

Supplemental Table 3. Expression for probe sets identified as differentially expressed in right ventricle of ligated hearts versus normal right ventricle.

Gene Annotation			Expression Data (log2) for all right ventricle samples										Comparison Data				
Symbol	Title	Probe Set ID	E6_RVa	E6_RVb	E8_RVa	E8_RVb	E8_RV_LaLa	E8_RV_LaLb	E10_RVa	E10_RVb	Mean (log2)	Present call (%)	Mean Difference (RV-LAL minus RV)	Fold Difference	P value		
---	---	AY013303.CDS2.S1_s_at	7.57	7.63	7.75	7.81	4.58	4.58	8.17	8.16	7.78	100	0	-3.2	-9.2	0.006	
---	---	AY013303.CDS3.S1_s_at	6.91	6.76	8.43	7.88	4.07	3.92	8.13	7.42	8.15	100	0	-4.16	-17.9	0.030	
SERPIN2	serpin peptidase inhibitor, clade B (ovalbumin), member 2	Gga.10034.1.S1_at	3.57	3.55	2.88	2.64	5.86	5.62	2.95	2.82	2.76	50	100	2.98	7.9	0.003	
---	---	Gga.10658.1.S1_at	8.9	8.76	6.17	6.49	8.46	8.32	5.23	4.65	6.33	100	100	2.06	4.2	0.023	
FZD7	frizzled homolog 7 (Drosophila)	Gga.110.1.S2_at	4.85	4.84	2.71	2.77	4.97	4.86	2.68	2.68	2.74	0	100	2.18	4.5	0.004	
KCTD3	potassium channel tetramerisation domain containing 3	Gga.11487.1.S1_s_at	7.36	7.36	5.12	5.09	7.54	7.69	6.19	5.48	5.1	100	100	2.51	5.7	0.015	
---	---	Gga.11496.1.S1_at	2.64	2.62	2.9	2.69	6.22	5.87	2.78	2.74	2.8	100	100	3.25	9.5	0.008	
---	---	Gga.12554.2.S1_a_at	7.08	6.88	7.74	7.71	5.53	5.41	8.49	8.34	7.72	100	0	-2.25	-4.8	0.010	
---	---	Gga.12631.1.S1_at	5.7	5.89	7.16	7.4	4.4	4.86	7.06	6.48	7.28	100	100	-2.65	-6.3	0.024	
LRCH2	leucine-rich repeats and calponin homology (CH) domain containing 2	Gga.13393.1.S1_s_at	6.93	6.63	4.48	4.57	7.93	7.77	3.55	3.99	4.52	100	100	3.33	10.1	0.003	
TTN	Titin	Gga.13915.1.S1_at	6.81	6.49	4.58	4.65	7.04	6.86	4.29	4.44	4.61	50	100	2.34	5.1	0.011	
SYNE2	spectrin repeat containing, nuclear envelope 2	Gga.15111.1.S1_s_at	5.02	5.09	3	2.88	4.99	4.95	2.84	3.03	2.94	100	100	2.03	4.1	0.009	
GNG11	guanine nucleotide binding protein (G protein), gamma 11	Gga.15320.1.S1_at	7.03	7.23	6.52	6.96	9.06	8.79	5.78	5.6	6.74	100	100	2.18	4.5	0.023	
---	---	Gga.15807.1.S1_at	8.19	8.09	6.24	6.3	8.43	8.17	6.25	6.54	6.27	100	100	2.03	4.1	0.035	
YTHDC1	YTH domain containing 1	Gga.16032.1.A1_at	2.64	2.64	5.6	5.63	2.62	2.64	4.38	4.85	5.62	100	100	-2.99	-7.9	0.000	
GLUD1	glutamate dehydrogenase 1	Gga.16450.1.S1_at	7.65	7.66	4.23	4.49	7.58	7.48	4.45	4.21	4.36	100	100	3.17	9.0	0.011	
---	---	Gga.16858.2.S1_a_at	11	11.07	9.23	9.29	11.66	11.76	8.89	8.72	9.26	100	100	2.45	5.5	0.002	
SYNE2	spectrin repeat containing, nuclear envelope 2	Gga.17077.1.S1_s_at	8.32	8.12	4.84	4.91	8.6	9.03	4.6	4.97	4.88	0	100	3.94	15.3	0.031	
GLIS2	GLIS family zinc finger 2	Gga.177.1.S1_at	3.84	3.71	2.26	2.23	4.55	4.25	2.23	2.24	2.24	4.4	100	2.16	4.5	0.042	
HERC2	hect domain and RLD 2	Gga.17764.1.S1_s_at	8.26	7.99	6.75	6.39	8.82	8.87	6.19	5.95	6.57	100	100	2.28	4.9	0.046	
BCKDHA	branched chain keto acid dehydrogenase E1, alpha polypeptide	Gga.188.1.S1_at	7.63	7.35	9.1	8.96	6.88	6.54	9.6	9.5	9.03	100	0	-2.32	-5.0	0.023	
ACOT9	acyl-CoA thioesterase 9	Gga.19408.1.S1_s_at	8.7	8.91	9.15	9.29	6.8	6.32	7.94	8.1	9.22	100	100	-2.66	-6.3	0.042	
---	---	Gga.19442.1.S1_at	7.4	7.73	8.8	8.82	6.39	6.49	9.14	8.93	8.81	100	100	-2.37	-5.2	0.012	
TTN	titin	Gga.19481.6.S1_at	9.29	9.07	6.87	6.75	10.22	10.34	6.38	6.46	6.81	100	100	3.47	11.1	0.001	
---	---	Gga.19967.1.S1_at	7.73	7.9	8.63	8.73	6.62	6.58	9.36	8.68	6.6	100	100	-2.08	-4.2	0.009	
GRB2	growth factor receptor-bound protein 2	Gga.2170.1.S1_at	8.93	9.2	6.47	6.12	8.48	8.6	6.58	6.85	6.29	50	100	2.25	4.8	0.032	
LMO4	LIM domain only 4	Gga.2310.1.S1_at	8.23	8.24	6.1	6.5	9.02	8.87	6.28	6.08	6.3	100	100	2.65	6.3	0.027	
---	---	Gga.2341.2.S1_at	4.12	3.94	5.99	6.18	3.78	3.66	5.88	5.63	6.08	100	100	-2.36	-5.1	0.005	
---	---	Gga.2501.1.A1_at	4.92	4.73	7.35	7.51	5.09	5.29	8.31	8.32	7.43	100	100	-2.24	-4.7	0.004	
NOV	nephroblastoma overexpressed gene	Gga.2587.1.S1_at	5.02	5.05	6.98	6.79	9.48	9.45	6.68	6.45	6.88	100	100	2.59	6.0	0.021	
ACVR1	activin A receptor, type I	Gga.2875.2.S1_a_at	8.06	8.02	9.02	9.04	6.49	6.39	9.18	9.1	9.03	100	100	-2.59	-6.0	0.009	
HOXA3	homeobox A3	Gga.3381.1.S2_at	5.48	5.73	4.2	3.97	6.32	6.19	3.21	3.25	4.08	100	100	2.17	4.5	0.008	
SERPINB10	serpin peptidase inhibitor, clade B (ovalbumin), member 10	Gga.415.1.S1_at	1.47	1.49	1.98	2.1	4.53	4.9	3.73	3.82	2.04	100	100	2.68	6.4	0.026	
ALB	albumin	Gga.4510.1.S1_a_at	3.89	3.91	4.79	4.34	8.78	8.52	6.55	6.55	4.56	100	100	4.09	17.0	0.010	
HRSPT12	heat-responsive protein 12	Gga.4700.1.S1_a_at	7.46	7.39	5.57	5.1	7.77	7.57	6.57	6.76	5.34	100	100	2.34	5.1	0.034	
LOC395914	lymphotactin	Gga.542.1.S1_at	7.14	6.96	3.56	3.71	5.65	5.71	7.58	7.24	3.63	100	100	2.05	4.1	0.008	
CABC1	chaperone, ABC1 activity of bc1 complex homolog (S. pombe)	Gga.6127.2.S1_a_at	8.22	8.2	9.32	9.37	7.34	7.23	9.81	9.53	9.35	100	100	-2.06	-4.2	0.005	
PAK4	p21(CDKN1A)-activated kinase 4	Gga.6761.1.S1_at	5.77	5.91	7.55	7.52	4.39	4.35	8.2	8.32	7.53	100	100	-3.16	-8.9	0.000	
---	---	Gga.6808.1.A1_at	8.16	7.9	8.85	9.25	6.86	6.56	9.54	9.37	9.05	100	100	-2.35	-5.1	0.014	
LOC420301	similar to stem cell antigen 2	Gga.7004.1.S1_at	4.89	5.17	4.07	4.29	8.09	7.83	7.45	7.08	4.18	100	100	3.78	13.7	0.002	
NDUFA12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	Gga.7183.1.S1_at	4.19	3.94	2.98	2.59	5.65	5.38	4.21	3.94	2.79	100	100	2.73	6.6	0.012	
LOC396260	mature avidin	Gga.729.1.S1_at	2.33	2.29	2.28	2.28	7.54	7.3	2.3	2.32	2.28	0	100	5.14	35.3	0.015	
---	---	Gga.8578.1.S1_at	5.87	5.72	3.42	3.7	6.3	6.15	2.34	2.78	3.56	100	100	2.66	6.3	0.010	
---	---	Gga.867.1.S1_at	9.91	9.96	9.9	9.87	7.62	7.53	9.12	9.09	9.88	100	100	-2.31	-5.0	0.006	
GIT1	G protein-coupled receptor kinase interactor 1	Gga.921.1.S1_at	5.57	6.26	6.58	6.83	3.89	3.73	6.92	7.08	6.7	100	100	-2.89	-7.4	0.006	
ATRX	alpha thalassemia/mental retardation syndrome X-linked	Gga.9668.1.S1_s_at	8.45	8.35	5.62	5.87	8.37	8.38	5.16	5.26	5.75	100	100	2.63	6.2	0.030	
TSPAN7	tetraspanin 7	Gga.9700.4.S1_a_at	8.43	8.61	10.16	10.18	7.98	7.9	10.27	10.33	10.17	100	100	-2.23	-4.7	0.007	
UMPS	uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)	GgaAffx.11425.1.S1_at	7.53	7.49	6.81	6.35	8.83	9.02	8.21	8.11	6.58	0	100	2.35	5.1	0.036	
KIAA0692	KIAA0692	GgaAffx.1423.1.S1_at	4.82	5.5	6.83	6.6	4.73	4.24	6.78	6.99	6.72	100	100	-2.23	-4.7	0.038	
ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	GgaAffx.1852.2.S1_s_at	4.77	5.33	7.52	7.55	5.31	5.16	7.77	7.99	7.53	100	100	-2.3	-4.9	0.018	
LOC418543	hypothetical gene supported by BX933825; CR407341	GgaAffx.20268.1.S1_s_at	11.64	11.66	7.67	7.84	10.98	10.84	4.31	4.33	7.76	100	100	3.16	8.9	0.002	
MGA	MAX gene associated	GgaAffx.22659.1.S1_at	3.19	3.59	4.5	4.42	2.3	2.59	4.63	4.47	4.46	0	100	-2.01	-4.0	0.033	
KLHL23	kelch-like 23 (Drosophila)	GgaAffx.23021.2.S1_s_at	7.26	6.6	6.65	6.54	8.73	8.63	7.05	6.92	6.59	100	100	2.09	4.3	0.001	
LOC423125 /// LOC768811	similar to scavenger receptor cysteine-rich type 1 protein CD163c-alpha /// similar to scavenger receptor cysteine-rich type 1 protein CD163c-alpha	GgaAffx.23339.2.S1_s_at	6.43	6.1	5.38	5.55	7.7	7.34	6.32	5.64	5.47	50	100	2.05	4.1	0.025	
FAM44A	family with sequence similarity 44, member A	GgaAffx.24441.1.S1_s_at	8.35	8.71	5.43	5.72	8.37	8.73	4.77	4.83	5.57	100	100	2.98	7.9	0.007	
---	---	GgaAffx.24621.1.S1_at	7.85	7.69	8.5	8.54	6.14	6.03	8.9	8.61	8.52	100	100	-2.44	-5.4	0.008	

FBXO3	F-box protein 3	GgaAffx.4835.1.S1_at	5.49	5.39	3.77	4.38	7.83	8.15	3.82	3.63	4.08	7.99	100	100	3.92	15.1	0.019
STEAP4	STEAP family member 4	GgaAffx.5682.1.S1_at	8.47	8.37	4.95	5.45	7.73	7.39	3.18	3.5	5.2	7.56	100	100	2.36	5.1	0.023
STEAP4	STEAP family member 4	GgaAffx.5682.2.S1_s_at	7.52	7.78	4.35	4.2	7.38	6.96	2.4	2.35	4.28	7.17	100	100	2.89	7.4	0.028
AKAP9	A kinase (PRKA) anchor protein (votiao) 9	GgaAffx.5870.1.S1_at	5.78	6.15	3.25	3.22	6.2	5.88	3.29	3.37	3.24	6.04	50	100	2.8	7.0	0.035
MMRN1	multimerin 1	GgaAffx.6568.1.S1_at	2.14	2.14	5.35	5.46	3.17	3.41	7.04	6.8	5.41	3.29	100	50	-2.11	-4.3	0.014
ZNF238	zinc finger protein 238	GgaAffx.6764.1.S1_at	7.82	7.78	7.95	8	5.38	5.37	7.95	7.91	7.97	5.38	100	100	-2.59	-6.0	0.004
CCNK	cyclin K	GgaAffx.7070.1.S1_s_at	3.96	4.12	5.95	5.77	3.37	2.93	6.45	6.46	5.86	3.15	100	100	-2.71	-6.5	0.029
SLC39A8	solute carrier family 39 (zinc transporter), member 8	GgaAffx.7796.1.S1_at	7.84	7.75	4.07	4.29	6.85	6.84	3	3.72	4.18	6.84	100	100	2.66	6.3	0.026
SUV39H2	suppressor of variegation 3-9 homolog 2 (Drosophila)	GgaAffx.8847.1.S1_at	6.11	6.09	3.55	4.01	6.21	5.89	4.25	2.92	3.78	6.05	0	100	2.27	4.8	0.021
CENTD1	centaurin, delta 1	GgaAffx.9098.1.S1_at	8.01	8.17	7.58	7.64	4.25	3.94	6.4	6.64	7.61	4.1	100	100	-3.51	-11.4	0.024

Abbreviations: RV, left ventricle; LAL, Left atrial ligation; "a" and "b" for RV samples indicate technical replicates.