

Appendix 1. Methods for Literature and Pathways Analysis Software Searches

Manual Literature Search

We performed MEDLINE searches from 1966 to April Week 2 2011 for papers describing gene expression in human fetal organs using the exploded MeSH terms [“fetus” OR “fetal development”] AND [“gene expression”, “gene expression profiling” OR “microarray analysis”] AND each of the following organs in turn: “heart”, “kidney”, “bladder”, “skin” and “intestine”. All search results were limited to human studies, English language, and normal fetal tissue samples from mid-trimester. Exclusion criteria were: non-human, non-English, cell culture, first or third trimester fetal samples, and abnormal fetal organs.

The literature search for placental and amniotic membrane gene expression studies was performed using the exploded MeSH terms [“microarray analysis” AND “placenta”] and [“microarray analysis” AND “amnion”], respectively. Inclusion criteria were: human, normal pregnancy, and tissue studies. Exclusion criteria were animal, abnormal pregnancy, and cell culture studies. Due to the lack of search results when a “second trimester” limit was added to the search terms, no gestational age limit was used.

Pathways Analysis Software Organ System Development and Function Gene Lists

We created lists of genes involved in organ system development and function using the pathways analysis software functions and disease search tool, and the terms “cardiovascular system”, “hair and skin”, “renal and urological system” and “digestive system”, and “fetal

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membranes". The placental gene list was formed using the terms "placenta", "trophoblast", "syncytiotrophoblast", or "cytotrophoblast". The pathways analysis software search was very broad based and included data from non-human and cell culture studies from both fetal and postnatal studies.

Categorization of Genes From the MEDLINE and Pathways Analysis Software Searches

After performing the MEDLINE and pathways analysis software searches, we categorized the genes as 1 to 3 in descending order of the human fetal relevance of the data used to select the genes.

Category 1 genes were based on Affymetrix microarray studies of normal mid-trimester human fetal organs identified from MEDLINE searches with available GEO datasets. The genes that were most consistently expressed in that fetal organ, either by being present in all samples in the dataset, or within the top quintile for expression value, were selected. The genes that were consistently expressed in the GEO data set and mapped to the appropriate organ system development and function in pathways analysis software were labeled Category 1 genes.

Category 2 genes were based on the manual literature searches, and included information from microarray, RT-PCR, immunohistochemistry, in situ hybridization and Northern blot studies.

Category 3 genes were based on the pathways analysis software organ system development and function searches, and included animal, non-fetal and cell culture data.

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Appendix 2. Amniotic Fluid Core Transcriptome Gene List

| Gene Symbol | Gene Name |
|-----------------------|---|
| ACTB | <i>actin, beta</i> |
| ACTG1 | <i>actin, gamma 1</i> |
| ACVR2A | <i>activin A receptor, type IIA</i> |
| AKAP2 /// PALM2-AKAP2 | <i>A kinase anchor protein 2</i> |
| AKIRIN2 | <i>akirin 2</i> |
| ALDH1B1 | <i>aldehyde dehydrogenase 1 family, member B1</i> |
| ALDOB | <i>aldolase B, fructose-bisphosphate</i> |
| AMD1 | <i>adenosylmethionine decarboxylase 1</i> |
| AMZ1 | <i>archaelysin family metallopeptidase 1</i> |
| ANAPC16 | <i>anaphase promoting complex subunit 16</i> |
| ANKRD12 | <i>ankyrin repeat domain 12</i> |
| ANKRD28 | <i>ankyrin repeat domain 28</i> |
| ANP32B | <i>acidic (leucine-rich) nuclear phosphoprotein 32 family, member B</i> |
| ANXA2 | <i>annexin A2</i> |
| AP2S1 | <i>adaptor-related protein complex 2, sigma 1 subunit</i> |
| APBB2 | <i>amyloid beta (A4) precursor protein-binding, family B, member 2</i> |
| APOL2 | <i>apolipoprotein L, 2</i> |
| APP | <i>amyloid beta (A4) precursor protein</i> |
| ARF6 | <i>ADP-ribosylation factor 6</i> |
| ARID4B | <i>AT rich interactive domain 4B (RBP1-like)</i> |

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|------------------------------------|--|
| <i>ARMCX6</i> /// <i>LOC653354</i> | <i>armadillo repeat containing, X-linked 6</i> |
| <i>ARPC2</i> | <i>actin related protein 2/3 complex, subunit 2, 34kDa</i> |
| <i>ATF7IP</i> | <i>activating transcription factor 7 interacting protein</i> |
| <i>ATMIN</i> | <i>ATM interactor</i> |
| <i>ATP6</i> | <i>ATP synthase F0 subunit 6</i> |
| <i>ATP5A1</i> | <i>ATP synthase, H⁺ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle</i> |
| <i>ATP8B1</i> | <i>ATPase, aminophospholipid transporter, class I, type 8B, member 1</i> |
| <i>ATXN7L3B</i> | <i>ataxin 7-like 3B</i> |
| <i>BASPI</i> | <i>brain abundant, membrane attached signal protein 1</i> |
| <i>BAT2L2</i> | <i>proline-rich coiled-coil 2C</i> |
| <i>BICD2</i> | <i>bicaudal D homolog 2 (<i>Drosophila</i>)</i> |
| <i>BRCC3</i> | <i>BRCA1/BRCA2-containing complex, subunit 3</i> |
| <i>BTF3</i> | <i>basic transcription factor 3</i> |
| <i>BTF3L4</i> | <i>basic transcription factor 3-like 4</i> |
| <i>BZW2</i> | <i>basic leucine zipper and W2 domains 2</i> |
| <i>CAMK2N1</i> | <i>calcium/calmodulin-dependent protein kinase II inhibitor 1</i> |
| <i>CAPZA2</i> | <i>capping protein (actin filament) muscle Z-line, alpha 2</i> |
| <i>CASP2</i> | <i>caspase 2, apoptosis-related cysteine peptidase</i> |
| <i>CASP6</i> | <i>caspase 6, apoptosis-related cysteine peptidase</i> |
| <i>CBX3</i> | <i>chromobox homolog 3</i> |
| <i>CCARI</i> | <i>cell division cycle and apoptosis regulator 1</i> |
| <i>CCDC152</i> | <i>coiled-coil domain containing 152</i> |

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| <i>CCDC72</i> | <i>coiled-coil domain containing 72</i> |
| <i>CCND2</i> | <i>cyclin D2</i> |
| <i>CCNG2</i> | <i>cyclin G2</i> |
| <i>CCNJ</i> | <i>cyclin J</i> |
| <i>CCT6A</i> | <i>chaperonin containing TCP1, subunit 6A (zeta 1)</i> |
| <i>CD3EAP</i> | <i>CD3e molecule, epsilon associated protein</i> |
| <i>CDC25B</i> | <i>cell division cycle 25 homolog B (S. pombe)</i> |
| <i>CDC27</i> | <i>cell division cycle 27 homolog (S. cerevisiae)</i> |
| <i>CDC42</i> | <i>cell division cycle 42 (GTP binding protein, 25kDa)</i> |
| <i>CDC42SE1</i> | <i>CDC42 small effector 1</i> |
| <i>CDC5L</i> | <i>CDC5 cell division cycle 5-like (S. pombe)</i> |
| <i>CDK12</i> | <i>cyclin-dependent kinase 12</i> |
| <i>CDK13</i> | <i>cyclin-dependent kinase 13</i> |
| <i>CDV3</i> | <i>CDV3 homolog (mouse)</i> |
| <i>CFL1</i> | <i>cofilin 1 (non-muscle)</i> |
| <i>CHCHD2</i> | <i>coiled-coil-helix-coiled-coil-helix domain containing 2</i> |
| <i>CHMP2B</i> | <i>chromatin modifying protein 2B</i> |
| <i>CMBL</i> | <i>carboxymethylenebutenolidase homolog (Pseudomonas)</i> |
| <i>COL1A1</i> | <i>collagen, type I, alpha 1</i> |
| <i>COL7A1</i> | <i>collagen, type VII, alpha 1</i> |
| <i>CORO1C</i> | <i>coronin, actin binding protein, 1C</i> |
| <i>COX1</i> | <i>cytochrome c oxidase subunit I</i> |

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| <i>COX2</i> | <i>cytochrome c oxidase subunit II</i> |
| <i>COX5A</i> | <i>cytochrome c oxidase subunit Va</i> |
| <i>CPSF2</i> | <i>cleavage and polyadenylation specific factor 2, 100kDa</i> |
| <i>CSDE1</i> | <i>cold shock domain containing E1, RNA-binding</i> |
| <i>CSRP2</i> | <i>cysteine and glycine-rich protein 2</i> |
| <i>CSTA</i> | <i>cystatin A (stefin A)</i> |
| <i>CTBP2</i> | <i>C-terminal binding protein 2</i> |
| <i>CTCFL /// HMGB1</i> | <i>CCCTC-binding factor (zinc finger protein)-like</i> |
| <i>CTSB</i> | <i>cathepsin B</i> |
| <i>CYP1A2</i> | <i>cytochrome P450, family 1, subfamily A, polypeptide 2</i> |
| <i>D4S234E /// FOXP1</i> | <i>DNA segment on chromosome 4 (unique) 234 expressed</i> |
| <i>DAB2</i> | <i>disabled homolog 2, mitogen-responsive phosphoprotein (<i>Drosophila</i>)</i> |
| <i>DALRD3</i> | <i>DALR anticodon binding domain containing 3</i> |
| <i>DAPPI</i> | <i>dual adaptor of phosphotyrosine and 3-phosphoinositides</i> |
| <i>DBR1</i> | <i>debranching enzyme homolog 1 (<i>S. cerevisiae</i>)</i> |
| <i>DBT</i> | <i>dihydrolipoamide branched chain transacylase E2</i> |
| <i>DCAF6</i> | <i>DDB1 and CUL4 associated factor 6</i> |
| <i>DCLRE1C</i> | <i>DNA cross-link repair 1C</i> |
| <i>DDOST</i> | <i>dolichyl-diphosphooligosaccharide--protein glycosyltransferase</i> |
| <i>DDX3X</i> | <i>DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked</i> |
| <i>DDX58</i> | <i>DEAD (Asp-Glu-Ala-Asp) box polypeptide 58</i> |
| <i>DDX59</i> | <i>DEAD (Asp-Glu-Ala-Asp) box polypeptide 59</i> |

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| <i>DGUOK</i> | <i>deoxyguanosine kinase</i> |
| <i>DLG5</i> | <i>discs, large homolog 5 (Drosophila)</i> |
| <i>DLGAP4</i> | <i>discs, large (Drosophila) homolog-associated protein 4</i> |
| <i>DNAH3</i> | <i>dynein, axonemal, heavy chain 3</i> |
| <i>DND1</i> | <i>dead end homolog 1 (zebrafish)</i> |
| <i>DNM1L</i> | <i>dynamin 1-like</i> |
| <i>DSPP</i> | <i>dentin sialophosphoprotein</i> |
| <i>E2F6</i> | <i>E2F transcription factor 6</i> |
| <i>EEF1A1</i> | <i>eukaryotic translation elongation factor 1 alpha 1</i> |
| <i>EEF1B2</i> | <i>eukaryotic translation elongation factor 1 beta 2</i> |
| <i>EEF1D</i> | <i>eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)</i> |
| <i>EFS</i> | <i>embryonal Fyn-associated substrate</i> |
| <i>EIF2S3</i> | <i>eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa</i> |
| <i>EIF3A</i> | <i>eukaryotic translation initiation factor 3, subunit A</i> |
| <i>EIF3E</i> | <i>eukaryotic translation initiation factor 3, subunit E</i> |
| <i>EIF3L</i> | <i>eukaryotic translation initiation factor 3, subunit L</i> |
| <i>EIF4A2</i> | <i>eukaryotic translation initiation factor 4A2</i> |
| <i>EIF4B</i> | <i>eukaryotic translation initiation factor 4B</i> |
| <i>EIF4E</i> | <i>eukaryotic translation initiation factor 4E</i> |
| <i>EIF5A</i> | <i>eukaryotic translation initiation factor 5A</i> |
| <i>ENGASE</i> | <i>endo-beta-N-acetylglucosaminidase</i> |
| <i>EPB41L1</i> | <i>erythrocyte membrane protein band 4.1-like 1</i> |

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| <i>EPB41L4A</i> | <i>erythrocyte membrane protein band 4.1 like 4A</i> |
| <i>F7</i> | <i>coagulation factor VII (serum prothrombin conversion accelerator)</i> |
| <i>FBXO44</i> | <i>F-box protein 44</i> |
| <i>FBXW12</i> | <i>F-box and WD repeat domain containing 12</i> |
| <i>FGFR1</i> | <i>fibroblast growth factor receptor 1</i> |
| <i>FGFR1OP</i> | <i>FGFR1 oncogene partner</i> |
| <i>FNBPI</i> | <i>formin binding protein 1</i> |
| <i>FNBPL</i> | <i>formin binding protein 1-like</i> |
| <i>FOLR1</i> | <i>folate receptor 1 (adult)</i> |
| <i>FOXN4</i> | <i>forkhead box N4</i> |
| <i>FTH1</i> | <i>ferritin, heavy polypeptide 1</i> |
| <i>FTL</i> | <i>ferritin, light polypeptide</i> |
| <i>G3BP1</i> | <i>GTPase activating protein (SH3 domain) binding protein 1</i> |
| <i>GALM</i> | <i>galactose mutarotase (aldose 1-epimerase)</i> |
| <i>GAPDH</i> | <i>glyceraldehyde-3-phosphate dehydrogenase</i> |
| <i>GDI2</i> | <i>GDP dissociation inhibitor 2</i> |
| <i>GJA1</i> | <i>gap junction protein, alpha 1, 43kDa</i> |
| <i>GK</i> | <i>glycerol kinase</i> |
| <i>GLRX3</i> | <i>glutaredoxin 3</i> |
| <i>GLTSCR2</i> | <i>glioma tumor suppressor candidate region gene 2</i> |
| <i>GLUL</i> | <i>glutamate-ammonia ligase</i> |
| <i>GPAA1</i> | <i>glycosylphosphatidylinositol anchor attachment protein 1 homolog (yeast)</i> |

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|---|---|
| <i>H3F3B</i> | <i>H3 histone, family 3B (H3.3B)</i> |
| <i>HAND1</i> | <i>heart and neural crest derivatives expressed 1</i> |
| <i>HHLA3</i> | <i>HERV-H LTR-associating 3</i> |
| <i>HMGB1</i> | <i>high-mobility group box 1</i> |
| <i>HMGB3</i> | <i>high-mobility group box 3</i> |
| <i>HMGN1</i> | <i>high-mobility group nucleosome binding domain 1</i> |
| <i>HMGN2</i> | <i>high-mobility group nucleosomal binding domain 2</i> |
| <i>HNRNPA1</i> | <i>heterogeneous nuclear ribonucleoprotein A1</i> |
| <i>HNRNPA1</i> /// <i>HNRNPA1L2</i> /// <i>HNRPA1L-2</i> /// <i>LOC644037</i> | <i>heterogeneous nuclear ribonucleoprotein A3</i> |
| <i>HNRNPA3</i> /// <i>HNRNPA3P1</i> | <i>heterogeneous nuclear ribonucleoprotein A3</i> |
| <i>HNRNPC</i> | <i>heterogeneous nuclear ribonucleoprotein C (C1/C2)</i> |
| <i>HNRNPH1</i> | <i>heterogeneous nuclear ribonucleoprotein H1 (H)</i> |
| <i>HNRNPH3</i> | <i>heterogeneous nuclear ribonucleoprotein H3 (2H9)</i> |
| <i>HNRNPK</i> | <i>heterogeneous nuclear ribonucleoprotein K</i> |
| <i>HNRNPL</i> | <i>heterogeneous nuclear ribonucleoprotein L</i> |
| <i>HNRNPM</i> | <i>heterogeneous nuclear ribonucleoprotein M</i> |
| <i>HNRNPR</i> | <i>heterogeneous nuclear ribonucleoprotein R</i> |
| <i>HNRNPU</i> | <i>heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)</i> |
| <i>HNRPDL</i> | <i>heterogeneous nuclear ribonucleoprotein D-like</i> |
| <i>HSP90AA1</i> | <i>heat shock protein 90kDa alpha (cytosolic), class A member 1</i> |
| <i>HSPD1</i> | <i>heat shock 60kDa protein 1 (chaperonin)</i> |

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| <i>HSPE1</i> | <i>heat shock 10kDa protein 1 (chaperonin 10)</i> |
| <i>HTRA3</i> | <i>HtrA serine peptidase 3</i> |
| <i>HUWE1</i> | <i>HECT, UBA and WWE domain containing 1</i> |
| <i>IARS</i> | <i>isoleucyl-tRNA synthetase</i> |
| <i>IBTK</i> | <i>inhibitor of Bruton agammaglobulinemia tyrosine kinase</i> |
| <i>IGF2BP2</i> | <i>insulin-like growth factor 2 mRNA binding protein 2</i> |
| <i>IPO7</i> | <i>importin 7</i> |
| <i>ITPR1PL2</i> | <i>inositol 1,4,5-triphosphate receptor interacting protein-like 2</i> |
| <i>IVNS1ABP</i> | <i>influenza virus NS1A binding protein</i> |
| <i>KCTD1</i> | <i>potassium channel tetramerisation domain containing 1</i> |
| <i>KCTD10</i> | <i>potassium channel tetramerisation domain containing 10</i> |
| <i>KDM6B</i> | <i>lysine (K)-specific demethylase 6B</i> |
| <i>KIAA0415</i> | <i>KIAA0415</i> |
| <i>KIAA1143</i> | <i>KIAA1143</i> |
| <i>KIR3DX1</i> | <i>killer cell immunoglobulin-like receptor, three domains, XI</i> |
| <i>KPNB1</i> | <i>karyopherin (importin) beta 1</i> |
| <i>KRT8</i> | <i>keratin 8</i> |
| <i>KTN1</i> | <i>kinectin 1 (kinesin receptor)</i> |
| <i>LDHA</i> | <i>lactate dehydrogenase A</i> |
| <i>LDHB</i> | <i>lactate dehydrogenase B</i> |
| <i>LRRC37A2</i> | <i>leucine rich repeat containing 37, member A3</i> |
| <i>LRRFIP1</i> | <i>leucine rich repeat (in FLII) interacting protein 1</i> |

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|-----------------|---|
| <i>LRRFIP1</i> | <i>leucine rich repeat (in FLII) interacting protein 1</i> |
| <i>LYRM2</i> | <i>LYR motif containing 2</i> |
| <i>LYRM7</i> | <i>Lyrm7 homolog (mouse)</i> |
| <i>LYSMD1</i> | <i>LysM, putative peptidoglycan-binding, domain containing 1</i> |
| <i>MAN2A1</i> | <i>mannosidase, alpha, class 2A, member 1</i> |
| <i>MARCKS</i> | <i>myristoylated alanine-rich protein kinase C substrate</i> |
| <i>MARVELD2</i> | <i>MARVEL domain containing 2</i> |
| <i>MAT2A</i> | <i>methionine adenosyltransferase II, alpha</i> |
| <i>MATR3</i> | <i>matrin 3</i> |
| <i>MAX</i> | <i>MYC associated factor X</i> |
| <i>MCL1</i> | <i>myeloid cell leukemia sequence 1 (BCL2 related)</i> |
| <i>MCM3AP</i> | <i>minichromosome maintenance complex component 3 associated protein</i> |
| <i>MED13</i> | <i>mediator complex subunit 13</i> |
| <i>MESDC2</i> | <i>mesoderm development candidate 2</i> |
| <i>MGEA5</i> | <i>meningioma expressed antigen 5 (hyaluronidase)</i> |
| <i>MINA</i> | <i>MYC induced nuclear antigen</i> |
| <i>MLL5</i> | <i>myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)</i> |
| <i>MORF4L1</i> | <i>mortality factor 4 like 1</i> |
| <i>MORF4L2</i> | <i>mortality factor 4 like 2</i> |
| <i>MPHOSPH8</i> | <i>M-phase phosphoprotein 8</i> |
| <i>MPV17L</i> | <i>MPV17 mitochondrial membrane protein-like</i> |

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| <i>MRPL44</i> | <i>mitochondrial ribosomal protein L44</i> |
| <i>MTUS2</i> | <i>microtubule associated tumor suppressor candidate 2</i> |
| <i>MUC4</i> | <i>mucin 4, cell surface associated</i> |
| <i>MUC5AC</i> | <i>mucin 5AC, oligomeric mucus/gel-forming</i> |
| <i>MUTED</i> | <i>muted homolog (mouse)</i> |
| <i>MXD1</i> | <i>MAX dimerization protein 1</i> |
| <i>MYH10</i> | <i>myosin, heavy chain 10, non-muscle</i> |
| <i>NAA40</i> | <i>N(alpha)-acetyltransferase 40, NatD catalytic subunit, homolog (S. cerevisiae)</i> |
| <i>NACA</i> | <i>nascent polypeptide-associated complex alpha subunit</i> |
| <i>NACAP1</i> | <i>nascent-polypeptide-associated complex alpha polypeptide pseudogene 1</i> |
| <i>NAP1L1</i> | <i>nucleosome assembly protein 1-like 1</i> |
| <i>NAT15</i> | <i>N-acetyltransferase 15 (GCN5-related, putative)</i> |
| <i>NAV2</i> | <i>neuron navigator 2</i> |
| <i>NBPF10</i> | <i>neuroblastoma breakpoint family, member 11</i> |
| <i>NBPF10</i> /// <i>NBPF15</i> /// <i>NBPF16</i> /// <i>NBPF8</i> /// <i>NBPF9</i> | <i>neuroblastoma breakpoint family, member 10</i> |
| <i>ND6</i> | <i>NADH dehydrogenase subunit 6 (complex I)</i> |
| <i>NDUFB1</i> | <i>NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa</i> |
| <i>NDUFB2</i> | <i>NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa</i> |
| <i>NDUFS2</i> | <i>NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase)</i> |

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| <i>NDUFS8</i> | <i>NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)</i> |
| <i>NFIB</i> | <i>nuclear factor I/B</i> |
| <i>NGFRAP1</i> | <i>nerve growth factor receptor (TNFRSF16) associated protein 1</i> |
| <i>NGRN</i> | <i>neugrin, neurite outgrowth associated</i> |
| <i>NIN</i> | <i>ninein (GSK3B interacting protein)</i> |
| <i>NKTR</i> | <i>natural killer-tumor recognition sequence</i> |
| <i>NLN</i> | <i>neurolysin (metallopeptidase M3 family)</i> |
| <i>NME1-NME2 /// NME2</i> | <i>non-metastatic cells 1, protein expressed in</i> |
| <i>NME7</i> | <i>non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)</i> |
| <i>NONO</i> | <i>non-POU domain containing, octamer-binding</i> |
| <i>NPIP</i> | <i>nuclear pore complex interacting protein</i> |
| <i>NPM1</i> | <i>nucleophosmin (nucleolar phosphoprotein B23, numatrin)</i> |
| <i>NR2F2</i> | <i>nuclear receptor subfamily 2, group F, member 2</i> |
| <i>NUDT4 /// NUDT4P1</i> | <i>nudix-type motif 4</i> |
| <i>NUTF2</i> | <i>nuclear transport factor 2</i> |
| <i>OCIAD1</i> | <i>OCIA domain containing 1</i> |
| <i>OFD1</i> | <i>oral-facial-digital syndrome 1</i> |
| <i>OPHN1</i> | <i>oligophrenin 1</i> |
| <i>ORAI2</i> | <i>ORAI calcium release-activated calcium modulator 2</i> |
| <i>PABPC3</i> | <i>poly(A) binding protein, cytoplasmic 3</i> |
| <i>PAK2</i> | <i>p21 protein (Cdc42/Rac)-activated kinase 2</i> |

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|---|---|
| <i>PCMTD1</i> | <i>protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1</i> |
| <i>PDCD6</i> | <i>programmed cell death 6</i> |
| <i>PDE4C</i> | <i>phosphodiesterase 4C, cAMP-specific</i> |
| <i>PECR</i> | <i>peroxisomal trans-2-enoyl-CoA reductase</i> |
| <i>PEX11B</i> | <i>peroxisomal biogenesis factor 11 beta</i> |
| <i>PFKFB3</i> | <i>6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3</i> |
| <i>PFN2</i> | <i>profilin 2</i> |
| <i>PGF</i> | <i>placental growth factor</i> |
| <i>PHAX</i> | <i>phosphorylated adaptor for RNA export</i> |
| <i>PICALM</i> | <i>phosphatidylinositol binding clathrin assembly protein</i> |
| <i>PKP4</i> | <i>plakophilin 4</i> |
| <i>PLCB3</i> | <i>phospholipase C, beta 3 (phosphatidylinositol-specific)</i> |
| <i>PLGLA</i> /// <i>PLGLB1</i> /// <i>PLGLB2</i> | <i>plasminogen-like A, B1, B2</i> |
| <i>PMS2L3</i> | <i>postmeiotic segregation increased 2 pseudogene 3</i> |
| <i>PNO1</i> | <i>partner of NOB1 homolog (<i>S. cerevisiae</i>)</i> |
| <i>POLH</i> | <i>polymerase (DNA directed), eta</i> |
| <i>POLRIB</i> | <i>polymerase (RNA) I polypeptide B, 128kDa</i> |
| <i>PPIA</i> | <i>peptidylprolyl isomerase A (cyclophilin A)</i> |
| <i>PPP1R13B</i> | <i>protein phosphatase 1, regulatory (inhibitor) subunit 13B</i> |
| <i>PQLC1</i> | <i>PQ loop repeat containing 1</i> |
| <i>PRDX6</i> | <i>peroxiredoxin 6</i> |

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| <i>PRELID1</i> | <i>PREL1 domain containing 1</i> |
| <i>PRKAR2A</i> | <i>protein kinase, cAMP-dependent, regulatory, type II, alpha</i> |
| <i>PRKCSH</i> | <i>protein kinase C substrate 80K-H</i> |
| <i>PRKD2</i> | <i>protein kinase D2</i> |
| <i>PROX1</i> | <i>prospero homeobox 1</i> |
| <i>PRR11</i> | <i>proline rich 11</i> |
| <i>PRSS1 /// PRSS2 /// PRSS3</i> | <i>protease, serine 1 (trypsin 1), protease, serine 2 (trypsin 2), protease, serine 3</i> |
| <i>PSMC2</i> | <i>proteasome (prosome, macropain) 26S subunit, ATPase, 2</i> |
| <i>PSMD4</i> | <i>proteasome (prosome, macropain) 26S subunit, non-ATPase, 4</i> |
| <i>PSME2</i> | <i>proteasome (prosome, macropain) activator subunit 2 (PA28 beta)</i> |
| <i>PTCD1</i> | <i>pentatricopeptide repeat domain 1</i> |
| <i>PTMA</i> | <i>prothymosin, alpha</i> |
| <i>PTP4A2</i> | <i>protein tyrosine phosphatase type IVA, member 2</i> |
| <i>PTPRO</i> | <i>protein tyrosine phosphatase, receptor type, O</i> |
| <i>QARS</i> | <i>glutaminyl-tRNA synthetase</i> |
| <i>RAB1A</i> | <i>RAB1A, member RAS oncogene family</i> |
| <i>RAB6A</i> | <i>RAB6A, member RAS oncogene family</i> |
| <i>RABGAPI</i> | <i>RAB GTPase activating protein 1</i> |
| <i>RAC1</i> | <i>ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)</i> |
| <i>RACGAPI</i> | <i>Rac GTPase activating protein 1</i> |
| <i>RAD52</i> | <i>RAD52 homolog (<i>S. cerevisiae</i>)</i> |

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| <i>RAP1A</i> | <i>RAP1A, member of RAS oncogene family</i> |
| <i>RAP2A</i> | <i>RAP2A, member of RAS oncogene family</i> |
| <i>RAP2B</i> | <i>RAP2B, member of RAS oncogene family</i> |
| <i>RASEF</i> | <i>RAS and EF-hand domain containing</i> |
| <i>RBM8A</i> | <i>RNA binding motif protein 8A</i> |
| <i>RBMS1</i> | <i>RNA binding motif, single stranded interacting protein 1</i> |
| <i>RECK</i> | <i>reversion-inducing-cysteine-rich protein with kazal motifs</i> |
| <i>RHEB</i> | <i>Ras homolog enriched in brain</i> |
| <i>RHOQ</i> | <i>ras homolog gene family, member Q</i> |
| <i>RND3</i> | <i>Rho family GTPase 3</i> |
| <i>RNPS1</i> | <i>RNA binding protein S1, serine-rich domain</i> |
| <i>RPL10A</i> | <i>ribosomal protein L10a</i> |
| <i>RPL12</i> | <i>ribosomal protein L12</i> |
| <i>RPL12</i> | <i>ribosomal protein L12</i> |
| <i>RPL14</i> | <i>ribosomal protein L14</i> |
| <i>RPL17</i> | <i>ribosomal protein L17</i> |
| <i>RPL19</i> | <i>ribosomal protein L19</i> |
| <i>RPL21</i> | <i>ribosomal protein L21</i> |
| <i>RPL22</i> | <i>ribosomal protein L22</i> |
| <i>RPL23</i> | <i>ribosomal protein L23</i> |
| <i>RPL23A</i> | <i>ribosomal protein L23a</i> |
| <i>RPL24</i> | <i>ribosomal protein L24</i> |

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| <i>RPL26</i> | <i>ribosomal protein L26</i> |
| <i>RPL27</i> | <i>ribosomal protein L27</i> |
| <i>RPL30</i> | <i>ribosomal protein L30</i> |
| <i>RPL31</i> | <i>ribosomal protein L31</i> |
| <i>RPL32</i> | <i>ribosomal protein L32</i> |
| <i>RPL35</i> | <i>ribosomal protein L35</i> |
| <i>RPL35A</i> | <i>ribosomal protein L35a</i> |
| <i>RPL36A</i> | <i>ribosomal protein L36a</i> |
| <i>RPL37</i> | <i>ribosomal protein L37</i> |
| <i>RPL37A</i> | <i>ribosomal protein L37a</i> |
| <i>RPL38</i> | <i>ribosomal protein L38</i> |
| <i>RPL39</i> | <i>ribosomal protein L39</i> |
| <i>RPL41</i> | <i>ribosomal protein L41</i> |
| <i>RPL5</i> | <i>ribosomal protein L5</i> |
| <i>RPL6</i> | <i>ribosomal protein L6</i> |
| <i>RPL7</i> | <i>ribosomal protein L7</i> |
| <i>RPL7L1</i> | <i>ribosomal protein L7-like 1</i> |
| <i>RPL9</i> | <i>ribosomal protein L9</i> |
| <i>RPRD2</i> | <i>regulation of nuclear pre-mRNA domain containing 2</i> |
| <i>RPS10</i> | <i>ribosomal protein S10</i> |
| <i>RPS11</i> | <i>ribosomal protein S11</i> |
| <i>RPS12</i> | <i>ribosomal protein S12</i> |

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| <i>RPS13</i> | <i>ribosomal protein S13</i> |
| <i>RPS14</i> | <i>ribosomal protein S14</i> |
| <i>RPS17</i> | <i>ribosomal protein S17</i> |
| <i>RPS18</i> | <i>ribosomal protein S18</i> |
| <i>RPS2</i> | <i>ribosomal protein S2</i> |
| <i>RPS20</i> | <i>ribosomal protein S20</i> |
| <i>RPS23</i> | <i>ribosomal protein S23</i> |
| <i>RPS25</i> | <i>ribosomal protein S25</i> |
| <i>RPS26</i> | <i>ribosomal protein S26</i> |
| <i>RPS27</i> | <i>ribosomal protein S27</i> |
| <i>RPS27A</i> | <i>ribosomal protein S27a</i> |
| <i>RPS28</i> | <i>ribosomal protein S28</i> |
| <i>RPS29</i> | <i>ribosomal protein S29</i> |
| <i>RPS3</i> | <i>ribosomal protein S3</i> |
| <i>RPS3A</i> | <i>ribosomal protein S3A</i> |
| <i>RPS4X</i> | <i>ribosomal protein S4, X-linked</i> |
| <i>RPS6</i> | <i>ribosomal protein S6</i> |
| <i>RPS6KB1</i> | <i>ribosomal protein S6 kinase, 70kDa, polypeptide 1</i> |
| <i>RPS7</i> | <i>ribosomal protein S7</i> |
| <i>RPSA</i> | <i>ribosomal protein SA</i> |
| <i>RSL24D1</i> | <i>ribosomal L24 domain containing 1</i> |
| <i>RUND C2A</i> | <i>RUN domain containing 2A</i> |

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| <i>RWDD4A</i> | <i>RWD domain containing 4</i> |
| <i>S100A10</i> | <i>S100 calcium binding protein A10</i> |
| <i>S100A7A</i> | <i>S100 calcium binding protein A7A</i> |
| <i>SAMD9</i> | <i>sterile alpha motif domain containing 9</i> |
| <i>SCD5</i> | <i>stearoyl-CoA desaturase 5</i> |
| <i>SDC4</i> | <i>syndecan 4</i> |
| <i>SEH1L</i> | <i>SEH1-like (<i>S. cerevisiae</i>)</i> |
| <i>SEPHS1</i> | <i>selenophosphate synthetase 1</i> |
| <i>SEPWI</i> | <i>selenoprotein W, 1</i> |
| <i>SERBP1</i> | <i>SERPINE1 mRNA binding protein 1</i> |
| <i>SET</i> | <i>SET nuclear oncogene</i> |
| <i>SFN</i> | <i>stratifin</i> |
| <i>SFPQ</i> | <i>splicing factor proline/glutamine-rich</i> |
| <i>SFRS2B</i> | <i>serine/arginine-rich splicing factor 8</i> |
| <i>SFTPB</i> | <i>surfactant protein B</i> |
| <i>SFTPC</i> | <i>surfactant protein C</i> |
| <i>SH3KBP1</i> | <i>SH3-domain kinase binding protein 1</i> |
| <i>SLAIN2</i> | <i>SLAIN motif family, member 2</i> |
| <i>SLC11A1</i> | <i>solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1</i> |
| <i>SLC25A16</i> | <i>solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16</i> |
| <i>SLC2A1</i> | <i>solute carrier family 2 (facilitated glucose transporter), member 1</i> |

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| <i>SLC2A14</i> /// <i>SLC2A3</i> | <i>solute carrier family 2 (facilitated glucose transporter) member 14, member 3</i> |
| <i>SLC2A3</i> | <i>solute carrier family 2 (facilitated glucose transporter), member 3</i> |
| <i>SLC30A5</i> | <i>solute carrier family 30 (zinc transporter), member 5</i> |
| <i>SLC35E1</i> | <i>solute carrier family 35, member E1</i> |
| <i>SLFN5</i> | <i>schlafen family member 5</i> |
| <i>SMARCE1</i> | <i>SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1</i> |
| <i>SNRPE</i> | <i>small nuclear ribonucleoprotein polypeptide E</i> |
| <i>SNW1</i> | <i>SNW domain containing 1</i> |
| <i>SNX15</i> | <i>sorting nexin 15</i> |
| <i>SP3</i> | <i>Sp3 transcription factor</i> |
| <i>SPG21</i> | <i>spastic paraplegia 21 (autosomal recessive, Mast syndrome)</i> |
| <i>SPN</i> | <i>sialophorin</i> |
| <i>SPRR1B</i> | <i>small proline-rich protein 1B</i> |
| <i>SPRR2B</i> | <i>small proline-rich protein 2A</i> |
| <i>SRP14</i> | <i>signal recognition particle 14kDa (homologous Alu RNA binding protein)</i> |
| <i>SRRM2</i> | <i>serine/arginine repetitive matrix 2</i> |
| <i>ST13</i> | <i>suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)</i> |
| <i>STK35</i> | <i>serine/threonine kinase 35</i> |
| <i>STK4</i> | <i>serine/threonine kinase 4</i> |
| <i>STRAP</i> | <i>serine/threonine kinase receptor associated protein</i> |

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| <i>STYX</i> | <i>serine/threonine/tyrosine interacting protein</i> |
| <i>SUDS3</i> | <i>suppressor of defective silencing 3 homolog (S. cerevisiae)</i> |
| <i>SUMO2</i> | <i>SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae)</i> |
| <i>SUMO4</i> | <i>SMT3 suppressor of mif two 3 homolog 4 (S. cerevisiae)</i> |
| <i>SYMPK</i> | <i>symplekin</i> |
| <i>TARDBP</i> | <i>TAR DNA binding protein</i> |
| <i>TATDN3</i> | <i>TatD DNase domain containing 3</i> |
| <i>TBC1D3 /// TBC1D3C /// TBC1D3F /// TBC1D3H</i> | <i>TBC1 domain family, member 3F</i> |
| <i>TBX3</i> | <i>T-box 3</i> |
| <i>TCTN2</i> | <i>tectonic family member 2</i> |
| <i>TDG</i> | <i>thymine-DNA glycosylase</i> |
| <i>TEAD1</i> | <i>TEA domain family member 1 (SV40 transcriptional enhancer factor)</i> |
| <i>TERF1</i> | <i>telomeric repeat binding factor (NIMA-interacting) 1</i> |
| <i>TES</i> | <i>testis derived transcript (3 LIM domains)</i> |
| <i>TFAP2C</i> | <i>transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)</i> |
| <i>TIMM8A</i> | <i>translocase of inner mitochondrial membrane 8 homolog A (yeast)</i> |
| <i>TJPI</i> | <i>tight junction protein 1 (zona occludens 1)</i> |
| <i>TM9SF3</i> | <i>transmembrane 9 superfamily member 3</i> |
| <i>TMBIM4</i> | <i>transmembrane BAX inhibitor motif containing 4</i> |
| <i>TMEFF2</i> | <i>transmembrane protein with EGF-like and two follistatin-like domains 2</i> |
| <i>TMEM106B</i> | <i>transmembrane protein 106B</i> |

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| <i>TMEM14B</i> /// <i>TMEM14C</i> | <i>transmembrane protein 14A, 14C</i> |
| <i>TMEM151B</i> | <i>transmembrane protein 151B</i> |
| <i>TMEM189</i> /// <i>TMEM189-UBE2V1</i> /// <i>UBE2V1</i> | <i>transmembrane protein 189, TMEM189-UBE2V readthrough</i> |
| <i>TMEM67</i> | <i>transmembrane protein 67</i> |
| <i>TMSB4X</i> /// <i>TMSL3</i> | <i>thymosin beta 4, X-linked, thymosin-like 3</i> |
| <i>TNPO1</i> | <i>transportin 1</i> |
| <i>TNPO3</i> | <i>transportin 3</i> |
| <i>TOMM20</i> | <i>translocase of outer mitochondrial membrane 20 homolog (yeast)</i> |
| <i>TOMM22</i> | <i>translocase of outer mitochondrial membrane 22 homolog (yeast)</i> |
| <i>TPM1</i> | <i>tropomyosin 1 (alpha)</i> |
| <i>TPM3</i> | <i>tropomyosin 3</i> |
| <i>TPMT</i> | <i>thiopurine S-methyltransferase</i> |
| <i>TPT1</i> | <i>tumor protein, translationally-controlled 1</i> |
| <i>TRIM16</i> | <i>tripartite motif-containing 16</i> |
| <i>TRIM4</i> | <i>tripartite motif-containing 4</i> |
| <i>TRIM65</i> | <i>tripartite motif-containing 65</i> |
| <i>TRMT5</i> | <i>TRM5 tRNA methyltransferase 5 homolog (<i>S. cerevisiae</i>)</i> |
| <i>TSPYLI</i> | <i>TSPY-like 1</i> |
| <i>TSR1</i> | <i>TSR1, 20S rRNA accumulation, homolog (<i>S. cerevisiae</i>)</i> |
| <i>TTC3</i> | <i>tetratricopeptide repeat domain 3</i> |
| <i>TUBA1B</i> | <i>tubulin, alpha 1b</i> |
| <i>TXN</i> | <i>thioredoxin</i> |

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| <i>UACA</i> | <i>uveal autoantigen with coiled-coil domains and ankyrin repeats</i> |
| <i>UBE4B</i> | <i>ubiquitination factor E4B (UFD2 homolog, yeast)</i> |
| <i>UBQLN4</i> | <i>ubiquilin 4</i> |
| <i>UBXN2A</i> | <i>UBX domain protein 2A</i> |
| <i>UPF3A</i> | <i>UPF3 regulator of nonsense transcripts homolog A (yeast)</i> |
| <i>UQCRH</i> | <i>ubiquinol-cytochrome c reductase hinge protein</i> |
| <i>UQCRQ</i> | <i>ubiquinol-cytochrome c reductase, complex III subunit VII, 9.5kDa</i> |
| <i>USP28</i> | <i>ubiquitin specific peptidase 28</i> |
| <i>USP34</i> | <i>ubiquitin specific peptidase 34</i> |
| <i>USP48</i> | <i>ubiquitin specific peptidase 48</i> |
| <i>USP6</i> | <i>ubiquitin specific peptidase 6 (Tre-2 oncogene)</i> |
| <i>VAMP2</i> | <i>vesicle-associated membrane protein 2 (synaptobrevin 2)</i> |
| <i>VAPA</i> | <i>VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa</i> |
| <i>VDAC2</i> | <i>voltage-dependent anion channel 2</i> |
| <i>VDAC3</i> | <i>voltage-dependent anion channel 3</i> |
| <i>XRCC2</i> | <i>X-ray repair complementing defective repair in Chinese hamster cells 2</i> |
| <i>YTHDF1</i> | <i>YTH domain family, member 1</i> |
| <i>YWHAB</i> | <i>tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide</i> |
| <i>YWHAE</i> | <i>tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide</i> |
| <i>YWHAQ</i> | <i>tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation</i> |

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| | <i>protein, theta polypeptide</i> |
| <i>YWHAZ</i> | <i>tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide</i> |
| <i>YY1</i> | <i>YY1 transcription factor</i> |
| <i>ZBTB44</i> | <i>zinc finger and BTB domain containing 44</i> |
| <i>ZBTB7A</i> | <i>zinc finger and BTB domain containing 7A</i> |
| <i>ZC3H11A</i> | <i>zinc finger CCCH-type containing 11A</i> |
| <i>ZCRB1</i> | <i>zinc finger CCHC-type and RNA binding motif 1</i> |
| <i>ZFAND6</i> | <i>zinc finger, AN1-type domain 6</i> |
| <i>ZFHX3</i> | <i>zinc finger homeobox 3</i> |
| <i>ZFP36L1</i> | <i>zinc finger protein 36, C3H type-like 1</i> |
| <i>ZNF107</i> | <i>zinc finger protein 107</i> |
| <i>ZNF160</i> | <i>zinc finger protein 665</i> |
| <i>ZNF238</i> | <i>zinc finger protein 238</i> |
| <i>ZNF252</i> | <i>zinc finger protein 252</i> |
| <i>ZNF320</i> | <i>zinc finger protein 320</i> |
| <i>ZNF337</i> | <i>zinc finger protein 337</i> |
| <i>ZNF445</i> | <i>zinc finger protein 445</i> |
| <i>ZNF490</i> | <i>zinc finger protein 490</i> |
| <i>ZNF506</i> | <i>zinc finger protein 506</i> |
| <i>ZNF528</i> | <i>zinc finger protein 528</i> |
| <i>ZNF548</i> | <i>zinc finger protein 548</i> |
| <i>ZNF552</i> | <i>zinc finger protein 552</i> |

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| | |
|---------|--|
| ZNF611 | <i>zinc finger protein 611</i> |
| ZNF652 | <i>zinc finger protein 652</i> |
| ZNF665 | <i>zinc finger protein 665</i> |
| ZNF721 | <i>zinc finger protein 721</i> |
| ZNF747 | <i>zinc finger protein 747</i> |
| ZNF808 | <i>zinc finger protein 808</i> |
| ZNF816A | <i>zinc finger protein 816</i> |
| ZNF827 | <i>zinc finger protein 827</i> |
| ZSCAN29 | <i>zinc finger and SCAN domain containing 29</i> |

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Appendix 3. Physiological Systems Gene Lists and Functional Annotations

| Category* | No. of Genes | Fisher P-Value | False Discovery Rate | Gene Symbols |
|--|--------------|-------------------|----------------------|--|
| Skeletal and muscular system development and function | 17 | 3.85E-04-2.44E-02 | 2.85E-02-1.59E-01 | <i>NACA, RPS6KB1, PAK2, CDC42, RECK, FGFR1, RAC1, SDC4, APP, PGF, CCND2, HMG B1, PPIA, TXN</i> (includes G:116484), <i>TPT1, ACVR2A, ZFHX3</i> |
| Growth of muscle | 4 | 3.85E-04 | 2.85E-02 | <i>ACVR2A, CCND2, NACA, RPS6KB1</i> |
| Polarization of podosomes | 2 | 5.94E-04 | 3.41E-02 | <i>CDC42, RAC1</i> |
| Growth of skeletal muscle | 3 | 1.52E-03 | 5.58E-02 | <i>ACVR2A, NACA, RPS6KB1</i> |
| Assembly of podosomes | 2 | 1.75E-03 | 5.98E-02 | <i>CDC42, RAC1</i> |
| Migration of vascular smooth muscle cells | 6 | 4.28E-03 | 1.04E-01 | <i>FGFR1, HMGB1, PPIA, RAC1, SDC4, TXN</i> |
| Formation of muscle cells | 5 | 6.11E-03 | 1.27E-01 | <i>FGFR1, HMGB1, RAC1, REC K, ZFHX3</i> |
| Formation of podosomes | 3 | 6.38E-03 | 1.31E-01 | <i>CDC42, PAK2, RAC1</i> |
| Tissue development | 20 | 3.85E-04-2.44E-02 | 2.85E-02-1.59E-01 | <i>NACA, TPM1</i> (includes EG:22003), <i>MYH10, RPS6KB1, GJA1, MGEA5, FGFR1, NR2F2, RAC1, HAND1, MAN2A1, PROX1,</i> |

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| Category* | No. of Genes | Fisher P-Value | False Discovery Rate | Gene Symbols |
|---|--------------|-----------------------|-----------------------|---|
| | | | | <i>APP, PGF, ARF6, CCND2, MAX, HMGB1, CTBP2, ACVR2A</i> |
| Growth of muscle | 4 | 3.85E-04 | 2.85E-02 | <i>ACVR2A,CCND2,NACA,RP S6KB1</i> |
| Growth of skeletal muscle | 3 | 1.52E-03 | 5.58E-02 | <i>ACVR2A,NACA,RPS6KB1</i> |
| Developmental process of cardiac muscle | 6 | 2.82E-03 | 7.89E-02 | <i>CCND2,HAND1,HMGB1,M GEA5,PROX1,TPM1</i> |
| Hematological system development and function or immune cell trafficking | 6 | 7.37E-04- 2.44E-02 | 3.66E-02- 1.59E-01 | <i>HMGB1,F7,ANXA2,HSPD1, APP,S100A10</i> |
| Activation of monocyte-derived macrophages | 3 | 7.37E-04 | 3.66E-02 | <i>ANXA2,HSPD1,S100A10</i> |
| Nervous system development and function | 20 | 3.45E-03- 2.44E-02 | 9.05E-02- 1.59E-01 | <i>MYH10, GJA1, CDC42, YWHAB, TBX3, FGFR1, VAPA, YWHAZ, BASP1, RAC1, PFN2, APP, OPHN1, ARF6, RHOQ, HMGB1, TARDBP, TXN (includes EG:116484), MARCKS, FNBP1</i> |
| Neurogenesis of neural stem cells | 2 | 3.45E-03 | 9.05E-02 | <i>APP,FGFR1</i> |
| Neurological process of hippocampal CA1 | 4 | 4.50E-03 | 1.07E-01 | <i>APP,HMGB1,OPHN1,RAC1</i> |

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| Category* | No. of Genes | Fisher P-Value | False Discovery Rate | Gene Symbols |
|--|--------------|-----------------------|-----------------------|---|
| region | | | | |
| Cell cycle progression of cortical neurons | 2 | 5.66E-03 | 1.21E-01 | <i>APP, YWHAB</i> |
| Embryonic development | 28 | 9.78E-03- 2.44E-02 | 1.59E-01- 1.59E-01 | <i>MYH10, TPM1 (includes EG:22003), CDC42, RPS6, HAND1, BTF3, APP, SLC2A3, AKIRIN2, XRCC2, YY1, SP3, HSPE1, DAB2, RPS6KB1, GJA1, POLR1B, CFL1, TJP1, TBX3, ATP5A1, FGFR1, RACGAP1, RAC1, MAN2A1, MESDC2, MAX, PP1A</i> |
| Developmental process of embryo | 19 | 9.78E-03 | 1.59E-01 | <i>AKIRIN2, ATP5A1, BTF3, DAB2, FGFR1, GJA1, HAND1, MAN2A1, MESDC2, MYH10, POLR1B, RACGAP1, RPS6, RPS6KB1, SP3, TBX3, TPM1, XRCC2, YY1</i> |
| Organismal development | 50 | 9.78E-03- 2.44E-02 | 1.59E-01- 1.59E-01 | <i>MYH10, NR2F2, PEX11B, HANND1, STYX, AKIRIN2, XRCC2, STK4, HMGB1, TARDBP, RPS6KB1, CDK13, GJA1, POLR1B, FGFR1, ATP5A1, MORF4L1, RPS4X, CCND2, MAX, PR, ELID1, CTSB, NGFRAP1, SUMO2, HMGB3, TPM1 (includes EG:22003), RPS6, BTF3, PROX1, APP, SLC2A3, PGF, YY1, TEAD1,</i> |

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| Category* | No. of Genes | Fisher P-Value | False Discovery Rate | Gene Symbols |
|---------------------------------|--------------|----------------|----------------------|--|
| | | | | <i>SP3, MXD1, CTBP2, DAB2, MARCKS, HNRNPC, TFAP2C, DSPP, TBX3, TJP1, RACGAP1, MAN2A1, MESDC2, KRT8, DNM1L, ACVR2A</i> |
| Developmental process of embryo | 19 | 9.78E-03 | 1.59E-01 | <i>AKIRIN2, ATP5A1, BTF3, DA B2, FGFR1, GJA1, HAND1, MAN2A1, MESDC2, MYH10, P OLR1B, RACGAP1, RPS6, RP S6KB1, SP3, TBX3, TPM1, XRC2, YY1</i> |

* Only individual functional annotations with $P < 0.01$ were reported.

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Appendix 4. Canonical Pathways Gene Lists

| Ingenuity Canonical Pathways | Genes |
|---|---|
| Mammalian target of rapamycin signaling | <i>RPS6KB1, RHEB, RAC1, RPS6, EIF4A2, EIF3E, EIF4E, PGF, RHOQ, RND3, EIF3A, FNBP1, EIF4B</i> |
| Regulation of Actin-based Motility by Rho | <i>PAK2, RHOQ, CDC42, RND3, CFL1, ARPC2, RAC1, PFN2, FNBP1</i> |
| Cell cycle: G2/M DNA damage checkpoint regulation | <i>CDC25B, YWHAQ, YWHAE, YWHAB, YWHAZ, SFN</i> |
| <i>PI3K/AKT</i> signaling | <i>YWHAQ, RPS6KB1, RHEB, YWHAE, YWHAB, YWHAZ, HSP90AA1, SFN, EIF4E, MCL1</i> |
| Semaphorin signaling in neurons | <i>PAK2, RHOQ, RND3, CFL1, RAC1, FNBP1</i> |
| Integrin signaling | <i>RAP2B, RAP2A, ARF6, PAK2, RHOQ, CDC42, RND3, ARPC2, RAC1, ACTG1, RAPIA, FNBP1</i> |
| <i>ERK5</i> signaling | <i>YWHAQ, RPS6KB1, YWHAE, YWHAB, YWHAZ, SFN</i> |
| Clathrin-mediated endocytosis signaling | <i>ARF6, CDC42, ARPC2, RAC1, DAB2, DNM1L, SH3KBP1, ACTG1, AP2S1, PGF</i> |
| Glycolysis or gluconeogenesis | <i>ALDH1B1, ALDOB, GAPDH, PECR, GALM, LDHA, LDHB</i> |
| Molecular mechanisms of cancer | <i>RAP2B, RAP2A, PAK2, CDC42, RAC1, PRKAR2A, RAPIA, CDC25B, CASP6, E2F6, RHOQ, MAX, CCND2, RND3, PLCB3, FNBP1</i> |
| <i>p70S6K</i> signaling | <i>YWHAQ, RPS6KB1, YWHAE, YWHAB, YWHAZ, PLCB3, RPS6, SFN</i> |

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Appendix 5. Functional Annotations Within Significant Molecular and Cellular Functions Categories*

| Category | No. of Genes | False Discovery Rate |
|--|--------------|----------------------|
| Protein synthesis | 80 | 9.21E-48-1.59E-01 |
| Elongation of protein | 51 | 9.21E-48 |
| Translation | 64 | 8.85E-39 |
| Synthesis of protein | 65 | 2.58E-31 |
| Metabolism of protein | 73 | 1.07E-24 |
| Translation of mammalian target of rapamycin | 7 | 5.31E-03 |
| Initiation of translation of protein | 7 | 2.78E-02 |
| Polymerization of actin | 6 | 4.04E-02 |
| Translation of protein | 8 | 4.40E-02 |
| RNA posttranscriptional modification | 41 | 2.03E-05-1.59E-01 |
| Splicing of RNA | 18 | 2.03E-05 |
| Processing of ribosomal RNA | 20 | 2.25E-05 |
| Modification of RNA | 21 | 3.59E-05 |
| Processing of RNA | 10 | 5.87E-05 |
| Modification of mRNA | 14 | 2.72E-03 |
| Splicing of mRNA | 9 | 4.94E-03 |
| Annealing of RNA | 3 | 9.11E-03 |
| Unwinding of mRNA | 3 | 9.11E-03 |

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| | | |
|---|----|-------------------|
| Processing of mRNA | 11 | 2.76E-02 |
| Alternative splicing of mRNA | 4 | 2.85E-02 |
| Binding of mRNA | 3 | 3.66E-02 |
| Gene expression | 82 | 1.46E-03-1.59E-01 |
| Recruitment of mRNA | 4 | 1.46E-03 |
| Translation of mRNA | 7 | 5.31E-03 |
| Expression of mRNA | 11 | 3.44E-02 |
| Binding of mRNA | 3 | 3.66E-02 |
| Transcription | 69 | 4.09E-02 |
| RNA trafficking | 4 | 1.46E-03-1.46E-03 |
| Recruitment of mRNA | 4 | 1.46E-03 |
| Cell cycle | 62 | 2.49E-03-1.59E-01 |
| G1/S phase transition of bone cancer cell lines | 5 | 2.49E-03 |
| Cell stage | 47 | 7.30E-03 |
| Interphase | 31 | 1.26E-02 |
| G1 phase of bone cancer cell lines | 6 | 1.47E-02 |
| Cell division process | 61 | 1.84E-02 |
| Cell cycle progression of cell lines | 18 | 2.00E-02 |
| Cell cycle progression of tumor cell lines | 14 | 2.01E-02 |
| Cell division process of cell lines | 34 | 3.44E-02 |
| Cell division process of eukaryotic cells | 41 | 4.06E-02 |
| Cell cycle progression of eukaryotic cells | 21 | 4.40E-02 |

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| | | |
|---|-----|-------------------|
| Arrest in G1/S phase transition of bone cancer cell lines | 3 | 4.53E-02 |
| Cell death | 104 | 3.02E-03-1.59E-01 |
| Cell death of central nervous system cells | 19 | 3.02E-03 |
| Apoptosis of cell lines | 58 | 1.26E-02 |
| Apoptosis of eukaryotic cells | 76 | 1.43E-02 |
| Cell death of eukaryotic cells | 88 | 1.43E-02 |
| Cell death | 104 | 1.77E-02 |
| Cell death of cell lines | 66 | 1.78E-02 |
| Apoptosis of tumor cell lines | 46 | 2.71E-02 |
| Apoptosis | 89 | 2.92E-02 |
| Cell death of brain cells | 15 | 3.41E-02 |
| Cell death of cerebral cortex cells | 13 | 3.41E-02 |
| Cell death of tumor cell lines | 51 | 3.56E-02 |
| DNA replication, recombination, and repair | 38 | 9.11E-03-1.59E-01 |
| Annealing of RNA | 3 | 9.11E-03 |
| Metabolism of DNA | 22 | 3.41E-02 |
| Posttranslational modification | 18 | 1.47E-02-1.59E-01 |
| Oxidation of protein | 5 | 1.47E-02 |
| Protein degradation | 5 | 1.47E-02-1.47E-02 |
| Oxidation of protein | 5 | 1.47E-02 |
| Cellular assembly and organization | 60 | 2.34E-02-1.59E-01 |
| Fusion of liposome | 3 | 2.34E-02 |

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| | | |
|--|-----|-------------------|
| Binding of ribosome | 3 | 3.28E-02 |
| Contraction of actin cytoskeleton | 2 | 3.41E-02 |
| Extension of actin cytoskeleton | 2 | 3.41E-02 |
| Induction of phospholipid vesicles | 2 | 3.41E-02 |
| Polarization of podosomes | 2 | 3.41E-02 |
| Polymerization of actin | 6 | 4.04E-02 |
| Polymerization of actin filaments | 6 | 4.76E-02 |
| Protein trafficking | 24 | 2.4E-02-9.05E-02 |
| Targeting of protein | 10 | 2.40E-02 |
| Transport of protein | 16 | 3.41E-02 |
| Cellular growth and proliferation | 117 | 3.1E-02-1.59E-01 |
| Growth of cells | 71 | 3.10E-02 |
| Re-entry into growth of leukemia cell lines | 2 | 3.41E-02 |
| Colony formation of cervical cancer cell lines | 4 | 4.00E-02 |
| Cellular movement | 63 | 3.41E-02-1.59E-01 |
| Invasion of cell lines | 24 | 3.41E-02 |
| Invasion of brain cancer cell lines | 6 | 4.26E-02 |
| Molecular transport | 39 | 3.41E-02-1.59E-01 |
| Transport of protein | 16 | 3.41E-02 |
| Quantity of phosphatidylinositol 4,5-diphosphate | 4 | 4.40E-02 |
| Cell morphology | 44 | 3.41E-02-1.59E-01 |
| Contraction of actin cytoskeleton | 2 | 3.41E-02 |

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| | | |
|--|----|-------------------|
| Extension of actin cytoskeleton | 2 | 3.41E-02 |
| Polarization of podosomes | 2 | 3.41E-02 |
| Ruffling of cervical cancer cell lines | 2 | 3.41E-02 |
| Shape change | 28 | 4.04E-02 |
| Cellular development | 58 | 3.41E-02-1.59E-01 |
| Re-entry into growth of leukemia cell lines | 2 | 3.41E-02 |
| Ruffling of cervical cancer cell lines | 2 | 3.41E-02 |
| Developmental process of tumor cell lines | 42 | 4.52E-02 |
| Energy production | 3 | 3.41E-02-1.57E-01 |
| Recovery of ATP | 2 | 3.41E-02 |
| Nucleic acid metabolism | 13 | 3.41E-02-1.59E-01 |
| Recovery of ATP | 2 | 3.41E-02 |
| Small molecule biochemistry | 35 | 3.41E-02-1.59E-01 |
| Recovery of ATP | 2 | 3.41E-02 |
| Quantity of phosphatidylinositol 4,5-diphosphate | 4 | 4.40E-02 |
| Antigen presentation | 4 | 3.66E-02-1.59E-01 |
| Activation of monocyte-derived macrophages | 3 | 3.66E-02 |
| Cell-to-cell signaling and interaction | 15 | 3.66E-02-1.59E-01 |
| Activation of monocyte-derived macrophages | 3 | 3.66E-02 |
| Cellular Function and Maintenance | 35 | 4.04E-02-1.59E-01 |
| Polymerization of actin | 6 | 4.04E-02 |
| Endocytosis of cells | 8 | 4.53E-02 |

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| | | |
|--|----|------------------|
| Polymerization of actin filaments | 6 | 4.76E-02 |
| Carbohydrate metabolism | 16 | 4.4E-02-1.59E-01 |
| Quantity of phosphatidylinositol 4,5-diphosphate | 4 | 4.40E-02 |
| Lipid metabolism | 13 | 4.4E-02-1.59E-01 |
| Quantity of phosphatidylinositol 4,5-diphosphate | 4 | 4.40E-02 |

mRNA, mammalian target of rapamycin; ATP, amniotic fluid transcriptome.

*Only functional annotations with a false discovery rate of < 0.05 were reported.

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Appendix 6. Genes identified by MEDLINE and Pathways Analysis Software Searches

Present in the Amniotic Fluid Transcriptome*

| Fetal organ (GEO accession number) | Number of Genes Present in AF Core Transcriptome[†] | | |
|---|---|-----------------------------|-----------------------------|
| | Category 1 Genes | Category 2 Genes | Category 3 Genes |
| Heart (GSE1789) | 32/671 | 2/98 | 38/ 2265 |
| Kidney or bladder (GSE6280) | 16/389 | 3/75 | 20/ 1020 |
| Placenta (GSE9984) | 7/96 [‡] | 1/47 | 8/196 |
| Intestine | - | 2/6 | 11/890 [§] |
| Skin | - | 1/13 | 28/1087 |
| Amnion | - | 1/45 | 0/58 |

AF, amniotic fluid.

*Includes only fetal organs not represented in the GNF Atlas. See Appendix 1 for gene-category definitions.

[†]The numerator is the number of Category “x” genes identified for that fetal organ present in the AF core transcriptome, and the denominator is the total number of Category “x” genes for that fetal organ.

[‡]Only second-trimester placenta data included.

[§]Excludes hepatic development and function.

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Appendix 7. MEDLINE Literature Search Results

| Organ | No. of Results From MEDLINE Search Query | Full-Text Articles Reviewed | Affymetrix Microarray Data Studies | Other Included Gene Expression Studies | Total Studies Included | No. Genes in Final List |
|-----------|---|-----------------------------------|--|---|------------------------------|-------------------------------|
| Amnion | 20 | 4 | 1 ⁽¹⁾ | 5 ⁽²⁻⁶⁾ | 6 | 45 |
| Bladder | 2 | 1 | 0 | 1 ⁽⁷⁾ | 1 | 4 |
| Intestine | 53 | 8 | 0 | 5 ⁽⁸⁻¹²⁾ | 5 | 6 |
| Heart | 105 | 23 | 2 ^(13, 14) | 5 ⁽¹⁵⁻¹⁹⁾ | 7 | 98 |
| Kidney | 101 | 35 | 2 ^(20, 21) | 16 ⁽²²⁻³⁸⁾ | 18 | 75 |
| Placenta | 206 | 10 | 2 ^(39, 40) | 1 ⁽⁴⁾ | 3 | 47 |
| Skin | 71 | 5 | 0 | 4 ⁽⁴¹⁻⁴⁴⁾ | 4 | 13 |

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Appendix 8. Category 1 Fetal Heart Genes (Common to GSE1789 and Ingenuity Cardiovascular Development and Function Category)

| | | | | |
|----------------|----------------|----------------|----------------|---------------|
| <i>ABAT</i> | <i>AGT</i> | <i>AP4S1</i> | <i>ATP7A</i> | <i>CACYBP</i> |
| <i>ABCA1</i> | <i>AGTR1</i> | <i>APC</i> | <i>ATPIF1</i> | <i>CALCR</i> |
| <i>ABCB4</i> | <i>AGTR2</i> | <i>APLNR</i> | <i>BAX</i> | <i>CALR</i> |
| <i>ABCC1</i> | <i>AIFM1</i> | <i>APOE</i> | <i>BAZ1B</i> | <i>CAPNS1</i> |
| <i>ABCG2</i> | <i>AIMP1</i> | <i>APP</i> | <i>BCL2</i> | <i>CARTPT</i> |
| <i>ACADM</i> | <i>AKT1</i> | <i>AQP1</i> | <i>BCL2L1</i> | <i>CASP3</i> |
| <i>ACE2</i> | <i>AKT3</i> | <i>ARG2</i> | <i>BCOR</i> | <i>CASP9</i> |
| <i>ACPI</i> | <i>ALCAM</i> | <i>ARHGAP1</i> | <i>BGN</i> | <i>CASQ2</i> |
| <i>ACTC1</i> | <i>ALDH2</i> | <i>ARID4B</i> | <i>BIRC5</i> | <i>CAT</i> |
| <i>ACTN1</i> | <i>ALDH1A2</i> | <i>ARNT</i> | <i>BMP5</i> | <i>CAV1</i> |
| <i>ACTN4</i> | <i>ALPK3</i> | <i>ASPH</i> | <i>BMP7</i> | <i>CAV2</i> |
| <i>ACVR1</i> | <i>ANGPT1</i> | <i>ATF2</i> | <i>BMPR1A</i> | <i>CBFB</i> |
| <i>ADAM9</i> | <i>ANGPTL2</i> | <i>ATF3</i> | <i>BNIP2</i> | <i>CBY1</i> |
| <i>ADAM17</i> | <i>ANK2</i> | <i>ATG5</i> | <i>BNIP3</i> | <i>CCNA2</i> |
| <i>ADAM19</i> | <i>ANK3</i> | <i>ATM</i> | <i>BRAF</i> | <i>CCND1</i> |
| <i>ADAMTS1</i> | <i>ANXA1</i> | <i>ATP1A1</i> | <i>BTG1</i> | <i>CCND2</i> |
| <i>ADAMTS9</i> | <i>ANXA2</i> | <i>ATP1A2</i> | <i>C3</i> | <i>CCND3</i> |
| <i>ADH5</i> | <i>ANXA3</i> | <i>ATP2A2</i> | <i>C1GALT1</i> | <i>CCT2</i> |
| <i>ADM</i> | <i>ANXA6</i> | <i>ATP2B4</i> | <i>C1QA</i> | <i>CD14</i> |
| <i>ADORAI</i> | <i>ANXA7</i> | <i>ATP5A1</i> | <i>CABIN1</i> | <i>CD34</i> |
| <i>AGGF1</i> | <i>AP3M2</i> | <i>ATP5B</i> | <i>CACNA1C</i> | <i>CD36</i> |
| <i>AGRN</i> | <i>AP3S2</i> | <i>ATP5J</i> | <i>CACNB3</i> | <i>CD40</i> |

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| | | | | |
|----------------|-----------------|-------------------|---------------|---------------|
| <i>CD44</i> | <i>COL18A1</i> | <i>CUL5</i> | <i>DNAJB6</i> | <i>EGLN3</i> |
| <i>CD47</i> | <i>COL1A1</i> | <i>CUL7</i> | <i>DOK5</i> | <i>ELK3</i> |
| <i>CD81</i> | <i>COL1A2</i> | <i>CX3CL1</i> | <i>DRAP1</i> | <i>ELN</i> |
| <i>CD99</i> | <i>COL2A1</i> | <i>CXADR</i> | <i>DSP</i> | <i>EMP1</i> |
| <i>CD151</i> | <i>COL3A1</i> | <i>CXCL2</i> | <i>DUSP1</i> | <i>EMP3</i> |
| <i>CDC42</i> | <i>COL4A1</i> | <i>CXCL12</i> | <i>DUSP6</i> | <i>ENG</i> |
| <i>CDH2</i> | <i>COL4A2</i> | <i>CXCR4</i> | <i>DVL1</i> | <i>ENO1</i> |
| <i>CDH5</i> | <i>COL5A1</i> | <i>CYCS</i> | <i>DVL2</i> | <i>ENPEP</i> |
| <i>CDK2</i> | <i>CORIN</i> | <i>CYP1B1</i> | <i>DVL3</i> | <i>ENPP2</i> |
| <i>CDK4</i> | <i>CREB1</i> | <i>CYP2J2</i> | <i>DYRK1A</i> | <i>ENTPD1</i> |
| <i>CDKN1A</i> | <i>CREM</i> | <i>CYR61</i> | <i>E2F1</i> | <i>EP300</i> |
| <i>CDKN1B</i> | <i>CRK</i> | <i>DAG1</i> | <i>ECE1</i> | <i>EPAS1</i> |
| <i>CDKN1C</i> | <i>CRKL</i> | <i>DCN</i> | <i>ECM1</i> | <i>EPHB4</i> |
| <i>CDKN2D</i> | <i>CRYAB</i> | <i>DDAH1</i> | <i>EDF1</i> | <i>EPOR</i> |
| <i>CELF2</i> | <i>CSRP3</i> | <i>DDR1</i> | <i>EDNRA</i> | <i>ERBB2</i> |
| <i>CENPF</i> | <i>CST3</i> | <i>DEFA1</i> | <i>EDNRB</i> | <i>ERBB3</i> |
| <i>CFLAR</i> | <i>CTBP1</i> | (includes others) | <i>EEF1A2</i> | <i>ERBB4</i> |
| <i>CITED2</i> | <i>CTBP2</i> | <i>DES</i> | <i>EFEMP2</i> | <i>F13A1</i> |
| <i>CLDN5</i> | <i>CTGF</i> | <i>DGKA</i> | <i>EFNA1</i> | <i>F2R</i> |
| <i>CLIC4</i> | <i>CTNNB1</i> | <i>DICER1</i> | <i>EFNB2</i> | <i>FABP3</i> |
| <i>CNNI</i> | <i>CTNNBIPI</i> | <i>DLC1</i> | <i>EGF</i> | <i>FABP4</i> |
| <i>COL11A1</i> | <i>CTSB</i> | <i>DLG1</i> | <i>EGFL7</i> | <i>FADD</i> |
| <i>COL15A1</i> | <i>CTTN</i> | <i>DMPK</i> | <i>EGLN2</i> | <i>FBN1</i> |

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| | | | | |
|---------------|----------------|---------------------------|---------------|-----------------|
| <i>FBXW7</i> | <i>GADD45A</i> | <i>GUCY1A3</i> | <i>HSPB8</i> | <i>INSR</i> |
| <i>FGF1</i> | <i>GAS1</i> | <i>GUCY1B3</i> | <i>HSPD1</i> | <i>IRSI</i> |
| <i>FGF7</i> | <i>GAS6</i> | <i>GYS1</i> | <i>HSPG2</i> | <i>IRS2</i> |
| <i>FGF9</i> | <i>GATA2</i> | <i>HAND1</i> | <i>HYOU1</i> | <i>IRX4</i> |
| <i>FGF12</i> | <i>GATA4</i> | <i>HBA1/HBA2</i> | <i>ICAM2</i> | <i>ITGA5</i> |
| <i>FGF13</i> | <i>GATA6</i> | <i>HBEGF</i> | <i>ID1</i> | <i>ITGA6</i> |
| <i>FGF18</i> | <i>GBPI</i> | <i>HDAC1</i> | <i>ID2</i> | <i>ITGA7</i> |
| <i>FGFR1</i> | <i>GCH1</i> | <i>HDAC9</i> | <i>ID3</i> | <i>ITGAE</i> |
| <i>FHL2</i> | <i>GCLC</i> | <i>HEXIM1</i> | <i>IFI16</i> | <i>ITGAV</i> |
| <i>FKBP1A</i> | <i>GCLM</i> | <i>HEY1</i> | <i>IFT52</i> | <i>ITGB1</i> |
| <i>FLNB</i> | <i>GJA1</i> | <i>HEY2</i> | <i>IFT57</i> | <i>ITGB3</i> |
| <i>FLT1</i> | <i>GJA4</i> | <i>HHEX</i> | <i>IFT88</i> | <i>ITGB5</i> |
| <i>FN1</i> | <i>GLRX3</i> | <i>HIF1A</i> | <i>IGF1</i> | <i>ITGB1BP2</i> |
| <i>FOXC1</i> | <i>GNA11</i> | <i>HIF3A</i> | <i>IGF2</i> | <i>JAG1</i> |
| <i>FOXM1</i> | <i>GNAQ</i> | <i>HMGB1</i> | <i>IGF1R</i> | <i>JAK2</i> |
| <i>FOXO1</i> | <i>GNAS</i> | <i>HMGB2</i> | <i>IGF2R</i> | <i>JAM3</i> |
| <i>FOXO3</i> | <i>GPC1</i> | <i>HMMR</i> | <i>IGFBP3</i> | <i>JARID2</i> |
| <i>FOXP1</i> | <i>GPX1</i> | <i>HMOX1</i> | <i>IGFBP4</i> | <i>JMJD6</i> |
| <i>FURIN</i> | <i>GRK5</i> | <i>HOPX</i> | <i>IKBKAP</i> | <i>JUN</i> |
| <i>FZD4</i> | <i>GRN</i> | <i>HRAS</i> | <i>IL15</i> | <i>JUNB</i> |
| <i>FZD5</i> | <i>GSK3A</i> | <i>HRC</i> | <i>IL6ST</i> | <i>JUND</i> |
| <i>GAA</i> | <i>GSK3B</i> | <i>HSPA1A/HS PA1B</i> | <i>ING4</i> | <i>JUP</i> |
| <i>GAB1</i> | <i>GSN</i> | | <i>INPP4B</i> | <i>KCNE1</i> |
| | | <i>HSPB7</i> | | |

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| | | | | |
|-----------------|-----------------|----------------|---------------|---------------|
| <i>KCNH2</i> | <i>LMO2</i> | <i>MFN2</i> | <i>MYOF</i> | <i>NR2F2</i> |
| <i>KCNJ8</i> | <i>LOX</i> | <i>MGP</i> | <i>NAB1</i> | <i>NR3C1</i> |
| <i>KCNMB4</i> | <i>LPL</i> | <i>MIF</i> | <i>NACA</i> | <i>NR3C2</i> |
| <i>KDR</i> | <i>LRPAP1</i> | <i>MITF</i> | <i>NCK1</i> | <i>NR4A1</i> |
| <i>KIT</i> | <i>MAP2K1</i> | <i>MKKS</i> | <i>NCL</i> | <i>NR4A3</i> |
| <i>KLF2</i> | <i>MAP2K6</i> | <i>MKL2</i> | <i>NCOA1</i> | <i>NRP1</i> |
| <i>KLF4</i> | <i>MAP3K7</i> | <i>MLYCD</i> | <i>NCOA3</i> | <i>NUPR1</i> |
| <i>KLF7</i> | <i>MAPK1</i> | <i>MMP2</i> | <i>NCOA6</i> | <i>ODC1</i> |
| <i>KLF10</i> | <i>MAPK7</i> | <i>MMP9</i> | <i>NCOR2</i> | <i>PAK2</i> |
| <i>KLF11</i> | <i>MAPK9</i> | <i>MMP14</i> | <i>NDST1</i> | <i>PAK4</i> |
| <i>KRIT1</i> | <i>MAPK14</i> | <i>MORF4L1</i> | <i>NDUFV2</i> | <i>PARP1</i> |
| <i>LAMA2</i> | <i>MAPKAPK2</i> | <i>MOSPD3</i> | <i>NFATC3</i> | <i>PAXIP1</i> |
| <i>LAMA4</i> | <i>MARCKSL1</i> | <i>MTDH</i> | <i>NFE2L2</i> | <i>PBRM1</i> |
| <i>LAMC1</i> | <i>MB</i> | <i>MTUS1</i> | <i>NIPBL</i> | <i>PDGFB</i> |
| <i>LDLR</i> | <i>MDK</i> | <i>MYBPC3</i> | <i>NISCH</i> | <i>PDGFC</i> |
| <i>LEMD3</i> | <i>MED1</i> | <i>MYH6</i> | <i>NKX2-5</i> | <i>PDGFRA</i> |
| <i>LEPR</i> | <i>MEF2A</i> | <i>MYH7</i> | <i>NLK</i> | <i>PEBP1</i> |
| <i>LEPROTL1</i> | <i>MEF2C</i> | <i>MYH9</i> | <i>NOTCH1</i> | <i>PECAM1</i> |
| <i>LGALS1</i> | <i>MEIS1</i> | <i>MYH10</i> | <i>NOTCH4</i> | <i>PGF</i> |
| <i>LGALS3</i> | <i>MEN1</i> | <i>MYL2</i> | <i>NOX4</i> | <i>PGK1</i> |
| <i>LGR4</i> | <i>MEOX2</i> | <i>MYL3</i> | <i>NPPA</i> | <i>PHC1</i> |
| <i>LIMS2</i> | <i>MFAP5</i> | <i>MYL4</i> | <i>NPPB</i> | <i>PIGF</i> |
| <i>LMNA</i> | <i>MFGE8</i> | <i>MYL7</i> | <i>NPR3</i> | <i>PIK3CB</i> |

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| | | | | |
|---|----------------|-----------------|-----------------|-----------------|
| <i>PIK3R1</i> | <i>PRDX3</i> | <i>RAF1</i> | <i>RNPEP</i> | <i>SERPINH1</i> |
| <i>PIM1</i> | <i>PRKARIA</i> | <i>RAMP1</i> | <i>ROCK1</i> | <i>SGK1</i> |
| <i>PIP5K1C</i> | <i>PRKD2</i> | <i>RAP1A</i> | <i>ROCK2</i> | <i>SGPL1</i> |
| <i>PKD1</i> | <i>PRKDC</i> | <i>RAP1B</i> | <i>ROR1</i> | <i>SHC1</i> |
| <i>PKD2</i> (includes <i>EG:18764</i>) | <i>PROCR</i> | <i>RAP1GDS1</i> | <i>RREB1</i> | <i>SIGMAR1</i> |
| | <i>PRRX1</i> | <i>RARA</i> | <i>RRM2</i> | <i>SIN3B</i> |
| <i>PKP2</i> | <i>PSEN1</i> | <i>RASA1</i> | <i>RTN4</i> | <i>SIRT1</i> |
| <i>PLA2G6</i> | <i>PTEN</i> | <i>RASSF1</i> | <i>RXRA</i> | <i>SKP2</i> |
| <i>PLA2G4A</i> | <i>PTGER3</i> | <i>RB1</i> | <i>RXRB</i> | <i>SLC12A2</i> |
| <i>PLAT</i> | <i>PTGER4</i> | <i>RB1CC1</i> | <i>RYR2</i> | <i>SLC22A5</i> |
| <i>PLAU</i> | <i>PTGES</i> | <i>RBL2</i> | <i>S100A4</i> | <i>SLC2A1</i> |
| <i>PLCB1</i> | <i>PTGIS</i> | <i>RBM15</i> | <i>SIPR1</i> | <i>SLC7A1</i> |
| <i>PLN</i> | <i>PTK2</i> | <i>RBPJ</i> | <i>SCD</i> | <i>SLIT2</i> |
| <i>PLOD3</i> | <i>PTN</i> | <i>RCAN1</i> | <i>SCG5</i> | <i>SLN</i> |
| <i>PLXND1</i> | <i>PTPN1</i> | <i>RELA</i> | <i>SCN5A</i> | <i>SMADI</i> |
| <i>PML</i> | <i>PTPN11</i> | <i>REM1</i> | <i>SCPEP1</i> | <i>SMAD2</i> |
| <i>PNPLA6</i> | <i>PTPRM</i> | <i>RGS2</i> | <i>SDC2</i> | <i>SMAD3</i> |
| <i>PPAP2B</i> | <i>PXN</i> | <i>RGS5</i> | <i>SDC4</i> | <i>SMAD4</i> |
| <i>PPP1CA</i> | <i>QKI</i> | <i>RGS19</i> | <i>SEMA3C</i> | <i>SMAD6</i> |
| <i>PPP2CA</i> | <i>RAB1A</i> | <i>RHOA</i> | <i>SEMA3F</i> | <i>SMAD7</i> |
| <i>PPP3CA</i> | <i>RAB4A</i> | <i>RHOB</i> | <i>SEMA5A</i> | <i>SMARCA4</i> |
| <i>PPP3CB</i> | <i>RAB9A</i> | <i>RHOC</i> | <i>SERPINF1</i> | <i>SMARCB1</i> |
| <i>PPP3R1</i> | <i>RAC1</i> | <i>RNHI</i> | <i>SERPING1</i> | <i>SMARCD3</i> |

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| | | | | |
|---------------|----------------|---------------|-----------------|---------------------------|
| <i>SMTN</i> | <i>SRI</i> | <i>TEAD4</i> | <i>TKT</i> | <i>TSC1</i> |
| <i>SNTA1</i> | <i>SRSF1</i> | <i>TEK</i> | <i>TM4SF1</i> | <i>TSC2</i> |
| <i>SNTB2</i> | <i>SRSF2</i> | <i>TFEB</i> | <i>TMOD1</i> | <i>TSPAN12</i> |
| <i>SOD1</i> | <i>ST3GAL4</i> | <i>TFPI</i> | <i>TNFAIP3</i> | <i>TSTA3</i> |
| <i>SOD2</i> | <i>STAB1</i> | <i>TGFBR2</i> | <i>TNFRSF1A</i> | <i>TTN</i> |
| <i>SOX4</i> | <i>STAT3</i> | <i>TGFBR3</i> | <i>TNFSF10</i> | <i>TUBA1C</i> |
| <i>SOX17</i> | <i>STK3</i> | <i>TGM2</i> | <i>TNIP2</i> | <i>TUBA3C/TU BA3D</i> |
| <i>SOX18</i> | <i>STX4</i> | <i>THBD</i> | <i>TNNC1</i> | <i>TUBA4A</i> |
| <i>SPARC</i> | <i>STX6</i> | <i>THBS2</i> | <i>TNNI1</i> | <i>TUBB3</i> |
| <i>SPEG</i> | <i>STX7</i> | <i>THBS4</i> | <i>TNNI3</i> | <i>TUBB6</i> |
| <i>SPP1</i> | <i>TAL1</i> | <i>THRA</i> | <i>TNNT2</i> | <i>TXN2</i> |
| <i>SPRED2</i> | <i>TAZ</i> | <i>THY1</i> | <i>TP53BP2</i> | <i>TXN</i> |
| <i>SPRY1</i> | <i>TBX2</i> | <i>TIE1</i> | <i>TPM1</i> | <i>TXND5</i> |
| <i>SPRY4</i> | <i>TCAP</i> | <i>TIMP1</i> | <i>TPM2</i> | |
| <i>SPTBN1</i> | <i>TCF21</i> | <i>TIMP3</i> | <i>TPT1</i> | |
| <i>SRF</i> | <i>TCF7L2</i> | <i>TIPARP</i> | <i>TRPC1</i> | |

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Appendix 9. Category 1 Kidney Genes (Common to GSE6280 and Pathways Analysis Software Renal and Urological System Category)

| | | | | |
|----------------|----------------|----------------|-----------------|---------------|
| <i>ABCA1</i> | <i>APOE</i> | <i>BRD4</i> | <i>CDKN1B</i> | <i>CYTH2</i> |
| <i>ABCC5</i> | <i>APP</i> | <i>BSG</i> | <i>CEBDP</i> | <i>DAB2</i> |
| <i>ABCG2</i> | <i>APRT</i> | <i>C5</i> | <i>CES2</i> | <i>DAPK1</i> |
| <i>ACPI</i> | <i>AQP1</i> | <i>C1GALT1</i> | <i>CKAP2</i> | <i>DDB1</i> |
| <i>ACTN4</i> | <i>AQP3</i> | <i>C1QBP</i> | <i>CLIP1</i> | <i>DDX17</i> |
| <i>ACVR2B</i> | <i>ARHGAP1</i> | <i>CADM1</i> | <i>CLU</i> | <i>DIRAS2</i> |
| <i>ADAMTS1</i> | <i>ARID5B</i> | <i>CALCA</i> | <i>COL18A1</i> | <i>DLG1</i> |
| <i>ADM</i> | <i>ARSB</i> | <i>CASP1</i> | <i>COL4A3</i> | <i>DLGAP5</i> |
| <i>ADNP</i> | <i>ATG5</i> | <i>CAT</i> | <i>CRK</i> | <i>DLST</i> |
| <i>ADORA1</i> | <i>AXL</i> | <i>CAVI</i> | <i>CSDA</i> | <i>DNM1</i> |
| <i>AFF1</i> | <i>B4GALT1</i> | <i>CAV2</i> | <i>CSF1R</i> | <i>DRD2</i> |
| <i>AGT</i> | <i>BAG6</i> | <i>CCND1</i> | <i>CTCF</i> | <i>DUSP1</i> |
| <i>AGTR1</i> | <i>BCAM</i> | <i>CCND3</i> | <i>CTNNA1</i> | <i>E2F1</i> |
| <i>AGTR2</i> | <i>BCL2</i> | <i>CD28</i> | <i>CTNNB1</i> | <i>E2F3</i> |
| <i>AHR</i> | <i>BCL6</i> | <i>CD44</i> | <i>CTNNBIP1</i> | <i>EDNRA</i> |
| <i>ALCAM</i> | <i>BECN1</i> | <i>CD46</i> | <i>CUL4A</i> | <i>EDNRB</i> |
| <i>ALDH1A1</i> | <i>BGN</i> | <i>CDC42</i> | <i>CX3CL1</i> | <i>EFNA1</i> |
| <i>ANGPT2</i> | <i>BIRC2</i> | <i>CDC25B</i> | <i>CXCL1</i> | <i>EFNA5</i> |
| <i>ANXA2</i> | <i>BIRC5</i> | <i>CDH1</i> | <i>CXCL10</i> | <i>EFNB2</i> |
| <i>ANXA4</i> | <i>BMP2</i> | <i>CDH16</i> | <i>CXCL12</i> | <i>EGF</i> |
| <i>APC</i> | <i>BMP7</i> | <i>CDK4</i> | <i>CXCR4</i> | <i>EGFR</i> |
| <i>APLNR</i> | <i>BNIP3</i> | <i>CDK2AP1</i> | <i>CYP4A11</i> | <i>ENTPD1</i> |

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| | | | | |
|---------------|----------------|----------------|---------------|----------------|
| <i>EPCAM</i> | <i>GAB1</i> | <i>HOXD11</i> | <i>ITGA9</i> | <i>LRP4</i> |
| <i>EPHB2</i> | <i>GAK</i> | <i>HRAS</i> | <i>ITGAV</i> | <i>LY96</i> |
| <i>ERBB2</i> | <i>GAS6</i> | <i>HSP90B1</i> | <i>ITGB1</i> | <i>MAFB</i> |
| <i>ERBB4</i> | <i>GEM</i> | <i>HSPD1</i> | <i>ITGB3</i> | <i>MAN2A1</i> |
| <i>ESM1</i> | <i>GHR</i> | <i>HSPG2</i> | <i>JMJD6</i> | <i>MAP2K3</i> |
| <i>EZR</i> | <i>GIT1</i> | <i>HYOU1</i> | <i>JUN</i> | <i>MAPK1</i> |
| <i>F10</i> | <i>GJA1</i> | <i>IFIH1</i> | <i>JUND</i> | <i>MAPK14</i> |
| <i>F2RL1</i> | <i>GLA</i> | <i>IFT88</i> | <i>KCNJ1</i> | <i>MAPT</i> |
| <i>FAS</i> | <i>GLI2</i> | <i>IGF1</i> | <i>KCNK5</i> | <i>MED28</i> |
| <i>FBLN1</i> | <i>GNAS</i> | <i>IGF2</i> | <i>KDR</i> | <i>MET</i> |
| <i>FBN1</i> | <i>GORASPI</i> | <i>IGF1R</i> | <i>KIF3A</i> | <i>MIF</i> |
| <i>FCER1G</i> | <i>GPC3</i> | <i>IGFBP3</i> | <i>KL</i> | <i>MLL</i> |
| <i>FGF1</i> | <i>GRB2</i> | <i>IL16</i> | <i>KLF5</i> | <i>MMP9</i> |
| <i>FGF2</i> | <i>GRN</i> | <i>IL13RA1</i> | <i>KLK6</i> | <i>MMP12</i> |
| <i>FGFR1</i> | <i>GSK3B</i> | <i>ILK</i> | <i>KNG1</i> | <i>MMP14</i> |
| <i>FGFR2</i> | <i>HBEGF</i> | <i>INSR</i> | <i>LICAM</i> | <i>MPDZ</i> |
| <i>FGFR4</i> | <i>HEG1</i> | <i>INVS</i> | <i>LAMA5</i> | <i>MST1</i> |
| <i>FLNA</i> | <i>HIF1A</i> | <i>IRAK3</i> | <i>LGALS3</i> | <i>MST4</i> |
| <i>FLNC</i> | <i>HIP1</i> | <i>IRF9</i> | <i>LIN7C</i> | <i>MT1E</i> |
| <i>FLT1</i> | <i>HIPK2</i> | <i>IRSI</i> | <i>LIPG</i> | <i>MT2A</i> |
| <i>FN1</i> | <i>HNF1B</i> | <i>ITGA5</i> | <i>LMNA</i> | <i>MTOR</i> |
| <i>FOXC1</i> | <i>HNRNPAB</i> | <i>ITGA6</i> | <i>LOX</i> | <i>MYO1E</i> |
| <i>FOXD1</i> | <i>HOXA11</i> | <i>ITGA8</i> | <i>LRP2</i> | <i>NDUFAB1</i> |

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| | | | | |
|--|----------------|----------------|------------------|----------------|
| <i>NEK9</i> | <i>PDGFRB</i> | <i>PPIA</i> | <i>RARB</i> | <i>SIX2</i> |
| <i>NF1</i> | <i>PDSS2</i> | <i>PPM1A</i> | <i>RARRES3</i> | <i>SKP2</i> |
| <i>NFAT5</i> | <i>PEG10</i> | <i>PPP2CA</i> | <i>RELA</i> | <i>SLC12A1</i> |
| <i>NFKBIA</i> | <i>PEMT</i> | <i>PPP3CA</i> | <i>RELN</i> | <i>SLC19A1</i> |
| <i>NID1</i> | <i>PFKM</i> | <i>PRKAR1A</i> | <i>REN</i> | <i>SLC2A1</i> |
| <i>NINL</i> | <i>PGF</i> | <i>PRKX</i> | <i>RET</i> | <i>SLC30A1</i> |
| <i>NPHS1</i> | <i>PIAS1</i> | <i>PRMT5</i> | <i>RHOA</i> | <i>SLIT2</i> |
| <i>NPHS2</i> | <i>PIKFYVE</i> | <i>PRNP</i> | <i>RLN1/RLN2</i> | <i>SLK</i> |
| <i>NPR1</i> | <i>PIM1</i> | <i>PSEN1</i> | <i>RND3</i> | <i>SMAD3</i> |
| <i>NR3C2</i> | <i>PKD1</i> | <i>PSEN2</i> | <i>RPGRIP1L</i> | <i>SMAD4</i> |
| <i>NRAS</i> | <i>PKD2</i> | <i>PTCH1</i> | <i>RPSA</i> | <i>SMO</i> |
| <i>NRIP1</i> <i>(includes EG:18764)</i> | | <i>PTEN</i> | <i>RTN4</i> | <i>SOD2</i> |
| <i>NRP1</i> | <i>PLAT</i> | <i>PTGER3</i> | <i>RXRA</i> | <i>SORBS1</i> |
| <i>ODC1</i> | <i>PLAU</i> | <i>PTGES</i> | <i>SALL1</i> | <i>SORLI</i> |
| <i>OTUB1</i> | <i>PLCE1</i> | <i>PTK2</i> | <i>SAT1</i> | <i>SORT1</i> |
| <i>PAFAH1B1</i> | <i>PLXNA1</i> | <i>PTP4A1</i> | <i>SCHIP1</i> | <i>SOSTDC1</i> |
| <i>PARP1</i> | <i>PLXND1</i> | <i>PTP4A3</i> | <i>SDC1</i> | <i>SPARC</i> |
| <i>PARVA</i> | <i>PMP22</i> | <i>PTPN1</i> | <i>SDC2</i> | <i>SPP1</i> |
| <i>PAX2</i> | <i>PNN</i> | <i>PTPRB</i> | <i>SDC4</i> | <i>SPRY1</i> |
| <i>PAX8</i> | <i>PODXL</i> | <i>PTTG1</i> | <i>SEMA3F</i> | <i>SPRY2</i> |
| <i>PBX1</i> | <i>POSTN</i> | <i>PTX3</i> | <i>SETMAR</i> | <i>ST6GAL1</i> |
| <i>PCSK5</i> | <i>PPARD</i> | <i>PXN</i> | <i>SFRP1</i> | <i>STAT3</i> |
| <i>PDCD6IP</i> | <i>PPARG</i> | <i>RARA</i> | <i>SGPL1</i> | <i>STC1</i> |

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| | | | | |
|---------------|-----------------|------------------|----------------|--------------|
| <i>STMN1</i> | <i>TGM2</i> | <i>TMEM123</i> | <i>TSC1</i> | <i>WASL</i> |
| <i>SULF1</i> | <i>THBS1</i> | <i>TNFAIP3</i> | <i>TSC2</i> | <i>WFS1</i> |
| <i>SUMO1</i> | <i>THY1</i> | <i>TNFRSF10B</i> | <i>TSC22D3</i> | <i>WISPI</i> |
| <i>TAC1</i> | <i>TIMELESS</i> | <i>TNFRSF1A</i> | <i>ULK1</i> | <i>WNT6</i> |
| <i>TACR1</i> | <i>TIMP1</i> | <i>TNIK</i> | <i>UMOD</i> | <i>WNT5A</i> |
| <i>TCF21</i> | <i>TIMP3</i> | <i>TNS1</i> | <i>UNC5B</i> | <i>WT1</i> |
| <i>TENC1</i> | <i>TIPARP</i> | <i>TP53</i> | <i>USP14</i> | <i>WWTR1</i> |
| <i>TFAP2B</i> | <i>TJP1</i> | <i>TP63</i> | <i>VDAC1</i> | <i>ZBTB5</i> |
| <i>TFDP1</i> | <i>TKT</i> | <i>TPM2</i> | <i>VEGFA</i> | <i>ZEB2</i> |
| <i>TGFA</i> | <i>TLR3</i> | <i>TPP2</i> | <i>VIM</i> | <i>ZHX2</i> |

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Appendix 10. Category 1 Placental Genes (Common to GSE9984 and Pathways Analysis Software Placental Terms)

| | | | | |
|---------------|---------------|-----------------|--------------------------------|----------------|
| <i>ABCA1</i> | <i>CUL7</i> | <i>HOPX</i> | <i>MYH10</i> | <i>RXRA</i> |
| <i>ADM</i> | <i>EED</i> | <i>HS6ST1</i> | <i>NCOA1</i> | <i>SMARCA5</i> |
| <i>AKT1</i> | <i>EGFR</i> | <i>HSF1</i> | <i>NCOA3</i> | <i>SOC3</i> |
| <i>ALKBH1</i> | <i>ENG</i> | <i>HSP90AB1</i> | <i>NCOA6</i> | <i>SOD1</i> |
| <i>ARNT</i> | <i>EPAS1</i> | <i>IGF2</i> | <i>NDRG1</i> | <i>SP1</i> |
| <i>ARPC3</i> | <i>ERVWE1</i> | <i>IGFBP1</i> | <i>PBRM1</i> | <i>SP3</i> |
| <i>ATF2</i> | <i>ETS2</i> | <i>IL6</i> | <i>PEA15</i> | <i>SPINT1</i> |
| <i>BIRC2</i> | <i>F3</i> | <i>INHBA</i> | <i>PEG10</i> | <i>STK3</i> |
| <i>BMP4</i> | <i>FGFR2</i> | <i>ITGAV</i> | <i>PKD2</i> | <i>STK4</i> |
| <i>C1QBP</i> | <i>FLT1</i> | <i>ITGB1</i> | (includes <i>EG:18764</i>) | <i>STK11</i> |
| <i>CCNE1</i> | <i>FN1</i> | <i>ITGB8</i> | <i>PNPLA6</i> | <i>TFAP2C</i> |
| <i>CDC42</i> | <i>FST</i> | <i>JUNB</i> | <i>PPARD</i> | <i>TFDP1</i> |
| <i>CDH1</i> | <i>FZD5</i> | <i>KRT8</i> | <i>PPARG</i> | <i>TFEB</i> |
| <i>CDKN1B</i> | <i>GAB1</i> | <i>KRT18</i> | <i>PTEN</i> | <i>TGFB3</i> |
| <i>CDKN1C</i> | <i>GATA2</i> | <i>LIFR</i> | <i>RAFI</i> | <i>UBA3</i> |
| <i>CEBPA</i> | <i>GCM1</i> | <i>MAP2K1</i> | <i>RB1</i> | <i>VCAM1</i> |
| <i>CEBPB</i> | <i>H19</i> | <i>MAPK1</i> | <i>RBPJ</i> | <i>VTN</i> |
| <i>CITED2</i> | <i>HBEGF</i> | <i>MAPK14</i> | <i>ROCK2</i> | <i>VWF</i> |
| <i>COMMD1</i> | <i>HIF1A</i> | <i>MED1</i> | <i>RPS6</i> | |
| <i>COMT</i> | <i>HIRA</i> | <i>MET</i> | | |

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Appendix 11. Category 2 (MEDLINE-Derived) Gene List for Fetal Organs Not Contained in GNF Atlas

| Organ | Reference |
|----------------------------|--------------------------|
| Skin gene list (n= 13) | |
| <i>KRT10</i> | Coolen 2010 |
| <i>IVL</i> | Coolen 2010, Lee 1999 |
| <i>KRT17</i> | Coolen 2010 |
| <i>FNI</i> | Coolen 2010 |
| <i>CSPG4</i> | Coolen 2010 |
| <i>SPRR1B</i> | Lee 1999 |
| <i>LOR</i> | Lee 1999 |
| <i>ITGB1</i> | Hertle 1991 |
| <i>ITGA2</i> | Hertle 1991 |
| <i>ITGA3</i> | Hertle 1991 |
| <i>ITGB1</i> | Hertle 1991 |
| <i>HOXA4</i> | Stelnicki 1998 |
| <i>HOXC4</i> | Stelnicki 1998 |
| Intestine gene list (n= 6) | |
| <i>MUC2</i> | Busine 1998, Busine 2000 |
| <i>MUC4</i> | Busine 1998 |
| <i>MUC5AC</i> | Buisine 2000 |
| <i>MUC6</i> | Buisine 2000 |
| <i>RET</i> | Tam 1996 |
| <i>XDH</i> | Saksela 1998 |
| Bladder gene list (n=4) | |
| <i>KRT18</i> | de la Rosette 2002 |
| <i>KRT8</i> | de la Rosette 2002 |
| <i>KRT13</i> | de la Rosette 2002 |
| <i>KRT19</i> | de la Rosette 2002 |
| Amnion gene list (n=45) | |
| <i>ALOX5</i> | Brown 1999 |
| <i>ALOX5AP</i> | Brown 1999 |
| <i>IL8</i> | Elliot 2001 |
| <i>MUC1</i> | Sood 2006 |
| <i>CD55</i> | Sood 2006 |
| <i>CD59</i> | Sood 2006 |
| <i>ID2</i> | Sood 2006 |
| <i>TGFB</i> | Han 2008 |

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| | |
|-------------------------|--------------------|
| <i>TGFBR1</i> | Han 2008 |
| <i>SMAD1</i> | Han 2008 |
| <i>SMAD5</i> | Han 2008 |
| <i>SMAD9</i> | Han 2008 |
| <i>BNC2</i> | Han 2008 |
| <i>PTHLH</i> | Han 2008 |
| <i>BMP2</i> | Han 2008 |
| <i>PTGS2</i> | Han 2008 |
| <i>LIMCH1</i> | Han 2008 |
| <i>RRAGD</i> | Han 2008 |
| <i>SLC38A5</i> | Han 2008 |
| <i>HK2</i> | Han 2008 |
| <i>CYP2J2</i> | Han 2008 |
| <i>ROR1</i> | Han 2008 |
| <i>COBLL1</i> | Han 2008 |
| <i>PKD1L2</i> | Han 2008 |
| <i>PHF17</i> | Han 2008 |
| <i>CCL5</i> | Han 2008 |
| <i>IRS2</i> | Han 2008 |
| <i>GNLY</i> | Han 2008 |
| <i>ADM</i> | Han 2008 |
| <i>HLA-G</i> | Han 2008 |
| <i>PRELID2</i> | Han 2008 |
| <i>TMPO</i> | Han 2008 |
| <i>FBLN1</i> | Moore 2009 |
| <i>EFEMP1</i> | Moore 2009 |
| <i>FBLN5</i> | Moore 2009 |
| <i>KIAA0826</i> | Moore 2009 |
| <i>NFIB</i> | Haddad 2006 |
| <i>N4BP2L2</i> | Haddad 2006 |
| <i>MT2A</i> | Haddad 2006 |
| <i>LIMCH1</i> | Haddad 2006 |
| <i>COL1A2</i> | Haddad 2006 |
| <i>MTAP</i> | Haddad 2006 |
| <i>DIO2</i> | Haddad 2006 |
| <i>LAMA2</i> | Haddad 2006 |
| <i>RWDD3</i> | Haddad 2006 |
| Kidney gene list (n=75) | |
| <i>AGT</i> | Li 2005 |
| <i>ApoM</i> | Zhang 2004 |
| <i>BMP7</i> | Jain 2007, Li 2005 |
| <i>PGM</i> | Jain 2007 |

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| | |
|-------------------|-----------------|
| <i>CA2</i> | Jain 2007 |
| <i>CADM1</i> | Jain 2007 |
| <i>CD24</i> | Ivanova 2010 |
| <i>CDCA7</i> | Li 2005 |
| <i>CDH1</i> | Li 2005 |
| <i>CDH6</i> | Li 2005 |
| <i>CKD1</i> | Jain 2007 |
| <i>COL13A1</i> | Jain 2007 |
| <i>COL4A1</i> | Li 2005 |
| <i>COL4A2</i> | Li 2005 |
| <i>COL4A3</i> | Feng 1994 |
| <i>COL5A1</i> | Li 2005 |
| <i>COL5A2</i> | Li 2005 |
| <i>CR1 (CD35)</i> | Appay 1990 |
| <i>CRABP2</i> | Li 2005 |
| <i>DDR2</i> | Li 2005 |
| <i>EEG1</i> | Li 2005 |
| <i>FBN2</i> | Jain 2007 |
| <i>FGFR3</i> | Li 2005 |
| <i>FLT-1</i> | Simon 1995 |
| <i>FRD1</i> | Li 2005 |
| <i>FRZB</i> | Li 2005 |
| <i>GATA3</i> | Jain 2007 |
| <i>GPC3</i> | Jain 2007 |
| <i>HDGF</i> | Li 2005 |
| <i>HOXA9</i> | Deszo 2008 |
| <i>HOXB9</i> | Deszo 2008 |
| <i>HSD11K</i> | Agarwal 1995 |
| <i>IGF BP1</i> | Suikarri 1992 |
| <i>IGF1R</i> | Li 2005 |
| <i>IGF2</i> | Li 2005 |
| <i>ITGA1</i> | Korhonen 1990 |
| <i>ITGA2</i> | Li 2005 |
| <i>ITGA2</i> | Li 2005 |
| <i>ITGA2B1</i> | Korhonen 1990 |
| <i>ITGA3B1</i> | Korhonen 1990 |
| <i>ITGA6B1</i> | Korhonen 1990 |
| <i>KCNMB2</i> | Deszo 2008 |
| <i>KDR</i> | Simon 1995 |
| <i>LHX1</i> | Li 2005 |
| <i>MDR1</i> | van Kalken 1992 |
| <i>MEOX1</i> | Li 2005 |

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| | |
|------------------------|---------------------------|
| <i>MT-1E</i> | Mididoddi 1996 |
| <i>MT-1F</i> | Mididoddi 1996 |
| <i>MT-1X</i> | Mididoddi 1996 |
| <i>MT-2A</i> | Mididoddi 1996 |
| <i>MUC1</i> | Leroy 2003 |
| <i>MUC3</i> | Leroy 2003 |
| <i>MUC6</i> | Leroy 2003 |
| <i>MYCN</i> | Li 2005 |
| <i>MYH9</i> | Arrondel 2002 |
| <i>NCAM1</i> | Li 2005 |
| <i>NCAM2</i> | Li 2005 |
| <i>NGFR</i> | Li 2005 |
| <i>NID1</i> | Deszo 2008 |
| <i>PDGFA</i> | Li 2005 |
| <i>PKD1</i> | Ibraghimov 1997, Ong 1999 |
| <i>PKD2</i> | Ong 1999 |
| <i>PODXL</i> | Jain 2007 |
| <i>RARG</i> | Li 2005 |
| <i>SDC1</i> | Li 2005 |
| <i>SET</i> | Li 2005 |
| <i>SLC37A4</i> | Ihara 2000 |
| <i>SLC47A2</i> | Deszo 2008 |
| <i>TGFA</i> | Li 2005 |
| <i>TGFBR2</i> | Li 2005 |
| <i>THBS1</i> | Li 2005 |
| <i>TIMP3</i> | Li 2005 |
| <i>VEGF</i> | Li 2005, Simon 1995 |
| <i>WNT5A</i> | Jain 2007 |
| <i>WT1</i> | Jain 2007 |
| Heart gene list (n=98) | |
| <i>ACTA1</i> | Mao 2005, Kong 2008 |
| <i>ANKRD2</i> | Kong 2008 |
| <i>ANLN</i> | Kong 2008 |
| <i>AURKB</i> | Kong 2008 |
| <i>BCAT1</i> | Kong 2008 |
| <i>BMP5</i> | Kong 2008 |
| <i>BMP7</i> | Kong 2008 |
| <i>BST2</i> | Kong 2008 |
| <i>BTG3</i> | Kong 2008 |
| <i>CASQ2</i> | Mao 2005 |
| <i>CCNA2</i> | Kong 2008 |
| <i>CCNB1</i> | Kong 2008 |

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| | |
|-----------------|---------------------|
| <i>CCNB2</i> | Kong 2008 |
| <i>CDC2</i> | Kong 2008 |
| <i>CDC20</i> | Kong 2008 |
| <i>CDC25B</i> | Kong 2008 |
| <i>CDC7</i> | Kong 2008 |
| <i>CDK6</i> | Kong 2008 |
| <i>CDKN1C</i> | Kong 2008 |
| <i>CDKN2D</i> | Kong 2008 |
| <i>CDKN3</i> | Kong 2008 |
| <i>CDT1</i> | Kong 2008 |
| <i>CENPF</i> | Kong 2008 |
| <i>CHRND</i> | Kong 2008 |
| <i>CKMT2</i> | Kong 2008 |
| <i>CKS2</i> | Kong 2008 |
| <i>CRIP1</i> | Kong 2008 |
| <i>CSPG2</i> | Kong 2008 |
| <i>CSRP2</i> | Kong 2008 |
| <i>CYR61</i> | Kong 2008 |
| <i>DACT1</i> | Kong 2008 |
| <i>DLK1</i> | Kong 2008 |
| <i>DUSP1</i> | Kong 2008 |
| <i>DUSP2</i> | Kong 2008 |
| <i>E2F2</i> | Kong 2008 |
| <i>EDN1</i> | Kong 2008 |
| <i>EFNB3</i> | Kong 2008 |
| <i>EPHA2</i> | Kong 2008 |
| <i>FBN2</i> | Kong 2008 |
| <i>FGF13</i> | Kong 2008 |
| <i>GAJ</i> | Kong 2008 |
| <i>GATA4</i> | von Kaisenberg 1998 |
| <i>GPC3</i> | Kong 2008 |
| <i>GSN</i> | Kong 2008 |
| <i>H1F0</i> | Kong 2008 |
| <i>H2AFX</i> | Kong 2008 |
| <i>HCAP-G</i> | Kong 2008 |
| <i>HDGF</i> | Kong 2008 |
| <i>HLF</i> | Kong 2008 |
| <i>HMG2</i> | Kong 2008 |
| <i>HOXB2</i> | Kong 2008 |
| <i>HYAL1</i> | Kong 2008 |
| <i>IER3</i> | Kong 2008 |
| <i>KIAA0074</i> | Kong 2008 |

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| | |
|-----------------|--------------------------|
| <i>KIF2</i> | Kong 2008 |
| <i>KNSL1</i> | Kong 2008 |
| <i>KNSL5</i> | Kong 2008 |
| <i>KNSL6</i> | Kong 2008 |
| <i>KPNA2</i> | Kong 2008 |
| <i>KRT18</i> | Kong 2008 |
| <i>MCM6</i> | Kong 2008 |
| <i>MDK</i> | Kong 2008 |
| <i>MYH6</i> | Razeghi 2001 |
| <i>MYH7</i> | Razeghi 2001 |
| <i>MYOM2</i> | Kong 2008 |
| <i>NCAM1</i> | Kong 2008 |
| <i>NPPA</i> | Razeghi 2001, Sasse 1993 |
| <i>NPPB</i> | Hyett 1996 |
| <i>NUF2R</i> | Kong 2008 |
| <i>NUSAP1</i> | Kong 2008 |
| <i>PIM1</i> | Kong 2008 |
| <i>PLU-1</i> | Kong 2008 |
| <i>PPBP</i> | Kong 2008 |
| <i>PRC1</i> | Kong 2008 |
| <i>RAB6KIFL</i> | Kong 2008 |
| <i>RAI2</i> | Kong 2008 |
| <i>ROR1</i> | Kong 2008 |
| <i>RRM2</i> | Kong 2008 |
| <i>SCGF</i> | Kong 2008 |
| <i>SMARCA1</i> | Kong 2008 |
| <i>SMC4L1</i> | Kong 2008 |
| <i>SNCA</i> | Kong 2008 |
| <i>SOX11</i> | Kong 2008 |
| <i>SPAG5</i> | Kong 2008 |
| <i>SPON1</i> | Kong 2008 |
| <i>STMN1</i> | Kong 2008 |
| <i>TCF8</i> | Kong 2008 |
| <i>TDGF1</i> | Mao 2005 |
| <i>TEAD4</i> | Kong 2008 |
| <i>TNMD</i> | Mao 2005 |
| <i>TNNI1</i> | Sasse 1993 |
| <i>TNNI3</i> | Sasse 1993 |
| <i>TNNT1</i> | Kong 2008 |
| <i>TNNT2</i> | Mao 2005 |
| <i>TOP2A</i> | Kong 2008 |
| <i>TOPK</i> | Kong 2008 |

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| <i>TTK</i> | Kong 2008 |
|------------------------------|-----------|
| <i>TYMS</i> | Kong 2008 |
| Placenta gene list (n=47)* | |
| <i>ADAM12</i> | |
| <i>ALPP/ALPPL2</i> | |
| <i>ANGPT2</i> | |
| <i>CAPN6</i> | |
| <i>CDH1</i> | |
| <i>CGA</i> | |
| <i>CGB</i> (includes others) | |
| <i>ALPP/ALPPL2</i> | |
| <i>ANGPT2</i> | |
| <i>CAPN6</i> | |
| <i>CDH1</i> | |
| <i>CGA</i> | |
| <i>CGB</i> (includes others) | |
| <i>COL1A2</i> | |
| <i>COL3A1</i> | |
| <i>CSH1/CSH2</i> | |
| <i>CSRP2</i> | |
| <i>CXCL14</i> | |
| <i>CYP19A1</i> | |
| <i>EBI3</i> | |
| <i>EFEMP1</i> | |
| <i>ENDOU</i> | |
| <i>ERVFRDE1</i> | |
| <i>ERVWE1</i> | |
| <i>ESRRG</i> | |
| <i>FBLN1</i> | |
| <i>FERMT2</i> | |
| <i>GH1</i> | |
| <i>GULP1</i> | |
| <i>HSD3B1</i> | |
| <i>INHBA</i> | |
| <i>INSL4</i> | |
| <i>KISS1</i> | |
| <i>LEP</i> | |
| <i>LIFR</i> | |
| <i>LUM</i> | |
| <i>PAGE4</i> | |
| <i>PAPPA</i> | |
| <i>PEG3</i> | |

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| |
|-----------------|
| <i>PKIB</i> |
| <i>PPAP2B</i> |
| <i>PRG2</i> |
| <i>PSG3</i> |
| <i>PSG5</i> |
| <i>PSG6</i> |
| <i>PSG9</i> |
| <i>RAI14</i> |
| <i>SERPINE1</i> |
| <i>SLC7A2</i> |
| <i>SMARCA1</i> |
| <i>TFPI</i> |
| <i>TFPI2</i> |
| <i>TIMP3</i> |

* Miura 2010 top 50 gene probes, corresponding to 47 genes.

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Appendix 12. Heart, Kidney, Bladder, Skin, Intestine, Placenta and Amnion Genes Present in the Amniotic Fluid Core Transcriptome

| Symbol | Entrez Gene Name | Category* |
|----------------|--|-----------|
| Heart | | |
| <i>ANXA2</i> | <i>Annexin A2</i> | 1 |
| <i>APP</i> | <i>Amyloid beta (A4) precursor protein</i> | 1 |
| <i>ARID4B</i> | <i>AT rich interactive domain 4B (RBP1-like)</i> | 1 |
| <i>ATP5A1</i> | <i>ATP synthase, H⁺ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle</i> | 1 |
| <i>CCND2</i> | <i>Cyclin D2</i> | 1 |
| <i>CDC42</i> | <i>Cell division cycle 42 (GTP binding protein, 25kDa)</i> | 1 |
| <i>COLIA1</i> | <i>Collagen, type I, alpha 1</i> | 1 |
| <i>CTBP2</i> | <i>C-terminal binding protein 2</i> | 1 |
| <i>CTSB</i> | <i>Cathepsin B</i> | 1 |
| <i>FGFR1</i> | <i>Fibroblast growth factor receptor 1</i> | 1 |
| <i>GJA1</i> | <i>Gap junction protein, alpha 1, 43kDa</i> | 1 |
| <i>GLRX3</i> | <i>Glutaredoxin 3</i> | 1 |
| <i>HAND1</i> | <i>Heart and neural crest derivatives expressed 1</i> | 1 |
| <i>HMGB1</i> | <i>High-mobility group box 1</i> | 1 |
| <i>HSPD1</i> | <i>Heat shock 60kDa protein 1 (chaperonin)</i> | 1 |
| <i>MORF4L1</i> | <i>Mortality factor 4 like 1</i> | 1 |
| <i>MYH10</i> | <i>Myosin, heavy chain 10, non-muscle</i> | 1 |
| <i>NACA</i> | <i>Nascent polypeptide-associated complex alpha subunit</i> | 1 |

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| | | |
|----------------|--|----------------|
| <i>NR2F2</i> | <i>Nuclear receptor subfamily 2, group F, member 2</i> | 1 |
| <i>PAK2</i> | <i>p21 protein (Cdc42/Rac)-activated kinase 2</i> | 1 |
| <i>PGF</i> | <i>Placental growth factor</i> | 1 |
| <i>PRKD2</i> | <i>Protein kinase D2</i> | 1 |
| <i>RAB1A</i> | <i>RAB1A, member RAS oncogene family</i> | 1 |
| <i>RAC1</i> | <i>Ras-related C3 botulinum toxin substrate 1</i> | 1 |
| <i>RAP1A</i> | <i>RAP1A, member of RAS oncogene family</i> | 1 |
| <i>SDC4</i> | <i>Syndecan 4</i> | 1 |
| <i>SLC2A1</i> | <i>Solute carrier family 2 (facilitated glucose transporter), member 1</i> | 1 |
| <i>TPM1</i> | <i>Tropomyosin 1 (alpha)</i> | 1 |
| <i>TPT1</i> | <i>Tumor protein, translationally-controlled 1</i> | 1 |
| <i>TXN</i> | <i>Thioredoxin</i> | 1 |
| <i>YY1</i> | <i>YY1 transcription factor</i> | 1 |
| <i>ZFP36L1</i> | <i>Zinc finger protein 36, C3H type-like 1</i> | 1 |
| <i>CDC25B</i> | <i>Cell division cycle 25 homolog B</i> | 2 |
| <i>CSRP2</i> | <i>Cystein and glycine-rich protein 2</i> | 2 |
| <i>F7</i> | <i>Coagulation factor VII (serum prothrombin conversion accelerator)</i> | 3 [†] |
| <i>PROX1</i> | <i>Prospero homeobox 1</i> | 3 |
| <i>RECK</i> | <i>Reversion-inducing-cysteine-rich protein with kazal motifs</i> | 3 |
| <i>STK4</i> | <i>Serine/threonine kinase 4</i> | 3 |
| <i>TBX3</i> | <i>T-box 3</i> | 3 |

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| | | |
|-------------------|--|----|
| <i>TEAD1</i> | <i>TEA domain family member 1 (SV40 transcriptional enhancer factor)</i> | 3 |
| Kidney or bladder | | |
| <i>ANXA2</i> | <i>annexin A2</i> | 1 |
| <i>APP</i> | <i>amyloid beta (A4) precursor protein</i> | 1 |
| <i>CDC42</i> | <i>cell division cycle 42 (GTP binding protein, 25kDa)</i> | 1 |
| <i>CDC25B</i> | <i>cell division cycle 25 homolog B (S. pombe)</i> | 1 |
| <i>DAB2</i> | <i>disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)</i> | 1 |
| <i>FGFR1</i> | <i>fibroblast growth factor receptor 1</i> | 1 |
| <i>GJA1</i> | <i>gap junction protein, alpha 1, 43kDa</i> | 1 |
| <i>HSPD1</i> | <i>heat shock 60kDa protein 1 (chaperonin)</i> | 1 |
| <i>MAN2A1</i> | <i>mannosidase, alpha, class 2A, member 1</i> | 1 |
| <i>PGF</i> | <i>placental growth factor</i> | 1 |
| <i>PPIA</i> | <i>peptidylprolyl isomerase A (cyclophilin A)</i> | 1 |
| <i>RND3</i> | <i>Rho family GTPase 3</i> | 1 |
| <i>RPSA</i> | <i>ribosomal protein SA</i> | 1 |
| <i>SDC4</i> | <i>syndecan 4</i> | 1 |
| <i>SLC2A1</i> | <i>solute carrier family 2 (facilitated glucose transporter), member 1</i> | 1 |
| <i>TJP1</i> | <i>tight junction protein 1 (zona occludens 1)</i> | 1 |
| <i>SET</i> | <i>SET nuclear oncogene</i> | 2 |
| <i>KRT8</i> | <i>keratin 8</i> | 2 |
| <i>DDX58</i> | <i>DEAD (Asp-Glu-Ala-Asp) box polypeptide 58</i> | 3* |

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| | | |
|---------------------------------|---|-----|
| <i>F7</i> | <i>coagulation factor VII (serum prothrombin conversion accelerator)</i> | 3 |
| <i>MLL5</i> | <i>myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)</i> | 3 |
| <i>TMEFF2</i> | <i>transmembrane protein with EGF-like and two follistatin-like domains 2</i> | 3 |
| Intestinal and digestive system | | |
| <i>MUC5AC/MUC5B</i> | <i>mucin 5AC/ mucin 5B</i> | 2 |
| <i>MUC 4</i> | <i>mucin 4</i> | 2 |
| <i>ACVR2A</i> | <i>activin A receptor, type IIA</i> | 3 |
| <i>APP</i> | <i>amyloid beta (A4) precursor protein</i> | 3 |
| <i>ARF6</i> | <i>ADP-ribosylation factor 6</i> | 3 |
| <i>COL1A1</i> | <i>collagen, type I, alpha 1</i> | 3 |
| <i>CYP1A2</i> | <i>cytochrome P450, family 1, subfamily A, polypeptide 2</i> | 3 |
| <i>EFS</i> | <i>embryonal Fyn-associated substrate</i> | 3 |
| <i>FGFR1</i> | <i>fibroblast growth factor receptor 1</i> | 3 |
| <i>FOLR1</i> | <i>folate receptor 1 (adult)</i> | 3 |
| <i>HMGB1</i> | <i>high-mobility group box 1</i> | 3 |
| <i>MAN2A1</i> | <i>mannosidase, alpha, class 2A, member 1</i> | 3 |
| <i>SP3</i> | <i>Sp3 transcription factor</i> | 3 |
| Skin and hair | | |
| <i>SPRR1B</i> | <i>small proline-rich protein 1B</i> | 2,3 |
| <i>ANXA2</i> | <i>annexin A2</i> | 3 |
| <i>APP</i> | <i>amyloid beta (A4) precursor protein</i> | 3 |

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| | | |
|---------------|--|---|
| <i>CCND2</i> | <i>cyclin D2</i> | 3 |
| <i>CCNG2</i> | <i>cyclin G2</i> | 3 |
| <i>CDC42</i> | <i>cell division cycle 42 (GTP binding protein, 25kDa)</i> | 3 |
| <i>CDC25B</i> | <i>cell division cycle 25 homolog B (S. pombe)</i> | 3 |
| <i>COL1A1</i> | <i>collagen, type I, alpha 1</i> | 3 |
| <i>COL7A1</i> | <i>collagen, type VII, alpha 1</i> | 3 |
| <i>CSTA</i> | <i>cystatin A (stefin A)</i> | 3 |
| <i>CYP1A2</i> | <i>cytochrome P450, family 1, subfamily A, polypeptide 2</i> | 3 |
| <i>DAB2</i> | <i>disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)</i> | 3 |
| <i>DDX58</i> | <i>DEAD (Asp-Glu-Ala-Asp) box polypeptide 58</i> | 3 |
| <i>FGFR1</i> | <i>fibroblast growth factor receptor 1</i> | 3 |
| <i>GJA1</i> | <i>gap junction protein, alpha 1, 43kDa</i> | 3 |
| <i>HMGB1</i> | <i>high-mobility group box 1</i> | 3 |
| <i>KRT8</i> | <i>keratin 8</i> | 3 |
| <i>MLL5</i> | <i>myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)</i> | 3 |
| <i>MUTED</i> | <i>muted homolog (mouse)</i> | 3 |
| <i>PPIA</i> | <i>peptidylprolyl isomerase A (cyclophilin A)</i> | 3 |
| <i>PTMA</i> | <i>prothymosin, alpha</i> | 3 |
| <i>RAC1</i> | <i>ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)</i> | 3 |
| <i>RAP1A</i> | <i>RAP1A, member of RAS oncogene family</i> | 3 |
| <i>SDC4</i> | <i>syndecan 4</i> | 3 |

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| | | |
|---------------|--|----------------|
| <i>SFN</i> | <i>stratifin</i> | 3 |
| <i>TFAP2C</i> | <i>Transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)</i> | 3 |
| <i>TMEFF2</i> | <i>transmembrane protein with EGF-like and two follistatin-like domains 2</i> | 3 |
| <i>TRIM16</i> | <i>tripartite motif-containing 16</i> | 3 |
| Placenta | | |
| <i>CDC42</i> | <i>cell division cycle 42 (GTP binding protein, 25kDa)</i> | 1 |
| <i>KRT8</i> | <i>keratin 8</i> | 1 |
| <i>MYH10</i> | <i>myosin, heavy chain 10, non-muscle</i> | 1 |
| <i>RPS6</i> | <i>ribosomal protein S6</i> | 1 |
| <i>SP3</i> | <i>Sp3 transcription factor</i> | 1 |
| <i>STK4</i> | <i>serine/threonine kinase 4</i> | 1 |
| <i>TFAP2C</i> | <i>transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)</i> | 1 |
| <i>CSRP2</i> | <i>cystein and glycine rich protein 2</i> | 2 |
| <i>HAND1</i> | <i>heart and neural crest derivatives expressed 1</i> | 3 [†] |
| Amnion | | |
| <i>NFIB</i> | <i>nuclear factor I/B</i> | 2 |

*See Appendix 1 for description of categorization of genes from MEDLINE and pathways analysis software searches.

[†] Category 3 genes for heart, kidney, and placenta are pathways analysis software-identified genes that were absent from the respective human Gene Expression Omnibus microarray datasets.

Hui L, Slonim DK, Wick HC, Johnson KL, Bianchi DW. Amniotic fluid transcriptome: a source of novel information about human fetal development. Obstet Gynecol 2011;119.

The authors provided this information as a supplement to their article.