

Supplementary Table 5. Gene ontology enrichment in modules.

	GO Biological Process	Go ID	GO Levels	Group	%Association Genes	Term P-value	Group P-value	Association Genes	All Association Genes	Term P-value BH-corrected	Group P-value BH-corrected
16th Module	positive regulation of mast cell degranulation	GO:0043306	4, 5, 6, 7, 8, 9, 10, 11, 12	Group2	10	0.004499286	0.008981208	FCER1A	ADORA2B, ADORA3, CRHR1, FCER1A, FCER1G, FGR, GAB2, MS4A1, MS4A2, SYK	0.007070306	0.013471813
	phosphate ion homeostasis	GO:0055062	8	Group1	10	0.004499286	0.010769128	SFRP4	ENPP1, FGF23, FGFR4, GCM2, SFRP4, SLC34A1, SLC34A2, SLC34A3, SLC9A3R1, TFAP2B	0.007070306	0.010769128
	positive regulation of epidermal cell differentiation	GO:0045606	4, 5, 6, 7, 8, 9, 10	Group1	7.142857075	0.006294135	0.010769128	SFRP4	ALOX15B, ATOH1, BMP4, CYP27B1, IL20, MBD4, MED1, NCOA3, NME2, NOTCH1, PRKCH, SFRP4, TRIM16, VDR	0.006923549	0.010769128
	ethanol oxidation	GO:0006069	4, 7	None	9.090909004	0.004948258	NaN	ADH1B	ACSS1, ACSS2, ADH1A, ADH1B, ADH1C, ADH4, ADH5, ADH6, ADH7, ALDH1A1, ALDH2	0.006803855	NaN
	cellular response to vitamin D	GO:0071305	6, 7, 8	Group0	6.666666508	0.006742414	0.000219694	TNNC1	BGLAP, CASR, CYP24A1, CYP27B1, IL15, ITGB1, MBD4, MED1, SFRP1, SNAI2, SNW1, TNC, TNNC1, TRIM24, VDR	0.006742414	0.000659082
	serotonin secretion	GO:0001820	4, 5, 6, 7, 8	Group2	8.333333015	0.005397057	0.008981208	FCER1A	CRH, FCER1A, FCER1G, HRH3, HTR1A, HTR1B, LILRB1, MAOB, P2RX1, SYK, XBP1, XBP1P1	0.006596403	0.013471813
	positive regulation of epithelial cell proliferation involved in lung morphogenesis	GO:0060501	5, 6, 7, 8, 9, 10, 11	Group0	20	0.002251817	0.000219694	WNT2	FGF7, FGFR2, FOXP2, SRSF6, WNT2	0.004953997	0.000659082
	atrial cardiac muscle tissue morphogenesis	GO:0055009	5, 6, 7, 8, 9, 10, 11	Group0	16.66666603	0.002701658	0.000219694	WNT2	BMP10, MYH6, PITX2, PROX1, TNN2, WNT2	0.00495304	0.000659082
	positive regulation of granulocyte macrophage colony-stimulating factor biosynthetic process	GO:0045425	6, 7, 8, 9	Group2	33.33333206	0.001351612	0.008981208	FCER1A	CD80, FCER1A, SYK	0.003716933	0.013471813
	lung induction	GO:0060492	4, 5, 6, 7, 8, 9, 10, 11, 12	Group0	33.33333206	0.001351612	0.000219694	WNT2	CTNNB1, WNT2, WNT2B	0.003716933	0.000659082
	diaphragm contraction	GO:0002086	5, 7, 9	Group0	33.33333206	0.001351612	0.000219694	TNNC1	GAA, TNNC1, TNNI3	0.003716933	0.000659082
	cellular response to prostaglandin D stimulus	GO:0071799	6, 7, 8	Group0	33.33333206	0.001351612	0.000219694	TNNC1	PTGDR, TNC, TNNC1	0.003716933	0.000659082
	regulation of muscle filament sliding speed	GO:0032972	3, 5, 6, 7, 8, 9	Group0	50	0.000901249	0.000219694	TNNC1	TNNC1, TNNI3	0.003304579	0.000659082
	positive regulation of type I hypersensitivity	GO:0001812	7, 8, 9, 10, 11	Group2	50	0.000901249	0.008981208	FCER1A	FCER1A, FCER1G	0.003304579	0.013471813
	positive regulation of keratinocyte apoptotic process	GO:1902174	6, 7, 8, 9	Group1	50	0.000901249	0.010769128	SFRP4	PIAS4, SFRP4	0.003304579	0.010769128

	positive regulation of interleukin-3 biosynthetic process	GO:0045401	6, 7, 8, 9	Group2	50	0.000901249	0.008981208	FCER1A	FCER1A, SYK	0.003304579	0.013471813
	mesenchymal-epithelial cell signaling involved in prostate gland development	GO:0060739	3, 4, 5, 6, 7, 8	Group0	50	0.000901249	0.000219694	TNNC1	TNC, TNNC1	0.003304579	0.000659082
	negative regulation of sodium-dependent phosphate transport	GO:2000119	4, 5, 6, 7, 8, 9, 10, 11	Group1	100	0.000450711	0.010769128	SFRP4	SFRP4	0.002478913	0.010769128
	epithelial tube branching involved in lung morphogenesis	GO:0060441	5, 6, 7, 8, 9	Group0	7.407407284	6.07931E-05	0.000219694	TNNC1, WNT2	BMP4, CELSR1, CTNNA1, CTSH, CTSZ, DAG1, FGF10, FGFR2, FOXA1, FOXA2, FOXF1, HHEX, HHIP, HOXA5, LAMA1, NKX2-1, RDH10, RSPO2, SHH, SOX2, TMTC3, TNC, TNF, TNNC1, VANGL2, WNT2, WNT2B	0.000668724	0.000659082

18th Module	phospholipase C-activating G-protein coupled acetylcholine receptor signaling pathway	GO:0007207	7, 8	None	33.33333206	0.001158599	NaN	GNA15	CHRM1, CHRM2, GNA15	0.002317199	NaN
	caritine biosynthetic process	GO:0045329	5, 6, 7, 8, 9	None	20	0.001930377	NaN	BBOX1	ACADM, ALDH9A1, BBOX1, SHMT1, TMLHE	0.001930377	NaN

19th Module	positive regulation of collagen biosynthetic process	GO:0032967	5, 6, 7, 8	Group1	4.166666508	0.028972409	3.00563E-07	WNT4	AMELX, BMP4, CTGF, ENG, EP300, F2, F2R, HDAC2, IHH, ITGA2, MKX, PDGFRB, PRDX5, RGCC, SCXA, SCXB, SERPINB7, SERPINF2, SUCO, TGFB1, TGFB3, UCN, UTS2, WNT4	0.028972409	1.50281E-06
	positive regulation vascular endothelial growth factor production	GO:0010575	4, 5, 6	Group1	4.761904716	0.025394844	3.00563E-07	IL1A	ADORA2B, ARNT, C3, C3AR1, C5, FLT4, GATA4, HIF1A, HPSE, IL1A, IL1B, IL6ST, ISL1, MIA3, NODAL, NOX1, PTGS2, RORA, SULF1, SULF2, TGFB1	0.026731414	1.50281E-06
	establishment of mitotic spindle localization	GO:0040001	4, 5, 6, 7	Group1	5.882352829	0.020605329	3.00563E-07	ESPL1	ARHGEF2, CDK5RAP2, CENPA, DYNLT1, ESPL1, EYA1, GSPM2, HTT, INSC, NDC80, NDE1, NUMA1, NUSAP1, PAFAH1B1, SLC6A4, SPDL1, ZW10	0.022894809	1.50281E-06

positive regulation of focal adhesion assembly	GO:0051894	4, 5, 6, 7, 8, 9, 10	Group1	5.882352829	0.020605329	3.00563E-07	WNT4	EPB41L5, HRG, ITGB1BP1, KDR, MYOC, NRG1, PPM1F, PTPRJ, ROCK1, S100A10, SDC4, SFRP1, SMAD3, TEK, TSC1, VEGFA, WNT4	0.022894809	1.50281E-06
mesonephric tubule development	GO:0072164	4, 5, 6, 7, 8, 9, 10	Group1	6.666666508	0.018202217	3.00563E-07	WNT4	GPC3, HNF1B, LHX1, OSR1, OXSR1, PAX2, PAX8, PKD1, PKD2, PRKD2, SIX1, WNT11, WNT4, WNT9B, WT1	0.021414373	1.50281E-06
extracellular negative regulation of signal transduction	GO:1900116	4, 5, 6, 7	Group4	7.142857075	0.016998568	0.032537531	ADH7	ADH7, AGTR2, CD46, CER1, DAND5, DKK1, ESR2, FBN1, FBN2, IL18BP, LRPAP1, LTBP1, MTRNR2, NBL1	0.02124821	0.032537531
positive regulation of interleukin-2 biosynthetic process	GO:0045086	6, 7, 8, 9	Group1	7.692307472	0.015793521	3.00563E-07	IL1A	CARD11, CD28, CD3E, CD4, CD80, CD86, GLMN, IL1A, IL1B, IRF4, PRKCC, STAT5A, STAT5B	0.021058028	1.50281E-06
positive regulation of meiosis	GO:0045836	4, 5, 6, 7, 8	Group1	7.692307472	0.015793521	3.00563E-07	WNT4	CAMK2B, DAZL, DMRT1, EIF4G3, MSX1, MSX2, NPM2, PIWIL2, PLCB1, PRDM9, UBE2B, WNT4, WNT5A	0.021058028	1.50281E-06
fever generation	GO:0001660	6, 7	Group1	8.333333015	0.014587074	3.00563E-07	IL1A	CNR1, EDNRB, IL1A, IL1B, IL1RN, PCDHA4, PCDHA@, PTGER3, PTGS2, TNF, TNFRSF11A, TNFSF11	0.020838677	1.50281E-06
ethanol oxidation	GO:0006069	4, 7	Group4	9.090909004	0.013379226	0.032537531	ADH7	ACSS1, ACSS2, ADH1A, ADH1B, ADH1C, ADH4, ADH5, ADH6, ADH7, ALDH1A1, ALDH2	0.020583425	0.032537531
negative regulation of fibroblast growth factor receptor signaling pathway	GO:0040037	4, 5, 6, 7, 8, 9, 10	Group1	9.090909004	0.013379226	3.00563E-07	WNT4	GATA3, GPC1, NGFR, SPRY1, SPRY2, SULF1, SULF2, TCF7L2, THBS1, WNT4, WNT5A	0.020583425	1.50281E-06
ossification involved in bone maturation	GO:0043931	4, 5, 6, 7, 8	Group3	9.090909004	0.013379226	0.020605329	RYR1	BMP2, GREM1, IGF1, LEP, LTF, PHOSPHO1, PLXNB1, RHOA, RYR1, SEMA4D, THBS3	0.020583425	0.025756661
pentose biosynthetic process	GO:0019322	6, 7	Group0	14.28571415	0.008533796	0.010959322	PGD	DDR2, G6PD, PGD, PHGDH, TALDO1, TKT, UBL4A	0.014222993	0.018265537
immature T cell proliferation in thymus	GO:0033080	7, 8, 9, 10, 11, 12	Group1	14.28571415	0.008533796	3.00563E-07	WNT4	BMP4, CDKN2A, ERBB2, FOXP3, IHH, SHH, WNT4	0.014222993	1.50281E-06
cellular response to caffeine	GO:0071313	6, 7	Group3	14.28571415	0.008533796	0.020605329	RYR1	CASQ2, CHEK1, GSTM2, RYR1, RYR2, RYR3, SLC8A1	0.014222993	0.025756661

positive regulation of p38MAPK cascade	GO:1900745	7, 8, 9, 10, 11	Group1	14.28571415	0.008533796	3.00563E-07	MAP3K4	BMP2, GADD45A, GADD45B, GADD45G, MAP3K4, VEGFA, XDH	0.014222993	1.50281E-06
ethanol catabolic process	GO:0006068	7	Group4	16.66666603	0.00731892	0.032537531	ADH7	ADH5, ADH7, ALDH1B1, ALDH2, ALDH3B1, ALDH3B2	0.013307128	0.032537531
negative regulation of Rho GTPase activity	GO:0034259	8, 9, 10, 11, 12, 13, 14, 15, 16	Group1	16.66666603	0.00731892	3.00563E-07	FZD10	ADCYAP1, ARFGEF1, FICD, FZD10, GMIP, HRAS	0.013307128	1.50281E-06
homologous chromosome segregation	GO:0045143	4, 5, 6, 7, 8	Group1	16.66666603	0.00731892	3.00563E-07	ESPL1	ESPL1, FMN2, HORMAD1, MLH1, MSH4, MSH5	0.013307128	1.50281E-06
metanephric mesenchymal cell differentiation	GO:0072162	6, 7, 8, 9, 10	Group1	16.66666603	0.00731892	3.00563E-07	WNT4	OSR1, OXSR1, PAX2, STAT1, TCF21, WNT4	0.013307128	1.50281E-06
pentose-phosphate shunt, oxidative branch	GO:0009051	6, 7, 9, 10, 11, 12, 13	Group0	20	0.006102635	0.010959322	PGD	G6PD, PGD, PGLS, PHGDH, UBL4A	0.01220527	0.018265537
somatotropin secreting cell differentiation	GO:0060126	4, 5, 6, 7, 8, 9, 10, 11, 12	Group1	20	0.006102635	3.00563E-07	WNT4	GHRHR, PITX2, POU1F1, PROP1, WNT4	0.01220527	1.50281E-06
thyroid-stimulating hormone-secreting cell differentiation	GO:0060129	4, 6, 7, 8, 9, 10, 11, 12	Group1	20	0.006102635	3.00563E-07	WNT4	BMP2, FGF13, FGF2, FGF8, WNT4	0.01220527	1.50281E-06
notochord formation	GO:0014028	3, 4, 5, 6, 7, 8, 9	Group1, Group2	25	0.004884938	3.005629479051135E-7, 3.9118554747208437E-5	EPHA2	CRB2, EFNA1, EPHA2, T	0.010855417	1.5028147395255675E-6, 9.77963868680211E-5
chorionic trophoblast cell differentiation	GO:0060718	4, 5	Group1	25	0.004884938	3.00563E-07	MAP3K4	DNMT3L, E2F7, E2F8, MAP3K4	0.010855417	1.50281E-06
D-gluconate metabolic process	GO:0019521	5, 6, 8, 9	Group0	33.33333206	0.003665827	0.010959322	PGD	IDNK, PGD, PHGDH	0.009164567	0.018265537
negative regulation of sister chromatid cohesion	GO:0045875	4, 5, 6, 7	Group1	33.33333206	0.003665827	3.00563E-07	ESPL1	ESPL1, RECQL4, WAPAL	0.009164567	1.50281E-06
axial mesoderm formation	GO:0048320	5, 6, 7, 8, 9	Group1, Group2	33.33333206	0.003665827	3.005629479051135E-7, 3.9118554747208437E-5	EPHA2	AXIN1, EPHA2, NODAL	0.009164567	1.5028147395255675E-6, 9.77963868680211E-5
positive regulation of dermatome development	GO:0061184	4, 5, 6, 7, 8	Group1	33.33333206	0.003665827	3.00563E-07	WNT4	WNT1, WNT3A, WNT4	0.009164567	1.50281E-06
renal vesicle induction	GO:0072034	4, 5, 6, 7, 8, 9, 10, 11, 12, 13	Group1	33.33333206	0.003665827	3.00563E-07	WNT4	SOX8, SOX9, WNT4	0.009164567	1.50281E-06
male germ-line sex determination	GO:0019100	5, 6, 7	Group1	50	0.002445302	3.00563E-07	MAP3K4	MAP3K4, SOX9	0.006986576	1.50281E-06
positive regulation of aldosterone biosynthetic process	GO:0032349	5, 6, 7, 8, 9, 10	Group1	50	0.002445302	3.00563E-07	WNT4	BMP6, WNT4	0.006986576	1.50281E-06
negative regulation of male gonad development	GO:2000019	3, 4, 5, 6, 7, 8, 9, 10	Group1	50	0.002445302	3.00563E-07	WNT4	ASMT, WNT4	0.006986576	1.50281E-06
notochord cell development	GO:0060035	4, 5, 6, 7, 8, 9	Group1, Group2	100	0.00122336	3.005629479051135E-7, 3.9118554747208437E-5	EPHA2	EPHA2	0.004077866	1.5028147395255675E-6, 9.77963868680211E-5
negative regulation of testicular blood vessel morphogenesis	GO:0061369	4, 5, 6, 7, 8, 9, 10, 11	Group1	100	0.00122336	3.00563E-07	WNT4	WNT4	0.004077866	1.50281E-06
positive regulation of cortisol biosynthetic process	GO:2000066	6, 7, 8, 9, 10, 11	Group1	100	0.00122336	3.00563E-07	WNT4	WNT4	0.004077866	1.50281E-06
negative regulation of testosterone biosynthetic process	GO:2000225	6, 7, 8, 9, 10	Group1	100	0.00122336	3.00563E-07	WNT4	WNT4	0.004077866	1.50281E-06

sex determination	GO:0007530	3, 4	Group1	8.695652008	0.000353281	3.00563E-07	MAP3K4, WNT4	AMH, CITED2, DHH, DMRT1, DMRT2, FGF9, FOXL2, IGF1R, INSR, INSR, MAP3K4, NR0B1, NR5A1, PTGDR, SF1, SOX3, SOX9, SRD5A1, SRY, TCF21, TMEM184A, WNT4, WT1	0.002355206	1.50281E-06
branching involved in mammary gland duct morphogenesis	GO:0060444	6, 7, 8, 9, 10	Group1, Group2	7.407407284	0.000488697	3.005629479051135E-7, 3.9118554747208437E-5	EPHA2, WNT4	BTRC, CAV3, CCL11, CSF1, CYP27B1, DDR1, EPHA2, ESR1, ETV4, ETV5, LRP5, LRP6, MBD4, MED1, MSX2, NCOA3, PGR, PHB2, PML, SLC12A2, SRC, TBX3, TFAP2C, TGFB1, VDR, WNT4, WNT5A	0.001954788	1.5028147395255675E-6, 9.77963868680211E-5
lens morphogenesis in camera-type eye	GO:0002089	3, 4, 6, 7, 8, 9, 10	Group2	8.333333015	0.000385116	3.91186E-05	EPHA2, PVRL3	BMP4, CITED2, CRYAA, CRYGB, CTNNA1, EPHA2, FGFR3, FOXE1, FOXE3, HIPK1, HIPK2, PITX3, POU2F1, PROX1, PVRL1, PVRL3, SHROOM2, SIX3, SKI, SOX1, SOX11, SOX2, TDRD7, TFAP2A	0.001925582	9.77964E-05
positive regulation of nuclear division	GO:0051785	4, 5, 6, 7	Group1	6.382978916	2.43279E-05	3.00563E-07	ESPL1, IL1A, WNT4	AURKA, BTC, CAMK2B, CD28, DAZL, DLGAP5, DMRT1, DRD3, EDN1, EDN3, EGF, EIF4G3, EPGN, EREG, ESPL1, FGF8, HOXA13, IGF1, IGF2, IL1A, IL1B, INS, INSR, LRP5, MSX1, MSX2, NFM2, NSMCE2, NUSAP1, PDGFB, PDGFRB, PHIP, PIWIL2, PLCB1, PLK1, PRDM9, PTEN, RB1, RGCC, SH2B1, SMC5, TERF1, TGFA, TNF, UBE2B, WNT4, WNT5A	0.000486558	1.50281E-06
non-canonical Wnt signaling pathway via MAPK cascade	GO:0038030	7, 8	Group1	28.5714283	2.96681E-05	3.00563E-07	FZD10, WNT4	DVL3, FZD10, FZD7, MYOC, NKD1, WNT4, WNT5A	0.000296681	1.50281E-06

20th Module										
cellular response to BMP stimulus	GO:0071773	4, 6	Group1	5	0.007702887	0.032020679	BMP2	ACVRL1, ADAMTS12, ADAMTS7, BMP2, CER1, COL2A1, DLX5, GARS, GATA3, GATA5, GATA6, HEYL, NOG, PHOX2B, RUNX2, SFRP1, SMAD1, SMAD5, TMEM100, TNMD	0.007702887	0.032020679

endocardial cushion morphogenesis	GO:0003203	5, 6, 7, 8, 9	Group1	5.882352829	0.006550616	0.032020679	BMP2	BMP2, BMPR1A, ENG, FGF8, HEY1, HEYL, ISL1, MSX1, MSX2, NOTCH1, RBPJ, SMAD4, SNAI2, SOX9, TBX2, TBX20, TWIST1	0.007146127	0.032020679
positive regulation of osteoblast proliferation	GO:0033690	4, 5, 6	Group1	11.11111069	0.003472442	0.032020679	BMP2	BMP2, CTHRC1, CYR61, GATA1, HPSE, ITGAV, LRP5, LTF, SOX8	0.005208663	0.032020679
atrioventricular valve morphogenesis	GO:0003181	4, 5, 6, 7, 8, 9, 10	Group1	10	0.003857648	0.032020679	BMP2	BMP2, CYR61, GATA4, HEY1, HEYL, JUP, NOTCH1, SMAD4, TBX5, ZFPM1	0.005143531	0.032020679
telencephalon regionalization	GO:0021978	4, 5, 6, 7, 8, 9, 10	Group1	9.090909004	0.00424273	0.032020679	BMP2	BHLHE22, BMP2, BMP4, EMX1, EMX2, EOMES, LHX2, NR2F1, NR2F2, PAX6, SHH	0.005091276	0.032020679
positive regulation of prostaglandin secretion	GO:0032308	5, 6, 7, 8, 9, 10, 11, 12, 13, 14	Group0	9.090909004	0.00424273	0.006166278	PLA2G10	AMH, IL1B, MAPK9, MIF, OXT, P2RX4, PLA2G10, S100A8, S100A9, TNFRSF11A, TNFSF11	0.005091276	0.012332557
negative regulation of calcium-independent cell-cell adhesion	GO:0051042	5, 6, 7	Group1	100	0.000386324	0.032020679	BMP2	BMP2	0.00463589	0.032020679
cellular response to magnesium ion	GO:0071286	6	None	50	0.000772524	NaN	FBP1	FBP1, RYR3	0.004635143	NaN
BMP signaling pathway involved in heart induction	GO:0003130	6, 7, 8, 9, 10, 11, 12, 13	Group1	33.33333206	0.001158599	0.032020679	BMP2	BMP2, BMP4, POU5F1	0.004634397	0.032020679
negative regulation of cardiac muscle cell differentiation	GO:2000726	6, 7, 8, 9, 10, 11	Group1	33.33333206	0.001158599	0.032020679	BMP2	BMP2, DKK1, PRICKLE1	0.004634397	0.032020679
negative regulation of aldosterone biosynthetic process	GO:0032348	5, 6, 7, 8, 9, 10	Group1	25	0.00154455	0.032020679	BMP2	BMP2, BMP5, DKK3, REST	0.004633651	0.032020679
corticotropin hormone secreting cell differentiation	GO:0060128	4, 5, 6, 7, 8, 9, 10, 11, 12	Group1	25	0.00154455	0.032020679	BMP2	BMP2, FGF13, FGF2, FGF8	0.004633651	0.032020679
negative regulation of cholesterol efflux	GO:0090370	6, 7, 8, 9, 10	Group0	25	0.00154455	0.006166278	PLA2G10	EGF, PLA2G10, SHH, SREBF2	0.004633651	0.012332557
negative regulation of cortisol biosynthetic process	GO:2000065	6, 7, 8, 9, 10, 11	Group1	25	0.00154455	0.032020679	BMP2	BMP2, BMP5, DKK3, REST	0.004633651	0.032020679
thyroid-stimulating hormone-secreting cell differentiation	GO:0060129	4, 6, 7, 8, 9, 10, 11, 12	Group1	20	0.001930377	0.032020679	BMP2	BMP2, FGF13, FGF2, FGF8, WNT4	0.004632905	0.032020679
negative regulation of Wnt signaling pathway involved in heart development	GO:0003308	5, 6, 7, 8, 9, 10, 11	Group1	16.66666603	0.00231608	0.032020679	BMP2	BMP2, DKK1, JUP, LRP6, MESP1, SOX17	0.004632159	0.032020679
bone mineralization involved in bone maturation	GO:0035630	5, 6, 7, 8, 9	Group1	16.66666603	0.00231608	0.032020679	BMP2	BMP2, GREM1, IGF1, LEP, LTF, PHOSPHO1	0.004632159	0.032020679

negative regulation of insulin-like growth factor receptor signaling pathway	GO:0043569	4, 5, 6, 7, 8, 9, 10	Group1	14.28571415	0.002701658	0.032020679	BMP2	ATXN1, ATXN7, BMP2, BMP5, CILP, IGFBP5, NKX3-1	0.004631414	0.032020679
positive regulation of arachidonic acid secretion	GO:0090238	5, 6, 7, 8, 9, 10, 11, 12, 13, 14	Group0	14.28571415	0.002701658	0.006166278	PLA2G10	AMH, MIF, PLA2G10, PLA2G6, PLA2R1, S100A8, S100A9	0.004631414	0.012332557
positive regulation of p38MAPK cascade	GO:1900745	7, 8, 9, 10, 11	Group1	14.28571415	0.002701658	0.032020679	BMP2	BMP2, GADD45A, GADD45B, GADD45G, MAP3K4, VEGFA, XDH	0.004631414	0.032020679

GO Biological Process: the name of the GO BP; Go ID: the name of the GO BP; GO Levels: the GO level the GO BP; Group: GO BPs were functionally grouped that reflects the relationships between the terms based on the similarity of their associated genes; Term Pvalue: p-value for the GO BP before BH-corrected; Group Pvalue: p-value for the GO BP group before BH-corrected; Annotated Genes: names of the annotated genes; All Association Genes: names of all the association genes in the group; Term Pvalue BH-corrected: p-value for the GO BP after BH-corrected; Group Pvalue BH-corrected: p-value for the GO BP group after BH-corrected;