Supplemental Material

Melanocortin-1 Receptor Positively Regulates Human Artery Endothelial Cell Migration

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Supplemental Methods

Quantitative real time PCR (qPCR)

We used single tube qPCR for assessing mRNA expression of the melanocortin receptors (MCRs), proopiomelanocortin (POMC), and prohormone convertases genes. Primers and probes were chosen among predesigned and validated Applied Biosystems TaqMan Gene Expression Assays (brand of Thermo Fisher Scientific, Waltham, MA, USA). Assay IDs were Hs00267168_s1 (MC1R), Hs00265039_s1 (MC2R), Hs00252036_s1 (MC3R), Hs00271877_s1 (MC4R), Hs00271882_s1 (MC5R), Hs01596743_m1 (POMC), Hs01026107_m1 (proprotein convertase subtilisin/kexin type 1, PCSK1), Hs01037347_m1 (PCSK2), Hs00159829_m1 (furin, PCSK3), Hs00159844_m1 (PCSK6), Hs00161638_m1 (secretogranin V, SCG5), and Hs99999902_m1 (ribosomal protein large P0, RPLP0, used as endogenous reference gene). Details on chromosome location on GRCh38 human genome assembly, genomic map, assay location on NCBI RefSeq and GenBank mRNA sequences, exon boundary, and amplicon length for each assay are available a: https://www.thermofisher.com/it/en/home/life-science/pcr/real-time-pcr/real-time-pcr-assays/taqman-gene-expression/single-tube-taqman-gene-expression-analysis.html.

Reaction conditions and thermocycling parameters were derived from the manufacturer's TaqMan Gene Expression Assays protocol (https://tools.thermofisher.com/content/sfs/manuals/cms_041280.pdf). Briefly, for all single reactions we used 1 µL of 20× TaqMan Gene Expression Assay, 10 µL of 2× TaqMan Gene Expression Universal Master Mix, and 20 ng of cDNA template, in a final volume of 20 µL. Reagents were handled with a MicroLab STAR automated liquid handling workstation (Hamilton Robotics, Bonaduz, Switzerland) to minimize dispensing error. Thermal cycling conditions were: an initial 10-minute denaturation step at 95°C, followed by 40 cycles of 15 seconds at 95°C (denaturation) and 1 minute at 60°C (annealing/extension), with standard ramp rate. Each assay were run in triplicate on a ViiA 7 Real-time PCR System (Applied Biosystems). Along with the assays, we run no-template controls in triplicate, which repeatedly resulted negative.

Efficiency of predesigned TaqMan Gene Expression Assays was extensively tested by the manufacturer and showed to be 100% ± 10%, with a $R^2 > 0.95$, when measured over 6 orders of magnitude (see the Applied Biosystems online *Application Note* https://assets.thermofisher.com/TFS-Assets/LSG/brochures/ap-taqman-gene-expression-assays.pdf).

Supplemental Figures

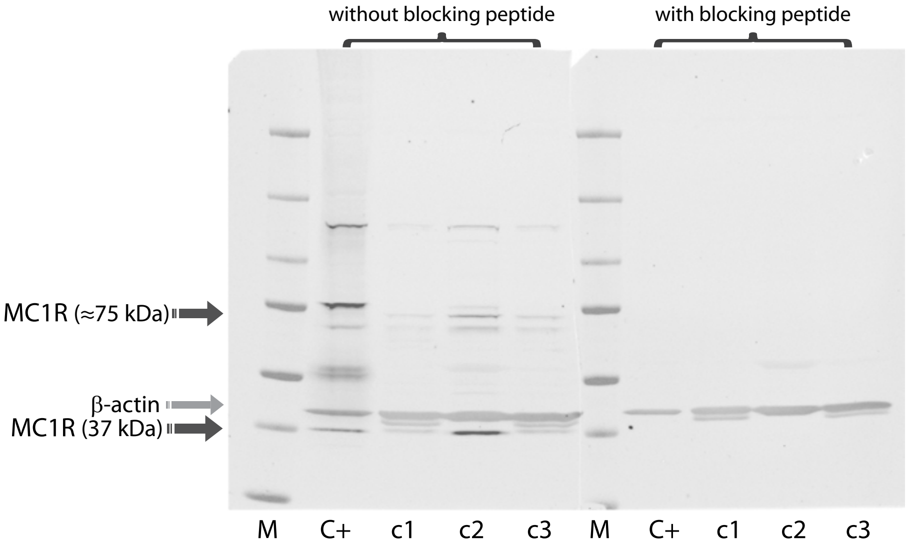

Fig. S1 | Full-length Western blot for assessment of the specificity of the anti-MC1R antibody by peptide block. HEK293 cells were transiently transfected with the MC1R full-length cDNA cloned in a pCMV6 mammalian expression vector. Total cell lysates from HEK293 transfected cells and from the three tested human aortic endothelial cells (HAoECs) were resolved and probed with the anti-MC1R antibody AMR-020 both with (*right blot*) or without (*left blot*) prior incubation with the MC1R antigenic peptide (Alomone Labs). A 37 kDa immunoreactive band, corresponding to the canonical fully active MC1R (indicated by the dark grey arrow), and ≈75 kDa bands, indicative of MC1R dimers (upper dark grey arrow), were detected in the positive control (transfected HEK293) and in the three HAoEC lysates analysed (*left blot*). Pre-absorption of the MC1R antibody with the blocking peptide (2-fold excess by weight) resulted in complete abrogation of the MC1R signal from all extracts, demonstrating antibody specificity (*right blot*). The β-actin immunoreactive band (light grey arrow) served as reference control. Lanes are: M, molecular weight marker; C+, HEK293 cells transiently transfected with the MC1R-pCMV6 construct; c1, c2, and c3 are the three different primary HAoECs (c1 – from ECACC, c2 – Lonza, and c3 – Promocell).

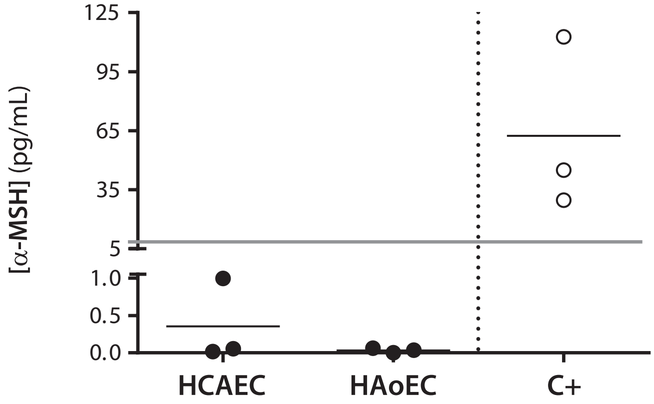

Fig. S2 | Human primary coronary artery (HCAEC) and aortic (HAoEC) endothelial cells do not release α-MSH. Filled dots denote primary cells (*n* = 3 for each type), while open dots indicate the positive control (C+) of the EIA kit (Phoenix Pharmaceuticals); the mean level detected in culture supernatants is also reported as an horizontal line. The grey horizontal line denotes the minimum detectable concentration of the ultrasensitive EIA assay, which is 8.9 pg/mL.

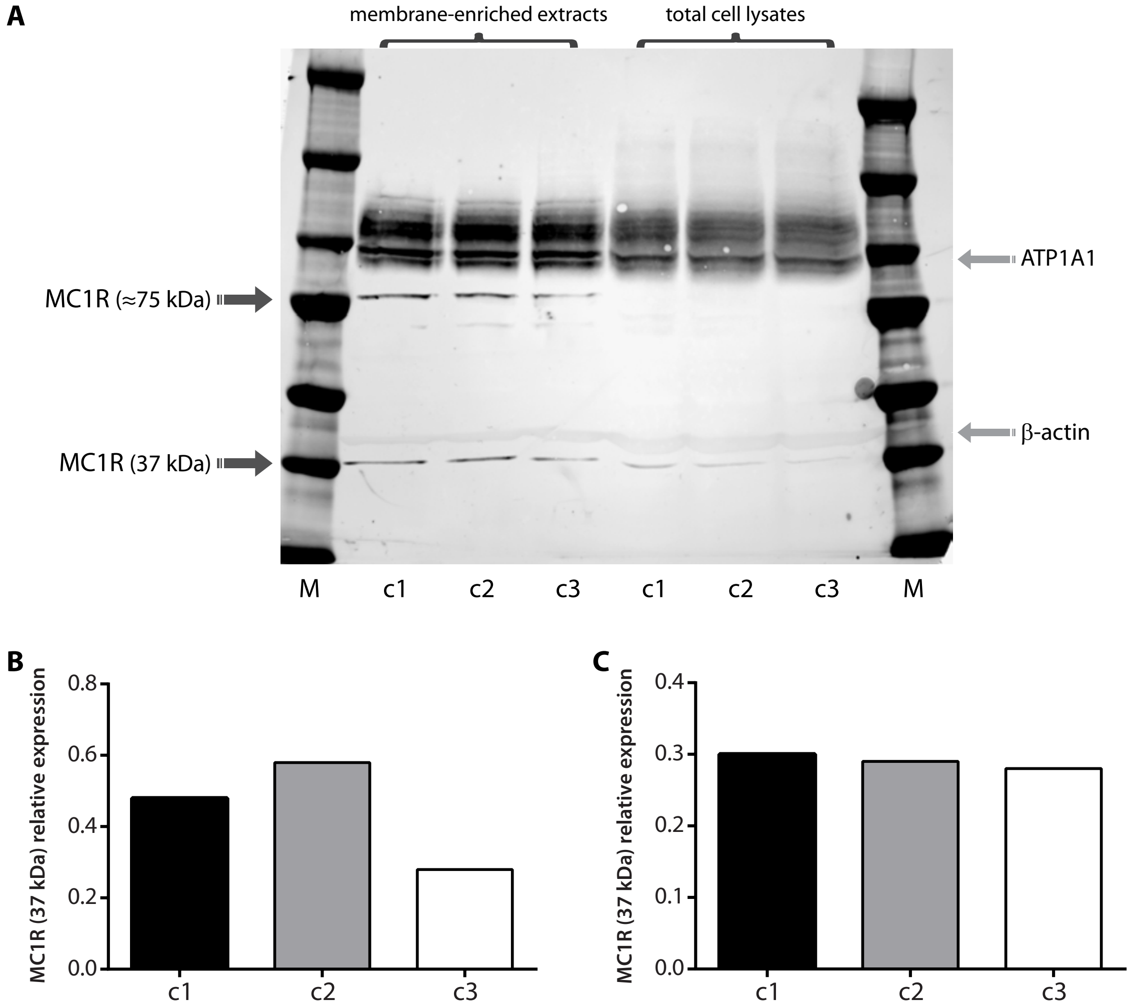

Fig. S3 | Western blot for detecting MC1R in human aortic endothelial cells (HAoECs). (**A**) Immunoblot analysis of membrane extracts (lanes 2-4 *on the left*) showed that all three studied primary HAoECs express MC1R on the plasma membrane. For comparison, we performed a side-by-side immunoblot of HAoEC total cell lysates (lanes 5-7 *on the right*), using an equal amount of protein extract (30 µg). Immunoreactive bands of 37 kDa and 75 kDa specific for monomeric and dimeric isoforms of MC1R, respectively, are indicated by grey arrows (*on the left*). Anti-ATPase Na+/K+ transporting subunit alpha 1 (ATP1A1) and anti-β-actin antibodies were used as reference controls (light grey arrows *on the right*). Lanes are: M, molecular weight marker; c1, c2, and c3, primary HAoECs (c1 – from ECACC, c2 – Lonza, and c3 – Promocell). Panels (**B**) and (**C**) show the densitometric analysis of the MC1R 37 kDa band, normalized to the indicated ATP1A1 band, in the membrane-enriched extracts and in the total cell lysates, respectively.

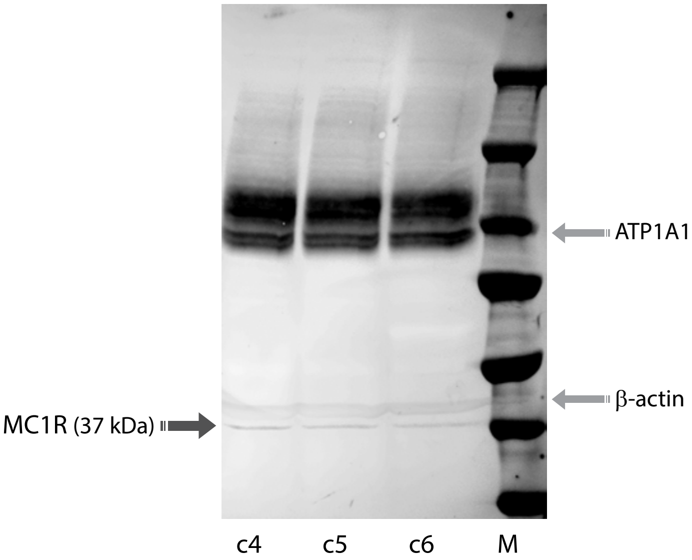

Fig. S4 | Western blot for detecting MC1R in human coronary artery endothelial cells (HCAECs). Immunoblot analysis of total cell lysates showed that all three studied primary HCAECs express the MC1R protein. The immunoreactive band of 37 kDa specific for the MC1R protein monomer is indicated by a grey arrow (*on the left*). The ATPase Na+/K+ transporting subunit alpha 1 (ATP1A1) protein and β-actin were probed as reference controls (light grey arrows *on the right*). Lanes are: c4, c5, and c6, primary HCAECs (c4 – from ECACC, c5 – Lonza, and c6 – Promocell); M, molecular weight marker.

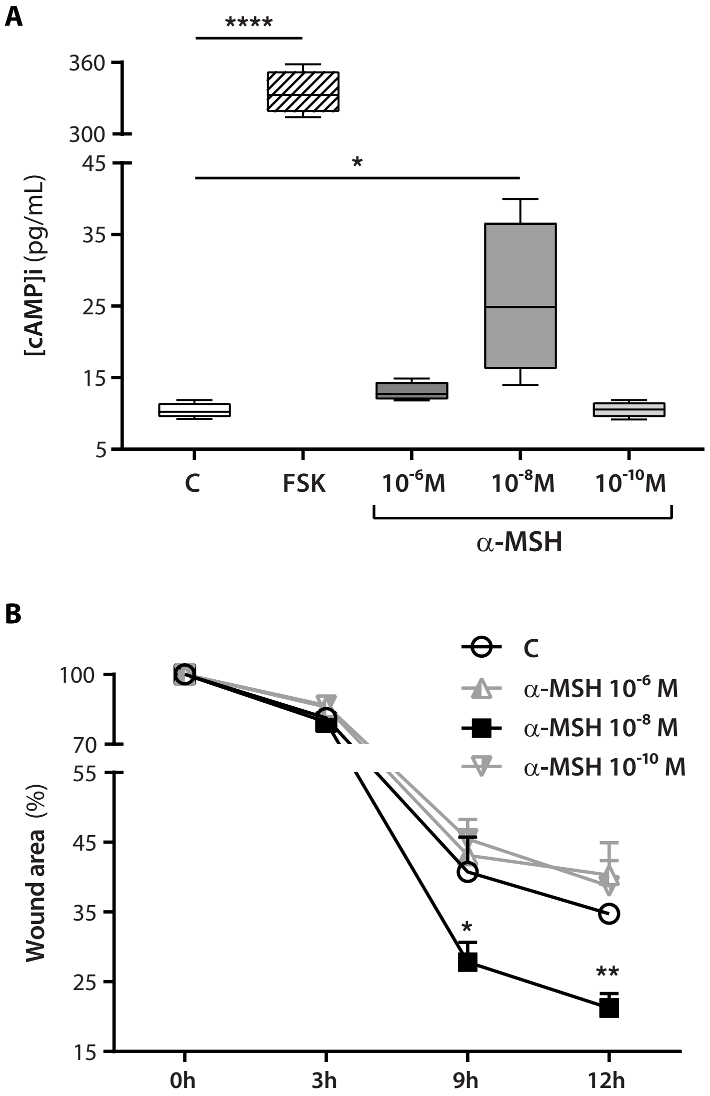

Fig. S5 | Dose-response assessment of α-MSH effects on intracellular cAMP biosynthesis and cell migration in human aortic endothelial cells (HAoECs). (**A**) Intracellular cAMP concentrations were measured in confluent HAoECs after treatment with α-MSH at the indicated decreasing concentrations for 5 min. Cells only pre-treated for 30 min with IBMX 0.1 mM (to inhibit cAMP degradation by PDEs) were used as negative controls (C), whereas cells stimulated with forskolin 10 µM (FSK, an activator of adenylyl cyclase) served as positive controls. Box and whiskers present the results of 4 independent experiments. Statistical significance of differences was assessed by one-way ANOVA [$F_{(4,15)} = 905.5$, $p<0.0001$] followed by Benjamini-Hochberg test (*$p<0.05$, ****$p<0.0001$). (**B**) Directional migration assay was performed stimulating cells with the indicated decreasing concentrations of α-MSH. Results are shown as mean ± SEM ($n = 3$). Statistical significance was assessed by two-way ANOVA [$F_{(9,32)} = 2.63$, $p=0.0211$, for interaction; $F_{(3,32)} = 14.1$, $p<0.0001$, treatment effect] with Dunnett's multiple comparisons test (*$p<0.05$, **$p<0.01$).

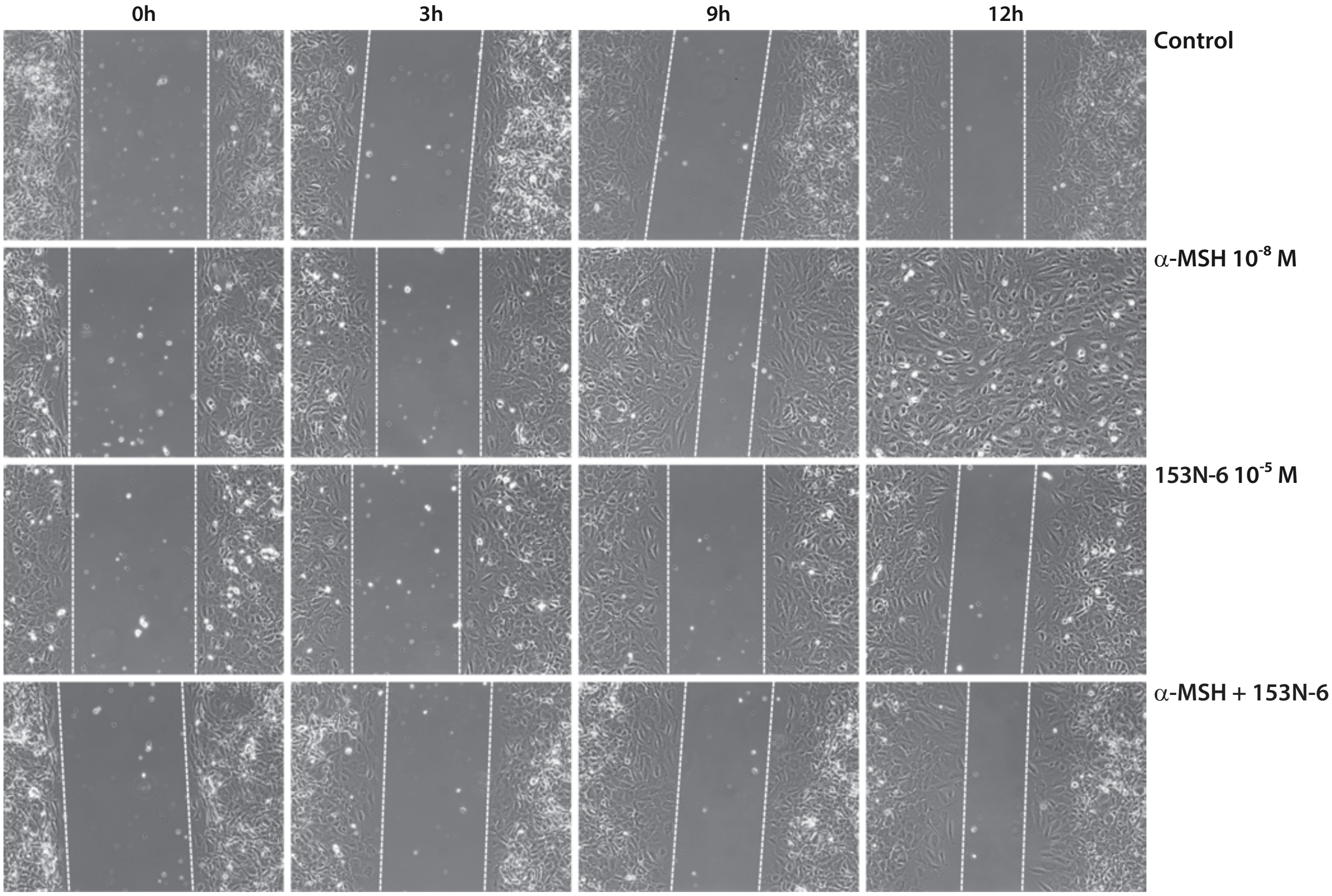

Fig. S6 | MC1R activation accelerates migration of human aortic endothelial cells (HAoECs). Representative sequential microphotographs, illustrating the influence of MC1R stimulation on HAoECs in a directional cell migration assay, were recorded by time-lapse confocal microscopy imaging (10×). Cells (c2 – Lonza) were seeded onto 24-well plates with culture inserts (IBIDI) and, after insert removal, allowed to migrate for 12h at 37°C and 5% CO_2 in the presence of 10^{-8} M α-MSH, with or without the MC1R-selective α-MSH antagonist 153N-6 10^{-5} M, or in medium alone (Control).

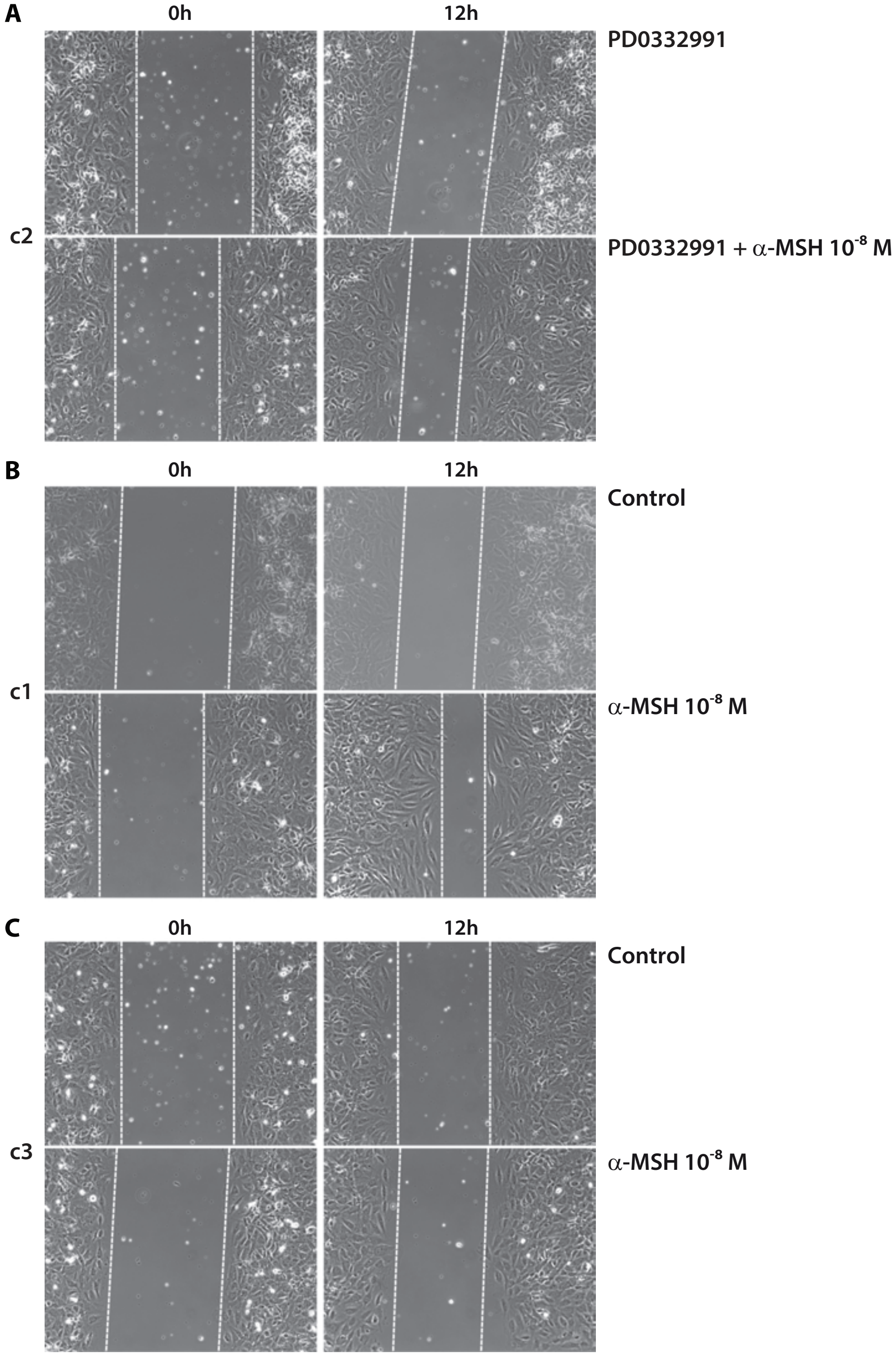

Fig. S7 | Control experiments for MC1R-mediated acceleration of human aortic endothelial cell (HAoEC) migration. Representative sequential microphotographs were recorded by time-lapse confocal microscopy imaging (10×). Cells were seeded as described in Fig. S6 legend, in the presence of 10^{-8} M α-MSH or in medium alone (Control). (**A**) Directional migration assay was performed in the presence of the proliferation inhibitor PD0332991 with HAoECs no. c2 (from Lonza). (**B**) The migration assay was repeated with HAoECs no. c1, the other cell line bearing wild-type *MC1R* alleles (from ECACC). (**C**) The migration assay was finally repeated with HAoECs no. c3, carrying a loss-of-function mutation in the *MC1R* gene (from Promocell).

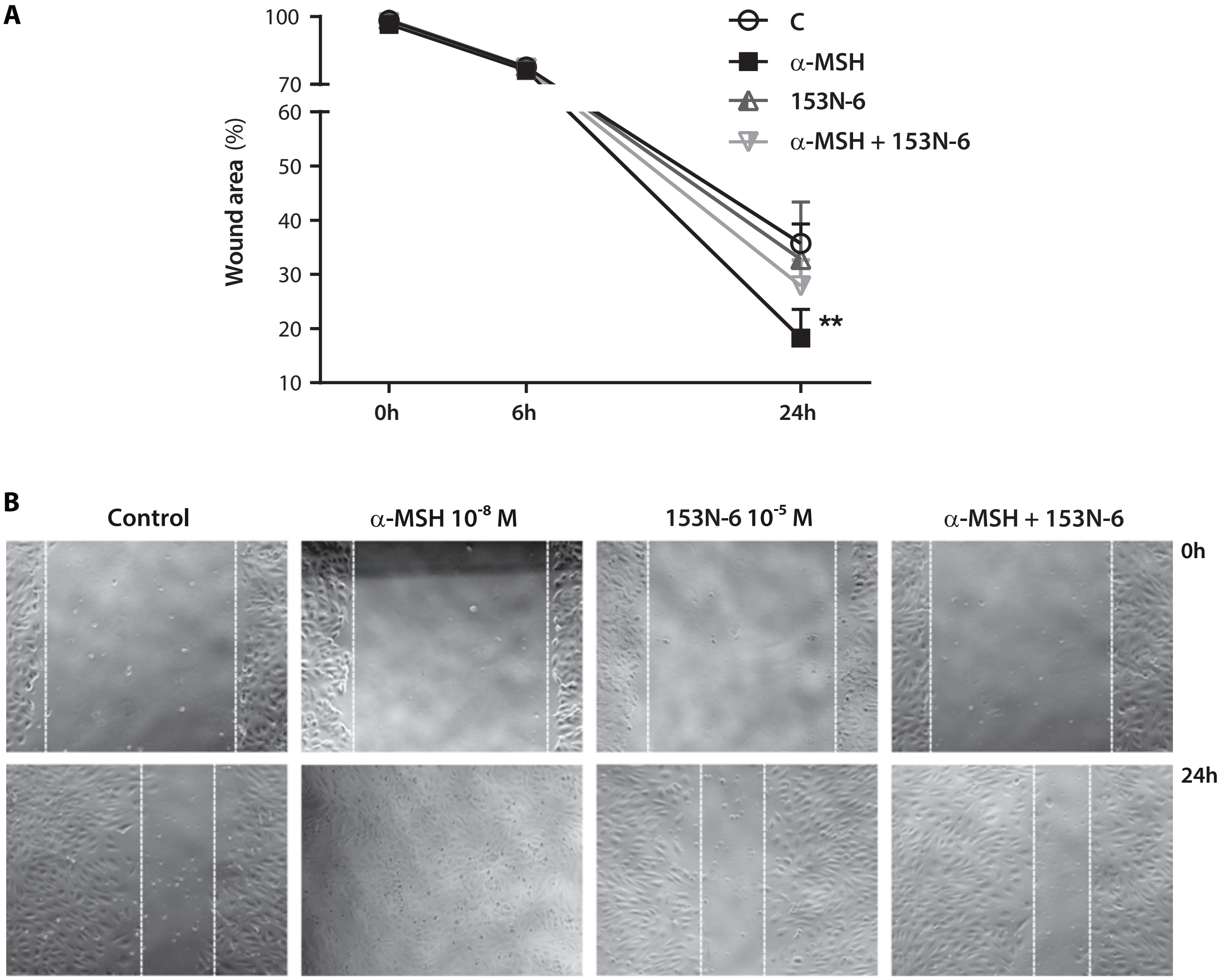

Fig. S8 | Human aortic endothelial cells (HAoECs) show accelerated migration upon activation of MC1R in *in vitro* scratch wound healing assay. (**A**) HAoECs (Lonza) were seeded into 6-well tissue culture plates at a density of 2.5 × 10^3 cells/cm^2 and grown to confluence. A "wound gap" in cell monolayers was created by scratching a straight line with a pipette tip, and HAoECs were allowed to migrate for 24 h at 37°C and 5% CO_2 in the presence of α-MSH 10^{-8} M, with or without the MC1R-selective α-MSH antagonist 153N-6 10^{-5} M, or medium alone (C). Plates were scanned by time-lapse confocal microscopy imaging (10×) at 0, 6, and 24 h, and images analysed with the NIH ImageJ software v1.38x. Results show the means ± SEM of 4-7 independent experiments. Statistical significance was assessed by two-way ANOVA followed by Bonferroni's multiple comparisons test (**$p<0.01$). (**B**) Representative microphotographs illustrating the influence of MC1R stimulation with α-MSH on HAoECs in the wound healing assay at 24h, recorded by time-lapse confocal microscopy imaging.

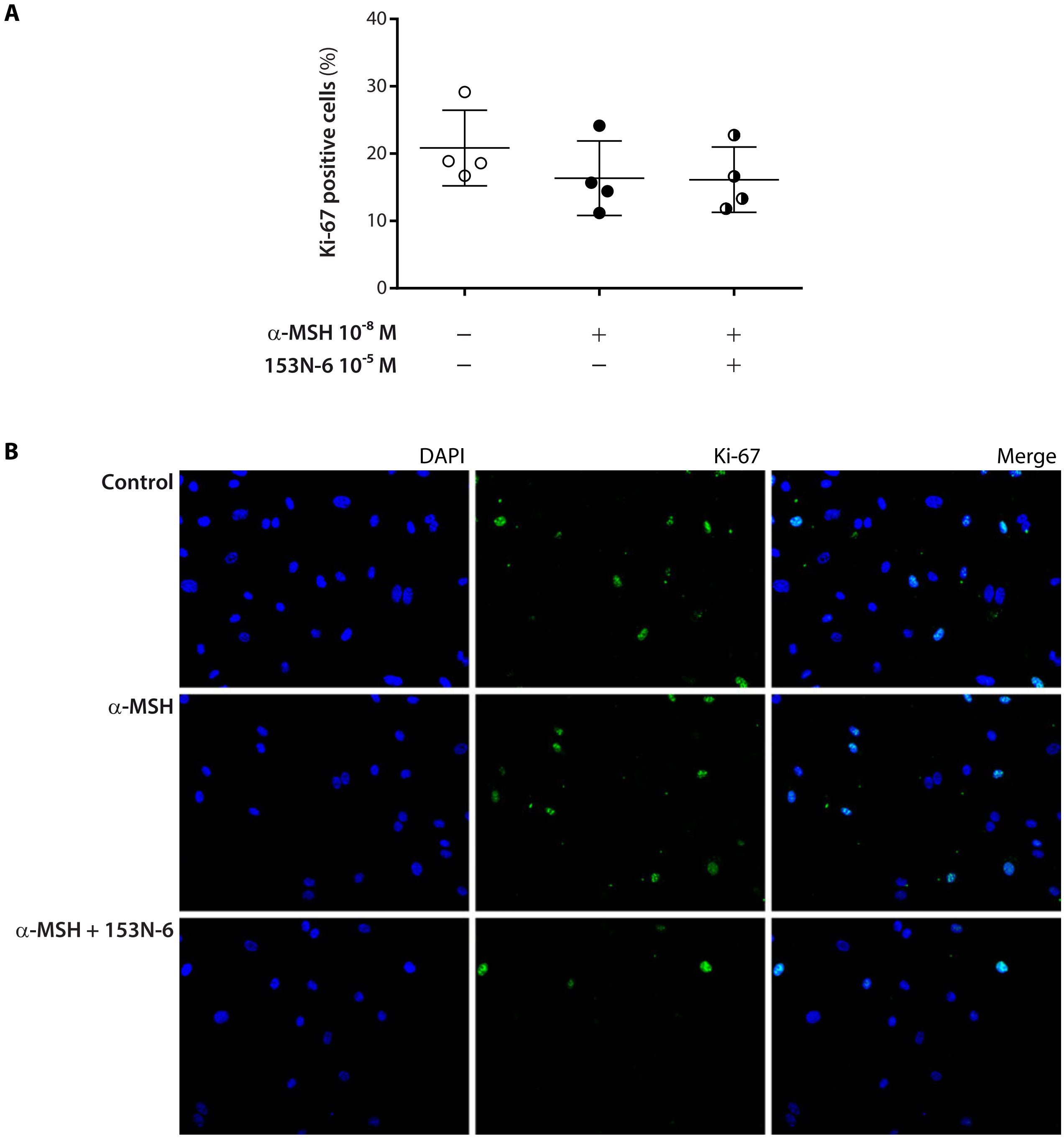

Fig. S9 | MC1R activation does not significantly influence HAoEC proliferation. (**A**) Quantification of Ki-67 positive cells in separate experiments showed no significant differences between control and stimulated HAoECs. Data are expressed as percentage of Ki-67 positive cells, counting 10 different fields for each treatment conditions using an ImageJ tool. Results are shown as a scatter dot plot with mean ± SD (*n* = 4 independent experiments); p = n.s. by one-way ANOVA. (**B**) Representative fluorescence microphotographs (20×) of cells double-stained with Ki-67 and DAPI cultured for 24h, illustrating the scarce influence of MC1R stimulation on cell proliferation.

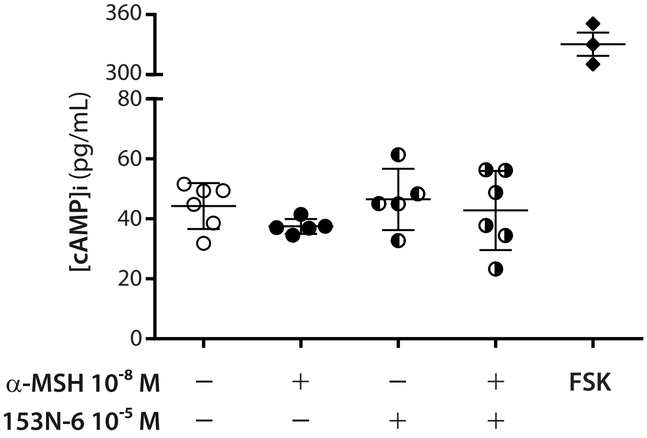

Fig. S10 | α-MSH does not increase intracellular cAMP biosynthesis in migrating human aortic endothelial cells (HAoECs). Intracellular cAMP production was detected during a directional cell migration assay in 24-well plates with culture inserts. After insert removal, HAoEC monolayers were stimulated with α-MSH 10^{-8} M, in the presence or not of the MC1R-selective competitive α-MSH antagonist 153N-6, for 5 min. Intracellular cAMP concentrations were measured using the cAMP Biotrak enzyme immunoassay (GE Healthcare). The scatter dot plot presents the results of 5–6 independent experiments, along with the mean ± SD; p = n.s. by one-way ANOVA and Tukey's multiple comparisons *post-hoc* test. Forskolin 10 µM (FSK) was used as positive control (*n* = 3).

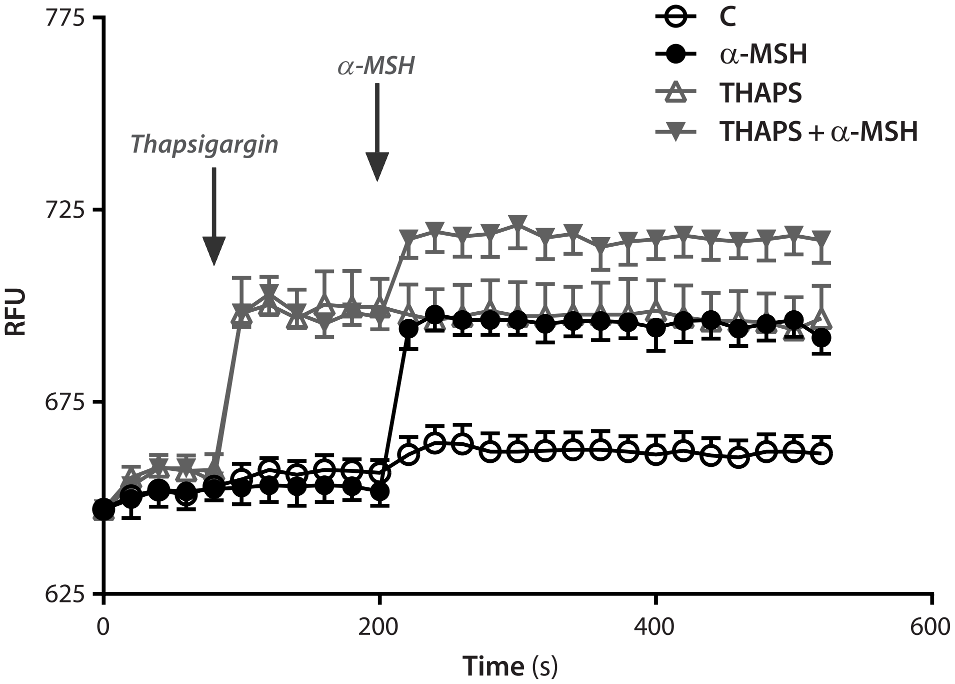

Fig. S11 | α-MSH increases intracellular calcium levels in confluent human aortic endothelial cells (HAoECs). Stimulation of HAoECs grown to confluence with α-MSH 10^{-8} M induced an increase in intracellular Ca^{2+} levels, similar to that induced by thapsigargin (THAPS) 10^{-8} M. A previous stimulation with thapsigargin 10^{-8} M prevented a further rise of intracellular Ca^{2+} in response to α-MSH 10^{-8} M. Intracellular Ca^{2+} was detected using the Fluo-4 NW fluorescent calcium indicator. Arrows indicate the time when either thapsigargin or α-MSH were added. Curves represent the means ± SEM of three separate experiments. RFU, relative fluorescence unit.

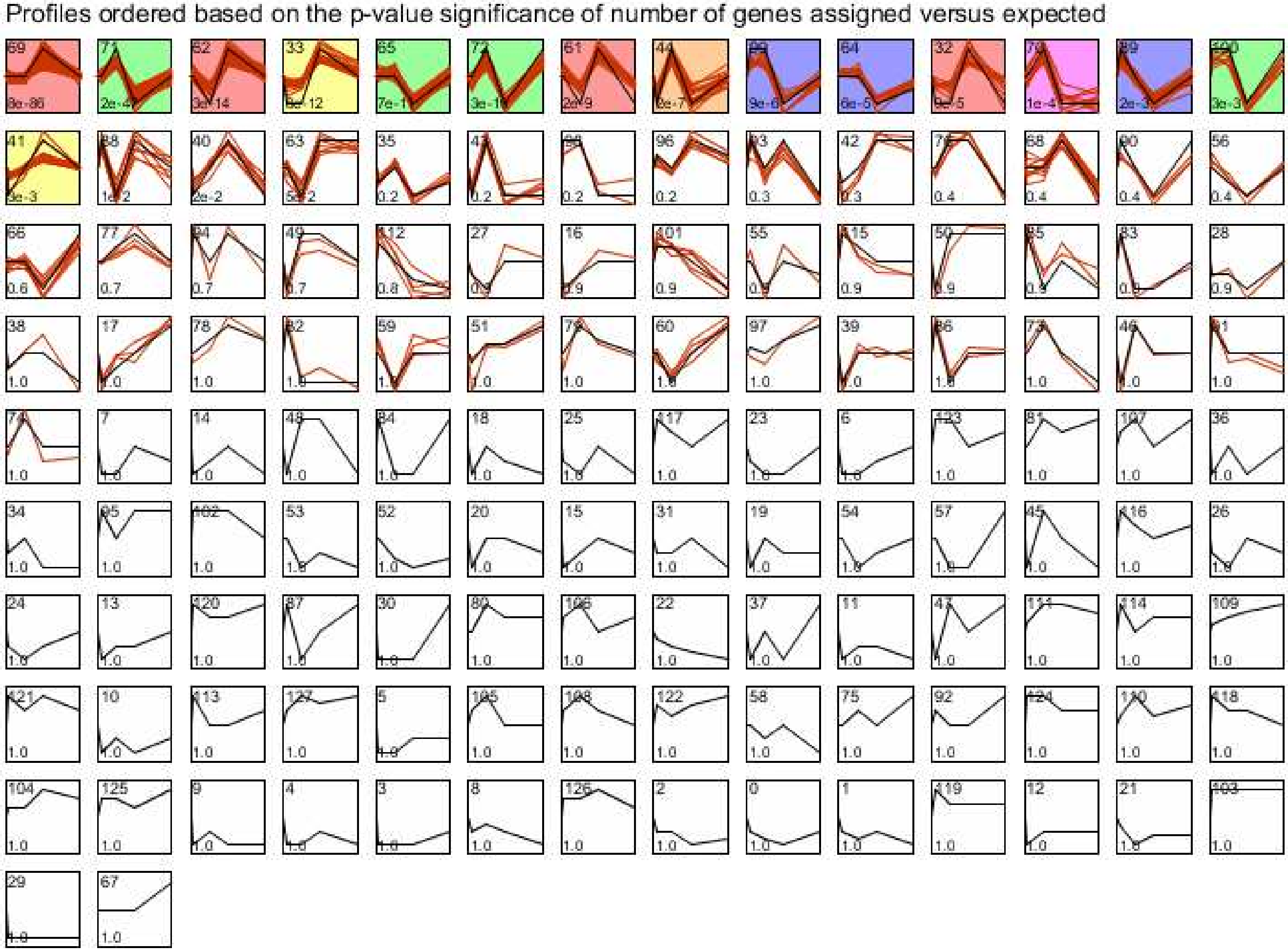

Fig. S12 | Schematic representation of temporal model profiles obtained by STEM analysis. Model profiles of gene expression ratios of α-MSH stimulated to non-stimulated cells are shown and ordered by significance. Each graph shows the enriched temporal expression patterns of co-regulated genes in α-MSH-stimulated migrating HAoECs. Black lines are the curve trend for each model profile, while the red lines are the genes that are attributed to the respective model profile. In the high left corner of each square is the number of the model profile computed by the STEM algorithm; in the low left corner is the significance (nominal *P*-value) of each model profile. Model profiles with a FDR < 0.05 have a coloured background and cluster profiles are displayed with the same colour background.

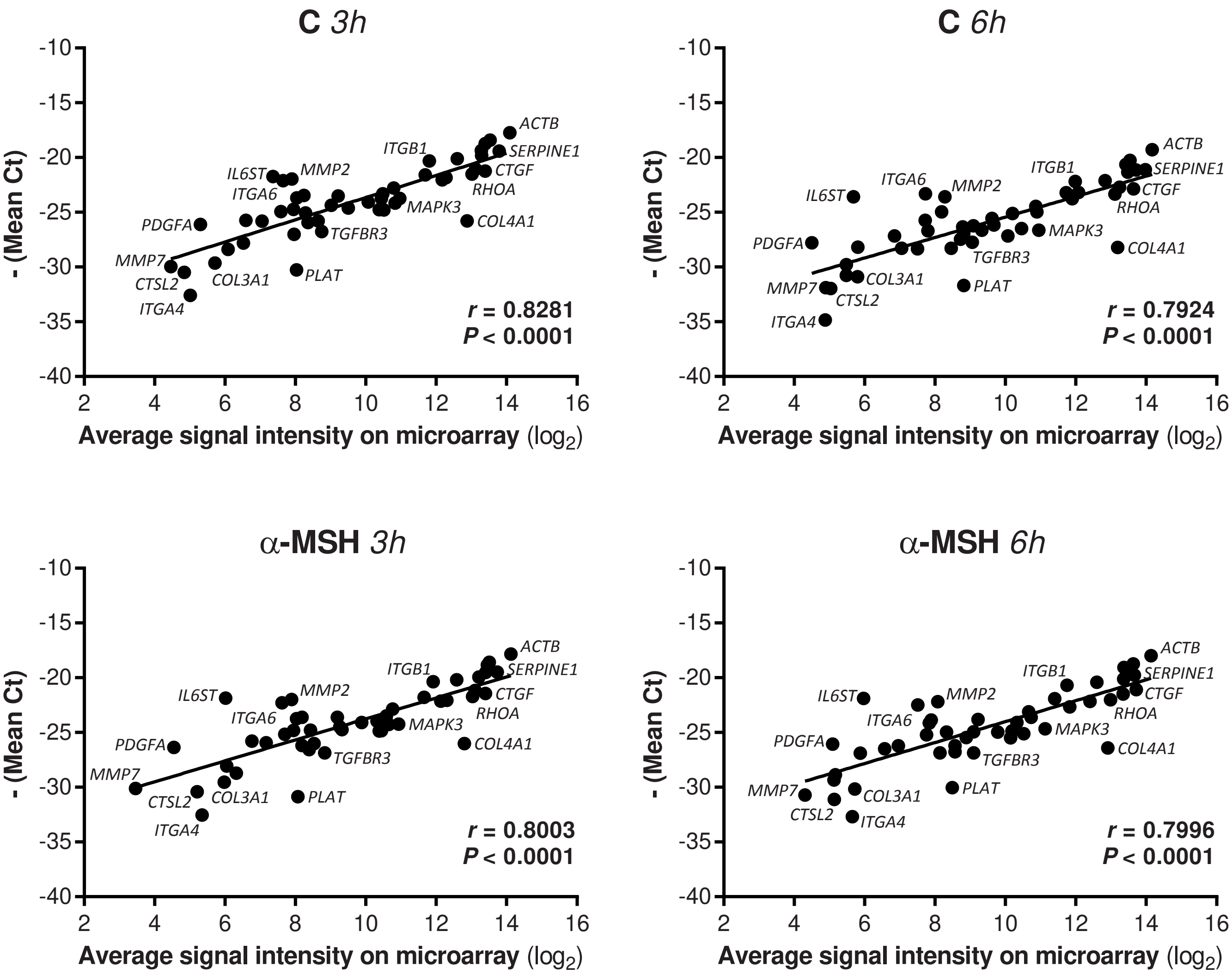

Fig. S13 | Validation of microarray data of non-stimulated and α-MSH-stimulated migrating human aortic endothelial cells (HAoECs) by RT-qPCR. We performed a technical confirmatory analysis of gene expression data of migrating HAoECs, using the Human Wound Healing RT^2 Profiler PCR Arrays (Qiagen). Microarray data were compared with those obtained by qPCR, the gold standard method for nucleic acid quantification. The four scatterplots show highly significant correlations between the raw signals detected with the two techniques at different time points (3 and 6h; *i.e.*, time points with the greatest treatment effect on gene expression) and cell treatment conditions (medium alone, C, and α-MSH). On the *y*-axis is the additive inverse mean Ct in C and α-MSH-treated cells at a given time point; on the *x*-axis is the log$_2$–transformed average raw signal intensity of microarrays (*n* = 3 independent experiments per treatment group). The Pearson's correlation coefficients (*r*) along with significance *P*-values are reported within the plots. Plots show data of 48 genes, spanning from low to high expression values, detected by both microarray and real-time PCR: *ACTA2*, *ACTB*, *B2M*, *CCL2*, *COL1A1*, *COL1A2*, *COL3A1*, *COL4A1*, *COL5A1*, *COL5A2*, *CTGF*, *CTSK*, *CTSL2*, *CXCL1*, *CXCL2*, *F3*, *FGF2*, *GAPDH*, *HBEGF*, *HPRT1*, *IL6*, *IL6ST*, *ITGA2*, *ITGA3*, *ITGA4*, *ITGA5*, *ITGA6*, *ITGAV*, *ITGB1*, *ITGB3*, *MAPK1*, *MAPK3*, *MIF*, *MMP1*, *MMP2*, *MMP7*, *PDGFA*, *PLAT*, *PLAU*, *PLAUR*, *PTEN*, *PTGS2*, *RHOA*, *RPL13A*, *SERPINE1*, *STAT3*, *TGFBR3*, and *TIMP1*. Results ensure microarray data were reliable and accurate on the greatest range of detection.

Supplemental Tables

Table S1 | Parameters used for STEM analysis

#Main Input:	
Gene Annotation Source	Human (EBI)
Gene Annotation File	gene_association.goa_human.gz
Cross Reference Source	User provided
Gene Location Source	Homo sapiens (Ensembl/BioMart)
Gene Location File	hsapiens.mart.gz
Clustering Method	STEM Clustering Method
Maximum Number of Model Profiles	624
Maximum Unit Change in Model Profiles between Time Points	2
Normalize Data	No normalization/add 0
Spot IDs included in the data file	true
#Repeat data	
Repeat Data is from	Different time periods
#Filtering:	
Maximum Number of Missing Values	0
Minimum Correlation between Repeats	0.3
Minimum Absolute Log Ratio Expression	0.4
Change should be based on	Maximum-Minimum
Pre-filtered Gene File	
#Model Profiles	
Maximum Correlation	0.9
Number of Permutations per Gene	0 (*)
Maximum Number of Candidate Model Profiles	1000000
Significance Level	0.05
Correction Method	False Discovery Rate
Permutation Test Should Permute Time Point 0	true
#Clustering Profiles:	
Clustering Minimum Correlation	0.7
Clustering Minimum Correlation Percentile	0

(*) The value = 0 for this parameter stands for "all possible permutations".

Table S2 | Mutational analysis of *MC1R* in primary human artery endothelial cells

Endothelial cell type	**SNP**	**Genotype**	***Position (nt)***	***Amino acid substitution***
HAoEC[c1]	-	-	-	-
HAoEC[c2]	-	-	-	-
HAoEC[c3]	rs885479	GA	*1868*	*Arg163Gln*
HCAEC[c4]	rs1805005	GT	*1558*	*Val60Leu*
HCAEC[c5]	rs1805005	GT	*1558*	*Val60Leu*
HCAEC[c6]	rs1805005	TT	*1558*	*Val60Leu*

HAoEC: human aortic endothelial cells; HCAEC: human carotid endothelial cells. Primary cell lines from: [c1,c4]ECACC, [c2,c5]Lonza, and [c3,c6]Promocell. Melanocortin-1 Receptor (*MC1R*) Ref. Seq. NM_002386.3.

Given that MC1R is a highly polymorphic gene and that many variants are known to affect its signal transduction, we analysed by Sanger sequencing the *MC1R* open reading frame (ORF) of three primary HCAEC and HAoEC to select those cells that bear the wild-type sequence. The intent here was to exclude from subsequent functional analysis those cells with gene polymorphisms that may hamper MC1R signalling and, hence, the cellular response to MC1R ligands. Sequence analysis revealed that all the three HCAECs bear a variant allele T in the rs1805005 (G/T) locus, whereas one HAoEC presented the variant allele A for the rs885479 (G/A) locus: these *MC1R* alleles has been reported to be associated with a decreased cAMP production in response to α-MSH stimulation. The other two HAoECs did not present any polymorphic or functional variant.

Table S3 | Full list of 637 genes and corresponding probes associated with distinct temporal expression profiles in response to MC1R activation in primary HAoEC

(a) 506 transcripts associated with 15 significant temporal profiles of differential expression

(b) 131 transcripts associated with 42 nonsignificant temporal profiles of differential expression

(**S3*a***) The 15 temporal profiles that showed a statistically significant enriched number of genes at a FDR < 0.05 (green coloured field) were grouped to form 6 different clusters of differential expression profiles, based on their similarity by a correlation coefficient ≥ 0.7. (**S3*b***) Genes associated with model profiles that had a FDR > 0.05 (red coloured field).

The table is available as supplemental format (TableS3.xlsx). Genes are sorted by cluster membership and p-value of the temporal profile and then listed in alphabetical order. For each of them the table reports NCBI and HGNC unique gene identifiers, the official and approved gene symbol and name, unique identifier(s) for Illumina probes, an integer identifying the cluster of significant temporal expression profiles, the profile number attributed by the STEM algorithm, significance p-value of each temporal expression profile, $\log_2$FC of α-MSH-treated to non-treated expression level at 0.5, 3, 6, and 12 h time points.

Table S4 | Gene set enrichment analysis of the 506 regulated genes, associating with 15 significant temporal profiles of differential expression

Gene sets that are deemed significantly enriched (FDR < 0.20 and with a number of genes for each corresponding term ≥ 3) are highlighted in bold, with their Benjamini-Hochberg adjusted *P*-values coloured in green.

The table is available as supplemental format (TableS4.xlsx). Gene sets are sorted by Benjamini-Hochberg adjusted p-value (FDR). For each gene set, the table reports: its functional annotation category (Gene Ontology, KEGG pathway, SP-PIR keyword), identifier, and annotation term; count, percentage, and list of modulated genes belonging to it; significance p-value and magnitude of gene-term enrichment; and FDR adjusted p-value.

Table S5 | Functionally annotated gene sets associated with clusters of temporal expression profiles

Gene sets that are deemed significantly enriched (FDR < 0.20 and with a number of genes for each corresponding term ≥ 3) are highlighted in bold, with their Benjamini-Hochberg adjusted *P*-values coloured in green.

The table is available as supplemental format (TableS5.xlsx). Gene sets are sorted by Benjamini-Hochberg adjusted p-value (FDR). For each gene set, the table reports: its functional annotation category (Gene Ontology, KEGG pathway, SP-PIR keyword), identifier, and annotation term; count, percentage, and list of modulated genes belonging to it; significance p-value and magnitude of gene-term enrichment, and FDR adjusted p-value.

Table S3*a* | Transcripts associated with 15 significant temporal profiles of differential expression. *These 15 profiles, showing a statistically significant enriched number of genes at a false discovery rate (FDR) < 0.05, were grouped to form 6 different clusters of differential expression profiles, based on their similarity by a correlation coefficient≥ 0.7.*

						FDR < 0.05					
Entrez GeneID	HGNC ID	Gene symbol	Gene Name	Illumina probe_ID	Cluster	Profile	Profile *P* -value	$\log_2$(FC) *at 0.5h*	$\log_2$(FC) *at 3h*	$\log_2$(FC) *at 6h*	$\log_2$(FC) *at 12h*
283693	51497	**ACTG1P17**	actin gamma 1 pseudogene 17	ILMN_3274790	1	69	8,1E-86	-0,26	-0,06	1,15	0,04
132	257	**ADK**	adenosine kinase	ILMN_3299579	1	69	8,1E-86	-0,09	-0,05	0,35	0,06
6718	388	**AKR1D1**	aldo-keto reductase family 1 member D1	ILMN_2157277	1	69	8,1E-86	0,08	0,03	0,38	-0,07
250	439	**ALPP**	alkaline phosphatase, placental	ILMN_1693789	1	69	8,1E-86	-0,10	-0,12	1,22	-0,10
374860	24165	**ANKRD30B**	ankyrin repeat domain 30B	ILMN_1730678	1	69	8,1E-86	-0,13	-0,07	0,66	-0,06
375248	24079	**ANKRD36**	ankyrin repeat domain 36	ILMN_3236021	1	69	8,1E-86	-0,11	-0,01	0,47	-0,01
723972	42949	**ANP32AP1**	acidic nuclear phosphoprotein 32 family member A pseudogene 1	ILMN_2056002	1	69	8,1E-86	0,03	-0,02	0,41	-0,06
90586	48869	**AOC4P**	amine oxidase, copper containing 4, pseudogene	ILMN_2219618	1	69	8,1E-86	-0,23	-0,15	0,98	0,09
339231	27902	**ARL16**	ADP ribosylation factor like GTPase 16	ILMN_1679917;ILMN_2188119	1	69	8,1E-86	0,06	-0,05	0,67	-0,03
79798	25781	**ARMC5**	armadillo repeat containing 5	ILMN_1697088	1	69	8,1E-86	0,03	-0,22	1,12	0,15
348110	28782	**ARPIN**	actin-related protein 2/3 complex inhibitor	ILMN_3265143	1	69	8,1E-86	-0,06	-0,21	1,02	-0,09
581	959	**BAX**	BCL2 associated X, apoptosis regulator	ILMN_2321064	1	69	8,1E-86	-0,02	-0,06	0,60	-0,07
9274	1006	**BCL7C**	BCL tumor suppressor 7C	ILMN_2371147	1	69	8,1E-86	-0,06	0,01	0,39	-0,11
618	1022	**BCYRN1**	brain cytoplasmic RNA 1	ILMN_1678757	1	69	8,1E-86	0,07	-0,19	0,83	0,11
645	1063	**BLVRB**	biliverdin reductase B	ILMN_1797793	1	69	8,1E-86	-0,15	-0,05	0,38	-0,07
8548	1065	**BLZF1**	basic leucine zipper nuclear factor 1	ILMN_2106656;ILMN_2106658	1	69	8,1E-86	-0,19	-0,10	1,09	-0,04
656	1075	**BMP8B**	bone morphogenetic protein 8b	ILMN_2123415	1	69	8,1E-86	-0,05	0,04	0,37	0,02
8019	1104	**BRD3**	bromodomain containing 3	ILMN_1785635	1	69	8,1E-86	-0,04	-0,14	0,49	-0,08
100129094	42540	**BTNL10**	butyrophilin like 10	ILMN_3187470	1	69	8,1E-86	-0,10	-0,06	0,37	0,00
157657	27232	**C8orf37**	chromosome 8 open reading frame 37	ILMN_2091084	1	69	8,1E-86	-0,14	-0,16	1,26	-0,17
117155	18810	**CATSPER2**	cation channel sperm associated 2	ILMN_2286014	1	69	8,1E-86	-0,31	-0,09	1,37	0,01
147372	29426	**CCBE1**	collagen and calcium binding EGF domains 1	ILMN_2122511;ILMN_1813528	1	69	8,1E-86	-0,03	-0,07	0,61	0,05
146059	1713	**CDAN1**	codanin 1	ILMN_2401906	1	69	8,1E-86	-0,14	-0,03	0,67	-0,07
84984	28209	**CEP19**	centrosomal protein 19	ILMN_1665217;ILMN_2288483	1	69	8,1E-86	-0,11	-0,01	0,57	-0,03
8837	1876	**CFLAR**	CASP8 and FADD like apoptosis regulator	ILMN_1789830	1	69	8,1E-86	-0,05	-0,14	1,09	0,25
1138	1959	**CHRNA5**	cholinergic receptor nicotinic alpha 5 subunit	ILMN_1770044;ILMN_2110751	1	69	8,1E-86	-0,01	-0,02	0,59	-0,06
56265	15771	**CPXM1**	carboxypeptidase X (M14 family), member 1	ILMN_1712046	1	69	8,1E-86	0,08	-0,07	0,35	0,03
1438	2435	**CSF2RA**	colony stimulating factor 2 receptor alpha subunit	ILMN_1721204	1	69	8,1E-86	-0,11	-0,24	0,88	0,02
1508	2527	**CTSB**	cathepsin B	ILMN_1696360;ILMN_2359742	1	69	8,1E-86	-0,07	-0,01	0,91	-0,29
91966	28089	**CXorf40A**	chromosome X open reading frame 40A	ILMN_2064655;ILMN_1759092	1	69	8,1E-86	-0,04	-0,14	0,43	0,03
157317	21252	**CYCSP55**	cytochrome c, somatic pseudogene 55	ILMN_1663751;ILMN_2061419	1	69	8,1E-86	0,07	-0,13	0,50	0,00
10395	2897	**DLC1**	DLC1 Rho GTPase activating protein	ILMN_1698020	1	69	8,1E-86	0,18	-0,14	0,82	-0,06
11144	2927	**DMC1**	DNA meiotic recombinase 1	ILMN_2162367	1	69	8,1E-86	-0,21	-0,04	1,26	-0,07
54943	1297	**DNAJC28**	DnaJ heat shock protein family (Hsp40) member C28	ILMN_1814204	1	69	8,1E-86	-0,03	-0,09	0,51	0,03
285605	19334	**DTWD2**	DTW domain containing 2	ILMN_2054554	1	69	8,1E-86	-0,11	-0,21	1,06	0,05
142679	18894	**DUSP19**	dual specificity phosphatase 19	ILMN_1722492	1	69	8,1E-86	-0,20	-0,23	1,17	0,19
503639	32189	**DUXAP10**	double homeobox A pseudogene 10	ILMN_2082893	1	69	8,1E-86	-0,11	-0,08	0,32	-0,07
503632	32182	**DUXAP3**	double homeobox A pseudogene 3	ILMN_2117809	1	69	8,1E-86	-0,17	0,05	1,07	-0,02
440275	19687	**EIF2AK4**	eukaryotic translation initiation factor 2 alpha kinase 4	ILMN_1755114	1	69	8,1E-86	0,05	-0,14	0,54	-0,02
1984	3300	**EIF5A**	eukaryotic translation initiation factor 5A	ILMN_1794522	1	69	8,1E-86	-0,09	0,06	0,33	0,01
2029	3360	**ENSA**	endosulfine alpha	ILMN_1700975;ILMN_2364700;ILMN_1760779	1	69	8,1E-86	0,04	-0,09	0,31	0,01
54751	24686	**FBLIM1**	filamin binding LIM protein 1	ILMN_2353143;ILMN_1691249	1	69	8,1E-86	-0,02	0,01	0,52	-0,09
2259	3671	**FGF14**	fibroblast growth factor 14	ILMN_3183544	1	69	8,1E-86	0,14	0,03	0,87	-0,01
55033	18625	**FKBP14**	FK506 binding protein 14	ILMN_2150294;ILMN_1665243	1	69	8,1E-86	0,03	-0,12	0,66	0,02
2218	3622	**FKTN**	fukutin	ILMN_2357386	1	69	8,1E-86	-0,04	-0,04	0,64	-0,18
2591	4125	**GALNT3**	polypeptide N-acetylgalactosaminyltransferase 3	ILMN_1671039	1	69	8,1E-86	-0,14	-0,18	0,48	-0,02
84296	28226	**GINS4**	GINS complex subunit 4	ILMN_1807501	1	69	8,1E-86	-0,08	-0,08	0,32	-0,07
283767	37444	**GOLGA6L1**	golgin A6 family-like 1	ILMN_3249230	1	69	8,1E-86	-0,07	0,06	0,57	0,04
727832	37225	**GOLGA6L6**	golgin A6 family-like 6	ILMN_3243175	1	69	8,1E-86	-0,14	-0,08	0,58	-0,05

27333	15448	**GOLIM4**	golgi integral membrane protein 4	ILMN_3245116;ILMN_2186216;ILMN_1795344	1	69	8,1E-86	-0,07	-0,04	0,35	-0,12
2825	4463	**GPR1**	G protein-coupled receptor 1	ILMN_2107004	1	69	8,1E-86	0,02	-0,11	1,13	0,14
653399	33606	**GSTTP2**	glutathione S-transferase theta pseudogene 2	ILMN_2246548	1	69	8,1E-86	0,04	-0,20	0,69	-0,02
8225	30189	**GTPBP6**	GTP binding protein 6 (putative)	ILMN_3247390	1	69	8,1E-86	0,06	-0,05	0,39	0,01
387751	25813	**GVINP1**	GTPase, very large interferon inducible pseudogene 1	ILMN_1668526	1	69	8,1E-86	-0,06	-0,14	0,34	-0,11
55142	25530	**HAUS2**	HAUS augmin like complex subunit 2	ILMN_1738482	1	69	8,1E-86	-0,12	-0,20	0,66	-0,04
9026	18415	**HIP1R**	huntingtin interacting protein 1 related	ILMN_1757910	1	69	8,1E-86	0,08	0,03	0,52	-0,12
28996	14402	**HIPK2**	homeodomain interacting protein kinase 2	ILMN_1687440	1	69	8,1E-86	0,02	-0,19	0,81	0,06
221092	25451	**HNRNPUL2**	heterogeneous nuclear ribonucleoprotein U like 2	ILMN_2072091	1	69	8,1E-86	-0,01	-0,10	0,52	-0,20
3455	5433	**IFNAR2**	interferon alpha and beta receptor subunit 2	ILMN_1791057;ILMN_1765146	1	69	8,1E-86	0,00	-0,05	0,34	-0,13
54756	17616	**IL17RD**	interleukin 17 receptor D	ILMN_2407851	1	69	8,1E-86	-0,31	-0,36	1,17	-0,03
58493	24994	**INIP**	INTS3 and NABP interacting protein	ILMN_2079098;ILMN_1688621	1	69	8,1E-86	0,01	-0,16	0,44	-0,10
1316	2235	**KLF6**	Kruppel like factor 6	ILMN_1700727;ILMN_1737406;ILMN_1735014	1	69	8,1E-86	-0,01	0,07	0,72	0,06
54813	19741	**KLHL28**	kelch like family member 28	ILMN_3251605;ILMN_1693401	1	69	8,1E-86	-0,11	-0,03	0,63	0,01
84458	29503	**LCOR**	ligand dependent nuclear receptor corepressor	ILMN_1689817;ILMN_2062381	1	69	8,1E-86	-0,01	-0,07	0,60	0,13
54741	29477	**LEPROT**	leptin receptor overlapping transcript	ILMN_1661537	1	69	8,1E-86	-0,08	-0,13	0,68	-0,14
10859	6605	**LILRB1**	leukocyte immunoglobulin like receptor B1	ILMN_2316974	1	69	8,1E-86	-0,14	-0,09	0,69	0,04
731789	44917	**LINC00202-2**	long intergenic non-protein coding RNA 202-2	ILMN_3233239	1	69	8,1E-86	-0,09	0,00	0,57	-0,01
100128782	27858	**LINC00476**	long intergenic non-protein coding RNA 476	ILMN_1738678	1	69	8,1E-86	-0,13	-0,16	0,45	-0,02
255031	22332	**LINC00957**	long intergenic non-protein coding RNA 957	ILMN_3269655	1	69	8,1E-86	0,00	-0,16	0,90	-0,05
401082	49636	**LINC01205**	long intergenic non-protein coding RNA 1205	ILMN_3260180	1	69	8,1E-86	0,02	-0,19	0,73	0,02
100128084		**LOC100128084**	hypothetical LOC100128084	ILMN_3187612	1	69	8,1E-86	-0,10	-0,12	0,86	0,17
100128274		**LOC100128274**	putative p150	ILMN_3253787	1	69	8,1E-86	-0,10	-0,20	0,42	-0,04
100128288		**LOC100128288**	uncharacterized LOC100128288 (ncRNA)	ILMN_3235637	1	69	8,1E-86	-0,25	0,00	1,27	0,08
100130276		**LOC100130276**	uncharacterized LOC100130276	ILMN_3267800	1	69	8,1E-86	-0,06	-0,15	0,75	0,15
100131541		**LOC100131541**	uncharacterized LOC100131541	ILMN_3285162	1	69	8,1E-86	-0,18	-0,11	0,56	0,05
100131541		**LOC100131541**	uncharacterized LOC100131541	ILMN_3205910	1	69	8,1E-86	-0,13	-0,07	0,48	0,05
100132585		**LOC100132585**	similar to speedy homolog A	ILMN_3237404	1	69	8,1E-86	-0,34	-0,10	1,18	0,11
100134159		**LOC100134159**	similar to Coiled-coil domain containing 144B	ILMN_3244728	1	69	8,1E-86	0,08	-0,07	0,83	0,02
100134868		**LOC100134868**	uncharacterized LOC100134868 (ncRNA)	ILMN_3249658	1	69	8,1E-86	-0,15	-0,26	0,97	-0,15
100190986		**LOC100190986**	uncharacterized LOC100190986 (ncRNA)	ILMN_3246910	1	69	8,1E-86	-0,09	-0,31	1,01	0,05
100272217		**LOC100272217**	uncharacterized LOC100272217 (ncRNA)	ILMN_1767263	1	69	8,1E-86	0,02	-0,06	0,52	-0,01
100286946		**LOC100286946**	ribosomal protein S3A pseudogene	ILMN_3227321	1	69	8,1E-86	-0,04	-0,03	0,46	-0,02
389765		**LOC389765**	kinesin family member 27 pseudogene	ILMN_3294134	1	69	8,1E-86	-0,25	-0,23	1,07	0,12
401261		**LOC401261**	uncharacterized LOC401261 (ncRNA)	ILMN_1771320	1	69	8,1E-86	-0,09	-0,07	0,39	0,01
440704		**LOC440704**	uncharacterized LOC440704 (ncRNA)	ILMN_1673421	1	69	8,1E-86	0,06	-0,10	0,66	0,05
641737		**LOC641737**	uncharacterized LOC641737	ILMN_2230162	1	69	8,1E-86	-0,08	-0,10	1,13	-0,15
642947		**LOC642947**	uncharacterized LOC642947	ILMN_2049343	1	69	8,1E-86	-0,09	-0,09	0,55	-0,19
730060		**LOC730060**	hypothetical LOC730060	ILMN_3225673	1	69	8,1E-86	-0,05	0,02	0,67	-0,02
653639	21069	**LYPLA2P1**	lysophospholipase II pseudogene 1	ILMN_1804306	1	69	8,1E-86	0,10	0,02	0,67	0,05
84061	28880	**MAGT1**	magnesium transporter 1	ILMN_1721349	1	69	8,1E-86	-0,12	-0,27	1,33	0,13
375449	19037	**MAST4**	microtubule associated serine/threonine kinase family member 4	ILMN_1738438	1	69	8,1E-86	-0,08	-0,01	0,40	-0,11
8930	6919	**MBD4**	methyl-CpG binding domain 4, DNA glycosylase	ILMN_2055310	1	69	8,1E-86	-0,22	-0,15	1,22	0,02
129642	25193	**MBOAT2**	membrane bound O-acyltransferase domain containing 2	ILMN_2347424	1	69	8,1E-86	-0,11	-0,08	0,36	-0,08
4204	6990	**MECP2**	methyl-CpG binding protein 2	ILMN_1824898	1	69	8,1E-86	-0,07	-0,12	0,40	0,03
9442	2377	**MED27**	mediator complex subunit 27	ILMN_3208140	1	69	8,1E-86	-0,03	-0,08	0,62	0,01
79157	25458	**MFSD11**	major facilitator superfamily domain containing 11	ILMN_1756152	1	69	8,1E-86	-0,20	-0,03	0,80	-0,02
84278	23672	**MFSD14C**	major facilitator superfamily domain containing 14C	ILMN_3235410	1	69	8,1E-86	-0,16	-0,05	1,07	-0,15
54471	25979	**MIEF1**	mitochondrial elongation factor 1	ILMN_1793203	1	69	8,1E-86	-0,06	-0,13	0,74	0,11
407021	31616	**MIR29A**	microRNA 29a	ILMN_1855278	1	69	8,1E-86	0,04	0,00	0,57	0,14
4494	7398	**MT1F**	metallothionein 1F	ILMN_1718766	1	69	8,1E-86	0,01	-0,07	0,36	0,10
4520	7428	**MTF1**	metal regulatory transcription factor 1	ILMN_1763828	1	69	8,1E-86	0,04	-0,08	0,55	0,09
55728	29851	**N4BP2**	NEDD4 binding protein 2	ILMN_1782273;ILMN_2222101	1	69	8,1E-86	-0,17	-0,16	0,66	0,03
100132406	31992	**NBPF10**	neuroblastoma breakpoint family member 10	ILMN_2155719	1	69	8,1E-86	-0,09	0,08	0,71	-0,22
400818	31991	**NBPF9**	neuroblastoma breakpoint family member 9	ILMN_2115490	1	69	8,1E-86	0,01	0,12	0,87	-0,08

126205	22940	**NLRP8**	NLR family pyrin domain containing 8	ILMN_2075794	1	69	8,1E-86	-0,21	0,02	1,48	-0,08
80224	20278	**NUBPL**	nucleotide binding protein like	ILMN_2048811	1	69	8,1E-86	-0,29	-0,13	1,15	0,10
64710	29923	**NUCKS1**	nuclear casein kinase and cyclin dependent kinase substrate 1	ILMN_1680692;ILMN_3251404	1	69	8,1E-86	-0,07	-0,33	0,76	-0,06
10204	13722	**NUTF2**	nuclear transport factor 2	ILMN_1655046	1	69	8,1E-86	-0,05	-0,08	0,54	0,16
80207	8142	**OPA3**	optic atrophy 3 (autosomal recessive, with chorea and spastic paraplegia)	ILMN_1652819;ILMN_2284591	1	69	8,1E-86	-0,05	-0,14	0,48	-0,11
202781	27328	**PAXIP1-AS1**	PAXIP1 antisense RNA 1 (head to head)	ILMN_3218292	1	69	8,1E-86	-0,17	-0,15	1,04	0,06
84054	14549	**PCDHB19P**	protocadherin beta 19 pseudogene	ILMN_1690237	1	69	8,1E-86	-0,01	-0,14	0,59	0,16
51449	20588	**PCYOX1**	prenylcysteine oxidase 1	ILMN_1679725;ILMN_2113535	1	69	8,1E-86	-0,20	-0,10	0,55	-0,15
51588	17002	**PIAS4**	protein inhibitor of activated STAT 4	ILMN_1802905	1	69	8,1E-86	-0,09	0,05	0,43	-0,05
54965	26046	**PIGX**	phosphatidylinositol glycan anchor biosynthesis class X	ILMN_1769508	1	69	8,1E-86	-0,17	-0,03	0,56	0,11
29990	18297	**PILRB**	paired immunoglobin-like type 2 receptor beta	ILMN_3204734	1	69	8,1E-86	0,13	-0,19	0,83	-0,04
87178	23166	**PNPT1**	polyribonucleotide nucleotidyltransferase 1	ILMN_1810608;ILMN_3251723;ILMN_2051408	1	69	8,1E-86	-0,08	-0,11	0,70	0,00
23509	14988	**POFUT1**	protein O-fucosyltransferase 1	ILMN_1776076;ILMN_2276758	1	69	8,1E-86	0,05	-0,06	0,48	0,07
56983	22954	**POGLUT1**	protein O-glucosyltransferase 1	ILMN_1811104	1	69	8,1E-86	0,03	-0,09	0,73	-0,06
27068	28883	**PPA2**	pyrophosphatase (inorganic) 2	ILMN_1687785;ILMN_2342455	1	69	8,1E-86	-0,06	-0,07	0,43	0,03
9701	19253	**PPP6R2**	protein phosphatase 6 regulatory subunit 2	ILMN_1655922	1	69	8,1E-86	-0,14	-0,37	0,95	-0,04
5576	9391	**PRKAR2A**	protein kinase cAMP-dependent type II regulatory subunit alpha	ILMN_1681888	1	69	8,1E-86	0,07	0,06	0,43	0,05
8073	9635	**PTP4A2**	protein tyrosine phosphatase type IVA, member 2	ILMN_1688490	1	69	8,1E-86	0,11	-0,07	0,61	-0,05
84109	15565	**QRFPR**	pyroglutamylated RFamide peptide receptor	ILMN_3241626	1	69	8,1E-86	0,04	-0,22	1,01	-0,05
646996	19799	**RAB42P1**	RAB42, member RAS oncogene family, pseudogene 1	ILMN_3247256	1	69	8,1E-86	-0,09	-0,01	0,92	0,01
166824	20796	**RASSF6**	Ras association domain family member 6	ILMN_2352245	1	69	8,1E-86	-0,22	-0,10	0,54	-0,09
84839	18286	**RAX2**	retina and anterior neural fold homeobox 2	ILMN_3239653;ILMN_1653412	1	69	8,1E-86	0,01	-0,09	0,49	-0,01
54933	16083	**RHBDL2**	rhomboid like 2	ILMN_2053538;ILMN_2053536	1	69	8,1E-86	-0,17	-0,18	0,61	0,04
22836	18757	**RHOBTB3**	Rho related BTB domain containing 3	ILMN_1744949	1	69	8,1E-86	0,19	-0,15	0,77	-0,10
246243	18466	**RNASEH1**	ribonuclease H1	ILMN_1726783	1	69	8,1E-86	0,14	-0,18	0,70	-0,03
107105261	48304	**RNU1-5P**	RNA, U1 small nuclear 5, pseudogene	ILMN_3236653	1	69	8,1E-86	0,00	-0,06	0,57	0,05
100151683	34016	**RNU4ATAC**	RNA, U4atac small nuclear (U12-dependent splicing)	ILMN_3240594	1	69	8,1E-86	-0,05	0,02	0,37	-0,11
100302741	34259	**RNU6-15P**	RNA, U6 small nuclear 15, pseudogene	ILMN_3310351	1	69	8,1E-86	-0,02	-0,07	0,39	0,06
285855	21370	**RPL7L1**	ribosomal protein L7 like 1	ILMN_1705908;ILMN_2220320	1	69	8,1E-86	-0,08	-0,13	0,64	0,01
729123	36762	**RPL7P21**	ribosomal protein L7 pseudogene 21	ILMN_3221790	1	69	8,1E-86	-0,01	-0,15	0,31	-0,05
64121	19902	**RRAGC**	Ras related GTP binding C	ILMN_1760121	1	69	8,1E-86	0,15	-0,09	0,50	-0,03
51282	10566	**SCAND1**	SCAN domain containing 1	ILMN_2372011;ILMN_1795317;ILMN_1794230	1	69	8,1E-86	-0,02	-0,13	0,42	0,04
107105265	51687	**SEPT14P3**	septin 14 pseudogene 3	ILMN_3235006	1	69	8,1E-86	-0,09	-0,07	0,64	0,01
6415	10752	**SEPW1**	selenoprotein W, 1	ILMN_2045994	1	69	8,1E-86	-0,02	0,07	0,70	0,00
79801	29547	**SHCBP1**	SHC binding and spindle associated 1	ILMN_2182482	1	69	8,1E-86	-0,06	-0,09	0,69	0,05
387700	23094	**SLC16A12**	solute carrier family 16 member 12	ILMN_2180929	1	69	8,1E-86	-0,02	-0,04	0,80	0,09
788	1421	**SLC25A20**	solute carrier family 25 member 20	ILMN_1783060	1	69	8,1E-86	-0,11	-0,07	0,31	-0,09
92014	23323	**SLC25A51**	solute carrier family 25 member 51	ILMN_2198499;ILMN_1772492	1	69	8,1E-86	-0,09	-0,11	0,59	-0,02
79939	20803	**SLC35E1**	solute carrier family 35 member E1	ILMN_2059173;ILMN_1752333;ILMN_3251379	1	69	8,1E-86	-0,12	-0,09	0,60	-0,04
57835	18168	**SLC4A5**	solute carrier family 4 member 5	ILMN_2273224	1	69	8,1E-86	-0,04	-0,15	0,69	-0,07
140771	17918	**SMCR5**	Smith-Magenis syndrome chromosome region, candidate 5 (non-protein coding)	ILMN_3240236	1	69	8,1E-86	-0,14	-0,08	1,04	0,19
201895	27321	**SMIM14**	small integral membrane protein 14	ILMN_2224907;ILMN_1713892	1	69	8,1E-86	0,03	-0,10	0,43	0,10
6617	11134	**SNAPC1**	small nuclear RNA activating complex polypeptide 1	ILMN_2093389;ILMN_1725346	1	69	8,1E-86	-0,10	0,06	0,44	0,08
100126798	34304	**SNAR-A1**	small ILF3/NF90-associated RNA A1	ILMN_1881909	1	69	8,1E-86	-0,23	-0,34	1,64	-0,39
677800	32600	**SNORA12**	small nucleolar RNA, H/ACA box 12	ILMN_3238435	1	69	8,1E-86	0,03	-0,14	0,44	-0,03
780853	33191	**SNORD3C**	small nucleolar RNA, C/D box 3C	ILMN_3241034	1	69	8,1E-86	-0,01	0,02	0,35	-0,09
6645	11169	**SNTB2**	syntrophin beta 2	ILMN_1808374;ILMN_1786766	1	69	8,1E-86	0,04	-0,19	0,83	0,15
147841	26913	**SPC24**	SPC24, NDC80 kinetochore complex component	ILMN_2181432	1	69	8,1E-86	-0,01	-0,08	0,33	-0,12
8405	11254	**SPOP**	speckle type BTB/POZ protein	ILMN_2397024	1	69	8,1E-86	-0,21	-0,15	0,59	-0,08
57522	17382	**SRGAP1**	SLIT-ROBO Rho GTPase activating protein 1	ILMN_1677432	1	69	8,1E-86	-0,10	0,00	0,31	-0,03
6752	11331	**SSTR2**	somatostatin receptor 2	ILMN_2152257	1	69	8,1E-86	-0,14	-0,31	0,97	0,02
442578	33845	**STAG3L3**	stromal antigen 3-like 3 (pseudogene)	ILMN_3239343	1	69	8,1E-86	0,00	0,07	0,66	0,01
100128126	44101	**STAU2-AS1**	STAU2 antisense RNA 1	ILMN_3178553	1	69	8,1E-86	0,06	-0,03	0,75	0,06
55342	16462	**STRBP**	spermatid perinuclear RNA binding protein	ILMN_1881526	1	69	8,1E-86	-0,11	-0,11	0,32	-0,09
57464	22209	**STRIP2**	striatin interacting protein 2	ILMN_2161286	1	69	8,1E-86	0,08	-0,16	0,75	0,07

94056	16273	**SYAP1**	synapse associated protein 1	ILMN_2089175;ILMN_1698470	1	69	8,1E-86	-0,01	-0,06	0,40	-0,06
55333	18955	**SYNJ2BP**	synaptojanin 2 binding protein	ILMN_1697793	1	69	8,1E-86	0,02	-0,11	0,70	0,11
8148	11547	**TAF15**	TATA-box binding protein associated factor 15	ILMN_1678707;ILMN_2402131	1	69	8,1E-86	-0,16	-0,06	0,41	-0,16
6925	11634	**TCF4**	transcription factor 4	ILMN_1814194	1	69	8,1E-86	0,01	-0,06	0,75	0,05
113277	28288	**TMEM106A**	transmembrane protein 106A	ILMN_3249244	1	69	8,1E-86	-0,28	-0,19	1,39	-0,22
80008	26260	**TMEM156**	transmembrane protein 156	ILMN_2095660	1	69	8,1E-86	-0,06	-0,08	0,32	-0,09
200728	26623	**TMEM17**	transmembrane protein 17	ILMN_2210386;ILMN_1783583	1	69	8,1E-86	-0,10	-0,06	0,60	0,03
8740	11930	**TNFSF14**	tumor necrosis factor superfamily member 14	ILMN_2363392	1	69	8,1E-86	-0,03	-0,07	0,54	0,04
10098	17753	**TSPAN5**	tetraspanin 5	ILMN_1799028	1	69	8,1E-86	-0,22	-0,11	0,50	-0,01
7428	12687	**VHL**	von Hippel-Lindau tumor suppressor	ILMN_2376625;ILMN_1738579;ILMN_1801984	1	69	8,1E-86	-0,07	-0,01	0,62	0,13
80335	28826	**WDR82**	WD repeat domain 82	ILMN_1679655	1	69	8,1E-86	-0,23	-0,10	0,69	-0,09
286451	28304	**YIPF6**	Yip1 domain family member 6	ILMN_1803939	1	69	8,1E-86	-0,01	-0,08	0,51	-0,09
26137	13503	**ZBTB20**	zinc finger and BTB domain containing 20	ILMN_1689456	1	69	8,1E-86	-0,11	-0,06	0,50	-0,07
7586	13101	**ZKSCAN1**	zinc finger with KRAB and SCAN domains 1	ILMN_2139052	1	69	8,1E-86	-0,07	-0,14	0,40	-0,03
7766	13016	**ZNF223**	zinc finger protein 223	ILMN_1815578	1	69	8,1E-86	-0,05	-0,23	0,71	-0,02
342908	19417	**ZNF404**	zinc finger protein 404	ILMN_1846517	1	69	8,1E-86	-0,04	-0,13	0,59	0,00
79088	20725	**ZNF426**	zinc finger protein 426	ILMN_1673804	1	69	8,1E-86	0,04	0,00	0,49	0,19
80264	20808	**ZNF430**	zinc finger protein 430	ILMN_2158164;ILMN_1780026	1	69	8,1E-86	-0,06	0,01	0,58	-0,07
58499	21684	**ZNF462**	zinc finger protein 462	ILMN_1686679	1	69	8,1E-86	0,03	-0,16	0,54	-0,11
116115	29415	**ZNF526**	zinc finger protein 526	ILMN_1756631	1	69	8,1E-86	-0,13	-0,12	0,49	-0,04
256051	26632	**ZNF549**	zinc finger protein 549	ILMN_1718042;ILMN_2227495	1	69	8,1E-86	-0,15	-0,04	0,53	-0,08
54811	25950	**ZNF562**	zinc finger protein 562	ILMN_1672940	1	69	8,1E-86	-0,12	0,03	0,46	-0,13
22834	29147	**ZNF652**	zinc finger protein 652	ILMN_2155322	1	69	8,1E-86	-0,02	-0,11	1,17	0,05
91120	28857	**ZNF682**	zinc finger protein 682	ILMN_2242998;ILMN_2313889	1	69	8,1E-86	-0,09	-0,09	0,55	-0,06
148203	32469	**ZNF738**	zinc finger protein 738	ILMN_3225102	1	69	8,1E-86	-0,14	-0,14	1,21	0,08
7627	13146	**ZNF75A**	zinc finger protein 75a	ILMN_3262849;ILMN_3186390	1	69	8,1E-86	-0,10	-0,12	0,84	-0,11
374928	30487	**ZNF773**	zinc finger protein 773	ILMN_1685365	1	69	8,1E-86	-0,05	-0,14	0,31	-0,05
79699	25820	**ZYG11B**	zyg-11 family member B, cell cycle regulator	ILMN_1656676	1	69	8,1E-86	-0,02	0,11	0,71	0,07
10005	15919	**ACOT8**	acyl-CoA thioesterase 8	ILMN_1679600	1	62	2,5E-14	0,05	-0,15	0,39	0,17
400986	32946	**ANKRD36C**	ankyrin repeat domain 36C	ILMN_1811117	1	62	2,5E-14	-0,09	-0,23	0,23	-0,05
26225	696	**ARL5A**	ADP ribosylation factor like GTPase 5A	ILMN_2332558;ILMN_1688526;ILMN_1771738	1	62	2,5E-14	0,07	-0,22	0,25	0,01
83734	20315	**ATG10**	autophagy related 10	ILMN_1748968;ILMN_2206098	1	62	2,5E-14	0,01	-0,12	0,32	0,05
80127	19855	**BBOF1**	basal body orientation factor 1	ILMN_1806456	1	62	2,5E-14	-0,06	-0,20	0,21	-0,04
1070	1868	**CETN3**	centrin 3	ILMN_2224031	1	62	2,5E-14	0,05	-0,23	0,41	-0,08
1906	3176	**EDN1**	endothelin 1	ILMN_1682775	1	62	2,5E-14	0,19	-0,22	0,42	-0,04
359845	28705	**FAM101B**	family with sequence similarity 101 member B	ILMN_1714418	1	62	2,5E-14	0,00	-0,42	0,18	-0,01
728640	44190	**FAM133CP**	family with sequence similarity 133 member C, pseudogene	ILMN_3304435	1	62	2,5E-14	0,10	-0,21	0,44	-0,05
8074	3680	**FGF23**	fibroblast growth factor 23	ILMN_1696488	1	62	2,5E-14	0,09	-0,13	0,36	-0,01
284802	15792	**FRG1BP**	FSHD region gene 1 family member B, pseudogene	ILMN_1688318	1	62	2,5E-14	-0,04	-0,25	0,30	-0,01
23493	4881	**HEY2**	hes related family bHLH transcription factor with YRPW motif 2	ILMN_1682034	1	62	2,5E-14	0,06	-0,21	0,30	-0,02
54617	26956	**INO80**	INO80 complex subunit	ILMN_3209317	1	62	2,5E-14	-0,04	-0,21	0,42	-0,06
81875	25745	**ISG20L2**	interferon stimulated exonuclease gene 20 like 2	ILMN_2090397	1	62	2,5E-14	-0,03	-0,19	0,34	-0,02
3673	6137	**ITGA2**	integrin subunit alpha 2	ILMN_1665792	1	62	2,5E-14	0,14	-0,26	0,53	0,03
147172	25390	**LRRC37BP1**	leucine rich repeat containing 37B pseudogene 1	ILMN_1802518;ILMN_3245600	1	62	2,5E-14	0,09	-0,18	0,50	0,08
57226	25229	**LYRM2**	LYR motif containing 2	ILMN_1703132	1	62	2,5E-14	0,07	-0,13	0,38	-0,03
4131	6836	**MAP1B**	microtubule associated protein 1B	ILMN_2377900;ILMN_1680154	1	62	2,5E-14	0,07	-0,23	0,44	0,09
4495	7399	**MT1G**	metallothionein 1G	ILMN_1715401	1	62	2,5E-14	0,08	-0,19	0,51	0,10
4792	7797	**NFKBIA**	NFKB inhibitor alpha	ILMN_1773154	1	62	2,5E-14	0,03	-0,20	0,28	0,10
23761	8999	PISD	phosphatidylserine decarboxylase	ILMN_1832879	1	62	2,5E-14	0,05	-0,26	0,16	0,05
5717	9556	**PSMD11**	proteasome 26S subunit, non-ATPase 11	ILMN_1800952	1	62	2,5E-14	0,11	-0,12	0,29	0,08
5872	9762	**RAB13**	RAB13, member RAS oncogene family	ILMN_1788180	1	62	2,5E-14	0,03	-0,32	0,36	-0,10
26866	37498	**RNU1-28P**	RNA, U1 small nuclear 28, pseudogene	ILMN_3240220	1	62	2,5E-14	0,01	-0,12	0,35	0,10
89970	29420	**RSPRY1**	ring finger and SPRY domain containing 1	ILMN_1763694	1	62	2,5E-14	0,14	-0,12	0,35	0,04
677768	32570	**SCARNA13**	small Cajal body-specific RNA 13	ILMN_3235325	1	62	2,5E-14	0,01	-0,16	0,37	-0,06
160728	19119	**SLC5A8**	solute carrier family 5 member 8	ILMN_1811221	1	62	2,5E-14	-0,06	-0,31	0,46	0,14

6606	11117	**SMN1**	survival of motor neuron 1, telomeric	ILMN_3215206	1	62	2,5E-14	0,12	-0,21	0,32	0,09
27099	24158	**SND1-IT1**	SND1 intronic transcript 1	ILMN_1655961	1	62	2,5E-14	0,11	-0,22	0,31	0,06
6629	11155	**SNRPB2**	small nuclear ribonucleoprotein polypeptide B2	ILMN_1690706;ILMN_1771620	1	62	2,5E-14	0,06	-0,15	0,32	0,01
6693	11249	**SPN**	sialophorin	ILMN_1801040	1	62	2,5E-14	-0,02	-0,29	0,62	0,07
6996	11700	**TDG**	thymine DNA glycosylase	ILMN_1777096;ILMN_1782331	1	62	2,5E-14	-0,03	-0,21	0,21	0,04
645233	49891	**TDGP1**	thymine-DNA glycosylase pseudogene 1	ILMN_3229033	1	62	2,5E-14	-0,10	-0,42	0,47	0,10
222068	22301	**TMED4**	transmembrane p24 trafficking protein 4	ILMN_1804148	1	62	2,5E-14	-0,02	-0,22	0,41	-0,05
84222	25317	**TMEM191A**	transmembrane protein 191A (pseudogene)	ILMN_3228529	1	62	2,5E-14	0,01	-0,19	0,47	0,05
286016	38069	**TPI1P2**	triosephosphate isomerase 1 pseudogene 2	ILMN_1684114	1	62	2,5E-14	0,08	-0,17	0,23	0,06
10475	10059	**TRIM38**	tripartite motif containing 38	ILMN_1697971	1	62	2,5E-14	-0,01	-0,17	0,27	-0,02
100874260	43554	**UBE2CP5**	ubiquitin conjugating enzyme E2 C pseudogene 5	ILMN_3303101;ILMN_3226495	1	62	2,5E-14	-0,03	-0,21	0,28	-0,03
7327	12483	**UBE2G2**	ubiquitin conjugating enzyme E2 G2	ILMN_1785179	1	62	2,5E-14	0,04	-0,24	0,19	-0,01
84858	23589	**ZNF503**	zinc finger protein 503	ILMN_1787265	1	62	2,5E-14	-0,05	-0,24	0,29	0,02
22848	19679	**AAK1**	AP2 associated kinase 1	ILMN_1688755	1	61	2,3E-09	-0,04	-0,24	0,54	-0,19
57730	29333	**ANKRD36B**	ankyrin repeat domain 36B	ILMN_1667932	1	61	2,3E-09	0,14	-0,13	0,40	-0,06
22809	790	**ATF5**	activating transcription factor 5	ILMN_1669113	1	61	2,3E-09	-0,04	-0,18	0,24	-0,15
401237	28245	**CASC15**	cancer susceptibility candidate 15 (non-protein coding)	ILMN_3247023	1	61	2,3E-09	0,02	-0,27	0,44	-0,13
113130	14626	**CDCA5**	cell division cycle associated 5	ILMN_1683450	1	61	2,3E-09	0,10	-0,13	0,20	-0,21
79366	8013	**HMGN5**	high mobility group nucleosome binding domain 5	ILMN_1749799	1	61	2,3E-09	0,02	-0,10	0,29	-0,12
100130764		**LOC100130764**	p150-like	ILMN_3256926	1	61	2,3E-09	0,13	-0,22	0,36	-0,21
2122	3498	**MECOM**	MDS1 and EVI1 complex locus	ILMN_1803367	1	61	2,3E-09	0,08	-0,12	0,34	-0,16
78988	14514	**MRPL57**	mitochondrial ribosomal protein L57	ILMN_1774312;ILMN_2203807	1	61	2,3E-09	0,02	-0,11	0,31	-0,11
644314	7401	**MT1IP**	metallothionein 1I, pseudogene	ILMN_2136089	1	61	2,3E-09	0,15	-0,13	0,37	-0,16
140851	16120	**MT1P3**	metallothionein 1 pseudogene 3	ILMN_1662640	1	61	2,3E-09	0,20	-0,13	0,47	-0,08
149934	16724	**NCOR1P1**	nuclear receptor corepressor 1 pseudogene 1	ILMN_2044027	1	61	2,3E-09	0,01	-0,16	0,25	-0,07
55051	20186	**NRDE2**	NRDE-2, necessary for RNA interference, domain containing	ILMN_1740165;ILMN_2374076	1	61	2,3E-09	0,06	-0,15	0,37	-0,14
56675	1167	**NRIP3**	nuclear receptor interacting protein 3	ILMN_1759563	1	61	2,3E-09	0,08	-0,14	0,29	-0,07
10432	14219	**RBM14**	RNA binding motif protein 14	ILMN_1657701	1	61	2,3E-09	0,06	-0,28	0,38	-0,16
653489	32416	**RGPD3**	RANBP2-like and GRIP domain containing 3	ILMN_1711073	1	61	2,3E-09	-0,05	-0,22	0,41	-0,18
56664	12654	**VTRNA1-1**	vault RNA 1-1	ILMN_1819384	1	61	2,3E-09	0,07	-0,29	0,61	-0,12
51101	24277	**ZC2HC1A**	zinc finger C2HC-type containing 1A	ILMN_1789558;ILMN_2057981	1	61	2,3E-09	0,17	-0,24	0,31	-0,14
10780	13027	**ZNF234**	zinc finger protein 234	ILMN_2103397;ILMN_1740197	1	61	2,3E-09	0,04	-0,15	0,31	-0,12
56987	14422	**BBX**	BBX, HMG-box containing	ILMN_1745415	1	32	9,1E-05	-0,18	-0,18	0,41	-0,06
55450	24190	**CAMK2N1**	calcium/calmodulin dependent protein kinase II inhibitor 1	ILMN_1794863	1	32	9,1E-05	-0,07	-0,15	0,27	-0,12
6347	10618	**CCL2**	C-C motif chemokine ligand 2	ILMN_1720048	1	32	9,1E-05	-0,21	-0,31	0,53	-0,42
404093	31350	**CUEDC1**	CUE domain containing 1	ILMN_1676665	1	32	9,1E-05	-0,13	-0,35	0,60	-0,16
160518	28338	**DENND5B**	DENN domain containing 5B	ILMN_1791593	1	32	9,1E-05	-0,12	-0,23	0,24	-0,17
8364	4787	**HIST1H4C**	histone cluster 1, H4c	ILMN_2075334	1	32	9,1E-05	-0,28	-0,45	0,76	-0,72
391356	33782	**PTRHD1**	peptidyl-tRNA hydrolase domain containing 1	ILMN_1692707	1	32	9,1E-05	-0,17	-0,22	0,20	-0,10
11267	17028	**SNF8**	SNF8, ESCRT-II complex subunit	ILMN_1766171	1	32	9,1E-05	-0,18	-0,15	0,23	-0,09
780854	33192	**SNORD3D**	small nucleolar RNA, C/D box 3D	ILMN_3242315	1	32	9,1E-05	-0,19	-0,17	0,38	-0,09
7049	11774	**TGFBR3**	transforming growth factor beta receptor 3	ILMN_1916457	1	32	9,1E-05	-0,19	-0,11	0,33	-0,05
126282	28279	**TNFAIP8L1**	TNF alpha induced protein 8 like 1	ILMN_1684346	1	32	9,1E-05	-0,28	-0,17	0,72	-0,32
23053	23528	**ZSWIM8**	zinc finger SWIM-type containing 8	ILMN_1803743	1	32	9,1E-05	-0,18	-0,24	0,32	-0,24
2	7	**A2M**	alpha-2-macroglobulin	ILMN_1745607	2	71	1,8E-47	-0,07	0,15	-0,33	0,04
653234	23659	**AGAP10P**	ArfGAP with GTPase domain, ankyrin repeat and PH domain 10 pseudogene	ILMN_3236344	2	71	1,8E-47	0,00	0,19	-0,28	-0,10
8227	18783	**AKAP17A**	A-kinase anchoring protein 17A	ILMN_1807737;ILMN_2117716	2	71	1,8E-47	-0,03	0,20	-0,23	-0,02
334	598	**APLP2**	amyloid beta precursor like protein 2	ILMN_2081465;ILMN_1710482	2	71	1,8E-47	-0,02	0,14	-0,33	0,04
351	620	**APP**	amyloid beta precursor protein	ILMN_1653283;ILMN_2404063;ILMN_2404065	2	71	1,8E-47	0,02	0,26	-0,46	-0,06
55738	15852	**ARFGAP1**	ADP ribosylation factor GTPase activating protein 1	ILMN_2406873;ILMN_1675709	2	71	1,8E-47	-0,06	0,18	-0,27	-0,02
9828	21726	**ARHGEF17**	Rho guanine nucleotide exchange factor 17	ILMN_1754562	2	71	1,8E-47	-0,09	0,21	-0,44	0,03
7832	1131	**BTG2**	BTG anti-proliferation factor 2	ILMN_1770085	2	71	1,8E-47	-0,04	0,25	-0,58	0,08
57805	23360	**CCAR2**	cell cycle and apoptosis regulator 2	ILMN_1804789	2	71	1,8E-47	-0,02	0,25	-0,19	-0,06
51363	18137	**CHST15**	carbohydrate sulfotransferase 15	ILMN_1670926	2	71	1,8E-47	-0,03	0,17	-0,35	-0,12
10106	17077	**CTDSP2**	CTD small phosphatase 2	ILMN_1692962	2	71	1,8E-47	0,00	0,19	-0,22	-0,03

220002	23014	**CYB561A3**	cytochrome b561 family member A3	ILMN_2129505	2	71	1,8E-47	0,06	0,25	-0,22	-0,02
23191	13759	**CYFIP1**	cytoplasmic FMR1 interacting protein 1	ILMN_2355462;ILMN_2355463	2	71	1,8E-47	-0,07	0,28	-0,29	0,02
8642	13681	**DCHS1**	dachsous cadherin-related 1	ILMN_1739640	2	71	1,8E-47	-0,02	0,19	-0,31	-0,07
22898	29134	**DENND3**	DENN domain containing 3	ILMN_1692742	2	71	1,8E-47	0,01	0,15	-0,29	0,00
9909	29044	**DENND4B**	DENN domain containing 4B	ILMN_3245066	2	71	1,8E-47	0,02	0,18	-0,30	0,03
57572	19189	**DOCK6**	dedicator of cytokinesis 6	ILMN_1801226	2	71	1,8E-47	-0,05	0,27	-0,28	0,06
8291	3097	**DYSF**	dysferlin	ILMN_1810420	2	71	1,8E-47	-0,09	0,24	-0,32	0,08
8662	3280	**EIF3B**	eukaryotic translation initiation factor 3 subunit B	ILMN_2379469;ILMN_2278729;ILMN_1715636	2	71	1,8E-47	-0,02	0,25	-0,21	-0,02
1981	3296	**EIF4G1**	eukaryotic translation initiation factor 4 gamma 1	ILMN_2370772;ILMN_1768470	2	71	1,8E-47	-0,03	0,20	-0,27	-0,04
57669	19819	**EPB41L5**	erythrocyte membrane protein band 4.1 like 5	ILMN_1770245;ILMN_2043306	2	71	1,8E-47	-0,10	0,15	-0,34	0,00
2086	3454	**ERV3-1**	endogenous retrovirus group 3 member 1	ILMN_2118663	2	71	1,8E-47	-0,04	0,18	-0,38	0,01
83986	14163	**FAM234A**	family with sequence similarity 234 member A	ILMN_1810055	2	71	1,8E-47	-0,07	0,27	-0,32	0,10
2194	3594	**FASN**	fatty acid synthase	ILMN_1784871	2	71	1,8E-47	-0,01	0,27	-0,29	-0,12
2314	3750	**FLII**	FLII, actin remodeling protein	ILMN_1737170	2	71	1,8E-47	-0,11	0,14	-0,35	-0,02
2548	4065	**GAA**	glucosidase alpha, acid	ILMN_2410783;ILMN_1765801	2	71	1,8E-47	-0,01	0,16	-0,33	-0,03
81544	28804	**GDPD5**	glycerophosphodiester phosphodiesterase domain containing 5	ILMN_1701643	2	71	1,8E-47	-0,06	0,15	-0,38	0,04
2817	4449	**GPC1**	glypican 1	ILMN_1801516	2	71	1,8E-47	-0,06	0,22	-0,18	0,08
9569	4661	**GTF2IRD1**	GTF2I repeat domain containing 1	ILMN_1712628	2	71	1,8E-47	-0,03	0,20	-0,24	-0,01
55127	25517	**HEATR1**	HEAT repeat containing 1	ILMN_1787762	2	71	1,8E-47	-0,02	0,19	-0,23	0,04
26173	24555	**INTS1**	integrator complex subunit 1	ILMN_1793854	2	71	1,8E-47	-0,09	0,23	-0,27	0,02
3915	6492	**LAMC1**	laminin subunit gamma 1	ILMN_1810852	2	71	1,8E-47	0,02	0,27	-0,23	0,03
55201	15715	**MAP1S**	microtubule associated protein 1S	ILMN_1796336	2	71	1,8E-47	0,00	0,21	-0,27	0,06
9862	22963	**MED24**	mediator complex subunit 24	ILMN_2388272;ILMN_1711853	2	71	1,8E-47	-0,02	0,24	-0,27	0,00
4213	7002	**MEIS3P1**	Meis homeobox 3 pseudogene 1	ILMN_2205896	2	71	1,8E-47	-0,10	0,18	-0,27	-0,02
4249	7049	**MGAT5**	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase	ILMN_1816244	2	71	1,8E-47	-0,07	0,23	-0,19	0,05
9961	7531	**MVP**	major vault protein	ILMN_2344373;ILMN_1803277	2	71	1,8E-47	-0,08	0,14	-0,30	0,00
4676	7640	**NAP1L4**	nucleosome assembly protein 1 like 4	ILMN_1804327	2	71	1,8E-47	0,02	0,28	-0,19	-0,02
84461	34410	**NEURL4**	neuralized E3 ubiquitin protein ligase 4	ILMN_2407811	2	71	1,8E-47	0,11	0,28	-0,19	0,08
4862	7895	**NPAS2**	neuronal PAS domain protein 2	ILMN_1765558	2	71	1,8E-47	-0,03	0,18	-0,24	0,02
728734	37490	**NPIPB8**	nuclear pore complex interacting protein family member B8	ILMN_1758798	2	71	1,8E-47	0,04	0,32	-0,29	0,01
64943	25717	**NT5DC2**	5'-nucleotidase domain containing 2	ILMN_1708743	2	71	1,8E-47	-0,02	0,19	-0,22	0,07
11054	15768	**OGFR**	opioid growth factor receptor	ILMN_1728224	2	71	1,8E-47	0,03	0,21	-0,28	-0,06
10401	16861	**PIAS3**	protein inhibitor of activated STAT 3	ILMN_1814966	2	71	1,8E-47	-0,08	0,25	-0,26	0,03
23396	8996	**PIP5K1C**	phosphatidylinositol-4-phosphate 5-kinase type 1 gamma	ILMN_1668514	2	71	1,8E-47	-0,03	0,17	-0,42	-0,10
23761	8999	**PISD**	phosphatidylserine decarboxylase	ILMN_1793934	2	71	1,8E-47	0,02	0,27	-0,18	0,04
5585	9405	**PKN1**	protein kinase N1	ILMN_2367710;ILMN_2367707	2	71	1,8E-47	-0,10	0,18	-0,26	-0,03
29941	17999	**PKN3**	protein kinase N3	ILMN_1797184	2	71	1,8E-47	-0,04	0,23	-0,26	0,05
57104	30802	**PNPLA2**	patatin like phospholipase domain containing 2	ILMN_1787923	2	71	1,8E-47	-0,11	0,30	-0,33	-0,11
5521	9305	**PPP2R2B**	protein phosphatase 2 regulatory subunit Bbeta	ILMN_2298365	2	71	1,8E-47	-0,03	0,27	-0,35	0,00
80209	20291	**PROSER1**	proline and serine rich 1	ILMN_2391551;ILMN_1795128	2	71	1,8E-47	-0,06	0,14	-0,37	-0,02
5725	9583	**PTBP1**	polypyrimidine tract binding protein 1	ILMN_1655154;ILMN_2333319	2	71	1,8E-47	0,04	0,32	-0,20	-0,03
25930	14406	**PTPN23**	protein tyrosine phosphatase, non-receptor type 23	ILMN_1654318	2	71	1,8E-47	0,04	0,16	-0,33	-0,04
9770	9883	**RASSF2**	Ras association domain family member 2	ILMN_2352303	2	71	1,8E-47	0,03	0,24	-0,47	-0,05
89941	21169	**RHOT2**	ras homolog family member T2	ILMN_1669310	2	71	1,8E-47	0,05	0,29	-0,21	0,00
255488	21578	**RNF144B**	ring finger protein 144B	ILMN_1752526	2	71	1,8E-47	0,03	0,21	-0,27	-0,04
9871	10706	**SEC24D**	SEC24 homolog D, COPII coat complex component	ILMN_1656386	2	71	1,8E-47	-0,02	0,23	-0,22	0,04
10801	7323	**SEPT9**	septin 9	ILMN_1769118	2	71	1,8E-47	-0,01	0,21	-0,19	0,01
124565	28237	**SLC38A10**	solute carrier family 38 member 10	ILMN_2277419;ILMN_1759743	2	71	1,8E-47	-0,09	0,13	-0,27	-0,12
6522	11028	**SLC4A2**	solute carrier family 4 member 2	ILMN_2078389	2	71	1,8E-47	0,09	0,23	-0,31	-0,01
27044	30646	**SND1**	staphylococcal nuclease and tudor domain containing 1	ILMN_1775111	2	71	1,8E-47	0,03	0,19	-0,28	0,00
6709	11273	**SPTAN1**	spectrin alpha, non-erythrocytic 1	ILMN_2095133	2	71	1,8E-47	-0,10	0,27	-0,31	-0,03
6720	11289	**SREBF1**	sterol regulatory element binding transcription factor 1	ILMN_1663035;ILMN_2328986	2	71	1,8E-47	-0,05	0,23	-0,21	-0,07
23166	18628	**STAB1**	stabilin 1	ILMN_1655987	2	71	1,8E-47	-0,05	0,23	-0,52	-0,06
6836	11476	**SURF4**	surfeit 4	ILMN_1690761	2	71	1,8E-47	0,10	0,28	-0,25	0,00
55638	26011	**SYBU**	syntabulin	ILMN_1738989	2	71	1,8E-47	-0,04	0,26	-0,18	0,11

101060321	29860	**TBC1D3G**	TBC1 domain family member 3G	ILMN_2068991	2	71	1,8E-47	-0,06	0,23	-0,40	-0,14
6904	11581	**TBCD**	tubulin folding cofactor D	ILMN_1673376;ILMN_1795400	2	71	1,8E-47	-0,11	0,16	-0,27	-0,09
64129	19168	**TINAGL1**	tubulointerstitial nephritis antigen like 1	ILMN_1807169	2	71	1,8E-47	0,06	0,22	-0,44	-0,09
25829	1310	**TMEM184B**	transmembrane protein 184B	ILMN_1747460	2	71	1,8E-47	-0,01	0,19	-0,42	-0,09
9772	28983	**TMEM94**	transmembrane protein 94	ILMN_2059211	2	71	1,8E-47	-0,08	0,10	-0,31	-0,06
26133	16181	**TRPC4AP**	transient receptor potential cation channel subfamily C member 4 associated protein	ILMN_2402805;ILMN_2402806	2	71	1,8E-47	0,01	0,32	-0,27	0,01
54795	17993	**TRPM4**	transient receptor potential cation channel subfamily M member 4	ILMN_1679401	2	71	1,8E-47	-0,03	0,31	-0,16	0,00
91373	28082	**UAP1L1**	UDP-N-acetylglucosamine pyrophosphorylase 1 like 1	ILMN_1653712	2	71	1,8E-47	0,00	0,29	-0,39	-0,09
8078	12628	**USP5**	ubiquitin specific peptidase 5	ILMN_1671494	2	71	1,8E-47	0,00	0,28	-0,34	0,03
6844	12643	**VAMP2**	vesicle associated membrane protein 2	ILMN_1713491	2	71	1,8E-47	-0,05	0,26	-0,22	0,04
23355	29122	**VPS8**	VPS8, CORVET complex subunit	ILMN_1678268;ILMN_2415170	2	71	1,8E-47	0,01	0,15	-0,27	0,05
84243	20712	**ZDHHC18**	zinc finger DHHC-type containing 18	ILMN_1668270	2	71	1,8E-47	0,06	0,17	-0,27	0,05
23053	23528	**ZSWIM8**	zinc finger SWIM-type containing 8	ILMN_1669433	2	71	1,8E-47	0,00	0,17	-0,35	-0,12
196527	25240	**ANO6**	anoctamin 6	ILMN_1674941	2	65	6,6E-11	0,05	0,01	-0,47	-0,08
162	554	**AP1B1**	adaptor related protein complex 1 beta 1 subunit	ILMN_1781983;ILMN_2387505	2	65	6,6E-11	-0,03	0,04	-0,39	-0,06
27032	13211	**ATP2C1**	ATPase secretory pathway Ca2+ transporting 1	ILMN_1758784;ILMN_2340565;ILMN_1696568	2	65	6,6E-11	0,00	0,13	-0,35	0,02
9331	929	**B4GALT6**	beta-1,4-galactosyltransferase 6	ILMN_1732555	2	65	6,6E-11	-0,02	-0,01	-0,43	-0,03
4059	6722	**BCAM**	basal cell adhesion molecule (Lutheran blood group)	ILMN_1790455	2	65	6,6E-11	-0,02	-0,07	-0,38	0,03
4179	6953	**CD46**	CD46 molecule	ILMN_2307744;ILMN_2307740	2	65	6,6E-11	0,00	0,05	-0,35	0,12
79009	17906	**DDX50**	DEAD-box helicase 50	ILMN_1712320	2	65	6,6E-11	0,06	-0,01	-0,55	-0,01
9993	2845	**DGCR2**	DiGeorge syndrome critical region gene 2	ILMN_1713301	2	65	6,6E-11	0,02	0,18	-0,57	0,11
55699	29685	**IARS2**	isoleucyl-tRNA synthetase 2, mitochondrial	ILMN_1671207	2	65	6,6E-11	0,03	-0,01	-0,31	0,10
3423	5389	**IDS**	iduronate 2-sulfatase	ILMN_3282829	2	65	6,6E-11	-0,09	0,05	-0,39	0,02
23633	6399	**KPNA6**	karyopherin subunit alpha 6	ILMN_1696021	2	65	6,6E-11	0,08	0,07	-0,31	0,10
3912	6486	**LAMB1**	laminin subunit beta 1	ILMN_2214790;ILMN_1658709	2	65	6,6E-11	0,02	0,05	-0,38	0,05
441228		**LOC441228**	exportin for tRNA pseudogene	ILMN_1743711	2	65	6,6E-11	-0,01	0,02	-0,42	-0,06
54545	18191	**MTMR12**	myotubularin related protein 12	ILMN_1802831	2	65	6,6E-11	0,12	0,02	-0,54	-0,04
29959	7993	**NRBP1**	nuclear receptor binding protein 1	ILMN_1670096	2	65	6,6E-11	0,01	0,11	-0,35	0,01
57575	13404	**PCDH10**	protocadherin 10	ILMN_1715458;ILMN_1688500	2	65	6,6E-11	0,06	0,15	-0,43	-0,02
55251	15882	**PCMTD2**	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	ILMN_1767848	2	65	6,6E-11	-0,04	0,03	-0,53	0,02
5138	8777	**PDE2A**	phosphodiesterase 2A	ILMN_1681356	2	65	6,6E-11	-0,01	0,08	-0,35	0,10
353511	30070	**PKD1P6**	polycystin 1, transient receptor potential channel interacting pseudogene 6	ILMN_3246247	2	65	6,6E-11	0,10	0,07	-0,33	-0,03
5327	9051	**PLAT**	plasminogen activator, tissue type	ILMN_1738742	2	65	6,6E-11	0,03	0,11	-0,29	-0,02
5431	9188	**POLR2B**	RNA polymerase II subunit B	ILMN_2088172	2	65	6,6E-11	0,04	0,06	-0,34	0,05
5054	8583	**SERPINE1**	serpin family E member 1	ILMN_1744381	2	65	6,6E-11	-0,07	0,09	-0,45	-0,07
8036	15454	**SHOC2**	SHOC2, leucine rich repeat scaffold protein	ILMN_2158242	2	65	6,6E-11	0,11	0,10	-0,31	0,04
23309	19354	**SIN3B**	SIN3 transcription regulator family member B	ILMN_1788315	2	65	6,6E-11	0,02	0,12	-0,53	0,02
2030	11003	**SLC29A1**	solute carrier family 29 member 1 (Augustine blood group)	ILMN_1723971;ILMN_2338963	2	65	6,6E-11	0,08	0,15	-0,31	0,05
6774	11364	**STAT3**	signal transducer and activator of transcription 3	ILMN_2410986;ILMN_1663618;ILMN_2401978	2	65	6,6E-11	0,00	-0,05	-0,43	-0,11
55578	20596	**SUPT20H**	SPT20 homolog, SAGA complex component	ILMN_1669555	2	65	6,6E-11	0,09	0,01	-0,30	0,12
6829	11469	**SUPT5H**	SPT5 homolog, DSIF elongation factor subunit	ILMN_1703866	2	65	6,6E-11	0,15	0,06	-0,36	-0,01
414060	24889	**TBC1D3C**	TBC1 domain family member 3C	ILMN_1693802	2	65	6,6E-11	0,00	-0,08	-0,44	-0,08
4591	7523	**TRIM37**	tripartite motif containing 37	ILMN_1711327;ILMN_1704383	2	65	6,6E-11	0,12	0,02	-0,35	0,05
64123	20822	**ADGRL4**	adhesion G protein-coupled receptor L4	ILMN_3240520	2	72	3,2E-10	-0,04	0,14	-0,28	0,16
375790	329	**AGRN**	agrin	ILMN_1770454	2	72	3,2E-10	-0,15	0,27	-0,38	0,09
406	701	**ARNTL**	aryl hydrocarbon receptor nuclear translocator like	ILMN_2405305	2	72	3,2E-10	0,02	0,19	-0,23	0,15
7461	2586	**CLIP2**	CAP-Gly domain containing linker protein 2	ILMN_1811682;ILMN_2352190	2	72	3,2E-10	-0,01	0,15	-0,29	0,10
1605	2666	**DAG1**	dystroglycan 1	ILMN_1658425	2	72	3,2E-10	-0,06	0,08	-0,26	0,19
60481	21308	**ELOVL5**	ELOVL fatty acid elongase 5	ILMN_2174369	2	72	3,2E-10	0,00	0,21	-0,30	0,19
138311	28290	**FAM69B**	family with sequence similarity 69 member B	ILMN_1757440;ILMN_1718446	2	72	3,2E-10	-0,08	0,17	-0,31	0,13
129804	26740	**FBLN7**	fibulin 7	ILMN_1735743	2	72	3,2E-10	-0,08	0,07	-0,26	0,17
8515	6135	**ITGA10**	integrin subunit alpha 10	ILMN_1700144	2	72	3,2E-10	-0,06	0,24	-0,33	0,13
79143	15505	**MBOAT7**	membrane bound O-acyltransferase domain containing 7	ILMN_1722218	2	72	3,2E-10	-0,03	0,26	-0,20	0,19
55666	18261	**NPLOC4**	NPL4 homolog, ubiquitin recognition factor	ILMN_1807600	2	72	3,2E-10	-0,02	0,18	-0,35	0,11
5426	9177	**POLE**	DNA polymerase epsilon, catalytic subunit	ILMN_1728199	2	72	3,2E-10	-0,09	0,13	-0,30	0,09

22904	29158	**SBNO2**	strawberry notch homolog 2	ILMN_1808811	2	72	3,2E-10	0,04	0,13	-0,25	0,23
1992	3311	**SERPINB1**	serpin family B member 1	ILMN_1679133	2	72	3,2E-10	-0,16	0,13	-0,31	0,08
51547	14935	**SIRT7**	sirtuin 7	ILMN_3237291	2	72	3,2E-10	-0,03	0,12	-0,29	0,08
124935	23087	**SLC43A2**	solute carrier family 43 member 2	ILMN_1787127	2	72	3,2E-10	-0,06	0,18	-0,31	0,09
23075	17070	**SWAP70**	SWAP switching B-cell complex 70kDa subunit	ILMN_1785175	2	72	3,2E-10	-0,11	0,08	-0,29	0,15
64759	21616	**TNS3**	tensin 3	ILMN_1667893	2	72	3,2E-10	-0,06	0,13	-0,28	0,18
389787	49299	**TPT1P9**	tumor protein, translationally-controlled 1 pseudogene 9	ILMN_1665823	2	72	3,2E-10	-0,08	0,04	-0,29	0,11
400406	49409	**ADAMTS7P3**	ADAMTS7 pseudogene 3	ILMN_1772239	2	100	2,9E-03	0,10	0,17	-0,31	0,07
65981	21259	**CAPRIN2**	caprin family member 2	ILMN_1681118;ILMN_2345739	2	100	2,9E-03	0,21	0,10	-0,26	0,11
51167	20147	**CYB5R4**	cytochrome b5 reductase 4	ILMN_1688158	2	100	2,9E-03	0,07	0,15	-0,25	0,18
100272217		**LOC100272217**	uncharacterized LOC100272217 (ncRNA)	ILMN_1770818	2	100	2,9E-03	0,23	0,18	-0,33	0,11
23241	23794	**PACS2**	phosphofurin acidic cluster sorting protein 2	ILMN_1719864	2	100	2,9E-03	0,11	0,25	-0,23	0,13
84255	20651	**SLC37A3**	solute carrier family 37 member 3	ILMN_2307598;ILMN_1779979;ILMN_1686535	2	100	2,9E-03	0,18	0,11	-0,34	0,06
91107	19020	**TRIM47**	tripartite motif containing 47	ILMN_1712708	2	100	2,9E-03	0,13	0,24	-0,30	0,20
253943	26465	**YTHDF3**	YTH N6-methyladenosine RNA binding protein 3	ILMN_1657470	2	100	2,9E-03	0,17	0,10	-0,31	0,19
57545	29253	**CC2D2A**	coiled-coil and C2 domain containing 2A	ILMN_2406586	3	99	9,4E-06	0,16	0,16	-0,27	0,06
9416	17347	**DDX23**	DEAD-box helicase 23	ILMN_1784218	3	99	9,4E-06	0,10	0,23	-0,17	-0,04
1793	2987	**DOCK1**	dedicator of cytokinesis 1	ILMN_1715789	3	99	9,4E-06	0,09	0,13	-0,40	-0,05
1857	3087	**DVL3**	dishevelled segment polarity protein 3	ILMN_2137464	3	99	9,4E-06	0,16	0,13	-0,40	-0,10
9695	18967	**EDEM1**	ER degradation enhancing alpha-mannosidase like protein 1	ILMN_1779828	3	99	9,4E-06	0,09	0,20	-0,31	0,00
955	3368	**ENTPD6**	ectonucleoside triphosphate diphosphohydrolase 6 (putative)	ILMN_2091792	3	99	9,4E-06	0,19	0,09	-0,21	-0,10
22992	13606	**KDM2A**	lysine demethylase 2A	ILMN_3237966	3	99	9,4E-06	0,19	0,27	-0,40	-0,09
648927		**LOC648927**	lysine acetyltransferase 7 pseudogene	ILMN_3274914	3	99	9,4E-06	0,11	0,26	-0,40	-0,04
4324	7161	**MMP15**	matrix metallopeptidase 15	ILMN_1718646	3	99	9,4E-06	0,16	0,07	-0,24	-0,09
23279	18017	**NUP160**	nucleoporin 160	ILMN_1652989	3	99	9,4E-06	0,11	0,25	-0,25	-0,04
6804	11433	**STX1A**	syntaxin 1A	ILMN_1760160	3	99	9,4E-06	0,07	0,18	-0,25	-0,09
10959	16996	**TMED2**	transmembrane p24 trafficking protein 2	ILMN_1654939	3	99	9,4E-06	0,14	0,11	-0,30	0,01
488	812	**ATP2A2**	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporting 2	ILMN_1687375;ILMN_1815666;ILMN_1655884	3	64	5,9E-05	0,03	0,11	-0,32	-0,08
1287	2207	**COL4A5**	collagen type IV alpha 5 chain	ILMN_1742534;ILMN_2375360	3	64	5,9E-05	0,08	0,02	-0,35	-0,09
2004	3325	**ELK3**	ELK3, ETS transcription factor	ILMN_1692335	3	64	5,9E-05	0,01	0,08	-0,47	-0,10
2590	4124	**GALNT2**	polypeptide N-acetylgalactosaminyltransferase 2	ILMN_1814606	3	64	5,9E-05	0,03	0,06	-0,35	-0,16
23303	14405	**KIF13B**	kinesin family member 13B	ILMN_1686562	3	64	5,9E-05	0,07	0,06	-0,34	-0,11
23367	29531	**LARP1**	La ribonucleoprotein domain family member 1	ILMN_1681590	3	64	5,9E-05	0,10	0,01	-0,35	-0,17
26509	3656	**MYOF**	myoferlin	ILMN_1810289;ILMN_3302919;ILMN_2370976	3	64	5,9E-05	0,11	0,08	-0,45	-0,16
55213	18243	**RCBTB1**	RCC1 and BTB domain containing protein 1	ILMN_1695317	3	64	5,9E-05	0,07	0,10	-0,32	-0,07
23353	18587	**SUN1**	Sad1 and UNC84 domain containing 1	ILMN_1772316	3	64	5,9E-05	-0,01	-0,04	-0,43	-0,18
85456	19081	**TNKS1BP1**	tankyrase 1 binding protein 1	ILMN_1690826	3	64	5,9E-05	0,04	0,07	-0,45	-0,13
54863	25981	**TOR4A**	torsin family 4 member A	ILMN_1813641	3	64	5,9E-05	0,00	0,19	-0,59	-0,13
377	654	**ARF3**	ADP ribosylation factor 3	ILMN_1682938	3	89	1,5E-03	0,41	-0,04	-0,39	-0,03
64225	24047	**ATL2**	atlastin GTPase 2	ILMN_1716384	3	89	1,5E-03	0,18	0,02	-0,23	-0,01
51272	19348	**BET1L**	Bet1 golgi vesicular membrane trafficking protein like	ILMN_2060652	3	89	1,5E-03	0,15	-0,04	-0,29	-0,05
65998	28449	**C11orf95**	chromosome 11 open reading frame 95	ILMN_1862180	3	89	1,5E-03	0,15	0,05	-0,32	0,00
51652	29865	**CHMP3**	charged multivesicular body protein 3	ILMN_2406043;ILMN_1683827	3	89	1,5E-03	0,10	-0,06	-0,31	-0,06
1847	3071	**DUSP5**	dual specificity phosphatase 5	ILMN_1656501	3	89	1,5E-03	0,22	-0,03	-0,24	-0,07
2624	4171	**GATA2**	GATA binding protein 2	ILMN_2102670	3	89	1,5E-03	0,22	0,05	-0,29	0,02
2697	4274	**GJA1**	gap junction protein alpha 1	ILMN_1727087	3	89	1,5E-03	0,20	-0,02	-0,25	0,01
57493	29227	**HEG1**	heart development protein with EGF like domains 1	ILMN_1666122	3	89	1,5E-03	0,18	-0,01	-0,32	0,00
100128337	39838	**IPO7P2**	importin 7 pseudogene 2	ILMN_3265761	3	89	1,5E-03	0,19	0,04	-0,26	0,09
1326	6860	**MAP3K8**	mitogen-activated protein kinase kinase kinase 8	ILMN_1741159	3	89	1,5E-03	0,23	0,02	-0,29	0,03
112950	19971	**MED8**	mediator complex subunit 8	ILMN_2339705	3	89	1,5E-03	0,23	-0,02	-0,20	0,08
29982	19692	**NRBF2**	nuclear receptor binding factor 2	ILMN_1719344	3	89	1,5E-03	0,17	-0,03	-0,23	-0,06
8050	21350	**PDHX**	pyruvate dehydrogenase complex component X	ILMN_1652357	3	89	1,5E-03	0,15	-0,11	-0,26	0,01
375133	33577	**PI4KAP2**	phosphatidylinositol 4-kinase alpha pseudogene 2	ILMN_1655126	3	89	1,5E-03	0,15	0,06	-0,25	-0,01
5591	9413	**PRKDC**	protein kinase, DNA-activated, catalytic polypeptide	ILMN_3235642	3	89	1,5E-03	0,21	-0,02	-0,35	-0,19
192683	30386	**SCAMP5**	secretory carrier membrane protein 5	ILMN_1753345	3	89	1,5E-03	0,14	-0,04	-0,30	-0,09

4088	6769	**SMAD3**	SMAD family member 3	ILMN_1682738	3	89	1,5E-03	0,19	0,05	-0,23	0,05
9675	29029	**TTI1**	TELO2 interacting protein 1	ILMN_1741398	3	89	1,5E-03	0,16	-0,01	-0,34	-0,02
7534	12855	**YWHAZ**	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta	ILMN_1801928	3	89	1,5E-03	0,19	0,06	-0,22	0,02
2182	3571	**ACSL4**	acyl-CoA synthetase long-chain family member 4	ILMN_1870457	4	33	8,2E-12	-0,08	-0,11	0,36	0,05
153222	24050	**CREBRF**	CREB3 regulatory factor	ILMN_1776788;ILMN_2195821	4	33	8,2E-12	-0,17	-0,20	0,30	0,10
64421	17642	**DCLRE1C**	DNA cross-link repair 1C	ILMN_1754211;ILMN_2321931	4	33	8,2E-12	-0,13	-0,13	0,30	-0,02
5610	9437	**EIF2AK2**	eukaryotic translation initiation factor 2 alpha kinase 2	ILMN_1706502	4	33	8,2E-12	-0,13	-0,12	0,30	0,02
51077	20220	**FCF1**	FCF1 rRNA-processing protein	ILMN_2189870;ILMN_2189869	4	33	8,2E-12	-0,10	-0,11	0,33	0,09
3652	6108	**IPP**	intracisternal A particle-promoted polypeptide	ILMN_1789106	4	33	8,2E-12	-0,21	-0,15	0,56	0,02
162073	27257	**ITPRIPL2**	inositol 1,4,5-trisphosphate receptor interacting protein-like 2	ILMN_1751034;ILMN_2219246	4	33	8,2E-12	-0,20	-0,10	0,34	0,04
3987	6616	**LIMS1**	LIM zinc finger domain containing 1	ILMN_1675387;ILMN_2381037	4	33	8,2E-12	-0,07	-0,14	0,39	0,18
100421561		**LOC100421561**	family with sequence similarity 133 member B pseudogene	ILMN_1771048	4	33	8,2E-12	-0,14	-0,28	0,58	0,09
4208	6996	**MEF2C**	myocyte enhancer factor 2C	ILMN_1742544	4	33	8,2E-12	-0,20	-0,24	0,51	0,24
4782	7786	**NFIC**	nuclear factor I C	ILMN_1675130	4	33	8,2E-12	-0,29	-0,21	0,38	0,05
54940	16074	**OCIAD1**	OCIA domain containing 1	ILMN_2330495;ILMN_1799604	4	33	8,2E-12	-0,19	-0,12	0,27	0,01
64282	30758	**PAPD5**	PAP associated domain containing 5	ILMN_1710571	4	33	8,2E-12	-0,10	-0,17	0,28	0,13
145482	20149	**PTGR2**	prostaglandin reductase 2	ILMN_2105253	4	33	8,2E-12	-0,25	-0,11	0,75	0,21
9584	15923	**RBM39**	RNA binding motif protein 39	ILMN_2411963	4	33	8,2E-12	-0,17	-0,09	0,28	0,06
79845	21147	**RNF122**	ring finger protein 122	ILMN_1691119	4	33	8,2E-12	-0,08	-0,03	0,37	0,11
389168	42933	**SETP14**	SET pseudogene 14	ILMN_3210917	4	33	8,2E-12	-0,17	-0,10	0,64	0,29
221322	21485	**TBC1D32**	TBC1 domain family member 32	ILMN_1805695;ILMN_2228196	4	33	8,2E-12	-0,10	-0,10	0,42	0,07
100131096	44360	**TNRC6C-AS1**	TNRC6C antisense RNA 1	ILMN_3216365	4	33	8,2E-12	-0,12	-0,08	0,32	0,09
54663	25529	**WDR74**	WD repeat domain 74	ILMN_2270845	4	33	8,2E-12	-0,40	-0,26	0,64	0,12
7707	12933	**ZNF148**	zinc finger protein 148	ILMN_2143822	4	33	8,2E-12	-0,21	-0,24	0,29	-0,05
162966	30951	**ZNF600**	zinc finger protein 600	ILMN_1678457	4	33	8,2E-12	-0,06	-0,11	0,41	0,16
23476	13575	**BRD4**	bromodomain containing 4	ILMN_1771061	4	41	3,0E-03	-0,21	-0,04	0,23	-0,05
27071	16500	**DAPP1**	dual adaptor of phosphotyrosine and 3-phosphoinositides 1	ILMN_2097410	4	41	3,0E-03	-0,39	-0,02	0,85	0,04
283932	27557	**FBXL19-AS1**	FBXL19 antisense RNA 1 (head to head)	ILMN_1710954;ILMN_3239236	4	41	3,0E-03	-0,18	-0,06	0,26	0,06
145438	20129	**FRMD6-AS1**	FRMD6 antisense RNA 1	ILMN_1690443	4	41	3,0E-03	-0,32	-0,16	0,38	-0,06
80895	15566	**ILKAP**	ILK associated serine/threonine phosphatase	ILMN_1684647	4	41	3,0E-03	-0,17	-0,02	0,26	-0,03
54923	26016	**LIME1**	Lck interacting transmembrane adaptor 1	ILMN_2183687	4	41	3,0E-03	-0,26	-0,01	0,21	-0,07
401149	49084	**LINC01061**	long intergenic non-protein coding RNA 1061	ILMN_3187283	4	41	3,0E-03	-0,16	-0,03	0,30	0,06
100131850		**LOC100131850**	hypothetical LOC100131850	ILMN_3281309	4	41	3,0E-03	-0,26	-0,01	0,30	0,07
8260	18704	**NAA10**	N(alpha)-acetyltransferase 10, NatA catalytic subunit	ILMN_1721977	4	41	3,0E-03	-0,27	-0,01	0,22	-0,03
260294	16609	**NSUN5P2**	NOP2/Sun RNA methyltransferase family member 5 pseudogene 2	ILMN_1681899	4	41	3,0E-03	-0,19	-0,03	0,25	0,00
81858	25321	**SHARPIN**	SHANK associated RH domain interactor	ILMN_1794780	4	41	3,0E-03	-0,21	0,08	0,21	-0,01
100506060	49864	**SMG1P7**	SMG1P7, nonsense mediated mRNA decay associated PI3K related kinase pseudogene 7	ILMN_3222998	4	41	3,0E-03	-0,29	-0,05	0,21	0,00
692084	32711	**SNORD13**	small nucleolar RNA, C/D box 13	ILMN_1892403	4	41	3,0E-03	-0,68	-0,25	1,13	0,00
780851	33189	**SNORD3A**	small nucleolar RNA, C/D box 3A	ILMN_3239574	4	41	3,0E-03	-0,17	0,00	0,33	0,11
9392	16836	**TGFBRAP1**	transforming growth factor beta receptor associated protein 1	ILMN_1696870	4	41	3,0E-03	-0,25	0,11	0,48	0,02
64417	26139	**TMEM267**	transmembrane protein 267	ILMN_2150465;ILMN_1694798	4	41	3,0E-03	-0,17	0,06	0,44	0,03
100134938	37278	**UPK3BL**	uroplakin 3B-like	ILMN_3236765	4	41	3,0E-03	-0,15	0,02	0,28	0,03
84225	20997	**ZMYND15**	zinc finger MYND-type containing 15	ILMN_1778136	4	41	3,0E-03	-0,21	0,02	0,20	0,01
729806	32471	**ZNF731P**	zinc finger protein 731, pseudogene	ILMN_3304012	4	41	3,0E-03	-0,13	0,03	0,39	0,11
440193	19967	**CCDC88C**	coiled-coil domain containing 88C	ILMN_3248352	5	44	1,9E-07	-0,10	0,24	-0,19	0,01
55743	20455	**CHFR**	checkpoint with forkhead and ring finger domains, E3 ubiquitin protein ligase	ILMN_1653828	5	44	1,9E-07	-0,13	0,14	-0,26	0,00
84940	21356	**CORO6**	coronin 6	ILMN_1813386	5	44	1,9E-07	-0,24	0,20	-0,20	0,02
644634	49509	**FAM231D**	family with sequence similarity 231 member D (ncRNA)	ILMN_3238281	5	44	1,9E-07	-0,22	0,19	-0,14	-0,02
360132	23568	**FKBP9P1**	FK506 binding protein 9 pseudogene 1	ILMN_2089977	5	44	1,9E-07	-0,19	0,25	-0,10	0,06
28964	4272	**GIT1**	GIT ArfGAP 1	ILMN_1733155	5	44	1,9E-07	-0,22	0,13	-0,40	-0,04
9807	18360	**IP6K1**	inositol hexakisphosphate kinase 1	ILMN_2392286;ILMN_1700231;ILMN_3187328	5	44	1,9E-07	-0,13	0,31	-0,09	0,01
3710	6182	**ITPR3**	inositol 1,4,5-trisphosphate receptor type 3	ILMN_1815500	5	44	1,9E-07	-0,14	0,26	-0,17	-0,01
613037		**LOC613037**	nuclear pore complex interacting protein member	ILMN_1696843;ILMN_2070052	5	44	1,9E-07	-0,31	0,22	-0,17	-0,07
23162	6884	**MAPK8IP3**	mitogen-activated protein kinase 8 interacting protein 3	ILMN_1811574	5	44	1,9E-07	-0,23	0,20	-0,31	-0,12
8775	7641	**NAPA**	NSF attachment protein alpha	ILMN_1713285	5	44	1,9E-07	-0,19	0,14	-0,30	-0,01

100132247	37233	**NPIPB5**	nuclear pore complex interacting protein family member B5	ILMN_3246766	5	44	1,9E-07	-0,26	0,14	-0,28	-0,11
23654	9104	**PLXNB2**	plexin B2	ILMN_1763447	5	44	1,9E-07	-0,14	0,19	-0,26	-0,04
54436	26009	**SH3TC1**	SH3 domain and tetratricopeptide repeats 1	ILMN_1756595	5	44	1,9E-07	-0,17	0,26	-0,28	0,04
11138	17791	**TBC1D8**	TBC1 domain family member 8	ILMN_1735495	5	44	1,9E-07	-0,17	0,13	-0,35	-0,01
8295	12347	**TRRAP**	transformation/transcription domain associated protein	ILMN_1660368	5	44	1,9E-07	-0,15	0,14	-0,27	-0,06
57507	29238	**ZNF608**	zinc finger protein 608	ILMN_1712798	5	44	1,9E-07	-0,18	0,23	-0,13	0,14
1277	2197	**COL1A1**	collagen type I alpha 1	ILMN_1701308	6	70	1,3E-04	0,05	0,29	-0,18	-0,34
1278	2198	**COL1A2**	collagen type I alpha 2 chain	ILMN_1785272;ILMN_2104356	6	70	1,3E-04	-0,11	0,19	-0,31	-0,20
1289	2209	**COL5A1**	collagen type V alpha 1	ILMN_1706505	6	70	1,3E-04	0,00	0,16	-0,18	-0,25
2975	4664	**GTF3C1**	general transcription factor IIIC subunit 1	ILMN_1789839	6	70	1,3E-04	-0,05	0,17	-0,25	-0,22
65123	26153	**INTS3**	integrator complex subunit 3	ILMN_1756086	6	70	1,3E-04	0,02	0,16	-0,26	-0,23
23189	19309	**KANK1**	KN motif and ankyrin repeat domains 1	ILMN_3244019	6	70	1,3E-04	-0,03	0,11	-0,18	-0,32
51621	13672	**KLF13**	Kruppel like factor 13	ILMN_1679929	6	70	1,3E-04	0,08	0,31	-0,07	-0,17
4054	6716	**LTBP3**	latent transforming growth factor beta binding protein 3	ILMN_1805395	6	70	1,3E-04	0,07	0,29	-0,23	-0,10
85358	14294	**SHANK3**	SH3 and multiple ankyrin repeat domains 3	ILMN_2317580;ILMN_2317581	6	70	1,3E-04	-0,05	0,14	-0,33	-0,26
51548	14934	**SIRT6**	sirtuin 6	ILMN_1654246	6	70	1,3E-04	-0,07	0,23	-0,23	-0,14
6777	11367	**STAT5B**	signal transducer and activator of transcription 5B	ILMN_1684034	6	70	1,3E-04	-0,01	0,15	-0,31	-0,19

Table S3*b* | Transcripts associated with 42 nonsignificant temporal profiles of differential expression. *These genes were associated with model profiles that had a FDR > 0.05.*

						FDR > 0.05					
Entrez GeneID	HGNC ID	Gene symbol	Gene Name	Illumina probe_ID	Cluster	Profile	Profile *P*-value	log$_2$(FC) *at 0.5h*	log$_2$(FC) *at 3h*	log$_2$(FC) *at 6h*	log$_2$(FC) *at 12h*
729198	33976	**ANAPC10P1**	anaphase promoting complex subunit 10 pseudogene 1	ILMN_3227485	na	88	0,01	0,21	-0,26	0,21	-0,19
10926	17364	**DBF4**	DBF4 zinc finger	ILMN_3191227	na	88	0,01	0,16	-0,27	0,16	0,05
11010	17001	**GLIPR1**	GLI pathogenesis related 1	ILMN_1769245	na	88	0,01	0,18	-0,09	0,32	0,03
100287497		**LOC100287497**	septin 7 pseudogene	ILMN_1691402	na	88	0,01	0,16	-0,28	0,29	-0,09
284821	23755	**RPL13AP7**	ribosomal protein L13a pseudogene 7	ILMN_1680208	na	88	0,01	0,16	-0,30	0,08	-0,03
29950	17932	**SERTAD1**	SERTA domain containing 1	ILMN_1794017	na	88	0,01	0,23	-0,13	0,32	0,09
9306	16833	**SOCS6**	suppressor of cytokine signaling 6	ILMN_1657077	na	88	0,01	0,31	-0,19	0,17	0,10
643136	25659	**ZC3H11B**	zinc finger CCCH-type containing 11B pseudogene	ILMN_1767514	na	88	0,01	0,21	-0,20	0,10	-0,08
367	644	**AR**	androgen receptor	ILMN_1767351	na	40	0,02	-0,11	0,02	0,37	-0,18
10309	18576	**CCNO**	cyclin O	ILMN_1676631	na	40	0,02	-0,13	-0,01	0,26	-0,14
3659	6116	**IRF1**	interferon regulatory factor 1	ILMN_1708375	na	40	0,02	-0,13	0,02	0,24	-0,19
143458	27046	**LDLRAD3**	low density lipoprotein receptor class A domain containing 3	ILMN_2129563	na	40	0,02	-0,21	0,03	0,23	-0,15
57555	14290	**NLGN2**	neuroligin 2	ILMN_1764158	na	40	0,02	-0,24	-0,10	0,17	-0,26
29901	30179	**SAC3D1**	SAC3 domain containing 1	ILMN_1776674	na	40	0,02	-0,19	0,06	0,17	-0,24
254863	28618	**TMEM256**	transmembrane protein 256	ILMN_2201533	na	40	0,02	-0,16	0,07	0,26	-0,06
2224	3631	**FDPS**	farnesyl diphosphate synthase	ILMN_1804248	na	63	0,05	0,08	-0,21	0,29	0,17
2268	3697	**FGR**	FGR proto-oncogene, Src family tyrosine kinase	ILMN_2272519	na	63	0,05	0,03	-0,34	0,14	0,24
9729	21636	**KIAA0408**	KIAA0408	ILMN_1661519	na	63	0,05	-0,06	-0,16	0,32	0,20
25945	17664	**NECTIN3**	nectin cell adhesion molecule 3	ILMN_1727633;ILMN_2188521	na	63	0,05	-0,14	-0,29	0,17	0,16
9749	20956	**PHACTR2**	phosphatase and actin regulator 2	ILMN_1790533	na	63	0,05	0,05	-0,37	0,23	0,19
286046	27806	**XKR6**	XK related 6	ILMN_3182020	na	63	0,05	0,04	-0,13	0,18	0,28
730051	33258	**ZNF814**	zinc finger protein 814	ILMN_1700182	na	63	0,05	0,04	-0,16	0,35	0,20
9253	8061	**NUMBL**	NUMB like, endocytic adaptor protein	ILMN_1651538	na	16	*ns*	-0,48	-0,15	0,13	0,03
		BU853937		ILMN_1825880	na	17	*ns*	-0,17	-0,02	0,09	0,23
83641	23726	**FAM107B**	family with sequence similarity 107 member B	ILMN_1758672	na	17	*ns*	-0,27	-0,02	-0,06	0,28
2537	4054	**IFI6**	interferon alpha inducible protein 6	ILMN_2347798;ILMN_1687384	na	17	*ns*	-0,20	0,00	0,01	0,26
645233	49891	**TDGP1**	thymine-DNA glycosylase pseudogene 1	ILMN_3240721	na	27	*ns*	-0,16	-0,43	0,20	0,05
90865	16028	**IL33**	interleukin 33	ILMN_1809099	na	28	*ns*	-0,16	-0,09	-0,42	-0,03
9149	3092	**DYRK1B**	dual specificity tyrosine phosphorylation regulated kinase 1B	ILMN_1696991;ILMN_2354617	na	35	*ns*	-0,18	0,04	-0,38	-0,09
2137	3518	**EXTL3**	exostosin like glycosyltransferase 3	ILMN_1778226	na	35	*ns*	-0,16	0,10	-0,31	-0,04
57523	20165	**NYNRIN**	NYN domain and retroviral integrase containing	ILMN_3236858	na	35	*ns*	-0,20	0,12	-0,31	-0,13
57649	20816	**PHF12**	PHD finger protein 12	ILMN_1730799	na	35	*ns*	-0,11	0,05	-0,41	-0,11
54872	25985	**PIGG**	phosphatidylinositol glycan anchor biosynthesis class G	ILMN_1769751	na	35	*ns*	-0,08	0,06	-0,35	-0,07
2653	4208	**GCSH**	glycine cleavage system protein H	ILMN_2090782	na	38	*ns*	-0,14	0,03	0,17	-0,33
767558	33955	**LUZP6**	leucine zipper protein 6	ILMN_3273491	na	39	*ns*	-0,49	0,04	0,08	-0,08
101059953	41983	**NPIPA8**	nuclear pore complex interacting protein family member A8	ILMN_3304111	na	39	*ns*	-0,42	0,13	-0,05	0,05
1499	2514	**CTNNB1**	catenin beta 1	ILMN_1757350;ILMN_1746396	na	42	*ns*	-0,21	-0,05	0,25	0,24
347292	35734	**RPL36P14**	ribosomal protein L36 pseudogene 14	ILMN_1654445	na	42	*ns*	-0,26	-0,10	0,27	0,13
4093	6774	**SMAD9**	SMAD family member 9	ILMN_1815385	na	42	*ns*	-0,19	-0,10	0,21	0,13
9684	20419	**LRRC14**	leucine rich repeat containing 14	ILMN_1678998	na	43	*ns*	-0,18	0,20	-0,19	-0,23
4642	7598	**MYO1D**	myosin ID	ILMN_1805999	na	43	*ns*	-0,22	0,19	-0,27	-0,15
80301	30026	**PLEKHO2**	pleckstrin homology domain containing O2	ILMN_1689968	na	43	*ns*	-0,15	0,23	-0,26	-0,11
26051	15850	**PPP1R16B**	protein phosphatase 1 regulatory subunit 16B	ILMN_1727098	na	43	*ns*	-0,16	0,17	-0,26	-0,14
5834	9723	**PYGB**	phosphorylase, glycogen; brain	ILMN_1778360	na	43	*ns*	-0,11	0,28	-0,13	-0,08
109	234	**ADCY3**	adenylate cyclase 3	ILMN_1676893	na	46	*ns*	-0,27	0,20	-0,01	0,00
643007	30973	**RPL36AP8**	ribosomal protein L36a pseudogene 8	ILMN_1724295	na	49	*ns*	-0,33	0,12	0,20	-0,09
57551	29259	**TAOK1**	TAO kinase 1	ILMN_1758087	na	49	*ns*	-0,64	0,34	0,38	0,01
57582	18865	**KCNT1**	potassium sodium-activated channel subfamily T member 1	ILMN_3285742	na	50	*ns*	-0,29	0,08	0,27	0,25
163882	26486	**CNST**	consortin, connexin sorting protein	ILMN_1670263	na	51	*ns*	-0,50	0,09	0,12	0,46
105369147		**LOC105369147**	uncharacterized LOC105369147 (ncRNA)	ILMN_1678246	na	51	*ns*	-0,07	0,10	0,08	0,33
643977		**FLJ32255**	uncharacterized LOC643977 (ncRNA)	ILMN_1745599	na	55	*ns*	0,09	-0,31	0,14	-0,18
874	1549	**CBR3**	carbonyl reductase 3	ILMN_1790819	na	56	*ns*	0,20	-0,15	-0,50	0,06
10631	16953	**POSTN**	periostin	ILMN_1790761;ILMN_2196328	na	56	*ns*	0,09	-0,06	-0,39	0,07
79718	29529	**TBL1XR1**	transducin (beta)-like 1 X-linked receptor 1	ILMN_1798657	na	56	*ns*	0,11	-0,14	-0,36	-0,03
79572	24113	**ATP13A3**	ATPase 13A3	ILMN_1663684	na	59	*ns*	0,09	-0,31	-0,01	0,01
3423	5389	**IDS**	iduronate 2-sulfatase	ILMN_1665332	na	59	*ns*	0,08	-0,27	0,15	0,06
646531	22635	**YBX1P2**	Y-box binding protein 1 pseudogene 2	ILMN_1669424	na	59	*ns*	0,13	-0,28	0,06	0,14
100131261	51933	**PNRC2P1**	proline rich nuclear receptor coactivator 2 pseudogene 1	ILMN_3289262	na	60	*ns*	-0,06	-0,19	-0,08	0,24
346950	31080	**RPL37P6**	ribosomal protein L37 pseudogene 6	ILMN_1786359	na	60	*ns*	0,04	-0,16	0,00	0,28
158135	18113	**TTLL11**	tubulin tyrosine ligase like 11	ILMN_1837102	na	60	*ns*	-0,07	-0,19	0,12	0,33
55075	15947	**UACA**	uveal autoantigen with coiled-coil domains and ankyrin repeats	ILMN_1703273;ILMN_1758209	na	60	*ns*	-0,02	-0,22	0,07	0,24
83464	24080	**APH1B**	aph-1 homolog B, gamma-secretase subunit	ILMN_1862217	na	66	*ns*	-0,04	0,01	-0,22	0,18
51719	20292	**CAB39**	calcium binding protein 39	ILMN_1765858	na	66	*ns*	0,00	-0,03	-0,24	0,16
988	1743	**CDC5L**	cell division cycle 5 like	ILMN_1652907	na	66	*ns*	-0,11	-0,03	-0,36	0,10
285464	26619	**CRIPAK**	cysteine rich PAK1 inhibitor	ILMN_2140700	na	66	*ns*	0,00	-0,05	-0,36	0,16
23136	3380	**EPB41L3**	erythrocyte membrane protein band 4.1 like 3	ILMN_2109197	na	66	*ns*	0,03	-0,05	-0,38	0,15
26959	23200	**HBP1**	HMG-box transcription factor 1	ILMN_1685415;ILMN_2160764	na	66	*ns*	-0,04	0,06	-0,18	0,22
9798	28977	**IST1**	IST1, ESCRT-III associated factor	ILMN_1740351	na	66	*ns*	-0,02	0,03	-0,15	0,26
11069	16626	**RAPGEF4**	Rap guanine nucleotide exchange factor 4	ILMN_1661802	na	66	*ns*	-0,08	0,04	-0,35	0,20
54885	24715	**TBC1D8B**	TBC1 domain family member 8B	ILMN_1701604	na	66	*ns*	-0,07	-0,07	-0,25	0,19
84798	29667	**C19orf48**	chromosome 19 open reading frame 48	ILMN_2383484;ILMN_1759184	na	68	*ns*	-0,09	0,01	0,27	-0,21
11335	1553	**CBX3**	chromobox 3	ILMN_1697665	na	68	*ns*	0,03	0,03	0,26	-0,14
643336	33952	**CDC42P2**	cell division cycle 42 pseudogene 2	ILMN_3282321	na	68	*ns*	-0,04	-0,06	0,33	-0,17
200185	28942	**KRTCAP2**	keratinocyte associated protein 2	ILMN_1658802	na	68	*ns*	0,16	0,07	0,34	-0,18
23429	10480	**RYBP**	RING1 and YY1 binding protein	ILMN_1721842	na	68	*ns*	-0,15	-0,11	0,34	-0,35
57108	30088	**SETD8P1**	SET domain containing 8 pseudogene 1	ILMN_3208881	na	68	*ns*	0,10	0,07	0,20	-0,22
9353	11086	**SLIT2**	slit guidance ligand 2	ILMN_1676449	na	68	*ns*	-0,06	0,02	0,34	-0,21
128710	16225	**SLX4IP**	SLX4 interacting protein	ILMN_1715625	na	68	*ns*	0,00	0,01	0,33	-0,14
54434	30579	**SSH1**	slingshot protein phosphatase 1	ILMN_1727671	na	68	*ns*	0,01	0,10	0,22	-0,19
6810	11439	**STX4**	syntaxin 4	ILMN_1680313	na	68	*ns*	-0,07	0,04	0,31	-0,24
115509	25173	**ZNF689**	zinc finger protein 689	ILMN_1759008	na	68	*ns*	0,02	-0,04	0,20	-0,28
54970	23700	**TTC12**	tetratricopeptide repeat domain 12	ILMN_2183784	na	73	*ns*	0,05	0,20	-0,02	-0,22
10318	16903	**TNIP1**	TNFAIP3 interacting protein 1	ILMN_1703650	na	74	*ns*	-0,06	0,29	-0,12	-0,09
92235	25034	**DUSP27**	dual specificity phosphatase 27 (putative)	ILMN_2318932	na	76	*ns*	-0,02	0,13	0,24	-0,19
26301	20460	**GBGT1**	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1	ILMN_1652906	na	76	*ns*	-0,06	0,14	0,25	-0,22
3187	5041	**HNRNPH1**	heterogeneous nuclear ribonucleoprotein H1 (H)	ILMN_3246409;ILMN_2101920	na	76	*ns*	-0,04	0,25	0,24	-0,19
647012	45095	**YY1P2**	YY1 transcription factor pseudogene 2	ILMN_3284530	na	76	*ns*	0,00	0,22	0,19	-0,18
4701	7691	**NDUFA7**	NADH:ubiquinone oxidoreductase subunit A7	ILMN_1675239	na	77	*ns*	-0,06	0,15	0,29	-0,15
4781	7785	**NFIB**	nuclear factor I B	ILMN_1778991	na	77	*ns*	-0,05	0,12	0,42	-0,11
5696	9545	**PSMB8**	proteasome subunit beta 8	ILMN_1767006;ILMN_1747195;ILMN_2390299	na	77	*ns*	-0,01	0,06	0,33	-0,11
10252	11269	**SPRY1**	sprouty RTK signaling antagonist 1	ILMN_1651610	na	77	*ns*	-0,06	0,20	0,73	-0,06
8693	4126	**GALNT4**	polypeptide N-acetylgalactosaminyltransferase 4	ILMN_1739297	na	78	*ns*	-0,09	0,06	0,41	0,18
5339	9069	**PLEC**	plectin	ILMN_1744268	na	79	*ns*	-0,17	0,42	0,11	-0,03
55165	1161	**CEP55**	centrosomal protein 55	ILMN_1747016	na	82	*ns*	0,26	-0,16	-0,10	-0,24
51144	18646	**HSD17B12**	hydroxysteroid 17-beta dehydrogenase 12	ILMN_1702168;ILMN_2094106	na	83	*ns*	0,17	-0,26	-0,16	-0,03
5062	8591	**PAK2**	p21 (RAC1) activated kinase 2	ILMN_1676385	na	85	*ns*	0,46	-0,18	0,22	-0,29
100422603	38850	**ST13P15**	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein) pseudogene 15	ILMN_1703102	na	85	*ns*	0,30	-0,12	0,08	-0,10
54165	18184	**DCUN1D1**	defective in cullin neddylation 1 domain containing 1	ILMN_1810719	na	86	*ns*	0,39	-0,25	-0,02	0,00
4616	4096	**GADD45B**	growth arrest and DNA damage inducible beta	ILMN_1718977	na	86	*ns*	0,33	-0,21	0,06	0,04
10951	1551	**CBX1**	chromobox 1	ILMN_1770244	na	90	*ns*	0,11	0,00	-0,32	0,15
51474	24636	**LIMA1**	LIM domain and actin binding 1	ILMN_1704369	na	90	*ns*	0,13	-0,03	-0,34	0,09
59277	13658	**NTN4**	netrin 4	ILMN_2113490;ILMN_1757019	na	90	*ns*	0,16	-0,04	-0,40	0,08
64151	24304	**NCAPG**	non-SMC condensin I complex subunit G	ILMN_1751444	na	91	*ns*	0,33	-0,07	-0,04	-0,17
25976	23696	**TIPARP**	TCDD inducible poly(ADP-ribose) polymerase	ILMN_1765578	na	91	*ns*	0,32	0,01	0,01	-0,12
890	1578	**CCNA2**	cyclin A2	ILMN_1786125	na	93	*ns*	0,24	-0,09	0,17	-0,26
991	1723	**CDC20**	cell division cycle 20	ILMN_1663390	na	93	*ns*	0,23	-0,08	0,16	-0,31
8318	1739	**CDC45**	cell division cycle 45	ILMN_1670238	na	93	*ns*	0,29	-0,02	0,11	-0,27
9232	9690	**PTTG1**	pituitary tumor-transforming 1	ILMN_1753196;ILMN_2042771	na	93	*ns*	0,22	-0,05	0,09	-0,22
100271106	35784	**RPS26P13**	ribosomal protein S26 pseudogene 13	ILMN_3236675	na	93	*ns*	0,09	0,01	0,18	-0,26
11065	15937	**UBE2C**	ubiquitin conjugating enzyme E2 C	ILMN_2301083;ILMN_1714730	na	93	*ns*	0,23	-0,13	0,22	-0,25
2647	4200	**BLOC1S1**	biogenesis of lysosomal organelles complex 1 subunit 1	ILMN_2157510	na	94	*ns*	0,29	-0,15	0,27	-0,11
27	77	**ABL2**	ABL proto-oncogene 2, non-receptor tyrosine kinase	ILMN_1741628;ILMN_1657870;ILMN_2240003	na	96	*ns*	0,19	-0,04	0,41	0,06
91526	25259	**ANKRD44**	ankyrin repeat domain 44	ILMN_2059844	na	96	*ns*	0,04	-0,09	0,33	0,09
7813	3501	**EVI5**	ecotropic viral integration site 5	ILMN_1746314	na	96	*ns*	0,03	-0,06	0,41	0,18
723790	29668	**HIST2H2AA4**	histone cluster 2, H2aa4	ILMN_3242900	na	96	*ns*	0,14	-0,08	0,51	0,12
10746	6854	**MAP3K2**	mitogen-activated protein kinase kinase kinase 2	ILMN_1765122	na	96	*ns*	0,06	-0,11	0,40	0,20
26871	10120	**RNU1-1**	RNA, U1 small nuclear 1	ILMN_3245678	na	96	*ns*	0,15	-0,07	0,60	0,28
654350	36112	**RPL9P25**	ribosomal protein L9 pseudogene 25	ILMN_3198499	na	97	*ns*	-0,03	-0,10	0,11	0,33
51280	15451	**GOLM1**	golgi membrane protein 1	ILMN_1766405	na	98	*ns*	0,13	0,24	-0,17	-0,11
3340	7680	**NDST1**	N-deacetylase and N-sulfotransferase 1	ILMN_1807283	na	98	*ns*	0,16	0,26	-0,24	-0,38
494513	29502	**DFNB59**	deafness, autosomal recessive 59	ILMN_1914857	na	101	*ns*	0,19	0,05	0,07	-0,28
3476	5461	**IGBP1**	immunoglobulin (CD79A) binding protein 1	ILMN_1717165	na	101	*ns*	0,22	0,16	-0,10	-0,34
4502	7406	**MT2A**	metallothionein 2A	ILMN_1686664	na	101	*ns*	0,26	0,13	0,09	-0,17
55069	25476	**TMEM248**	transmembrane protein 248	ILMN_1729130	na	101	*ns*	0,21	0,17	-0,07	-0,23

10024	12327	**TROAP**	trophinin associated protein	ILMN_1700337	na	101	*ns*	0,14	0,12	0,08	-0,27
1503	2519	**CTPS1**	CTP synthase 1	ILMN_1783285	na	112	*ns*	0,21	0,13	-0,04	-0,19
400322	4870	**HERC2P2**	hect domain and RLD 2 pseudogene 2	ILMN_1754880	na	112	*ns*	0,19	-0,03	-0,25	-0,21
389674	32234	**HNRNPA1P4**	heterogeneous nuclear ribonucleoprotein A1 pseudogene 4	ILMN_1690586	na	112	*ns*	0,22	0,06	-0,20	-0,24
5999	10000	**RGS4**	regulator of G-protein signaling 4	ILMN_1758067	na	112	*ns*	0,24	0,05	-0,18	-0,14
8553	1046	**BHLHE40**	basic helix-loop-helix family member e40	ILMN_1768534	na	115	*ns*	0,33	0,05	-0,04	-0,14
7153	11989	**TOP2A**	topoisomerase (DNA) II alpha	ILMN_1686097	na	115	*ns*	0,30	0,03	-0,10	-0,12

Entrez GeneID	Species specific, unique integer identifying genes assigned by Entrez Gene, the gene-specific database at the National Center for Biotechnology Information (NCBI)
HGNC ID	Unique identifier for each gene curated by the Human Genome Organisation (HUGO) Gene Nomenclature Committee (HGNC)
Gene symbol	Official, approved gene symbol
Gene Name	Official, approved full gene name
Illumina probe_ID	Reporter name, *i.e.* unique identifier(s) for the probe across all species and Illumina products
Cluster	Number of the cluster profile grouping significant temporal expression profiles, based on their similarity by a correlation coefficient > 0.7
Profile	Number of the model profile attributed by the STEM algorithm, in order of significance (*P* -value)
Profile *P* -value	*P* -value (nominal) significance of the number of genes assigned to each temporal expression profile *vs.* expected
$\log_2$(FC)	Log_2 transformation of fold changes in gene expression at indicated time points, calculated as the ratios of α-MSH-treated to non-treated gene expression values
Footnote	The first sheet lists the 506 genes associated with 15 temporal profiles that showed a statistically significant enrichment at a FDR < 0.05 The first sheet lists the 131 genes associated with model profiles that showed a nonsignificant enrichment (FDR > 0.05)

Table S4 | Functional enrichment analysis of the 506 regulated genes, associating with 15 significant temporal profiles of differential expression

Category	Geneset/ Pathway ID	Term	Count	%	*P* -value	Fold Enrichment	Benjamini Hochberg	Genes
SP_PIR_KEYWORDS		**phosphoprotein**	197	46,8	4,80E-08	1,36	**0,00002**	MEF2C, DLC1, STAT5B, PTPN23, BBX, MED24, INTS1, IARS2, INTS3, WDR82, HMGN5, WDR74, APP, CD46, NAA10, MAP3K8, SUPT5H, CDCA5, BCL7C, KIF13B, STAG3L3, POLE, PTBP1, MECP2, ZNF503, MECOM, DCLRE1C, LILRB1, SSTR2, ATP2C1, FLII, TMEM184B, TGFBRAP1, RAB13, EIF2AK2, EIF2AK4, NFKBIA, SLC29A1, TCF4, GIT1, DVL3, NRBF2, KLF13, RGPD3, SMAD3, OCIAD1, PPA2, TNKS1BP1, ATP2A2, BET1L, AP1B1, HIP1R, GJA1, NAP1L4, BLZF1, ZNF148, SHARPIN, BRD4, IP6K1, STX1A, ZBTB20, SNAPC1, ARHGEF17, PAPD5, MMP15, SMN1, VPS8, MTMR12, MAST4, DNAJC28, TAF15, MED8, ADK, EPB41L5, SERPINB1, RBM39, SRGAP1, YWHAZ, USP5, ZDHHC18, ALPP, ZNF652, DAPP1, FASN, BRD3, NBPF10, SWAP70, NUCKS1, ITPR3, STAT3, CAPRIN2, HNRNPUL2, PDE2A, PSMD11, STAB1, RASSF2, LIME1, OGFR, ZNF462, RBM14, ILKAP, NRBP1, INO80, EIF5A, NSUN5P2, KANK1, TRIM47, PRKAR2A, DYSF, DDX23, ELOVL5, AAK1, SND1, SLC4A2, SPN, PNPLA2, ARNTL, TRIM37, TNS3, KDM2A, GTF2IRD1, NEURL4, CLIP2, VAMP2, MVP, SEPT9, ARFGAP1, PACS2, PNPT1, SNRPB2, SLC38A10, TRRAP, ENSA, ELK3, RRAGC, SPC24, EIF3B, DOCK1, SYAP1, ENTPD6, HIST1H4C, STRBP, SH3TC1, SREBF1, GOLIM4, ITGA2, HEATR1, DOCK6, SHANK3, DDX50, CYFIP1, ATL2, PIP5K1C, ZKSCAN1, BCAM, LARP1, DGCR2, ACOT8, PKN3, HEY2, SNTB2, DENND5B, GPC1, SLC43A2, NBPF9, TRPM4, CCDC88C, PKN1, EIF4G1, IFNAR2, SLC35E1, HIPK2, GAA, KPNA6, MFSD11, LCOR, CHFR, SHCBP1, NUP160, PRKDC, APLP2, N4BP2, ZNF600, ZNF608, MYOF, GTF3C1, MAP1B, SIRT6, SIRT7, SUN1, MAP1S, CDAN1, MAPK8IP3, DENND4B, LOC648927, NFIC, CUEDC1, SPTAN1
SP_PIR_KEYWORDS		**nucleus**	124	29,5	4,62E-06	1,45	**0,00090**	MEF2C, FGF14, STAT5B, BBX, EIF5A, INTS1, INO80, MED24, INTS3, WDR82, HMGN5, RCBTB1, WDR74, GATA2, TRIM47, SIN3B, DDX23, NAA10, SND1, ZNF773, MED27, CTDSP2, SUPT5H, CDCA5, STAG3L3, PTBP1, POLE, MECP2, ZNF503, ARNTL, ISG20L2, MECOM, DCLRE1C, ZNF234, KDM2A, MTF1, PIAS4, PIAS3, GTF2IRD1, FLII, MVP, ZNF430, SNRPB2, NFKBIA, ELK3, TRRAP, RRAGC, SPC24, ZNF223, SNF8, HIST1H4C, ZNF426, TCF4, SPOP SREBF1, KLF6, NPLOC4, NRBF2, KLF13, GINS4, SMAD3, HEATR1, ZNF526, TNKS1BP1, ATF5, TDG, DDX50, SHOC2, ZKSCAN1, NAP1L4, BLZF1, ZNF682, ZNF738, PKN3, ZNF148, ZNF404, HEY2, BRD4, LOC441228, IP6K1, ZBTB20, SNAPC1, MBD4, PAPD5, ZNF549, SMN1, TAF15, MED8, HIPK2, RBM39, DMC1, LCOR, CHFR, NUP160, PRKDC, ZNF75A, FCF1, POLR2B, ZNF652, APLP2, NPAS2, ZNF600, RAX2, GTF3C1, MYOF, ZNF562, BRD3, SWAP70, NUCKS1, VHL, SIRT6, SUN1, SIRT7, STAT3, DUSP5, HNRNPUL2, MAP1S, RASSF2, ZNF462, OGFR, RBM14, NFIC, LOC648927, SCAND1
SP_PIR_KEYWORDS		**alternative splicing**	188	44,7	0,00004	1,26	**0,00579**	MEF2C, DLC1, FGF14, LTBP3, BBX, NT5DC2, TNFSF14, EIF5A, INTS3, NSUN5P2, LOC100132585, IL17RD, WDR74, SIN3B, APP, DYSF, IDS, CD46, ZNF773, MED27, CCBE1, SLC4A2, SUPT5H, BCL7C, SLC4A5, SCAMP5, OPA3, STAG3L3, PTBP1, MECP2, CORO6, PISD, ZNF503, PNPLA2, ARNTL, MECOM, DCLRE1C, LILRB1, TRIM37, TNS3, SSTR2, KDM2A, CATSPER2, ATP2C1, GTF2IRD1, CC2D2A, PCMTD2, SURF4, CLIP2, NEURL4, COL1A1, EIF2AK4, SEPT9, ARFGAP1, PACS2, ITGA10, SLC38A10, ANKRD30B, ENSA, TRRAP, DUSP19, EIF3B, SNF8, HEG1, STRBP, PPP2R2B, TCF4, SREBF1, PLAT, GIT1, KLF6, CFLAR, NPLOC4, PTGR2, NRBF2, GINS4, RGPD3, ARMC5, UAP1L1, TINAGL1, OCIAD1, SHANK3, PPA2, TNKS1BP1, NUBPL, ATP2A2, CYFIP1, RHOT2, RHBDL2, AP1B1, ATL2, SHOC2, LARP1, ZYG11B, BLZF1, ZNF682, RSPRY1, SHARPIN, KLHL28, SNTB2, CHST15, BRD4, DENND5B, SEC24D, NBPF9, CSF2RA, PILRB, SLC43A2, ANKRD36B, TRPM4, STX1A, ZBTB20, PIGX, CCDC88C, NLRP8, PKN1, FBLIM1, MBD4, PAPD5, ZNF549, SMN1, VPS8, MTMR12, EIF4G1, MAST4, IFNAR2, TAF15, ADK, MED8, TBCD, HIPK2, SLC35E1, EPB41L5, MFSD11, RBM39, DENND3, LCOR, CHFR, SRGAP1, GALNT3, ATG10, SBNO2, NUP160, FAM69B, TBC1D8, USP5, SLC37A3, HAUS2, PRKDC, APLP2, ANKRD36, N4BP2, TMED4, DAPP1, ZNF608, ACSL4, GTF3C1, MYOF, ZNF562, MT1G, BRD3, NBPF10, NUCKS1, VHL, GDPD5, SIRT6, SIRT7, SUN1, STAT3, CAPRIN2, COL4A5, RASSF6, PDE2A, STAB1, CDAN1, BAX, MBOAT7, PTP4A2, FBLN7, TRPC4AP, LIME1, MAPK8IP3, OGFR, ZNF462, CUEDC1, NFIC, RBM14, POFUT1, SPTAN1
GOTERM_CC_FAT	**GO:0012505**	**endomembrane system**	35	8,3	0,00004	2,13	**0,01325**	ARFGAP1, GALNT2, NRBP1, NUP160, AP1B1, HIP1R, EIF5A, GJA1, EDEM1, APP, TMED2, AAK1, LOC441228, MYOF, SEC24D, SCAMP5, SREBF1, NPLOC4, STX1A, PIGX, RGPD3, SMAD3, SUN1, ITPR3, MAGT1, ATP2A2, ATP2C1, BAX, HIPK2, KPNA6, MAPK8IP3, NUTF2, VAMP2, MGAT5, MVP
GOTERM_CC_FAT	**GO:0048471**	**perinuclear region of cytoplasm**	18	4,3	0,00012	2,98	**0,02021**	GALNT3, CYB5R4, GALNT2, NRBP1, HIP1R, MAP1B, ITGA2, GDPD5, SUN1, TRIM37, APP, PKN3, MAP1S, ARF3, CYFIP1, LAMB1, SEC24D, SEPT9
SP_PIR_KEYWORDS		**Transcription**	65	15,4	0,00024	1,57	**0,02301**	MEF2C, STAT5B, BBX, MED24, ZKSCAN1, HMGN5, RCBTB1, GATA2, SIN3B, ZNF738, ZNF682, ZNF148, SND1, ZNF773, HEY2, ZNF404, MED27, SUPT5H, ZBTB20, SNAPC1, MECP2, ZNF503, ARNTL, MECOM, ZNF549, ZNF234, BTG2, MTF1, PIAS4, KDM2A, PIAS3, GTF2IRD1, MED8, HIPK2, FLII, RBM39, LCOR, SBNO2, ZNF430, ZNF75A, TRRAP, ELK3, POLR2B, ZNF652, NPAS2, ZNF600, RAX2, ZNF223, SNF8, ZNF426, TCF4, ZNF562, GTF3C1, SREBF1, KLF6, NRBF2, KLF13, SMAD3, STAT3, ZNF526, ATF5, ZNF462, RBM14, LOC648927, NFIC
KEGG_PATHWAY	**hsa04512**	**ECM-receptor interaction**	9	2,1	0,00023	5,34	**0,02476**	COL1A2, DAG1, ITGA10, ITGA2, AGRN, LAMC1, COL1A1, LAMB1, COL5A1
SP_PIR_KEYWORDS		**transcription regulation**	63	15,0	0,00039	1,56	**0,02983**	MEF2C, STAT5B, BBX, MED24, ZKSCAN1, HMGN5, RCBTB1, GATA2, SIN3B, ZNF738, ZNF682, ZNF148, SND1, ZNF773, HEY2, ZNF404, MED27, SUPT5H, ZBTB20, SNAPC1, MECP2, ZNF503, ARNTL, MECOM, ZNF549, ZNF234, BTG2, MTF1, PIAS4, KDM2A, PIAS3, GTF2IRD1, MED8, HIPK2, FLII, RBM39, LCOR, ZNF430, SBNO2, ZNF75A, TRRAP, ELK3, ZNF652, NPAS2, ZNF600, RAX2, ZNF223, SNF8, ZNF426, TCF4, ZNF562, SREBF1, KLF6, NRBF2, KLF13, SMAD3, STAT3, ZNF526, ATF5, ZNF462, RBM14, LOC648927, NFIC
SP_PIR_KEYWORDS		**cytoplasm**	92	21,9	0,00075	1,38	**0,04752**	DLC1, ILKAP, NRBP1, HIP1R, STAT5B, TNFSF14, EIF5A, RNASEH1, SHOC2, IL17RD, KANK1, TRIM47, BLZF1, PKN3, SHARPIN, LYPLA2P1, NAA10, SND1, MAP3K8, SNTB2, LOC441228, IP6K1, SEC24D, NBPF9, KIF13B, STAG3L3, NLRP8, FBLIM1, PKN1, PAPD5, SMN1, MTMR12, TRIM37, MAST4, HIPK2, EPB41L5, CC2D2A, PCMTD2, FLII, SERPINB1, CLIP2, TGFBRAP1, AKR1D1, MVP, SEPT9, ARFGAP1, ATG10, YWHAZ, HAUS2, CETN3, DAG1, NFKBIA, ENSA, RRAGC, N4BP2, DOCK1, EIF3B, DAPP1, SNF8, FASN, STRBP, PPP2R2B, GIT1, SEPW1, IPP, DVL3, NPLOC4, PTGR2, NRBF2, NBPF10, SWAP70, VHL, GINS4, RGPD3, SMAD3, GDPD5, SIRT7, SHANK3, STAT3, CAPRIN2, TNKS1BP1, ATF5, MAP1S, ARF3, BAX, PTP4A2, BLVRB, MAPK8IP3, CYFIP1, NUTF2, OGFR, RBM14, SPTAN1
GOTERM_BP_FAT	**GO:0045944**	**positive regulation of transcription from RNA polymerase II promoter**	22	5,2	0,00005	2,75	**0,05438**	SREBF1, MEF2C, KLF6, KLF13, STAT5B, NFKBIA, SMAD3, PRKDC, ARNTL, MECOM, STAT3, GATA2, APP, NPAS2, MTF1, ZNF148, HIPK2, ZNF462, AGRN, NFIC, RBM14, SUPT5H
SP_PIR_KEYWORDS		**acetylation**	75	17,8	0,00124	1,43	**0,06680**	MEF2C, ILKAP, NRBP1, ATL2, AP1B1, STAT5B, INO80, INTS1, EIF5A, IARS2, WDR82, NAP1L4, MT1P3, LARP1, SLC25A20, PRKAR2A, ACOT8, ZNF148, NAA10, SND1, BRD4, SUPT5H, LOC441228, PTBP1, MECP2, PKN1, CORO6, ARNTL, MECOM, SMN1, EIF4G1, TAF15, PIAS4, ADK, KPNA6, FLII, SERPINB1, VAMP2, RBM39, EIF2AK2, EIF2AK4, MVP, SEPT9, ARFGAP1, YWHAZ, LIMS1, USP5, PNPT1, PRKDC, TRRAP, ENSA, EIF3B, SYAP1, FASN, HIST1H4C, ACSL4, MYOF, PDHX, MT1G, MT1F, NPLOC4, MAP1B, SMAD3, SIRT7, OCIAD1, PPA2, HNRNPUL2, ATP2A2, PSMD11, BAX, CYFIP1, NUTF2, OGFR, LOC648927, SPTAN1
SP_PIR_KEYWORDS		**metal-thiolate cluster**	4	1,0	0,00151	16,70	**0,07073**	MT1IP, MT1G, MT1P3, MT1F
GOTERM_BP_FAT	**GO:0006357**	**regulation of transcription from RNA polymerase II promoter**	34	8,1	0,00004	2,17	**0,08021**	MEF2C, STAT5B, NFKBIA, PRKDC, GATA2, BLZF1, APP, NPAS2, ZNF148, SNF8, MED27, HEY2, AGRN, TCF4, SUPT5H, SREBF1, KLF6, KLF13, VHL, MECP2, SMAD3, ARNTL, MECOM, STAT3, IFNAR2, ATF5, PIAS4, MTF1, MED8, HIPK2, ZNF462, NFIC, LCOR, RBM14
SP_PIR_KEYWORDS		**dna-binding**	56	13,3	0,00209	1,50	**0,08648**	MEF2C, STAT5B, BBX, INO80, ZKSCAN1, HMGN5, GATA2, ZNF738, ZNF682, ZNF148, ZNF773, HEY2, ZNF404, ZBTB20, SNAPC1, POLE, MECP2, PAPD5, MBD4, ARNTL, MECOM, ZNF549, ZNF234, TAF15, PIAS4, KDM2A, MTF1, GTF2IRD1, LCOR, DMC1, ZNF430, PRKDC, ZNF75A, ELK3, ZNF652, APLP2, NPAS2, ZNF600, RAX2, ZNF223, HIST1H4C, ZNF426, STRBP, TCF4, ZNF562, GTF3C1, SREBF1, KLF6, SWAP70, KLF13, STAT3, ZNF526, ATF5, MAP1S, ZNF462, NFIC
GOTERM_CC_FAT	**GO:0043233**	**organelle lumen**	57	13,5	0,00158	1,49	**0,08854**	MEF2C, A2M, MED24, INTS1, IARS2, INTS3, HMGN5, WDR74, GATA2, BLZF1, APP, ZNF148, BRD4, LOC441228, SUPT5H, ZBTB20, PTBP1, POLE, MBD4, ARNTL, ISG20L2, SMN1, TNS3, PIAS4, KDM2A, PIAS3, MED8, HIPK2, FKBP14, FLII, RBM39, CHFR, PACS2, PRKDC, TRRAP, ELK3, FCF1, POLR2B, NPAS2, HIST1H4C, TCF4, PDHX, GTF3C1, PTGR2, GOLIM4, SMAD3, SIRT6, HEATR1, SIRT7, ITPR3, STAT3, ATF5, DDX50, TDG, TRPC4AP, LOC648927, RBM14
KEGG_PATHWAY	**hsa05200**	**Pathways in cancer**	16	3,8	0,00186	2,43	**0,09651**	DVL3, FGF14, VHL, STAT5B, NFKBIA, SMAD3, FGF23, ITGA2, MECOM, STAT3, PIAS4, PIAS3, BAX, LAMC1, LAMB1, CSF2RA
GOTERM_CC_FAT	**GO:0031974**	**membrane-enclosed lumen**	58	13,8	0,00149	1,49	**0,09938**	MEF2C, A2M, MED24, INTS1, IARS2, INTS3, HMGN5, WDR74, GATA2, BLZF1, APP, ZNF148, BRD4, LOC441228, SUPT5H, ZBTB20, PTBP1, POLE, MBD4, ARNTL, ISG20L2, SMN1, TNS3, PIAS4, KDM2A, PIAS3, MED8, HIPK2, FKBP14, FLII, RBM39, CHFR, PACS2, PNPT1, PRKDC, TRRAP, ELK3, FCF1, POLR2B, NPAS2, HIST1H4C, TCF4, PDHX, GTF3C1, PTGR2, GOLIM4, SMAD3, SIRT6, HEATR1, SIRT7, ITPR3, STAT3, ATF5, DDX50, TDG, TRPC4AP, RBM14, LOC648927
GOTERM_BP_FAT	**GO:0045941**	**positive regulation of transcription**	26	6,2	0,00051	2,14	**0,10145**	MEF2C, STAT5B, PRKDC, NFKBIA, GATA2, APP, NPAS2, ZNF148, AGRN, TCF4, SUPT5H, SREBF1, DVL3, KLF6, KLF13, VHL, SMAD3, SIRT7, ARNTL, MECOM, STAT3, MTF1, HIPK2, ZNF462, NFIC, RBM14
GOTERM_BP_FAT	**GO:0046907**	**intracellular transport**	29	6,9	0,00044	2,04	**0,10947**	ARFGAP1, YWHAZ, NRBP1, NUP160, AP1B1, ATL2, NFKBIA, EIF5A, NAPA, SLC25A20, APP, LOC441228, SEC24D, RHOBTB3, KIF13B, STX1A, RGPD3, ARNTL, TINAGL1, ATP2A2, MAP1S, ATP2C1, BAX, KPNA6, RHOT2, BET1L, TRPC4AP, NUTF2, VAMP2
GOTERM_BP_FAT	**GO:0009891**	**positive regulation of biosynthetic process**	30	7,1	0,00050	2,00	**0,10952**	MEF2C, EDN1, STAT5B, NFKBIA, PRKDC, EIF5A, GATA2, APP, NPAS2, ZNF148, AGRN, TCF4, SUPT5H, SPN, SREBF1, KLF6, DVL3, KLF13, VHL, SMAD3, ITGA2, SIRT7, ARNTL, MECOM, STAT3, MTF1, HIPK2, ZNF462, NFIC, RBM14
SP_PIR_KEYWORDS		**cytoplasmic vesicle**	13	3,1	0,00303	2,74	**0,11151**	SREBF1, STX1A, DYSF, TMED2, AP1B1, HIP1R, CD46, PTPN23, SNTB2, VAMP2, RAB13, MYOF, SCAMP5
GOTERM_BP_FAT	**GO:0006355**	**regulation of transcription, DNA-dependent**	59	14,0	0,00064	1,54	**0,11431**	MEF2C, STAT5B, MED24, ZKSCAN1, HMGN5, GATA2, BLZF1, APP, SIN3B, ZNF738, ZNF682, ZNF148, ZNF773, HEY2, ZNF404, MED27, SUPT5H, MECP2, ARNTL, MECOM, ZNF549, ZNF234, IFNAR2, PIAS4, MTF1, GTF2IRD1 MED8, HIPK2, LCOR, ZNF430, SBNO2, PRKDC, NFKBIA, ZNF75A, ELK3, NPAS2, RAX2, ZNF223, SNF8, ZNF426, MEIS3P1, AGRN, TCF4, ZNF562, SREBF1, DVL3, KLF6, VHL, KLF13, SMAD3, SIRT6, SIRT7, STAT3, ATF5, ZNF462, RBM14, LOC648927, NFIC, SCAND1
GOTERM_BP_FAT	**GO:0010557**	**positive regulation of macromolecule biosynthetic process**	29	6,9	0,00041	2,05	**0,11638**	MEF2C, STAT5B, NFKBIA, EIF5A, PRKDC, GATA2, APP, NPAS2, ZNF148, AGRN, TCF4, SUPT5H, SPN, SREBF1, KLF6, DVL3, KLF13, VHL, SMAD3, ITGA2, SIRT7, ARNTL, MECOM, STAT3, MTF1, HIPK2, ZNF462, NFIC, RBM14
GOTERM_CC_FAT	**GO:0031981**	**nuclear lumen**	48	11,4	0,00141	1,58	**0,11650**	MEF2C, PRKDC, INTS1, MED24, INTS3, TRRAP, ELK3, HMGN5, FCF1, POLR2B, WDR74, GATA2, NPAS2, ZNF148, HIST1H4C, BRD4, TCF4, SUPT5H, LOC441228, GTF3C1, ZBTB20, PTGR2, PTBP1, POLE, SMAD3, SIRT6, MBD4, HEATR1, ARNTL, ISG20L2, SIRT7, ITPR3, STAT3, SMN1, ATF5, TNS3, PIAS4, KDM2A, PIAS3, MED8, HIPK2, DDX50, TDG, FLII, RBM39, CHFR, RBM14, LOC648927
GOTERM_CC_FAT	**GO:0070013**	**intracellular organelle lumen**	55	13,1	0,00263	1,47	**0,12369**	MEF2C, MED24, INTS1, IARS2, INTS3, HMGN5, WDR74, GATA2, BLZF1, ZNF148, BRD4, LOC441228, SUPT5H, ZBTB20, PTBP1, POLE, MBD4, ISG20L2, ARNTL, SMN1, TNS3, PIAS4, KDM2A, PIAS3, MED8, HIPK2, FKBP14, FLII, RBM39, CHFR, PACS2, PRKDC, TRRAP, ELK3, FCF1, POLR2B, NPAS2, HIST1H4C, TCF4, PDHX, GTF3C1, PTGR2, GOLIM4, SMAD3, SIRT6, HEATR1, SIRT7, ITPR3, STAT3, ATF5, DDX50, TDG, TRPC4AP, LOC648927, RBM14
GOTERM_BP_FAT	**GO:0010628**	**positive regulation of gene expression**	26	6,2	0,00078	2,07	**0,12782**	MEF2C, STAT5B, PRKDC, NFKBIA, GATA2, APP, NPAS2, ZNF148, AGRN, TCF4, SUPT5H, SREBF1, DVL3, KLF6, KLF13, VHL, SMAD3, SIRT7, ARNTL, MECOM, STAT3, MTF1, HIPK2, ZNF462, NFIC, RBM14
GOTERM_CC_FAT	**GO:0044420**	**extracellular matrix part**	9	2,1	0,00313	3,67	**0,12861**	COL1A2, DAG1, AGRN, LAMC1, COL1A1, LAMB1, COL5A1, SPN, COL4A5
GOTERM_BP_FAT	**GO:0010604**	**positive regulation of macromolecule metabolic process**	35	8,3	0,00040	1,89	**0,13197**	DLC1, MEF2C, ATG10, STAT5B, NFKBIA, PRKDC, EIF5A, GJA1, GATA2, APP, NPAS2, ZNF148, AGRN, TCF4, SUPT5H, SPN, SREBF1, KLF6, DVL3, KLF13, VHL, SMAD3, ITGA2, ARNTL, SIRT7, MECOM, STAT3, PIAS4, MTF1, PIAS3, PSMD11, HIPK2, ZNF462, NFIC, RBM14
SP_PIR_KEYWORDS		**activator**	21	5,0	0,00401	2,02	**0,13254**	SREBF1, MEF2C, KLF6, KLF13, STAT5B, MED24, ELK3, TRRAP, ARNTL, STAT3, GATA2, ATF5, MTF1, MED8, MED27, FLII, RBM39, TCF4, SUPT5H, LCOR, NFIC
GOTERM_CC_FAT	**GO:0046930**	**pore complex**	8	1,9	0,00371	4,02	**0,13507**	NUP160, BAX, RGPD3, KPNA6, EIF5A, NUTF2, LOC441228, MVP
GOTERM_CC_FAT	**GO:0005635**	**nuclear envelope**	13	3,1	0,00126	3,02	**0,13708**	SREBF1, NUP160, RGPD3, EIF5A, SMAD3, SUN1, ITPR3, HIPK2, KPNA6, NUTF2, LOC441228, MYOF, MVP
GOTERM_BP_FAT	**GO:0051254**	**positive regulation of RNA metabolic process**	24	5,7	0,00030	2,31	**0,14570**	SREBF1, MEF2C, KLF6, DVL3, KLF13, STAT5B, SMAD3, NFKBIA, PRKDC, ARNTL, MECOM, STAT3, GATA2, APP, NPAS2, MTF1, ZNF148, HIPK2, ZNF462, AGRN, TCF4, SUPT5H, NFIC, RBM14
GOTERM_BP_FAT	**GO:0031328**	**positive regulation of cellular biosynthetic process**	30	7,1	0,00039	2,03	**0,15083**	MEF2C, EDN1, STAT5B, NFKBIA, PRKDC, EIF5A, GATA2, APP, NPAS2, ZNF148, AGRN, TCF4, SUPT5H, SPN, SREBF1, KLF6, DVL3, KLF13, VHL, SMAD3, ITGA2, SIRT7, ARNTL, MECOM, STAT3, MTF1, HIPK2, ZNF462, NFIC, RBM14

GOTERM_BP_FAT	**GO:0051252**	**regulation of RNA metabolic process**	59	14,0	0,00110	1,51	**0,16273**	MEF2C, STAT5B, MED24, ZKSCAN1, HMGN5, GATA2, BLZF1, APP, SIN3B, ZNF738, ZNF682, ZNF148, ZNF773, HEY2, ZNF404, MED27, SUPT5H, MECP2, ARNTL, MECOM, ZNF549, ZNF234, IFNAR2, PIAS4, MTF1, GTF2IRD1 MED8, HIPK2, LCOR, ZNF430, SBNO2, PRKDC, NFKBIA, ZNF75A, ELK3, NPAS2, RAX2, ZNF223, SNF8, ZNF426, MEIS3P1, AGRN, TCF4, ZNF562, SREBF1, DVL3, KLF6, VHL, KLF13, SMAD3, SIRT6, SIRT7, STAT3, ATF5, ZNF462, RBM14, LOC648927, NFIC, SCAND1
GOTERM_CC_FAT	**GO:0005643**	**nuclear pore**	7	1,7	0,00611	4,23	**0,16417**	NUP160, RGPD3, KPNA6, EIF5A, NUTF2, LOC441228, MVP
GOTERM_CC_FAT	**GO:0005604**	**basement membrane**	7	1,7	0,00575	4,28	**0,16796**	DAG1, AGRN, LAMC1, LAMB1, COL5A1, SPN, COL4A5
GOTERM_CC_FAT	**GO:0031201**	**SNARE complex**	4	1,0	0,00682	10,04	**0,16863**	STX1A, BET1L, NAPA, SCAMP5
GOTERM_BP_FAT	**GO:0045893**	**positive regulation of transcription, DNA-dependent**	24	5,7	0,00026	2,33	**0,16877**	SREBF1, MEF2C, KLF6, DVL3, KLF13, STAT5B, SMAD3, NFKBIA, PRKDC, ARNTL, MECOM, STAT3, GATA2, APP, NPAS2, MTF1, ZNF148, HIPK2, ZNF462, AGRN, TCF4, SUPT5H, NFIC, RBM14
GOTERM_BP_FAT	**GO:0006350**	**transcription**	66	15,7	0,00125	1,46	**0,17061**	MEF2C, STAT5B, BBX, MED24, ZKSCAN1, HMGN5, RCBTB1, GATA2, SIN3B, ZNF738, ZNF682, ZNF148, SND1, ZNF773, HEY2, ZNF404, MED27, SUPT5H, ZBTB20, SNAPC1, MECP2, ZNF503, ARNTL, ZNF549, ZNF234, BTG2, MTF1, PIAS4, KDM2A, PIAS3, GTF2IRD1, MED8, HIPK2, FLII, RBM39, LCOR, SBNO2, ZNF430, ZNF75A, TRRAP, ELK3, POLR2B, ZNF652, RRAGC, NPAS2, ZNF600, RAX2, ZNF223, SNF8, ZNF426, TCF4, ZNF562, GTF3C1, SREBF1, KLF6, NRBF2, KLF13, SMAD3, SIRT7, STAT3, ZNF526, ATF5, ZNF462, RBM14, LOC648927, NFIC
GOTERM_CC_FAT	**GO:0019867**	**outer membrane**	8	1,9	0,00746	3,53	**0,17123**	BAX, RHOT2, GJA1, ITGA2, SYNJ2BP, ACSL4, ITPR3, PPP2R2B
GOTERM_CC_FAT	**GO:0005654**	**nucleoplasm**	31	7,4	0,00565	1,68	**0,18037**	MEF2C, PRKDC, MED24, INTS1, TRRAP, INTS3, HMGN5, POLR2B, NPAS2, HIST1H4C, TCF4, LOC441228, SUPT5H, GTF3C1, PTBP1, POLE, SMAD3, SIRT6, ARNTL, ITPR3, SMN1, ATF5, KDM2A, PIAS3, MED8, HIPK2, TDG, RBM39, CHFR, LOC648927, RBM14
GOTERM_BP_FAT	**GO:0045449**	**regulation of transcription**	78	18,5	0,00143	1,39	**0,18088**	MEF2C, STAT5B, BBX, MED24, ZKSCAN1, HMGN5, RCBTB1, GATA2, BLZF1, APP, SIN3B, ZNF682, ZNF738, ZNF148, SND1, ZNF773, MED27, HEY2, ZNF404, SUPT5H, ZBTB20, SNAPC1, MECP2, ZNF503, ARNTL, MECOM, ZNF549, ZNF234, IFNAR2, BTG2, MTF1, KDM2A, PIAS4, PIAS3, GTF2IRD1, MED8, HIPK2, FLII, TGFBRAP1, RBM39, LCOR, SBNO2, ZNF430, PRKDC, NFKBIA, ZNF75A, ELK3, TRRAP, ZNF652, NPAS2, ZNF600, RAX2, ZNF223, SNF8, ZNF426, MEIS3P1, AGRN, TCF4, ZNF562, SREBF1, KLF6, DVL3, NRBF2, VHL, KLF13, SMAD3, SIRT6, SIRT7, STAT3, ZNF526, ATF5, TGFBR3, ZNF462, RBM14, LOC648927, NFIC, POFUT1, SCAND1
GOTERM_BP_FAT	**GO:0051173**	**positive regulation of nitrogen compound metabolic process**	27	6,4	0,00155	1,94	**0,18415**	MEF2C, EDN1, STAT5B, NFKBIA, PRKDC, GATA2, APP, NPAS2, ZNF148, AGRN, TCF4, SUPT5H, SREBF1, DVL3, KLF6, KLF13, VHL, SMAD3, SIRT7, ARNTL, MECOM, STAT3, MTF1, HIPK2, ZNF462, NFIC, RBM14
GOTERM_CC_FAT	**GO:0005794**	**Golgi apparatus**	30	7,1	0,00870	1,64	**0,18485**	GALNT3, ARFGAP1, GALNT2, AP1B1, GJA1, NAPA, IL17RD, BLZF1, APP, PKN3, TMED2, ZNF148, SND1, FASN, ENTPD6, CHST15, B4GALT6, SEC24D, RNF122, RHOBTB3, SCAMP5, SREBF1, FKTN, GOLIM4, ATP2C1, ARF3, MAPK8IP3, BET1L, RAB13, MGAT5
SP_PIR_KEYWORDS		golgi apparatus	22	5,2	0,00745	1,87	0,21536	GALNT3, SREBF1, ARFGAP1, GALNT2, FKTN, AP1B1, GOLIM4, IL17RD, BLZF1, TMED2, ATP2C1, ARF3, SURF4, ENTPD6, BET1L, CHST15, B4GALT6, MGAT5, SEC24D, RNF122, SCAMP5, RHOBTB3
GOTERM_BP_FAT	GO:0045935	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	26	6,2	0,00210	1,93	0,22855	MEF2C, STAT5B, PRKDC, NFKBIA, GATA2, APP, NPAS2, ZNF148, AGRN, TCF4, SUPT5H, SREBF1, DVL3, KLF6, KLF13, VHL, SMAD3, SIRT7, ARNTL, MECOM, STAT3, MTF1, HIPK2, ZNF462, NFIC, RBM14
GOTERM_CC_FAT	GO:0044451	nucleoplasm part	21	5,0	0,01257	1,80	0,24236	MEF2C, SMAD3, PRKDC, MED24, INTS1, INTS3, TRRAP, ARNTL, POLR2B, SMN1, ATF5, NPAS2, PIAS3, MED8, HIPK2, RBM39, TCF4, CHFR, LOC648927, RBM14, GTF3C1
GOTERM_CC_FAT	GO:0005912	adherens junction	9	2,1	0,01613	2,77	0,27177	DLC1, GIT1, TNS3, LIMS1, EPB41L5, FBLIM1, GJA1, ITGA2, SPTAN1
GOTERM_CC_FAT	GO:0045202	synapse	15	3,6	0,01722	2,02	0,27454	PLAT, YWHAZ, STX1A, MAP1B, CAMK2N1, SHANK3, APP, MAP1S, PIAS3, CHRNA5, SNTB2, CYFIP1, AGRN, VAMP2, SCAMP5
SP_PIR_KEYWORDS		Signal-anchor	17	4,0	0,01071	2,02	0,27549	GALNT3, GALNT2, FKTN, GOLIM4, TNFSF14, PNPLA2, SUN1, EDEM1, GOLGA6L6, GOLGA6L1, DYSF, ENTPD6, LIME1, CHST15, B4GALT6, ACSL4, MGAT5, MYOF
GOTERM_CC_FAT	GO:0031410	cytoplasmic vesicle	23	5,5	0,01554	1,71	0,27624	PLAT, SREBF1, A2M, YWHAZ, STX1A, AP1B1, HIP1R, PTPN23, GOLIM4, PKN1, GJA1, APP, DYSF, TMED2, SND1, FASN, SNTB2, VAMP2, CTSB, RAB13, MYOF, SEC24D, SCAMP5
SP_PIR_KEYWORDS		acetylated amino end	7	1,7	0,01492	3,51	0,30608	YWHAZ, PRKAR2A, EIF5A, HIST1H4C, MT1G, MT1P3, MT1F
GOTERM_CC_FAT	GO:0031968	organelle outer membrane	7	1,7	0,02175	3,21	0,30760	BAX, RHOT2, GJA1, SYNJ2BP, ACSL4, ITPR3, PPP2R2B
GOTERM_CC_FAT	GO:0031975	envelope	22	5,2	0,02096	1,69	0,31042	SREBF1, NUP160, RGPD3, PNPT1, SMAD3, ITGA2, GJA1, EIF5A, SYNJ2BP, SUN1, ITPR3, SLC25A20, BAX, HIPK2, RHOT2, KPNA6, NUTF2, LOC441228, ACSL4, PPP2R2B, MYOF, MVP
SP_PIR_KEYWORDS		magnesium	17	4,0	0,01614	1,93	0,31091	ILKAP, NT5DC2, ITGA2, ITGA10, RNASEH1, ALPP, PPA2, POLR2B, DCLRE1C, MAST4, ATP2A2, ATP2C1, ADK, MAP3K8, ENTPD6, B4GALT6, ACSL4
SP_PIR_KEYWORDS		trimer	4	1,0	0,01450	7,71	0,31536	COL1A2, COL1A1, COL5A1, COL4A5
GOTERM_CC_FAT	GO:0031982	vesicle	23	5,5	0,02390	1,64	0,32016	PLAT, SREBF1, A2M, YWHAZ, STX1A, AP1B1, HIP1R, PTPN23, GOLIM4, PKN1, GJA1, APP, DYSF, TMED2, SND1, FASN, SNTB2, VAMP2, CTSB, RAB13, MYOF, SEC24D, SCAMP5
SP_PIR_KEYWORDS		zinc	59	14,0	0,01430	1,35	0,32985	ZKSCAN1, MT1P3, TRIM47, GATA2, APP, ZNF682, ZNF148, SHARPIN, RSPRY1, ZNF773, ZNF404, ZBTB20, POLE, FBLIM1, ZNF503, MMP15, MECOM, ZNF549, VPS8, ZNF234, TRIM37, TRIM38, TNS3, MTF1, TAF15, PIAS4, KDM2A, PIAS3, CPXM1, CHFR, ARFGAP1, LIMS1, ZNF430, USP5, ZDHHC18, ZNF75A, ALPP, POLR2B, ZNF652, ZNF600, ZNF223, ZNF426, ZNF608, RNF122, ZNF562, MT1G, MT1F, GIT1, RNF144B, KLF6, NPLOC4, KLF13, SIRT6, SIRT7, ZNF526, ZNF462, RBM14, LOC648927, ZMYND15
GOTERM_CC_FAT	GO:0070161	anchoring junction	9	2,1	0,02804	2,50	0,35212	DLC1, GIT1, TNS3, LIMS1, EPB41L5, FBLIM1, GJA1, ITGA2, SPTAN1
SP_PIR_KEYWORDS		Synaptosome	4	1,0	0,02535	6,26	0,36498	STX1A, CYFIP1, VAMP2, CAMK2N1
SP_PIR_KEYWORDS		laminin egf-like domain	4	1,0	0,02137	6,68	0,37295	STAB1, AGRN, LAMC1, LAMB1
SP_PIR_KEYWORDS		er-golgi transport	6	1,4	0,02501	3,62	0,37450	ARFGAP1, BLZF1, TMED2, ARF3, NAPA, SEC24D
SP_PIR_KEYWORDS		zinc-finger	47	11,2	0,02389	1,37	0,37515	ARFGAP1, ZNF430, USP5, ZNF75A, ZDHHC18, ZKSCAN1, POLR2B, ZNF652, TRIM47, GATA2, ZNF600, ZNF682, RSPRY1, SHARPIN, ZNF148, ZNF773, ZNF223, ZNF404, ZNF426, ZNF608, ZNF562, RNF122, GIT1, RNF144B, KLF6, ZBTB20, NPLOC4, KLF13, POLE, ZNF503, MECOM, ZNF549, ZNF526, VPS8, ZNF234, TRIM37, TRIM38, MTF1, TAF15, PIAS4, KDM2A, PIAS3, ZNF462, CHFR, RBM14, LOC648927, ZMYND15
SP_PIR_KEYWORDS		hydroxylysine	4	1,0	0,02331	6,46	0,38305	COL1A2, COL1A1, COL5A1, COL4A5
SP_PIR_KEYWORDS		triple helix	4	1,0	0,02331	6,46	0,38305	COL1A2, COL1A1, COL5A1, COL4A5
GOTERM_CC_FAT	GO:0005581	collagen	4	1,0	0,03608	5,45	0,40309	COL1A2, COL1A1, COL5A1, COL4A5
SP_PIR_KEYWORDS		calcium	25	5,9	0,03168	1,56	0,40659	GALNT3, TRPM4, GALNT2, LTBP3, PCDH10, CETN3, ITGA2, ITGA10, MMP15, ITPR3, DCHS1, ATP2A2, IDS, CATSPER2, ATP2C1, CCBE1, FKBP14, FBLN7, RHOT2, HEG1, SNTB2, ENTPD6, B4GALT6, ANO6, SPTAN1
GOTERM_BP_FAT	GO:0045892	negative regulation of transcription, DNA-dependent	17	4,0	0,00450	2,21	0,40882	MEF2C, SBNO2, VHL, MECP2, SMAD3, SIRT6, SIRT7, STAT3, SIN3B, PIAS4, ZNF148, HIPK2, HEY2, TCF4, LCOR, NFIC, SUPT5H
SP_PIR_KEYWORDS		metal-binding	74	17,6	0,03105	1,25	0,41345	CYB5R4, ILKAP, NT5DC2, RNASEH1, ZKSCAN1, MT1P3, GATA2, TRIM47, APP, ZNF682, IDS, ZNF148, SHARPIN, RSPRY1, ZNF773, MAP3K8, ZNF404, CTDSP2, ZBTB20, POLE, FBLIM1, ZNF503, MMP15, MECOM, ZNF549, VPS8, TRIM37, ZNF234, TNS3, TRIM38, MAST4, MTF1, KDM2A, PIAS4, TAF15, ATP2C1, PIAS3, ADK, CPXM1, CHFR, ARFGAP1, LIMS1, ZNF430, USP5, ZDHHC18, ZNF75A, ALPP, POLR2B, ZNF652, ZNF600, ZNF223, ZNF426 ZNF608, B4GALT6, RNF122, ZNF562, MT1G, MT1IP, MT1F, GIT1, KLF6, RNF144B, NPLOC4, KLF13, SIRT6, SIRT7, PPA2, ZNF526, PDE2A, ATP2A2, ZNF462, RBM14, LOC648927, ZMYND15
GOTERM_CC_FAT	GO:0031967	organelle envelope	21	5,0	0,03595	1,62	0,41461	SREBF1, NUP160, RGPD3, PNPT1, SMAD3, GJA1, EIF5A, SYNJ2BP, SUN1, ITPR3, SLC25A20, BAX, HIPK2, RHOT2, KPNA6, NUTF2, LOC441228, ACSL4, PPP2R2B, MYOF, MVP
GOTERM_CC_FAT	GO:0000139	Golgi membrane	9	2,1	0,04160	2,31	0,42440	ARFGAP1, GALNT2, AP1B1, ATP2C1, MAPK8IP3, GJA1, MGAT5, SEC24D, SCAMP5
GOTERM_CC_FAT	GO:0005741	mitochondrial outer membrane	6	1,4	0,04012	3,18	0,42462	BAX, RHOT2, GJA1, SYNJ2BP, ACSL4, PPP2R2B
SP_PIR_KEYWORDS		protein transport	17	4,0	0,03497	1,76	0,42529	ARFGAP1, ATG10, AP1B1, NUP160, EIF5A, NAPA, BLZF1, TMED2, ARF3, SNF8, KPNA6, BET1L, NUTF2, RAB13, SEC24D, MVP, SCAMP5
SP_PIR_KEYWORDS		hydroxyproline	4	1,0	0,03695	5,42	0,43067	COL1A2, COL1A1, COL5A1, COL4A5
GOTERM_CC_FAT	GO:0005783	endoplasmic reticulum	29	6,9	0,04523	1,44	0,44019	CYB5R4, PACS2, ATL2, UBE2G2, EIF5A, GJA1, NAPA, EDEM1, TMED4, IDS, ELOVL5, ACSL4, SEC24D, RNF122, SREBF1, NPLOC4, YIPF6, VHL, PIGX, ITPR3, MAGT1, ATP2A2, BAX, SURF4, FKBP14, MAPK8IP3, TGFBR3, TRPC4AP, POFUT1
GOTERM_BP_FAT	GO:0051253	negative regulation of RNA metabolic process	17	4,0	0,00526	2,18	0,44161	MEF2C, SBNO2, VHL, MECP2, SMAD3, SIRT6, SIRT7, STAT3, SIN3B, PIAS4, ZNF148, HIPK2, HEY2, TCF4, LCOR, NFIC, SUPT5H
SP_PIR_KEYWORDS		transcription factor	5	1,2	0,04054	3,85	0,44915	MEF2C, SNAPC1, NFIC, GTF3C1, STAT3
SP_PIR_KEYWORDS		Apoptosis	14	3,3	0,04231	1,84	0,45151	MEF2C, PACS2, RNF144B, CFLAR, STAG3L3, MECOM, APP, DOCK1, MAP1S, BAX, HIPK2, SLC5A8, PPP2R2B, BCL7C
GOTERM_BP_FAT	GO:0045321	leukocyte activation	13	3,1	0,00623	2,49	0,48095	KLF6, YWHAZ, SBNO2, SWAP70, EDN1, STAT5B, SMAD3, TNFSF14, PRKDC, DCLRE1C, BAX, SPN, KIF13B
GOTERM_BP_FAT	GO:0009612	response to mechanical stimulus	6	1,4	0,00694	4,96	0,48548	CCL2, BTG2, MAP1B, ITGA2, STRBP, COL1A1
GOTERM_BP_FAT	GO:0016192	vesicle-mediated transport	23	5,5	0,00679	1,85	0,49388	ARFGAP1, YWHAZ, STX1A, NRBP1, ATL2, AP1B1, HIP1R, NAPA, TINAGL1, GATA2, BLZF1, APP, DOCK1, TMED2, STAB1, ARF3, MAPK8IP3, BET1L, VAMP2, RAB13, SEC24D, RHOBTB3, SCAMP5
GOTERM_BP_FAT	GO:0007179	transforming growth factor beta receptor signaling pathway	6	1,4	0,00926	4,63	0,57217	CCL2, LTBP3, COL1A2, SMAD3, TGFBR3, TGFBRAP1
GOTERM_MF_FAT	GO:0008134	transcription factor binding	24	5,7	0,00155	2,05	0,57833	YWHAZ, VHL, MECP2, SMAD3, NFKBIA, PRKDC, MED24, ELK3, ARNTL, TRRAP, STAT3, GATA2, ATF5, SIN3B, PIAS4, MTF1, PIAS3, SND1, HIPK2, MED27, TCF4, LCOR, RBM14, SCAND1
KEGG_PATHWAY	hsa05222	Small cell lung cancer	6	1,4	0,02509	3,56	0,60282	PIAS4, PIAS3, NFKBIA, ITGA2, LAMC1, LAMB1
GOTERM_BP_FAT	GO:0010629	negative regulation of gene expression	20	4,8	0,01283	1,84	0,66162	MEF2C, SBNO2, VHL, MECP2, SMAD3, SIRT6, SIRT7, ELK3, STAT3, SIN3B, PIAS4, ZNF148, BAX, SND1, HIPK2, HEY2, TCF4, SUPT5H, LCOR, NFIC
GOTERM_BP_FAT	GO:0009628	response to abiotic stimulus	16	3,8	0,01359	2,01	0,66842	STX1A, CCL2, MAP1B, PRKDC, PKN1, ITGA2, GJA1, MBD4, INTS3, DCLRE1C, APP, BTG2, BAX, COL1A1, STRBP, MYOF
GOTERM_BP_FAT	GO:0000122	negative regulation of transcription from RNA polymerase II promoter	13	3,1	0,01267	2,26	0,67198	MEF2C, VHL, MECP2, SMAD3, STAT3, PIAS4, ZNF148, HEY2, HIPK2, TCF4, LCOR, NFIC, SUPT5H
GOTERM_BP_FAT	GO:0032268	regulation of cellular protein metabolic process	19	4,5	0,01449	1,86	0,67830	DLC1, A2M, ATG10, CCDC88C, EDN1, NFKBIA, PKN1, ITGA2, EIF5A, EIF4G1, PRKAR2A, APP, EIF3B, PIAS4, PIAS3, PSMD11, BAX, MAPK8IP3, EIF2AK4
GOTERM_BP_FAT	GO:0010608	posttranscriptional regulation of gene expression	11	2,6	0,01607	2,42	0,70289	EIF4G1, APP, EIF3B, VHL, CCDC88C, SND1, SMAD3, PRKDC, EIF5A, ITGA2, EIF2AK4
GOTERM_BP_FAT	GO:0001568	blood vessel development	12	2,9	0,01713	2,27	0,71358	PLAT, VHL, BAX, CCBE1, HEY2, EDN1, COL1A2, TGFBR3, ELK3, COL1A1, POFUT1, COL5A1

KEGG_PATHWAY	hsa04510	Focal adhesion	9	2,1	0,04539	2,23	0,71796	DOCK1, COL1A2, ITGA10, ITGA2, PIP5K1C, LAMC1, COL1A1, LAMB1, COL5A1
GOTERM_BP_FAT	GO:0043062	extracellular structure organization	9	2,1	0,02473	2,56	0,73113	APP, VHL, MAP1B, COL1A2, AGRN, LAMC1, COL1A1, COL5A1, APLP2
GOTERM_BP_FAT	GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	7	1,7	0,02371	3,15	0,73410	CCL2, LTBP3, HIPK2, COL1A2, SMAD3, TGFBR3, TGFBRAP1
GOTERM_BP_FAT	GO:0008219	cell death	25	5,9	0,02195	1,61	0,73567	MEF2C, DLC1, PACS2, FGF14, GJA1, PRKDC, NFKBIA, RRAGC, APP, DOCK1, SHARPIN, PPP2R2B, BCL7C, CFLAR, RNF144B, STAG3L3, ARHGEF17, SMAD3, SMN1, MAP1S, BAX, HIPK2, SLC5A8, RHOT2, EIF2AK2
GOTERM_BP_FAT	GO:0012501	programmed cell death	22	5,2	0,02336	1,67	0,73817	DLC1, MEF2C, PACS2, RNF144B, CFLAR, STAG3L3, SMAD3, NFKBIA, PRKDC, ARHGEF17, GJA1, RRAGC, APP, DOCK1, MAP1S, SHARPIN, BAX, HIPK2, SLC5A8, RHOT2, EIF2AK2, BCL7C
GOTERM_BP_FAT	GO:0031589	cell-substrate adhesion	7	1,7	0,01905	3,31	0,73954	DLC1, LIMS1, ITGA10, ITGA2, BCAM, LAMC1, LAMB1
GOTERM_BP_FAT	GO:0030198	extracellular matrix organization	7	1,7	0,02472	3,12	0,73987	APP, VHL, COL1A2, LAMC1, COL1A1, COL5A1, APLP2
GOTERM_BP_FAT	GO:0001775	cell activation	13	3,1	0,02170	2,10	0,74169	KLF6, YWHAZ, SBNO2, SWAP70, EDN1, STAT5B, SMAD3, TNFSF14, PRKDC, DCLRE1C, BAX, SPN, KIF13B
GOTERM_BP_FAT	GO:0016481	negative regulation of transcription	18	4,3	0,02110	1,82	0,74221	MEF2C, SBNO2, VHL, MECP2, SMAD3, SIRT6, SIRT7, ELK3, STAT3, SIN3B, PIAS4, ZNF148, HIPK2, HEY2, TCF4, LCOR, NFIC, SUPT5H
GOTERM_BP_FAT	GO:0016265	death	25	5,9	0,02303	1,60	0,74273	MEF2C, DLC1, PACS2, FGF14, GJA1, PRKDC, NFKBIA, RRAGC, APP, DOCK1, SHARPIN, PPP2R2B, BCL7C, CFLAR, RNF144B, STAG3L3, ARHGEF17, SMAD3, SMN1, MAP1S, BAX, HIPK2, SLC5A8, RHOT2, EIF2AK2
GOTERM_BP_FAT	GO:0045184	establishment of protein localization	26	6,2	0,02623	1,57	0,74341	ARFGAP1, ATG10, STX1A, YWHAZ, AP1B1, NUP160, RGPD3, NFKBIA, EIF5A, ITGA2, NAPA, ARNTL, BLZF1, TMED2, ARF3, SNF8, KPNA6, TRPC4AP, BET1L, NUTF2, RAB13, COL1A1, SEC24D, MVP, KIF13B, SCAMP5
GOTERM_BP_FAT	GO:0046649	lymphocyte activation	10	2,4	0,02838	2,33	0,74662	DCLRE1C, KLF6, SWAP70, BAX, STAT5B, SMAD3, PRKDC, TNFSF14, SPN, KIF13B
GOTERM_BP_FAT	GO:0001944	vasculature development	12	2,9	0,02013	2,21	0,74747	PLAT, VHL, BAX, CCBE1, HEY2, EDN1, COL1A2, TGFBR3, ELK3, COL1A1, POFUT1, COL5A1
GOTERM_BP_FAT	GO:0033554	cellular response to stress	21	5,0	0,02080	1,72	0,74790	SREBF1, ATG10, POLE, MAP1B, PRKDC, PKN1, MBD4, SIRT7, INTS3, DCLRE1C, DUSP19, BTG2, BAX, HIPK2, TDG, MAPK8IP3, RBM14, EIF2AK2, MYOF, EIF2AK4, SCAMP5
GOTERM_BP_FAT	GO:0010558	negative regulation of macromolecule biosynthetic process	20	4,8	0,02739	1,69	0,75021	MEF2C, SBNO2, VHL, EDN1, MECP2, SMAD3, SIRT6, SIRT7, ELK3, STAT3, SIN3B, PIAS4, ZNF148, HIPK2, HEY2, TCF4, SUPT5H, LCOR, NFIC, EIF2AK4
GOTERM_BP_FAT	GO:0045934	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	19	4,5	0,02803	1,72	0,75027	MEF2C, SBNO2, VHL, EDN1, MECP2, SMAD3, SIRT6, SIRT7, ELK3, STAT3, SIN3B, PIAS4, ZNF148, HIPK2, HEY2, TCF4, SUPT5H, LCOR, NFIC
GOTERM_BP_FAT	GO:0009611	response to wounding	19	4,5	0,03649	1,66	0,76410	PLAT, KLF6, A2M, YWHAZ, CCL2, STAT5B, MAP1B, SMAD3, ITGA2, ELK3, MECOM, COL5A1, STAT3, DYSF, STAB1, CD46, BAX, SERPINE1, CTSB
GOTERM_BP_FAT	GO:0016044	membrane organization	15	3,6	0,03642	1,82	0,76975	ARFGAP1, NPLOC4, AP1B1, HIP1R, NAPA, COL5A1, GATA2, APP, DYSF, DOCK1, STAB1, BAX, AGRN, VAMP2, SEC24D
GOTERM_BP_FAT	GO:0010552	positive regulation of specific transcription from RNA polymerase II promoter	5	1,2	0,03401	4,06	0,77273	MEF2C, GATA2, SMAD3, NFKBIA, PRKDC
GOTERM_BP_FAT	GO:0006915	apoptosis	21	5,0	0,03615	1,62	0,77363	DLC1, MEF2C, PACS2, RNF144B, CFLAR, STAG3L3, NFKBIA, SMAD3, ARHGEF17, GJA1, RRAGC, APP, DOCK1, MAP1S, SHARPIN, BAX, HIPK2, SLC5A8, RHOT2, EIF2AK2, BCL7C
GOTERM_BP_FAT	GO:0001776	leukocyte homeostasis	4	1,0	0,04174	5,15	0,77479	BAX, STAT5B, TNFSF14, MECOM
GOTERM_BP_FAT	GO:0009890	negative regulation of biosynthetic process	20	4,8	0,04109	1,62	0,77512	MEF2C, SBNO2, VHL, EDN1, MECP2, SMAD3, SIRT6, SIRT7, ELK3, STAT3, SIN3B, PIAS4, ZNF148, HIPK2, HEY2, TCF4, SUPT5H, LCOR, NFIC, EIF2AK4
GOTERM_BP_FAT	GO:0008104	protein localization	28	6,7	0,04044	1,47	0,77536	ARFGAP1, YWHAZ, ATG10, NUP160, AP1B1, NFKBIA, EIF5A, NAPA, BLZF1, TMED2, SNF8, SEC24D, SCAMP5, KIF13B, STX1A, RGPD3, ITGA2, ARNTL, ARF3, BAX, MAPK8IP3, BET1L, TRPC4AP, KPNA6, NUTF2, COL1A1, RAB13, MVP
GOTERM_BP_FAT	GO:0010212	response to ionizing radiation	5	1,2	0,03997	3,86	0,77716	DCLRE1C, CCL2, BAX, PRKDC, INTS3
GOTERM_BP_FAT	GO:0015031	protein transport	25	5,9	0,03928	1,52	0,77717	ARFGAP1, ATG10, YWHAZ, STX1A, AP1B1, NUP160, RGPD3, NFKBIA, EIF5A, NAPA, ARNTL, BLZF1, TMED2, ARF3, SNF8, KPNA6, TRPC4AP, BET1L, NUTF2, RAB13, COL1A1, SEC24D, MVP, KIF13B, SCAMP5
GOTERM_BP_FAT	GO:0015931	nucleobase, nucleoside, nucleotide and nucleic acid transport	7	1,7	0,03517	2,87	0,77738	SLC29A1, NUP160, RGPD3, GJA1, EIF5A, LOC441228, MVP
GOTERM_BP_FAT	GO:0051172	negative regulation of nitrogen compound metabolic process	19	4,5	0,03177	1,70	0,77798	MEF2C, SBNO2, VHL, EDN1, MECP2, SMAD3, SIRT6, SIRT7, ELK3, STAT3, SIN3B, PIAS4, ZNF148, HIPK2, HEY2, TCF4, SUPT5H, LCOR, NFIC
GOTERM_BP_FAT	GO:0031327	negative regulation of cellular biosynthetic process	20	4,8	0,03397	1,65	0,77918	MEF2C, SBNO2, VHL, EDN1, MECP2, SMAD3, SIRT6, SIRT7, ELK3, STAT3, SIN3B, PIAS4, ZNF148, HIPK2, HEY2, TCF4, SUPT5H, LCOR, NFIC, EIF2AK4
GOTERM_BP_FAT	GO:0006984	ER-nuclear signaling pathway	4	1,0	0,03886	5,29	0,77949	ATG10, ATP2A2, EIF2AK2, EIF2AK4
GOTERM_BP_FAT	GO:0034976	response to endoplasmic reticulum stress	4	1,0	0,03608	5,45	0,77950	ATG10, EIF2AK2, EIF2AK4, SCAMP5
GOTERM_BP_FAT	GO:0007507	heart development	10	2,4	0,04313	2,15	0,78052	DLC1, DVL3, EDN1, GAA, TGFBR3, PRKDC, GJA1, MECOM, POFUT1, COL5A1
GOTERM_BP_FAT	GO:0070482	response to oxygen levels	8	1,9	0,03275	2,63	0,78095	PLAT, CYB5R4, CCL2, VHL, STAT5B, EDN1, SMAD3, ITGA2
GOTERM_BP_FAT	GO:0010605	negative regulation of macromolecule metabolic process	24	5,7	0,04444	1,51	0,78521	MEF2C, A2M, SBNO2, VHL, EDN1, MECP2, SMAD3, SIRT6, SIRT7, ELK3, STAT3, SIN3B, PIAS4, ZNF148, PSMD11, SND1, BAX, HIPK2, HEY2, TCF4, SUPT5H, LCOR, NFIC, EIF2AK4
GOTERM_BP_FAT	GO:0007167	enzyme linked receptor protein signaling pathway	14	3,3	0,03392	1,90	0,78575	PLAT, CCL2, LTBP3, HIPK2, STAT5B, COL1A2, SMAD3, FGF23, TGFBR3, SHOC2, TGFBRAP1, AGRN, STAT3, PILRB
GOTERM_BP_FAT	GO:0006259	DNA metabolic process	18	4,3	0,04664	1,65	0,79616	SWAP70, POLE, GINS4, PRKDC, RNASEH1, MBD4, PAPD5, INTS3, LOC100130764, TNKS1BP1, DCLRE1C, BTG2, BAX, TDG, DMC1, LOC648927, NFIC, RBM14
GOTERM_BP_FAT	GO:0006936	muscle contraction	8	1,9	0,04746	2,42	0,79687	SSTR2, DYSF, EDN1, GAA, DAG1, GJA1, FLII, MYOF
GOTERM_BP_FAT	GO:0051098	regulation of binding	8	1,9	0,04746	2,42	0,79687	BAX, HIPK2, SMAD3, NFKBIA, TGFBR3, ITGA2, ZNF462, BRD4
GOTERM_MF_FAT	GO:0016628	oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor	4	1,0	0,00867	9,20	0,91080	PTGR2, BLVRB, FASN, AKR1D1
GOTERM_MF_FAT	GO:0005201	extracellular matrix structural constituent	7	1,7	0,01369	3,56	0,92195	COL1A2, LAMC1, COL1A1, TINAGL1, LAMB1, COL5A1, COL4A5
GOTERM_MF_FAT	GO:0003702	RNA polymerase II transcription factor activity	12	2,9	0,02435	2,15	0,93521	SREBF1, MEF2C, ATF5, KLF13, ZNF148, MED8, GTF2IRD1, SNF8, SMAD3, MED24, LCOR, RBM14
GOTERM_MF_FAT	GO:0000287	magnesium ion binding	18	4,3	0,03012	1,74	0,94092	ILKAP, NT5DC2, ITGA2, ITGA10, RNASEH1, ALPP, PPA2, POLR2B, RRAGC, DCLRE1C, MAST4, ATP2A2, ATP2C1, ADK, MAP3K8, ENTPD6, B4GALT6, ACSL4
GOTERM_MF_FAT	GO:0046332	SMAD binding	5	1,2	0,02039	4,75	0,94268	HIPK2, COL1A2, SMAD3, TGFBR3, TGFBRAP1

Table S5.*1* | Functionally annotated gene sets associated with Cluster #1 of temporal expression profiles

Category	Geneset/ Pathway ID	Term	Count	%	*P* -value	Fold Enrichment	Benjamini Hochberg	Genes
SP_PIR_KEYWORDS		**metal-thiolate cluster**	4	1,90	0,00016	35,62	**0,0212**	MT1IP, MT1G, MT1P3, MT1F
SP_PIR_KEYWORDS		**dna-binding**	35	16,67	0,00010	2,00	**0,0270**	ZNF430, BBX, INO80, ZNF75A, ZKSCAN1, HMGN5, ZNF652, RAX2, ZNF682, ZNF738, ZNF773, ZNF223, ZNF404, HEY2, HIST1H4C, ZNF426, STRBP, TCF4, ZNF562, KLF6, ZBTB20, SNAPC1, MECP2, MBD4, MECOM, ZNF549, ZNF526, ZNF234, ATF5, PIAS4, TAF15, MTF1, ZNF462, LCOR, DMC1
SP_PIR_KEYWORDS		**nucleus**	59	28,10	0,00110	1,47	**0,0694**	FGF14, BBX, INO80, EIF5A, ZKSCAN1, WDR82, HMGN5, BLZF1, ZNF738, ZNF682, ZNF773, HEY2, ZNF404, MED27, CDCA5, ZBTB20, SNAPC1, STAG3L3, MECP2, MBD4, ZNF503, ISG20L2, MECOM, ZNF549, SMN1, ZNF234, MTF1, TAF15, PIAS4, HIPK2, LCOR, DMC1, ZNF430, SNRPB2, NFKBIA, ZNF75A, ZNF652, RRAGC, SPC24, RAX2, ZNF223, SNF8, ZNF426, HIST1H4C, TCF4, ZNF562, SPOP, KLF6, BRD3, NUCKS1, VHL, GINS4, ZNF526, ATF5, HNRNPUL2, TDG, ZNF462, RBM14, SCAND1
SP_PIR_KEYWORDS		**Transcription**	34	16,19	0,00143	1,75	**0,0721**	ZNF430, BBX, ZNF75A, ZKSCAN1, HMGN5, ZNF652, RAX2, ZNF682, ZNF738, ZNF773, ZNF223, SNF8, ZNF404, MED27, HEY2, ZNF426, TCF4, ZNF562, KLF6, ZBTB20, SNAPC1, MECP2, ZNF503, MECOM, ZNF549, ZNF526, ZNF234, ATF5, PIAS4, MTF1, HIPK2, ZNF462, LCOR, RBM14
SP_PIR_KEYWORDS		**transcription regulation**	34	16,19	0,00099	1,79	**0,0826**	ZNF430, BBX, ZNF75A, ZKSCAN1, HMGN5, ZNF652, RAX2, ZNF682, ZNF738, ZNF773, ZNF223, SNF8, ZNF404, MED27, HEY2, ZNF426, TCF4, ZNF562, KLF6, ZBTB20, SNAPC1, MECP2, ZNF503, MECOM, ZNF549, ZNF526, ZNF234, ATF5, PIAS4, MTF1, HIPK2, ZNF462, LCOR, RBM14
SP_PIR_KEYWORDS		**acetylated amino end**	6	2,86	0,00244	6,41	**0,0873**	PRKAR2A, EIF5A, HIST1H4C, MT1G, MT1P3, MT1F
SP_PIR_KEYWORDS		**chelation**	3	1,43	0,00232	40,07	**0,0966**	MT1G, MT1P3, MT1F
SP_PIR_KEYWORDS		**cadmium**	3	1,43	0,00232	40,07	**0,0966**	MT1G, MT1P3, MT1F
GOTERM_BP_FAT	**GO:0051252**	**regulation of RNA metabolic process**	33	15,71	0,00018	1,95	**0,1236**	ZNF430, NFKBIA, ZNF75A, ZKSCAN1, HMGN5, BLZF1, RAX2, ZNF682, ZNF738, ZNF773, ZNF223, SNF8, ZNF404, MED27, HEY2, ZNF426, TCF4, ZNF562, KLF6, VHL, MECP2, MECOM, ZNF549, ZNF234, IFNAR2, ATF5, PIAS4, MTF1, HIPK2, ZNF462, LCOR, RBM14, SCAND1
KEGG_PATHWAY	**hsa05200**	**Pathways in cancer**	9	4,29	0,00244	3,58	**0,1425**	PIAS4, VHL, FGF14, BAX, NFKBIA, FGF23, ITGA2, MECOM, CSF2RA
GOTERM_BP_FAT	**GO:0045449**	**regulation of transcription**	41	19,52	0,00044	1,69	**0,1486**	ZNF430, BBX, NFKBIA, ZNF75A, ZKSCAN1, HMGN5, ZNF652, BLZF1, RAX2, ZNF682, ZNF738, ZNF773, ZNF223, SNF8, ZNF404, MED27, HEY2, ZNF426, TCF4, ZNF562, KLF6, ZBTB20, SNAPC1, VHL, MECP2, ZNF503, MECOM, ZNF549, ZNF526, ZNF234, ATF5, IFNAR2, PIAS4, MTF1, HIPK2, TGFBR3, ZNF462, RBM14, LCOR, POFUT1, SCAND1
GOTERM_BP_FAT	**GO:0006355**	**regulation of transcription, DNA-dependent**	33	15,71	0,00012	2,00	**0,1592**	ZNF430, NFKBIA, ZNF75A, ZKSCAN1, HMGN5, BLZF1, RAX2, ZNF682, ZNF738, ZNF773, ZNF223, SNF8, ZNF404, MED27, HEY2, ZNF426, TCF4, ZNF562, KLF6, VHL, MECP2, MECOM, ZNF549, ZNF234, IFNAR2, ATF5, PIAS4, MTF1, HIPK2, ZNF462, LCOR, RBM14, SCAND1
GOTERM_BP_FAT	**GO:0006357**	**regulation of transcription from RNA polymerase II promoter**	18	8,57	0,00037	2,66	**0,1650**	KLF6, VHL, MECP2, NFKBIA, MECOM, ATF5, IFNAR2, BLZF1, PIAS4, MTF1, HIPK2, MED27, HEY2, SNF8, ZNF462, TCF4, LCOR, RBM14
GOTERM_BP_FAT	GO:0006350	transcription	34	16,19	0,00117	1,74	0,2902	ZNF430, BBX, ZNF75A, ZKSCAN1, HMGN5, ZNF652, RRAGC, RAX2, ZNF682, ZNF738, ZNF773, ZNF223, SNF8, ZNF404, MED27, HEY2, ZNF426, TCF4, ZNF562, KLF6, ZBTB20, SNAPC1, MECP2, ZNF503, ZNF549, ZNF526, ZNF234, ATF5, PIAS4, MTF1, HIPK2, ZNF462, LCOR, RBM14
SP_PIR_KEYWORDS		metal binding	3	1,43	0,01327	16,87	0,3544	MT1G, MT1P3, MT1F
GOTERM_MF_FAT	GO:0003677	DNA binding	38	18,10	0,00178	1,63	0,4259	ZNF430, BBX, INO80, ZNF75A, ZKSCAN1, HMGN5, ZNF652, BLZF1, RAX2, ZNF682, ZNF738, ZNF773, ZNF223, ZNF404, HEY2, HIST1H4C, ZNF426, STRBP, TCF4, ZNF562, KLF6, ZBTB20, SNAPC1, MECP2, MBD4, MECOM, ZNF549, ZNF526, ZNF234, ATF5, PIAS4, TAF15, MTF1, TDG, ZNF462, LCOR, DMC1, SCAND1
GOTERM_MF_FAT	GO:0046870	cadmium ion binding	3	1,43	0,00418	29,96	0,4801	MT1G, MT1P3, MT1F
KEGG_PATHWAY	hsa04210	Apoptosis	4	1,90	0,02653	5,99	0,5712	CFLAR, PRKAR2A, BAX, NFKBIA
SP_PIR_KEYWORDS		zinc	30	14,29	0,03177	1,46	0,6093	ZNF430, ZNF75A, ZKSCAN1, ALPP, MT1P3, ZNF652, ZNF682, RSPRY1, ZNF773, ZNF223, ZNF404, ZNF426, ZNF562, MT1G, MT1F, KLF6, ZBTB20, FBLIM1, ZNF503, MECOM, ZNF549, ZNF526, ZNF234, TRIM38, PIAS4, TAF15, MTF1, CPXM1, ZNF462, RBM14
SP_PIR_KEYWORDS		alternative splicing	82	39,05	0,04870	1,17	0,6955	DLC1, FGF14, BBX, TNFSF14, EIF5A, LOC100132585, IL17RD, ZYG11B, BLZF1, ZNF682, RSPRY1, KLHL28, ZNF773, CCBE1, MED27, SNTB2, DENND5B, NBPF9, CSF2RA, BCL7C, PILRB, ANKRD36B, SLC4A5, OPA3, ZBTB20, PIGX, STAG3L3, NLRP8, MECP2, FBLIM1, PISD, ZNF503, MBD4, MECOM, ZNF549, SMN1, LILRB1, IFNAR2, MAST4, SSTR2, TAF15, CATSPER2, ADK, HIPK2, SLC35E1, MFSD11, LCOR, EIF2AK4, SRGAP1, GALNT3, ATG10, HAUS2, ANKRD30B, ENSA, ANKRD36, N4BP2, TMED4, DUSP19, SNF8, STRBP, TCF4, ZNF562, MT1G, KLF6, CFLAR, BRD3, NBPF10, NUCKS1, VHL, RGPD3, GINS4, ARMC5, PPA2, NUBPL, RASSF6, CDAN1, BAX, PTP4A2, RHBDL2, ZNF462, RBM14, CUEDC1, POFUT1
SP_PIR_KEYWORDS		zinc-finger	24	11,43	0,04859	1,49	0,7288	KLF6, ZBTB20, ZNF430, ZNF75A, ZKSCAN1, ZNF503, MECOM, ZNF549, ZNF652, ZNF526, ZNF234, TRIM38, ZNF682, PIAS4, TAF15, MTF1, RSPRY1, ZNF773, ZNF223, ZNF404, ZNF462, ZNF426, RBM14, ZNF562
GOTERM_MF_FAT	GO:0008134	transcription factor binding	12	5,71	0,01319	2,34	0,7488	ATF5, MTF1, PIAS4, VHL, HIPK2, MED27, MECP2, NFKBIA, TCF4, LCOR, RBM14, SCAND1
GOTERM_BP_FAT	GO:0009394	2'-deoxyribonucleotide metabolic process	3	1,43	0,01586	15,34	0,8341	ADK, TDG, MBD4
GOTERM_BP_FAT	GO:0009612	response to mechanical stimulus	4	1,90	0,01496	7,67	0,8403	CCL2, MAP1B, ITGA2, STRBP
GOTERM_BP_FAT	GO:0042127	regulation of cell proliferation	15	7,14	0,01382	2,05	0,8426	DLC1, CCL2, VHL, EDN1, NFKBIA, ITGA2, EIF5A, MECOM, SSTR2, BAX, HIPK2, HEY2, TGFBR3, SCAND1, SPN
GOTERM_BP_FAT	GO:0009891	positive regulation of biosynthetic process	13	6,19	0,02708	2,01	0,8654	KLF6, VHL, EDN1, ITGA2, EIF5A, NFKBIA, MECOM, MTF1, HIPK2, ZNF462, TCF4, RBM14, SPN
GOTERM_BP_FAT	GO:0051098	regulation of binding	6	2,86	0,01374	4,21	0,8675	BAX, HIPK2, NFKBIA, TGFBR3, ITGA2, ZNF462
GOTERM_BP_FAT	GO:0001568	blood vessel development	7	3,33	0,02616	3,07	0,8697	VHL, BAX, CCBE1, HEY2, EDN1, TGFBR3, POFUT1
GOTERM_BP_FAT	GO:0001944	vasculature development	7	3,33	0,02898	2,99	0,8708	VHL, BAX, CCBE1, HEY2, EDN1, TGFBR3, POFUT1
GOTERM_BP_FAT	GO:0010604	positive regulation of macromolecule metabolic process	16	7,62	0,01254	2,00	0,8711	DLC1, KLF6, ATG10, VHL, NFKBIA, ITGA2, EIF5A, MECOM, PIAS4, MTF1, PSMD11, HIPK2, ZNF462, TCF4, RBM14, SPN
GOTERM_BP_FAT	GO:0012502	induction of programmed cell death	9	4,29	0,00985	3,01	0,8734	DLC1, CFLAR, BAX, HIPK2, TNFSF14, EIF5A, MBD4, SCAND1, SPN
GOTERM_BP_FAT	GO:0010942	positive regulation of cell death	9	4,29	0,04856	2,22	0,8748	DLC1, CFLAR, BAX, HIPK2, TNFSF14, EIF5A, MBD4, SCAND1, SPN
GOTERM_BP_FAT	GO:0048514	blood vessel morphogenesis	6	2,86	0,04604	3,05	0,8759	VHL, BAX, CCBE1, HEY2, EDN1, POFUT1
GOTERM_BP_FAT	GO:0043068	positive regulation of programmed cell death	9	4,29	0,04749	2,23	0,8764	DLC1, CFLAR, BAX, HIPK2, TNFSF14, EIF5A, MBD4, SCAND1, SPN
GOTERM_BP_FAT	GO:0001776	leukocyte homeostasis	3	1,43	0,04350	8,95	0,8771	BAX, TNFSF14, MECOM
GOTERM_BP_FAT	GO:0010941	regulation of cell death	14	6,67	0,03800	1,84	0,8771	DLC1, CFLAR, CCL2, VHL, NFKBIA, TNFSF14, EIF5A, MBD4, ATF5, BAX, HIPK2, CTSB, SCAND1, SPN
GOTERM_BP_FAT	GO:0007584	response to nutrient	5	2,38	0,04080	3,83	0,8774	SSTR2, CCL2, MAP1B, ITGA2, ENSA
GOTERM_BP_FAT	GO:0006916	anti-apoptosis	6	2,86	0,04227	3,13	0,8779	CFLAR, ATF5, CCL2, VHL, BAX, NFKBIA
GOTERM_BP_FAT	GO:0010557	positive regulation of macromolecule biosynthetic process	12	5,71	0,03957	1,97	0,8784	KLF6, MTF1, VHL, HIPK2, NFKBIA, EIF5A, ITGA2, ZNF462, TCF4, MECOM, RBM14, SPN
GOTERM_BP_FAT	GO:0051101	regulation of DNA binding	5	2,38	0,02580	4,44	0,8801	HIPK2, NFKBIA, TGFBR3, ITGA2, ZNF462
GOTERM_BP_FAT	GO:0043067	regulation of programmed cell death	14	6,67	0,03706	1,85	0,8802	DLC1, CFLAR, CCL2, VHL, NFKBIA, TNFSF14, EIF5A, MBD4, ATF5, BAX, HIPK2, CTSB, SCAND1, SPN
GOTERM_BP_FAT	GO:0043065	positive regulation of apoptosis	9	4,29	0,04592	2,25	0,8831	DLC1, CFLAR, BAX, HIPK2, TNFSF14, EIF5A, MBD4, SCAND1, SPN
GOTERM_BP_FAT	GO:0000122	negative regulation of transcription from RNA polymerase II promoter	7	3,33	0,03692	2,83	0,8890	PIAS4, VHL, HIPK2, HEY2, MECP2, TCF4, LCOR
GOTERM_BP_FAT	GO:0032270	positive regulation of cellular protein metabolic process	7	3,33	0,02107	3,23	0,8916	DLC1, ATG10, PIAS4, PSMD11, NFKBIA, EIF5A, ITGA2
GOTERM_BP_FAT	GO:0009262	deoxyribonucleotide metabolic process	3	1,43	0,02557	11,93	0,8921	ADK, TDG, MBD4
GOTERM_BP_FAT	GO:0031667	response to nutrient levels	6	2,86	0,03597	3,27	0,8925	SSTR2, CCL2, MAP1B, ITGA2, ENSA, EIF2AK4
GOTERM_MF_FAT	GO:0003712	transcription cofactor activity	9	4,29	0,02835	2,48	0,8939	ATF5, MTF1, PIAS4, HIPK2, MED27, MECP2, TCF4, RBM14, SCAND1
GOTERM_BP_FAT	GO:0032268	regulation of cellular protein metabolic process	11	5,24	0,01243	2,49	0,8982	DLC1, ATG10, PRKAR2A, PIAS4, PSMD11, BAX, EDN1, NFKBIA, EIF5A, ITGA2, EIF2AK4
GOTERM_BP_FAT	GO:0044265	cellular macromolecule catabolic process	13	6,19	0,03582	1,93	0,9014	ATG10, VHL, UBE2G2, PNPT1, RNASEH1, MBD4, ZYG11B, PIAS4, PSMD11, BAX, TDG, PCYOX1, SPOP
GOTERM_BP_FAT	GO:0051247	positive regulation of protein metabolic process	7	3,33	0,02526	3,09	0,9033	DLC1, ATG10, PIAS4, PSMD11, NFKBIA, EIF5A, ITGA2

GOTERM_BP_FAT	GO:0042981	regulation of apoptosis	14	6,67	0,03463	1,87	0,9037	DLC1, CFLAR, CCL2, VHL, NFKBIA, TNFSF14, EIF5A, MBD4, ATF5, BAX, HIPK2, CTSB, SCAND1, SPN
GOTERM_BP_FAT	GO:0006917	induction of apoptosis	9	4,29	0,00968	3,02	0,9064	DLC1, CFLAR, BAX, HIPK2, TNFSF14, EIF5A, MBD4, SCAND1, SPN
GOTERM_BP_FAT	GO:0031328	positive regulation of cellular biosynthetic process	13	6,19	0,02455	2,04	0,9112	KLF6, VHL, EDN1, ITGA2, EIF5A, NFKBIA, MECOM, MTF1, HIPK2, ZNF462, TCF4, RBM14, SPN
GOTERM_CC_FAT	GO:0046930	pore complex	4	1,90	0,04229	5,13	0,9998	BAX, RGPD3, EIF5A, NUTF2

Table S5.*2* | Functionally annotated gene sets associated with Cluster #2 of temporal expression profiles

Category	Geneset/ Pathway ID	Term	Count	%	*P*-value	Fold Enrichment	Benjamini Hochberg	Genes
SP_PIR_KEYWORDS		**phosphoprotein**	71	59,17	6,43E-07	1,61	**0,0001**	NRBP1, AP1B1, PTPN23, INTS1, PIP5K1C, MED24, BCAM, IARS2, NAP1L4, TRIM47, DGCR2, APP, DYSF, ELOVL5, PKN3, SND1, CD46, SLC4A2, SUPT5H, GPC1, SLC43A2, TRPM4, PTBP1, POLE, PKN1, ARHGEF17, PNPLA2, ARNTL, VPS8, MTMR12, EIF4G1, TRIM37, TNS3, ATP2C1, GTF2IRD1, EPB41L5, GAA, KPNA6, FLII, SERPINB1, CLIP2, NEURL4, TMEM184B, VAMP2, MVP, SEPT9, ARFGAP1, PACS2, USP5, SLC38A10, ZDHHC18, APLP2, SLC29A1, EIF3B, FASN, SREBF1, SWAP70, HEATR1, SIRT7, DOCK6, STAT3, CAPRIN2, PDE2A, MAP1S, STAB1, RASSF2, DDX50, CYFIP1, OGFR, DENND4B, SPTAN1
GOTERM_CC_FAT	**GO:0048471**	**perinuclear region of cytoplasm**	11	9,17	0,00007	4,93	**0,0150**	TRIM37, CYB5R4, APP, NRBP1, PKN3, MAP1S, CYFIP1, GDPD5, LAMB1, SEC24D, SEPT9
SP_PIR_KEYWORDS		**alternative splicing**	63	52,50	0,00103	1,38	**0,0728**	AP1B1, NT5DC2, SHOC2, SIN3B, APP, DYSF, IDS, CD46, SLC4A2, CHST15, SUPT5H, SEC24D, SLC43A2, TRPM4, PTBP1, PKN1, PISD, PNPLA2, ARNTL, VPS8, MTMR12, TRIM37, EIF4G1, TNS3, ATP2C1, GTF2IRD1, TBCD, PCMTD2, EPB41L5, SURF4, CLIP2, NEURL4, DENND3, SEPT9, ARFGAP1, PACS2, SBNO2, FAM69B, USP5, SLC37A3, ITGA10, SLC38A10, APLP2, EIF3B, PPP2R2B, PLAT, SREBF1, NPLOC4, GDPD5, SIRT7, UAP1L1, TINAGL1, STAT3, CAPRIN2, PDE2A, STAB1, MBOAT7, FBLN7, RHOT2, TRPC4AP, CYFIP1, OGFR, SPTAN1
SP_PIR_KEYWORDS		**Serine protease inhibitor**	5	4,17	0,00140	10,28	**0,0739**	APP, A2M, SERPINE1, SERPINB1, APLP2
SP_PIR_KEYWORDS		**laminin egf-like domain**	4	3,33	0,00077	21,92	**0,0813**	STAB1, AGRN, LAMC1, LAMB1
KEGG_PATHWAY	**hsa04512**	**ECM-receptor interaction**	5	4,17	0,00273	8,18	**0,1205**	DAG1, ITGA10, AGRN, LAMC1, LAMB1
SP_PIR_KEYWORDS		**cell adhesion**	9	7,50	0,00407	3,51	**0,1388**	APP, DGCR2, PCDH10, FBLN7, ITGA10, BCAM, LAMC1, LAMB1, DCHS1
SP_PIR_KEYWORDS		**protease inhibitor**	5	4,17	0,00402	7,68	**0,1625**	APP, A2M, SERPINE1, SERPINB1, APLP2
SP_PIR_KEYWORDS		**cytoplasm**	32	26,67	0,00728	1,58	**0,1820**	ARFGAP1, NRBP1, DAG1, SHOC2, TRIM47, EIF3B, PKN3, SND1, FASN, PPP2R2B, LOC441228, SEC24D, NPLOC4, SWAP70, PKN1, GDPD5, SIRT7, STAT3, CAPRIN2, MTMR12, TRIM37, MAP1S, EPB41L5, PCMTD2, CYFIP1, SERPINB1, FLII, OGFR, CLIP2, MVP, SEPT9, SPTAN1
SP_PIR_KEYWORDS		**acetylation**	27	22,50	0,00701	1,68	**0,1983**	ARFGAP1, NRBP1, AP1B1, USP5, INTS1, IARS2, NAP1L4, EIF3B, SND1, FASN, LOC441228, SUPT5H, NPLOC4, PTBP1, PKN1, SIRT7, ARNTL, EIF4G1, KPNA6, CYFIP1, SERPINB1, FLII, OGFR, VAMP2, MVP, SPTAN1, SEPT9
KEGG_PATHWAY	hsa04610	Complement and coagulation cascades	4	3,33	0,01240	7,97	0,2541	PLAT, A2M, CD46, SERPINE1
SP_PIR_KEYWORDS		cytoplasmic vesicle	6	5,00	0,01471	4,14	0,3039	SREBF1, DYSF, AP1B1, CD46, PTPN23, VAMP2
SP_PIR_KEYWORDS		calcium	11	9,17	0,02334	2,25	0,4052	TRPM4, IDS, ATP2C1, PCDH10, FBLN7, RHOT2, ITGA10, B4GALT6, ANO6, DCHS1, SPTAN1
GOTERM_BP_FAT	GO:0046907	intracellular transport	14	11,67	0,00059	3,03	0,4059	ARFGAP1, NRBP1, AP1B1, ARNTL, TINAGL1, APP, MAP1S, ATP2C1, TRPC4AP, KPNA6, RHOT2, VAMP2, LOC441228, SEC24D
SP_PIR_KEYWORDS		golgi apparatus	9	7,50	0,02602	2,52	0,4098	ARFGAP1, SREBF1, AP1B1, ATP2C1, SURF4, CHST15, B4GALT6, MGAT5, SEC24D
SP_PIR_KEYWORDS		polymorphism	81	67,50	0,02924	1,15	0,4197	CYB5R4, A2M, NRBP1, NT5DC2, PTPN23, INTS1, MED24, BCAM, IARS2, TRIM47, DGCR2, APP, DYSF, PKN3, CD46, SERPINE1, SLC4A2, LOC441228, GPC1, ANO6, SEC24D, POLE, ARHGEF17, PKN1, PNPLA2, VPS8, EIF4G1, TRIM37, TNS3, BTG2, ATP2C1, PIAS3, GTF2IRD1, TBCD, EPB41L5, GAA, FLII, SERPINB1, CLIP2, NEURL4, LAMC1, DENND3, MVP, SEPT9, ARFGAP1, PACS2, FAM69B, DAG1, ITGA10, SLC38A10, APLP2, DCHS1, SLC29A1, NPAS2, EIF3B, FASN, AGRN, B4GALT6, PPP2R2B, LAMB1, PLAT, SREBF1, SWAP70, GDPD5, HEATR1, SIRT7, UAP1L1, TINAGL1, DOCK6, STAT3, CAPRIN2, PDE2A, MAP1S, STAB1, MBOAT7, RASSF2, FBLN7, RHOT2, CYFIP1, OGFR, SPTAN1
GOTERM_CC_FAT	GO:0012505	endomembrane system	13	10,83	0,01622	2,15	0,5050	ARFGAP1, SREBF1, NPLOC4, NRBP1, AP1B1, APP, ATP2C1, KPNA6, VAMP2, LOC441228, MGAT5, SEC24D, MVP
GOTERM_CC_FAT	GO:0031410	cytoplasmic vesicle	12	10,00	0,00997	2,41	0,5122	PLAT, SREBF1, APP, A2M, DYSF, AP1B1, SND1, FASN, PTPN23, PKN1, VAMP2, SEC24D
GOTERM_CC_FAT	GO:0031982	vesicle	12	10,00	0,01341	2,31	0,5160	PLAT, SREBF1, APP, A2M, DYSF, AP1B1, SND1, FASN, PTPN23, PKN1, VAMP2, SEC24D
SP_PIR_KEYWORDS		proteoglycan	3	2,50	0,04210	9,13	0,5171	APP, AGRN, GPC1
GOTERM_CC_FAT	GO:0005605	basal lamina	3	2,50	0,00734	22,78	0,5471	AGRN, LAMC1, LAMB1
GOTERM_CC_FAT	GO:0005604	basement membrane	4	3,33	0,02197	6,62	0,5489	DAG1, AGRN, LAMC1, LAMB1
GOTERM_MF_FAT	GO:0004867	serine-type endopeptidase inhibitor activity	5	4,17	0,00495	7,20	0,7801	APP, A2M, SERPINE1, SERPINB1, APLP2
GOTERM_BP_FAT	GO:0016044	membrane organization	9	7,50	0,00498	3,36	0,8879	ARFGAP1, APP, NPLOC4, DYSF, AP1B1, STAB1, AGRN, VAMP2, SEC24D
GOTERM_MF_FAT	GO:0019899	enzyme binding	9	7,50	0,04170	2,28	0,9256	A2M, PIAS3, SERPINE1, SHOC2, CYFIP1, LAMB1, SUPT5H, DOCK6, STAT3
GOTERM_BP_FAT	GO:0050885	neuromuscular process controlling balance	3	2,50	0,02450	12,21	0,9340	APP, GAA, APLP2
GOTERM_MF_FAT	GO:0030414	peptidase inhibitor activity	5	4,17	0,02763	4,33	0,9421	APP, A2M, SERPINE1, SERPINB1, APLP2
GOTERM_BP_FAT	GO:0030182	neuron differentiation	8	6,67	0,03269	2,60	0,9458	APP, BTG2, MAP1S, CYFIP1, PIP5K1C, AGRN, LAMB1, STAT3
GOTERM_BP_FAT	GO:0022610	biological adhesion	11	9,17	0,02347	2,23	0,9490	APP, DGCR2, ATP2C1, STAB1, PCDH10, FBLN7, ITGA10, BCAM, LAMC1, LAMB1, DCHS1
GOTERM_BP_FAT	GO:0031589	cell-substrate adhesion	4	3,33	0,03077	5,81	0,9524	ITGA10, BCAM, LAMC1, LAMB1
GOTERM_MF_FAT	GO:0005509	calcium ion binding	13	10,83	0,04072	1,87	0,9580	TRPM4, IDS, ATP2C1, PCDH10, DAG1, FBLN7, RHOT2, ITGA10, B4GALT6, ANO6, DCHS1, STAT3, SPTAN1
GOTERM_BP_FAT	GO:0033500	carbohydrate homeostasis	3	2,50	0,04549	8,72	0,9667	CYB5R4, SERPINE1, STAT3
GOTERM_BP_FAT	GO:0042593	glucose homeostasis	3	2,50	0,04549	8,72	0,9667	CYB5R4, SERPINE1, STAT3
GOTERM_BP_FAT	GO:0007155	cell adhesion	11	9,17	0,02326	2,24	0,9680	APP, DGCR2, ATP2C1, STAB1, PCDH10, FBLN7, ITGA10, BCAM, LAMC1, LAMB1, DCHS1
GOTERM_MF_FAT	GO:0004866	endopeptidase inhibitor activity	5	4,17	0,02325	4,57	0,9723	APP, A2M, SERPINE1, SERPINB1, APLP2
GOTERM_BP_FAT	GO:0045944	positive regulation of transcription from RNA polymerase II promoter	7	5,83	0,04442	2,69	0,9733	SREBF1, NPAS2, APP, AGRN, ARNTL, SUPT5H, STAT3
GOTERM_BP_FAT	GO:0010970	microtubule-based transport	3	2,50	0,01717	14,73	0,9776	APP, MAP1S, RHOT2
GOTERM_BP_FAT	GO:0048193	Golgi vesicle transport	5	4,17	0,01310	5,44	0,9788	ARFGAP1, NRBP1, AP1B1, VAMP2, SEC24D
GOTERM_BP_FAT	GO:0048589	developmental growth	4	3,33	0,02263	6,55	0,9820	APP, SERPINE1, INTS1, CYFIP1

Table S5.*3* | Functionally annotated gene sets associated with Cluster #3 of temporal expression profiles

Category	Geneset/ Pathway ID	Term	Count	%	*P* -value	Fold Enrichment	Benjamini Hochberg	Genes
GOTERM_CC_FAT	**GO:0012505**	**endomembrane system**	11	28,21	0,00001	5,80	**0,0011**	GALNT2, STX1A, ATP2A2, NUP160, TMED2, SMAD3, GJA1, SUN1, EDEM1, MYOF, SCAMP5
GOTERM_BP_FAT	**GO:0016192**	**vesicle-mediated transport**	9	23,08	0,00004	6,41	**0,0260**	GATA2, STX1A, YWHAZ, DOCK1, ATL2, TMED2, ARF3, BET1L, SCAMP5
SP_PIR_KEYWORDS		**phosphoprotein**	25	64,10	0,00041	1,79	**0,0549**	YWHAZ, NUP160, ATL2, GJA1, PRKDC, ELK3, LARP1, DOCK1, DDX23, MAP3K8, ENTPD6, MYOF, KIF13B, DVL3, STX1A, NRBF2, SMAD3, MMP15, SUN1, TNKS1BP1, KDM2A, ATP2A2, MED8, BET1L, LOC648927
GOTERM_CC_FAT	**GO:0031201**	**SNARE complex**	3	7,69	0,00089	65,10	**0,0695**	STX1A, BET1L, SCAMP5
GOTERM_CC_FAT	**GO:0031090**	**organelle membrane**	9	23,08	0,00302	3,39	**0,1505**	GALNT2, STX1A, ATP2A2, TMED2, SMAD3, GJA1, SUN1, EDEM1, SCAMP5
SP_PIR_KEYWORDS		golgi apparatus	6	15,38	0,00452	5,30	0,2683	GALNT2, TMED2, ARF3, BET1L, ENTPD6, SCAMP5
SP_PIR_KEYWORDS		cytoplasmic vesicle	4	10,26	0,00989	8,74	0,2902	STX1A, TMED2, MYOF, SCAMP5
SP_PIR_KEYWORDS		protein transport	5	12,82	0,01243	5,36	0,2919	NUP160, TMED2, ARF3, BET1L, SCAMP5
SP_PIR_KEYWORDS		Signal-anchor	5	12,82	0,00766	6,17	0,2980	GALNT2, ENTPD6, SUN1, EDEM1, MYOF
GOTERM_BP_FAT	GO:0045184	establishment of protein localization	8	20,51	0,00180	4,26	0,3038	STX1A, YWHAZ, NUP160, TMED2, ARF3, BET1L, KIF13B, SCAMP5
SP_PIR_KEYWORDS		nucleus	15	38,46	0,01803	1,82	0,3419	NRBF2, NUP160, SMAD3, PRKDC, ELK3, SUN1, TNKS1BP1, DUSP5, RCBTB1, GATA2, DDX23, KDM2A, MED8, LOC648927, MYOF
GOTERM_CC_FAT	GO:0031410	cytoplasmic vesicle	6	15,38	0,01579	3,85	0,3494	STX1A, YWHAZ, TMED2, GJA1, MYOF, SCAMP5
GOTERM_CC_FAT	GO:0031982	vesicle	6	15,38	0,01868	3,69	0,3537	STX1A, YWHAZ, TMED2, GJA1, MYOF, SCAMP5
GOTERM_CC_FAT	GO:0005794	Golgi apparatus	7	17,95	0,01433	3,31	0,3734	GALNT2, TMED2, ARF3, GJA1, BET1L, ENTPD6, SCAMP5
GOTERM_BP_FAT	GO:0046907	intracellular transport	7	17,95	0,00394	4,37	0,3787	STX1A, YWHAZ, ATP2A2, ATL2, NUP160, BET1L, KIF13B
GOTERM_CC_FAT	GO:0005635	nuclear envelope	4	10,26	0,01200	8,05	0,3868	NUP160, SMAD3, SUN1, MYOF
GOTERM_BP_FAT	GO:0015031	protein transport	8	20,51	0,00171	4,30	0,4026	STX1A, YWHAZ, NUP160, TMED2, ARF3, BET1L, KIF13B, SCAMP5
GOTERM_BP_FAT	GO:0008104	protein localization	8	20,51	0,00391	3,72	0,4457	STX1A, YWHAZ, NUP160, TMED2, ARF3, BET1L, KIF13B, SCAMP5
SP_PIR_KEYWORDS		coiled coil	9	23,08	0,03029	2,32	0,4547	STX1A, NRBF2, ATL2, MED8, CC2D2A, BET1L, SUN1, COL4A5, KIF13B
GOTERM_CC_FAT	GO:0031301	integral to organelle membrane	3	7,69	0,03353	10,06	0,4987	GALNT2, SUN1, EDEM1
GOTERM_CC_FAT	GO:0012506	vesicle membrane	3	7,69	0,04861	8,19	0,5199	STX1A, TMED2, GJA1
GOTERM_CC_FAT	GO:0031300	intrinsic to organelle membrane	3	7,69	0,04576	8,47	0,5318	GALNT2, SUN1, EDEM1
GOTERM_CC_FAT	GO:0030659	cytoplasmic vesicle membrane	3	7,69	0,04188	8,90	0,5370	STX1A, TMED2, GJA1
GOTERM_BP_FAT	GO:0010552	positive regulation of specific transcription from RNA polymerase II promoter	3	7,69	0,00798	21,58	0,5529	GATA2, SMAD3, PRKDC
GOTERM_BP_FAT	GO:0060627	regulation of vesicle-mediated transport	3	7,69	0,02153	12,81	0,6967	GATA2, STX1A, SCAMP5
GOTERM_BP_FAT	GO:0010551	regulation of specific transcription from RNA polymerase II promoter	3	7,69	0,02070	13,08	0,7167	GATA2, SMAD3, PRKDC
KEGG_PATHWAY	hsa04110	Cell cycle	3	7,69	0,03917	8,72	0,7216	YWHAZ, SMAD3, PRKDC
GOTERM_BP_FAT	GO:0045321	leukocyte activation	4	10,26	0,01914	6,78	0,7260	YWHAZ, SMAD3, PRKDC, KIF13B
GOTERM_BP_FAT	GO:0006887	exocytosis	3	7,69	0,03010	10,69	0,7319	STX1A, YWHAZ, SCAMP5
GOTERM_BP_FAT	GO:0051050	positive regulation of transport	4	10,26	0,01542	7,35	0,7378	GATA2, STX1A, SMAD3, SCAMP5
GOTERM_BP_FAT	GO:0051276	chromosome organization	5	12,82	0,02652	4,23	0,7409	RCBTB1, TNKS1BP1, KDM2A, PRKDC, LOC648927
GOTERM_BP_FAT	GO:0043193	positive regulation of gene-specific transcription	3	7,69	0,01790	14,14	0,7436	GATA2, SMAD3, PRKDC
GOTERM_BP_FAT	GO:0001775	cell activation	4	10,26	0,02978	5,71	0,7540	YWHAZ, SMAD3, PRKDC, KIF13B
GOTERM_BP_FAT	GO:0042110	T cell activation	3	7,69	0,03559	9,76	0,7670	SMAD3, PRKDC, KIF13B
GOTERM_BP_FAT	GO:0002252	immune effector process	3	7,69	0,03980	9,18	0,7836	GALNT2, YWHAZ, PRKDC
GOTERM_BP_FAT	GO:0032583	regulation of gene-specific transcription	3	7,69	0,03980	9,18	0,7836	GATA2, SMAD3, PRKDC
GOTERM_MF_FAT	GO:0008134	transcription factor binding	5	12,82	0,02926	4,08	0,9890	GATA2, YWHAZ, SMAD3, PRKDC, ELK3

Table S5.*4* | Functionally annotated gene sets associated with Cluster #4 of temporal expression profiles

Category	Geneset/ Pathway ID	Term	Count	%	*P* -value	Fold Enrichment	Benjamini Hochberg	Genes
GOTERM_CC_FAT	**GO:0031974**	**membrane-enclosed lumen**	7	23,33	0,02020	2,84	**0,1746**	WDR74, MEF2C, PTGR2, ZNF148, RBM39, BRD4, FCF1
GOTERM_CC_FAT	**GO:0043233**	**organelle lumen**	7	23,33	0,01845	2,89	**0,1965**	WDR74, MEF2C, PTGR2, ZNF148, RBM39, BRD4, FCF1
GOTERM_CC_FAT	**GO:0005730**	**nucleolus**	5	16,67	0,00947	5,39	**0,2004**	WDR74, PTGR2, ZNF148, BRD4, FCF1
GOTERM_CC_FAT	**GO:0070013**	**intracellular organelle lumen**	7	23,33	0,01658	2,96	**0,2304**	WDR74, MEF2C, PTGR2, ZNF148, RBM39, BRD4, FCF1
SP_PIR_KEYWORDS		**acetylation**	10	33,33	0,00581	2,70	**0,2395**	MEF2C, ILKAP, LIMS1, ZNF148, NAA10, RBM39, BRD4, ACSL4, OCIAD1, EIF2AK2
GOTERM_CC_FAT	GO:0031981	nuclear lumen	7	23,33	0,00617	3,63	0,2525	WDR74, MEF2C, PTGR2, ZNF148, RBM39, BRD4, FCF1
SP_PIR_KEYWORDS		phosphoprotein	18	60,00	0,00393	1,77	0,3096	MEF2C, ILKAP, PAPD5, NSUN5P2, OCIAD1, DCLRE1C, WDR74, ZNF600, DAPP1, ZNF148, SHARPIN, NAA10, LIME1, TGFBRAP1, BRD4, RBM39, EIF2AK2, NFIC
SP_PIR_KEYWORDS		nucleus	11	36,67	0,04592	1,83	0,6687	WDR74, DCLRE1C, MEF2C, ZNF600, ZNF148, NAA10, PAPD5, RBM39, BRD4, NFIC, FCF1
SP_PIR_KEYWORDS		immune response	3	10,00	0,03653	9,54	0,6884	DCLRE1C, LIME1, OCIAD1
GOTERM_BP_FAT	GO:0000122	negative regulation of transcription from RNA polymerase II promoter	3	10,00	0,04792	8,03	0,9998	MEF2C, ZNF148, NFIC

Table S5.*5* | Functionally annotated gene sets associated with Cluster #5 of temporal expression profiles

Category	Geneset/ Pathway ID	Term	Count	%	*P* -value	Fold Enrichment	Benjamini Hochberg	Genes
SP_PIR_KEYWORDS		phosphoprotein	9	64,29	0,04061	1,83	0,8452	GIT1, CCDC88C, MAPK8IP3, ZNF608, TRRAP, IP6K1, CHFR, ITPR3, SH3TC1

Table S5.*6* | Functionally annotated gene sets associated with Cluster #6 of temporal expression profiles

Category	Geneset/ Pathway ID	Term	Count	%	*P* -value	Fold Enrichment	Benjamini Hochberg	Genes
GOTERM_MF_FAT	**GO:0019838**	**growth factor binding**	4	36,36	0,00003	54,95	**0,0007**	LTBP3, COL1A2, COL1A1, COL5A1
SP_PIR_KEYWORDS		**Ehlers-Danlos syndrome**	3	27,27	0,00001	476,90	**0,0007**	COL1A2, COL1A1, COL5A1
GOTERM_MF_FAT	**GO:0048407**	**platelet-derived growth factor binding**	3	27,27	0,00002	393,42	**0,0009**	COL1A2, COL1A1, COL5A1
GOTERM_CC_FAT	**GO:0005583**	**fibrillar collagen**	3	27,27	0,00002	355,06	**0,0010**	COL1A2, COL1A1, COL5A1
SP_PIR_KEYWORDS		**triple helix**	3	27,27	0,00011	169,22	**0,0021**	COL1A2, COL1A1, COL5A1
SP_PIR_KEYWORDS		**hydroxylysine**	3	27,27	0,00011	169,22	**0,0021**	COL1A2, COL1A1, COL5A1
SP_PIR_KEYWORDS		**trimer**	3	27,27	0,00008	201,77	**0,0022**	COL1A2, COL1A1, COL5A1
SP_PIR_KEYWORDS		**hydroxyproline**	3	27,27	0,00016	141,78	**0,0022**	COL1A2, COL1A1, COL5A1
SP_PIR_KEYWORDS		**pyroglutamic acid**	3	27,27	0,00025	114,04	**0,0027**	COL1A2, COL1A1, COL5A1
GOTERM_CC_FAT	**GO:0005581**	**collagen**	3	27,27	0,00020	121,73	**0,0045**	COL1A2, COL1A1, COL5A1
SP_PIR_KEYWORDS		**hydroxylation**	3	27,27	0,00059	73,89	**0,0054**	COL1A2, COL1A1, COL5A1
KEGG_PATHWAY	**hsa04512**	**ECM-receptor interaction**	3	27,27	0,00080	45,40	**0,0064**	COL1A2, COL1A1, COL5A1
SP_PIR_KEYWORDS		**collagen**	3	27,27	0,00106	55,22	**0,0083**	COL1A2, COL1A1, COL5A1
KEGG_PATHWAY	**hsa04510**	**Focal adhesion**	3	27,27	0,00454	18,97	**0,0180**	COL1A2, COL1A1, COL5A1
GOTERM_MF_FAT	**GO:0005201**	**extracellular matrix structural constituent**	3	27,27	0,00118	50,32	**0,0203**	COL1A2, COL1A1, COL5A1
GOTERM_CC_FAT	**GO:0044420**	**extracellular matrix part**	3	27,27	0,00224	36,42	**0,0331**	COL1A2, COL1A1, COL5A1
SP_PIR_KEYWORDS		**extracellular matrix**	3	27,27	0,00658	21,77	**0,0444**	COL1A2, COL1A1, COL5A1
SP_PIR_KEYWORDS		**chromosomal rearrangement**	3	27,27	0,00874	18,80	**0,0522**	COL1A2, COL1A1, SHANK3
GOTERM_BP_FAT	**GO:0030199**	**collagen fibril organization**	3	27,27	0,00016	139,94	**0,0540**	COL1A2, COL1A1, COL5A1
GOTERM_BP_FAT	**GO:0043588**	**skin development**	3	27,27	0,00016	139,94	**0,0540**	COL1A2, COL1A1, COL5A1
SP_PIR_KEYWORDS		**coiled coil**	5	45,45	0,01512	4,33	**0,0804**	COL1A2, COL1A1, COL5A1, SHANK3, KANK1
GOTERM_CC_FAT	**GO:0031012**	**extracellular matrix**	3	27,27	0,01826	12,35	**0,1529**	COL1A2, COL1A1, COL5A1
GOTERM_CC_FAT	**GO:0005578**	**proteinaceous extracellular matrix**	3	27,27	0,01583	13,31	**0,1644**	COL1A2, COL1A1, COL5A1
SP_PIR_KEYWORDS		**disease mutation**	4	36,36	0,04360	4,40	**0,1998**	STAT5B, COL1A2, COL1A1, COL5A1
GOTERM_BP_FAT	GO:0030198	extracellular matrix organization	3	27,27	0,00203	39,02	0,3005	COL1A2, COL1A1, COL5A1
GOTERM_BP_FAT	GO:0007398	ectoderm development	3	27,27	0,00724	20,39	0,3463	COL1A2, COL1A1, COL5A1
GOTERM_BP_FAT	GO:0008544	epidermis development	3	27,27	0,00622	22,06	0,3547	COL1A2, COL1A1, COL5A1
GOTERM_BP_FAT	GO:0001944	vasculature development	3	27,27	0,01133	16,17	0,3934	COL1A2, COL1A1, COL5A1
GOTERM_BP_FAT	GO:0048729	tissue morphogenesis	3	27,27	0,00596	22,55	0,4082	COL1A2, COL1A1, SHANK3
GOTERM_BP_FAT	GO:0001568	blood vessel development	3	27,27	0,01081	16,56	0,4203	COL1A2, COL1A1, COL5A1

GOTERM_BP_FAT	GO:0043062	extracellular structure organization	3	27,27	0,00491	24,90	0,4380	COL1A2, COL1A1, COL5A1
GOTERM_BP_FAT	GO:0001501	skeletal system development	3	27,27	0,01789	12,72	0,5053	LTBP3, COL1A2, COL1A1
GOTERM_BP_FAT	GO:0007167	enzyme linked receptor protein signaling pathway	3	27,27	0,02040	11,87	0,5149	LTBP3, STAT5B, COL1A2

Category	Studied annotation categories: Gene Ontology (GO) terms (BP: Biological Process; CC: Cellular Component; and MF: Molecular Function), KEGG pathways, and the Swiss Prot (SP)-Protein Information Resource (PIR) keywords
Geneset/Pathway ID	Unique identifier of the GO gene set or KEGG pathway (functional annotation terms)
Term	Enriched annotation term associated with genes modulated by α-MSH
Count	Number of modulated genes involved in the process/function/pathway
%	Percentage of modulated genes involved in the process/function/pathway
***P* -value**	Significance of gene–term enrichment with a modified Fisher's exact test (EASE score)
Fold Enrichment	Magnitude of enrichment in the modulated genes
Benjamini Hochberg	Corrected enrichment *P* -value controlling for family-wide false discovery rate (FDR) by the Benjamini-Hochberg procedure. *P* -values corrected for FDR < 0.25 are highlighted in bold green.
Genes	Modulated genes involved in the process/function/pathway