

Supplementary Material

Correlation of gene expression and clinical parameters identifies a set of genes reflecting systolic dysfunction and morphological alterations

Running title: Correlation of gene expression with LV parameters in DCM

Eric Witt^{1,5}, Elke Hammer^{1,5}, Marcus Dörr², Kerstin Weitmann³, Daniel Beug^{2,5}, Kristin Lehnert^{2,5}, Matthias Nauck^{4, 5}, Uwe Völker^{1,5}, Stephan B. Felix^{2,5,a}, Sabine Ameling^{1,5,a}

¹ Interfaculty Institute for Genetics and Functional Genomics, University Medicine Greifswald, Felix-Hausdorff-Straße 8, D-17475 Greifswald, Germany

² Department for Internal Medicine B, University Medicine Greifswald, Ferdinand-Sauerbruch-Str., D-17475 Greifswald, Germany

³ Institute for Community Medicine, University Medicine Greifswald, Ellernholzstr. 1, D-17475 Greifswald, Germany

⁴ Institute of Clinical Chemistry and Laboratory Medicine, University Medicine Greifswald, Ferdinand-Sauerbruch-Str., 17475 Greifswald, Germany

⁵ DZHK (German Centre for Cardiovascular Research), partner site Greifswald, Greifswald, Germany

^a corresponding author

Corresponding authors:

Prof. Dr. Stephan B. Felix
Department of Internal Medicine B
University Medicine Greifswald
Ferdinand-Sauerbruch-Str.
17475 Greifswald
Phone: +49-3834-8680500, Fax: +49-3834-8680502
E-mail: felix@uni-greifswald.de

Sabine Ameling, PhD
Interfaculty Institute for Genetics and Functional Genomics
University Medicine Greifswald
Felix-Hausdorff-Str. 8
D – 17475 Greifswald, Germany
Phone: +49-3834-420 5818, Fax: +49-3834-420 5809
E-mail: amelings@uni-greifswald.de

Content:

1. Supplemental Tables

Supplemental Table S1 Correlation between expression of known heart failure markers and LVEF, LVEDDI, and NT-proBNP

Supplemental Table S2 All significant correlations between gene expression and LVEF, LVEDDI, or NT-proBNP

Supplemental Table S3 Top Canonical Pathways of genes significantly correlating with NT-proBNP, LVEDDI or LVEF ($p < .0.01$)

1. Supplemental Tables

Supplemental Table S1 Correlation of Heart failure markers.

Spearman coefficient ρ and p -value are given.

Gene name	probe set ID	Description	LVEF		LVEDDI		NT-proBNP		ref.
			p -value	ρ	p -value	ρ	p -value	ρ	
ACE2	222257_s_at	angiotensin I converting enzyme 2	<0.001	-0.58	<0.001	0.53	<0.001	0.59	(6, 13, 19, 20)
ACTA1	203872_at	actin, alpha 1, skeletal muscle	0.008	-0.35	0.021	0.31	0.010	0.41	(7)
ACTA2	200974_at	actin, alpha 2, smooth muscle, aorta	0.002	-0.41	0.001	0.42	0.848	0.03	(7)
ACTC1	205132_at	actin, alpha, cardiac muscle 1	0.776	0.03	0.028	-0.29	0.575	0.09	(7)
ACTN1	208636_at	actinin, alpha 1	<0.001	-0.65	0.003	0.40	0.012	0.41	(7)
ACTN2	203861_s_at	actinin, alpha 2	0.391	-0.11	0.417	0.11	0.059	0.30	(7)
ADM	202912_at	adrenomedullin	0.246	0.15	0.426	-0.10	0.247	-0.19	(12)
ADRB2	206170_at	beta-2 adrenergic receptor	<0.001	0.45	<0.001	-0.46	0.070	-0.30	(3)
APOA1	204450_x_at	apolipoprotein A-I	0.001	-0.42	0.022	0.31	0.194	0.22	(2)
ATP2A2	209186_at	ATPase, Ca ⁺⁺ transporting, cardiac muscle, slow twitch 2	0.006	0.36	0.003	-0.38	0.022	-0.37	(14)
CD40	35150_at	CD40 molecule, TNF receptor superfamily member 5	0.574	0.07	0.706	0.05	0.159	0.23	(15)
COL1A1	1556499_s_at	collagen, type I, alpha 1	0.010	-0.34	0.008	0.35	0.071	0.29	(21)
COL1A2	202404_s_at	collagen, type I, alpha 2	0.002	-0.40	0.049	0.27	0.126	0.25	(21)
COL3A1	215076_s_at	collagen, type III, alpha 1	<0.001	-0.46	0.012	0.34	0.014	0.40	(15, 21)
CORIN	220356_at	corin, serine peptidase	0.003	0.39	0.001	-0.42	<0.001	-0.64	(10, 12)

Gene name	probe set ID	Description	LVEF		LVEDDI		NT-proBNP		ref.
			<i>p</i> -value	ρ	<i>p</i> -value	ρ	<i>p</i> -value	ρ	
CTGF	209101_at	connective tissue growth factor	<0.001	-0.44	0.268	0.15	0.131	0.25	(1)
DES	202222_s_at	desmin	0.057	-0.25	0.051	0.26	0.312	0.16	(7)
DSP	200606_at	desmoplakin	<0.001	0.44	0.005	-0.37	0.002	-0.49	(18)
EDN1	222802_at	endothelin 1	0.133	-0.20	0.011	0.34	0.596	-0.08	(12)
FABP3	205738_s_at	fatty acid binding protein 3, muscle and heart	0.895	0.01	0.015	-0.32	0.279	0.17	(15)
FAS	204780_s_at	Fas cell surface death receptor	0.108	0.21	0.630	-0.06	0.819	-0.03	(12)
FN1	210495_x_at	fibronectin 1	0.010	-0.35	0.001	0.43	0.078	0.29	(9)
ICAM2	213620_s_at	intercellular adhesion molecule 2	0.897	-0.01	0.081	0.23	0.806	0.04	(2)
ICAM3	204949_at	intercellular adhesion molecule 3	0.026	0.30	0.001	-0.43	0.205	-0.21	(2)
LGALS3	208949_s_at	lectin, galactoside-binding, soluble, 3	0.697	0.05	0.007	-0.36	0.281	-0.17	(12)
LMNA	1554600_s_at	lamin A/C	0.032	0.29	0.003	-0.39	0.005	-0.45	(4, 17)
MMP2	201069_at	matrix metalloproteinase 2	0.876	-0.02	0.409	0.11	0.539	0.10	(12, 23)
MMP9	203936_s_at	matrix metalloproteinase 9	0.125	-0.20	0.983	≈0.00	0.844	0.03	(12, 15, 23)
MYBPC1	214087_s_at	myosin binding protein C, slow type	<0.001	0.45	0.024	-0.30	0.025	-0.36	(7)
MYBPC3	208040_s_at	myosin binding protein C, cardiac	0.803	0.03	0.046	-0.26	0.525	-0.10	(7)
MYH6	214468_at	myosin, heavy chain 6, cardiac muscle, alpha	<0.001	0.44	<0.001	-0.63	0.108	-0.26	(5, 11, 16, 22)
MYH7	216265_x_at	myosin, heavy chain 7, cardiac muscle, beta	0.644	0.06	0.002	-0.41	0.198	0.21	(5, 7, 11, 16, 22)

Gene name	probe set ID	Description	LVEF		LVEDDI		NT-proBNP		ref.
			p-value	ρ	p-value	ρ	p-value	ρ	
MYH7B	233949_s_at	myosin, heavy chain 7B, cardiac muscle, beta	0.234	0.16	0.419	-0.11	0.624	-0.08	(5, 7, 11, 16, 22)
MYL6	214002_at	myosin, light chain 6, alkali, smooth muscle and non-muscle	0.642	-0.06	0.944	$\approx$ 0.00	0.215	-0.20	(15)
MYL7	219942_at	myosin, light chain 7, regulatory	0.398	0.11	0.137	-0.20	0.383	0.14	(15)
NPPA	209957_s_at	natriuretic peptide A	<0.001	-0.56	0.001	0.43	<0.001	0.60	(15)
NPPB	206801_at	natriuretic peptide B	<0.001	-0.59	<0.001	0.48	<0.001	0.64	(2, 12, 15, 20)
PLN	204938_s_at	phospholamban	<0.001	0.44	0.006	-0.37	0.782	0.05	(8, 14)
POSTN	210809_s_at	periostin, osteoblast specific factor	0.010	-0.34	0.032	0.28	0.054	0.31	(23)
PTX3	206157_at	pentraxin 3, long	0.528	-0.08	0.505	0.09	0.546	0.10	(12)
RYR2	207557_s_at	ryanodine receptor 2 (cardiac)	0.002	0.40	0.045	-0.27	0.639	-0.08	(14)
SELP	206049_at	selectin P (granule membrane protein 140kDa, antigen CD62)	0.129	0.20	0.624	-0.06	0.461	-0.12	(2, 15)
SPP1	209875_s_at	secreted phosphoprotein 1	0.001	-0.43	0.238	0.16	0.260	0.19	(2)
TIMP1	201666_at	TIMP metalloproteinase inhibitor 1	0.009	-0.34	0.025	0.30	0.319	0.16	(12, 15)
TNNC1	209904_at	troponin C type 1 (slow)	0.617	0.06	0.065	-0.25	0.224	0.20	(2, 7, 12, 15)
TNNI3	205742_at	troponin I type 3 (cardiac)	0.233	-0.16	0.763	-0.04	0.068	0.29	(2, 7, 12, 15)
TNNT2	215389_s_at	troponin T type 2 (cardiac)	0.002	0.39	0.013	-0.33	0.969	$\approx$ 0.00	(2, 7, 12, 15)
TNNT3	205693_at	troponin T type 3 (skeletal, fast)	0.135	0.20	0.776	-0.03	0.917	0.01	(2, 7, 12, 15)

Gene name	probe set ID	Description	LVEF		LVEDDI		NT-proBNP		ref.
			<i>p</i> -value	ρ	<i>p</i> -value	ρ	<i>p</i> -value	ρ	
TTN	208195_at	titin	0.012	0.33	0.132	-0.20	0.684	-0.06	(7)
VCAM1	203868_s_at	vascular cell adhesion molecule 1	0.661	0.06	0.864	0.02	0.658	-0.07	(15)
APOA2	not detected	apolipoprotein A-2	NA	NA	NA	NA	NA	NA	(2)
CA125	not detected	cancer antigen 125	NA	NA	NA	NA	NA	NA	(2)
CRP	not detected	c-reactive protein	NA	NA	NA	NA	NA	NA	(2, 12, 15)
GDF15	not detected	growth/differentiation factor 15	NA	NA	NA	NA	NA	NA	(12)
IL2R	not detected	interleukin-2 receptor	NA	NA	NA	NA	NA	NA	(2, 15)
IL6	not detected	interleukin-6	NA	NA	NA	NA	NA	NA	(2, 12, 15)
MMP-1	not detected	Collagenase I	NA	NA	NA	NA	NA	NA	(12)
MPO	not detected	myeloperoxidase	NA	NA	NA	NA	NA	NA	(12)
MYL1	not detected	myosin light chain 1/3, skeletal muscle isoform	NA	NA	NA	NA	NA	NA	(15)
ST2	not detected	interleukin-1 receptor-like 1	NA	NA	NA	NA	NA	NA	(12)
TNF	not detected	tumor necrosis factor	NA	NA	NA	NA	NA	NA	(2, 12, 15)

References

1. **Ahmed MS, Øie E, Vinge LE, Yndestad A, Øystein Andersen G, Andersson Y, Attramadal T, Attramadal H.** Connective tissue growth factor—a novel mediator of angiotensin II-stimulated cardiac fibroblast activation in heart failure in rats. *J Mol Cell Cardiol* 36: 393–404, 2004.
2. **Bielecka-Dąbrowa A, Wierzbicka M, Dąbrowa M, Goch A.** New methods in laboratory diagnostics of dilated cardiomyopathy. *Cardiol J* 15: 388–395, 2008.

3. **Brodde O-E, Michel MC, Zerkowski H-R.** Signal transduction mechanisms controlling cardiac contractility and their alterations in chronic heart failure. *Cardiovasc Res* 30: 570–584, 1995.
4. **Brodsky GL, Muntoni F, Miocic S, Sinagra G, Sewry C, Mestroni L.** Lamin A/C Gene mutation associated with dilated cardiomyopathy with variable skeletal muscle involvement. *Circulation* 101: 473–476, 2000.
5. **Carniel E, Taylor MRG, Sinagra G, Di Lenarda A, Ku L, Fain PR, Boucek MM, Cavanaugh J, Miocic S, Slavov D, Graw SL, Feiger J, Zhu XZ, Dao D, Ferguson DA, Bristow MR, Mestroni L.** Alpha-myosin heavy chain: a sarcomeric gene associated with dilated and hypertrophic phenotypes of cardiomyopathy. *Circulation* 112: 54–59, 2005.
6. **Chamsi-Pasha MAR, Shao Z, Tang WHW.** Angiotensin-converting enzyme 2 as a therapeutic target for heart failure. *Curr Heart Fail Rep* 11: 58–63, 2014.
7. **Chang AN, Potter JD.** Sarcomeric protein mutations in dilated cardiomyopathy. *Heart Fail Rev* 10: 225–235, 2005.
8. **Cordero-Reyes AM, Youker K, Estep JD, Torre-Amione G, Nagueh SF.** Molecular and cellular correlates of cardiac function in end-stage DCM: a study using speckle tracking echocardiography [eng]. *JACC. Cardiovascular imaging* 7: 441–452, 2014.
9. **Franz M, Berndt A, Neri D, Galler K, Grün K, Porrmann C, Reinbothe F, Mall G, Schlattmann P, Renner A, Figulla HR, Jung C, Kütke F.** Matrix metalloproteinase-9, tissue inhibitor of metalloproteinase-1, B⁺ tenascin-C and ED-A⁺ fibronectin in dilated cardiomyopathy: potential impact on disease progression and patients' prognosis. *Int J Cardiol* 168: 5344–5351, 2013.
10. **Gladysheva IP, Wang D, McNamee RA, Hounq AK, Mohamad AA, Fan TM, Reed GL.** Corin overexpression improves cardiac function, heart failure, and survival in mice with dilated cardiomyopathy. *Hypertension* 61: 327–332, 2013.
11. **Hang CT, Yang J, Han P, Cheng H-L, Shang C, Ashley E, Zhou B, Chang C-P.** Chromatin regulation by Brg1 underlies heart muscle development and disease. *Nature* 466: 62–67, 2010.
12. **Iqbal N, Wentworth B, Choudhary R, Landa, Alejandro De La Parra, Kipper B, Fard A, Maisel AS.** Cardiac biomarkers: new tools for heart failure management. *Cardiovasc Diagn Ther* 2: 147–164, 2012.
13. **Jiang F, Yang J, Zhang Y, Dong M, Wang S, Zhang Q, Liu FF, Zhang K, Zhang C.** Angiotensin-converting enzyme 2 and angiotensin 1-7: novel therapeutic targets. *Nat Rev Cardiol* 11: 413–426, 2014.
14. **Kubo H, Margulies KB, Piacentino V, Gaughan JP, Houser SR.** Patients with end-stage congestive heart failure treated with -adrenergic receptor antagonists have improved ventricular myocyte calcium regulatory protein abundance. *Circulation* 104: 1012–1018, 2001.
15. **Lee DS, Vasan RS.** Novel markers for heart failure diagnosis and prognosis. *Curr Opin Cardiol* 20: 201–210, 2005.
16. **Lowes BD, Minobe W, Abraham WT, Rizeq MN, Bohlmeier TJ, Quaife RA, Roden RL, Dutcher DL, Robertson AD, Voelkel NF, Badesch DB, Groves BM, Gilbert EM, Bristow MR.** Changes in gene expression in the intact human heart. Downregulation of alpha-myosin heavy chain in hypertrophied, failing ventricular myocardium. *J Clin Invest* 100: 2315–2324, 1997.

17. **Mohapatra B, Jimenez S, Lin JH, Bowles KR, Coveler KJ, Marx JG, Chrisco MA, Murphy RT, Lurie PR, Schwartz RJ, Elliott PM, Vatta M, McKenna W, Towbin JA, Bowles NE.** Mutations in the muscle LIM protein and α -actinin-2 genes in dilated cardiomyopathy and endocardial fibroelastosis. *Mol Genet Metab* 80: 207–215, 2003.
18. **Norgett EE.** Recessive mutation in desmoplakin disrupts desmoplakin-intermediate filament interactions and causes dilated cardiomyopathy, woolly hair and keratoderma. *Hum Mol Genet* 9: 2761–2766, 2000.
19. **Parajuli N, Ramprasath T, Patel VB, Wang W, Putko B, Mori J, Oudit GY.** Targeting angiotensin-converting enzyme 2 as a new therapeutic target for cardiovascular diseases. *Can J Physiol Pharmacol* 92: 558–565, 2014.
20. **Patel SK, Velkoska E, Burrell LM.** Emerging markers in cardiovascular disease: where does angiotensin-converting enzyme 2 fit in?. *Clin Exp Pharmacol Physiol* 40: 551–559, 2013.
21. **Satoh M, Nakamura M, Akatsu T, Shimoda Y, Segawa I, Hiramori K.** Myocardial osteopontin expression is associated with collagen fibrillogenesis in human dilated cardiomyopathy. *Eur J Heart Fail* 7: 755–762, 2005.
22. **Shih Y-H, Zhang Y, Ding Y, Ross CA, Li H, Olson TM, Xu X.** Cardiac transcriptome and dilated cardiomyopathy genes in zebrafish. *Circ Genom Precis Med* 8: 261–269, 2015.
23. **Zhao S, Wu H, Xia W, Chen X, Zhu S, Zhang S, Shao Y, Ma W, Di Yang, Zhang J.** Periostin expression is upregulated and associated with myocardial fibrosis in human failing hearts. *J Cardiol* 63: 373–378, 2014.

Supplemental Table 2. All significantly correlated genes with LVEF, LVEDDI, or NT-proBNP

Gene Symbol	Annotation	Category	Identifier	LVEF			Identifier	LVEDDI			Identifier	NT-proBNP		
				p-value	pBH	p		p-value	pBH	p		p-value	pBH	p
AAMDC	adipogenesis associated, Mth938 domain containing	Gene Expression	221599_at	0.001	0.054	0.429	221599_at	<0.001	0.010	-0.567	221599_at	0.245	0.874	-0.193
ABCA11P	ATP-binding cassette, sub-family A (ABC1), member 11, pseudogene	Fatty Acid Metabolism	220159_at	0.008	0.139	0.354	220159_at	0.017	0.178	-0.322	220159_at	0.096	0.757	-0.274
ABCA17P	ATP-binding cassette, sub-family A (ABC1), member 17, pseudogene	Fatty Acid Metabolism	231164_at	0.026	0.229	0.300	231164_at	0.004	0.104	-0.380	231164_at	0.209	0.849	-0.208
ABCA6	ATP-binding cassette, sub-family A (ABC1), member 6	Fatty Acid Metabolism	217504_at	0.007	0.132	0.359	217504_at	0.089	0.375	-0.231	217504_at	0.222	0.858	-0.202
ABCA8	ATP-binding cassette, sub-family A (ABC1), member 8	Signal Transduction	204719_at	<0.001	0.047	0.439	204719_at	<0.001	0.054	-0.441	204719_at	0.029	0.561	-0.356
ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	Signal Transduction	209994_s_at	0.001	0.062	0.420	209994_s_at	0.039	0.260	-0.279	209994_s_at	0.057	0.663	-0.312
ABCG2	ATP-binding cassette, sub-family G (WHITE), member 2 (Junior blood group)	Signal Transduction	209735_at	<0.001	0.043	-0.446	209735_at	<0.001	0.047	0.454	209735_at	0.047	0.633	0.325
ABHD11	abhydrolase domain containing 11	Signal Transduction	221927_s_at	0.176	0.521	-0.185	221927_s_at	0.008	0.130	0.355	221927_s_at	0.060	0.672	0.308
ABHD2	abhydrolase domain containing 2	Signal Transduction	228490_at	<0.001	0.040	-0.453	221815_at	0.742	0.896	-0.045	221815_at	0.006	0.382	0.441
ABHD6	abhydrolase domain containing 6	Signal Transduction	45288_at	0.004	0.100	0.382	45288_at	<0.001	0.055	-0.439	45288_at	0.004	0.352	-0.464
ABI2	abl-interactor 2	Signal Transduction	225098_at	0.116	0.436	-0.214	225098_at	0.040	0.262	0.278	225098_at	0.006	0.382	0.440
ABRA	actin-binding Rho activating protein	Gene Expression	1552731_at	0.007	0.134	-0.357	1552731_at	0.030	0.232	0.294	1552731_at	0.025	0.528	0.365
ACACB	acetyl-CoA carboxylase beta	Fatty Acid Metabolism	49452_at	0.243	0.598	0.160	49452_at	0.008	0.127	-0.358	49452_at	0.374	0.922	-0.148
ACAT1	acetyl-CoA acetyltransferase 1	Fatty Acid Metabolism	205412_at	0.045	0.293	0.272	205412_at	0.004	0.097	-0.388	205412_at	0.128	0.796	-0.251
ACE2	angiotensin I converting enzyme 2	Cardiac Muscle	222257_s_at	<0.001	0.005	-0.575	222257_s_at	<0.001	0.018	0.526	222257_s_at	<0.001	0.136	0.589
ACOT9	acyl-CoA thioesterase 9	Fatty Acid Metabolism	221641_s_at	<0.001	0.033	-0.465	221641_s_at	0.644	0.850	0.063	221641_s_at	0.028	0.556	0.358
ACSL1	acyl-CoA synthetase long-chain family member 1	Fatty Acid Metabolism	201963_at	<0.001	0.042	0.447	201963_at	0.003	0.093	-0.391	201963_at	0.029	0.561	-0.356

Gene			LVEF				LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
ACSS3	acyl-CoA synthetase short-chain family member 3	Fatty Acid Metabolism	229222_at	0.018	0.193	0.319	229222_at	<0.001	0.019	-0.519	229222_at	0.021	0.503	-0.376
ACTA1	actin, alpha 1, skeletal muscle	Actin Cytoskeleton	203872_at	0.008	0.139	-0.354	203872_at	0.021	0.196	0.311	203872_at	0.010	0.435	0.414
ACTA2	actin, alpha 2, smooth muscle, aorta	Actin Cytoskeleton	200974_at	0.002	0.065	-0.414	200974_at	0.001	0.065	0.423	200974_at	0.848	0.990	0.032
ACTN1	actinin, alpha 1	Cardiac Muscle	208636_at	<0.001	<0.001	-0.649	208637_x_at	<0.001	0.046	0.456	208636_at	0.012	0.449	0.407
ACTRT3	actin-related protein T3	Actin Cytoskeleton	223665_at	0.250	0.606	0.158	223665_at	0.004	0.102	-0.384	223665_at	0.037	0.593	-0.340
ADAM17	ADAM metalloproteinase domain 17	Actin Cytoskeleton	205745_x_at	0.321	0.668	-0.136	205745_x_at	0.363	0.685	-0.125	205745_x_at	0.010	0.433	0.415
ADAM19	ADAM metalloproteinase domain 19	ECM Organization	209765_at	0.033	0.256	-0.288	209765_at	0.008	0.131	0.354	209765_at	0.018	0.490	0.384
ADAM23	ADAM metalloproteinase domain 23	Cell Adhesion	244463_at	0.008	0.134	0.357	206046_at	0.003	0.088	-0.397	206046_at	0.023	0.523	-0.369
ADAMTS15	ADAM metalloproteinase with thrombospondin type 1 motif, 15	ECM Organization	229004_at	<0.001	0.044	0.444	229004_at	0.002	0.083	-0.403	229004_at	0.027	0.550	-0.360
ADAMTS5	ADAM metalloproteinase with thrombospondin type 1 motif, 5	ECM Organization	229357_at	0.002	0.063	0.417	219935_at	0.139	0.450	-0.202	219935_at	0.009	0.410	-0.424
ADCK2	aarF domain containing kinase 2 adenylate cyclase activating polypeptide 1 (pituitary) receptor	Signal Transduction	44120_at	0.896	0.969	-0.018	44120_at	0.001	0.063	-0.429	44120_at	0.289	0.899	-0.176
ADCYAP1R1	type I adhesion G protein-coupled receptor	Signal Transduction	226690_at	<0.001	0.053	0.432	226690_at	0.038	0.254	-0.282	226690_at	0.092	0.747	-0.277
ADGRA3	A3 adhesion G protein-coupled receptor	Signal Transduction	210473_s_at	<0.001	0.043	0.445	210473_s_at	0.023	0.206	-0.306	210473_s_at	0.107	0.776	-0.265
ADGRD1	D1 alcohol dehydrogenase 5 (class III), chi polypeptide	Signal Transduction	232267_at	0.274	0.628	0.150	232267_at	0.003	0.091	-0.393	232267_at	0.042	0.616	-0.333
ADH5	alcohol dehydrogenase 5 (class III), chi polypeptide	Fatty Acid Metabolism	208847_s_at	0.079	0.371	0.239	208847_s_at	0.001	0.065	-0.423	208847_s_at	0.382	0.924	-0.146
ADIPOR1	adiponectin receptor 1	Fatty Acid Metabolism	217748_at	0.083	0.380	-0.236	217748_at	0.003	0.094	0.390	217748_at	0.910	0.994	-0.019
ADORA1	adenosine A1 receptor	Stress Response	205481_at	0.369	0.703	0.124	205481_at	0.005	0.108	-0.375	205481_at	0.505	0.953	-0.111
ADRB1	adrenoceptor beta 1	Signal Transduction	229277_at	0.007	0.130	0.360	229309_at	0.001	0.061	-0.431	229309_at	0.098	0.761	-0.273
ADRB2	adrenoceptor beta 2, surface	Signal Transduction	206170_at	<0.001	0.042	0.449	206170_at	<0.001	0.042	-0.464	206170_at	0.070	0.695	-0.297
AGBL5	ATP/GTP binding protein-like 5	Cell Division	218480_at	0.004	0.098	-0.384	238889_at	0.056	0.303	0.259	238889_at	0.009	0.416	0.422
AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2	Metabolic Process	210678_s_at	0.349	0.688	-0.129	210678_s_at	0.003	0.085	0.400	210678_s_at	0.987	0.999	-0.003

Gene			LVEF				LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3	Fatty Acid Metabolism	223182_s_at	0.172	0.515	0.187	223184_s_at	0.006	0.113	-0.370	223184_s_at	0.100	0.766	-0.271
AGTPBP1	ATP/GTP binding protein 1	Signal Transduction	204500_s_at	<0.001	0.032	0.467	204500_s_at	<0.001	0.043	-0.462	204500_s_at	0.036	0.585	-0.343
AK4	adenylate kinase 4	Metabolic Process	230630_at	0.130	0.458	-0.207	230630_at	0.209	0.533	0.172	230630_at	0.009	0.416	0.421
AKAP13	A kinase (PRKA) anchor protein 13	Signal Transduction	208325_s_at	<0.001	0.041	-0.450	221718_s_at	0.003	0.091	0.393	221718_s_at	0.014	0.463	0.396
AKAP7	A kinase (PRKA) anchor protein 7	Signal Transduction	205771_s_at	0.001	0.062	0.421	205771_s_at	<0.001	0.026	-0.497	205771_s_at	<0.001	0.153	-0.573
AKIRIN2	akirin 2	Immune/Acute Phase Response	223145_s_at	0.007	0.130	-0.360	223145_s_at	0.127	0.433	0.208	223145_s_at	0.215	0.854	0.206
ALDH18A1	aldehyde dehydrogenase 18 family, member A1	Carbohydrate Metabolism	222416_at	0.002	0.077	-0.403	222416_at	0.743	0.897	0.045	222416_at	0.344	0.915	0.157
ALDH1L1	aldehyde dehydrogenase 1 family, member L1	Carbohydrate Metabolism	205208_at	0.007	0.134	-0.357	205208_at	0.153	0.468	0.195	205208_at	0.574	0.966	-0.094
ALDH3A2	aldehyde dehydrogenase 3 family, member A2	Fatty Acid Metabolism	202053_s_at	0.015	0.185	-0.326	202053_s_at	0.004	0.103	0.381	202053_s_at	0.062	0.677	0.306
ALDH7A1	aldehyde dehydrogenase 7 family, member A1	Metabolic Process	208951_at	0.070	0.352	0.246	208951_at	0.894	0.961	0.018	208951_at	0.009	0.414	-0.422
ALG10	ALG10, alpha-1,2-glucosyltransferase	Carbohydrate Metabolism	1552306_at	0.288	0.640	0.146	1552306_at	0.002	0.083	-0.403	1552306_at	0.966	0.998	0.007
AMD1	adenosylmethionine decarboxylase 1	Metabolic Process	201196_s_at	0.007	0.131	0.359	201196_s_at	0.075	0.348	-0.242	201196_s_at	0.223	0.859	-0.202
AMFR	autocrine motility factor receptor, E3 ubiquitin protein ligase	Protein Folding	202204_s_at	0.216	0.571	-0.169	202204_s_at	0.009	0.135	0.352	202204_s_at	0.541	0.961	0.102
ANAPC11	anaphase promoting complex subunit 11	Cell Division	226414_s_at	0.159	0.500	0.192	226414_s_at	<0.001	0.055	-0.439	226414_s_at	0.167	0.828	-0.229
ANGPTL1	angiopoietin-like 1	Signal Transduction	224339_s_at	<0.001	0.009	-0.535	224339_s_at	<0.001	0.033	0.478	239183_at	0.003	0.329	0.475
ANKRD1	ankyrin repeat domain 1 (cardiac muscle)	Cardiac Muscle	206029_at	0.002	0.070	-0.410	206029_at	0.285	0.614	0.147	206029_at	0.342	0.915	0.158
ANKRD10	ankyrin repeat domain 10	Signal Transduction	223251_s_at	0.004	0.101	-0.381	223251_s_at	0.750	0.899	0.044	223251_s_at	0.842	0.990	0.033
ANKRD13C	ankyrin repeat domain 13C	Signal Transduction	227375_at	0.004	0.097	0.385	1554471_a_at	0.005	0.107	0.376	1554471_a_at	0.368	0.921	0.150
ANKRD6	ankyrin repeat domain 6	Signal Transduction	204671_s_at	0.107	0.423	0.220	204671_s_at	0.006	0.116	-0.366	204672_s_at	0.221	0.858	-0.203
ANKRD9	ankyrin repeat domain 9	Protein Translation	227959_at	0.002	0.077	-0.404	227959_at	0.335	0.661	0.132	227959_at	0.378	0.923	0.147

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
ANXA3	annexin A3	Metabolic Process	209369_at	0.006	0.123	0.365	209369_at	0.098	0.391	-0.225	209369_at	0.033	0.572	-0.348
ANXA4	annexin A4	Apoptosis	201301_s_at	0.002	0.077	-0.402	201301_s_at	0.027	0.222	0.299	201301_s_at	0.045	0.625	0.328
ANXA6	annexin A6	Signal Transduction	200982_s_at	0.396	0.722	-0.117	200982_s_at	0.002	0.081	0.406	200982_s_at	0.818	0.986	0.039
AP1S2	adaptor-related protein complex 1, sigma 2 subunit	Immune/Acute Phase Response	228415_at	<0.001	0.036	-0.461	228415_at	0.001	0.058	0.434	228415_at	0.003	0.345	0.468
APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2	ECM Organization	40148_at	0.017	0.191	-0.321	213419_at	0.016	0.173	0.325	213419_at	0.002	0.290	0.486
APH1B	APH1B gamma secretase subunit	Apoptosis	226358_at	0.053	0.313	0.262	226358_at	<0.001	0.046	-0.456	226358_at	0.016	0.473	-0.389
APLN	apelin	Immune/Acute Phase Response	244166_at	0.226	0.582	0.166	244166_at	0.008	0.129	-0.356	244166_at	0.089	0.741	-0.280
APLP2	amyloid beta (A4) precursor-like protein 2	Signal Transduction	211404_s_at	<0.001	0.009	-0.535	211404_s_at	0.002	0.076	0.410	208702_x_at	0.670	0.974	0.071
APOA1	apolipoprotein A-I	Signal Transduction	204450_x_at	0.001	0.062	-0.420	204450_x_at	0.022	0.199	0.310	204450_x_at	0.194	0.838	0.215
APP	amyloid beta (A4) precursor protein	Cell Division	214953_s_at	0.827	0.945	-0.030	214953_s_at	0.002	0.076	0.410	214953_s_at	0.940	0.996	-0.013
AQP4	aquaporin 4	Signal Transduction	226228_at	0.001	0.059	0.423	210906_x_at	0.001	0.062	-0.431	226228_at	0.003	0.336	-0.470
AQR	aquarius intron-binding spliceosomal factor	Gene Expression	212584_at	0.042	0.287	-0.275	212584_at	0.004	0.105	0.380	212584_at	0.661	0.974	-0.073
ARF3	ADP-ribosylation factor 3	Signal Transduction	200734_s_at	0.729	0.903	0.048	200734_s_at	0.008	0.129	0.356	200734_s_at	0.906	0.993	0.020
ARF4	ADP-ribosylation factor 4	Protein Translation	201096_s_at	0.003	0.089	-0.391	201096_s_at	0.543	0.799	0.084	201096_s_at	0.691	0.975	0.066
ARFGEF3	ARFGEF family member 3	Signal Transduction	227479_at	0.474	0.770	0.099	227479_at	0.005	0.111	-0.372	227479_at	0.754	0.982	-0.052
ARHGAP1	Rho GTPase activating protein 1	Signal Transduction	202117_at	0.013	0.172	-0.334	202117_at	0.009	0.135	0.352	202117_at	<0.001	0.170	0.556
ARHGAP24	Rho GTPase activating protein 24	Signal Transduction	223422_s_at	0.006	0.124	-0.364	223422_s_at	0.754	0.901	0.043	223422_s_at	0.170	0.831	0.227
ARHGAP27	Rho GTPase activating protein 27	Signal Transduction	225618_at	0.151	0.490	0.196	225618_at	0.001	0.061	-0.432	225618_at	0.032	0.566	-0.350
ARHGEF9	Cdc42 guanine nucleotide exchange factor (GEF) 9	Signal Transduction	203264_s_at	0.858	0.956	-0.025	203264_s_at	<0.001	0.046	0.457	203264_s_at	0.325	0.909	0.164
ARL13B	ADP-ribosylation factor-like 13B	Signal Transduction	228201_at	0.081	0.375	-0.238	228201_at	0.007	0.119	0.364	228201_at	0.037	0.593	0.340

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
ARPC3	actin related protein 2/3 complex, subunit 3, 21kDa	Actin Cytoskeleton	208736_at	0.006	0.117	-0.369	208736_at	0.190	0.513	0.179	208736_at	0.026	0.539	0.363
ARSD	arylsulfatase D	Metabolism	230131_x_at	0.225	0.580	-0.166	230131_x_at	0.006	0.114	0.369	230131_x_at	0.592	0.968	0.089
ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	Fatty Acid Metabolism	213702_x_at	0.328	0.673	0.134	213702_x_at	0.007	0.123	-0.360	213702_x_at	0.516	0.955	0.108
ASB1	ankyrin repeat and SOCS box containing 1	Signal Transduction	212819_at	0.002	0.077	0.403	212819_at	0.002	0.070	-0.417	212819_at	0.032	0.566	-0.350
ASB4	ankyrin repeat and SOCS box containing 4	Protein Folding	235619_at	0.205	0.557	0.174	235619_at	<0.001	0.048	-0.452	235619_at	0.414	0.932	-0.136
ASPH	aspartate beta-hydroxylase	Signal Transduction	224996_at	0.105	0.420	0.221	224996_at	0.022	0.201	-0.308	224996_at	<0.001	0.170	-0.556
ASPN	asporin	ECM Organization	219087_at	0.001	0.054	-0.430	224396_s_at	0.002	0.074	0.413	219087_at	0.053	0.648	0.316
ATAD1	ATPase family, AAA domain containing 1	Signal Transduction	236072_at	0.142	0.477	0.201	236072_at	0.002	0.083	-0.403	236072_at	0.510	0.954	-0.110
ATF6B	activating transcription factor 6 beta	Gene Expression	1554487_a_at	0.003	0.081	0.399	1554487_a_at	0.008	0.126	-0.358	1554487_a_at	0.321	0.908	-0.165
ATG12	autophagy related 12	Protein Folding	213930_at	0.026	0.230	0.299	213930_at	0.008	0.131	-0.355	213930_at	0.364	0.919	-0.151
ATM	ATM serine/threonine kinase	Cell Division	212672_at	0.006	0.118	0.368	212672_at	0.522	0.788	-0.088	212672_at	0.186	0.833	0.219
ATMIN	ATM interactor	Gene Expression	201855_s_at	0.056	0.322	0.259	201855_s_at	0.001	0.062	-0.430	201855_s_at	0.665	0.974	-0.072
ATOH8	atonal homolog 8 (Drosophila)	Gene Expression	228890_at	0.033	0.254	-0.288	228890_at	0.643	0.850	0.064	228890_at	0.004	0.356	0.463
ATP1A2	ATPase, Na+/K+ transporting, alpha 2 polypeptide	Signal Transduction	203295_s_at	0.018	0.194	-0.318	203295_s_at	0.077	0.352	0.241	203295_s_at	0.009	0.416	0.420
ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	Cardiac Muscle	212361_s_at	0.006	0.123	0.365	212361_s_at	0.004	0.099	-0.386	212361_s_at	0.023	0.522	-0.371
ATP5A1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	Fatty Acid Metabolism	213738_s_at	0.489	0.780	0.095	213738_s_at	0.008	0.128	-0.357	213738_s_at	0.500	0.953	0.113
ATP5C1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	Respiratory Electron Chain Transport	213366_x_at	0.398	0.724	0.116	213366_x_at	0.007	0.121	-0.362	213366_x_at	0.595	0.968	0.089
ATP5E	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	Signal Transduction	217801_at	0.007	0.130	0.360	217801_at	<0.001	0.051	-0.448	217801_at	0.327	0.909	-0.163
ATP5F1	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit B1	Signal Transduction	211755_s_at	0.189	0.536	0.180	211755_s_at	0.003	0.083	-0.402	211755_s_at	0.704	0.976	-0.064

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
ATP5G1	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit C1 (subunit 9)	Respiratory Electron Chain Transport	208972_s_at	0.029	0.242	0.294	208972_s_at	<0.001	0.024	-0.501	208972_s_at	0.641	0.972	-0.078
ATP5G3	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit C3 (subunit 9)	Respiratory Electron Chain Transport	207508_at	0.059	0.328	0.257	228168_at	<0.001	0.023	-0.503	228168_at	0.133	0.799	-0.248
ATP5I	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit E	Signal Transduction	209492_x_at	<0.001	0.029	0.475	209492_x_at	0.074	0.346	-0.243	209492_x_at	0.973	0.998	-0.006
ATP5J	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit F6	Signal Transduction	202325_s_at	0.002	0.077	0.404	202325_s_at	<0.001	0.026	-0.494	202325_s_at	0.362	0.919	-0.152
ATP5O	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	Respiratory Electron Chain Transport	216954_x_at	0.337	0.679	0.132	216954_x_at	0.010	0.140	-0.348	216954_x_at	0.411	0.931	-0.137
ATP5S	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit s (factor B)	Respiratory Electron Chain Transport	1554177_a_at	0.261	0.618	0.154	1554177_a_at	0.008	0.127	-0.358	1554177_a_at	0.208	0.847	-0.209
ATP6AP2	ATPase, H+ transporting, lysosomal accessory protein 2	Signal Transduction	201444_s_at	0.001	0.062	-0.419	201444_s_at	0.007	0.124	0.360	201444_s_at	0.047	0.633	0.325
ATP6V0E1	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1	Respiratory Electron Chain Transport	214150_x_at	0.513	0.795	0.090	214150_x_at	0.005	0.107	-0.377	214150_x_at	0.601	0.968	0.087
ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	Respiratory Electron Chain Transport	202874_s_at	0.019	0.197	-0.316	202874_s_at	0.004	0.103	0.382	202874_s_at	0.059	0.668	0.310
ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	Signal Transduction	235864_at	0.043	0.287	-0.274	235864_at	0.056	0.303	0.259	235864_at	0.004	0.358	0.456
ATP8B1	ATPase, aminophospholipid transporter, class I, type 8B, member 1	Signal Transduction	226302_at	0.023	0.215	-0.307	226302_at	0.002	0.083	0.403	226302_at	0.347	0.915	0.156
ATPIF1	ATPase inhibitory factor 1	Respiratory Electron Chain Transport	218671_s_at	0.441	0.750	0.106	218671_s_at	0.007	0.123	-0.360	218671_s_at	0.443	0.938	0.128
ATRX	alpha thalassemia/mental retardation syndrome X-linked	Gene Expression	208859_s_at	0.606	0.848	-0.071	208859_s_at	0.705	0.878	0.052	208859_s_at	0.009	0.416	0.420
ATXN1L	ataxin 1-like	ECM Organization	227373_at	0.005	0.116	-0.370	227373_at	<0.001	0.043	0.462	227373_at	<0.001	0.194	0.544
AURKAIP1	aurora kinase A interacting protein 1	Protein Translation	227546_x_at	0.003	0.085	0.395	227546_x_at	0.557	0.806	-0.081	227546_x_at	0.278	0.896	-0.180

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
AZIN1	antizyme inhibitor 1	Amino Acid Metabolism Immune/Acute Phase Response	212461_at	0.002	0.062	-0.418	212461_at	0.011	0.148	0.342	201772_at	0.007	0.393	0.437
B2M	beta-2-microglobulin		201891_s_at	0.357	0.695	0.127	201891_s_at	0.004	0.100	-0.385	201891_s_at	0.517	0.955	0.108
B3GALNT1	beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)	Metabolic Process	211812_s_at	0.652	0.870	-0.062	211812_s_at	0.523	0.788	-0.088	211812_s_at	0.010	0.429	-0.417
B4GALT6	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6 BMP and activin membrane-bound inhibitor	Carbohydrate Metabolism	235333_at	0.003	0.082	0.397	235333_at	<0.001	0.051	-0.445	235333_at	<0.001	0.170	-0.558
BAMBI	BTG3 associated nuclear protein	Signal Transduction	203304_at	0.002	0.075	-0.405	203304_at	0.011	0.150	0.340	203304_at	0.198	0.842	0.213
BANP	Bardet-Biedl syndrome 1	Cell Division	233186_s_at	0.006	0.124	-0.364	233186_s_at	0.333	0.660	0.133	233186_s_at	0.108	0.776	0.265
BBS1	Bardet-Biedl syndrome 1	Cell Division	218471_s_at	0.006	0.119	0.368	218471_s_at	0.573	0.813	0.077	218471_s_at	0.137	0.800	-0.245
BBS4	Bardet-Biedl syndrome 4	Fatty Acid Metabolism	212745_s_at	0.008	0.143	-0.352	212745_s_at	0.190	0.513	0.179	212745_s_at	0.717	0.979	0.061
BBX	bobby sox homolog (Drosophila) BRCA2 and CDKN1A interacting protein	Gene Expression	232008_s_at	0.003	0.084	-0.396	232008_s_at	0.036	0.249	0.284	223134_at	0.007	0.394	0.436
BCCIP	branched chain keto acid dehydrogenase E1, beta polypeptide B-cell CLL/lymphoma 11A (zinc finger protein)	Cell Division	227896_at	0.003	0.090	-0.390	227896_at	0.004	0.097	0.387	227896_at	0.243	0.872	0.194
BCKDHB	branched chain keto acid dehydrogenase E1, beta polypeptide B-cell CLL/lymphoma 11A (zinc finger protein)	Carbohydrate Metabolism	210653_s_at	0.308	0.657	0.140	210653_s_at	0.139	0.449	-0.202	210653_s_at	0.008	0.408	-0.427
BCL11A	BCL2-like 11 (apoptosis facilitator) BCL2-associated transcription factor 1	Gene Expression	210347_s_at	0.007	0.130	0.360	210347_s_at	<0.001	0.011	-0.552	210347_s_at	0.022	0.512	-0.373
BCL2L11	BCL2-like 11 (apoptosis facilitator) BCL2-associated transcription factor 1	Apoptosis	225606_at	<0.001	0.019	0.498	225606_at	0.031	0.236	-0.291	225606_at	0.160	0.819	-0.232
BCLAF1	biglycan	Gene Expression	214499_s_at	0.004	0.095	-0.387	214499_s_at	0.011	0.147	0.343	214499_s_at	<0.001	0.134	0.602
BGN	biglycan	ECM Organization	213905_x_at	0.018	0.197	-0.317	213905_x_at	<0.001	0.057	0.436	201261_x_at	0.047	0.633	0.325
BICD2	bicaudal D homolog 2 (Drosophila) BH3 interacting domain death agonist	Cell Division	209203_s_at	0.018	0.193	-0.319	209203_s_at	0.534	0.793	0.085	209203_s_at	0.003	0.315	0.479
BID	bridging integrator 3	Signal Transduction	211725_s_at	0.797	0.933	0.036	211725_s_at	0.001	0.065	-0.423	211725_s_at	0.220	0.857	-0.203
BIN3	bridging integrator 3	Actin Cytoskeleton	222199_s_at	0.010	0.153	-0.346	222199_s_at	0.006	0.116	0.366	222199_s_at	0.188	0.834	0.218
BIRC2	baculoviral IAP repeat containing 2	Protein Folding	202076_at	0.023	0.215	0.307	202076_at	0.001	0.058	-0.434	202076_at	0.177	0.833	-0.224
BIRC3	baculoviral IAP repeat containing 3	Protein Folding	210538_s_at	0.004	0.098	0.383	210538_s_at	0.003	0.085	-0.400	210538_s_at	0.029	0.561	-0.355

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
BLM	Bloom syndrome, RecQ helicase-like	Stress Response	205733_at	<0.001	0.025	0.482	205733_at	0.005	0.106	-0.378	205733_at	0.198	0.842	-0.213
BMP5	bone morphogenetic protein 5	Cardiac Muscle	205430_at	0.004	0.095	0.386	205430_at	0.147	0.459	-0.198	205430_at	0.855	0.991	-0.031
BMP7	bone morphogenetic protein 7	ECM Organization	209590_at	<0.001	0.010	0.529	209590_at	0.004	0.097	-0.388	209590_at	0.013	0.457	-0.402
BRCC3	BRCA1/BRCA2-containing complex, subunit 3	Protein Folding	216521_s_at	0.009	0.149	-0.348	216521_s_at	0.102	0.397	0.223	216521_s_at	0.042	0.618	0.332
BRD2	bromodomain containing 2	Gene Expression	208685_x_at	0.231	0.586	-0.164	208685_x_at	0.006	0.112	0.371	208685_x_at	0.240	0.871	0.195
BRD7	bromodomain containing 7	Cell Division	222737_s_at	0.001	0.062	-0.421	222737_s_at	0.114	0.416	0.215	222737_s_at	0.066	0.690	0.302
BRF2	BRF2, RNA polymerase III transcription initiation factor 50 kDa subunit	Gene Expression	218955_at	0.177	0.521	-0.185	218955_at	0.005	0.108	0.374	218955_at	0.520	0.956	-0.107
BTG1	B-cell translocation gene 1, anti-proliferative	Apoptosis	200920_s_at	0.002	0.063	-0.416	200920_s_at	0.409	0.718	0.113	200920_s_at	0.183	0.833	0.220
BTN2A1	butyrophilin, subfamily 2, member A1	Metabolic Process	203944_x_at	0.002	0.064	-0.415	203944_x_at	0.055	0.301	0.261	203944_x_at	0.249	0.875	0.191
C1GALT1C1L	C1GALT1-specific chaperone 1 like	Protein Folding	241710_at	0.149	0.486	0.197	241710_at	0.007	0.123	-0.360	241710_at	0.047	0.632	-0.325
C3	complement component 3	Immune/Acute Phase Response	217767_at	0.052	0.311	0.263	217767_at	0.178	0.497	-0.184	217767_at	0.002	0.277	-0.499
CACNA2D1	calcium channel, voltage-dependent, alpha 2/delta subunit 1	Cardiac Muscle	227623_at	0.103	0.417	-0.222	227623_at	0.005	0.106	0.378	227623_at	0.045	0.626	0.327
CACNA2D3	calcium channel, voltage-dependent, alpha 2/delta subunit 3	Cardiac Muscle	219714_s_at	<0.001	0.036	0.460	219714_s_at	0.073	0.343	-0.244	219714_s_at	0.182	0.833	-0.221
CACNB2	calcium channel, voltage-dependent, beta 2 subunit	Signal Transduction	213714_at	0.005	0.116	0.370	213714_at	0.002	0.067	-0.421	213714_at	<0.001	0.239	-0.524
CACYBP	calcyclin binding protein	Cardiac Muscle	201381_x_at	<0.001	0.024	0.486	210691_s_at	0.001	0.065	-0.427	210691_s_at	0.017	0.485	-0.386
CADPS2	Ca++-dependent secretion activator 2	Cell Adhesion	219572_at	0.011	0.163	0.339	219572_at	<0.001	0.026	-0.496	219572_at	0.928	0.995	0.015
CALD1	caldesmon 1	Actin Cytoskeleton	201617_x_at	0.001	0.058	-0.425	201617_x_at	0.015	0.168	0.328	201616_s_at	0.014	0.463	0.397
CALR	calreticulin	Cardiac Muscle	214316_x_at	0.030	0.244	0.293	214316_x_at	0.007	0.121	-0.362	214316_x_at	0.319	0.908	-0.166
CALU	calumenin	Metabolic Process	200757_s_at	0.007	0.133	-0.358	200757_s_at	0.168	0.485	0.188	200757_s_at	0.657	0.974	0.074
CAMK2D	calcium/calmodulin-dependent protein kinase II delta	Signal Transduction	231793_s_at	0.019	0.201	-0.314	231793_s_at	0.084	0.367	0.235	231793_s_at	0.009	0.416	0.420
CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2, beta	Signal Transduction	213812_s_at	0.010	0.154	-0.346	213812_s_at	0.053	0.296	0.263	213812_s_at	0.092	0.747	0.277
CAMTA1	calmodulin binding transcription activator 1	Gene Expression	225692_at	0.001	0.054	0.430	225692_at	0.001	0.065	-0.426	225692_at	0.381	0.923	-0.146

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
CAND1	cullin-associated and neddylation-dissociated 1	Protein Folding	208839_s_at	0.008	0.140	-0.353	208839_s_at	0.001	0.065	0.425	208839_s_at	0.702	0.976	0.064
CANT1	calcium activated nucleotidase 1	Signal Transduction	46323_at	0.003	0.081	-0.398	46323_at	0.476	0.761	0.098	46323_at	0.587	0.968	0.091
CAP2	CAP, adenylate cyclase-associated protein, 2 (yeast)	Actin Cytoskeleton	212551_at	0.002	0.074	-0.407	212551_at	0.150	0.464	0.196	212551_at	0.022	0.520	0.372
CAPN3	calpain 3, (p94)	Apoptosis	210944_s_at	0.036	0.266	-0.283	210944_s_at	0.037	0.253	0.282	210944_s_at	0.003	0.337	0.470
CARD18	caspase recruitment domain family, member 18	Immune/Acute Phase Response	231733_at	<0.001	0.016	0.511	231733_at	<0.001	0.048	-0.450	231733_at	0.372	0.922	-0.148
CARF	calcium responsive transcription factor	Gene Expression	219834_at	0.003	0.089	-0.391	219834_at	0.058	0.308	0.257	219834_at	0.709	0.977	0.062
CASC3	cancer susceptibility candidate 3	Gene Expression	207842_s_at	0.734	0.906	0.047	207842_s_at	0.005	0.106	-0.378	207842_s_at	0.401	0.928	-0.140
CASP3	caspase 3, apoptosis-related cysteine peptidase	Amino Acid Metabolism	202763_at	0.008	0.136	-0.356	202763_at	0.067	0.329	0.249	202763_at	0.597	0.968	0.088
CASQ1	calsequestrin 1 (fast-twitch, skeletal muscle)	Signal Transduction	219645_at	0.031	0.249	-0.291	219645_at	0.002	0.080	0.406	219645_at	0.068	0.693	0.299
CBLB	Cbl proto-oncogene B, E3 ubiquitin protein ligase	Protein Folding	209682_at	0.055	0.318	0.260	209682_at	<0.001	0.054	-0.441	209682_at	0.009	0.416	-0.420
CBR4	carbonyl reductase 4	Fatty Acid Metabolism	244052_at	0.931	0.980	0.012	244052_at	0.007	0.122	-0.361	244052_at	0.522	0.958	0.107
CBX2	chromobox homolog 2	Gene Expression	240084_at	0.863	0.958	-0.024	240084_at	0.005	0.108	0.374	240084_at	0.112	0.780	0.262
CBX5	chromobox homolog 5	Cell Division	209715_at	0.031	0.248	0.291	209715_at	0.007	0.121	-0.362	209715_at	0.719	0.979	-0.060
CCDC3	coiled-coil domain containing 3	Fatty Acid Metabolism	223316_at	0.004	0.103	-0.380	223316_at	0.013	0.159	0.334	223316_at	0.978	0.998	-0.005
CCDC80	coiled-coil domain containing 80	ECM Organization	225242_s_at	0.008	0.140	-0.353	225242_s_at	0.006	0.116	0.366	225242_s_at	0.535	0.959	0.104
CCND1	cyclin D1	Cell Division	208712_at	<0.001	0.047	-0.439	208711_s_at	0.006	0.115	0.367	208711_s_at	0.013	0.457	0.400
CCND3	cyclin D3	Cell Division	201700_at	0.009	0.150	-0.347	201700_at	0.407	0.717	0.114	201700_at	0.782	0.984	0.046
CCNI	cyclin I	Cell Division	208656_s_at	0.009	0.149	-0.348	208656_s_at	0.341	0.667	0.131	208656_s_at	0.038	0.594	0.338
CCNK	cyclin K	Cell Division	225824_at	0.003	0.089	0.391	225824_at	0.032	0.237	-0.290	225824_at	0.754	0.982	0.052
CCNL1	cyclin L1	Cell Division	1555411_a_at	0.161	0.501	0.192	1555411_a_at	0.009	0.139	-0.349	1555411_a_at	0.097	0.760	-0.273
CCSAP	centriole, cilia and spindle-associated protein	Cell Division	225904_at	<0.001	0.041	-0.450	225904_at	0.015	0.171	0.326	225904_at	0.458	0.940	0.124
CD109	CD109 molecule	Fatty Acid Metabolism	229900_at	0.155	0.495	0.194	229900_at	0.006	0.113	-0.369	229900_at	0.061	0.674	-0.307
CD151	CD151 molecule (Raph blood group)	Cell Adhesion	204306_s_at	0.206	0.558	-0.173	204306_s_at	0.006	0.118	0.365	204306_s_at	0.566	0.965	0.096
CD36	CD36 molecule (thrombospondin receptor)	Signal Transduction	228766_at	<0.001	0.037	0.458	228766_at	0.029	0.229	-0.295	228766_at	0.336	0.911	-0.160

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
CD3EAP	CD3e molecule, epsilon associated protein	Signal Transduction	205264_at	0.008	0.140	0.354	205264_at	0.020	0.190	-0.315	205264_at	<0.001	0.097	-0.662
CD47	CD47 molecule	Cell Adhesion	213857_s_at	0.814	0.939	-0.032	213857_s_at	0.004	0.103	-0.381	213857_s_at	0.094	0.754	-0.275
		Immune/Acute Phase												
CD86	CD86 molecule	Response	205685_at	0.006	0.124	0.364	205685_at	0.021	0.196	-0.311	205685_at	0.049	0.637	-0.322
CDC16	cell division cycle 16	Cell Division	209659_s_at	0.189	0.537	0.180	209659_s_at	0.009	0.138	-0.349	209659_s_at	0.794	0.984	-0.044
CDC42	cell division cycle 42	Actin Cytoskeleton	210232_at	0.120	0.444	0.212	210232_at	0.007	0.121	-0.362	210232_at	0.015	0.466	-0.394
CDC42SE2	CDC42 small effector 2	Signal Transduction	229026_at	0.171	0.514	0.187	229026_at	0.002	0.075	-0.410	229026_at	0.219	0.855	-0.204
CDC5L	cell division cycle 5-like	Cell Division	209055_s_at	0.293	0.646	-0.144	209055_s_at	0.009	0.134	0.352	209055_s_at	0.581	0.967	0.092
CDC47L	cell division cycle associated 7-like	Cell Division	225081_s_at	0.008	0.136	0.356	225081_s_at	<0.001	0.032	-0.479	225081_s_at	0.125	0.795	-0.253
CDK11B	cyclin-dependent kinase 11B	Cell Division	212401_s_at	0.149	0.487	0.197	212401_s_at	<0.001	0.043	-0.462	212401_s_at	0.387	0.924	-0.144
CDK6	cyclin-dependent kinase 6	Cell Division	243000_at	0.055	0.319	0.260	243000_at	<0.001	0.046	-0.457	243000_at	0.217	0.855	-0.205
	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	Cell Division												
CDKN1A	cat eye syndrome chromosome region, candidate 2	Cell Division	202284_s_at	<0.001	0.011	-0.524	202284_s_at	0.028	0.225	0.297	202284_s_at	0.012	0.449	0.408
CECR2	cadherin, EGF LAG seven-pass G-type receptor 2	Apoptosis	239752_at	0.001	0.057	0.427	239752_at	<0.001	0.047	-0.455	223729_at	0.663	0.974	-0.073
CELSR2	centromere protein V	Signal Transduction	36499_at	0.005	0.116	0.371	36499_at	0.021	0.196	-0.311	36499_at	0.044	0.623	-0.330
CENPV	centrosomal protein 112kDa	Cell Division	226610_at	0.447	0.754	0.105	226610_at	0.008	0.132	-0.353	226610_at	0.087	0.739	-0.282
CEP112	centrosomal protein 192kDa	Cell Division	213644_at	0.005	0.112	0.373	213644_at	0.018	0.182	-0.320	213644_at	0.581	0.967	-0.092
CEP192	centrosomal protein 85kDa	Cell Division	218827_s_at	<0.001	0.047	0.439	218827_s_at	0.002	0.070	-0.417	218827_s_at	<0.001	0.159	-0.567
CEP85	centrosomal protein 85kDa-like	Cell Division	227818_at	0.477	0.772	-0.098	227818_at	0.856	0.946	-0.025	227818_at	0.010	0.426	-0.418
CEP85L		Cell Division	228007_at	<0.001	0.025	0.481	228007_at	0.001	0.065	-0.425	228007_at	0.022	0.522	-0.371
CFDP1	craniofacial development protein 1	Apoptosis	203166_at	0.821	0.943	-0.031	203166_at	0.389	0.703	0.118	203166_at	0.010	0.433	0.415
CHADL	chondroadherin-like	ECM Organization	1557123_a_at	0.076	0.366	0.241	1557123_a_at	<0.001	0.011	-0.550	1557123_a_at	0.069	0.693	-0.299
		Carbohydrate												
CHDH	choline dehydrogenase	Metabolism	229954_at	<0.001	0.022	0.492	229954_at	0.033	0.239	-0.289	1559591_s_at	0.002	0.289	-0.489
	calcium homeostasis endoplasmic reticulum protein	Gene Expression												
CHERP	chromogranin B	Protein Translation	202230_s_at	0.108	0.424	0.219	202230_s_at	0.005	0.109	-0.373	202230_s_at	0.075	0.709	-0.293
CHGB	charged multivesicular body protein 1A	Cell Division	204260_at	0.047	0.299	0.269	204260_at	<0.001	0.041	-0.466	204260_at	0.174	0.832	-0.225
	charged multivesicular body protein 1B	Cell Division												
CHMP1A		Cell Division	201933_at	0.001	0.054	-0.430	201933_at	0.132	0.442	0.205	201933_at	0.328	0.909	-0.163
CHMP1B		Cell Division	218177_at	0.600	0.845	-0.072	218177_at	0.920	0.971	-0.014	218177_at	0.007	0.402	-0.432
CHAC1	chromatin accessibility complex 1	Gene Expression	231764_at	0.002	0.065	0.414	231764_at	0.378	0.695	-0.121	231764_at	0.143	0.800	-0.242

Gene			LVEF				LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
CHST12	carbohydrate (chondroitin 4) sulfotransferase 12	Carbohydrate Metabolism	218927_s_at	0.007	0.134	-0.357	218927_s_at	0.034	0.241	0.288	218927_s_at	0.567	0.965	0.096
CHST9	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9	Carbohydrate Metabolism	224400_s_at	<0.001	0.023	0.490	224400_s_at	0.004	0.103	-0.381	223737_x_at	0.013	0.457	-0.400
CHTOP	chromatin target of PRMT1	Gene Expression	202560_s_at	0.363	0.700	-0.125	202560_s_at	0.007	0.124	0.359	209927_s_at	0.008	0.404	0.429
CKAP4	cytoskeleton-associated protein 4	Protein Translation	200998_s_at	<0.001	0.039	-0.454	200998_s_at	0.397	0.710	0.116	200998_s_at	0.592	0.968	0.089
CLCN4	chloride channel, voltage-sensitive 4	Signal Transduction	205148_s_at	0.094	0.402	0.228	205148_s_at	0.861	0.948	-0.024	205148_s_at	0.005	0.359	-0.453
CLCNKB	chloride channel, voltage-sensitive Kb	Signal Transduction	1554748_at	0.073	0.359	0.244	1554748_at	<0.001	0.010	-0.560	1554748_at	0.711	0.979	-0.062
CLIC5	chloride intracellular channel 5	Signal Transduction	217628_at	0.010	0.154	-0.346	217628_at	0.001	0.058	0.434	217628_at	0.287	0.899	0.177
CNDP2	CNDP dipeptidase 2	Carbohydrate Metabolism	217752_s_at	0.037	0.270	0.282	217752_s_at	0.002	0.079	-0.407	217752_s_at	0.753	0.982	-0.053
CNGA1	(metallopeptidase M20 family) cyclic nucleotide gated channel alpha 1	Signal Transduction	206417_at	0.002	0.066	0.413	206417_at	0.628	0.843	-0.067	206417_at	0.260	0.883	-0.187
CNN1	calponin 1, basic, smooth muscle	Cardiac Muscle	203951_at	0.002	0.077	-0.404	203951_at	0.025	0.213	0.303	203951_at	0.133	0.799	0.248
CNN3	calponin 3, acidic	Actin Cytoskeleton	228297_at	0.314	0.662	0.138	228297_at	<0.001	0.051	-0.448	228297_at	0.572	0.966	-0.094
CNTN4	contactin 4	Cell Adhesion	229084_at	0.828	0.945	0.030	229084_at	0.233	0.562	0.163	229084_at	0.007	0.402	0.432
COA5	cytochrome c oxidase assembly factor 5	Respiratory Electron Chain Transport	225410_at	0.045	0.292	0.272	225410_at	0.002	0.072	-0.414	225410_at	0.063	0.678	-0.305
COL16A1	collagen, type XVI, alpha 1	Cell Adhesion	204345_at	0.003	0.093	-0.388	204345_at	0.091	0.378	0.230	204345_at	0.271	0.892	0.183
COL1A1	collagen, type I, alpha 1	ECM Organization	1556499_s_at	0.010	0.157	-0.344	1556499_s_at	0.008	0.129	0.356	1556499_s_at	0.072	0.700	0.296
COL1A2	collagen, type I, alpha 2	ECM Organization	202404_s_at	0.002	0.077	-0.404	202403_s_at	0.005	0.110	0.373	202403_s_at	0.118	0.789	0.258
COL21A1	collagen, type XXI, alpha 1	ECM Organization	208096_s_at	<0.001	0.049	-0.437	208096_s_at	0.031	0.235	0.292	208096_s_at	0.082	0.724	0.286
COL27A1	collagen, type XXVII, alpha 1	ECM Organization	225293_at	<0.001	0.051	0.434	225293_at	0.009	0.139	-0.349	225293_at	0.976	0.998	-0.005
COL28A1	collagen, type XXVIII, alpha 1	ECM Organization	239921_at	<0.001	0.022	0.492	239921_at	0.071	0.337	-0.246	239921_at	0.281	0.897	-0.179
COL3A1	collagen, type III, alpha 1	ECM Organization	215076_s_at	<0.001	0.037	-0.459	201852_x_at	0.005	0.108	0.375	215076_s_at	0.014	0.460	0.398
COL4A1	collagen, type IV, alpha 1	ECM Organization	211980_at	<0.001	0.051	-0.434	211980_at	<0.001	0.048	0.450	211980_at	0.033	0.574	0.347
COL4A3BP	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	Immune/Acute Phase Response	223465_at	0.003	0.086	-0.394	223465_at	0.005	0.107	0.376	223465_at	0.982	0.998	0.004
COL4A4	collagen, type IV, alpha 4	ECM Organization	229779_at	0.145	0.481	-0.199	229779_at	0.004	0.103	0.381	229779_at	0.146	0.805	0.240
COL5A2	collagen, type V, alpha 2	ECM Organization	221729_at	<0.001	0.037	-0.458	221730_at	0.003	0.088	0.397	221729_at	0.123	0.794	0.254
COL6A3	collagen, type VI, alpha 3	ECM Organization	201438_at	0.002	0.074	-0.407	201438_at	0.417	0.723	0.111	201438_at	0.430	0.936	0.131

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
COMT	catechol-O-methyltransferase	Stress Response	208818_s_at	0.017	0.189	-0.322	208818_s_at	0.005	0.106	0.378	208818_s_at	0.212	0.853	0.207
COPB1	coatamer protein complex, subunit beta 1	Protein Folding	201359_at	0.006	0.116	-0.369	201359_at	0.080	0.357	0.239	201359_at	0.936	0.995	-0.013
COPB2	coatamer protein complex, subunit beta 2 (beta prime)	Protein Folding	201098_at	0.003	0.086	-0.394	201098_at	0.219	0.545	0.168	201098_at	0.132	0.797	0.249
COPS5	COP9 signalosome subunit 5	Protein Folding	201652_at	0.499	0.785	0.093	201652_at	0.004	0.100	-0.385	201652_at	0.153	0.812	-0.236
COPS6	COP9 signalosome subunit 6	Protein Folding	201405_s_at	0.161	0.501	0.192	201405_s_at	0.005	0.108	-0.375	201405_s_at	0.372	0.922	-0.148
COQ3	coenzyme Q3 methyltransferase	Metabolic Process	221227_x_at	0.013	0.174	0.332	221227_x_at	0.002	0.071	-0.415	221227_x_at	0.536	0.959	-0.103
COQ7	coenzyme Q7 homolog, ubiquinone (yeast)	Gene Expression	210820_x_at	0.048	0.301	0.268	210820_x_at	0.005	0.107	-0.377	210820_x_at	0.507	0.954	-0.111
CORIN	corin, serine peptidase	Actin Cytoskeleton	239260_at	0.003	0.086	0.394	239260_at	0.001	0.066	-0.422	239260_at	<0.001	0.107	-0.643
COX17	COX17 cytochrome c oxidase copper chaperone	Respiratory Electron Chain Transport	203880_at	0.001	0.058	0.425	203880_at	0.105	0.401	-0.221	203880_at	0.624	0.971	0.082
COX20	COX20 cytochrome c oxidase assembly factor	Respiratory Electron Chain Transport	206848_at	0.498	0.785	-0.093	206848_at	0.325	0.652	0.135	206848_at	0.004	0.352	0.465
COX4I1	cytochrome c oxidase subunit IV isoform 1	Respiratory Electron Chain Transport	200086_s_at	0.200	0.552	0.175	200086_s_at	0.003	0.091	-0.394	202698_x_at	0.478	0.946	0.118
COX5A	cytochrome c oxidase subunit Va	Respiratory Electron Chain Transport	203663_s_at	0.052	0.312	0.263	203663_s_at	<0.001	0.043	-0.462	203663_s_at	0.782	0.984	-0.046
COX6C	cytochrome c oxidase subunit VIc	Respiratory Electron Chain Transport	201754_at	0.157	0.496	0.194	201754_at	0.002	0.083	-0.404	201754_at	0.715	0.979	-0.061
COX7C	cytochrome c oxidase subunit VIIc	Respiratory Electron Chain Transport	213846_at	0.006	0.119	0.367	217491_x_at	0.007	0.126	-0.359	213846_at	0.454	0.940	-0.125
CPEB4	cytoplasmic polyadenylation element binding protein 4	Amino Acid Metabolism	224829_at	0.001	0.055	-0.429	224829_at	0.101	0.395	0.224	224828_at	0.009	0.425	0.419
CPSF3L	cleavage and polyadenylation specific factor 3-like	Gene Expression	233563_s_at	0.125	0.450	-0.209	233563_s_at	0.006	0.113	0.370	233563_s_at	0.798	0.984	0.043
CRADD	CASP2 and RIPK1 domain containing adaptor with death domain	Signal Transduction	209833_at	0.012	0.167	-0.337	209833_at	0.008	0.130	0.356	209833_at	0.404	0.929	0.139
CRCP	CGRP receptor component	Gene Expression	203899_s_at	0.302	0.652	-0.142	203899_s_at	0.005	0.109	0.374	203899_s_at	0.680	0.975	0.069
CREB1	cAMP responsive element binding protein 1	Cardiac Muscle	237289_at	0.005	0.112	0.373	237289_at	0.018	0.182	-0.319	237289_at	0.375	0.923	-0.148

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
CREB3L1	cAMP responsive element binding protein 3-like 1	ECM Organization	213059_at	<0.001	0.029	0.475	213059_at	0.034	0.243	-0.286	213059_at	0.028	0.558	-0.358
CREB5	cAMP responsive element binding protein 5	Gene Expression	242329_at	0.018	0.197	-0.317	242329_at	<0.001	0.027	0.492	242329_at	0.004	0.356	0.463
CREBBP	CREB binding protein	Signal Transduction	202160_at	0.023	0.214	0.307	202160_at	0.009	0.137	-0.350	202160_at	0.178	0.833	-0.223
CREM	cAMP responsive element modulator	Fatty Acid	209967_s_at	0.005	0.111	-0.374	209967_s_at	0.083	0.365	0.236	209967_s_at	0.427	0.935	0.132
CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	Metabolism	202551_s_at	0.021	0.208	-0.311	202551_s_at	0.115	0.417	0.215	202551_s_at	0.007	0.394	0.436
CRLS1	cardiolipin synthase 1	Signal Transduction	232118_at	0.021	0.208	-0.311	202551_s_at	0.115	0.417	0.215	202551_s_at	0.007	0.394	0.436
CRYZ	crystallin, zeta (quinone reductase)	Fatty Acid	232118_at	0.007	0.126	-0.359	232118_at	0.007	0.126	-0.359	232118_at	0.830	0.988	-0.036
CRYZL1	crystallin, zeta (quinone reductase)-like 1	Metabolism	202950_at	0.010	0.153	-0.346	202950_at	0.323	0.651	0.136	202950_at	0.680	0.975	-0.069
CSDE1	cold shock domain containing E1, RNA-binding	Fatty Acid	219767_s_at	0.005	0.108	0.376	219767_s_at	0.102	0.397	-0.223	219767_s_at	0.459	0.941	-0.124
CSE1L	CSE1 chromosome segregation 1-like (yeast)	Metabolism	202646_s_at	0.004	0.094	-0.389	202646_s_at	0.004	0.094	-0.389	202646_s_at	0.876	0.992	0.026
CSNK2A1	casein kinase 2, alpha 1 polypeptide	Apoptosis	201112_s_at	0.016	0.172	-0.326	201112_s_at	0.016	0.172	-0.326	201112_s_at	0.002	0.286	-0.491
CSPP1	centrosome and spindle pole associated protein 1	Apoptosis	212073_at	0.008	0.130	-0.355	212073_at	0.008	0.130	-0.355	212073_at	0.604	0.968	0.087
CSRP2	cysteine and glycine-rich protein 2	Cell Division	220072_at	0.005	0.116	-0.370	220072_at	0.089	0.375	0.232	220072_at	0.035	0.578	0.345
CSRP2BP	CSRP2 binding protein	Cell Adhesion	207030_s_at	0.106	0.423	0.220	207030_s_at	<0.001	0.014	-0.541	207030_s_at	0.298	0.901	-0.173
CSRP3	cysteine and glycine-rich protein 3 (cardiac LIM protein)	Cell Division	225432_s_at	<0.001	0.043	0.446	225432_s_at	0.006	0.114	-0.368	225432_s_at	0.010	0.426	-0.418
CSTF3	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa	Cardiac Muscle	205553_s_at	0.025	0.226	-0.301	205553_s_at	0.450	0.747	0.104	205553_s_at	0.007	0.393	0.436
CTBP1	C-terminal binding protein 1	Gene Expression	229665_at	0.006	0.120	0.367	229665_at	<0.001	0.023	-0.506	229665_at	0.563	0.965	0.096
CTCF	CCCTC-binding factor (zinc finger protein)	Cell Division	213980_s_at	0.268	0.624	0.152	213980_s_at	0.001	0.066	-0.421	213980_s_at	0.241	0.871	-0.194
CTDSP2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	Cell Division	202521_at	0.007	0.134	0.358	202521_at	0.015	0.167	-0.329	202521_at	0.324	0.909	-0.164
CTGF	connective tissue growth factor	Gene Expression	203445_s_at	<0.001	0.014	0.517	203445_s_at	0.123	0.429	-0.210	203445_s_at	0.304	0.902	-0.171
		Signal Transduction	209101_at	<0.001	0.044	-0.444	209101_at	0.268	0.598	0.152	209101_at	0.131	0.797	0.249

Gene			LVEF				LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
CTU2	cytosolic thioridylase subunit 2	Amino Acid	1561502_x_at	0.005	0.112	0.374	1561502_x_at	0.070	0.336	-0.246	1561502_x_at	0.413	0.932	-0.136
CUL2	homolog (S. pombe)	Metabolism	203079_s_at	0.027	0.234	0.298	203079_s_at	0.002	0.072	-0.414	203079_s_at	0.045	0.625	-0.328
CUL4A	cullin 2	Cell Division	201424_s_at	0.039	0.275	0.279	201424_s_at	0.006	0.113	-0.370	201424_s_at	0.092	0.747	-0.277
CUL4B	cullin 4A	Protein Folding	202214_s_at	0.002	0.063	-0.417	202214_s_at	0.053	0.295	0.263	202214_s_at	0.907	0.993	0.020
CUL5	cullin 4B	Cell Division	230393_at	0.005	0.116	0.370	230393_at	0.036	0.247	-0.285	230393_at	0.024	0.525	-0.366
CUX1	cullin 5	Protein Folding	214743_at	0.120	0.444	-0.212	214743_at	0.017	0.180	0.321	214743_at	0.002	0.290	0.487
CWC27	cut-like homeobox 1	Gene Expression	1558841_at	0.010	0.155	0.345	1558841_at	0.845	0.941	-0.027	1558841_at	0.675	0.974	-0.070
CXXC5	CWC27 spliceosome-associated protein homolog (S. cerevisiae)	Gene Expression	224516_s_at	0.027	0.233	0.298	224516_s_at	0.024	0.209	-0.305	224516_s_at	0.004	0.352	-0.466
CYB5A	CXXC finger protein 5	Gene Expression	209366_x_at	0.003	0.093	0.388	209366_x_at	0.011	0.148	-0.342	209366_x_at	0.030	0.564	-0.353
CYB5D1	cytochrome b5 type A (microsomal)	Respiratory Electron Chain Transport	1552711_a_at	0.009	0.149	0.348	1552711_a_at	0.126	0.432	-0.209	1552711_a_at	0.374	0.922	-0.148
CYGB	cytochrome b5 domain containing 1	Respiratory Electron Chain Transport	226632_at	0.493	0.782	0.094	226632_at	0.009	0.134	0.352	226632_at	0.112	0.780	-0.262
CYP2J2	cytoglobin	Fatty Acid Metabolism	205073_at	0.003	0.085	-0.395	205073_at	0.012	0.153	0.338	205073_at	0.008	0.410	0.424
CYTH3	cytochrome P450, family 2, subfamily J, polypeptide 2	Metabolic Process	225147_at	0.714	0.898	0.050	225147_at	0.003	0.083	-0.402	225147_at	0.743	0.982	0.055
DAAM1	cytohesin 3	Signal Transduction	226666_at	0.011	0.160	0.341	226666_at	0.014	0.164	-0.331	226666_at	0.004	0.358	-0.461
DACH1	dishevelled associated activator of morphogenesis 1	Actin Cytoskeleton	228915_at	0.002	0.069	0.410	228915_at	0.265	0.595	-0.153	228915_at	0.244	0.874	-0.193
DAP	dachshund family transcription factor 1	Gene Expression	201095_at	0.006	0.120	-0.367	201095_at	<0.001	0.051	0.446	201095_at	0.058	0.664	0.311
DAZAP1	death-associated protein	Apoptosis	226620_x_at	0.098	0.407	0.226	229813_x_at	<0.001	0.026	-0.498	226620_x_at	0.574	0.966	-0.094
DBT	DAZ associated protein 1	Gene Expression	205369_x_at	0.028	0.235	-0.297	205369_x_at	0.003	0.091	0.393	205369_x_at	0.055	0.656	0.315
DCAF6	dihydrolipoamide branched chain transacylase E2	Amino Acid Metabolism	217908_s_at	0.079	0.372	0.239	217908_s_at	0.008	0.130	-0.355	217908_s_at	0.053	0.647	-0.317
DCLK1	DDB1 and CUL4 associated factor 6	Gene Expression	205399_at	0.003	0.091	0.390	205399_at	0.747	0.898	-0.044	205399_at	0.325	0.909	-0.164
DDAH1	doublecortin-like kinase 1	Signal Transduction	209094_at	<0.001	0.011	-0.527	209094_at	<0.001	0.037	0.472	209094_at	<0.001	0.097	0.671
DDO	dimethylarginine	Amino Acid Metabolism	207418_s_at	0.009	0.151	0.347	207418_s_at	0.912	0.968	0.015	207418_s_at	0.069	0.693	-0.299

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
DDX17	DEAD (Asp-Glu-Ala-Asp) box helicase 17	Gene Expression	208151_x_at	0.003	0.089	0.391	208151_x_at	0.216	0.542	-0.169	208151_x_at	0.588	0.968	0.090
DDX19A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19A	Gene Expression	202577_s_at	0.007	0.130	-0.360	202577_s_at	0.119	0.423	0.212	202577_s_at	0.104	0.775	0.268
DDX27	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	Gene Expression	219108_x_at	0.393	0.721	0.118	219108_x_at	0.005	0.110	-0.373	219108_x_at	0.662	0.974	-0.073
DDX39B	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B	Cardiac Muscle	200041_s_at	0.154	0.494	-0.195	200041_s_at	0.003	0.090	0.395	200041_s_at	0.252	0.878	0.190
DDX52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	Gene Expression	213637_at	0.809	0.937	-0.033	213637_at	0.654	0.855	0.062	213637_at	0.005	0.360	0.452
DECR1	2,4-dienoyl CoA reductase 1, mitochondrial	Fatty Acid Metabolism	202447_at	0.001	0.062	0.418	202447_at	0.003	0.088	-0.397	202447_at	0.030	0.563	-0.354
DEDD2	death effector domain containing 2	Apoptosis	225434_at	0.334	0.677	-0.133	225434_at	0.004	0.103	0.381	225434_at	0.784	0.984	0.046
DEGS1	delta(4)-desaturase, sphingolipid 1	Fatty Acid Metabolism	209250_at	0.006	0.122	0.366	209250_at	0.197	0.520	-0.176	209250_at	0.588	0.968	-0.090
DENND1A	DENN/MADD domain containing 1A	Signal Transduction	226849_at	0.006	0.123	0.365	226849_at	0.003	0.087	-0.397	226849_at	0.571	0.965	-0.095
DGCR14	DiGeorge syndrome critical region gene 14	Gene Expression	204383_at	0.256	0.612	-0.156	204383_at	0.005	0.109	0.374	204383_at	0.868	0.991	0.028
DHFR	dihydrofolate reductase	Metabolic Process	202534_x_at	0.098	0.408	0.225	202534_x_at	0.004	0.104	-0.380	202534_x_at	0.650	0.973	-0.076
DHRS12	dehydrogenase/reductase (SDR family) member 12	Stress Response	204800_s_at	<0.001	0.040	0.453	204800_s_at	0.339	0.665	-0.131	204800_s_at	0.128	0.796	-0.251
DHX30	DEAH (Asp-Glu-Ala-His) box helicase 30	Protein Translation	239772_x_at	0.001	0.062	0.420	239772_x_at	0.830	0.935	0.030	239772_x_at	0.918	0.995	-0.017
DIO2	deiodinase, iodothyronine, type II	Metabolic Process	203699_s_at	0.002	0.065	-0.414	203700_s_at	0.003	0.087	0.398	203699_s_at	<0.001	0.211	0.538
DIP2A	DIP2 disco-interacting protein 2 homolog A (Drosophila)	Apoptosis	215529_x_at	0.022	0.212	0.308	215529_x_at	0.002	0.077	-0.408	215529_x_at	0.500	0.953	-0.112
DKK3	dickkopf WNT signaling pathway inhibitor 3	Signal Transduction	221127_s_at	0.495	0.783	0.094	221127_s_at	0.001	0.059	-0.433	221127_s_at	0.395	0.927	0.141
DLG1	discs, large homolog 1 (Drosophila)	Signal Transduction	202514_at	0.061	0.333	-0.254	202514_at	0.694	0.872	0.054	202514_at	0.002	0.307	0.481
DLK1	delta-like 1 homolog (Drosophila)	Signal Transduction	209560_s_at	<0.001	0.033	0.466	209560_s_at	0.170	0.487	-0.188	209560_s_at	0.204	0.844	-0.211
DNAJA2	DnaJ (Hsp40) homolog, subfamily A, member 2	Protein Folding	231508_s_at	0.334	0.677	0.133	231508_s_at	0.003	0.085	-0.401	231508_s_at	0.478	0.946	-0.118
DNAJA3	DnaJ (Hsp40) homolog, subfamily A, member 3	Protein Folding	1554078_s_at	0.324	0.670	0.136	1554078_s_at	0.201	0.523	-0.175	205963_s_at	0.006	0.376	-0.445

Gene			LVEF				LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
DNAJA4	DnaJ (Hsp40) homolog, subfamily A, member 4	Protein Folding	225061_at	0.001	0.062	-0.420	225061_at	0.261	0.591	0.154	225061_at	0.082	0.726	0.286
DNAJB4	DnaJ (Hsp40) homolog, subfamily B, member 4	Protein Folding	203810_at	<0.001	0.047	-0.439	203810_at	0.023	0.205	0.306	203810_at	0.236	0.868	0.197
DNAJB5	DnaJ (Hsp40) homolog, subfamily B, member 5	Protein Folding	212817_at	0.038	0.272	-0.281	212817_at	0.008	0.008	0.575	212817_at	0.030	0.564	0.353
DNAJC13	DnaJ (Hsp40) homolog, subfamily C, member 13	Signal Transduction	1560020_at	0.864	0.958	-0.024	1560020_at	0.478	0.762	0.097	1560020_at	<0.001	0.211	0.539
DNAJC14	DnaJ (Hsp40) homolog, subfamily C, member 14	Protein Folding	223420_at	0.013	0.171	0.334	223420_at	<0.001	0.019	-0.518	223420_at	0.005	0.358	-0.454
DNAJC15	DnaJ (Hsp40) homolog, subfamily C, member 15	Fatty Acid Metabolism	227808_at	0.051	0.309	-0.264	227808_at	0.007	0.123	0.361	227808_at	0.771	0.983	0.049
DNAJC19	DnaJ (Hsp40) homolog, subfamily C, member 19	Protein Folding	225358_at	0.063	0.338	0.252	225358_at	0.016	0.175	-0.324	225358_at	0.005	0.358	-0.454
DNAJC27	DnaJ (Hsp40) homolog, subfamily C, member 27	Protein Folding	227859_at	0.373	0.706	0.122	227859_at	0.002	0.080	-0.407	227859_at	0.089	0.740	-0.280
DNAJC4	DnaJ (Hsp40) homolog, subfamily C, member 4	Protein Folding	213919_at	0.019	0.199	0.315	213919_at	0.003	0.083	-0.402	213919_at	0.739	0.982	-0.056
DOK5	docking protein 5	Signal Transduction	214844_s_at	0.342	0.683	-0.131	214844_s_at	0.007	0.121	0.363	214844_s_at	0.235	0.868	0.197
DPH7	diphthamide biosynthesis 7	Metabolism	225586_at	0.001	0.062	-0.418	225586_at	0.790	0.918	0.037	225586_at	0.405	0.930	0.139
DSP	desmoplakin	ECM Organization	200606_at	<0.001	0.050	0.436	200606_at	0.005	0.110	-0.372	200606_at	0.002	0.290	-0.485
DSTN	destrin (actin depolymerizing factor)	Actin Cytoskeleton	201022_s_at	0.238	0.592	0.162	201022_s_at	0.010	0.140	-0.348	201022_s_at	0.934	0.995	0.014
DTNA	dystrobrevin, alpha	Signal Transduction	210091_s_at	0.002	0.063	-0.416	210091_s_at	0.040	0.261	0.278	210091_s_at	0.901	0.993	0.021
DTNBP1	dystrobrevin binding protein 1	Actin Cytoskeleton	223445_at	0.001	0.059	0.424	223445_at	0.102	0.397	-0.223	223445_at	0.213	0.853	-0.206
DUSP1	dual specificity phosphatase 1	Signal Transduction	201041_s_at	<0.001	0.024	-0.487	201041_s_at	0.034	0.242	0.287	201041_s_at	0.218	0.855	0.204
DUSP27	dual specificity phosphatase 27 (putative)	Signal Transduction	232252_at	0.011	0.159	-0.342	232252_at	0.120	0.423	0.212	232252_at	0.002	0.290	0.488
DUSP5	dual specificity phosphatase 5	Signal Transduction	209457_at	<0.001	0.018	-0.503	209457_at	0.099	0.393	0.225	209457_at	0.052	0.642	0.319
DUSP7	dual specificity phosphatase 7	Signal Transduction	213848_at	0.017	0.192	0.320	213848_at	<0.001	0.032	-0.481	213848_at	0.340	0.914	-0.159
DUT	deoxyuridine triphosphatase	Metabolic Process	208956_x_at	0.442	0.751	0.106	208956_x_at	0.007	0.121	-0.362	208956_x_at	0.300	0.901	-0.172
DYNC1LI1	dynein, cytoplasmic 1, light intermediate chain 1	Cell Division	217976_s_at	0.010	0.154	-0.345	217976_s_at	0.061	0.317	0.254	217976_s_at	0.994	1.000	0.001

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
EBP	emopamil binding protein (sterol isomerase)	Signal Transduction	213789_at	0.171	0.514	0.187	202735_at	<0.001	0.034	-0.477	213789_at	0.055	0.653	-0.315
ECHDC2	enoyl CoA hydratase domain containing 2	Fatty Acid Metabolism	218552_at	0.006	0.120	0.367	218552_at	0.103	0.399	-0.222	218552_at	0.186	0.833	-0.219
EDNRA	endothelin receptor type A	Signal Transduction	204463_s_at	0.082	0.377	-0.237	204463_s_at	0.265	0.595	0.153	204463_s_at	0.002	0.277	0.501
EEF1D	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	Gene Expression	214394_x_at	0.364	0.700	0.125	214394_x_at	0.003	0.085	-0.400	214394_x_at	0.352	0.915	0.155
EEF2K	eukaryotic elongation factor 2 kinase	Protein Translation	225545_at	0.010	0.154	0.345	225545_at	0.079	0.356	-0.239	225545_at	0.018	0.486	-0.385
EFHD2	EF-hand domain family, member D2	Cell Adhesion	217992_s_at	0.001	0.062	-0.418	217992_s_at	0.630	0.844	0.066	217992_s_at	0.863	0.991	0.029
EGF	epidermal growth factor	Signal Transduction	206254_at	0.298	0.650	0.143	206254_at	0.100	0.393	-0.224	206254_at	0.006	0.377	-0.443
EGLN3	egl-9 family hypoxia-inducible factor 3	Apoptosis	222847_s_at	<0.001	0.043	-0.447	222847_s_at	0.014	0.164	0.330	219232_s_at	<0.001	0.211	0.535
EIF1	eukaryotic translation initiation factor 1	Protein Translation	211956_s_at	0.454	0.758	0.103	211956_s_at	0.002	0.070	-0.416	211956_s_at	0.229	0.864	0.199
EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4	Protein Translation	225164_s_at	0.364	0.700	0.125	225164_s_at	0.002	0.077	-0.409	225164_s_at	0.779	0.984	-0.047
EIF2B4	eukaryotic translation initiation factor 2B, subunit 4 delta, 67kDa	Protein Translation	215482_s_at	0.398	0.724	0.116	215482_s_at	0.008	0.129	-0.356	215482_s_at	0.640	0.972	-0.078
EIF3M	eukaryotic translation initiation factor 3, subunit M	Protein Translation	202231_at	0.032	0.253	0.289	202231_at	<0.001	0.025	-0.499	202231_at	0.235	0.866	-0.197
EIF4A1	eukaryotic translation initiation factor 4A1	Gene Expression	211787_s_at	0.001	0.054	-0.430	201530_x_at	0.114	0.415	0.216	211787_s_at	0.377	0.923	0.147
EIF4B	eukaryotic translation initiation factor 4B	Protein Translation	211938_at	0.001	0.062	0.421	211938_at	0.011	0.150	-0.340	211938_at	0.382	0.924	-0.145
EIF4E3	eukaryotic translation initiation factor 4E family member 3	Protein Translation	225939_at	0.070	0.353	0.246	225939_at	0.006	0.112	-0.371	225939_at	0.387	0.924	-0.144
EIF4EBP2	eukaryotic translation initiation factor 4E binding protein 2	Protein Translation	224645_at	0.008	0.139	0.354	224645_at	0.038	0.256	-0.281	224645_at	0.556	0.964	0.098
ELF1	E74-like factor 1 (ets domain transcription factor)	Gene Expression	212420_at	0.026	0.227	-0.301	212420_at	0.024	0.208	0.305	212420_at	0.004	0.358	0.456
ELK4	ELK4, ETS-domain protein (SRF accessory protein 1)	Gene Expression	205994_at	0.699	0.891	0.053	205994_at	0.008	0.126	-0.358	205994_at	0.874	0.992	0.027

Gene			LVEF				LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
ELL2	elongation factor, RNA polymerase II, 2	Gene Expression	226099_at	0.701	0.891	0.053	226099_at	0.006	0.112	-0.371	226099_at	0.265	0.888	-0.185
ELL3	elongation factor RNA polymerase II-like 3	Gene Expression	219517_at	0.283	0.637	0.147	219517_at	0.008	0.131	-0.355	219517_at	0.670	0.974	-0.071
EMC3	ER membrane protein complex subunit 3	Protein Folding	228775_at	0.229	0.584	0.165	228775_at	<0.001	0.040	-0.468	228775_at	0.224	0.859	-0.202
EMP2	epithelial membrane protein 2	Cell Adhesion	225078_at	0.004	0.096	0.386	225078_at	0.060	0.314	-0.255	225078_at	0.007	0.400	-0.434
ENAH	enabled homolog (Drosophila)	Cell Adhesion	222433_at	0.009	0.148	-0.349	222433_at	0.008	0.128	0.357	228310_at	0.001	0.257	0.511
ENO2	enolase 2 (gamma, neuronal)	Carbohydrate Metabolism	201313_at	0.059	0.329	-0.256	201313_at	0.004	0.103	0.382	201313_at	0.194	0.838	0.215
EP300-AS1	EP300 antisense RNA 1	Amino Acid Metabolism	1562921_at	<0.001	0.008	0.541	1562921_at	<0.001	0.005	-0.596	1562921_at	0.001	0.277	-0.503
EPB41L5	erythrocyte membrane protein band 4.1 like 5	Metabolism	225855_at	0.004	0.098	-0.384	225855_at	0.512	0.782	0.090	225855_at	0.198	0.842	0.213
EPHA4	EPH receptor A4	Actin Cytoskeleton	227449_at	0.190	0.537	-0.180	227449_at	0.007	0.119	0.364	227449_at	0.355	0.917	0.154
EPS15L1	epidermal growth factor receptor pathway substrate 15-like 1	Cell Adhesion	222113_s_at	0.007	0.134	0.357	222113_s_at	0.570	0.813	-0.078	222113_s_at	0.599	0.968	0.088
ERLIN2	ER lipid raft associated 2	Signal Transduction	238615_at	0.293	0.646	0.144	238615_at	0.866	0.950	0.023	238615_at	0.004	0.352	-0.465
ERO1L	ERO1-like (S. cerevisiae)	Amino Acid Metabolism	222646_s_at	0.003	0.094	-0.387	222646_s_at	0.957	0.985	0.007	222646_s_at	0.386	0.924	0.144
ESCO1	establishment of sister chromatid cohesion N-acetyltransferase 1	Metabolism	235645_at	0.065	0.344	-0.250	235645_at	0.237	0.567	0.162	235645_at	0.005	0.362	0.450
ESYT2	extended synaptotagmin-like protein 2	Protein Translation	224698_at	0.386	0.717	0.119	224698_at	0.253	0.583	-0.156	224698_at	0.009	0.425	-0.419
ETV1	ets variant 1	Metabolic Process	221911_at	0.001	0.062	-0.419	221911_at	0.229	0.295	0.295	221911_at	0.023	0.523	0.369
ETV5	ets variant 5	Gene Expression	203349_s_at	<0.001	0.031	-0.470	203349_s_at	0.031	0.233	0.293	203349_s_at	0.976	0.998	0.005
EVI5	ecotropic viral integration site 5	Gene Expression	208297_s_at	0.125	0.451	-0.209	208297_s_at	<0.001	0.044	0.460	208297_s_at	0.011	0.446	0.411
EXOSC10	exosome component 10	Cell Division	207541_s_at	0.317	0.665	0.137	207541_s_at	0.006	0.115	-0.367	207541_s_at	0.756	0.982	-0.052
EXT1	exostosin glycosyltransferase 1	Gene Expression	201995_at	<0.001	0.014	-0.517	230183_at	<0.001	0.022	0.508	201995_at	<0.001	0.128	0.607
F5	coagulation factor V (proaccelerin, labile factor)	Signal Transduction	231029_at	0.021	0.207	0.311	231029_at	0.489	0.769	-0.095	231029_at	<0.001	0.252	-0.520
FABP6	fatty acid binding protein 6, ileal	Immune/Acute Phase Response	210445_at	0.003	0.092	0.388	210445_at	0.005	0.107	-0.377	210445_at	0.719	0.979	-0.060
FAHD1	fumarylacetoacetate hydrolase domain containing 1	Fatty Acid Metabolism	227960_s_at	0.066	0.345	0.250	227960_s_at	<0.001	0.023	-0.504	227960_s_at	0.243	0.872	-0.194

Gene			LVEF				LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
FAHD2A	fumarylacetoacetate hydrolase domain containing 2A	Metabolic Process	222056_s_at	0.033	0.255	0.288	222056_s_at	0.002	0.083	-0.404	222056_s_at	0.034	0.576	-0.347
FAM213A	family with sequence similarity 213, member A	Stress Response	228155_at	<0.001	0.037	0.458	228155_at	<0.001	0.028	-0.490	228155_at	0.002	0.289	-0.490
FARP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	Signal Transduction	201911_s_at	0.002	0.071	-0.409	201911_s_at	0.203	0.526	0.174	201911_s_at	0.034	0.577	0.345
FBRSL1	fibrosin-like 1	Gene Expression	225703_at	0.010	0.155	0.345	225703_at	<0.001	0.032	-0.480	225703_at	0.038	0.594	-0.339
FBXL4	F-box and leucine-rich repeat protein 4	Protein Folding	235450_at	<0.001	0.051	0.434	235450_at	0.004	0.099	-0.385	209943_at	0.004	0.356	-0.462
FBXO9	F-box protein 9	Protein Folding	1566509_s_at	<0.001	0.041	-0.451	210638_s_at	0.006	0.115	0.368	1566509_s_at	0.054	0.649	0.316
FBXW7	F-box and WD repeat domain containing 7, E3 ubiquitin protein ligase	Fatty Acid Metabolism	229419_at	0.156	0.496	0.194	229419_at	0.007	0.124	-0.359	229419_at	0.603	0.968	-0.087
FCER1A	Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide	Signal Transduction	211734_s_at	0.003	0.081	0.398	211734_s_at	0.052	0.294	-0.264	211734_s_at	0.443	0.938	-0.128
FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	Signal Transduction	203561_at	0.115	0.434	0.215	203561_at	0.001	0.062	-0.429	203561_at	0.070	0.694	-0.298
FCGR2B	Fc fragment of IgG, low affinity IIb, receptor (CD32)	Signal Transduction	210889_s_at	0.062	0.335	0.254	210889_s_at	<0.001	0.046	-0.457	210889_s_at	0.595	0.968	-0.089
FECH	ferrochelatase	Metabolic Process	203116_s_at	0.164	0.506	-0.190	203116_s_at	0.005	0.109	0.373	203116_s_at	0.705	0.976	0.063
FEM1A	fem-1 homolog a (C. elegans)	Protein Folding	228435_at	0.002	0.078	0.402	228435_at	<0.001	0.026	-0.494	223175_s_at	0.059	0.668	-0.310
FERMT2	fermitin family member 2	Stress Response	214212_x_at	0.075	0.364	-0.242	214212_x_at	0.588	0.822	0.074	214212_x_at	0.007	0.393	0.436
FEZ1	fasciculation and elongation protein zeta 1 (zygin I)	Cell Adhesion	205973_at	<0.001	0.020	0.496	203562_at	<0.001	0.053	-0.443	203562_at	0.043	0.618	-0.331
FEZ2	fasciculation and elongation protein zeta 2 (zygin II)	Signal Transduction	202305_s_at	0.003	0.081	-0.398	202305_s_at	0.010	0.142	0.346	202305_s_at	0.025	0.528	0.366
FGF1	fibroblast growth factor 1 (acidic)	ECM Organization	205117_at	0.001	0.062	-0.419	205117_at	0.001	0.061	0.432	205117_at	0.020	0.503	0.377
FGFR2	fibroblast growth factor receptor 2	Cardiac Muscle	208229_at	0.181	0.527	0.183	208229_at	0.002	0.073	-0.413	208229_at	0.434	0.937	-0.130
FHL1	four and a half LIM domains 1	Signal Transduction	210299_s_at	0.005	0.109	-0.376	214505_s_at	<0.001	0.026	0.497	201539_s_at	0.019	0.497	0.382
FILIP1	filamin A interacting protein 1	Actin Cytoskeleton	1570515_a_at	0.190	0.538	-0.179	1570515_a_at	0.026	0.218	0.301	1570515_a_at	0.010	0.429	0.416
FITM2	fat storage-inducing transmembrane protein 2	Fatty Acid Metabolism	1559788_at	0.016	0.189	0.322	1559788_at	0.004	0.102	-0.383	1559788_at	0.077	0.714	-0.291
FKBP11	FK506 binding protein 11, 19 kDa	Amino Acid Metabolism	219117_s_at	0.007	0.133	-0.358	219117_s_at	0.571	0.813	0.078	219117_s_at	0.126	0.796	0.252

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
FKBP14	FK506 binding protein 14, 22 kDa	Protein Folding	219390_at	<0.001	0.031	-0.470	219390_at	0.043	0.271	0.274	219390_at	0.025	0.536	0.364
FKBP3	FK506 binding protein 3, 25kDa	Amino Acid Metabolism	218003_s_at	0.081	0.375	0.238	218003_s_at	0.004	0.102	-0.383	218003_s_at	0.979	0.998	0.004
FKBP7	FK506 binding protein 7	Amino Acid Metabolism	224002_s_at	0.635	0.861	0.066	224002_s_at	0.006	0.118	-0.365	224002_s_at	0.259	0.882	-0.187
FMOD	fibromodulin	ECM Organization	202709_at	0.002	0.063	-0.417	202709_at	0.005	0.108	0.375	202709_at	0.985	0.999	0.003
FN1	fibronectin 1	ECM Organization	212464_s_at	0.005	0.107	-0.377	211719_x_at	0.001	0.065	0.425	211719_x_at	0.078	0.719	0.289
FNDC3B	fibronectin type III domain containing 3B	ECM Organization	218618_s_at	0.002	0.077	-0.404	218618_s_at	0.023	0.204	0.307	218618_s_at	0.002	0.279	0.496
FNIP1	folliculin interacting protein 1	Stress Response	243861_at	0.005	0.110	-0.375	243861_at	0.509	0.781	0.091	243861_at	0.572	0.965	0.094
FOSL2	FOS-like antigen 2	Apoptosis	225262_at	0.002	0.077	-0.403	225262_at	0.010	0.140	0.348	225262_at	0.743	0.982	-0.055
FOXK2	forkhead box K2	Gene Expression	226224_at	0.481	0.774	0.097	226224_at	0.005	0.105	-0.380	226224_at	0.685	0.975	0.068
FOXN3-AS1	FOXN3 antisense RNA 1	Cell Division	227887_at	<0.001	0.016	-0.511	227887_at	0.061	0.317	0.254	227887_at	0.102	0.771	0.269
FRMD3	FERM domain containing 3	Actin Cytoskeleton	229893_at	<0.001	0.028	-0.477	229893_at	<0.001	0.011	0.548	229893_at	0.033	0.572	0.348
FRRS1L	ferric-chelate reductase 1-like	Signal Transduction	213904_at	0.006	0.118	0.368	213904_at	0.005	0.106	-0.378	213904_at	0.013	0.457	-0.403
FRZB	frizzled-related protein	Apoptosis	203697_at	0.013	0.172	-0.333	203697_at	<0.001	0.040	0.467	203697_at	0.085	0.735	0.283
FSTL1	folliculin-like 1	Signal Transduction	208782_at	<0.001	0.030	-0.473	208782_at	0.451	0.748	0.104	208782_at	0.142	0.800	0.243
FSTL3	folliculin-like 3 (secreted glycoprotein)	Signal Transduction	203592_s_at	<0.001	0.045	-0.442	203592_s_at	<0.001	0.048	0.453	203592_s_at	0.002	0.290	0.488
FUS	FUS RNA binding protein	Gene Expression	215744_at	0.005	0.110	0.375	215744_at	0.047	0.281	-0.270	215744_at	0.410	0.931	0.137
FYN	FYN proto-oncogene, Src family tyrosine kinase	Signal Transduction	210105_s_at	0.802	0.935	-0.035	210105_s_at	0.002	0.083	0.403	210105_s_at	0.081	0.723	0.287
FYTDD1	forty-two-three domain containing 1	Gene Expression	224642_at	0.004	0.098	-0.383	224642_at	0.591	0.823	0.074	224642_at	0.358	0.917	0.153
G0S2	G0/G1 switch 2	Apoptosis	213524_s_at	0.004	0.094	0.387	213524_s_at	0.003	0.085	-0.401	213524_s_at	0.008	0.404	-0.428
G2E3	G2/M-phase specific E3 ubiquitin protein ligase	Protein Folding	223254_s_at	0.001	0.055	-0.428	223254_s_at	0.973	0.989	0.005	223254_s_at	0.286	0.899	0.177
GABRA4	gamma-aminobutyric acid (GABA) A receptor, alpha 4	Signal Transduction	208463_at	<0.001	0.023	-0.490	208463_at	<0.001	0.022	0.510	233437_at	<0.001	0.213	0.534
GABRB1	gamma-aminobutyric acid (GABA) A receptor, beta 1	Signal Transduction	207010_at	0.006	0.118	-0.369	207010_at	<0.001	0.048	0.452	1557256_a_at	<0.001	0.237	0.526
GADD45A	growth arrest and DNA-damage- inducible, alpha	Cell Division	203725_at	0.331	0.675	-0.133	203725_at	0.004	0.094	0.389	203725_at	0.146	0.805	0.240
GALNT16	polypeptide N- acetylgalactosaminyltransferase 16	Carbohydrate Metabolism	230418_s_at	<0.001	0.039	0.454	230418_s_at	0.015	0.169	-0.327	230418_s_at	0.005	0.360	-0.451

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	ρ	Identifier	p-value	pBH	ρ	Identifier	p-value	pBH	ρ
GALNT2	polypeptide N-acetylgalactosaminyltransferase 2	Carbohydrate Metabolism	217788_s_at	0.181	0.527	-0.183	217788_s_at	0.058	0.308	0.257	217788_s_at	0.009	0.425	0.419
GAREM	GRB2 associated, regulator of MAPK1	Cell Division	228115_at	0.002	0.070	0.410	228115_at	0.007	0.121	-0.361	228115_at	0.005	0.359	-0.453
GARNL3	GTPase activating Rap/RanGAP domain-like 3	Signal Transduction	223604_at	0.006	0.124	-0.364	223604_at	<0.001	0.048	0.452	223604_at	0.019	0.497	0.380
GAS1	growth arrest-specific 1	Cell Division	204457_s_at	0.008	0.140	0.353	204457_s_at	0.191	0.514	-0.179	204457_s_at	0.062	0.674	-0.306
GCLM	glutamate-cysteine ligase, modifier subunit	Carbohydrate Metabolism	236140_at	0.002	0.077	0.403	236140_at	0.050	0.290	-0.266	236140_at	0.328	0.909	-0.162
GCOM1	GRINL1A complex locus 1	Signal Transduction	212243_at	0.006	0.120	-0.367	212241_at	0.002	0.077	0.409	212241_at	0.022	0.518	0.372
GDAP1	ganglioside induced differentiation associated protein 1	Metabolic Process	226269_at	0.009	0.144	-0.351	226269_at	0.007	0.121	0.362	226269_at	0.095	0.755	0.275
GDI1	GDP dissociation inhibitor 1	Signal Transduction	201864_at	0.117	0.438	-0.214	201864_at	0.009	0.136	0.351	201864_at	0.946	0.996	-0.011
GDPD1	glycerophosphodiester phosphodiesterase domain containing 1	Fatty Acid Metabolism	238681_at	0.155	0.496	0.194	238681_at	0.003	0.087	-0.398	238681_at	0.127	0.796	-0.252
GEMIN8	gem (nuclear organelle) associated protein 8	Gene Expression	219252_s_at	0.004	0.101	-0.381	219252_s_at	0.531	0.791	0.086	219252_s_at	0.589	0.968	0.090
GFOD1	glucose-fructose oxidoreductase domain containing 1	Carbohydrate Metabolism	1554486_a_at	0.004	0.095	-0.386	1554486_a_at	0.018	0.185	0.318	1554486_a_at	0.207	0.846	0.209
GGTLC1	gamma-glutamyltransferase light chain 1	Stress Response	211416_x_at	0.662	0.875	0.060	211416_x_at	0.010	0.140	0.348	211416_x_at	0.548	0.962	-0.100
GHR	growth hormone receptor	Fatty Acid Metabolism	205498_at	0.006	0.125	0.363	205498_at	0.400	0.712	-0.116	205498_at	0.648	0.973	-0.076
GJA1	gap junction protein, alpha 1, 43kDa	Signal Transduction	201667_at	0.029	0.241	0.295	201667_at	0.008	0.130	-0.355	201667_at	0.250	0.875	-0.191
GKAP1	G kinase anchoring protein 1	Signal Transduction	234192_s_at	0.177	0.521	0.185	234192_s_at	0.008	0.129	-0.356	234192_s_at	0.499	0.953	-0.113
GLA	galactosidase, alpha	Fatty Acid Metabolism	214430_at	0.003	0.086	-0.394	214430_at	0.029	0.228	0.295	214430_at	0.411	0.931	0.137
GLG1	golgi glycoprotein 1	ECM Organization	214730_s_at	0.036	0.266	-0.283	207966_s_at	<0.001	0.043	0.463	214730_s_at	0.005	0.376	0.446
GLRB	glycine receptor, beta	Amino Acid Metabolism	205280_at	0.003	0.090	-0.390	205280_at	0.033	0.240	0.288	205280_at	0.182	0.833	0.221
GLRX2	glutaredoxin 2	Stress Response	219933_at	0.098	0.407	0.226	219933_at	0.008	0.126	-0.358	219933_at	0.522	0.958	-0.107

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
GLRX5	glutaredoxin 5	Metabolic Process Fatty Acid	221932_s_at	0.156	0.496	0.194	221932_s_at	<0.001	0.046	-0.456	221932_s_at	0.444	0.938	-0.127
GM2A	GM2 ganglioside activator	Metabolism	235678_at	0.002	0.077	0.402	235678_at	0.002	0.069	-0.418	235678_at	0.309	0.904	-0.169
GMFB	glia maturation factor, beta	Signal Transduction	202543_s_at	0.148	0.485	0.198	202543_s_at	0.009	0.136	-0.351	202543_s_at	0.046	0.627	-0.327
GNA12	guanine nucleotide binding protein (G protein) alpha 12	Signal Transduction	224681_at	0.862	0.957	0.024	224681_at	0.199	0.521	-0.176	224681_at	0.001	0.257	-0.514
GNAL	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type	Signal Transduction	206355_at	0.004	0.097	0.385	206355_at	0.050	0.290	-0.266	206355_at	0.005	0.369	-0.448
GNAQ	guanine nucleotide binding protein (G protein), q polypeptide	Signal Transduction	224862_at	0.079	0.371	-0.239	224862_at	0.003	0.093	0.390	224862_at	0.603	0.968	0.087
GNG12	guanine nucleotide binding protein (G protein), gamma 12	Signal Transduction	222834_s_at	<0.001	0.041	-0.451	222834_s_at	0.073	0.344	0.243	222834_s_at	0.326	0.909	0.163
GNG5	guanine nucleotide binding protein (G protein), gamma 5	Signal Transduction	207157_s_at	0.088	0.391	0.232	207157_s_at	0.002	0.074	-0.412	207157_s_at	0.629	0.971	0.081
GOLGA3	golgin A3	Cell Adhesion	202106_at	0.165	0.507	-0.190	202106_at	0.935	0.978	0.011	202106_at	0.008	0.404	0.428
GOLIM4	golgi integral membrane protein 4	Unspecified	204324_s_at	<0.001	0.042	-0.449	204324_s_at	0.005	0.110	0.373	204324_s_at	0.030	0.563	0.354
GORASP1	golgi reassembly stacking protein 1, 65kDa	Protein Folding	215749_s_at	0.035	0.264	-0.285	215749_s_at	0.002	0.075	0.410	215749_s_at	0.202	0.843	0.212
GOSR1	golgi SNAP receptor complex member 1	Signal Transduction	204630_s_at	0.034	0.258	-0.287	204630_s_at	0.770	0.909	-0.040	204630_s_at	0.008	0.404	0.429
GOSR2	golgi SNAP receptor complex member 2	Signal Transduction	213180_s_at	0.008	0.141	-0.353	213144_at	0.014	0.164	0.331	213144_at	0.008	0.407	0.428
GPC5	glypican 5	Metabolic Process	207174_at	0.010	0.155	0.345	207174_at	0.090	0.376	-0.231	207174_at	0.036	0.587	-0.343
GPIHBP1	glycosylphosphatidylinositol anchored high density lipoprotein binding protein 1	Signal Transduction	238062_at	0.381	0.712	0.120	238062_at	0.957	0.985	0.007	238062_at	0.006	0.382	-0.440
GPN2	GPN-loop GTPase 2	Gene Expression	218799_at	0.007	0.130	-0.360	218799_at	0.056	0.303	0.259	218799_at	0.493	0.951	0.114
GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2	Amino Acid Metabolism	224839_s_at	0.004	0.095	0.387	224839_s_at	0.046	0.278	-0.271	224839_s_at	0.028	0.560	-0.357
GRK5	G protein-coupled receptor kinase 5	Apoptosis	204396_s_at	0.236	0.591	0.162	204396_s_at	<0.001	0.037	-0.472	204396_s_at	0.075	0.709	-0.292
GRSF1	G-rich RNA sequence binding factor 1	Gene Expression	201501_s_at	0.106	0.423	0.220	201501_s_at	0.002	0.071	-0.415	201501_s_at	0.324	0.909	-0.164
GSDMC	gasdermin C	Apoptosis	234305_s_at	<0.001	0.052	0.433	234305_s_at	0.001	0.065	-0.424	234305_s_at	0.021	0.508	-0.375

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
GSPT1	G1 to S phase transition 1	Cell Division	234975_at	0.003	0.087	0.393	234975_at	0.416	0.722	-0.112	234975_at	0.173	0.832	-0.225
GSS	glutathione synthetase	Amino Acid Metabolism	211630_s_at	0.315	0.662	-0.138	211630_s_at	0.004	0.100	0.385	211630_s_at	0.676	0.974	0.070
GSTM1	glutathione S-transferase mu 1	Metabolic Process	215333_x_at	0.003	0.085	0.395	215333_x_at	0.700	0.876	0.053	215333_x_at	0.449	0.940	-0.126
GSX1	GS homeobox 1	Gene Expression	216497_at	0.009	0.148	0.349	216497_at	0.642	0.849	-0.064	216497_at	0.590	0.968	-0.090
GTF2F1	general transcription factor IIF, polypeptide 1, 74kDa	Gene Expression	202356_s_at	0.400	0.725	-0.116	202356_s_at	0.007	0.121	0.363	202356_s_at	0.914	0.994	-0.018
GTF2F2	general transcription factor IIF, polypeptide 2, 30kDa	Gene Expression	209595_at	0.007	0.133	0.358	209595_at	0.224	0.551	-0.166	209595_at	0.358	0.917	-0.153
GTF2I	general transcription factor Ili	Gene Expression	201065_s_at	0.021	0.206	-0.311	201065_s_at	0.915	0.969	0.015	201065_s_at	0.008	0.404	0.428
GTF3A	general transcription factor IIIA	Gene Expression	201338_x_at	0.127	0.454	0.208	201338_x_at	<0.001	0.023	-0.503	201338_x_at	0.360	0.918	-0.152
GTF3C5	general transcription factor IIIC, polypeptide 5, 63kDa	Gene Expression	217876_at	0.017	0.190	0.322	217876_at	0.006	0.113	-0.369	217876_at	0.131	0.796	-0.249
GTF3C6	general transcription factor IIIC, polypeptide 6, alpha 35kDa	Gene Expression	225083_at	0.134	0.466	0.204	225083_at	<0.001	0.045	-0.458	225083_at	0.680	0.975	-0.069
GTPBP10	GTP-binding protein 10 (putative)	Protein Translation	234311_s_at	0.056	0.321	0.259	234311_s_at	0.002	0.082	-0.405	234311_s_at	0.303	0.902	-0.171
GUCY1A2	guanylate cyclase 1, soluble, alpha 2	Signal Transduction	236335_at	0.431	0.743	-0.108	236335_at	0.008	0.131	0.355	236335_at	0.861	0.991	-0.029
GUK1	guanylate kinase 1	Metabolic Process	200075_s_at	0.007	0.127	-0.362	200075_s_at	0.089	0.375	0.232	200075_s_at	0.553	0.963	0.099
GXYLT2	glucoside xylosyltransferase 2	Carbohydrate Metabolism	235371_at	0.006	0.124	-0.364	235371_at	0.457	0.752	0.102	235371_at	0.676	0.974	-0.070
H2AFJ	H2A histone family, member J	Gene Expression	225245_x_at	0.754	0.915	0.043	225245_x_at	0.010	0.141	-0.347	225245_x_at	0.936	0.995	-0.013
H2AFZ	H2A histone family, member Z	Gene Expression	200853_at	0.080	0.374	0.238	213911_s_at	<0.001	0.016	-0.533	213911_s_at	0.148	0.806	-0.239
HADHB	hydroxyacyl-CoA dehydrogenase/3- ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), beta subunit	Fatty Acid Metabolism	201007_at	0.002	0.073	0.408	201007_at	0.007	0.119	-0.364	201007_at	0.688	0.975	-0.067
HAND2-AS1	HAND2 antisense RNA 1 (head to head)	Cardiac Muscle	219791_s_at	0.007	0.131	-0.359	219791_s_at	0.027	0.223	0.298	219791_s_at	0.002	0.286	0.493
HAPLN1	hyaluronan and proteoglycan link protein 1	ECM Organization	205523_at	<0.001	0.047	-0.441	205523_at	0.163	0.480	0.190	205523_at	0.046	0.627	0.326
HARS	histidyl-tRNA synthetase	Amino Acid Metabolism	202042_at	0.008	0.138	-0.355	202042_at	0.003	0.087	0.399	202042_at	0.007	0.400	0.434
HAUS3	HAUS augmin-like complex, subunit 3	Cell Division	210054_at	0.275	0.628	0.150	210054_at	0.003	0.091	-0.393	210054_at	0.495	0.953	-0.114
HBEGF	heparin-binding EGF-like growth factor	Signal Transduction	203821_at	0.066	0.347	-0.249	203821_at	<0.001	0.022	0.510	38037_at	0.008	0.410	0.424

Gene			LVEF				LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
HCN4	hyperpolarization activated cyclic nucleotide gated potassium channel 4	Cardiac Muscle	230208_at	0.009	0.149	0.348	230208_at	0.459	0.753	-0.102	230208_at	0.922	0.995	-0.017
HDAC4	histone deacetylase 4	Gene Expression	204225_at	0.006	0.121	0.366	204225_at	0.198	0.520	-0.176	204225_at	0.667	0.974	-0.072
HDAC9	histone deacetylase 9	Gene Expression	230968_at	0.186	0.533	-0.181	230968_at	0.646	0.851	0.063	230968_at	0.009	0.412	0.423
HEATR6	HEAT repeat containing 6 homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain	Unspecified	1557121_s_at	0.001	0.057	-0.426	1557121_s_at	0.003	0.086	0.399	1557121_s_at	0.191	0.837	0.217
HERPUD1	member 1	Protein Folding	217168_s_at	0.184	0.530	0.182	217168_s_at	<0.001	0.053	-0.443	217168_s_at	0.012	0.450	-0.406
HERPUD2	HERPUD family member 2	Protein Folding	222751_at	0.235	0.589	0.163	222751_at	0.002	0.075	-0.411	222751_at	0.022	0.519	-0.372
HEXB	hexosaminidase B (beta polypeptide)	Carbohydrate	201944_at	0.001	0.062	-0.418	201944_at	0.084	0.367	0.235	201944_at	0.023	0.524	0.368
HEXIM1	hexamethylene bis-acetamide inducible 1	Immune/Acute Phase Response	202814_s_at	0.113	0.431	0.216	202814_s_at	<0.001	0.042	-0.464	202814_s_at	0.167	0.828	-0.228
HEY2	hes-related family bHLH transcription factor with YRPW motif 2	Cardiac Muscle	219743_at	<0.001	0.029	0.475	219743_at	<0.001	0.023	-0.506	219743_at	0.003	0.329	-0.474
HEYL	hes-related family bHLH transcription factor with YRPW motif-like	Gene Expression	226828_s_at	0.010	0.153	-0.346	226828_s_at	0.239	0.569	0.161	226828_s_at	0.397	0.927	0.141
HFE2	hemochromatosis type 2 (juvenile) 3-hydroxyisobutyrate	Signal Transduction	228621_at	0.004	0.104	-0.379	228621_at	0.005	0.108	0.376	228621_at	0.734	0.981	0.057
HIBADH	dehydrogenase	Metabolic Process	224812_at	0.005	0.108	0.376	224812_at	<0.001	0.056	-0.437	224812_at	0.016	0.473	-0.390
HINT1	histidine triad nucleotide binding protein 1	Amino Acid Metabolism	200093_s_at	0.289	0.641	0.146	1555961_a_at	<0.001	0.046	-0.456	208826_x_at	0.163	0.821	-0.231
HIPK2	homeodomain interacting protein kinase 2	Cell Division	240294_at	0.004	0.095	-0.387	240294_at	0.011	0.150	0.340	240294_at	0.014	0.463	0.396
HIPK3	homeodomain interacting protein kinase 3	Signal Transduction	210148_at	0.002	0.077	0.403	210148_at	0.504	0.777	-0.092	210148_at	0.087	0.739	-0.281
HIST1H4F	histone cluster 1, H4f	ECM Organization	232035_at	0.001	0.062	-0.419	232035_at	0.014	0.162	0.332	232035_at	0.014	0.459	0.399
HIST3H2A	histone cluster 3, H2a	Gene Expression	221582_at	0.001	0.058	0.425	221582_at	0.020	0.191	-0.314	221582_at	0.161	0.820	-0.232
HIVEP3	human immunodeficiency virus type I enhancer binding protein 3	Gene Expression	244764_at	0.003	0.086	0.393	244764_at	0.011	0.149	-0.341	244764_at	0.070	0.694	-0.298
HLF	hepatic leukemia factor	Gene Expression	204754_at	<0.001	0.043	0.447	204754_at	0.191	0.514	-0.179	204754_at	0.294	0.901	-0.174
HMGB1	high mobility group box 1	Immune/Acute Phase Response	224731_at	0.257	0.613	0.156	224731_at	0.007	0.121	-0.362	224731_at	0.277	0.894	-0.180

Gene			LVEF				LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
HMGB3	high mobility group box 3	Immune/Acute Phase Response	203744_at	0.003	0.092	-0.389	203744_at	0.957	0.985	0.007	203744_at	0.849	0.990	0.032
HMGN3	high mobility group nucleosomal binding domain 3	Gene Expression	209377_s_at	0.559	0.822	0.081	209377_s_at	0.005	0.107	-0.377	209377_s_at	0.556	0.964	-0.098
HMGN4	high mobility group nucleosomal binding domain 4	Gene Expression	202579_x_at	0.007	0.131	-0.359	202579_x_at	0.213	0.537	0.171	202579_x_at	0.308	0.904	0.169
HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1	Protein Translation	225932_s_at	0.018	0.195	0.318	205292_s_at	0.004	0.103	-0.381	225932_s_at	0.417	0.933	-0.135
HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)	Gene Expression	200751_s_at	0.317	0.664	-0.137	214737_x_at	<0.001	0.047	0.455	212626_x_at	0.352	0.915	0.155
HNRNPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	Amino Acid Metabolism	221481_x_at	0.009	0.147	0.350	200073_s_at	<0.001	0.044	-0.460	221481_x_at	0.878	0.992	0.026
HNRNPK	heterogeneous nuclear ribonucleoprotein K	Protein Translation	200775_s_at	0.009	0.149	-0.348	200775_s_at	0.966	0.987	-0.006	200775_s_at	0.817	0.986	-0.039
HNRNPM	heterogeneous nuclear ribonucleoprotein M	Protein Translation	1555844_s_at	0.067	0.348	0.249	1555844_s_at	0.003	0.085	-0.399	1555844_s_at	0.451	0.940	0.126
HNRNPUL2	heterogeneous nuclear ribonucleoprotein U-like 2	Protein Translation	225405_at	0.592	0.841	0.074	225405_at	0.010	0.140	-0.347	225405_at	0.722	0.979	-0.059
HOGA1	4-hydroxy-2-oxoglutarate aldolase 1	Carbohydrate Metabolism	239093_at	0.001	0.053	-0.431	239093_at	0.027	0.223	0.298	239093_at	<0.001	0.128	0.613
HOOK1	hook microtubule-tethering protein 1	Cell Division	225792_at	0.098	0.408	0.225	225792_at	<0.001	0.007	-0.585	225792_at	0.005	0.376	-0.446
HOOK2	hook microtubule-tethering protein 2	Cell Division	218780_at	0.335	0.678	-0.133	218780_at	0.009	0.137	0.350	218780_at	0.441	0.938	0.128
HP	haptoglobin	Immune/Acute Phase Response	206697_s_at	0.202	0.554	0.175	206697_s_at	0.002	0.070	-0.416	206697_s_at	0.112	0.780	-0.262
HPRT1	hypoxanthine phosphoribosyltransferase 1	Metabolic Process	202854_at	0.006	0.120	-0.367	202854_at	0.279	0.610	0.148	202854_at	0.568	0.965	0.095
HRASLS5	HRAS-like suppressor family, member 5	Metabolic Process	231050_at	0.086	0.386	0.234	231050_at	0.181	0.501	-0.183	231050_at	0.005	0.360	-0.451
HSD11B1	hydroxysteroid (11-beta) dehydrogenase 1	Fatty Acid Metabolism	205404_at	0.139	0.472	0.202	205404_at	0.964	0.987	0.006	205404_at	0.003	0.318	-0.478
HSDL2	hydroxysteroid dehydrogenase like 2	Metabolic Process	209512_at	<0.001	0.018	0.506	209513_s_at	0.101	0.395	-0.224	209512_at	0.016	0.468	-0.391
HSF2	heat shock transcription factor 2	Protein Folding	209657_s_at	0.237	0.592	0.162	209657_s_at	0.011	0.148	-0.343	209657_s_at	0.008	0.404	-0.429
HSP90B1	heat shock protein 90kDa beta (Grp94), member 1	Protein Folding	200598_s_at	0.006	0.125	-0.364	200598_s_at	0.469	0.759	0.099	200598_s_at	0.118	0.788	0.258

Gene			LVEF				LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
HSPA2	heat shock 70kDa protein 2	Cell Division	211538_s_at	0.003	0.090	-0.390	211538_s_at	0.051	0.290	0.265	211538_s_at	0.027	0.548	0.360
HSPA4	heat shock 70kDa protein 4	Protein Folding	208815_x_at	0.003	0.093	-0.388	208814_at	0.037	0.252	0.282	208814_at	0.017	0.476	0.388
HSPA4L	heat shock 70kDa protein 4-like	Protein Folding	1556194_a_at	0.003	0.083	-0.396	205543_at	0.002	0.067	0.420	205543_at	0.034	0.576	0.346
HSPH1	heat shock 105kDa/110kDa protein 1	Protein Folding	208744_x_at	0.003	0.089	-0.392	208744_x_at	0.041	0.265	0.277	208744_x_at	0.016	0.473	0.390
HTATIP2	HIV-1 Tat interactive protein 2, 30kDa	Metabolic Process	209448_at	0.226	0.580	0.166	209448_at	0.002	0.070	-0.417	209448_at	0.143	0.800	-0.242
HTRA1	HtrA serine peptidase 1	ECM Organization	201185_at	<0.001	0.036	-0.461	201185_at	0.005	0.106	0.379	201185_at	0.195	0.839	0.215
HYLS1	hydroletharus syndrome 1	Cell Division	227687_at	0.426	0.740	0.110	227687_at	<0.001	0.035	-0.476	227687_at	0.985	0.999	0.003
HYPK	huntingtin interacting protein K	Apoptosis	218680_x_at	0.003	0.089	0.391	218680_x_at	0.002	0.077	-0.408	218680_x_at	0.595	0.968	0.089
IBA57	IBA57, iron-sulfur cluster assembly homolog (S. cerevisiae)	Protein Folding	231983_at	0.026	0.229	-0.300	231983_at	0.009	0.137	0.350	231983_at	0.176	0.833	0.224
ICAM3	intercellular adhesion molecule 3 interactor of little elongation	ECM Organization	204949_at	0.026	0.228	0.301	204949_at	0.001	0.065	-0.425	204949_at	0.205	0.844	-0.210
ICE1	complex ELL subunit 1 interactor of little elongation	Gene Expression	209654_at	0.162	0.503	0.191	209654_at	<0.001	0.047	-0.454	209654_at	0.178	0.833	-0.223
ICE2	complex ELL subunit 2 isoprenylcysteine carboxyl	Gene Expression	242639_at	0.005	0.116	-0.370	218713_at	0.005	0.110	-0.372	242639_at	0.328	0.909	0.162
ICMT	methyltransferase	Protein Translation	201609_x_at	<0.001	0.007	-0.552	201609_x_at	0.020	0.192	0.313	201609_x_at	0.003	0.336	0.470
ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein isocitrate dehydrogenase 1 (NADP+),	Gene Expression	209291_at	<0.001	0.034	-0.463	209291_at	0.015	0.170	0.327	209291_at	0.098	0.762	0.273
IDH1	soluble	Stress Response	201193_at	0.013	0.174	0.332	201193_at	0.002	0.083	-0.404	201193_at	<0.001	0.153	-0.578
IER3	immediate early response 3	Apoptosis	201631_s_at	<0.001	0.002	-0.621	201631_s_at	0.003	0.085	0.400	201631_s_at	0.026	0.542	0.362
IFT20	intraflagellar transport 20	Cell Division	210312_s_at	0.002	0.065	-0.413	210312_s_at	0.899	0.963	0.018	210312_s_at	0.182	0.833	0.221
IFT46	intraflagellar transport 46	Cell Division	218483_s_at	0.069	0.351	-0.247	218483_s_at	0.007	0.124	0.360	218483_s_at	0.541	0.961	-0.102
IFT81	intraflagellar transport 81	Cell Division	219372_at	0.170	0.512	0.188	219372_at	0.203	0.526	-0.174	219372_at	0.007	0.396	-0.435
IGFBP3	insulin-like growth factor binding protein 3	Signal Transduction	210095_s_at	0.004	0.099	-0.383	210095_s_at	0.090	0.376	0.231	210095_s_at	0.620	0.969	-0.083
IL17RD	interleukin 17 receptor D interleukin 1 receptor accessory	Signal Transduction	227997_at	<0.001	0.041	0.451	227997_at	0.208	0.532	-0.172	227997_at	0.048	0.635	-0.324
IL1RAPL1	protein-like 1	Signal Transduction	220663_at	<0.001	0.030	0.473	220663_at	0.012	0.151	-0.340	220663_at	0.148	0.806	-0.239
IL20RA	interleukin 20 receptor, alpha	Apoptosis	219115_s_at	0.048	0.301	0.268	219115_s_at	0.006	0.112	-0.371	219115_s_at	<0.001	0.211	-0.536
IL6R	interleukin 6 receptor	Immune/Acute Phase Response	226333_at	0.041	0.281	0.277	226333_at	<0.001	0.047	-0.455	226333_at	0.014	0.457	-0.399

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	ρ	Identifier	p-value	pBH	ρ	Identifier	p-value	pBH	ρ
IMMP2L	IMP2 inner mitochondrial membrane peptidase-like (<i>S. cerevisiae</i>)	Respiratory Electron Chain Transport	227153_at	0.002	0.076	0.404	227153_at	0.005	0.107	-0.377	227153_at	0.071	0.696	-0.297
IMPA2	inositol(myo)-1(or 4)-monophosphatase 2	Signal Transduction Amino Acid	203126_at	<0.001	0.051	0.434	203126_at	0.003	0.090	-0.394	203126_at	0.003	0.334	-0.472
IMPACT	impact RWD domain protein	Metabolism	222698_s_at	0.006	0.120	-0.367	222698_s_at	0.937	0.978	-0.011	222698_s_at	0.277	0.894	0.180
ING5	inhibitor of growth family, member 5	Signal Transduction	228287_at	0.713	0.897	0.051	228287_at	0.008	0.131	-0.355	228287_at	0.709	0.977	0.062
INPP5F	inositol polyphosphate-5-phosphatase F	Signal Transduction	230363_s_at	<0.001	0.026	-0.480	230363_s_at	0.075	0.347	0.242	230363_s_at	0.871	0.992	0.027
INTS8	integrator complex subunit 8	Gene Expression Amino Acid	218905_at	0.331	0.675	0.134	218905_at	0.003	0.091	-0.393	218905_at	0.185	0.833	-0.219
IPO5	importin 5	Metabolism	211955_at	0.005	0.110	-0.375	211955_at	0.021	0.196	0.311	211955_at	0.132	0.797	0.249
IPO7	importin 7	Immune/Acute Phase Response	200994_at	0.003	0.092	0.388	200994_at	0.616	0.836	-0.069	200994_at	0.718	0.979	0.060
IPP	intracisternal A particle-promoted polypeptide	Actin Cytoskeleton	241434_at	0.010	0.152	0.347	241434_at	0.416	0.723	-0.112	241434_at	0.140	0.800	-0.244
IRAK2	interleukin-1 receptor-associated kinase 2	Signal Transduction	231779_at	0.060	0.329	0.256	231779_at	<0.001	0.053	-0.442	231779_at	0.121	0.793	-0.256
IRF2BPL	interferon regulatory factor 2 binding protein-like	Immune/Acute Phase Response	223474_at	0.316	0.664	0.138	223474_at	0.005	0.108	-0.375	223474_at	0.173	0.832	-0.225
ISCU	iron-sulfur cluster assembly enzyme	Metabolic Process	209075_s_at	0.121	0.445	0.212	209075_s_at	0.009	0.138	-0.349	209075_s_at	0.915	0.994	0.018
ISG20L2	interferon stimulated exonuclease gene 20kDa-like 2	Gene Expression	208114_s_at	0.004	0.095	-0.386	208114_s_at	0.014	0.164	0.330	208114_s_at	0.038	0.594	0.340
ITGB6	integrin, beta 6	Cell Adhesion	226535_at	0.003	0.081	0.399	239517_at	0.009	0.135	-0.352	226535_at	0.025	0.532	-0.364
ITLN1	intelectin 1 (galactofuranose binding)	Carbohydrate	223597_at	0.001	0.061	0.422	223597_at	0.061	0.315	-0.255	223597_at	0.467	0.945	-0.121
ITM2B	integral membrane protein 2B	Metabolism	217732_s_at	0.044	0.290	0.273	217732_s_at	0.003	0.092	-0.392	217732_s_at	0.155	0.813	-0.235
ITSN1	intersectin 1 (SH3 domain protein)	Metabolic Process	35776_at	0.010	0.154	0.345	35776_at	0.031	0.236	-0.291	35776_at	0.117	0.787	-0.259
ITSN2	intersectin 2	Signal Transduction	209907_s_at	0.006	0.119	0.368	209907_s_at	<0.001	0.007	-0.580	209907_s_at	0.522	0.958	-0.107
JAK1	Janus kinase 1	Immune/Acute Phase Response	1552610_a_at	0.157	0.496	0.193	1552610_a_at	0.008	0.127	-0.357	1552610_a_at	0.536	0.959	-0.103
JAK2	Janus kinase 2	Cardiac Muscle	205842_s_at	0.002	0.076	-0.405	205842_s_at	<0.001	0.041	0.465	205842_s_at	<0.001	0.128	0.615
JARID2	jumonji, AT rich interactive domain 2	Cardiac Muscle	203297_s_at	<0.001	0.037	0.459	203297_s_at	0.305	0.633	-0.141	203297_s_at	0.793	0.984	-0.044

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
JAZF1	JAZF zinc finger 1	Gene Expression	225800_at	0.001	0.059	-0.424	225800_at	0.161	0.476	0.192	225800_at	0.037	0.592	0.341
JMJD1C	jumonji domain containing 1C	Gene Expression	224933_s_at	0.104	0.419	-0.221	224933_s_at	0.169	0.486	0.188	224933_s_at	0.006	0.376	0.445
JTB	jumping translocation breakpoint	Apoptosis	210434_x_at	0.343	0.683	-0.130	200048_s_at	<0.001	0.040	-0.467	200048_s_at	0.511	0.954	-0.110
JUN	jun proto-oncogene	Gene Expression	201464_x_at	0.002	0.063	-0.417	201464_x_at	0.159	0.474	0.192	201464_x_at	0.592	0.968	0.089
KALRN	kalirin, RhoGEF kinase	Actin Cytoskeleton	230596_at	0.535	0.810	-0.085	230596_at	0.329	0.656	0.134	230596_at	0.001	0.272	0.504
KARS	lysyl-tRNA synthetase	Amino Acid												
KAT2B	K(lysine) acetyltransferase 2B	Metabolism	200840_at	0.757	0.917	0.043	200840_at	0.003	0.092	-0.393	200840_at	0.448	0.940	0.126
KATNAL1	K(lysine) acetyltransferase 2B	Gene Expression	203845_at	0.024	0.219	0.305	203845_at	0.008	0.128	-0.357	203845_at	0.118	0.788	-0.258
	katanin p60 subunit A-like 1	Cell Division	223790_at	<0.001	0.025	-0.484	223790_at	0.001	0.065	0.427	223790_at	0.020	0.503	0.377
	potassium channel modulatory factor 1													
KCMF1	factor 1	Protein Folding	222471_s_at	0.014	0.179	0.329	222471_s_at	0.004	0.098	-0.386	222471_s_at	0.626	0.971	-0.081
	potassium channel, voltage gated													
KCND3	Shal related subfamily D, member 3	Cardiac Muscle	215014_at	0.004	0.106	0.378	215014_at	0.515	0.783	-0.090	215014_at	0.364	0.919	-0.151
KCNIP2	Kv channel interacting protein 2	Signal Transduction	223727_at	<0.001	0.041	0.450	223727_at	0.002	0.074	-0.412	223727_at	0.006	0.385	-0.440
	potassium channel, calcium activated intermediate/small conductance subfamily N alpha, member 2													
KCNN2	member 2	Signal Transduction	220116_at	<0.001	0.042	0.449	220116_at	0.007	0.121	-0.362	220116_at	0.033	0.571	-0.349
	potassium channel tetramerization domain containing 1													
KCTD1	domain containing 1	Gene Expression	226245_at	0.008	0.141	0.353	226245_at	0.167	0.484	-0.189	226245_at	0.513	0.954	-0.109
	potassium channel tetramerization domain containing 2													
KCTD2	domain containing 2	Protein Folding	34858_at	<0.001	0.004	-0.596	34858_at	0.004	0.098	0.386	34858_at	0.239	0.870	0.195
KDM1B	lysine (K)-specific demethylase 1B	Gene Expression	227021_at	0.392	0.721	-0.118	227021_at	0.003	0.093	0.390	227021_at	0.250	0.875	-0.191
KDM2A	lysine (K)-specific demethylase 2A	Gene Expression	208988_at	0.507	0.791	0.091	208988_at	0.008	0.126	-0.358	208988_at	0.990	1.000	-0.002
KDM5A	lysine (K)-specific demethylase 5A	Gene Expression	215698_at	0.001	0.062	-0.418	215698_at	0.012	0.154	0.337	215698_at	0.632	0.971	0.080
KIAA0141	KIAA0141	Apoptosis	201977_s_at	0.006	0.119	-0.368	201977_s_at	<0.001	0.025	0.499	201977_s_at	0.521	0.957	0.107
KIAA0368	KIAA0368	Cell Division	214356_s_at	0.048	0.301	0.268	214356_s_at	0.002	0.068	-0.419	214356_s_at	0.498	0.953	0.113
KIAA0907	KIAA0907	Gene Expression	202220_at	0.208	0.560	0.172	202220_at	0.005	0.108	-0.375	202220_at	0.504	0.953	-0.112
KIAA1598	KIAA1598	Signal Transduction	221802_s_at	0.562	0.825	0.080	221802_s_at	0.235	0.565	-0.162	221802_s_at	0.005	0.360	-0.451

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
KIDINS220	kinase D-interacting substrate, 220kDa	Signal Transduction	242032_at	<0.001	0.040	-0.453	212163_at	<0.001	0.026	0.494	212163_at	0.007	0.400	0.434
KIF13A	kinesin family member 13A	Cell Division	232837_at	<0.001	0.043	-0.445	232837_at	0.003	0.090	0.394	232837_at	0.029	0.561	0.356
KIF18B	kinesin family member 18B	Cell Division	222039_at	0.032	0.253	0.289	222039_at	<0.001	0.053	-0.443	222039_at	0.018	0.496	-0.382
KIF5B	kinesin family member 5B	Carbohydrate Metabolism	201992_s_at	0.003	0.086	-0.394	201992_s_at	0.037	0.254	0.282	201991_s_at	0.009	0.413	0.422
KIFAP3	kinesin-associated protein 3	Signal Transduction	203333_at	<0.001	0.011	-0.525	203333_at	0.015	0.170	0.327	203333_at	0.107	0.776	0.266
KIZ	kizuna centrosomal protein	Cell Division	228291_s_at	0.050	0.306	0.265	228291_s_at	0.006	0.117	-0.365	228291_s_at	0.964	0.998	0.008
KLF12	Kruppel-like factor 12	Gene Expression	227261_at	0.005	0.108	0.376	227261_at	0.503	0.777	-0.092	227261_at	0.497	0.953	-0.113
KLF7	Kruppel-like factor 7 (ubiquitous)	Gene Expression	1555420_a_at	0.001	0.062	-0.418	1555420_a_at	0.066	0.329	0.249	1555420_a_at	0.006	0.376	0.444
KLHL13	kelch-like family member 13	Protein Folding	227875_at	0.011	0.159	-0.342	227875_at	<0.001	0.040	0.468	227875_at	0.167	0.828	0.228
KLHL42	kelch-like family member 42	Cell Division	225732_at	0.002	0.077	-0.403	225732_at	0.060	0.313	0.256	225732_at	0.781	0.984	0.047
KLHL7	kelch-like family member 7	Protein Folding	223250_at	0.011	0.162	0.340	223250_at	0.006	0.115	-0.367	223250_at	0.003	0.334	-0.472
KMT2C	lysine (K)-specific methyltransferase 2C	Gene Expression	232940_s_at	0.049	0.304	-0.266	232940_s_at	<0.001	0.051	0.445	232940_s_at	0.025	0.536	0.364
KMT2E	lysine (K)-specific methyltransferase 2E	Gene Expression	223190_s_at	0.065	0.342	-0.251	223189_x_at	0.142	0.454	0.200	223189_x_at	0.001	0.260	0.510
KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	Metabolic Process	211762_s_at	0.009	0.146	-0.350	211762_s_at	0.886	0.957	-0.020	211762_s_at	0.613	0.969	0.084
KPNB1	karyopherin (importin) beta 1 Kirsten rat sarcoma viral oncogene	Apoptosis	208974_x_at	0.003	0.088	-0.392	208974_x_at	0.206	0.530	0.173	208974_x_at	0.059	0.668	0.310
KRAS	homolog	Actin Cytoskeleton	204010_s_at	0.437	0.747	0.107	204010_s_at	0.003	0.091	-0.393	204010_s_at	0.573	0.966	-0.094
LACTB2	lactamase, beta 2	Gene Expression	222714_s_at	<0.001	0.028	0.476	222714_s_at	<0.001	0.006	-0.592	218701_at	<0.001	0.253	-0.519
LAMA2	laminin, alpha 2	ECM Organization	216840_s_at	0.005	0.116	-0.370	216840_s_at	0.002	0.075	0.411	216840_s_at	0.049	0.635	0.323
LAMTOR5	late endosomal/lysosomal adaptor, MAPK and MTOR activator 5	Signal Transduction	202299_s_at	0.127	0.454	0.208	202299_s_at	0.002	0.077	-0.408	202299_s_at	0.554	0.963	-0.099
LAMTOR5- AS1	LAMTOR5 antisense RNA 1	Amino Acid Metabolism	237065_s_at	0.001	0.062	-0.419	237065_s_at	0.003	0.087	0.398	237065_s_at	0.758	0.982	0.052
LAPTM4B	lysosomal protein transmembrane 4 beta	Signal Transduction	214039_s_at	0.099	0.409	0.225	214039_s_at	0.002	0.073	-0.414	214039_s_at	0.624	0.971	-0.082
LARP4B	La ribonucleoprotein domain family, member 4B	Gene Expression	208952_s_at	<0.001	0.044	0.444	208952_s_at	<0.001	0.043	-0.461	228196_s_at	0.294	0.901	-0.174
LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	Immune/Acute Phase Response	205269_at	0.188	0.535	0.180	205269_at	0.008	0.129	-0.356	205269_at	0.699	0.976	-0.065

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
LGALS3	lectin, galactoside-binding, soluble, 3	Immune/Acute Phase Response	208949_s_at	0.698	0.890	0.054	208949_s_at	0.007	0.123	-0.360	208949_s_at	0.281	0.897	-0.179
LGALS8	lectin, galactoside-binding, soluble, 8	Carbohydrate Metabolism	208933_s_at	0.594	0.842	0.074	208933_s_at	0.135	0.444	0.204	208933_s_at	<0.001	0.194	0.543
LGALSL	lectin, galactoside-binding-like	Carbohydrate Metabolism	226188_at	<0.001	0.050	-0.436	226188_at	0.073	0.343	0.244	226188_at	0.023	0.522	0.370
LIMD1	LIM domains containing 1	Signal Transduction	234687_x_at	0.004	0.098	0.383	234687_x_at	0.228	0.556	0.165	234687_x_at	0.275	0.894	-0.181
LIN54	lin-54 DREAM MuvB core complex component	Cell Division	235809_at	0.115	0.435	0.215	235809_at	0.021	0.196	-0.311	235809_at	0.005	0.360	-0.450
LIPT1	lipoyltransferase 1	Metabolic Process	205571_at	0.011	0.159	0.342	205571_at	0.048	0.284	-0.268	205571_at	0.003	0.336	-0.470
LMCD1	LIM and cysteine-rich domains 1	Cardiac Muscle	227317_at	0.093	0.401	0.229	227317_at	0.006	0.113	-0.369	227317_at	0.453	0.940	-0.125
LMNA	lamin A/C	ECM Organization	212086_x_at	0.032	0.251	0.290	212086_x_at	0.003	0.093	-0.391	212086_x_at	0.005	0.376	-0.446
LMO4	LIM domain only 4	Gene Expression	227155_at	0.439	0.748	0.107	227155_at	<0.001	0.056	-0.437	227155_at	0.296	0.901	-0.174
LMOD1	leiomodoin 1 (smooth muscle)	Actin Cytoskeleton	203766_s_at	0.004	0.101	-0.381	203766_s_at	0.047	0.281	0.269	203766_s_at	0.883	0.993	-0.025
LMOD2	leiomodoin 2 (cardiac)	Actin Cytoskeleton	239057_at	0.202	0.554	-0.175	239057_at	0.007	0.123	0.360	239057_at	0.018	0.491	0.383
LONRF3	LON peptidase N-terminal domain and ring finger 3	Protein Folding	242931_at	<0.001	0.016	0.510	242931_at	0.037	0.250	-0.283	242931_at	0.584	0.968	-0.091
LOXL1	lysyl oxidase-like 1	ECM Organization	203570_at	<0.001	0.044	-0.444	203570_at	0.259	0.588	0.155	203570_at	0.704	0.976	0.064
LPAR5	lysophosphatidic acid receptor 5	Signal Transduction	230252_at	0.004	0.095	0.386	230252_at	<0.001	0.023	-0.504	230252_at	0.008	0.404	-0.428
LPCAT4	lysophosphatidylcholine acyltransferase 4	Metabolic Process	40472_at	0.009	0.148	0.349	40472_at	0.137	0.446	-0.203	40472_at	<0.001	0.233	-0.528
LPL	lipoprotein lipase	ECM Organization	203548_s_at	0.003	0.086	-0.393	203548_s_at	0.004	0.103	0.382	203548_s_at	0.004	0.358	0.457
LPP	LIM domain containing preferred translocation partner in lipoma	Cell Adhesion	202822_at	0.017	0.191	-0.321	202822_at	<0.001	0.048	0.450	202822_at	0.013	0.457	0.400
LPP-AS2	LPP antisense RNA 2	Cell Adhesion	1556827_at	0.005	0.107	-0.377	1556827_at	0.008	0.132	0.353	1556827_at	0.001	0.272	0.504
LRCH3	leucine-rich repeats and calponin homology (CH) domain containing 3	Signal Transduction	214739_at	0.009	0.146	0.350	214739_at	0.508	0.780	0.091	214739_at	0.887	0.993	-0.024
LRP4	low density lipoprotein receptor-related protein 4	Signal Transduction	212850_s_at	0.366	0.702	0.124	212850_s_at	<0.001	0.044	-0.460	212850_s_at	0.159	0.817	-0.233
LRRC1	leucine rich repeat containing 1	Signal Transduction	218816_at	<0.001	0.043	-0.445	218816_at	0.016	0.172	0.325	218816_at	<0.001	0.217	0.532
LRRC39	leucine rich repeat containing 39	Cardiac Muscle	227532_at	0.001	0.062	0.421	227532_at	0.053	0.295	-0.263	227532_at	0.194	0.838	-0.215
LRRFIP1	leucine rich repeat (in FLII) interacting protein 1	Gene Expression	201861_s_at	0.008	0.141	-0.353	201862_s_at	0.005	0.109	0.374	211452_x_at	0.005	0.376	0.445

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
LRRN3	leucine rich repeat neuronal 3	ECM Organization	209840_s_at	0.022	0.211	0.308	209840_s_at	0.133	0.442	-0.205	209840_s_at	0.010	0.426	-0.418
LSAMP	limbic system-associated membrane protein	Cell Adhesion	228218_at	<0.001	0.006	0.565	228218_at	0.004	0.102	-0.383	228218_at	0.003	0.351	-0.466
LSM8	LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae)	Gene Expression	219119_at	0.128	0.456	0.208	219119_at	0.006	0.116	-0.367	219119_at	0.956	0.997	0.009
LTBP2	latent transforming growth factor beta binding protein 2	ECM Organization	204682_at	<0.001	0.018	-0.507	223690_at	0.001	0.065	0.424	204682_at	0.069	0.694	0.298
LUC7L	LUC7-like (S. cerevisiae)	Gene Expression	223295_s_at	0.036	0.265	0.284	223295_s_at	0.004	0.102	-0.383	223295_s_at	0.696	0.976	0.065
LUC7L2	LUC7-like 2 (S. cerevisiae)	Gene Expression	217842_at	0.105	0.421	0.221	217842_at	0.005	0.108	-0.374	217842_at	0.718	0.979	0.060
LUC7L3	LUC7-like 3 (S. cerevisiae)	Gene Expression	208835_s_at	0.009	0.149	-0.348	208835_s_at	0.958	0.985	0.007	208835_s_at	0.030	0.563	0.354
LYRM4	LYR motif containing 4	Metabolic Process	222672_at	0.288	0.640	-0.146	222672_at	0.008	0.131	0.354	222672_at	0.889	0.993	-0.023
LYRM7	LYR motif containing 7	Respiratory Electron Chain Transport	231840_x_at	0.004	0.101	0.381	240344_x_at	0.002	0.075	-0.411	228841_at	0.069	0.693	-0.299
MAD2L1BP	MAD2L1 binding protein	Cell Division	203094_at	0.006	0.124	-0.364	203094_at	0.975	0.990	-0.004	203094_at	0.603	0.968	0.087
MAF	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog	Gene Expression	229327_s_at	0.062	0.336	0.253	229327_s_at	<0.001	0.030	-0.486	209348_s_at	0.009	0.425	-0.418
MAFB	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog B	Gene Expression	218559_s_at	0.008	0.138	0.354	218559_s_at	0.001	0.065	-0.425	218559_s_at	0.085	0.734	-0.284
MAFK	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog K	Gene Expression	226206_at	<0.001	0.047	-0.441	226206_at	0.125	0.431	0.209	226206_at	0.066	0.690	0.302
MAGI1	membrane associated guanylate kinase, WW and PDZ domain containing 1	Signal Transduction	206144_at	0.546	0.815	-0.083	206144_at	0.003	0.090	0.395	206144_at	0.453	0.940	0.125
MALSU1	mitochondrial assembly of ribosomal large subunit 1	Protein Translation	226385_s_at	0.017	0.192	0.320	226385_s_at	<0.001	0.057	-0.436	226385_s_at	0.293	0.901	-0.175
MALT1	MALT1 paracaspase	Signal Transduction	208309_s_at	0.627	0.859	0.067	208309_s_at	0.003	0.090	-0.394	208309_s_at	0.185	0.833	-0.219
MAN2A2	mannosidase, alpha, class 2A, member 2	Carbohydrate Metabolism	202032_s_at	0.043	0.287	0.274	219999_at	<0.001	0.035	-0.474	202032_s_at	0.011	0.446	-0.411
MAP1B	microtubule-associated protein 1B	Signal Transduction	226084_at	<0.001	0.042	-0.449	226084_at	0.005	0.108	0.375	226084_at	<0.001	0.134	0.599

Gene			LVEF				LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
MAP2K3	mitogen-activated protein kinase kinase 3	Cardiac Muscle	215499_at	0.006	0.121	-0.366	215499_at	0.497	0.774	-0.093	215499_at	0.292	0.900	0.175
MAP2K6	mitogen-activated protein kinase kinase 6	Cardiac Muscle	205698_s_at	<0.001	0.019	0.497	205698_s_at	0.009	0.135	-0.351	205698_s_at	0.182	0.833	-0.221
MAP3K12	mitogen-activated protein kinase kinase kinase 12	Signal Transduction	230921_s_at	0.005	0.110	0.375	230921_s_at	0.005	0.106	-0.379	230921_s_at	0.364	0.919	-0.151
MAP3K3	mitogen-activated protein kinase kinase kinase 3	Signal Transduction	227131_at	<0.001	0.025	-0.483	203514_at	0.014	0.164	0.331	227131_at	0.029	0.561	0.355
MAP3K5	mitogen-activated protein kinase kinase kinase 5	Signal Transduction	203837_at	0.009	0.149	0.348	203837_at	0.002	0.074	-0.412	203837_at	0.305	0.902	-0.171
MAP4	microtubule-associated protein 4	Actin Cytoskeleton	200835_s_at	0.001	0.056	-0.427	200835_s_at	0.003	0.089	0.396	212566_at	0.001	0.254	0.518
MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	Signal Transduction	222548_s_at	0.007	0.130	0.360	222548_s_at	0.108	0.405	-0.219	222548_s_at	0.973	0.998	0.006
MAP9	microtubule-associated protein 9	Cell Division	239415_at	0.914	0.974	0.015	239415_at	0.007	0.119	0.364	239415_at	0.633	0.971	0.080
MAPK8	mitogen-activated protein kinase 8	Signal Transduction	229664_at	<0.001	0.019	0.498	229664_at	0.009	0.134	-0.353	229664_at	0.010	0.438	-0.413
MAPRE2	microtubule-associated protein, RP/EB family, member 2	Actin Cytoskeleton	202501_at	0.016	0.187	-0.323	202501_at	0.045	0.276	0.272	202501_at	0.004	0.358	0.456
MARC2	mitochondrial amidoxime reducing component 2	Metabolic Process	221636_s_at	0.418	0.735	0.111	221636_s_at	0.043	0.269	-0.275	221636_s_at	0.008	0.408	-0.426
MARCH11	membrane-associated ring finger (C3HC4) 11	Protein Folding	239359_at	<0.001	0.025	0.484	239359_at	<0.001	0.032	-0.480	239359_at	0.014	0.457	-0.399
MARCH3	membrane-associated ring finger (C3HC4) 3, E3 ubiquitin protein ligase	Protein Folding	213256_at	<0.001	0.030	-0.471	213256_at	0.190	0.513	0.179	213256_at	0.059	0.668	0.309
MARCH5	membrane-associated ring finger (C3HC4) 5	Protein Folding	226394_at	0.017	0.191	0.320	226394_at	0.004	0.103	-0.381	226394_at	0.162	0.820	-0.231
MARCH8	membrane-associated ring finger (C3HC4) 8, E3 ubiquitin protein ligase	Protein Folding	221824_s_at	0.665	0.876	0.060	221824_s_at	0.001	0.065	-0.424	221824_s_at	0.849	0.990	-0.032
MARK3	MAP/microtubule affinity-regulating kinase 3	Signal Transduction	202569_s_at	0.057	0.323	0.258	202569_s_at	0.002	0.074	-0.413	202569_s_at	0.403	0.928	-0.139
MARS	methionyl-tRNA synthetase	Amino Acid Metabolism	213671_s_at	0.007	0.134	-0.357	213671_s_at	0.984	0.993	0.003	213671_s_at	0.807	0.985	-0.041
MATR3	matrin 3	Immune/Acute Phase Response	1558093_s_at	0.010	0.153	-0.346	1558093_s_at	0.008	0.131	0.354	1558093_s_at	0.077	0.713	0.291

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
MBP	myelin basic protein	Signal Transduction	210136_at	0.030	0.246	-0.292	210136_at	0.008	0.130	0.355	210136_at	0.226	0.862	0.201
MCAM	melanoma cell adhesion molecule	Cell Adhesion	210869_s_at	<0.001	0.007	-0.547	210869_s_at	0.005	0.107	0.377	209086_x_at	0.004	0.358	0.456
MCL1	myeloid cell leukemia 1	Apoptosis	200797_s_at	0.001	0.062	-0.420	200798_x_at	0.002	0.070	0.417	200798_x_at	0.006	0.376	0.445
MCM6	minichromosome maintenance complex component 6	Cell Division	201930_at	0.001	0.058	-0.425	201930_at	0.080	0.359	0.238	201930_at	0.717	0.979	-0.061
MCUR1	mitochondrial calcium uniporter regulator 1	Signal Transduction	227451_s_at	0.221	0.575	0.168	227451_s_at	0.917	0.970	0.014	227451_s_at	0.010	0.429	-0.416
MDFIC	MyoD family inhibitor domain containing	Signal Transduction	1559942_at	<0.001	0.040	-0.453	211675_s_at	<0.001	0.022	0.512	1559942_at	0.002	0.277	0.501
MDM1	Mdm1 nuclear protein homolog (mouse)	Cell Division	220397_at	0.046	0.295	0.271	220397_at	<0.001	0.028	-0.489	220397_at	0.020	0.503	-0.378
ME2	malic enzyme 2, NAD(+)-dependent, mitochondrial	Carbohydrate Metabolism	209397_at	0.038	0.272	0.281	209397_at	0.005	0.106	-0.378	209397_at	0.548	0.962	-0.100
MED13	mediator complex subunit 13	Gene Expression	223780_s_at	0.033	0.256	-0.288	223780_s_at	0.001	0.065	0.424	223780_s_at	0.267	0.889	0.184
MED17	mediator complex subunit 17	Gene Expression	221517_s_at	0.003	0.080	-0.399	221517_s_at	0.040	0.263	0.278	221517_s_at	0.938	0.995	0.013
MED30	mediator complex subunit 30	Gene Expression	227787_s_at	0.005	0.109	-0.375	227787_s_at	0.043	0.271	0.274	227787_s_at	0.188	0.834	0.218
MEF2C	myocyte enhancer factor 2C	Cardiac Muscle	209200_at	0.002	0.080	-0.400	209200_at	0.034	0.242	0.287	209200_at	0.071	0.696	0.297
MEIS2	Meis homeobox 2	Cardiac Muscle	207480_s_at	0.871	0.960	-0.022	207480_s_at	0.010	0.140	-0.348	207480_s_at	0.753	0.982	0.053
MESDC2	mesoderm development candidate 2	Protein Folding	224675_at	0.544	0.814	-0.084	224675_at	0.008	0.127	-0.358	224675_at	0.467	0.945	-0.121
METTL14	methyltransferase like 14	Gene Expression	227601_at	0.007	0.133	-0.358	227601_at	0.358	0.681	0.126	227601_at	0.180	0.833	0.222
METTL20	methyltransferase like 20	Fatty Acid Metabolism	1554582_a_at	0.106	0.421	0.221	1554582_a_at	0.005	0.106	-0.379	1554582_a_at	0.112	0.780	-0.262
MFHAS1	malignant fibrous histiocyoma amplified sequence 1	Signal Transduction	225478_at	0.042	0.287	0.275	225478_at	0.007	0.122	-0.361	225478_at	0.257	0.879	-0.188
MFSD8	major facilitator superfamily domain containing 8	Signal Transduction	228282_at	0.029	0.241	-0.295	228282_at	<0.001	0.043	0.462	228282_at	0.304	0.902	0.171
MIB2	mindbomb E3 ubiquitin protein ligase 2	Protein Folding	226644_at	0.007	0.129	0.361	226644_at	0.026	0.216	-0.302	226644_at	0.007	0.402	-0.431
MICA	MHC class I polypeptide-related sequence A	Immune/Acute Phase Response	205905_s_at	0.003	0.085	-0.395	205905_s_at	0.195	0.518	0.177	205905_s_at	0.790	0.984	0.045
MICAL2	microtubule associated monooxygenase, calponin and LIM domain containing 2	Actin Cytoskeleton	206275_s_at	0.010	0.154	-0.345	212473_s_at	<0.001	0.034	0.477	206275_s_at	0.132	0.797	0.248
MID1	midline 1	Protein Folding	203637_s_at	0.167	0.510	-0.189	203637_s_at	0.005	0.108	0.376	203637_s_at	0.327	0.909	0.163
MKKS	McKusick-Kaufman syndrome	Cell Division	218138_at	0.144	0.480	0.200	218138_at	<0.001	0.014	-0.538	218138_at	0.113	0.781	-0.261

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
MKNK2	MAP kinase interacting serine/threonine kinase 2	Signal Transduction	218205_s_at	0.288	0.640	0.146	218205_s_at	0.003	0.085	-0.400	218205_s_at	0.998	1.000	-0.001
MLH1	mutL homolog 1	Apoptosis	202520_s_at	<0.001	0.024	-0.487	202520_s_at	<0.001	0.048	0.453	202520_s_at	0.017	0.476	0.388
MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	Gene Expression	1563321_s_at	0.152	0.491	-0.196	1563321_s_at	0.007	0.123	0.360	1563321_s_at	0.077	0.714	0.290
MLPH	melanophilin	Actin Cytoskeleton	218211_s_at	<0.001	0.028	0.477	218211_s_at	<0.001	0.026	-0.497	218211_s_at	0.033	0.571	-0.349
MLX	MLX, MAX dimerization protein	Gene Expression	210752_s_at	0.001	0.061	0.422	210752_s_at	<0.001	0.010	-0.562	210752_s_at	0.005	0.363	-0.450
MMAA	methylmalonic aciduria (cobalamin deficiency) cbIA type	Fatty Acid Metabolism	236347_at	0.035	0.262	-0.285	236347_at	0.009	0.139	0.349	236347_at	0.505	0.953	0.111
MNDA	myeloid cell nuclear differentiation antigen	Signal Transduction	204959_at	0.800	0.934	0.035	204959_at	0.001	0.065	-0.425	204959_at	0.831	0.988	-0.036
MOG	myelin oligodendrocyte glycoprotein	Signal Transduction	214650_x_at	0.020	0.205	0.312	214650_x_at	0.001	0.065	-0.424	214650_x_at	0.012	0.450	-0.405
MOSPD1	motile sperm domain containing 1	Gene Expression	218853_s_at	0.025	0.223	0.303	218853_s_at	0.006	0.113	-0.369	218853_s_at	0.049	0.635	-0.322
MPHOSPH9	M-phase phosphoprotein 9	Cell Division	206205_at	0.466	0.766	0.100	206205_at	0.009	0.137	-0.350	206205_at	0.194	0.838	-0.215
MPP3	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)	Signal Transduction	206186_at	0.005	0.110	0.375	206186_at	0.004	0.100	-0.384	206186_at	0.138	0.800	-0.245
MPRIP	myosin phosphatase Rho interacting protein	Actin Cytoskeleton	212197_x_at	0.002	0.063	-0.417	212197_x_at	0.001	0.061	0.432	212197_x_at	0.031	0.565	0.352
MPV17	MpV17 mitochondrial inner membrane protein	Stress Response	203466_at	0.044	0.290	-0.273	203466_at	0.003	0.090	0.394	203466_at	0.300	0.901	0.172
MPZL2	myelin protein zero-like 2	Cell Adhesion	230518_at	0.174	0.517	-0.186	230518_at	0.617	0.837	0.069	230518_at	0.006	0.377	0.442
MRC1	mannose receptor, C type 1	Signal Transduction	204438_at	0.001	0.055	0.428	204438_at	0.010	0.141	-0.347	204438_at	<0.001	0.211	-0.537
MRPL2	mitochondrial ribosomal protein L2	Protein Translation	229884_s_at	0.551	0.818	-0.082	229884_s_at	<0.001	0.023	0.503	229884_s_at	0.872	0.992	-0.027
MRPL20	mitochondrial ribosomal protein L20	Protein Translation	220526_s_at	0.416	0.733	0.112	220526_s_at	0.005	0.106	-0.378	220526_s_at	0.768	0.983	0.049
MRPL30	mitochondrial ribosomal protein L30	Protein Translation	223996_s_at	<0.001	0.024	0.486	224971_at	<0.001	0.051	-0.447	224971_at	0.104	0.774	-0.268
MRPL33	mitochondrial ribosomal protein L33	Protein Translation	203781_at	0.007	0.130	0.360	203781_at	0.071	0.337	-0.246	203781_at	0.653	0.973	-0.075

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
MRPL41	mitochondrial ribosomal protein L41	Protein Translation	227186_s_at	0.171	0.514	0.187	225423_x_at	0.008	0.127	-0.357	225423_x_at	0.093	0.749	-0.277
MRPL44	mitochondrial ribosomal protein L44	Protein Translation	218202_x_at	0.010	0.153	0.346	218202_x_at	0.018	0.182	-0.319	218202_x_at	0.102	0.770	-0.270
MRPL52	mitochondrial ribosomal protein L52	Protein Translation	221997_s_at	0.888	0.967	-0.019	221997_s_at	0.009	0.138	-0.349	221997_s_at	0.775	0.984	-0.048
MRPS10	mitochondrial ribosomal protein S10	Protein Translation	224247_s_at	0.263	0.619	-0.154	224247_s_at	0.792	0.918	-0.036	224247_s_at	0.010	0.426	0.417
MRPS11	mitochondrial ribosomal protein S11	Protein Translation	211595_s_at	0.398	0.724	0.116	211595_s_at	0.003	0.093	-0.391	211595_s_at	0.031	0.565	-0.352
MRPS15	mitochondrial ribosomal protein S15	Protein Translation	223292_s_at	0.555	0.819	0.081	223292_s_at	0.007	0.121	-0.363	223292_s_at	0.878	0.992	-0.026
MRPS17	mitochondrial ribosomal protein S17	Protein Translation	218982_s_at	0.275	0.629	0.150	218982_s_at	0.008	0.130	-0.355	218982_s_at	0.685	0.975	0.068
MRPS24	mitochondrial ribosomal protein S24	Protein Translation	224948_at	0.015	0.182	0.327	224948_at	<0.001	0.002	-0.628	224948_at	0.042	0.616	-0.333
MRPS25	mitochondrial ribosomal protein S25	Protein Translation	224873_s_at	0.029	0.241	0.295	224869_s_at	0.003	0.093	-0.390	224873_s_at	0.324	0.909	-0.164
MRPS33	mitochondrial ribosomal protein S33	Protein Translation	218654_s_at	0.005	0.109	0.375	218654_s_at	0.425	0.729	-0.110	218654_s_at	0.851	0.990	0.031
MRS2	MRS2 magnesium transporter	Signal Transduction	218536_at	0.234	0.588	0.163	218536_at	0.169	0.486	-0.188	218536_at	0.004	0.358	-0.458
MSI2	musashi RNA-binding protein 2	Gene Expression	1552364_s_at	0.007	0.127	0.362	1552364_s_at	0.064	0.324	-0.251	1552364_s_at	0.291	0.900	-0.175
MTCH1	mitochondrial carrier 1	Signal Transduction	221619_s_at	0.163	0.505	0.191	221619_s_at	<0.001	0.011	-0.548	221619_s_at	0.530	0.959	-0.105
MT-CO1	cytochrome c oxidase subunit I	Respiratory Electron Chain Transport	1553538_s_at	0.584	0.836	0.076	1553538_s_at	0.007	0.121	-0.362	1553538_s_at	0.505	0.953	0.111
MTERF3	mitochondrial transcription termination factor 3	Gene Expression	219363_s_at	0.108	0.424	0.219	219363_s_at	0.002	0.083	-0.403	219363_s_at	0.142	0.800	-0.242
MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	Metabolic Process Carbohydrate	238762_at	0.438	0.747	0.107	238762_at	0.004	0.102	-0.384	238762_at	0.194	0.838	-0.215
MTMR1	myotubularin related protein 1	Metabolism	216095_x_at	0.704	0.893	0.052	216095_x_at	0.001	0.062	-0.431	216095_x_at	0.342	0.914	0.158
MT-ND4	NADH dehydrogenase, subunit 4 (complex I)	Respiratory Electron Chain Transport	224373_s_at	0.381	0.713	0.120	224373_s_at	0.010	0.140	-0.348	224373_s_at	0.496	0.953	0.113

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
MTSS1	metastasis suppressor 1	Signal Transduction	203037_s_at	0.040	0.279	0.278	203037_s_at	0.005	0.107	-0.377	203037_s_at	0.008	0.408	-0.426
MUM1	melanoma associated antigen (mutated) 1	Immune/Acute Phase Response	221290_s_at	0.506	0.790	0.092	221290_s_at	0.003	0.093	-0.390	221290_s_at	0.480	0.946	-0.118
MXD4	MAX dimerization protein 4	Gene Expression	210778_s_at	0.002	0.080	-0.400	210778_s_at	0.133	0.442	0.205	210778_s_at	0.070	0.695	0.297
MXRA8	matrix-remodelling associated 8 v-myb avian myeloblastosis viral oncogene homolog-like 1	ECM Organization	213422_s_at	0.082	0.377	-0.237	213422_s_at	0.005	0.107	0.377	213422_s_at	0.589	0.968	-0.090
MYBL1		Cell Division	213906_at	0.002	0.077	-0.404	213906_at	0.009	0.134	0.352	213906_at	0.016	0.473	0.389
MYBPC1	myosin binding protein C, slow type	Cell Adhesion	214087_s_at	<0.001	0.039	0.455	214087_s_at	0.024	0.211	-0.304	214087_s_at	0.025	0.530	-0.365
MYEF2	myelin expression factor 2	Gene Expression	222771_s_at	0.010	0.153	-0.346	232676_x_at	<0.001	0.041	0.466	222771_s_at	0.136	0.800	0.246
MYH10	myosin, heavy chain 10, non-muscle	Stress Response	213067_at	0.006	0.122	-0.366	212372_at	0.002	0.076	0.409	213067_at	0.018	0.486	0.385
MYH11	myosin, heavy chain 11, smooth muscle	Cardiac Muscle	201497_x_at	0.060	0.332	-0.255	201497_x_at	0.003	0.093	0.392	201497_x_at	0.476	0.946	0.119
MYH6	myosin, heavy chain 6, cardiac muscle, alpha	Cardiac Muscle	214468_at	<0.001	0.047	0.441	214468_at	<0.001	0.002	-0.634	214468_at	0.108	0.776	-0.265
MYH7	myosin, heavy chain 7, cardiac muscle, beta	Cardiac Muscle	204737_s_at	0.510	0.792	0.091	216265_x_at	0.002	0.074	-0.412	216265_x_at	0.198	0.842	0.213
MYL12A	myosin, light chain 12A, regulatory, non-sarcomeric	Signal Transduction	201318_s_at	0.200	0.551	-0.176	201318_s_at	0.417	0.723	-0.111	201318_s_at	0.009	0.416	0.421
MYL2	myosin, light chain 2, regulatory, cardiac, slow	Cardiac Muscle	209742_s_at	0.314	0.662	0.138	209742_s_at	0.001	0.065	-0.426	209742_s_at	0.657	0.974	0.074
MYL3	myosin, light chain 3, alkali; ventricular, skeletal, slow	Cardiac Muscle	205589_at	0.013	0.173	0.333	205589_at	<0.001	0.034	-0.476	205589_at	0.547	0.962	-0.101
MYLK3	myosin light chain kinase 3	Cardiac Muscle	238834_at	0.004	0.100	0.382	238834_at	0.003	0.090	-0.395	238834_at	0.287	0.899	-0.177
MYLK4	myosin light chain kinase family, member 4	Signal Transduction	1561504_s_at	<0.001	0.005	0.575	1561504_s_at	<0.001	0.018	-0.521	1561504_s_at	0.001	0.257	-0.512
MYOCD	myocardin	Cardiac Muscle	229339_at	0.009	0.149	-0.348	229339_at	0.111	0.411	0.217	229339_at	0.011	0.449	0.408
MYOT	myotilin	Actin Cytoskeleton	219728_at	0.013	0.171	-0.334	219728_at	0.010	0.142	0.346	219728_at	0.015	0.468	0.392
MZT2A	mitotic spindle organizing protein 2A	Cell Division	213166_x_at	<0.001	0.024	0.486	213166_x_at	<0.001	0.011	-0.549	213166_x_at	0.113	0.781	-0.262
N4BP1	NEDD4 binding protein 1	Protein Folding	32069_at	0.066	0.346	0.250	32069_at	<0.001	0.056	-0.437	32069_at	0.390	0.925	-0.143
NAMPT	nicotinamide phosphoribosyltransferase	Protein Translation	217738_at	0.006	0.125	0.363	217738_at	0.090	0.377	-0.231	217738_at	0.074	0.709	-0.293
NANP	N-acetylneuraminic acid phosphatase	Carbohydrate Metabolism	228073_at	0.089	0.392	-0.232	228073_at	0.679	0.867	-0.057	228073_at	0.006	0.382	-0.440
NAV2	neuron navigator 2	Signal Transduction	218330_s_at	0.001	0.054	-0.430	218330_s_at	0.073	0.344	0.244	218330_s_at	0.877	0.992	0.026

Gene			LVEF				LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
NBPF10	neuroblastoma breakpoint family, member 15	Unspecified	201104_x_at	0.002	0.063	0.417	201104_x_at	0.834	0.936	0.029	201104_x_at	0.677	0.974	-0.070
NCKAP1	NCK-associated protein 1	Apoptosis	217465_at	0.008	0.137	0.355	217465_at	0.060	0.313	-0.255	217465_at	0.607	0.969	0.086
NCKAP1L	NCK-associated protein 1-like	Actin Cytoskeleton	238668_at	0.093	0.401	0.229	238668_at	<0.001	0.048	-0.453	238668_at	0.634	0.971	-0.080
NCOA4	nuclear receptor coactivator 4	Signal Transduction	210774_s_at	0.028	0.240	0.296	210774_s_at	<0.001	0.048	-0.453	210774_s_at	0.467	0.945	-0.121
NDE1	nudE neurodevelopment protein 1	Cell Division	227249_at	0.001	0.057	-0.427	227249_at	0.210	0.534	0.172	227249_at	0.019	0.497	0.381
NDUFA1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa	Respiratory Electron Chain Transport	202298_at	0.075	0.365	0.242	202298_at	0.008	0.129	-0.356	202298_at	0.711	0.978	0.062
NDUFA4	NDUFA4, mitochondrial complex associated	Respiratory Electron Chain Transport	217773_s_at	0.068	0.350	0.248	217773_s_at	0.004	0.103	-0.381	217773_s_at	0.578	0.967	-0.093
NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa	Respiratory Electron Chain Transport	202001_s_at	0.043	0.289	0.274	202001_s_at	0.001	0.065	-0.423	202001_s_at	0.928	0.995	0.015
NDUFAF6	NADH dehydrogenase (ubiquinone) complex I, assembly factor 6	Respiratory Electron Chain Transport	235509_at	0.289	0.641	0.146	235509_at	<0.001	0.032	-0.483	235509_at	0.278	0.895	-0.180
NDUFB1	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa	Respiratory Electron Chain Transport	206790_s_at	0.147	0.484	0.198	206790_s_at	0.004	0.103	-0.381	206790_s_at	0.966	0.998	-0.007
NDUFB10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa	Respiratory Electron Chain Transport	228301_x_at	0.076	0.366	0.241	228301_x_at	<0.001	0.032	-0.481	228301_x_at	0.490	0.950	-0.115
NDUFB2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa	Respiratory Electron Chain Transport	218200_s_at	0.218	0.572	0.169	218200_s_at	0.003	0.091	-0.393	218200_s_at	0.737	0.982	0.056
NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa	Respiratory Electron Chain Transport	203621_at	0.058	0.327	0.257	203621_at	0.003	0.089	-0.396	203621_at	0.451	0.940	-0.126
NDUFB6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa	Respiratory Electron Chain Transport	203613_s_at	<0.001	0.049	0.437	203613_s_at	0.637	0.847	-0.065	203613_s_at	0.027	0.548	-0.361
NDUFB8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	Respiratory Electron Chain Transport	201227_s_at	0.039	0.276	0.279	201227_s_at	0.005	0.107	-0.376	201227_s_at	0.818	0.986	-0.039

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
NDUFC2	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa	Respiratory Electron Chain Transport	218101_s_at	0.001	0.057	0.426	218101_s_at	0.003	0.085	-0.401	218101_s_at	0.330	0.909	-0.162
NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)	Fatty Acid Metabolism	203606_at	0.220	0.574	0.168	203606_at	<0.001	0.010	-0.567	203606_at	0.602	0.968	0.087
NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa	Respiratory Electron Chain Transport	226616_s_at	0.001	0.061	0.421	226616_s_at	0.124	0.429	-0.210	226616_s_at	0.510	0.954	-0.110
NEBL	nebullette	Cardiac Muscle	241782_at	0.008	0.138	0.355	241782_at	0.669	0.862	-0.059	241782_at	0.527	0.959	-0.106
NECAB3	N-terminal EF-hand calcium binding protein 3	Metabolic Process	210720_s_at	0.004	0.097	-0.385	210720_s_at	0.140	0.450	0.202	210720_s_at	0.847	0.990	0.032
NEK1	NIMA-related kinase 1	Signal Transduction	213328_at	0.002	0.063	-0.417	213328_at	0.042	0.266	0.276	213328_at	0.008	0.408	0.426
NES	nestin	ECM Organization	218678_at	<0.001	0.039	-0.454	218678_at	<0.001	0.051	0.446	218678_at	0.002	0.306	0.482
NEU1	sialidase 1 (lysosomal sialidase)	Fatty Acid Metabolism	208926_at	0.010	0.153	-0.346	208926_at	0.069	0.334	0.247	208926_at	0.765	0.983	0.050
NEU3	sialidase 3 (membrane sialidase)	Metabolism	235474_at	0.055	0.318	-0.260	235474_at	0.003	0.093	0.391	235474_at	0.094	0.754	0.275
NEXN	nexilin (F actin binding protein)	Actin Cytoskeleton	1552309_a_at	0.285	0.638	-0.147	1552309_a_at	0.153	0.468	0.195	1552309_a_at	0.001	0.257	0.515
NFATC2IP	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein	Signal Transduction	229235_at	0.069	0.351	0.247	229235_at	0.002	0.072	-0.415	229235_at	0.427	0.935	-0.132
NFRKB	nuclear factor related to kappaB binding protein	Cell Division	213028_at	0.830	0.946	-0.030	213028_at	0.009	0.137	-0.350	213028_at	0.102	0.771	-0.269
NGFRAP1	nerve growth factor receptor (TNFRSF16) associated protein 1	Apoptosis	217963_s_at	0.105	0.420	0.221	217963_s_at	<0.001	0.034	-0.477	217963_s_at	0.729	0.981	0.058
NGLY1	N-glycanase 1	Amino Acid Metabolism	220742_s_at	0.834	0.947	0.029	220742_s_at	0.003	0.091	-0.393	220742_s_at	0.906	0.993	-0.020
NID1	nidogen 1	Cell Adhesion	202007_at	0.942	0.982	0.010	202007_at	0.004	0.098	0.387	202007_at	0.344	0.915	0.157
NIPBL	Nipped-B homolog (Drosophila)	Gene Expression	242352_at	0.002	0.077	-0.403	242352_at	0.060	0.313	0.255	242352_at	0.034	0.576	0.346
NKIRAS1	NFKB inhibitor interacting Ras-like 1	Signal Transduction	225930_at	0.035	0.264	0.284	225930_at	0.001	0.065	-0.426	225930_at	0.025	0.528	-0.365
NKTR	natural killer cell triggering receptor NLR family, CARD domain containing	Protein Folding Immune/Acute Phase	202379_s_at	0.035	0.264	-0.284	202379_s_at	0.753	0.900	0.043	202379_s_at	0.008	0.404	0.429
NLRC3	3	Response	236295_s_at	0.005	0.112	0.373	236295_s_at	0.103	0.399	-0.222	236295_s_at	0.053	0.647	-0.317
NMRK1	nicotinamide riboside kinase 1	Metabolic Process	219147_s_at	0.678	0.882	0.057	219147_s_at	0.186	0.507	-0.181	219147_s_at	0.002	0.279	-0.494

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
NMRK2	nicotinamide riboside kinase 2	Metabolic Process	221051_s_at	0.009	0.151	-0.347	221051_s_at	0.095	0.385	0.227	221051_s_at	0.236	0.868	0.196
NMT2	N-myristoyltransferase 2	Signal Transduction	215069_at	0.073	0.359	0.244	215069_at	0.002	0.077	-0.409	215069_at	0.320	0.908	0.165
NOL11	nucleolar protein 11	Gene Expression	221970_s_at	0.256	0.611	0.156	221970_s_at	0.007	0.124	-0.359	221970_s_at	0.522	0.958	-0.107
NOP16	NOP16 nucleolar protein	Protein Translation	209327_s_at	0.329	0.674	0.134	213833_x_at	0.001	0.062	-0.429	213833_x_at	0.074	0.706	-0.294
NOP56	NOP56 ribonucleoprotein	Gene Expression	200874_s_at	0.533	0.809	-0.086	200874_s_at	0.008	0.127	0.357	200874_s_at	0.926	0.995	0.016
NOSTRIN	nitric oxide synthase trafficking	Gene Expression	226992_at	<0.001	0.050	0.435	226992_at	0.434	0.736	-0.107	226992_at	0.706	0.977	-0.063
NOX4	NADPH oxidase 4	Respiratory Electron Chain Transport	219773_at	0.002	0.076	-0.405	219773_at	0.003	0.087	0.398	219773_at	0.040	0.603	0.336
NPC2	Niemann-Pick disease, type C2	Metabolic Process	200701_at	<0.001	0.053	-0.432	200701_at	0.021	0.195	0.312	200701_at	0.253	0.878	0.190
NPPA	natriuretic peptide A	Signal Transduction	209957_s_at	<0.001	0.006	-0.561	209957_s_at	0.001	0.058	0.434	209957_s_at	<0.001	0.134	0.595
NPPB	natriuretic peptide B	Cardiac Muscle	206801_at	<0.001	0.004	-0.589	206801_at	<0.001	0.031	0.484	206801_at	<0.001	0.107	0.641
NPY6R	neuropeptide Y receptor Y6 (pseudogene)	Signal Transduction	210444_at	0.235	0.590	-0.163	210444_at	0.002	0.083	0.404	210444_at	0.133	0.799	0.248
NRBF2	nuclear receptor binding factor 2	Gene Expression	223650_s_at	0.003	0.089	-0.391	223650_s_at	0.148	0.461	0.198	223650_s_at	0.350	0.915	0.155
NRIP1	nuclear receptor interacting protein 1	Signal Transduction	202600_s_at	0.316	0.664	-0.138	202600_s_at	0.750	0.899	0.044	202600_s_at	0.010	0.426	0.417
NSDHL	NAD(P) dependent steroid dehydrogenase-like	Signal Transduction	215093_at	0.013	0.170	0.334	215093_at	<0.001	0.051	-0.448	215093_at	0.319	0.908	-0.166
NSF	N-ethylmaleimide-sensitive factor	Signal Transduction	202395_at	0.003	0.082	-0.397	202395_at	<0.001	0.051	0.445	202395_at	0.839	0.990	0.034
NSG1	neuron specific gene family member 1	Apoptosis	209569_x_at	<0.001	0.033	0.464	209570_s_at	0.010	0.143	-0.346	209570_s_at	0.353	0.916	-0.155
NSUN3	NOP2/Sun domain family, member 3	Amino Acid Metabolism	219458_s_at	<0.001	0.051	-0.434	219458_s_at	0.330	0.657	0.133	219458_s_at	0.732	0.981	0.057
NSUN5	NOP2/Sun domain family, member 5	Gene Expression	213773_x_at	0.004	0.101	-0.381	213773_x_at	0.591	0.823	0.074	203802_x_at	0.666	0.974	-0.072
NUAK1	NUAK family, SNF1-like kinase, 1	Signal Transduction	204589_at	0.576	0.832	-0.077	204589_at	0.413	0.721	0.112	204589_at	0.004	0.358	0.455
NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	Cell Division	222424_s_at	0.226	0.580	0.166	222424_s_at	<0.001	0.037	-0.472	222424_s_at	0.093	0.748	-0.277
NUDT3	nudix (nucleoside diphosphate linked moiety X)-type motif 3	Metabolic Process	229803_s_at	<0.001	0.036	0.460	229803_s_at	0.014	0.164	-0.331	229803_s_at	0.332	0.909	-0.161
NUDT4	nudix (nucleoside diphosphate linked moiety X)-type motif 4	Signal Transduction	212183_at	0.013	0.170	0.335	212181_s_at	0.006	0.113	-0.370	212183_at	<0.001	0.134	-0.594

Gene			LVEF				LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
NUFIP2	nuclear fragile X mental retardation protein interacting protein 2	Stress Response	224958_at	<0.001	0.024	0.487	224958_at	0.003	0.093	-0.390	224958_at	0.299	0.901	-0.173
NUP98	nucleoporin 98kDa	Cell Division	210793_s_at	0.566	0.827	0.079	210793_s_at	0.010	0.142	-0.346	210793_s_at	0.855	0.991	0.031
NUPL1	nucleoporin like 1	Protein Translation	223984_s_at	0.317	0.665	-0.137	223984_s_at	0.004	0.097	-0.387	223984_s_at	0.450	0.940	0.126
NUTF2	nuclear transport factor 2	Gene Expression	202397_at	0.007	0.127	-0.362	202397_at	0.003	0.085	0.401	202397_at	0.192	0.838	0.216
OARD1	O-acyl-ADP-ribose deacylase 1	Metabolic Process	213322_at	0.446	0.753	0.105	213322_at	0.008	0.126	-0.358	213322_at	0.687	0.975	-0.067
		Amino Acid												
OAZ1	ornithine decarboxylase antizyme 1	Metabolism	200077_s_at	0.150	0.488	0.197	200077_s_at	<0.001	0.016	-0.533	200077_s_at	0.798	0.984	-0.043
		Amino Acid												
ODC1	ornithine decarboxylase 1	Metabolism	200790_at	<0.001	0.007	-0.545	200790_at	0.020	0.192	0.313	200790_at	0.257	0.879	0.188
	O-linked N-acetylglucosamine (GlcNAc) transferase	Apoptosis	207563_s_at	0.006	0.120	-0.366	207563_s_at	0.085	0.369	0.234	207563_s_at	0.760	0.982	0.051
OPTN	optineurin	Signal Transduction	202074_s_at	0.780	0.925	-0.039	202074_s_at	<0.001	0.051	-0.446	202074_s_at	0.871	0.992	-0.027
	olfactory receptor, family 7, subfamily D, member 2	Signal Transduction	1562337_at	0.303	0.654	0.141	1562337_at	0.023	0.206	-0.306	1562337_at	0.003	0.315	-0.479
ORMDL3	ORMDL sphingolipid biosynthesis regulator 3	Metabolic Process	223259_at	<0.001	0.045	-0.443	223259_at	0.176	0.495	0.185	223259_at	0.072	0.700	0.296
OSBPL1A	oxysterol binding protein-like 1A	Metabolic Process	208158_s_at	0.007	0.130	0.360	208158_s_at	0.005	0.107	-0.376	208158_s_at	0.100	0.766	-0.271
	purinergic receptor P2X, ligand gated ion channel, 5	Signal Transduction	210448_s_at	0.006	0.119	-0.368	210448_s_at	0.040	0.262	0.278	210448_s_at	0.019	0.497	0.380
P2RX5	prolyl 4-hydroxylase, alpha	Amino Acid												
P4HA1	polypeptide I	Metabolism	207543_s_at	0.002	0.077	-0.402	207543_s_at	0.094	0.382	0.228	207543_s_at	0.095	0.755	0.275
	poly(A) binding protein, cytoplasmic 1	Gene Expression	215157_x_at	<0.001	0.047	-0.440	215157_x_at	0.016	0.172	0.325	215157_x_at	0.062	0.676	0.306
PABPC1	p21 protein (Cdc42/Rac)-activated kinase 1	Actin Cytoskeleton	226507_at	0.958	0.987	-0.007	226507_at	0.002	0.074	-0.413	226507_at	0.975	0.998	-0.005
	p21 protein (Cdc42/Rac)-activated kinase 6	Actin Cytoskeleton	1555310_a_at	0.167	0.511	0.189	1555310_a_at	0.004	0.102	-0.383	1555310_a_at	<0.001	0.211	-0.537
PAK1	peptidylglycine alpha-amidating monooxygenase	Fatty Acid												
PAK6		Metabolism	212958_x_at	0.654	0.871	0.062	212958_x_at	0.008	0.129	-0.356	212958_x_at	0.432	0.936	0.131
PAM		Fatty Acid												
PANK2	pantothenate kinase 2	Metabolism	218809_at	0.067	0.348	0.248	218809_at	0.003	0.085	-0.401	218809_at	0.230	0.864	0.199
	pregnancy-associated plasma protein A, pappalysin 1	Signal Transduction	228128_x_at	0.195	0.545	-0.177	228128_x_at	0.006	0.114	0.369	224940_s_at	0.231	0.864	0.199
PAPPA														
PARD3	par-3 family cell polarity regulator	Cell Adhesion	221526_x_at	0.003	0.087	-0.393	221526_x_at	0.095	0.384	0.228	221526_x_at	0.149	0.806	0.239

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
PARD6B	par-6 family cell polarity regulator beta	Cell Division	235165_at	0.010	0.152	0.347	235165_at	0.133	0.442	-0.205	235165_at	0.002	0.286	-0.492
PARP12	poly (ADP-ribose) polymerase family, member 12	Gene Expression	218543_s_at	0.982	0.995	-0.003	218543_s_at	0.013	0.161	-0.333	218543_s_at	<0.001	0.211	-0.536
PARVA	parvin, alpha	Actin Cytoskeleton	217890_s_at	<0.001	0.030	-0.472	217890_s_at	0.117	0.419	0.214	217890_s_at	0.505	0.953	0.111
PARVB	parvin, beta	Actin Cytoskeleton	229822_at	0.003	0.089	0.392	229822_at	<0.001	0.022	-0.510	229822_at	0.014	0.459	-0.398
PAWR	PRKC, apoptosis, WT1, regulator	Apoptosis	204005_s_at	0.734	0.906	0.047	204005_s_at	0.002	0.070	-0.417	204005_s_at	0.565	0.965	0.096
PAXIP1	PAX interacting (with transcription-activation domain) protein 1	Cell Division	212825_at	0.100	0.412	0.224	212825_at	0.072	0.340	-0.245	212825_at	0.007	0.402	-0.431
PAXIP1-AS1	PAXIP1 antisense RNA 1 (head to head)	Cell Division	235587_at	0.175	0.519	0.186	235587_at	<0.001	0.048	-0.451	235587_at	0.012	0.449	-0.408
PBX2	pre-B-cell leukemia homeobox 2	Gene Expression	202876_s_at	0.320	0.667	0.137	202876_s_at	0.069	0.334	-0.247	202876_s_at	0.004	0.358	-0.456
PCBP2	poly(rC) binding protein 2	Gene Expression	213264_at	<0.001	0.007	0.555	213264_at	<0.001	0.018	-0.523	213264_at	0.002	0.290	-0.486
PCDH7	protocadherin 7	Cell Adhesion	210273_at	0.346	0.686	-0.129	210273_at	0.005	0.106	0.378	210273_at	0.824	0.988	0.037
PCDH9	protocadherin 9	Cell Adhesion	219737_s_at	0.020	0.202	-0.314	219737_s_at	0.135	0.444	0.204	219737_s_at	0.008	0.404	0.429
PCGF5	polycomb group ring finger 5	Gene Expression	229996_s_at	0.797	0.933	0.035	229996_s_at	<0.001	0.037	-0.473	229996_s_at	0.854	0.991	0.031
PCSK5	proprotein convertase subtilisin/kexin type 5	Respiratory Electron Chain Transport	205559_s_at	0.007	0.131	-0.359	213652_at	0.009	0.136	0.351	205559_s_at	0.511	0.954	0.110
PCYOX1	prenylcysteine oxidase 1	Metabolic Process	225274_at	<0.001	0.037	0.459	225274_at	0.010	0.145	-0.344	225274_at	0.011	0.446	-0.411
PDAP1	PDGFA associated protein 1	Signal Transduction	202290_at	0.720	0.900	-0.049	202290_at	0.005	0.107	0.376	202290_at	0.416	0.933	0.136
PDCD2	programmed cell death 2	Apoptosis	213581_at	<0.001	0.007	-0.545	204025_s_at	0.004	0.103	-0.382	204025_s_at	0.395	0.927	-0.141
PDE11A	phosphodiesterase 11A	Signal Transduction	237248_at	0.005	0.109	0.376	237248_at	0.007	0.124	-0.360	237248_at	0.040	0.603	-0.336
PDE1C	phosphodiesterase 1C, calmodulin-dependent 70kDa	Signal Transduction	216869_at	0.006	0.124	-0.364	216869_at	0.182	0.502	0.183	216869_at	0.203	0.843	0.211
PDE3A	phosphodiesterase 3A, cGMP-inhibited	Apoptosis	236300_at	0.002	0.065	0.413	236300_at	0.233	0.562	-0.163	236300_at	0.013	0.457	-0.403
PDE4A	phosphodiesterase 4A, cAMP-specific	Signal Transduction	204735_at	0.005	0.107	0.377	204735_at	0.004	0.103	-0.381	204735_at	0.034	0.576	-0.346
PDE4DIP	phosphodiesterase 4D interacting protein	Cell Division	214099_s_at	0.002	0.068	-0.412	214099_s_at	0.166	0.482	0.189	214099_s_at	0.019	0.497	0.381
PDE7A	phosphodiesterase 7A	Signal Transduction	230444_at	0.211	0.564	0.171	230444_at	<0.001	0.047	-0.455	230444_at	0.593	0.968	-0.089
PDE7B	phosphodiesterase 7B	Signal Transduction	230109_at	0.001	0.062	0.419	230109_at	0.011	0.146	-0.344	230109_at	0.011	0.446	-0.409

Gene			LVEF				LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
PDGFA	platelet-derived growth factor alpha polypeptide	Signal Transduction	229830_at	0.852	0.955	0.026	229830_at	0.006	0.112	-0.371	229830_at	0.731	0.981	-0.057
PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	Carbohydrate Metabolism	1555864_s_at	0.109	0.425	0.219	1555864_s_at	0.003	0.092	-0.392	1555864_s_at	0.885	0.993	-0.024
PDIK1L	PDLIM1 interacting kinase 1 like	Signal Transduction	227255_at	<0.001	0.047	0.439	227255_at	0.146	0.458	-0.198	227255_at	0.196	0.840	-0.214
PDLIM1	PDZ and LIM domain 1	Stress Response	208690_s_at	0.151	0.490	-0.196	208690_s_at	0.148	0.461	0.197	208690_s_at	0.004	0.358	0.456
PDLIM5	PDZ and LIM domain 5	Actin Cytoskeleton	216804_s_at	0.002	0.063	-0.415	216804_s_at	0.048	0.285	0.268	216804_s_at	0.048	0.635	0.324
PDPK1	3-phosphoinositide dependent protein kinase 1	Actin Cytoskeleton	204524_at	0.003	0.089	-0.391	204524_at	0.413	0.721	0.112	204524_at	0.402	0.928	0.140
PDS5A	PDS5 cohesin associated factor A	Cell Division	213983_s_at	<0.001	0.032	-0.467	212140_at	0.019	0.186	-0.317	213983_s_at	0.007	0.400	0.434
PDZRN3	PDZ domain containing ring finger 3	Protein Folding	212915_at	0.002	0.063	0.415	212915_at	0.016	0.175	-0.324	212915_at	0.007	0.394	-0.436
PDZRN3-AS1	PDZRN3 antisense RNA 1	Protein Folding	238165_at	0.088	0.391	0.232	238165_at	0.236	0.565	-0.162	238165_at	0.003	0.328	-0.475
PECR	peroxisomal trans-2-enoyl-CoA reductase	Fatty Acid Metabolism	223619_x_at	<0.001	0.037	0.459	223619_x_at	<0.001	0.006	-0.590	223619_x_at	0.009	0.411	-0.423
PEF1	penta-EF-hand domain containing 1 pellino E3 ubiquitin protein ligase	Protein Folding	217923_at	<0.001	0.041	-0.451	217923_at	0.028	0.225	0.297	217923_at	0.398	0.927	0.141
PELI3	family member 3	Protein Folding	235431_s_at	0.323	0.669	0.136	235431_s_at	0.005	0.106	-0.378	235431_s_at	0.315	0.908	-0.167
PERM1	PPARGC1 and ESRR induced regulator, muscle 1	Gene Expression	224501_at	0.379	0.711	0.121	224501_at	0.013	0.157	-0.335	224501_at	0.008	0.404	-0.429
PGAM2	phosphoglycerate mutase 2 (muscle)	Carbohydrate Metabolism	205736_at	0.006	0.119	0.368	205736_at	0.147	0.460	-0.198	205736_at	0.082	0.726	-0.286
PGK1	phosphoglycerate kinase 1	Carbohydrate Metabolism	200738_s_at	0.298	0.650	0.143	200738_s_at	0.005	0.111	-0.372	200738_s_at	0.567	0.965	0.096
PGM1	phosphoglucomutase 1	Carbohydrate Metabolism	201968_s_at	0.012	0.169	0.336	201968_s_at	0.007	0.121	-0.362	201968_s_at	0.749	0.982	-0.054
PGM3	phosphoglucomutase 3	Carbohydrate Metabolism	210041_s_at	0.004	0.106	-0.378	210041_s_at	0.015	0.171	0.326	210041_s_at	0.338	0.912	0.159
PGM5	phosphoglucomutase 5	Carbohydrate Metabolism	226303_at	0.001	0.055	-0.428	226303_at	0.019	0.186	0.317	226303_at	0.404	0.928	0.139
PGPEP1	pyroglutamyl-peptidase I	Amino Acid Metabolism	219891_at	0.024	0.222	0.303	219891_at	<0.001	0.036	-0.473	219891_at	0.297	0.901	-0.173
PHACTR1	phosphatase and actin regulator 1	Actin Cytoskeleton	226397_s_at	<0.001	0.013	0.518	226397_s_at	0.006	0.114	-0.368	226397_s_at	0.053	0.647	-0.317

Gene			LVEF				LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
PHF20	PHD finger protein 20	Signal Transduction	235389_at	0.007	0.130	0.360	235389_at	0.034	0.242	-0.287	235389_at	0.880	0.992	-0.025
PHF20L1	PHD finger protein 20-like 1	Gene Expression	231967_at	0.006	0.120	-0.366	231967_at	0.002	0.070	0.416	227523_s_at	0.007	0.402	0.431
PHF21A	PHD finger protein 21A	Gene Expression	203278_s_at	0.757	0.917	0.043	203278_s_at	0.006	0.116	-0.366	203278_s_at	0.886	0.993	-0.024
PHLDA1	pleckstrin homology-like domain, family A, member 1	Apoptosis	217996_at	<0.001	0.023	-0.488	217999_s_at	<0.001	0.029	0.487	225842_at	0.029	0.561	0.356
PHLDA2	pleckstrin homology-like domain, family A, member 2	Metabolic Process	209803_s_at	0.006	0.117	-0.369	209803_s_at	0.292	0.621	0.145	209803_s_at	0.556	0.964	-0.098
PHLDB2	pleckstrin homology-like domain, family B, member 2	Stress Response	238419_at	0.002	0.063	-0.416	238419_at	0.086	0.370	0.234	238419_at	0.121	0.793	0.255
PI4K2A	phosphatidylinositol 4-kinase type 2 alpha	Carbohydrate Metabolism	209345_s_at	0.004	0.098	-0.384	209345_s_at	0.079	0.356	0.239	209345_s_at	0.131	0.796	0.250
PIAS2	protein inhibitor of activated STAT, 2	Protein Folding	1555514_a_at	0.168	0.511	-0.189	1555514_a_at	0.001	0.063	0.428	1555514_a_at	0.181	0.833	0.222
PICALM	phosphatidylinositol binding clathrin assembly protein	Unspecified	212506_at	0.008	0.142	-0.352	212506_at	0.115	0.417	0.215	212506_at	0.046	0.628	0.326
PID1	phosphotyrosine interaction domain containing 1	Fatty Acid Metabolism	219093_at	<0.001	0.009	0.533	219093_at	0.012	0.154	-0.337	219093_at	0.087	0.739	-0.282
PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	Immune/Acute Phase Response	226459_at	0.004	0.106	0.378	226459_at	0.136	0.445	-0.204	226459_at	<0.001	0.170	-0.556
PIK3C2B	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 beta	Signal Transduction	204484_at	0.681	0.884	0.057	204484_at	0.052	0.295	0.263	204484_at	0.005	0.360	0.451
PIK3CA	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit alpha	Cardiac Muscle	235980_at	0.041	0.283	-0.276	235980_at	0.005	0.110	0.372	235980_at	0.746	0.982	0.054
PIK3CD	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit delta	Signal Transduction	203879_at	0.021	0.208	0.310	203879_at	<0.001	0.041	-0.465	203879_at	0.638	0.971	-0.079
PIM3	Pim-3 proto-oncogene, serine/threonine kinase	Apoptosis	224739_at	0.701	0.891	0.053	224739_at	0.009	0.136	-0.351	224739_at	0.178	0.833	-0.223
PIN4	peptidylprolyl cis/trans isomerase, NIMA-interacting 4	Gene Expression	214224_s_at	0.007	0.130	0.360	214224_s_at	0.049	0.287	-0.267	214224_s_at	0.510	0.954	-0.110
PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	Carbohydrate Metabolism	205632_s_at	0.004	0.102	0.381	205632_s_at	0.015	0.167	-0.328	205632_s_at	0.088	0.739	-0.281
PKNOX2	PBX/knotted 1 homeobox 2	Actin Cytoskeleton	63305_at	<0.001	0.019	0.498	63305_at	0.020	0.192	-0.313	63305_at	0.001	0.272	-0.506
PKP2	plakophilin 2	Cell Adhesion	207717_s_at	0.007	0.130	0.360	207717_s_at	0.905	0.966	-0.016	207717_s_at	0.344	0.915	-0.157
PKP4	plakophilin 4	Cell Adhesion	201928_at	0.046	0.296	0.270	201928_at	0.002	0.075	-0.412	201928_at	0.185	0.833	-0.220

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
PLCE1	phospholipase C, epsilon 1	Signal Transduction	205111_s_at	<0.001	0.007	-0.553	205112_at	<0.001	0.045	0.458	205111_s_at	<0.001	0.136	0.583
PLCL2	phospholipase C-like 2	Signal Transduction	213309_at	0.002	0.070	0.410	213309_at	<0.001	0.026	-0.496	213309_at	0.050	0.638	-0.321
PLD1	phospholipase D1, phosphatidylcholine-specific	Fatty Acid Metabolism	226636_at	0.006	0.118	0.369	226636_at	0.566	0.810	-0.079	226636_at	0.759	0.982	0.051
PLD6	phospholipase D family, member 6 pleckstrin homology domain containing, family A (phosphoinositide binding specific)	Cell Division	227037_at	0.043	0.287	0.274	227037_at	<0.001	0.039	-0.470	227037_at	<0.001	0.237	-0.526
PLEKHA1	member 1 pleckstrin homology domain containing, family A (phosphoinositide binding specific)	Metabolic Process	219024_at	0.614	0.853	0.070	219024_at	0.007	0.121	-0.362	219024_at	0.695	0.976	-0.066
PLEKHA2	member 2 pleckstrin homology domain containing, family A member 7	Cell Adhesion	238013_at	0.031	0.246	-0.292	238013_at	0.003	0.090	0.395	238013_at	0.127	0.796	0.252
PLEKHA7	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1	Cell Adhesion	228450_at	0.005	0.112	-0.373	228450_at	0.104	0.400	0.222	228450_at	<0.001	0.136	0.586
PLEKHH1		Actin Cytoskeleton	225726_s_at	0.022	0.210	0.309	225726_s_at	<0.001	0.011	-0.555	225726_s_at	0.142	0.800	-0.243
PLN	phospholamban	Signal Transduction	204938_s_at	<0.001	0.050	0.436	204939_s_at	<0.001	0.041	-0.465	204939_s_at	0.619	0.969	-0.083
PLP1	proteolipid protein 1	Fatty Acid Metabolism	210198_s_at	0.009	0.146	0.350	210198_s_at	0.384	0.699	-0.120	210198_s_at	0.448	0.940	-0.126
PNMA1	paraneoplastic Ma antigen 1	Immune/Acute Phase Response	218224_at	0.001	0.059	-0.423	218224_at	0.289	0.617	0.145	218224_at	0.565	0.965	0.096
PNPO	pyridoxamine 5'-phosphate oxidase	Metabolic Process	218511_s_at	0.096	0.405	0.227	218511_s_at	<0.001	0.038	-0.471	218511_s_at	0.078	0.718	-0.289
POLG	polymerase (DNA directed), gamma	Cell Division	203366_at	0.272	0.626	0.151	203366_at	0.006	0.113	-0.370	203366_at	0.771	0.983	-0.049
POLR1B	polymerase (RNA) I polypeptide B, 128kDa	Gene Expression	223403_s_at	0.001	0.054	0.430	223403_s_at	0.006	0.113	-0.370	223403_s_at	0.358	0.917	-0.153
POLR1E	polymerase (RNA) I polypeptide E, 53kDa	Gene Expression	218997_at	<0.001	0.050	-0.435	218997_at	<0.001	0.048	0.453	218997_at	<0.001	0.194	0.544
POLR2D	polymerase (RNA) II (DNA directed) polypeptide D	Gene Expression	203664_s_at	0.565	0.826	0.079	203664_s_at	0.009	0.136	-0.351	203664_s_at	0.282	0.897	-0.179
POLR2H	polymerase (RNA) II (DNA directed) polypeptide H	Gene Expression	209302_at	0.923	0.977	0.013	209302_at	0.005	0.107	-0.377	209302_at	0.590	0.968	-0.090

Gene			LVEF				LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
PPAP2A	phosphatidic acid phosphatase type 2A	Fatty Acid Metabolism	209147_s_at	0.007	0.130	-0.360	209147_s_at	0.014	0.164	0.330	209147_s_at	0.547	0.962	0.101
PPARA	peroxisome proliferator-activated receptor alpha	Fatty Acid Metabolism	1560981_a_at	0.236	0.590	-0.163	1560981_a_at	0.218	0.544	0.169	1560981_a_at	<0.001	0.167	0.562
PPCS	phosphopantothoenoylcysteine synthetase	Amino Acid Metabolism	218341_at	<0.001	0.048	-0.438	218341_at	0.727	0.889	0.048	218341_at	0.459	0.941	0.124
PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	Cell Adhesion	203735_x_at	0.274	0.628	0.150	203735_x_at	0.322	0.651	-0.136	203735_x_at	0.009	0.416	-0.421
PPID	peptidylprolyl isomerase D	Apoptosis	204186_s_at	0.004	0.100	-0.382	204186_s_at	0.547	0.801	0.083	204186_s_at	0.204	0.844	0.210
PPIG	peptidylprolyl isomerase G (cyclophilin G)	Gene Expression	208994_s_at	0.231	0.587	-0.164	208994_s_at	0.033	0.238	0.289	208994_s_at	0.005	0.376	0.445
PPIL1	peptidylprolyl isomerase (cyclophilin)-like 1	Gene Expression	222500_at	0.091	0.395	0.230	222500_at	<0.001	0.044	-0.460	222500_at	0.082	0.724	-0.286
PPIL6	peptidylprolyl isomerase (cyclophilin)-like 6	Amino Acid Metabolism	1553684_at	0.246	0.601	0.159	1553684_at	0.210	0.534	-0.171	1553684_at	0.002	0.286	-0.491
PPIP5K2	diphosphoinositol pentakisphosphate kinase 2	Carbohydrate Metabolism	203253_s_at	0.294	0.646	0.144	203253_s_at	0.004	0.096	-0.388	203253_s_at	0.082	0.726	-0.286
PPM1A	protein phosphatase, Mg2+/Mn2+ dependent, 1A	Cell Division	203966_s_at	<0.001	0.043	0.446	203966_s_at	0.014	0.162	-0.332	203966_s_at	0.580	0.967	-0.092
PPM1L	protein phosphatase, Mg2+/Mn2+ dependent, 1L	Signal Transduction	228457_at	0.001	0.061	0.422	228457_at	0.002	0.074	-0.412	228457_at	0.052	0.643	-0.318
PPOX	protoporphyrinogen oxidase	Signal Transduction	238117_at	0.258	0.614	-0.155	238117_at	0.003	0.092	0.392	238117_at	0.298	0.901	0.173
PPP1CC	protein phosphatase 1, catalytic subunit, gamma isozyme	Metabolic Process	200726_at	0.021	0.208	0.311	200726_at	<0.001	0.022	-0.508	200726_at	0.147	0.806	-0.240
PPP1R15A	protein phosphatase 1, regulatory subunit 15A	Apoptosis	202014_at	0.011	0.162	-0.339	202014_at	0.003	0.094	0.390	37028_at	0.398	0.927	0.141
PPP1R1A	protein phosphatase 1, regulatory (inhibitor) subunit 1A	Signal Transduction	205478_at	<0.001	0.027	0.478	235129_at	<0.001	0.038	-0.470	235129_at	0.020	0.503	-0.377
PPP1R2	protein phosphatase 1, regulatory (inhibitor) subunit 2	Signal Transduction	202166_s_at	0.006	0.124	-0.364	202166_s_at	0.057	0.305	0.258	202166_s_at	0.977	0.998	0.005
PPP1R3C	protein phosphatase 1, regulatory subunit 3C	Metabolic Process	204284_at	0.001	0.061	-0.422	204284_at	0.121	0.425	0.212	204284_at	0.002	0.290	0.485
PPP2CA	protein phosphatase 2, catalytic subunit, alpha isozyme	Apoptosis	208652_at	0.012	0.164	-0.338	208652_at	0.003	0.089	0.396	208652_at	0.188	0.834	0.218
PPP2R2B	protein phosphatase 2, regulatory subunit B, beta	Apoptosis	213849_s_at	0.013	0.172	-0.333	213849_s_at	0.002	0.080	0.407	213849_s_at	0.013	0.457	0.400
PPP2R2D	protein phosphatase 2, regulatory subunit B, delta	Signal Transduction	225066_at	0.003	0.090	-0.390	225066_at	0.231	0.560	0.164	225066_at	0.587	0.968	0.091

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
PPP2R5E	protein phosphatase 2, regulatory subunit B', epsilon isoform	Signal Transduction	229322_at	0.010	0.154	-0.345	229322_at	0.035	0.244	0.286	229322_at	0.393	0.927	0.142
PPP6C	protein phosphatase 6, catalytic subunit	Cell Division	225429_at	0.002	0.078	0.402	225429_at	0.011	0.147	-0.343	225429_at	0.012	0.449	-0.407
PPWD1	peptidylprolyl isomerase domain and WD repeat containing 1	Gene Expression	213483_at	0.318	0.666	0.137	213483_at	<0.001	0.047	-0.454	213483_at	0.911	0.994	-0.019
PRDM16	PR domain containing 16	Gene Expression	232424_at	0.018	0.193	0.319	232424_at	0.001	0.065	-0.425	232424_at	0.584	0.968	-0.091
PRDM4	PR domain containing 4	Gene Expression	49485_at	0.012	0.170	0.335	49485_at	0.004	0.102	-0.383	49485_at	0.015	0.466	-0.394
PRDX5	peroxiredoxin 5	Stress Response	1560587_s_at	0.004	0.095	0.386	1560587_s_at	0.001	0.065	-0.424	222994_at	0.299	0.901	-0.173
PRDX6	peroxiredoxin 6	Stress Response	200844_s_at	0.029	0.241	0.295	200844_s_at	<0.001	0.040	-0.467	200844_s_at	0.092	0.747	-0.277
PRICKLE1	prickle homolog 1 (Drosophila)	Cardiac Muscle	226065_at	0.019	0.197	-0.316	226065_at	0.005	0.107	0.377	226065_at	0.027	0.552	0.359
PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	Fatty Acid Metabolism	207709_at	0.021	0.208	-0.311	207709_at	0.002	0.077	0.409	207709_at	0.024	0.524	0.367
PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	Fatty Acid Metabolism	214474_at	0.006	0.124	-0.364	214474_at	0.160	0.475	0.192	214474_at	0.195	0.839	0.215
PRKACB	protein kinase, cAMP-dependent, catalytic, beta	Signal Transduction	202742_s_at	0.022	0.210	-0.309	202742_s_at	0.002	0.067	0.421	202742_s_at	0.019	0.497	0.381
PRMT1	protein arginine methyltransferase 1	Gene Expression	206445_s_at	0.782	0.926	-0.038	206445_s_at	0.003	0.091	0.393	206445_s_at	0.501	0.953	-0.112
PRMT2	protein arginine methyltransferase 2	Gene Expression	228725_x_at	0.001	0.058	-0.425	202098_s_at	0.019	0.186	0.317	228725_x_at	0.403	0.928	0.139
PRMT9	protein arginine methyltransferase 9	Metabolism	228536_at	0.001	0.059	-0.423	228536_at	0.214	0.539	0.170	228536_at	0.740	0.982	-0.055
PROS1	protein S (alpha)	Immune/Acute Phase Response	207808_s_at	0.002	0.069	-0.410	207808_s_at	0.047	0.281	0.269	207808_s_at	0.012	0.450	0.405
PRPSAP1	phosphoribosyl pyrophosphate synthetase-associated protein 1	Metabolic Process	202529_at	0.004	0.106	0.378	202529_at	0.008	0.126	-0.358	202529_at	0.008	0.408	-0.426
PRRX1	paired related homeobox 1	Signal Transduction	226695_at	0.002	0.074	-0.407	226695_at	0.430	0.733	0.108	226695_at	0.230	0.864	0.199
PRSS23	protease, serine, 23	Protein Translation	202458_at	0.001	0.059	-0.423	202458_at	0.027	0.220	0.300	202458_at	0.174	0.832	0.225
PSAP	prosaposin	Fatty Acid Metabolism	200871_s_at	0.365	0.701	0.125	200871_s_at	0.006	0.115	-0.367	200871_s_at	0.568	0.965	-0.095
PSMC3IP	PSMC3 interacting protein	Cell Division	213951_s_at	0.490	0.780	0.095	213951_s_at	0.009	0.136	-0.351	213951_s_at	0.675	0.974	0.070
PSMD10	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	Protein Folding	1554577_a_at	0.547	0.816	-0.083	1554577_a_at	0.002	0.073	0.414	1554577_a_at	0.832	0.988	0.036

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
PSMD2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	Protein Folding	200830_at	0.877	0.962	-0.021	200830_at	0.006	0.114	-0.368	200830_at	0.699	0.976	-0.065
PSMD7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	Protein Folding	201705_at	0.911	0.973	0.015	201705_at	0.010	0.140	-0.348	201705_at	0.844	0.990	-0.033
PSMG3	proteasome (prosome, macropain) assembly chaperone 3	Protein Folding Immune/Acute Phase	223363_at	0.564	0.826	-0.079	223363_at	0.004	0.104	-0.380	223363_at	0.367	0.920	-0.150
PSPC1	paraspeckle component 1	Response	218371_s_at	0.341	0.682	0.131	218371_s_at	0.001	0.058	-0.434	218371_s_at	0.590	0.968	-0.090
PTCH1	patched 1	Cell Division	209815_at	0.001	0.059	0.424	209815_at	0.069	0.334	-0.247	209815_at	0.566	0.965	-0.096
PTEN	phosphatase and tensin homolog	Apoptosis	204054_at	0.982	0.995	-0.003	204054_at	0.004	0.104	-0.380	204054_at	0.241	0.871	-0.194
PTGDS	prostaglandin D2 synthase 21kDa (brain)	Fatty Acid Metabolism	211748_x_at	0.002	0.063	0.415	211748_x_at	0.042	0.267	-0.276	212187_x_at	0.111	0.779	-0.263
PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	Fatty Acid Metabolism	238669_at	0.289	0.642	0.145	238669_at	0.010	0.140	-0.348	238669_at	0.355	0.917	-0.154
PTOV1-AS1	PTOV1 antisense RNA 1	Gene Expression	240615_at	<0.001	0.007	0.545	240615_at	0.005	0.106	-0.378	240615_at	0.034	0.577	-0.345
PTP4A2	protein tyrosine phosphatase type IVA, member 2	Protein Translation	208617_s_at	0.236	0.591	0.162	208617_s_at	0.001	0.062	-0.431	208617_s_at	0.353	0.916	-0.154
PTPN1	protein tyrosine phosphatase, non- receptor type 1	Signal Transduction	202716_at	<0.001	0.016	-0.511	202716_at	0.007	0.121	0.362	202716_at	<0.001	0.136	0.587
PTPN11	protein tyrosine phosphatase, non- receptor type 11	Carbohydrate Metabolism	209896_s_at	<0.001	0.022	-0.491	209895_at	0.019	0.189	0.315	209896_s_at	<0.001	0.239	0.524
PTPN14	protein tyrosine phosphatase, non- receptor type 14	Signal Transduction	244533_at	0.293	0.645	-0.144	244533_at	0.242	0.572	0.160	244533_at	0.002	0.277	0.499
PTPRK	protein tyrosine phosphatase, receptor type, K	Cell Adhesion	203038_at	0.009	0.149	0.349	203038_at	0.108	0.405	-0.219	203038_at	0.312	0.905	0.168
PTPRS	protein tyrosine phosphatase, receptor type, S	Signal Transduction	229465_s_at	0.001	0.054	0.430	226571_s_at	0.221	0.548	-0.167	226571_s_at	0.341	0.914	0.158
PTRH2	peptidyl-tRNA hydrolase 2	Apoptosis	218732_at	0.249	0.605	0.158	218732_at	0.004	0.100	-0.385	218732_at	0.471	0.946	-0.120
PUM1	pumilio RNA-binding family member 1	Cell Division	201165_s_at	0.008	0.141	-0.353	201165_s_at	0.552	0.804	0.082	201165_s_at	0.480	0.946	0.118
PUM2	pumilio RNA-binding family member 2	Gene Expression	216221_s_at	<0.001	0.033	0.466	216221_s_at	0.387	0.702	-0.119	216221_s_at	0.219	0.855	-0.204
PVR	poliovirus receptor	Cell Adhesion	1556582_at	0.006	0.118	0.369	1556582_at	0.648	0.852	-0.063	1556582_at	0.236	0.868	-0.196

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
PWP1	PWP1 homolog (S. cerevisiae)	Amino Acid Metabolism	201606_s_at	0.003	0.090	-0.390	201607_at	0.005	0.108	0.375	201606_s_at	0.032	0.571	0.349
PYGM	phosphorylase, glycogen, muscle	Carbohydrate Metabolism	205577_at	<0.001	0.048	0.438	205577_at	0.115	0.417	-0.215	205577_at	0.024	0.524	-0.368
QPCT	glutaminyl-peptide cyclotransferase	Amino Acid Metabolism	205174_s_at	<0.001	0.037	-0.457	205174_s_at	0.003	0.093	0.390	205174_s_at	0.013	0.457	0.402
RAB1B	RAB1B, member RAS oncogene family	Metabolic Process	220964_s_at	0.695	0.889	-0.054	220964_s_at	0.007	0.120	0.364	220964_s_at	0.867	0.991	0.028
RAB22A	RAB22A, member RAS oncogene family	Signal Transduction	218360_at	0.009	0.149	-0.348	218360_at	0.308	0.636	0.140	218360_at	0.182	0.833	0.221
RAB27A	RAB27A, member RAS oncogene family	Stress Response	222294_s_at	0.090	0.393	0.231	222294_s_at	0.002	0.082	-0.405	222294_s_at	0.040	0.605	-0.335
RAB31	RAB31, member RAS oncogene family	Signal Transduction	217762_s_at	<0.001	0.005	-0.573	217763_s_at	0.032	0.238	0.290	217762_s_at	0.044	0.625	0.329
RAB7A	RAB7A, member RAS oncogene family	Fatty Acid Metabolism	227602_at	0.007	0.128	0.362	211961_s_at	0.005	0.106	0.378	211960_s_at	0.861	0.991	-0.029
RABGAP1	RAB GTPase activating protein 1	Cell Division	204028_s_at	0.009	0.149	-0.348	204028_s_at	0.561	0.808	0.080	204028_s_at	0.642	0.972	0.078
RAE1	ribonucleic acid export 1	Cell Division	201558_at	0.624	0.858	0.068	201558_at	0.003	0.090	-0.396	201558_at	0.886	0.993	0.024
RAI1	retinoic acid induced 1	Gene Expression	226143_at	0.004	0.106	0.378	226143_at	0.022	0.200	-0.309	226143_at	0.143	0.800	-0.242
RALA	v-ral simian leukemia viral oncogene homolog A (ras related)	Actin Cytoskeleton	224880_at	0.044	0.289	0.273	214435_x_at	0.001	0.066	-0.422	214435_x_at	0.070	0.695	-0.297
RALB	v-ral simian leukemia viral oncogene homolog B	Apoptosis	202100_at	0.008	0.138	0.355	202100_at	0.235	0.565	-0.162	202100_at	0.547	0.962	-0.101
RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	Signal Transduction	227533_at	0.006	0.117	0.369	227533_at	0.003	0.087	-0.398	227224_at	0.041	0.608	-0.335
RAN	RAN, member RAS oncogene family	Cell Division	200750_s_at	0.004	0.103	-0.380	200750_s_at	0.082	0.363	0.237	200750_s_at	0.140	0.800	0.244
RANBP2	RAN binding protein 2	Cell Division	201711_x_at	0.029	0.243	-0.294	201711_x_at	0.089	0.375	0.232	201711_x_at	0.001	0.257	0.510
RAP2A	RAP2A, member of RAS oncogene family	Actin Cytoskeleton	221830_at	0.002	0.076	-0.404	221830_at	0.150	0.464	0.196	221830_at	0.016	0.475	0.389
RASD1	RAS, dexamethasone-induced 1	Signal Transduction	223467_at	<0.001	0.047	0.439	223467_at	<0.001	0.026	-0.498	223467_at	0.006	0.389	-0.438
RASGRP2	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	Signal Transduction	214369_s_at	0.015	0.185	0.325	214369_s_at	<0.001	0.032	-0.480	214369_s_at	0.135	0.800	-0.247
RASSF3	Ras association (RalGDS/AF-6) domain family member 3	Signal Transduction	230466_s_at	0.004	0.106	0.378	227167_s_at	<0.001	0.052	-0.444	230466_s_at	0.281	0.897	-0.179
RBBP8	retinoblastoma binding protein 8	Cell Division	203344_s_at	0.008	0.138	-0.355	203344_s_at	0.889	0.959	0.019	203344_s_at	0.676	0.974	0.070

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
RBFOX1	RNA binding protein, fox-1 homolog (C. elegans) 1	Gene Expression	1553422_s_at	<0.001	0.043	0.447	1553422_s_at	0.083	0.366	-0.236	1553422_s_at	0.113	0.781	-0.262
RBFOX2	RNA binding protein, fox-1 homolog (C. elegans) 2	Gene Expression	212104_s_at	0.015	0.182	-0.328	212104_s_at	0.002	0.075	0.411	212104_s_at	<0.001	0.239	0.523
RBKS	ribokinase	Metabolism	219222_at	0.002	0.065	0.414	57540_at	0.002	0.071	-0.415	57540_at	0.080	0.722	-0.288
RBM17	RNA binding motif protein 17	Gene Expression	224780_at	0.036	0.266	0.283	224781_s_at	0.005	0.107	-0.376	224780_at	0.560	0.965	-0.097
RBM26	RNA binding motif protein 26	Gene Expression	226316_at	0.554	0.819	-0.082	226316_at	0.010	0.141	-0.347	226316_at	0.674	0.974	0.070
RBM6	RNA binding motif protein 6	Gene Expression	228030_at	0.083	0.381	0.236	228030_at	0.009	0.138	-0.349	228030_at	0.428	0.936	-0.132
RBMS1	RNA binding motif, single stranded interacting protein 1	Cell Division	207266_x_at	0.006	0.119	-0.368	207266_x_at	0.002	0.067	0.420	207266_x_at	0.405	0.930	0.139
RBMX	RNA binding motif protein, X-linked	Protein Translation	213762_x_at	0.010	0.152	0.347	213762_x_at	0.016	0.174	-0.324	213762_x_at	0.142	0.800	-0.243
RCAN1	regulator of calcineurin 1	Signal Transduction	208370_s_at	0.009	0.146	-0.350	208370_s_at	0.142	0.453	0.201	208370_s_at	0.307	0.904	0.170
REPIN1	replication initiator 1	Cell Division	219041_s_at	0.005	0.114	0.372	219041_s_at	<0.001	0.048	-0.451	219041_s_at	0.001	0.257	-0.511
RET	ret proto-oncogene	Signal Transduction	211421_s_at	0.001	0.055	0.428	211421_s_at	0.073	0.343	-0.244	211421_s_at	<0.001	0.159	-0.566
RFC5	replication factor C (activator 1) 5, 36.5kDa	Signal Transduction	213734_at	0.949	0.985	0.009	213734_at	0.007	0.121	-0.362	213734_at	0.882	0.992	-0.025
RFX3	regulatory factor X, 3 (influences HLA class II expression)	Gene Expression	243868_at	<0.001	0.047	-0.439	243868_at	0.254	0.584	0.156	243868_at	0.391	0.925	0.143
RFX5	regulatory factor X, 5 (influences HLA class II expression)	Gene Expression	202963_at	<0.001	0.007	-0.556	202963_at	0.207	0.531	0.173	202963_at	0.072	0.701	0.295
RFX7	regulatory factor X, 7	Gene Expression	218430_s_at	0.005	0.116	-0.370	218430_s_at	<0.001	0.018	0.523	218430_s_at	0.085	0.734	0.284
RGS3	regulator of G-protein signaling 3	Signal Transduction	203823_at	<0.001	0.030	-0.471	203823_at	0.038	0.254	0.281	203823_at	0.407	0.931	0.138
RGS4	regulator of G-protein signaling 4	Signal Transduction	204337_at	<0.001	0.009	-0.531	204337_at	0.002	0.083	0.404	204337_at	0.023	0.522	0.370
RGS5	regulator of G-protein signaling 5	Signal Transduction	209070_s_at	0.410	0.730	-0.113	209070_s_at	0.002	0.075	0.411	209070_s_at	0.790	0.984	0.045
RHEB	Ras homolog enriched in brain	Signal Transduction	213409_s_at	0.611	0.852	0.070	213409_s_at	0.008	0.132	-0.354	213409_s_at	0.714	0.979	-0.061
RHOBTB1	Rho-related BTB domain containing 1	Signal Transduction	212651_at	<0.001	0.048	-0.438	212651_at	0.552	0.804	0.082	212651_at	0.102	0.770	0.270
RHOF	ras homolog family member F (in filopodia)	Signal Transduction	219045_at	0.079	0.371	0.239	219045_at	<0.001	0.029	-0.487	219045_at	0.206	0.845	-0.209

Gene			LVEF				LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
RHOQ	ras homolog family member Q	Actin Cytoskeleton	212117_at	0.668	0.878	0.059	212117_at	0.006	0.115	-0.368	212117_at	0.395	0.927	-0.141
RHOT1	ras homolog family member T1	Signal Transduction	218323_at	0.052	0.312	0.263	222148_s_at	<0.001	0.057	-0.437	222148_s_at	0.345	0.915	-0.157
RICTOR	RPTOR independent companion of MTOR, complex 2	Actin Cytoskeleton	228248_at	0.246	0.601	-0.159	228248_at	0.007	0.124	0.359	228248_at	0.262	0.884	0.186
RMDN1	regulator of microtubule dynamics 1	Cell Division	218549_s_at	0.200	0.551	0.176	218549_s_at	<0.001	0.055	-0.440	218549_s_at	0.331	0.909	-0.162
RMDN2	regulator of microtubule dynamics 2	Cell Division	235349_at	0.245	0.600	-0.159	235349_at	0.567	0.811	0.079	235349_at	0.008	0.408	-0.425
RNASEH2B	ribonuclease H2, subunit B	Cell Division	229210_at	0.002	0.075	-0.405	229210_at	0.603	0.830	0.071	229210_at	0.334	0.911	0.161
RND3	Rho family GTPase 3	Actin Cytoskeleton	212724_at	0.019	0.197	-0.316	212724_at	<0.001	0.041	0.465	212724_at	0.011	0.446	0.409
RNF123	ring finger protein 123	Protein Folding	224186_s_at	0.008	0.139	-0.354	221063_x_at	0.009	0.137	0.350	224186_s_at	0.471	0.946	0.120
RNF165	ring finger protein 165	Protein Folding	230143_at	<0.001	0.034	0.464	230143_at	0.058	0.306	-0.258	230143_at	0.098	0.763	-0.272
RNF168	ring finger protein 168, E3 ubiquitin protein ligase	Protein Folding	226832_at	0.034	0.261	0.286	226832_at	0.003	0.089	-0.396	226832_at	0.485	0.948	-0.116
RNF170	ring finger protein 170	Protein Folding	1554312_at	0.005	0.107	0.377	1554312_at	0.103	0.399	-0.222	1554312_at	0.623	0.970	-0.082
RNF187	ring finger protein 187	Protein Folding	1569294_at	<0.001	0.048	0.439	1569294_at	0.243	0.573	-0.160	1569294_at	0.407	0.931	-0.138
RNF207	ring finger protein 207	Cardiac Muscle	1555870_at	0.011	0.162	0.340	1555870_at	0.002	0.083	-0.403	1555870_at	0.067	0.692	-0.301
RNF217	ring finger protein 217	Protein Folding	226885_at	0.004	0.100	-0.382	226885_at	0.088	0.373	0.233	226885_at	0.398	0.927	0.141
RNF41	ring finger protein 41, E3 ubiquitin protein ligase	Protein Folding	201961_s_at	<0.001	0.043	-0.446	201961_s_at	0.007	0.123	0.360	201961_s_at	0.079	0.719	0.289
RNF43	ring finger protein 43	Protein Folding	218704_at	0.103	0.417	0.222	218704_at	0.006	0.112	-0.371	218704_at	0.172	0.832	-0.226
RNF5	ring finger protein 5, E3 ubiquitin protein ligase	Signal Transduction	209111_at	0.002	0.078	0.401	209111_at	0.066	0.329	-0.249	209111_at	0.384	0.924	-0.145
RNFT1	ring finger protein, transmembrane 1	Protein Folding	227268_at	0.045	0.292	0.272	227268_at	0.006	0.112	-0.371	227268_at	0.007	0.402	-0.431
RNLS	renalase, FAD-dependent amine oxidase	Stress Response	223824_at	<0.001	0.037	0.458	223824_at	<0.001	0.046	-0.458	223824_at	<0.001	0.128	-0.612
RNMT	RNA (guanine-7-) methyltransferase	Gene Expression	202684_s_at	0.032	0.250	-0.290	202684_s_at	0.006	0.113	0.370	202684_s_at	0.473	0.946	0.120
ROPN1B	rhophilin associated tail protein 1B	Signal Transduction	220425_x_at	<0.001	0.048	0.438	220425_x_at	0.029	0.228	-0.295	220425_x_at	0.036	0.585	-0.343
ROR1	receptor tyrosine kinase-like orphan receptor 1	Signal Transduction	232060_at	0.014	0.176	-0.331	205805_s_at	0.006	0.114	0.368	232060_at	0.006	0.380	0.442
RORC	RAR-related orphan receptor C	Apoptosis	228806_at	0.460	0.762	0.102	228806_at	0.004	0.102	-0.383	228806_at	0.267	0.890	-0.184
RPL10A	ribosomal protein L10a	Protein Translation	229563_s_at	0.370	0.704	0.123	229563_s_at	0.007	0.121	-0.362	229563_s_at	0.477	0.946	0.119
RPL10L	ribosomal protein L10-like	Protein Translation	217559_at	0.236	0.590	0.163	217559_at	0.264	0.594	-0.153	217559_at	0.008	0.404	-0.429
RPL14	ribosomal protein L14	Protein Translation	213588_x_at	0.031	0.248	0.291	213588_x_at	0.004	0.103	-0.381	219138_at	0.327	0.909	-0.163
RPL22	ribosomal protein L22	Protein Translation	208768_x_at	0.009	0.145	0.351	208768_x_at	0.096	0.387	-0.226	208768_x_at	0.376	0.923	0.147

Gene			LVEF				LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
RPL23	ribosomal protein L23	Protein Translation	200888_s_at	0.760	0.918	0.042	200888_s_at	0.008	0.128	-0.357	200888_s_at	0.596	0.968	0.089
RPL24	ribosomal protein L24	Protein Translation	214143_x_at	0.204	0.557	0.174	214143_x_at	0.006	0.117	-0.366	214143_x_at	0.757	0.982	0.052
RPL27	ribosomal protein L27	Protein Translation	200025_s_at	0.017	0.191	0.321	200025_s_at	0.008	0.131	-0.355	200025_s_at	0.709	0.977	-0.062
RPL27A	ribosomal protein L27a	Protein Translation	223707_at	0.283	0.637	-0.147	223707_at	0.039	0.259	0.280	223707_at	0.003	0.329	0.474
RPL30	ribosomal protein L30	Protein Translation	200062_s_at	0.181	0.526	0.183	200062_s_at	0.005	0.110	-0.373	200062_s_at	0.928	0.995	0.015
RPL32	ribosomal protein L32	Protein Translation	200674_s_at	0.314	0.662	0.138	200674_s_at	0.003	0.088	-0.397	200674_s_at	0.468	0.946	0.121
RPL36A	ribosomal protein L36a	Protein Translation	201406_at	0.005	0.116	0.370	201406_at	0.240	0.570	-0.161	201406_at	0.353	0.916	-0.154
RPL37	ribosomal protein L37	Protein Translation	200092_s_at	0.049	0.303	0.267	200092_s_at	0.009	0.136	-0.351	200092_s_at	0.805	0.985	0.041
RPL37A	ribosomal protein L37a	Protein Translation	214041_x_at	0.764	0.919	0.041	214041_x_at	0.004	0.098	-0.386	214041_x_at	0.500	0.953	0.113
RPL38	ribosomal protein L38	Protein Translation	202028_s_at	0.326	0.671	0.135	202028_s_at	0.006	0.115	-0.368	202028_s_at	0.614	0.969	-0.084
RPL39	ribosomal protein L39	Protein Translation	208695_s_at	0.284	0.638	0.147	208695_s_at	0.010	0.140	-0.348	208695_s_at	0.497	0.953	0.113
RPL5	ribosomal protein L5	Protein Translation	213080_x_at	0.353	0.691	0.128	213080_x_at	0.006	0.117	-0.366	213080_x_at	0.422	0.934	0.134
RPL7	ribosomal protein L7	Protein Translation	212042_x_at	0.249	0.604	0.158	212042_x_at	0.004	0.097	-0.387	212042_x_at	0.998	1.000	0.001
RPP40	ribonuclease P/MRP 40kDa subunit regulation of nuclear pre-mRNA	Protein Translation	213427_at	0.226	0.582	0.166	213427_at	0.001	0.065	-0.424	213427_at	0.057	0.661	-0.312
RPRD2	domain containing 2	Gene Expression	226527_at	0.005	0.109	0.376	226527_at	0.169	0.487	-0.188	226527_at	0.168	0.828	-0.228
RPS11	ribosomal protein S11	Protein Translation	213350_at	0.224	0.579	0.167	213350_at	0.009	0.137	-0.350	213350_at	0.340	0.914	-0.159
RPS15A	ribosomal protein S15a	Protein Translation	200781_s_at	0.277	0.631	0.149	200781_s_at	0.004	0.103	-0.381	200781_s_at	0.614	0.969	-0.084
RPS17	ribosomal protein S17	Protein Translation	212578_x_at	0.121	0.444	0.212	212578_x_at	<0.001	0.023	-0.504	212578_x_at	0.841	0.990	-0.034
RPS20	ribosomal protein S20	Protein Translation	200949_x_at	0.263	0.619	0.154	200949_x_at	0.001	0.065	-0.426	200949_x_at	0.699	0.976	0.065
RPS21	ribosomal protein S21	Protein Translation	200834_s_at	0.603	0.847	0.072	200834_s_at	0.006	0.117	-0.365	200834_s_at	0.754	0.982	-0.052
RPS23	ribosomal protein S23	Protein Translation	200926_at	0.050	0.306	0.266	200926_at	<0.001	0.057	-0.436	200926_at	0.874	0.992	-0.027
RPS25	ribosomal protein S25	Protein Translation	200091_s_at	0.001	0.053	0.432	200091_s_at	0.048	0.283	-0.268	200091_s_at	0.765	0.983	-0.050
RPS27	ribosomal protein S27	Protein Translation	200741_s_at	0.073	0.361	0.243	200741_s_at	0.010	0.140	-0.348	200741_s_at	0.908	0.993	-0.019
RPS27L	ribosomal protein S27-like	Protein Translation	218007_s_at	0.051	0.308	0.265	218007_s_at	<0.001	0.048	-0.451	218007_s_at	0.699	0.976	-0.065
RPS28	ribosomal protein S28	Protein Translation	208904_s_at	0.174	0.517	0.186	208904_s_at	0.002	0.080	-0.407	208904_s_at	0.510	0.954	0.110
RPS3A	ribosomal protein S3A	Protein Translation	216823_at	0.041	0.283	0.276	216823_at	0.004	0.099	-0.386	216823_at	0.089	0.740	-0.280
RPS4Y1	ribosomal protein S4, Y-linked 1	Protein Translation	201909_at	0.532	0.807	0.086	201909_at	0.005	0.107	-0.376	201909_at	0.164	0.822	-0.230
RPS6KA5	ribosomal protein S6 kinase, 90kDa, polypeptide 5	Protein Translation	204633_s_at	0.664	0.876	0.060	204633_s_at	0.007	0.121	-0.363	204633_s_at	0.247	0.875	-0.192
RRAS2	related RAS viral (r-ras) oncogene homolog 2	Signal Transduction	212590_at	<0.001	0.007	-0.544	212590_at	0.014	0.164	0.330	212590_at	0.002	0.289	0.489
RREB1	ras responsive element binding protein 1	Gene Expression	228487_s_at	0.169	0.512	0.188	228487_s_at	0.008	0.132	-0.353	228487_s_at	0.963	0.998	-0.008
RSF1	remodeling and spacing factor 1	Gene Expression	222540_s_at	0.044	0.289	-0.273	222540_s_at	0.010	0.140	0.347	222540_s_at	0.008	0.404	0.429
RSRC1	arginine/serine-rich coiled-coil 1	Gene Expression	219507_at	0.041	0.281	-0.277	219507_at	0.599	0.827	0.072	219507_at	0.003	0.329	0.473

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
RTCA	RNA 3'-terminal phosphate cyclase	Gene Expression	238087_at	0.157	0.497	0.193	238087_at	<0.001	0.052	-0.444	238087_at	0.815	0.986	0.039
RUNX1T1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	Gene Expression	205529_s_at	<0.001	0.046	0.442	205529_s_at	0.518	0.785	-0.089	205529_s_at	0.649	0.973	-0.076
RXRA	retinoid X receptor, alpha	Cardiac Muscle	202449_s_at	0.118	0.439	0.213	202449_s_at	0.007	0.122	-0.361	202449_s_at	0.016	0.468	-0.392
RYR2	ryanodine receptor 2 (cardiac)	Signal Transduction Immune/Acute Phase	207557_s_at	0.002	0.072	0.408	214044_at	0.045	0.275	-0.272	207557_s_at	0.267	0.889	-0.184
S1PR3	sphingosine-1-phosphate receptor 3	Response	228176_at	0.004	0.097	0.385	228176_at	0.050	0.290	-0.266	228176_at	0.004	0.358	-0.456
SAMM50	SAMM50 sorting and assembly machinery component	Respiratory Electron Chain Transport	201569_s_at	0.716	0.898	-0.050	201569_s_at	0.004	0.098	-0.386	201569_s_at	0.573	0.966	-0.094
SARS	seryl-tRNA synthetase	Gene Expression	231894_at	0.946	0.984	0.009	231894_at	0.010	0.140	-0.348	231894_at	0.102	0.771	-0.269
SCAF11	SR-related CTD-associated factor 11 scavenger receptor class A, member	Gene Expression	206989_s_at	0.003	0.086	-0.394	206989_s_at	0.511	0.781	0.090	206989_s_at	0.328	0.909	0.162
SCARA5	5 scavenger receptor class F, member	Signal Transduction	235849_at	0.002	0.077	0.402	235849_at	0.666	0.861	-0.059	235849_at	0.503	0.953	-0.112
SCARF1	1	Cell Adhesion	206995_x_at	0.004	0.095	0.387	206995_x_at	0.011	0.147	-0.343	206995_x_at	0.456	0.940	-0.124
SCLT1	sodium channel and clathrin linker 1	Cell Division	1569190_at	0.004	0.098	-0.384	1569190_at	0.020	0.192	0.314	1569190_at	0.110	0.778	0.263
SCO1	SCO1 cytochrome c oxidase assembly protein	Respiratory Electron Chain Transport	223221_at	0.003	0.086	-0.394	223221_at	0.005	0.110	0.373	223221_at	0.203	0.843	0.211
SDC2	syndecan 2	ECM Organization	212154_at	0.002	0.070	-0.410	212158_at	0.004	0.104	0.380	212154_at	0.646	0.973	-0.077
SDHAF1	succinate dehydrogenase complex assembly factor 1	Respiratory Electron Chain Transport	44669_at	0.009	0.148	-0.349	44669_at	0.487	0.768	0.095	44669_at	0.123	0.794	0.254
SDHC	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	Respiratory Electron Chain Transport	238191_at	0.008	0.136	0.356	238191_at	0.016	0.172	-0.326	238191_at	0.850	0.990	0.032
SDK1	sidekick cell adhesion molecule 1	Cell Adhesion	229912_at	0.003	0.080	0.400	229912_at	0.002	0.083	-0.404	229912_at	0.006	0.376	-0.444
SEC11A	SEC11 homolog A (S. cerevisiae)	Signal Transduction	201290_at	0.457	0.760	0.102	201290_at	0.005	0.107	-0.377	201290_at	0.995	1.000	0.001
SEC23IP	SEC23 interacting protein	Protein Folding	209175_at	0.015	0.185	0.325	209175_at	0.002	0.080	-0.406	209175_at	0.100	0.766	-0.271
SEC31A	SEC31 homolog A (S. cerevisiae)	Immune/Acute Phase Response	200945_s_at	<0.001	0.041	-0.449	210616_s_at	<0.001	0.028	0.490	200945_s_at	0.006	0.377	0.443

Gene			LVEF				LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
SEC61B	Sec61 beta subunit	Protein Translation	203133_at	0.011	0.161	0.340	203133_at	<0.001	0.052	-0.445	203133_at	0.097	0.758	-0.273
SEC62	SEC62 homolog (S. cerevisiae)	Protein Translation	1552789_at	0.147	0.484	0.198	1552789_at	0.002	0.077	-0.409	1552789_at	0.431	0.936	-0.131
SEH1L	SEH1-like (S. cerevisiae)	Cell Division	221931_s_at	0.167	0.510	0.189	221931_s_at	0.003	0.085	-0.401	221931_s_at	0.930	0.995	-0.015
SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	Metabolic Process	230265_at	0.916	0.975	0.014	230265_at	0.009	0.135	-0.352	230265_at	0.275	0.894	-0.181
SELM	selenoprotein M	Metabolic Process	226051_at	0.010	0.155	-0.345	226051_at	0.077	0.352	0.240	226051_at	0.573	0.966	0.094
SEMA5A	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	Apoptosis	213169_at	0.171	0.514	-0.187	229427_at	0.002	0.069	0.418	229427_at	0.104	0.775	0.268
SEPT11	septin 11	Stress Response	201307_at	<0.001	0.050	-0.435	201307_at	<0.001	0.048	0.452	201307_at	0.010	0.426	0.417
SEPT2	septin 2	Actin Cytoskeleton	200778_s_at	0.016	0.189	-0.322	200778_s_at	0.002	0.074	0.412	200778_s_at	0.897	0.993	0.022
SERINC3	serine incorporator 3	Signal Transduction	221473_x_at	0.002	0.075	-0.406	221473_x_at	0.055	0.301	0.260	221473_x_at	0.343	0.915	0.158
SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1	ECM Organization	213572_s_at	0.360	0.697	0.126	228726_at	<0.001	0.026	-0.495	213572_s_at	0.607	0.969	-0.086
SERPINE2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	ECM Organization	212190_at	<0.001	0.015	-0.513	212190_at	<0.001	0.022	0.510	212190_at	<0.001	0.213	0.534
SERPINI1	serpin peptidase inhibitor, clade I (neuroserpin), member 1	Cell Adhesion	205352_at	<0.001	0.007	-0.555	205352_at	<0.001	0.055	0.439	205352_at	0.050	0.638	0.321
SESN1	sestrin 1	Stress response	218346_s_at	0.021	0.208	0.311	218346_s_at	0.055	0.301	-0.260	218346_s_at	0.001	0.257	-0.513
SESN3	sestrin 3	Stress response	225123_at	0.026	0.229	-0.300	225123_at	0.002	0.083	0.404	225123_at	0.479	0.946	0.118
SESTD1	SEC14 and spectrin domains 1	Signal Transduction	226763_at	0.051	0.308	-0.265	226763_at	0.095	0.385	0.227	226763_at	0.006	0.377	0.442
SET	SET nuclear proto-oncogene	Cell Division	210231_x_at	0.461	0.762	0.101	213048_s_at	0.003	0.084	-0.402	210231_x_at	0.003	0.335	0.471
SETD8	SET domain containing (lysine methyltransferase) 8	Gene Expression	228443_s_at	0.011	0.163	0.339	228443_s_at	0.001	0.062	-0.430	228443_s_at	0.124	0.795	-0.254
SETDB2	SET domain, bifurcated 2	Gene Expression	238684_at	<0.001	0.048	0.438	238684_at	0.034	0.241	-0.288	238684_at	0.622	0.970	0.082
SF3B1	splicing factor 3b, subunit 1, 155kDa	Gene Expression	229303_at	<0.001	0.037	-0.456	229303_at	0.014	0.164	0.331	229303_at	0.017	0.475	0.388
SFRP4	secreted frizzled-related protein 4	Signal Transduction	204051_s_at	0.002	0.079	-0.401	204051_s_at	0.002	0.075	0.410	204051_s_at	0.370	0.922	0.149
SGK1	serum/glucocorticoid regulated kinase 1	Signal Transduction	201739_at	<0.001	0.050	-0.436	201739_at	0.063	0.321	0.252	201739_at	0.140	0.800	0.244

Gene				LVEF			LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	ρ	Identifier	p-value	pBH	ρ	Identifier	p-value	pBH	ρ
SH2B3	SH2B adaptor protein 3	Signal Transduction	203320_at	0.005	0.112	0.373	203320_at	0.807	0.925	-0.034	203320_at	0.706	0.977	-0.063
SH3GL2	SH3-domain GRB2-like 2	Signal Transduction	205751_at	0.008	0.138	-0.355	205751_at	0.043	0.271	0.274	205751_at	0.004	0.352	0.464
SH3GLB1	SH3-domain GRB2-like endophilin B1	Apoptosis	210101_x_at	<0.001	0.018	-0.505	209091_s_at	0.113	0.414	0.216	210101_x_at	0.390	0.925	0.143
SH3KBP1	SH3-domain kinase binding protein 1	Apoptosis	223082_at	<0.001	0.006	0.561	1554168_a_at	<0.001	0.016	-0.533	1554168_a_at	<0.001	0.153	-0.576
SHB	Src homology 2 domain containing adaptor protein B	Signal Transduction	204656_at	0.144	0.480	-0.200	204656_at	0.003	0.089	0.396	204656_at	0.003	0.345	0.468
SHISA8	shisa family member 8	Signal Transduction	244467_at	0.001	0.062	0.419	244467_at	<0.001	0.018	-0.524	244467_at	0.081	0.722	-0.287
SHROOM3	shroom family member 3	Cell Adhesion	228400_at	0.003	0.092	-0.388	225548_at	<0.001	0.032	0.479	225548_at	0.008	0.408	0.426
		Carbohydrate												
SIAE	sialic acid acetyltransferase	Metabolism	224391_s_at	<0.001	0.029	0.473	224391_s_at	0.232	0.561	-0.164	224391_s_at	0.007	0.402	-0.432
SIAH2	siah E3 ubiquitin protein ligase 2	Protein Folding	209339_at	0.015	0.183	-0.327	209339_at	0.009	0.135	0.352	209339_at	0.398	0.927	0.141
SIRT4	sirtuin 4	Stress response	220047_at	0.006	0.122	0.366	220047_at	0.003	0.092	-0.392	220047_at	0.013	0.457	-0.401
SIVA1	SIVA1, apoptosis-inducing factor	Apoptosis	222030_at	0.363	0.700	0.125	222030_at	0.122	0.427	-0.211	222030_at	0.005	0.358	-0.454
SKI	SKI proto-oncogene	Signal Transduction	204270_at	0.354	0.692	0.127	204270_at	0.004	0.099	-0.385	204270_at	0.814	0.986	-0.039
SKP1	S-phase kinase-associated protein 1	Cell Division	200718_s_at	0.374	0.706	0.122	200718_s_at	0.008	0.126	-0.358	200718_s_at	0.494	0.952	0.114
SLAIN2	SLAIN motif family, member 2	Cell Division	224845_s_at	0.925	0.978	0.013	224845_s_at	0.004	0.102	0.383	224845_s_at	0.490	0.950	0.115
	solute carrier family 16 (monocarboxylate transporter), member 5	Signal Transduction	206600_s_at	<0.001	0.047	-0.440	206600_s_at	0.850	0.944	0.026	206600_s_at	0.088	0.739	0.281
SLC16A5	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	Amino Acid Metabolism	213664_at	0.001	0.062	0.419	213664_at	0.415	0.722	-0.112	213664_at	0.330	0.909	-0.162
SLC1A1	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 24	Signal Transduction	204342_at	0.005	0.116	0.371	204342_at	0.113	0.414	-0.216	204342_at	0.010	0.435	-0.414
SLC25A24	solute carrier family 25 (S-adenosylmethionine carrier), member 26	Signal Transduction	225862_at	0.229	0.584	0.165	225862_at	0.002	0.071	-0.415	225862_at	0.100	0.766	-0.271
SLC25A26	solute carrier family 25 (pyrimidine nucleotide carrier), member 36	Signal Transduction	201919_at	0.002	0.075	0.406	201919_at	0.022	0.199	-0.309	201919_at	0.133	0.799	-0.248

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
SLC25A5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	Signal Transduction	200657_at	<0.001	0.038	-0.456	200657_at	0.002	0.074	0.412	200657_at	0.009	0.416	0.422
SLC26A2	solute carrier family 26 (anion exchanger), member 2	Signal Transduction	205097_at	0.016	0.187	-0.324	205097_at	0.116	0.417	0.214	205097_at	0.008	0.410	0.424
SLC2A10	solute carrier family 2 (facilitated glucose transporter), member 10	Signal Transduction	221024_s_at	0.834	0.947	-0.029	221024_s_at	0.165	0.481	-0.190	221024_s_at	0.006	0.376	-0.444
SLC31A1	solute carrier family 31 (copper transporter), member 1	Signal Transduction	203971_at	0.715	0.898	-0.050	203971_at	0.002	0.083	-0.403	203971_at	0.774	0.984	-0.048
SLC31A2	solute carrier family 31 (copper transporter), member 2	Signal Transduction	204204_at	0.051	0.309	0.264	204204_at	0.004	0.103	-0.382	204204_at	0.008	0.410	-0.424
SLC38A1	solute carrier family 38, member 1	Metabolism	218237_s_at	0.001	0.055	0.429	224579_at	0.011	0.147	-0.343	218237_s_at	0.141	0.800	-0.243
SLC44A1	solute carrier family 44 (choline transporter), member 1	Signal Transduction	228486_at	0.002	0.063	-0.416	228486_at	0.002	0.071	0.415	228486_at	0.109	0.776	0.264
SLC5A1	solute carrier family 5 (sodium/glucose cotransporter), member 1	Carbohydrate Metabolism	242773_at	0.050	0.306	0.266	242773_at	0.002	0.067	-0.420	242773_at	0.007	0.393	-0.437
SLC5A3	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	Respiratory Electron Chain Transport	213164_at	0.009	0.151	-0.347	213164_at	0.104	0.399	0.222	213164_at	0.930	0.995	-0.015
SLC6A6	solute carrier family 6 (neurotransmitter transporter), member 6	Amino Acid Metabolism	228754_at	<0.001	0.042	-0.448	228754_at	0.011	0.148	0.342	228754_at	0.027	0.552	0.359
SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	Amino Acid Metabolism	212295_s_at	0.144	0.480	-0.200	212295_s_at	0.763	0.905	0.041	212295_s_at	0.003	0.345	0.468
SLC7A6	solute carrier family 7 (amino acid transporter light chain, y+L system), member 6	Amino Acid Metabolism	203580_s_at	0.003	0.088	0.392	203578_s_at	0.003	0.093	-0.391	203578_s_at	0.282	0.897	-0.179
SLC7A6OS	solute carrier family 7, member 6 opposite strand	Gene Expression	232057_at	0.009	0.144	-0.351	232057_at	0.813	0.928	0.033	232057_at	0.213	0.853	0.206
SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	Signal Transduction	241752_at	0.045	0.294	-0.271	241752_at	<0.001	0.022	0.510	241752_at	0.079	0.719	0.289
SLIRP	SRA stem-loop interacting RNA binding protein	Gene Expression	221434_s_at	0.898	0.970	0.018	221434_s_at	0.005	0.107	-0.376	221434_s_at	0.895	0.993	0.022

Gene				LVEF				LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	p		Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
SMAD2	SMAD family member 2	Signal Transduction	203076_s_at	<0.001	0.012	-0.522		203076_s_at	0.009	0.136	0.351	203076_s_at	0.041	0.609	0.334
SMAD6	SMAD family member 6	Immune/Acute Phase Response	207069_s_at	0.008	0.142	-0.352		207069_s_at	0.116	0.417	0.215	207069_s_at	0.137	0.800	0.245
SMAD7	SMAD family member 7	Cardiac Muscle	204790_at	<0.001	0.031	-0.469		204790_at	<0.001	0.010	0.562	204790_at	0.014	0.463	0.396
SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	Gene Expression	202303_x_at	<0.001	0.047	-0.439		202303_x_at	0.120	0.423	0.212	202303_x_at	0.105	0.775	0.267
SMDT1	single-pass membrane protein with aspartate-rich tail 1	Signal Transduction	225795_at	<0.001	0.005	0.574		225794_s_at	0.002	0.070	-0.417	225795_at	0.434	0.937	-0.130
SMEK2	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	Fatty Acid Metabolism	222270_at	0.102	0.415	0.223		222270_at	0.009	0.138	-0.349	222270_at	0.304	0.902	-0.171
SMOC2	SPARC related modular calcium binding 2	ECM Organization	223235_s_at	<0.001	0.019	-0.497		223235_s_at	0.032	0.238	0.290	223235_s_at	0.055	0.657	0.314
SMU1	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	Gene Expression	222618_at	0.632	0.861	0.066		222618_at	0.009	0.137	-0.350	222618_at	0.235	0.868	-0.197
SMYD1	SET and MYND domain containing 1	Gene Expression	228406_at	0.002	0.069	0.410		228406_at	0.027	0.223	-0.298	228406_at	0.131	0.796	-0.249
SMYD2	SET and MYND domain containing 2	Gene Expression	212922_s_at	0.009	0.147	-0.349		212922_s_at	0.009	0.139	0.348	212922_s_at	0.104	0.775	0.268
SNAP47	synaptosomal-associated protein, 47kDa	Signal Transduction	225244_at	<0.001	0.043	-0.447		225244_at	0.002	0.080	0.406	225244_at	0.016	0.475	0.389
SNCA	synuclein, alpha (non A4 component of amyloid precursor)	Actin Cytoskeleton	204466_s_at	<0.001	0.001	-0.631		204466_s_at	0.003	0.092	0.392	204466_s_at	0.047	0.633	0.325
SNRNP25	small nuclear ribonucleoprotein 25kDa (U11/U12)	Gene Expression	218493_at	0.090	0.394	0.231		218493_at	0.004	0.100	-0.385	218493_at	0.013	0.457	-0.403
SNRNP35	small nuclear ribonucleoprotein 35kDa (U11/U12)	Protein Translation	205300_s_at	0.004	0.098	0.384		205300_s_at	0.024	0.206	-0.306	205300_s_at	0.386	0.924	0.144
SNRPC	small nuclear ribonucleoprotein polypeptide C	Protein Translation	201342_at	0.008	0.141	0.353		201342_at	0.562	0.809	-0.080	201342_at	0.823	0.987	0.038
SNRPE	small nuclear ribonucleoprotein polypeptide E	Protein Translation	203316_s_at	0.083	0.380	0.236		203316_s_at	0.010	0.140	-0.348	203316_s_at	0.540	0.961	-0.102
SNRPN	small nuclear ribonucleoprotein polypeptide N	Gene Expression	206042_x_at	0.073	0.359	-0.244		206042_x_at	0.132	0.441	0.206	206042_x_at	0.009	0.412	0.423
SNX15	sorting nexin 15	Signal Transduction	205482_x_at	0.095	0.403	0.228		205482_x_at	0.003	0.087	-0.398	205482_x_at	0.237	0.869	-0.196

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
SNX3	sorting nexin 3	Signal Transduction	210648_x_at	0.218	0.572	0.169	210648_x_at	<0.001	0.051	-0.446	210648_x_at	0.479	0.946	0.118
SOCS2	suppressor of cytokine signaling 2	Signal Transduction	203373_at	0.002	0.066	-0.413	203373_at	0.012	0.153	0.337	203373_at	0.004	0.352	0.465
SOD2	superoxide dismutase 2, mitochondrial	Stress Response	1566342_at	0.770	0.922	0.040	1566342_at	0.006	0.114	-0.369	1566342_at	0.602	0.968	0.087
SORT1	sortilin 1	Carbohydrate Metabolism	212807_s_at	<0.001	0.017	-0.508	212807_s_at	0.071	0.338	0.245	212807_s_at	0.002	0.279	0.497
SPCS2	signal peptidase complex subunit 2 homolog (S. cerevisiae)	Signal Transduction	201239_s_at	0.022	0.210	0.309	201240_s_at	0.005	0.108	-0.374	201239_s_at	0.410	0.931	-0.137
SPEG	SPEG complex locus	Signal Transduction	205265_s_at	<0.001	0.007	-0.557	205265_s_at	0.134	0.444	0.204	205265_s_at	0.344	0.915	0.157
SPEN	spen family transcriptional repressor	Gene Expression	201996_s_at	0.013	0.174	-0.332	201996_s_at	0.062	0.318	0.254	201996_s_at	0.006	0.377	0.442
SPG21	spastic paraplegia 21 (autosomal recessive, Mast syndrome)	Signal Transduction	215383_x_at	0.002	0.068	0.412	215383_x_at	0.024	0.210	-0.304	215383_x_at	0.563	0.965	-0.096
SPHKAP	SPHK1 interactor, AKAP domain containing	Signal Transduction	228509_at	<0.001	0.052	0.432	228509_at	0.133	0.443	-0.205	228509_at	0.008	0.410	-0.424
SPINT2	serine peptidase inhibitor, Kunitz type, 2	Signal Transduction	210715_s_at	0.004	0.099	-0.383	210715_s_at	0.059	0.310	0.257	210715_s_at	0.118	0.788	0.258
SPIRE1	spire-type actin nucleation factor 1	Actin Cytoskeleton	1554807_a_at	0.002	0.074	-0.406	1554807_a_at	0.159	0.474	0.192	1554807_a_at	0.027	0.551	0.359
SPOCK1	sparc/osteonectin, cwcv and kazal- like domains proteoglycan (testican) 1	ECM Organization	202363_at	0.003	0.082	-0.397	202363_at	0.002	0.083	0.403	202363_at	0.411	0.931	0.137
SPON1	spondin 1, extracellular matrix protein	Cell Adhesion	213993_at	0.004	0.106	-0.378	213993_at	0.008	0.128	0.357	213993_at	0.272	0.892	0.182
SPP1	secreted phosphoprotein 1	Signal Transduction	209875_s_at	0.001	0.056	-0.427	209875_s_at	0.238	0.568	0.161	209875_s_at	0.260	0.883	0.187
SPTBN1	spectrin, beta, non-erythrocytic 1	Actin Cytoskeleton	200671_s_at	0.004	0.098	-0.383	200671_s_at	0.012	0.154	0.337	215918_s_at	0.006	0.377	0.442
SPTLC3	serine palmitoyltransferase, long chain base subunit 3	Fatty Acid Metabolism	227752_at	0.013	0.171	0.334	227752_at	0.001	0.062	-0.430	227752_at	0.124	0.795	-0.254
SRI	sorcin	Cardiac Muscle	208921_s_at	0.251	0.608	0.157	208921_s_at	0.002	0.069	-0.418	208921_s_at	0.720	0.979	-0.060
SRPK1	SRSF protein kinase 1	Signal Transduction	202200_s_at	0.117	0.438	0.214	202200_s_at	<0.001	0.029	-0.488	202200_s_at	0.612	0.969	-0.085
SRSF3	serine/arginine-rich splicing factor 3	Gene Expression	232392_at	0.007	0.131	0.359	232392_at	<0.001	0.046	-0.455	232392_at	0.385	0.924	-0.145

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
SSBP2	single-stranded DNA binding protein 2	Gene Expression	203787_at	<0.001	0.041	-0.451	210829_s_at	<0.001	0.014	0.540	210829_s_at	0.169	0.829	0.228
SSPN	sarcospan	Cell Adhesion	204964_s_at	0.002	0.072	-0.408	204964_s_at	0.002	0.075	0.410	204964_s_at	0.010	0.435	0.414
SSR3	signal sequence receptor, gamma (translocon-associated protein gamma)	Signal Transduction	237817_at	0.124	0.448	0.210	237817_at	<0.001	0.040	-0.467	237817_at	0.943	0.996	0.012
SSRP1	structure specific recognition protein 1	Gene Expression	200956_s_at	0.019	0.197	-0.316	200956_s_at	0.459	0.753	0.102	200956_s_at	0.004	0.358	0.460
SSTR5-AS1	SSTR5 antisense RNA 1	Carbohydrate Metabolism	1557146_a_at	0.031	0.247	0.292	1557146_a_at	0.005	0.107	-0.376	1557146_a_at	0.010	0.433	-0.415
SSU72	SSU72 RNA polymerase II CTD phosphatase homolog (S. cerevisiae)	Gene Expression	223051_at	0.081	0.375	0.238	223051_at	0.001	0.065	-0.424	227244_s_at	0.438	0.937	-0.129
ST3GAL4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	Metabolic Process	203759_at	<0.001	0.034	-0.463	203759_at	0.083	0.365	0.236	203759_at	0.092	0.747	0.278
ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	Fatty Acid Metabolism	203217_s_at	0.006	0.126	0.363	203217_s_at	0.003	0.090	-0.395	203217_s_at	0.495	0.953	-0.114
ST3GAL6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	Metabolic Process	210942_s_at	<0.001	0.011	-0.526	210942_s_at	0.022	0.198	0.310	213355_at	0.344	0.915	0.157
ST5	suppression of tumorigenicity 5	Signal Transduction	202440_s_at	0.743	0.909	0.045	202440_s_at	0.346	0.670	-0.129	202440_s_at	0.009	0.416	-0.421
ST6GALNAC4	ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-acetylglactosaminide alpha-2,6-sialyltransferase 4	Fatty Acid Metabolism	221551_x_at	0.098	0.408	-0.225	221551_x_at	0.008	0.132	0.354	221551_x_at	0.138	0.800	0.245
STAG2	stromal antigen 2	Cell Division	209022_at	0.093	0.400	-0.229	209022_at	<0.001	0.057	0.436	209022_at	0.250	0.875	0.191
STC1	stanniocalcin 1	Cardiac Muscle	204595_s_at	0.013	0.170	-0.335	204595_s_at	0.005	0.106	0.379	204595_s_at	0.021	0.512	0.374
STK17A	serine/threonine kinase 17a	Apoptosis	202695_s_at	0.004	0.102	-0.381	202695_s_at	0.003	0.092	0.392	202695_s_at	0.033	0.571	0.349
STK25	serine/threonine kinase 25	Signal Transduction	201314_at	0.008	0.142	-0.352	201314_at	0.775	0.912	0.039	201314_at	0.575	0.967	0.094
STK38	serine/threonine kinase 38	Signal Transduction	202951_at	0.120	0.443	-0.212	202951_at	0.176	0.494	0.185	202951_at	0.009	0.416	0.420
STK38L	serine/threonine kinase 38 like	Signal Transduction	212572_at	0.004	0.101	-0.382	212572_at	0.013	0.159	0.334	212565_at	0.029	0.561	0.356
STRADB	STE20-related kinase adaptor beta serine/threonine kinase receptor associated protein	Apoptosis	223266_at	0.015	0.182	0.328	223266_at	<0.001	0.054	-0.441	223266_at	0.087	0.739	-0.282
STRAP	striatin interacting protein 2	Gene Expression	200870_at	0.740	0.908	0.046	200870_at	0.004	0.098	-0.386	200870_at	0.786	0.984	0.045
STRIP2	striatin interacting protein 2	Actin Cytoskeleton	231880_at	<0.001	0.021	0.494	231880_at	0.089	0.375	-0.231	231880_at	0.023	0.522	-0.370

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
STX17	syntaxin 17	Signal Transduction	226662_at	<0.001	0.027	0.479	226662_at	0.005	0.107	-0.377	226662_at	0.264	0.887	-0.185
STXBP6	syntaxin binding protein 6 (amisyn)	Cell Adhesion	230560_at	<0.001	0.020	0.496	230560_at	<0.001	0.054	-0.440	230560_at	<0.001	0.155	-0.571
SUGCT	succinyl-CoA:glutarate-CoA transferase	Metabolic Process	219655_at	0.024	0.220	0.304	219655_at	<0.001	0.055	-0.439	219655_at	0.061	0.673	-0.308
SULT1C2	sulfotransferase family, cytosolic, 1C, member 2	Metabolic Process	211470_s_at	0.137	0.469	0.203	211470_s_at	0.005	0.108	-0.375	211470_s_at	0.212	0.853	-0.207
SUV39H2	homolog 2 (Drosophila)	Gene Expression	1554572_a_at	0.002	0.077	-0.402	1554572_a_at	0.012	0.151	0.339	1554572_a_at	0.014	0.463	0.398
SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	Gene Expression	209024_s_at	0.021	0.209	-0.310	209025_s_at	0.058	0.308	0.257	209024_s_at	0.001	0.257	0.513
SYNPO	synaptopodin	Actin Cytoskeleton	202796_at	<0.001	0.036	-0.460	202796_at	0.085	0.369	0.234	202796_at	0.224	0.859	0.202
SYNPO2L	synaptopodin 2-like	Actin Cytoskeleton	219804_at	0.172	0.514	-0.187	219804_at	0.423	0.728	0.110	219804_at	0.004	0.358	0.459
TAB2	TGF-beta activated kinase 1/MAP3K7 binding protein 2	Signal Transduction	212184_s_at	<0.001	0.044	0.445	212184_s_at	0.017	0.179	-0.322	212184_s_at	0.029	0.561	-0.355
TADA2B	transcriptional adaptor 2B	Gene Expression	226240_at	0.237	0.591	0.162	226240_at	0.001	0.065	-0.425	226240_at	0.479	0.946	-0.118
TBC1D5	TBC1 domain family, member 5	Signal Transduction	201814_at	0.002	0.075	0.405	201814_at	0.006	0.115	-0.367	201814_at	0.078	0.716	-0.290
TBCE	tubulin folding cofactor E	Protein Folding	203714_s_at	0.007	0.132	0.359	203714_s_at	<0.001	0.018	-0.522	203714_s_at	0.090	0.745	-0.279
TBL1XR1	transducin (beta)-like 1 X-linked receptor 1	Signal Transduction	223013_at	0.015	0.185	-0.326	223013_at	0.002	0.071	0.416	222633_at	0.006	0.389	0.439
TBX5	T-box 5	Cardiac Muscle	240715_at	0.451	0.756	0.104	240715_at	0.002	0.070	-0.417	240715_at	0.648	0.973	-0.076
TCEB1	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	Gene Expression	202824_s_at	0.033	0.255	0.288	202824_s_at	<0.001	0.039	-0.469	202824_s_at	0.477	0.946	-0.119
TCF24	transcription factor 24	Gene Expression	242522_at	0.074	0.362	0.243	242522_at	0.001	0.058	-0.434	242522_at	0.098	0.763	-0.272
TCF3	transcription factor 3	Gene Expression	202648_at	0.028	0.236	0.297	202648_at	0.010	0.140	-0.348	202648_at	0.945	0.996	0.012
TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	Gene Expression	216035_x_at	0.003	0.088	0.392	216035_x_at	0.809	0.926	-0.033	216035_x_at	0.924	0.995	-0.016
TESC	tescalcin	Signal Transduction	218872_at	0.004	0.098	0.384	218872_at	0.396	0.709	-0.117	218872_at	0.179	0.833	-0.222
TET2	tet methylcytosine dioxygenase 2	Cell Division	235461_at	0.157	0.496	-0.194	235461_at	<0.001	0.043	0.462	235461_at	0.041	0.610	0.334
TFDP2	transcription factor Dp-2 (E2F dimerization partner 2)	Gene Expression	203588_s_at	0.594	0.842	0.073	203588_s_at	<0.001	0.027	-0.491	203588_s_at	0.208	0.848	-0.208
TGFB111	transforming growth factor beta 1 induced transcript 1	Signal Transduction	209651_at	0.048	0.301	-0.268	209651_at	0.002	0.074	0.412	209651_at	0.062	0.677	0.306

Gene			LVEF				LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
TGM2	transglutaminase 2	ECM Organization	201042_at	<0.001	0.052	-0.432	201042_at	<0.001	0.050	0.448	201042_at	0.576	0.967	0.093
THBS1	thrombospondin 1	Cell Division	201110_s_at	0.007	0.134	-0.358	201110_s_at	0.010	0.144	0.345	201110_s_at	0.891	0.993	0.023
THBS2	thrombospondin 2	Cell Adhesion	203083_at	<0.001	0.007	-0.554	203083_at	0.145	0.457	0.199	203083_at	0.280	0.896	0.179
THBS4	thrombospondin 4	Cell Division	204776_at	0.033	0.255	-0.288	204776_at	0.007	0.121	0.363	204776_at	0.241	0.871	0.195
THRB	thyroid hormone receptor, beta	Signal Transduction	228716_at	0.067	0.348	-0.249	228716_at	0.004	0.098	0.387	228716_at	0.729	0.981	0.058
TIA1	TIA1 cytotoxic granule-associated RNA binding protein	Apoptosis	201446_s_at	0.003	0.093	-0.388	201446_s_at	0.512	0.781	0.090	201446_s_at	0.468	0.946	0.121
TIMP1	TIMP metalloproteinase inhibitor 1	ECM Organization Carbohydrate	201666_at	0.009	0.149	-0.348	201666_at	0.025	0.214	0.302	201666_at	0.320	0.908	0.165
TKTL1	transketolase-like 1	Metabolism	214183_s_at	<0.001	0.025	0.483	214183_s_at	0.085	0.369	-0.234	214183_s_at	0.004	0.356	-0.464
TLN1	talin 1	Actin Cytoskeleton	236132_at	0.004	0.103	0.380	236132_at	0.014	0.164	-0.331	236132_at	0.097	0.761	-0.273
TLR3	toll-like receptor 3	Signal Transduction	206271_at	0.004	0.100	0.382	206271_at	0.011	0.147	-0.343	206271_at	0.007	0.402	-0.433
TLR8	toll-like receptor 8	Immune/Acute Phase Response	229560_at	0.610	0.851	0.070	229560_at	0.004	0.097	-0.388	229560_at	0.841	0.990	-0.034
TMBIM4	transmembrane BAX inhibitor motif containing 4	Apoptosis	222845_x_at	0.894	0.969	0.018	222845_x_at	0.006	0.115	-0.367	222845_x_at	0.941	0.996	-0.012
TMBIM6	transmembrane BAX inhibitor motif containing 6	Apoptosis	200803_s_at	0.152	0.491	0.196	200803_s_at	0.009	0.136	-0.351	200803_s_at	0.194	0.838	-0.215
TMCO3	transmembrane and coiled-coil domains 3	Signal Transduction	226050_at	<0.001	0.030	-0.472	226050_at	0.029	0.228	0.295	226050_at	0.144	0.800	0.241
TMED4	transport domain containing 4	Signal Transduction	224676_at	0.005	0.116	-0.370	224676_at	0.009	0.136	0.351	224676_at	0.295	0.901	0.174
TMEFF2	transmembrane protein with EGF-like and two follistatin-like domains 2	Stress Response	223557_s_at	0.001	0.057	0.426	223557_s_at	0.047	0.281	-0.269	223557_s_at	0.438	0.937	-0.129
TMEM231	transmembrane protein 231	Signal Transduction	219182_at	<0.001	0.006	-0.568	219182_at	0.133	0.442	0.205	219182_at	0.532	0.959	0.104
TMEM237	transmembrane protein 237	Signal Transduction	1553956_at	<0.001	0.018	-0.506	1553956_at	0.384	0.700	0.119	1553956_at	0.855	0.991	0.031
TMEM47	transmembrane protein 47	Cell Adhesion	209655_s_at	<0.001	0.008	-0.542	209655_s_at	0.006	0.115	0.367	209655_s_at	0.168	0.828	0.228
TMEM67	transmembrane protein 67	Cell Division	1552765_x_at	0.002	0.075	0.405	1552763_at	0.020	0.192	-0.313	238229_at	0.308	0.904	-0.169
TMEM68	transmembrane protein 68	Metabolic Process	227936_at	0.223	0.577	0.167	227936_at	0.166	0.483	-0.189	227936_at	0.007	0.393	-0.436
TMF1	TATA element modulatory factor 1	Apoptosis	227685_at	0.195	0.545	-0.178	227685_at	0.009	0.135	0.352	227685_at	0.631	0.971	-0.080
TMOD1	tropomodulin 1	Cardiac Muscle	203661_s_at	0.018	0.193	0.319	203661_s_at	0.002	0.075	-0.412	203661_s_at	0.126	0.796	-0.253

Gene			LVEF				LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
TNFAIP8	tumor necrosis factor, alpha-induced protein 8	Apoptosis	210260_s_at	0.029	0.241	0.295	210260_s_at	<0.001	0.011	-0.554	210260_s_at	0.002	0.286	-0.491
TNFRSF11B	tumor necrosis factor receptor superfamily, member 11b	Signal Transduction	204932_at	0.034	0.257	-0.287	204932_at	<0.001	0.048	0.450	204932_at	0.002	0.290	0.486
TNFRSF12A	tumor necrosis factor receptor superfamily, member 12A	Apoptosis	218368_s_at	0.003	0.090	-0.390	218368_s_at	0.001	0.066	0.422	218368_s_at	0.006	0.376	0.444
TNFRSF18	tumor necrosis factor receptor superfamily, member 18	Signal Transduction	224553_s_at	0.013	0.172	0.333	224553_s_at	0.001	0.062	-0.430	224553_s_at		0.440	0.938 -0.129
TNIK	TRAF2 and NCK interacting kinase	Actin Cytoskeleton	213109_at	0.567	0.828	-0.079	213109_at	0.004	0.103	0.382	213109_at	0.189	0.836	0.217
TNNT2	troponin T type 2 (cardiac)	Cardiac Muscle	215389_s_at	0.003	0.081	0.399	215389_s_at	0.014	0.162	-0.332	215389_s_at	0.970	0.998	-0.006
TNPO1	transportin 1	Protein Translation	209226_s_at	<0.001	0.005	-0.576	209226_s_at	0.006	0.113	0.370	207657_x_at	0.027	0.548	0.360
TNRC6A	trinucleotide repeat containing 6A	Gene Expression	224705_s_at	0.001	0.062	0.421	224704_at	0.022	0.200	-0.309	224705_s_at	0.194	0.838	0.215
TOB2	transducer of ERBB2, 2	Signal Transduction	222243_s_at	0.064	0.342	0.251	222243_s_at	0.002	0.071	-0.415	222243_s_at	0.072	0.700	-0.295
TOMM40	translocase of outer mitochondrial membrane 40 homolog (yeast)	Signal Transduction	202264_s_at	0.644	0.867	-0.064	202264_s_at	0.003	0.084	0.402	202264_s_at	0.496	0.953	0.113
TOMM7	translocase of outer mitochondrial membrane 7 homolog (yeast)	Signal Transduction	201812_s_at	0.016	0.188	0.323	201812_s_at	<0.001	0.035	-0.475	201812_s_at	0.151	0.808	-0.237
TP53BP1	tumor protein p53 binding protein 1	Stress Response	203050_at	0.009	0.150	0.347	203050_at	<0.001	0.017	-0.528	203050_at	0.181	0.833	-0.222
TP53I3	tumor protein p53 inducible protein 3	Respiratory Electron Chain Transport	210609_s_at	0.008	0.140	0.354	210609_s_at	0.017	0.181	-0.320	210609_s_at	0.305	0.902	-0.171
TPM1	tropomyosin 1 (alpha)	Cardiac Muscle	210986_s_at	0.009	0.149	-0.348	210986_s_at	0.462	0.755	0.101	210986_s_at	0.174	0.832	0.225
TPM3	tropomyosin 3	Actin Cytoskeleton	214365_at	0.028	0.237	-0.296	214365_at	0.159	0.475	0.192	214365_at	0.004	0.358	0.455
TPPP	tubulin polymerization promoting protein	Cell Division	230104_s_at	0.229	0.584	0.165	230104_s_at	0.003	0.089	-0.396	230104_s_at	0.141	0.800	-0.243
TPRKB	TP53RK binding protein	Amino Acid Metabolism	219030_at	<0.001	0.039	0.455	219030_at	0.003	0.083	-0.402	219030_at	0.004	0.358	-0.458
TPST2	tyrosylprotein sulfotransferase 2	Metabolic Process	204079_at	0.992	0.997	-0.001	204079_at	<0.001	0.026	-0.494	204079_at	0.827	0.988	-0.037
TRDN	triadin	Cardiac Muscle	222287_at	0.031	0.248	-0.291	222287_at	0.006	0.113	0.370	222287_at	0.290	0.900	0.176
TRIB1	tribbles pseudokinase 1	Signal Transduction	202241_at	<0.001	0.019	-0.499	202241_at	0.007	0.122	0.361	202241_at	<0.001	0.136	0.584

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	ρ	Identifier	p-value	pBH	ρ	Identifier	p-value	pBH	ρ
TRIB2	tribbles pseudokinase 2	Signal Transduction	202479_s_at	0.008	0.138	-0.355	202479_s_at	<0.001	0.028	0.489	202479_s_at	0.115	0.786	0.260
TRIM41	tripartite motif containing 41	Protein Folding	226445_s_at	0.012	0.170	-0.335	226445_s_at	0.086	0.370	0.234	226445_s_at	0.005	0.371	0.447
TRIM55	tripartite motif containing 55	Signal Transduction	236175_at	0.005	0.113	-0.372	236175_at	0.294	0.623	0.144	236175_at	0.674	0.974	0.070
	tripartite motif containing 63, E3													
TRIM63	ubiquitin protein ligase	Protein Folding	236972_at	0.030	0.244	0.294	236972_at	<0.001	0.048	-0.451	236972_at	0.306	0.903	-0.170
TRIM7	tripartite motif containing 7	Protein Folding	239694_at	0.009	0.147	0.350	239694_at	0.002	0.072	-0.414	239694_at	0.189	0.836	-0.217
TRIM8	tripartite motif containing 8	Protein Folding	221012_s_at	0.015	0.182	0.328	221012_s_at	0.001	0.065	-0.424	221012_s_at	0.299	0.901	-0.173
	thyroid hormone receptor interactor 6													
TRIP6		Cell Adhesion	209129_at	0.003	0.092	-0.388	209129_at	0.090	0.376	0.231	209129_at	0.943	0.996	0.012
	tRNA methyltransferase 11 homolog (S. cerevisiae)	Amino Acid												
TRMT11		Metabolism	218877_s_at	0.008	0.139	-0.354	218877_s_at	1.000	1.000	0.000	218877_s_at	0.844	0.990	0.033
	tRNA methyltransferase 1 homolog (S. cerevisiae)-like	Amino Acid												
TRMT1L		Metabolism	223404_s_at	0.138	0.470	0.203	223404_s_at	0.002	0.069	-0.418	223404_s_at	0.570	0.965	-0.095
TSC22D1	TSC22 domain family, member 1	Gene Expression	215111_s_at	<0.001	0.040	0.452	215111_s_at	<0.001	0.026	-0.493	215111_s_at	0.011	0.441	-0.412
TSC22D3	TSC22 domain family, member 3	Stress Response	208763_s_at	0.004	0.102	-0.381	208763_s_at	0.057	0.305	0.259	208763_s_at	0.326	0.909	0.163
	TSEN15 tRNA splicing endonuclease subunit													
TSEN15		Gene Expression	230257_s_at	0.348	0.687	0.129	230257_s_at	0.005	0.105	-0.379	230257_s_at	0.371	0.922	-0.149
	TSEN2 tRNA splicing endonuclease subunit													
TSEN2		Gene Expression	244391_at	0.020	0.203	0.313	244391_at	<0.001	0.045	-0.459	244391_at	0.178	0.833	-0.223
	TSEN34 tRNA splicing endonuclease subunit													
TSEN34		Gene Expression	218132_s_at	0.005	0.113	-0.373	218132_s_at	0.034	0.242	0.287	218132_s_at	0.966	0.998	0.007
TSPAN17	tetraspanin 17	Signal Transduction	225235_at	0.002	0.075	-0.406	225235_at	0.636	0.846	0.065	225235_at	0.867	0.991	0.028
		Immune/Acute Phase Response												
TSPAN2	tetraspanin 2		214606_at	0.071	0.355	0.245	214606_at	0.014	0.163	-0.331	227233_at	<0.001	0.153	-0.573
TSPAN5	tetraspanin 5	Signal Transduction	209890_at	0.013	0.175	-0.332	209890_at	0.068	0.332	0.248	209890_at	0.001	0.257	0.512
TSPAN7	tetraspanin 7	Signal Transduction	202242_at	0.016	0.187	0.323	202242_at	0.472	0.760	-0.099	202242_at	0.005	0.359	-0.453
	thiosulfate sulfurtransferase (rhodanese)													
TST		Metabolic Process	209605_at	0.009	0.151	0.347	209605_at	<0.001	0.030	-0.485	209605_at	0.046	0.627	-0.327
TTC1	tetratricopeptide repeat domain 1	Protein Folding	201434_at	<0.001	0.033	0.465	201434_at	<0.001	0.002	-0.653	201434_at	0.017	0.480	-0.387
TTC17	tetratricopeptide repeat domain 17	Actin Cytoskeleton	218972_at	0.224	0.579	0.167	218972_at	0.753	0.900	-0.043	218972_at	0.007	0.402	-0.433
TTC3	tetratricopeptide repeat domain 3	Protein Folding	208073_x_at	0.204	0.557	-0.174	208073_x_at	0.003	0.087	0.399	208073_x_at	0.153	0.812	0.236

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
TTC5	tetratricopeptide repeat domain 5	Gene Expression	226557_at	0.009	0.147	-0.350	226557_at	0.034	0.242	0.287	226557_at	0.490	0.950	0.115
TTI2	TELO2 interacting protein 2	Cell Division	219124_at	0.104	0.419	0.222	219124_at	0.006	0.115	-0.367	219124_at	0.124	0.795	-0.254
TUBA1C	tubulin, alpha 1c	Cell Division	211750_x_at	<0.001	0.041	-0.451	211750_x_at	0.028	0.225	0.297	211750_x_at	0.750	0.982	0.053
TUBA4A	tubulin, alpha 4a	Cell Division	212242_at	0.009	0.149	-0.348	212242_at	0.300	0.628	0.142	212242_at	0.626	0.971	0.081
TXLNA	taxilin alpha	Immune/Acute Phase Response	231169_at	0.213	0.565	0.171	231169_at	0.001	0.066	-0.422	231169_at	0.182	0.833	-0.221
TXNDC12	thioredoxin domain containing 12 (endoplasmic reticulum)	Apoptosis	223017_at	0.002	0.072	-0.408	225642_at	0.007	0.007	0.578	223017_at	0.329	0.909	-0.162
TYMS	thymidylate synthetase	Cell Division	202589_at	<0.001	0.040	-0.453	202589_at	0.348	0.672	0.129	202589_at	0.137	0.800	0.246
TYW1	tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)	Amino Acid Metabolism	218347_at	<0.001	0.046	-0.442	218347_at	0.319	0.646	0.137	218347_at	0.787	0.984	-0.045
TYW3	tRNA-yW synthesizing protein 3 homolog (S. cerevisiae)	Amino Acid Metabolism	227141_at	0.002	0.065	-0.414	227141_at	0.028	0.225	0.297	227141_at	0.292	0.900	0.175
UACA	uveal autoantigen with coiled-coil domains and ankyrin repeats	Apoptosis	223279_s_at	0.026	0.228	-0.301	223279_s_at	0.007	0.123	0.360	223279_s_at	0.006	0.389	0.438
UAP1	UDP-N-acetylglucosamine pyrophosphorylase 1	Carbohydrate Metabolism	209340_at	0.005	0.114	0.371	209340_at	<0.001	0.003	-0.611	209340_at	0.002	0.277	-0.502
UBA5	ubiquitin-like modifier activating enzyme 5	Protein Folding	222579_at	0.004	0.099	0.383	222579_at	0.785	0.916	-0.038	222579_at	0.364	0.919	-0.151
UBAC2	UBA domain containing 2	Protein Folding	224298_s_at	<0.001	0.041	-0.451	224298_s_at	0.139	0.449	0.202	224298_s_at	0.003	0.342	0.469
UBAP1	ubiquitin associated protein 1	Protein Folding	46270_at	0.002	0.079	0.401	46270_at	0.015	0.170	-0.327	46270_at	0.150	0.808	-0.238
UBAP2	ubiquitin associated protein 2	Protein Folding	219192_at	<0.001	0.013	0.519	219192_at	0.014	0.164	-0.330	221839_s_at	0.815	0.986	-0.039
UBC	ubiquitin C	Protein Folding	211296_x_at	0.845	0.951	0.027	211296_x_at	0.010	0.140	-0.348	211296_x_at	0.443	0.938	0.128
UBE2B	ubiquitin-conjugating enzyme E2B	Protein Folding	228588_s_at	0.068	0.348	0.248	228588_s_at	0.006	0.115	-0.367	228588_s_at	0.451	0.940	-0.126
UBE2D2	ubiquitin-conjugating enzyme E2D 2	Protein Folding	201345_s_at	<0.001	0.030	0.472	201345_s_at	0.037	0.250	-0.283	201345_s_at	0.232	0.864	-0.198
UBE2D3	ubiquitin-conjugating enzyme E2D 3	Protein Folding	200668_s_at	0.792	0.932	-0.036	200668_s_at	0.004	0.097	-0.388	200668_s_at	0.379	0.923	-0.147
UBE2F	ubiquitin-conjugating enzyme E2F (putative)	Protein Folding	225783_at	0.049	0.304	0.266	225783_at	0.003	0.090	-0.394	225783_at	0.157	0.817	-0.234
UBE2H	ubiquitin-conjugating enzyme E2H	Protein Folding	221962_s_at	<0.001	0.047	-0.441	221962_s_at	<0.001	0.020	0.517	222421_at	0.003	0.336	0.470
UBE2J1	ubiquitin-conjugating enzyme E2, J1	Protein Folding	222435_s_at	0.002	0.077	-0.404	222435_s_at	0.643	0.850	0.064	222435_s_at	0.938	0.995	0.013
UBE2J2	ubiquitin-conjugating enzyme E2, J2	Protein Folding	225209_s_at	0.007	0.134	-0.357	225209_s_at	0.945	0.981	0.009	225209_s_at	0.717	0.979	0.061

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
UBE2K	ubiquitin-conjugating enzyme E2K	Protein Folding	202347_s_at	0.940	0.982	0.010	202347_s_at	0.001	0.065	-0.427	202347_s_at	0.824	0.988	-0.037
UBE2L3	ubiquitin-conjugating enzyme E2L 3	Protein Folding	200682_s_at	0.005	0.113	0.372	200682_s_at	0.942	0.980	-0.010	200682_s_at	0.373	0.922	0.148
UBE2Q2	ubiquitin-conjugating enzyme E2Q family member 2	Protein Folding	224747_at	0.006	0.121	-0.366	224747_at	0.625	0.842	0.067	224747_at	0.422	0.934	0.134
UBE2QL1	ubiquitin-conjugating enzyme E2Q family-like 1	Protein Folding	226612_at	0.106	0.422	0.220	226612_at	0.007	0.123	-0.360	226612_at	0.146	0.805	-0.240
UBE2S	ubiquitin-conjugating enzyme E2S	Protein Folding	202779_s_at	0.005	0.112	-0.373	202779_s_at	0.049	0.286	0.267	202779_s_at	0.191	0.838	0.216
UBE2W	ubiquitin-conjugating enzyme E2W (putative)	Protein Folding	218521_s_at	0.003	0.083	-0.396	218521_s_at	0.004	0.104	0.380	218521_s_at	0.073	0.704	0.294
UBE2Z	ubiquitin-conjugating enzyme E2Z	Protein Folding	217750_s_at	0.107	0.423	-0.220	217750_s_at	<0.001	0.054	0.441	217750_s_at	0.102	0.770	0.270
UBE4B	ubiquitination factor E4B	Protein Folding	202317_s_at	0.003	0.087	0.393	202317_s_at	0.066	0.329	-0.249	202317_s_at	0.737	0.982	-0.056
UBL3	ubiquitin-like 3	Protein Folding	201535_at	0.006	0.118	0.369	201535_at	0.353	0.676	-0.127	201535_at	0.116	0.787	-0.259
UBL5	ubiquitin-like 5	Protein Folding	218011_at	0.534	0.809	0.086	218011_at	0.008	0.131	-0.354	218011_at	0.721	0.979	0.060
UBR2	ubiquitin protein ligase E3 component n-recognin 2	Protein Folding	212760_at	0.003	0.081	0.398	212760_at	0.037	0.250	-0.283	212760_at	0.238	0.869	-0.196
UBXN2B	UBX domain protein 2B	Protein Folding	238903_at	0.002	0.079	-0.401	238903_at	0.588	0.822	0.075	238903_at	0.076	0.712	0.292
UBXN4	UBX domain protein 4	Protein Folding	212007_at	0.002	0.063	-0.416	212007_at	0.458	0.753	0.102	212007_at	0.003	0.329	0.473
UCHL5	ubiquitin carboxyl-terminal hydrolase L5	Protein Folding	219960_s_at	0.007	0.127	0.362	219960_s_at	<0.001	0.055	-0.438	219960_s_at	0.002	0.286	-0.492
UGCG	UDP-glucose ceramide glucosyltransferase	Fatty Acid Metabolism	204881_s_at	0.005	0.116	-0.370	204881_s_at	0.422	0.727	0.110	204881_s_at	0.301	0.901	0.172
UGGT2	UDP-glucose glycoprotein glucosyltransferase 2	Protein Folding	235749_at	<0.001	0.033	-0.466	235749_at	0.013	0.159	0.334	235749_at	0.114	0.784	0.260
UHRF1BP1	UHRF1 binding protein 1	Protein Folding	226135_at	0.003	0.082	0.397	226135_at	0.005	0.110	-0.373	226135_at	0.082	0.725	-0.286
UNC5B	unc-5 homolog B (C. elegans)	Signal Transduction	41856_at	0.128	0.456	-0.208	41856_at	0.003	0.083	0.402	41856_at	0.127	0.796	0.252
UNKL	unkempt family zinc finger-like	Protein Folding	229908_s_at	0.002	0.076	0.405	229908_s_at	0.004	0.103	-0.382	229908_s_at	0.033	0.572	-0.348
UQCR11	ubiquinol-cytochrome c reductase, complex III subunit XI	Respiratory Electron Chain Transport	202090_s_at	0.147	0.483	0.198	202090_s_at	0.003	0.087	-0.397	202090_s_at	0.993	1.000	-0.002
UQCRB	ubiquinol-cytochrome c reductase binding protein	Respiratory Electron Chain Transport	205849_s_at	0.003	0.086	0.394	205849_s_at	0.004	0.103	-0.381	244293_at	0.057	0.660	-0.312

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
USP14	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	Protein Folding	201672_s_at	0.020	0.205	0.312	201672_s_at	0.009	0.138	-0.350	201672_s_at	0.306	0.903	-0.170
USP15	ubiquitin specific peptidase 15	Protein Folding	210681_s_at	0.004	0.095	-0.386	210681_s_at	0.012	0.154	0.337	210681_s_at	0.708	0.977	0.063
USP28	ubiquitin specific peptidase 28	Protein Folding	230623_x_at	<0.001	0.051	0.434	230623_x_at	0.017	0.179	-0.321	230623_x_at	0.537	0.960	-0.103
USP30	ubiquitin specific peptidase 30	Protein Folding	223602_at	0.057	0.323	0.258	223602_at	0.004	0.102	-0.383	223602_at	0.831	0.988	0.036
USP46-AS1	USP46 antisense RNA 1	Protein Folding	235667_at	<0.001	0.049	-0.436	235667_at	0.282	0.611	0.147	235667_at	0.027	0.548	0.361
USP47	ubiquitin specific peptidase 47	Protein Folding	223119_s_at	0.007	0.133	0.358	223701_s_at	0.153	0.468	0.195	223701_s_at	0.009	0.425	0.418
USP48	ubiquitin specific peptidase 48	Protein Folding	220079_s_at	0.255	0.611	0.156	220079_s_at	0.004	0.103	-0.382	220079_s_at	0.914	0.994	0.018
USP53	ubiquitin specific peptidase 53	Protein Folding	237465_at	0.007	0.126	-0.363	237465_at	0.551	0.803	0.082	237465_at	0.180	0.833	0.222
UTP11L	UTP11-like, U3 small nucleolar ribonucleoprotein (yeast)	Apoptosis	218235_s_at	0.002	0.064	0.415	218235_s_at	0.502	0.776	-0.092	218235_s_at	0.286	0.899	-0.177
VANGL2	VANGL planar cell polarity protein 2	Actin Cytoskeleton	226029_at	0.003	0.089	0.391	226029_at	0.020	0.190	-0.314	226029_at	0.623	0.970	0.082
VAR52	valyl-tRNA synthetase 2, mitochondrial	Amino Acid Metabolism	226200_at	0.003	0.094	0.387	226200_at	0.025	0.211	-0.304	226200_at	0.508	0.954	0.110
VCAN	versican	Cell Adhesion	221731_x_at	<0.001	0.017	-0.508	204619_s_at	0.033	0.240	0.288	221731_x_at	0.038	0.594	0.339
VEGFA	vascular endothelial growth factor A	ECM Organization	212171_x_at	0.031	0.246	-0.292	212171_x_at	0.002	0.068	0.419	212171_x_at	0.115	0.786	0.260
VGLL4	vestigial-like family member 4	Gene Expression	214004_s_at	0.008	0.139	-0.354	214004_s_at	0.092	0.379	0.230	214004_s_at	0.005	0.363	0.449
VIT	vitrin	ECM Organization	227899_at	0.006	0.120	0.367	227899_at	0.418	0.724	-0.111	227899_at	0.027	0.548	-0.360
VLDLR-AS1	VLDLR antisense RNA 1	Signal Transduction	1558212_at	0.032	0.253	-0.289	1558212_at	0.002	0.068	0.419	1558212_at	0.137	0.800	0.245
VOPP1	vesicular, overexpressed in cancer, prosurvival protein 1	Gene Expression	208091_s_at	0.004	0.106	-0.378	208091_s_at	0.002	0.075	0.410	208091_s_at	0.387	0.924	0.144
VPS35	vacuolar protein sorting 35 homolog (S. cerevisiae)	Immune/Acute Phase Response	222387_s_at	0.198	0.549	-0.176	222387_s_at	0.066	0.327	0.250	222387_s_at	0.005	0.371	0.447
VPS4A	vacuolar protein sorting 4 homolog A (S. cerevisiae)	Cell Division	217913_at	0.921	0.977	0.014	217913_at	0.005	0.107	-0.378	217913_at	0.788	0.984	0.045
VRK2	vaccinia related kinase 2	Stress Response	205126_at	0.006	0.126	0.363	205126_at	0.010	0.144	-0.345	205126_at	0.002	0.286	-0.491
VSNL1	visinin-like 1	Carbohydrate Metabolism	203797_at	<0.001	0.009	-0.533	203798_s_at	0.002	0.080	0.406	203797_at	0.011	0.448	0.409
WAC	WW domain containing adaptor with coiled-coil	Gene Expression	219679_s_at	0.064	0.342	-0.251	219679_s_at	0.065	0.325	0.251	230154_at	0.004	0.358	0.455
WDR33	WD repeat domain 33	Gene Expression	218851_s_at	<0.001	0.002	0.612	218851_s_at	0.008	0.127	-0.357	218851_s_at	0.008	0.408	-0.425
WHAMM	WAS protein homolog associated with actin, golgi membranes and microtubules	Cell Adhesion	228953_at	0.297	0.649	0.143	228953_at	0.001	0.066	-0.421	228953_at	0.500	0.953	-0.113

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
WIBG	within bgcn homolog (Drosophila)	Gene Expression	242304_at	<0.001	0.024	0.487	242304_at	0.035	0.243	-0.286	242304_at	0.020	0.503	-0.377
WIPI1	WD repeat domain, phosphoinositide interacting 1	Signal Transduction	203827_at	0.027	0.232	-0.298	203827_at	0.048	0.285	0.268	203827_at	0.009	0.412	0.423
WLS	wntless Wnt ligand secretion mediator	Signal Transduction	228950_s_at	0.020	0.205	-0.312	228950_s_at	0.006	0.113	0.370	228950_s_at	0.926	0.995	0.016
WNT5A	wingless-type MMTV integration site family, member 5A	ECM Organization	213425_at	<0.001	0.023	0.488	231227_at	<0.001	0.046	-0.456	213425_at	0.004	0.358	-0.459
WNT9A	wingless-type MMTV integration site family, member 9A	Signal Transduction	230643_at	0.005	0.116	-0.371	230643_at	0.014	0.162	0.332	230643_at	0.014	0.459	0.398
WRAP73	WD repeat containing, antisense to TP73	Cell Division	219322_s_at	0.004	0.098	-0.384	219322_s_at	0.088	0.373	0.232	219322_s_at	0.696	0.976	-0.065
WWC3	WWC family member 3	Signal Transduction	219520_s_at	0.364	0.700	-0.125	219520_s_at	0.904	0.965	0.017	219520_s_at	0.004	0.358	0.462
WWOX	WW domain containing oxidoreductase	Signal Transduction	210695_s_at	0.003	0.085	0.395	219077_s_at	0.049	0.287	-0.267	219077_s_at	0.003	0.328	-0.475
WWTR1	WW domain containing transcription regulator 1	Gene Expression	202132_at	<0.001	0.022	-0.492	202132_at	0.005	0.111	0.372	202132_at	0.008	0.408	0.426
XIRP1	xin actin-binding repeat containing 1	Actin Cytoskeleton	235042_at	0.008	0.138	-0.355	235042_at	0.078	0.354	0.240	235042_at	0.052	0.643	0.318
XPR1	receptor 1	Signal Transduction	222581_at	<0.001	0.017	-0.508	222581_at	<0.001	0.051	0.447	226615_at	0.003	0.328	0.476
YBX3	Y box binding protein 3	Gene Expression	201161_s_at	<0.001	0.018	-0.504	201161_s_at	<0.001	0.023	0.506	201160_s_at	0.002	0.277	0.500
YLPM1	YLP motif containing 1	Gene Expression	214659_x_at	0.057	0.324	-0.258	214659_x_at	0.050	0.288	0.266	214659_x_at	0.004	0.358	0.459
YRDC	yrnC N(6)- threonylcarbamoyltransferase domain containing	Amino Acid Metabolism	218647_s_at	<0.001	0.018	-0.506	218647_s_at	0.035	0.244	0.286	218647_s_at	0.678	0.975	0.069
YWHAB	tyrosine 3- monooxygenase/tryptophan 5- monooxygenase activation protein, beta	Apoptosis	217717_s_at	0.002	0.079	-0.401	217717_s_at	0.002	0.075	0.411	217717_s_at	0.280	0.896	0.180
YWHAQ	tyrosine 3- monooxygenase/tryptophan 5- monooxygenase activation protein, theta	Signal Transduction	200693_at	<0.001	<0.001	-0.648	200693_at	<0.001	0.023	0.506	200693_at	0.012	0.449	0.406
YY1	YY1 transcription factor	Gene Expression	201901_s_at	0.010	0.155	-0.345	201901_s_at	0.599	0.827	0.072	201901_s_at	0.641	0.972	0.078

Gene Symbol	Annotation	Category	LVEF				LVEDDI				NT-proBNP			
			Identifier	p-value	pBH	p	Identifier	p-value	pBH	p	Identifier	p-value	pBH	p
ZBED5	zinc finger, BED-type containing 5	Gene Expression	218263_s_at	0.004	0.104	0.379	218263_s_at	0.077	0.352	-0.240	218263_s_at	0.100	0.766	-0.271
ZBED6	zinc finger, BED-type containing 6	Gene Expression	243648_at	0.079	0.372	-0.239	243648_at	0.243	0.573	0.160	243648_at	0.002	0.279	0.495
ZBTB18	zinc finger and BTB domain containing 18	Gene Expression	212774_at	0.030	0.243	0.294	212774_at	<0.001	0.051	-0.446	212774_at	0.226	0.862	-0.201
ZBTB20	zinc finger and BTB domain containing 20	Gene Expression	227082_at	0.079	0.373	-0.239	227082_at	0.001	0.065	0.426	226252_at	0.007	0.404	0.431
ZBTB33	zinc finger and BTB domain containing 33	Gene Expression	226255_at	0.003	0.088	0.393	226255_at	0.498	0.774	-0.093	226255_at	0.452	0.940	-0.125
ZBTB38	zinc finger and BTB domain containing 38	Gene Expression	1558733_at	0.003	0.081	-0.399	1558733_at	0.022	0.199	0.310	1558733_at	<0.001	0.136	0.589
ZBTB42	zinc finger and BTB domain containing 42	Gene Expression	229691_at	<0.001	0.033	-0.466	229691_at	0.159	0.475	0.192	229691_at	0.603	0.968	0.087
ZBTB43	zinc finger and BTB domain containing 43	Gene Expression	227991_x_at	<0.001	0.039	0.454	227991_x_at	0.168	0.485	-0.189	227991_x_at	0.275	0.894	-0.181
ZBTB44	zinc finger and BTB domain containing 44	Gene Expression	1554469_at	0.067	0.348	0.249	1554469_at	0.006	0.115	-0.367	1554469_at	0.595	0.968	-0.089
ZBTB46	zinc finger and BTB domain containing 46	Gene Expression	227329_at	0.023	0.215	0.307	227329_at	0.004	0.101	-0.384	227329_at	0.124	0.795	-0.254
ZBTB47	zinc finger and BTB domain containing 47	Gene Expression	226500_at	0.006	0.119	-0.368	226500_at	0.108	0.406	0.219	226500_at	0.100	0.766	0.271
ZC3H11A	zinc finger CCCH-type containing 11A	Gene Expression	205787_x_at	0.097	0.407	-0.226	205787_x_at	0.449	0.746	0.104	205787_x_at	0.007	0.394	0.436
ZC3H8	zinc finger CCCH-type containing 8	Apoptosis	223506_at	0.410	0.730	0.113	223506_at	0.009	0.138	-0.349	223506_at	0.354	0.916	-0.154
ZDHC13	zinc finger, DHHC-type containing 13	Signal Transduction	219296_at	<0.001	0.006	-0.560	219296_at	0.092	0.379	0.230	219296_at	0.970	0.998	0.006
ZDHC3	zinc finger, DHHC-type containing 3	Fatty Acid Metabolism	218077_s_at	0.064	0.342	-0.251	218077_s_at	0.002	0.081	0.405	218077_s_at	0.784	0.984	0.046
ZEB1	zinc finger E-box binding homeobox 1	Amino Acid Metabolism	212758_s_at	0.028	0.235	-0.297	212758_s_at	0.004	0.103	0.381	212758_s_at	0.004	0.358	0.461
ZFP36L2	ZFP36 ring finger protein-like 2	Cell Division	201368_at	0.029	0.242	0.294	201368_at	0.001	0.065	-0.424	201368_at	0.122	0.793	-0.255
ZMYM4	zinc finger, MYM-type 4	Actin Cytoskeleton	202049_s_at	0.004	0.098	-0.383	202049_s_at	0.442	0.740	0.106	202049_s_at	0.007	0.402	0.433
ZMYM6	zinc finger, MYM-type 6	Actin Cytoskeleton	227595_at	0.003	0.089	-0.391	227595_at	0.306	0.634	0.140	227595_at	0.466	0.945	0.122
ZNF146	zinc finger protein 146	Gene Expression	200050_at	0.647	0.868	0.063	200050_at	0.005	0.107	-0.376	200050_at	0.830	0.988	-0.036
ZNF180	zinc finger protein 180	Gene Expression	219495_s_at	0.224	0.578	0.167	219495_s_at	0.007	0.119	-0.364	219495_s_at	0.409	0.931	-0.138
ZNF189	zinc finger protein 189	Gene Expression	207513_s_at	0.388	0.718	-0.119	207513_s_at	0.208	0.532	-0.172	207513_s_at	0.008	0.408	0.427
ZNF197	zinc finger protein 197	Gene Expression	205855_at	0.001	0.062	0.420	205855_at	0.041	0.265	-0.277	205855_at	0.772	0.984	-0.048

Gene			LVEF				LVEDDI				NT-proBNP			
Symbol	Annotation	Category	Identifier	p-value	pBH	ρ	Identifier	p-value	pBH	ρ	Identifier	p-value	pBH	ρ
ZNF20	zinc finger protein 20	Gene Expression	213916_at	0.002	0.073	-0.407	213916_at	0.351	0.674	0.128	213916_at	0.894	0.993	0.022
ZNF226	zinc finger protein 226	Gene Expression	233461_x_at	<0.001	0.036	-0.460	233461_x_at	0.664	0.861	0.060	233461_x_at	0.011	0.449	0.408
ZNF230	zinc finger protein 230	Protein Folding	1557322_at	0.359	0.696	-0.126	1557322_at	0.008	0.130	0.355	1557322_at	0.089	0.740	0.280
ZNF274	zinc finger protein 274	Gene Expression	204937_s_at	0.268	0.623	-0.152	204937_s_at	0.004	0.103	0.381	204937_s_at	0.133	0.799	0.248
ZNF280D	zinc finger protein 280D	Gene Expression	229013_at	0.053	0.314	0.262	229013_at	0.005	0.107	-0.376	229013_at	0.117	0.787	-0.259
ZNF320	zinc finger protein 320	Gene Expression	241704_x_at	0.002	0.075	0.406	241704_x_at	0.416	0.723	-0.112	241704_x_at	0.697	0.976	-0.065
ZNF322	zinc finger protein 322	Cell Division	219376_at	0.008	0.135	-0.356	219376_at	0.855	0.946	0.025	219376_at	0.476	0.946	0.119
ZNF395	zinc finger protein 395	Gene Expression	218149_s_at	0.101	0.413	0.223	218149_s_at	0.006	0.117	-0.365	218149_s_at	0.117	0.787	-0.258
ZNF418	zinc finger protein 418	Gene Expression	243439_at	0.010	0.158	0.342	243439_at	0.003	0.090	-0.395	243439_at	0.105	0.775	-0.267
ZNF462	zinc finger protein 462	Gene Expression	226575_at	0.671	0.879	-0.058	226575_at	0.281	0.610	0.148	226575_at	0.005	0.373	0.447
ZNF518B	zinc finger protein 518B	Gene Expression	230715_at	0.862	0.957	0.024	230715_at	0.934	0.977	-0.011	230715_at	0.008	0.410	0.424
ZNF552	zinc finger protein 552	Gene Expression	219741_x_at	0.001	0.062	0.419	219741_x_at	0.008	0.132	-0.354	219741_x_at	0.016	0.468	-0.391
ZNF554	zinc finger protein 554	Gene Expression	242864_at	0.178	0.523	0.184	242864_at	0.009	0.139	-0.348	242864_at	0.273	0.893	-0.182
ZNF562	zinc finger protein 562	Gene Expression	235200_at	0.247	0.602	-0.159	235200_at	0.349	0.672	-0.129	235200_at	0.007	0.402	0.432
ZNF586	zinc finger protein 586	Gene Expression	219711_at	0.006	0.125	-0.363	219711_at	0.093	0.381	0.229	219711_at	0.648	0.973	0.076
ZNF593	zinc finger protein 593	Gene Expression	204175_at	0.004	0.100	-0.382	204175_at	0.530	0.791	0.086	204175_at	0.326	0.909	0.163
ZNF610	zinc finger protein 610	Gene Expression	235953_at	0.376	0.708	-0.122	235953_at	0.009	0.137	0.350	235953_at	0.116	0.787	0.259
ZNF703	zinc finger protein 703	Cell Division	222760_at	0.569	0.829	0.078	222760_at	0.004	0.103	-0.382	222760_at	0.007	0.394	-0.436
ZNF720	zinc finger protein 720	Gene Expression	238510_at	0.492	0.782	0.095	238510_at	0.008	0.133	-0.353	238510_at	0.864	0.991	0.029
ZNF75A	zinc finger protein 75a	Gene Expression	227670_at	0.070	0.352	0.246	227670_at	0.016	0.173	-0.325	227670_at	0.009	0.416	-0.420
ZNF785	zinc finger protein 785	Gene Expression	1554770_x_at	0.977	0.993	-0.004	1554770_x_at	0.004	0.097	-0.388	1554770_x_at	0.329	0.909	0.162
ZNF81	zinc finger protein 81	Gene Expression	240079_at	0.024	0.219	-0.305	240079_at	0.007	0.121	0.363	240079_at	0.029	0.561	0.355
ZNF827	zinc finger protein 827	Gene Expression	228046_at	0.110	0.427	-0.218	228046_at	0.952	0.983	0.008	228046_at	0.006	0.376	0.444
ZNF846	zinc finger protein 846	Gene Expression	1569157_s_at	0.025	0.225	0.302	1569157_s_at	0.006	0.113	-0.370	1569157_s_at	0.027	0.548	-0.360
ZNF883	zinc finger protein 883	Gene Expression	230876_at	0.458	0.761	0.102	230876_at	0.002	0.083	-0.403	230876_at	0.217	0.855	-0.205
ZNF93	zinc finger protein 93	Gene Expression	208119_s_at	0.530	0.806	0.087	208119_s_at	0.003	0.085	-0.401	208119_s_at	0.471	0.946	-0.120
ZNRD1-AS1	ZNRD1 antisense RNA 1	Gene Expression	242557_at	0.103	0.417	0.222	242557_at	0.052	0.293	-0.264	242557_at	0.002	0.306	-0.482
ZPR1	ZPR1 zinc finger	Cell Division	200054_at	0.001	0.053	-0.431	200054_at	0.074	0.345	0.243	200054_at	0.637	0.971	0.079
	zinc finger and SCAN domain													
ZSCAN18	containing 18	Gene Expression	218312_s_at	0.059	0.328	-0.257	218312_s_at	0.002	0.081	0.405	218312_s_at	0.970	0.998	0.006
	zinc finger and SCAN domain													
ZSCAN25	containing 25	Gene Expression	242621_at	0.005	0.113	0.372	242621_at	0.730	0.890	-0.047	242621_at	0.563	0.965	-0.097
ZXDC	ZXD family zinc finger C	Gene Expression	218639_s_at	0.807	0.937	0.034	218639_s_at	0.008	0.132	-0.354	218639_s_at	0.992	1.000	-0.002

Significant correlation between genes and left ventricular ejection fraction (LVEF), left ventricular diameter at diastole index (LVEDDI) or serum NT-pro BNP was assumed by a nominal p -value<0.01. Additionally, Benjamini-Hochberg corrected p -values (p_{BH}) and Spearman correlation coefficient ρ (rho) are given. Gene symbol and annotation was derived by UniGene database (NETAFFX).

Supplemental Table 3. Top canonical pathways of genes significantly correlating with NT-proBNP, LVEDDI or LVEF ($p < 0.01$).

Canonical Pathways	BNP - log (p - value) Ratio	BNP molecules	LVEDDI - log (p - value) Ratio	LVEDDI molecules	LVEF - log (p - value) Ratio	LVEF molecules
Choline Degradation I	3.6	1.0 CHDH, ALDH7A1	0.0 NA	NA	1.1	0.5 CHDH
Role of JAK2 in Hormone-like Cytokine Signaling	2.7	0.1 PTPN11, PTPN1, SOCS2, JAK2	0.6	0.1 JAK1, PTPN1, JAK2	2.4	0.2 GHR, PTPN11, SH2B3, PTPN1, SOCS2, JAK2
Ephrin Receptor Signaling	2.7	0.1 RRAS2, PAK6, PTPN11, KALRN, GNA12, EGF, JAK2, CREB5, GNAL	2.2	0.1 FYN, RALA, PAK6, PDGFA, CREBBP, GNAQ, ACP1, EPHA4, KRAS, JAK2, CREB5, FGF1, VEGFA, PAK1, CDC42, SDC2, GNG5	1.6	0.1 RAP2A, RGS3, ITSN1, RALB, JAK2, FGF1, RRAS2, PTPN11, SDC2, CREB1, ARPC3, MAP4K4, GNAL, GNG12
JAK/Stat Signaling	2.5	0.1 PIK3C2B, RRAS2, PTPN11, PTPN1, SOCS2, JAK2	1.9	0.1 PIK3CA, PIAS2, RALA, JAK1, PTPN1, GNAQ, FGFR2, KRAS, PIK3CD, JAK2	2.1	0.1 RAP2A, JUN, RRAS2, PTPN11, RALB, CDKN1A, PTPN1, SOCS2, JAK2, ATM
Regulation of the Epithelial-Mesenchymal Transition Pathway	2.4	0.0 PIK3C2B, ADAM17, RRAS2, PTPN11, EGF, PARD6B, JAK2, ZEB1, WNT5A	0.8	0.1 MAP2K6, SMAD2, PIK3CA, RALA, JAK1, FGFR2, KRAS, ZEB1, JAK2, FGF1, APH1B, PIK3CD, WNT5A	1.2	0.1 MAP2K6, RAP2A, SMAD2, WNT9A, RALB, PARD6B, JAK2, FGF1, RRAS2, PTPN11, MAP2K3, TCF7L2, ATM, WNT5A
ERK5 Signaling	2.3	0.1 RRAS2, PTPN11, GNA12, EGF, CREB5	2.2	0.1 YWHAQ, RALA, YWHAB, CREBBP, GNAQ, RPS6KA5, KRAS, CREB5, ELK4	3.0	0.1 YWHAQ, RAP2A, RRAS2, PTPN11, SGK1, YWHAB, RALB, CREB1, MEF2C, MAP3K3
Thrombin Signaling	2.2	0.0 PIK3C2B, RRAS2, CAMK2D, PLCE1, PTPN11, GNA12, EGF, GNAL, MYL12A	1.5	0.1 PIK3CA, RALA, MPRIP, MYL2, GNAQ, FGFR2, KRAS, PLCL2, RHOQ, PLCE1, RND3, RHOT1, PIK3CD, GNG5, RHOF, ARHGEF9, MYL3	0.6	0.1 RAP2A, RRAS2, PLCE1, MPRIP, PTPN11, RALB, CREB1, PDPK1, PLCL2, GNG12, GNAL, ATM
ErbB Signaling	2.2	0.1 PIK3C2B, RRAS2, PAK6, PTPN11, HBEGF, EGF	1.8	0.1 MAP2K6, PIK3CA, PAK1, RALA, PAK6, CDC42, MAPK8, FGFR2, HBEGF, KRAS, PIK3CD	1.7	0.1 MAP2K6, RAP2A, JUN, RRAS2, PTPN11, RALB, MAPK8, PDPK1, MAP2K3, ATM
FAK Signaling	2.1	0.1 PIK3C2B, RRAS2, PAK6, PTPN11, EGF, CAPN3	1.8	0.1 FYN, PIK3CA, PAK1, RALA, PAK6, ACTA2, FGFR2, KRAS, PIK3CD, ACTG2, PTEN	1.3	0.1 RAP2A, RRAS2, PTPN11, ACTA2, RALB, PDPK1, TLN1, ACTA1, ATM
CREB Signaling in Neurons	2.1	0.0 PIK3C2B, RRAS2, CAMK2D, PLCE1, PTPN11, GNA12, CACNB2, CREB5, GNAL	1.1	0.1 PRKACB, PIK3CA, RALA, POLR2D, CREBBP, GNAQ, FGFR2, POLR2H, KRAS, PLCL2, CREB5, PLCE1, CACNA2D1, PIK3CD, CACNB2, GNG5	0.6	0.1 RAP2A, RRAS2, PLCE1, PTPN11, RALB, CREB1, CACNB2, PLCL2, CACNA2D3, GNG12, GNAL, ATM
Integrin Signaling	2.0	0.0 PIK3C2B, RRAS2, TSPAN5, PAK6, PTPN11, TSPAN7, TSPAN2, CAPN3, MYL12A	3.2	0.1 FYN, PIK3CA, RALA, MPRIP, PAK6, MYL2, MAPK8, MYLK3, FGFR2, KRAS, PTEN, PAK1, RHOQ, ACTA2, RND3, CDC42, ARF3, RHOT1, PIK3CD, ACTG2, ITGB6, RHOF, ACTN1	1.7	0.1 RAP2A, PARVA, MPRIP, RALB, MAPK8, MYLK3, TLN1, RRAS2, PTPN11, ACTA2, ARF4, ARPC3, ILKAP, ITGB6, ACTN1, ACTA1, ATM
GM-CSF Signaling	2.0	0.1 PIK3C2B, CAMK2D, RRAS2, PTPN11, JAK2	1.0	0.1 PIK3CA, RALA, FGFR2, PIK3CD, KRAS, JAK2, CCND1	1.2	0.1 RAP2A, RRAS2, PTPN11, RALB, JAK2, CCND1, ATM

Canonical Pathways	BNP		BNP molecules	LVEDDI		LVEDDI molecules	LVEF		LVEF molecules
	log (p-value)	Ratio		log (p-value)	Ratio		log (p-value)	Ratio	
Telomerase Signaling	1.9	0.1	PIK3C2B, HDAC9, RRAS2, PTPN11, EGF, ELF1	0.6	0.1	PIK3CA, RALA, PPP2CA, PPM1L, PPP2R2B, FGFR2, PIK3CD, KRAS	1.7	0.1	RAP2A, HSP90B1, RRAS2, HDAC4, PTPN11, RALB, CDKN1A, PPM1L, PDPK1, PPP2R5E, ATM
Angiopoietin Signaling	1.9	0.1	PIK3C2B, ANGPTL1, RRAS2, PAK6, PTPN11	1.2	0.1	ANGPTL1, PIK3CA, PAK1, RALA, PAK6, FGFR2, PIK3CD, KRAS	0.7	0.1	ANGPTL1, RAP2A, RRAS2, PTPN11, RALB, ATM
Pancreatic Adenocarcinoma Signaling	1.9	0.0	PIK3C2B, PTPN11, HBEGF, EGF, JAK2, PLD6	2.6	0.1	SMAD2, PIK3CA, RALA, JAK1, MAPK8, FGFR2, HBEGF, KRAS, JAK2, PLD6, CCND1, VEGFA, CDC42, PIK3CD	0.7	0.1	SMAD2, PTPN11, CDKN1A, MAPK8, JAK2, CCND1, PLD1, ATM
Glioma Signaling	1.9	0.0	PIK3C2B, CAMK2D, RRAS2, PTPN11, EGF, IDH1	1.1	0.1	PIK3CA, RALA, PDGFA, CDK6, FGFR2, KRAS, PIK3CD, CCND1, PTEN, IDH1	0.5	0.1	RAP2A, RRAS2, PTPN11, RALB, CDKN1A, CCND1, ATM
Macropinocytosis Signaling	1.9	0.1	MRC1, PIK3C2B, RRAS2, PTPN11, EGF	1.9	0.1	MRC1, PIK3CA, PAK1, RALA, CDC42, PDGFA, FGFR2, KRAS, PIK3CD, ITGB6	1.0	0.1	MRC1, RAP2A, RRAS2, PTPN11, RALB, ITGB6, ATM
Renal Cell Carcinoma Signaling	1.8	0.1	PIK3C2B, RRAS2, PAK6, PTPN11, EGLN3	3.4	0.1	VEGFA, PAK1, PIK3CA, RALA, PAK6, CDC42, CUL2, CREBBP, FGFR2, KRAS, PIK3CD, UBC, ELOC	1.0	0.1	RAP2A, RRAS2, JUN, PTPN11, RALB, EGLN3, ATM
Endothelin-1 Signaling	1.8	0.0	PIK3C2B, PLCE1, RRAS2, PTPN11, GNA12, EDNRA, PLD6, GNAL	0.7	0.1	PIK3CA, RALA, PTGS1, GNAQ, MAPK8, FGFR2, KRAS, PLD6, PLCL2, PLCE1, CASQ1, GUCY1A2, PIK3CD	1.0	0.1	CASP6, RAP2A, PLCE1, RRAS2, JUN, PTPN11, CASP3, RALB, MAPK8, PLCL2, GNAL, PLD1, ATM
Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis	1.8	0.0	PIK3C2B, RRAS2, CAMK2D, PLCE1, PTPN11, DAAM1, TLR3, JAK2, CREB5, TNFRSF11B, WNT5A	1.5	0.1	MAP2K6, SFRP4, PIK3CA, RALA, FN1, FRZB, PDGFA, CREBBP, IL6R, GNAQ, TLR8, FGFR2, KRAS, JAK2, PLCL2, CREB5, CCND1, VEGFA, PLCE1, DKK3, PIK3CD, WNT5A, TNFRSF11B, IRAK2	1.0	0.1	MAP2K6, RAP2A, SFRP4, FN1, WNT9A, RALB, PLCL2, JAK2, CCND1, PLCE1, RRAS2, JUN, PTPN11, CREB1, MAP2K3, TLR3, IL1RAPL1, TCF7L2, WNT5A, ATM
Prolactin Signaling	1.8	0.1	PIK3C2B, RRAS2, PTPN11, SOCS2, JAK2	1.1	0.1	FYN, PIK3CA, RALA, CREBBP, FGFR2, PIK3CD, KRAS, JAK2	1.7	0.1	RAP2A, JUN, RRAS2, PTPN11, RALB, PDPK1, SOCS2, JAK2, ATM
Sphingosine-1-phosphate Signaling	1.8	0.0	S1PR3, ASAH2B, PIK3C2B, PLCE1, PTPN11, GNA12	2.0	0.1	PIK3CA, PLCE1, RHOQ, RND3, RHOT1, PDGFA, CASQ1, GNAQ, FGFR2, PIK3CD, PLCL2, RHOF, ASAH1	0.5	0.1	S1PR3, CASP6, PLCE1, PTPN11, CASP3, PLCL2, ATM
NRF2-mediated Oxidative Stress Response	1.8	0.0	PIK3C2B, RRAS2, PTPN11, DNAJC19, MAF, DNAJC14, DNAJC13, DNAJA3	3.0	0.1	MAP2K6, PIK3CA, USP14, RALA, CREBBP, MAF, MAPK8, HERPUD1, FGFR2, KRAS, DNAJC15, MAP3K5, SOD2, ACTA2, DNAJC4, DNAJC14, UBE2K, PIK3CD, DNAJA2, ACTG2, DNAJB5	2.0	0.1	MAP2K6, RAP2A, GSTM1, DNAJB4, RALB, MAPK8, DNAJA4, MAP3K5, MAFK, RRAS2, JUN, ACTA2, PTPN11, MAP2K3, GCLM, ACTA1, ATM
Lipoate Salvage and Modification	1.8	1.0	LIPT1	0.0	NA	NA	0.0	NA	NA
Neuregulin Signaling	1.8	0.1	ADAM17, RRAS2, PTPN11, HBEGF, EGF	0.3	0.1	RALA, HBEGF, KRAS, RNF41, PTEN	1.2	0.1	RAP2A, HSP90B1, RRAS2, PTPN11, RALB, PDPK1, TMEFF2, RNF41

Canonical Pathways	BNP		BNP molecules	LVEDDI		LVEDDI molecules	LVEF		LVEF molecules
	log (p - value)	Ratio		log (p - value)	Ratio		log (p - value)	Ratio	
Wnt/Ca+ pathway	1.8	0.1	PLCE1, CREB5, ROR1, WNT5A	1.1	0.1	PLCE1, CREBBP, PLCL2, CREB5, ROR1, WNT5A	0.5	0.1	PLCE1, CREB1, PLCL2, WNT5A
ERK/MAPK Signaling	1.8	0.0	PIK3C2B, RRAS2, PAK6, PTPN11, PPP1R3C, VRK2, CREB5, ELF1	2.2	0.1	PRKACB, FYN, PIK3CA, RALA, PAK6, PPP2CA, YWHAB, CREBBP, FGFR2, RPS6KA5, KRAS, MKNK2, CREB5, YWHAB, PPP1CC, PAK1, PPM1L, PPP2R2B, PIK3CD	1.1	0.1	YWHAB, RAP2A, RRAS2, PTPN11, DUSP1, YWHAB, PPP1R3C, VRK2, PPM1L, CREB1, RALB, TLN1, PPP2R5E, ATM
HER-2 Signaling in Breast Cancer	1.7	0.1	PIK3C2B, RRAS2, PTPN11, EGF, PARD6B	1.7	0.1	PIK3CA, RALA, CDC42, CDK6, FGFR2, KRAS, PIK3CD, MAP3K5, ITGB6, CCND1	2.4	0.1	RAP2A, RRAS2, PTPN11, RALB, CDKN1A, PARD6B, MAP3K5, PARD3, ITGB6, CCND1, ATM
Role of Tissue Factor in Cancer	1.7	0.0	PIK3C2B, RRAS2, PTPN11, GNA12, HBEGF, JAK2	2.3	0.1	FYN, PIK3CA, RALA, GNAQ, FGFR2, HBEGF, KRAS, RPS6KA5, JAK2, PTEN, VEGFA, PAK1, CDC42, PIK3CD	0.6	0.1	RAP2A, CTGF, RRAS2, PTPN11, CASP3, RALB, JAK2, ATM
Tec Kinase Signaling	1.7	0.0	PIK3C2B, PTPN11, PAK6, GTF2I, GNA12, JAK2, GNAL	2.3	0.1	FYN, PIK3CA, JAK1, PAK6, MAPK8, GNAQ, FGFR2, JAK2, PAK1, RHOQ, RND3, ACTA2, RHOT1, PIK3CD, ACTG2, GNG5, RHOF	0.4	0.1	PTPN11, ACTA2, MAPK8, FCER1A, JAK2, GNG12, ACTA1, GNAL, ATM
CXCR4 Signaling	1.7	0.0	PIK3C2B, RRAS2, PTPN11, PAK6, GNA12, GNAL, MYL12A	2.0	0.1	PIK3CA, RALA, MYL2, PAK6, MAPK8, GNAQ, FGFR2, KRAS, PAK1, RHOQ, RND3, RHOT1, PIK3CD, GNG5, RHOF, MYL3	0.4	0.1	RAP2A, JUN, RRAS2, PTPN11, RALB, MAPK8, GNG12, GNAL, ATM
Aldosterone Signaling in Epithelial Cells	1.7	0.0	PIK3C2B, ICMT, PLCE1, PTPN11, DNAJC19, DNAJC14, DNAJC13	0.8	0.1	PIK3CA, PLCE1, DNAJC4, DNAJC27, DNAJC14, FGFR2, KRAS, PIK3CD, DNAJC15, PLCL2, DNAJB5, HSPA4L	1.9	0.1	ICMT, DNAJB4, SGK1, HSPH1, PDPK1, PIP5K1B, PLCL2, HSPA2, HSPA4, HSP90B1, PLCE1, PTPN11, DUSP1, HSPA4L, ATM
IL-6 Signaling	1.7	0.0	PIK3C2B, RRAS2, PTPN11, JAK2, TNFRSF11B, MCL1	2.1	0.1	MAP2K6, CSNK2A1, PIK3CA, RALA, IL6R, MAPK8, FGFR2, KRAS, JAK2, VEGFA, COL1A1, PIK3CD, TNFRSF11B, MCL1	2.5	0.1	MAP2K6, RAP2A, ABCB1, RALB, MAPK8, JAK2, JUN, RRAS2, PTPN11, MAP2K3, IL1RAPL1, MAP4K4, ATM, MCL1
Ceramide Signaling	1.6	0.0	S1PR3, PIK3C2B, RRAS2, PTPN11, TNFRSF11B	2.0	0.1	DIABLO, PIK3CA, RALA, PPP2CA, PPM1L, PPP2R2B, MAPK8, FGFR2, KRAS, PIK3CD, TNFRSF11B	1.8	0.1	S1PR3, RAP2A, JUN, RRAS2, PTPN11, RALB, PPM1L, MAPK8, PPP2R5E, ATM
CNTF Signaling	1.6	0.1	PIK3C2B, RRAS2, PTPN11, JAK2	1.6	0.1	PIK3CA, RALA, JAK1, FGFR2, PIK3CD, KRAS, RPS6KA5, JAK2	1.0	0.1	RAP2A, RRAS2, PTPN11, RALB, JAK2, ATM
Gf±12/13 Signaling	1.6	0.0	PIK3C2B, RRAS2, PTPN11, GNA12, LPAR5, MYL12A	1.3	0.1	PIK3CA, RALA, MYL2, CDC42, LPAR5, MAPK8, FGFR2, KRAS, PIK3CD, MAP3K5, LPAR3, MYL3	1.2	0.1	RAP2A, JUN, RRAS2, PTPN11, RALB, LPAR5, MAPK8, MEF2C, MAP3K5, LPAR3, ATM
Thrombopoietin Signaling	1.6	0.1	PIK3C2B, RRAS2, PTPN11, JAK2	0.8	0.1	PIK3CA, RALA, FGFR2, KRAS, PIK3CD, JAK2	1.4	0.1	RAP2A, JUN, RRAS2, PTPN11, RALB, JAK2, ATM

Canonical Pathways	BNP		BNP molecules	LVEDDI		LVEDDI molecules	LVEF		LVEF molecules
	log (p-value)	Ratio		log (p-value)	Ratio		log (p-value)	Ratio	
Axonal Guidance Signaling	1.5	0.0	PIK3C2B, ADAM17, KALRN, PAK6, C9orf3, GNA12, EGF, RRAS2, PLCE1, PTPN11, ADAMTS5, GNAL, MYL12A, WNT5A	0.7	0.1	PRKACB, FYN, PIK3CA, RALA, MYL2, PDGFA, UNC5B, EPHA4, KRAS, VEGFA, PAK1, PLCE1, SDC2, ADAM19, ADAM23, GNG5, MYL3, ADAMTS15, PAPP, PAK6, COP55, SEMA5A, GNAQ, FGFR2, PLCL2, CDC42, BMP7, PIK3CD, WNT5A	0.9	0.1	RAP2A, RGS3, ITSN1, BRCC3, SEMA6D, PLCE1, SDC2, ADAM23, ARPC3, TUBA1C, CHMP1A, ADAMTS5, GNG12, ATM, ADAMTS15, WNT9A, C9orf3, PTCH1, RALB, TUBA4A, PLCL2, BMP5, RRAS2, PTPN11, BMP7, AFG3L2, GNAL, WNT5A
RAN Signaling	1.5	0.1	RANBP2, CSE1L	0.2	0.1	TNPO1	3.2	0.3	KPNB1, TNPO1, RAN, KPN2, IPO5
PAK Signaling	1.5	0.0	PIK3C2B, RRAS2, PAK6, PTPN11, MYL12A	2.1	0.1	PIK3CA, PAK1, RALA, PAK6, MYL2, CDC42, PDGFA, MAPK8, FGFR2, KRAS, PIK3CD, MYL3	0.7	0.1	RAP2A, RRAS2, PTPN11, CASP3, RALB, MAPK8, ATM
Insulin Receptor Signaling	1.5	0.0	PIK3C2B, RRAS2, PTPN11, PPP1R3C, PTPN1, JAK2	2.6	0.1	PRKACB, FYN, PIK3CA, EIF2B4, RALA, JAK1, MAPK8, FGFR2, KRAS, JAK2, VAMP2, PTEN, PPP1CC, RHOQ, PTPN1, PIK3CD	1.5	0.1	RAP2A, RRAS2, INPP5F, PTPN11, SGK1, PPP1R3C, RALB, PTPN1, MAPK8, PDPK1, JAK2, ATM
Lipoate Biosynthesis and Incorporation II	1.5	0.5	LIPT1	0.0	NA	NA	0.0	NA	NA
Actin Cytoskeleton Signaling	1.5	0.0	PIK3C2B, ABI2, RRAS2, PTPN11, PAK6, GNA12, EGF, MYL12A	3.0	0.1	MYH10, PIK3CA, MYH6, RALA, FN1, MPRI, PAK6, MYL2, PDGFA, MYLK3, FGFR2, KRAS, MYH7, MYH11, FGF1, PAK1, ACTA2, CDC42, PIK3CD, ACTG2, NCKAP1L, ACTN1, MYL3	2.4	0.1	RAP2A, MYH10, MYH6, FN1, MPRI, RALB, MYLK3, TLN1, PIP5K1B, FGF1, RRAS2, ACTA2, PTPN11, ARPC3, ARHGAP24, ACTN1, GNG12, ACTA1, ATM, NCKAP1
Ovarian Cancer Signaling	1.5	0.0	PIK3C2B, RRAS2, PTPN11, EGF, EDNRA, WNT5A	1.5	0.1	PRKACB, GJA1, PIK3CA, RALA, PTGS1, FGFR2, KRAS, CCND1, MLH1, PTEN, VEGFA, PIK3CD, WNT5A	1.1	0.1	RAP2A, RRAS2, PTPN11, MSH2, WNT9A, RALB, CCND1, MLH1, TCF7L2, WNT5A, ATM
IGF-1 Signaling	1.5	0.0	PIK3C2B, RRAS2, PTPN11, SOCS2, JAK2	2.0	0.1	YWHAQ, PRKACB, PIK3CA, CSNK2A1, RALA, JAK1, YWHAB, MAPK8, FGFR2, KRAS, PIK3CD, JAK2	3.3	0.1	YWHAQ, RAP2A, JUN, RRAS2, CTGF, PTPN11, YWHAB, RALB, IGFBP3, MAPK8, SOCS2, PDPK1, JAK2, ATM
UVA-Induced MAPK Signaling	1.5	0.0	PIK3C2B, PLCE1, RRAS2, PTPN11, PARP12	1.0	0.1	PIK3CA, RALA, PLCE1, MAPK8, FGFR2, RPS6KA5, KRAS, PIK3CD, PLCL2	1.5	0.1	RAP2A, JUN, RRAS2, PLCE1, PTPN11, CASP3, RALB, MAPK8, PLCL2, ATM
Role of JAK1 and JAK3 in ¹³ c Cytokine Signaling	1.4	0.1	PIK3C2B, RRAS2, PTPN11, JAK2	1.1	0.1	PIK3CA, RALA, JAK1, FGFR2, PIK3CD, KRAS, JAK2	0.9	0.1	RAP2A, RRAS2, PTPN11, RALB, JAK2, ATM
Superpathway of Inositol Phosphate Compounds	1.4	0.0	SET, PIK3C2B, PLCE1, PTPN11, DUSP27, PTPN1, PIK3AP1, NUDT4	1.1	0.1	FYN, PIK3CA, PPP1R1A, SEC16A, ACP1, FGFR2, PAWR, NUDT15, PTEN, SET, PPP1CC, PLCE1, PTPN1, SGPP2, PIK3CD, NUDT4, PPIP5K2	1.2	0.1	PPP1R1A, NUDT3, PIP5K1B, DUSP5, PLCE1, INPP5F, PI4K2A, PTPN11, DUSP1, SGPP2, PTPN1, CD86, PIK3AP1, ILKAP, PPP2R5E, ATM

Canonical Pathways	BNP		BNP molecules	LVEDDI		LVEDDI molecules	LVEF		LVEF molecules
	log (p-value)	Ratio		log (p-value)	Ratio		log (p-value)	Ratio	
Dendritic Cell Maturation	1.4	0.0	PIK3C2B, PLCE1, PTPN11, TLR3, JAK2, CREB5, TNFRSF11B	1.5	0.1	B2M, PIK3CA, FCGR2A, CREBBP, MAPK8, FGFR2, PLCL2, JAK2, FCGR2B, CREB5, COL1A2, COL1A1, PLCE1, PIK3CD, TNFRSF11B, COL3A1	0.6	0.1	COL1A2, PLCE1, PTPN11, CREB1, MAPK8, CD86, TLR3, JAK2, PLCL2, COL3A1, ATM
G-Protein Coupled Receptor Signaling	1.4	0.0	S1PR3, PIK3C2B, RRAS2, CAMK2D, PTPN11, NPR3, PLD6, CREB5, GNAL	1.2	0.1	PRKACB, FYN, PIK3CA, RALA, GTPD1, PDE7A, PTGER3, CREBBP, GNAQ, PDE4A, RGS4, FGFR2, KRAS, PLD6, CREB5, ADRB1, PIK3CD, PDE11A, ADORA1, ADRB2	1.5	0.1	RAP2A, PDE3A, RALB, PDE4A, RGS4, PDPK1, PDE1C, S1PR3, ADRB1, RRAS2, PDE7B, PTPN11, DUSP1, CREB1, PTH1R, PDE11A, GNAL, ADRA1A, ADRB2, ATM
IL-9 Signaling	1.4	0.1	PIK3C2B, PTPN11, SOCS2	0.7	0.1	PIK3CA, JAK1, FGFR2, PIK3CD	0.5	0.1	PTPN11, SOCS2, ATM
ErbB4 Signaling	1.4	0.1	PIK3C2B, ADAM17, RRAS2, PTPN11	0.7	0.1	PIK3CA, RALA, FGFR2, APH1B, KRAS, PIK3CD	0.8	0.1	RAP2A, RRAS2, PTPN11, RALB, PDPK1, ATM
Cardiomyocyte Differentiation via BMP Receptors	1.4	0.1	NPPB, NPPA	2.6	0.3	NPPB, MYL2, MYH7, BMP7, NPPA	3.7	0.3	NPPB, SMAD6, MEF2C, BMP7, NPPA, BMP5
G Beta Gamma Signaling	1.4	0.0	RRAS2, GNA12, HBEGF, CACNB2, GNAL	1.2	0.1	PRKACB, PAK1, RALA, CDC42, CACNA2D1, GNAQ, HBEGF, KRAS, CACNB2, GNG5	0.8	0.1	RAP2A, RRAS2, RALB, PDPK1, CACNB2, CACNA2D3, GNG12, GNAL
SPINK1 General Cancer Pathway	1.4	0.0	PIK3C2B, RRAS2, PTPN11, JAK2	1.3	0.1	PIK3CA, RALA, JAK1, IL6R, FGFR2, PIK3CD, KRAS, JAK2	0.8	0.1	RAP2A, RRAS2, PTPN11, RALB, JAK2, ATM
3-phosphoinositide Biosynthesis	1.4	0.0	SET, PIK3C2B, PTPN11, DUSP27, PTPN1, PIK3AP1, NUDT4	0.9	0.1	FYN, PIK3CA, PPP1R1A, FGFR2, ACP1, PAWR, NUDT15, PTEN, SET, PPP1CC, SGPP2, PTPN1, PIK3CD, NUDT4	1.4	0.1	PPP1R1A, NUDT3, PIP5K1B, DUSP5, INPP5F, PI4K2A, PTPN11, DUSP1, SGPP2, PTPN1, CD86, PIK3AP1, ILKAP, PPP2R5E, ATM
Neurotrophin/TRK Signaling	1.3	0.0	PIK3C2B, RRAS2, PTPN11, CREB5	2.6	0.1	MAP2K6, PIK3CA, RALA, CDC42, CREBBP, MAPK8, FGFR2, KRAS, PIK3CD, MAP3K5, CREB5	3.5	0.1	MAP2K6, RAP2A, JUN, RRAS2, PTPN11, RALB, CREB1, MAPK8, PDPK1, MAP2K3, MAP3K5, ATM
GDNF Family Ligand-Receptor Interactions	1.3	0.0	PIK3C2B, RRAS2, PTPN11, RET	1.3	0.1	DOK5, PIK3CA, RALA, CDC42, MAPK8, FGFR2, PIK3CD, KRAS	1.9	0.1	RAP2A, JUN, RRAS2, PTPN11, RALB, CREB1, MAPK8, RET, ATM
IL-15 Signaling	1.3	0.0	PIK3C2B, RRAS2, PTPN11, JAK2	0.9	0.1	PIK3CA, RALA, JAK1, FGFR2, PIK3CD, KRAS, JAK2	0.8	0.1	RAP2A, RRAS2, PTPN11, RALB, JAK2, ATM
IL-8 Signaling	1.3	0.0	PIK3C2B, RRAS2, PTPN11, GNA12, EGF, HBEGF, PLD6	1.9	0.1	PIK3CA, NOX4, RALA, MYL2, MAPK8, HBEGF, FGFR2, KRAS, PLD6, CCND1, VEGFA, RHOQ, RND3, RHOT1, PIK3CD, GNG5, RHOF, IRAK2	0.9	0.1	RAP2A, NOX4, JUN, RRAS2, CCND3, PTPN11, RALB, MAPK8, MAP4K4, CCND1, PLD1, GNG12, ATM
D-myo-inositol-5-phosphate Metabolism	1.3	0.0	SET, PLCE1, PTPN11, DUSP27, PTPN1, NUDT4	0.8	0.1	SET, PPP1CC, PLCE1, PPP1R1A, SGPP2, PTPN1, ACP1, PAWR, NUDT4, NUDT15, PTEN	1.0	0.1	DUSP5, PLCE1, INPP5F, PTPN11, DUSP1, PPP1R1A, NUDT3, SGPP2, PTPN1, ILKAP, PPP2R5E
Relaxin Signaling	1.3	0.0	PIK3C2B, PTPN11, NPR3, GNA12, PLD6, GNAL	1.2	0.1	PRKACB, PIK3CA, GTPD1, PDE7A, PDE4A, GNAQ, FGFR2, PLD6, VEGFA, GUCY1A2, PIK3CD, PDE11A, GNG5	0.9	0.1	JUN, PTPN11, PDE7B, PDE3A, CREB1, PDE4A, PDE11A, GNG12, GNAL, ATM, PDE1C

Canonical Pathways	BNP		BNP molecules	LVEDDI		LVEDDI molecules	LVEF		LVEF molecules
	log (p - value)	Ratio		log (p - value)	Ratio		log (p - value)	Ratio	
Non-Small Cell Lung Cancer Signaling	1.3	0.0	PIK3C2B, RRAS2, PTPN11, EGF	1.2	0.1	PIK3CA, RALA, CDK6, FGFR2, KRAS, PIK3CD, RXRA, CCND1	1.1	0.1	RAP2A, RRAS2, PTPN11, RALB, PDPK1, CCND1, ATM
RhoA Signaling	1.3	0.0	GNA12, LPAR5, SEPT11, ARHGAP1, MYL12A	1.7	0.1	MPRIP, MYL2, ACTA2, RND3, LPAR5, MYLK3, SEPT11, ACTG2, ARHGAP1, LPAR3, MYL3, SEPT2	1.3	0.1	MPRIP, ACTA2, LPAR5, MYLK3, ARPC3, SEPT11, PIP5K1B, LPAR3, ACTA1, PLD1
Thyroid Hormone Metabolism I (via Deiodination)	1.3	0.3	DIO2	0.9	0.3	DIO2	0.9	0.3	DIO2
Thyronamine and Iodothyronamine Metabolism	1.3	0.3	DIO2	0.9	0.3	DIO2	0.9	0.3	DIO2
4-hydroxyproline Degradation I	1.3	0.3	HOGA1	0.0	NA	NA	0.9	0.3	HOGA1
Rac Signaling	1.3	0.0	PIK3C2B, ABI2, RRAS2, PAK6, PTPN11	1.4	0.1	PIK3CA, PAK1, NOX4, RALA, PAK6, CDC42, MAPK8, FGFR2, KRAS, PIK3CD, ELK4	2.4	0.1	RAP2A, NOX4, RALB, MAPK8, PIP5K1B, PLD1, JUN, RRAS2, PTPN11, ARPC3, PARD3, ATM, NCKAP1
Growth Hormone Signaling	1.3	0.0	PIK3C2B, PTPN11, SOCS2, JAK2	0.4	0.1	PIK3CA, FGFR2, RPS6KA5, PIK3CD, JAK2	1.0	0.1	GHR, PTPN11, IGFBP3, PDPK1, SOCS2, JAK2, ATM
Huntington's Disease Signaling	1.3	0.0	PIK3C2B, HDAC9, PTPN11, EGF, GOSR1, CREB5, GOSR2, CAPN3	2.2	0.1	ATP5PF, PIK3CA, ATP5MC1, POLR2D, ATP5F1A, CREBBP, MAPK8, GNAQ, POLR2H, FGFR2, CREB5, VAMP2, ATP5F1E, TGM2, NSF, ATP5F1C, CASQ1, PIK3CD, GNG5, UBC, ATP5PB, SNCA	2.0	0.1	ATP5PF, HDAC4, CASP3, SGK1, MAPK8, PDPK1, UBE2S, HSPA2, ATP5F1E, TGM2, NSF, HSPA4, CASP6, JUN, PTPN11, CREB1, GOSR2, SNCA, GNG12, ATM
Fc γ RIIB Signaling in B Lymphocytes	1.3	0.0	PIK3C2B, RRAS2, PTPN11, CACNB2	1.6	0.1	PIK3CA, RALA, CACNA2D1, MAPK8, FGFR2, KRAS, PIK3CD, CACNB2, FCGR2B	1.8	0.1	RAP2A, RRAS2, PTPN11, RALB, MAPK8, PDPK1, CACNB2, CACNA2D3, ATM
Estrogen-Dependent Breast Cancer Signaling	1.3	0.0	PIK3C2B, RRAS2, PTPN11, CREB5	1.2	0.1	PIK3CA, RALA, CREBBP, FGFR2, KRAS, PIK3CD, CREB5, CCND1	1.4	0.1	RAP2A, RRAS2, JUN, PTPN11, CREB1, RALB, CCND1, ATM
Antiproliferative Role of Somatostatin Receptor 2	1.3	0.0	PIK3C2B, RRAS2, PTPN11, NPR3	0.9	0.1	PIK3CA, RALA, GUCY1A2, FGFR2, KRAS, PIK3CD, GNG5	1.0	0.1	RAP2A, RRAS2, PTPN11, RALB, CDKN1A, GNG12, ATM
Erythropoietin Signaling	1.3	0.0	PIK3C2B, RRAS2, PTPN11, JAK2	0.6	0.1	PIK3CA, RALA, FGFR2, KRAS, PIK3CD, JAK2	1.4	0.1	RAP2A, RRAS2, JUN, PTPN11, RALB, PDPK1, JAK2, ATM
Semaphorin Signaling in Neurons	1.3	0.1	PAK6, DPYSL4, ARHGAP1	2.4	0.2	FYN, PAK1, RHOQ, PAK6, RND3, RHOT1, RHOF, ARHGAP1	0.0	NA	NA
Endocannabinoid Developing Neuron Pathway	1.3	0.0	PIK3C2B, RRAS2, PTPN11, CREB5, GNAL	1.6	0.1	PRKACB, MAP2K6, PIK3CA, RALA, CREBBP, MAPK8, FGFR2, KRAS, PIK3CD, GNG5, CREB5, CCND1	1.5	0.1	MAP2K6, RAP2A, RRAS2, PTPN11, RALB, CREB1, MAPK8, MAP2K3, CCND1, GNAL, ATM
GNRH Signaling	1.3	0.0	CAMK2D, RRAS2, PAK6, HBEGF, CACNB2, CREB5	2.4	0.1	MAP2K6, PRKACB, RALA, PAK6, CREBBP, MAPK8, GNAQ, HBEGF, KRAS, MAP3K5, CREB5, MAP3K12, PAK1, CDC42, CACNA2D1, CACNB2, GNG5	1.4	0.1	MAP2K6, RAP2A, RALB, MAPK8, MAP3K5, MAP3K12, JUN, RRAS2, CREB1, CACNB2, MAP2K3, MAP3K3, CACNA2D3

Canonical Pathways	BNP		BNP molecules	LVEDDI		LVEDDI molecules	LVEF		LVEF molecules
	log (p-value)	Ratio		log (p-value)	Ratio		log (p-value)	Ratio	
Glioblastoma Multiforme Signaling	1.3	0.0	PIK3C2B, PLCE1, RRAS2, PTPN11, EGF, WNT5A	2.4	0.1	PIK3CA, RALA, PDGFA, CDK6, FGFR2, KRAS, PLCL2, CCND1, PTEN, RHOQ, PLCE1, RND3, CDC42, RHOT1, PIK3CD, RHOF, WNT5A	0.8	0.1	RAP2A, RRAS2, PLCE1, PTPN11, WNT9A, RALB, CDKN1A, PLCL2, CCND1, WNT5A, ATM
Role of JAK family kinases in IL-6-type Cytokine Signaling	1.2	0.1	PTPN11, JAK2	1.5	0.2	JAK1, IL6R, MAPK8, JAK2	1.0	0.1	PTPN11, MAPK8, JAK2
CDP-diacylglycerol Biosynthesis I	1.2	0.1	LPCAT4, MBOAT1	1.5	0.2	AGPAT2, CRLS1, MBOAT1, AGPAT3	0.0	0.0	LPCAT4
Phagosome Formation	1.2	0.0	MRC1, PIK3C2B, PLCE1, PTPN11, TLR3	2.3	0.1	MRC1, PIK3CA, FN1, FCGR2A, TLR8, FGFR2, PLCL2, FCGR2B, PLCE1, RHOQ, RND3, RHOT1, PIK3CD, RHOF	0.6	0.1	MRC1, PLCE1, FN1, PTPN11, FCER1A, TLR3, PLCL2, ATM
IL-17 Signaling	1.2	0.0	PIK3C2B, RRAS2, PTPN11, JAK2	1.4	0.1	MAP2K6, PIK3CA, RALA, JAK1, MAPK8, FGFR2, KRAS, PIK3CD, JAK2	2.5	0.1	MAP2K6, RAP2A, JUN, RRAS2, PTPN11, TIMP1, RALB, MAPK8, MAP2K3, JAK2, ATM
Acute Phase Response Signaling	1.2	0.0	C3, RRAS2, PTPN11, SOCS2, JAK2, TNFRSF11B	1.0	0.1	MAP2K6, HP, PIK3CA, SOD2, FN1, RALA, IL6R, MAPK8, KRAS, PIK3CD, MAP3K5, JAK2, TNFRSF11B	1.9	0.1	MAP2K6, RAP2A, FN1, RALB, MAPK8, PDPK1, MAP3K5, JAK2, HNRNPK, APOA1, RRAS2, JUN, PTPN11, SOCS2, MAP2K3
PI3K Signaling in B Lymphocytes	1.2	0.0	CAMK2D, PLCE1, C3, RRAS2, PIK3AP1	1.8	0.1	FYN, PIK3CA, PLCE1, RALA, ATF6B, KRAS, PIK3CD, PLEKHA2, MALT1, PLEKHA1, PLCL2, FCGR2B, PTEN	1.1	0.1	RAP2A, JUN, RRAS2, PLCE1, RALB, CREB1, PDPK1, ATF6B, PIK3AP1, PLCL2
Apoptosis Signaling	1.2	0.0	RRAS2, LMNA, CAPN3, MCL1	2.1	0.1	DIABLO, RALA, MAPK8, BID, LMNA, KRAS, MAP3K5, SPTAN1, BIRC3, BIRC2, MCL1	2.4	0.1	RAP2A, CASP6, RRAS2, CASP3, RALB, MAPK8, MAP3K5, MAP4K4, BIRC3, BCL2L11, MCL1
Phosphatidylglycerol Biosynthesis II (Non-plastidic)	1.2	0.1	LPCAT4, MBOAT1	1.4	0.1	AGPAT2, CRLS1, MBOAT1, AGPAT3	0.0	0.0	LPCAT4
Role of NFAT in Cardiac Hypertrophy	1.2	0.0	PIK3C2B, HDAC9, PLCE1, CAMK2D, RRAS2, PTPN11, CACNB2	0.8	0.1	MAP2K6, PRKACB, PIK3CA, RALA, MAPK8, GNAQ, FGFR2, KRAS, PLCL2, PLCE1, CACNA2D1, PIK3CD, CACNB2, GNG5, SLC8A1	1.3	0.1	MAP2K6, RAP2A, HDAC4, RALB, MAPK8, PLCL2, RCAN1, RRAS2, PLCE1, PTPN11, MAP2K3, CACNB2, MEF2C, CACNA2D3, GNG12, ATM
PDGF Signaling	1.1	0.0	PIK3C2B, RRAS2, PTPN11, JAK2	2.1	0.1	PIK3CA, CSNK2A1, RALA, JAK1, PDGFA, MAPK8, FGFR2, ACP1, KRAS, PIK3CD, JAK2	1.5	0.1	RAP2A, JUN, RRAS2, INPP5F, PTPN11, RALB, MAPK8, JAK2, ATM
cAMP-mediated signaling	1.1	0.0	S1PR3, CAMK2D, NPR3, PLD6, CREB5, AKAP7, GNAL	0.8	0.1	PRKACB, GTPBP1, PDE7A, PTGER3, CREBBP, PDE4A, RGS4, PLD6, CREB5, AKAP7, AKAP13, ADRB1, PDE11A, ADORA1, ADRB2	1.6	0.1	PDE3A, PDE4A, RGS4, CNGA1, AKAP7, PDE1C, S1PR3, AKAP13, ADRB1, PDE7B, DUSP1, CREB1, PTH1R, CREM, PDE11A, GNAL, ADRB2
P2Y Purigenic Receptor Signaling Pathway	1.1	0.0	PIK3C2B, PLCE1, RRAS2, PTPN11, CREB5	1.7	0.1	PRKACB, PIK3CA, RALA, CREBBP, GNAQ, FGFR2, KRAS, PLCL2, CREB5, PLCE1, P2RY1, PIK3CD, GNG5	1.0	0.1	RAP2A, JUN, RRAS2, PLCE1, PTPN11, RALB, CREB1, PLCL2, GNG12, ATM

Canonical Pathways	BNP		BNP molecules	LVEDDI		LVEDDI molecules	LVEF		LVEF molecules
	log (p-value)	Ratio		log (p-value)	Ratio		log (p-value)	Ratio	
Acute Myeloid Leukemia Signaling	1.1	0.0	PIK3C2B, RRAS2, PTPN11, IDH1	0.9	0.1	MAP2K6, PIK3CA, RALA, FGFR2, KRAS, PIK3CD, CCND1, IDH1	1.5	0.1	MAP2K6, RAP2A, RRAS2, PTPN11, RALB, MAP2K3, CCND1, TCF7L2, ATM
TR/RXR Activation	1.1	0.0	PIK3C2B, PTPN11, TBL1XR1, DIO2	1.6	0.1	HP, PIK3CA, ADRB1, FGFR2, PIK3CD, TBL1XR1, RXRA, THRB, DIO2, NCOA4	0.5	0.1	AKR1C1/AKR1C2, ADRB1, COL6A3, PTPN11, DIO2, ATM
Myo-inositol Biosynthesis	1.1	0.2	IMPA2	0.7	0.2	IMPA2	1.7	0.4	INPP5F, IMPA2
CTLA4 Signaling in Cytotoxic T Lymphocytes	1.1	0.0	PIK3C2B, PTPN11, AP1S2, JAK2	2.0	0.1	B2M, FYN, PIK3CA, PPP2CA, AP1S2, PPM1L, PPP2R2B, FGFR2, PIK3CD, JAK2, LCP2	1.1	0.1	PTPN11, AP1S2, AP1M1, PPM1L, CD86, JAK2, PPP2R5E, ATM
Melanoma Signaling	1.1	0.0	PIK3C2B, RRAS2, PTPN11	1.5	0.1	PIK3CA, RALA, FGFR2, KRAS, PIK3CD, CCND1, PTEN	1.7	0.1	RAP2A, RRAS2, PTPN11, RALB, CDKN1A, CCND1, ATM
Regulation of Cellular Mechanics by Calpain Protease	1.1	0.0	RRAS2, EGF, CAPN3	0.7	0.1	RALA, CDK6, KRAS, CCND1, ACTN1	1.7	0.1	RAP2A, RRAS2, RALB, TLN1, CCND1, CNGA1, ACTN1
Prostate Cancer Signaling	1.1	0.0	PIK3C2B, RRAS2, PTPN11, CREB5	1.2	0.1	PIK3CA, RALA, CREBBP, FGFR2, KRAS, PIK3CD, CREB5, CCND1, PTEN	1.8	0.1	RAP2A, HSP90B1, RRAS2, PTPN11, RALB, CREB1, CDKN1A, PDPK1, CCND1, ATM
B Cell Receptor Signaling	1.0	0.0	PIK3C2B, CAMK2D, RRAS2, PTPN11, PIK3AP1, CREB5	1.5	0.1	MAP2K6, PIK3CA, RALA, FCGR2A, CREBBP, MAPK8, FGFR2, KRAS, MAP3K5, MALT1, FCGR2B, CREB5, PTEN, MAP3K12, CDC42, PIK3CD	2.2	0.1	MAP2K6, RAP2A, RALB, MAPK8, PDPK1, MAP3K5, MAP3K12, RRAS2, JUN, PTPN11, INPP5F, CREB1, MEF2C, PIK3AP1, MAP2K3, MAP3K3, ATM
UDP-N-acetyl-D-glucosamine Biosynthesis II	1.0	0.2	UAP1	0.6	0.2	UAP1	1.6	0.3	PGM3, UAP1
Cardiac Hypertrophy Signaling	1.0	0.0	PIK3C2B, PLCE1, RRAS2, PTPN11, GNA12, GNAL, MYL12A	3.4	0.1	PRKACB, MAP2K6, PIK3CA, RALA, EIF2B4, MYL2, CREBBP, IL6R, MAPK8, GNAQ, FGFR2, KRAS, PLCL2, MAP3K5, MAP3K12, RHOQ, PLCE1, ADRB1, RND3, RHOT1, PIK3CD, GNG5, RHOF, MYL3, ADRB2	2.5	0.1	MAP2K6, RAP2A, RALB, MAPK8, PLCL2, MAP3K5, MAP3K12, PLCE1, ADRB1, RRAS2, JUN, PTPN11, CREB1, MEF2C, MAP2K3, MAP3K3, GNAL, GNG12, ADRA1A, ADRB2, ATM
Production of Nitric Oxide and Reactive Oxygen Species in Macrophages	1.0	0.0	PPARA, PIK3C2B, PTPN11, PPP1R3C, JAK2, TNFRSF11B	2.1	0.1	PIK3CA, JAK1, PPP2CA, CREBBP, MAPK8, FGFR2, JAK2, MAP3K5, MAP3K12, PPP1CC, RHOQ, RND3, RHOT1, PPM1L, PPP2R2B, PIK3CD, RHOF, TNFRSF11B	1.0	0.1	MAP3K12, JUN, APOA1, PTPN11, PPP1R3C, PPM1L, MAPK8, PPP2R5E, MAP3K5, JAK2, PCYOX1, MAP3K3, ATM
SAPK/JNK Signaling	1.0	0.0	PIK3C2B, RRAS2, PTPN11, GNA12	1.7	0.1	MAP3K12, PIK3CA, RALA, GADD45A, CDC42, MAPK8, FGFR2, KRAS, PIK3CD, MAP3K5, GNG5	2.4	0.1	MAP3K12, RAP2A, JUN, RRAS2, PTPN11, RALB, MAPK8, MAP3K5, MAP4K4, MAP3K3, HNRNPK, ATM

Canonical Pathways	BNP			LVEDDI			LVEF		
	log (p - value)	Ratio	BNP molecules	log (p - value)	Ratio	LVEDDI molecules	log (p - value)	Ratio	LVEF molecules
Protein Kinase A Signaling	1.0	0.0	CAMK2D, PLCE1, PTPN11, PTPN14, PPP1R3C, PTPN1, PLD6, CREB5, AKAP7, MYL12A	1.6	0.1	PRKACB, MYH10, MYL2, GDDPD1, PDE7A, MYLK3, PDE4A, ACP1, AKAP7, PTEN, YWHAQ, PPP1CC, PLCE1, PTPN1, DUSP7, CDC16, PDE11A, ANAPC11, GNG5, MYL3, PLN, YWHAB, CREBBP, GNAQ, PLD6, PLCL2, CREB5, AKAP13, KDELR3	2.1	0.1	MYH10, PDE3A, PPP1R3C, MYLK3, PDE4A, AKAP7, YWHAQ, DUSP5, PLCE1, PDE7B, PTPN1, CREB1, PDE11A, GNG12, PLN, PTPRK, YWHAB, RYR2, PTCH1, PLCL2, CNGA1, PDE1C, AKAP13, PYGM, PTPN11, DUSP1, CREM, PTPRS, TCF7L2
p53 Signaling	1.0	0.0	PIK3C2B, HDAC9, PTPN11, SERPINE2	1.3	0.1	PIK3CA, KAT2B, GADD45A, COQ8A, MAPK8, FGFR2, PIK3CD, CCND1, PTEN, SERPINE2	2.3	0.1	CASP6, JUN, PTPN11, THBS1, CCNK, CDKN1A, MAPK8, HIPK2, CCND1, ATM, SERPINE2, TP53I3
Endometrial Cancer Signaling	1.0	0.0	PIK3C2B, RRAS2, PTPN11	1.6	0.1	PIK3CA, RALA, FGFR2, KRAS, PIK3CD, CCND1, MLH1, PTEN	1.8	0.1	RAP2A, RRAS2, PTPN11, RALB, PDPK1, CCND1, MLH1, ATM
IL-2 Signaling	1.0	0.0	PIK3C2B, RRAS2, PTPN11	1.6	0.1	PIK3CA, CSNK2A1, JAK1, RALA, MAPK8, FGFR2, PIK3CD, KRAS	1.4	0.1	RAP2A, JUN, RRAS2, PTPN11, RALB, MAPK8, ATM
Signaling by Rho Family GTPases	1.0	0.0	PIK3C2B, PTPN11, PAK6, GNA12, SEPT11, GNAL, MYL12A	2.2	0.1	PIK3CA, NOX4, PAK6, MYL2, MAPK8, GNAQ, FGFR2, SEPT11, MAP3K12, PAK1, RHOQ, ACTA2, RND3, CDC42, RHOT1, PIK3CD, ACTG2, GNG5, RHOF, ARHGEF9, SEPT2, MYL3	0.8	0.1	NOX4, MAPK8, PIP5K1B, SEPT11, PLD1, MAP3K12, JUN, ACTA2, PTPN11, ARPC3, PARD3, GNG12, GNAL, ACTA1, ATM
Apelin Cardiomyocyte Signaling Pathway	1.0	0.0	PIK3C2B, PLCE1, PTPN11, MYL12A	1.6	0.1	PLN, PIK3CA, PLCE1, MYL2, MAPK8, FGFR2, PIK3CD, PLCL2, SLC8A1, ATP2A2, MYL3	0.6	0.1	PLN, PLCE1, PTPN11, MAPK8, PLCL2, ATP2A2, ATM
Calcium Signaling	1.0	0.0	HDAC9, CAMK2D, TPM3, CACNB2, ASPH, CREB5	1.6	0.1	PRKACB, CALR, MYH10, MYH6, MYL2, CREBBP, TRDN, MYH7, MYH11, CREB5, ATP2A2, ACTA2, CASQ1, CACNA2D1, CACNB2, SLC8A1, MYL3	1.6	0.1	RAP2A, MYH10, MYH6, HDAC4, RYR2, TNNT2, TPM1, ATP2A2, RCAN1, ACTA2, CREB1, MEF2C, CACNB2, CACNA2D3, CAMKK2, ACTA1
Adrenomedullin signaling pathway	0.9	0.0	PIK3C2B, PLCE1, C3, RRAS2, PTPN11, NPR3	1.3	0.1	MAP2K6, PRKACB, CRCP, PIK3CA, RALA, MAPK8, MYLK3, GNAQ, FGFR2, KRAS, PLCL2, KCNN2, PLCE1, GUCY1A2, PIK3CD, RXRA	0.9	0.1	MAP2K6, RAP2A, RRAS2, PLCE1, PTPN11, CASP3, RALB, MYLK3, MAPK8, MAP2K3, KCNN2, PLCL2, ATM
Colorectal Cancer Metastasis Signaling	0.9	0.0	PIK3C2B, RRAS2, PTPN11, EGF, JAK2, TLR3, WNT5A	2.1	0.1	PRKACB, SMAD2, PIK3CA, RALA, JAK1, PTGER3, IL6R, MAPK8, TLR8, FGFR2, KRAS, JAK2, CCND1, MLH1, VEGFA, RHOQ, RND3, RHOT1, PIK3CD, GNG5, RHOF, WNT5A	1.4	0.1	RAP2A, SMAD2, CASP3, WNT9A, RALB, MAPK8, JAK2, CCND1, MLH1, RRAS2, JUN, PTPN11, MSH2, TLR3, GNG12, TCF7L2, WNT5A, ATM

Canonical Pathways	BNP		BNP molecules	LVEDDI		LVEDDI molecules	LVEF		LVEF molecules
	log (p-value)	Ratio		log (p-value)	Ratio		log (p-value)	Ratio	
Clathrin-mediated Endocytosis Signaling	0.9	0.0	PIK3C2B, PTPN11, AP1S2, EGF, SH3GL2, SH3KBP1	1.3	0.1	CSNK2A1, PIK3CA, PDGFA, AP1S2, RAB7A, FGFR2, FGF1, VEGFA, ACTA2, CDC42, AMPH, PIK3CD, ACTG2, ITGB6, UBC, SH3KBP1	1.6	0.1	PICALM, AP1S2, AP1M1, RAB7A, SH3GLB1, SH3GL2, PCYOX1, FGF1, APOA1, PTPN11, ACTA2, ARPC3, ITGB6, SH3KBP1, ACTA1, ATM
Virus Entry via Endocytic Pathways	0.9	0.0	PIK3C2B, RRAS2, PTPN11, AP1S2	1.9	0.1	B2M, FYN, PIK3CA, RALA, ACTA2, CDC42, AP1S2, FGFR2, KRAS, PIK3CD, ACTG2, ITGB6	1.8	0.1	RAP2A, RRAS2, ITSN1, PTPN11, ACTA2, AP1S2, AP1M1, RALB, ITGB6, ACTA1, ATM
Myc Mediated Apoptosis Signaling	0.9	0.0	PIK3C2B, RRAS2, PTPN11	1.9	0.1	YWHAQ, PIK3CA, RALA, YWHAB, MAPK8, FGFR2, BID, KRAS, PIK3CD	2.1	0.1	YWHAQ, RAP2A, RRAS2, PTPN11, CASP3, YWHAB, RALB, MAPK8, ATM
ErbB2-ErbB3 Signaling	0.9	0.0	PIK3C2B, RRAS2, PTPN11	1.1	0.1	PIK3CA, RALA, FGFR2, KRAS, PIK3CD, CCND1, PTEN	1.7	0.1	RAP2A, RRAS2, JUN, PTPN11, RALB, PDPK1, CCND1, ATM
Paxillin Signaling	0.9	0.0	PIK3C2B, RRAS2, PAK6, PTPN11	2.2	0.1	PAK1, PIK3CA, RALA, ACTA2, PAK6, CDC42, MAPK8, FGFR2, KRAS, PIK3CD, ACTG2, ITGB6, ACTN1	2.1	0.1	RAP2A, PARVA, RRAS2, PTPN11, ACTA2, RALB, MAPK8, TLN1, ITGB6, ACTN1, ACTA1, ATM
HGF Signaling	0.9	0.0	PIK3C2B, RRAS2, PTPN11, ELF1	1.4	0.1	MAP3K12, PIK3CA, PAK1, RALA, CDC42, MAPK8, FGFR2, KRAS, PIK3CD, MAP3K5, CCND1	2.1	0.1	MAP3K12, RAP2A, JUN, RRAS2, PTPN11, RALB, CDKN1A, MAPK8, MAP3K5, CCND1, MAP3K3, ATM
Glioma Invasiveness Signaling	0.9	0.0	PIK3C2B, RRAS2, PTPN11	1.8	0.1	PIK3CA, RALA, RHOQ, RND3, RHOT1, FGFR2, KRAS, PIK3CD, RHOF	0.9	0.1	RAP2A, RRAS2, PTPN11, TIMP1, RALB, ATM
PKC δ Signaling in T Lymphocytes	0.9	0.0	PIK3C2B, CAMK2D, RRAS2, PTPN11, CACNB2	1.2	0.1	MAP3K12, FYN, PIK3CA, RALA, CACNA2D1, MAPK8, FGFR2, KRAS, CACNB2, PIK3CD, MAP3K5, MALT1, LCP2	1.4	0.1	MAP3K12, RAP2A, RRAS2, JUN, PTPN11, RALB, MAPK8, CD86, CACNB2, MAP3K5, MAP3K3, CACNA2D3, ATM
NGF Signaling	0.9	0.0	PIK3C2B, RRAS2, PTPN11, CREB5	1.7	0.1	MAP3K12, PIK3CA, RALA, CDC42, CREBBP, MAPK8, FGFR2, RPS6KA5, KRAS, PIK3CD, MAP3K5, CREB5	1.6	0.1	MAP3K12, RAP2A, RRAS2, PTPN11, RALB, CREB1, MAPK8, PDPK1, MAP3K5, MAP3K3, ATM
HIF1 α Signaling	0.9	0.0	PIK3C2B, RRAS2, PTPN11, EGLN3	1.3	0.1	VEGFA, PIK3CA, RALA, CUL2, COPS5, CREBBP, MAPK8, FGFR2, KRAS, PIK3CD, ELOC	0.7	0.1	RAP2A, RRAS2, JUN, PTPN11, RALB, MAPK8, EGLN3, ATM
Apelin Endothelial Signaling Pathway	0.8	0.0	PIK3C2B, RRAS2, PTPN11, GNAL	0.4	0.1	PIK3CA, RALA, PRKAA2, MAPK8, FGFR2, PIK3CD, KRAS	1.6	0.1	RAP2A, JUN, RRAS2, HDAC4, PTPN11, PRKAB2, RALB, MAPK8, MEF2C, GNAL, ATM
eNOS Signaling	0.8	0.0	PIK3C2B, PTPN11, LPAR5, SLC7A1, AQP4	0.6	0.1	VEGFA, PRKACB, PIK3CA, GNAQ, GUCY1A2, LPAR5, PRKAA2, FGFR2, PIK3CD, AQP4, LPAR3	1.3	0.1	HSPA4, HSP90B1, PTPN11, CASP3, PRKAB2, LPAR5, PDPK1, AQP4, LPAR3, CNGA1, HSPA2, NOSTRIN, ATM
RhoGDI Signaling	0.8	0.0	PAK6, GNA12, ARHGAP1, GNAL, MYL12A	2.2	0.1	GDI1, PAK6, MYL2, CREBBP, GNAQ, PAK1, RHOQ, RND3, ACTA2, RHOT1, CDC42, ACTG2, GNG5, RHOF, ARHGAP1, ARHGEF9, MYL3	0.0	0.0	ACTA2, ARPC3, PIP5K1B, GNG12, ACTA1, GNAL

Canonical Pathways	BNP		BNP molecules	LVEDDI		LVEDDI molecules	LVEF		LVEF molecules
	log (p - value)	Ratio		log (p - value)	Ratio		log (p - value)	Ratio	
HIPPO signaling	0.8	0.0	DLG1, PPP1R3C, WWTR1	1.6	0.1	YWHAQ, SMAD2, PPP1CC, YWHAB, PPP2CA, WWTR1, PPM1L, PPP2R2B, SKP1	1.4	0.1	YWHAQ, SMAD2, YWHAB, PPP1R3C, WWTR1, PPM1L, PPP2R5E, PARD3
Thyroid Cancer Signaling	0.8	0.0	RRAS2, RET	0.7	0.1	RALA, KRAS, RXRA, CCND1	1.8	0.1	RAP2A, RRAS2, RALB, RET, CCND1, TCF7L2
Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis	0.8	0.0	PIK3C2B, ADAM17, PTPN11, ADAMTS5, TNFRSF11B, WNT5A	0.7	0.1	MAP2K6, SFRP4, PIK3CA, FRZB, MAPK8, FGFR2, MAP3K5, COL1A1, DKK3, BMP7, PIK3CD, BIRC3, TNFRSF11B, WNT5A, BIRC2	2.0	0.1	MAP2K6, SFRP4, SPP1, WNT9A, TAB2, MAPK8, SMAD6, MAP3K5, BMP5, JUN, PTPN11, MAP2K3, BMP7, IL1RAPL1, BIRC3, ADAMTS5, TCF7L2, WNT5A, ATM
PPAR α /RXR α Activation	0.8	0.0	PPARA, PLCE1, RRAS2, LPL, JAK2	1.7	0.1	MAP2K6, PRKACB, SMAD2, RALA, CREBBP, MAPK8, GNAQ, KRAS, PLCL2, JAK2, ADIPOR1, CAND1, PLCE1, LPL, PRKAA2, RXRA	4.0	0.1	MAP2K6, RAP2A, SMAD2, PRKAB2, CD36, RALB, MAPK8, PLCL2, JAK2, CAND1, HSP90B1, JUN, RRAS2, PLCE1, GHR, APOA1, LPL, MEF2C, MAP2K3, IL1RAPL1, MAP4K4
Molecular Mechanisms of Cancer	0.8	0.0	PIK3C2B, RRAS2, CAMK2D, PAK6, PTPN11, GNA12, JAK2, GNAL, WNT5A	2.7	0.1	PRKACB, MAP2K6, FYN, PIK3CA, JAK1, RALA, KRAS, MAP3K5, JAK2, CCND1, DIABLO, PAK1, RHOT1, BID, RHOF, BIRC3, SMAD2, PAK6, CREBBP, CDK6, MAPK8, SMAD7, GNAQ, FGFR2, RHOQ, RND3, CDC42, APH1B, PIK3CD, BMP7, ARHGEF9, BIRC2, WNT5A	2.2	0.1	MAP2K6, RAP2A, TAB2, JAK2, MAP3K5, CCND1, CASP6, JUN, CCND3, HIPK2, BIRC3, ATM, SMAD2, CASP3, WNT9A, PTCH1, RALB, SMAD6, SMAD7, MAPK8, BMP5, RRAS2, PTPN11, CDKN1A, BMP7, MAP2K3, GNAL, BCL2L11, WNT5A
FGF Signaling	0.7	0.0	PIK3C2B, PTPN11, CREB5	1.8	0.1	MAP2K6, PIK3CA, CREBBP, MAPK8, FGFR2, RPS6KA5, PIK3CD, MAP3K5, CREB5, FGF1	1.3	0.1	MAP2K6, PTPN11, CREB1, MAPK8, MAP2K3, MAP3K5, ATM, FGF1
14-3-3-mediated Signaling	0.7	0.0	PIK3C2B, PLCE1, RRAS2, PTPN11	1.4	0.1	YWHAQ, PIK3CA, RALA, PLCE1, YWHAB, MAPK8, FGFR2, KRAS, PIK3CD, MAP3K5, PLCL2, SNCA	2.8	0.1	YWHAQ, RAP2A, PLCE1, RRAS2, JUN, PTPN11, YWHAB, RALB, MAPK8, TUBA4A, TUBA1C, MAP3K5, PLCL2, SNCA, ATM
p70S6K Signaling	0.7	0.0	PIK3C2B, PLCE1, RRAS2, PTPN11	2.0	0.1	PIK3CA, JAK1, RALA, PPP2CA, YWHAB, GNAQ, FGFR2, KRAS, PLCL2, YWHAQ, PLCE1, PPP2R2B, PPM1L, PIK3CD	2.4	0.1	YWHAQ, RAP2A, RRAS2, PLCE1, PTPN11, YWHAB, PPM1L, RALB, PDPK1, PPP2R5E, EEF2K, PLCL2, PLD1, ATM
HMGB1 Signaling	0.7	0.0	PIK3C2B, RRAS2, PTPN11, TNFRSF11B	2.4	0.1	MAP2K6, PIK3CA, RALA, MAPK8, FGFR2, KRAS, HMGB1, KAT2B, RHOQ, RND3, CDC42, RHOT1, PIK3CD, RHOF, TNFRSF11B	1.0	0.1	MAP2K6, RAP2A, JUN, RRAS2, PTPN11, IL17D, RALB, MAPK8, MAP2K3, ATM
LPS-stimulated MAPK Signaling	0.7	0.0	PIK3C2B, RRAS2, PTPN11	1.7	0.1	MAP2K6, PIK3CA, PAK1, RALA, CDC42, MAPK8, FGFR2, KRAS, PIK3CD, MAP3K5	2.5	0.1	MAP2K6, RAP2A, JUN, RRAS2, PTPN11, RALB, CREB1, MAPK8, MAP2K3, MAP3K5, ATM

Canonical Pathways	BNP		BNP molecules	LVEDDI		LVEDDI molecules	LVEF		LVEF molecules
	log (p - value)	Ratio		log (p - value)	Ratio		log (p - value)	Ratio	
Phospholipase C Signaling	0.7	0.0	HDAC9, PLCE1, RRAS2, PLD6, CREB5, MYL12A	2.0	0.1	FYN, RALA, MPRIP, MYL2, FCGR2A, CREBBP, GNAQ, KRAS, PLD6, CREB5, FCGR2B, TGM2, PLCE1, RHOQ, RND3, RHOT1, GNG5, RHOF, ARHGEF9, LCP2, MYL3	0.3	0.0	TGM2, RAP2A, RRAS2, PLCE1, HDAC4, MPRIP, RALB, CREB1, MEF2C, GNG12, PLD1
Xenobiotic Metabolism Signaling	0.7	0.0	PIK3C2B, CAMK2D, RRAS2, PTPN11, MAF, NRIP1, ALDH7A1	0.5	0.1	MAP2K6, PIK3CA, RALA, SULT1C2, PPP2CA, CREBBP, MAF, MAPK8, FGFR2, KRAS, MAP3K5, MAP3K12, ALDH3A2, PPM1L, PPP2R2B, PIK3CD, RXRA	1.5	0.1	MAP2K6, RAP2A, GSTM1, ABCB1, HDAC4, RALB, MAPK8, CHST12, MAP3K5, MAP3K12, HSP90B1, ALDH1L1, RRAS2, UST, PTPN11, PPM1L, ALDH18A1, MAP2K3, PPP2R5E, MAP3K3, ATM
Human Embryonic Stem Cell Pluripotency	0.7	0.0	S1PR3, PIK3C2B, PTPN11, WNT5A	0.4	0.1	SMAD2, PIK3CA, PDGFA, SMAD7, FGFR2, PIK3CD, BMP7, WNT5A	1.5	0.1	S1PR3, SMAD2, PTPN11, WNT9A, SMAD7, SMAD6, PDPK1, BMP7, BMP5, TCF7L2, WNT5A, ATM
ILK Signaling	0.7	0.0	PIK3C2B, PTPN11, FERMT2, CREB5, DSP	9.2	0.2	MAP2K6, MYH10, PIK3CA, MYH6, FN1, MYL2, PPP2CA, MYH11, RICTOR, CCND1, PTEN, VEGFA, TGFB1I1, RHOT1, PPM1L, ACTG2, RHOF, MYL3, ACTN1, DSP, CREBBP, MAPK8, FGFR2, RPS6KA5, MYH7, CREB5, RHOQ, ACTA2, RND3, CDC42, PPP2R2B, PIK3CD, ITGB6	3.7	0.1	MAP2K6, MYH10, MYH6, PARVA, FN1, CASP3, MAPK8, PDPK1, CCND1, JUN, PTPN11, ACTA2, CREB1, PPM1L, ILKAP, PPP2R5E, ITGB6, DSP, ACTN1, ACTA1, ATM
Hereditary Breast Cancer Signaling	0.7	0.0	PIK3C2B, HDAC9, RRAS2, PTPN11	3.3	0.1	PIK3CA, RALA, POLR2D, FANCG, CREBBP, CDK6, POLR2H, FGFR2, KRAS, RFC5, CCND1, MLH1, PTEN, GADD45A, XPC, PIK3CD, BLM, UBC	1.7	0.1	RAP2A, BRD7, RRAS2, HDAC4, PTPN11, MSH2, RALB, CDKN1A, XPC, BLM, CCND1, MLH1, ATM
Neuroinflammation Signaling Pathway	0.6	0.0	PIK3C2B, PTPN11, GABRA4, GABRB1, TLR3, JAK2, CREB5	1.4	0.1	B2M, PIK3CA, NOX4, JAK1, GABRA4, CREBBP, IL6R, MAPK8, TLR8, FGFR2, JAK2, CREB5, GABRE, APP, HMGB1, SOD2, GABRB1, APH1B, PIK3CD, BIRC3, SNCA, BIRC2, IRAK2	0.0	0.0	NOX4, CASP3, GABRA4, MAPK8, JAK2, JUN, PTPN11, CREB1, GABRB1, CD86, TLR3, SNCA, BIRC3, ATM
Endocannabinoid Cancer Inhibition Pathway	0.6	0.0	PIK3C2B, PTPN11, CREB5, GNAL	1.0	0.1	VEGFA, PRKACB, MAP2K6, PIK3CA, CREBBP, CASQ1, GNAQ, PRKAA2, FGFR2, PIK3CD, CREB5, CCND1	1.9	0.1	MAP2K6, PRKAB2, CASP3, CCND1, CASP6, CCND3, PTPN11, CREB1, CDKN1A, MAP2K3, CAMKK2, GNAL, TCF7L2, ATM
Valine Degradation I	0.6	0.1	BCKDHB	1.3	0.2	HIBADH, HADHB, DBT	1.4	0.2	ABAT, HIBADH, HADHB
Induction of Apoptosis by HIV1	0.6	0.0	SLC25A5, TNFRSF11B	2.6	0.1	DIABLO, SLC25A4, MAPK8, BID, MAP3K5, SLC25A5, BIRC3, BIRC2, TNFRSF11B	0.9	0.1	CASP3, MAPK8, MAP3K5, SLC25A5, BIRC3

Canonical Pathways	BNP		LVEDDI - log (p - value)	Ratio		LVEF - log (p - value)	Ratio		
	log (p - value)	Ratio BNP		LVEDDI	LVEDDI molecules		LVEF	LVEF molecules	
Actin Nucleation by ARP-WASP Complex	0.6	0.0	RRAS2, GNA12	1.5	0.1	RHOQ, RALA, RND3, RHOT1, CDC42, KRAS, RHOF	0.5	0.1	RAP2A, RRAS2, RALB, ARPC3
Ephrin A Signaling	0.6	0.0	PIK3C2B, PTPN11	1.5	0.1	FYN, PAK1, PIK3CA, CDC42, FGFR2, PIK3CD, EPHA4	0.0	0.0	PTPN11, ATM
VEGF Signaling	0.6	0.0	PIK3C2B, RRAS2, PTPN11	1.7	0.1	VEGFA, PIK3CA, RALA, EIF1, EIF2B4, ACTA2, FGFR2, KRAS, PIK3CD, ACTG2, ACTN1	0.9	0.1	RAP2A, RRAS2, ACTA2, PTPN11, RALB, ACTN1, ACTA1, ATM
Protein Ubiquitination Pathway	0.6	0.0	UBE2H, DNAJC19, USP47, DNAJC14, DNAJC13, UCHL5	4.5	0.1	B2M, USP14, PSMD7, UBE2Z, FBXW7, UBE2W, DNAJC15, SKP1, ELOC, UBE2F, USP48, PSMD10, UBE2B, DNAJC4, UBE2K, UCHL5, ANAPC11, BIRC3, AMFR, HSPA4L, DNAJC27, USP30, UBE2H, CUL2, PSMD2, DNAJC14, UBC, UBE2D3, DNAJB5, BIRC2	2.3	0.1	USP28, USP15, UBE4B, DNAJB4, USP53, HSPH1, UBR2, UBE2W, UBE2S, HSPA2, HSPA4, UBE2L3, HSP90B1, UBE2D2, UBE2J1, UBE2H, USP47, UCHL5, BIRC3, UBE2Q2, HSPA4L, UBE2J2
Tight Junction Signaling	0.6	0.0	YBX3, GOSR1, GOSR2, TNFRSF11B	4.1	0.1	PRKACB, MYH10, MYH6, MYL2, PPP2CA, MPP5, YBX3, MYH7, MYH11, VAMP2, PTEN, NSF, ACTA2, CDC42, PPM1L, PPP2R2B, ACTG2, SPTAN1, CSTF3, MYL3, TNFRSF11B	0.9	0.1	MYH10, NSF, MYH6, JUN, ACTA2, PPM1L, YBX3, PPP2R5E, GOSR2, CSTF3, ACTA1
Caveolar-mediated Endocytosis Signaling	0.5	0.0	PTPN1, EGF	1.2	0.1	B2M, FYN, ACTA2, COPA, PTPN1, ACTG2, ITGB6	1.4	0.1	ITSN1, ACTA2, PTPN1, COPB2, ITGB6, COPB1, ACTA1
Germ Cell-Sertoli Cell Junction Signaling	0.5	0.0	PIK3C2B, RRAS2, PAK6, PTPN11	3.2	0.1	MAP2K6, PIK3CA, RALA, PAK6, MAPK8, FGFR2, KRAS, MAP3K5, MAP3K12, PAK1, RHOQ, ACTA2, RND3, CDC42, RHOT1, PIK3CD, ACTG2, CLINT1, RHOF, ACTN1	2.5	0.1	MAP2K6, RAP2A, RALB, MAPK8, TUBA4A, PDPK1, MAP3K5, MAP3K12, RRAS2, PTPN11, ACTA2, TUBA1C, MAP2K3, MAP3K3, ACTN1, ACTA1, ATM
Fc Epsilon RI Signaling	0.5	0.0	PIK3C2B, RRAS2, PTPN11	0.8	0.1	MAP2K6, FYN, PIK3CA, RALA, MAPK8, FGFR2, KRAS, PIK3CD, LCP2	1.6	0.1	MAP2K6, RAP2A, RRAS2, INPP5F, PTPN11, RALB, MAPK8, FCER1A, PDPK1, MAP2K3, ATM
Hypoxia Signaling in the Cardiovascular System	0.5	0.0	UBE2H, CREB5	3.6	0.2	VEGFA, UBE2B, UBE2H, COP55, CREBBP, UBE2K, UBE2Z, UBE2W, CREB5, UBE2D3, UBE2F, PTEN	4.0	0.2	UBE2L3, HSP90B1, UBE2D2, UBE2J1, JUN, UBE2H, CREB1, UBE2W, UBE2S, UBE2Q2, UBE2J2, ATM
Ethanol Degradation IV	0.5	0.0	ALDH7A1	1.5	0.2	ACSS3, ALDH3A2, CYGB, ACSL1	0.5	0.1	ALDH1L1, ACSL1
Sertoli Cell-Sertoli Cell Junction Signaling	0.5	0.0	SPTBN1, DLG1, RRAS2, YBX3	1.4	0.1	PRKACB, RALA, MAPK8, YBX3, KRAS, MAP3K5, PTEN, MAP3K12, ACTA2, CDC42, GUCY1A2, ACTG2, SPTAN1, CLINT1, ACTN1	2.1	0.1	SPTBN1, RAP2A, RALB, MAPK8, TUBA4A, YBX3, MAP3K5, MAP3K12, JUN, RRAS2, ACTA2, MAP2K3, TUBA1C, MAP3K3, ACTN1, ACTA1
Agrin Interactions at Neuromuscular Junction	0.5	0.0	RRAS2, PAK6	2.0	0.1	PAK1, RALA, PAK6, ACTA2, CDC42, LAMA2, MAPK8, KRAS, ACTG2	1.7	0.1	RAP2A, RRAS2, JUN, ACTA2, RALB, LAMA2, MAPK8, ACTA1

Canonical Pathways	BNP		BNP molecules	LVEDDI		LVEDDI molecules	LVEF		LVEF molecules
	log (p-value)	Ratio		log (p-value)	Ratio		log (p-value)	Ratio	
PI3K/AKT Signaling	0.5	0.0	RRAS2, JAK2, MCL1	3.2	0.1	RHEB, PIK3CA, JAK1, RALA, PPP2CA, YWHAB, KRAS, MAP3K5, JAK2, CCND1, PTEN, YWHAQ, PPM1L, PPP2R2B, PIK3CD, MCL1	3.2	0.1	RAP2A, YWHAB, RALB, PDPK1, MAP3K5, JAK2, CCND1, YWHAQ, HSP90B1, RRAS2, INPP5F, PPM1L, CDKN1A, PPP2R5E, MCL1
Cellular Effects of Sildenafil (Viagra)	0.5	0.0	PLCE1, NPPA, MYL12A	3.1	0.1	PRKACB, MYH10, MYH6, MPRIP, MYL2, PDE4A, MYH7, PLCL2, KCNN2, MYH11, PLCE1, ACTA2, GUCY1A2, ACTG2, NPPA, MYL3	1.8	0.1	MYH10, MYH6, PLCE1, MPRIP, ACTA2, PDE3A, PDE4A, KCNN2, PLCL2, NPPA, ACTA1, PDE1C
Androgen Signaling	0.4	0.0	GNA12, CACNB2, GNAL	2.1	0.1	PRKACB, CALR, POLR2D, CREBBP, GNAQ, POLR2H, GTF2F1, CCND1, NCOA4, TGFBI1, KAT2B, CACNA2D1, CACNB2, GNG5	0.4	0.1	HSPA4, JUN, CACNB2, CACNA2D3, CCND1, GNG12, GNAL
Iron homeostasis signaling pathway	0.4	0.0	ATP6V1D, EGF, JAK2	2.1	0.1	SMAD2, JAK1, ATP6V1C1, PDGFA, IL6R, HJV, JAK2, SKP1, LYRM4, HP, FECH, BMP7, ISCU, ATP6V0E1	0.0	0.0	SMAD2, BMP7, JAK2, HJV, BMP5
Cardiac I ² -adrenergic Signaling	0.4	0.0	PPP1R3C, PLD6, AKAP7	3.7	0.1	PRKACB, PLN, GDDPD1, PDE7A, PPP2CA, PPP1R1A, PDE4A, PLD6, AKAP7, ATP2A2, AKAP13, PPP1CC, ADRB1, PPM1L, PPP2R2B, SLC8A1, GNG5, PDE11A	3.3	0.1	PLN, PPP1R1A, PDE3A, PPP1R3C, RYR2, PDE4A, ATP2A2, AKAP7, PDE1C, AKAP13, ADRB1, PDE7B, PPM1L, PPP2R5E, PDE11A, GNG12
Small Cell Lung Cancer Signaling	0.4	0.0	PIK3C2B, PTPN11	1.6	0.1	PIK3CA, CDK6, FGFR2, BID, PIK3CD, RXRA, CCND1, BIRC2, PTEN	0.0	0.0	PTPN11, CCND1, ATM
Regulation of Actin-based Motility by Rho	0.4	0.0	PAK6, MYL12A	2.9	0.1	PAK1, RHOQ, MPRIP, PAK6, MYL2, ACTA2, RND3, CDC42, RHOT1, ACTG2, RHOF, MYL3	0.4	0.1	MPRIP, ACTA2, ARPC3, PIP5K1B, ACTA1
mTOR Signaling	0.4	0.0	PIK3C2B, RRAS2, PTPN11, PLD6	7.5	0.1	PIK3CA, RALA, RPS3A, PPP2CA, RPS27, RPS23, KRAS, RICTOR, RPS11, VEGFA, RPS28, RPS20, RHOT1, PPM1L, PRKAA2, RHOF, RPS17, RPS19, RHEB, FGFR2, RPS6KA5, RPS21, PLD6, EIF3M, RPS4Y1, RHOQ, RND3, RPS27L, PPP2R2B, RPS15A, PIK3CD	0.8	0.1	RAP2A, PRKAB2, RALB, PDPK1, PLD1, RRAS2, PTPN11, PPM1L, EIF4A1, RPS25, PPP2R5E, EIF4B, ATM
Death Receptor Signaling	0.4	0.0	LMNA, PARP12	2.2	0.1	DIABLO, ACTA2, CRADD, MAPK8, BID, LMNA, MAP3K5, ACTG2, SPTAN1, BIRC3, BIRC2	1.2	0.1	CASP6, ACTA2, CASP3, MAPK8, MAP3K5, MAP4K4, BIRC3, ACTA1
Sumoylation Pathway	0.3	0.0	RANBP2, ZEB1	2.6	0.1	CTBP1, GDI1, RHOQ, RND3, RHOT1, CREBBP, MAPK8, MAP3K5, ZEB1, RFC5, RHOF, SNCA	0.4	0.1	JUN, MAPK8, RAN, MAP3K5, SNCA

Canonical Pathways	BNP		BNP molecules	LVEDDI		LVEDDI molecules	LVEF		LVEF molecules
	log (p - value)	Ratio		log (p - value)	Ratio		log (p - value)	Ratio	
ATM Signaling	0.3	0.0	ZEB1, CREB5	3.6	0.1	PPP2CA, CREBBP, MAPK8, ZEB1, CBX5, CREB5, RNF168, PPP1CC, GADD45A, PPP2R2B, PPM1L, BID, TP53BP1, BLM	1.9	0.1	JUN, CREB1, CDKN1A, PPM1L, RBBP8, MAPK8, TP53BP1, PPP2R5E, BLM, ATM
AMPK Signaling	0.3	0.0	PIK3C2B, PTPN11, AK4, CREB5	1.6	0.1	PRKACB, RAB27A, PIK3CA, ACACB, RAB9B, PPP2CA, CREBBP, RAB7A, FGFR2, CREB5, CCND1, KAT2B, ADRB1, PPM1L, PPP2R2B, PRKAA2, PIK3CD, ADRB2	2.7	0.1	PRKAB2, RAB7A, PDPK1, CCND1, RAB22A, BRD7, ADRB1, PTPN11, CDKN1A, PPM1L, CREB1, PPM1A, ILKAP, MAP2K3, PPP2R5E, EEF2K, CAMKK2, ADRA1A, ADRB2, ATM
Mechanisms of Viral Exit from Host Cells	0.3	0.0	SH3GL2	1.3	0.1	CHMP4A, ACTA2, CHMP4C, ACTG2, VPS4A	1.0	0.1	ACTA2, SH3GLB1, SH3GL2, ACTA1
Role of PKR in Interferon Induction and Antiviral Response	0.3	0.0	TLR3	0.0	0.0	MAP2K6, BID	1.5	0.1	MAP2K6, CASP3, TAB2, MAP2K3, TLR3
Regulation of eIF4 and p70S6K Signaling	0.3	0.0	PIK3C2B, RRAS2, PTPN11	5.2	0.1	RPS19, PIK3CA, EIF2B4, RALA, RPS3A, PPP2CA, RPS27, RPS23, FGFR2, RPS21, KRAS, RPS11, EIF3M, RPS28, RPS4Y1, EIF1, RPS20, RPS27L, PPM1L, PPP2R2B, PIK3CD, RPS15A, RPS17	1.2	0.1	PABPC1, RAP2A, RRAS2, EIF4EBP2, PTPN11, RALB, PPM1L, EIF4A1, PDPK1, RPS25, PPP2R5E, ATM
tRNA Splicing	0.3	0.0	PLD6	2.4	0.2	TSEN15, PDE7A, GPD1, PDE4A, PLD6, TSEN2, PDE11A	2.0	0.1	PDE7B, TSEN34, PDE3A, PDE4A, PDE11A, PDE1C
RANK Signaling in Osteoclasts	0.3	0.0	PIK3C2B, PTPN11	1.2	0.1	MAP2K6, MAP3K12, PIK3CA, MAPK8, FGFR2, PIK3CD, MAP3K5, BIRC3, BIRC2	1.7	0.1	MAP2K6, MAP3K12, JUN, PTPN11, TAB2, MAPK8, MAP3K5, MAP3K3, BIRC3, ATM
EIF2 Signaling	0.3	0.0	PIK3C2B, RPL27A, RRAS2, PTPN11	12.3	0.2	RPL24, EIF2AK4, PIK3CA, RALA, EIF2B4, RPS3A, RPS27, RPS23, RPL39, KRAS, CCND1, RPL7, RPS11, RPS28, VEGFA, RPL14, PPP1CC, EIF1, RPS20, ACTG2, RPS17, RPL32, RPS19, NOX4, RPL30, FGFR2, RPL23, RPS21, RPL37A, EIF3M, RPL10A, RPL27, RPS4Y1, ACTA2, RPS27L, PPP1R15A, RPL5, PIK3CD, RPS15A, RPL37, RPL38	1.0	0.1	PABPC1, RAP2A, RPL22, NOX4, RRAS2, ACTA2, PTPN11, RPL36A, RALB, EIF4A1, PDPK1, RPS25, CCND1, ACTA1, ATM
Cholecystokinin/Gastrin-mediated Signaling	0.3	0.0	RRAS2, GNA12	1.4	0.1	MAP2K6, RALA, RHOQ, RND3, RHOT1, GNAQ, MAPK8, KRAS, EPHA4, RHOF	1.3	0.1	MAP2K6, RAP2A, JUN, RRAS2, RALB, CREM, MAPK8, MAP2K3, MEF2C
TNFR1 Signaling	0.3	0.0	PAK6	2.5	0.2	PAK1, CRADD, PAK6, CDC42, MAPK8, BID, BIRC3, BIRC2	1.1	0.1	CASP6, JUN, CASP3, MAPK8, BIRC3

Canonical Pathways	BNP		BNP molecules	LVEDDI		LVEDDI molecules	LVEF		LVEF molecules
	log (p-value)	Ratio		log (p-value)	Ratio		log (p-value)	Ratio	
Hepatic Fibrosis / Hepatic Stellate Cell Activation	0.2	0.0	EGF, EDNRA, TNFRSF11B	4.8	0.1	MYH10, SMAD2, COL5A2, MYH6, FN1, COL4A1, MYL2, PDGFA, IL6R, SMAD7, FGFR2, MYH7, COL4A3BP, MYH11, FGF1, VEGFA, COL1A2, COL1A1, ACTA2, COL4A4, COL27A1, MYL3, COL3A1, TNFRSF11B	4.5	0.1	MYH10, SMAD2, COL5A2, MYH6, FN1, CTGF, COL4A1, SMAD7, BAMBI, COL4A3BP, COL28A1, FGF1, COL1A2, COL16A1, COL21A1, COL6A3, ACTA2, TIMP1, IGFBP3, IL1RAPL1, COL27A1, COL3A1
CD27 Signaling in Lymphocytes	0.2	0.0	SIVA1	0.9	0.1	MAP2K6, MAP3K12, MAPK8, BID, MAP3K5	2.6	0.2	MAP2K6, MAP3K12, JUN, CASP3, MAPK8, MAP2K3, MAP3K5, MAP3K3
Unfolded protein response	0.2	0.0	UBXN4	1.7	0.1	SEL1L, CALR, PPP1R15A, MAPK8, DNAJA2, MAP3K5, AMFR	1.9	0.1	HSPA4, HSP90B1, UBXN4, HSPH1, MAPK8, MAP3K5, HSPA2
Mitochondrial Dysfunction	0.0	0.0	COX11	12.3	0.2	NDUFA4, ATP5MC1, COX6C, PRDX5, NDUFB5, NDUFB8, ATP5S, NDUFA1, ATP5F1E, NDUFB10, PDHA1, SOD2, NDUFS6, ATP5PB, ATP5MC3, COX4I1, MT-CO1, ATP5PF, ATP5F1A, GLRX2, ATP5PO, MAPK8, MT-ND4, UQCR11, NDUFB1, VDAC3, APP, UQCRB, ATP5F1C, COX11, NDUFA6, COX5A, APH1B, SNCA, NDUFB2	2.4	0.1	ATP5PF, COX17, CASP3, PRDX5, COX7C, NDUFV3, MAPK8, SDHC, ATP5F1E, UQCRB, COX11, NDUFB6, MT-CO3, CYB5A, SNCA, ATP5ME
Oxidative Phosphorylation	0.0	0.0	COX11	10.9	0.2	NDUFA4, ATP5MC1, COX6C, NDUFB5, NDUFB8, ATP5S, NDUFA1, ATP5F1E, NDUFB10, NDUFS6, ATP5PB, ATP5MC3, COX4I1, ATP5PF, MT-CO1, ATP5F1A, ATP5PO, MT-ND4, UQCR11, NDUFB1, UQCRB, ATP5F1C, COX11, NDUFA6, COX5A, NDUFB2	2.5	0.1	ATP5PF, COX17, COX11, NDUFV3, COX7C, NDUFB6, MT-CO3, SDHC, CYB5A, ATP5ME, ATP5F1E, UQCRB
Sirtuin Signaling Pathway	0.0	0.0	PPARA, POLR1E, SLC25A5	6.4	0.1	NDUFA4, TOMM40, TIMM13, ATP5MC1, NDUFB5, NDUFB8, NDUFA1, SIRT4, ATP5F1E, NDUFB10, PDHA1, TOMM7, SOD2, GADD45A, XPC, NDUFS6, PRKAA2, ATP5PB, PGK1, ATG12, ATP5PF, SLC25A4, POLR1B, ATP5F1A, POLR1E, TIMM8B, MT-ND4, NDUFB1, VDAC3, APP, TIMM17A, ATP5F1C, NDUFA6, TP53BP1, SLC25A5, NDUFB2	1.6	0.1	PPID, ATP5PF, POLR1B, NDUFV3, POLR1E, TUBA4A, RBBP8, SMARCA5, PGAM2, SDHC, SIRT4, ATP5F1E, JUN, GABARAPL1, XPC, NDUFB6, TUBA1C, NAMPT, TP53BP1, SLC25A5, BCL2L11

Canonical Pathways	BNP		BNP molecules	LVEDDI		LVEDDI molecules	LVEF		LVEF molecules
	log (p-value)	Ratio		log (p-value)	Ratio		log (p-value)	Ratio	
GP6 Signaling Pathway	0.0	0.0	PIK3C2B, PTPN11	2.6	0.1	FYN, PIK3CA, COL5A2, COL4A1, LAMA2, FGFR2, COL4A3BP, COL1A2, COL1A1, COL4A4, PIK3CD, COL27A1, LCP2, RASGRP2, COL3A1	3.0	0.1	COL5A2, COL4A1, LAMA2, PDPK1, TLN1, COL4A3BP, COL28A1, COL1A2, COL16A1, COL21A1, PTPN11, COL6A3, COL27A1, COL3A1, ATM
Epithelial Adherens Junction Signaling	0.0	0.0	RRAS2, EGF	2.6	0.1	MYH10, MYH6, RALA, MYL2, KRAS, MYH7, MYH11, PTEN, FGF1, MAGI1, ACTA2, CDC42, ACTG2, CLINT1, ACTN1, MYL3	2.1	0.1	RAP2A, MYH10, MYH6, RALB, TUBA4A, FGF1, RRAS2, ACTA2, ARPC3, TUBA1C, PARD3, TCF7L2, ACTN1, ACTA1
Inhibition of Angiogenesis by TSP1	0.0	NA	NA	2.2	0.2	VEGFA, FYN, CD47, SDC2, MAPK8, GUCY1A2	2.4	0.2	JUN, CASP3, THBS1, SDC2, CD36, MAPK8
Acetate Conversion to Acetyl-CoA	0.0	NA	NA	1.9	0.5	ACSS3, ACSL1	0.8	0.3	ACSL1
Heme Biosynthesis from Uroporphyrinogen-III	0.0	NA	NA	1.9	0.5	PPOX, FECH	0.0	NA	NA
TGF- β Signaling	0.0	0.0	RRAS2	1.8	0.1	MAP2K6, SMAD2, RALA, CDC42, SKI, CREBBP, SMAD7, MAPK8, KRAS, BMP7	2.5	0.1	MAP2K6, SMAD2, RAP2A, JUN, RRAS2, RALB, SMAD7, SMAD6, MAPK8, MAP2K3, BMP7
Assembly of RNA Polymerase III Complex	0.0	NA	NA	1.6	0.2	GTF3C5, GTF3A, BRF2	0.0	NA	NA
RAR Activation	0.0	0.0	DHRS7C, JAK2, NRIP1	1.6	0.1	PRKACB, SMAD2, CSNK2A1, PIK3CA, CREBBP, MAPK8, SMAD7, DHRS7C, MAP3K5, JAK2, PTEN, PRMT1, VEGFA, KAT2B, PIK3CD, RXRA	1.1	0.1	SMAD2, PRMT2, SMAD6, SMAD7, MAPK8, DHRS7C, PDPK1, MAP3K5, JAK2, BRD7, JUN, DUSP1, IGFBP3
Cell Cycle Regulation by BTG Family Proteins	0.0	NA	NA	1.5	0.1	PPP2CA, PPP2R2B, PPM1L, CCND1, PRMT1	1.1	0.1	PPM1L, BTG1, PPP2R5E, CCND1
Apelin Liver Signaling Pathway	0.0	NA	NA	1.4	0.2	COL1A2, COL1A1, MAPK8, COL3A1	1.0	0.1	COL1A2, MAPK8, COL3A1
Fc γ Receptor-mediated Phagocytosis in Macrophages and Monocytes	0.0	0.0	PLD6	1.4	0.1	FYN, PAK1, ACTA2, CDC42, FCGR2A, PLD6, ACTG2, LCP2, PTEN	0.4	0.1	ACTA2, ARPC3, TLN1, ACTA1, PLD1
Pyridoxal 5'-phosphate Salvage Pathway	0.0	NA	NA	1.4	0.1	MAP2K6, PAK1, PNPO, PRKAA2, MAPK8, CDK6, GRK5	0.5	0.1	MAP2K6, SGK1, MAPK8, MAP2K3
Acetyl-CoA Biosynthesis I (Pyruvate Dehydrogenase)	0.0	NA	NA	1.4	0.3	PDHA1, DBT	0.0	NA	NA
Wnt/ β -catenin Signaling	0.0	0.0	WNT5A	1.4	0.1	SFRP4, CSNK2A1, GJA1, FRZB, DKK3, FRAT1, PPP2CA, PPP2R2B, PPM1L, CREBBP, GNAQ, UBC, CCND1, WNT5A	0.4	0.1	SFRP4, JUN, FRAT1, WNT9A, PPM1L, PPP2R5E, CCND1, TCF7L2, WNT5A
Superpathway of Cholesterol Biosynthesis	0.0	NA	NA	1.3	0.1	NSDHL, EBP, ACAT1, HADHB	0.0	0.0	HADHB
Sulfite Oxidation IV	0.0	NA	NA	1.3	1.0	SUOX	0.0	NA	NA
PTEN Signaling	0.0	0.0	RRAS2	1.1	0.1	PIK3CA, CSNK2A1, RALA, MAGI1, CDC42, FGFR2, KRAS, PIK3CD, CCND1, PTEN	1.3	0.1	RAP2A, RRAS2, GHR, INPP5F, CASP3, RALB, CDKN1A, PDPK1, CCND1, BCL2L11
Endoplasmic Reticulum Stress Pathway	0.0	NA	NA	1.1	0.1	CALR, MAPK8, MAP3K5	1.9	0.2	HSP90B1, CASP3, MAPK8, MAP3K5
BMP signaling pathway	0.0	0.0	RRAS2	1.0	0.1	PRKACB, RALA, CREBBP, MAPK8, SMAD7, KRAS, BMP7	2.4	0.1	RAP2A, JUN, RRAS2, RALB, CREB1, SMAD7, SMAD6, MAPK8, BMP7, BMP5
Parkinson's Signaling	0.0	NA	NA	0.7	0.1	MAPK8, SNCA	1.5	0.2	CASP3, MAPK8, SNCA
GADD45 Signaling	0.0	NA	NA	0.6	0.1	GADD45A, CCND1	2.0	0.2	CCND3, CDKN1A, CCND1, ATM

Canonical Pathways	BNP		BNP molecules	LVEDDI		LVEDDI molecules	LVEF		LVEF molecules
	log (p - value)	Ratio		log (p - value)	Ratio		log (p - value)	Ratio	
Remodeling of Epithelial Adherens Junctions	0.0	0.0	MAPRE2	0.6	0.1	RALA, ACTA2, RAB7A, ACTG2, ACTN1	1.5	0.1	ACTA2, RAB7A, TUBA4A, ARPC3, TUBA1C, ACTN1, ACTA1
Osteoarthritis Pathway	0.0	0.0	S1PR3, CREB5, ADAMTS5	0.5	0.1	HMGB1, VEGFA, SMAD2, FN1, FRZB, ANKH, CREBBP, CASQ1, SMAD7, PRKAA2, CREB5, HTRA1	2.9	0.1	SMAD2, SPP1, HDAC4, FN1, PRKAB2, CASP3, ITLN1, PTCH1, SMAD7, SMAD6, S1PR3, CASP6, CREB1, PTH1R, MEF2C, NAMPT, IL1RAPL1, HTRA1, ADAMTS5, TCF7L2
Role of MAPK Signaling in the Pathogenesis of Influenza	0.0	0.0	RRAS2	0.5	0.1	MAP2K6, RALA, MAPK8, KRAS, MAP3K5	1.6	0.1	MAP2K6, RAP2A, RRAS2, CASP3, RALB, MAPK8, MAP2K3, MAP3K5
Role of BRCA1 in DNA Damage Response	0.0	NA	NA	0.4	0.1	GADD45A, FANCG, BLM, RFC5, MLH1	1.6	0.1	BRD7, MSH2, CDKN1A, RBBP8, BLM, BRCC3, MLH1, ATM
Glycogen Degradation II	0.0	NA	NA	0.3	0.1	PGM1	1.7	0.2	PYGM, PGM3, PGM5
Glycogen Degradation III	0.0	NA	NA	0.3	0.1	PGM1	1.6	0.2	PYGM, PGM3, PGM5
Dermatan Sulfate Degradation (Metazoa)	0.0	NA	NA	0.2	0.1	GM2A	1.4	0.2	IDS, GM2A, HEXB
Adenine and Adenosine Salvage VI	0.0	NA	NA	0.0	NA	NA	1.3	1.0	ADK

Top Canonical Pathways are given for genes significantly ($p < 0.01$) correlating with LVEF, LVEDDI or BNP. The p -value of the Fisher's exact test and the ratio of the number of genes from the list that maps to the pathway divided by the total number of the genes that map to the same pathway were given to return the measure of association in IPA. Additionally, the enrichment of genes as indicated by the negative log (p -value) was colored. Dark red indicates high enrichment of genes and white color of the negative log (p -value) indicates no enrichment.