

Table S1. Genes that are differentially expressed in biopsies of failure-prone Ren2 rats as compared to compensated Ren2 rats

Probe set ID ^a	FC ^b (HF/comp)	FC ^b (comp/contr)	FC ^b (HF/contr)	Ttest ^c (HF,comp)	ttest ^c (comp,contr)	ttest ^c (HF,contr)	Gene name
1383637_at	2.38	-3.06	-1.29	0.000016	0.000007	0.034115	Transcribed sequences
1385381_at	2.28	-1.91	1.20	0.038761	0.138775	0.658911	Transcribed sequences
1390530_at	2.07	-2.07	-1.00	0.025325	0.009386	0.999806	Transcribed sequences
1391387_s_at	2.00	-3.55	-1.77	0.045059	0.000006	0.027763	Transcribed sequences
1394011_at	1.92	-1.59	1.21	0.023178	0.017873	0.464874	Transcribed sequences
1378315_at	1.91	-2.81	-1.47	0.018390	0.000572	0.141974	Transcribed sequence with moderate similarity to protein pdb:1LBG (E. coli) B Chain B, Lactose Operon Repressor
1395036_at	1.83	-1.62	1.13	0.005896	0.023006	0.262097	Similar to Ac2-190 (LOC312952), mRNA
1379740_at	1.82	-1.32	1.38	0.025179	0.090286	0.191486	Transcribed sequences
1379345_at	1.80	-1.68	1.07	0.017815	0.018960	0.664513	Similar to type XV collagen (LOC298069), mRNA
1394419_at	1.73	-1.17	1.48	0.013232	0.391831	0.066245	Similar to RIKEN cDNA 6530401L14 gene (LOC296060), mRNA
1398706_at	1.69	-1.13	1.49	0.012983	0.308701	0.061366	Transcribed sequence with moderate similarity to protein pdb:1LBG (E. coli) B Chain B, Lactose Operon Repressor
1374029_at	1.67	-1.06	1.58	0.005357	0.567933	0.031042	Transcribed sequences
1368429_at	1.66	-1.66	-1.00	0.000959	0.048662	0.997913	TAF9-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31 kD
1398587_at	1.66	-1.83	-1.10	0.011620	0.014845	0.557088	Transcribed sequences
1388527_at	1.66	-1.25	1.33	0.037074	0.190260	0.204989	Transcribed sequences
1392795_at	1.65	-1.18	1.40	0.003974	0.452570	0.155797	Transcribed sequences
1373697_at	1.65	2.16	3.57	0.010724	0.001765	0.001148	Similar to Myosin binding protein C, fast-type (LOC292879), mRNA
1384899_at	1.65	-1.63	1.01	0.020374	0.020346	0.934120	Transcribed sequences
1378614_at	1.64	-1.09	1.51	0.009899	0.717726	0.094550	Transcribed sequences
1376964_at	1.63	-1.20	1.36	0.005509	0.177978	0.032373	Similar to Ofd1 protein (LOC302661), mRNA
1379130_at	1.63	1.12	1.83	0.022482	0.603545	0.025922	Transcribed sequences
1397889_at	1.63	1.01	1.64	0.032654	0.974625	0.081607	Transcribed sequences
1388904_at	1.62	-2.00	-1.24	0.006148	0.000430	0.012235	hypothetical protein
1381556_at	1.62	-1.92	-1.19	0.043902	0.004195	0.439074	Transcribed sequences
1367744_at	1.61	-1.54	1.05	0.006968	0.019714	0.724155	melanoma antigen, family D, 2
1378937_at	1.60	-1.38	1.16	0.038643	0.048431	0.407622	Transcribed sequences
1382183_at	1.59	-1.37	1.16	0.003473	0.002520	0.257826	Transcribed sequences
1369203_at	1.58	-1.06	1.49	0.046910	0.789679	0.124743	Wnt inhibitory factor 1
1389979_at	1.57	-1.08	1.45	0.008233	0.664369	0.166651	Similar to transportin-SR; importin 12 (LOC296954), mRNA
1385326_at	1.55	-1.30	1.19	0.009515	0.143862	0.192234	Similar to 60S RIBOSOMAL PROTEIN L29 (P23) (LOC305052), mRNA
1397676_at	1.53	-1.75	-1.14	0.021689	0.001925	0.495306	Transcribed sequences
1377342_s_at	1.52	1.03	1.57	0.002968	0.811404	0.013940	rapostlin
1386989_at	1.52	-2.23	-1.47	0.048220	0.000377	0.033489	endothelial differentiation, sphingolipid G-protein-coupled receptor, 5
1376704_a_at	1.51	-1.54	-1.02	0.020797	0.015053	0.873952	Similar to mage-g1 (LOC309259), mRNA
1368553_at	1.50	-1.35	1.11	0.001911	0.148546	0.590619	activin A receptor type II-like 1
1392578_at	1.50	-1.19	1.26	0.019991	0.281248	0.209915	matrix Gla protein
1384147_at	1.49	-1.35	1.11	0.011960	0.001260	0.486286	Similar to eIF-1A (LOC317163), mRNA
1386156_at	1.49	-1.76	-1.18	0.025787	0.006253	0.294632	Transcribed sequences
1371566_at	1.48	1.81	2.68	0.014288	0.001446	0.003009	Similar to F-box protein FBL2 (LOC363083), mRNA
1392516_a_at	1.48	-1.20	1.24	0.026032	0.252736	0.076396	Transcribed sequence with moderate similarity to protein sp:P00722 (E. coli) BGAL_ECOLI Beta-galactosidase
1373864_at	1.48	-1.37	1.08	0.027008	0.076428	0.694600	Similar to Traf2 and NCK interacting kinase, splice variant 4 (LOC301363), mRNA
1392778_at	1.48	-3.73	-2.51	0.048926	0.005024	0.047714	Transcribed sequences
1382598_at	1.47	-1.55	-1.05	0.000125	0.000028	0.276510	heat shock factor 2
1392702_at	1.47	-1.23	1.19	0.001133	0.048095	0.014768	Transcribed sequence with weak similarity to protein sp:P16415 (H.sapiens) ZF36_HUMAN Zinc finger protein ZFP-36
1378637_at	1.47	-1.27	1.16	0.015599	0.162289	0.423729	Transcribed sequences
1398479_at	1.47	-2.43	-1.66	0.018770	0.000004	0.002911	Transcribed sequence with strong similarity to protein sp:Q15413 (H.sapiens) RYR3_HUMAN Ryanodine receptor 3
1384824_at	1.47	-1.55	-1.05	0.019924	0.053908	0.788114	Transcribed sequences
1376034_at	1.47	-1.08	1.36	0.031931	0.582794	0.106602	Transcribed sequence with strong similarity to protein ref:NP_055534.1 (H.sapiens)
1384000_at	1.46	-1.09	1.34	0.021094	0.527076	0.135644	Similar to sox-4 protein - mouse (LOC364712), mRNA
1396028_at	1.46	1.00	1.47	0.047853	0.986617	0.053122	Transcribed sequences
1368370_at	1.45	-1.11	1.31	0.010093	0.510775	0.141433	adenylyl cyclase 4
1398355_at	1.45	-1.30	1.12	0.016380	0.000193	0.442462	transient receptor potential-related protein, ChaK
1394605_at	1.45	-1.34	1.09	0.021277	0.069657	0.566168	Transcribed sequence with moderate similarity to protein pdb:1LBG (E. coli) B Chain B, Lactose Operon Repressor
1380393_at	1.45	-2.72	-1.88	0.021715	0.000105	0.002444	Similar to crystallin, zeta (LOC362061), mRNA
1368990_at	1.44	-1.13	1.27	0.023593	0.252290	0.213999	cytochrome P450, subfamily 1B, polypeptide 1
1379866_at	1.44	-1.66	-1.15	0.049391	0.008213	0.458497	Transcribed sequences
1377669_at	1.43	-1.85	-1.29	0.045170	0.000937	0.020055	low Mr GTP-binding protein
1370866_at	1.42	-1.54	-1.09	0.009390	0.000136	0.405982	ribosomal protein L41
1369144_a_at	1.42	-1.05	1.35	0.011685	0.725768	0.085181	potassium voltage gated channel, Shal-related family, member 3
1383154_at	1.42	-1.17	1.21	0.015048	0.086950	0.181894	Similar to SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c2 isoform a
1383730_at	1.42	-1.05	1.35	0.038985	0.744846	0.151871	Similar to hypothetical protein (LOC309196), mRNA
1373077_at	1.41	-1.10	1.28	0.010766	0.246646	0.075495	Similar to hypothetical protein D11Erd497e (LOC287278), mRNA
1370397_at	1.41	-1.29	1.09	0.049573	0.113588	0.667928	cytochrome P450, family 4, subfamily a, polypeptide 3
1368356_a_at	1.40	-1.47	-1.05	0.016812	0.025585	0.678705	leucyl-specific aminopeptidase PILS
1384112_at	1.40	-1.13	1.23	0.037457	0.091115	0.224045	5 nucleotidase
1373263_at	1.39	-1.46	-1.05	0.019257	0.021054	0.661030	Similar to RIKEN cDNA 5730436H21 (LOC309192), mRNA
1392422_at	1.39	-1.35	1.03	0.020023	0.026127	0.780475	Similar to Disrupted in bipolar disorder 1 homolog (LOC367083), mRNA

1389074_at	1.38	-1.22	1.13	0.000261	0.186895	0.395762	Similar to mKIAA0769 protein (LOC308864), mRNA
1375358_at	1.38	-1.45	-1.05	0.005373	0.008663	0.671917	Transcribed sequence with moderate similarity to protein pdb:1LBG (E. coli) B Chain B, Lactose Operon Repressor
1389203_at	1.38	1.10	1.52	0.011345	0.354287	0.019944	Similar to cDNA sequence BC003251 (LOC363604), mRNA
1372789_at	1.37	-1.46	-1.07	0.005190	0.007791	0.584783	zinc finger protein 1
1373673_at	1.37	-1.06	1.29	0.020481	0.622614	0.108849	Transcribed sequence with moderate similarity to protein sp:P01903 (H.sapiens) HA2R_HUMAN HLA class II histocompatibility antigen, DR alpha chain precursor
1388618_at	1.37	-1.35	1.02	0.023760	0.110108	0.902310	Similar to Nidogen 2 (LOC302248), mRNA
1384453_at	1.37	1.03	1.41	0.023991	0.859288	0.026672	Transcribed sequences
1393361_at	1.37	-1.15	1.20	0.036569	0.377803	0.064446	Similar to chromosome 16 open reading frame 33; minus -99 protein (LOC287170), mRNA
1376213_at	1.37	-1.15	1.19	0.040025	0.369804	0.342365	Transcribed sequences
1397750_at	1.36	-1.70	-1.24	0.002114	0.010715	0.273616	Transcribed sequence with moderate similarity to protein pdb:1LBG (E. coli) B Chain B, Lactose Operon Repressor
1368323_at	1.36	-1.48	-1.09	0.005690	0.002562	0.314936	tissue factor pathway inhibitor
1379431_at	1.36	-1.26	1.08	0.010603	0.074062	0.502835	Transcribed sequences
1393251_at	1.36	-1.24	1.09	0.028133	0.138487	0.452779	Transcribed sequence with moderate similarity to protein sp:P00722 (E. coli) BGAL_ECOLI Beta-galactosidase
1387195_at	1.36	-1.53	-1.13	0.037324	0.007647	0.231288	suppression of tumorigenicity 14
1395327_at	1.35	2.17	2.94	0.011445	0.000090	0.000516	Lysosomal integral membrane protein-2
1372476_at	1.35	1.32	1.79	0.011648	0.001426	0.002928	putative fatty acid desaturase
1390885_at	1.35	-1.33	1.01	0.013787	0.080336	0.903876	Transcribed sequences
1378094_at	1.35	1.23	1.65	0.013973	0.116445	0.000014	Similar to RIKEN cDNA C820004H04 (LOC360713), mRNA
1375573_at	1.35	1.21	1.64	0.018458	0.089383	0.003872	Transcribed sequences
1372237_at	1.35	-2.05	-1.51	0.024551	0.000812	0.016987	Transcribed sequences
1379296_at	1.35	-1.50	-1.11	0.034045	0.004441	0.414585	Transcribed sequences
1371166_at	1.34	1.11	1.49	0.003104	0.096521	0.003422	nitric oxide synthase 3, endothelial cell
1378842_at	1.34	1.07	1.43	0.015999	0.653300	0.027479	Similar to gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1; GABA(A) receptor-associated protein like 1 (LOC297644), mRNA
1368712_at	1.34	-1.57	-1.18	0.019867	0.000250	0.223913	zinc finger protein 386 (Kruppel-like)
1374546_at	1.34	-1.37	-1.02	0.023989	0.059455	0.871380	Transcribed sequences
1389353_at	1.34	-1.17	1.15	0.025431	0.272603	0.222666	Transcribed sequences
1385553_at	1.34	1.00	1.35	0.028651	0.983207	0.050788	Similar to KIAA2010 protein (LOC314388), mRNA
1377723_at	1.34	-1.86	-1.39	0.031103	0.000070	0.036944	Transcribed sequences
1374247_at	1.33	-1.06	1.25	0.004181	0.578495	0.135708	Similar to stabilin-1 (LOC290559), mRNA
1393694_at	1.33	-1.42	-1.06	0.014451	0.015288	0.480561	Transcribed sequences
1398455_at	1.33	-1.01	1.32	0.028137	0.906149	0.069972	Similar to putative NFkB activating protein (LOC365252), mRNA
1381279_at	1.33	-1.29	1.03	0.039071	0.022327	0.814412	Similar to receptor-interacting protein 2 (LOC362491), mRNA
1383599_at	1.33	-1.48	-1.11	0.045720	0.000251	0.442543	Similar to retinoblastoma-binding protein mRbAp48 (LOC313048), mRNA
1387887_at	1.33	-1.30	1.02	0.046774	0.062744	0.891164	ribosomal protein L14
1367715_at	1.33	1.48	1.96	0.046931	0.027744	0.001522	tumor necrosis factor receptor superfamily, member 1a
1371295_at	1.33	-1.32	1.01	0.047771	0.053393	0.957744	Similar to 40S ribosomal protein S20 (LOC367130), mRNA
1379251_at	1.32	-1.34	-1.01	0.021646	0.022239	0.904436	Transcribed sequences
1385798_at	1.32	-2.17	-1.65	0.032402	0.000093	0.000961	Transcribed sequences
1369633_at	1.32	-1.83	-1.39	0.040950	0.000016	0.031232	chemokine (C-X-C motif) ligand 12
1379258_at	1.31	-1.29	1.02	0.003568	0.027712	0.880455	Similar to KLHL5 protein (LOC305351), mRNA
1389214_at	1.31	-1.13	1.17	0.016042	0.259998	0.031816	Similar to Lama4 protein (LOC309816), mRNA
1381612_at	1.31	-1.25	1.05	0.016541	0.050870	0.630886	Transcribed sequences
1393613_at	1.31	-1.10	1.19	0.019765	0.575825	0.348615	Transcribed sequences
1383011_at	1.31	-1.46	-1.12	0.029704	0.000725	0.296630	Transcribed sequence with moderate similarity to protein ref:NP_114414.1 (H.sapiens) CDA02 protein [Homo sapiens]
1380190_at	1.31	1.03	1.35	0.045659	0.851562	0.127638	coagulation factor VIII
1393309_at	1.31	-1.15	1.14	0.047422	0.142669	0.358057	Transcribed sequences
1389569_at	1.30	-1.27	1.03	0.003310	0.006347	0.750814	Similar to BRIX (LOC294799), mRNA
1383147_at	1.30	-1.46	-1.12	0.007386	0.001946	0.228673	Transcribed sequences
1398454_at	1.30	-1.15	1.13	0.010322	0.205374	0.201145	Transcribed sequences
1388393_at	1.30	-1.00	1.29	0.038651	0.964748	0.037263	proteolipid protein 2
1395978_at	1.30	-1.31	-1.01	0.048396	0.030554	0.946955	Transcribed sequences
1371958_at	-1.30	1.26	-1.03	0.026599	0.105909	0.888711	Similar to polymyositis scleroderma overlap syndrome (PM-SCL) antigen 1 a (LOC294975), mRNA
1369084_a_at	-1.30	1.35	1.03	0.029031	0.001318	0.811259	Bcl-2-related ovarian killer protein
1389230_at	-1.30	-2.35	-3.07	0.033563	0.000232	0.001053	Similar to hypothetical protein CLONE24945 (LOC309945), mRNA
1374495_at	-1.31	1.46	1.12	0.001661	0.003671	0.409206	Similar to LBA (LOC310700), mRNA
1379754_at	-1.31	1.89	1.44	0.009238	0.000038	0.012183	Transcribed sequences
1385016_at	-1.31	1.27	-1.03	0.022694	0.066800	0.853863	Transcribed sequences
1393146_at	-1.31	1.06	-1.23	0.031971	0.536894	0.133001	Transcribed sequences
1379628_at	-1.31	-1.25	-1.65	0.038042	0.023836	0.000323	Transcribed sequences
1389516_at	-1.31	1.32	1.01	0.039329	0.067901	0.950904	Transcribed sequences
1395707_at	-1.31	1.06	-1.24	0.043588	0.571976	0.167018	Transcribed sequence with strong similarity to protein sp:P00722 (E. coli) BGAL_ECOLI Beta-galactosidase
1380800_at	-1.31	1.39	1.06	0.044827	0.005958	0.656435	Transcribed sequences
1370163_at	-1.32	2.03	1.54	0.008418	0.000037	0.002023	ornithine decarboxylase 1
1373407_at	-1.32	1.02	-1.29	0.017381	0.805660	0.002727	Transcribed sequences
1392447_at	-1.32	1.24	-1.06	0.023536	0.068761	0.610873	Transcribed sequences
1393482_at	-1.32	1.64	1.24	0.034356	0.005353	0.176539	Transcribed sequences
1394968_at	-1.32	-1.13	-1.50	0.037157	0.375181	0.036809	Similar to PHD-like zinc finger protein (LOC363505), mRNA
1367759_at	-1.33	1.11	-1.20	0.013588	0.214608	0.073372	H1 histone family, member 0
1387390_at	-1.33	-1.20	-1.59	0.041035	0.155836	0.009081	granzyme K
1377768_at	-1.34	1.01	-1.32	0.033799	0.919178	0.028180	vitamin A-deficient testicular protein 5

1397528_at	-1.34	-1.10	-1.48	0.036546	0.425735	0.013897	Similar to splicing factor, arginine/serine-rich 2, interacting protein; SC35-interacting protein 1 (LOC312030), mRNA
1387074_at	-1.34	-1.14	-1.53	0.049955	0.397725	0.133771	regulator of G-protein signaling protein 2
1393485_at	-1.35	1.67	1.23	0.007134	0.001521	0.103821	Transcribed sequences
1389045_at	-1.35	1.33	-1.01	0.018779	0.054177	0.945951	Transcribed sequences
1368003_at	-1.35	-1.25	-1.70	0.030600	0.216713	0.059724	aldehyde dehydrogenase family 1, subfamily A2
1379668_at	-1.35	1.08	-1.25	0.033118	0.354322	0.119877	Similar to CG11306-PA (LOC361174), mRNA
1385586_at	-1.36	1.03	-1.32	0.000112	0.724635	0.035235	Transcribed sequences
1397686_at	-1.36	-1.16	-1.57	0.026248	0.098134	0.006994	Transcribed sequences
1389246_at	-1.37	1.92	1.40	0.027713	0.000715	0.017520	Transcribed sequence with moderate similarity to protein ref:NP_001488.2 (H.sapiens) UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase 1, membrane-bound form
1372873_at	-1.37	1.03	-1.32	0.035613	0.768886	0.010294	Hypothetical LOC307390 (LOC307390), mRNA
1388793_at	-1.38	1.31	-1.05	0.011781	0.063892	0.767053	Similar to N-acetylglucosaminyl transferase component Gpi1 (LOC287159), mRNA
1372176_at	-1.38	1.43	1.03	0.032545	0.011018	0.801850	protein kinase C, alpha
1389101_at	-1.38	-1.40	-1.94	0.033775	0.051641	0.012396	cyclin C
1382104_at	-1.39	1.21	-1.15	0.037929	0.187066	0.108131	Similar to putative WDC146 (LOC307524), mRNA
1397029_at	-1.39	1.21	-1.16	0.038761	0.143341	0.316478	Transcribed sequences
1372025_at	-1.40	1.20	-1.17	0.003353	0.209015	0.469337	Transcribed sequences
1377411_at	-1.40	1.24	-1.13	0.033902	0.253515	0.597597	Transcribed sequences
1393164_at	-1.41	-1.04	-1.46	0.006700	0.853807	0.273590	Similar to mitochondrial ribosomal protein S27; mitochondrial 28S ribosomal protein S27 (LOC361883), mRNA
1387234_at	-1.41	1.19	-1.18	0.030396	0.136990	0.320342	alpha-2-glycoprotein 1, zinc
1379295_at	-1.42	-1.08	-1.53	0.028599	0.632766	0.053750	Transcribed sequence with moderate similarity to protein ref:NP_113686.1 (H.sapiens) guanine nucleotide binding protein-gamma transducing activity polypeptide 2; gamma-T2 subunit; G protein cone gamma 8 subunit [Homo sapiens]
1370160_at	-1.43	1.65	1.16	0.043886	0.016068	0.153111	cytoplasmic aminopeptidase P
1390042_at	-1.45	1.97	1.36	0.031023	0.006672	0.078402	Similar to 1110007F12Rik protein (LOC362334), mRNA
1395349_at	-1.45	1.70	1.18	0.037616	0.012296	0.520314	Transcribed sequences
1372248_at	-1.46	-1.94	-2.83	0.037788	0.001987	0.002246	Similar to Sestrin 1 (p53-regulated protein PA26) (LOC294518), mRNA
1379418_at	-1.48	1.10	-1.35	0.006891	0.401710	0.058057	Transcribed sequences
1379592_at	-1.48	1.23	-1.21	0.047814	0.301792	0.423305	Similar to Calcium-binding mitochondrial carrier protein Aralar2 (Solute carrier family 25, member 13) (Citrin) (LOC296855), mRNA
1371776_at	-1.48	-1.37	-2.04	0.049236	0.339359	0.169994	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1
1385017_at	-1.50	1.44	-1.05	0.029697	0.135366	0.912817	Similar to Zinc finger protein 70 (Zinc finger protein N27C7-1) (LOC311303), mRNA
1376484_at	-1.52	1.72	1.13	0.005431	0.000754	0.500198	Transcribed sequences
1392299_at	-1.52	1.07	-1.41	0.019570	0.614400	0.107575	C-terminal PDZ domain ligand of neuronal nitric oxide synthase
1384131_at	-1.55	1.29	-1.20	0.044024	0.124015	0.302209	Similar to ARL6IP2 (LOC298757), mRNA
1397687_at	-1.56	1.32	-1.18	0.013440	0.050806	0.485139	Transcribed sequences
1369639_at	-1.62	1.60	-1.01	0.017843	0.037970	0.973466	gap junction membrane channel protein alpha 1
1376467_at	-1.62	1.33	-1.22	0.025023	0.116420	0.088712	Similar to leukemia associated gene protein (LOC301119), mRNA
1378199_at	-1.67	-2.33	-3.88	0.037125	0.000668	0.000696	Transcribed sequence with moderate similarity to protein sp:P00722 (E. coli) BGAL_ECOLI Beta-galactosidase
1387876_at	-1.68	1.49	-1.12	0.045175	0.103465	0.559897	signal transducer and activator of transcription 5B
1398393_at	-1.69	1.30	-1.29	0.016153	0.072280	0.342048	Transcribed sequences
1397993_at	-1.70	1.54	-1.10	0.038348	0.120177	0.744743	Transcribed sequences
1377297_at	-1.71	1.21	-1.41	0.012174	0.218315	0.097241	Similar to HSPC182 protein (LOC298681), mRNA
1393163_at	-1.72	1.57	-1.10	0.020595	0.016121	0.741572	Transcribed sequences
1380564_at	-1.75	1.30	-1.34	0.013096	0.126405	0.172063	LOC360567 (LOC360567), mRNA
1383457_at	-1.77	1.78	1.01	0.004783	0.005447	0.967851	Transcribed sequences
1374120_at	-1.85	1.09	-1.69	0.000148	0.366340	0.013336	Transcribed sequences
1385205_at	-1.87	-5.66	-10.56	0.017596	0.000000	0.000002	Transcribed sequences
1381396_s_at	-1.92	-1.20	-2.31	0.003745	0.441159	0.065123	Kruppel-like factor 15

^aProbe Set ID, Affymetrix probe set number (www.affymetrix.com).

^bFC, fold change.

^ctest, *t* test with $P < 0.05$ considered statistically significant.

Table S2. Left ventricular weights and hemodynamic parameters in LIMP-2 KO and WT mice at baseline, and after 14 and 28 days of AngII treatment

		Baseline	Day 14	Day 28
LV mass index (mg/g) 14 d	KO (<i>n</i> = 4)	3.7 ± 0.1	4.0 ± 0.1 ^a	na
	WT (<i>n</i> = 5)	3.5 ± 0.2	4.6 ± 0.2	na
LV mass index (mg/g) 28 d	KO (<i>n</i> = 11)	3.9 ± 0.1	na	4.4 ± 0.2 ^b
	WT (<i>n</i> = 10)	4.2 ± 0.2	na	5.5 ± 0.3 ^c
Dfp/sys 14 d AngII (mmHg/s)	KO (<i>n</i> = 4)	62.6 ± 6.5	60.9 ± 6.2 ^b	na
	WT (<i>n</i> = 5)	61.1 ± 4.6	114.5 ± 10.1*	na
Dfp/sys 28 d AngII (mmHg/s)	KO (<i>n</i> = 11)	72.5 ± 1.8	na	77.9 ± 6.4
	WT (<i>n</i> = 10)	74.0 ± 2.1	na	87.6 ± 3.6 ^c

Echocardiographic parameters in LIMP-2 KO and WT mice at baseline, and after 7, 10, 14, and 28 d of AngII treatment

		Baseline	Day 7	Day 10	Day 14	Day 28
IVSd ^d (cm)	KO (<i>n</i> = 11)	0.10 ± 0.00	0.09 ± 0.00 ^{a,c}	0.09 ± 0.01	0.10 ± 0.01 ^a	0.10 ± 0.01 ^b
	WT (<i>n</i> = 10)	0.10 ± 0.01	0.10 ± 0.00	0.11 ± 0.00	0.13 ± 0.01	0.13 ± 0.00 ^c
LVIDd ^d (cm)	KO (<i>n</i> = 11)	0.34 ± 0.01	0.35 ± 0.01 ^a	0.37 ± 0.00 ^{a,c}	0.38 ± 0.01 ^{b,c}	0.38 ± 0.01 ^{b,c}
	WT (<i>n</i> = 10)	0.34 ± 0.01	0.31 ± 0.01	0.32 ± 0.01	0.33 ± 0.02	0.33 ± 0.01
LVPWd ^d (cm)	KO (<i>n</i> = 11)	0.10 ± 0.01	0.09 ± 0.00 ^a	0.10 ± 0.00 ^a	0.09 ± 0.01 ^b	0.09 ± 0.00 ^b
	WT (<i>n</i> = 10)	0.10 ± 0.00	0.13 ± 0.01	0.16 ± 0.01	0.15 ± 0.01	0.15 ± 0.01 ^c
LVAd ^e (cm)	KO (<i>n</i> = 11)	0.21 ± 0.01	na	na	0.27 ± 0.01 ^{b,c}	0.28 ± 0.02 ^{a,c}
	WT (<i>n</i> = 10)	0.21 ± 0.01	na	na	0.23 ± 0.01	0.22 ± 0.00
LVLd ^e (cm)	KO (<i>n</i> = 11)	0.73 ± 0.01	na	na	0.85 ± 0.02 ^{a,c}	0.84 ± 0.03 ^{a,c}
	WT (<i>n</i> = 10)	0.73 ± 0.01	na	na	0.79 ± 0.02 ^c	0.79 ± 0.02 ^c
FS ^d (%)	KO (<i>n</i> = 11)	28.7 ± 1.9	27.4 ± 2.6	27.6 ± 2.3	20.1 ± 3.1	22.2 ± 3.0
	WT (<i>n</i> = 10)	27.4 ± 2.1	30.5 ± 1.7	31.1 ± 2.9	25.8 ± 1.9	25.5 ± 2.9

Averages ± SEM

^aP < 0.05 versus age-matched WT.

^bP < 0.001 versus age-matched WT.

^cP < 0.005 versus baseline KO or WT.

^dMeasured from short axis: IVSd, interventricular septum in diastole; LVIDd, left ventricular inner diameter in diastole; LVPWd, left ventricular posterior wall thickness in diastole; FS (%), percentage of fractional shortening.

^eMeasured from long axis: LVAd, left ventricular area in diastole; LVLd, left ventricular length in diastole.