

SUPPLEMENT FIGURES AND LEGENDS

Supplemental Figure 1- Gross morphology of HSRA Model. (A) Image of abdominal region from two-kidney rat HSRA-C (two-kidney) rats that demonstrate no urogenital abnormalities. (B) Image of abdominal region in one-kidney rat HSRA-S (one-kidney) with failure of the right kidney and right ureter to develop. In this case, no other urogenital abnormalities were observed [e.g., presence of testis (thick arrow), epididymis, and seminal vesicles). (C) Image of abdominal region in one-kidney rat HSRA-S with no development of the left kidney, ipsilateral ureter, testis, epididymis, and seminal vesicles (not shown). (D) Frequency of left/right unilateral renal agenesis in male and female animals (n=487). (E) Frequency of bilateral and unilateral agenesis determined by time-breeding and embryos dissection (n=29 pregnant female; n= 130 embryos). *, $p < 0.05$ right side agenesis vs left agenesis using chi-squared test.

Supplemental Figure 2 – Pregnancy efficiency and litter size among all mating comparisons. Kidney status (i.e. single kidney versus two-kidney) correlates with other urogenital abnormalities including the failure of the ipsilateral ureter, testis, epididymis, and seminal vesicles or uterine horn and ovaries. (A) Pregnancy rate depends on kidney status of female and male. A failed pregnancy would be defined as a female housed with a male for more than 2 months without birth of any pups. (B) Number of offspring depends on kidney status of female and male. The median litter size is denoted by line in box. The whiskers denote range. -S denotes one kidney and -C denotes two-kidney. *, $p < 0.05$ compared to other groups using chi-squared test (panel A) or one-way ANOVA (panel B).

Supplemental Figure 3– Protein composition by SDS-PAGE and measurement of conscious blood pressure. (A) Composition of proteinuria in HSRA-S at month 5, 15, and 20 by SDS-PAGE. A fixed percentage of total urine volume (0.015%) was loaded for each sample to directly compare across time. (B) Composition of proteinuria in all groups at month 20 by SDS-PAGE. The same amount of protein (5ug) was loaded for each sample (3 random samples from each group). (C) Conscious blood pressure measured by indwelling catheter at month 20. The specific numbers of animals used for each experiment are shown below the x-axis. *, $p < 0.05$ compared to –C using ANOVA and Dunnett’s.

Supplemental Figure 4– Measurement of renal blood flow autoregulation and renal vascular resistance. (A) Autoregulation of renal blood flow (RBF) measured at month 5. Both the HSRA-S and –C animals properly autoregulate RBF as perfusion pressure is increased from 50 to 150 mm Hg. RBF autoregulatory index for HSRA-S was 0.3 ± 0.07 and –C was 0.27 ± 0.07 . An AI of 0 indicates perfect autoregulation of RBF; an AI of 1 is characteristic of a circulation with a fixed vascular resistance. (B) Calculation of renal vascular resistance (RVR) at month 5, 15, and 20. The specific numbers of animals used for each experiment are shown below the x-axis. *, $p < 0.05$ compared to –C using ANOVA and Dunnett’s.

Supplemental Figure 5– Time course estimation of single nephron glomerular filtration rate (GFR) from month 5- 20. (A) GFR normalized to nephron number. (B) GFR normalized to nephron number and kidney weight. The calculation of nephron number from week 4 was used to calculate snGFR (Fig. 2) $n=6-13$; *, $p < 0.05$ compared to –C.

Supplemental Figure 6– Tubular Injury and infiltration of immune cells (macrophages, T-cells, and B-cells) and representative immunohistochemistry (IHC) kidney images at month 20 in HSRA-S, -C, -UNX3, and –UNX8. (A) Semi-quantitative measurement of tubular injury and protein markers. Tubular injury was analyzed for degree of tubular atrophy, vacuolization, dilation, and protein casts on a scale from 0 (normal) to 4 (severe with > 75% tubules demonstrating injury). Neutrophil gelatinase-associated lipocalin (NGAL), a marker of tubular injury, confirmed that HSRA-S demonstrated significant more tubular injury compared to –C, -UNX3, and –UNX8. (B) Quantification of macrophages (CD-68) and IHC images. (C) Quantification of T-cells (CD-43) and IHC images. (D) Quantification of B-cells (CD-22) and IHC images. (E) Western blot analysis of key pro-inflammatory markers. In particular, TGF- β 1 and TNF- α demonstrated significant up-regulation in the –S compared –C, -UNX3, and –UNX8. The –UNX3 group also demonstrated increased levels of TGF- β 1 and NF κ B (p65) compared to –C, but not the –UNX8 group. **The arrows denote the location of punctate staining of immune cells.** *, p<0.05 compared to –C using one-way ANOVA using Dunnett's, †, p<0.05 compared to other groups (one-way ANOVA using Bonferroni).

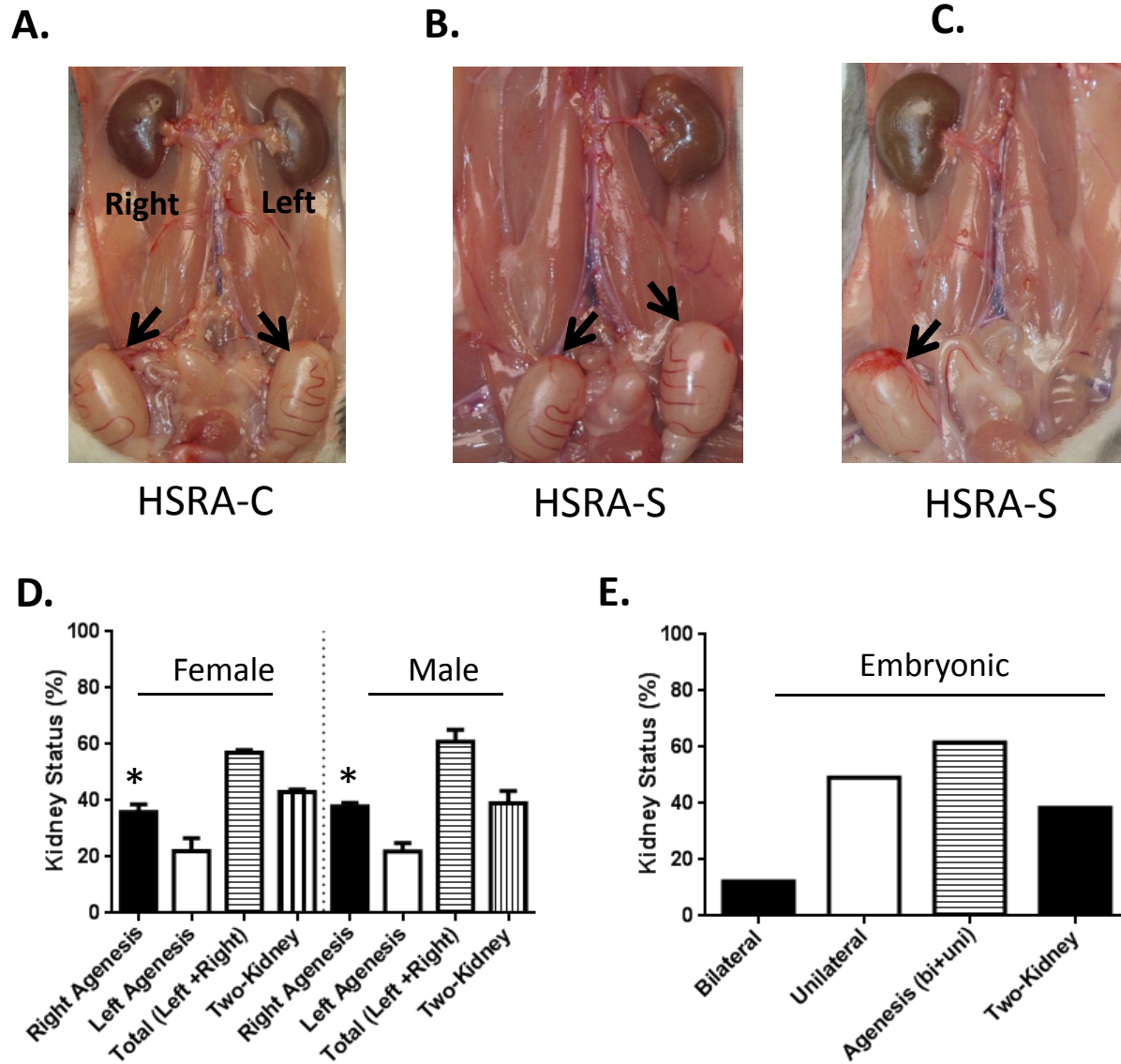
Supplemental Figure 7– Top two gene networks associated with gene expression differences between HSRA-S and HSRA-C kidney at month 1 using Ingenuity Pathway Analysis. (A) Network 1 associated organ injury and reproductive system disease. (B) Network 2 associated cardiovascular system and tissue development. Top diseases and biofunctions of associated genes networks were linked with connective tissue/reproductive development and function (7.29×10^{-4} - 2.57×10^{-2} , n=18 genes) and cardiovascular/organ system development (1.51×10^{-2} - 2.57×10^{-2} , n=38 genes). Genes shown in red denote up-regulation in the HSRA-S kidney and

those shown in green denote down-regulation. Boxes denoted with Fx are annotated functions associated with genes connected by solid lines.

Supplemental Figure 8 – Overview of mechanism of renal injury exhibited by HSRA model.

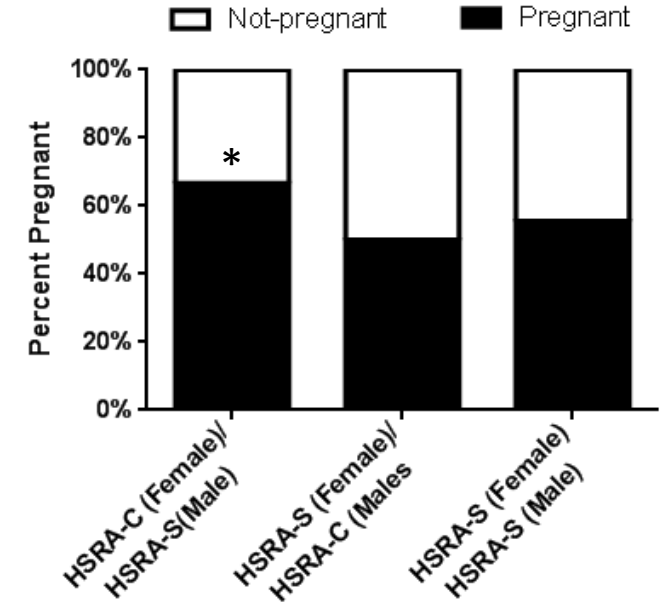
Genetic factors (yet to be determined) predispose HSRA animals to exhibit a high incidence of unilateral renal agenesis. Animals that develop with a single kidney (HSRA-S) exhibit reduced nephrons compared to littermates that are born with both kidneys (HSRA-C). The –C animals appear normal and exhibit no propensity to develop renal injury or hypertension. HSRA-S animals develop progressive injury via hyperfiltration and glomerular hypertrophy that leads to glomerular injury and increased proteinuria. Increased proteinuria, combined with tubular injury, results in reduced blood flow, promotes tubular injury (e.g. epithelial mesenchymal transition), inflammation, tubulointerstitial fibrosis, and culminates in reduced renal function and increased blood pressure. This mechanism of injury between the HSRA-S model and uninephrectomy appears similar with respect to glomerular injury (hyperfiltration); however, the reduced nephrons composition and vascular changes seen in the HSRA-S model exacerbate kidney injury and decline in renal function over and above that seen in UNX models.

Supplemental Figure 1- Gross View of One Kidney Model

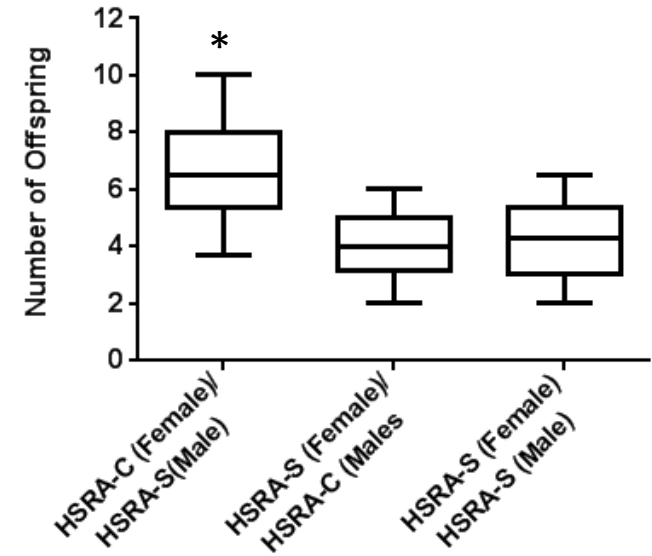


Supplemental Figure 2- Pregnancy Efficiency and Litter Size

A.

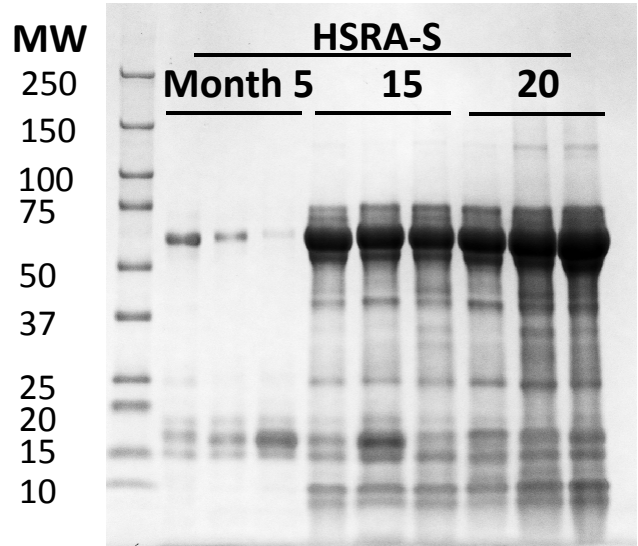


B.

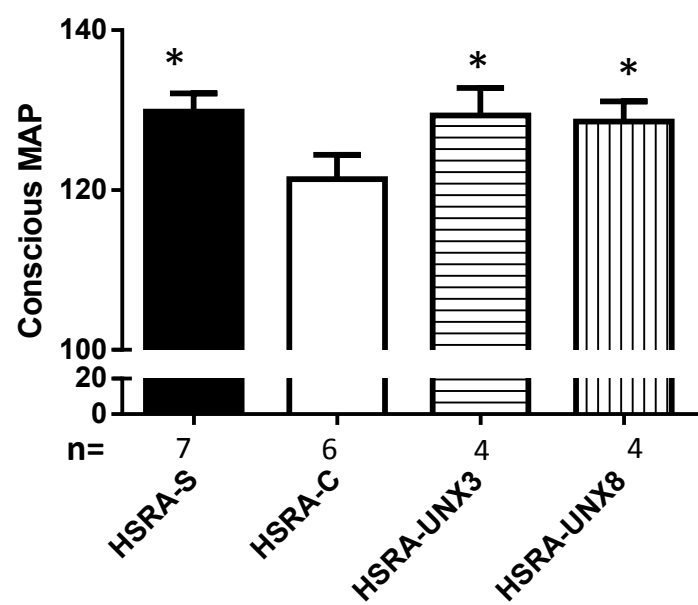


Supplemental Figure 3- Protein composition via SDS-PAGE and Conscious BP at Month 20

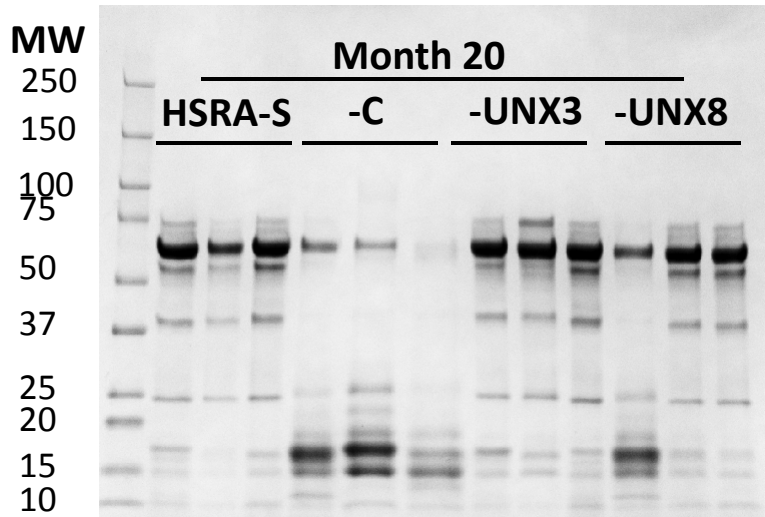
A.



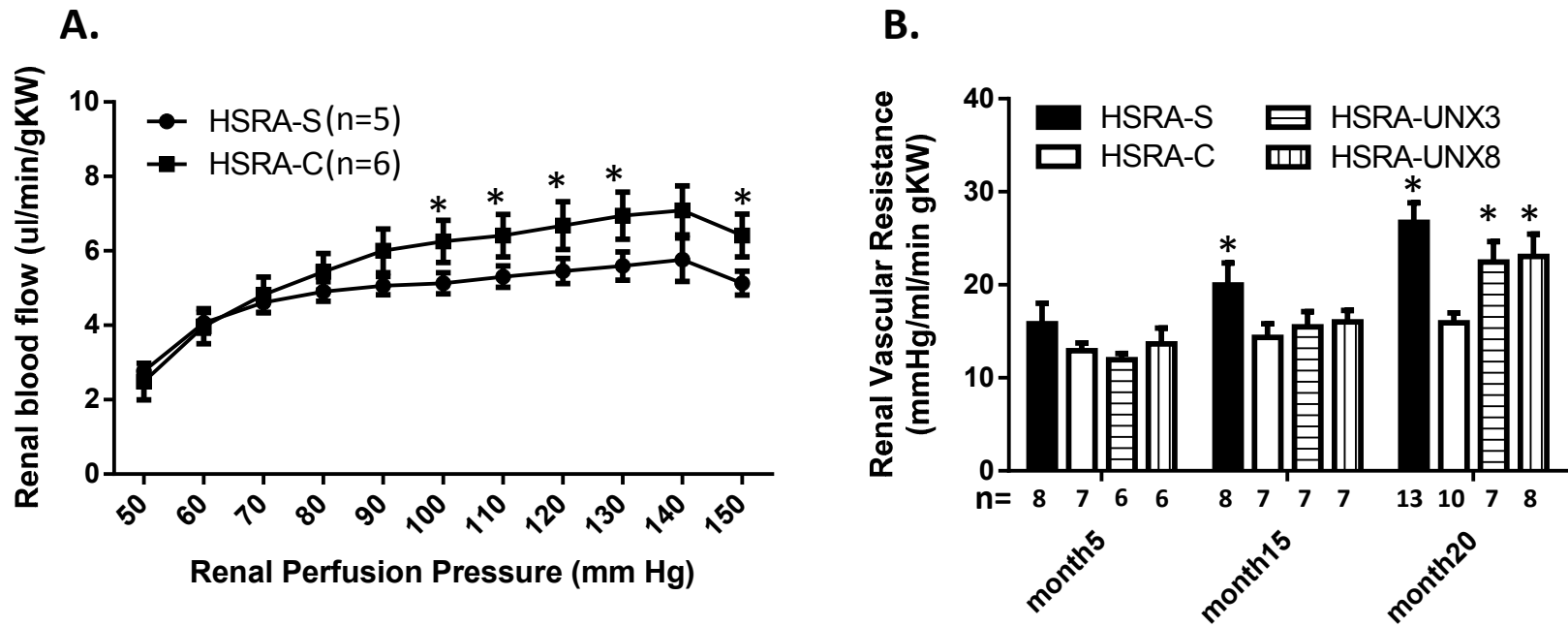
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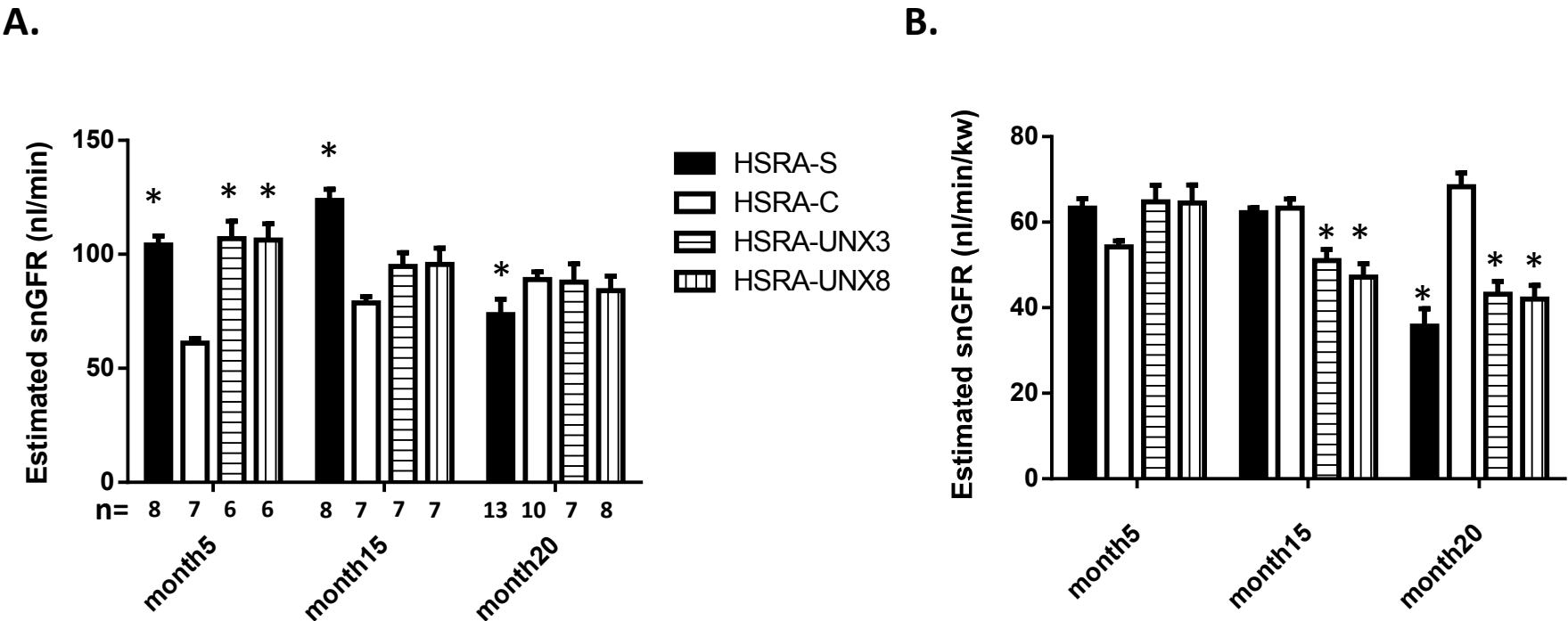
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Supplemental Figure 4- RBF Autoregulation and RVR

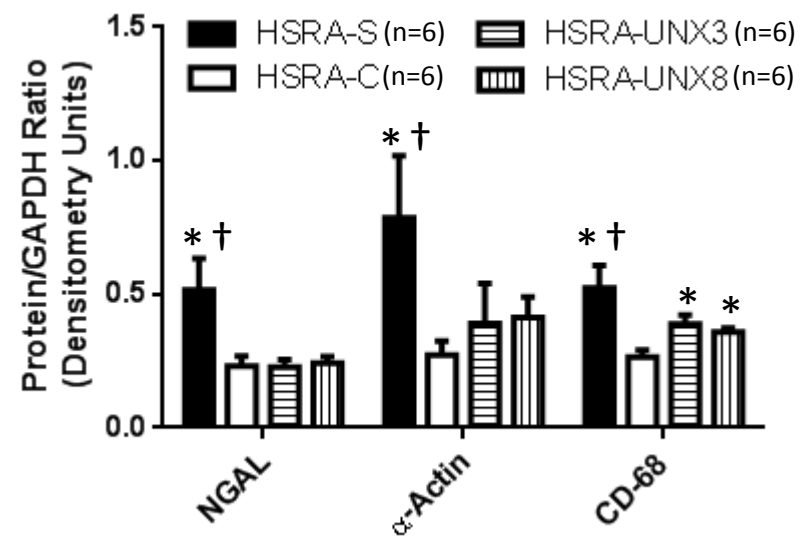
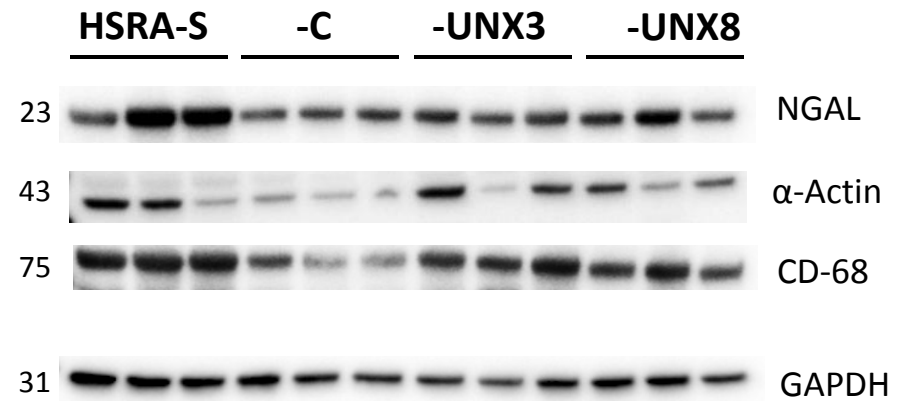
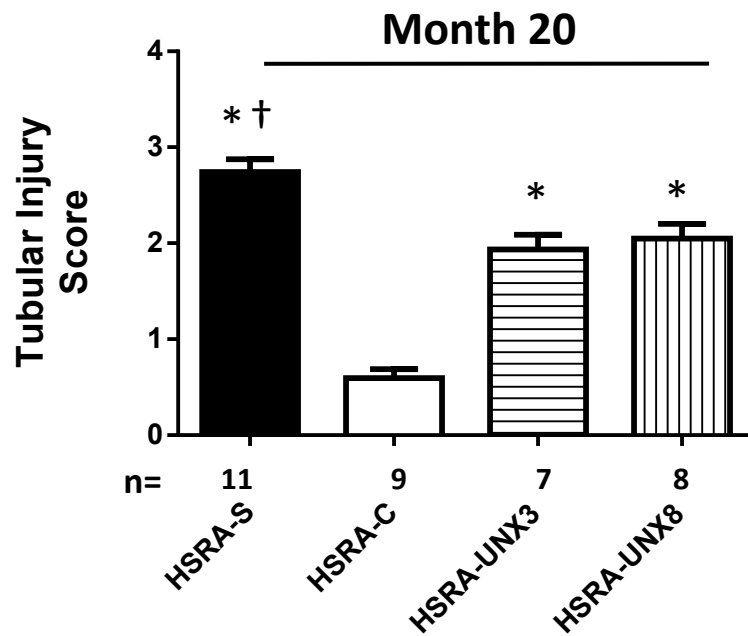


Supplemental Figure 5- Time Course Estimation of Single Nephron GFR



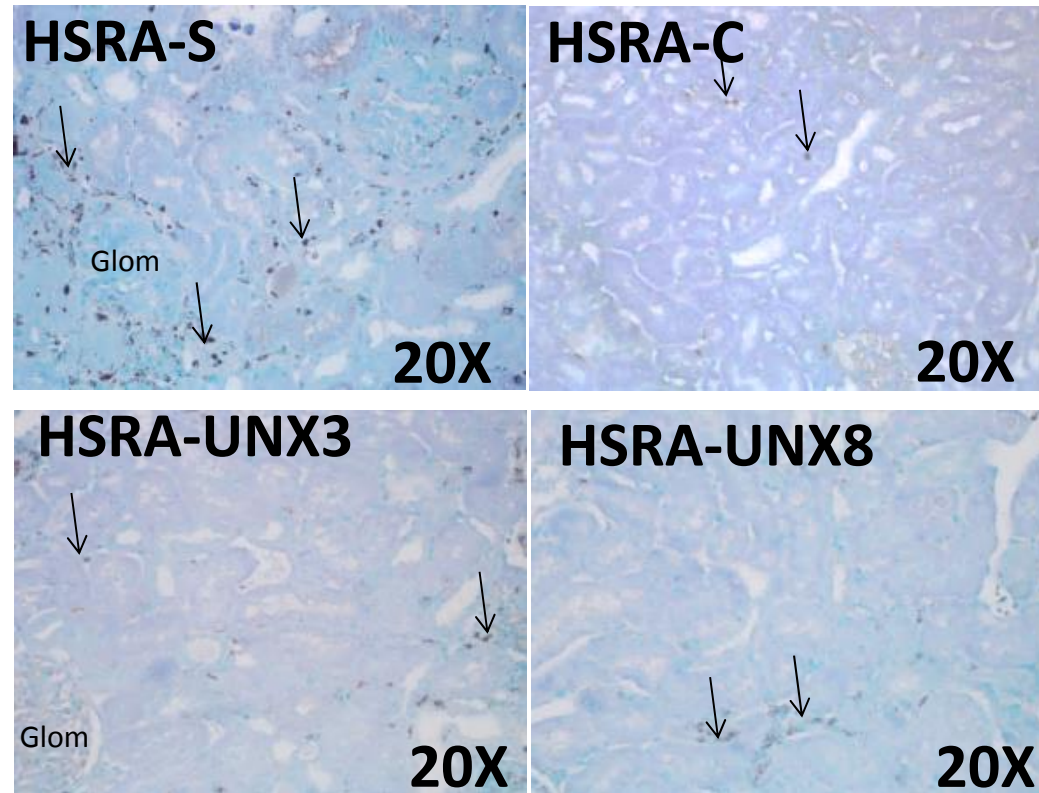
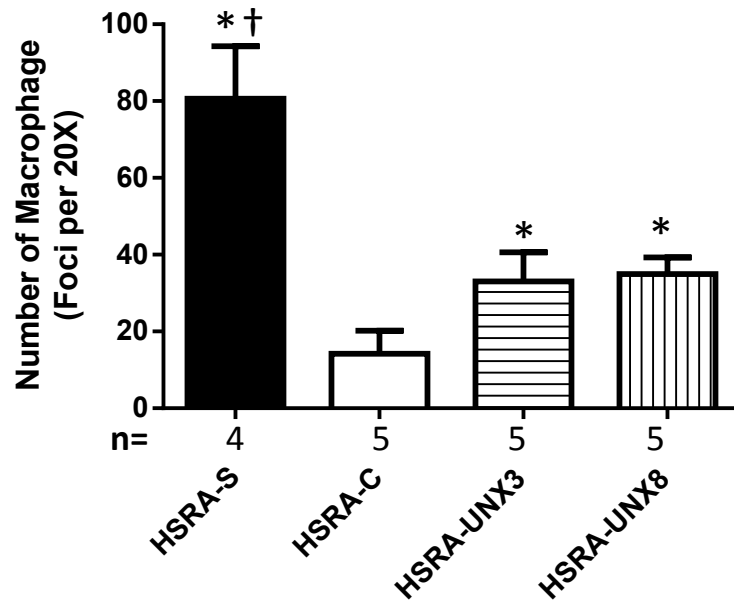
Supplemental Figure 6- Tubular Injury and Immune Cell Infiltration

A.



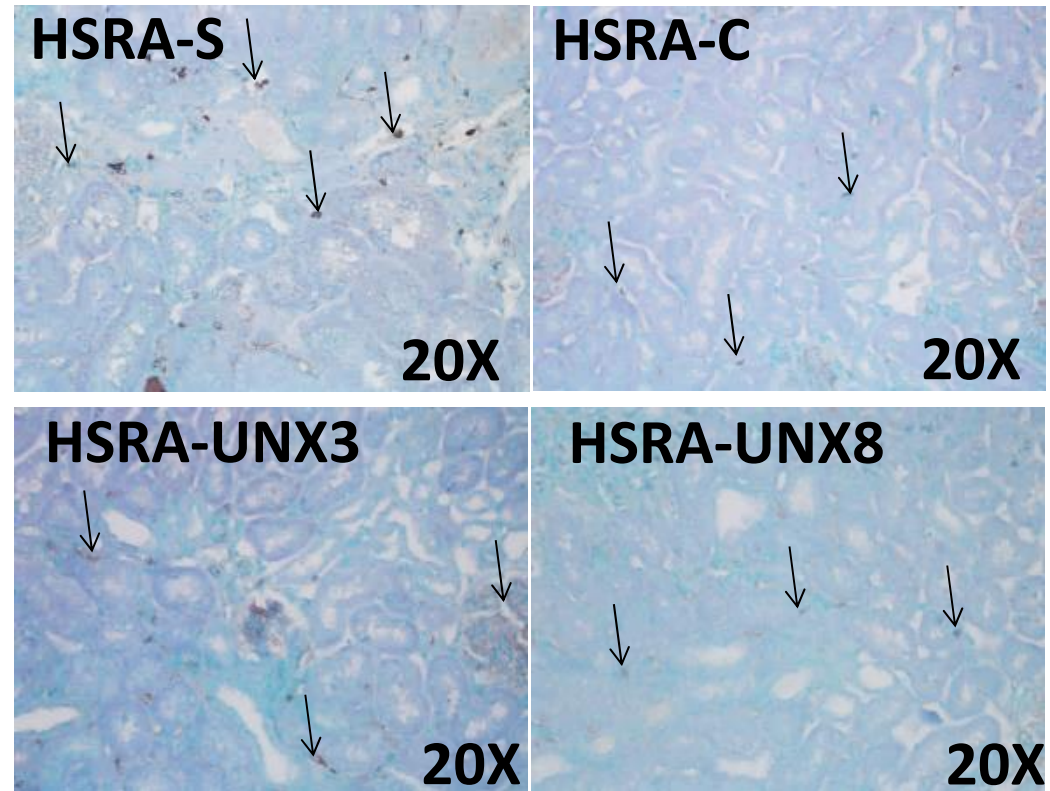
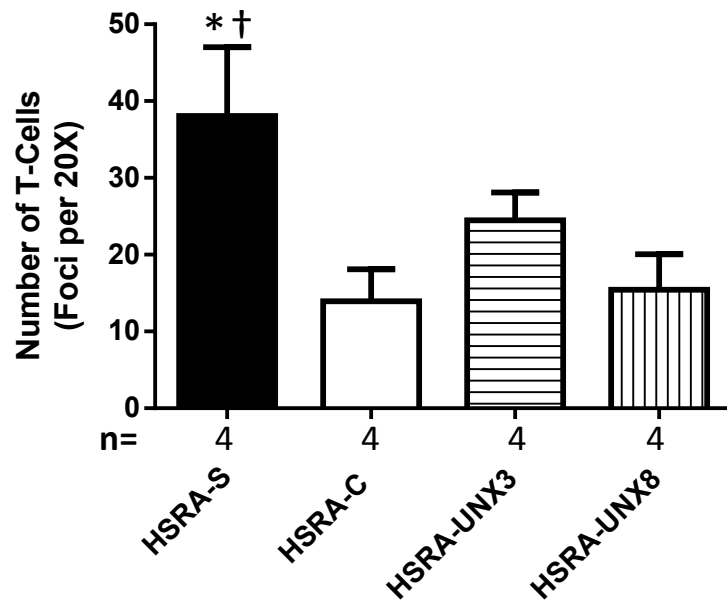
Supplemental Figure 6- Tubular Injury and Immune Cell Infiltration

B.



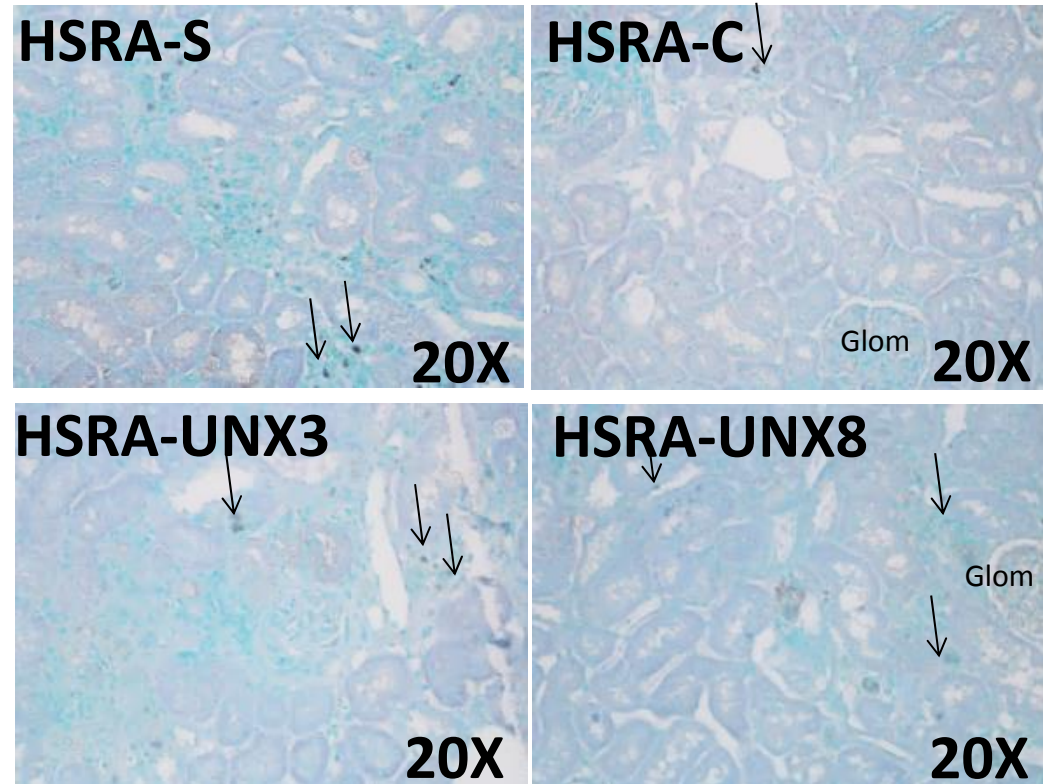
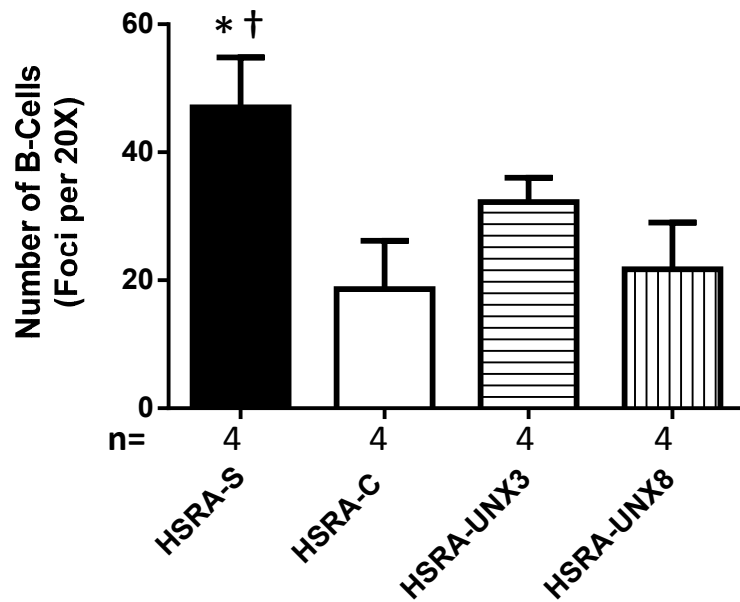
Supplemental Figure 6- Tubular Injury and Immune Cell Infiltration

C.



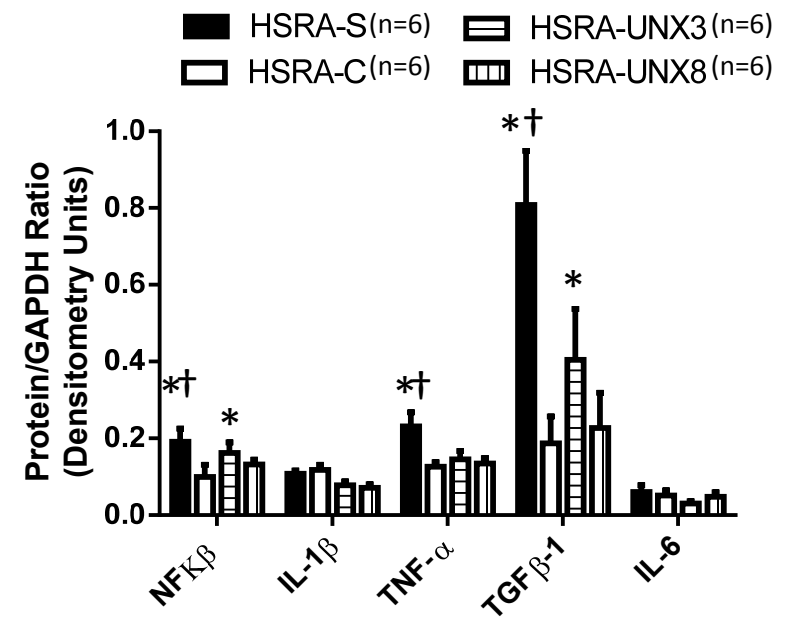
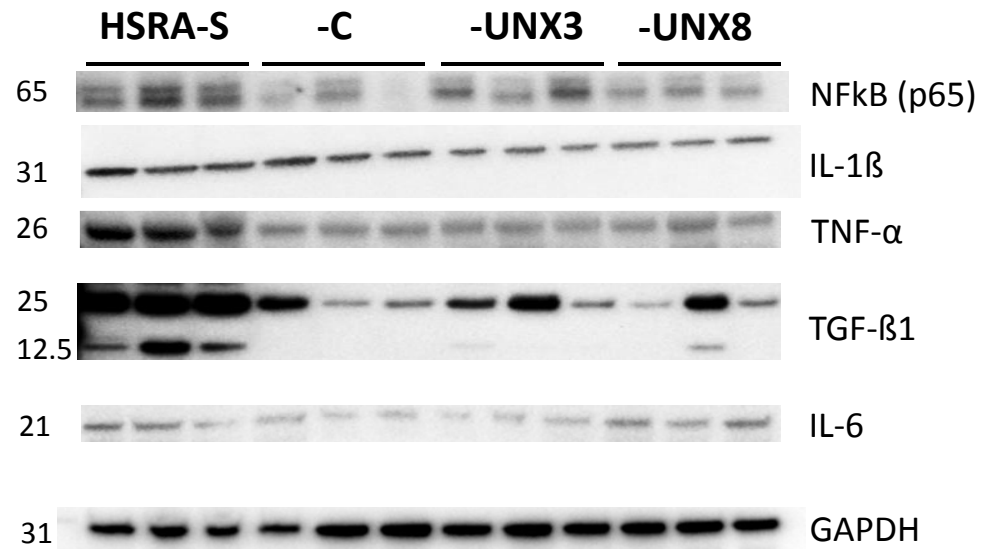
Supplemental Figure 6-Tubular Injury and Immune Cell Infiltration

D.



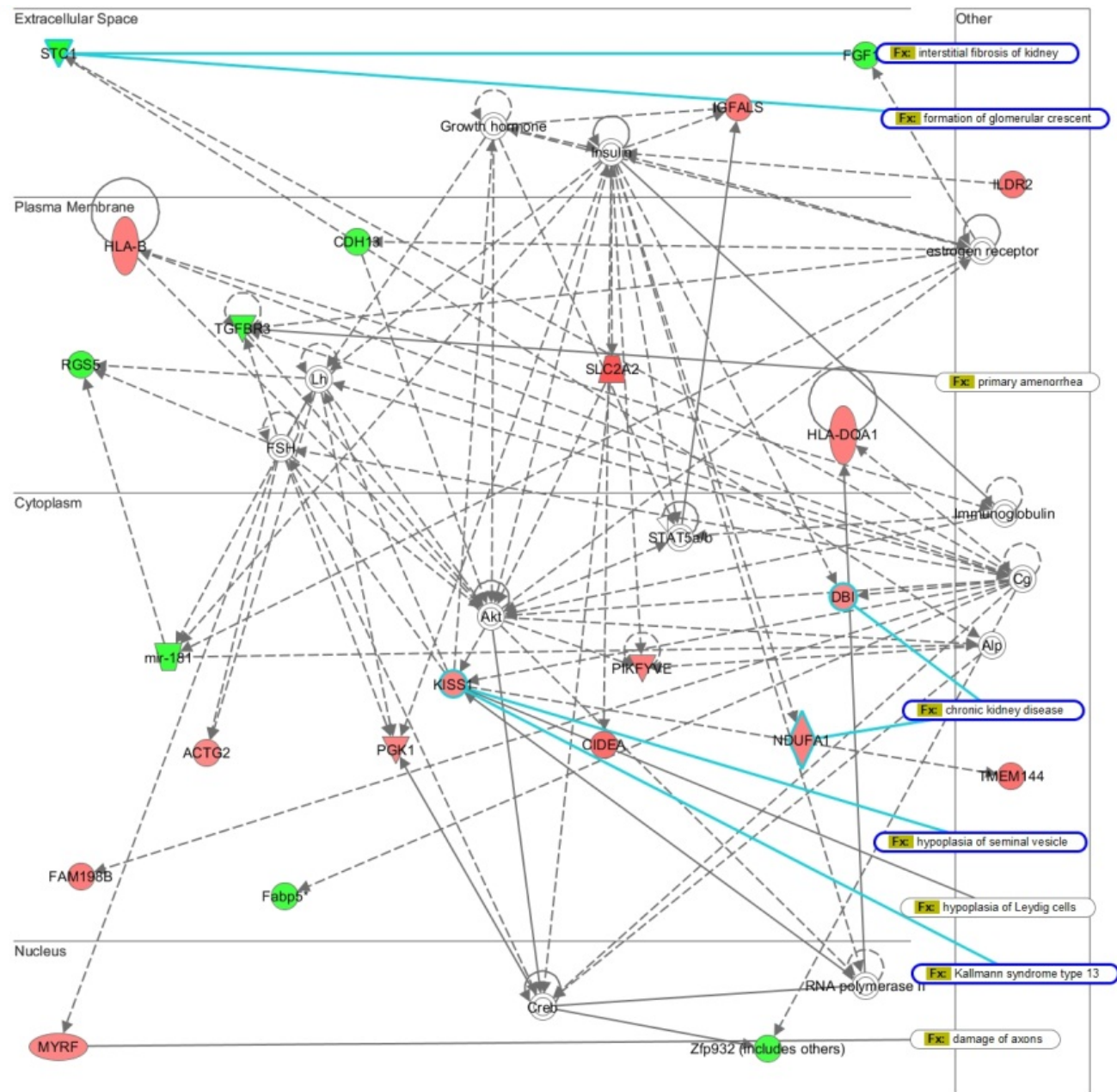
Supplemental Figure 6- Tubular Injury and Immune Cell Infiltration

E.



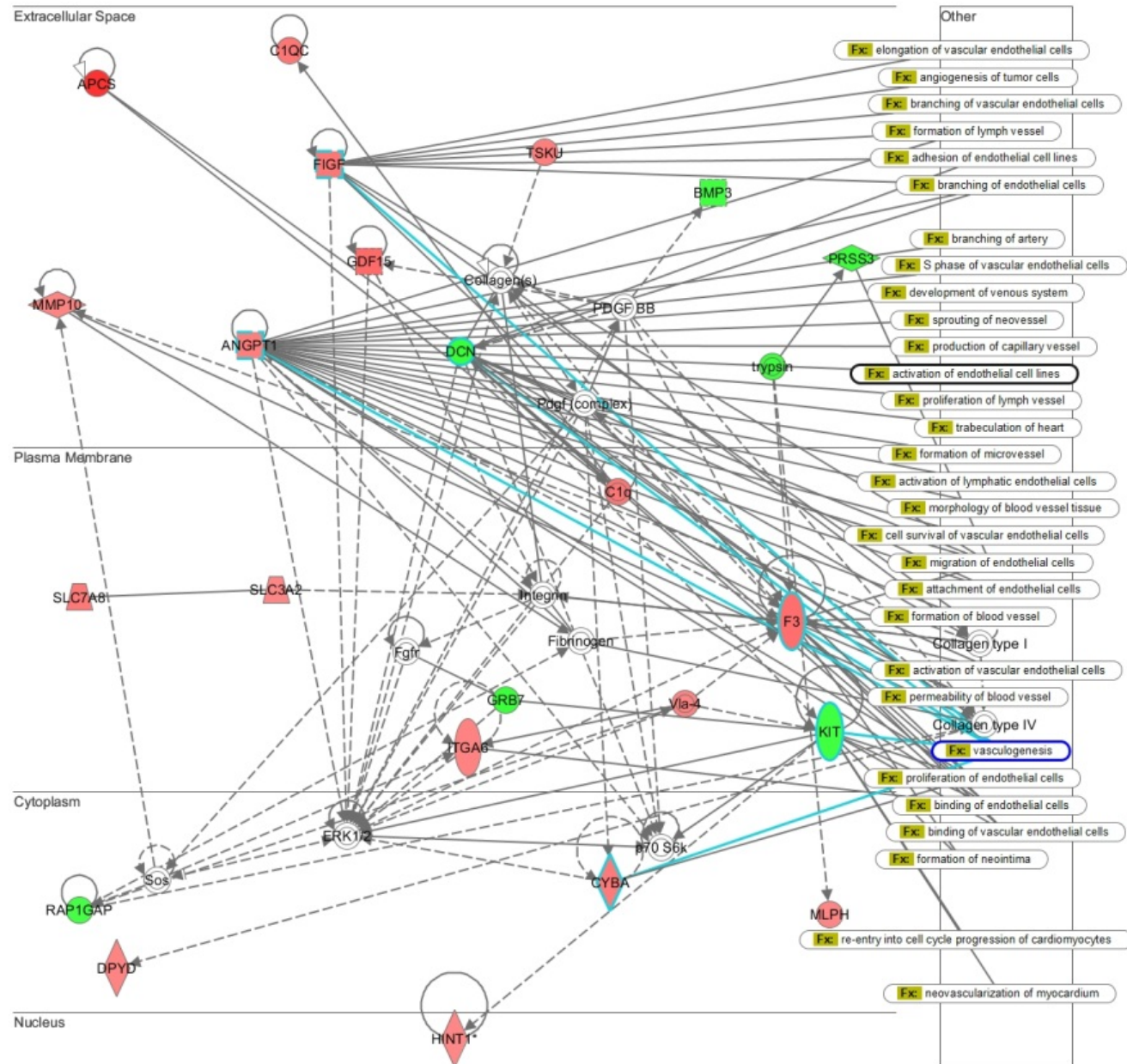
Supplemental Figure 7- IPA of kidney from HSRA-S and -C at month 1

A.



Supplemental Figure 7- IPA of kidney from HSRA-S and -C at month 1

B.



Supplemental Figure 8

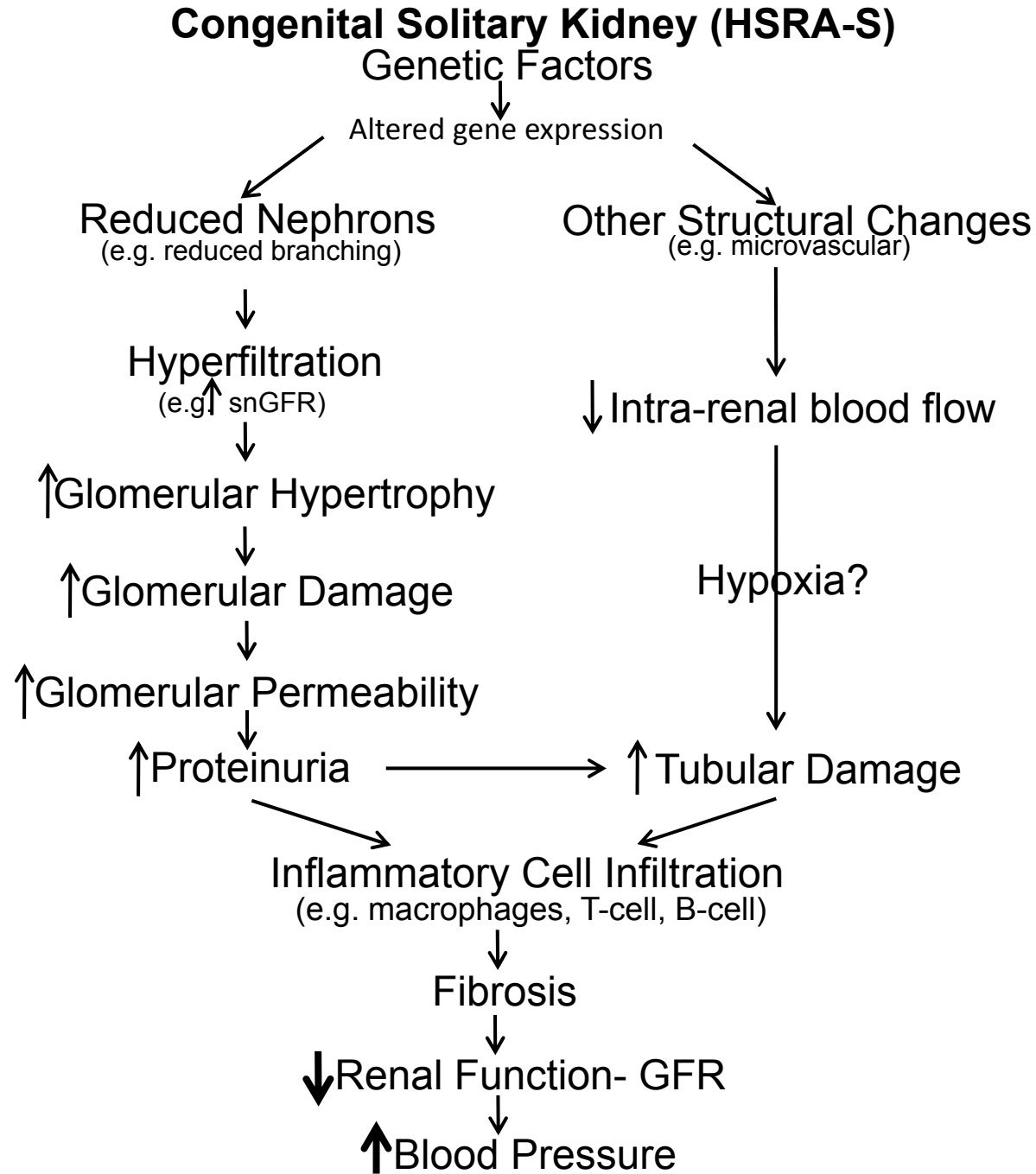


Table S1-AllGenes-P<0.02-FC>20%

Probe Set ID	HSRA-CM	HSRA-SM	gene_assignment	mrna_assignment	Fold change	P value	T value	Adjusted P value 2	T value 2
10770048	6.09846	7.14527	Apcs	ENSRNOT00000012092	2.065953255	0.0138	-3.44356	0.57	-3.44356
10814630	7.31556	8.06542	Slc2a2	NM_012879	1.681625843	0.0183	-3.21575	0.566	-3.21575
10781207	5.95326	6.70207	Adra1a	ENSRNOT00000012736	1.68040669	0.0135	-3.46063	0.565	-3.46063
10923270	7.18337	7.8402	Obfc2a	NM_001014216	1.576613545	0.00548	-4.23486	0.569	-4.23486
10925936	7.06853	7.71517	Epb41l3	NM_053927	1.565519094	0.0118	-3.57273	0.566	-3.57273
10769086	6.23405	6.82845	LOC680415	ENSRNOT00000059368	1.509852648	0.00278	-4.87529	0.576	-4.87529
10797937	4.00269	4.5951			1.507765293	0.00849	-3.84721	0.585	-3.84721
10934509	5.32332	5.91471	Tsx	ENSRNOT00000003922	1.506695271	0.0194	-3.16838	0.565	-3.16838
10787517	5.60499	6.18491	Gdf15	NM_019216	1.494766116	0.00429	-4.45901	0.557	-4.45901
10843362	9.05376	9.63056	Slc34a3	NM_139338	1.491544843	0.0195	-3.16525	0.566	-3.16525
10802416	5.90918	6.46744	Cidea	NM_001170467	1.472488761	0.00131	-5.66038	0.496	-5.66038
10714103	5.19488	5.75307	Mpeg1	NM_022617	1.472429156	0.00914	-3.78398	0.59	-3.78398
10753214	7.05123	7.60357	Rcan1	NM_153724	1.466457725	0.00675	-4.04699	0.603	-4.04699
10818708	7.26276	7.80133	F3	ENSRNOT00000015836	1.452536106	0.00353	-4.64454	0.569	-4.64454
10891834	9.45755	9.99591	Lgmn	NM_022226	1.452319145	0.0152	-3.36595	0.57	-3.36595
10878938	5.36869	5.90627	Plk3	NM_022187	1.451542974	0.0176	-3.24778	0.564	-3.24778
10854239	5.40745	5.92936		ENSRNOT00000036735	1.435850024	0.0127	-3.50893	0.564	-3.50893
10764415	4.83945	5.35632	Aspm	NM_001105955	1.430852294	0.015	-3.37236	0.568	-3.37236
10925255	7.97475	8.49129	Spp2	NM_053577	1.4305197	0.0187	-3.19588	0.565	-3.19588
10752007	8.54206	9.05822	Dgkg	ENSRNOT00000002452	1.430147886	0.00244	-5.00707	0.565	-5.00707
10872260	7.5841	8.09929	Ak2	NM_001033967	1.429186344	0.00418	-4.48439	0.567	-4.48439
10823838	5.69	6.19957	Tmem144	NM_001108551	1.423624277	0.0125	-3.52703	0.561	-3.52703
10765446	3.3084	3.80458	RGD1560672	NM_001109073	1.4104774	0.0119	-3.5662	0.564	-3.5662
10843438	7.47937	7.97229	Uap1l1	NM_001134516	1.407283306	0.00133	-5.6489	0.489	-5.6489
10855003	3.62485	4.11546	Tas2r139	ENSRNOT00000037220	1.405037165	0.000261	-7.6517	0.761	-7.6517
10930299	4.46048	4.95077		ENSRNOT00000054648	1.40472734	0.00702	-4.01329	0.596	-4.01329
10843424	8.98009	9.46936	Dpp7	NM_031973	1.403736711	0.00986	-3.72016	0.59	-3.72016
10881829	7.82099	8.30588	Car6	NM_001134841	1.399483562	0.0107	-3.65598	0.569	-3.65598
10881955	7.62051	8.10318	Tas1r1	NM_053305	1.397328973	0.0141	-3.42421	0.571	-3.42421
10937725	7.78836	8.25788	Figf	ENSRNOT00000068601	1.384649038	0.0167	-3.28896	0.571	-3.28896
10880731	4.82156	5.28988	C1qc	NM_001008524	1.383496761	0.00799	-3.89999	0.594	-3.89999
10757962	7.43361	7.89759	Asl	NM_021577	1.379342914	0.0153	-3.35647	0.568	-3.35647
10765364	6.47282	6.93651	Ildr2	ENSRNOT00000031367	1.379063249	0.0128	-3.50471	0.564	-3.50471
10802956	6.46697	6.92773	Pqlc1	NM_001013189	1.376264572	0.01	-3.70748	0.586	-3.70748
10732449	3.62883	4.08413	Msln1	ENSRNOT00000060286	1.371060133	0.00462	-4.39154	0.569	-4.39154
10701250	6.51026	6.96226			1.367931247	0.0198	-3.15212	0.568	-3.15212
10783648	8.88798	9.3273	Slc7a8	NM_053442	1.355967164	0.00902	-3.79594	0.589	-3.79594
10713152	7.46298	7.89839	Slc25a45	XM_001071416	1.352290273	0.0185	-3.20572	0.565	-3.20572
10732239	5.42635	5.85868	Igfals	NM_053329	1.349403739	0.0103	-3.68607	0.579	-3.68607
10723734	2.87695	3.30549		ENSRNOT00000041628	1.345871806	0.0141	-3.42383	0.57	-3.42383
10707338	5.04766	5.47207	Gas2	NM_001127504	1.342026591	0.0105	-3.66729	0.571	-3.66729
10825153	4.67212	5.09594	Fcgr1a	NM_001100836	1.341479778	0.0104	-3.67951	0.569	-3.67951
10811571	7.46432	7.8737	Cyba	NM_024160	1.328109026	0.00363	-4.61766	0.57	-4.61766
10745595	5.59136	5.99905	Sifn13	NM_001013970	1.32655561	0.00959	-3.74342	0.59	-3.74342
10816017	5.81265	6.21859	Fam198b	ENSRNOT00000013524	1.324951887	0.00937	-3.76329	0.59	-3.76329
10786028	6.0052	6.41012	Gpr183	NM_001109386	1.324014425	0.0184	-3.2115	0.566	-3.2115
10730830	4.45588	4.85708		ENSRNOT00000038101	1.320608735	0.00847	-3.84998	0.588	-3.84998
10908084	5.36631	5.75523	Vstm5	NM_001144870	1.309410334	0.00654	-4.07512	0.601	-4.07512

Table S1-AllGenes-P<0.02-FC>20%

Probe Set ID	HSRA-CM	HSRA-SM	gene_assignment	mrna_assignment	Fold change	P value	T value	Adjusted P value 2	T value 2
10807700	3.96843	4.35609	Pmfbp1	NM_134393	1.308269858	0.00347	-4.66125	0.582	-4.66125
10927780	8.13689	8.52241	Slc40a1	NM_133315	1.306331873	0.017	-3.27602	0.568	-3.27602
10754145	9.66176	10.04695	Igsf11	NM_001013120	1.306035995	0.0176	-3.24775	0.563	-3.24775
10723822	7.01621	7.39848	Tsku	NM_001009965	1.303387523	0.00104	-5.91837	0.522	-5.91837
10923996	5.87744	6.2596	Pikfyve	BC089984	1.303295374	0.00981	-3.72415	0.59	-3.72415
10770082	3.41087	3.79093	Ifi204	NM_001012029	1.301391125	0.0081	-3.88799	0.592	-3.88799
10903529	6.1778	6.55094	Angpt1	ENSRNOT00000007979	1.29517293	0.00977	-3.72749	0.591	-3.72749
10772272	5.9852	6.35814			1.294989347	0.0113	-3.61046	0.566	-3.61046
10831099	4.1044	4.47677	RT1-CE5	NM_001008843	1.294481158	0.0000233	-11.7267	0.226	-11.7267
10733697	6.73606	7.10774	Slc36a1	ENSRNOT00000016755	1.293865442	0.00459	-4.39752	0.57	-4.39752
10828351	5.92905	6.29804	RT1-Ba	NM_001008831	1.291449785	0.0122	-3.54767	0.565	-3.54767
10722524	4.16624	4.53159	Peg12	NM_001170562	1.288196445	0.0132	-3.47921	0.562	-3.47921
10825328	6.83457	7.19821	Phgdh	NM_031620	1.286665678	0.0103	-3.68972	0.58	-3.68972
10905933	8.60594	8.96748	RGD1304694	ENSRNOT00000042070	1.284789681	0.015	-3.3763	0.568	-3.3763
10804301	6.31005	6.67028	LOC683071	ENSRNOT00000065149	1.283626795	0.00821	-3.87627	0.591	-3.87627
10717270	2.16981	2.52753		ENSRNOT00000061221	1.281394839	0.00719	-3.99158	0.594	-3.99158
10837342	4.27209	4.62854	Ube2l6	NM_001024755	1.280274749	0.00129	-5.68202	0.499	-5.68202
10931991	6.89457	7.24809	Ndufa1	NM_001108813	1.277674198	0.0177	-3.24212	0.563	-3.24212
10809001	7.57723	7.9302	Pdp2	ENSRNOT00000016462	1.277180195	0.00769	-3.93258	0.601	-3.93258
10878880	4.87904	5.22918	Nasp	NM_001005543	1.274682879	0.000928	-6.04532	0.521	-6.04532
10890494	8.11132	8.46069	RGD1305721	NM_001108031	1.273997664	0.016	-3.32497	0.569	-3.32497
10842472	3.73098	4.079			1.272816062	0.00731	-3.97691	0.594	-3.97691
10865972	2.72018	3.06781			1.272471309	0.00858	-3.83862	0.583	-3.83862
10782144	7.70265	8.04771	Clybl	NM_001100685	1.270208955	0.00905	-3.79223	0.589	-3.79223
10873314	3.70746	4.04943		ENSRNOT00000055904	1.267486691	0.0161	-3.31813	0.569	-3.31813
10812042	3.82512	4.1667		GENSCAN00000041458	1.267144799	0.0122	-3.54712	0.565	-3.54712
10876829	5.23421	5.57448		ENSRNOT00000023703	1.265990853	0.00583	-4.17788	0.588	-4.17788
10710340	3.21424	3.55338	Abca15	NM_001106293	1.265009165	0.0153	-3.35988	0.568	-3.35988
10871048	3.11932	3.4567		ENSRNOT00000053202	1.263458371	0.00787	-3.91355	0.598	-3.91355
10912282	2.78223	3.11934		GENSCAN00000008639	1.263223529	0.0143	-3.41363	0.571	-3.41363
10850390	7.67149	8.0043	Snx5	NM_001106518	1.259465694	0.0106	-3.66227	0.569	-3.66227
10787275	4.95348	5.28626	Ankrd41	ENSRNOT00000023065	1.259442806	0.00496	-4.32503	0.57	-4.32503
10811554	3.51374	3.84611	Trhr2	ENSRNOT00000017317	1.259074211	0.00738	-3.96958	0.594	-3.96958
10766378	6.19919	6.53122	Srp9	NM_001126095	1.258777142	0.00414	-4.49268	0.57	-4.49268
10928976	4.28379	4.61552		ENSRNOT00000030232	1.258528709	0.000501	-6.78706	0.505	-6.78706
10734264	5.88698	6.21755	LOC100360307	XM_002724502	1.257510185	0.00798	-3.90075	0.597	-3.90075
10933587	7.5447	7.87495	Lamtor1	NM_199102	1.257225037	0.0193	-3.17297	0.567	-3.17297
10723866	6.25814	6.58817	Dgat2	NM_001012345	1.25703907	0.0118	-3.57462	0.565	-3.57462
10887359	4.33158	4.65326	Trmt61a	NM_001007706	1.249789953	0.00634	-4.10303	0.592	-4.10303
10812216	7.53891	7.86033	Glrx	ENSRNOT00000016372	1.249554634	0.015	-3.37336	0.568	-3.37336
10856357	7.46855	7.78873	St3gal5	NM_031337	1.248486757	0.00942	-3.75811	0.587	-3.75811
10700120	7.20783	7.52763			1.248162866	0.0175	-3.25	0.566	-3.25
10751218	3.56584	3.88436	Gap43	NM_017195	1.247055531	0.00884	-3.81301	0.587	-3.81301
10901413	6.66392	6.98214	Txnrd1	NM_031614	1.246791244	0.00547	-4.2352	0.571	-4.2352
10844005	5.3994	5.71712	Fcnb	ENSRNOT00000012494	1.246361971	0.0112	-3.61977	0.569	-3.61977
10836849	8.43752	8.75485	Itga6	NM_053725	1.246024251	0.0173	-3.2579	0.563	-3.2579
10789557	5.78317	6.09788		ENSRNOT00000039584	1.243762255	0.0198	-3.15207	0.567	-3.15207
10794798	3.96513	4.27978	Hmgbl-ps2	NR_024023	1.243714929	0.00428	-4.46098	0.559	-4.46098

Table S1-AllGenes-P<0.02-FC>20%

Probe Set ID	HSRA-CM	HSRA-SM	gene_assignment	mrna_assignment	Fold change	P value	T value	Adjusted P value 2	T value 2
10923857	7.03397	7.34787	Eef1b2	NM_001108799	1.24306345	0.0124	-3.53269	0.563	-3.53269
10814847	4.65622	4.9694	Sox2	NM_001109181	1.242437959	0.0192	-3.17684	0.567	-3.17684
10889961	8.59534	8.90723	Cfl2	NM_001108982	1.241334438	0.00144	-5.56142	0.476	-5.56142
10923358	6.3394	6.6511	Mars2	XM_001066991	1.241165757	0.0175	-3.25135	0.566	-3.25135
10810375	2.90183	3.2135		ENSRNOT000000045124	1.241149664	0.00114	-5.8146	0.519	-5.8146
10882840	6.47266	6.78357	RGD1562291	ENSRNOT000000061693	1.240495563	0.00798	-3.90124	0.598	-3.90124
10822253	3.16995	3.47907	Car13	NM_001134993	1.238959432	0.00294	-4.82121	0.584	-4.82121
10904699	2.27855	2.58654		GENSCAN000000044033	1.237982512	0.0114	-3.60413	0.568	-3.60413
10868125	8.17362	8.48157	Rragd	ENSRNOT000000068028	1.23794663	0.00317	-4.74827	0.597	-4.74827
10717019	7.48856	7.7959	RGD1309903	XM_001072524	1.237427473	0.00542	-4.24391	0.574	-4.24391
10866144	4.46235	4.7681	Klra7	XM_003753950	1.236056089	0.00994	-3.71314	0.59	-3.71314
10705928	3.96493	4.26952	Wdr62	NM_001191623	1.235069036	0.0128	-3.50449	0.563	-3.50449
10839506	6.74679	7.05102	Mtfr1	NM_001100977	1.234758735	0.000385	-7.12561	0.535	-7.12561
10907904	2.19091	2.49503	Mmp10	NM_133514	1.234662771	0.00843	-3.85401	0.588	-3.85401
10871305	5.74994	6.0525	Tesk2	NM_133396	1.233327746	0.00115	-5.80148	0.509	-5.80148
10748932	3.82272	4.1245	Ush1g	NM_001105850	1.232670307	0.0187	-3.19725	0.565	-3.19725
10704895	6.57208	6.87248	Zfp180	NM_144757	1.231491804	0.00687	-4.03182	0.601	-4.03182
10715452	5.48897	5.78927	Avpi1	ENSRNOT000000019978	1.231403112	0.0107	-3.65689	0.57	-3.65689
10764007	5.27014	5.56868	Kiss1	NM_181692	1.229898334	0.00159	-5.45312	0.458	-5.45312
10916734	7.16593	7.46416	C2cd2l	NM_001011996	1.229633212	0.00525	-4.27351	0.578	-4.27351
10934610	9.05777	9.35502	Pgk1	NM_053291	1.228806138	0.0144	-3.40728	0.568	-3.40728
10742431	6.55089	6.84698	Rufy1	NM_001100727	1.227811456	0.00939	-3.76078	0.59	-3.76078
10872940	8.60247	8.89784	Fuca1	NM_012562	1.227200866	0.00591	-4.16661	0.587	-4.16661
10818660	6.27328	6.56846	Dpyd	NM_031027	1.227041841	0.012	-3.56098	0.563	-3.56098
10746256	6.55492	6.84866	Utp18	NM_001135039	1.2258147	0.0185	-3.20678	0.566	-3.20678
10732207	10.03044	10.32244	Sepx1	NM_001044285	1.224341512	0.00915	-3.78361	0.589	-3.78361
10789237	3.31782	3.60966	Defa6	NM_001033076	1.224205136	0.0026	-4.94403	0.562	-4.94403
10762735	6.14263	6.43416	RGD1311899	BC088751	1.223943949	0.012	-3.55744	0.562	-3.55744
10933535	6.35179	6.64263	Nhs	NM_001191733	1.223350286	0.00372	-4.59348	0.557	-4.59348
10728647	6.57894	6.86839	Mrf	NM_001170487	1.222172856	0.00879	-3.81778	0.588	-3.81778
10903538	3.6979	3.98667	Rspo2	NM_001130575	1.221600413	0.0177	-3.24232	0.564	-3.24232
10794544	7.46438	7.75286		ENSRNOT000000060493	1.221355796	0.0163	-3.30654	0.571	-3.30654
10798945	3.53325	3.82084	LOC296884	NM_001177442	1.2206074	0.0146	-3.39699	0.567	-3.39699
10722982	7.10908	7.3965	Pex11a	NM_053487	1.220458269	0.000527	-6.72421	0.481	-6.72421
10925303	4.5949	4.88179	Mlph	NM_001012135	1.220006466	0.00997	-3.71059	0.591	-3.71059
10728507	10.05001	10.33651	Slc3a2	NM_019283	1.219674468	0.00329	-4.71266	0.589	-4.71266
10864446	3.9814	4.26769	Shq1	NM_001134713	1.219502568	0.000292	-7.4934	0.711	-7.4934
10738522	4.47085	4.75689	Nags	NM_001107053	1.219290972	0.00046	-6.89623	0.516	-6.89623
10723413	7.47906	7.76462	Fam108c1	NM_001100736	1.218877316	0.0185	-3.20735	0.566	-3.20735
10896234	8.09429	8.37953	Atp6v1c1	NM_001011992	1.218616366	0.0011	-5.85311	0.526	-5.85311
10855371	5.7292	6.01403	RGD1559747	NR_027235	1.218267083	0.00727	-3.98263	0.591	-3.98263
10916060	3.57751	3.86026	Ddx25	NM_031630	1.21651113	0.00856	-3.84004	0.583	-3.84004
10745249	6.19087	6.47347	Tmem199	NM_001024992	1.216381669	0.0164	-3.3036	0.571	-3.3036
10790348	3.23757	3.51897		GENSCAN000000025919	1.215367079	0.00793	-3.90684	0.597	-3.90684
10888210	7.1399	7.42129	Lrpprc	ENSRNOT00000008200	1.215364814	0.00247	-4.99435	0.563	-4.99435
10871487	6.34498	6.62595		ENSRNOT000000027844	1.215015054	0.00273	-4.89493	0.573	-4.89493
10807464	5.4217	5.7012	Pla2g15	NM_001004277	1.213775754	0.00295	-4.81679	0.583	-4.81679
10782761	3.61597	3.89518		ENSRNOT000000030299	1.213525891	0.0114	-3.60334	0.568	-3.60334

Table S1-AllGenes-P<0.02-FC>20%

Probe Set ID	HSRA-CM	HSRA-SM	gene_assignment	mrna_assignment	Fold change	P value	T value	Adjusted P value 2	T value 2
10927922	3.74816	4.02538	Dnah7	ENSRNOT00000016465	1.211859822	0.0094	-3.76006	0.588	-3.76006
10933279	7.46969	7.74621	Hccs	NM_001191732	1.211276412	0.0148	-3.3857	0.569	-3.3857
10797256	7.65722	7.93336	Pfn3	NM_001109487	1.21094954	0.00478	-4.35948	0.574	-4.35948
10885116	4.75044	5.02564		ENSRNOT00000046038	1.210160375	0.000849	-6.14771	0.517	-6.14771
10920991	6.17278	6.44735		ENSRNOT00000034355	1.209631205	0.00237	-5.03828	0.566	-5.03828
10862834	8.73122	9.00531	Hint1	NM_001109607	1.20923388	0.000339	-7.29299	0.55	-7.29299
10790119	5.86819	6.14133	Phf7	NM_001012211	1.208432555	0.000383	-7.13178	0.559	-7.13178
10880415	7.53838	7.81148	Dhdds	NM_001011978	1.208398342	0.00805	-3.89392	0.592	-3.89392
10779159	7.10253	7.37452	Mrps16	NM_001109518	1.207475781	0.00801	-3.89735	0.593	-3.89735
10836035	4.46411	4.73607	Arhgap15	NM_001013917	1.207444191	0.0166	-3.29444	0.57	-3.29444
10733676	8.54046	8.81216	Hint1	NM_001109607	1.207229257	0.000409	-7.04636	0.543	-7.04636
10931154	7.84275	8.11427	Dbi	NM_031853	1.207078695	0.00523	-4.27585	0.579	-4.27585
10844183	9.05805	9.32955	Crat	NM_001004085	1.207064867	0.0167	-3.28606	0.568	-3.28606
10783193	4.39948	4.67082	Rnase1	NM_001029904	1.206925154	0.0125	-3.52336	0.563	-3.52336
10834157	5.49474	5.7655	Rnf208	NM_001109195	1.20644176	0.0132	-3.48101	0.563	-3.48101
10867364	5.31205	5.58127		ENSRNOT00000035699	1.205154181	0.0101	-3.70547	0.586	-3.70547
10777950	6.39358	6.66136	Rnf185	NM_001024271	1.20395124	0.00914	-3.78407	0.591	-3.78407
10852649	2.7965	3.06333		NM_130400	1.20316124	0.00694	-4.02278	0.6	-4.02278
10856436	8.50442	8.77116	Suc1g1	ENSRNOT00000007624	1.203087926	0.0138	-3.44235	0.57	-3.44235
10851664	4.82588	5.09194	Spata25	NM_001025769	1.202518344	0.00758	-3.94542	0.602	-3.94542
10725993	7.17481	7.44086	Sephs2	NM_001079889	1.202504039	0.0192	-3.17835	0.567	-3.17835
10799539	6.86507	7.13087	Nudt5	NM_001007733	1.202307224	0.000747	-6.29814	0.496	-6.29814
10883196	3.80192	4.06761	LOC100322897	NM_001170709	1.202206016	0.0182	-3.22029	0.566	-3.22029
10863549	4.56965	4.83492	Actg2	NM_012893	1.201864004	0.00849	-3.84792	0.586	-3.84792
10817977	6.42259	6.68618	Bcas2	NM_001106458	1.200465918	0.0158	-3.3311	0.57	-3.3311
					n=169				
10873170	7.13269	6.81073	Rap1gap	BC089979	0.799978495	0.0148	3.383815	0.567	3.383815
10911531	5.9963	5.6713	Pygo1	NM_001191117	0.79829365	0.0114	3.601137	0.568	3.601137
10875532	5.93649	5.61001	Pdp1	NM_019372	0.797477365	0.0146	3.395566	0.565	3.395566
10916101	2.99675	2.66802	LOC100360049	JQ031758	0.796233594	0.01	3.707495	0.587	3.707495
10783501	5.25882	4.92829		ENSRNOT00000060356	0.795245826	0.00832	3.864386	0.595	3.864386
10713602	10.18205	9.85139		ENSRNOT00000054147	0.795173049	0.00662	4.064892	0.599	4.064892
10769168	4.90668	4.57572		ENSRNOT00000054127	0.795007765	0.0175	3.248916	0.564	3.248916
10703434	6.62922	6.29742	LOC688452	ENSRNOT00000014598	0.794544637	0.0171	3.269664	0.568	3.269664
10839868	5.84356	5.51077		ENSRNOT00000053440	0.793997705	0.00143	5.56394	0.48	5.56394
10893424	5.68659	5.35136	Zfp347	NM_133390	0.792658031	0.00807	3.891624	0.592	3.891624
10775647	7.6697	7.33322	Fras1	NM_001191595	0.79197067	0.00704	4.010717	0.596	4.010717
10744641	4.95574	4.61796	Pitpnm3	ENSRNOT00000041067	0.791256011	0.0146	3.397272	0.568	3.397272
10752764	6.16319	5.82461	RGD1563888	NM_001108312	0.790815115	0.0167	3.289694	0.571	3.289694
10724967	6.36494	6.02618	Dkk3	ENSRNOT00000022301	0.790719509	0.00661	4.065496	0.6	4.065496
10719922	6.31243	5.97346	Cyp2s1	NM_001107495	0.790605783	0.0128	3.507468	0.564	3.507468
10748513	5.3844	5.04226	Arsg	NM_001047877	0.788869619	0.00811	3.887283	0.591	3.887283
10931566	3.92154	3.57702	Fabp5	NM_145878	0.787568629	0.0173	3.260155	0.563	3.260155
10931568	3.92154	3.57702	Fabp5	NM_145878	0.787568629	0.0173	3.260155	0.564	3.260155
10839730	5.3909	5.04521	Zc3h6	NM_001107772	0.786932349	0.0116	3.590164	0.569	3.590164
10799671	8.31846	7.97138		ENSRNOT00000057851	0.786172509	0.000756	6.284821	0.491	6.284821
10829046	5.01184	4.66369	Glpi1r	ENSRNOT00000001527	0.785588384	0.0172	3.265179	0.567	3.265179
10808274	5.65248	5.30291	Cdh13	NM_138889	0.784817517	0.0144	3.408713	0.571	3.408713

Table S1-AllGenes-P<0.02-FC>20%

Probe Set ID	HSRA-CM	HSRA-SM	gene_assignment	mrna_assignment	Fold change	P value	T value	Adjusted P value 2	T value 2
10851670	8.25593	7.90007	Pltp	NM_001168543	0.781404436	0.0179	3.233935	0.566	3.233935
10852641	5.21989	4.86148	LOC690826	ENSRNOT00000060488	0.780019879	0.000716	6.349726	0.486	6.349726
10775573	6.00642	5.64743	Bmp3	ENSRNOT00000038872	0.779711187	0.0177	3.243042	0.564	3.243042
10781995	3.20868	2.84968	7SK RNA	ENSRNOT00000053541	0.779703915	0.000552	6.666609	0.488	6.666609
10747979	8.30399	7.94427	Dcald	NM_001007724	0.779316366	0.0119	3.567787	0.565	3.567787
10802427	4.92949	4.56892	Slmo1	NM_001109570	0.778858721	0.0167	3.286545	0.569	3.286545
10891402	3.58088	3.21822	Dio2	NM_031720	0.777728498	0.00898	3.799099	0.59	3.799099
10725914	5.93529	5.57002	RGD1564195	ENSRNOT00000049044	0.776319921	0.0102	3.694316	0.582	3.694316
10891916	5.13617	4.76583	Serpina10	NM_133617	0.773600698	0.015	3.376329	0.568	3.376329
10812297	5.34871	4.97756	RGD1560883	ENSRNOT00000018479	0.773167074	0.000557	6.653764	0.479	6.653764
10762224	6.63018	6.25884		ENSRNOT00000053049	0.773063362	0.00152	5.502989	0.465	5.502989
10776437	6.09907	5.72496	Kit	NM_022264	0.771580219	0.00492	4.332504	0.57	4.332504
10864773	6.92032	6.54354		ENSRNOT00000053840	0.770159781	0.00593	4.163521	0.587	4.163521
10892704	6.92032	6.54354		ENSRNOT00000053840	0.770159781	0.00593	4.163521	0.585	4.163521
10732644	5.48306	5.10131	Stc2	NM_022230	0.767509162	0.0103	3.68423	0.579	3.68423
10810553	4.66002	4.27613	B3gnt9	XM_226431	0.766369998	0.0142	3.417737	0.57	3.417737
10932394	6.11531	5.72456	Porcn	NM_001173355	0.762736022	0.000294	7.486133	0.66	7.486133
10791989	5.79241	5.40122	Pragmin	NM_001107315	0.762500167	0.0199	3.149614	0.567	3.149614
10801197	5.26793	4.87446	LOC690826	ENSRNOT00000060488	0.761292338	0.000878	6.109504	0.513	6.109504
10700231	9.40172	9.00787			0.761096001	0.00102	5.937747	0.523	5.937747
10862184	3.24062	2.84407	Prss2	NM_012729	0.75967437	0.00186	5.28665	0.502	5.28665
10910872	4.79478	4.39636	Igdcc4	BC168991	0.758688509	0.0161	3.319942	0.569	3.319942
10751871	6.09797	5.69929	Fgf12	ENSRNOT00000002650	0.758554101	0.0131	3.48453	0.564	3.48453
10754179	5.05621	4.65694	Popdc2	NM_199113	0.758242905	0.0197	3.155399	0.567	3.155399
10808601	8.72511	8.32464	Rpl13	BC086577	0.757607162	0.000136	8.608301	0.659	8.608301
10807935	4.7728	4.37147		GENSCAN00000037874	0.757158399	0.00605	4.145182	0.583	4.145182
10788685	4.29228	3.88959			0.75644654	0.019	3.185894	0.567	3.185894
10764367	5.5295	5.12628	Mir181b-1	NR_031899	0.756168723	0.00834	3.862833	0.594	3.862833
10737999	8.19042	7.7827	Grb7	NM_053403	0.753810644	0.00459	4.396545	0.568	4.396545
10839197	7.29612	6.88731	Casc4	ENSRNOT00000038291	0.753248274	0.0128	3.504887	0.565	3.504887
10862359	6.47993	6.06971	Y RNA	ENSRNOT00000053328	0.752505362	0.00443	4.429798	0.567	4.429798
10724672	3.75258	3.34006	Olr255	NM_001000947	0.751308978	0.0166	3.292367	0.57	3.292367
10929041	8.31619	7.90304	Slc23a3	NM_001109006	0.750980079	0.0126	3.520649	0.562	3.520649
10899139	9.95752	9.53959	Aqp6	ENSRNOT00000000323	0.748494864	0.00415	4.490804	0.569	4.490804
10925526	7.07999	6.66169	Sned1	ENSRNOT00000022479	0.748305321	0.0135	3.462319	0.565	3.462319
10701349	1.84721	1.42627			0.746940076	0.0152	3.364739	0.57	3.364739
10911268	8.01437	7.59333			0.746885061	0.0102	3.693985	0.581	3.693985
10852719	5.98713	5.56438		ENSRNOT00000062069	0.746000409	0.00686	4.032603	0.602	4.032603
10721700	7.74171	7.3148		ENSRNOT00000052978	0.743853569	0.0106	3.661748	0.567	3.661748
10867142	6.78777	6.36078	Eya1	ENSRNOT00000064946	0.743809283	0.00336	4.692962	0.573	4.692962
10771070	8.37635	7.94774	Tgfbr3	ENSRNOT00000002867	0.742978275	0.0123	3.540522	0.562	3.540522
10868881	6.22552	5.7962	Col15a1	ENSRNOT00000059992	0.742608726	0.0183	3.217057	0.567	3.217057
10847162	3.13137	2.6992	Olr674	NM_001000352	0.741145134	0.00114	5.811625	0.513	5.811625
10895075	11.58499	11.15251	Dcn	NM_024129	0.740981996	0.00723	3.986633	0.592	3.986633
10889260	6.84195	6.40306	Fam84a	NM_001127299	0.737699389	0.000769	6.264716	0.488	6.264716
10765437	9.42597	8.98678	Rgs5	ENSRNOT00000003705	0.73755002	0.0167	3.290422	0.571	3.290422
10809503	5.58456	5.14488		ENSRNOT00000052385	0.737294495	0.0156	3.341105	0.572	3.341105
10833468	4.1097	3.66902	RGD1563833	ENSRNOT00000066263	0.736786425	0.00767	3.935958	0.602	3.935958

Table S1-AllGenes-P<0.02-FC>20%

Probe Set ID	HSRA-CM	HSRA-SM	gene_assignment	mrna_assignment	Fold change	P value	T value	Adjusted P value 2	T value 2
10752978	4.4235	3.96976	Krtap21-1	ENSRNOT00000061592	0.730146289	0.016	3.321831	0.569	3.321831
10706941	5.88054	5.42625	Car11	NM_175708	0.729874194	0.000699	6.378464	0.498	6.378464
10796917	5.39679	4.93984	LOC501406	XM_003748688	0.728525043	0.00337	4.690013	0.571	4.690013
10730310	7.63915	7.1737	Marveld1	NM_001107590	0.724241495	0.0136	3.452574	0.565	3.452574
10807698	2.45627	1.98697			0.722314656	0.00323	4.729633	0.586	4.729633
10747847	6.30458	5.82434	RGD1307966	ENSRNOT00000028563	0.716857255	0.0148	3.38499	0.569	3.38499
10753557	3.72113	3.21777	Olr1537	NM_001001352	0.705461264	0.0111	3.621631	0.569	3.621631
10889415	5.96333	5.45709	Sox11	ENSRNOT00000045963	0.704052806	0.0103	3.687176	0.579	3.687176
10737722	6.82263	6.29135	Hoxb5	NM_001191925	0.691941202	0.00000953	13.66961	0.279	13.66961
10838117	7.31665	6.78142	Pamr1	NM_001107755	0.690049052	0.000845	6.153393	0.525	6.153393
10912003	5.17244	4.63081	Tpbg	NM_031807	0.686997175	0.0191	3.182878	0.568	3.182878
10759447	4.17795	3.63442	5S ribosomal RNA	ENSRNOT00000054474	0.68608731	0.0124	3.532315	0.562	3.532315
10759457	4.17795	3.63442	5S ribosomal RNA	ENSRNOT00000054474	0.68608731	0.0124	3.532315	0.563	3.532315
10741009	5.00372	4.45679	Ntn3	NM_053732	0.684476256	0.017	3.27426	0.568	3.27426
10807923	4.33273	3.76657		GENSCAN00000037874	0.675414562	0.00134	5.634384	0.489	5.634384
10862505	6.97308	6.40452	LOC500124	BC078992	0.674291432	0.00367	4.60755	0.567	4.60755
10781273	8.37149	7.79197	Stc1	NM_031123	0.669183075	0.0129	3.4976	0.562	3.4976
10727232	7.24645	6.6548	Ano1	NM_001107564	0.663582206	0.0127	3.511189	0.564	3.511189
10765040	6.87527	6.27687	Gas5	GAS5	0.660486042	0.00658	4.070036	0.601	4.070036
10703310	9.09589	8.49019	Smoc2	ENSRNOT00000019317	0.657150209	0.00972	3.732017	0.59	3.732017
10929727	3.43206	2.66196	U6 spliceosomal RNA	ENSRNOT00000053323	0.586375535	0.00594	4.161051	0.585	4.161051
10764460	5.67644	4.89702	Kcnt2	ENSRNOT00000064223	0.582601011	0.00867	3.828963	0.584	3.828963
10722461	5.45095	4.66746	Small nucleolar RNA SNORD116	ENSRNOT00000053974	0.580957532	0.0117	3.576585	0.57	3.576585
10806506	4.60077	3.64523	LOC685411, F1M023_RAT	ENSRNOT00000041115	0.515648425	0.0104	3.68159	0.58	3.68159
10779233	4.1	3.12999	Spetex-2B	NM_001011697	0.510502815	0.0156	3.341317	0.573	3.341317
10749886	5.26663	4.02582			0.423137248	0.00599	4.154495	0.587	4.154495
10722431	4.55023	3.29539	Small nucleolar RNA SNORD116	ENSRNOT00000052564	0.419038683	0.00799	3.899352	0.593	3.899352
10722421	4.60545	3.17617	Small nucleolar RNA SNORD116	ENSRNOT00000053882	0.371315509	0.0104	3.679809	0.574	3.679809
10722439	4.60545	3.17617	Small nucleolar RNA SNORD116	ENSRNOT00000053882	0.371315509	0.0104	3.679809	0.575	3.679809
10722445	4.60545	3.17617	Small nucleolar RNA SNORD116	ENSRNOT00000053882	0.371315509	0.0104	3.679809	0.57	3.679809
10722447	4.60545	3.17617	Small nucleolar RNA SNORD116	ENSRNOT00000053882	0.371315509	0.0104	3.679809	0.571	3.679809
10722453	4.60545	3.17617	Small nucleolar RNA SNORD116	ENSRNOT00000053882	0.371315509	0.0104	3.679809	0.572	3.679809
10722455	4.60545	3.17617	Small nucleolar RNA SNORD116	ENSRNOT00000053882	0.371315509	0.0104	3.679809	0.573	3.679809
10722457	4.60545	3.17617	Small nucleolar RNA SNORD116	ENSRNOT00000053882	0.371315509	0.0104	3.679809	0.577	3.679809
10722463	4.60545	3.17617	Small nucleolar RNA SNORD116	ENSRNOT00000053882	0.371315509	0.0104	3.679809	0.579	3.679809
10722469	4.60545	3.17617	Small nucleolar RNA SNORD116	ENSRNOT00000053882	0.371315509	0.0104	3.679809	0.578	3.679809
10722477	4.60545	3.17617	Small nucleolar RNA SNORD116	ENSRNOT00000053882	0.371315509	0.0104	3.679809	0.58	3.679809
					n=107				
					n=276				

TableS2-KidneyDevelopment

Number	Gene ID	Fold-Change (HSRA-C vs -S)	P_value	Type Kidney or Urogenital Malformation/ Syndrome
1	Aph1a	1.06	0.004	
2	Arsb	1.14	0.006	
3	Eya1	-1.34	0.003	Kidney development
4	Ezr	1.17	0.009	
5	Fras1	-1.26	0.007	Fraser syndrome 1/CAKUT
6	Glis2	-1.13	0.018	Nephronophthisis/ renal atrophy and fibrosis (Glis2-/-)
7	Igf2	-1.10	0.015	
8	Kiss1	1.23	0.002	Kallman syndrome- unilateral renal agenesis
9	Lama5	-1.16	0.018	nephrogenesis/ PKD
10	Pkd1	-1.14	0.008	PKD
11	Ptcd2	1.08	0.009	
12	Pygo1	-1.25	0.011	nephrogenesis/UB branching
13	Robo2	-1.18	0.010	nephrogenesis/UB branching
14	Smo	-1.11	0.010	CAKUT
15	Smoc2	-1.52	0.009	
16	Sox11	-1.42	0.010	nephrogenesis/UB branching

TableS3-Angiogenesis Genes

Number	Gene ID	Fold-Change (HSRA-C vs -S)	P-value	Angiogenesis
1	Angpt1	1.30	0.0098	Angiopoietins are proteins with important roles in vascular development and angiogenesis.
2	Aph1a	1.06	0.0037	
3	Arhgap24	-1.10	0.0112	
4	Arhgdia	-1.11	0.0037	
5	Atpif1	1.10	0.0186	
6	Cd36	1.08	0.0142	
7	Cdh13	-1.27	0.0144	
8	Cdh5	-1.16	0.0029	
9	Col15a1	-1.35	0.0183	
10	Csf2	1.19	0.0146	
11	Dcn	-1.35	0.0072	decorin plays a role in the formation of new blood vessels (angiogenesis), wound healing, bone development, inflammation,
12	Eya1	-1.34	0.0034	
13	F3	1.45	0.0035	
14	Figf	1.38	0.0167	
15	Foxo1	-1.10	0.0126	
16	Fshr	1.15	0.0189	
17	Hmgb1	1.08	0.0172	
18	Hoxb5	-1.45	0.0000	
19	Hoxd3	-1.17	0.0018	
20	Igf2	-1.10	0.0122	
21	Igf2r	1.18	0.0145	vegfd
22	Il15	-1.20	0.0054	
23	Il19	1.12	0.0042	
24	Lama5	-1.16	0.0180	
25	Mir27a	-1.15	0.0107	
26	Nppa	1.13	0.0196	
27	Nr2f2	-1.14	0.0193	
28	Nrg1	1.18	0.0179	
29	Pgk1	1.23	0.0144	
30	Rcan1	1.47	0.0068	a regulatory protein in the calcineurin/NFAT signal transduction pathway, in vascular morphology to gain further insight into these mechanisms.
31	Rgs5	-1.36	0.0167	
32	Robo4	-1.12	0.0010	RGS5 is an endogenous regulator of Hedgehog-mediated signaling and that RGS proteins are potential targets for novel therapeutics in Hh-mediated diseases.
33	Smoc2	-1.52	0.0097	SMOC2 are matricellular proteins thought to influence growth factor signaling, migration, proliferation, and angiogenesis.
34	Tdg	1.11	0.0073	
35	Tgfbr3	-1.35	0.0123	
36	Vhl	-1.14	0.0159	
37	Yars	1.13	0.0025	
38	Zeb1	-1.10	0.0029	