Supplementary table

Table 1S - Summary of significant associations found between expression profile and GO term trees.

Hier. Clust. Pearson 0H-48H		**Hier. Clust. Euclid. 0H-48H**		**Hier. Clust. Euclid. 0H-4H**	
All GO terms					
Genes	**Associated terms**	**Genes**	**Associated terms**	**Genes**	**Associated terms**
p= 0.0046* CIRBP FOXD1 GABPB2 KLF4 PHLDA1 PTGS2 SOX4	-transcription factor activity -regulation of transcription DNA-dependent -nucleus	p= 0.032^{+} ABCC3 ANXA4 CAMKK2 G6PC GPR147 KCNAB2 LIM2 MGC4809 MYL9 PKD2L1 SEC14L1 SLC7A4 TMEFF1	-ATP bonding -intracellular -golgi apparatus -calcium ion binding -integral to membrane -transport -transporter activity	p= 0.016$^{\&}$ AKR1C1 HMGCS1 OASL	-transferase activity -cytoplasm
p= 0.028* ABCC3 AKR1C1 AKR1C3 ANXA4 CAMKK2 CROT DHCR7 FDFT1 G6PD HMGCS1 HSD17B7 IDI1 KCNAB2 MGC4809 MYL9 OASL PECR PTGER4 SC4MOL SEC14L1 SQLE	-immune response -ATP binding -intracellular -transferase activity -calcium ion binding -lipid metabolism -cytoplasm -trans-l,2-dihydrobenzene-1,2-diol dehydrogenase -aldo-keto reductase activity -electron transporter activity -binding -fatty acid metabolism -metabolism -sterol biosynthesis -peroxisome -endoplsmic reticulum -integral to membrane -steroid biosynthesis -oxidoreductase activity -isoprenoid biosynthesis -cholesterol biosynthesis -magnesium ion binding -transport -transporter activity -microsome	p= 0.037* APBA1 FLRT3 KBTBD4 LDLR MSR1 NINJ2 PTPRF	-cell adhesion -protein binding -integral to plasma membrane -receptor activity -lipid transporter activity	p= 0.037$^{\&}$ CLIC3 PPP2R2B SLC12A3	-signal transduction -chloride transport -ion transport -membrane fraction
GO molecular function terms					
p= 0.027^{+} FOXD1 GABPB2 KLF4 PTPRF SOX4	-protein binding -zinc ion binding -transcription factor activity	p= 0.013* ANXA4 LDLR MGC4809 MYL9 PKD2L1	-calcium ion binding	p= 0.025^{+} ANXA4 LDLR MGC4809 MYL9 PKD2L1	-calcium ion binding
GO biological process terms					
p= 0.01* DNAJB1 HSPA1B	-response to unfolded proteins -protein folding	p= 0.045^{+} (0,068) FOXD1 SOX4	-regulation of transcription, DNA-dependent	p=0.045^{+} (0,079) FOXD1 SOX4	-regulation of transcription, DNA-dependent
p=0.032^{+} FOXD1 GABPB2 SOX4	-regulation of transcription, DNA-dependent	p= 0.0045* AKR1C3 FDFT1 IDI1	-isoprenoid biosynthesis -cholesterol biosynthesis	p= 0.003* DHCR7 HMGCS1	-cholesterol biosynthesis
p=0.031^{+} ABCC3 CROT HSD17B7 PECR SC4MOL SEC14L1 SQLE	-transport -sterol biosynthesis -fatty acid metabolism -metabolism	p= 0.017* C11orf8 FLRT3 NINJ2	-neurogenesis -cell adhesion	p= 0.013* C3 IL18 OASL PTGER4	-immune response -G-protein coupled receptor protein signaling
p= 0.005* AKR1C3 DHCR7 FDFT1 HMGCS1	-lipid metabolism -isoprenoid biosynthesis -cholesterol biosynthesis	p= 0.0093* C3 IL18 OASL PTGER4	-immune response -G-protein coupled receptor protein signaling		

IDI1 LDLR					
GO cell component terms					
p= 0.024* CIRBP FOXD1 GABPB2 KLF4 PHLDA1 PTGS2 PTPRF SOX4	-nucleus	p= 0.035$^+$ ABCC3 DTR FLRT3 LDLR NINJ2 SLC12A3	-integral to plasma membrane -membrane fraction	p= 0.0042* ABCC3 DTR FLRT3 LDLR NINJ2 SLC12A3	-nucleus
p= 0.0002* CAMKK2 SEC14L1 SMURF	-intracellular	p= 0.0087* DHCR7 SC4MOL	-endoplasmic reticulum -integral to membrane	p= 0.024* G6PC GPR147 SLC7A4 TMEFF1	-integral to membrane
		p= 0.014$^+$ AKR1C1 HMGCS1 OASL	-cytoplasm	p= 0.017* HMGCS1 OASL	-cytoplasm
		p= 0.041$^+$ VEGF CXCL2	-soluble fraction	P= 0.014$^+$ C3 IL18	-extracellular
				p= 0.041$^+$ VEGF CXCL2	-soluble fraction
				p= 0.03* SMURF1 CAMKK2	-intracellular
GO molecular function + biological process terms					
p= 0.0085* DNAJB1 HSPA1B	-response to unfolded protein -protein folding	p= 0.031* CROT HMGCS1 OASL	-transferase activity	p= 0.006* FDFT1 G6PD IDI1 SC4MOL	-isoprenoid biosynthesis -cholesterol biosynthesis -magnesium ion binding -oxidoreductase activity
p= 0.006* ASB9 G6PD HSD17B7 IDI1 SC4MOL	-isoprenoid biosynthesis -cholesterol biosynthesis -magnesium ion binding -steroid biosynthesis -oxidoreductase activity -metabolism -sterol biosynthesis	p= 0.028* ABCC3 G6PC SEC14L1 SLC7A4	-transport -transporter activity	p= 0.006* FOXD1 SOX4	-transcription factor activity -regulation of transcription, DNA-dependent
p= 0.034$^+$ FOXD1 GABPB2 KLF4 PTPRF SOX4	-transcription factor activity -regulation of transcription, DNA-dependent -protein binding	p= 0.0063* CLIC3 PPP2R2B SLC12A3	-signal transduction -chloride transport -ion transport	p= 0.013* C3 IL18 PTGER4	-immune response -G-protein coupled receptor protein signaling
		p= 0.0063* FDFT1 IDI1	-isoprenoid biosynthesis -cholesterol biosynthesis -magnesium ion binding		
		p= 0.0056$^+$ DHCR7 G6PD SC4MOL	-oxidoreductase activity		
		p= 0.0084* ANXA4 LDLR LPIN1 MGC4809 MYL9 PKD2L1 SMURF1	-molecular function unknown -calcium ion binding		
		p= 0,0084* ABPA1 CRSP2 FLRT3 KBTBD4 MSR1 NINJ2 ZHX2 ZNF297B ZNF81	-zinc ion binding -transcription factor activity -regulation of transcription, DNA-dependent -cell adhesion -protein binding -neurogenesis -DNA binding -receptor activity		
		p= 0,031* C3 IL18 PTGER4	-immune response -G-protein coupled receptor protein signaling		
GO molecular function + cell component terms					

p= 0.009* CIRBP FOXD1 KLF4 PHLDA1 PTGS2 SOX4	-nucleus -transcription factor activity	p=0.0035* CIRBP PHLDA1	-nucleus	p= 0.0035* CIRBP PHLDA1	-nucleus
p= 0.011* NUDT6 PPP3CC	-hydrolase activity	p= 0.0059* FOXD1 SOX4	-nucleus -transcription factor activity	p= 0.011* ZNF81 ZHX2	-nucleus -zinc ion binding -transcription factor activity
p= 0.0003* GPR147 TMEFF1 LIM2 SLC7A4	-integral to membrane	p= 0.022* DTR MSR1	-integral to plasma membrane -receptor activity	p=0.0059* FOXD1 SOX4	-nucleus -transcription factor activity
p= 0.027* DHCR7 FDFT1 HSD17B7 SC4MOL	-endoplasmic reticulum -integral to membrane -oxidoreductase activity	p= 0.0015* GPR147 LIM2 SLC7A4 TMEFF1	-integral to membrane	p= 0.022* NUDT6 PPP3CC	-hydrolase activity
p= 0.011* SEC14L1 SMURF1	-intracellular	p= 0.0047* ANXA4 CAMKK2 LDLR MGC4809 MYL9 PKD2L1	-calcium ion binding	p= 0.011* DTR MSR1	-integral to plasma membrane -receptor activity
				p= 0.0028* HMGCS1 OASL	-transferase activity -cytoplasm
				p= 0.011* C3 IL18	-extracellular
				p= 0.0084* GPR147 LIM2 SLC7A4 TMEFF1	-integral to membrane
				p= 0.025* ANXA4 CAMKK2 LDLR MGC4809 MYL9 PKD2L1	-calcium ion binding
GO biological process + cell component terms					
p= 0.0012* CIRBP FOXD1 GABPB2 PHLDA1 SOX4	-nucleus -regulation of transcription, DNA-dependent	p= 0.0013* CIRBP PHLDA1	-nucleus	p= 0.0013* CIRBP PHLDA1	-nucleus
p= 0.012* DNAJB1 HSPA1B	-response to unfolded protein -protein folding -nucleus	p= 0.0064* CLIC3 SLC12A3	-chloride transport -ion transport -membrane fraction	p= 0.0051* CLIC3 CRSP2 FLRT3 HSPA1B LPIN1 NINJ2 SLC12A3 TREX1	-chloride transport -ion transport -membrane fraction -nucleus -cell adhesion -integral to plasma membrane
p= 0.024* DHCR7 FDFT1 HSD17B7 SC4MOL	-metabolism -endoplasmic reticulum -integral to membrane -steroid biosynthesis -cholesterol biosynthesis	p= 0.014* C11orf8 FLRT3 NINJ2	-neurogenesis -cell adhesion -integral to plasma membrane		
p= 0.0038* CHST3 PKD2L1	-integral to membrane				
p= 0.018* GPR147 LIM2 TMEFF1	-integral to membrane				
p= 0.0004* CAMKK2 SEC14L1 SMURF1	-intracellular				

FDR correction for multiple testing: *: significant when FDR= 5%; $^{+}$: significant when FDR= 10%; $^{\&}$: significant when FDR= 15%.