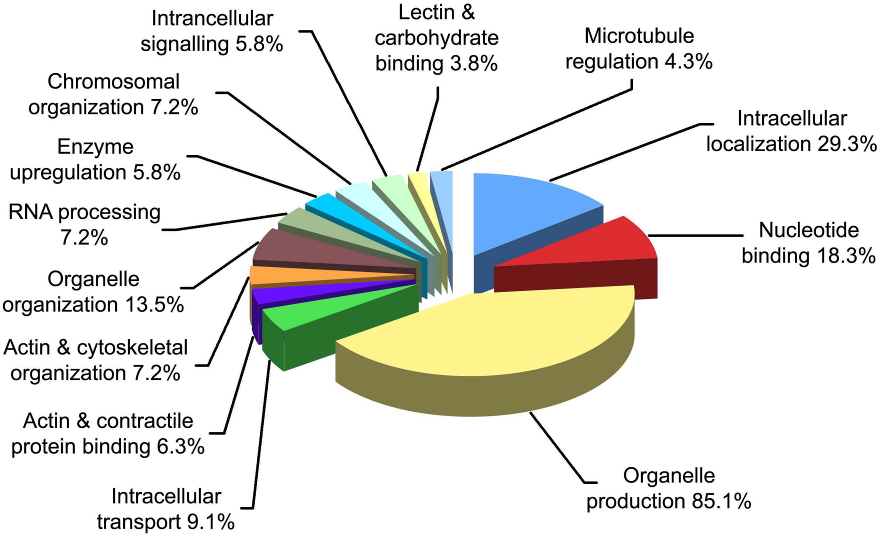
Supplementary Figure

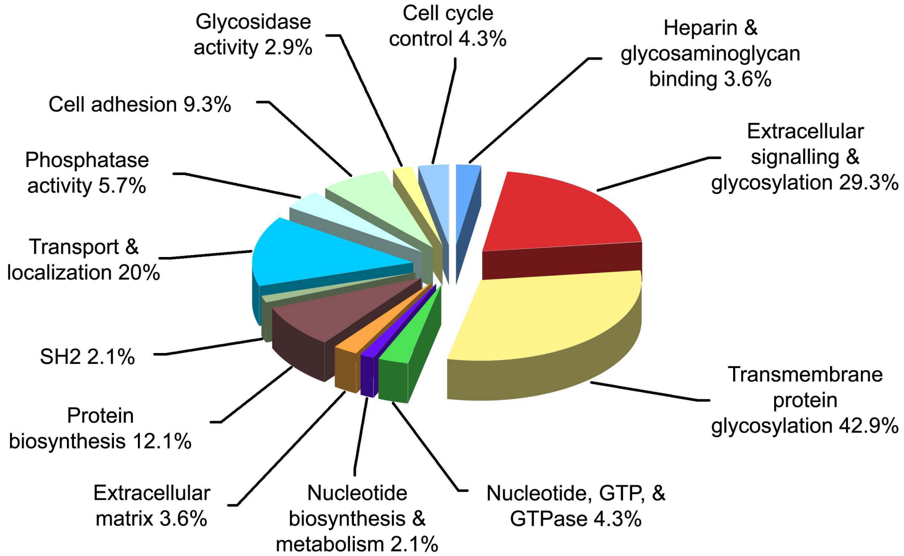
Figure E1 Gene ontology clustering of significant genes between respective groups as assessed by DAVID 2007. Numbers represent the percent of our significantly expressed genes in a particular cluster compared to the total number of significant genes. Individual genes may be representative of more than one gene ontologic category (thus total percentages will not add to 100%).

Figure E1

Band *vs.* Sham



Deband *vs.* Band



Deband *vs.* Sham Deband

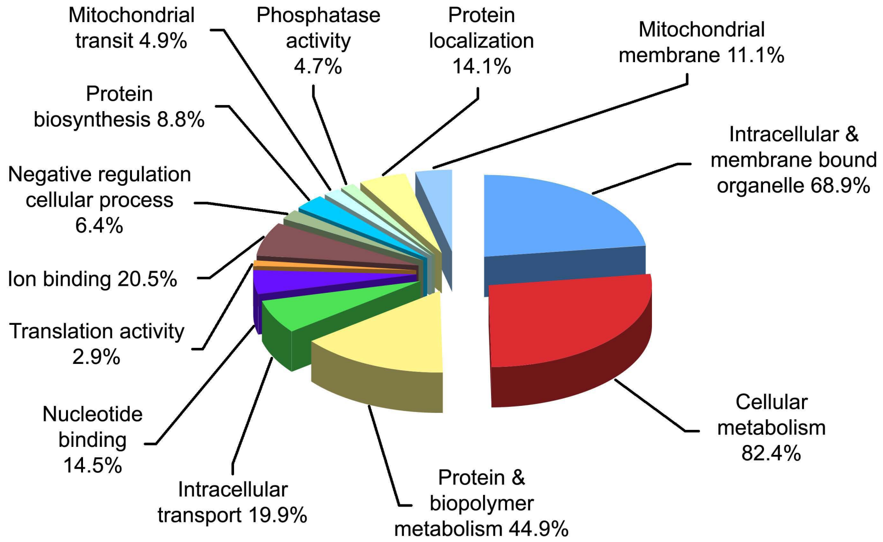


Table E1 (Supplemental): Echocardiographic measurements at each time points for each of the experimental groups.

Echocardiographic measurements: IVSd,s, Interventricular septum in diastole and systole; LVIDd,s, Left ventricular internal diameter in diastole and systole; LVPWd,s, Left ventricular posterior wall in diastole and systole; LVFS, Left ventricular fractional shortening; LVEF, left ventricular ejection fraction; LVMass, Left ventricular mass corrected and uncorrected. *P<0.05 vs. Baseline, †P<0.05 vs. 4wks Banded

	Sham	Band	Sham Deband	Deband
Baseline:				
IVS; d (mm)	0.63 +/- 0.02	0.57 +/- 0.02	0.66 +/- 0.02	0.56 +/- 0.02
LVID; d (mm)	4.2 +/- 0.06	4.23 +/- 0.08	4.12 +/- 0.08	4.14 +/- 0.06
LV PW; d (mm)	0.56 +/- 0.02	0.57 +/- 0.02	0.6 +/- 0.02	0.56 +/- 0.02
IVS; s (mm)	0.69 +/- 0.02	0.67 +/- 0.02	0.73 +/- 0.02	0.64 +/- 0.02
LVID; s (mm)	3.22 +/- 0.09	3.16 +/- 0.08	3.15 +/- 0.13	3.13 +/- 0.1
LV PW; s (mm)	0.71 +/- 0.02	0.73 +/- 0.03	0.72 +/- 0.03	0.69 +/- 0.01
LV FS (%)	23.1 +/- 1.2	25 +/- 1.8	23.5 +/- 1.9	23.9 +/- 1.9
LV EF (%)	46.6 +/- 2.1	49.5 +/- 2.7	47 +/- 3.2	47.7 +/- 3.2
LV Mass (mg) (Uncorr.)	90.9 +/- 4	87.8 +/- 2.7	92.9 +/- 2.1	83.4 +/- 2.8
LV Mass (mg) (Corr.)	72.7 +/- 3.2	70.2 +/- 2.2	74.3 +/- 1.7	66.7 +/- 2.2
4 Weeks Banded:				
IVS; d (mm)	0.62 +/- 0.02	0.72 +/- 0.02*	0.66 +/- 0.02	0.66 +/- 0.02*
LVID; d (mm)	4.23 +/- 0.14	4.47 +/- 0.09*	4.19 +/- 0.07	4.44 +/- 0.07*
LV PW; d (mm)	0.58 +/- 0.02	0.67 +/- 0.02*	0.59 +/- 0.01	0.62 +/- 0.01*
IVS; s (mm)	0.68 +/- 0.02	0.78 +/- 0.02*	0.74 +/- 0.02	0.73 +/- 0.02*
LVID; s (mm)	3.23 +/- 0.16	3.58 +/- 0.15*	3.23 +/- 0.11	3.54 +/- 0.11*
LV PW; s (mm)	0.71 +/- 0.03	0.84 +/- 0.04*	0.74 +/- 0.03	0.77 +/- 0.02*
LV FS (%)	23.6 +/- 1.7	20.7 +/- 2.3*	23.4 +/- 1.5	19.8 +/- 1.8*
LV EF (%)	47.1 +/- 3	41.7 +/- 3.7*	46.9 +/- 2.4	40.4 +/- 3.1*
LV Mass (mg) (Uncorr)	92.9 +/- 5.5	125 +/- 4.9*	97 +/- 1.8	109.9 +/- 3*
LV Mass (mg) (Corr)	74.3 +/- 4.4	100 +/- 3.9*	77.6 +/- 1.4	87.9 +/- 2.4*
1 Week Debanded:				
IVS; d (mm)			0.69 +/- 0.02	0.58 +/- 0.02†
LVID; d (mm)			4.23 +/- 0.06	4.37 +/- 0.08†
LV PW; d (mm)			0.58 +/- 0.01	0.58 +/- 0.01†
IVS; s (mm)			0.73 +/- 0.02	0.66 +/- 0.02†
LVID; s (mm)			3.28 +/- 0.07	3.47 +/- 0.13†
LV PW; s (mm)			0.72 +/- 0.02	0.69 +/- 0.02†
LV FS (%)			21.3 +/- 1.2	20.3 +/- 1.6
LV EF (%)			43.5 +/- 2.1	41.4 +/- 2.8
LV Mass (mg) (Uncorrected)			100.8 +/- 2.2	94 +/- 3.7†
LV Mass (mg) (Corrected)			80.6 +/- 1.8	75.2 +/- 3†

Table E2 – A. (Supplemental): Genes most differentially expressed in each comparison: Deband vs. Band

Direction (Deband)	Accession No.	Symbol	Name	Fold Δ
+	NM_030679	Myh1	myosin, heavy polypeptide 1, skeletal muscle, adult	2.742
+	U01063	Plk1	polo-like kinase 1 (Drosophila)	2.475
+	NM_016677	Hpcal1	hippocalcin-like 1	2.074
+	NM_001012336	Mdk	midkine	2.044
+	NM_029948	Pramef12	PRAME family member 12	1.979
+	NM_147089	Olfr572	olfactory receptor 572	1.978
+	AK036567	Mgat5	mannoside acetylglucosaminyltransferase 5	1.962
+	AK083490	Arfrp1	ADP-ribosylation factor related protein 1	1.916
+	NM_009303	Syngr1	synaptogyrin 1	1.845
+	NM_182991	5330410G16R	RIKEN cDNA 5330410G16 gene	1.730
+	NM_172817	Zfp647	zinc finger protein 647	1.713
+	NM_007472	Aqp1	aquaporin 1	1.673
+	AC124532	Calcoco1	calcium binding and coiled coil domain 1	1.638
+	NM_146201	Zfp553	zinc finger protein 553	1.628
+	NM_001002272	Tro	trophinin	1.626
+	NM_011601	Tlm	T lymphoma oncogene	1.596
+	NM_007444	Amd2	S-adenosylmethionine decarboxylase 2	1.550
+	AC155922	Rps6ka5	ribosomal protein S6 kinase, polypeptide 5	1.538
+	XM_925008	Slc44a5	solute carrier family 44, member 5	1.538
+	AC161037	Hnrpul1	heterogeneous nuclear ribonucleoprotein U-like 1	1.530
-	NM_020581	Angptl4	angiopoietin-like 4	2.550
-	NM_008725	Nppa	natriuretic peptide precursor type A	2.052
-	XM_621314	Dsp	desmoplakin	1.928
-	XM_283556	Fer1l3	fer-1-like 3, myoferlin (C. elegans)	1.758
-	NM_001013390	Scn4b	sodium channel, type IV, beta	1.701
-	NM_021453	Pga5	pepsinogen 5, group I	1.651
-	NM_024478	Grpel1	GrpE-like 1, mitochondrial	1.645
-	NM_053176	Hrg	histidine-rich glycoprotein	1.625
-	NM_019662	Rrad	Ras-related associated with diabetes	1.623
-	NM_171826	Cldnd1	claudin domain containing 1	1.614
-	NM_133786	Smc4	structural maintenance of chromosomes 4	1.607
-	NM_023733	Crot	carnitine O-octanoyltransferase	1.605
-	AC1017091	Lama2	laminin, alpha 2	1.601
-	NM_029977	Polq	polymerase (DNA directed), theta	1.592
-	NM_134072	Akr1c14	aldo-keto reductase family 1, member C14	1.585
-	NM_012037	Vat1	vesicle amine transport protein 1 homolog	1.584
-	NM_145406	Slc10a3	solute carrier family 10, member 3	1.576
-	NM_175277	Bola3	bolA-like 3 (E. coli)	1.555
-	NM_008961	Pter	phosphotriesterase related	1.554
-	NM_008937	Prox1	prospero-related homeobox 1	1.551

Table E2 – B. (Supplemental): Genes most differentially expressed in each comparison: Band vs. Sham

Direction	Accession No.	Symbol	Name	Fold Δ
+	XM_001002752	Zc3h7b	zinc finger CCCH type containing 7B	1.884
+	NM_008725	Nppa	natriuretic peptide precursor type A	1.754
+	NM_007489	Arntl	aryl hydrocarbon receptor nuclear translocator-like	1.645
+	NM_013468	Ankrd1	ankyrin repeat domain 1 (cardiac muscle)	1.557
+	NM_015784	Postn	periostin, osteoblast specific factor	1.534
+	AC034265	Ankrd23	ankyrin repeat domain 23	1.530
+	NM_134129	Prpf19	PRP19/PSO4 pre-mRNA processing factor 19 homolog	1.497
+	NM_133357	Krt75	keratin 75	1.480
+	NM_010480	Hsp90aa1	heat shock protein 90kDa alpha, class A member 1	1.454
+	NM_031260	Mov10l1	Moloney leukemia virus 10-like 1	1.445
+	NM_021453	Pga5	pepsinogen 5, group I	1.445
+	NM_009221	Snca	synuclein, alpha	1.439
+	NM_007564	Zfp36l1	zinc finger protein 36, C3H type-like 1	1.424
+	NM_172621	Clic5	chloride intracellular channel 5	1.414
+	NM_133744	Ccdc71	coiled-coil domain containing 71	1.413
+	NM_178701	Lrrc8d	leucine rich repeat containing 8D	1.410
+	NM_009007	Rac1	RAS-related C3 botulinum substrate 1	1.394
+	NM_173442	Gcnt1	glucosaminyl (N-acetyl) transferase 1, core 2	1.388
+	NM_029614	Prss23	protease, serine, 23	1.378
+	NM_008524	Lum	lumican	1.365
-	NM_007606	Car3	carbonic anhydrase 3	2.672
-	NM_030679	Myh1	myosin, heavy polypeptide 1, skeletal muscle, adult	2.131
-	NM_010005	Cyp2d10	cytochrome P450, family 2, subfam. d, polypeptide 10	2.051
-	NM_009416	Tpm2	tropomyosin 2, beta	2.016
-	U01063	Plk1	polo-like kinase 1 (Drosophila)	1.982
-	NM_017370	Hp	haptoglobin	1.971
-	NM_147089	Olfr572	olfactory receptor 572	1.925
-	NM_001012336	Mdk	midkine	1.911
-	NM_011066	Per2	period homolog 2 (Drosophila)	1.867
-	BC004722	Malat1	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	1.859
-	NM_013900	Mfi2	antigen p97 (melanoma associated)	1.727
-	NM_010404	Hap1	huntingtin-associated protein 1	1.627
-	NM_177709	Tusc5	tumor suppressor candidate 5	1.597
-	XM_981394	Rhobtb1	Rho-related BTB domain containing 1	1.586
-	AK083490	Arfrp1	ADP-ribosylation factor related protein 1	1.567
-	NM_016693	Map3k6	mitogen-activated protein kinase kinase kinase 6	1.562
-	NM_009920	Cnih2	cornichon homolog 2 (Drosophila)	1.549
-	NM_025866	Cdca7	cell division cycle associated 7	1.534
-	NM_001025156	Ccdc93	coiled-coil domain containing 93	1.524
-	NM_009119	Sap18	Sin3-associated polypeptide 18	1.520

Table E2 - C (Supplemental): Genes most differentially expressed in each comparison: Deband vs. Sham Deband

Direction	Accession No.	Symbol	Name	Fold Δ
+	NM_133777	Ube2s	ubiquitin-conjugating enzyme E2S	1.967
+	AK036567	Mgat5	mannoside acetylglucosaminyltransferase 5	1.731
+	NM_029948	Pramef12	PRAME family member 12	1.704
+	NM_011202	Ptpn11	protein tyrosine phosphatase, non-receptor type 11	1.620
+	NM_144791	Tor1aip1	torsin A interacting protein 1	1.507
+	AB009392	Hnrpl	heterogeneous nuclear ribonucleoprotein L	1.505
+	NM_010890	Nedd4	neural precursor cell, developmentally down-reg gene 4	1.501
+	NM_028004	Ttn	titin	1.497
+	NM_001024955	Pik3r1	phosphatidylinositol 3-kinase, reg. sub., polypeptide 1	1.496
+	NM_008609	Mmp15	matrix metallopeptidase 15	1.492
+	NM_146087	Csnk1a1	casein kinase 1, alpha 1	1.483
+	NM_173364	Zfp445	zinc finger protein 445	1.480
+	NM_025403	Nola3	nucleolar protein family A, member 3	1.472
+	NM_152134	Homer1	homer homolog 1 (Drosophila)	1.469
+	NM_011601	Tlm	T lymphoma oncogene	1.466
+	NM_009652	Akt1	thymoma viral proto-oncogene 1	1.464
+	NM_146201	Zfp553	zinc finger protein 553	1.464
+	NM_173028	Vps13a	vacuolar protein sorting 13A (yeast)	1.464
+	NM_008714	Notch1	Notch gene homolog 1 (Drosophila)	1.447
+	NM_029657	Mgrn1	mahogunin, ring finger 1	1.445
-	NM_020581	Angptl4	angiopoietin-like 4	1.875
-	NM_001013390	Scn4b	sodium channel, type IV, beta	1.744
-	XM_001001760	Gan	giant axonal neuropathy	1.671
-	NM_145741	Gdf10	growth differentiation factor 10	1.651
-	NM_178882	D2hgdh	D-2-hydroxyglutarate dehydrogenase	1.578
-	NM_012037	Vat1	vesicle amine transport protein 1 homolog	1.572
-	XM_001006025	Rpl19	ribosomal protein L19	1.558
-	NM_010937	Nras	neuroblastoma ras oncogene	1.553
-	NM_008937	Prox1	prospero-related homeobox 1	1.540
-	XM_915717	Ube2e1	ubiquitin-conjugating enzyme E2E 1, UBC4/5 homolog	1.539
-	XR_001538	Tfb2m	transcription factor B2, mitochondrial	1.527
-	NM_053176	Hrg	histidine-rich glycoprotein	1.524
-	NM_025276	Evpl	envoplakin	1.520
-	AK041640	Zfpn1a4	zinc finger protein, subfamily 1A, 4 (Eos)	1.517
-	NM_019794	Dnaja2	DnaJ (Hsp40) homolog, subfamily A, member 2	1.516
-	XM_621314	Dsp	desmoplakin	1.514
-	NM_027777	Pex1	peroxisome biogenesis factor 1	1.505
-	NM_007666	Cdh6	cadherin 6	1.502
-	NM_133786	Smc4	structural maintenance of chromosomes 4	1.501
-	NM_012010	Eif2s3x	eukaryotic translation initiation factor 2, subunit 3	1.491

Table E3 (Supplemental): Significant gene ontologies and GSEA categories identified by SAFE analysis in LVH regression (excluding those identified in LVH progression)

	GO Categories	GSEA Categories
GO:0015629	actin cytoskeleton	actin pathway
GO:0007411	axon guidance	adrenergic
GO:0003824	catalytic activity	akt pathway
GO:0006968	cellular defense response	alk pathway
GO:0004197	cysteine-type endopeptidase activity	bcl2 family and reg network
GO:0004519	endonuclease activity	carm-er pathway
GO:0005789	endoplasmic reticulum membrane	cell cycle
GO:0016251	RNA polymerase II transcription factor	creb pathway
GO:0004364	glutathione transferase activity	death pathway
GO:0006811	ion transport	differentiation pathway in PC12 cells
GO:0007254	JNK cascade	erk5 pathway
GO:0000287	magnesium ion binding	G alpha I pathway
GO:0006120	mitochondrial electron transport, NADH to ubiquinone	glutamine down
GO:0005554	molecular_function unknown	il2rb pathway
GO:0008137	NADH dehydrogenase (ubiquinone)	IL4 receptor in B-lymphocytes
GO:0003954	NADH dehydrogenase activity	INS
GO:0045786	negative regulation of cell cycle	interleukin 4 pathway
GO:0009968	negative regulation signal transduction	mapk pathway
GO:0030182	neuron cell differentiation	monocyte pathway
GO:0005643	nuclear pore	mRNA processing
GO:0000786	nucleosome	mRNA splicing
GO:0005634	nucleus	mtor pathway
GO:0016491	oxidoreductase activity	p53 hypoxia pathway
GO:0003755	peptidyl-prolyl cis-trans isomerase	p53 signalling
GO:0007204	positive regulation of cytosolic [Ca++]	phosphoinositide-3-kinase pathway
GO:0006470	protein amino acid dephosphorylation	PIP3 signaling in B lymphocytes
GO:0006412	protein biosynthesis	protein modification
GO:0006457	protein folding	ptdins pathway
GO:0004722	protein serine/threonine phosphatase	pyruvate metabolism
GO:0004725	protein tyrosine phosphatase activity	rarrxr pathway
GO:0016567	protein ubiquitination	RNA polymerase
GO:0015992	proton transport	stress pathway
GO:0008217	regulation of blood pressure	tid pathway
GO:0042127	regulation of cell proliferation	wnt pathway
GO:0006446	regulation of translational initiation	
GO:0006950	response to stress	
GO:0005840	ribosome	
GO:0003723	RNA binding	
GO:0008380	RNA splicing	
GO:0006814	sodium ion transport	
GO:0030528	transcription regulator activity	
GO:0003743	translation initiation factor activity	
GO:0006512	ubiquitin cycle	
GO:0000151	ubiquitin ligase complex	
GO:0006511	ubiquitin-dependent protein catabolism	
GO:0004842	ubiquitin-protein ligase activity	
GO:0030018	Z disc	
GO:0008270	zinc ion binding	

Table E4 (Supplemental): Significant gene ontologies and GSEA categories identified by SAFE analysis in both LVH progression and regression

GO:0005516	calmodulin binding
GO:0003677	DNA binding
GO:0005874	microtubule
GO:0005762	mitochondrial large ribosomal subunit
GO:0003704	specific RNA polymerase II transcription factor activity
GO:0004221	ubiquitin thiolesterase activity