

Supplemental Table 2. Expression data for probe sets identified as differentially expressed in left ventricle of ligated hearts versus normal left ventricle.

Gene Annotation		Expression Data (log2) for all left ventricle samples										Comparison Data					
Symbol	Title	probe set	E6_LVa	E6_LVb	E8_LVa	E8_LVb	E8_LV_LaLa	E8_LV_LALb	E10_LVa	E10_LVb	Mean (log2)		Present call (%)		Mean Difference	Fold Difference	P value
											E8-LV	E8-LV-LAL	E8-LV	E8-LV-LAL	(LV-LAL minus LV)		
---	---	AY013303.CDS1.S1_s_at	10.01	9.93	11.75	11.8	8.87	8.83	11.22	11.22	11.77	8.85	100	100	-2.92	-7.6	0.000
SERPIN2	serpin peptidase inhibitor, clade B (ovalbumin), member 2	Gga.10034.2.S1_a_at	2.73	2.79	2.7	2.72	5	4.76	2.72	2.68	2.71	4.88	50	100	2.17	4.5	0.034
FBLN5	fibulin 5	Gga.10096.1.S1_at	5.86	5.42	6.3	6.14	8.7	8.62	5.76	5.23	6.22	8.66	100	100	2.44	5.4	0.005
SERPINA10	serpin peptidase inhibitor, clade A (alpha-1 antitrypsin, antitrypsin), member 10	Gga.10644.1.S1_at	2.64	2.65	2.6	2.55	5.44	5.05	2.58	2.55	2.58	5.25	0	100	2.67	6.4	0.043
---	---	Gga.10720.1.S1_at	4.86	4.65	5.75	5.88	8.47	8.26	7.86	8.09	5.82	8.36	100	100	2.55	5.9	0.005
FZD7	frizzled homolog 7 (Drosophila)	Gga.110.1.S2_at	3.11	2.99	2.69	2.91	5.08	5.28	2.66	2.64	2.8	5.18	100	100	2.38	5.2	0.004
---	---	Gga.11602.1.S1_at	6.04	5.33	5.05	5.18	8.52	8.82	5.23	5.74	5.12	8.67	0	100	3.55	11.7	0.010
FGG	fibrinogen gamma chain	Gga.1165.1.S1_at	3.41	3.06	2.65	2.73	7.94	7.86	3.13	3	2.69	7.9	0	100	5.21	37.0	0.000
SERPIND1	serpin peptidase inhibitor, clade D (heparin cofactor), member 1	Gga.1166.1.S1_at	2.07	2.07	2.19	2.05	5.19	5.26	2.35	2.39	2.12	5.23	50	100	3.1	8.6	0.002
SPP2	secreted phosphoprotein 2, 24kDa	Gga.1170.1.S1_a_at	2.83	2.72	2.4	2.41	7	7.15	3.67	3.4	2.41	7.07	0	100	4.67	25.5	0.009
---	---	Gga.11937.1.S1_at	9.06	8.93	10.4	10.44	8.11	8.43	10.91	10.84	10.42	8.27	100	100	-2.15	-4.4	0.044
ANGPTL1	angiotensin-like 1	Gga.12111.1.S1_at	7.84	7.95	6.18	5.91	8.9	8.93	5.78	5.89	6.05	8.91	100	100	2.87	7.3	0.028
---	---	Gga.12554.2.S1_a_at	7.33	7.43	8.46	8.5	5.7	5.47	9.37	9.29	8.48	5.59	100	0	-2.9	-7.5	0.022
---	---	Gga.12631.1.S1_at	5.92	5.31	6.98	7	4.6	4.81	6.59	6.79	6.99	4.71	100	100	-2.28	-4.9	0.027
---	---	Gga.12912.1.S1_at	8.47	8.69	9.9	9.79	7.54	7.44	9.42	9.27	9.85	7.49	100	100	-2.36	-5.1	0.001
---	---	Gga.13827.1.S1_at	7.81	7.57	4.5	4.6	6.59	6.83	3.21	4.47	4.55	6.71	100	100	2.17	4.5	0.016
---	---	Gga.14974.1.S1_at	6.8	6.72	6.08	6.19	8.17	8.2	4.45	3.51	6.13	8.18	100	100	2.05	4.1	0.008
PRRX1	paired related homeobox 1	Gga.1546.1.S1_at	6.33	6.72	4.3	4.17	7.63	7.94	3.62	3.59	4.23	7.78	100	100	3.55	11.7	0.011
PRRX1	Paired related homeobox 1	Gga.1546.1.S2_a_at	7.83	7.53	5.23	5.84	8.77	8.27	4.92	5.29	5.54	8.52	100	100	2.98	7.9	0.019
---	---	Gga.15847.1.S1_at	7.4	7.77	8.48	8.67	6.5	6.02	9.13	9.14	8.58	6.26	100	100	-2.32	-5.0	0.039
---	---	Gga.16108.1.S1_at	5.18	5.35	4.41	4.18	6.47	6.28	4.12	4.06	4.3	6.38	100	100	2.08	4.2	0.006
KRT14	keratin 14	Gga.16196.1.S1_at	7.16	7.18	5.04	5.29	7.21	7.44	4.73	4.85	5.16	7.33	100	100	2.16	4.5	0.007
GAL10	Gal 10	Gga.16863.1.S1_s_at	1.68	1.71	1.67	1.66	7.37	7.67	1.69	1.66	1.67	7.52	0	100	5.85	57.7	0.016
TTN	Titin	Gga.17020.1.S1_at	5.01	4.92	5.06	5.28	7.88	7.98	3.67	3.63	5.17	7.93	100	100	2.76	6.8	0.009
SYNE2	spectrin repeat containing, nuclear envelope 2	Gga.17077.1.S1_s_at	5.72	5.4	5.31	5.08	8.28	8.29	4.83	4.91	5.2	8.28	0	100	3.09	8.5	0.024
PRNPIP	prion protein interacting protein	Gga.18185.1.S1_at	5.08	5.13	7.36	7.17	4.64	4.67	7	6.96	7.26	4.65	100	0	-2.61	-6.1	0.019
---	---	Gga.18781.1.S1_at	2.94	2.6	2.53	2.49	5.11	5.55	2.49	2.48	2.51	5.33	0	100	2.82	7.1	0.049
BCKDHA	branched chain keto acid dehydrogenase E1, alpha polypeptide	Gga.188.1.S1_at	7.57	7.46	9.49	9.46	6.33	6.71	10.32	10.36	9.48	6.52	100	0	-2.95	-7.7	0.040
RSPO3	R-spondin 3 homolog (Xenopus laevis)	Gga.19305.1.S1_at	10.93	10.81	8.37	8.2	10.38	10.59	6.29	6.15	8.28	10.48	100	100	2.2	4.6	0.004
---	---	Gga.19442.1.S1_at	7.73	6.66	8.85	8.77	6.48	6.51	9.23	9.28	8.81	6.49	100	100	-2.31	-5.0	0.002
LOC770705	Similar to pol	Gga.19447.1.S1_at	10.96	11.02	12.29	12.33	10.21	10.08	11.77	11.81	12.31	10.15	100	100	-2.17	-4.5	0.011
LOC770705	Similar to pol	Gga.19447.2.S1_s_at	8.74	8.71	10.54	10.47	7.65	7.58	9.9	10.02	10.51	7.61	100	100	-2.89	-7.4	0.000
TTN	titin	Gga.19481.6.S1_at	7.63	7.37	7.89	7.72	9.81	9.93	5.34	5.05	7.8	9.87	100	100	2.06	4.2	0.003
---	---	Gga.19752.1.S1_at	4.07	5.17	3.75	3.51	6.01	6.1	4.81	5.19	3.63	6.05	0	100	2.42	5.4	0.016
---	---	Gga.19967.1.S1_at	8.43	8.26	9.21	9.14	6.2	5.76	9.82	9.86	9.17	5.98	100	100	-3.19	-9.1	0.039
---	---	Gga.2341.2.S1_at	4.8	4.82	6.77	7.08	4.03	3.59	6.55	6.91	6.92	3.81	100	100	-3.11	-8.6	0.010
MAP2K2	mitogen-activated protein kinase kinase 2	Gga.2391.1.S1_at	8.15	8.02	9	9.17	6.82	6.79	9.92	9.86	9.09	6.8	100	100	-2.28	-4.9	0.021
TF	transferrin	Gga.2551.2.S1_a_at	8.77	8.56	8.39	8.29	11.1	11.21	8.91	8.92	8.34	11.16	100	100	2.82	7.1	0.001
NOV	nephroblastoma overexpressed gene	Gga.2587.1.S1_at	5.37	5.56	3.67	3.62	7.67	7.73	4.51	4.83	3.65	7.7	100	100	4.06	16.7	0.000
TTR	transthyretin	Gga.2620.1.S1_at	7.25	6.83	3.27	3.37	9.33	9.27	6.03	6.21	3.32	9.3	50	100	5.98	63.1	0.000
ACVR1	activin A receptor, type I	Gga.2875.2.S1_a_at	8.6	8.38	8.82	8.86	6.8	6.84	9.5	9.57	8.84	6.82	100	100	-2.02	-4.1	0.000
COL8A1	collagen, type VIII, alpha 1	Gga.3013.1.S1_at	2.06	2.06	3.7	3.13	5.61	5.29	7.22	7.69	3.42	5.45	100	100	2.03	4.1	0.044
HPGDS	hematopoietic prostaglandin D synthase	Gga.3137.1.S1_at	7.12	7.56	6.25	6.19	8.25	8.31	6.64	6.76	6.22	8.28	100	100	2.06	4.2	0.000
CA2	carbonic anhydrase II	Gga.3986.2.S1_a_at	10.02	10	9.99	10.03	12.46	12.46	9.75	9.78	10.01	12.46	100	100	2.45	5.5	0.005
FETUB	fetuin B	Gga.4055.1.S1_at	2.41	2.43	2.41	2.4	8.29	8.07	2.44	2.4	2.41	8.18	0	100	5.78	54.9	0.011
BCMO1	beta-carotene 15,15'-monooxygenase 1	Gga.41.1.S1_at	5.97	5.67	2.92	3.12	5.68	5.9	5.36	5.4	3.02	5.79	0	100	2.77	6.8	0.003
DCTN2	dynactin 2 (p50)	Gga.4314.1.S1_at	9.62	9.72	10.69	10.8	8.61	8.61	11.07	11.1	10.74	8.61	100	100	-2.13	-4.4	0.017
ALB	albumin	Gga.4510.1.S1_a_at	3.53	3.88	3.99	4.22	11.41	11.48	7.68	7.54	4.1	11.45	100	100	7.34	162.0	0.005
FGB	fibrinogen beta chain	Gga.4557.1.S1_at	3.93	4.13	3.41	3.48	7.57	7.9	4.02	3.98	3.45	7.74	50	100	4.29	19.6	0.019
GAL9	Gal 9	Gga.4562.1.S1_s_at	2.35	2.36	2.36	2.34	5.61	5.97	2.36	2.35	2.35	5.79	100	100	3.44	10.9	0.033
FMO6P	flavin containing monooxygenase 6 pseudogene	Gga.4564.1.S1_a_at	3.48	3.05	3.96	3.74	6.29	6.18	4.7	4.63	3.85	6.24	0	100	2.39	5.2	0.010
CSDE1	cold shock domain containing E1, RNA-binding	Gga.4570.1.S1_at	12.49	12.62	13.14	13.14	11.1	11.03	13.53	13.49	13.14	11.06	100	100	-2.08	-4.2	0.011
YWHAH	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	Gga.4816.1.A1_at	7.93	7.82	6.7	7.05	8.97	9.29	6.93	6.92	6.88	9.13	100	100	2.26	4.8	0.011
MSX2	msh homeobox 2	Gga.4977.1.S1_at	7.4	7.47	4.39	3.98	6.49	6.58	3.95	3.93	4.18	6.54	100	100	2.35	5.1	0.046
FBP1	fructose-1,6-bisphosphatase 1	Gga.5139.1.S1_at	7.87	7.72	7.3	7.35	9.65	9.62	7.33	6.74	7.33	9.63	100	100	2.31	5.0	0.000
SEPHS1	Selenophosphate synthetase 1	Gga.5144.1.A1_at	2.74	2.85	2.75	2.79	4.79	4.9	2.75	2.69	2.77	4.85	100	100	2.07	4.2	0.008
GPD1	Glycerol-3-phosphate dehydrogenase 1 (soluble)	Gga.5289.1.S1_at	5.56	5.27	5.19	5.16	8.08	7.94	5.63	5.71	5.18	8.01	100	100	2.83	7.1	0.011
---	---	Gga.6080.1.A1_at	3.04	3.24	4.93	5.48	2.98	2.44	5.91	5.21	2.71	100	0	-2.49	-5.6	0.023	
---	---	Gga.6155.1.S1_at	9.06	9.19	9.52	9.55	7.56	7.37	9.54	9.56	9.54	7.47	100	100	-2.07	-4.2	0.024
RYR1	ryanodine receptor 1 (skeletal)	Gga.659.1.S1_at	6.37	6.55	7.87	7.83	5.34	5.31	7.98	8.07	7.85	5.33	100	100	-2.52	-5.7	0.000
---	---	Gga.6808.1.A1_at	8.61	8.58	9.6	9.65	6.55	6.89	10.49	10.53	9.63	6.72	100	100	-2.91	-7.5	0.034
LOC420301	similar to stem cell antigen 2	Gga.7004.1.S1_at	3.55	3.51	3.55	3.71	6.17	6	5.1	5.07	3.63	6.09	100	100	2.45	5.5	0.002
---	---	Gga.7352															

TNNI3	troponin I type 3 (cardiac)	Gga.820.1.S1_at	12.28	12.44	13.3	13.34	11.26	11.36	13.51	13.46	13.32	11.31	100	100	-2.01	-4.0	0.007
---	---	Gga.840.2.S1_a_at	12.39	12.49	13.3	13.28	10.96	10.93	13.87	13.84	13.29	10.95	100	100	-2.34	-5.1	0.000
DBN1	drebrin 1	Gga.9093.1.S1_a_at	8.01	8.11	9.55	9.5	7.38	7.62	9.23	8.98	9.52	7.5	100	100	-2.02	-4.1	0.030
GIT1	G protein-coupled receptor kinase interactor 1	Gga.921.1.S1_at	5.99	5.55	7.43	7.07	4.78	4.28	7.65	7.66	7.25	4.53	100	100	-2.72	-6.6	0.016
---	---	Gga.9326.1.S1_at	4.19	4.44	4.4	4.38	6.67	6.48	5.5	4.48	4.39	6.58	100	100	2.19	4.6	0.026
---	---	Gga.9909.1.S1_at	7.43	7.52	8.72	8.74	6.36	6.34	9.19	9.29	8.73	6.35	100	0	-2.38	-5.2	0.000
MTCH1	mitochondrial carrier homolog 1 (C. elegans)	GgaAffx.117.2.S1_s_at	3.7	3.7	3.71	3.69	1.74	1.63	3.93	3.71	3.7	1.68	100	0	-2.02	-4.1	0.016
PRPS2	phosphoribosyl pyrophosphate synthetase 2	GgaAffx.13038.1.S1_s_at	4.09	4.72	2.56	2.64	6.44	6.33	3.46	2.9	2.6	6.39	0	100	3.78	13.7	0.000
KIAA0692	KIAA0692	GgaAffx.1423.1.S1_at	5.94	5.75	7.24	6.78	4.54	4.87	7.39	7.07	7.01	4.71	100	100	-2.3	-4.9	0.019
LOC418543	hypothetical gene supported by BX933825; CR407341	GgaAffx.20268.1.S1_s_at	6.73	7.04	4.98	5.25	10.23	10.23	2.34	2.67	5.12	10.23	0	100	5.11	34.5	0.017
KIAA0430	KIAA0430	GgaAffx.20448.1.S1_s_at	5.88	6.07	5.28	5.56	3.04	2.88	5.45	5.23	5.42	2.96	100	100	-2.46	-5.5	0.011
---	---	GgaAffx.20839.1.S1_s_at	9.84	9.79	10.62	10.55	7.22	7.11	9.77	9.55	10.59	7.17	100	100	-3.42	-10.7	0.001
---	---	GgaAffx.21330.1.S1_at	5.43	5.45	3.93	3.67	6.3	6.23	3.63	3.61	3.8	6.27	0	100	2.47	5.5	0.024
---	---	GgaAffx.21332.1.S1_s_at	6.06	6.43	8.24	8.52	3.95	3.81	3.65	3.61	8.38	3.88	100	0	-4.5	-22.6	0.005
LINGO3	leucine rich repeat and Ig domain containing 3	GgaAffx.22179.1.S1_at	8.28	8.5	9.57	9.62	7.18	7.29	9.47	9.39	9.6	7.24	100	100	-2.36	-5.1	0.004
DOT1L	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	GgaAffx.22303.1.S1_at	4.58	4.4	6.39	6.32	3.25	2.97	6.64	6.95	6.36	3.11	100	100	-3.25	-9.5	0.021
MGA	MAX gene associated	GgaAffx.22659.1.S1_at	3.82	3.69	4.47	4.9	2.54	2.71	4.91	4.66	4.69	2.63	100	0	-2.06	-4.2	0.040
PAK4	p21(CDKN1A)-activated kinase 4	GgaAffx.24395.1.S1_at	4.94	5.41	7.2	7.22	4.74	4.48	7.76	7.67	7.21	4.61	100	0	-2.61	-6.1	0.031
UPF1	UPF1 regulator of nonsense transcripts homolog (yeast)	GgaAffx.25781.1.S1_s_at	8.25	7.68	8.74	8.68	6.64	6.47	9.05	9.11	8.71	6.55	100	100	-2.16	-4.5	0.015
LOC768852	similar to Ac1147	GgaAffx.26780.1.S1_s_at	1.95	1.98	1.95	1.93	6.34	6.71	1.95	1.93	1.94	6.53	0	100	4.59	24.1	0.026
TRIM36	tripartite motif-containing 36	GgaAffx.5168.1.S1_at	5.58	5.47	6.4	6.57	4.55	4.39	6.58	6.8	6.48	4.47	100	100	-2.02	-4.1	0.003
ABCF3	ATP-binding cassette, sub-family F (GCN20), member 3	GgaAffx.5344.3.S1_s_at	8.04	8.09	8.6	8.73	6.59	6.46	8.61	8.65	8.66	6.53	100	100	-2.14	-4.4	0.002
ZNF238	zinc finger protein 238	GgaAffx.6764.1.S1_at	5.54	5.68	7.93	7.9	5.52	5.73	7.99	8.01	7.92	5.63	100	100	-2.29	-4.9	0.026
CCNK	cyclin K	GgaAffx.7070.1.S1_s_at	5.05	5.07	6.46	6.45	3.62	3.57	7.17	7.48	6.46	3.59	100	100	-2.86	-7.3	0.006
---	---	GgaAffx.9072.1.A1_at	2.61	2.74	2.57	2.55	5.46	5.25	2.55	2.53	2.56	5.36	0	100	2.8	7.0	0.024
CENTD1	centaurin, delta 1	GgaAffx.9098.1.S1_at	8.14	8.14	8.8	8.5	5.01	5.14	8.38	8.28	8.65	5.07	100	100	-3.58	-12.0	0.011
CENTD1	centaurin, delta 1	GgaAffx.9099.1.S1_at	7.52	7.41	7.42	6.86	4.57	4.94	7.19	7.37	7.14	4.76	100	100	-2.39	-5.2	0.029

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