

Supplemental Table 2: Sexually dimorphic genes were annotated according to their biological process and molecular function and analysed for significantly enriched categories (FDR <5%, fold-change >2; Fisher's exact test, $p < 0.05$).

Overview

Table	Dataset	Description
a.	MoAg2	Mouse hearts, 2 month old, Agilent platform, Biological Process
b.	MoAg2	Mouse hearts, 2 month old, Agilent platform, Molecular Function
c.	MoAg8	Mouse hearts, 8 month old, Agilent platform, Biological Process
d.	MoAg8	Mouse hearts, 8 month old, Agilent platform, Molecular Function
e.	HuAg<40	Human myocardium of donors <40 years old, Agilent platform, Biological Process
f.	HuAg<40	Human myocardium of donors <40 years old, Agilent platform, Molecular Function
g.	HuAg50-65	Human myocardium of donors 50-65 years old, Agilent platform, Biological Process
h.	HuAg50-65	Human myocardium of donors 50-65 years old, Agilent platform, Molecular Function
i.	HuAffy	Human myocardium*, Affymetrix platform, Biological Process
j.	HuAffy	Human myocardium*, Affymetrix platform, Molecular Function

* data obtained from Cardiogenomics, NHLBI Program for Genomic Applications, Harvard Medical School. URL: <http://www.cardiogenomics.org>

a. Mouse hearts, 2 months old, Agilent platform, Biological Process

Category	Term	Count	%	PValue	Genes
GOTERM_BP_ALL	calcium-mediated signaling	4	5.13%	0.00017	Cd4, Cd3e, Lat, Cd8a,
GOTERM_BP_ALL	cell activation	9	11.54%	0.00002	Cd4, Ccnd3, Sftpd, Cd5, Cd3e, Rag1, Lat, Cd3g, Cd8a,
GOTERM_BP_ALL	cellular defense response	5	6.41%	0.00142	Cd4, Sftpd, Tcrb-V13, Lat, Cd8a,
GOTERM_BP_ALL	chemotaxis	4	5.13%	0.04144	Sftpd, Ccr7, Ccl25, Ccl28,
GOTERM_BP_ALL	defense response	17	21.79%	0.00000	Ccnd3, Cd4, Cd5, Tacstd1, Tcrb-V13, Sh2d1a, Ly6d, Ccr7, Ccl25, Lat, Cd3g, Cd8a, Orm1, Sftpd, Cd3e, Rag1, Ccl28,
GOTERM_BP_ALL	hemopoiesis	5	6.41%	0.03510	Cd4, Zfpn1a1, Cd3e, Rag1, Cd8a,
GOTERM_BP_ALL	hemopoietic or lymphoid organ development	5	6.41%	0.04928	Cd4, Zfpn1a1, Cd3e, Rag1, Cd8a,
GOTERM_BP_ALL	immune cell activation	9	11.54%	0.00002	Cd4, Ccnd3, Sftpd, Cd5, Cd3e, Rag1, Lat, Cd3g, Cd8a,
GOTERM_BP_ALL	immune response	15	19.23%	0.00002	Ccnd3, Cd4, Cd5, Tcrb-V13, Sh2d1a, Ccr7, Ccl25, Lat, Cd3g, Cd8a, Orm1, Sftpd, Cd3e, Rag1, Ccl28,
GOTERM_BP_ALL	induction of apoptosis	4	5.13%	0.03310	Cidec, Nr4a1, Cd5, Trp53inp1,
GOTERM_BP_ALL	induction of programmed cell death	4	5.13%	0.03310	Cidec, Nr4a1, Cd5, Trp53inp1,
GOTERM_BP_ALL	lymphocyte activation	9	11.54%	0.00001	Cd4, Ccnd3, Sftpd, Cd5, Cd3e, Rag1, Lat, Cd3g, Cd8a,
GOTERM_BP_ALL	lymphocyte differentiation	4	5.13%	0.01500	Cd4, Cd3e, Rag1, Cd8a,
GOTERM_BP_ALL	organismal physiological process	18	23.08%	0.00058	Ccnd3, Cd4, Cd5, Tcrb-V13, Sh2d1a, Ccr7, Ccl25, Lat, Cd3g, Cd8a, Orm1, Sftpd, Sftpc, Camk4, Cd3e, Snca, Rag1, Ccl28,
GOTERM_BP_ALL	positive regulation of biological process	12	15.38%	0.00364	Gfi1, Cd4, Cidec, Sftpd, Nr4a1, Cd5, Zfpn1a1, Trp53inp1, Cd3e, Nusap1, Kcnn4, Cd8a,

Category	Term	Count	%	PValue	Genes
GOTERM_BP_ALL	positive regulation of calcium-mediated signaling	3	3.85%	0.00100	Cd4, Cd3e, Cd8a,
GOTERM_BP_ALL	positive regulation of cellular physiological process	9	11.54%	0.02005	Cd4, Cidec, Sftpd, Nr4a1, Cd5, Zfpn1a1, Trp53inp1, Cd3e, Nusap1,
GOTERM_BP_ALL	positive regulation of cellular process	11	14.10%	0.00323	Gfi1, Cd4, Cidec, Sftpd, Nr4a1, Cd5, Zfpn1a1, Trp53inp1, Cd3e, Nusap1, Cd8a,
GOTERM_BP_ALL	positive regulation of physiological process	10	12.82%	0.00837	Cd4, Cidec, Sftpd, Nr4a1, Cd5, Zfpn1a1, Trp53inp1, Cd3e, Nusap1, Kcnn4,
GOTERM_BP_ALL	positive regulation of signal transduction	3	3.85%	0.01800	Cd4, Cd3e, Cd8a,
GOTERM_BP_ALL	positive regulation of T cell activation	3	3.85%	0.04485	Cd4, Cd5, Cd3e,
GOTERM_BP_ALL	regulation of calcium-mediated signaling	3	3.85%	0.00100	Cd4, Cd3e, Cd8a,
GOTERM_BP_ALL	regulation of cell activation	5	6.41%	0.00225	Cd4, Sftpd, Cd5, Cd3e, Lat,
GOTERM_BP_ALL	regulation of immune response	5	6.41%	0.01225	Cd4, Sftpd, Cd5, Cd3e, Lat,
GOTERM_BP_ALL	regulation of liquid surface tension	2	2.56%	0.02602	Sftpd, Sftpc,
GOTERM_BP_ALL	regulation of lymphocyte activation	5	6.41%	0.00225	Cd4, Sftpd, Cd5, Cd3e, Lat,
GOTERM_BP_ALL	regulation of T cell activation	5	6.41%	0.00103	Cd4, Sftpd, Cd5, Cd3e, Lat,
GOTERM_BP_ALL	response to abiotic stimulus	7	8.97%	0.02421	Gfi1, Sftpd, Ccr7, Ccl25, Gys2, Snca, Ccl28,
GOTERM_BP_ALL	response to biotic stimulus	18	23.08%	0.00000	Ccnd3, Cd4, Cd5, Tacstd1, Tcrb-V13, Sh2d1a, Ly6d, Ccr7, Ccl25, Lat, Cd3g, Cd8a, Orm1, Sftpd, Krt2-8, Cd3e, Rag1, Ccl28,
GOTERM_BP_ALL	response to chemical stimulus	6	7.69%	0.03102	Sftpd, Ccr7, Ccl25, Gys2, Snca, Ccl28,
GOTERM_BP_ALL	response to external stimulus	9	11.54%	0.00309	Gfi1, Cd4, Sftpd, Tcrb-V13, Ccr7, Ccl25, Ccl28, Lat, Cd8a,
GOTERM_BP_ALL	response to other organism	9	11.54%	0.00206	Cd4, Sftpd, Orm1, Tcrb-V13, Sh2d1a, Krt2-8, Ccl25, Lat, Cd8a,
GOTERM_BP_ALL	response to pest, pathogen or parasite	9	11.54%	0.00159	Cd4, Sftpd, Orm1, Tcrb-V13, Sh2d1a, Krt2-8, Ccl25, Lat, Cd8a,
GOTERM_BP_ALL	response to stimulus	22	28.21%	0.00009	Ccnd3, Cd4, Cd5, Tacstd1, Tcrb-V13, Sh2d1a, Ly6d, Ccr7, Ccl25, Lat, Cd3g, Cd8a, Gfi1, Sftpd, Orm1, Trp53inp1, Krt2-8, Cd3e, Gys2, Snca, Rag1, Ccl28,
GOTERM_BP_ALL	response to wounding	6	7.69%	0.04140	Cd4, Sftpd, Tcrb-V13, Ccl25, Lat, Cd8a,
GOTERM_BP_ALL	second-messenger-mediated signaling	4	5.13%	0.01041	Cd4, Cd3e, Lat, Cd8a,
GOTERM_BP_ALL	T cell activation	8	10.26%	0.00000	Cd4, Ccnd3, Sftpd, Cd5, Cd3e, Lat, Cd3g, Cd8a,
GOTERM_BP_ALL	T cell proliferation	3	3.85%	0.04174	Ccnd3, Sftpd, Cd3e,
GOTERM_BP_ALL	taxis	4	5.13%	0.04144	Sftpd, Ccr7, Ccl25, Ccl28,

b. Mouse hearts, 2 months old, Agilent platform, Molecular Function

Category	Term	Count	%	PValue	Genes
Category	Term	Count	%	PValue	Genes
GOTERM_MF_ALL	ion binding	23	29.49%	0.02518	Def6, Clstn3, Car3, Scd1, Cd6, Fxyd2, Cyp2b10, Cyp2f2, Cyp2a4, Bcl11b, Gfi1, Sftpd, Nr4a1, Zfpn1a1, Fasn, Camk4, Kcna3, Rag1, Dntt, Rasgrp1, Itk, Car5b, Ltf,
GOTERM_MF_ALL	receptor binding	7	8.97%	0.04694	Cd4, Ccl25, Ccl28, Scgb3a1, Nsg2, Cd3g, Cd8a,
GOTERM_MF_ALL	metal ion binding	23	29.49%	0.02518	Def6, Clstn3, Car3, Scd1, Cd6, Fxyd2, Cyp2b10, Cyp2f2, Cyp2a4, Bcl11b, Gfi1, Sftpd, Nr4a1, Zfpn1a1, Fasn, Camk4, Kcna3, Rag1, Dntt, Rasgrp1, Itk, Car5b, Ltf,
GOTERM_MF_ALL	MHC protein binding	2	2.56%	0.04416	Cd4, Cd8a,
GOTERM_MF_ALL	hydrolyase activity	3	3.85%	0.03887	Fasn, Car3, Car5b,

Category	Term	Count	%	PValue	Genes
GOTERM_MF_ALL	iron ion binding	5	6.41%	0.03736	Scd1, Cyp2b10, Cyp2f2, Cyp2a4, Ltf,
GOTERM_MF_ALL	binding	53	67.95%	0.01539	Clstn3, Car3, Myb, Ccl25, Kcnn4, Lat, Abcg3, Zfpn1a1, Fasn, Orm1, Gys2, Dntt, Ccl28, Def6, Scd1, Cd6, Cyp2b10, Cyp2f2, Bcl11b, Sept1, Nusap1, Lck, Cd4, Ccnd3, Cidec, Myef2, Ccr7, Fxyd2, Cd3g, Cd8a, Gfi1, Nr4a1, Sftpd, Arpp21, Rag1, Snca, Igh-VJ558, Rasgrp1, Nsg2, Ucp1, Ltf, Car5b, Tox, Cyp2a4, Satb1, Txk, U46068, Krt2-8, Camk4, Cd3e, Kcna3, Scgb3a1, Itk,
GOTERM_MF_ALL	cation binding	22	28.21%	0.01940	Def6, Clstn3, Car3, Scd1, Cd6, Fxyd2, Cyp2b10, Cyp2f2, Cyp2a4, Bcl11b, Gfi1, Sftpd, Zfpn1a1, Fasn, Nr4a1, Camk4, Kcna3, Rag1, Rasgrp1, Itk, Car5b, Ltf,

c. Mouse hearts, 8 months old, Agilent platform, Biological Process

Category	Term	Count	%	PValue	Genes
GOTERM_BP_ALL	taxis	3	9.68%	0.03656	Ccl7, Spp1, Cxcl5,
GOTERM_BP_ALL	immune response	9	29.03%	0.00007	Chi3l3, Saa3, Orm1, Igh-6, Ccl7, Igj, Serpina3n, Spp1, Cxcl5,
GOTERM_BP_ALL	inflammatory response	4	12.90%	0.00667	Chi3l3, Ccl7, Spp1, Cxcl5,
GOTERM_BP_ALL	N-acetylglucosamine catabolism	2	6.45%	0.02553	Chi3l3, Chi3l1,
GOTERM_BP_ALL	response to biotic stimulus	9	29.03%	0.00019	Chi3l3, Saa3, Orm1, Igh-6, Ccl7, Igj, Serpina3n, Spp1, Cxcl5,
GOTERM_BP_ALL	glucosamine catabolism	2	6.45%	0.02553	Chi3l3, Chi3l1,
GOTERM_BP_ALL	acute-phase response	3	9.68%	0.00258	Saa3, Orm1, Serpina3n,
GOTERM_BP_ALL	response to pest, pathogen or parasite	9	29.03%	0.00000	Chi3l3, Saa3, Orm1, Igh-6, Ccl7, Igj, Serpina3n, Spp1, Cxcl5,
GOTERM_BP_ALL	organismal physiological process	12	38.71%	0.00004	Chi3l3, Saa3, Orm1, Igh-6, Ccl7, Igj, Ptgs, Serpina3n, Spp1, Sftpc, Cxcl5, Nppb,
GOTERM_BP_ALL	chitin metabolism	2	6.45%	0.02553	Chi3l3, Chi3l1,
GOTERM_BP_ALL	response to other organism	9	29.03%	0.00000	Chi3l3, Saa3, Orm1, Igh-6, Ccl7, Igj, Serpina3n, Spp1, Cxcl5,
GOTERM_BP_ALL	chitin catabolism	2	6.45%	0.02553	Chi3l3, Chi3l1,
GOTERM_BP_ALL	chemotaxis	3	9.68%	0.03656	Ccl7, Spp1, Cxcl5,
GOTERM_BP_ALL	response to wounding	4	12.90%	0.03802	Chi3l3, Ccl7, Spp1, Cxcl5,
GOTERM_BP_ALL	behavior	4	12.90%	0.01781	Ccl7, Ptgs, Spp1, Cxcl5,
GOTERM_BP_ALL	amino sugar catabolism	2	6.45%	0.02553	Chi3l3, Chi3l1,
GOTERM_BP_ALL	cellular polysaccharide catabolism	2	6.45%	0.03056	Chi3l3, Chi3l1,
GOTERM_BP_ALL	defense response	9	29.03%	0.00016	Chi3l3, Saa3, Orm1, Igh-6, Ccl7, Igj, Serpina3n, Spp1, Cxcl5,
GOTERM_BP_ALL	polysaccharide catabolism	2	6.45%	0.03056	Chi3l3, Chi3l1,
GOTERM_BP_ALL	response to stress	9	29.03%	0.00059	Chi3l3, Saa3, Orm1, Igh-6, Ccl7, Igj, Serpina3n, Spp1, Cxcl5,
GOTERM_BP_ALL	response to stimulus	10	32.26%	0.00510	Chi3l3, Saa3, Orm1, Igh-6, Ccl7, Igj, Ptgs, Serpina3n, Spp1, Cxcl5,

d. Mouse hearts, 8 months old, Agilent platform, Molecular Function

Category	Term	Count	%	PValue	Genes
GOTERM_MF_ALL	hydrolase activity, acting on glycosyl bonds	3	9.68%	0.02431	Chi3l3, Gla, Chi3l1,
GOTERM_MF_ALL	antigen binding	3	9.68%	0.00480	Igh-6, Igj, Igh-VJ558,
GOTERM_MF_ALL	carbonate dehydratase activity	2	6.45%	0.04687	Car2, Car5b,
GOTERM_MF_ALL	chitinase activity	2	6.45%	0.02370	Chi3l3, Chi3l1,

e. Human myocardium of donors <40 years old, Agilent platform, Biological Process

Category	Term	Count	%	PValue	Genes
GOTERM_BP_ALL	regulation of cell differentiation	4	4.35%	0.01651	FADS1, ZBTB16, ALOX15B, PPARD,
GOTERM_BP_ALL	chemotaxis	6	6.52%	0.00555	CCL11, CCL7, CCL22, PLAU, IL8, FOSL1,
GOTERM_BP_ALL	negative regulation of programmed cell death	5	5.43%	0.03419	HSPA1A, HSP90B1, IER3, HSPA5, BCL2A1,
GOTERM_BP_ALL	negative regulation of physiological process	16	17.39%	0.00027	HSP90B1, RARRES1, IER3, PLAU, ALOX15B, HSPA5, IL6, HSPA1A, ZBTB16, VCL, GADD45A, FOSB, IL8, PTGFRN, BCL2A1, PPARD,
GOTERM_BP_ALL	icosanoid metabolism	3	3.26%	0.03729	FADS1, ALOX15B, CYP2J2,
GOTERM_BP_ALL	defense response	17	18.48%	0.00384	IGHG1, CCL7, CCL22, CD163, HP, FOSL1, DEFA1, IL6, DGKD, SERPINA3, CCL11, PTX3, TREM1, ITGB1, IL8, IL24, IL1RN,
GOTERM_BP_ALL	negative regulation of biological process	16	17.39%	0.00120	HSP90B1, RARRES1, IER3, PLAU, ALOX15B, HSPA5, IL6, HSPA1A, ZBTB16, VCL, GADD45A, FOSB, IL8, PTGFRN, BCL2A1, PPARD,
GOTERM_BP_ALL	death	13	14.13%	0.00245	HSP90B1, IER3, ALOX15B, HSPA5, IL6, ZBTB16, HSPA1A, GADD45A, TNFRSF11B, PHLDA1, IL24, BCL2A1, PPARD,
GOTERM_BP_ALL	fatty acid metabolism	5	5.43%	0.02905	FADS1, ALOX15B, CYP2J2, CROT, PPARD,
GOTERM_BP_ALL	anti-apoptosis	5	5.43%	0.02186	HSPA1A, HSP90B1, IER3, HSPA5, BCL2A1,
GOTERM_BP_ALL	negative regulation of apoptosis	5	5.43%	0.03419	HSPA1A, HSP90B1, IER3, HSPA5, BCL2A1,

f. Human myocardium of donors <40 years old, Agilent platform, Molecular Function

Category	Term	Count	%	PValue	Genes
GOTERM_MF_ALL	receptor binding	12	13.04%	0.00702	IL6, CCL11, HSP90B1, NPPA, CCL7, TNFRSF11B, CCL22, AREG, IL8, IL24, PPARD, IL1RN,
GOTERM_MF_ALL	sequence-specific DNA binding	8	8.70%	0.01754	NR1D1, RXRG, ELF3, FOSB, CREM, ATF3, PPARD, FOSL1,
GOTERM_MF_ALL	G-protein-coupled receptor binding	4	4.35%	0.01721	CCL11, CCL7, CCL22, IL8,
GOTERM_MF_ALL	unfolded protein binding	5	5.43%	0.04626	HSPA1A, FKBP5, HSP90B1, DNAJB5, HSPA5,
GOTERM_MF_ALL	heparin binding	4	4.35%	0.03056	THBS2, POSTN, CCL7, THBS1,
GOTERM_MF_ALL	cytokine activity	9	9.78%	0.00023	IL6, CCL11, CCL7, TNFRSF11B, CCL22, AREG, IL8, IL24, IL1RN,
GOTERM_MF_ALL	chemokine receptor binding	4	4.35%	0.01134	CCL11, CCL7, CCL22, IL8,
GOTERM_MF_ALL	chemokine activity	4	4.35%	0.01134	CCL11, CCL7, CCL22, IL8,
GOTERM_MF_ALL	protein dimerization activity	7	7.61%	0.00145	ZBTB16, FOSB, ITGB1, CREM, ATF3, PPARD, FOSL1,

g. Human myocardium of donors 50-65 years old, Agilent platform, Biological Process

Category	Term	Count	%	PValue	Genes
GOTERM_BP_ALL	anti-apoptosis	5	4.13%	0.03772	HMGB1, NPM1, HSPA5, ANXA5, TGM2,
GOTERM_BP_ALL	cell adhesion	13	10.74%	0.01984	TTN, TNC, ATP2A2, CHST10, CCL11, POSTN, ITGA5, ITGB1, CD44, TGM2, WISP2, ZYX, ITGA3,
GOTERM_BP_ALL	cell organization and biogenesis	21	17.36%	0.03524	KRT5, KRT8, TUBA1, MYH9, HIST1H1C, NPM1, CNN1, YWHAH, NPPB, HMGB1, KLF6, DGKD, CNN3, CLTB, KIF22, TIMP1, TUBA3, XPO7, WISP2, ATXN7, RPLP0,
GOTERM_BP_ALL	cellular morphogenesis	7	5.79%	0.04822	KLF6, DGKD, MYH9, TIMP1, YWHAH, WISP2, NPPB,
GOTERM_BP_ALL	muscle contraction	8	6.61%	0.00131	CNN3, TTN, CRYAB, CNN1, ACTA2, ACTG2, TNNT2, MRCL3, ANKRD2,
GOTERM_BP_ALL	negative regulation of apoptosis	6	4.96%	0.01506	HMGB1, NPM1, HSPA5, ANXA5, TGM2, YWHAH,
GOTERM_BP_ALL	negative regulation of biological process	14	11.57%	0.03282	GNAI2, KRT5, NPM1, MLLT7, HSPA5, YWHAH, NPPB, CDKN1A, HMGB1, MYC, TIMP1, ANXA5, TGM2, CSDA,
GOTERM_BP_ALL	negative regulation of cellular process	13	10.74%	0.04149	KRT5, NPM1, MLLT7, HSPA5, YWHAH, NPPB, CDKN1A, HMGB1, MYC, TIMP1, TGM2, ANXA5, CSDA,
GOTERM_BP_ALL	negative regulation of physiological process	13	10.74%	0.02606	KRT5, NPM1, MLLT7, HSPA5, YWHAH, NPPB, CDKN1A, HMGB1, MYC, TIMP1, TGM2, ANXA5, CSDA,
GOTERM_BP_ALL	negative regulation of programmed cell death	6	4.96%	0.01506	HMGB1, NPM1, HSPA5, ANXA5, TGM2, YWHAH,
GOTERM_BP_ALL	organ development	12	9.92%	0.01870	TAGLN, KLF6, MDK, TTN, POSTN, TNFRSF11B, CD1D, TIMP1, NPPB, COL3A1, COL1A1, ANKRD2,
GOTERM_BP_ALL	organelle organization and biogenesis	13	10.74%	0.04037	KRT5, KRT8, TUBA1, HIST1H1C, NPM1, CNN1, YWHAH, HMGB1, CNN3, KIF22, TUBA3, ATXN7, RPLP0,
GOTERM_BP_ALL	organismal physiological process	29	23.97%	0.00599	IFI30, GUCY2D, HLA-DRA, MYH9, HLA-DQA1, YWHAH, TNNT2, NPPB, ANKRD2, COL3A1, FOSL1, CXCL3, CNN3, DGKD, KLF6, ITGB1, LPL, SERPINE1, MRCL3, COL1A1, ATXN7, TTN, CNN1, ACTA2, ACTG2, CCL11, OPN1SW, CD1D, CRYAB, ANXA5,
GOTERM_BP_ALL	regulation of organismal physiological process	6	4.96%	0.01758	TTN, CD1D, CNN1, TNNT2, NPPB, MRCL3,
GOTERM_BP_ALL	response to abiotic stimulus	10	8.26%	0.02812	DEFA1, GNAI2, DGKD, TTN, CCL11, OPN1SW, PLP2, CSDA, CXCL3, FOSL1,
GOTERM_BP_ALL	response to external stimulus	11	9.09%	0.04183	GNAI2, MDK, CCL11, OPN1SW, PLP2, CD1D, ITGB1, ANXA5, SERPINE1, CXCL3, FOSL1,
GOTERM_BP_ALL	response to stimulus	29	23.97%	0.01374	GNAI2, IFI30, GUCY2D, HLA-DRA, MYH9, NPM1, HLA-DQA1, FOSL1, CXCL3, GSTT1, KLF6, DGKD, PLP2, ITGB1, UNG2, SERPINE1, ATXN7, COL1A1, TTN, MDK, DEFA1, HMGB1, CCL11, XRCC4, OPN1SW, CD1D, CRYAB, ANXA5, CSDA,
GOTERM_BP_ALL	sensory perception	8	6.61%	0.03777	GUCY2D, CCL11, OPN1SW, MYH9, CRYAB, ATXN7, COL1A1, CXCL3,
GOTERM_BP_ALL	smooth muscle contraction	3	2.48%	0.02765	CNN3, CNN1, MRCL3,

h. Human myocardium of donors 50-65 years old, Agilent platform, Molecular Function

Category	Term	Count	%	PValue	Genes
GOTERM_MF_ALL	unfolded protein binding	6	4.96%	0.03280	FKBP5, NPM1, DNAJA4, CRYAB, PPIB, HSPA5,
GOTERM_MF_ALL	structural constituent of cytoskeleton	5	4.13%	0.01682	KRT18, KRT5, ACTB, MSN, ACTA2, ACTG2,
GOTERM_MF_ALL	actin binding	8	6.61%	0.01011	TAGLN, CNN3, MYO1C, MYH9, CNN1, MSN, YWHAH, TNNT2,
GOTERM_MF_ALL	cytoskeletal protein binding	9	7.44%	0.01948	TAGLN, CNN3, TTN, MYO1C, MYH9, CNN1, MSN, YWHAH, TNNT2,
GOTERM_MF_ALL	protein binding	54	44.63%	0.02188	GNAI2, MYO1C, MYH9, HSPA5, NPPB, CDKN1A, TNNT2, EIF3S2, MAP2K3, EIF1AY, CNN3, ITGA3, KRT5, TTN, MDK, TUBA1, FKBP5, CNN1, ATP2A2, HMGB1, CCL11, PICALM, MYC, CD1D, CRYAB, PPIB, ACTB, TNC, NPM1, YWHAH, FOSL1, CXCL3, DGKD, POSTN, PLP2, TNFRSF11B, TRIM25, ITGB1, CD44, CAND2, ATXN7, RPLP0, TAGLN, YWHAZ, MSN, ACTA2, ACTG2, MCM7, ITGA5, MARCH3, DNAJA4, ANXA5, WISP2, ZYX, CSDA,
GOTERM_MF_ALL	pattern binding	5	4.13%	0.03250	MDK, POSTN, HRG, CD44, LPL,
GOTERM_MF_ALL	glycosaminoglycan binding	5	4.13%	0.02441	MDK, POSTN, HRG, CD44, LPL,
GOTERM_MF_ALL	enzyme inhibitor activity	8	6.61%	0.00725	HRG, TIMP1, HSPA5, ANXA5, CAST, YWHAH, CDKN1A, SERPINE1,
GOTERM_MF_ALL	structural molecule activity	16	13.22%	0.00088	KRT5, KRT18, KRT8, TTN, TUBA1, ACTB, MSN, ACTA2, ACTG2, ANKRD2, COL3A1, RPL3, RPS4Y1, CRYAB, TUBA3, COL1A1, RPLP0,
GOTERM_MF_ALL	polysaccharide binding	5	4.13%	0.02771	MDK, POSTN, HRG, CD44, LPL,
GOTERM_MF_ALL	protein heterodimerization activity	4	3.31%	0.02074	KRT5, NPM1, CD1D, ITGB1,

i. Human myocardium, Affymetrix platform, Biological Process

Category	Term	Count	%	PValue	Genes
GOTERM_BP_ALL	sexual reproduction	3	17.65%	0.00865	USP9Y, EREG, SMCY,
GOTERM_BP_ALL	gametogenesis	3	17.65%	0.00569	USP9Y, EREG, SMCY,
GOTERM_BP_ALL	reproduction	3	17.65%	0.01393	USP9Y, EREG, SMCY,

j. Human myocardium, Affymetrix platform, Molecular Function

Category	Term	Count	%	PValue	Genes
GOTERM_MF_ALL	RNA binding	3	17.65%	0.03963	DDX3Y, EIF1AY, RPS4Y1,
GOTERM_MF_ALL	nucleic acid binding	6	35.29%	0.03519	DDX3Y, EIF1AY, ZFY, RPS4Y1, POLR2J2, SMCY,