

Supplemental Information

Clinical Summary and Rationale for the Designation of Non-Tolerant (n=5)

Patient #3, a multiparous female with 29% PRA by flow cytometry pre-operatively (0% by cytotoxicity), required immunosuppression resumption due to Banff 1A acute rejection documented by a biopsy at month 25. This was performed because a 24-month protocol biopsy at the time of complete withdrawal had shown “borderline acute rejection”. Stable renal function accompanied both biopsies (i.e. subclinical rejection). Patient #1 had a normal pre-withdrawal protocol biopsy but developed findings of Banff 1A acute rejection on the next biopsy done after 1 year off meds (Table 1), all without renal dysfunction, i.e. subclinical rejection, (Figure 2C and D). The third withdrawal failure (Patient #4) also had subclinical Banff 1A acute rejection in the 36-month protocol biopsy after 1 year off immunosuppression despite a normal 24-month biopsy. Of the 2 other non-tolerant subjects never withdrawn, one (Patient #7) developed electron-dense immune complex deposit glomerulonephritis and proteinuria (2 gm/day) 12 months post-transplantation and was considered to have recurrent disease, unsuspected preoperatively. Finally, Patient #10 developed proteinuria (4 gm/day) 18 months post-transplantation with the transplant biopsy showing focal segmental glomerulosclerosis, possibly the cause of his native ESRD (not biopsied pre-transplant). Both these patients had immunosuppression continued, consistent with clinical practice.

Non-Protocol Related Adverse Events (No adverse events were protocol related)

Adverse events included a skin rash that developed in 8 of the first 10 recipients after the second dose of AI, resolving within 72 hours. Two experienced transient cutaneous herpes zoster. Another (Patient #4, Table 1) developed diabetic vasculopathy consisting of a foot ulcer which progressed to requiring a right below knee amputation. Also, a left proximal radial artery thrombosis occurred requiring a distal bypass which salvaged the hand. Patient #1 (Table 1) developed an early post-operative lymphocele requiring operative drainage, and one year later

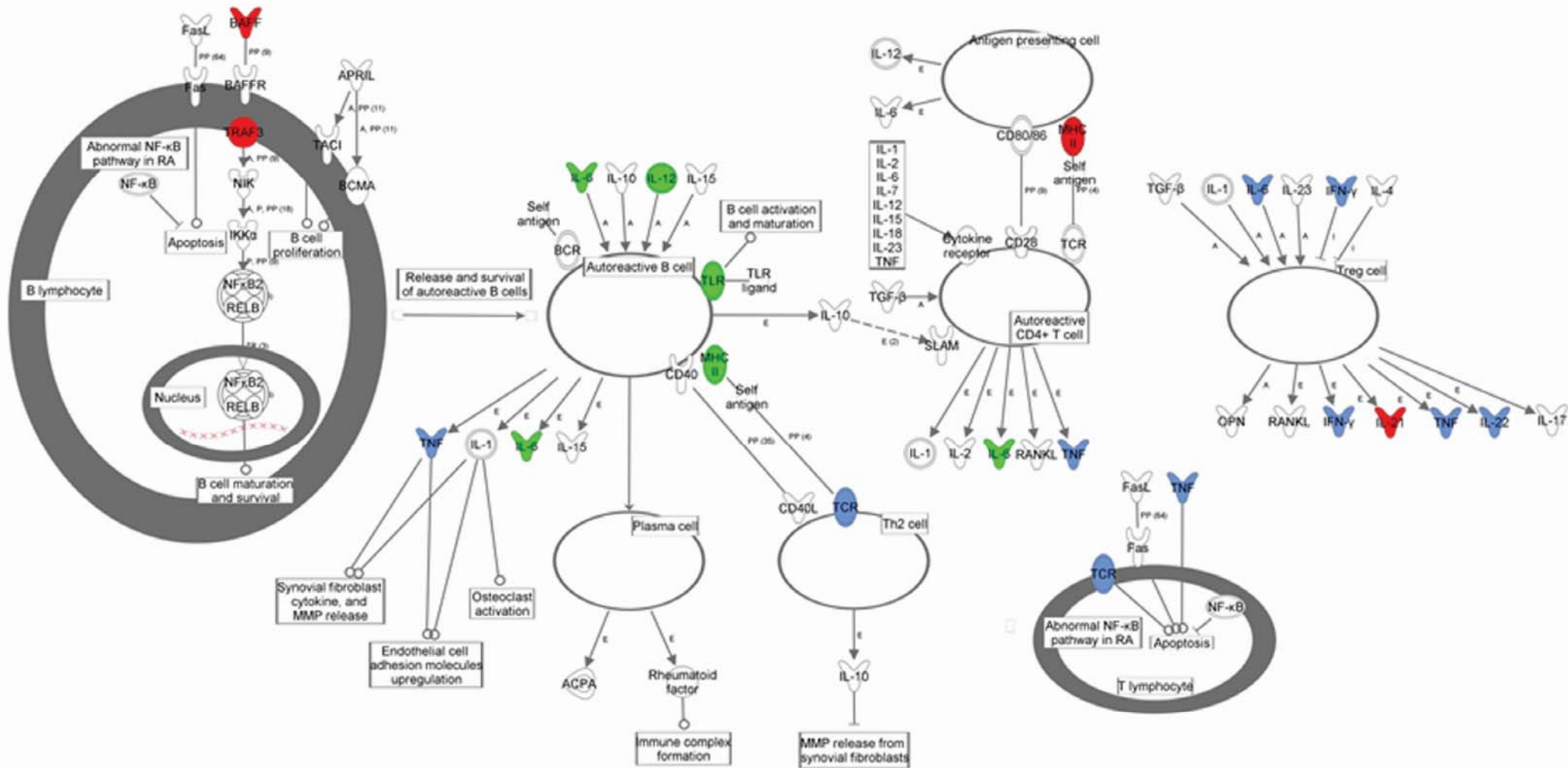
sustained a traumatic brachial vein thrombosis at work and a small pulmonary embolism requiring 6 months of warfarin therapy. This delayed IS withdrawal until month 30 rather than month 24 when a (normal) pre-withdrawal biopsy could be safely performed. No adverse events occurred in the donors.

Supplemental Figure Legends

Supplemental Figure 1. An example of the T and B Cell signaling pathway showing genes in the pathway that are unique and common to the 1 year and 2 Year tolerant vs. non-tolerant patients. Genes in red are unique to year 1, genes in blue are unique to year 2 and genes in green are shared at 1 and 2 years.

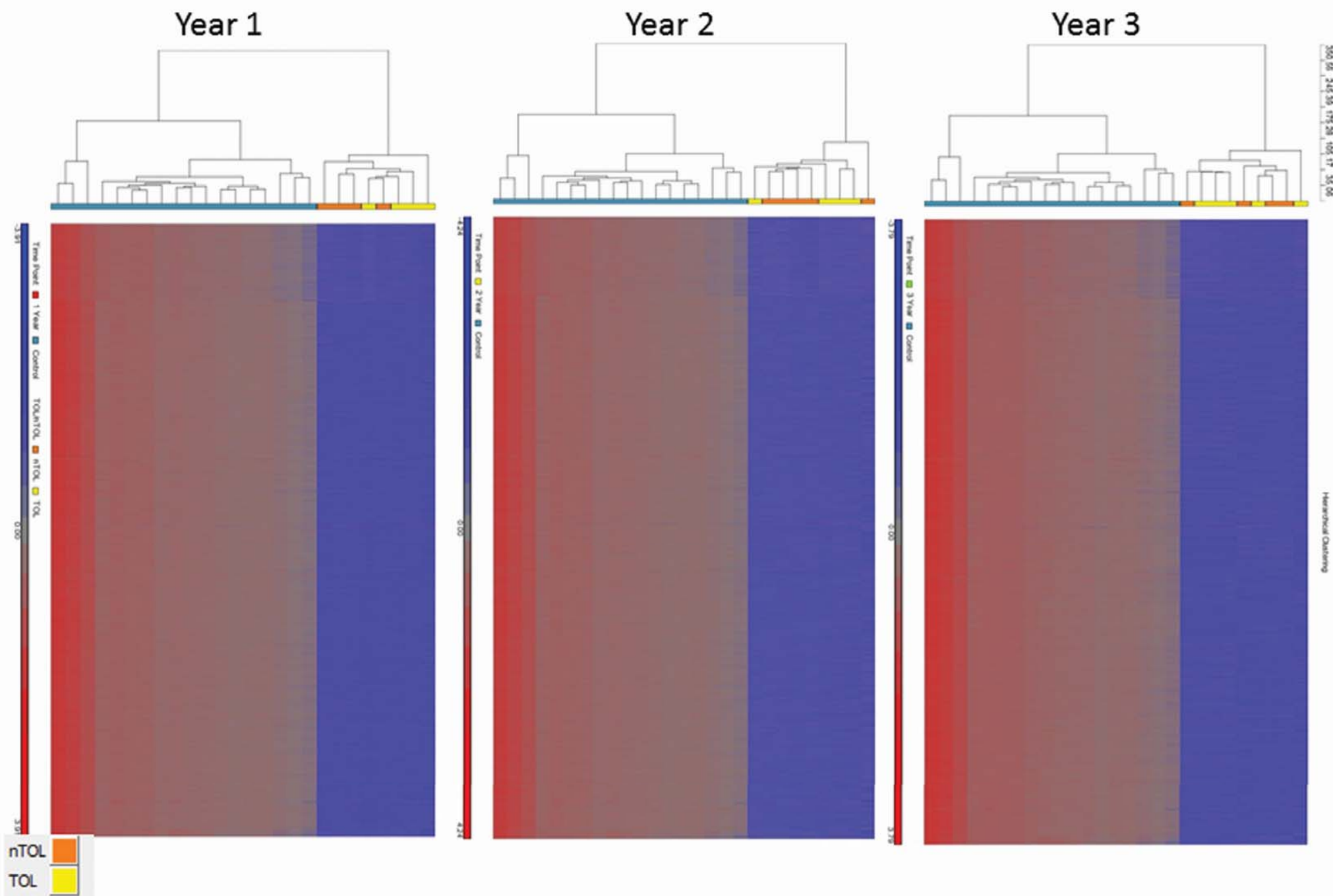
Supplemental Figure 2. **(A)** Unsupervised clustering of global gene expression (~33000 probesets) from the Controls, TOL and nTOL patients at Year 1, 2 and 3 shows that there are no major differences between the TOL and nTOL patients, but shows clear differences between the Control group and the TOL and nTOL patients suggesting that the TOL and nTOL patients show a clear suppression of gene expression at all time points. Red indicates upregulation and blue indicates downregulation. **(B)** Supervised clustering of the Controls, TOL and nTOL patients at Year 1, 2 and 3 based on the 783 gene core set shows a clear separation of the TOL and nTOL patients especially at the 3 Year time point where the gene expression reflects changes after immunosuppression withdrawal in the TOL group.

SUPPLEMENTAL FIGURE 1 - An example of the T and B Cell signaling pathway showing genes in the pathway that are unique and common to the 1 year and 2 Year tolerant vs. non-tolerant patients.



SUPPLEMENTAL FIGURE 2: UNSUPERVISED AND SUPERVISED GENOMIC CLUSTERING HEAT MAPS

A. Unsupervised Clustering of global gene expression from the Controls, TOL and nTOL patients at Year 1, 2 and 3



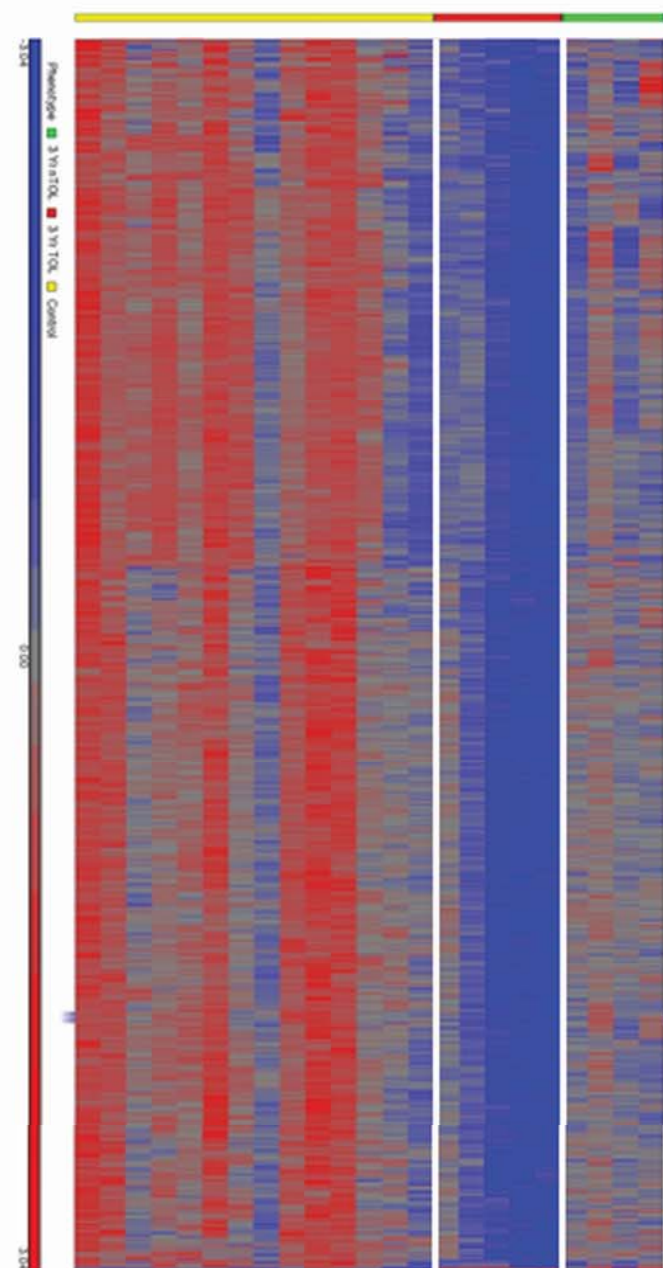
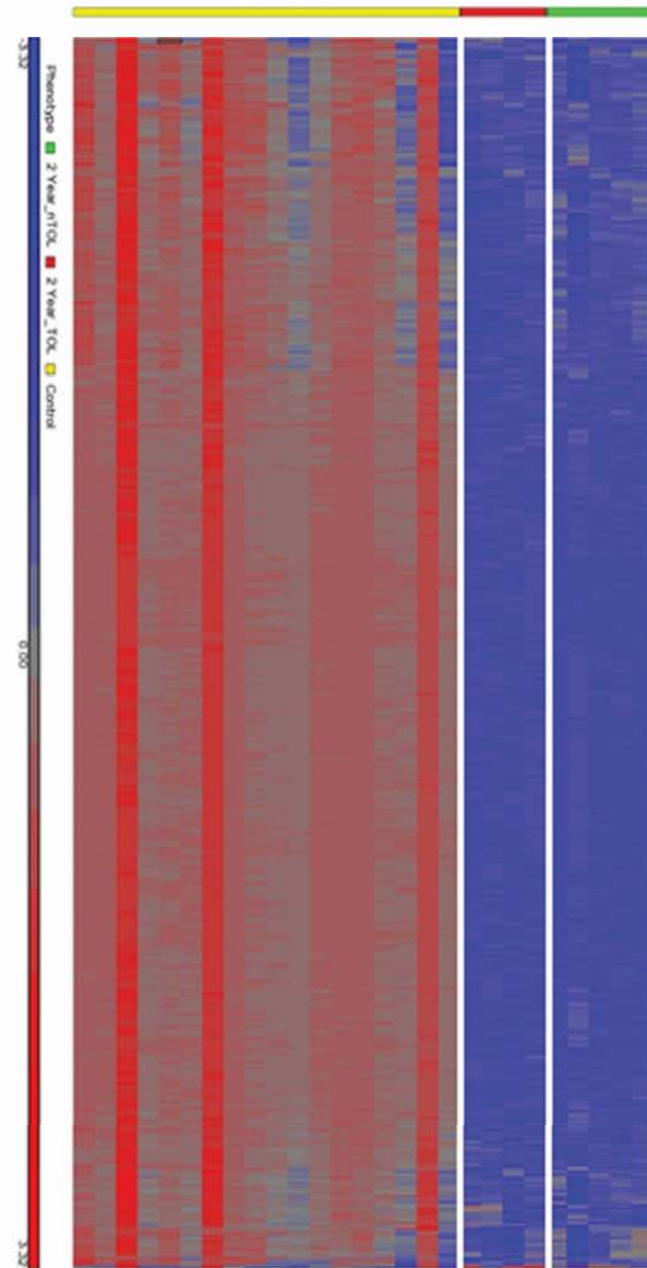
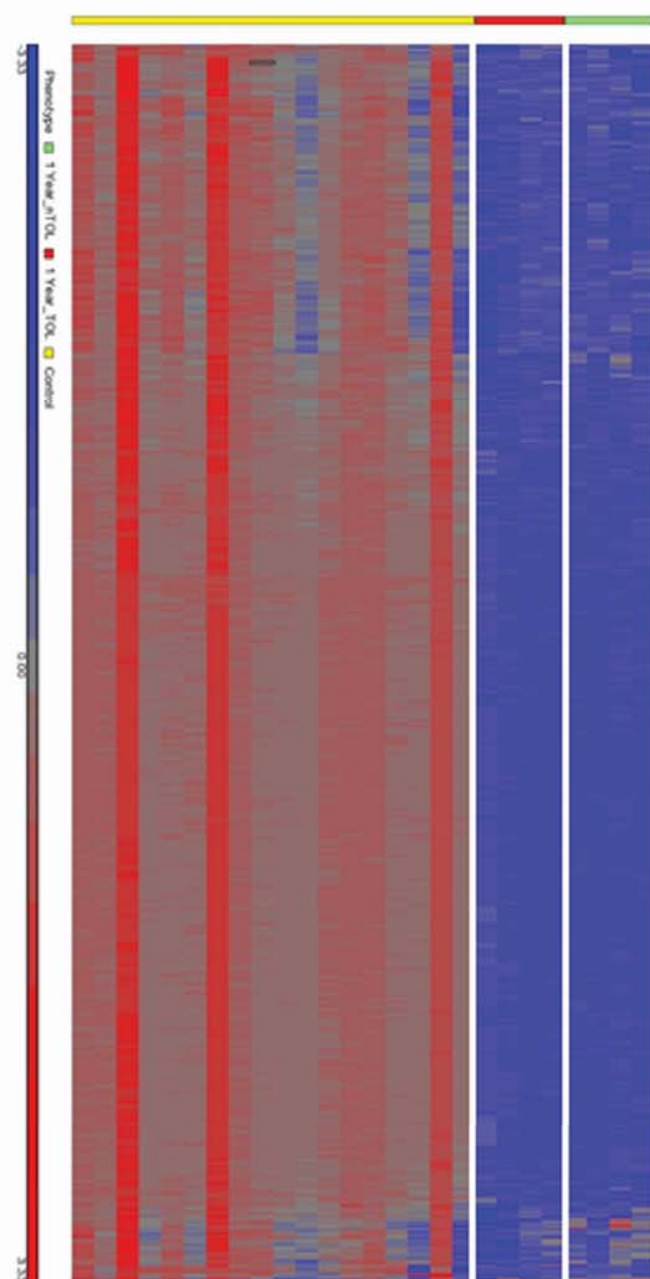
B. Supervised Clustering of the Controls, TOL and nTOL patients at Year 1, 2 and 3 based on the core set of 783 genes

3 Yr nTOL
3 Yr TOL
Control

1 Year

2 Year

3 Year



SUPPLEMENTAL TABLE 1: -- Sequential Detection of Effector vs Naïve B Cells

ie. CD19⁺ CD27⁺ IgD/M⁺ Cells vs CD19⁺ CD27⁻ IgD/M⁺ Cells ^a

	CD19 ⁺ CD27 ⁺ IgD/M ⁺ Cells												CD19 ⁺ CD27 ⁻ IgD/M ⁺ Cells											
	Normals + Pre-Tx	Post-Tx (months)											Normal + Pre-Tx	Post-Tx (months)										
		3	6	12	18	24	30	36	42	48	54	60		3	6	12	18	24	30	36	42	48	54	60
	9.1	2.3	4.5	1.1	0.6	1.0	3.1	3.5	3.0	1.7	0.0	3.6	69.7	97.1	94.5	92.1	93.8	95.5	95.7	88.1	93.4	95.9	94.0	94.4
	16.1	1.5	3.4	1.7	5.4	1.3	1.3	1.8	12.7	4.2	1.2	4.7	58.1	96.3	88.0	95.8	93.5	96.7	93.6	97.1	62.4	70.4	73.7	69.1
	8.0			2.1	0.4	1.5	1.9	0.7	1.2	2.6	2.7		79.9			89.5	93.9	91.2	95.9	93.4	94.0	90.3	89.5	
	7.6			2.8	0.5	0.6	1.9	0.8	1.8	2.9			70.6			85.7	96.4	96.0	90.7	94.0	90.6	90.2		
	10.6				2.8	1.3	0.9	1.0	1.2	2.6			63.3				87.4	96.0	97.6	89.5	97.8	90.5		
	4.1					3.3	0.5	1.8	0.5				81.8				94.7	92.1	90.4	96.3	95.7			
	6.2					4.1		1.8	2.5				78.0					88.4		86.7	92.8			
	14.5								1.9				66.7					91.8			89.6			
	10.9								2.9				66.5					95.1			94.0			
	8.8												80.1											
	9.6												70.7											
	10.6												78.3											
	23.0												63.4											
	16.7												58.7											
	6.6												80.4											
	5.8												78.7											
	9.5												67.3											
	6.1												62.8											
	25.1												61.9											
	28.4												58.1											
	3.0												61.1											
	3.9												60.5											
	8.1												67.3											
	6.7												82.0											
	12.6												73.5											
	5.2												79.7											
Ave.	10.6	1.9	4.0	1.9	1.9	1.9	1.6	1.6	3.1	2.8	1.3	4.2	70.0	96.7	91.3	90.8	93.3	93.6	94.0	92.2	90.0	87.5	85.7	81.8
SD	6.5	0.6	0.8	0.7	2.2	1.3	0.9	1.0	3.7	0.9	1.4	0.8	8.3	0.6	4.6	4.3	3.1	2.9	2.9	4.1	10.6	9.8	10.7	17.9

a. See Text and Figure 2D.

**SUPPLEMENTAL
TABLE 2:**

: Canonical pathways for the 1095 differentially expressed genes at Year 1 (TOL patients vs. nTOL patients)

Ingenuity Canonical Pathways	-log(p-value)	p-value	Ratio	Molecules
Altered T Cell and B Cell Signaling in Rheumatoid Arthritis	4.1E00	7.94328E-05	1.28E-01	TLR4,IFNG (includes EG:15978),HLA-DMA,TLR1,IL12A,CXCL13,HLA-DRA,HLA-DQA1,FCER1G,IL22,TNF
Allograft Rejection Signaling	3.88E00	0.000131826	1.36E-01	IFNG (includes EG:15978),HLA-DMA,HLA-DRA,HLA-DQA1,FCER1G,TNF,HLA-DPB1,HLA-DPA1
Glutathione-mediated Detoxification	3.07E00	0.000851138	2.17E-01	GSTM1,GSTM2,GSTM5,GSTA4,GSTO2
Type I Diabetes Mellitus Signaling	3.03E00	0.000933254	9.65E-02	IFNG (includes EG:15978),HLA-DMA,IL12A,MYD88,HLA-DRA,SOC56,HLA-DQA1,IFNGR2,FCER1G,BID,TNF
Cytotoxic T Lymphocyte-mediated Apoptosis of Target Cells	2.98E00	0.001047129	1.35E-01	HLA-DMA,HLA-DRA,HLA-DQA1,FCER1G,BID,HLA-DPB1,HLA-DPA1
Antigen Presentation Pathway	2.94E00	0.001148154	1.5E-01	IFNG (includes EG:15978),HLA-DMA,HLA-DRA,HLA-DQA1,HLA-DPB1,HLA-DPA1
T Helper Cell Differentiation	2.75E00	0.001778279	1.16E-01	IFNG (includes EG:15978),HLA-DMA,IL12A,HLA-DRA,HLA-DQA1,IFNGR2,FCER1G,TNF
OX40 Signaling Pathway	2.73E00	0.001862087	1.15E-01	HLA-DMA,CD4,HLA-DRA,HLA-DQA1,FCER1G,HLA-DPB1,HLA-DPA1
Xenobiotic Metabolism Signaling	2.53E00	0.002951209	6.77E-02	GSTM1,FTL,GSTM5,CHST7,NQO2,GSTA4,CHST15,PTGES3,HMOX1,CAMK2A,GSTM2,ALDH1A3,PPP2R2B,PIK3CB,GSTO2,ABCC3,TNF,AHR
D-glucuronate Degradation I	2.48E00	0.003311311	6.67E-01	AKR1A1,CRYL1
Graft-versus-Host Disease Signaling	2.48E00	0.003311311	1.3E-01	IFNG (includes EG:15978),HLA-DMA,HLA-DRA,HLA-DQA1,FCER1G,TNF
Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses	2.46E00	0.003467369	9.47E-02	TLR4,TLR1,IL12A,C3,MYD88,C1QA,PIK3CB,C3AR1,TNF
MSP-RON Signaling Pathway	2.43E00	0.003715352	1.28E-01	TLR4,IFNG (includes EG:15978),IL12A,IL3RA,PIK3CB,TNF
Acute Phase Response Signaling	2.37E00	0.004265795	7.56E-02	HMOX1,FTL,C3,MYD88,SOC56,SERPINF1,PIK3CB,SERPINA1,SERPINE1,TNF,A2M,HNF1A,C2
Methylglyoxal Degradation III	2.29E00	0.005128614	2.73E-01	AKR1A1,AKR1C1/AKR1C2,AKR1C4
Aryl Hydrocarbon Receptor Signaling	2.28E00	0.005248075	7.8E-02	GSTM1,SRC,GSTM2,GSTM5,ALDH1A3,NQO2,GSTA4,GSTO2,TNF,PTGES3,AHR
Communication between Innate and Adaptive Immune Cells	2.24E00	0.005754399	8.6E-02	TLR4,IFNG (includes EG:15978),TLR1,IL12A,CD4,HLA-DRA,FCER1G,TNF
Crosstalk between Dendritic Cells and Natural Killer Cells	2.11E00	0.007762471	8.89E-02	TLR4,IFNG (includes EG:15978),IL12A,CAMK2A,IL3RA,HLA-DRA,TNF,MICA
CTLA4 Signaling in Cytotoxic T Lymphocytes	2E00	0.01	8.42E-02	HLA-DMA,CD4,HLA-DRA,PPP2R2B,HLA-DQA1,FCER1G,PIK3CB,CTLA4
Ceramide Degradation	1.98E00	0.010471285	3.33E-01	NAAA,ASA2
Breast Cancer Regulation by Stathmin1	1.97E00	0.010715193	6.6E-02	GNB4,ARHGEF4,CAMK2A,ARHGEF12,ADCY1,PPP2R2B,RAC1,GNB5 (includes EG:10681),PPP1R14A,PIK3CB,TRPC5,TSG101,GN5
B Cell Development	1.92E00	0.012022644	1.38E-01	HLA-DMA,IGKC,HLA-DRA,HLA-DQA1
iNOS Signaling	1.89E00	0.012882496	1.09E-01	TLR4,IFNG (includes EG:15978),MYD88,IFNGR2,IRAK3
Phospholipase C Signaling	1.77E00	0.016982437	6.15E-02	SRC,ARHGEF4,ARHGEF12,GNB5 (includes EG:10681),RAC1,PPP1R14A,GN5,GNB4,HMOX1,PLA2G6,PLA2G4D,ADCY1,LYN,FCER1G,MARCKS
G Protein Signaling Mediated by Tubby	1.76E00	0.017378008	1.14E-01	GNB4,GNB5 (includes EG:10681),ABL1,GN5
iCOS-iCOSL Signaling in T Helper Cells	1.69E00	0.020417379	7.14E-02	HLA-DMA,CAMK2A,CD4,HLA-DRA,HLA-DQA1,RAC1,FCER1G,PIK3CB
Sphingosine and Sphingosine-1-phosphate Metabolism	1.67E00	0.021379621	2.5E-01	NAAA,ASA2
Complement System	1.67E00	0.021379621	1.21E-01	C3,C1QA,C3AR1,C2
Role of NFAT in Regulation of the Immune Response	1.66E00	0.021877616	5.98E-02	AKAP5,HLA-DMA,GNB4,CD4,HLA-DRA,HLA-DQA1,GNB5 (includes EG:10681),FCER1G,LYN,PIK3CB,GN5

Colorectal Cancer Metastasis Signaling	1.61E00	0.024547089	5.79E-02	TLR1, SRC, IFNG (includes EG:15978), GNB5 (includes EG:10681), RAC1, HNF1A, GNG5, TLR4, GNB4, ADCY1, FZD3, PIK3CB, TNF, TCF7L2
Cardiac β -adrenergic Signaling	1.6E00	0.025118864	6.57E-02	AKAP5, GNB4, PPP2R2B, ADCY1, GNB5 (includes EG:10681), PPP1R14A, PDE5A, GNG5, AKAP11
LPS/IL-1 Mediated Inhibition of RXR Function	1.6E00	0.025118864	5.86E-02	TLR4, GSTM1, GSTM2, GSTM5, ALDH1A3, MYD88, CHST7, GSTA4, PLTP, ABCC3, GSTO2, TNF, CHST15
Coagulation System	1.58E00	0.02630268	1.14E-01	F2R, SERPINA1, SERPINE1, A2M
Role of Cytokines in Mediating Communication between Immune Cells	1.52E00	0.030199517	9.62E-02	IFNG (includes EG:15978), IL12A, IL26, IL22, TNF
CD28 Signaling in T Helper Cells	1.47E00	0.033884416	6.56E-02	HLA-DMA, CD4, HLA-DRA, HLA-DQA1, RAC1, FCER1G, PIK3CB, CTLA4
Prostanoid Biosynthesis	1.46E00	0.034673685	2.22E-01	TBXAS1, PTGES3
PKC θ Signaling in T Lymphocytes	1.44E00	0.036307805	6.3E-02	HLA-DMA, CAMK2A, CD4, HLA-DRA, HLA-DQA1, RAC1, FCER1G, PIK3CB
NRF2-mediated Oxidative Stress Response	1.43E00	0.037153523	5.88E-02	HMOX1, GSTM1, AKR1A1, FTL, GSTM2, GSTM5, NQO2, GSTA4, PIK3CB, GSTO2, BACH1
TREM1 Signaling	1.43E00	0.037153523	8.77E-02	TLR4, TLR1, MYD88, TNF, ITGAX
HMGB1 Signaling	1.43E00	0.037153523	7.22E-02	TLR4, IFNG (includes EG:15978), RAC1, IFNGR2, PIK3CB, SERPINE1, TNF
Docosahexaenoic Acid (DHA) Signaling	1.42E00	0.03801894	9.76E-02	SERPINF1, BID, PIK3CB, BCL2A1
Hepatic Cholestasis	1.41E00	0.038904514	6.38E-02	TLR4, IFNG (includes EG:15978), TJP2, MYD88, ADCY1, IRAK3, ABCC3, TNF, HNF1A
Differential Regulation of Cytokine Production in Intestinal Epithelial Cells by IL-	1.39E00	0.040738028	1.3E-01	IFNG (includes EG:15978), IL12A, TNF
Eicosanoid Signaling	1.37E00	0.042657952	9.84E-02	PLA2G6, LTA4H, PLA2G4D, PTGIR, ALOX5, TBXAS1
Calcium-induced T Lymphocyte Apoptosis	1.35E00	0.044668359	8.2E-02	HLA-DMA, CD4, HLA-DRA, HLA-DQA1, FCER1G
VDR/RXR Activation	1.33E00	0.046773514	7.59E-02	IFNG (includes EG:15978), IGFBP6, IL12A, CAMP (includes EG:12796), IGFBP5, VDR
Autoimmune Thyroid Disease Signaling	1.32E00	0.047863009	7.55E-02	HLA-DMA, HLA-DRA, HLA-DQA1, FCER1G

Pathway p-values < 0.05 were considered significant

Pathway Ratio: The number of molecules in a given pathway that meet cutoff criteria, divided by total number of molecules that make up that pathway.

**SUPPLEMENTAL
TABLE 3:**

Canonical pathways for the 857 differentially expressed genes at Year 2 (TOL patients vs. nTOL patients)

Ingenuity Canonical Pathways	-log(p-value)	p-value	Ratio	Molecules
Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis	2.68E00	0.0020893	7.07E-02	TRAF3,PIK3CA,FN1 (includes EG:100005469),NFKBIE,TLR8,FZD9,IL6,CREB3L4,WNT10A,F2RL1,TLR5,TRAF4,PLCB3,PRKCE,DKK4,FIGF,DKK1,PLCD4,TNFSF13B,WNT11,RYK (includes EG:140585),ADAMTS4
UDP-N-acetyl-D-galactosamine Biosynthesis II	2.54E00	0.002884	3.33E-01	HK1,GNPDA1,UAP1
Reelin Signaling in Neurons	2.48E00	0.0033113	1.1E-01	BLK,ARHGEF5,MAP3K9,PIK3CA,MAPK8,LRP8,MAPK8IP3,CDK5R1,ITGB3
Endoplasmic Reticulum Stress Pathway	2.34E00	0.0045709	2.22E-01	CASP12,CASP9,MAPK8,EIF2AK3
Molecular Mechanisms of Cancer	2.23E00	0.0058884	6.39E-02	RAPGEF1,PIK3CA,NFKBIE,ARHGEF7,CTNNA1,MAPK8,PSENEN,FZD9,PSEN2,CRK,RHOH,SIN3A,CHEK1,PTK2,ARHGEF5,PRKAR2B,CASP9,BMPR1A,PRKCE,PLCB3,BMP6,BCL2L11,BIRC2
Small Cell Lung Cancer Signaling	2.2E00	0.0063096	9.52E-02	PTK2,TRAF3,PIK3CA,CASP9,NFKBIE,TRAF4,SIN3A,BIRC2
NGF Signaling	2.07E00	0.0085114	9.01E-02	MAP3K9,TRIO,PIK3CA,SMPD4,TRAF4,MAPK8,CRK,CREB3L4,SMPD2,MAP3K2
Leukocyte Extravasation Signaling	2.05E00	0.0089125	7.45E-02	PTK2,NOX1,VAV2,CLDN10,PIK3CA,SPN,EZR,ACTA2,CTNNA1,MAPK8,PRKCE,CRK,MM P12,RHOH
Sphingosine-1-phosphate Signaling	2.04E00	0.0091201	8.7E-02	PTK2,CASP12,PIK3CA,CASP9,SMPD4,PLCB3,CASP4,SMPD2,RHOH,PLCD4
Role of PI3K/AKT Signaling in the Pathogenesis of Influenza	2.02E00	0.0095499	1.04E-01	PIK3CA,CCR5,CASP9,IFNA8,NFKBIE,IFNA21,CRK
Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis	1.98E00	0.0104713	7.08E-02	ADAM17,PIK3CA,NFKBIE,MAPK8,FZD9,IL6,ITGB3,CASP9,WNT10A,BMPR1A,DKK4,DK K1,BMP6,WNT11,ADAMTS4,BIRC2
Altered T Cell and B Cell Signaling in Rheumatoid Arthritis	1.86E00	0.0138038	9.3E-02	IL21,TRAF3,IL12A,TLR5,TLR8,HLA-DQB1,IL6,TNFSF13B
CD27 Signaling in Lymphocytes	1.85E00	0.0141254	1.09E-01	MAP3K9,CASP9,CD70,NFKBIE,MAPK8,MAP3K2
T Helper Cell Differentiation	1.81E00	0.0154882	1.01E-01	IL21,IL4R,IL12A,IL21R,CXCR5,HLA-DQB1,IL6
Lymphotoxin β Receptor Signaling	1.74E00	0.018197	1.07E-01	NFKBID,TRAF3,PIK3CA,CASP9,TRAF4,BIRC2
Apoptosis Signaling	1.72E00	0.0190546	8.7E-02	CASP12,CASP9,NFKBIE,MAPK8,PRKCE,LMNA,BCL2L11,BIRC2
Role of Hypercytokinemia/hyperchemokineemia in the Pathogenesis of Influenza	1.68E00	0.020893	1.22E-01	CCR5,IL12A,IFNA8,IFNA21,IL6
Parkinson's Signaling	1.64E00	0.0229087	1.88E-01	SEPT5,CASP9,MAPK8
ILK Signaling	1.61E00	0.0245471	7.03E-02	PTK2,PARVB,PIK3CA,FN1 (includes EG:100005469),KRT18,PPP2R5D,PPP2R5B,ACTA2,MAPK8,FIGF,CREB3L4,RHOH,ITGB3
Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses	1.59E00	0.025704	8.42E-02	PIK3CA,IL12A,TLR5,TLR8,MAPK8,PRKCE,IFNA21,IL6
Xenobiotic Metabolism Signaling	1.58E00	0.0263027	6.39E-02	GSTM1,MAP3K9,PIK3CA,FMO6P,GSTM5,PPP2R5D,PPP2R5B,MAPK8,UGT8,IL6,CUL3 (includes EG:26554),PRKCE,CYP2B6,CHST13,EIF2AK3,ALDH5A1,MAP3K2
Axonal Guidance Signaling	1.56E00	0.0275423	5.58E-02	TUBB1,ADAM17,PIK3CA,ARHGEF7,GNB5 (includes EG:10681),FZD9,CRK,EIF4E,EFNA1,PTK2,ADAM30,SRGAP3,PRKAR2B,ADAM12,WNT1 0A,TUBB8,ADAM19,PRKCE,PLCB3,FIGF,BMP6,PLCD4,WNT11,SEMA7A
Sphingomyelin Metabolism	1.55E00	0.0281838	2.86E-01	SMPD4,SMPD2
Activation of IRF by Cytosolic Pattern Recognition Receptors	1.53E00	0.0295121	9.52E-02	TRAF3,IFNA8,NFKBIE,MAPK8,IFNA21,IL6
Huntington's Disease Signaling	1.5E00	0.0316228	6.19E-02	PIK3CA,HSPA9,CLTC,MAPK8,GNB5 (includes EG:10681),CASP4,CREB3L4,SIN3A,CDK5R1,HSPA1L,CASP12,CASP9,PLCB3,PRKCE
IL-17A Signaling in Airway Cells	1.44E00	0.0363078	8.7E-02	PIK3CA,NFKBIE,MAPK8,CCL20,IL6,CXCL6
Paxillin Signaling	1.42E00	0.0380189	7.27E-02	PTK2,PIK3CA,ITGA2B,ARHGEF7,ACTA2,MAPK8,CRK,ITGB3
TWEAK Signaling	1.41E00	0.0389045	1.08E-01	TRAF3,CASP9,NFKBIE,BIRC2
Amyloid Processing	1.41E00	0.0389045	9.62E-02	PRKAR2B,PRKCE,PSEN2,PSENEN,CDK5R1
Phosphatidylethanolamine Biosynthesis III	1.41E00	0.0389045	1E00	PTDSS2

P2Y Purigenic Receptor Signaling Pathway	1.4E00	0.0398107	7.2E-02	PIK3CA,ITGA2B,PRKAR2B,GNB5 (includes EG:10681),PRKCE,PLCB3,CREB3L4,PLCD4,ITGB3
HGF Signaling	1.4E00	0.0398107	7.84E-02	PTK2,RAPGEF1,MAP3K9,PIK3CA,MAPK8,PRKCE,IL6,MAP3K2
Angiopoietin Signaling	1.39E00	0.040738	8.45E-02	PTK2,PIK3CA,CASP9,NFKBIE,ANGPT4,CRK
p70S6K Signaling	1.38E00	0.0416869	7.38E-02	PIK3CA,IL4R,F2RL1,PPP2R5D,PPP2R5B,PRKCE,PLCB3,PLCD4,AGT
Cell Cycle Regulation by BTG Family Proteins	1.33E00	0.0467735	1.11E-01	PPP2R5D,PPP2R5B,BTG1,HOXB9

Pathway p-values < 0.05 were considered significant

Pathway Ratio: The number of molecules in a given pathway that meet cutoff criteria, divided by total number of molecules that make up that pathway.

**SUPPLEMENTAL
TABLE 4:**

Canonical pathways for the 783 core set genes at Year 3 (TOL patients vs. Healthy Controls)

Ingenuity Canonical Pathways	-log(p-value)	p-value	Ratio	Molecules
T Helper Cell Differentiation	2.96E00	0.001096478	1.16E-01	STAT4,IL21,ICOS,CD80,HLA-DOB,CXCR5,HLA-DQB1,ICOSLG
B Cell Development	2.88E00	0.001318257	1.72E-01	CD80,IGKC,HLA-DOB,HLA-DQB1,CD79A
Systemic Lupus Erythematosus Signaling	2.6E00	0.002511886	6.14E-02	LSM14B,IGKC,PRPF39,TXNL4A,IL37,PRPF38B,CD79A,SNRPN,KNG1,CD80,SNRNP25,CD72,IFNA2,LSM3
Triacylglycerol Degradation	2.36E00	0.004365158	1.6E-01	NDST3,NDST4,PNLIPRP3,PNLIP
Cell Cycle: G1/S Checkpoint Regulation	2E00	0.01	9.38E-02	NRG1,RPL11,MYC,RPL5,E2F5,GNL3
Altered T Cell and B Cell Signaling in Rheumatoid Arthritis	1.88E00	0.013182567	8.14E-02	IL21,CD80,HLA-DOB,HLA-DQB1,IL37,CSF2,CD79A
Growth Hormone Signaling	1.71E00	0.019498446	8.45E-02	RPS6KB1,RPS6KA6,GHR,IGF1,PRKD3,PRKD1
Role of Cytokines in Mediating Communication between Immune Cells	1.64E00	0.022908677	9.62E-02	IL21,IFNB1,IFNA2,IL37,CSF2
EIF2 Signaling	1.59E00	0.025703958	5.49E-02	RPL11,RPL4,RPL27A,RPS3A,RPL5,RPL7A,RPL32,EIF2B3,RPL9,EIF2A
Glutamate Removal from Folates	1.51E00	0.030902954	1E00	GGH
Estrogen-mediated S-phase Entry	1.42E00	0.03801894	1.11E-01	MYC,E2F5,ESR2
Role of Hypercytokinemia in the Pathogenesis of Influenza	1.42E00	0.03801894	9.76E-02	IFNB1,IFNA2,IL37,CCL3
Dermatan Sulfate Biosynthesis (Late Stages)	1.42E00	0.03801894	9.76E-02	NDST3,SULT1C4,SULT1C2,NDST4
Communication between Innate and Adaptive Immune Cells	1.39E00	0.040738028	6.45E-02	CD80,HLA-DRB3,IFNB1,IL37,CCL3,CSF2
Chondroitin Sulfate Biosynthesis (Late Stages)	1.35E00	0.044668359	9.09E-02	NDST3,SULT1C4,SULT1C2,NDST4
Graft-versus-Host Disease Signaling	1.32E00	0.047863009	8.7E-02	CD80,HLA-DOB,HLA-DQB1,IL37

Pathway p-values < 0.05 were considered significant

Pathway Ratio: The number of molecules in a given pathway that meet cutoff criteria, divided by total number of molecules that make up that pathway.

SUPPLEMENTAL TABLE 5: Annotated Gene list for the 783 core set genes at Year 3 (TOL patients vs. Healthy Controls)

#	Transcript ID	unigene	gene_assignment	Gene Symbol	RefSeq	GO_biological process	GO_cellular component	GO_molecular function
1	8083409	NM_207365 // Hs.144710 // heart intestine placenta skin uterus normal fetus adul	NM_207365 // AADACL2 // // arylacetamide deacetylase-like 2 // 3q25.1 // 344752 /// ENST00	AADACL2	NM_207365	NM_207365 // GO:0008152 // metabolic process // inferred from electronic annotation //	NM_207365 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_207365 // GO:0004091 // carboxylesterase activity // inferred from electronic annota
2	8103706	NM_016228 // Hs.529735 // ascites bone brain cervix connective tissue ear embryon	NM_016228 // AADAT // aminoadipate aminotransferase // 4q33 // 51166 /// NM_182662 // A	AADAT	NM_016228	NM_016228 // GO:0006103 // 2-oxoglutarate metabolic process // inferred from direct ass	NM_016228 // GO:0005739 // mitochondrion // inferred from electronic annotation /// NM	NM_016228 // GO:0016212 // kynurenine-oxoglutarate transaminase activity // inferred fr
3	8140752	NM_000443 // Hs.654403 // adrenal gland blood brain embryonic tissue heart intesti	NM_000443 // ABCB4 // ATP-binding cassette, sub-family B (MDR/TAP), member 4 // 7q21.1	ABCB4	NM_000443	NM_000443 // GO:0006629 // lipid metabolic process // traceable author statement /// N	NM_000443 // GO:0000139 // Golgi membrane // inferred from sequence or structural simil	NM_000443 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
4	8123137	NM_005891 // Hs.571037 // adrenal gland ascites bladder blood bone bone marrow br	NM_005891 // ACAT2 // acetyl-CoA acetyltransferase 2 // 6q25.3 // 39 /// ENST0000036704	ACAT2	NM_005891	NM_005891 // GO:0006629 // lipid metabolic process // inferred by curator /// ENST00000	NM_005891 // GO:0005737 // cytoplasm // inferred from direct assay /// ENST0000036704 8	NM_005891 // GO:0003985 // acetyl-CoA C-acetyltransferase activity // inferred from dir
5	8117219	NM_018473 // Hs.9676 // // adrenal gland ascites bladder blood bone bone marrow brai	NM_018473 // ACOT13 // acyl-CoA thioesterase 13 // 6p22.3 // 55856 /// NM_001160094 //	ACOT13	NM_018473	NM_018473 // GO:0051289 // protein homotetramerization // inferred from physical intera	NM_018473 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_018	NM_018473 // GO:0016291 // acyl-CoA thioesterase activity // inferred from direct assay
6	7952503	NM_001612 // Hs.169222 // blood brain placenta testis germ cell tumor normal fetu	NM_001612 // ACRV1 // acrosomal vesicle protein 1 // 11q23-q24 // 56 /// NM_020069 // A	ACRV1	NM_001612	NM_001612 // GO:0007275 // multicellular organismal development // traceable author sta	NM_001612 // GO:0001669 // acrosomal vesicle // inferred from electronic annotation //	---
7	7975406	NM_003813 // Hs.178748 // bone intestine testis chondrosarcoma normal adult /// EN	NM_003813 // ADAM21 // // ADAM metalloproteinase domain 21 // 14q24.1 // 8747 /// ENST000000	ADAM21	NM_003813	NM_003813 // GO:0006508 // proteolysis // inferred from electronic annotation /// NM_0	NM_003813 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0038	NM_003813 // GO:0004222 // metalloendopeptidase activity // inferred from electronic an

8	8146051	NR_001448 // Hs.369765 // brain connective tissue testis germ cell tumor normal so	NR_001448 // ADAM5P // ADAM metallopeptidase domain 5, pseudogene // 8p11.22 // 255926	ADAM5P	NR_001448	NR_001448 // GO:0006508 // proteolysis // inferred from electronic annotation BC02	---	NR_001448 // GO:0004222 // metalloendopeptidase activity // inferred from electronic an
9	8145334	NM_003817 // Hs.116147 // kidney muscle testis normal fetus adult /// ENST00000175	NM_003817 // ADAM7 // ADAM metallopeptidase domain 7 // 8p21.2 // 8756 /// ENST00000175	ADAM7	NM_003817	NM_003817 // GO:0006508 // proteolysis // inferred from electronic annotation ENST	NM_003817 // GO:0016020 // membrane // inferred from electronic annotation NM_0038	NM_003817 // GO:0004222 // metalloendopeptidase activity // inferred from electronic an
10	8145317	NM_014479 // Hs.521459 // blood connective tissue intestine kidney lung lymph node	NM_014479 // ADAMDEC1 // ADAM-like, decysin 1 // 8p21.2 // 27299 /// NM_001145271 // AD	ADAMDEC1	NM_014479	NM_014479 // GO:0006508 // proteolysis // inferred from electronic annotation NM_0	NM_014479 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_014479 // GO:0004222 // metalloendopeptidase activity // non-traceable author statem
11	8054254	NM_002285 // Hs.444414 // blood bone bone marrow brain cervix connective tissue e	NM_002285 // AFF3 // AF4/FMR2 family, member 3 // 2q11.2-q12 // 3899 /// NM_001025108 /	AFF3	NM_002285	NM_002285 // GO:0007275 // multicellular organismal development // traceable author sta	NM_002285 // GO:0005634 // nucleus // inferred from electronic annotation NM_00102	NM_002285 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
12	8095663	NM_001133 // Hs.168718 // heart kidney liver mammary gland liver tumor normal fet	NM_001133 // AFM // afamin // 4q13.3 // 173 /// ENST00000226355 // AFM // afamin // 4q1	AFM	NM_001133	NM_001133 // GO:0006810 // transport // inferred from electronic annotation ENST00	NM_001133 // GO:0005576 // extracellular region // inferred from electronic annotation	---
13	8136370	NM_178563 // Hs.648616 // ascites brain eye intestine kidney liver lung pancreas	NM_178563 // AGBL3 // ATP/GTP binding protein-like 3 // 7q33 // 340351 /// ENST000000436	AGBL3	NM_178563	NM_178563 // GO:0006508 // proteolysis // inferred from electronic annotation ENST	NM_178563 // GO:0005737 // cytoplasm // inferred from electronic annotation ENST00	NM_178563 // GO:0004181 // metallocarboxypeptidase activity // inferred from electronic
14	8136614	NM_018238 // Hs.724527 // adrenal gland bladder blood bone marrow brain cervix co	NM_018238 // AGK // acylglycerol kinase // 7q34 // 55750 /// ENST00000355413 // AGK //	AGK	NM_018238	NM_018238 // GO:0007205 // activation of protein kinase C activity by G-protein coupled	NM_018238 // GO:0005739 // mitochondrion // inferred from electronic annotation NM	NM_018238 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
15	8138381	NM_006408 // Hs.530009 // ascites bladder bone marrow cervix eye heart intestine	NM_006408 // AGR2 // anterior gradient homolog 2 (Xenopus laevis) // 7p21.3 // 10551 //	AGR2	NM_006408	NM_006408 // GO:0070254 // mucus secretion // inferred from sequence or structural simi	NM_006408 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_006408 // GO:0005515 // protein binding // inferred from physical interaction /// E
16	8169492	NM_000686 // Hs.405348 // brain heart kidney lung testis uterus germ cell tumor	NM_000686 // AGTR2 // angiotensin II receptor, type 2 // Xq22-q23 // 186 /// ENST000003	AGTR2	NM_000686	NM_000686 // GO:0001974 // blood vessel remodeling // traceable author	NM_000686 // GO:0005886 // plasma membrane // not recorded /// NM_000686 //	NM_000686 // GO:0004872 // receptor activity // inferred from electronic annotation //

						statement /// N	GO:0005887	
17	8102249	NM_031279 // Hs.106576 // brain embryonic tissue eye kidney liver nerve testis g	NM_031279 // AGXT2L1 // alanine-glyoxylate aminotransferase 2-like 1 // 4q25 // 64850 /	AGXT2L1	NM_031279	NM_031279 // GO:0006520 // cellular amino acid metabolic process // non-traceable autho	NM_031279 // GO:0005575 // cellular_component // no biological data available /// NM_0	NM_031279 // GO:0008453 // alanine-glyoxylate transaminase activity // non-traceable au
18	7924491	NM_022831 // Hs.156625 // adipose tissue adrenal gland ascites blood bone brain c	NM_022831 // AIDA // axin interactor, dorsalization associated // 1q41 // 64853 /// ENS	AIDA	NM_022831	NM_022831 // GO:0007275 // multicellular organismal development // inferred from electr	NM_022831 // GO:0005575 // cellular_component // no biological data available /// ENST	NM_022831 // GO:0005515 // protein binding // inferred from electronic annotation ///
19	7976578	NM_152327 // Hs.667462 // bone brain embryonic tissue intestine kidney lung mamma	NM_152327 // AK7 // adenylate kinase 7 // 14q32.2 // 122481 /// ENST00000267584 // AK7	AK7	NM_152327	NM_152327 // GO:0006139 // nucleobase, nucleoside, nucleotide and nucleic acid metabolism	---	NM_152327 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
20	7906988	ENST00000354775 // Hs.2533 // adipose tissue adrenal gland ascites bladder blood b	ENST00000354775 // ALDH9A1 // aldehyde dehydrogenase 9 family, member A1 // 1q23.1 // 2	ALDH9A1	ENST00000354775	ENST00000354775 // GO:0001822 // kidney development // inferred from electronic annotat	ENST00000354775 // GO:0005634 // nucleus // inferred from direct assay /// ENST0000035	ENST00000354775 // GO:0004029 // aldehyde dehydrogenase (NAD) activity // inferred from
21	8166006	NM_182680 // Hs.654436 // connective tissue soft tissue muscle tissue tumor adult ///	NM_182680 // AMELX // amelogenin, X-linked // Xp22.31-p22.1 // 265 /// NM_001142 // AME	AMELX	NM_182680	NM_182680 // GO:0001649 // osteoblast differentiation // inferred from sequence or stru	NM_182680 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_182680 // GO:0005515 // protein binding // inferred from physical interaction /// N
22	8095508	NM_212557 // Hs.453069 // brain normal adult /// ENST00000339336 // Hs.453069 // brai	NM_212557 // AMTN // amelotin // 4q13.3 // 401138 /// ENST00000339336 // AMTN // amelot	AMTN	NM_212557	NM_212557 // GO:0007155 // cell adhesion // inferred from electronic annotation /// NM	NM_212557 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_212557 // GO:0003674 // molecular_function // no biological data available /// ENST
23	7903407	NM_020978 // Hs.484588 // brain connective tissue eye heart intestine kidney lary	NM_020978 // AMY2B // amylase, alpha 2B (pancreatic) // 1p21 // 280 /// NM_017619 // RN	AMY2B	NM_020978	NM_020978 // GO:0005975 // carbohydrate metabolic process // inferred from electronic a	NM_020978 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_020978 // GO:0004556 // alpha-amylase activity // inferred from electronic annotatio
24	7973084	NM_001145 // Hs.283749 // adipose tissue ascites bladder blood bone brain cervix	NM_001145 // ANG // angiogenin, ribonuclease, RNase A family, 5 // 14q11.1-q11.2 // 283	ANG	NM_001145	NM_001145 // GO:0001525 // angiogenesis // inferred from direct assay /// NM_001145 //	NM_001145 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_001145 // GO:0003677 // DNA binding // inferred by curator /// NM_001145 // GO:0003

25	8008609	NM_153228 // Hs.673040 // adrenal gland brain mammary gland placenta stomach testi	NM_153228 // ANKFN1 // ankyrin-repeat and fibronectin type III domain containing 1 // 1	ANKFN1	NM_153228	---	---	---
26	8053737	---	NR_003366 // ANKRD20B // ankyrin repeat domain 20B // 2q11.1 // 729171 /// ENST00000456	ANKRD20B	NR_003366	---	---	---
27	8001113	NR_026556 // Hs.97414 // ascites testis gastrointestinal tumor normal adult /// ENS	NR_026556 // ANKRD26P1 // ankyrin repeat domain 26 pseudogene 1 // 16q11.2 // 124149 //	ANKRD26P1	NR_026556	---	---	---
28	7943231	NM_017704 // Hs.29052 // adrenal gland ascites bladder blood bone brain connectiv	NM_017704 // ANKRD49 // ankyrin repeat domain 49 // 11q21 // 54851 /// ENST00000302755	ANKRD49	NM_017704	NM_017704 // GO:0045893 // positive regulation of transcription, DNA-dependent // infer	NM_017704 // GO:0005634 // nucleus // inferred by curator /// ENST00000302755 // GO:00	NM_017704 // GO:0016563 // transcription activator activity // inferred from direct ass
29	7955117	NM_012404 // Hs.532658 // --- /// ENST00000266594 // Hs.532658 // --- /// BC069122 // H	NM_012404 // ANP32D // acidic (leucine-rich) nuclear phosphoprotein 32 family, member D	ANP32D	NM_012404	---	---	---
30	7927294	NR_003601 // Hs.538515 // brain muscle testis thymus normal adult	NR_003601 // ANTXML // anthrax toxin receptor-like // 10q11.22 // 195977	ANTXML	NR_003601	---	NR_003601 // GO:0016020 // membrane // inferred from electronic annotation /// NR_0036	NR_003601 // GO:0004872 // receptor activity // inferred from electronic annotation //
31	8047300	NM_001159 // Hs.406238 // adipose tissue adrenal gland bladder bone brain connecti	NM_001159 // AOX1 // aldehyde oxidase 1 // 2q33 // 316 /// ENST00000374700 // AOX1 // a	AOX1	NM_001159	NM_001159 // GO:0006800 // oxygen and reactive oxygen species metabolic process // trac	NM_001159 // GO:0005737 // cytoplasm // inferred from electronic annotation /// ENST00	NM_001159 // GO:0004031 // aldehyde oxidase activity // inferred from electronic annota
32	7973813	NM_007077 // Hs.293411 // bone brain connective tissue embryonic tissue intestine	NM_007077 // AP4S1 // adaptor-related protein complex 4, sigma 1 subunit // 14q12 // 11	AP4S1	NM_007077	---	NM_007077 // GO:0005794 // Golgi apparatus // inferred from electronic annotation ///	NM_007077 // GO:0005215 // transporter activity // traceable author statement /// NM_0
33	8072721	NM_030642 // Hs.326561 // mammary gland placenta testis normal adult /// ENST000002	NM_030642 // APOL5 // apolipoprotein L, 5 // 22q12.3 // 80831 /// ENST00000249044 // AP	APOL5	NM_030642	NM_030642 // GO:0006629 // lipid metabolic process // non-traceable author statement /	NM_030642 // GO:0005575 // cellular componen t // no biological data available /// NM_0	NM_030642 // GO:0005515 // protein binding // inferred from physical interaction /// N
34	8160602	NR_036579 // Hs.20158 // ascites bladder blood bone bone marrow brain cervix con	NR_036579 // APTX // aprataxin // 9p13.3 // 54840 /// NM_001195249 // APTX // aprataxin	APTX	NR_036579	NR_036579 // GO:0000012 // single strand break repair // inferred from direct assay //	NR_036579 // GO:0000785 // chromatin // inferred from direct assay /// NR_036579 // GO	NR_036579 // GO:0003682 // chromatin binding // inferred from direct assay /// NR_0365

35	8081989	NM_001012659 // Hs.224976 // germ cell tumor /// ENST00000334384 // Hs.224976 // germ c	NM_001012659 // ARGFX // arginine-fifty homeobox // 3q13.33 // 503582 /// ENST000003343	ARGFX	NM_001012659	NM_001012659 // GO:0006355 // regulation of transcription, DNA-dependent // inferred fr	NM_001012659 // GO:0005634 // nucleus // inferred from electronic annotation /// ENST0	NM_001012659 // GO:0003700 // sequence-specific DNA binding transcription factor activi
36	8096160	NM_001025616 // Hs.444229 // adipose tissue ascites bladder blood brain connective	NM_001025616 // ARHGAP24 // Rho GTPase activating protein 24 // 4q22.1 // 83478 /// NM_	ARHGAP24	NM_001025616	NM_001025616 // GO:0001525 // angiogenesis // inferred from electronic annotation ///	NM_001025616 // GO:0005622 // intracellular // inferred from electronic annotation ///	NM_001025616 // GO:0005096 // GTPase activator activity // inferred from electronic ann
37	7917850	NM_004815 // Hs.483238 // adipose tissue bladder bone brain connective tissue embr	NM_004815 // ARHGAP29 // Rho GTPase activating protein 29 // 1p22.1 // 9411 /// ENST000	ARHGAP29	NM_004815	NM_004815 // GO:0007165 // signal transduction // inferred from electronic annotation	NM_004815 // GO:0005622 // intracellular // inferred from electronic annotation /// EN	NM_004815 // GO:0005096 // GTPase activator activity // inferred from electronic annota
38	7974621	NM_002892 // Hs.161000 // bladder blood bone bone marrow brain connective tissue	NM_002892 // ARID4A // AT rich interactive domain 4A (RBP1-like) // 14q23.1 // 5926 ///	ARID4A	NM_002892	NM_002892 // GO:0006333 // chromatin assembly or disassembly // inferred from electronic annotation	NM_002892 // GO:0000785 // chromatin // inferred from electronic annotation /// NM_002	NM_002892 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
39	7927732	NM_032199 // Hs.535297 // bladder blood bone marrow brain cervix connective tissue	NM_032199 // ARID5B // AT rich interactive domain 5B (MRF1-like) // 10q21.2 // 84159 //	ARID5B	NM_032199	NM_032199 // GO:0001822 // kidney development // inferred from electronic annotation /	NM_032199 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_032199 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
40	8168855	NR_028407 // Hs.9728 // adrenal gland blood bone bone marrow brain connective tiss	NR_028407 // ARMCMX4 // armadillo repeat containing, X-linked 4 // Xq22.1 // 100131755 /	ARMCMX4	NR_028407	---	NR_028407 // GO:0016020 // membrane // inferred from electronic annotation /// NR_0284	---
41	8048120	NM_004044 // Hs.90280 // adipose tissue adrenal gland ascites bladder blood bone	NM_004044 // ATIC // 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IM	ATIC	NM_004044	NM_004044 // GO:0006139 // nucleobase, nucleoside, nucleotide and nucleic acid metabol	NM_004044 // GO:0005739 // mitochondrion // inferred from electronic annotation /// EN	NM_004044 // GO:0003937 // IMP cyclohydrolase activity // inferred from electronic anno
42	8142100	NM_020725 // Hs.489603 // adrenal gland bladder bone bone marrow brain cervix con	NM_020725 // ATXN7L1 // ataxin 7-like 1 // 7q22.3 // 222255 /// NM_138495 // ATXN7L1 //	ATXN7L1	NM_020725	---	---	---
43	8046078	NM_020981 // Hs.657258 // connective tissue germ cell tumor normal soft tissue muscl	NM_020981 // B3GALT1 // UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide	B3GALT1	NM_020981	NM_020981 // GO:0006486 // protein glycosylation // inferred from direct assay /// NM_	NM_020981 // GO:0000139 // Golgi membrane // inferred from electronic annotation /// N	NM_020981 // GO:0008378 // galactosyltransferase activity // inferred from electronic a

44	8128247	NM_021813 // Hs.269764 // blood brain embryonic tissue eye heart intestine larynx	NM_021813 // BACH2 // BTB and CNC homology 1, basic leucine zipper transcription factor	BACH2	NM_021813	NM_021813 // GO:0006355 // regulation of transcription, DNA-dependent // inferred from	NM_021813 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00117	NM_021813 // GO:0003700 // sequence-specific DNA binding transcription factor activity
45	8096617	NM_017935 // Hs.480400 // blood bone marrow brain connective tissue intestine lung	NM_017935 // BANK1 // B-cell scaffold protein with ankyrin repeats 1 // 4q24 // 55024 /	BANK1	NM_017935	NM_017935 // GO:0042113 // B cell activation // inferred from electronic annotation //	---	---
46	8061859	NR_026760 // Hs.434194 // muscle normal adult /// AY180924 // Hs.434194 // muscle no	NR_026760 // BASE // breast cancer and salivary gland expression gene // 20q11.21 // 31	BASE	NR_026760	---	---	---
47	8164649	NM_013318 // Hs.724374 // adipose tissue adrenal gland ascites bladder blood bone	NM_013318 // BAT2L1 // HLA-B associated transcript 2-like 1 // 9q34.13 // 84726 /// ENS	BAT2L1	NM_013318	---	---	NM_013318 // GO:0005515 // protein binding // inferred from physical interaction /// E
48	7964852	NM_032735 // Hs.280782 // bone marrow brain cervix connective tissue embryonic tiss	NM_032735 // BEST3 // bestrophin 3 // 12q14.2-q15 // 144453 /// NM_152439 // BEST3 // b	BEST3	NM_032735	NM_032735 // GO:0008150 // biological_process // no biological data available /// NM_0	NM_032735 // GO:0005886 // plasma membrane // inferred from electronic annotation ///	NM_032735 // GO:0003674 // molecular_function // no biological data available /// NM_0
49	7979241	NM_001202 // Hs.68879 // adipose tissue bone brain connective tissue embryonic tiss	NM_001202 // BMP4 // bone morphogenetic protein 4 // 14q22-q23 // 652 /// NM_130851 //	BMP4	NM_001202	NM_001202 // GO:0000186 // activation of MAPKK activity // inferred from direct assay	NM_001202 // GO:0005576 // extracellular region // inferred from sequence or structural	NM_001202 // GO:0005125 // cytokine activity // inferred from direct assay /// NM_0012
50	8058075	NM_033030 // Hs.169797 // bladder brain connective tissue testis bladder carcinoma	NM_033030 // BOLL // bol, boule-like (Drosophila) // 2q33 // 66037 /// NM_197970 // BOL	BOLL	NM_033030	NM_033030 // GO:0006417 // regulation of translation // inferred from electronic annota	NM_033030 // GO:0005737 // cytoplasm // inferred from direct assay /// NM_197970 // GO	NM_033030 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
51	8075600	NM_174932 // Hs.372939 // brain esophagus pancreas skin esophageal tumor glioma n	NM_174932 // BPIL2 // bactericidal/permeability-increasing protein-like 2 // 22q12.3 //	BPIL2	NM_174932	---	NM_174932 // GO:0005576 // extracellular region // non-traceable author statement ///	NM_174932 // GO:0001530 // lipopolysaccharide binding // non-traceable author statement
52	7929201	NM_003972 // Hs.500526 // adrenal gland ascites bladder blood bone bone marrow br	NM_003972 // BTAF1 // BTAF1 RNA polymerase II, B-TFIID transcription factor-associated,	BTAF1	NM_003972	NM_003972 // GO:0016481 // negative regulation of transcription // non-traceable author	NM_003972 // GO:0005634 // nucleus // non-traceable author statement /// ENST000002659	NM_003972 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
53	8089519	NM_181780 // Hs.445162 // blood brain kidney lymph node pharynx thymus trachea g	NM_181780 // BTLA // B and T lymphocyte associated // 3q13.2 // 151888 /// NM_001085357	BTLA	NM_181780	NM_181780 // GO:0002768 // immune response-regulating cell surface receptor signaling p	NM_181780 // GO:0005886 // plasma membrane // not recorded /// NM_181780 // GO:0005887	NM_181780 // GO:0004872 // receptor activity // inferred from electronic annotation //

54	8128553	NM_147147 // Hs.221660 // blood bone marrow brain connective tissue ear embryonic	NM_147147 // BVES // blood vessel epicardial substance // 6q21 // 11149 /// NM_007073 /	BVES	NM_147147	NM_147147 // GO:0001921 // positive regulation of receptor recycling // inferred from s	NM_147147 // GO:0005886 // plasma membrane // inferred from sequence or structural simi	NM_147147 // GO:0005198 // structural molecule activity // inferred from direct assay
55	8131583	NM_001159767 // Hs.487635 // adipose tissue adrenal gland ascites bladder blood bo	NM_001159767 // BZW2 // basic leucine zipper and W2 domains 2 // 7p21.1 // 28969 /// NM	BZW2	NM_001159767	NM_001159767 // GO:0007275 // multicellular organismal development // inferred from ele	---	NM_001159767 // GO:0005515 // protein binding // inferred from physical interaction //
56	7934505	NM_001001791 // Hs.585453 // brain heart kidney lung placenta testis lung tumor	NM_001001791 // C10orf55 // chromosome 10 open reading frame 55 // 10q22.2 // 414236 //	C10orf55	NM_001001791	NM_001145031 // GO:0001525 // angiogenesis // inferred from electronic annotation ///	NM_001145031 // GO:0005576 // extracellular region // inferred from electronic annotati	NM_001145031 // GO:0004252 // serine-type endopeptidase activity // inferred from elect
57	7936201	NM_025145 // Hs.288927 // bone brain connective tissue embryonic tissue intestine	NM_025145 // C10orf79 // chromosome 10 open reading frame 79 // 10q25.1 // 80217 /// EN	C10orf79	NM_025145	---	---	---
58	7939087	BC047775 // Hs.502208 // adrenal gland blood bone bone marrow brain cervix connec	BC047775 // C11orf46 // chromosome 11 open reading frame 46 // 11p14.1 // 120534 /// NM	C11orf46	BC047775	---	---	---
59	7950128	NM_014042 // Hs.38044 // blood bone bone marrow brain cervix connective tissue em	NM_014042 // C11orf51 // chromosome 11 open reading frame 51 // 11q13.4 // 25906 /// NM	C11orf51	NM_014042	NM_001145308 // GO:0007605 // sensory perception of sound // inferred from sequence or	NM_014042 // GO:0005622 // intracellular // inferred from direct assay /// NM_00114530	NM_001145308 // GO:0016206 // catechol O-methyltransferase activity // inferred from se
60	7943842	NM_018195 // Hs.195060 // adipose tissue adrenal gland bladder blood bone bone mar	NM_018195 // C11orf57 // chromosome 11 open reading frame 57 // 11q23.1 // 55216 /// NM	C11orf57	NM_018195	NR_028383 // GO:0006626 // protein targeting to mitochondrion // traceable author state	NR_028383 // GO:0005739 // mitochondrion // inferred from electronic annotation /// NR	NR_028383 // GO:0005515 // protein binding // inferred from physical interaction /// N
61	7942783	BC002752 // Hs.503357 // adrenal gland ascites bone brain connective tissue embryo	BC002752 // C11orf67 // chromosome 11 open reading frame 67 // 11q14.1 // 28971 /// BC0	C11orf67	BC002752	BC015664 // GO:0016180 // snRNA processing // inferred from direct assay /// ENST000000	BC015664 // GO:0005634 // nucleus // inferred from electronic annotation /// BC015664	BC015664 // GO:0005515 // protein binding // inferred from physical interaction /// EN
62	7958666	NM_013300 // Hs.436618 // adrenal gland ascites blood bone bone marrow brain cerv	NM_013300 // C12orf24 // chromosome 12 open reading frame 24 // 12q24.11 // 29902 /// N	C12orf24	NM_013300	---	NM_001164372 // GO:0043234 // protein complex // inferred from direct assay	NM_001164372 // GO:0000166 // nucleotide binding // inferred from electronic annotation
63	7954794	NM_001031748 // Hs.648205 // muscle testis normal fetus adult /// ENST00000324616 /	NM_001031748 // C12orf40 // chromosome 12 open reading frame 40 // 12q12 // 283461 ///	C12orf40	NM_001031748	---	---	---

64	7965900	NM_001099336 // Hs.534649 // brain lymph node testis thymus germ cell tumor leukem	NM_001099336 // C12orf42 // chromosome 12 open reading frame 42 // 12q23.2 // 374470 //	C12orf42	NM_001099336	---	---	---
65	7957688	ENST00000342887 // Hs.436197 // lung testis trachea normal /// AK126100 // Hs.436197	ENST00000342887 // C12orf63 // chromosome 12 open reading frame 63 // 12q23.1 // 374467	C12orf63	ENST00000342887	---	---	---
66	7968866	NM_182508 // Hs.16970 // brain lung pharynx trachea uterus normal fetus adult //	NM_182508 // C13orf30 // chromosome 13 open reading frame 30 // 13q14.11 // 144809 ///	C13orf30	NM_182508	---	---	---
67	7972665	BC132748 // Hs.508623 // brain connective tissue heart lung placenta non-neoplasia	BC132748 // C13orf39 // chromosome 13 open reading frame 39 // 13q33.1 // 196541 /// NM	C13orf39	BC132748	---	---	---
68	7972670	NM_001146197 // Hs.368382 // brain liver testis normal /// ENST00000322527 // Hs.368	NM_001146197 // C13orf40 // chromosome 13 open reading frame 40 // 13q33.1 // 643677 //	C13orf40	NM_001146197	---	---	---
69	7987526	NM_001080791 // Hs.654661 // ascites blood bone bone marrow brain cervix connecti	NM_001080791 // C15orf57 // chromosome 15 open reading frame 57 // 15q15.1 // 90416 ///	C15orf57	NM_001080791	---	---	---
70	8003566	NM_001214 // Hs.633032 // normal fetus /// ENST00000408886 // Hs.633032 // normal fet	NM_001214 // C16orf3 // chromosome 16 open reading frame 3 // 16q24.3 // 750 /// ENST00	C16orf3	NM_001214	NM_001214 // GO:0008150 // biological_process // no biological data available /// ENST	NM_001214 // GO:0005575 // cellular_component // no biological data available /// ENST	NM_001214 // GO:0003674 // molecular_function // no biological data available /// ENST
71	8007530	AK125817 // Hs.252707 // testis germ cell tumor normal fetus /// ENST00000449302 //	AK125817 // C17orf105 // chromosome 17 open reading frame 105 // 17q21.31 // 284067 ///	C17orf105	AK125817	---	---	---
72	8004802	NM_017622 // Hs.129563 // adipose tissue adrenal gland bladder blood bone brain c	NM_017622 // C17orf59 // chromosome 17 open reading frame 59 // 17p13.1 // 54785 /// EN	C17orf59	NM_017622	---	---	---
73	8012207	BC030270 // Hs.534591 // ascites bladder blood bone marrow brain connective tissue	BC030270 // C17orf61 // chromosome 17 open reading frame 61 // 17p13.1 // 254863 /// AK	C17orf61	BC030270	AK290117 // GO:0017121 // phospholipid scrambling // non-traceable author statement //	BC030270 // GO:0005743 // mitochondrial inner membrane // inferred from electronic anno	AK290117 // GO:0005509 // calcium ion binding // non-traceable author statement /// AK
74	8008914	NM_181707 // Hs.129312 // brain connective tissue liver lung pancreas testis germ	NM_181707 // C17orf64 // chromosome 17 open reading frame 64 // 17q23.2 // 124773 /// B	C17orf64	NM_181707	---	---	---

75	8009662	NM_152460 // Hs.350775 // kidney ovary testis germ cell tumor normal ovarian tumor	NM_152460 // C17orf77 // chromosome 17 open reading frame 77 // 17q25.1 // 146723 /// E	C17orf77	NM_152460	---	NM_152460 // GO:0005576 // extracellular region // inferred from electronic annotation	---
76	8021152	AB027121 // Hs.334493 // ---	AB027121 // C18orf12 // chromosome 18 open reading frame 12 // 18q21.1 // 84322	C18orf12	AB027121	---	---	---
77	7907396	NM_139240 // Hs.517991 // brain connective tissue embryonic tissue eye heart liver	NM_139240 // C1orf105 // chromosome 1 open reading frame 105 // 1q24.3 // 92346 /// ENS	C1orf105	NM_139240	---	---	---
78	7922152	BC026073 // Hs.567557 // bone brain connective tissue embryonic tissue eye lung p	BC026073 // C1orf114 // chromosome 1 open reading frame 114 // 1q24 // 57821 /// NM_021	C1orf114	BC026073	---	---	---
79	7913852	NM_024037 // Hs.149305 // adipose tissue adrenal gland bladder blood bone brain c	NM_024037 // C1orf135 // chromosome 1 open reading frame 135 // 1p36.11 // 79000 /// EN	C1orf135	NM_024037	---	---	---
80	7924180	NM_001024601 // Hs.153274 // brain testis normal fetus adult /// ENST00000332912 //	NM_001024601 // C1orf227 // chromosome 1 open reading frame 227 // 1q32.3 // 149643 ///	C1orf227	NM_001024601	---	---	---
81	7910630	BC116455 // Hs.23198 // adrenal gland ascites bone marrow brain cervix connective	BC116455 // C1orf31 // chromosome 1 open reading frame 31 // 1q42.2 // 388753 /// BC064	C1orf31	BC116455	---	BC116455 // GO:0005739 // mitochondrion // inferred from electronic annotation /// BC0	BC116455 // GO:0004129 // cytochrome-c oxidase activity // inferred from electronic ann
82	7968052	NM_178540 // Hs.362854 // bone pharynx testis chondrosarcoma normal adult /// ENST	NM_178540 // C1QTNF9 // C1q and tumor necrosis factor related protein 9 // 13q12.12 //	C1QTNF9	NM_178540	ENST0000038214 1 // GO:0035023 // regulation of Rho protein signal transduction // infer	NM_178540 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_178540 // GO:0005179 // hormone activity // inferred from electronic annotation ///
83	8061224	NM_178483 // Hs.112794 // testis germ cell tumor normal fetus /// ENST00000377428 //	NM_178483 // C20orf79 // chromosome 20 open reading frame 79 // 20p11.23 // 140856 ///	C20orf79	NM_178483	NM_178483 // GO:0008152 // metabolic process // inferred from electronic annotation //	---	NM_178483 // GO:0016491 // oxidoreductase activity // inferred from electronic annotati
84	8067932	NR_027790 // Hs.473394 // bone bone marrow brain connective tissue ear embryonic t	NR_027790 // C21orf34 // chromosome 21 open reading frame 34 // 21q21.1 // 388815 /// N	C21orf34	NR_027790	---	---	---

85	8058108	NR_004862 // Hs.204619 // adrenal gland blood bone brain cervix ear embryonic tis	NR_004862 // C2orf60 // chromosome 2 open reading frame 60 // 2q33.1 // 129450 /// NM_0	C2orf60	NR_004862	---	---	---
86	8081903	NM_033364 // Hs.341906 // brain embryonic tissue eye kidney lung mouth muscle ne	NM_033364 // C3orf15 // chromosome 3 open reading frame 15 // 3q12-q13.3 // 89876 /// E	C3orf15	NM_033364	---	NM_033364 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_033	NM_033364 // GO:0005515 // protein binding // inferred from physical interaction /// E
87	8078605	NM_178339 // Hs.475945 // eye mammary gland muscle testis thymus trachea uterus	NM_178339 // C3orf35 // chromosome 3 open reading frame 35 // 3p22.2 // 339883 /// NM_1	C3orf35	NM_178339	---	NM_178339 // GO:0016020 // membrane // inferred from electronic annotation /// NM_1783	---
88	8081073	NM_173824 // Hs.518099 // adipose tissue ascites blood brain connective tissue emb	NM_173824 // C3orf38 // chromosome 3 open reading frame 38 // 3p11.1 // 285237 /// NM_0	C3orf38	NM_173824	NM_173824 // GO:0006915 // apoptosis // inferred from electronic annotation /// NM_001	NM_001195308 // GO:0005634 // nucleus // inferred from direct assay	NM_001195308 // GO:0003677 // DNA binding // inferred from electronic annotation /// N
89	8093137	NM_001077657 // Hs.631933 // connective tissue heart muscle normal soft tissue/musc	NM_001077657 // C3orf43 // chromosome 3 open reading frame 43 // 3q29 // 255798 /// ENS	C3orf43	NM_001077657	---	NM_001077657 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0	---
90	8083463	ENST00000446603 // Hs.58586 // connective tissue heart normal soft tissue/muscle tis	ENST00000446603 // C3orf79 // chromosome 3 open reading frame 79 // 3q25.2 // 152118 //	C3orf79	ENST00000446603	---	---	---
91	8096568	NM_032149 // Hs.97501 // connective tissue testis normal soft tissue/muscle tissue t	NM_032149 // C4orf17 // chromosome 4 open reading frame 17 // 4q23 // 84103 /// ENST000	C4orf17	NM_032149	---	---	---
92	8102389	NM_018392 // Hs.380346 // bladder blood bone marrow brain connective tissue ear e	NM_018392 // C4orf21 // chromosome 4 open reading frame 21 // 4q25 // 55345 /// ENST000	C4orf21	NM_018392	---	NM_018392 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0183	NM_018392 // GO:0008270 // zinc ion binding // inferred from electronic annotation ///
93	8095767	BC117342 // Hs.24510 // bladder brain kidney placenta normal primitive neuroectode	BC117342 // C4orf26 // chromosome 4 open reading frame 26 // 4q21.1 // 152816 /// ENST0	C4orf26	BC117342	---	BC117342 // GO:0005576 // extracellular region // inferred from electronic annotation	---

94	8103684	NM_017867 // Hs.406756 // adrenal gland blood bone bone marrow brain cervix conne	NM_017867 // C4orf27 // chromosome 4 open reading frame 27 // 4q33 // 54969 /// ENST000	C4orf27	NM_017867	---	NM_017867 // GO:0005634 // nucleus // inferred from direct assay /// ENST0000039338 1 /	---
95	8095451	NM_214711 // Hs.518795 // eye mammary gland muscle testis breast (mammary gland) tu	NM_214711 // C4orf40 // chromosome 4 open reading frame 40 // 4q13.3 // 401137 /// ENST	C4orf40	NM_214711	---	NM_214711 // GO:0005576 // extracellular region // inferred from electronic annotation	---
96	8095467	NM_152997 // Hs.320147 // connective tissue heart intestine liver lung lymph node	NM_152997 // C4orf7 // chromosome 4 open reading frame 7 // 4q13 4q13 // 260436 /// ENS	C4orf7	NM_152997	---	NM_152997 // GO:0005576 // extracellular region // inferred from electronic annotation	---
97	8104758	BC022250 // Hs.13528 // bone bone marrow brain cervix connective tissue embryonic	BC022250 // C5orf23 // chromosome 5 open reading frame 23 // 5p13.3 // 79614 /// ENST00	C5orf23	BC022250	---	BC022250 // GO:0043234 // protein complex // inferred from direct assay /// ENST000003	---
98	8111960	NM_198566 // Hs.661641 // bone brain connective tissue embryonic tissue eye intest	NM_198566 // C5orf34 // chromosome 5 open reading frame 34 // 5p12 // 375444 /// BC0368	C5orf34	NM_198566	---	---	---
99	8105456	NM_153706 // Hs.85950 // adrenal gland bladder brain embryonic tissue esophagus he	NM_153706 // C5orf35 // chromosome 5 open reading frame 35 // 5q11.2 // 133383 /// NM_0	C5orf35	NM_153706	---	---	---
100	8111584	BC144069 // Hs.586199 // blood bone bone marrow brain cervix connective tissue em	BC144069 // C5orf42 // chromosome 5 open reading frame 42 // 5p13.2 // 65250 /// NM_023	C5orf42	BC144069	---	BC144069 // GO:0016020 // membrane // inferred from electronic annotation /// BC144069	---
101	8105647	NM_001093755 // Hs.591760 // adrenal gland ascites bladder blood bone brain conne	NM_001093755 // C5orf44 // chromosome 5 open reading frame 44 // 5q12.3 // 80006 /// NM	C5orf44	NM_001093755	---	---	---
102	8114970	NM_206966 // Hs.660038 // brain embryonic tissue heart liver mammary gland muscle	NM_206966 // C5orf46 // chromosome 5 open reading frame 46 // 5q32 // 389336 /// ENST00	C5orf46	NM_206966	---	NM_206966 // GO:0005576 // extracellular region // inferred from electronic annotation	---
103	8107702	BC130495 // Hs.177983 // brain testis germ cell tumor normal fetus /// ENST00000357	BC130495 // C5orf48 // chromosome 5 open reading frame 48 // 5q23.2 // 389320 /// ENST0	C5orf48	BC130495	---	---	---

10 4	8115600	NM_022090 // Hs.529464 // brain connective tissue esophagus heart intestine liver	NM_022090 // C5orf54 // chromosome 5 open reading frame 54 // 5q33.3 // 63920 /// ENST0	C5orf54	NM_022090	---	NM_022090 // GO:0005739 // mitochondrion // inferred from electronic annotation /// EN	---
10 5	8126259	AJ420538 // Hs.227457 // adrenal gland ascites bladder blood bone bone marrow bra	AJ420538 // C6orf130 // chromosome 6 open reading frame 130 // 6p21.1 // 221443 /// AK2	C6orf130	AJ420538	---	---	---
10 6	8120300	NM_138569 // Hs.449276 // --- /// NM_138569 // Hs.591803 // brain connective tissue h	NM_138569 // C6orf142 // chromosome 6 open reading frame 142 // 6p12.1 // 90523 /// ENS	C6orf142	NM_138569	---	---	---
10 7	8129476	NM_001010876 // Hs.448372 // brain eye normal /// ENST00000368143 // Hs.448372 // bra	NM_001010876 // C6orf191 // chromosome 6 open reading frame 191 // 6q22.33 // 253582 //	C6orf191	NM_001010876	---	NM_001010876 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0	---
10 8	8123884	NR_026737 // Hs.61389 // bladder bone marrow connective tissue heart kidney lung	NR_026737 // C6orf52 // chromosome 6 open reading frame 52 // 6p24.1 // 347744 /// NR_0	C6orf52	NR_026737	---	---	---
10 9	8136181	NM_145268 // Hs.351816 // eye testis normal fetus /// ENST00000297819 // Hs.351816 /	NM_145268 // C7orf45 // chromosome 7 open reading frame 45 // 7q32.2 // 136263 /// ENST	C7orf45	NM_145268	---	NM_145268 // GO:0016020 // membrane // inferred from electronic annotation /// NM_1452	---
11 0	8136535	NM_197964 // Hs.718441 // ascites blood bone brain connective tissue embryonic tis	NM_197964 // C7orf55 // chromosome 7 open reading frame 55 // 7q34 // 154791 /// ENST00	C7orf55	NM_197964	---	NM_197964 // GO:0005739 // mitochondrion // inferred from electronic annotation /// EN	AK297642 // GO:0005515 // protein binding // inferred from physical interaction /// AK
11 1	8151898	NM_177965 // Hs.548157 // bone brain embryonic tissue eye intestine lung parathyr	NM_177965 // C8orf37 // chromosome 8 open reading frame 37 // 8q22.1 // 157657 /// BC03	C8orf37	NM_177965	---	---	---
11 2	8146225	NM_001135674 // Hs.655320 // adrenal gland bone bone marrow brain cervix connectiv	NM_001135674 // C8orf40 // chromosome 8 open reading frame 40 // 8p11.21 // 114926 ///	C8orf40	NM_001135674	---	NM_001135674 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0	---
11 3	8144721	NM_001007090 // Hs.I04941 // bladder bone brain embryonic tissue eye heart kidney	NM_001007090 // C8orf48 // chromosome 8 open reading frame 48 // 8p22 // 157773 /// ENS	C8orf48	NM_001007090	---	---	NM_001007090 // GO:0005515 // protein binding // inferred from physical interaction //

11 4	8152734	BC137357 // Hs.683919 // testis normal /// AK093040 // Hs.683919 // testis normal	BC137357 // C8orf54 // chromosome 8 open reading frame 54 // 8q24.13 // 439941 /// AK09	C8orf54	BC137357	---	---	---
11 5	8149318	ENST00000443854 // Hs.404138 // ---	ENST00000443854 // C8orf8 // chromosome 8 open reading frame 8 // 8p23-p22 // 83647	C8orf8	ENST00000443854	---	---	---
11 6	8160036	NM_033428 // Hs.7517 // adipose tissue ascites bladder blood bone bone marrow bra	NM_033428 // C9orf123 // chromosome 9 open reading frame 123 // 9p24.1 // 90871 /// ENS	C9orf123	NM_033428	---	NM_033428 // GO:0016020 // membrane // inferred from electronic annotation NM_0334 ///	---
11 7	8154973	NM_203299 // Hs.148250 // blood larynx pharynx testis germ cell tumor head and nec	NM_203299 // C9orf131 // chromosome 9 open reading frame 131 // 9p13.3 // 138724 /// NM	C9orf131	NM_203299	---	---	---
11 8	8160900	NR_024481 // Hs.721061 // testis normal fetus	NR_024481 // C9orf144 // transmembrane protein C9orf144B pseudogene // 9p13.2 // 389715	C9orf144	NR_024481	---	---	---
11 9	8159838	NM_152569 // Hs.190877 // brain kidney prostate testis leukemia normal fetus adu	NM_152569 // C9orf66 // chromosome 9 open reading frame 66 // 9p24.3 // 157983 /// ENST	C9orf66	NM_152569	---	---	---
12 0	8159919	NM_001039395 // Hs.179615 // bladder brain connective tissue embryonic tissue intes	NM_001039395 // C9orf68 // chromosome 9 open reading frame 68 // 9p24.2 // 55064 /// EN	C9orf68	NM_001039395	---	---	---
12 1	8154416	AY422473 // Hs.17267 // bone brain cervix connective tissue heart liver lung lym	AY422473 // C9orf93 // chromosome 9 open reading frame 93 // 9p22.3 // 203238 /// BC144	C9orf93	AY422473	---	---	---
12 2	7905131	NM_012113 // Hs.528988 // brain ear embryonic tissue eye heart lung lymph ovary	NM_012113 // CA14 // carbonic anhydrase XIV // 1q21 // 23632 /// ENST00000369111 // CA1	CA14	NM_012113	---	NM_012113 // GO:0016020 // membrane // inferred from electronic annotation NM_0121 ///	NM_012113 // GO:0004089 // carbonate dehydratase activity // inferred from electronic a
12 3	8142585	NM_017954 // Hs.649459 // adipose tissue bladder bone brain connective tissue embr	NM_017954 // CADPS2 // Ca++-dependent secretion activator 2 // 7q31.3 // 93664 /// NM_0	CADPS2	NM_017954	NM_017954 // GO:0015031 // protein transport // inferred from electronic annotation //	NM_017954 // GO:0030054 // cell junction // inferred from electronic annotation /// NM	NM_017954 // GO:0005515 // protein binding // inferred from electronic annotation ///

124	7930861	NR_026939 // Hs.89387 // brain connective tissue embryonic tissue eye intestine lu	NR_026939 // CASC2 // cancer susceptibility candidate 2 // 10q26.11 // 255082 /// NR_02	CASC2	NR_026939	---	---	---
125	7980861	NM_024764 // Hs.131755 // bladder brain liver mammary gland ovary pancreas placen	NM_024764 // CATSPERB // cation channel, sperm-associated, beta // 14q32.12 // 79820 //	CATSPERB	NM_024764	NM_024764 // GO:0007275 // multicellular organismal development // inferred from electr	NM_024764 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0247	NM_024764 // GO:0005515 // protein binding // inferred from electronic annotation ///
126	7927889	NM_018237 // Hs.49853 // adrenal gland ascites bladder blood bone bone marrow bra	NM_018237 // CCAR1 // cell division cycle and apoptosis regulator 1 // 10q21.3 // 55749	CCAR1	NM_018237	NM_018237 // GO:0006915 // apoptosis // inferred from electronic annotation /// NM_018	NM_018237 // GO:0005634 // nucleus // inferred from direct assay /// NM_018237 // GO:0	NM_018237 // GO:0003676 // nucleic acid binding // inferred from electronic annotation
127	8090133	NM_022757 // Hs.645028 // adipose tissue bladder blood bone bone marrow brain cer	NM_022757 // CCDC14 // coiled-coil domain containing 14 // 3q21.1 // 64770 /// BX537652	CCDC14	NM_022757	---	---	---
128	8057377	NM_173648 // Hs.324341 // adrenal gland eye heart liver lung lymph node muscle p	NM_173648 // CCDC141 // coiled-coil domain containing 141 // 2q31.2 // 285025 /// ENST0	CCDC141	NM_173648	---	---	NM_173648 // GO:0005515 // protein binding // inferred from physical interaction /// E
129	8081462	NM_032600 // Hs.164799 // testis uterus germ cell tumor normal fetus /// ENST000002	NM_032600 // CCDC54 // coiled-coil domain containing 54 // 3q13.12 // 84692 /// ENST000	CCDC54	NM_032600	---	---	---
130	7933760	NM_005436 // Hs.591360 // adipose tissue adrenal gland ascites bladder blood bone	NM_005436 // CCDC6 // coiled-coil domain containing 6 // 10q21 // 8030 /// ENST00000263	CCDC6	NM_005436	NM_005436 // GO:0008150 // biological_process // no biological data available /// ENST	NM_005436 // GO:0005737 // cytoplasm // inferred from direct assay /// NM_005436 // GO	NM_005436 // GO:0005200 // structural constituent of cytoskeleton // traceable author s
131	7942941	NM_001156474 // Hs.144913 // brain connective tissue eye lung pharynx prostate te	NM_001156474 // CCDC81 // coiled-coil domain containing 81 // 11q14.2 // 60494 /// NM_0	CCDC81	NM_001156474	---	---	---
132	7942896	NM_173556 // Hs.567774 // brain testis germ cell tumor normal fetus adult /// ENST	NM_173556 // CCDC83 // coiled-coil domain containing 83 // 11q14.1-q14.2 // 220047 ///	CCDC83	NM_173556	---	---	---
133	8014369	NM_002983 // Hs.514107 // adrenal gland blood brain eye heart intestine kidney l	NM_002983 // CCL3 // chemokine (C-C motif) ligand 3 // 17q12 // 6348 /// ENST0000022524	CCL3	NM_002983	NM_002983 // GO:0006874 // cellular calcium ion homeostasis // traceable author stateme	NM_002983 // GO:0005576 // extracellular region // not recorded /// NM_002983 // GO:00	NM_002983 // GO:0004871 // signal transducer activity // traceable author statement //

13 4	8014391	NM_021006 // Hs.512683 // blood bone bone marrow brain connective tissue intestine	NM_021006 // CCL3L1 // chemokine (C-C motif) ligand 3-like 1 // 17q21.1 // 6349 /// NM_	CCL3L1	NM_021006	NM_001001437 // GO:0006935 // chemotaxis // non-traceable author statement /// NM_0010	NM_001001437 // GO:0005576 // extracellular region // not recorded /// NM_001001437 //	NM_001001437 // GO:0008009 // chemokine activity // non-traceable author statement ///
13 5	7983969	NM_004701 // Hs.194698 // adrenal gland ascites bladder blood bone bone marrow br	NM_004701 // CCNB2 // cyclin B2 // 15q22.2 // 9133 /// ENST00000288207 // CCNB2 // cycl	CCNB2	NM_004701	NM_004701 // GO:0001701 // in utero embryonic development // inferred from electronic a	NM_004701 // GO:0005624 // membrane fraction // inferred from electronic annotation //	NM_004701 // GO:0005515 // protein binding // inferred from physical interaction /// E
13 6	7962831	NM_001240 // Hs.279906 // brain eye kidney larynx liver lung placenta prostate	NM_001240 // CCNT1 // cyclin T1 // 12q13.11 // 904 /// ENST00000261900 // CCNT1 // cycl	CCNT1	NM_001240	NM_001240 // GO:0000079 // regulation of cyclin-dependent protein kinase activity // tr	NM_001240 // GO:0005634 // nucleus // inferred from direct assay /// NM_001240 // GO:0	NM_001240 // GO:0003677 // DNA binding // inferred from direct assay /// NM_001240 //
13 7	8045381	NM_058241 // Hs.591241 // adipose tissue adrenal gland blood bone brain connective	NM_058241 // CCNT2 // cyclin T2 // 2q21.3 // 905 /// NM_001241 // CCNT2 // cyclin T2 //	CCNT2	NM_058241	NM_058241 // GO:0000079 // regulation of cyclin-dependent protein kinase activity // tr	NM_058241 // GO:0005634 // nucleus // inferred from direct assay /// NM_058241 // GO:0	---
13 8	8104449	NM_012073 // Hs.1600 // adipose tissue adrenal gland ascites bladder blood bone b	NM_012073 // CCT5 // chaperonin containing TCP1, subunit 5 (epsilon) // 5p15.2 // 22948	CCT5	NM_012073	NM_012073 // GO:0006457 // protein folding // inferred from electronic annotation ///	NM_012073 // GO:0005634 // nucleus // inferred from direct assay /// NM_012073 // GO:0	NM_012073 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
13 9	8161004	NM_001782 // Hs.116481 // bladder blood brain connective tissue heart intestine k	NM_001782 // CD72 // CD72 molecule // 9p13.3 // 971 /// ENST00000396757 // CD72 // CD72	CD72	NM_001782	NM_001782 // GO:0007155 // cell adhesion // traceable author statement /// ENST0000039	NM_001782 // GO:0005887 // integral to plasma membrane // inferred from direct assay /	NM_001782 // GO:0004888 // transmembrane receptor activity // non-traceable author stat
14 0	8029136	NM_001783 // Hs.631567 // blood connective tissue eye heart intestine liver lung	NM_001783 // CD79A // CD79a molecule, immunoglobulin-associated alpha // 19q13.2 // 973	CD79A	NM_001783	NM_001783 // GO:0007166 // cell surface receptor linked signaling pathway // inferred f	NM_001783 // GO:0005771 // multivesicular body // inferred from sequence or structural	NM_001783 // GO:0004888 // transmembrane receptor activity // inferred from electronic
14 1	8089771	NM_005191 // Hs.838 // blood connective tissue lung lymph node mammary gland thymu	NM_005191 // CD80 // CD80 molecule // 3q13.3-q21 // 941 /// ENST00000264246 // CD80 //	CD80	NM_005191	NM_005191 // GO:0007267 // cell-cell signaling // inferred by curator /// NM_005191 //	NM_005191 // GO:0005886 // plasma membrane // not recorded /// NM_005191 // GO:0009897	NM_005191 // GO:0005515 // protein binding // inferred from physical interaction /// N
14 2	8006850	NM_016507 // Hs.416108 // ascites bladder bone bone marrow brain cervix connectiv	NM_016507 // CDK12 // cyclin-dependent kinase 12 // 17q12 // 51755 /// NM_015083 // CDK	CDK12	NM_016507	NM_016507 // GO:0046777 // protein autophosphorylation // inferred from direct assay /	NM_016507 // GO:0005634 // nucleus // inferred from direct assay /// NM_016507 // GO:0	NM_016507 // GO:0000166 // nucleotide binding // inferred from electronic annotation /

14 3	8101031	NM_003948 // Hs.591698 // brain kidney liver lung muscle pancreas pharynx testis	NM_003948 // CDKL2 // cyclin-dependent kinase-like 2 (CDC2-related kinase) // 4q21.1 //	CDKL2	NM_003948	NM_003948 // GO:0006468 // protein phosphorylation // inferred from electronic annotation	NM_003948 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00394	NM_003948 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
14 4	8175531	NM_004065 // Hs.446675 // adipose tissue blood brain connective tissue embryonic ti	NM_004065 // CDR1 // cerebellar degeneration-related protein 1, 34kDa // Xq27.1-q27.2 /	CDR1	NM_004065	---	---	AK096486 // GO:0000166 // nucleotide binding // inferred from electronic annotation //
14 5	8157534	NM_007018 // Hs.653263 // ascites blood bone bone marrow brain connective tissue	NM_007018 // CEP110 // centrosomal protein 110kDa // 9q33.2 // 11064 /// ENST0000023834	CEP110	NM_007018	NM_007018 // GO:0007049 // cell cycle // inferred from electronic annotation /// NM_00	NM_007018 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_007	NM_007018 // GO:0005515 // protein binding // inferred from electronic annotation ///
14 6	7988537	NM_001194998 // Hs.597323 // bladder blood bone brain embryonic tissue eye heart	NM_001194998 // CEP152 // centrosomal protein 152kDa // 15q21.1 // 22995 /// NM_014985	CEP152	NM_001194998	---	NM_001194998 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_00	---
14 7	8113050	NM_004365 // Hs.591767 // ascites bladder blood bone bone marrow brain connective	NM_004365 // CETN3 // centrin, EF-hand protein, 3 // 5q14.3 // 1070 /// ENST00000283122	CETN3	NM_004365	NM_004365 // GO:0007049 // cell cycle // inferred from electronic annotation /// NM_00	NM_004365 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_004	NM_004365 // GO:0005509 // calcium ion binding // inferred from electronic annotation
14 8	8178115	NM_001710 // Hs.69771 // adipose tissue adrenal gland bladder blood bone bone marr	NM_001710 // CFB // complement factor B // 6p21.3 // 629 /// ENST00000417261 // CFB //	CFB	NM_001710	NM_001710 // GO:0006508 // proteolysis // inferred from electronic annotation /// NM_0	NM_001710 // GO:0005576 // extracellular region // not recorded /// NM_001710 // GO:00	NM_001710 // GO:0001848 // complement binding // traceable author statement /// NM_001
14 9	8002865	NM_006324 // Hs.461361 // adrenal gland ascites blood bone bone marrow brain cerv	NM_006324 // CFDP1 // craniofacial development protein 1 // 16q22.2-q22.3 // 10428 ///	CFDP1	NM_006324	NM_006324 // GO:0006916 // anti-apoptosis // inferred from electronic annotation /// N	NM_006324 // GO:0005575 // cellular_component // no biological data available /// ENST	NM_006324 // GO:0003674 // molecular_function // no biological data available /// ENST
15 0	7908481	NM_021023 // Hs.709217 // connective tissue larynx liver lung muscle testis uteru	NM_021023 // CFHR3 // complement factor H-related 3 // 1q32 // 10878 /// NM_001166624 /	CFHR3	NM_021023	---	NM_021023 // GO:0005576 // extracellular region // inferred from electronic annotation	---
15 1	7974418	NM_006568 // Hs.59106 // adipose tissue adrenal gland ascites bladder blood bone	NM_006568 // CGRRF1 // cell growth regulator with ring finger domain 1 // 14q22.2 // 10	CGRRF1	NM_006568	NM_006568 // GO:0006950 // response to stress // traceable author statement /// NM_006	---	NM_006568 // GO:0005515 // protein binding // inferred from electronic annotation ///

15 2	8150550	NM_004198 // Hs.103128 // brain eye lymph muscle placenta skin testis germ cell	NM_004198 // CHRNA6 // cholinergic receptor, nicotinic, alpha 6 // 8p11.21 // 8973 ///	CHRNA6	NM_004198	NM_004198 // GO:0006810 // transport // traceable author statement /// NM_004198 // GO	NM_004198 // GO:0005886 // plasma membrane // not recorded /// NM_004198 // GO:0005892	NM_004198 // GO:0004872 // receptor activity // inferred from electronic annotation //
15 3	8054702	NM_152515 // Hs.434250 // adrenal gland bladder blood bone bone marrow brain cerv	NM_152515 // CKAP2L // cytoskeleton associated protein 2-like // 2q13 // 150468 /// ENS	CKAP2L	NM_152515	---	---	---
15 4	8106689	NM_001825 // Hs.80691 // adipose tissue adrenal gland brain embryonic tissue heart	NM_001825 // CKMT2 // creatine kinase, mitochondrial 2 (sarcomeric) // 5q13.3 // 1160 /	CKMT2	NM_001825	NM_001825 // GO:0006600 // creatine metabolic process // not recorded /// NM_001825 //	NM_001825 // GO:0005739 // mitochondrion // inferred from electronic annotation /// NM	NM_001825 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
15 5	8103877	NM_024949 // Hs.333179 // blood bone brain connective tissue embryonic tissue eye	NM_001111319 // CLDN22 // claudin 22 // 4q35.1 // 53842 /// NM_024949 // WWC2 // WW and	CLDN22	NM_001111319	NM_001111319 // GO:0016338 // calcium- independent cell- cell adhesion // inferred from s	NM_001111319 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001111319 // GO:0005198 // structural molecule activity // inferred from electronic
15 6	8103879	---	NM_001185149 // CLDN24 // claudin 24 // 4q35.1 // 100132463 /// ENST00000329738 // CLDN	CLDN24	NM_001185149	---	NM_001185149 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001185149 // GO:0005198 // structural molecule activity // inferred from electronic
15 7	7998898	NM_021195 // Hs.533779 // brain embryonic tissue eye intestine lung mammary gland	NM_021195 // CLDN6 // claudin 6 // 16p13.3 // 9074 /// ENST00000328796 // CLDN6 // clau	CLDN6	NM_021195	NM_021195 // GO:0016338 // calcium- independent cell- cell adhesion // inferred from sequ	NM_021195 // GO:0005886 // plasma membrane // inferred from electronic annotation ///	NM_021195 // GO:0005198 // structural molecule activity // inferred from electronic ann
15 8	7961083	NM_005127 // Hs.85201 // adipose tissue adrenal gland bladder blood bone bone marr	NM_005127 // CLEC2B // C-type lectin domain family 2, member B // 12p13-p12 // 9976 ///	CLEC2B	NM_005127	---	NM_005127 // GO:0005887 // integral to plasma membrane // traceable author statement /	NM_005127 // GO:0005488 // binding // inferred from electronic annotation /// NM_00512
15 9	8099368	NM_052964 // Hs.678910 // blood brain kidney muscle spleen kidney tumor leukemia	NM_052964 // CLNK // cytokine-dependent hematopoietic cell linker // 4p16.1 // 116449 /	CLNK	NM_052964	NM_052964 // GO:0006955 // immune response // non-traceable author statement /// NM_05	NM_052964 // GO:0005622 // intracellular // non- traceable author statement /// ENST000	NM_052964 // GO:0005070 // SH3/SH2 adaptor activity // non- traceable author statement
16 0	7937016	NM_152311 // Hs.242014 // ascites intestine kidney liver stomach colorectal tumor	NM_152311 // CLRN3 // clarin 3 // 10q26.2 // 119467 /// ENST00000368671 // CLRN3 // cla	CLRN3	NM_152311	---	NM_152311 // GO:0016020 // membrane // inferred from electronic annotation /// NM_1523	---

16 1	7978343	NM_001836 // Hs.135626 // mammary gland breast (mammary gland) tumor adult /// ENST00	NM_001836 // CMA1 // chymase 1, mast cell // 14q11.2 // 1215 /// ENST00000250378 // CMA	CMA1	NM_001836	NM_001836 // GO:0006508 // proteolysis // inferred from electronic annotation /// NM_0	NM_001836 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_001836 // GO:0004252 // serine-type endopeptidase activity // inferred from direct a
16 2	7957106	NM_014515 // Hs.133350 // adrenal gland ascites bladder blood bone bone marrow br	NM_014515 // CNOT2 // CCR4-NOT transcription complex, subunit 2 // 12q15 // 4848 /// EN	CNOT2	NM_014515	NM_014515 // GO:0006358 // regulation of transcription from RNA polymerase II promoter,	NM_014515 // GO:0005634 // nucleus // non-traceable author statement /// NM_014515 //	NM_014515 // GO:0005515 // protein binding // inferred from physical interaction /// N
16 3	7954899	NM_001843 // Hs.143434 // adipose tissue brain connective tissue ear embryonic tiss	NM_001843 // CNTN1 // contactin 1 // 12q11-q12 // 1272 /// NM_175038 // CNTN1 // contac	CNTN1	NM_001843	NM_001843 // GO:0007155 // cell adhesion // inferred from electronic annotation /// NM	NM_001843 // GO:0005624 // membrane fraction // traceable author statement /// NM_0018	NM_001843 // GO:0005515 // protein binding // inferred from electronic annotation ///
16 4	7943319	NM_014361 // Hs.656783 // brain connective tissue embryonic tissue eye liver lung	NM_014361 // CNTN5 // contactin 5 // 11q21-q22.2 // 53942 /// NM_175566 // CNTN5 // con	CNTN5	NM_014361	NM_014361 // GO:0007155 // cell adhesion // inferred from electronic annotation /// NM	NM_014361 // GO:0005886 // plasma membrane // inferred from electronic annotation ///	NM_014361 // GO:0005515 // protein binding // inferred from physical interaction /// N
16 5	8100127	NM_130902 // Hs.479656 // bladder brain connective tissue skin testis bladder carc	NM_130902 // COX7B2 // cytochrome c oxidase subunit VIIb2 // 4p12 // 170712 /// ENST000	COX7B2	NM_130902	---	NM_130902 // GO:0005739 // mitochondrion // inferred from electronic annotation /// NM	NM_130902 // GO:0004129 // cytochrome-c oxidase activity // inferred from electronic an
16 6	7971444	NM_001872 // Hs.512937 // brain connective tissue embryonic tissue liver mammary gl	NM_001872 // CPB2 // carboxypeptidase B2 (plasma) // 13q14.11 // 1361 /// NM_016413 //	CPB2	NM_001872	NM_001872 // GO:0006508 // proteolysis // inferred from electronic annotation /// NM_0	NM_001872 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_001872 // GO:0004181 // metalloproteinase activity // inferred from electronic
16 7	7909350	NM_001006658 // Hs.445757 // blood brain connective tissue intestine kidney liver	NM_001006658 // CR2 // complement component (3d/Epstein Barr virus) receptor 2 // 1q32	CR2	NM_001006658	NM_001006658 // GO:0006955 // immune response // non-traceable author statement /// NM	NM_001006658 // GO:0005886 // plasma membrane // non-traceable author statement /// NM	NM_001006658 // GO:0004875 // complement receptor activity // non-traceable author stat
16 8	8151092	NM_000756 // Hs.75294 // adrenal gland brain connective tissue muscle pancreas pla	NM_000756 // CRH // corticotropin releasing hormone // 8q13 // 1392 /// ENST00000276571	CRH	NM_000756	NM_000756 // GO:0006704 // glucocorticoid biosynthetic process // inferred from electro	NM_000756 // GO:0005576 // extracellular region // not recorded /// NM_000756 // GO:00	NM_000756 // GO:0005102 // receptor binding // traceable author statement /// NM_00075
16 9	8058520	NM_006891 // Hs.546247 // embryonic tissue eye ovary normal ovarian tumor fetus a	NM_006891 // CRYGD // crystallin, gamma D // 2q33-q35 // 1421 /// ENST00000264376 // CR	CRYGD	NM_006891	NM_006891 // GO:0007601 // visual perception // inferred from mutant phenotype /// NM	NM_006891 // GO:0005625 // soluble fraction // inferred from direct assay /// ENST00000	NM_006891 // GO:0005212 // structural constituent of eye lens // non-traceable author s

17 0	8107887	NM_000758 // Hs.1349 // blood bone intestine lung chondrosarcoma germ cell tumor	NM_000758 // CSF2 // colony stimulating factor 2 (granulocyte- macrophage) // 5q31.1 //	CSF2	NM_000758	NM_000758 // GO:0006955 // immune response // inferred from electronic annotation ///	NM_000758 // GO:0005576 // extracellular region // not recorded /// NM_000758 // GO:00	NM_000758 // GO:0005125 // cytokine activity // inferred from electronic annotation //
17 1	8175353	NM_001017438 // Hs.676560 // liver liver tumor adult /// NM_152582 // Hs.632281 // bo	NM_001017438 // CT45A6 // cancer/testis antigen family 45, member A6 // Xq26.3 // 54146	CT45A6	NM_001017438	---	---	---
17 2	8022508	NM_172241 // Hs.406709 // kidney placenta testis normal adult /// ENST00000391403 /	NM_172241 // CTAGE1 // cutaneous T-cell lymphoma-associated antigen 1 // 18p11.2 // 646	CTAGE1	NM_172241	NM_172241 // GO:0008150 // biological_process // no biological data available /// ENST	NM_172241 // GO:0005575 // cellular_componen t // no biological data available /// NM_1	---
17 3	8129560	NM_198495 // Hs.720693 // ascites heart kidney liver muscle ovary pancreas prost	NM_198495 // CTAGE4 // CTAGE family, member 4 // 7q35 // 100128553 /// NM_001145659 //	CTAGE4	NM_198495	NM_198495 // GO:0008150 // biological_process // no biological data available /// NM_1	NM_198495 // GO:0005575 // cellular_componen t // no biological data available /// NM_1	---
17 4	7904018	NM_018704 // Hs.724560 // adrenal gland bladder blood bone brain cervix connectiv	NM_018704 // CTTNBP2NL // CTTNBP2 N-terminal like // 1p13.2 // 55917 /// ENST0000027127	CTTNBP2NL	NM_018704	---	NM_018704 // GO:0015629 // actin cytoskeleton // inferred from direct assay /// ENST00	NM_018704 // GO:0005515 // protein binding // inferred from physical interaction /// E
17 5	8094988	NM_025087 // Hs.479703 // bone connective tissue intestine kidney mouth nerve pha	NM_025087 // CWH43 // cell wall biogenesis 43 C- terminal homolog (S. cerevisiae) // 4p1	CWH43	NM_025087	NM_025087 // GO:0006506 // GPI anchor biosynthetic process // inferred from electronic	NM_025087 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0250	---
17 6	7944335	NM_001716 // Hs.113916 // blood connective tissue esophagus intestine lung lymph	NM_001716 // CXCR5 // chemokine (C-X-C motif) receptor 5 // 11q23.3 // 643 /// NM_03296	CXCR5	NM_001716	NM_001716 // GO:0006928 // cellular component movement // traceable author statement /	NM_001716 // GO:0005886 // plasma membrane // not recorded /// NM_001716 // GO:0005887	NM_001716 // GO:0004872 // receptor activity // inferred from electronic annotation //
17 7	8049471	NM_020311 // Hs.471751 // bladder bone bone marrow brain connective tissue embryon	NM_020311 // CXCR7 // chemokine (C-X-C motif) receptor 7 // 2q37.3 // 57007 /// ENST000	CXCR7	NM_020311	NM_020311 // GO:0008150 // biological_process // no biological data available /// NM_0	NM_020311 // GO:0005886 // plasma membrane // not recorded /// NM_020311 // GO:0016021	NM_020311 // GO:0004872 // receptor activity // inferred from electronic annotation //
17 8	8170319	NM_004709 // Hs.106688 // brain eye lung non-neoplasia normal fetus adult /// ENS	NM_004709 // CXorf1 // chromosome X open reading frame 1 // Xq27.3 // 9142 /// ENST0000	CXorf1	NM_004709	NM_004709 // GO:0008150 // biological_process // no biological data available /// ENST	NM_004709 // GO:0005575 // cellular_componen t // no biological data available /// ENST	NM_004709 // GO:0003674 // molecular_function // no biological data available /// ENST

179	8169221	NM_001169154 // Hs.128836 // lung testis uterus normal uterine tumor fetus adult	NM_001169154 // CXorf41 // chromosome X open reading frame 41 // Xq22.3 // 139212 /// N	CXorf41	NM_001169154	---	---	---
180	8168569	NM_021118 // Hs.444230 // testis normal fetus /// ENST00000329312 // Hs.444230 // tes	NM_021118 // CYLC1 // cyclin, basic protein of sperm head cytoskeleton 1 // Xq21.1 //	CYLC1	NM_021118	NM_021118 // GO:0007275 // multicellular organismal development // inferred from electr	NM_021118 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_021	NM_021118 // GO:0005198 // structural molecule activity // non-traceable author stateme
181	8126770	NM_016593 // Hs.387367 // adrenal gland brain cervix connective tissue embryonic ti	NM_016593 // CYP39A1 // cytochrome P450, family 39, subfamily A, polypeptide 1 // 6p21.	CYP39A1	NM_016593	NM_016593 // GO:0006699 // bile acid biosynthetic process // inferred from direct assay	NM_016593 // GO:0005783 // endoplasmic reticulum // inferred from electronic annotation	NM_016593 // GO:0004497 // monooxygenase activity // inferred from electronic annotatio
182	8134655	NM_022820 // Hs.306220 // brain ovary testis normal ovarian tumor fetus adult ///	NM_022820 // CYP3A43 // cytochrome P450, family 3, subfamily A, polypeptide 43 // 7q21.	CYP3A43	NM_022820	NM_022820 // GO:0055114 // oxidation reduction // inferred from electronic annotation	NM_022820 // GO:0005783 // endoplasmic reticulum // inferred from electronic annotation	NM_022820 // GO:0004497 // monooxygenase activity // inferred from sequence or structur
183	7915896	NR_002788 // Hs.591431 // mammary gland prostate breast (mammary gland) tumor normal	NR_002788 // CYP4Z2P // cytochrome P450, family 4, subfamily Z, polypeptide 2 pseudogen	CYP4Z2P	NR_002788	---	NR_002788 // GO:0016020 // membrane // inferred from electronic annotation /// NR_0027	NR_002788 // GO:0004497 // monooxygenase activity // inferred from electronic annotatio
184	7969959	NM_172370 // Hs.381382 // --- /// NM_001161814 // Hs.381382 // --- /// NM_001161812 //	NM_172370 // DAOA // D-amino acid oxidase activator // 13q33.2 13q34 // 267012 /// NM_0	DAOA	NM_172370	---	NM_172370 // GO:0005794 // Golgi apparatus // inferred from electronic annotation ///	---
185	7962481	NM_001004329 // Hs.302764 // bone brain kidney glioma kidney tumor non-neoplasia	NM_001004329 // DBX2 // developing brain homeobox 2 // 12q12 // 440097 /// ENST00000332	DBX2	NM_001004329	NM_001004329 // GO:0006355 // regulation of transcription, DNA-dependent // inferred fr	NM_001004329 // GO:0005634 // nucleus // inferred from electronic annotation /// ENST0	NM_001004329 // GO:0003700 // sequence-specific DNA binding transcription factor activi
186	7947322	NM_181807 // Hs.592000 // muscle pharynx testis normal fetus adult /// ENST0000045	NM_181807 // DCDC1 // doublecortin domain containing 1 // 11p13 // 341019 /// ENST00000	DCDC1	NM_181807	NM_181807 // GO:0023034 // intracellular signaling pathway // inferred from electronic	---	---
187	7943521	NM_001001711 // Hs.591941 // brain testis germ cell tumor normal fetus adult /// E	NM_001001711 // DDI1 // DNA-damage inducible 1 homolog 1 (S. cerevisiae) // 11q22.3 //	DDI1	NM_001001711	NM_001001711 // GO:0006508 // proteolysis // inferred from electronic annotation /// E	---	NM_001001711 // GO:0004190 // aspartic-type endopeptidase activity // inferred from ele

18 8	7906900	AY423733 // Hs.275757 // adipose tissue adrenal gland bone bone marrow brain conne	AY423733 // DDR2 // discoidin domain receptor tyrosine kinase 2 // 1q23.3 // 4921 // A	DDR2	AY423733	AY423733 // GO:0001558 // regulation of cell growth // inferred from electronic annotat	AY423733 // GO:0005887 // integral to plasma membrane // inferred from electronic annot	AY423733 // GO:0000166 // nucleotide binding // inferred from electronic annotation //
18 9	7943690	NM_004398 // Hs.591931 // adrenal gland bladder blood bone bone marrow brain conn	NM_004398 // DDX10 // DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 // 11q22-q23 // 1662 //	DDX10	NM_004398	---	---	NM_004398 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
19 0	8044745	NM_006773 // Hs.363492 // adipose tissue adrenal gland ascites bladder blood bone	NM_006773 // DDX18 // DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 // 2q14.1 // 8886 // E	DDX18	NM_006773	---	---	NM_006773 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
19 1	8034806	NM_005804 // Hs.311609 // adipose tissue adrenal gland ascites bladder blood bone	NM_005804 // DDX39 // DEAD (Asp-Glu-Ala-Asp) box polypeptide 39 // 19p13.12 // 10212 //	DDX39	NM_005804	NM_005804 // GO:0000398 // nuclear mRNA splicing, via spliceosome // inferred from gene	NM_005804 // GO:0005634 // nucleus // inferred from electronic annotation /// ENST0000	NM_005804 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
19 2	8014574	NM_007010 // Hs.590937 // ascites bladder blood bone bone marrow brain cervix co	NM_007010 // DDX52 // DEAD (Asp-Glu-Ala-Asp) box polypeptide 52 // 17q21.1 // 11056 ///	DDX52	NM_007010	---	NM_007010 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00701	NM_007010 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
19 3	8166440	NM_182699 // Hs.434416 // testis normal fetus /// ENST00000327968 // Hs.434416 // tes	NM_182699 // DDX53 // DEAD (Asp-Glu-Ala-Asp) box polypeptide 53 // Xp22.11 // 168400 //	DDX53	NM_182699	---	NM_182699 // GO:0005634 // nucleus // inferred from electronic annotation /// ENST0000	NM_182699 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
19 4	8061504	NM_001037730 // Hs.580793 // --- /// ENST00000400552 // Hs.580793 // --- /// DQ012019 /	NM_001037730 // DEFB115 // defensin, beta 115 // 20q11.1 // 245929 /// ENST00000400552	DEFB115	NM_001037730	NM_001037730 // GO:0042742 // defense response to bacterium // inferred from electronic	NM_001037730 // GO:0005576 // extracellular region // inferred from electronic annotati	---
19 5	8065563	NM_001011878 // Hs.272294 // normal fetus /// NM_001171832 // Hs.272294 // normal fet	NM_001011878 // DEFB121 // defensin, beta 121 // 20q11.1 // 245934 /// NM_001171832 //	DEFB121	NM_001011878	NM_001011878 // GO:0042742 // defense response to bacterium // inferred from electronic	NM_001011878 // GO:0005576 // extracellular region // inferred from electronic annotati	NM_001011878 // GO:0003674 // molecular_function // no biological data available /// N
19 6	8060314	NM_139074 // Hs.99362 // testis normal fetus /// ENST00000382388 // Hs.99362 // testi	NM_139074 // DEFB127 // defensin, beta 127 // 20p13 // 140850 /// ENST00000382388 // DE	DEFB127	NM_139074	NM_139074 // GO:0042742 // defense response to bacterium // traceable author statement	NM_139074 // GO:0005575 // cellular_componen t // no biological data available /// NM_1	---
19 7	8126931	NM_001166478 // Hs.558270 // --- /// ENST00000398721 // Hs.558270 // --- /// DQ012023 /	NM_001166478 // DEFB133 // defensin, beta 133 // 6p12.3 // 403339 /// ENST00000398721 /	DEFB133	NM_001166478	NM_001166478 // GO:0042742 // defense response to bacterium // inferred from electronic	NM_001166478 // GO:0005576 // extracellular region // inferred from electronic annotati	---

19 8	8144687	NM_001033017 // Hs.558284 // --- /// ENST00000382208 // Hs.558284 // --- /// DQ012025 /	NM_001033017 // DEFB135 // defensin, beta 135 // 8p23.1 // 613209 /// ENST00000382208 /	DEFB135	NM_001033017	NM_001033017 // GO:0042742 // defense response to bacterium // inferred from electronic	NM_001033017 // GO:0005576 // extracellular region // inferred from electronic annotati	---
19 9	7916898	NM_001114120 // Hs.445098 // ascites bladder blood bone bone marrow brain connect	NM_001114120 // DEPDC1 // DEP domain containing 1 // 1p31.2 // 55635 /// NM_017779 // D	DEPDC1	NM_001114120	NM_001114120 // GO:0007165 // signal transduction // inferred from electronic annotatio	NM_001114120 // GO:0005622 // intracellular // inferred from electronic annotation ///	NM_001114120 // GO:0005096 // GTPase activator activity // inferred from electronic ann
20 0	8168098	NM_198512 // Hs.454355 // skin normal /// ENST00000333026 // Hs.454355 // skin normal	NM_198512 // DGAT2L6 // diacylglycerol O- acyltransferase 2-like 6 // Xq13.1 // 347516 /	DGAT2L6	NM_198512	NM_198512 // GO:0008610 // lipid biosynthetic process // inferred from electronic annot	NM_198512 // GO:0005783 // endoplasmic reticulum // inferred from electronic annotation	NM_198512 // GO:0008415 // acyltransferase activity // inferred from electronic annotat
20 1	8091562	NM_020865 // Hs.446270 // adipose tissue adrenal gland ascites blood bone bone mar	NM_020865 // DHX36 // DEAH (Asp-Glu-Ala-His) box polypeptide 36 // 3p13-q23 // 170506 /	DHX36	NM_020865	---	NM_020865 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_02086	NM_020865 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
20 2	7980485	NM_013989 // Hs.202354 // bone brain cervix connective tissue ear embryonic tissue	NM_013989 // DIO2 // deiodinase, iodothyronine, type II // 14q24.2-q24.3 // 1734 /// NM	DIO2	NM_013989	NM_013989 // GO:0001514 // selenocysteine incorporation // non-traceable author stateme	NM_013989 // GO:0005886 // plasma membrane // not recorded /// NM_013989 // GO:0016020	NM_013989 // GO:0004800 // thyroxine 5'-deiodinase activity // inferred from direct ass
20 3	7971967	NM_014953 // Hs.643464 // adipose tissue adrenal gland ascites bladder blood bone	NM_014953 // DIS3 // DIS3 mitotic control homolog (S. cerevisiae) // 13q22.1 // 22894 /	DIS3	NM_014953	NM_014953 // GO:0006364 // rRNA processing // traceable author statement /// NM_001128	NM_014953 // GO:0000178 // exosome (RNase complex) // traceable author statement /// N	NM_014953 // GO:0003723 // RNA binding // inferred from electronic annotation /// NM_0
20 4	7938702	NR_026750 // Hs.720645 // eye intestine kidney testis colorectal tumor liver tumor	NR_026750 // DKFZp686O24166 // hypothetical protein DKFZp686O24166 // 11p15.1 // 374383	DKFZp686O2416 6	NR_026750	---	NR_026750 // GO:0016020 // membrane // inferred from electronic annotation /// NR_0267	NR_026750 // GO:0005198 // structural molecule activity // inferred from electronic ann
20 5	7938481	NM_015881 // Hs.292156 // adrenal gland ascites bone brain connective tissue ear	NM_015881 // DKK3 // dickkopf homolog 3 (Xenopus laevis) // 11p15.2 // 27122 /// NM_013	DKK3	NM_015881	NM_015881 // GO:0007275 // multicellular organismal development // inferred from electr	NM_015881 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_015881 // GO:0016564 // transcription repressor activity // inferred from direct ass
20 6	8096274	NM_004407 // Hs.652366 // bone connective tissue ear embryonic tissue normal fetus	NM_004407 // DMP1 // dentin matrix acidic phosphoprotein 1 // 4q21 // 1758 /// NM_00107	DMP1	NM_004407	NM_004407 // GO:0001503 // ossification // inferred from electronic annotation /// NM_	NM_004407 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_004407 // GO:0005178 // integrin binding // traceable author statement /// NM_00440

20 7	8107474	NM_005509 // Hs.181042 // adrenal gland ascites blood bone bone marrow brain cerv	NM_005509 // DMXL1 // Dmx-like 1 // 5q22 // 1657 /// ENST00000311085 // DMXL1 // Dmx-li	DMXL1	NM_005509	---	---	---
20 8	8088322	NM_198564 // Hs.201378 // blood connective tissue lung pancreas pharynx testis tr	NM_198564 // DNAH12 // dynein, axonemal, heavy chain 12 // 3p14.3 // 201625 /// NM_1785	DNAH12	NM_198564	NM_198564 // GO:0007018 // microtubule-based movement // inferred from electronic annot	NM_198564 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_198	NM_198564 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
20 9	8043043	NM_001370 // Hs.249972 // bone brain connective tissue intestine kidney liver lun	NM_001370 // DNAH6 // dynein, axonemal, heavy chain 6 // 2p11.2 // 1768 /// ENST00000038	DNAH6	NM_001370	NM_001370 // GO:0007018 // microtubule-based movement // inferred from electronic annot	NM_001370 // GO:0005874 // microtubule // inferred from electronic annotation /// NM_0	NM_001370 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
21 0	8119243	NM_001371 // Hs.520106 // brain connective tissue lymph node placenta prostate tes	NM_001371 // DNAH8 // dynein, axonemal, heavy chain 8 // 6p21.2 // 1769 /// ENST00000035	DNAH8	NM_001371	NM_001371 // GO:0001539 // ciliary or flagellar motility // non-traceable author statem	NM_001371 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_001	NM_001371 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
21 1	8001185	NM_005880 // Hs.368078 // adipose tissue adrenal gland ascites bladder blood bone	NM_005880 // DNAJA2 // DnaJ (Hsp40) homolog, subfamily A, member 2 // 16q12.1 // 10294	DNAJA2	NM_005880	NM_005880 // GO:0006457 // protein folding // inferred from electronic annotation ///	NM_005880 // GO:0016020 // membrane // inferred from electronic annotation /// ENST000	NM_005880 // GO:0005524 // ATP binding // inferred from electronic annotation /// NM_0
21 2	8070097	NM_017833 // Hs.458308 // blood bone brain embryonic tissue lung pharynx stomach	NM_017833 // DNAJC28 // DnaJ (Hsp40) homolog, subfamily C, member 28 // 21q22.11 // 549	DNAJC28	NM_017833	---	---	NM_017833 // GO:0031072 // heat shock protein binding // inferred from electronic annot
21 3	8088371	NM_004944 // Hs.476453 // adrenal gland blood brain connective tissue eye intestin	NM_004944 // DNASE1L3 // deoxyribonuclease I-like 3 // 3p14.3 // 1776 /// ENST0000003183	DNASE1L3	NM_004944	NM_004944 // GO:0006259 // DNA metabolic process // traceable author statement /// NM	NM_004944 // GO:0005634 // nucleus // inferred from electronic annotation /// ENST0000	NM_004944 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
21 4	7902623	NM_021233 // Hs.129142 // lung muscle prostate skin testis normal prostate cancer	NM_021233 // DNASE2B // deoxyribonuclease II beta // 1p22.3 // 58511 /// NM_058248 // D	DNASE2B	NM_021233	NM_021233 // GO:0006259 // DNA metabolic process // inferred from electronic annotation	NM_021233 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_021233 // GO:0004520 // endodeoxyribonuclease activity // inferred from electronic a
21 5	7953665	NM_199286 // Hs.131358 // germ cell tumor /// AY317075 // Hs.131358 // germ cell tumor	NM_199286 // DPPA3 // developmental pluripotency associated 3 // 12p13.31 // 359787 ///	DPPA3	NM_199286	---	NM_199286 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_19928	---

21 6	8020779	NM_001943 // Hs.412597 // adipose tissue ascites bladder bone bone marrow brain c	NM_001943 // DSG2 // desmoglein 2 // 18q12.1 // 1829 /// ENST00000261590 // DSG2 // des	DSG2	NM_001943	NM_001943 // GO:0007155 // cell adhesion // inferred from electronic annotation /// NM	NM_001943 // GO:0005886 // plasma membrane // not recorded /// NM_001943 // GO:0005886	NM_001943 // GO:0005509 // calcium ion binding // inferred from electronic annotation
21 7	8147101	NM_001951 // Hs.445758 // blood bone brain embryonic tissue eye heart intestine	NM_001951 // E2F5 // E2F transcription factor 5, p130-binding // 8q21.2 // 1875 /// NM_	E2F5	NM_001951	NM_001951 // GO:0006355 // regulation of transcription, DNA- dependent // inferred from	NM_001951 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00195	NM_001951 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
21 8	8115543	NM_024007 // Hs.573143 // adipose tissue bone marrow brain connective tissue ear e	NM_024007 // EBF1 // early B-cell factor 1 // 5q34 // 1879 /// ENST00000313708 // EBF1	EBF1	NM_024007	NM_024007 // GO:0006355 // regulation of transcription, DNA- dependent // inferred from	NM_024007 // GO:0005634 // nucleus // inferred from electronic annotation /// ENST0000	NM_024007 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
21 9	8080980	NM_018029 // Hs.658858 // blood connective tissue embryonic tissue eye liver lymph	NM_018029 // EBLN2 // endogenous Borna-like N element-2 // 3p13 // 55096 /// AY036895 /	EBLN2	NM_018029	---	---	NM_018029 // GO:0005515 // protein binding // inferred from physical interaction /// A
22 0	7973093	NM_006683 // Hs.304757 // prostate testis normal adult /// ENST00000326842 // Hs.304	NM_006683 // EDDM3A // epididymal protein 3A // 14q11.2 // 10876 /// ENST00000326842 //	EDDM3A	NM_006683	NM_006683 // GO:0007321 // sperm displacement // traceable author statement /// ENST00	NM_006683 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_006683 // GO:0003676 // nucleic acid binding // inferred from electronic annotation
22 1	7965436	NM_003566 // Hs.567367 // adrenal gland ascites blood bone brain cervix connectiv	NM_003566 // EEA1 // early endosome antigen 1 // 12q22 // 8411 /// ENST00000322349 // E	EEA1	NM_003566	NM_003566 // GO:0006906 // vesicle fusion // inferred from mutant phenotype /// NM_003	NM_003566 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_003566 // GO:0005515 // protein binding // inferred from physical interaction /// N
22 2	8047771	NM_001959 // Hs.421608 // adipose tissue adrenal gland ascites bladder blood bone	NM_001959 // EE1B2 // eukaryotic translation elongation factor 1 beta 2 // 2q33.3 // 1	EE1B2	NM_001959	NM_001959 // GO:0006414 // translational elongation // not recorded /// NM_001959 // G	NM_001959 // GO:0005829 // cytosol // not recorded /// NM_001959 // GO:0005853 // euka	NM_001959 // GO:0003746 // translation elongation factor activity // non-traceable auth
22 3	8150691	NM_024593 // Hs.23245 // brain embryonic tissue eye heart lung ovary pancreas ph	NM_024593 // EFCAB1 // EF-hand calcium binding domain 1 // 8q11.21 // 79645 /// NR_0246	EFCAB1	NM_024593	---	---	NM_024593 // GO:0005509 // calcium ion binding // inferred from electronic annotation
22 4	8008995	NM_173503 // Hs.152670 // testis normal fetus /// NM_001144933 // Hs.152670 // testis	NM_173503 // EFCAB3 // EF-hand calcium binding domain 3 // 17q23.2 // 146779 /// NM_001	EFCAB3	NM_173503	---	---	NM_173503 // GO:0005509 // calcium ion binding // inferred from electronic annotation
22 5	7901931	NM_032437 // Hs.652324 // bone bone marrow brain cervix connective tissue embryoni	NM_032437 // EFCAB7 // EF-hand calcium binding domain 7 // 1p31.3 // 84455 /// ENST0000	EFCAB7	NM_032437	---	---	NM_032437 // GO:0005509 // calcium ion binding // inferred from electronic annotation

22 6	8085732	NM_144715 // Hs.670883 // brain connective tissue embryonic tissue kidney lung pha	NM_144715 // EFHB // EF-hand domain family, member B // 3p24.3 // 151651 /// ENST000002	EFHB	NM_144715	---	---	NM_144715 // GO:0005509 // calcium ion binding // inferred from electronic annotation
22 7	8083333	NM_032025 // Hs.655782 // adipose tissue adrenal gland ascites bladder blood bone	NM_032025 // EIF2A // eukaryotic translation initiation factor 2A, 65kDa // 3q25.1 // 8	EIF2A	NM_032025	NM_032025 // GO:0006417 // regulation of translation // inferred from mutant phenotype	NM_032025 // GO:0005737 // cytoplasm // inferred from direct assay /// NM_032025 // GO	NM_032025 // GO:0000049 // tRNA binding // inferred from mutant phenotype /// NM_03202
22 8	7915640	NM_020365 // Hs.533549 // ascites blood bone bone marrow brain cervix connective	NM_020365 // EIF2B3 // eukaryotic translation initiation factor 2B, subunit 3 gamma, 58	EIF2B3	NM_020365	NM_020365 // GO:0006413 // translational initiation // inferred from direct assay ///	NM_020365 // GO:0005737 // cytoplasm // inferred from direct assay /// NM_020365 // GO	NM_020365 // GO:0003743 // translation initiation factor activity // inferred from dire
22 9	7901342	NM_021952 // Hs.213050 // brain embryonic tissue eye lung nerve pancreas pituitar	NM_021952 // ELAVL4 // ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu	ELAVL4	NM_021952	NM_021952 // GO:0006396 // RNA processing // traceable author statement /// NM_021952	---	NM_021952 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
23 0	8020930	NM_018255 // Hs.8739 // adipose tissue adrenal gland ascites bladder blood bone ma	NM_018255 // ELP2 // elongation protein 2 homolog (S. cerevisiae) // 18q12.2 // 55250 /	ELP2	NM_018255	NM_018255 // GO:0006357 // regulation of transcription from RNA polymerase II promoter	NM_018255 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_01825	NM_018255 // GO:0003677 // DNA binding // inferred from direct assay /// NM_018255 //
23 1	8029988	NM_022142 // Hs.104894 // brain connective tissue eye placenta testis germ cell tu	NM_022142 // ELSPBP1 // epididymal sperm binding protein 1 // 19q13.33 // 64100 /// ENS	ELSPBP1	NM_022142	NM_022142 // GO:0007338 // single fertilization // inferred from electronic annotation	NM_022142 // GO:0005576 // extracellular region // inferred from electronic annotation	---
23 2	8096875	NM_001977 // Hs.435765 // bone marrow brain connective tissue embryonic tissue eye	NM_001977 // ENPEP // glutamyl aminopeptidase (aminopeptidase A) // 4q25 // 2028 /// EN	ENPEP	NM_001977	NM_001977 // GO:0001525 // angiogenesis // inferred from electronic annotation /// NM_	NM_001977 // GO:0005886 // plasma membrane // non-traceable author statement /// NM_00	NM_001977 // GO:0004177 // aminopeptidase activity // traceable author statement /// N
23 3	8147883	NM_020189 // Hs.492555 // adrenal gland ascites bladder blood bone bone marrow br	NM_020189 // ENY2 // enhancer of yellow 2 homolog (Drosophila) // 8q23.1 // 56943 /// N	ENY2	NM_020189	NM_020189 // GO:0006810 // transport // inferred from electronic annotation /// NM_020	NM_020189 // GO:0000124 // SAGA complex // inferred from direct assay /// NM_020189 //	NM_020189 // GO:0003713 // transcription coactivator activity // inferred from direct a
23 4	8045619	NM_015630 // Hs.23270 // adrenal gland bone bone marrow brain connective tissue em	NM_015630 // EPC2 // enhancer of polycomb homolog 2 (Drosophila) // 2q23.1 // 26122 ///	EPC2	NM_015630	NM_015630 // GO:0006281 // DNA repair // inferred from electronic annotation /// NM_01	NM_015630 // GO:0005634 // nucleus // inferred from electronic annotation /// ENST0000	---

23 5	8107044	NM_022350 // Hs.482910 // adrenal gland ascites bladder blood bone bone marrow br	NM_022350 // ERAP2 // endoplasmic reticulum aminopeptidase 2 // 5q15 // 64167 /// NM_00	ERAP2	NM_022350	NM_022350 // GO:0008217 // regulation of blood pressure // traceable author statement	NM_022350 // GO:0005783 // endoplasmic reticulum // inferred from electronic annotation	NM_022350 // GO:0004177 // aminopeptidase activity // inferred from direct assay /// N
23 6	8173506	NM_017669 // Hs.47558 // bone bone marrow brain embryonic tissue intestine kidney	NM_017669 // ERCC6L // excision repair cross-complementing rodent repair deficiency, co	ERCC6L	NM_017669	NM_017669 // GO:0007049 // cell cycle // inferred from electronic annotation /// NM_01	NM_017669 // GO:0000777 // condensed chromosome kinetochore // inferred from electronic	NM_017669 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
23 7	8112285	NM_000082 // Hs.435237 // ascites bladder blood bone marrow brain connective tissu	NM_000082 // ERCC8 // excision repair cross-complementing rodent repair deficiency, com	ERCC8	NM_000082	NM_000082 // GO:0000209 // protein polyubiquitination // inferred from direct assay //	NM_000082 // GO:0000109 // nucleotide-excision repair complex // inferred from direct a	NM_000082 // GO:0003678 // DNA helicase activity // inferred from direct assay /// NM_
23 8	8140909	---	NM_014590 // ERVWE1 // endogenous retroviral family W, env(C7), member 1 // 7q21.2 // 3	ERVWE1	NM_014590	NM_014590 // GO:0006949 // syncytium formation // traceable author statement /// NM_01	NM_014590 // GO:0005886 // plasma membrane // inferred from electronic annotation ///	NM_014590 // GO:0005198 // structural molecule activity // inferred from electronic ann
23 9	7979583	NM_001040275 // Hs.660607 // brain embryonic tissue lung testis germ cell tumor lu	NM_001040275 // ESR2 // estrogen receptor 2 (ER beta) // 14q23.2 // 2100 /// NM_001437	ESR2	NM_001040275	NM_001040275 // GO:0001541 // ovarian follicle development // inferred from electronic	NM_001040275 // GO:0005634 // nucleus // traceable author statement /// NM_001040275 /	NM_001040275 // GO:0003677 // DNA binding // traceable author statement /// NM_0010402
24 0	8138289	NM_004956 // Hs.22634 // adrenal gland bone bone marrow brain connective tissue em	NM_004956 // ETV1 // ets variant 1 // 7p21.3 // 2115 /// NM_001163147 // ETV1 // ets va	ETV1	NM_004956	NM_004956 // GO:0006355 // regulation of transcription, DNA-dependent // inferred from	NM_004956 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00116	NM_004956 // GO:0003700 // sequence-specific DNA binding transcription factor activity
24 1	7968658	NM_181503 // Hs.294041 // adipose tissue ascites bladder blood bone bone marrow b	NM_181503 // EXOSC8 // exosome component 8 // 13q13.1 // 11340 /// ENST00000389704 // E	EXOSC8	NM_181503	NM_181503 // GO:0006364 // rRNA processing // inferred from electronic annotation ///	NM_181503 // GO:0000178 // exosome (RNase complex) // inferred from electronic annotati	NM_181503 // GO:0000175 // 3'-5'-exoribonuclease activity // inferred from electronic a
24 2	8127393	NM_001142800 // Hs.25067 // bone brain embryonic tissue eye kidney mammary gland	NM_001142800 // EYS // eyes shut homolog (Drosophila) // 6q12 // 346007 /// ENST0000050	EYS	NM_001142800	NM_001142800 // GO:0007601 // visual perception // inferred from electronic annotation	NM_001142800 // GO:0005576 // extracellular region // inferred from electronic annotati	NM_001142800 // GO:0005509 // calcium ion binding // inferred from electronic annotatio
24 3	7923917	NM_005449 // Hs.723317 // adipose tissue blood bone brain connective tissue esopha	NM_005449 // FAIM3 // Fas apoptotic inhibitory molecule 3 // 1q32.1 // 9214 /// NM_0011	FAIM3	NM_005449	NM_005449 // GO:0006916 // anti-apoptosis // traceable author statement /// NM_005449	NM_005449 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0054	---

24 4	7985488	BC112329 // Hs.80624 // adipose tissue ascites bladder blood bone marrow brain co	BC112329 // FAM103A1 // family with sequence similarity 103, member A1 // 15q25.2 // 83	FAM103A1	BC112329	---	---	---
24 5	8064557	AK293638 // Hs.29341 // adrenal gland ascites bladder blood bone bone marrow brai	AK293638 // FAM113A // family with sequence similarity 113, member A // 20p13 // 64773	FAM113A	AK293638	---	---	AK293638 // GO:0005515 // protein binding // inferred from physical interaction /// AK
24 6	8082066	NM_014367 // Hs.584881 // adrenal gland bladder blood bone bone marrow brain conn	NM_014367 // FAM162A // family with sequence similarity 162, member A // 3q21.1 // 2635	FAM162A	NM_014367	---	NM_014367 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0143	---
24 7	7973918	NM_173607 // Hs.446357 // adipose tissue adrenal gland ascites bladder blood bone	NM_173607 // FAM177A1 // family with sequence similarity 177, member A1 // 14q13.2 // 2	FAM177A1	NM_173607	---	---	---
24 8	7963203	NM_001145475 // Hs.133187 // brain connective tissue lymph node testis normal soft	NM_001145475 // FAM186A // family with sequence similarity 186, member A // 12q13.12 //	FAM186A	NM_001145475	---	---	---
24 9	8096425	NM_001145065 // Hs.654735 // brain connective tissue embryonic tissue intestine kid	NM_001145065 // FAM190A // family with sequence similarity 190, member A // 4q22.1 // 4	FAM190A	NM_001145065	---	---	---
25 0	8091469	NM_152394 // Hs.147128 // brain prostate testis normal fetus adult /// ENST0000029	NM_152394 // FAM194A // family with sequence similarity 194, member A // 3q25.1 // 1318	FAM194A	NM_152394	---	---	---
25 1	7971400	NM_182542 // Hs.668747 // adrenal gland brain connective tissue embryonic tissue ey	NM_182542 // FAM194B // family with sequence similarity 194, member B // 13q14.13 // 22	FAM194B	NM_182542	---	---	---
25 2	8121605	NM_153036 // Hs.350750 // placenta normal adult /// ENST00000368597 // Hs.350750 // p	NM_153036 // FAM26D // family with sequence similarity 26, member D // 6q22.1 // 221301	FAM26D	NM_153036	---	NM_153036 // GO:0016020 // membrane // inferred from electronic annotation /// NM_1530	---
25 3	8095819	AK090914 // Hs.109590 // adipose tissue ascites bladder blood bone bone marrow br	NM_001136570 // FAM47E // family with sequence similarity 47, member E // 4q21.1 // 100	FAM47E	NM_001136570	AK090914 // GO:0005975 // carbohydrate metabolic process // inferred from electronic an	AK090914 // GO:0005624 // membrane fraction // traceable author statement /// AK090914	AK090914 // GO:0003824 // catalytic activity // inferred from electronic annotation //

25 4	7944023	NM_182495 // Hs.446760 // muscle trachea normal adult /// ENST00000389586 // Hs.4467	NM_182495 // FAM55B // family with sequence similarity 55, member B // 11q23.3 // 12040	FAM55B	NM_182495	---	NM_182495 // GO:0016020 // membrane // inferred from electronic annotation /// NM_1824	---
25 5	7962146	NM_001135811 // Hs.505154 // adipose tissue adrenal gland ascites bladder blood bo	NM_001135811 // FAM60A // family with sequence similarity 60, member A // 12p11 // 5851	FAM60A	NM_001135811	---	---	---
25 6	8156090	NR_026851 // Hs.215235 // testis normal /// AK128229 // Hs.215235 // testis normal	NR_026851 // FAM75D5 // FAM75-like protein FLJ46321 pseudogene // 9q21.32 // 347127 ///	FAM75D5	NR_026851	---	---	---
25 7	8041519	NM_001170792 // Hs.591566 // adrenal gland blood brain connective tissue embryonic	NM_001170792 // FAM82A1 // family with sequence similarity 82, member A1 // 2p22.2 // 1	FAM82A1	NM_001170792	---	NM_001170792 // GO:0000922 // spindle pole // inferred from electronic annotation ///	NM_001170792 // GO:0005488 // binding // inferred from electronic annotation /// NM_00
25 8	8171260	NM_174951 // Hs.382062 // normal fetus /// NM_001171186 // Hs.382062 // normal fetus	NM_174951 // FAM9A // family with sequence similarity 9, member A // Xp22.32 // 171482	FAM9A	NM_174951	---	NM_174951 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_17495	---
25 9	7974166	NM_020937 // Hs.509229 // brain connective tissue embryonic tissue intestine kidney	NM_020937 // FANCM // Fanconi anemia, complementation group M // 14q21.2 // 57697 /// E	FANCM	NM_020937	NM_020937 // GO:0006281 // DNA repair // inferred from electronic annotation /// ENST0	NM_020937 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_02093	NM_020937 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
26 0	8150002	NM_172366 // Hs.659190 // bone marrow brain connective tissue eye kidney liver lu	NM_172366 // FBXO16 // F-box protein 16 // 8p21.1 // 157574 /// ENST00000380254 // FBXO	FBXO16	NM_172366	AK098243 // GO:0006355 // regulation of transcription, DNA-dependent // inferred by cur	AK098243 // GO:0005622 // intracellular // inferred from electronic annotation /// AK0	AK098243 // GO:0003677 // DNA binding // inferred from direct assay /// AK098243 // GO
26 1	8033420	NM_002002 // Hs.465778 // blood brain intestine lymph node spleen thymus tonsil	NM_002002 // FCER2 // Fc fragment of IgE, low affinity II, receptor for (CD23) // 19p13	FCER2	NM_002002	NM_002002 // GO:0002925 // positive regulation of humoral immune response mediated by c	NM_002002 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_002002 // GO:0004872 // receptor activity // inferred from electronic annotation //
26 2	7921298	NM_030764 // Hs.437393 // blood connective tissue lung lymph lymph node mouth spl	NM_030764 // FCRL2 // Fc receptor-like 2 // 1q21 // 79368 /// ENST00000361516 // FCRL2	FCRL2	NM_030764	NM_030764 // GO:0007267 // cell-cell signaling // non-traceable author statement /// E	NM_030764 // GO:0005625 // soluble fraction // traceable author statement /// NM_03076	NM_030764 // GO:0004872 // receptor activity // inferred from electronic annotation //

26 3	8152742	NM_001039112 // Hs.632058 // brain pharynx head and neck tumor normal fetus adult	NM_001039112 // FER1L6 // fer-1-like 6 (C. elegans) // 8q24.1 // 654463 /// ENST0000039	FER1L6	NM_001039112	---	NM_001039112 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0	---
26 4	8097910	NM_005141 // Hs.300774 // bladder blood brain cervix embryonic tissue eye heart	NM_005141 // FGB // fibrinogen beta chain // 4q28 // 2244 /// NM_001184741 // FGB // fi	FGB	NM_005141	NM_005141 // GO:0007165 // signal transduction // inferred from electronic annotation	NM_005141 // GO:0005576 // extracellular region // not recorded /// NM_005141 // GO:00	NM_005141 // GO:0005102 // receptor binding // inferred from electronic annotation ///
26 5	7965541	NM_018351 // Hs.506381 // bone marrow brain cervix connective tissue embryonic tiss	NM_018351 // FGD6 // FYVE, RhoGEF and PH domain containing 6 // 12q22 // 55785 /// ENST	FGD6	NM_018351	NM_018351 // GO:0007010 // cytoskeleton organization // inferred from sequence or struc	NM_018351 // GO:0001726 // ruffle // inferred from sequence or structural similarity /	NM_018351 // GO:0005085 // guanyl-nucleotide exchange factor activity // inferred from
26 6	8139632	NM_001042762 // Hs.137516 // adrenal gland blood bone bone marrow brain cervix co	NM_001042762 // FIGNL1 // fidgetin-like 1 // 7p12.1 // 63979 /// NM_022116 // FIGNL1 //	FIGNL1	NM_001042762	NM_001042762 // GO:0046034 // ATP metabolic process // inferred from sequence or struct	---	NM_001042762 // GO:0000166 // nucleotide binding // inferred from electronic annotation
26 7	8089112	NM_182909 // Hs.104672 // adipose tissue ascites bladder bone brain connective tis	NM_182909 // FILIP1L // filamin A interacting protein 1-like // 3q12.1 // 11259 /// NM_	FILIP1L	NM_182909	NM_182909 // GO:0008150 // biological_process // no biological data available /// NM_0	NM_182909 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_18290	NM_182909 // GO:0003674 // molecular_function // no biological data available /// NM_0
26 8	8134460	AK054626 // Hs.632300 // adrenal gland brain pancreas prostate spleen testis germ	AK054626 // FLJ30064 // hypothetical protein LOC644975 // 7q21.3 // 644975	FLJ30064	AK054626	---	---	---
26 9	8076813	BC041833 // Hs.632786 // intestine testis colorectal tumor normal adult	BC041833 // FLJ32756 // hypothetical LOC642757 // 22q13.31 // 642757	FLJ32756	BC041833	---	---	---
27 0	8049957	AK095698 // Hs.653239 // brain embryonic tissue liver uterus normal embryoid body	AK095698 // FLJ38379 // hypothetical FLJ38379 // 2q37.3 // 285097	FLJ38379	AK095698	---	---	---
27 1	8047492	AK297413 // Hs.686898 // brain nerve ovary testis trachea germ cell tumor normal	AK297413 // FLJ39061 // hypothetical protein FLJ39061 // 2q33.1 // 165057 /// AK295603	FLJ39061	AK297413	---	---	---
27 2	7960436	AK126822 // Hs.586786 // brain embryonic tissue lung mammary gland mouth placenta	AK126822 // FLJ44874 // FLJ44874 protein // 12p13.31 // 399990	FLJ44874	AK126822	---	---	---
27 3	8105731	AK127903 // Hs.673805 // spleen normal fetus	AK127903 // FLJ46010 // FLJ46010 protein // 5q12.3 // 401191	FLJ46010	AK127903	---	---	---

27 4	8065071	NM_198391 // Hs.41296 // adrenal gland bladder brain connective tissue ear embryo	NM_198391 // FLRT3 // fibronectin leucine rich transmembrane protein 3 // 20p11 // 2376	FLRT3	NM_198391	NM_198391 // GO:0007155 // cell adhesion // inferred from electronic annotation /// NM	NM_198391 // GO:0005578 // proteinaceous extracellular matrix // non-traceable author s	NM_198391 // GO:0005057 // receptor signaling protein activity // non-traceable author
27 5	7907286	NM_002021 // Hs.1424 // brain embryonic tissue eye heart intestine kidney liver	NM_002021 // FMO1 // flavin containing monooxygenase 1 // 1q24.3 // 2326 /// ENST0000003	FMO1	NM_002021	NM_002021 // GO:0006082 // organic acid metabolic process // inferred from direct assay	NM_002021 // GO:0005783 // endoplasmic reticulum // inferred from electronic annotation	NM_002021 // GO:0004497 // monooxygenase activity // inferred from electronic annotation
27 6	7903530	NM_001144937 // Hs.258253 // mammary gland placenta testis breast (mammary gland) tu	NM_001144937 // FNDC7 // fibronectin type III domain containing 7 // 1p13.3 // 163479 /	FNDC7	NM_001144937	---	NM_001144937 // GO:0005576 // extracellular region // inferred from electronic annotation	---
27 7	8080994	NM_001124759 // Hs.722640 // --- /// ENST00000308062 // Hs.722640 // --- /// ENST0000004	NM_001124759 // FRG2C // FSHD region gene 2 family, member C // 3p12.3 // 100288801 /// ENST0000004	FRG2C	NM_001124759	---	NM_001124759 // GO:0005634 // nucleus // inferred from electronic annotation /// ENST0	---
27 8	7987426	NM_152597 // Hs.129598 // brain embryonic tissue heart kidney mammary gland ovary	NM_152597 // FSIP1 // fibrous sheath interacting protein 1 // 15q14 // 161835 /// ENST0	FSIP1	NM_152597	---	---	NM_152597 // GO:0005515 // protein binding // inferred from electronic annotation ///
27 9	8121152	NM_006581 // Hs.49117 // brain connective tissue eye kidney lung muscle pancreas	NM_006581 // FUT9 // fucosyltransferase 9 (alpha (1,3) fucosyltransferase) // 6q16 // 1	FUT9	NM_006581	NM_006581 // GO:0005975 // carbohydrate metabolic process // traceable author statement /// NM_006581	NM_006581 // GO:0005794 // Golgi apparatus // traceable author statement /// NM_006581	NM_006581 // GO:0008417 // fucosyltransferase activity // traceable author statement /
28 0	8100109	NM_000807 // Hs.116250 // brain connective tissue intestine liver lung liver tumor	NM_000807 // GABRA2 // gamma-aminobutyric acid (GABA) A receptor, alpha 2 // 4p12 // 25	GABRA2	NM_000807	NM_000807 // GO:0001505 // regulation of neurotransmitter levels // inferred from mutant	NM_000807 // GO:0005886 // plasma membrane // inferred from electronic annotation ///	NM_000807 // GO:0004872 // receptor activity // inferred from electronic annotation //
28 1	8175696	NM_000808 // Hs.123024 // brain connective tissue larynx testis head and neck tumor	NM_000808 // GABRA3 // gamma-aminobutyric acid (GABA) A receptor, alpha 3 // Xq28 // 25	GABRA3	NM_000808	NM_000808 // GO:0006810 // transport // traceable author statement /// NM_000808 // GO	NM_000808 // GO:0005886 // plasma membrane // inferred from electronic annotation ///	NM_000808 // GO:0004872 // receptor activity // inferred from electronic annotation //
28 2	8137437	NR_033169 // Hs.647077 // brain testis normal fetus adult /// NM_145292 // Hs.64707	NR_033169 // GALNTL5 // UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglactos	GALNTL5	NR_033169	---	NR_033169 // GO:0000139 // Golgi membrane // inferred from electronic annotation /// N	NR_033169 // GO:0016757 // transferase activity, transferring glycosyl groups // infer

28 3	8044236	NM_181453 // Hs.436505 // ascites bladder blood bone bone marrow brain cervix co	NM_181453 // GCC2 // GRIP and coiled-coil domain containing 2 // 2q12.3 // 9648 /// NR_	GCC2	NM_181453	NM_181453 // GO:0006622 // protein targeting to lysosome // inferred from mutant phenot	NM_181453 // GO:0000139 // Golgi membrane // inferred from electronic annotation /// N	NM_181453 // GO:0005515 // protein binding // inferred from physical interaction /// N
28 4	8096027	NR_026555 // Hs.104215 // connective tissue eye prostate normal prostate cancer so	NR_026555 // GDEP // gene differentially expressed in prostate // 4q21.1 // 118425 ///	GDEP	NR_026555	---	---	---
28 5	8151032	NM_003878 // Hs.78619 // adrenal gland ascites blood bone bone marrow brain cervi	NM_003878 // GGH // gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	GGH	NM_003878	NM_003878 // GO:0006541 // glutamine metabolic process // inferred from electronic anno	NM_003878 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_003878 // GO:0008238 // exopeptidase activity // traceable author statement /// NM_
28 6	8105121	NM_000163 // Hs.125180 // adipose tissue adrenal gland bladder bone brain connecti	NM_000163 // GHR // growth hormone receptor // 5p13-p12 // 2690 /// ENST00000230882 //	GHR	NM_000163	NM_000163 // GO:0000187 // activation of MAPK activity // inferred from sequence or str	NM_000163 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_000163 // GO:0004872 // receptor activity // inferred from electronic annotation //
28 7	7902518	NM_017655 // Hs.659356 // bladder brain connective tissue intestine kidney liver	NM_017655 // GIPC2 // GIPC PDZ domain containing family, member 2 // 1p31.1 // 54810 //	GIPC2	NM_017655	---	NM_017655 // GO:0005737 // cytoplasm // inferred from electronic annotation /// ENST00	NM_017655 // GO:0005515 // protein binding // inferred from electronic annotation ///
28 8	8101256	NM_033214 // Hs.98008 // brain prostate testis germ cell tumor normal fetus adult	NM_033214 // GK2 // glycerol kinase 2 // 4q13 // 2712 /// ENST00000358842 // GK2 // gly	GK2	NM_033214	NM_033214 // GO:0005975 // carbohydrate metabolic process // inferred from electronic a	NM_033214 // GO:0005737 // cytoplasm // non-traceable author statement /// NM_033214 /	NM_033214 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
28 9	8091120	NR_033289 // Hs.135904 // adrenal gland ascites blood bone brain cervix connectiv	NR_033289 // GK5 // glycerol kinase 5 (putative) // 3q23 // 256356 /// NM_001039547 //	GK5	NR_033289	NR_033289 // GO:0005975 // carbohydrate metabolic process // inferred from electronic a	---	NR_033289 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
29 0	8052753	NM_182536 // Hs.16757 // connective tissue heart lung stomach chondrosarcoma gastr	NM_182536 // GKN2 // gastroke 2 // 2p13.3 // 200504 /// ENST00000328895 // GKN2 // ga	GKN2	NM_182536	---	NM_182536 // GO:0005576 // extracellular region // inferred from electronic annotation	---
29 1	8103778	NM_006529 // Hs.413099 // blood brain connective tissue lymph node mammary gland t	NM_006529 // GLRA3 // glycine receptor, alpha 3 // 4q33-q34 // 8001 /// NM_001042543 //	GLRA3	NM_006529	NM_006529 // GO:0006811 // ion transport // inferred from electronic annotation /// NM	NM_006529 // GO:0005886 // plasma membrane // inferred from electronic annotation ///	NM_006529 // GO:0004872 // receptor activity // inferred from electronic annotation //

29 2	8098006	NM_000824 // Hs.32973 // adrenal gland bone brain connective tissue eye heart kid	NM_000824 // GLRB // glycine receptor, beta // 4q31.3 // 2743 /// NM_001166060 // GLRB	GLRB	NM_000824	NM_000824 // GO:0001964 // startle response // inferred from mutant phenotype /// NM_0	NM_000824 // GO:0005624 // membrane fraction // inferred from electronic annotation //	NM_000824 // GO:0004872 // receptor activity // inferred from electronic annotation //
29 3	7948354	NM_145016 // Hs.254271 // bone marrow brain embryonic tissue leukemia lymphoma nor	NM_145016 // GLYATL2 // glycine-N-acyltransferase-like 2 // 11q12.1 // 219970 /// ENST0	GLYATL2	NM_145016	---	NM_145016 // GO:0005739 // mitochondrion // inferred from electronic annotation /// EN	NM_145016 // GO:0008415 // acyltransferase activity // inferred from electronic annotat
29 4	8020164	NM_182978 // Hs.136295 // bladder brain connective tissue embryonic tissue eye hea	NM_182978 // GNAL // guanine nucleotide binding protein (G protein), alpha activating a	GNAL	NM_182978	NM_182978 // GO:0007165 // signal transduction // traceable author statement /// NM_18	NM_182978 // GO:0005886 // plasma membrane // not recorded /// NM_002071 // GO:0005886	NM_182978 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
29 5	8080419	NM_206825 // Hs.313544 // adrenal gland ascites bladder blood bone bone marrow br	NM_206825 // GNL3 // guanine nucleotide binding protein-like 3 (nucleolar) // 3p21.1 //	GNL3	NM_206825	NM_206825 // GO:0042127 // regulation of cell proliferation // inferred from sequence o	NM_206825 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_206825 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
29 6	7985472	NR_003246 // Hs.498345 // bladder bone brain connective tissue eye heart kidney	NR_003246 // GOLGA6L5 // golgin A6 family-like 5 (pseudogene) // 15q25.2 // 374650 ///	GOLGA6L5	NR_003246	---	---	---
29 7	8089930	NM_004487 // Hs.213389 // adipose tissue adrenal gland ascites bladder blood bone	NM_004487 // GOLGB1 // golgin B1 // 3q13 // 2804 /// ENST00000340645 // GOLGB1 // golgi	GOLGB1	NM_004487	NM_004487 // GO:0007030 // Golgi organization // traceable author statement /// ENST00	NM_004487 // GO:0000139 // Golgi membrane // inferred from electronic annotation /// N	NM_004487 // GO:0005515 // protein binding // inferred from physical interaction /// E
29 8	8165663	AK172782 // Hs.42586 // adipose tissue adrenal gland ascites blood bone bone marro	AK172782 // GPAM // glycerol-3-phosphate acyltransferase, mitochondrial // 10q25.2 // 5	GPAM	AK172782	AK172782 // GO:0006631 // fatty acid metabolic process // inferred from electronic anno	AK172782 // GO:0005739 // mitochondrion // inferred from electronic annotation /// AK1	AK172782 // GO:0004366 // glycerol-3-phosphate O-acyltransferase activity // inferred f
29 9	8016077	NR_036474 // Hs.463129 // adipose tissue adrenal gland ascites bladder blood bone	NR_036474 // GPATCH8 // G patch domain containing 8 // 17q21.31 // 23131 /// NM_0010029	GPATCH8	NR_036474	NR_036474 // GO:0008150 // biological_process // no biological data available /// NM_0	NR_036474 // GO:0005575 // cellular_component // no biological data available /// NR_0	NR_036474 // GO:0003674 // molecular_function // no biological data available /// NR_0
30 0	8058450	NM_005279 // Hs.184907 // adipose tissue bone marrow brain cervix connective tissue	NM_005279 // GPR1 // G protein-coupled receptor 1 // 2q33.3 // 2825 /// NM_001098199 //	GPR1	NM_005279	NM_005279 // GO:0007186 // G-protein coupled receptor protein signaling pathway // trac	NM_005279 // GO:0005886 // plasma membrane // inferred from electronic annotation ///	NM_005279 // GO:0004872 // receptor activity // inferred from electronic annotation //
30 1	8120124	NM_153839 // Hs.724860 // brain lung skin normal /// ENST00000467205 // Hs.724860 //	NM_153839 // GPR111 // G protein-coupled receptor 111 // 6p12.3 // 222611 /// ENST000000	GPR111	NM_153839	NM_153839 // GO:0007186 // G-protein coupled receptor protein signaling pathway	NM_153839 // GO:0005886 // plasma membrane // inferred from electronic	NM_153839 // GO:0004930 // G-protein coupled receptor activity // inferred from electro

						// trac	annotation ///	
30 2	8030731	NM_001506 // Hs.515555 // placenta normal adult /// ENST00000270590 // Hs.515555 // p	NM_001506 // GPR32 // G protein-coupled receptor 32 // 19q13.3 // 2854 /// ENST00000270	GPR32	NM_001506	NM_001506 // GO:0007186 // G-protein coupled receptor protein signaling pathway // trac	NM_001506 // GO:0005886 // plasma membrane // inferred from electronic annotation ///	NM_001506 // GO:0004872 // receptor activity // inferred from electronic annotation //
30 3	8091515	NM_023915 // Hs.591292 // adrenal gland bladder brain embryonic tissue eye heart	NM_023915 // GPR87 // G protein-coupled receptor 87 // 3q24 // 53836 /// ENST0000026084	GPR87	NM_023915	NM_023915 // GO:0008150 // biological_process // no biological data available /// ENST	NM_023915 // GO:0005886 // plasma membrane // inferred from electronic annotation ///	NM_023915 // GO:0004872 // receptor activity // inferred from electronic annotation //
30 4	8105348	NM_001008397 // Hs.289044 // ascites bladder bone bone marrow brain cervix connec	NM_001008397 // GPX8 // glutathione peroxidase 8 (putative) // 5q11.2 // 493869 /// ENS	GPX8	NM_001008397	NM_001008397 // GO:0006979 // response to oxidative stress // inferred from electronic	NM_001008397 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0	NM_001008397 // GO:0004602 // glutathione peroxidase activity // inferred from electron
30 5	8169717	NM_007325 // Hs.377070 // adrenal gland brain embryonic tissue eye kidney liver l	NM_007325 // GRIA3 // glutamate receptor, ionotropic, AMPA 3 // Xq25 // 2892 /// NM_00	GRIA3	NM_007325	NM_007325 // GO:0001919 // regulation of receptor recycling // inferred from electronic	NM_007325 // GO:0005624 // membrane fraction // inferred from electronic annotation //	NM_007325 // GO:0004872 // receptor activity // inferred from electronic annotation //
30 6	8064928	NM_017545 // Hs.193640 // brain kidney liver mammary gland pancreas liver tumor n	NM_017545 // HAO1 // hydroxyacid oxidase (glycolate oxidase) 1 // 20p12 // 54363 /// EN	HAO1	NM_017545	NM_017545 // GO:0001561 // fatty acid alpha-oxidation // inferred from direct assay //	NM_017545 // GO:0005777 // peroxisome // traceable author statement /// ENST0000037878	NM_017545 // GO:0003973 // (S)-2-hydroxy-acid oxidase activity // inferred from direct
30 7	8115455	NM_012206 // Hs.129711 // brain eye intestine kidney uterus colorectal tumor kidn	NM_012206 // HAVCR1 // hepatitis A virus cellular receptor 1 // 5q33.2 // 26762 /// NM_	HAVCR1	NM_012206	NM_012206 // GO:0044419 // interspecies interaction between organisms // inferred from	NM_012206 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0122	NM_012206 // GO:0004872 // receptor activity // inferred from electronic annotation //
30 8	8017186	NM_022070 // Hs.591183 // adrenal gland ascites bone bone marrow brain cervix con	NM_022070 // HEATR6 // HEAT repeat containing 6 // 17q23.1 // 63897 /// ENST00000184956	HEATR6	NM_022070	---	---	NM_022070 // GO:0005488 // binding // inferred from electronic annotation /// ENST0000
30 9	7943197	NM_001098672 // Hs.669645 // mouth muscle pharynx head and neck tumor normal adult	NM_001098672 // HEPHL1 // hephaestin-like 1 // 11q21 // 341208 /// ENST00000315765 // H	HEPHL1	NM_001098672	NM_001098672 // GO:0006811 // ion transport // inferred from electronic annotation ///	NM_001098672 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0	NM_001098672 // GO:0005507 // copper ion binding // inferred from electronic annotation

31 0	8088285	NM_003865 // Hs.171980 // intestine lung ovary uterus germ cell tumor non-neoplasia	NM_003865 // HESX1 // HESX homeobox 1 // 3p14.3 // 8820 /// ENST00000295934 // HESX1 //	HESX1	NM_003865	NM_003865 // GO:0006355 // regulation of transcription, DNA-dependent // inferred from	NM_003865 // GO:0005634 // nucleus // inferred from electronic annotation /// ENST0000	NM_003865 // GO:0003677 // DNA binding // traceable author statement /// NM_003865 //
31 1	7917612	NM_001017975 // Hs.454818 // brain embryonic tissue muscle testis uterus germ cell	NM_001017975 // HFM1 // HFM1, ATP-dependent DNA helicase homolog (S. cerevisiae) // 1p2	HFM1	NM_001017975	---	---	NM_001017975 // GO:0000166 // nucleotide binding // inferred from electronic annotation
31 2	8178833	NM_002120 // Hs.1802 // blood brain connective tissue heart intestine kidney lung	NM_002120 // HLA-DOB // major histocompatibility complex, class II, DO beta // 6p21.3 /	HLA-DOB	NM_002120	NM_002120 // GO:0002504 // antigen processing and presentation of peptide or polysaccha	NM_002120 // GO:0005764 // lysosome // inferred from direct assay /// NM_002120 // GO:	NM_002120 // GO:0032395 // MHC class II receptor activity // traceable author statement
31 3	8178826	ENST00000399084 // Hs.409934 // adipose tissue adrenal gland bladder blood bone bo	ENST00000399084 // HLA-DQB1 // major histocompatibility complex, class II, DQ beta 1 //	HLA-DQB1	ENST00000399084	ENST00000399084 // GO:0002504 // antigen processing and presentation of peptide or poly	ENST00000399084 // GO:0005622 // intracellular // inferred from electronic annotation	ENST00000399084 // GO:0005515 // protein binding // inferred from electronic annotation
31 4	8180003	---	NM_022555 // HLA-DRB3 // major histocompatibility complex, class II, DR beta 3 // 6p21.	HLA-DRB3	NM_022555	NM_022555 // GO:0002504 // antigen processing and presentation of peptide or polysaccha	NM_022555 // GO:0005765 // lysosomal membrane // inferred from direct assay /// NM_022	NM_022555 // GO:0032395 // MHC class II receptor activity // non-traceable author state
31 5	7899898	NM_145205 // Hs.568628 // brain testis germ cell tumor normal fetus adult /// NM_1	NM_145205 // HMGB4 // high-mobility group box 4 // 1p35.1 // 127540 /// NR_033264 // HM	HMGB4	NM_145205	---	NM_145205 // GO:0005634 // nucleus // inferred from electronic annotation /// NR_03326	NM_145205 // GO:0003677 // DNA binding // inferred from electronic annotation /// NR_0
31 6	8173812	NM_030763 // Hs.282204 // adrenal gland bone bone marrow brain cervix ear embryon	NM_030763 // HMGN5 // high-mobility group nucleosome binding domain 5 // Xq13.3 // 7936	HMGN5	NM_030763	NM_030763 // GO:0006355 // regulation of transcription, DNA-dependent // non-traceable	NM_030763 // GO:0000785 // chromatin // inferred from electronic annotation /// NM_030	NM_030763 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
31 7	8080991	NM_194247 // Hs.516539 // adipose tissue adrenal gland ascites bladder blood bone	NM_194247 // HNRNPA3 // heterogeneous nuclear ribonucleoprotein A3 // 2q31.2 // 220988	HNRNPA3	NM_194247	NM_194247 // GO:0006397 // mRNA processing // inferred from electronic annotation ///	NM_194247 // GO:0005634 // nucleus // inferred from direct assay /// NM_194247 // GO:0	NM_194247 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
31 8	7912552	NM_001013631 // Hs.502617 // uterus uterine tumor /// ENST00000317869 // Hs.502617 //	NM_001013631 // HNRNPCL1 // heterogeneous nuclear ribonucleoprotein C-like 1 // 1p36.21	HNRNPCL1	NM_001013631	---	NM_001013631 // GO:0030529 // ribonucleoprotein complex // inferred from electronic ann	NM_001013631 // GO:0000166 // nucleotide binding // inferred from electronic annotation

31 9	7955887	---	NM_018953 // HOXC5 // homeobox C5 // 12q13.3 // 3222 /// NR_003084 // HOXC5 // homeobox	HOXC5	NM_018953	NM_018953 // GO:0006357 // regulation of transcription from RNA polymerase II promoter	NM_018953 // GO:0005634 // nucleus // inferred from electronic annotation /// NR_00308	NM_018953 // GO:0003700 // sequence-specific DNA binding transcription factor activity
32 0	8176681	NR_003509 // Hs.592255 // testis normal /// NR_003510 // Hs.662281 // brain connectiv	NR_003509 // HSFY2 // heat shock transcription factor, Y linked 2 // Yq11.222 // 159119	HSFY2	NR_003509	NR_003509 // GO:0006355 // regulation of transcription, DNA-dependent // inferred from	NR_003509 // GO:0005634 // nucleus // inferred from electronic annotation /// NR_00350	NR_003509 // GO:0003700 // sequence-specific DNA binding transcription factor activity
32 1	7972420	AY956767 // Hs.627166 // ---	AY956767 // HSP90AB6P // heat shock protein 90kDa alpha (cytosolic), class B member 6 (	HSP90AB6P	AY956767	---	---	---
32 2	7986407	AY956768 // Hs.656611 // brain lung prostate normal prostate cancer adult /// ENST	AY956768 // HSP90B2P // heat shock protein 90kDa beta (Grp94), member 2 (pseudogene) //	HSP90B2P	AY956768	AY956768 // GO:0006457 // protein folding // inferred from electronic annotation /// A	AY956768 // GO:0005783 // endoplasmic reticulum // inferred from electronic annotation	AY956768 // GO:0005524 // ATP binding // inferred from electronic annotation /// AY956
32 3	8105323	NM_006308 // Hs.41707 // brain connective tissue eye heart liver lung muscle pro	NM_006308 // HSPB3 // heat shock 27kDa protein 3 // 5q11.2 // 8988 /// ENST00000302005	HSPB3	NM_006308	NM_006308 // GO:0006986 // response to unfolded protein // traceable author statement	NM_006308 // GO:0005634 // nucleus // inferred from direct assay /// NM_006308 // GO:0	---
32 4	8170166	NM_014500 // Hs.204475 // adrenal gland ascites bladder blood bone brain cervix	NM_014500 // HTATSF1 // HIV-1 Tat specific factor 1 // Xq26.3 // 27336 /// NM_001163280	HTATSF1	NM_014500	NM_014500 // GO:0006357 // regulation of transcription from RNA polymerase II promoter	NM_014500 // GO:0005634 // nucleus // inferred from direct assay /// NM_014500 // GO:0	NM_014500 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
32 5	8095435	NM_002159 // Hs.250959 // eye liver muscle salivary gland testis head and neck tum	NM_002159 // HTN1 // histatin 1 // 4q13 // 3346 /// ENST00000246896 // HTN1 // histatin	HTN1	NM_002159	NM_002159 // GO:0031214 // biomineral tissue development // inferred from electronic an	NM_002159 // GO:0005576 // extracellular region // non-traceable author statement ///	NM_002159 // GO:0005515 // protein binding // inferred from physical interaction /// E
32 6	8081067	NM_000866 // Hs.248136 // bone marrow pancreas placenta normal adult /// ENST0000003	NM_000866 // HTR1F // 5-hydroxytryptamine (serotonin) receptor 1F // 3p12 // 3355 /// E	HTR1F	NM_000866	NM_000866 // GO:0007187 // G-protein signaling, coupled to cyclic nucleotide second mes	NM_000866 // GO:0005886 // plasma membrane // not recorded /// NM_000866 // GO:0005887	NM_000866 // GO:0004872 // receptor activity // inferred from electronic annotation //
32 7	8135827	NM_012269 // Hs.28673 // placenta germ cell tumor normal fetus adult /// ENST0000002	NM_012269 // HYAL4 // hyaluronoglucosaminidas e 4 // 7q31.3 // 23553 /// ENST00000223026	HYAL4	NM_012269	NM_012269 // GO:0005975 // carbohydrate metabolic process // inferred from electronic a	NM_012269 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0122	NM_012269 // GO:0004415 // hyaluronoglucosaminidase activity // inferred from electron

32 8	8047702	NM_012092 // Hs.56247 // blood brain heart lung pharynx thymus thyroid uterus g	NM_012092 // ICOS // inducible T-cell co-stimulator // 2q33 // 29851 // ENST0000031638	ICOS	NM_012092	NM_012092 // GO:0006955 // immune response // non-traceable author statement /// ENST0	NM_012092 // GO:0005576 // extracellular region // inferred from electronic annotation	---
32 9	8070720	NM_015259 // Hs.14155 // adrenal gland ascites bladder blood brain connective tiss	NM_015259 // ICOSLG // inducible T-cell co-stimulator ligand // 21q22.3 // 23308 // EN	ICOSLG	NM_015259	NM_015259 // GO:0006952 // defense response // non-traceable author statement /// NM_0	NM_015259 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0152	NM_015259 // GO:0005102 // receptor binding // traceable author statement /// ENST0000
33 0	8154627	NM_024013 // Hs.37026 // --- /// NM_006900 // Hs.533471 // --- /// BC112300 // Hs.37026	NM_024013 // IFNA1 // interferon, alpha 1 // 9p22 // 3439 /// NM_006900 // IFNA13 // in	IFNA1	NM_024013	NM_006900 // GO:0006952 // defense response // inferred from electronic annotation ///	NM_006900 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_006900 // GO:0005125 // cytokine activity // inferred from electronic annotation //
33 1	8160419	NM_006900 // Hs.533471 // --- /// BC112002 // Hs.37026 // --- /// BC093988 // Hs.533471	NM_006900 // IFNA13 // interferon, alpha 13 // 9p22 // 3447 /// BC112002 // IFNA1 // in	IFNA13	NM_006900	NM_006900 // GO:0006952 // defense response // inferred from electronic annotation ///	NM_006900 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_006900 // GO:0005125 // cytokine activity // inferred from electronic annotation //
33 2	8160422	NM_000605 // Hs.211575 // --- /// ENST00000380206 // Hs.211575 // --- /// M54886 // Hs.	NM_000605 // IFNA2 // interferon, alpha 2 // 9p22 // 3440 /// ENST00000380206 // IFNA2	IFNA2	NM_000605	NM_000605 // GO:0006917 // induction of apoptosis // traceable author statement /// NM	NM_000605 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_000605 // GO:0005125 // cytokine activity // inferred from electronic annotation //
33 3	8160360	NM_002176 // Hs.93177 // --- /// ENST00000380232 // Hs.93177 // --- /// M28622 // Hs.93	NM_002176 // IFNB1 // interferon, beta 1, fibroblast // 9p21 // 3456 /// ENST0000038023	IFNB1	NM_002176	NM_002176 // GO:0006917 // induction of apoptosis // inferred from direct assay /// NM	NM_002176 // GO:0005576 // extracellular region // inferred by curator /// NM_002176 /	NM_002176 // GO:0003714 // transcription corepressor activity // inferred from direct a
33 4	7965873	NM_001111283 // Hs.160562 // adrenal gland blood bone brain connective tissue ear	NM_001111283 // IGF1 // insulin-like growth factor 1 (somatomedin C) // 12q23.2 // 3479	IGF1	NM_001111283	NM_001111283 // GO:0001501 // skeletal system development // traceable author statement	NM_001111283 // GO:0005576 // extracellular region // not recorded /// NM_001111283 //	NM_001111283 // GO:0005158 // insulin receptor binding // inferred from physical intera
33 5	8043465	BC029444 // Hs.449621 // adipose tissue adrenal gland bladder blood bone bone marr	BC029444 // IGKC // immunoglobulin kappa constant // 2p12 // 3514 /// BC029444 // IGKC	IGKC	BC029444	BC029444 // GO:0006955 // immune response // non-traceable author statement /// BC0294	BC029444 // GO:0005576 // extracellular region // not recorded /// BC029444 // GO:0005	BC029444 // GO:0003823 // antigen binding // non-traceable author statement /// BC0294
33 6	8043423	---	ENST00000390243 // IGKV4-1 // immunoglobulin kappa variable 4-1 // 2p12 // 28908	IGKV4-1	ENST00000390243	ENST00000390243 // GO:0006955 // immune response // non-traceable author statement	ENST00000390243 // GO:0005576 // extracellular region // not recorded /// ENST00000390	ENST00000390243 // GO:0003823 // antigen binding // non-traceable author statement

33 7	7923885	NM_014002 // Hs.321045 // ascites bladder blood bone bone marrow brain cervix co	NM_014002 // IKBKE // inhibitor of kappa light polypeptide gene enhancer in B-cells, ki	IKBKE	NM_014002	NM_014002 // GO:0006468 // protein phosphorylation // inferred from direct assay /// N	NM_014002 // GO:0005634 // nucleus // inferred from direct assay /// NM_014002 // GO:0	NM_014002 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
33 8	7936826	NM_022466 // Hs.501289 // adipose tissue ascites blood bone bone marrow brain con	NM_022466 // IKZF5 // IKAROS family zinc finger 5 (Pegasus) // 10q26 // 64376 /// ENST0	IKZF5	NM_022466	NM_022466 // GO:0045449 // regulation of transcription // inferred from electronic anno	NM_022466 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_022466 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
33 9	8044532	NM_014439 // Hs.166371 // intestine placenta normal fetus /// NM_173202 // Hs.166371	NM_014439 // IL1F7 // interleukin 1 family, member 7 (zeta) // 2q12-q14.1 // 27178 ///	IL1F7	NM_014439	NM_014439 // GO:0006955 // immune response // non-traceable author statement /// NM_17	NM_014439 // GO:0005576 // extracellular region // non-traceable author statement ///	NM_014439 // GO:0005125 // cytokine activity // inferred from electronic annotation //
34 0	8102707	NM_021803 // Hs.567559 // testis normal adult /// ENST00000264497 // Hs.567559 // tes	NM_021803 // IL21 // interleukin 21 // 4q26-q27 // 59067 /// ENST00000264497 // IL21 //	IL21	NM_021803	NM_021803 // GO:0006955 // immune response // inferred from electronic annotation ///	NM_021803 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_021803 // GO:0005125 // cytokine activity // inferred from electronic annotation //
34 1	8129848	NM_052962 // Hs.126891 // lung placenta testis normal adult /// NM_181309 // Hs.126	NM_052962 // IL22RA2 // interleukin 22 receptor, alpha 2 // 6q25.1 // 116379 /// NM_181	IL22RA2	NM_052962	NM_052962 // GO:0007596 // blood coagulation // inferred from electronic annotation //	NM_052962 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_052962 // GO:0004872 // receptor activity // inferred from electronic annotation //
34 2	8142332	NM_032549 // Hs.655722 // blood bone marrow brain connective tissue embryonic tissu	NM_032549 // IMP2L // IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)	IMP2L	NM_032549	NM_032549 // GO:0001541 // ovarian follicle development // inferred from electronic ann	NM_032549 // GO:0005739 // mitochondrion // inferred from electronic annotation /// NM	NM_032549 // GO:0008233 // peptidase activity // inferred from sequence or structural s
34 3	7916785	NM_005478 // Hs.251380 // --- /// ENST00000304526 // Hs.251380 // --- /// AF133816 // H	NM_005478 // INSL5 // insulin-like 5 // 1p31.3 // 10022 /// ENST00000304526 // INSL5 //	INSL5	NM_005478	NM_005478 // GO:0008150 // biological_process // no biological data available /// ENST	NM_005478 // GO:0005575 // cellular_component // no biological data available /// NM_0	NM_005478 // GO:0005179 // hormone activity // non-traceable author statement /// ENST
34 4	8089954	NM_001023570 // Hs.604110 // blood bone bone marrow brain cervix connective tissue	NM_001023570 // IQCB1 // IQ motif containing B1 // 3q13.33 3q21.1 // 9657 /// NM_001023	IQCB1	NM_001023570	NM_001023570 // GO:0045494 // photoreceptor cell maintenance // inferred from mutant ph	NM_001023570 // GO:0001750 // photoreceptor outer segment // inferred from electronic a	NM_001023570 // GO:0005516 // calmodulin binding // inferred from direct assay /// NM_
34 5	8093258	NM_032263 // Hs.591675 // adrenal gland bladder blood bone bone marrow brain conn	NM_032263 // IQCG // IQ motif containing G // 3q29 // 84223 /// NM_001134435 // IQCG //	IQCG	NM_032263	---	---	---
34 6	8168291	NM_012278 // Hs.109999 // brain heart intestine lung muscle ovary placenta prost	NM_012278 // ITGB1BP2 // integrin beta 1 binding protein (melusin) 2 // Xq12-q13.1 // 2	ITGB1BP2	NM_012278	NM_012278 // GO:0007165 // signal transduction // traceable author statement ///	NM_012278 // GO:0030018 // Z disc // inferred from electronic annotation ///	NM_012278 // GO:0005509 // calcium ion binding // inferred from electronic annotation

						NM_01	ENST00000	
34 7	8173755	NM_004867 // Hs.17109 // adipose tissue adrenal gland blood bone bone marrow brain	NM_004867 // ITM2A // integral membrane protein 2A // Xq13.3- Xq21.2 // 9452 /// NM_0011	ITM2A	NM_004867	---	NM_004867 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0048	NM_004867 // GO:0005515 // protein binding // inferred from physical interaction /// N
34 8	8114938	NM_014790 // Hs.723185 // blood bone brain connective tissue ear embryonic tissue	NM_014790 // JAKMIP2 // janus kinase and microtubule interacting protein 2 // 5q32 // 9	JAKMIP2	NM_014790	---	NM_014790 // GO:0005794 // Golgi apparatus // inferred from electronic annotation ///	---
34 9	8078196	NM_144633 // Hs.475656 // bladder brain intestine liver lung lymph node muscle s	NM_144633 // KCNH8 // potassium voltage-gated channel, subfamily H (eag-related), membe	KCNH8	NM_144633	NM_144633 // GO:0006355 // regulation of transcription, DNA- dependent // inferred from	NM_144633 // GO:0016020 // membrane // inferred from electronic annotation /// NM_1446	NM_144633 // GO:0000155 // two- component sensor activity // inferred from electronic an
35 0	8126163	NM_031460 // Hs.162282 // blood bone ear heart intestine lung pancreas placenta	NM_031460 // KCNK17 // potassium channel, subfamily K, member 17 // 6p21.1 // 89822 ///	KCNK17	NM_031460	NM_031460 // GO:0006811 // ion transport // inferred from electronic annotation /// NM	NM_031460 // GO:0016020 // membrane // non- traceable author statement /// NM_031460 //	NM_031460 // GO:0005244 // voltage-gated ion channel activity // inferred from electron
35 1	7898833	NM_001009999 // Hs.591518 // adrenal gland ascites bladder blood bone bone marrow	NM_001009999 // KDM1A // lysine (K)- specific demethylase 1A // 1p36.12 // 23028 /// NM_	KDM1A	NM_001009999	NM_001009999 // GO:0007275 // multicellular organismal development // inferred from ele	NM_001009999 // GO:0005634 // nucleus // inferred from direct assay /// NM_015013 // G	NM_001009999 // GO:0003682 // chromatin binding // inferred from direct assay /// NM_0
35 2	8121161	NM_015323 // Hs.149367 // adrenal gland ascites bladder blood bone bone marrow br	NM_015323 // KIAA0776 // KIAA0776 // 6q16.1 // 23376 /// ENST000000369278 // KIAA0776 //	KIAA0776	NM_015323	NM_015323 // GO:0031397 // negative regulation of protein ubiquitination // inferred fr	NM_015323 // GO:0005737 // cytoplasm // inferred from direct assay /// NM_015323 // GO	NM_015323 // GO:0005515 // protein binding // inferred from physical interaction /// N
35 3	8091550	NM_020776 // Hs.4045 // bone brain connective tissue eye kidney lung mammary glan	NM_020776 // KIAA1328 // KIAA1328 // 18q12.2 // 57536 /// ENST000000280020 // KIAA1328 /	KIAA1328	NM_020776	---	---	---
35 4	7943376	NM_020802 // Hs.156352 // bone brain connective tissue embryonic tissue eye heart	NM_020802 // KIAA1377 // KIAA1377 // 11q22.1 // 57562 /// ENST000000263468 // KIAA1377 /	KIAA1377	NM_020802	---	---	NM_020802 // GO:0005515 // protein binding // inferred from physical interaction /// E
35 5	8089372	NM_020890 // Hs.591308 // blood brain cervix embryonic tissue esophagus heart int	NM_020890 // KIAA1524 // KIAA1524 // 3q13.13 // 57650 /// ENST000000295746 // KIAA1524 /	KIAA1524	NM_020890	---	NM_020890 // GO:0005737 // cytoplasm // inferred from direct assay ///	NM_020890 // GO:0005515 // protein binding // inferred from physical interaction /// E

							NM_020890 // GO	
35 6	8039884	NM_020535 // Hs.676464 // --- /// ENST00000400846 // Hs.676464 // --- /// AF204903 // H	NM_020535 // KIR2DL5A // killer cell immunoglobulin-like receptor, two domains, long cy	KIR2DL5A	NM_020535	---	NM_020535 // GO:0005886 // plasma membrane // inferred from electronic annotation ///	NM_020535 // GO:0004872 // receptor activity // inferred from electronic annotation //
35 7	8039871	NM_001083539 // Hs.683173 // blood lung spleen lung tumor normal adult /// NM_0132	NM_001083539 // KIR3DS1 // killer cell immunoglobulin-like receptor, three domains, sho	KIR3DS1	NM_001083539	NM_001083539 // GO:0006955 // immune response // non-traceable author statement /// NM	NM_001083539 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001083539 // GO:0004872 // receptor activity // inferred from electronic annotation
35 8	7965322	NM_000899 // Hs.1048 // ascites bladder blood bone brain connective tissue embryo	NM_000899 // KITLG // KIT ligand // 12q22 // 4254 /// NM_003994 // KITLG // KIT ligand	KITLG	NM_000899	NM_000899 // GO:0001541 // ovarian follicle development // inferred from electronic ann	NM_000899 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_000899 // GO:0005125 // cytokine activity // inferred from electronic annotation //
35 9	8167912	NM_007250 // Hs.646614 // adrenal gland bone brain connective tissue embryonic tiss	NM_007250 // KLF8 // Kruppel-like factor 8 // Xp11.21 // 11279 /// NM_001159296 // KLF8	KLF8	NM_007250	NM_007250 // GO:0045449 // regulation of transcription // inferred from electronic anno	NM_007250 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_007250 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
36 0	7974229	NM_014315 // Hs.509264 // adipose tissue adrenal gland blood bone brain cervix co	NM_014315 // KLHDC2 // kelch domain containing 2 // 14q21.3 // 23588 /// ENST0000029830	KLHDC2	NM_014315	---	NM_014315 // GO:0005634 // nucleus // inferred from electronic annotation /// ENST0000	NM_014315 // GO:0005515 // protein binding // inferred from physical interaction /// E
36 1	8168622	NM_019117 // Hs.49075 // brain connective tissue embryonic tissue eye heart kidney	NM_019117 // KLHL4 // kelch-like 4 (Drosophila) // Xq21.3 // 56062 /// NM_057162 // KLH	KLHL4	NM_019117	NM_019117 // GO:0008150 // biological process // no biological data available /// NM_0	NM_019117 // GO:0005737 // cytoplasm // inferred from sequence or structural similarity	NM_019117 // GO:0003674 // molecular function // no biological data available /// NM_0
36 2	7961151	NM_007360 // Hs.387787 // blood brain cervix connective tissue kidney liver lung	NM_007360 // KLRK1 // killer cell lectin-like receptor subfamily K, member 1 // 12p13.2	KLRK1	NM_007360	NM_007360 // GO:0002223 // stimulatory C-type lectin receptor signaling pathway // infe	NM_007360 // GO:0005887 // integral to plasma membrane // traceable author statement /	NM_007360 // GO:0004872 // receptor activity // inferred from electronic annotation //
36 3	8084679	NM_000893 // Hs.77741 // brain kidney liver mammary gland prostate spleen stomach	NM_000893 // KNG1 // kininogen 1 // 3q27 // 3827 /// NM_001102416 // KNG1 // kininogen	KNG1	NM_000893	NM_000893 // GO:0006939 // smooth muscle contraction // traceable author statement ///	NM_000893 // GO:0005576 // extracellular region // not recorded /// NM_000893 // GO:00	NM_000893 // GO:0004869 // cysteine-type endopeptidase inhibitor activity // inferred f

36 4	8121632	NM_002269 // Hs.182971 // brain embryonic tissue eye intestine kidney liver lung	NM_002269 // KPNA5 // karyopherin alpha 5 (importin alpha 6) // 6q22.1 // 3841 /// ENST	KPNA5	NM_002269	NM_002269 // GO:0006607 // NLS-bearing substrate import into nucleus // traceable autho	NM_002269 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00226	NM_002269 // GO:0005515 // protein binding // inferred from physical interaction /// N
36 5	8069813	NM_181621 // Hs.58152 // heart normal fetus /// ENST00000399889 // Hs.58152 // heart	NM_181621 // KRTAP13-2 // keratin associated protein 13-2 // 21q22.1 // 337959 /// ENST	KRTAP13-2	NM_181621	---	NM_181621 // GO:0005882 // intermediate filament // inferred from electronic annotation	---
36 6	8069827	NM_181608 // Hs.553692 // --- /// ENST00000334055 // Hs.553692 // --- /// AB180041 // H	NM_181608 // KRTAP19-2 // keratin associated protein 19-2 // 21q22.1 // 337969 /// ENST	KRTAP19-2	NM_181608	---	NM_181608 // GO:0005882 // intermediate filament // inferred from electronic annotation	---
36 7	8069841	NM_181612 // Hs.553695 // --- /// ENST00000334046 // Hs.553695 // --- /// AB096947 // H	NM_181612 // KRTAP19-6 // keratin associated protein 19-6 // 21q22.1 // 337973 /// ENST	KRTAP19-6	NM_181612	---	NM_181612 // GO:0005882 // intermediate filament // inferred from electronic annotation	---
36 8	7994237	NM_016309 // Hs.337730 // adipose tissue adrenal gland ascites bladder blood bone	NM_016309 // LCMT1 // leucine carboxyl methyltransferase 1 // 16p12.1 // 51451 /// NM_0	LCMT1	NM_016309	NM_016309 // GO:0006464 // protein modification process // traceable author statement	---	NM_016309 // GO:0003880 // protein C-terminal carboxyl O-methyltransferase activity //
36 9	7938788	NM_002301 // Hs.654377 // brain connective tissue kidney lung placenta testis ger	NM_002301 // LDHC // lactate dehydrogenase C // 11p15.1 // 3948 /// NM_017448 // LDHC /	LDHC	NM_002301	NM_002301 // GO:0006096 // glycolysis // inferred from electronic annotation /// NM_00	NM_002301 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_017	NM_002301 // GO:0004459 // L-lactate dehydrogenase activity // inferred from electronic
37 0	7910706	NM_006499 // Hs.4082 // adipose tissue adrenal gland bladder blood bone bone marrow	NM_006499 // LGALS8 // lectin, galactoside-binding, soluble, 8 // 1q43 // 3964 /// NM_2	LGALS8	NM_006499	NM_018072 // GO:0006364 // rRNA processing // inferred from electronic annotation ///	NM_006499 // GO:0005615 // extracellular space // traceable author statement /// NM_00	NM_006499 // GO:0005529 // sugar binding // inferred from electronic annotation /// NM
37 1	8127380	NM_016571 // Hs.149585 // eye liver ovary uterus normal ovarian tumor uterine tum	NM_016571 // LGSN // lengsin, lens protein with glutamine synthetase domain // 6pter-q2	LGSN	NM_016571	NM_016571 // GO:0006542 // glutamine biosynthetic process // inferred from electronic a	---	NM_016571 // GO:0003824 // catalytic activity // inferred from electronic annotation /
37 2	8094688	NM_006859 // Hs.550502 // adipose tissue adrenal gland ascites bladder bone brain	NM_006859 // LIAS // lipoic acid synthetase // 4p14 // 11019 /// NM_194451 // LIAS // I	LIAS	NM_006859	NM_006859 // GO:0006954 // inflammatory response // inferred from sequence or structura	NM_006859 // GO:0005634 // nucleus // inferred from direct assay /// NM_006859 // GO:0	NM_006859 // GO:0016740 // transferase activity // inferred from electronic annotation

37 3	8111677	NM_002310 // Hs.133421 // adipose tissue adrenal gland ascites brain connective tis	NM_002310 // LIFR // leukemia inhibitory factor receptor alpha // 5p13- p12 // 3977 ///	LIFR	NM_002310	NM_002310 // GO:0007166 // cell surface receptor linked signaling pathway // traceable	NM_002310 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_002310 // GO:0004872 // receptor activity // inferred from electronic annotation //
37 4	8069521	NM_198996 // Hs.139907 // bone connective tissue embryonic tissue testis normal pr	NM_198996 // LIPI // lipase, member I // 21q11.2 // 149998 /// ENST00000344577 // LIPI	LIPI	NM_198996	NM_198996 // GO:0016042 // lipid catabolic process // inferred from electronic annotati	NM_198996 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_198996 // GO:0016787 // hydrolase activity // inferred from electronic annotation /
37 5	8088739	NM_198271 // Hs.350621 // bone embryonic tissue heart liver mouth muscle nerve c	NM_198271 // LMOD3 // leiomodoin 3 (fetal) // 3p14.1 // 56203 /// ENST00000420581 // LMO	LMOD3	NM_198271	---	NM_198271 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_198	NM_198271 // GO:0005523 // tropomyosin binding // inferred from electronic annotation
37 6	8100362	NM_001126328 // Hs.518760 // ascites blood brain connective tissue embryonic tissue	NM_001126328 // LNX1 // ligand of numb-protein X 1 // 4q12 // 84708 /// NM_032622 // LN	LNX1	NM_001126328	NM_001126328 // GO:0042787 // protein ubiquitination involved in ubiquitin- dependent pr	NM_001126328 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_	NM_001126328 // GO:0004842 // ubiquitin-protein ligase activity // inferred from electr
37 7	8039975	AF274944 // Hs.542229 // ---	AF274944 // LOC100128185 // PNAS- 19 // 2p25.3 // 100128185	LOC100128185	AF274944	---	---	---
37 8	8040483	ENST00000450853 // Hs.651096 // testis normal	ENST00000450853 // LOC100129278 // tudor domain-containing protein 6-like // 2p24.1 //	LOC100129278	ENST0000045085 3	---	---	---
37 9	7981237	---	NR_033943 // LOC100129345 // hypothetical LOC100129345 // 14q32.2 // 100129345 /// ENST	LOC100129345	NR_033943	---	---	---
38 0	8055911	---	AF130063 // LOC100129449 // PRO2055 // 2q23.3 // 100129449	LOC100129449	AF130063	---	---	---
38 1	8149084	AK057771 // Hs.490892 // brain embryonic tissue non-neoplasia normal fetus adult	AK057771 // LOC100131112 // hypothetical LOC100131112 // 8p23.1 // 100131112	LOC100131112	AK057771	---	---	---
38 2	8155503	BC006438 // Hs.649184 // brain muscle ovary testis normal soft tissue/muscle tissu	BC006438 // LOC100132167 // hypothetical LOC100132167 // 9p12 // 100132167 /// BC006438	LOC100132167	BC006438	---	---	---

38 3	8002760	---	ENST00000412576 // LOC100132346 // 10 kDa heat shock protein, mitochondrial-like // 16q	LOC100132346	ENST00000412576	---	---	---
38 4	8111930	NR_034127 // Hs.649468 // blood brain cervix connective tissue embryonic tissue he	NR_034127 // LOC100132356 // hypothetical LOC100132356 // 5p12 // 100132356	LOC100132356	NR_034127	---	---	---
38 5	7976554	---	BX247990 // LOC100133207 // hypothetical LOC100133207 // 14q32.13 // 100133207 /// XR_1	LOC100133207	BX247990	---	---	---
38 6	7945950	---	XM_003120677 // LOC100293160 // peptidyl-prolyl cis-trans isomerase A-like // --- // 10	LOC100293160	XM_003120677	---	---	---
38 7	8088472	---	XM_003118868 // LOC100506946 // peptidyl-prolyl cis-trans isomerase A-like // --- // 10	LOC100506946	XM_003118868	---	---	---
38 8	7981726	---	XM_003119591 // LOC100508797 // hypothetical protein LOC100508797 // --- // 100508797	LOC100508797	XM_003119591	---	---	---
38 9	8142692	NM_001024603 // Hs.444163 // brain testis glioma normal fetus /// ENST00000419423 /	NM_001024603 // LOC154872 // hypothetical protein LOC154872 // 7q31.33 // 154872 /// EN	LOC154872	NM_001024603	---	---	---
39 0	8005225	NR_003190 // Hs.419859 // adipose tissue bone brain cervix connective tissue eye	NR_003190 // LOC162632 // ubiquitin specific peptidase 6 (Tre-2 oncogene) pseudogene //	LOC162632	NR_003190	---	---	---
39 1	7967210	NR_002809 // Hs.524804 // ascites bladder blood bone bone marrow brain cervix co	NR_002809 // LOC338799 // hypothetical LOC338799 // 12q24.31 // 338799 /// AK095700 //	LOC338799	NR_002809	---	---	---
39 2	8158164	NR_024425 // Hs.632678 // brain non-neoplasia adult /// ENST00000443493 // Hs.632678	NR_024425 // LOC389791 // hypothetical LOC389791 // 9q34.11 // 389791 /// ENST000004434	LOC389791	NR_024425	---	NR_024425 // GO:0016020 // membrane // inferred from electronic annotation NR_0244	---
39 3	8006237	BC062632 // Hs.709813 // brain intestine liver mammary gland mouth muscle pancrea	BC062632 // LOC400590 // hypothetical LOC400590 // 17q11.2 // 400590 /// XR_109453 // L	LOC400590	BC062632	---	---	---

39 4	8140869	---	NM_001161528 // LOC401387 // leucine-rich repeat and death domain-containing protein //	LOC401387	NM_001161528	NM_001161528 // GO:0007165 // signal transduction // inferred from electronic annotation	---	NM_001161528 // GO:0005515 // protein binding // inferred from electronic annotation /
39 5	7985560	NR_033579 // Hs.498322 // adrenal gland brain embryonic tissue larynx mammary gland	NR_033579 // LOC440297 // chondroitin sulfate proteoglycan 4 pseudogene // 15q25.2 // 4	LOC440297	NR_033579	---	---	---
39 6	7919580	AK125737 // Hs.710283 // brain stomach normal fetus adult /// AK125737 // Hs.710283	AK125737 // LOC440570 // hypothetical LOC440570 // 1p36.13 // 440570 /// AK125737 // LO	LOC440570	AK125737	---	---	---
39 7	8149396	---	ENST00000358192 // LOC442381 // similar to seven transmembrane helix receptor // 8p23.1	LOC442381	ENST00000358192	---	---	---
39 8	8022320	ENST00000432570 // Hs.448833 // bone brain connective tissue embryonic tissue esoph	NR_002555 // LOC613037 // nuclear pore complex interacting protein pseudogene // 16p11.	LOC613037	NR_002555	ENST00000419180 // GO:0008150 // biological_process // no biological data available //	ENST00000432570 // GO:0005576 // extracellular region // inferred from electronic annot	ENST00000419180 // GO:0003674 // molecular_function // no biological data available //
39 9	7903561	AY312144 // Hs.724774 // brain connective tissue testis normal soft tissue/muscle t	AY312144 // LOC642864 // spermatogenesis-related protein 7 // 1p13.3 // 642864	LOC642864	AY312144	---	---	---
40 0	8161415	---	ENST00000456982 // LOC644249 // hypothetical LOC644249 // 9q12 // 644249 /// ENST000004	LOC644249	ENST00000456982	---	---	---
40 1	7986603	NR_027053 // Hs.510697 // bone brain eye kidney lymph node nerve ovary parathyro	NR_027053 // LOC646214 // p21 protein (Cdc42/Rac)-activated kinase 2 pseudogene // 15q1	LOC646214	NR_027053	---	---	---
40 2	8043476	---	ENST00000493819 // LOC652493 // ig kappa chain V-I region HK102-like // --- // 652493	LOC652493	ENST00000493819	---	---	---
40 3	8051864	NM_001101330 // Hs.602756 // testis normal fetus	NM_001101330 // LOC728819 // hCG1645220 // 2p21 // 728819	LOC728819	NM_001101330	---	---	---
40 4	7968976	NM_001164211 // Hs.507971 // adrenal gland bladder blood bone brain cervix connec	NM_001164211 // LRCH1 // leucine-rich repeats and calponin homology (CH) domain contain	LRCH1	NM_001164211	---	---	NM_001164211 // GO:0005515 // protein binding // inferred from electronic annotation /

40 5	7934779	NM_001017924 // Hs.450425 // brain eye normal adult /// ENST00000372113 // Hs.450425	NM_001017924 // LRIT2 // leucine-rich repeat, immunoglobulin-like and transmembrane dom	LRIT2	NM_001017924	---	NM_001017924 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0	NM_001017924 // GO:0005515 // protein binding // inferred from electronic annotation /
40 6	8096839	NM_198506 // Hs.308127 // brain eye normal adult /// ENST00000379920 // Hs.308127 //	NM_198506 // LRIT3 // leucine-rich repeat, immunoglobulin-like and transmembrane domain	LRIT3	NM_198506	---	NM_198506 // GO:0016020 // membrane // inferred from electronic annotation /// NM_1985	NM_198506 // GO:0005515 // protein binding // inferred from electronic annotation ///
40 7	8117243	NM_017640 // Hs.649550 // blood bone brain connective tissue embryonic tissue esop	NM_017640 // LRRC16A // leucine rich repeat containing 16A // 6p22.2 // 55604 /// NM_00	LRRC16A	NM_017640	NM_017640 // GO:0046415 // urate metabolic process // inferred from mutant phenotype /	NM_017640 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_001	---
40 8	7996546	NM_018296 // Hs.125139 // adipose tissue brain connective tissue heart intestine k	NM_018296 // LRRC36 // leucine rich repeat containing 36 // 16q22.1 // 55282 /// NM_001	LRRC36	NM_018296	---	---	---
40 9	8006336	NM_052888 // Hs.514071 // brain cervix embryonic tissue eye kidney lung mammary g	NM_052888 // LRRC37B // leucine rich repeat containing 37B // --- // 114659 /// ENST000	LRRC37B	NM_052888	---	NM_052888 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0528	NM_052888 // GO:0005515 // protein binding // inferred from electronic annotation ///
41 0	8049534	NM_001137550 // Hs.471779 // adipose tissue ascites bladder blood bone bone marrow	NM_001137550 // LRRFIP1 // leucine rich repeat (in FLII) interacting protein 1 // 2q37.	LRRFIP1	NM_001137550	NM_001137550 // GO:0006357 // regulation of transcription from RNA polymerase II promot	NM_001137550 // GO:0005634 // nucleus // non- traceable author statement /// NM_0011375	NM_001137550 // GO:0003677 // DNA binding // inferred from electronic annotation /// N
41 1	7917008	NM_001105659 // Hs.644625 // bladder brain connective tissue kidney skin testis b	NM_001105659 // LRRIQ3 // leucine-rich repeats and IQ motif containing 3 // 1p31.1 // 1	LRRIQ3	NM_001105659	---	---	---
41 2	8083808	NM_001080460 // Hs.319484 // brain connective tissue lung normal soft tissue/muscle	NM_001080460 // LRRIQ4 // leucine-rich repeats and IQ motif containing 4 // 3q26.2 // 3	LRRIQ4	NM_001080460	---	---	NM_001080460 // GO:0005515 // protein binding // inferred from electronic annotation /
41 3	8067380	NM_144703 // Hs.105379 // ascites blood bone brain cervix connective tissue embryo	NM_144703 // LSM14B // LSM14B, SCD6 homolog B (S. cerevisiae) // 20q13.33 // 149986 ///	LSM14B	NM_144703	NM_144703 // GO:0006417 // regulation of translation // inferred from electronic annota	NM_144703 // GO:0030529 // ribonucleoprotein complex // inferred from electronic annota	---

41 4	8078008	NM_014463 // Hs.111632 // adrenal gland ascites bladder blood bone bone marrow br	NM_014463 // LSM3 // LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae) // 3	LSM3	NM_014463	NM_014463 // GO:0006397 // mRNA processing // traceable author statement /// NM_014463	NM_014463 // GO:0005634 // nucleus // traceable author statement /// NM_014463 // GO:0	NM_014463 // GO:0003723 // RNA binding // inferred from electronic annotation /// NM_0
41 5	7998174	NM_018032 // Hs.16803 // adipose tissue adrenal gland ascites bladder blood bone	NM_018032 // LUC7L // LUC7-like (S. cerevisiae) // 16p13.3 // 55692 /// NM_201412 // LU	LUC7L	NM_018032	NM_018032 // GO:0045843 // negative regulation of striated muscle tissue development //	NM_018032 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_20141	NM_018032 // GO:0005515 // protein binding // inferred from physical interaction /// N
41 6	8169467	NM_016383 // Hs.242183 // testis normal fetus /// ENST00000371920 // Hs.242183 // tes	NM_016383 // LUZP4 // leucine zipper protein 4 // Xq23 // 51213 /// ENST00000371920 //	LUZP4	NM_016383	---	NM_016383 // GO:0005634 // nucleus // inferred from electronic annotation /// ENST00000	---
41 7	8107859	NM_181705 // Hs.115467 // adrenal gland bladder blood bone bone marrow brain conn	NM_181705 // LYRM7 // Lym7 homolog (mouse) // 5q23.3 // 90624 /// ENST00000379380 // L	LYRM7	NM_181705	---	NM_181705 // GO:0005739 // mitochondrion // inferred from electronic annotation /// EN	---
41 8	7907032	NM_032858 // Hs.651245 // brain eye heart liver mammary gland placenta prostate	NM_032858 // MAEL // maelstrom homolog (Drosophila) // 1q24.1 // 84944 /// ENST00000367	MAEL	NM_032858	NM_032858 // GO:0000122 // negative regulation of transcription from RNA polymerase II	NM_032858 // GO:0000785 // chromatin // inferred from electronic annotation /// NM_032	NM_032858 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
41 9	8166576	ENST00000379029 // Hs.224079 // germ cell tumor	ENST00000379029 // MAGEB5 // melanoma antigen family B, 5 // Xp21.3 // 347541	MAGEB5	ENST00000379029	ENST00000379029 // GO:0008150 // biological_process // no biological data available	ENST00000379029 // GO:0005575 // cellular_component // no biological data available	ENST00000379029 // GO:0003674 // molecular_function // no biological data available
42 0	8175562	NM_016249 // Hs.123536 // bone bone marrow brain placenta salivary gland skin tes	NM_016249 // MAGEC2 // melanoma antigen family C, 2 // Xq27 // 51438 /// ENST0000024745	MAGEC2	NM_016249	---	NM_016249 // GO:0005634 // nucleus // inferred from direct assay /// NM_016249 // GO:0	---
42 1	8105899	NM_001038603 // Hs.724697 // blood brain embryonic tissue eye intestine liver lun	NM_001038603 // MARVELD2 // MARVEL domain containing 2 // 5q13.2 // 153562 /// ENST00000	MARVELD2	NM_001038603	NM_001038603 // GO:0007605 // sensory perception of sound // inferred from electronic a	NM_001038603 // GO:0005886 // plasma membrane // inferred from electronic annotation /	---
42 2	8123176	NM_002377 // Hs.99900 // --- /// ENST00000252660 // Hs.99900 // --- /// M13150 // Hs.99	NM_002377 // MAS1 // MAS1 oncogene // 6q25.3-q26 // 4142 /// ENST00000252660 // MAS1 //	MAS1	NM_002377	NM_002377 // GO:0001933 // negative regulation of protein phosphorylation // inferred f	NM_002377 // GO:0005886 // plasma membrane // inferred from direct assay /// NM_002377	NM_002377 // GO:0001595 // angiotensin receptor activity // inferred from sequence or s

42 3	8069332	NR_002776 // Hs.655095 // bladder brain embryonic tissue eye kidney larynx liver	NR_002776 // MCM3AP-AS // MCM3AP antisense RNA (non-protein coding) // 21q22.3 // 11404	MCM3AP-AS	NR_002776	ENST0000039770 8 // GO:0006260 // DNA replication // traceable author statement /// ENS	ENST0000039770 8 // GO:0005634 // nucleus // inferred from direct assay /// ENST0000039	ENST00000397708 // GO:0000166 // nucleotide binding // inferred from electronic annotat
42 4	7978192	NM_138476 // Hs.220963 // blood bone brain ear embryonic tissue eye heart intest	NM_138476 // MDP1 // magnesium-dependent phosphatase 1 // 14q12 // 145553 /// ENST00000	MDP1	NM_138476	---	---	NM_138476 // GO:0004725 // protein tyrosine phosphatase activity // inferred from elect
42 5	8127854	NM_002395 // Hs.21160 // adrenal gland bladder blood bone bone marrow brain cervi	NM_002395 // ME1 // malic enzyme 1, NADP(+)-dependent, cytosolic // 6q12 // 4199 /// EN	ME1	NM_002395	NM_002395 // GO:0005975 // carbohydrate metabolic process // non-traceable author state	NM_002395 // GO:0005625 // soluble fraction // inferred from electronic annotation ///	NM_002395 // GO:0004470 // malic enzyme activity // inferred from direct assay /// NM_
42 6	8110886	NM_032286 // Hs.13885 // adrenal gland ascites bladder blood bone bone marrow bra	NM_032286 // MED10 // mediator complex subunit 10 // 5p15.31 // 84246 /// ENST000002557	MED10	NM_032286	NM_032286 // GO:0006357 // regulation of transcription from RNA polymerase II promoter	NM_032286 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_03228	NM_032286 // GO:0016455 // RNA polymerase II transcription mediator activity // inferre
42 7	8113039	NM_002397 // Hs.649965 // adipose tissue blood bone marrow brain connective tissue	NM_002397 // MEF2C // myocyte enhancer factor 2C // 5q14 // 4208 /// NM_001193350 // ME	MEF2C	NM_002397	NM_002397 // GO:0002634 // regulation of germinal center formation // inferred from seq	NM_002397 // GO:0005634 // nucleus // inferred from direct assay /// NM_002397 // GO:0	NM_002397 // GO:0003700 // sequence-specific DNA binding transcription factor activity
42 8	8013341	NM_001198695 // Hs.296049 // adrenal gland bone brain cervix connective tissue emb	NM_001198695 // MFAP4 // microfibrillar-associated protein 4 // 17p11.2 // 4239 /// NM_	MFAP4	NM_001198695	NM_001198695 // GO:0007155 // cell adhesion // non-traceable author statement /// NM_0	NM_001198695 // GO:0001527 // microfibril // non-traceable author statement /// NM_001	NM_001198695 // GO:0003674 // molecular_function // no biological data available /// N
42 9	8138527	---	NM_207342 // MGC87042 // STEAP family protein MGC87042 // 7p15.3 // 256227 /// NM_00116	MGC87042	NM_207342	---	NM_207342 // GO:0016020 // membrane // inferred from electronic annotation /// NM_2073	NM_207342 // GO:0005506 // iron ion binding // inferred from electronic annotation ///
43 0	8063921	---	NR_029780 // MIR1-1 // microRNA 1-1 // 20q13.33 // 406904	MIR1-1	NR_029780	---	---	---
43 1	8045453	---	NR_029672 // MIR128-1 // microRNA 128-1 // 2q21.3 // 406915	MIR128-1	NR_029672	---	---	---
43 2	7939463	---	NR_029697 // MIR129-2 // microRNA 129-2 // 11p11.2 // 406918	MIR129-2	NR_029697	---	---	---
43 3	8022498	---	NR_029675 // MIR133A1 // microRNA 133a-1 // 18q11.2 // 406922	MIR133A1	NR_029675	---	---	---
43 4	8087883	---	NR_029677 // MIR135A1 // microRNA 135a-1 // 3p21.1 // 406925	MIR135A1	NR_029677	---	---	---

43 5	7917944	---	NR_029679 // MIR137 // microRNA 137 // 1p21.3 // 406928	MIR137	NR_029679	---	---	---
43 6	8059211	---	NR_029688 // MIR153-1 // microRNA 153-1 // 2q35 // 406944	MIR153-1	NR_029688	---	---	---
43 7	7969576	NR_027350 // Hs.24115 // blood embryonic tissue kidney liver lymph node pharynx p	NR_027350 // MIR17HG // MIR17 host gene (non-protein coding) // 13q31.3 // 407975 /// N	MIR17HG	NR_027350	---	---	---
43 8	7923175	---	NR_029626 // MIR181A1 // microRNA 181a-1 // 1q32.1 // 406995	MIR181A1	NR_029626	---	---	---
43 9	8034099	---	NR_029586 // MIR199A1 // microRNA 199a-1 // 19p13.2 // 406976	MIR199A1	NR_029586	---	---	---
44 0	7977214	---	NR_029620 // MIR203 // microRNA 203 // 14q32.33 // 406986	MIR203	NR_029620	---	---	---
44 1	8175683	U92285 // Hs.22785 // adipose tissue bladder bone marrow brain connective tissue e	NR_029638 // MIR224 // microRNA 224 // Xq28 // 407009 /// U92285 // GABRE // gamma-amin	MIR224	NR_029638	U92285 // GO:0006810 // transport traceable author statement /// U92285 // GO:00068	U92285 // GO:0005886 // plasma membrane // inferred from electronic annotation /// U92	U92285 // GO:0004890 // GABA-A receptor activity // inferred from electronic annotation
44 2	8156573	AF043897 // Hs.434253 // adrenal gland ascites bladder blood bone brain cervix c	NR_029496 // MIR24-1 // microRNA 24-1 // 9q22.32 // 407012 /// NR_036109 // MIR3074 //	MIR24-1	NR_029496	AF043897 // GO:0006508 // proteolysis // inferred from direct assay /// AF043897 // GO	AF043897 // GO:0005737 // cytoplasm // inferred from electronic annotation	AF043897 // GO:0004177 // aminopeptidase activity // inferred from direct assay /// AF
44 3	7976830	---	NR_029841 // MIR299 // microRNA 299 // 14q32.31 // 407023	MIR299	NR_029841	---	---	---
44 4	8142975	---	NR_029503 // MIR29A // microRNA 29a // 7q32.3 // 407021	MIR29A	NR_029503	---	---	---
44 5	7976832	---	NR_029890 // MIR323 // microRNA 323 // 14q32.31 // 442897	MIR323	NR_029890	---	---	---
44 6	7976856	---	NR_030156 // MIR410 // microRNA 410 // 14q32.31 // 574434	MIR410	NR_030156	---	---	---
44 7	7976854	---	NR_030155 // MIR412 // microRNA 412 // 14q32.31 // 574433	MIR412	NR_030155	---	---	---
44 8	8157444	---	NR_030255 // MIR455 // microRNA 455 // 9q32 // 619556	MIR455	NR_030255	---	---	---
44 9	7976840	---	NR_030162 // MIR487A // microRNA 487a // 14q32.31 // 619555	MIR487A	NR_030162	---	---	---

45 0	8175248	---	NR_029509 // MIR92A2 // microRNA 92a-2 // Xq26.2 // 407049	MIR92A2	NR_029509	---	---	---
45 1	8142882	---	NR_029512 // MIR96 // microRNA 96 // 7q32.2 // 407053	MIR96	NR_029512	---	---	---
45 2	8173007	---	NR_029484 // MIRLET7F2 // microRNA let-7f-2 // Xp11.22 // 406889	MIRLET7F2	NR_029484	---	---	---
45 3	8087881	---	NR_029660 // MIRLET7G // microRNA let-7g // 3p21.1 // 406890	MIRLET7G	NR_029660	---	---	---
45 4	7944223	NM_001197104 // Hs.258855 // adrenal gland ascites bladder blood bone bone marrow	NM_001197104 // MLL // myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, D	MLL	NM_001197104	NM_001197104 // GO:0006306 // DNA methylation // inferred from electronic annotation /	NM_001197104 // GO:0005634 // nucleus // inferred from direct assay /// NM_001197104 /	NM_001197104 // GO:0003677 // DNA binding // inferred from electronic annotation /// N
45 5	8160332	NM_004529 // Hs.591085 // adrenal gland ascites bladder blood bone bone marrow br	NM_004529 // MLLT3 // myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Dr	MLLT3	NM_004529	NM_004529 // GO:0006355 // regulation of transcription, DNA-dependent // inferred from	NM_004529 // GO:0005634 // nucleus // inferred from direct assay /// NM_004529 // GO:0	NM_004529 // GO:0005515 // protein binding // inferred from physical interaction /// E
45 6	8151684	ENST00000286614 // Hs.546267 // brain connective tissue embryonic tissue eye heart	ENST00000286614 // MMP16 // matrix metalloproteinase 16 (membrane-inserted) // 8q21.3 //	MMP16	ENST00000286614	ENST00000286614 // GO:0006508 // proteolysis // inferred from electronic annotation //	ENST00000286614 // GO:0005576 // extracellular region // inferred from electronic annot	ENST00000286614 // GO:0004222 // metalloendopeptidase activity // inferred from electro
45 7	7937961	NM_021801 // Hs.204732 // brain connective tissue uterus normal soft tissue muscle	NM_021801 // MMP26 // matrix metalloproteinase 26 // 11p15 // 56547 /// ENST00000380390	MMP26	NM_021801	NM_021801 // GO:0006508 // proteolysis // non-traceable author statement /// NM_021801	NM_021801 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_021801 // GO:0004222 // metalloendopeptidase activity // inferred from electronic an
45 8	8095894	NM_020236 // Hs.532019 // ascites bladder blood bone bone marrow brain connective	NM_020236 // MRPL1 // mitochondrial ribosomal protein L1 // 4q21.1 // 65008 /// ENST000	MRPL1	NM_020236	NM_020236 // GO:0006396 // RNA processing // inferred from electronic annotation /// N	NM_020236 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_020236 // GO:0003723 // RNA binding // inferred from electronic annotation /// NM_0
45 9	7973327	NM_181304 // Hs.355935 // bone bone marrow brain embryonic tissue esophagus eye h	NM_181304 // MRPL52 // mitochondrial ribosomal protein L52 // 14q11.2 // 122704 /// NM_	MRPL52	NM_181304	NM_181304 // GO:0006412 // translation // inferred from sequence or structural similari	NM_181304 // GO:0005634 // nucleus // inferred from direct assay /// NM_181304 // GO:0	NM_181304 // GO:0003735 // structural constituent of ribosome // inferred from sequence
46 0	7905163	NM_018997 // Hs.405880 // adipose tissue adrenal gland ascites bladder blood bone	NM_018997 // MRPS21 // mitochondrial ribosomal protein S21 // 1q21 // 54460 /// NM_0319	MRPS21	NM_018997	NM_018997 // GO:0006412 // translation // non-traceable author statement /// NM_031901	NM_018997 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_018997 // GO:0003735 // structural constituent of ribosome // non-traceable author s

46 1	7947934	NM_014342 // Hs.269944 // adrenal gland ascites bladder blood bone bone marrow br	NM_014342 // MTCH2 // mitochondrial carrier homolog 2 (C. elegans) // 11p11.2 // 23788	MTCH2	NM_014342	NM_014342 // GO:0055085 // transmembrane transport // inferred from electronic annotation	NM_014342 // GO:0005739 // mitochondrion // inferred from electronic annotation /// NM	NM_014342 // GO:0005488 // binding // inferred from electronic annotation /// ENST0000
46 2	8151917	NM_015942 // Hs.308613 // adrenal gland blood bone brain cervix connective tissue	NM_015942 // MTERFD1 // MTERF domain containing 1 // 8q22.1 // 51001 /// ENST0000028702	MTERFD1	NM_015942	NM_015942 // GO:0045892 // negative regulation of transcription, DNA-dependent // infer	NM_015942 // GO:0005634 // nucleus // inferred from direct assay /// NM_015942 // GO:0	NM_015942 // GO:0010843 // promoter binding // inferred from direct assay /// ENST0000
46 3	8095705	NM_001144978 // Hs.721011 // adrenal gland connective tissue embryonic tissue testis	NM_001144978 // MTHFD2L // methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-	MTHFD2L	NM_001144978	NM_001144978 // GO:0000105 // histidine biosynthetic process // inferred from electronic	---	NM_001144978 // GO:0004477 // methenyltetrahydrofolate cyclohydrolase activity // infer
46 4	8148317	NM_002467 // Hs.202453 // adipose tissue adrenal gland ascites bladder blood bone	NM_002467 // MYC // v-myc myelocytomatosis viral oncogene homolog (avian) // 8q24.21 //	MYC	NM_002467	NM_002467 // GO:0001658 // branching involved in ureteric bud morphogenesis // inferred	NM_002467 // GO:0005634 // nucleus // inferred from direct assay /// NM_002467 // GO:0	NM_002467 // GO:0003677 // DNA binding // traceable author statement /// NM_002467 //
46 5	8012726	NM_005963 // Hs.689619 // bone heart larynx liver mouth muscle pharynx spleen t	NM_005963 // MYH1 // myosin, heavy chain 1, skeletal muscle, adult // 17p13.1 // 4619 /	MYH1	NM_005963	---	NM_005963 // GO:0005730 // nucleolus // inferred from direct assay /// NM_005963 // GO	NM_005963 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
46 6	7966379	NM_000432 // Hs.75535 // bone embryonic tissue eye heart kidney larynx liver lun	NM_000432 // MYL2 // myosin, light chain 2, regulatory, cardiac, slow // 12q24.11 // 46	MYL2	NM_000432	NM_000432 // GO:0006942 // regulation of striated muscle contraction // traceable autho	NM_000432 // GO:0005856 // cytoskeleton // inferred from direct assay /// NM_000432 //	NM_000432 // GO:0003774 // motor activity // inferred from electronic annotation /// N
46 7	8047127	NM_001130158 // Hs.439620 // adrenal gland ascites bladder bone bone marrow brain	NM_001130158 // MYO1B // myosin IB // 2q12-q34 // 4430 /// NM_012223 // MYO1B // myosin	MYO1B	NM_001130158	---	NM_001130158 // GO:0016459 // myosin complex // inferred from electronic annotation //	NM_001130158 // GO:0000166 // nucleotide binding // inferred from electronic annotation
46 8	7916592	NM_001085487 // Hs.477495 // adipose tissue blood bone bone marrow brain embryonic	NM_001085487 // MYSM1 // Myb-like, SWIRM and MPN domains 1 // 1p32.1 // 114803 /// ENST	MYSM1	NM_001085487	NM_001085487 // GO:0016568 // chromatin modification // inferred from electronic annota	NM_001085487 // GO:0005634 // nucleus // inferred from direct assay /// NM_001085487 /	NM_001085487 // GO:0003677 // DNA binding // inferred from electronic annotation /// N
46 9	8144866	NM_000015 // Hs.2 // bone connective tissue intestine liver liver tumor normal so	NM_000015 // NAT2 // N-acetyltransferase 2 (arylamine N-acetyltransferase) // 8p22 // 1	NAT2	NM_000015	NM_000015 // GO:0008152 // metabolic process // inferred from electronic annotation //	NM_000015 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_000	NM_000015 // GO:0004060 // arylamine N-acetyltransferase activity // inferred from elec

47 0	8054511	BC064430 // Hs.128499 // blood bone brain cervix embryonic tissue eye heart inte	BC064430 // NCRNA00116 // non- protein coding RNA 116 // 2q13 // 205251 /// BC133660 //	NCRNA00116	BC064430	---	BC064430 // GO:0016020 // membrane // inferred from electronic annotation /// BC064430	---
47 1	8170963	AY168775 // Hs.391764 // normal fetus	AY168775 // NCRNA00204 // non- protein coding RNA 204 // Xq28 // 100132967	NCRNA00204	AY168775	---	---	---
47 2	8097038	NM_004784 // Hs.480596 // adrenal gland blood brain embryonic tissue eye lung mus	NM_004784 // NDST3 // N-deacetylase/N- sulfotransferase (heparan glucosaminy) 3 // 4q26	NDST3	NM_004784	---	NM_004784 // GO:0000139 // Golgi membrane // inferred from electronic annotation /// N	NM_004784 // GO:0008146 // sulfotransferase activity // inferred from electronic annota
47 3	8102450	NM_022569 // Hs.591700 // brain lung lung tumor normal /// ENST00000264363 // Hs.591	NM_022569 // NDST4 // N-deacetylase/N- sulfotransferase (heparan glucosaminy) 4 // 4q26	NDST4	NM_022569	---	NM_022569 // GO:0000139 // Golgi membrane // inferred from electronic annotation /// N	NM_022569 // GO:0008146 // sulfotransferase activity // inferred from electronic annota
47 4	8163930	NM_014222 // Hs.495039 // ascites blood bone bone marrow brain connective tissue	NM_014222 // NDUFA8 // NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa //	NDUFA8	NM_014222	NM_014222 // GO:0006120 // mitochondrial electron transport, NADH to ubiquinone // non-	NM_014222 // GO:0005739 // mitochondrion // inferred from electronic annotation /// NM	NM_014222 // GO:0008137 // NADH dehydrogenase (ubiquinone) activity // non-traceable au
47 5	7900228	NM_004552 // Hs.632385 // adrenal gland ascites bladder blood bone bone marrow br	NM_004552 // NDUFS5 // NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coen	NDUFS5	NM_004552	NM_004552 // GO:0006120 // mitochondrial electron transport, NADH to ubiquinone // non-	NM_004552 // GO:0005739 // mitochondrion // inferred from direct assay /// NM_004552 /	NM_004552 // GO:0008137 // NADH dehydrogenase (ubiquinone) activity // non-traceable au
47 6	8055711	NM_001164507 // Hs.588655 // adrenal gland bone brain connective tissue embryonic t	NM_001164507 // NEB // nebulin // 2q22 // 4703 /// NM_001164508 // NEB // nebulin // 2q	NEB	NM_001164507	NM_001164507 // GO:0007517 // muscle organ development // traceable author statement /	NM_001164507 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM	NM_001164507 // GO:0003779 // actin binding // inferred from electronic annotation ///
47 7	8023828	NM_138966 // Hs.465407 // bladder brain eye prostate skin germ cell tumor normal	NM_138966 // NETO1 // neuropilin (NRP) and tolloid (TLL)-like 1 // 18q22.2 // 81832 ///	NETO1	NM_138966	NM_138966 // GO:0007613 // memory // inferred from sequence or structural similarity /	NM_138966 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_138966 // GO:0004872 // receptor activity // inferred from electronic annotation //
47 8	7918891	NM_005599 // Hs.46296 // bone marrow brain embryonic tissue eye kidney lung mouth	NM_005599 // NHLH2 // necient helix loop helix 2 // 1p12-p11 // 4808 /// NM_001111061	NHLH2	NM_005599	NM_005599 // GO:0007275 // multicellular organismal development // inferred from electr	NM_005599 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00111	NM_005599 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0

47 9	8157021	NM_015469 // Hs.530275 // adrenal gland ascites bladder blood bone bone marrow br	NM_015469 // NIPSNAP3A // nipsnap homolog 3A (C. elegans) // 9q31.1 // 25934 /// ENST00	NIPSNAP3A	NM_015469	---	NM_015469 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_015	---
48 0	8157027	NM_018376 // Hs.720820 // adipose tissue bone marrow brain embryonic tissue eye he	NM_018376 // NIPSNAP3B // nipsnap homolog 3B (C. elegans) // 9q31.1 // 55335 /// ENST00	NIPSNAP3B	NM_018376	---	NM_018376 // GO:0005739 // mitochondrion // inferred from electronic annotation /// EN	---
48 1	8174684	NM_001173487 // Hs.437084 // bladder bone brain cervix connective tissue ear embr	NM_001173487 // NKRF // NFkB repressing factor // Xq24 // 55922 /// NM_017544 // NKRF /	NKRF	NM_001173487	NM_001173487 // GO:0016481 // negative regulation of transcription // inferred from dir	NM_001173487 // GO:0005622 // intracellular // inferred from electronic annotation ///	NM_001173487 // GO:0003677 // DNA binding // inferred from electronic annotation /// N
48 2	8100464	NM_006681 // Hs.418367 // bone marrow brain cervix connective tissue embryonic tiss	NM_006681 // NMU // neuromedin U // 4q12 // 10874 /// ENST00000264218 // NMU // neurome	NMU	NM_006681	NM_006681 // GO:0001696 // gastric acid secretion // inferred from electronic annotatio	NM_006681 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_006681 // GO:0005102 // receptor binding // traceable author statement /// NM_00668
48 3	7935146	NM_022451 // Hs.74899 // ascites bladder blood bone brain cervix connective tissu	NM_022451 // NOL11 // nucleolar complex associated 3 homolog (S. cerevisiae) // 10q23.3	NOL11	NM_022451	NM_022451 // GO:0045444 // fat cell differentiation // inferred from electronic annotat	NM_022451 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_02245	NM_022451 // GO:0005488 // binding // inferred from electronic annotation /// ENST0000
48 4	8009366	NM_015462 // Hs.463936 // adrenal gland ascites bladder blood bone bone marrow br	NM_015462 // NOL11 // nucleolar protein 11 // 17q24.2 // 25926 /// ENST00000253247 // N	NOL11	NM_015462	---	NM_015462 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_01546	---
48 5	8054486	NM_000272 // Hs.280388 // bone brain cervix connective tissue embryonic tissue eye	NM_000272 // NPHP1 // nephronophthisis 1 (juvenile) // 2q13 // 4867 /// NM_207181 // NP	NPHP1	NM_000272	NM_000272 // GO:0007165 // signal transduction // non-traceable author statement /// N	NM_000272 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_000	NM_000272 // GO:0005198 // structural molecule activity // non-traceable author stateme
48 6	8098146	NM_006174 // Hs.519058 // brain kidney mammary gland testis thymus breast (mammary	NM_006174 // NPY5R // neuropeptide Y receptor Y5 // 4q31-q32 // 4889 /// ENST0000033856	NPY5R	NM_006174	NM_006174 // GO:0002675 // positive regulation of acute inflammatory response // inferr	NM_006174 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_006	NM_006174 // GO:0001601 // peptide YY receptor activity // inferred from electronic ann
48 7	8145736	NM_013958 // Hs.453951 // blood bone brain connective tissue embryonic tissue eye	NM_013958 // NRG1 // neuregulin 1 // 8p12 // 3084 /// NM_001160004 // NRG1 // neureguli	NRG1	NM_013958	NM_013958 // GO:0006916 // anti-apoptosis // inferred from direct assay /// NM_013958	NM_013958 // GO:0005576 // extracellular region // non-traceable author statement ///	NM_013958 // GO:0003712 // transcription cofactor activity // inferred from direct assa

48 8	7960331	NM_031474 // Hs.530816 // brain eye heart intestine kidney larynx mammary gland	NM_031474 // NRIP2 // nuclear receptor interacting protein 2 // 12p13.33 // 83714 /// E	NRIP2	NM_031474	NM_031474 // GO:0000122 // negative regulation of transcription from RNA polymerase II	NM_031474 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_03147	NM_031474 // GO:0004190 // aspartic-type endopeptidase activity // inferred from electr
48 9	8139947	NR_033323 // Hs.436034 // adipose tissue adrenal gland ascites blood bone brain c	NR_033323 // NSUN5P2 // NOP2/Sun domain family, member 5 pseudogene 2 // 7q11.23 // 260	NSUN5P2	NR_033323	---	---	NR_033323 // GO:0008168 // methyltransferase activity // inferred from electronic annot
49 0	8050480	NM_001002006 // Hs.120319 // testis germ cell tumor normal fetus adult /// NM_03325	NM_001002006 // NT5C1B // 5'-nucleotidase, cytosolic IB // 2p24.2 // 93034 /// NM_03325	NT5C1B	NM_001002006	NM_001002006 // GO:0009117 // nucleotide metabolic process // inferred from electronic	NM_001002006 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_001002006	NM_001002006 // GO:0000166 // nucleotide binding // inferred from electronic annotation
49 1	8011832	NM_002532 // Hs.584784 // adipose tissue adrenal gland ascites bladder blood bone	NM_002532 // NUP88 // nucleoporin 88kDa // 17p13.2 // 4927 /// ENST00000225696 // NUP88	NUP88	NM_002532	NM_002532 // GO:0015031 // protein transport // inferred from electronic annotation //	NM_002532 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00253	NM_002532 // GO:0005215 // transporter activity // traceable author statement /// ENST
49 2	8168940	NR_002216 // Hs.454283 // brain testis normal	NR_002216 // NXF4 // nuclear RNA export factor 4 pseudogene // Xq22 // 55999	NXF4	NR_002216	---	---	---
49 3	8166104	NM_003611 // Hs.6483 // adrenal gland ascites bladder blood brain cervix connecti	NM_003611 // OFD1 // oral-facial-digital syndrome 1 // Xp22 // 8481 /// ENST00000340096	OFD1	NM_003611	NM_003611 // GO:0007067 // mitosis // inferred from sequence or structural similarity	NM_003611 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00361	NM_003611 // GO:0005515 // protein binding // inferred from physical interaction /// N
49 4	7948111	NM_001005491 // Hs.554525 // --- /// ENST00000312345 // Hs.554525 // --- /// BC136890 /	NM_001005491 // OR10AG1 // olfactory receptor, family 10, subfamily AG, member 1 // 11q	OR10AG1	NM_001005491	NM_001005491 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001005491 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001005491 // GO:0004872 // receptor activity // inferred from electronic annotation
49 5	8026494	NM_001004465 // Hs.553579 // --- /// ENST00000322107 // Hs.553579 // ---	NM_001004465 // OR10H4 // olfactory receptor, family 10, subfamily H, member 4 // 19p13	OR10H4	NM_001004465	NM_001004465 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001004465 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001004465 // GO:0004872 // receptor activity // inferred from electronic annotation
49 6	7973030	NM_001004480 // Hs.553575 // --- /// ENST00000315519 // Hs.553575 // ---	NM_001004480 // OR11H6 // olfactory receptor, family 11, subfamily H, member 6 // 14q11	OR11H6	NM_001004480	NM_001004480 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001004480 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001004480 // GO:0004872 // receptor activity // inferred from electronic annotation
49 7	8117724	NM_013936 // Hs.247862 // germ cell tumor adult /// ENST00000383555 // Hs.247862 // ge	NM_013936 // OR12D2 // olfactory receptor, family 12, subfamily D, member 2 // 6p22.2-p	OR12D2	NM_013936	NM_013936 // GO:0007608 // sensory perception of smell // inferred from electronic	NM_013936 // GO:0005886 // plasma membrane // inferred from electronic	NM_013936 // GO:0004872 // receptor activity // inferred from electronic annotation //

						anno	annotation ///	
49 8	8162936	NM_001004481 // Hs.553789 // --- /// ENST00000318797 // Hs.553789 // --- /// BC136824 /	NM_001004481 // OR13C2 // olfactory receptor, family 13, subfamily C, member 2 // 9q31.	OR13C2	NM_001004481	NM_001004481 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001004481 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001004481 // GO:0004872 // receptor activity // inferred from electronic annotation
49 9	8157016	NM_001004484 // Hs.553683 // --- /// ENST00000318763 // Hs.553683 // --- /// BC140916 /	NM_001004484 // OR13D1 // olfactory receptor, family 13, subfamily D, member 1 // 9q31.	OR13D1	NM_001004484	NM_001004484 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001004484 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001004484 // GO:0004872 // receptor activity // inferred from electronic annotation
50 0	8169947	NM_001004486 // Hs.553711 // --- /// NM_001004486 // Hs.714693 // --- /// ENST000003386	NM_001004486 // OR13H1 // olfactory receptor, family 13, subfamily H, member 1 // Xq26.	OR13H1	NM_001004486	NM_001004486 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001004486 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001004486 // GO:0004872 // receptor activity // inferred from electronic annotation
50 1	8157681	NM_001005236 // Hs.567736 // --- /// ENST00000373686 // Hs.567736 // --- /// ENST0000003	NM_001005236 // OR1L1 // olfactory receptor, family 1, subfamily L, member 1 // 9q33.2	OR1L1	NM_001005236	NM_001005236 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001005236 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001005236 // GO:0004872 // receptor activity // inferred from electronic annotation
50 2	8157688	NM_001004453 // Hs.553790 // --- /// ENST00000373684 // Hs.553790 // --- /// ENST0000003	NM_001004453 // OR1L6 // olfactory receptor, family 1, subfamily L, member 6 // 9q33.2	OR1L6	NM_001004453	NM_001004453 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001004453 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001004453 // GO:0004872 // receptor activity // inferred from electronic annotation
50 3	7911258	NM_001004687 // Hs.690412 // normal /// ENST00000359959 // Hs.690412 // normal /// BC13	NM_001004687 // OR2L3 // olfactory receptor, family 2, subfamily L, member 3 // 1q44 //	OR2L3	NM_001004687	NM_001004687 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001004687 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001004687 // GO:0004872 // receptor activity // inferred from electronic annotation
50 4	7925751	NM_001004693 // Hs.553585 // --- /// ENST00000330500 // Hs.553585 // --- /// BC136937 /	NM_001004693 // OR2T10 // olfactory receptor, family 2, subfamily T, member 10 // 1q44	OR2T10	NM_001004693	NM_001004693 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001004693 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001004693 // GO:0004872 // receptor activity // inferred from electronic annotation
50 5	7939916	NM_001005274 // Hs.554530 // --- /// ENST00000314721 // Hs.554530 // --- /// BC140748 /	NM_001005274 // OR4A16 // olfactory receptor, family 4, subfamily A, member 16 // 11q11	OR4A16	NM_001005274	NM_001005274 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001005274 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001005274 // GO:0004872 // receptor activity // inferred from electronic annotation
50 6	7948105	NM_001004700 // Hs.553620 // --- /// ENST00000302231 // Hs.553620 // --- /// BC140727 /	NM_001004700 // OR4C11 // olfactory receptor, family 4, subfamily C, member 11 // 11q11	OR4C11	NM_001004700	NM_001004700 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001004700 // GO:0005886 // plasma membrane // inferred from electronic	NM_001004700 // GO:0004872 // receptor activity // inferred from electronic annotation

							annotation /	
50 7	7948090	NM_001005270 // Hs.553669 // --- ENST00000335238 // Hs.553669 // --- BC136850 /	NM_001005270 // OR4C12 // olfactory receptor, family 4, subfamily C, member 12 // 11p11	OR4C12	NM_001005270	NM_001005270 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001005270 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001005270 // GO:0004872 // receptor activity // inferred from electronic annotation
50 8	7948039	NM_001005513 // Hs.554533 // --- ENST00000360720 // Hs.554533 // --- ENST000004	NM_001005513 // OR4C45 // olfactory receptor, family 4, subfamily C, member 45 // 11p11	OR4C45	NM_001005513	NM_001005513 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001005513 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001005513 // GO:0004872 // receptor activity // inferred from electronic annotation
50 9	7986532	NM_001001674 // Hs.554589 // --- ENST00000332238 // Hs.554589 // --- BC137064 /	NM_001001674 // OR4F15 // olfactory receptor, family 4, subfamily F, member 15 // 15q26	OR4F15	NM_001001674	NM_001001674 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001001674 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001001674 // GO:0004872 // receptor activity // inferred from electronic annotation
51 0	7939930	NM_001004059 // Hs.553621 // --- ENST00000312422 // Hs.553621 // ---	NM_001004059 // OR4S2 // olfactory receptor, family 4, subfamily S, member 2 // 11q11 /	OR4S2	NM_001004059	NM_001004059 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001004059 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001004059 // GO:0004872 // receptor activity // inferred from electronic annotation
51 1	7939867	NM_001004727 // Hs.553565 // --- ENST00000302329 // Hs.553565 // --- BC136935 /	NM_001004727 // OR4X2 // olfactory receptor, family 4, subfamily X, member 2 // 11p11.2	OR4X2	NM_001004727	NM_001004727 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001004727 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001004727 // GO:0004872 // receptor activity // inferred from electronic annotation
51 2	7937948	NM_001005169 // Hs.553727 // --- ENST00000450052 // Hs.553727 // ---	NM_001005169 // OR52I1 // olfactory receptor, family 52, subfamily I, member 1 // 11p15	OR52I1	NM_001005169	NM_001005169 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001005169 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001005169 // GO:0004872 // receptor activity // inferred from electronic annotation
51 3	7939940	NM_001001967 // Hs.553743 // --- ENST00000361760 // Hs.553743 // ---	NM_001001967 // OR5D13 // olfactory receptor, family 5, subfamily D, member 13 // 11q11	OR5D13	NM_001001967	NM_001001967 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001001967 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001001967 // GO:0004872 // receptor activity // inferred from electronic annotation
51 4	7939936	---	ENST00000333984 // OR5D3P // olfactory receptor, family 5, subfamily D, member 3 pseudo	OR5D3P	ENST00000333984	---	---	---
51 5	7939948	NM_001004739 // Hs.528356 // --- ENST00000378397 // Hs.528356 // ---	NM_001004739 // OR5L2 // olfactory receptor, family 5, subfamily L, member 2 // 11q11 /	OR5L2	NM_001004739	NM_001004739 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001004739 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001004739 // GO:0004872 // receptor activity // inferred from electronic annotation

51 6	7948150	NM_001004740 // Hs.553751 // ---	NM_001004740 // OR5M1 // olfactory receptor, family 5, subfamily M, member 1 // 11q12.1	OR5M1	NM_001004740	NM_001004740 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001004740 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001004740 // GO:0004872 // receptor activity // inferred from electronic annotation
51 7	7939988	NM_001004742 // Hs.553631 // --- /// ENST00000312240 // Hs.553631 // --- /// BC136982 /	NM_001004742 // OR5M3 // olfactory receptor, family 5, subfamily M, member 3 // 11q12.1	OR5M3	NM_001004742	NM_001004742 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001004742 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001004742 // GO:0004872 // receptor activity // inferred from electronic annotation
51 8	7948125	NM_001004746 // Hs.553627 // --- /// ENST00000313264 // Hs.553627 // --- /// BC136876 /	NM_001004746 // OR5T2 // olfactory receptor, family 5, subfamily T, member 2 // 11q12.1	OR5T2	NM_001004746	NM_001004746 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001004746 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001004746 // GO:0004872 // receptor activity // inferred from electronic annotation
51 9	7948107	NM_001001960 // Hs.554526 // --- /// ENST00000344514 // Hs.554526 // ---	NM_001001960 // OR5W2 // olfactory receptor, family 5, subfamily W, member 2 // 11q11 /	OR5W2	NM_001001960	NM_001001960 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001001960 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001001960 // GO:0004872 // receptor activity // inferred from electronic annotation
52 0	7963865	NM_001005493 // Hs.554555 // --- /// ENST00000358433 // Hs.554555 // ---	NM_001005493 // OR6C6 // olfactory receptor, family 6, subfamily C, member 6 // 12q13.2	OR6C6	NM_001005493	NM_001005493 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001005493 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001005493 // GO:0004872 // receptor activity // inferred from electronic annotation
52 1	8033742	BC137147 // Hs.446910 // thyroid head and neck tumor /// X89673 // Hs.381327 // ---	BC137147 // OR7D4 // olfactory receptor, family 7, subfamily D, member 4 // 19p13.2 //	OR7D4	BC137147	BC137147 // GO:0007608 // sensory perception of smell // inferred from electronic annot	BC137147 // GO:0005886 // plasma membrane // inferred from electronic annotation /// B	BC137147 // GO:0004872 // receptor activity // inferred from electronic annotation ///
52 2	7948119	NM_001004064 // Hs.554523 // --- /// NM_001004064 // Hs.554523 // --- /// ENST000003015	NM_001004064 // OR8J3 // olfactory receptor, family 8, subfamily J, member 3 // 11q12.1	OR8J3	NM_001004064	NM_001004064 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001004064 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001004064 // GO:0004872 // receptor activity // inferred from electronic annotation
52 3	7939977	NM_001005202 // Hs.553629 // --- /// ENST00000312711 // Hs.553629 // ---	NM_001005202 // OR8K3 // olfactory receptor, family 8, subfamily K, member 3 // 11q12.1	OR8K3	NM_001005202	NM_001005202 // GO:0007608 // sensory perception of smell // inferred from electronic a	NM_001005202 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001005202 // GO:0004872 // receptor activity // inferred from electronic annotation
52 4	7995354	NM_014321 // Hs.49760 // adrenal gland ascites blood bone brain cervix connective	NM_014321 // ORC6 // origin recognition complex, subunit 6 // 16q12 // 23594 /// ENST00	ORC6	NM_014321	NM_014321 // GO:0006260 // DNA replication // not recorded /// ENST0000021909 7 // GO:0	NM_014321 // GO:000808 // origin recognition complex // inferred from direct assay //	NM_014321 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0

52 5	8057689	---	NM_022353 // OSGEPL1 // O-sialoglycoprotein endopeptidase-like 1 // 2q32.2 // 64172 ///	OSGEPL1	NM_022353	NM_022353 // GO:0006508 // proteolysis // inferred from electronic annotation /// ENST	NM_022353 // GO:0005739 // mitochondrion // inferred from electronic annotation /// EN	NM_022353 // GO:0004222 // metalloendopeptidase activity // inferred from electronic an
52 6	7962029	NM_183378 // Hs.674588 // liver muscle testis normal fetus adult /// ENST000003181	NM_183378 // OVCH1 // ovochymase 1 // 12p11.22 // 341350 /// ENST00000318184 // OVCH1 /	OVCH1	NM_183378	NM_183378 // GO:0006508 // proteolysis // inferred from electronic annotation /// ENST	NM_183378 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_183378 // GO:0004252 // serine-type endopeptidase activity // inferred from electron
52 7	8078173	NM_138381 // Hs.655449 // adrenal gland blood bone brain cervix connective tissue	NM_138381 // OXNAD1 // oxidoreductase NAD- binding domain containing 1 // 3p25-p24 // 92	OXNAD1	NM_138381	NM_138381 // GO:0055114 // oxidation reduction // inferred from electronic annotation	NM_138381 // GO:0005739 // mitochondrion // inferred from electronic annotation /// EN	NM_138381 // GO:0016491 // oxidoreductase activity // inferred from electronic annotati
52 8	7990165	NM_020214 // Hs.270244 // adipose tissue adrenal gland blood bone brain cervix co	NM_020214 // PARP6 // poly (ADP-ribose) polymerase family, member 6 // 15q23 // 56965 /	PARP6	NM_020214	---	---	NM_020214 // GO:0003950 // NAD+ ADP-ribosyltransferase activity // inferred from electr
52 9	8170488	NM_173493 // Hs.160594 // bone testis chondrosarcoma normal fetus adult /// ENST00	NM_173493 // PASD1 // PAS domain containing 1 // Xq28 // 139135 /// ENST00000370357 //	PASD1	NM_173493	---	NM_173493 // GO:0005634 // nucleus // inferred from direct assay /// NM_173493 // GO:0	NM_173493 // GO:0004871 // signal transducer activity // inferred from electronic annot
53 0	7965112	NM_002583 // Hs.643130 // adipose tissue adrenal gland bone brain cervix connectiv	NM_002583 // PAWR // PRKC, apoptosis, WT1, regulator // 12q21 // 5074 /// ENST000003288	PAWR	NM_002583	NM_002583 // GO:0000122 // negative regulation of transcription from RNA polymerase II	NM_002583 // GO:0005634 // nucleus // inferred from direct assay /// NM_002583 // GO:0	NM_002583 // GO:0003714 // transcription corepressor activity // traceable author state
53 1	8161211	NM_016734 // Hs.654464 // eye lymph lymph node mammary gland muscle spleen tonsil	NM_016734 // PAX5 // paired box 5 // 9p13 // 5079 /// ENST00000358127 // PAX5 // paired	PAX5	NM_016734	NM_016734 // GO:0000122 // negative regulation of transcription from RNA polymerase II	NM_016734 // GO:0005634 // nucleus // inferred from electronic annotation /// ENST0000	NM_016734 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
53 2	8129876	NM_021635 // Hs.302016 // --- /// BC069109 // Hs.302016 // ---	NM_021635 // PBOV1 // prostate and breast cancer overexpressed 1 // 6q23-q24 // 59351 /	PBOV1	NM_021635	---	NM_021635 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_02163	---
53 3	7971922	NM_203487 // Hs.654709 // blood bone brain ear embryonic tissue eye intestine ki	NM_203487 // PCDH9 // protocadherin 9 // 13q21.32 // 5101 /// NM_020403 // PCDH9 // pro	PCDH9	NM_203487	NM_203487 // GO:0007155 // cell adhesion // inferred from electronic annotation /// NM	NM_203487 // GO:0005886 // plasma membrane // inferred from electronic annotation ///	NM_203487 // GO:0005509 // calcium ion binding // inferred from electronic annotation

53 4	8108724	NM_018930 // Hs.657953 // adrenal gland brain connective tissue eye liver mouth n	NM_018930 // PCDHB10 // protocadherin beta 10 // 5q31 // 56126 /// ENST00000239446 // P	PCDHB10	NM_018930	NM_018930 // GO:0007155 // cell adhesion // inferred from electronic annotation /// NM	NM_018930 // GO:0005886 // plasma membrane // inferred from electronic annotation ///	NM_018930 // GO:0005509 // calcium ion binding // inferred from electronic annotation
53 5	8108703	NM_018939 // Hs.283085 // brain connective tissue esophagus eye kidney liver lung	NM_018939 // PCDHB6 // protocadherin beta 6 // 5q31 // 56130 /// ENST00000231136 // PCD	PCDHB6	NM_018939	NM_018939 // GO:0007155 // cell adhesion // inferred from electronic annotation /// NM	NM_018939 // GO:0005886 // plasma membrane // inferred from electronic annotation ///	NM_018939 // GO:0005509 // calcium ion binding // inferred from electronic annotation
53 6	8144812	NM_006197 // Hs.491148 // adipose tissue adrenal gland ascites bladder blood bone	NM_006197 // PCM1 // pericentriolar material 1 // 8p22-p21.3 // 5108 /// ENST0000032508	PCM1	NM_006197	NM_006197 // GO:0022027 // interkinetic nuclear migration // inferred from sequence or	NM_006197 // GO:0000242 // pericentriolar material // inferred from sequence or structu	NM_006197 // GO:0005515 // protein binding // inferred from physical interaction /// N
53 7	8100458	NM_152401 // Hs.223712 // blood brain connective tissue testis germ cell tumor nor	NM_152401 // PDCL2 // phosducin-like 2 // 4q12 // 132954 /// ENST00000295645 // PDCL2 /	PDCL2	NM_152401	---	---	---
53 8	8057486	NM_005019 // Hs.191046 // brain cervix connective tissue ear embryonic tissue esop	NM_005019 // PDE1A // phosphodiesterase 1A, calmodulin-dependent // 2q32.1 // 5136 ///	PDE1A	NM_005019	NM_005019 // GO:0007165 // signal transduction // inferred from electronic annotation	NM_005019 // GO:0005829 // cytosol // not recorded /// NM_001003683 // GO:0005829 // c	NM_005019 // GO:0004117 // calmodulin-dependent cyclic-nucleotide phosphodiesterase act
53 9	8000501	NR_003610 // Hs.513695 // adipose tissue ascites bladder blood bone brain connect	NR_003610 // PDXDC2P // pyridoxal-dependent decarboxylase domain containing 2, pseudoge	PDXDC2P	NR_003610	NR_003610 // GO:0019752 // carboxylic acid metabolic process // inferred from electroni	AK294177 // GO:0005634 // nucleus // inferred from electronic annotation /// AK294177	NR_003610 // GO:0016829 // lyase activity // inferred from electronic annotation /// N
54 0	7959070	NM_002567 // Hs.433863 // adipose tissue adrenal gland ascites bladder blood bone	NM_002567 // PEBP1 // phosphatidylethanolamin e binding protein 1 // 12q24.23 // 5037 //	PEBP1	NM_002567	NM_002567 // GO:0001505 // regulation of neurotransmitter levels // inferred from elect	NM_002567 // GO:0005615 // extracellular space // inferred from electronic annotation	NM_002567 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
54 1	8091446	NM_053024 // Hs.91747 // adrenal gland ascites bladder blood bone bone marrow bra	NM_053024 // PFN2 // profilin 2 // 3q25.1 // 5217 /// NM_002628 // PFN2 // profilin 2 /	PFN2	NM_053024	NM_053024 // GO:0008064 // regulation of actin polymerization or depolymerization // no	NM_053024 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_053	NM_053024 // GO:0003779 // actin binding // non-traceable author statement /// NM_0530
54 2	8081590	NM_001134439 // Hs.477114 // bladder blood bone bone marrow brain cervix connecti	NM_001134439 // PHLDB2 // pleckstrin homology-like domain, family B, member 2 // 3q13.2	PHLDB2	NM_001134439	---	NM_001134439 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_	---

54 3	8005157	NM_004278 // Hs.499793 // adrenal gland ascites blood bone brain embryonic tissue	NM_004278 // PIGL // phosphatidylinositol glycan anchor biosynthesis, class L // 17p12-	PIGL	NM_004278	NM_004278 // GO:0006506 // GPI anchor biosynthetic process // non- traceable author stat	NM_004278 // GO:0005783 // endoplasmic reticulum // non- traceable author statement ///	NM_004278 // GO:0000225 // N- acetylglucosaminylphosphatidylinosit ol deacetylase activit
54 4	7913252	NM_032409 // Hs.389171 // adipose tissue adrenal gland blood bone brain cervix co	NM_032409 // PINK1 // PTEN induced putative kinase 1 // 1p36 // 65018 /// NM_005216 //	PINK1	NM_032409	NM_032409 // GO:0006468 // protein phosphorylation // inferred from direct assay /// N	NM_032409 // GO:0005739 // mitochondrion // inferred from direct assay /// NM_032409 /	NM_032409 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
54 5	7999769	NR_036447 // Hs.650717 // brain embryonic tissue eye intestine lung prostate skin	NR_036447 // PKD1P1 // polycystic kidney disease 1 (autosomal dominant) pseudogene 1 //	PKD1P1	NR_036447	NM_006985 // GO:0015031 // protein transport // inferred from electronic annotation //	NR_036447 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00698	---
54 6	7961604	NM_033123 // Hs.97542 // brain testis germ cell tumor normal fetus adult /// ENST0	NM_033123 // PLCZ1 // phospholipase C, zeta 1 // 12p12.3 // 89869 /// ENST00000266505 /	PLCZ1	NM_033123	NM_033123 // GO:0006816 // calcium ion transport // inferred from electronic annotation	NM_033123 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_03312	NM_033123 // GO:0004435 // phosphoinositide phospholipase C activity // inferred from e
54 7	7957514	NM_001004330 // Hs.591013 // eye kidney larynx lung lymph node trachea head and n	NM_001004330 // PLEKHG7 // pleckstrin homology domain containing, family G (with RhoGef	PLEKHG7	NM_001004330	NM_001004330 // GO:0035023 // regulation of Rho protein signal transduction // inferred	NM_001004330 // GO:0005622 // intracellular // inferred from electronic annotation ///	NM_001004330 // GO:0005089 // Rho guanyl-nucleotide exchange factor activity // inferre
54 8	7930777	NM_000936 // Hs.501135 // adipose tissue connective tissue heart liver lung lymph	NM_000936 // PNLIP // pancreatic lipase // 10q26.1 // 5406 /// ENST00000369221 // PNLIP	PNLIP	NM_000936	NM_000936 // GO:0009791 // post-embryonic development // inferred from electronic annot	NM_000936 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_000936 // GO:0004806 // triglyceride lipase activity // inferred from electronic ann
54 9	7930760	NM_001011709 // Hs.276724 // brain larynx lung mammary gland pharynx skin breast	NM_001011709 // PNLIPRP3 // pancreatic lipase-related protein 3 // 10q25.3 // 119548 //	PNLIPRP3	NM_001011709	NM_001011709 // GO:0016042 // lipid catabolic process // inferred from electronic annot	NM_001011709 // GO:0005576 // extracellular region // inferred from electronic annotati	NM_001011709 // GO:0004806 // triglyceride lipase activity // inferred from electronic
55 0	8173869	NM_024921 // Hs.267038 // bladder eye intestine larynx liver lung mammary gland	NM_024921 // POF1B // premature ovarian failure, 1B // Xq21.2 // 79983 /// ENST00000262	POF1B	NM_024921	---	---	NM_024921 // GO:0003779 // actin binding // inferred from electronic annotation /// EN
55 1	7942527	NM_006591 // Hs.82502 // bladder blood bone bone marrow brain cervix connective t	NM_006591 // POLD3 // polymerase (DNA- directed), delta 3, accessory subunit // 11q14 //	POLD3	NM_006591	NM_006591 // GO:0000731 // DNA synthesis involved in DNA repair // non- traceable author	NM_006591 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00659	NM_006591 // GO:0003887 // DNA- directed DNA polymerase activity // non-traceable author
55 2	8084488	NM_006232 // Hs.432574 // adrenal gland ascites bladder blood bone bone marrow br	NM_006232 // POLR2H // polymerase (RNA) // (DNA directed) polypeptide H // 3q28 // 5437	POLR2H	NM_006232	NM_006232 // GO:0006350 // transcription // inferred from electronic	NM_006232 // GO:0005634 // nucleus // inferred from direct assay /// NM_006232 //	NM_006232 // GO:0003899 // DNA- directed RNA polymerase activity // non-traceable author

						annotation /// NM	GO:0	
55 3	8036276	NM_006233 // Hs.47062 // adrenal gland ascites bladder blood bone marrow brain ce	NM_006233 // POLR2I // polymerase (RNA) // (DNA directed) polypeptide I, 14.5kDa // 19q	POLR2I	NM_006233	NM_006233 // GO:0006366 // transcription from RNA polymerase II promoter // inferred fr	NM_006233 // GO:0005634 // nucleus // inferred from direct assay /// NM_006233 // GO:0	NM_006233 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
55 4	8061171	NM_006466 // Hs.472227 // adrenal gland blood brain cervix connective tissue embryo	NM_006466 // POLR3F // polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa // 20p	POLR3F	NM_006466	NM_006466 // GO:0006350 // transcription // inferred from electronic annotation /// NM	NM_006466 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00646	NM_006466 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
55 5	8140297	NM_001099415 // Hs.712563 // adipose tissue ascites bladder blood bone bone marrow	NM_001099415 // POM121C // POM121 membrane glycoprotein C // 7q11.2 // 100101267 /// NM	POM121C	NM_001099415	NM_001099415 // GO:0015031 // protein transport // inferred from electronic annotation	NM_001099415 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00	NM_001099415 // GO:0005515 // protein binding // inferred from physical interaction //
55 6	8150276	NM_001102559 // Hs.567619 // adipose tissue adrenal gland blood bone brain cervix	NM_001102559 // PPAPDC1B // phosphatidic acid phosphatase type 2 domain containing 1B /	PPAPDC1B	NM_001102559	---	NM_001102559 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0	NM_001102559 // GO:0008195 // phosphatidate phosphatase activity // inferred from elect
55 7	8166314	NM_006240 // Hs.211589 // adrenal gland brain cervix muscle testis adrenal tumor c	NM_006240 // PPEF1 // protein phosphatase, EF- hand calcium binding domain 1 // Xp22 //	PPEF1	NM_006240	NM_006240 // GO:0006470 // protein dephosphorylation // traceable author statement ///	---	NM_006240 // GO:0004722 // protein serine/threonine phosphatase activity // inferred fr
55 8	7965166	NM_003625 // Hs.506216 // adipose tissue bone brain connective tissue eye kidney	NM_003625 // PPFA2 // protein tyrosine phosphatase, receptor type, f polypeptide (PTPR	PPFA2	NM_003625	NM_003625 // GO:0007160 // cell- matrix adhesion // traceable author statement /// ENST	NM_003625 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_003	NM_003625 // GO:0005515 // protein binding // inferred from physical interaction /// E
55 9	7954940	NM_016488 // Hs.444157 // adrenal gland ascites bladder blood bone bone marrow br	NM_016488 // PPHLN1 // peripilin 1 // 12q12 // 51535 /// NM_001143787 // PPHLN1 // per	PPHLN1	NM_016488	NM_016488 // GO:0031424 // keratinization // inferred from electronic annotation /// N	NM_016488 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_01648	---
56 0	8128726	NM_173672 // Hs.32234 // ascites blood brain eye intestine kidney liver lung ma	NM_173672 // PPIL6 // peptidylprolyl isomerase (cyclophilin)-like 6 // 6q21 // 285755 /	PPIL6	NM_173672	NM_173672 // GO:0006457 // protein folding // inferred from electronic annotation ///	---	NM_173672 // GO:0003755 // peptidyl-prolyl cis-trans isomerase activity // inferred fro

56 1	8125527	---	AF275684 // PPP1R2P1 // protein phosphatase 1, regulatory (inhibitor) subunit 2 pseudog	PPP1R2P1	AF275684	AF275684 // GO:0005975 // carbohydrate metabolic process // inferred from electronic an	---	AF275684 // GO:0004864 // phosphoprotein phosphatase inhibitor activity // inferred fro
56 2	8082869	NM_002718 // Hs.518155 // ascites bone brain connective tissue ear embryonic tissu	NM_002718 // PPP2R3A // protein phosphatase 2, regulatory subunit B", alpha // 3q22.1	PPP2R3A	NM_002718	NM_002718 // GO:0006470 // protein dephosphorylation // inferred from sequence or struc	NM_002718 // GO:0000159 // protein phosphatase type 2A complex // inferred from direct	NM_002718 // GO:0005509 // calcium ion binding // inferred from electronic annotation
56 3	8105633	NM_015342 // Hs.121432 // adrenal gland ascites bladder blood bone bone marrow br	NM_015342 // PPWD1 // peptidylprolyl isomerase domain and WD repeat containing 1 // 5q1	PPWD1	NM_015342	NM_015342 // GO:0006397 // mRNA processing // inferred from electronic annotation ///	NM_015342 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_01534	NM_015342 // GO:0003755 // peptidyl-prolyl cis-trans isomerase activity // inferred fro
56 4	7927280	NM_005972 // Hs.524719 // intestine mouth head and neck tumor normal adult /// ENST	NM_005972 // PPYR1 // pancreatic polypeptide receptor 1 // 10q11.2 // 5540 /// ENST0000	PPYR1	NM_005972	NM_005972 // GO:0007186 // G- protein coupled receptor protein signaling pathway // trac	NM_005972 // GO:0005886 // plasma membrane // not recorded /// NM_005972 // GO:0005887	NM_005972 // GO:0001601 // peptide YY receptor activity // inferred from electronic ann
56 5	7897978	NM_001024661 // Hs.531192 // testis normal /// NM_001099854 // Hs.449964 // normal fe	NM_023013 // PRAMEF1 // PRAME family member 1 // 1p36.21 // 65121 /// NM_001024661 // P	PRAMEF1	NM_023013	---	---	---
56 6	7978407	NM_002742 // Hs.508999 // bone bone marrow brain connective tissue ear embryonic t	NM_002742 // PRKD1 // protein kinase D1 // 14q11 // 5587 /// ENST00000331968 // PRKD1 /	PRKD1	NM_002742	NM_002742 // GO:0006468 // protein phosphorylation // inferred from electronic annotati	NM_002742 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_002	NM_002742 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
56 7	8051547	NM_005813 // Hs.660757 // adrenal gland bladder blood bone brain connective tissue	NM_005813 // PRKD3 // protein kinase D3 // 2p21 // 23683 /// ENST00000379066 // PRKD3 /	PRKD3	NM_005813	NM_005813 // GO:0006468 // protein phosphorylation // inferred from electronic annotati	NM_005813 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_005	NM_005813 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
56 8	8135162	NM_024653 // Hs.406395 // adipose tissue blood brain connective tissue embryonic ti	NM_024653 // PRKRIP1 // PRKR interacting protein 1 (IL11 inducible) // 7q22.1 // 79706	PRKRIP1	NM_024653	NM_024653 // GO:0006469 // negative regulation of protein kinase activity // inferred f	NM_024653 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_02465	NM_024653 // GO:0003725 // double-stranded RNA binding // inferred from electronic anno
56 9	7903519	NM_018061 // Hs.342307 // adrenal gland ascites bladder blood bone bone marrow br	NM_018061 // PRPF38B // PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	PRPF38B	NM_018061	NM_018061 // GO:0006397 // mRNA processing // inferred from electronic annotation ///	NM_018061 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_01806	---

57 0	7974146	NM_017922 // Hs.274337 // bladder blood bone brain connective tissue ear embryoni	NM_017922 // PRPF39 // PRP39 pre-mRNA processing factor 39 homolog (S. cerevisiae) // 1	PRPF39	NM_017922	NM_017922 // GO:0006397 // mRNA processing // inferred from electronic annotation ///	NM_017922 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_017922 // GO:0005488 // binding // inferred from electronic annotation /// ENST0000
57 1	8037259	NM_203287 // Hs.646353 // connective tissue lung placenta vascular normal soft tis	NM_203287 // PSG11 // pregnancy specific beta-1-glycoprotein 11 // 19q13.2 // 5680 ///	PSG11	NM_203287	NM_203287 // GO:0007565 // female pregnancy // traceable author statement /// NM_00278	NM_203287 // GO:0005576 // extracellular region // inferred from electronic annotation	---
57 2	8020691	NM_144662 // Hs.464813 // blood connective tissue pharynx testis leukemia lymphoma	NM_144662 // PSMA8 // proteasome (prosome, macropain) subunit, alpha type, 8 // 18q11.2	PSMA8	NM_144662	NM_144662 // GO:0006511 // ubiquitin-dependent protein catabolic process // inferred fr	NM_144662 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_14466	NM_144662 // GO:0004298 // threonine-type endopeptidase activity // inferred from elect
57 3	8177938	---	NM_014068 // PSORS1C1 // psoriasis susceptibility 1 candidate 1 // 6p21.3 // 170679 ///	PSORS1C1	NM_014068	---	---	---
57 4	7931159	NM_153336 // Hs.281004 // blood bone brain connective tissue embryonic tissue hear	NM_153336 // PSTK // phosphoseryl-tRNA kinase // 10q26.13 // 118672 /// ENST00000368887	PSTK	NM_153336	NM_153336 // GO:0006412 // translation // inferred from electronic annotation /// ENST	---	NM_153336 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
57 5	8120431	NM_003463 // Hs.227777 // adipose tissue adrenal gland ascites bladder blood bone	NM_003463 // PTP4A1 // protein tyrosine phosphatase type IVA, member 1 // 6q12 // 7803	PTP4A1	NM_003463	NM_003463 // GO:0006470 // protein dephosphorylation // inferred from electronic annota	NM_003463 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_003	NM_003463 // GO:0004725 // protein tyrosine phosphatase activity // non-traceable autho
57 6	7933437	NM_001042389 // Hs.440733 // brain connective tissue heart liver pancreas stomach	NM_001042389 // PTPN20A // protein tyrosine phosphatase, non-receptor type 20A // 10q11	PTPN20A	NM_001042389	NM_001042389 // GO:0006470 // protein dephosphorylation // inferred from electronic ann	NM_001042389 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00	NM_001042389 // GO:0004725 // protein tyrosine phosphatase activity // inferred from el
57 7	7933379	NM_001042357 // Hs.499552 // connective tissue pancreas pituitary gland testis chon	NM_001042357 // PTPN20B // protein tyrosine phosphatase, non-receptor type 20B // 10q11	PTPN20B	NM_001042357	NM_001042389 // GO:0006470 // protein dephosphorylation // inferred from electronic ann	NM_001042389 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00	NM_001042389 // GO:0004725 // protein tyrosine phosphatase activity // inferred from el
57 8	7964872	NM_001109754 // Hs.434375 // adipose tissue bladder brain cervix connective tissue	NM_001109754 // PTPRB // protein tyrosine phosphatase, receptor type, B // 12q15-q21 //	PTPRB	NM_001109754	NM_001109754 // GO:0001525 // angiogenesis // inferred from electronic annotation ///	NM_001109754 // GO:0005887 // integral to plasma membrane // traceable author statement	NM_001109754 // GO:0005001 // transmembrane receptor protein tyrosine phosphatase activ

579	8135774	NM_002851 // Hs.489824 // adrenal gland brain connective tissue embryonic tissue ey	NM_002851 // PTPRZ1 // protein tyrosine phosphatase, receptor-type, Z polypeptide 1 //	PTPRZ1	NM_002851	NM_002851 // GO:0006470 // protein dephosphorylation // inferred from electronic annota	NM_002851 // GO:0005578 // proteinaceous extracellular matrix // inferred from electron	NM_002851 // GO:0005001 // transmembrane receptor protein tyrosine phosphatase activity
580	8087271	NM_017730 // Hs.297389 // adipose tissue adrenal gland bladder blood bone bone mar	NM_017730 // QRIC1 // glutamine-rich 1 // 3p21.31 // 54870 /// NM_198880 // QRIC1 //	QRICH1	NM_017730	NM_017730 // GO:0008150 // biological_process // no biological data available /// NM_1	NM_017730 // GO:0005575 // cellular_component // no biological data available /// NM_1	NM_017730 // GO:0003674 // molecular_function // no biological data available /// NM_1
581	8045425	NM_015361 // Hs.412462 // bladder blood bone bone marrow brain cervix connective	NM_015361 // R3HDM1 // R3H domain containing 1 // 2q21.3 // 23518 /// ENST00000264160 /	R3HDM1	NM_015361	---	---	NM_015361 // GO:0003676 // nucleic acid binding // inferred from electronic annotation
582	7936567	NM_014904 // Hs.173656 // adrenal gland blood bone bone marrow brain connective ti	NM_014904 // RAB11FIP2 // RAB11 family interacting protein 2 (class I) // 10q26.11 // 2	RAB11FIP2	NM_014904	NM_014904 // GO:0015031 // protein transport // inferred from electronic annotation //	NM_014904 // GO:0005768 // endosome // inferred from direct assay /// NM_014904 // GO:	NM_014904 // GO:0005515 // protein binding // inferred from physical interaction /// N
583	7950743	NM_014488 // Hs.40758 // adrenal gland blood bone brain connective tissue embryoni	NM_014488 // RAB30 // RAB30, member RAS oncogene family // 11q12-q14 // 27314 /// ENST0	RAB30	NM_014488	NM_014488 // GO:0007264 // small GTPase mediated signal transduction // inferred from e	NM_014488 // GO:0005795 // Golgi stack // traceable author statement /// NM_014488 //	NM_014488 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
584	8107942	NM_005732 // Hs.655835 // adipose tissue adrenal gland blood bone bone marrow brai	NM_005732 // RAD50 // RAD50 homolog (S. cerevisiae) // 5q31 // 10111 /// ENST0000026533	RAD50	NM_005732	NM_005732 // GO:0000019 // regulation of mitotic recombination // inferred from direct	NM_005732 // GO:0000784 // nuclear chromosome, telomeric region // inferred from direct	NM_005732 // GO:0000014 // single-stranded DNA specific endodeoxyribonuclease activity
585	8130151	NM_139165 // Hs.511818 // brain cervix eye liver muscle skin spleen cervical tum	NM_139165 // RAET1E // retinoic acid early transcript 1E // 6q25.1 // 135250 /// ENST00	RAET1E	NM_139165	NM_139165 // GO:0006955 // immune response // inferred from electronic annotation ///	NM_139165 // GO:0005886 // plasma membrane // non-traceable author statement /// NM_13	NM_139165 // GO:0005515 // protein binding // inferred from physical interaction /// E
586	7907657	NM_152663 // Hs.644008 // bladder brain connective tissue embryonic tissue eye hea	NM_152663 // RALGPS2 // Ral GEF with PH domain and SH3 binding motif 2 // 1q25.2 // 551	RALGPS2	NM_152663	NM_152663 // GO:0007264 // small GTPase mediated signal transduction // inferred from e	NM_152663 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_152663 // GO:0005085 // guanyl-nucleotide exchange factor activity // inferred from
587	8100943	NM_201431 // Hs.590920 // bladder brain embryonic tissue eye intestine kidney liv	NM_201431 // RASSF6 // Ras association (RalGDS/AF-6) domain family member 6 // 4q13.3 /	RASSF6	NM_201431	NM_201431 // GO:0006915 // apoptosis // inferred from electronic annotation /// NM_201	---	NM_201431 // GO:0005515 // protein binding // inferred from electronic annotation ///

58 8	8065230	NM_006606 // Hs.69330 // adipose tissue adrenal gland ascites blood bone brain ce	NM_006606 // RBBP9 // retinoblastoma binding protein 9 // 20p11.2 // 10741 /// ENST0000	RBBP9	NM_006606	NM_006606 // GO:0042127 // regulation of cell proliferation // inferred from electronic	NM_006606 // GO:0005634 // nucleus // inferred from direct assay /// NM_006606 // GO:0	NM_006606 // GO:0005515 // protein binding // inferred from electronic annotation ///
58 9	8051215	NM_022128 // Hs.11916 // adrenal gland bone bone marrow brain connective tissue em	NM_022128 // RBKS // ribokinase // 2p23.3 // 64080 /// ENST00000302188 // RBKS // ribok	RBKS	NM_022128	NM_022128 // GO:0005975 // carbohydrate metabolic process // inferred from electronic a	---	NM_022128 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
59 0	8079842	NM_005777 // Hs.696735 // adrenal gland ascites blood bone bone marrow brain cerv	NM_005777 // RBM6 // RNA binding motif protein 6 // 3p21.3 // 10180 /// NM_001167582 //	RBM6	NM_005777	NM_005777 // GO:0006396 // RNA processing // traceable author statement /// NM_0011675	NM_005777 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_005777 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
59 1	8121649	NM_173560 // Hs.352276 // adrenal gland connective tissue liver lung pancreas pros	NM_173560 // RFX6 // regulatory factor X, 6 // 6q22.1 // 222546 /// ENST00000332958 //	RFX6	NM_173560	NM_173560 // GO:0003309 // pancreatic B cell differentiation // inferred from sequence	NM_173560 // GO:0005634 // nucleus // inferred from sequence or structural similarity	NM_173560 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_1
59 2	7989132	NM_022841 // Hs.282855 // adrenal gland ascites bladder blood bone brain cervix	NM_022841 // RFX7 // regulatory factor X, 7 // 15q21.3 // 64864 /// ENST00000423270 //	RFX7	NM_022841	NM_022841 // GO:0006355 // regulation of transcription, DNA-dependent // inferred from	NM_022841 // GO:0005634 // nucleus // inferred from electronic annotation /// ENST0000	NM_022841 // GO:0003677 // DNA binding // inferred from electronic annotation /// ENST
59 3	7907986	NM_001137669 // Hs.121200 // brain prostate testis thyroid head and neck tumor nor	NM_001137669 // RGSL1 // regulator of G-protein signaling like 1 // 1q25 // 353299 ///	RGSL1	NM_001137669	---	NM_001137669 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0	NM_001137669 // GO:0004871 // signal transducer activity // inferred from electronic an
59 4	7946340	NM_024557 // Hs.231850 // adipose tissue adrenal gland brain embryonic tissue eye	NM_024557 // RIC3 // resistance to inhibitors of cholinesterase 3 homolog (C. elegans)	RIC3	NM_024557	NM_024557 // GO:0007204 // elevation of cytosolic calcium ion concentration // inferred	NM_024557 // GO:0000139 // Golgi membrane // inferred from electronic annotation /// N	NM_024557 // GO:0033130 // acetylcholine receptor binding // inferred from electronic a
59 5	8050079	NM_002936 // Hs.568006 // adipose tissue adrenal gland ascites bladder blood bone	NM_002936 // RNASEH1 // ribonuclease H1 // 2p25 // 246243 /// ENST00000315212 // RNASEH	RNASEH1	NM_002936	NM_002936 // GO:0006264 // mitochondrial DNA replication // inferred from electronic an	NM_002936 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00293	NM_002936 // GO:0000287 // magnesium ion binding // inferred from electronic annotation
59 6	8001423	NM_015272 // Hs.298382 // blood bone brain connective tissue embryonic tissue eye	NM_015272 // RPGRIP1L // RPGRIP1-like // 16q12.2 // 23322 /// NM_001127897 // RPGRIP1L	RPGRIP1L	NM_015272	NM_015272 // GO:0001701 // in utero embryonic development // inferred from electronic a	NM_015272 // GO:0005737 // cytoplasm // inferred from direct assay /// NM_015272 // GO	NM_015272 // GO:0031870 // thromboxane A2 receptor binding // inferred from physical in

59 7	7898875	NM_000975 // Hs.719951 // adipose tissue adrenal gland ascites bladder blood bone	NM_000975 // RPL11 // ribosomal protein L11 // 1p36.1-p35 // 6135 /// ENST00000374550 /	RPL11	NM_000975	NM_000975 // GO:0006364 // rRNA processing // inferred from mutant phenotype /// NM_00	NM_000975 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_000975 // GO:0003723 // RNA binding // traceable author statement /// NM_000975 //
59 8	7938295	NM_000990 // Hs.523463 // adipose tissue adrenal gland ascites bladder blood bone	NM_000990 // RPL27A // ribosomal protein L27a // 11p15 // 6157 /// ENST00000314138 // R	RPL27A	NM_000990	NM_000990 // GO:0006412 // translation // traceable author statement /// NM_000990 //	NM_000990 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_000990 // GO:0003723 // RNA binding // traceable author statement /// NM_000990 //
59 9	8085407	NM_001007073 // Hs.265174 // adipose tissue adrenal gland ascites bladder blood bo	NM_001007073 // RPL32 // ribosomal protein L32 // 3p25-p24 // 6161 /// NM_001007074 //	RPL32	NM_001007073	NM_001007073 // GO:0006414 // translational elongation // not recorded /// NM_00100707	NM_001007073 // GO:0005622 // intracellular // inferred from electronic annotation ///	NM_001007073 // GO:0003735 // structural constituent of ribosome // inferred from elect
60 0	7989932	NM_000968 // Hs.186350 // adipose tissue adrenal gland ascites bladder blood bone	NM_000968 // RPL4 // ribosomal protein L4 // 15q22 // 6124 /// ENST00000307961 // RPL4	RPL4	NM_000968	NM_000968 // GO:0006412 // translation // traceable author statement /// NM_000968 //	NM_000968 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_000968 // GO:0003723 // RNA binding // traceable author statement /// NM_000968 //
60 1	8076511	NM_000969 // Hs.532359 // adipose tissue adrenal gland ascites bladder blood bone	NM_000969 // RPL5 // ribosomal protein L5 // 1p22.1 // 6125 /// ENST00000370321 // RPL5	RPL5	NM_000969	NM_000969 // GO:0006364 // rRNA processing // inferred from mutant phenotype /// NM_00	NM_000969 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_000969 // GO:0003723 // RNA binding // traceable author statement /// NM_000969 //
60 2	8171834	NM_000661 // Hs.412370 // adipose tissue adrenal gland ascites bladder blood bone	NM_000661 // RPL9 // ribosomal protein L9 // 4p13 // 6133 /// ENST00000295955 // RPL9 /	RPL9	NM_000661	NM_000661 // GO:0006412 // translation // traceable author statement /// NM_000661 //	NM_000661 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_000661 // GO:0003723 // RNA binding // traceable author statement /// NM_000661 //
60 3	8097782	NM_001006 // Hs.356572 // adipose tissue adrenal gland ascites bladder blood bone	NM_001006 // RPS3A // ribosomal protein S3A // 4q31.2-q31.3 // 6189 /// ENST00000274065	RPS3A	NM_001006	NM_001006 // GO:0006412 // translation // inferred by curator /// NM_001006 // GO:0006	NM_001006 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_001006 // GO:0003723 // RNA binding // non-traceable author statement /// NM_001006
60 4	8036029	---	ENST00000334591 // RPS4XP21 // ribosomal protein S4X pseudogene 21 // 19q13.11 // 12623	RPS4XP21	ENST0000033459 1	---	---	---
60 5	8173825	NM_014496 // Hs.234478 // brain connective tissue embryonic tissue eye kidney lung	NM_014496 // RPS6KA6 // ribosomal protein S6 kinase, 90kDa, polypeptide 6 // Xq21 // 27	RPS6KA6	NM_014496	NM_014496 // GO:0006468 // protein phosphorylation // inferred from electronic annotati	NM_014496 // GO:0005654 // nucleoplasm // not recorded /// NM_014496 // GO:0005829 //	NM_014496 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
60 6	8008887	NM_003161 // Hs.463642 // adrenal gland bladder blood bone bone marrow brain cerv	NM_003161 // RPS6KB1 // ribosomal protein S6 kinase, 70kDa, polypeptide 1 // 17q23.1 //	RPS6KB1	NM_003161	NM_003161 // GO:0000082 // G1/S transition of mitotic cell cycle // inferred from mutan	NM_003161 // GO:0005625 // soluble fraction // inferred from electronic	NM_003161 // GO:0000166 // nucleotide binding // inferred from electronic annotation /

							annotation ///	
60 7	8167897	NM_016656 // Hs.50282 // adrenal gland bladder blood brain cervix embryonic tissue	NM_016656 // RRAGB // Ras-related GTP binding B // Xp11.21 // 10325 /// NM_006064 // RR	RRAGB	NM_016656	NM_016656 // GO:0007165 // signal transduction // traceable author statement /// NM_01	NM_016656 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_01665	NM_016656 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
60 8	8121622	NM_001010892 // Hs.160380 // brain heart lung mouth pharynx pituitary gland testi	NM_001010892 // RSPH4A // radial spoke head 4 homolog A (Chlamydomonas) // 6q22.1 // 34	RSPH4A	NM_001010892	NM_001010892 // GO:0003341 // cilium movement // inferred from mutant phenotype /// NM	NM_001010892 // GO:0001534 // radial spoke // inferred from sequence or structural simi	NM_001010892 // GO:0003674 // molecular_function // no biological data available /// N
60 9	7920249	NM_001045479 // Hs.647713 // --- /// ENST00000368725 // Hs.647713 // --- /// ENST000003	NM_001045479 // S100A7L2 // S100 calcium binding protein A7-like 2 // 1q21.3 // 645922	S100A7L2	NM_001045479	---	---	NM_001045479 // GO:0005509 // calcium ion binding // inferred from electronic annotatio
61 0	7946986	NM_000331 // Hs.632144 // adipose tissue eye intestine kidney liver lung mammary	NM_000331 // SAA1 // serum amyloid A1 // 11p15.1 // 6288 /// NM_001178006 // SAA1 // se	SAA1	NM_000331	NM_000331 // GO:0006953 // acute-phase response // non- traceable author statement ///	NM_000331 // GO:0005576 // extracellular region // not recorded /// NM_000331 // GO:00	NM_000331 // GO:0001664 // G- protein-coupled receptor binding // inferred from direct a
61 1	7970569	NM_014363 // Hs.159492 // adipose tissue blood bone bone marrow brain connective t	NM_014363 // SACS // spastic ataxia of Charlevoix-Saguenay (sacsin) // 13q12 // 26278 /	SACS	NM_014363	NM_014363 // GO:0006457 // protein folding // non-traceable author statement /// NM_01	NM_014363 // GO:0005634 // nucleus // inferred from direct assay /// NM_014363 // GO:0	NM_014363 // GO:0005524 // ATP binding // inferred from electronic annotation /// NM_0
61 2	7902617	NM_001010971 // Hs.591445 // brain heart intestine kidney lung lymph node muscle	NM_001010971 // SAMD13 // sterile alpha motif domain containing 13 // 1p31.1 // 148418	SAMD13	NM_001010971	---	---	---
61 3	7963923	NR_026723 // Hs.505676 // adrenal gland ascites bladder blood bone bone marrow br	NR_026723 // SARNP // SAP domain containing ribonucleoprotein // 12q13.2 // 84324 /// N	SARNP	NR_026723	NR_026723 // GO:0006355 // regulation of transcription, DNA- dependent // non- traceable	NR_026723 // GO:0005634 // nucleus // non- traceable author statement /// NM_033082 //	NR_026723 // GO:0003676 // nucleic acid binding // non-traceable author statement ///
61 4	7917976	NM_194292 // Hs.591447 // ascites bladder bone bone marrow brain cervix embryonic	NM_194292 // SASS6 // spindle assembly 6 homolog (C. elegans) // 1p21.2 // 163786 /// E	SASS6	NM_194292	NM_194292 // GO:0007049 // cell cycle // inferred from electronic annotation /// NM_19	NM_194292 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_194	---
61 5	7985480	NR_003011 // Hs.513091 // ascites bladder blood brain cervix eye heart intestine	NR_003011 // SCARNA15 // small Cajal body-specific RNA 15 // 15q25.2 // 677778 /// ENST	SCARNA15	NR_003011	---	---	---

61 6	7929816	NM_005063 // Hs.558396 // adipose tissue adrenal gland ascites bladder blood bone	NM_005063 // SCD // stearoyl-CoA desaturase (delta-9-desaturase) // 10q24.31 // 6319 //	SCD	NM_005063	NM_005063 // GO:0006633 // fatty acid biosynthetic process // inferred from electronic	NM_005063 // GO:0005783 // endoplasmic reticulum // inferred from direct assay /// NM	NM_005063 // GO:0004768 // stearoyl-CoA 9-desaturase activity // inferred from electron
61 7	7969493	NM_144777 // Hs.534699 // adipose tissue adrenal gland ascites brain connective tis	NM_144777 // SCEL // sciellin // 13q22 // 8796 /// NM_003843 // SCEL // sciellin // 13q	SCEL	NM_144777	NM_144777 // GO:0008544 // epidermis development // inferred from sequence or structura	NM_144777 // GO:0001533 // cornified envelope // traceable author statement /// NM_144	NM_144777 // GO:0005515 // protein binding // inferred from physical interaction /// N
61 8	8089203	NM_020654 // Hs.529551 // blood bone bone marrow brain connective tissue embryonic	NM_020654 // SENP7 // SUMO1/sentrin specific peptidase 7 // 3q12 // 57337 /// NM_001077	SENP7	NM_020654	NM_020654 // GO:0006508 // proteolysis // inferred from electronic annotation /// NM_0	NM_020654 // GO:0005622 // intracellular // inferred from direct assay /// NM_020654 /	NM_020654 // GO:0008233 // peptidase activity // inferred from electronic annotation /
61 9	8057394	NM_178123 // Hs.30977 // adipose tissue adrenal gland bladder blood bone brain ce	NM_178123 // SESTD1 // SEC14 and spectrin domains 1 // 2q31.2 // 91404 /// ENST00000428	SESTD1	NM_178123	NM_178123 // GO:0051925 // regulation of calcium ion transport via voltage-gated calciu	NM_178123 // GO:0034704 // calcium channel complex // inferred from physical interactio	NM_178123 // GO:0001786 // phosphatidylserine binding // inferred from direct assay //
62 0	7917674	NM_001122821 // Hs.436687 // adipose tissue adrenal gland ascites bladder blood bo	NM_001122821 // SET // SET nuclear oncogene // 9q34 // 6418 /// NM_003011 // SET // SET	SET	NM_001122821	NM_001122821 // GO:0006260 // DNA replication // traceable author statement /// NM_001	NM_001122821 // GO:0005634 // nucleus // inferred from direct assay /// NM_001122821 /	NM_001122821 // GO:0004864 // phosphoprotein phosphatase inhibitor activity // traceabl
62 1	8139087	NM_003014 // Hs.658169 // adrenal gland bladder bone brain cervix connective tissu	NM_003014 // SFRP4 // secreted frizzled-related protein 4 // 7p14.1 // 6424 /// ENST000	SFRP4	NM_003014	NM_003014 // GO:0002092 // positive regulation of receptor internalization // inferred	NM_003014 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_003014 // GO:0003674 // molecular function // no biological data available /// NM_0
62 2	8128394	NM_032870 // Hs.520287 // adipose tissue adrenal gland ascites bladder blood bone	NM_032870 // SFRS18 // splicing factor, arginine/serine-rich 18 // 6q16.3 // 25957 ///	SFRS18	NM_032870	---	NM_032870 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_03287	---
62 3	8085754	NM_001012410 // Hs.105153 // bladder blood bone bone marrow brain cervix embryoni	NM_001012410 // SGOL1 // shugoshin-like 1 (S. pombe) // 3p24.3 // 151648 /// NM_0010124	SGOL1	NM_001012410	NM_001012410 // GO:0007049 // cell cycle // inferred from electronic annotation /// NM	NM_001012410 // GO:0000775 // chromosome, centromeric region // inferred from direct as	NM_001012410 // GO:0005515 // protein binding // inferred from physical interaction //
62 4	8021187	NM_001039535 // Hs.134726 // adrenal gland blood bone marrow brain cervix embryoni	NM_001039535 // SKA1 // spindle and kinetochore associated complex subunit 1 // 18q21.1	SKA1	NM_001039535	NM_001039535 // GO:0000090 // mitotic anaphase // inferred from mutant phenotype /// N	NM_001039535 // GO:0000940 // condensed chromosome outer kinetochore // inferred from d	NM_001039535 // GO:0005515 // protein binding // inferred from physical interaction //

62 5	8016414	NM_003726 // Hs.316931 // blood brain connective tissue intestine kidney liver lu	NM_003726 // SKAP1 // src kinase associated phosphoprotein 1 // 17q21.32 // 8631 /// NM	SKAP1	NM_003726	NM_003726 // GO:0045944 // positive regulation of transcription from RNA polymerase II	NM_003726 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00372	NM_003726 // GO:0003823 // antigen binding // inferred from physical interaction /// N
62 6	7921625	NM_001184714 // Hs.492348 // blood bone marrow connective tissue intestine lung ly	NM_001184714 // SLAMF6 // SLAM family member 6 // 1q23.2 // 114836 /// NM_052931 // SLA	SLAMF6	NM_001184714	---	NM_001184714 // GO:0005886 // plasma membrane // inferred from electronic annotation /	NM_001184714 // GO:0004872 // receptor activity // inferred from electronic annotation
62 7	7956658	NM_004731 // Hs.439643 // bladder blood brain connective tissue eye kidney lymph	NM_004731 // SLC16A7 // solute carrier family 16, member 7 (monocarboxylic acid transpo	SLC16A7	NM_004731	NM_004731 // GO:0006848 // pyruvate transport // traceable author statement /// NM_004	NM_004731 // GO:0005624 // membrane fraction // inferred from electronic annotation //	NM_004731 // GO:0005477 // pyruvate secondary active transmembrane transporter activity
62 8	8124351	NM_001098486 // Hs.327179 // brain kidney liver normal fetus /// NM_006632 // Hs.32	NM_001098486 // SLC17A3 // solute carrier family 17 (sodium phosphate), member 3 // 6p2	SLC17A3	NM_001098486	NM_001098486 // GO:0006796 // phosphate metabolic process // traceable author statement	NM_001098486 // GO:0005624 // membrane fraction // traceable author statement /// NM_0	NM_001098486 // GO:0005436 // sodium:phosphate symporter activity // traceable author s
62 9	7940737	NM_001039752 // Hs.188982 // liver liver tumor normal fetus adult /// ENST000003327	NM_001039752 // SLC22A10 // solute carrier family 22, member 10 // 11q12.3 // 387775 //	SLC22A10	NM_001039752	NM_001039752 // GO:0055085 // transmembrane transport // inferred from electronic annot	NM_001039752 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0	NM_001039752 // GO:0005215 // transporter activity // inferred from electronic annotati
63 0	8129666	NM_145176 // Hs.486508 // ascites brain connective tissue embryonic tissue esophagu	NM_145176 // SLC2A12 // solute carrier family 2 (facilitated glucose transporter), memb	SLC2A12	NM_145176	NM_145176 // GO:0008643 // carbohydrate transport // inferred from electronic annotatio	NM_145176 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_145	NM_145176 // GO:0005215 // transporter activity // inferred from electronic annotation
63 1	7926486	NM_001145195 // Hs.350895 // brain eye kidney kidney tumor non-neoplasia normal f	NM_001145195 // SLC39A12 // solute carrier family 39 (zinc transporter), member 12 // 1	SLC39A12	NM_001145195	NM_001145195 // GO:0006811 // ion transport // inferred from electronic annotation ///	NM_001145195 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0	NM_001145195 // GO:0046873 // metal ion transmembrane transporter activity // inferred
63 2	8169504	NM_007231 // Hs.522109 // intestine liver lung mammary gland muscle pancreas phar	NM_007231 // SLC6A14 // solute carrier family 6 (amino acid transporter), member 14 //	SLC6A14	NM_007231	NM_007231 // GO:0006520 // cellular amino acid metabolic process // traceable author st	NM_007231 // GO:0005887 // integral to plasma membrane // inferred from electronic anno	NM_007231 // GO:0005328 // neurotransmitter:sodium symporter activity // inferred from
63 3	8038326	NM_014037 // Hs.130949 // blood bone brain embryonic tissue lung mammary gland mo	NM_014037 // SLC6A16 // solute carrier family 6, member 16 // 19q13.1- q13.4 // 28968 //	SLC6A16	NM_014037	NM_014037 // GO:0006836 // neurotransmitter transport // non- traceable author statement	NM_014037 // GO:0005622 // intracellular // non- traceable author statement /// NM_0140	NM_014037 // GO:0005326 // neurotransmitter transporter activity // non-traceable autho

63 4	8091863	NM_014926 // Hs.101745 // brain uterus germ cell tumor glioma normal fetus adult	NM_014926 // SLITRK3 // SLIT and NTRK-like family, member 3 // 3q26.1 // 22865 /// ENST	SLITRK3	NM_014926	NM_014926 // GO:0007409 // axonogenesis // inferred from electronic annotation /// ENS	NM_014926 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0149	NM_014926 // GO:0005515 // protein binding // inferred from electronic annotation ///
63 5	8106006	NM_000344 // Hs.535788 // adrenal gland blood brain cervix connective tissue eye	NM_000344 // SMN1 // survival of motor neuron 1, telomeric // 5q13 // 6606 /// NM_01741	SMN1	NM_000344	NM_017411 // GO:0000245 // spliceosome assembly // non- traceable author statement ///	NM_017411 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_01741	NM_017411 // GO:0003723 // RNA binding // inferred from electronic annotation /// NM_0
63 6	8171791	NM_014332 // Hs.86492 // brain eye heart liver lung mammary gland muscle prostat	NM_014332 // SMPX // small muscle protein, X- linked // Xp22.1 // 23676 /// ENST00000379	SMPX	NM_014332	NM_014332 // GO:0006941 // striated muscle contraction // traceable author statement /	NM_014332 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_01433	---
63 7	8174715	NR_002584 // Hs.675255 // stomach gastrointestinal tumor adult	NR_002584 // SNORA69 // small nucleolar RNA, H/ACA box 69 // Xq24 // 26779	SNORA69	NR_002584	---	---	---
63 8	8108420	NR_002915 // Hs.684893 // ---	NR_002915 // SNORA74A // small nucleolar RNA, H/ACA box 74A // 5q31.2 // 26821	SNORA74A	NR_002915	---	---	---
63 9	8090565	NR_002992 // Hs.711399 // uterus uterine tumor adult	NR_002992 // SNORA7B // small nucleolar RNA, H/ACA box 7B // 3q21.3 // 677797	SNORA7B	NR_002992	---	---	---
64 0	7976810	---	NR_003231 // SNORD113-3 // small nucleolar RNA, C/D box 113-3 // 14q32.31 // 767563	SNORD113-3	NR_003231	---	---	---
64 1	7982026	---	NR_003302 // SNORD115-10 // small nucleolar RNA, C/D box 115-10 // 15q11.2 // 100033447	SNORD115-10	NR_003302	---	---	---
64 2	7982068	---	NR_003346 // SNORD115-31 // small nucleolar RNA, C/D box 115-31 // 15q11.2 // 100033805	SNORD115-31	NR_003346	---	---	---
64 3	7982072	---	NR_003348 // SNORD115-33 // small nucleolar RNA, C/D box 115-33 // 15q11.2 // 100033807	SNORD115-33	NR_003348	---	---	---

64 4	7982088	---	NR_003356 // SNORD115-41 // small nucleolar RNA, C/D box 115-41 // 15q11.2 // 100033815	SNORD115-41	NR_003356	---	---	---
64 5	7982020	AF400492 // Hs.555970 // adrenal gland bladder bone brain connective tissue ear e	NR_003299 // SNORD115-7 // small nucleolar RNA, C/D box 115-7 // 15q11.2 // 100033444 /	SNORD115-7	NR_003299	AF400492 // GO:0008380 // RNA splicing // traceable author statement	AF400492 // GO:0005634 // nucleus // inferred from electronic annotation /// AF400492	AF400492 // GO:0003723 // RNA binding // inferred from electronic annotation /// AF400
64 6	7981974	---	NR_003328 // SNORD116-13 // small nucleolar RNA, C/D box 116-13 // 15q11.2 // 100033425	SNORD116-13	NR_003328	---	---	---
64 7	7982004	---	NR_003361 // SNORD116-28 // small nucleolar RNA, C/D box 116-28 // 15q11.2 // 100033820	SNORD116-28	NR_003361	---	---	---
64 8	8159004	BX641050 // Hs.499839 // adipose tissue adrenal gland ascites bladder blood bone	NR_002447 // SNORD24 // small nucleolar RNA, C/D box 24 // 9q34 // 26820 /// BX641050 /	SNORD24	NR_002447	BX641050 // GO:0006412 // translation // traceable author statement /// BX641050 // GO	BX641050 // GO:0005624 // membrane fraction // inferred from direct assay /// BX641050	BX641050 // GO:0003723 // RNA binding // traceable author statement /// BX641050 // GO
64 9	8159006	---	NR_000017 // SNORD36B // small nucleolar RNA, C/D box 36B // 9q34 // 26814	SNORD36B	NR_000017	---	---	---
65 0	7991735	NM_024571 // Hs.15277 // adrenal gland ascites blood bone bone marrow brain cervi	NM_024571 // SNRNP25 // small nuclear ribonucleoprotein 25kDa (U11/U12) // 16p13.3 // 7	SNRNP25	NM_024571	NM_024571 // GO:0006397 // mRNA processing // inferred from electronic annotation ///	NM_024571 // GO:0005634 // nucleus // inferred from direct assay /// NM_024571 // GO:0	---
65 1	7993281	NM_001080530 // Hs.585745 // adipose tissue blood bone marrow brain connective tiss	NM_001080530 // SNX29 // sorting nexin 29 // 16p13.13-p13.12 // 92017 /// ENST000003060	SNX29	NM_001080530	NM_001080530 // GO:0007154 // cell communication // inferred from electronic annotation	---	NM_001080530 // GO:0005515 // protein binding // inferred from electronic annotation /
65 2	7903203	NR_033716 // Hs.197015 // adrenal gland ascites bladder bone bone marrow brain ce	NR_033716 // SNX7 // sorting nexin 7 // 1p21.3 // 51375 /// NM_015976 // SNX7 // sortin	SNX7	NR_033716	NR_033716 // GO:0007154 // cell communication // inferred from electronic annotation /	---	NR_033716 // GO:0005515 // protein binding // inferred from physical interaction /// N
65 3	8121066	NM_030960 // Hs.161241 // brain testis normal fetus adult /// ENST00000237201 // Hs	NM_030960 // SPACA1 // sperm acrosome associated 1 // 6q15 // 81833 /// ENST00000237201	SPACA1	NM_030960	---	NM_030960 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0309	---

65 4	8013671	NM_006461 // Hs.514033 // adrenal gland ascites blood bone bone marrow brain cerv	NM_006461 // SPAG5 // sperm associated antigen 5 // 17q11.2 // 10615 /// ENST0000032176	SPAG5	NM_006461	NM_006461 // GO:0007049 // cell cycle // non-traceable author statement /// NM_006461	NM_006461 // GO:0000777 // condensed chromosome kinetochore // inferred from electronic	NM_006461 // GO:0005515 // protein binding // inferred from physical interaction /// E
65 5	8170282	NM_001009613 // Hs.535082 // testis normal /// ENST00000446864 // Hs.535082 // testis	NM_001009613 // SPANXN4 // SPANX family, member N4 // Xq27.3 // 441525 /// ENST000000446	SPANXN4	NM_001009613	---	---	---
65 6	8172800	NM_001009616 // Hs.535218 // kidney normal fetus /// ENST00000375511 // Hs.535218 //	NM_001009616 // SPANXN5 // SPANX family, member N5 // Xp11.22 // 494197 /// ENST00000037	SPANXN5	NM_001009616	---	---	---
65 7	7909768	NM_138796 // Hs.171130 // brain connective tissue eye kidney lung mammary gland p	NM_138796 // SPATA17 // spermatogenesis associated 17 // 1q41 // 128153 /// ENST00000036	SPATA17	NM_138796	---	NM_138796 // GO:0005737 // cytoplasm // inferred from electronic annotation /// ENST00	NM_138796 // GO:0005516 // calmodulin binding // inferred from electronic annotation /
65 8	8056572	NM_020675 // Hs.421956 // adrenal gland bladder blood bone bone marrow brain embr	NM_020675 // SPC25 // SPC25, NDC80 kinetochore complex component, homolog (S. cerevisia	SPC25	NM_020675	NM_020675 // GO:0007049 // cell cycle // inferred from electronic annotation /// NM_02	NM_020675 // GO:0000777 // condensed chromosome kinetochore // inferred from direct ass	NM_020675 // GO:0005515 // protein binding // inferred from physical interaction /// E
65 9	8041138	NM_182756 // Hs.511956 // brain connective tissue eye intestine kidney mammary gla	NM_182756 // SPDYA // speedy homolog A (Xenopus laevis) // 2p23.2 // 245711 /// NM_0011	SPDYA	NM_182756	NM_182756 // GO:0000082 // G1/S transition of mitotic cell cycle // inferred from direc	NM_182756 // GO:0005634 // nucleus // inferred from direct assay /// NM_001142634 // G	NM_182756 // GO:0019901 // protein kinase binding // inferred from physical interaction
66 0	8141750	NM_001031618 // Hs.433879 // ascites brain cervix embryonic tissue eye intestine	NM_001031618 // SPDYE2 // speedy homolog E2 (Xenopus laevis) // 7q22.1 // 441273 /// NM	SPDYE2	NM_001031618	---	---	---
66 1	8104856	NM_024867 // Hs.298863 // bladder blood bone brain embryonic tissue eye intestine	NM_024867 // SPEF2 // sperm flagellar 2 // 5p13.2 // 79925 /// NM_144722 // SPEF2 // sp	SPEF2	NM_024867	NM_024867 // GO:0006139 // nucleobase, nucleoside, nucleotide and nucleic acid metaboli	---	NM_024867 // GO:0005524 // ATP binding // inferred from electronic annotation /// NM_0
66 2	8089627	NM_144718 // Hs.477144 // blood bone bone marrow brain connective tissue ear embr	NM_144718 // SPICE1 // spindle and centriole associated protein 1 // 3q13.2 // 152185 /	SPICE1	NM_144718	NM_144718 // GO:0007049 // cell cycle // inferred from electronic annotation /// NM_14	NM_144718 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_144	NM_144718 // GO:0005515 // protein binding // inferred from physical interaction /// E

66 3	8173198	NM_019003 // Hs.460725 // blood bone embryonic tissue eye lung leukemia normal p	NM_019003 // SPIN2A // spindlin family, member 2A // Xp11.1 // 54466 /// ENST0000037490	SPIN2A	NM_019003	NM_019003 // GO:0007049 // cell cycle // inferred from electronic annotation /// NM_01	NM_019003 // GO:0005575 // cellular_component // no biological data available /// ENST	NM_019003 // GO:0003674 // molecular_function // no biological data available /// ENST
66 4	8109057	NM_001040433 // Hs.631798 // testis germ cell tumor adult /// ENST00000377906 // Hs.6	NM_001040433 // SPINK9 // serine peptidase inhibitor, Kazal type 9 // 5q32 // 643394 //	SPINK9	NM_001040433	---	NM_001040433 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_001040433 // GO:0004867 // serine-type endopeptidase inhibitor activity // inferred
66 5	8066530	NM_006652 // Hs.370724 // testis normal fetus adult /// AY372172 // Hs.370724 // tes	NM_006652 // SPINT3 // serine peptidase inhibitor, Kunitz type, 3 // --- // 10816 /// A	SPINT3	NM_006652	---	NM_006652 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_006652 // GO:0004867 // serine-type endopeptidase inhibitor activity // inferred fro
66 6	7920205	NM_005988 // Hs.355542 // brain cervix connective tissue esophagus larynx lung mo	NM_005988 // SPRR2A // small proline-rich protein 2A // 1q21-q22 // 6700 /// ENST000003	SPRR2A	NM_005988	NM_005988 // GO:0008544 // epidermis development // non-traceable author statement ///	NM_005988 // GO:0001533 // cornified envelope // non-traceable author statement /// NM	NM_005988 // GO:0005488 // binding // inferred from direct assay /// ENST00000392653 /
66 7	7920196	NM_006945 // Hs.505327 // brain connective tissue esophagus intestine larynx lung	NM_006945 // SPRR2D // small proline-rich protein 2D // 1q21-q22 // 6703 /// NM_0010174	SPRR2D	NM_006945	NM_006945 // GO:0008544 // epidermis development // non-traceable author statement ///	NM_006945 // GO:0001533 // cornified envelope // non-traceable author statement /// NM	---
66 8	7983051	NM_016642 // Hs.709819 // bladder brain eye heart kidney lung mammary gland sple	NM_016642 // SPTBN5 // spectrin, beta, non-erythrocytic 5 // 15q21 // 51332 /// ENST000	SPTBN5	NM_016642	NM_016642 // GO:0030036 // actin cytoskeleton organization // non-traceable author stat	NM_016642 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_016	NM_016642 // GO:0003779 // actin binding // non-traceable author statement /// ENST000
66 9	8107578	NM_152546 // Hs.107622 // ascites bladder blood bone brain connective tissue embr	NM_152546 // SRFBP1 // serum response factor binding protein 1 // 5q23.1 // 153443 ///	SRFBP1	NM_152546	NM_152546 // GO:0045449 // regulation of transcription // inferred from electronic anno	NM_152546 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_15254	NM_152546 // GO:0005515 // protein binding // inferred from electronic annotation ///
67 0	7902269	NM_004768 // Hs.479693 // adipose tissue adrenal gland ascites bladder blood bone	NM_004768 // SRSF11 // serine/arginine-rich splicing factor 11 // 1p31 // 9295 /// NM_0	SRSF11	NM_004768	NM_004768 // GO:0006397 // mRNA processing // inferred from electronic annotation ///	NM_004768 // GO:0005634 // nucleus // inferred from direct assay /// NM_004768 // GO:0	NM_004768 // GO:0000166 // nucleotide binding // inferred from electronic annotation /
67 1	8022625	NM_001007559 // Hs.404263 // adipose tissue adrenal gland ascites bladder blood bo	NM_001007559 // SS18 // synovial sarcoma translocation, chromosome 18 // 18q11.2 // 676	SS18	NM_001007559	NM_001007559 // GO:0000226 // microtubule cytoskeleton organization // inferred from el	NM_001007559 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00	NM_001007559 // GO:0005515 // protein binding // inferred from physical interaction //

67 2	8046201	NM_003142 // Hs.632535 // adipose tissue adrenal gland ascites bladder blood bone	NM_003142 // SSB // Sjogren syndrome antigen B (autoantigen La) // 2q31.1 // 6741 /// E	SSB	NM_003142	NM_003142 // GO:0006396 // RNA processing // inferred from electronic annotation /// N	NM_003142 // GO:0005634 // nucleus // inferred from direct assay /// NM_003142 // GO:0	NM_003142 // GO:0000049 // tRNA binding // traceable author statement /// NM_003142 //
67 3	7948211	AB209132 // Hs.523680 // adipose tissue adrenal gland ascites bladder blood bone	AB209132 // SSRP1 // structure specific recognition protein 1 // 11q12 // 6749 /// ENST	SSRP1	AB209132	AB209132 // GO:0006260 // DNA replication // inferred from electronic annotation /// A	AB209132 // GO:0005634 // nucleus // inferred from direct assay /// AB209132 // GO:000	AB209132 // GO:0003677 // DNA binding // inferred from electronic annotation /// AB209
67 4	8167254	NM_005635 // Hs.434142 // bone bone marrow brain connective tissue liver placenta	NM_005635 // SSX1 // synovial sarcoma, X breakpoint 1 // Xp11.23 // 6756 /// ENST000003	SSX1	NM_005635	NM_005635 // GO:0006355 // regulation of transcription, DNA- dependent // inferred from	NM_005635 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_005635 // GO:0003676 // nucleic acid binding // inferred from electronic annotation
67 5	7929012	NM_020799 // Hs.16229 // adrenal gland blood bone brain cervix connective tissue	NM_020799 // STAMBPL1 // STAM binding protein-like 1 // 10q23.31 // 57559 /// ENST000000	STAMBPL1	NM_020799	---	---	NM_020799 // GO:0004221 // ubiquitin thiolesterase activity // inferred from electronic
67 6	7990839	NM_181900 // Hs.513075 // adrenal gland bone brain embryonic tissue esophagus eye	NM_181900 // STARD5 // StAR-related lipid transfer (START) domain containing 5 // 15q26	STARD5	NM_181900	NM_181900 // GO:0006869 // lipid transport // inferred from electronic annotation ///	NM_181900 // GO:0005829 // cytosol // not recorded /// NM_004513 // GO:0005576 // extr	NM_181900 // GO:0008289 // lipid binding // inferred from electronic annotation /// NM
67 7	8057771	NM_003151 // Hs.80642 // blood bone marrow brain connective tissue embryonic tissue	NM_003151 // STAT4 // signal transducer and activator of transcription 4 // 2q32.2-q32.	STAT4	NM_003151	NM_003151 // GO:0006355 // regulation of transcription, DNA- dependent // inferred from	NM_003151 // GO:0005634 // nucleus // inferred from direct assay /// NM_003151 // GO:0	NM_003151 // GO:0003700 // sequence-specific DNA binding transcription factor activity
67 8	7927915	NM_152709 // Hs.37636 // brain embryonic tissue eye intestine lung lymph node mam	NM_152709 // STOX1 // storkhead box 1 // 10q22.1 // 219736 /// NM_001130162 // STOX1 //	STOX1	NM_152709	---	NM_152709 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_15270	NM_152709 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
67 9	8089026	NM_001001850 // Hs.679768 // skin normal /// ENST00000315099 // Hs.679768 // skin nor	NM_001001850 // STX19 // syntaxin 19 // 3q11 // 415117 /// ENST00000315099 // STX19 //	STX19	NM_001001850	NM_001001850 // GO:0006886 // intracellular protein transport // inferred from electron	NM_001001850 // GO:0016020 // membrane // inferred from electronic annotation /// ENST	NM_001001850 // GO:0005484 // SNAP receptor activity // inferred from electronic annota
68 0	8083422	NM_033050 // Hs.279575 // blood kidney liver leukemia liver tumor normal neonate	NM_033050 // SUCNR1 // succinate receptor 1 // 3q25.1 // 56670 /// ENST00000362032 // S	SUCNR1	NM_033050	NM_033050 // GO:0008150 // biological_process // no biological data available /// ENST	NM_033050 // GO:0005886 // plasma membrane // inferred from electronic annotation ///	NM_033050 // GO:0004872 // receptor activity // inferred from electronic annotation //

68 1	8044212	NM_001056 // Hs.436123 // bladder blood brain connective tissue intestine kidney	NM_001056 // SULT1C2 // sulfotransferase family, cytosolic, 1C, member 2 // 2q12.3 // 6	SULT1C2	NM_001056	NM_001056 // GO:0009308 // amine metabolic process // traceable author statement /// N	NM_001056 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_001	NM_001056 // GO:0008146 // sulfotransferase activity // inferred from direct assay ///
68 2	8044225	NM_006588 // Hs.312644 // adipose tissue brain connective tissue embryonic tissue h	NM_006588 // SULT1C4 // sulfotransferase family, cytosolic, 1C, member 4 // 2q12.3 // 2	SULT1C4	NM_006588	NM_006588 // GO:0051923 // sulfation // inferred from direct assay /// ENST00000272452	NM_006588 // GO:0005575 // cellular_component // no biological data available /// NM_0	NM_006588 // GO:0008146 // sulfotransferase activity // inferred from direct assay ///
68 3	8034583	NM_001105578 // Hs.655173 // lymph placenta skin testis uterus germ cell tumor ly	NM_001105578 // SYCE2 // synaptonemal complex central element protein 2 // 19p13.2 // 2	SYCE2	NM_001105578	NM_001105578 // GO:0007049 // cell cycle // inferred from electronic annotation /// NM	NM_001105578 // GO:0000801 // central element // inferred from sequence or structural s	NM_001105578 // GO:0005515 // protein binding // inferred from electronic annotation /
68 4	8129615	NM_138327 // Hs.375030 // stomach gastrointestinal tumor adult /// ENST00000275216 //	NM_138327 // TAAR1 // trace amine associated receptor 1 // 6q23.2 // 134864 /// ENST000	TAAR1	NM_138327	NM_138327 // GO:0007186 // G-protein coupled receptor protein signaling pathway // trac	NM_138327 // GO:0005886 // plasma membrane // not recorded /// NM_138327 // GO:0016021	NM_138327 // GO:0004872 // receptor activity // inferred from electronic annotation //
68 5	8134420	NM_003182 // Hs.2563 // brain connective tissue embryonic tissue eye kidney nerve	NM_003182 // TAC1 // tachykinin, precursor 1 // 7q21-q22 // 6863 /// NM_013996 // TAC1	TAC1	NM_003182	NM_003182 // GO:0002675 // positive regulation of acute inflammatory response // inferr	NM_003182 // GO:0005576 // extracellular region // not recorded /// NM_003182 // GO:00	NM_003182 // GO:0031835 // substance P receptor binding // inferred from electronic ann
68 6	8020702	NM_005640 // Hs.369519 // ascites bone marrow brain cervix connective tissue embryo	NM_005640 // TAF4B // TAF4b RNA polymerase II, TATA box binding protein (TBP)-associate	TAF4B	NM_005640	NM_005640 // GO:0006355 // regulation of transcription, DNA-dependent // non-traceable	NM_005640 // GO:0005634 // nucleus // non-traceable author statement /// NM_005640 //	NM_005640 // GO:0003677 // DNA binding // inferred from direct assay /// NM_005640 //
68 7	8099506	NM_153365 // Hs.479223 // adrenal gland bladder blood bone brain connective tissue	NM_153365 // TAPT1 // transmembrane anterior posterior transformation 1 // 4p15.32 // 2	TAPT1	NM_153365	NM_153365 // GO:0001701 // in utero embryonic development // inferred from electronic a	NM_153365 // GO:0016020 // membrane // inferred from electronic annotation /// NM_1533	NM_153365 // GO:0004872 // receptor activity // inferred from electronic annotation //
68 8	8142624	NM_016945 // Hs.272395 // --- /// ENST00000249284 // Hs.272395 // --- /// BC095524 // H	NM_016945 // TAS2R16 // taste receptor, type 2, member 16 // 7q31.1-q31.3 7q31 // 50833	TAS2R16	NM_016945	NM_016945 // GO:0001580 // detection of chemical stimulus involved in sensory perceptio	NM_016945 // GO:0005783 // endoplasmic reticulum // inferred from direct assay /// NM_	NM_016945 // GO:0004872 // receptor activity // inferred from electronic annotation //
68 9	7961298	NM_181429 // Hs.553716 // --- /// ENST00000334266 // Hs.553716 // --- /// BC131742 // H	NM_181429 // TAS2R42 // taste receptor, type 2, member 42 // 12p13 // 353164 /// ENST00	TAS2R42	NM_181429	NM_181429 // GO:0050896 // response to stimulus // inferred from electronic annotation	NM_181429 // GO:0016020 // membrane // inferred from electronic annotation ///	NM_181429 // GO:0004872 // receptor activity // inferred from electronic annotation //

							NM_1814	
69 0	7961245	NM_023917 // Hs.272391 // --- /// ENST00000240691 // Hs.272391 // --- /// BC095519 // H	NM_023917 // TAS2R9 // taste receptor, type 2, member 9 // 12p13 // 50835 /// ENST00000	TAS2R9	NM_023917	NM_023917 // GO:0008150 // biological_process // no biological data available /// NM_0	NM_023917 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0239	NM_023917 // GO:0004872 // receptor activity // inferred from electronic annotation //
69 1	8169035	NM_024863 // Hs.194329 // adipose tissue ascites bladder blood bone bone marrow b	NM_024863 // TCEAL4 // transcription elongation factor A (SII)-like 4 // Xq22.2 // 7992	TCEAL4	NM_024863	NM_024863 // GO:0045449 // regulation of transcription // inferred from electronic anno	NM_024863 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00100	---
69 2	8023159	NM_016427 // Hs.375035 // testis normal /// ENST00000332567 // Hs.375035 // testis no	NM_016427 // TCEB3B // transcription elongation factor B polypeptide 3B (elongin A2) //	TCEB3B	NM_016427	NM_016427 // GO:0006354 // RNA elongation // inferred from electronic annotation /// N	NM_016427 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_01642	NM_016427 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
69 3	8108954	NM_006706 // Hs.723884 // ascites bladder blood bone bone marrow brain cervix co	NM_006706 // TCERG1 // transcription elongation regulator 1 // 5q31 // 10915 /// NM_001	TCERG1	NM_006706	NM_006706 // GO:0006366 // transcription from RNA polymerase II promoter // traceable a	NM_006706 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00104	NM_006706 // GO:0003702 // RNA polymerase II transcription factor activity // traceable
69 4	7939184	NM_018393 // Hs.655341 // adipose tissue adrenal gland blood bone marrow brain con	NM_018393 // TCP11L1 // t-complex 11 (mouse)- like 1 // 11p13 // 55346 /// NM_001145541	TCP11L1	NM_018393	NM_001326 // GO:0006378 // mRNA polyadenylation // traceable author statement /// NM_0	NM_001326 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_001326 // GO:0003723 // RNA binding // traceable author statement /// NM_001326 //
69 5	8093096	ENST00000442633 // Hs.710321 // bone brain esophagus eye liver lung mammary gland	NM_152773 // TCTEX1D2 // Tctex1 domain containing 2 // 3q29 // 255758 /// ENST000004426	TCTEX1D2	NM_152773	---	ENST0000044263 3 // GO:0016020 // membrane // inferred from electronic annotation /// E	NM_152773 // GO:0005515 // protein binding // inferred from physical interaction /// B
69 6	8169385	NR_002718 // Hs.592361 // brain embryonic tissue intestine kidney liver spleen te	NR_002718 // TDGF3 // teratocarcinoma-derived growth factor 3, pseudogene // Xq22.3 //	TDGF3	NR_002718	NR_002718 // GO:0001570 // vasculogenesis // inferred from electronic annotation /// N	NR_002718 // GO:0005575 // cellular componen t // no biological data available /// NR_0	NR_002718 // GO:0008083 // growth factor activity // non-traceable author statement //
69 7	7930631	NM_198795 // Hs.333132 // brain liver pancreas prostate testis trachea liver tumo	NM_198795 // TDRD1 // tudor domain containing 1 // 10q25.3 // 56165 /// ENST00000251864	TDRD1	NM_198795	NM_198795 // GO:0007126 // meiosis // inferred from electronic annotation /// NM_19879	NM_198795 // GO:0005737 // cytoplasm // inferred from sequence or structural similarity	NM_198795 // GO:0003676 // nucleic acid binding // inferred from electronic annotation

69 8	7907749	NM_173533 // Hs.197354 // brain intestine larynx lung pharynx testis colorectal t	NM_173533 // TDRD5 // tudor domain containing 5 // 1q25.2 // 163589 /// ENST00000367614	TDRD5	NM_173533	---	---	NM_173533 // GO:0003676 // nucleic acid binding // inferred from electronic annotation
69 9	8120082	NM_001010870 // Hs.656983 // brain connective tissue eye kidney liver mammary gland	NM_001010870 // TDRD6 // tudor domain containing 6 // 6p12.3 // 221400 /// NM_001168359	TDRD6	NM_001010870	NM_001010870 // GO:0007275 // multicellular organismal development // inferred from ele	NM_001010870 // GO:0005737 // cytoplasm // inferred from sequence or structural similar	NM_001010870 // GO:0003676 // nucleic acid binding // inferred from electronic annotati
70 0	8168646	NM_138960 // Hs.592220 // brain testis normal adult /// NM_139214 // Hs.112148 // te	NM_138960 // TGIF2LX // TGFB-induced factor homeobox 2-like, X-linked // Xq21.31 // 903	TGIF2LX	NM_138960	NM_138960 // GO:0006355 // regulation of transcription, DNA-dependent // inferred from	NM_138960 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_13921	NM_138960 // GO:0003700 // sequence-specific DNA binding transcription factor activity
70 1	8176397	NM_139214 // Hs.112148 // testis normal fetus /// NM_138960 // Hs.592220 // brain te	NM_139214 // TGIF2LY // TGFB-induced factor homeobox 2-like, Y-linked // Yp11.2 // 9065	TGIF2LY	NM_139214	NM_139214 // GO:0006355 // regulation of transcription, DNA-dependent // inferred from	NM_139214 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_13896	NM_139214 // GO:0003700 // sequence-specific DNA binding transcription factor activity
70 2	8051746	NR_028102 // Hs.468254 // adrenal gland bone bone marrow brain cervix connective t	NR_028102 // THUMPD2 // THUMP domain containing 2 // 2p22.1 2p22-p21 // 80745 /// NM_02	THUMPD2	NR_028102	---	---	NR_028102 // GO:0008168 // methyltransferase activity // inferred from electronic annot
70 3	7998952	NM_033208 // Hs.718663 // bladder bone marrow brain kidney lung muscle parathyroi	NM_033208 // TIGD7 // tigger transposable element derived 7 // 16p13.3 // 91151 /// NM_	TIGD7	NM_033208	NM_033208 // GO:0045449 // regulation of transcription // inferred from electronic anno	NM_033208 // GO:0000775 // chromosome, centromeric region // inferred from electronic a	NM_033208 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
70 4	8147830	NM_030788 // Hs.652230 // blood brain lung skin thyroid head and neck tumor norma	NM_030788 // TM7SF4 // transmembrane 7 superfamily member 4 // 8q23 // 81501 /// ENST00	TM7SF4	NM_030788	NM_030788 // GO:0030316 // osteoclast differentiation // inferred from sequence or stru	NM_030788 // GO:0005886 // plasma membrane // inferred from electronic annotation ///	---
70 5	7982552	NM_152453 // Hs.179646 // brain pharynx testis germ cell tumor normal fetus adult	NM_152453 // TMCO5A // transmembrane and coiled-coil domains 5A // 15q14 // 145942 ///	TMCO5A	NM_152453	---	NM_152453 // GO:0016020 // membrane // inferred from electronic annotation /// NM_1524	---
70 6	8016841	NM_001099640 // Hs.173233 // adipose tissue brain connective tissue embryonic tissue	NM_001099640 // TMEM100 // transmembrane protein 100 // 17q22 // 55273 /// NM_018286 //	TMEM100	NM_001099640	NM_001099640 // GO:0008150 // biological_process // no biological data available /// N	NM_001099640 // GO:0005575 // cellular_componen t // no biological data available /// N	NM_001099640 // GO:0003674 // molecular_function // no biological data available /// N
70 7	8077728	ENST00000245046 // Hs.475392 // adipose tissue adrenal gland ascites bladder blood	ENST00000245046 // TMEM111 // transmembrane protein 111 // 3p25.3 // 55831 /// AK092352	TMEM111	ENST00000245046	ENST00000245046 // GO:0008150 // biological_process // no biological data available //	ENST00000245046 // GO:0005575 // cellular_componen t // no biological data available //	ENST00000245046 // GO:0003674 // molecular_function // no biological data available

70 8	7943369	NM_032021 // Hs.44004 // adrenal gland bone brain ear eye heart intestine kidney	NM_032021 // TMEM133 // transmembrane protein 133 // 11q22.1 // 83935 /// ENST000003031	TMEM133	NM_032021	---	NM_032021 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0320	---
70 9	7944554	NM_001198670 // Hs.643516 // bone brain connective tissue embryonic tissue eye int	NM_001198670 // TMEM136 // transmembrane protein 136 // 11q23.3 // 219902 /// NM_174926	TMEM136	NM_001198670	---	NM_001198670 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0	---
71 0	8159379	NM_032928 // Hs.356744 // adrenal gland ascites blood bone brain cervix connectiv	NM_032928 // TMEM141 // transmembrane protein 141 // 9q34.3 // 85014 /// ENST0000029007	TMEM141	NM_032928	---	NM_032928 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0329	---
71 1	8027876	NM_032635 // Hs.9234 // adipose tissue adrenal gland ascites blood bone brain cer	NM_032635 // TMEM147 // transmembrane protein 147 // 19q13.1 // 10430 /// ENST000002222	TMEM147	NM_032635	---	NM_032635 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0326	NM_032635 // GO:0005515 // protein binding // inferred from physical interaction /// E
71 2	8165642	NM_053045 // Hs.724611 // adrenal gland blood bone brain cervix connective tissue	NM_053045 // TMEM203 // transmembrane protein 203 // 9q34.3 // 94107 /// ENST0000034366	TMEM203	NM_053045	---	NM_053045 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0530	---
71 3	8100701	NM_182502 // Hs.407122 // cervix esophagus larynx mouth muscle pharynx esophageal	NM_182502 // TMPRSS11B // transmembrane protease, serine 11B // 4q13.2 // 132724 /// EN	TMPRSS11B	NM_182502	NM_182502 // GO:0006508 // proteolysis // inferred from electronic annotation /// ENST	NM_182502 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_182502 // GO:0004252 // serine-type endopeptidase activity // inferred from electron
71 4	8100688	NM_207407 // Hs.677557 // esophagus eye mouth placenta esophageal tumor head and n	NM_207407 // TMPRSS11F // transmembrane protease, serine 11F // 4q13.2 // 389208 /// EN	TMPRSS11F	NM_207407	NM_207407 // GO:0006508 // proteolysis // inferred from electronic annotation /// ENST	NM_207407 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_207407 // GO:0004252 // serine-type endopeptidase activity // inferred from electron
71 5	8174189	NM_021992 // Hs.56145 // bone brain ear embryonic tissue eye heart kidney liver	NM_021992 // TMSB15A // thymosin beta 15a // Xq21.33-q22.3 // 11013 /// D82345 // TMSB1	TMSB15A	NM_021992	NM_021992 // GO:0030036 // actin cytoskeleton organization // inferred from electronic	NM_021992 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_021	NM_021992 // GO:0003779 // actin binding // inferred from electronic annotation /// D8

71 6	8169073	NM_194324 // Hs.675540 // brain intestine kidney liver thymus uterus normal soft	NM_194324 // TMSB15B // thymosin beta 15B // Xq22.2 // 286527 /// NR_003238 // H2BFXP /	TMSB15B	NM_194324	NM_194324 // GO:0030036 // actin cytoskeleton organization // inferred from electronic	NM_194324 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_194	NM_194324 // GO:0003779 // actin binding // inferred from electronic annotation /// NM
71 7	8126839	NM_014452 // Hs.443577 // adipose tissue adrenal gland bladder bone bone marrow br	NM_014452 // TNFRSF21 // tumor necrosis factor receptor superfamily, member 21 // 6p21.	TNFRSF21	NM_014452	NM_014452 // GO:0007165 // signal transduction // inferred from electronic annotation	NM_014452 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0144	NM_014452 // GO:0004872 // receptor activity // inferred from electronic annotation //
71 8	8073032	NM_020243 // Hs.595072 // adrenal gland ascites bladder blood bone bone marrow br	NM_020243 // TOMM22 // translocase of outer mitochondrial membrane 22 homolog (yeast) /	TOMM22	NM_020243	NM_020243 // GO:0006626 // protein targeting to mitochondrion // traceable author state	NM_020243 // GO:0000299 // integral to membrane of membrane fraction // inferred from d	NM_020243 // GO:0004872 // receptor activity // inferred from electronic annotation //
71 9	8140739	AB007455 // Hs.274329 // adipose tissue adrenal gland bone marrow brain cervix emb	AB007455 // TP53TG1 // TP53 target 1 (non-protein coding) // 7q21.1 // 11257 /// NR_015	TP53TG1	AB007455	AB007455 // GO:0006950 // response to stress // traceable author statement /// AB00745	AB007455 // GO:0005634 // nucleus // non-traceable author statement /// NR_015381 // G	AB007455 // GO:0003674 // molecular_function // no biological data available /// NR_01
72 0	8151475	NM_001025252 // Hs.368433 // adrenal gland ascites bladder blood bone bone marrow	NM_001025252 // TPD52 // tumor protein D52 // 8q21 // 7163 /// NM_001025253 // TPD52 //	TPD52	NM_001025252	NM_001025252 // GO:0009653 // anatomical structure morphogenesis // traceable author st	NM_001025252 // GO:0005737 // cytoplasm // inferred from direct assay /// NM_001025252	NM_001025252 // GO:0005509 // calcium ion binding // inferred from direct assay /// NM
72 1	7957205	NM_173353 // Hs.376337 // brain testis germ cell tumor normal /// ENST00000333850 //	NM_173353 // TPH2 // tryptophan hydroxylase 2 // 12q21.1 // 121278 /// ENST00000333850	TPH2	NM_173353	NM_173353 // GO:0009072 // aromatic amino acid family metabolic process // inferred fro	---	NM_173353 // GO:0004510 // tryptophan 5-monoxygenase activity // inferred from electro
72 2	7909545	NM_145759 // Hs.523930 // adipose tissue blood bone marrow brain cervix embryonic	NM_145759 // TRAF5 // TNF receptor-associated factor 5 // 1q32 // 7188 /// NM_004619 //	TRAF5	NM_145759	NM_145759 // GO:0007165 // signal transduction // inferred from electronic annotation	NM_145759 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_004	NM_145759 // GO:0004842 // ubiquitin-protein ligase activity // inferred from electroni
72 3	7939912	NM_024114 // Hs.195715 // brain placenta skin uterus germ cell tumor normal skin	NM_024114 // TRIM48 // tripartite motif-containing 48 // 11q11 // 79097 /// ENST0000041	TRIM48	NM_024114	---	NM_024114 // GO:0005622 // intracellular // inferred from electronic annotation /// EN	NM_024114 // GO:0005515 // protein binding // inferred from electronic annotation ///
72 4	8051226	NM_017910 // Hs.468026 // adipose tissue ascites blood bone brain cervix connecti	NM_017910 // TRMT61B // tRNA methyltransferase 61 homolog B (S. cerevisiae) // 2p23.2 /	TRMT61B	NM_017910	NM_017910 // GO:0008033 // tRNA processing // inferred from electronic annotation ///	ENST0000033405 6 // GO:0005634 // nucleus // inferred from direct assay	NM_017910 // GO:0008168 // methyltransferase activity // inferred from electronic annot

72 5	8174556	NM_012471 // Hs.657709 // brain placenta thyroid head and neck tumor normal adult	NM_012471 // TRPC5 // transient receptor potential cation channel, subfamily C, member	TRPC5	NM_012471	NM_012471 // GO:0006811 // ion transport // inferred from electronic annotation /// NM	NM_012471 // GO:0005887 // integral to plasma membrane // traceable author statement /	NM_012471 // GO:0005216 // ion channel activity // inferred from electronic annotation
72 6	7904203	NM_000549 // Hs.406687 // connective tissue pancreas pituitary gland normal soft ti	NM_000549 // TSHB // thyroid stimulating hormone, beta // 1p13 // 7252 /// ENST00000256	TSHB	NM_000549	NM_000549 // GO:0007186 // G-protein coupled receptor protein signaling pathway // trac	NM_000549 // GO:0005576 // extracellular region // not recorded /// ENST0000025659 2 //	NM_000549 // GO:0005179 // hormone activity // inferred from electronic annotation ///
72 7	8107270	NM_033035 // Hs.389874 // bone marrow brain connective tissue eye lung salivary gl	NM_033035 // TSLP // thymic stromal lymphopoietin // 5q22.1 // 85480 /// NR_033425 // T	TSLP	NM_033035	---	NM_033035 // GO:0005576 // extracellular region // inferred from electronic annotation	NM_033035 // GO:0005125 // cytokine activity // inferred from electronic annotation //
72 8	7964927	NM_004616 // Hs.170563 // ascites bladder bone bone marrow brain cervix connectiv	NM_004616 // TSPAN8 // tetraspanin 8 // 12q14.1-q21.1 // 7103 /// ENST00000247829 // TS	TSPAN8	NM_004616	NM_004616 // GO:0006486 // protein glycosylation // traceable author statement /// NM	NM_004616 // GO:0005764 // lysosome // traceable author statement /// NM_004616 // GO:	NM_004616 // GO:0004871 // signal transducer activity // traceable author statement //
72 9	8129097	NM_003309 // Hs.486292 // blood bone brain cervix connective tissue ear eye hear	NM_003309 // TSPYL1 // TSPY-like 1 // 6q22.1 // 7259	TSPYL1	NM_003309	NM_003309 // GO:0006334 // nucleosome assembly // inferred from electronic annotation	NM_003309 // GO:0005575 // cellular componen t // no biological data available /// NM_0	NM_003309 // GO:0003674 // molecular_function // no biological data available
73 0	7939434	NM_018259 // Hs.191186 // adrenal gland bladder blood bone bone marrow brain cerv	NM_018259 // TTC17 // tetratricopeptide repeat domain 17 // 11p11.2 // 55761 /// ENST00	TTC17	NM_018259	---	---	NM_018259 // GO:0005488 // binding // inferred from electronic annotation /// ENST0000
73 1	8104812	NM_144725 // Hs.435742 // brain embryonic tissue eye lung mammary gland ovary pha	NM_144725 // TTC23L // tetratricopeptide repeat domain 23-like // 5p13.2 // 153657 ///	TTC23L	NM_144725	---	---	NM_144725 // GO:0005488 // binding // inferred from electronic annotation /// ENST0000
73 2	8103064	NM_031956 // Hs.378893 // brain connective tissue kidney lung ovary pharynx place	NM_031956 // TTC29 // tetratricopeptide repeat domain 29 // 4q31.22 // 83894 /// ENST00	TTC29	NM_031956	---	---	NM_031956 // GO:0005488 // binding // inferred from electronic annotation /// ENST0000
73 3	8023920	NM_006701 // Hs.465498 // adipose tissue adrenal gland ascites bladder blood bone	NM_006701 // TXNL4A // thioredoxin-like 4A // 18q23 // 10907 /// ENST00000269601 // TXN	TXNL4A	NM_006701	NM_006701 // GO:0000245 // spliceosome assembly // traceable author statement /// NM_0	NM_006701 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00670	NM_006701 // GO:0005515 // protein binding // inferred from physical interaction /// E
73 4	8019842	NM_001071 // Hs.592338 // adrenal gland ascites bladder blood bone bone marrow br	NM_001071 // TYMS // thymidylate synthetase // 18p11.32 // 7298 /// ENST00000323274 //	TYMS	NM_001071	NM_001071 // GO:0006139 // nucleobase, nucleoside, nucleotide and nucleic acid	---	NM_001071 // GO:0000166 // nucleotide binding // inferred from electronic annotation /

						metaboli		
73 5	7990054	NM_018003 // Hs.108049 // adipose tissue adrenal gland ascites bladder bone brain	NM_018003 // UACA // uveal autoantigen with coiled-coil domains and ankyrin repeats //	UACA	NM_018003	NM_018003 // GO:0008150 // biological_process // no biological data available /// NM_0	NM_018003 // GO:0005576 // extracellular region // non-traceable author statement ///	NM_018003 // GO:0003674 // molecular_function // no biological data available /// NM_0
73 6	7906863	NM_003115 // Hs.492859 // adipose tissue ascites bladder blood bone bone marrow b	NM_003115 // UAP1 // UDP-N-acetylglucosamine pyrophosphorylase 1 // 1q23.3 // 6675 ///	UAP1	NM_003115	NM_003115 // GO:0006048 // UDP-N-acetylglucosamine biosynthetic process // traceable au	NM_003115 // GO:0005634 // nucleus // inferred from direct assay /// NM_003115 // GO:0	NM_003115 // GO:0003977 // UDP-N-acetylglucosamine diphosphorylase activity // not reco
73 7	7968670	NM_016617 // Hs.643655 // adipose tissue adrenal gland ascites bladder blood bone	NM_016617 // UFM1 // ubiquitin-fold modifier 1 // 13q13.3 // 51569 /// ENST00000239878	UFM1	NM_016617	NM_016617 // GO:0071569 // protein ufmylation // inferred from direct assay /// ENST00	NM_016617 // GO:0005634 // nucleus // inferred from direct assay /// NM_016617 // GO:0	NM_016617 // GO:0005515 // protein binding // inferred from physical interaction /// E
73 8	8100760	NM_024743 // Hs.122583 // bladder brain intestine kidney liver muscle pancreas p	NM_024743 // UGT2A3 // UDP glucuronosyltransferase 2 family, polypeptide A3 // 4q13.2 /	UGT2A3	NM_024743	NM_024743 // GO:0008152 // metabolic process // inferred from electronic annotation //	NM_024743 // GO:0016020 // membrane // inferred from electronic annotation /// NM_0247	NM_024743 // GO:0015020 // glucuronosyltransferase activity // inferred from direct ass
73 9	8043820	NM_014044 // Hs.13370 // blood bone bone marrow brain cervix connective tissue em	NM_014044 // UNC50 // unc-50 homolog (C. elegans) // 2q11.2 // 25972 /// ENST0000035776	UNC50	NM_014044	NM_014044 // GO:0007166 // cell surface receptor linked signaling pathway // inferred f	NM_014044 // GO:0000139 // Golgi membrane // inferred from electronic annotation /// N	NM_014044 // GO:0003723 // RNA binding // inferred from electronic annotation /// ENST
74 0	7984132	NM_006537 // Hs.458499 // adipose tissue adrenal gland ascites bladder blood bone	NM_006537 // USP3 // ubiquitin specific peptidase 3 // 15q22.3 // 9960 /// ENST00000380	USP3	NM_006537	NM_006537 // GO:0000278 // mitotic cell cycle // inferred from mutant phenotype /// NM	NM_006537 // GO:0000790 // nuclear chromatin // inferred from direct assay /// NM_0065	NM_006537 // GO:0004221 // ubiquitin thiolesterase activity // inferred from mutant phe
74 1	7938448	NM_017944 // Hs.577256 // adrenal gland ascites bladder blood bone bone marrow br	NM_017944 // USP47 // ubiquitin specific peptidase 47 // 11p15.3 // 55031 /// ENST00000	USP47	NM_017944	NM_017944 // GO:0006511 // ubiquitin-dependent protein catabolic process // inferred fr	NM_017944 // GO:0019005 // SCF ubiquitin ligase complex // inferred from direct assay	NM_017944 // GO:0004221 // ubiquitin thiolesterase activity // inferred from electronic
74 2	8171013	NM_003372 // Hs.436803 // adrenal gland ascites bladder blood bone bone marrow br	NM_003372 // VBP1 // von Hippel-Lindau binding protein 1 // Xq28 // 7411 /// ENST000002	VBP1	NM_003372	NM_003372 // GO:0006457 // protein folding // inferred from electronic annotation ///	NM_003372 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00337	NM_003372 // GO:0051082 // unfolded protein binding // inferred from electronic annotat

74 3	8122865	NM_003381 // Hs.53973 // brain connective tissue embryonic intestine lung m	NM_003381 // VIP // vasoactive intestinal peptide // 6q25 // 7432 /// NM_194435 // VIP	VIP	NM_003381	NM_003381 // GO:0007186 // G-protein coupled receptor protein signaling pathway // trac	NM_003381 // GO:0005576 // extracellular region // not recorded /// NM_194435 // GO:00	NM_003381 // GO:0005184 // neuropeptide hormone activity // traceable author statement
74 4	7911174	NM_173858 // Hs.553686 // --- /// BC126341 // Hs.553686 // ---	NM_173858 // VN1R5 // vomeronasal 1 receptor 5 (gene/pseudogene) // 1q44 // 317705 ///	VN1R5	NM_173858	NM_173858 // GO:0019236 // response to pheromone // inferred from electronic annotation	NM_173858 // GO:0005886 // plasma membrane // inferred from electronic annotation ///	NM_173858 // GO:0004872 // receptor activity // inferred from electronic annotation //
74 5	8074934	NM_013378 // Hs.136713 // bone marrow connective tissue kidney lymph node pharynx	NM_013378 // VPRED3 // pre-B lymphocyte 3 // 22q11.23 22q11 // 29802 /// ENST0000024894	VPRED3	NM_013378	---	NM_013378 // GO:0005783 // endoplasmic reticulum // non-traceable author statement ///	---
74 6	8142671	NM_003941 // Hs.143728 // adrenal gland ascites bladder bone bone marrow brain ce	NM_003941 // WASL // Wiskott-Aldrich syndrome-like // 7q31.3 // 8976 /// ENST0000022302	WASL	NM_003941	NM_003941 // GO:0006461 // protein complex assembly // inferred from electronic annotat	NM_003941 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00394	NM_003941 // GO:0003779 // actin binding // inferred from electronic annotation /// NM
74 7	8094638	NM_025132 // Hs.438482 // adrenal gland bladder blood bone brain connective tissue	NM_025132 // WDR19 // WD repeat domain 19 // 4p14 // 57728 /// ENST00000399820 // WDR19	WDR19	NM_025132	NM_025132 // GO:0030030 // cell projection organization // inferred from electronic ann	NM_025132 // GO:0005737 // cytoplasm // inferred from electronic annotation /// NM_025	NM_025132 // GO:0005488 // binding // inferred from electronic annotation /// ENST0000
74 8	8091922	NM_178824 // Hs.213762 // bone marrow brain lung ovary placenta testis trachea g	NM_178824 // WDR49 // WD repeat domain 49 // 3q26.1 // 151790 /// ENST00000308378 // WD	WDR49	NM_178824	ENST0000047625 7 // GO:0006928 // cellular component movement // traceable author statem	ENST0000047625 7 // GO:0005576 // extracellular region // inferred from electronic annot	ENST00000476257 // GO:0004867 // serine-type endopeptidase inhibitor activity // inferr
74 9	7988990	NM_182758 // Hs.122125 // bladder embryonic tissue esophagus eye intestine kidney	NM_182758 // WDR72 // WD repeat domain 72 // 15q21.3 // 256764 /// ENST00000396328 // W	WDR72	NM_182758	---	---	---
75 0	8066569	NM_147197 // Hs.374924 // testis normal /// ENST00000356562 // Hs.374924 // testis no	NM_147197 // WFDC11 // WAP four-disulfide core domain 11 // 20q13.12 // 259239 /// ENST	WFDC11	NM_147197	---	NM_147197 // GO:0005576 // extracellular region // inferred from electronic annotation	---
75 1	8041197	NM_001127401 // Hs.515890 // adipose tissue adrenal gland ascites bladder blood bo	NM_001127401 // YPEL5 // yippee-like 5 (Drosophila) // 2p23.1 // 51646 /// NM_001127400	YPEL5	NM_001127401	NM_001127401 // GO:0055114 // oxidation reduction // inferred from electronic annotatio	---	NM_001127401 // GO:0008113 // peptide-methionine-(S)-S-oxide reductase activity // infe

75 2	8107375	NM_022828 // Hs.231942 // adipose tissue adrenal gland ascites blood bone marrow b	NM_022828 // YTHDC2 // YTH domain containing 2 // 5q22.2 // 64848 /// ENST00000161863 /	YTHDC2	NM_022828	---	---	NM_022828 // GO:000166 // nucleotide binding // inferred from electronic annotation /
75 3	7970887	NM_001136571 // Hs.569254 // testis normal /// ENST00000345108 // Hs.569254 // testis	NM_001136571 // ZAR1L // zygote arrest 1-like // 13q13.1 // 646799 /// ENST00000345108	ZAR1L	NM_001136571	---	---	---
75 4	7946635	NM_021211 // Hs.655066 // adipose tissue adrenal gland bladder blood bone bone mar	NM_021211 // ZBED5 // zinc finger, BED-type containing 5 // 11p15.3 // 58486 /// NM_001	ZBED5	NM_021211	---	---	NM_021211 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
75 5	7976101	NM_024824 // Hs.325846 // adrenal gland bladder blood bone bone marrow brain cerv	NM_024824 // ZC3H14 // zinc finger CCH-type containing 14 // 14q31.3 // 79882 /// NM_0	ZC3H14	NM_024824	---	NM_024824 // GO:0005634 // nucleus // inferred from electronic annotation /// NM_00116	NM_024824 // GO:0003723 // RNA binding // inferred from electronic annotation /// NM_0
75 6	8173261	NM_001178032 // Hs.28249 // adrenal gland blood bone brain cervix connective tissu	NM_001178032 // ZC4H2 // zinc finger, C4H2 domain containing // Xq11.2 // 55906 /// NM	ZC4H2	NM_001178032	---	---	NM_001178032 // GO:0005515 // protein binding // inferred from physical interaction //
75 7	8039625	NM_052882 // Hs.348622 // --- /// ENST00000269834 // Hs.348622 // --- /// AF365931 // H	NM_052882 // ZIM3 // zinc finger, imprinted 3 // --- // 114026 /// ENST00000269834 // Z	ZIM3	NM_052882	NM_052882 // GO:0006355 // regulation of transcription, DNA-dependent // inferred from	NM_052882 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_052882 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
75 8	8133049	NM_016220 // Hs.50216 // bladder blood bone brain connective tissue embryonic tiss	NM_016220 // ZNF107 // zinc finger protein 107 // 7q11.2 // 51427 /// NM_001013746 // Z	ZNF107	NM_016220	NM_016220 // GO:0008150 // biological_process // no biological data available /// NM_0	NM_016220 // GO:0005575 // cellular_component // no biological data available /// NM_0	NM_016220 // GO:0003674 // molecular_function // no biological data available /// NM_0
75 9	8035765	NM_021030 // Hs.659932 // adrenal gland ascites blood bone marrow brain embryonic	NM_021030 // ZNF14 // zinc finger protein 14 // 19p13.11 // 7561 /// ENST00000344099 //	ZNF14	NM_021030	NM_021030 // GO:0006355 // regulation of transcription, DNA-dependent // inferred from	NM_021030 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_021030 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
76 0	8117630	NM_003447 // Hs.535177 // ascites kidney mammary gland ovary pancreas placenta pr	NM_003447 // ZNF165 // zinc finger protein 165 // 6p21.3 // 7718 /// ENST00000252206 //	ZNF165	NM_003447	NM_003447 // GO:0006355 // regulation of transcription, DNA-dependent // non-traceable	NM_003447 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_003447 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
76 1	8025488	---	NM_003451 // ZNF177 // zinc finger protein 177 // 19p13.2 // 7730 /// NM_001172650 // Z	ZNF177	NM_003451	NM_003451 // GO:0000122 // negative regulation of transcription from RNA polymerase II	NM_003451 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_003451 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0

76 2	8124498	NR_002722 // Hs.8198 // bone brain connective tissue embryonic tissue eye heart i	NR_002722 // ZNF204P // zinc finger protein 204, pseudogene // 6p21.3 // 7754 /// NR_02	ZNF204P	NR_002722	---	---	---
76 3	8029399	NM_001032372 // Hs.145956 // adrenal gland bladder blood brain connective tissue e	NM_001032372 // ZNF226 // zinc finger protein 226 // 19q13.2 // 7769 /// NM_001032373 /	ZNF226	NM_001032372	NM_001032372 // GO:0006355 // regulation of transcription, DNA- dependent // inferred fr	NM_001032372 // GO:0005622 // intracellular // inferred from electronic annotation ///	NM_001032372 // GO:0003677 // DNA binding // inferred from electronic annotation /// N
76 4	8005106	X52357 // Hs.684886 // ---	X52357 // ZNF29P // zinc finger protein 29, pseudogene // 17p12 // 7577	ZNF29P	X52357	---	---	---
76 5	8065517	NM_015655 // Hs.633621 // bladder bone brain cervix connective tissue embryonic ti	NM_015655 // ZNF337 // zinc finger protein 337 // 20p11.1 // 26152 /// ENST00000376436	ZNF337	NM_015655	NM_015655 // GO:0006355 // regulation of transcription, DNA- dependent // inferred from	NM_015655 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_015655 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
76 6	8039044	NR_028343 // Hs.147765 // adrenal gland bladder blood brain connective tissue embr	NR_028343 // ZNF415 // zinc finger protein 415 // 19q13.42 // 55786 /// NM_001164309 //	ZNF415	NR_028343	NR_028343 // GO:0045449 // regulation of transcription // inferred from electronic anno	NR_028343 // GO:0005622 // intracellular // inferred from electronic annotation /// NR	NR_028343 // GO:0003677 // DNA binding // inferred from electronic annotation /// NR_0
76 7	8027292	NM_133473 // Hs.687547 // adipose tissue adrenal gland brain embryonic tissue eye	NM_133473 // ZNF431 // zinc finger protein 431 // 19p12 // 170959 /// ENST00000311048 /	ZNF431	NM_133473	NM_133473 // GO:0006355 // regulation of transcription, DNA- dependent // inferred from	NM_133473 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_133473 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_1
76 8	8038942	NM_014650 // Hs.655934 // blood brain cervix connective tissue embryonic tissue ey	NM_014650 // ZNF432 // zinc finger protein 432 // 19q13.41 // 9668 /// ENST00000221315	ZNF432	NM_014650	NM_014650 // GO:0006355 // regulation of transcription, DNA- dependent // inferred from	NM_014650 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_014650 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
76 9	8157105	NM_021224 // Hs.370379 // adrenal gland ascites blood bone brain cervix embryonic	NM_021224 // ZNF462 // zinc finger protein 462 // 9q31.2 // 58499 /// ENST00000277225 /	ZNF462	NM_021224	NM_021224 // GO:0043392 // negative regulation of DNA binding // inferred from electron	NM_021224 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_021224 // GO:0008270 // zinc ion binding // inferred from electronic annotation ///
77 0	8030908	NM_144684 // Hs.147025 // adrenal gland bone brain embryonic tissue eye heart int	NM_144684 // ZNF480 // zinc finger protein 480 // 19q13.41 // 147657 /// ENST0000046824	ZNF480	NM_144684	NM_144684 // GO:0006355 // regulation of transcription, DNA- dependent // inferred from	NM_144684 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_144684 // GO:0003676 // nucleic acid binding // inferred from electronic annotation
77 1	8027345	NM_020855 // Hs.232108 // kidney muscle testis germ cell tumor normal fetus adult	NM_020855 // ZNF492 // zinc finger protein 492 // 19p12 // 57615 /// ENST00000456783 //	ZNF492	NM_020855	NM_020855 // GO:0006355 // regulation of transcription, DNA- dependent // inferred from	NM_020855 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_020855 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0

77 2	8031732	NR_002166 // Hs.446620 // adipose tissue adrenal gland blood bone brain cervix em	NM_173631 // ZNF547 // zinc finger protein 547 // 19q13.43 // 284306 /// NR_002166 // T	ZNF547	NM_173631	NM_173631 // GO:0006355 // regulation of transcription, DNA- dependent // inferred from	NM_173631 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_173631 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_1
77 3	8033767	NM_152476 // Hs.631613 // bone brain skin testis chondrosarcoma germ cell tumor s	NM_152476 // ZNF560 // zinc finger protein 560 // 19p13.2 // 147741 /// ENST00000301480	ZNF560	NM_152476	NM_152476 // GO:0006355 // regulation of transcription, DNA- dependent // inferred from	NM_152476 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_152476 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_1
77 4	8038989	NM_198457 // Hs.696848 // ascites bladder brain connective tissue embryonic tissue	NM_198457 // ZNF600 // zinc finger protein 600 // 19q13.41 // 162966 /// ENST0000033823	ZNF600	NM_198457	NM_198457 // GO:0045449 // regulation of transcription // inferred from electronic anno	NM_198457 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_198457 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_1
77 5	7967863	NM_183238 // Hs.720299 // connective tissue eye kidney lymph node pharynx placenta	NM_183238 // ZNF605 // zinc finger protein 605 // 12q24.33 // 100289635 /// NM_00116471	ZNF605	NM_183238	NM_183238 // GO:0006355 // regulation of transcription, DNA- dependent // inferred from	NM_183238 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_183238 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_1
77 6	7910190	NR_033184 // Hs.30323 // brain cervix embryonic tissue eye heart intestine kidney	NR_033184 // ZNF678 // zinc finger protein 678 // 1q42.13 // 339500 /// NM_178549 // ZN	ZNF678	NR_033184	NR_033184 // GO:0045449 // regulation of transcription // inferred from electronic anno	NR_033184 // GO:0005622 // intracellular // inferred from electronic annotation /// NR	NR_033184 // GO:0003677 // DNA binding // inferred from electronic annotation /// NR_0
77 7	8035855	NM_138286 // Hs.187337 // skin uterus skin tumor uterine tumor /// NM_138286 // Hs.3	NM_138286 // ZNF681 // zinc finger protein 681 // 19p12 // 148213 /// ENST00000402377 /	ZNF681	NM_138286	NM_138286 // GO:0006355 // regulation of transcription, DNA- dependent // inferred from	NM_138286 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_138286 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_1
77 8	8132917	NM_182633 // Hs.660834 // brain eye lung mammary gland mouth placenta prostate s	NM_182633 // ZNF713 // zinc finger protein 713 // 7p11.2 // 349075 /// ENST00000429591	ZNF713	NM_182633	NM_182633 // GO:0006355 // regulation of transcription, DNA- dependent // inferred from	NM_182633 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_182633 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_1
77 9	8098745	NM_001137608 // Hs.698668 // embryonic tissue testis thymus germ cell tumor normal	NM_001137608 // ZNF732 // zinc finger protein 732 // 4p16.3 // 654254 /// AK302099 // Z	ZNF732	NM_001137608	NM_001137608 // GO:0006355 // regulation of transcription, DNA- dependent // inferred fr	NM_001137608 // GO:0005622 // intracellular // inferred from electronic annotation ///	NM_001137608 // GO:0003677 // DNA binding // inferred from electronic annotation /// N
78 0	8078380	NM_001137674 // Hs.585139 // heart intestine kidney liver lymph node mouth pancre	NM_001137674 // ZNF860 // zinc finger protein 860 // 3p23 // 344787 /// ENST00000360311	ZNF860	NM_001137674	NM_001137674 // GO:0006355 // regulation of transcription, DNA- dependent // inferred fr	NM_001137674 // GO:0005622 // intracellular // inferred from electronic annotation ///	NM_001137674 // GO:0003677 // DNA binding // inferred from electronic annotation /// N

78 1	8035842	NM_003430 // Hs.654471 // blood brain connective tissue embryonic tissue esophagus	NM_003430 // ZNF91 // zinc finger protein 91 // 19p12 // 7644 /// ENST00000300619 // ZN	ZNF91	NM_003430	NM_003430 // GO:0006355 // regulation of transcription, DNA- dependent // non- traceable	NM_003430 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_003430 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
78 2	8117640	NM_025231 // Hs.656641 // adipose tissue adrenal gland blood bone brain connective	NM_025231 // ZSCAN16 // zinc finger and SCAN domain containing 16 // 6p22.1 // 80345 //	ZSCAN16	NM_025231	NM_025231 // GO:0006355 // regulation of transcription, DNA- dependent // inferred from	NM_025231 // GO:0005622 // intracellular // inferred from electronic annotation /// NM	NM_025231 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_0
78 3	8031799	NM_152677 // Hs.469663 // placenta uterus normal adult /// ENST00000318203 // Hs.469	NM_152677 // ZSCAN4 // zinc finger and SCAN domain containing 4 // 19q13.43 // 201516 /	ZSCAN4	NM_152677	NM_152677 // GO:0006355 // regulation of transcription, DNA- dependent // inferred from	NM_152677 // GO:0000784 // nuclear chromosome, telomeric region // inferred from sequen	NM_152677 // GO:0003677 // DNA binding // inferred from electronic annotation /// NM_1