SUPPLEMENTARY APPENDIX

Early growth response 1 regulates hematopoietic support and proliferation in human primary bone marrow stromal cells

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1. Supplemental Materials and Methods

BM-MNC isolation

Bone marrow mononuclear cells (BM-MNC) from BM aspiration samples were isolated by density gradient centrifugation (LSM 1077 Lymphocyte, PAA, Pasching, Austria) either with or without prior incubation with RosetteSep Human Mesenchymal Stem Cell Enrichment Cocktail (STEMCELL Technologies, Vancouver, Canada) for lineage depletion (CD3, CD14, CD19, CD38, CD66b, glycophorin A).

BM-MNCs from fetal long bones and adult hip bones were isolated as reported previously [1] by gently crushing bones (femora, tibiae, fibulae, humeri, radii and ulna) in PBS+0.5% FCS subsequent passing of the cell suspension through a 40-µm filter. Bone fragments were digested with 0.25% collagenase type I (STEMCELL Technologies) for 45 minutes at 37°C. Excess PBS was added to the solution and cells were filtered through a 40 µm filter. Then, cell suspensions were washed once with PBS+0.5% FCS and erythrocytes were lysed with IOtest 3 lysing solution (Beckman Coulter, Brea, California, United States) according to manufacturer's instructions.

Generation of EGR1 knockdown and EGR1 overexpressing stroma cells

Sorted BMSCs ($CD45^{-}CD271^{+}CD140a^{-}$) were cultured in standard MSC culture medium [StemMACS MSC Expansion Media, human (Miltenyi Biotec, Bergisch Gladbach, Germany) + 1% antibiotic-antimycotic solution (Sigma, St. Louis, USA)]. Medium was changed weekly and cells were passaged at 80% confluency after trypsinization (0.05% trypsin/EDTA, Invitrogen, Carlsbad, USA). EGR1 knockdown BMSCs, EGR1 overexpressing BMSCs and their respective controls were generated by infecting stromal cells (passage 2-4) with shEGR1-GFP, scramble control-GFP (both from OriGene, Rockville, United States), EGR1-

P2A-GFP and GFP-encoding lentivirus VSV-G (Virus Core Facility, Lund Stem Cell Center, Lund University, Lund, Sweden) at a MOI of 5. Lentiviral vectors carrying shEGR1 (TL313277) and scramble control (TR30021) were from OriGene. Three days after infection, GFP expressing cells were sorted by flow cytometry, followed by expansion in culture. For assessment of growth kinetics, population doubling times (PD) were calculated as PD = [culture duration] / [$\log_2$ (final cell number)-$\log_2$ (initial cell number)], with culture duration expressed in days.

Flow cytometry and fluorescence activated cell sorting (FACS)

Lineage-depleted BM-MNCs were incubated in blocking buffer [DPBS w/o Ca^{2+}, Mg^{2+}, 3.3 mg/ml human normal immunoglobulin (Gammanorm, Octapharm, Stockholm, Sweden), 1% FBS (Invitrogen)], followed by staining with monoclonal antibodies against CD271, CD140a, and CD45. Sorting gates were set according to the corresponding fluorescence-minus-one (FMO) controls and cells were sorted on a FACS Aria II or Aria III (BD Bioscience, Erembodegem, Belgium). Dead cells were excluded by 7-Amino-actinomycin (7-AAD, Sigma) staining and doublets were excluded by gating on FSC-H versus FSC-W and SSC-H versus SSC-W.

For sorting of BM cells for RNA-seq analysis, antibody incubations were performed in PBS/ 0.5% FCS for 20 minutes on ice in the dark. Cell populations of interest were sorted using a FACS Aria III Cell Sorter (BD). Dead cells were gated out using 7AAD (Stem-Kit Reagents) after MNC selection and doublets exclusion. Cells were directly sorted into 800µl Trizol (Ambion) for isolation of RNA for RNA-seq analysis. RNA for qPCR analysis of sorted cells was isolated as described below.

Cultured cells were harvested, washed, and unspecific binding was blocked with human normal immunoglobulin. Cells were stained (45 min, 4˚C) with combinations of antibodies and samples were analyzed on a LSRII or LSRFortessa (BD).

ROS levels were measured by incubating cells with CellROX Deep Red Reagent (Thermo Fisher Scientific, Waltham, USA) at a final concentration of 5 µM at 37°C for 30 minutes followed by FACS analysis.

Cell cycle analysis was performed by flow cytometry (LSRII, BD) using Lysis buffer with 10 µl/ml DAPI and Stabilization buffer according to the manufacturer's instruction (ChemoMetec, Lillerod, Denmark).

Antibodies

For FACS analysis and cell sorting the following antibodies were used: CD45-FITC (fluorescein isothiocyanate) (clone 2D1), CD34-FITC (clone 581), HLA-DR-FITC (clone L243), CD14-PE (clone MϕP9), CD19-PE (clone SJ25C1), CD73-PE (clone AD2), HLA-class I-PE (clone G46-2.6), CD90-APC (allophycocyanin) (clone 5E10), CD45-APC-Cy7 (clone 2D1), CD34-PE-Cy7 (clone 8G12) (all BD Bioscience), CD271-APC (clone ME20.4-1.H4, Miltenyi). Matching isotype controls were from BD Bioscience and R&D Systems. For unconjugated primary antibodies, goat anti-mouse IgG2a-FITC and goat anti-mouse IgM-FITC (Jackson ImmunoResearch Laboratories, Inc., Suffolk, UK) were used as secondary antibodies. Neutralizing antibody specific to CCL28 (clone MM0153-9G34), VCAM1 (clone B-K9) and IgG control (clone 15-6E10A7) were from Abcam (Cambridge, UK).

For RNA-seq cell sorting, the following antibody were used CD45 (clone HI30), CD271 (clone ME20.4), CD235a (clone HI264), CD31 (clone WM59), CD9 (clone HI9a) from Biolegend, and CD105 (clone SN6) from eBioscience.

CFU-F (colony-forming unit, fibroblast) assay

FACS-sorted cells were cultured at plating densities of 10-50 cells/cm^2 when assaying EGR1 knockdown and EGR1 overexpressing stromal cells and their respective controls. Colonies were counted after 14 days (1% Crystal Violet, Sigma). Generally, assays were set up in duplicates or triplicates.

***In vitro* differentiation assays**

Cultured BM mesenchymal stromal cells were differentiated towards the adipogenic, osteoblastic, and chondrogenic lineage as described previously [2]. Briefly, cells were cultured for 14 days in AdipoDiff medium (Miltenyi) and cells were stained with Oil Red O (Sigma). For osteogenic differentiation, cells were cultured in osteogenesis induction medium for 21 days and calcium depositions were detected by Alizarin Red staining (Sigma). Osteogenesis induction medium: standard MSC medium supplemented with 0.05 mM L-ascorbic-acid-2-phosphate (Wako Chemicals, Neuss, Germany), 0.1 µM dexamethasone and 10 mM β-glycerophosphate (both from Sigma).

Chondrogenic differentiation was induced by culturing cell pellets (2.5×10^5 cells/pellet) for 28 days in chondrogenesis induction medium. Chondrogenesis induction medium: DMEM-high glucose supplemented with 0.1 µM dexamethasone, 1 mM sodium pyruvate, 0.35 mM L-proline (all from Sigma), 0.17 mM ascorbic acid, 1% ITS+ culture supplements (BD Biosciences) and 0.01 µg/ml TGF-ß3 (R&D Systems).

Pellets were paraformaldehyde (PFA)-fixed, and frozen in O.C.T. Compound (Sakura, Zoeterwoude, Netherlands). Cryo sections were stained with antibodies against aggrecan, and nuclei were stained with 4',6-diamidino-2-phenylindole (DAPI, Invitrogen). Sections were

analyzed with an Olympus BX51 (Olympus, Solna Sweden) fluorescence microscope and a DP70 Olympus digital camera (DP manager software Version 1.1.1.71).

Cytokines

Stem cell factor (SCF), thrombopoietin (TPO), and FLT3-ligand (FLT3L), all at 25 ng/ml, [STF25] and 100 ng/ml of CCL28 were used in the CB co-culture expansion experiments. All growth factors were from Peprotech, Rocky Hill, USA.

Quantitative real-time PCR

RNA from sorted primary BM $lin^-CD45^-CD271^+CD140a^-$ and $lin^-CD45^-CD271^+CD140a^+$ and $lin^-CD45^-CD271^-CD140a^-$ populations was isolated from three individual donors. RNA was isolated using QIAshredder Homogenizers columns and the RNeasy Micro Kit (both from Qiagen, Hilden, Germany) according to the manufacturer's protocol. The concentration and purity of RNA was determined by Nanodrop (Thermo Fisher Scientific). cDNA was synthesized using SuperScript VILO cDNA synthesis kit (Life Technologies, Carlsbad, USA) on a C1000^{TM} Thermal Cycler (Bio-Rad, Hercules, CA, USA). Quantitative real-time PCR analysis was carried out using Fast SYBR master mix (Applied Biosystems by Life Technologies) according to the manufacturer's instructions. The crossing point of each sample was measured and analyzed with StepOne Software v2.1 (Applied Biosystems). Each gene-specific mRNA was normalized to the housekeeping gene *Glyceraldehyde 3-phosphate dehydrogenase (GAPDH)* mRNA. The expression of each mRNA was determined using the $2^{-\Delta\Delta CT}$ threshold cycle method.

ROS inbibitor treatment

For the ROS inhibition assay experiments, L-ascorbic acid, citric acid monohydrate, 4-Aminobenzoic acid, LY2228820, apocynin and N-acetylcystein (NAC) were added to the cultures. ROS inhibitors used: L-ascorbic acid (Sigma, St. Louis, USA) at 0.378 mg/ml, citric acid monohydrate (Thermo Fisher, Pittsburgh, USA) at 0.158 mg/ml, myeloperoxidase (MPO) blocker 4-Aminobenzoic acid (Sigma) at 100 µM, p38 mitogen-activated protein kinase (MAPK) inhibitor LY2228820 (Selleckchem, Houston, USA) at 500 nM, NAPDH oxidase inhibitor apocynin at 100 µM and N-acetylcystein (NAC) at 10 mM. Inhibitors were dissolved in dimethyl sulfoxide (DMSO) (Sigma, St. Louis, USA).

In vivo HSC repopulation assay

Eight- to twelve-week old NOD.Cg-PrkdcscidIl2rgtmlWjl/SzJ (NOD/SCID-IL2Rγc null; NSG) mice (Jackson Laboratory, Bar Harbor, USA) were sublethally irradiated (250 cGy) 6 hours prior to transplantation. The culture equivalent of 50,000 input $CD34^+$ cells of *ex vivo* co-cultured CB $CD34^+$ cells was injected intravenously and human hematopoietic engraftment was assessed 8, 12 and 16 weeks after transplantation by flow cytometry (human-specific antibodies against CD45, CD15/CD33/CD66b and CD19). All animal procedures were approved by the local ethical committee on animal experiments.

CCL28 ELISA

The levels of secreted CCL28 protein were quantified using the CCL28 Human ELISA Kit (Abcam, Cambridge, UK) according to the manufacturer's instructions. Culture supernatants were collected, centrifuged at 1,000× g for 15 min at 4° C, and assayed by ELISA. Microplate readings were analyzed with the SoftMax Pro 6.4 software (Molecular Devices, CA, USA).

Illumina microarray data analysis

Total RNA isolated from shEGR1-GFP, scramble-GFP, EGR1-OE-GFP and control-GFP stroma cells were subjected to a two-round amplification using the TargetAmp 2-round biotin-aRNA amplification kit (Epicentre Biotechnologies, Madison, USA). Microarray analysis was performed by the SCIBLU Swegene center at Lund University using Illumina Human HT-12 expression v4 BeadChips comprising of 48,107 probes according to the manufacturer's instructions. Microarray data were initially pre-processed and normalized using Quantile Normalization method [3]. These analyses were performed using GenomeStudio software V2011.1. Non-annotated probe sets and probe sets with signal intensities below the median of the negative control intensities in 20% of the samples that did not belong to one condition were excluded. To identify significantly differentially expressed genes between shEGR1-GFP and scramble-GFP cells, between EGR1OE-GFP and control-GFP cells, we used significance analysis of microarrays (SAM) method with the q value of 0 for the comparison between EGR1 OE and control-GFP and q value of 10 for the comparison between shEGR1-GFP and scramble-GFP cells [4]. SAM analyses were performed using TMEV v4.0 software [5]. Up and down-regulated genes were tested for enriched GO terms using DAVID Bioinformatics Resources 6.8.

RNA-seq

RNA of sorted cells was extracted according to the manufacturer's instructions for RNA isolation with GenElute LPA (Sigma). cDNA was prepared using the SMARTer procedure (SMARTer Ultra Low RNA Kit, Clonetech, Takara, St-Germain-en-Laye, France). Library preparation and RNA-seq was performed as previously described and validated for low input [6].

Proteome analysis

Non-transfected control, scrambled control and shEGR1 BM stromal cells were prepared for proteomic analysis as previously reported [7]. For sample preparation, cells were lysed with 0.1% RapiGest (Waters) in 100 µl 50 mM ammonium bicarbonate and extracted proteins were reduced/alkylated and digested with sequencing grade modified trypsin (Promega). Protein digests were differentially dimethyl labelled on columns as previously described [7]. Briefly, samples were labelled by flushing the columns with labelling reagent (light, intermediate or heavy using CH_2O + $NaBH_3CN$, CD_2O + $NaBH_3CN$ or $^{13}CD_2O$ + $NaBD_3CN$, respectively). Sample complexity was reduced by fractionation using OFFGEL isoelectric focusing (Agilent). The 12 fractions resolved were acidified and desalted with C18 Ultra-Micro SpinColumns (Harvard). Samples were reconstituted in 4% acetonitrile/0.1% formic acid prior to MS analysis.

MS analyses were carried out on an Orbitrap Fusion Tribrid MS system (Thermo Scientific) equipped with a Proxeon Easy-nLC 1000 (Thermo Fisher). On a 110 min gradient, one full scan spectrum from m/z 375 to 1500 at resolution 60,000 FWHM was followed by MS/MS scans (resolution 15,000 FWHM) of the most intense ions (up to 15) from the full scan MS.

MS raw data files were processed with MaxQuant (version 1.5.0.0) [8]. The derived peak list was searched using the in-built Andromeda search engine in MaxQuant against the Uniprot human database (downloaded 2016.10.13) together with 265 frequently observed contaminants (Andromeda configured database) and reversed sequences of all entries. A 1% false discovery rate (FDR) was required at both the protein level and the peptide level. Criteria for top differentially expressed proteins was set as the product of log2 ratios of shEGR1 to the two controls. The protein identification was reported as an indistinguishable "protein group" if no unique peptide sequence to a single database entry was identified.

Deposition of gene expression and proteomics data

Normalized illumina array data have been deposited in the GEO database (GSE122831). RNA-seq data can be accessed at the European Genome-phenome Archive: EGAS00001002736. The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE [9] partner repository with the dataset identifier PXD011767.

Primer sequences for qRT-PCR analysis*

GAPDH	F	5'- CACTCCACCTTTGACGC -3'
	R	5'- GGTCCAGGGGTCTTACTCC -3'
EGR1	F	5'- ACCCCTCTGTCTACTATTAAGGC-3'
	R	5'- TGGGACTGGTAGCTGGTATTG-3'
EGR2	F	5'- TCAACATTGACATGACTGGAGAG-3'
	R	5'- AGTGAAGGTCTGGTTTCTAGGT-3'
EGR3	F	5'- GCGACCTCTACTCAGAGCC-3'
	R	5'- CTTGGCCGATTGGTAATCCTG-3'
EGR4	F	5'- GGAGGCTCGTTTTCCCGTAAT-3'
	R	5'- TGGGATAGAGTCTGTTGGCTG-3'

*All primers were obtained from Life Technologies.

2. Supplemental Figures

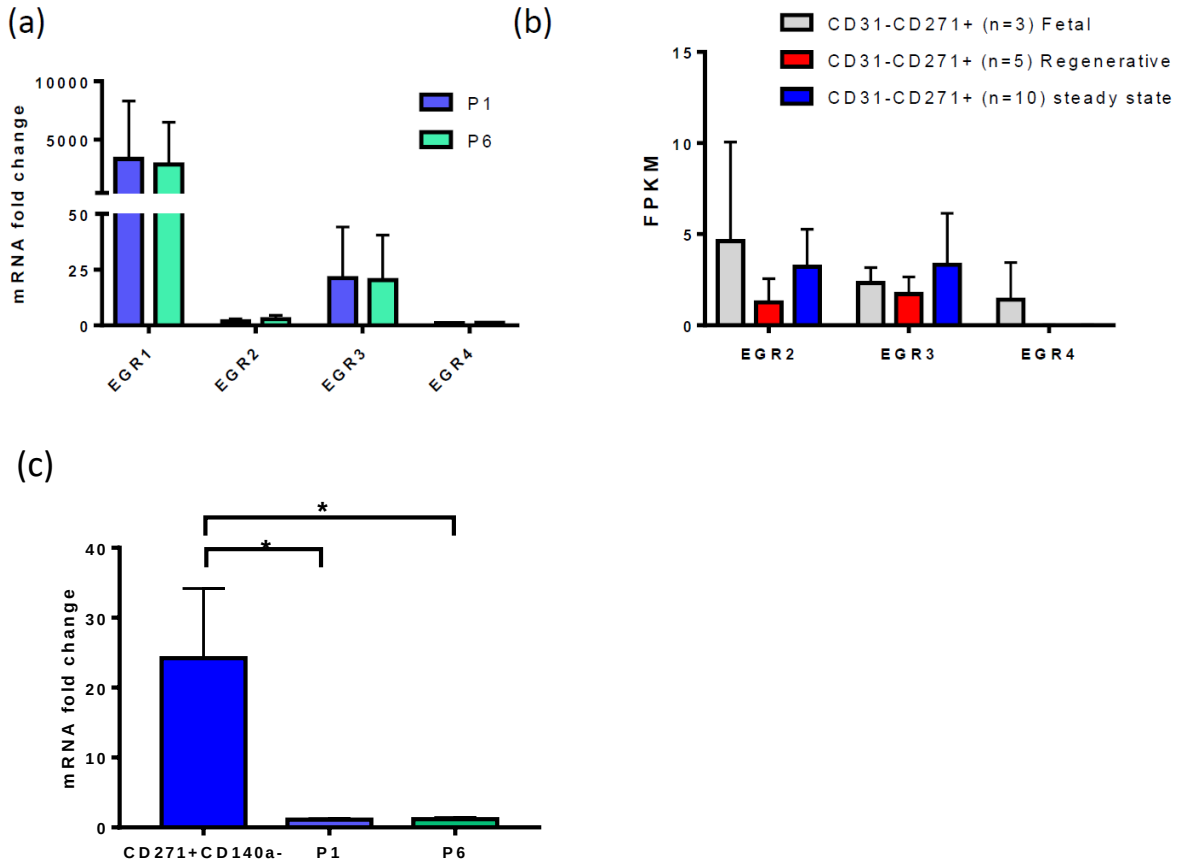

Figure S1

(a) Quantitative rtPCR of EGR1-4 expression in passage 1 (P1) and passage 6 (P6) BMSCs. Results are shown as fold mRNA change after standardizing with GAPDH levels. Data are shown as mean ± SD (n=3). (b) Transcript analysis by massive parallel RNA sequencing of EGR2-4 expression in BMSCs ($CD31^-CD271^+$) isolated from human fetal, regenerative and steady-state BMSCs. Data are shown as mean ± SD for (a) and mean ± SEM for (b), n=3-10. (c) EGR1 expression differences in freshly isolated $Lin^-/CD45^-/CD271^+/CD140a^-$ compared to cultured stromal cells in passage 1 (P1) and passage 6 (P6). Gene expression is calculated relative to P1 MSCs. Data are shown as mean ± SD (n=3). *:$p< 0.05$

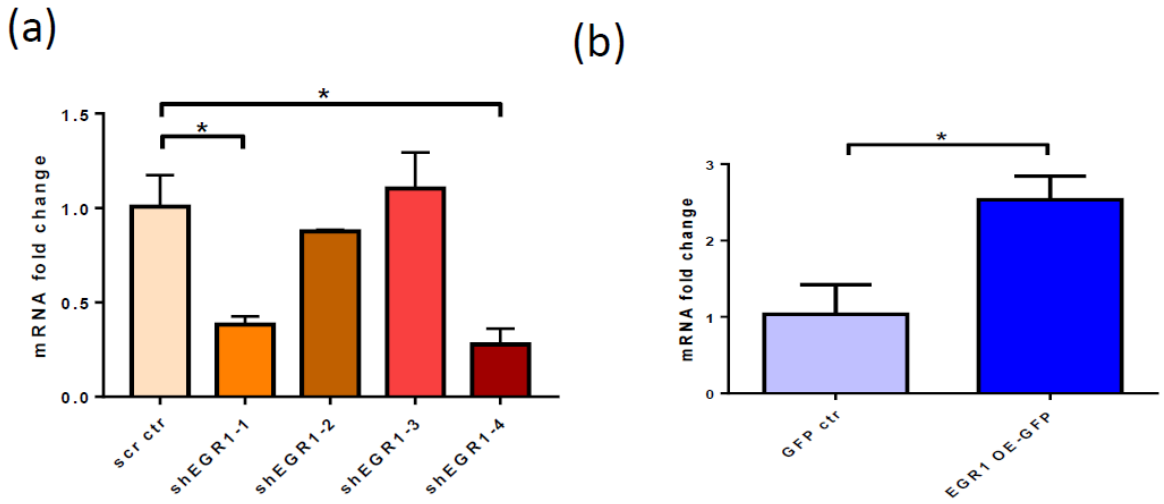

Figure S2

Quantitative rtPCR of EGR1 expression in BMSCs 72 h after infection with lentiviral particles encoding shEGR1 1-4 (a) or EGR1 overexpression plasmid (b). Data are shown as mean ± SD (n=3). *:$p< 0.05$

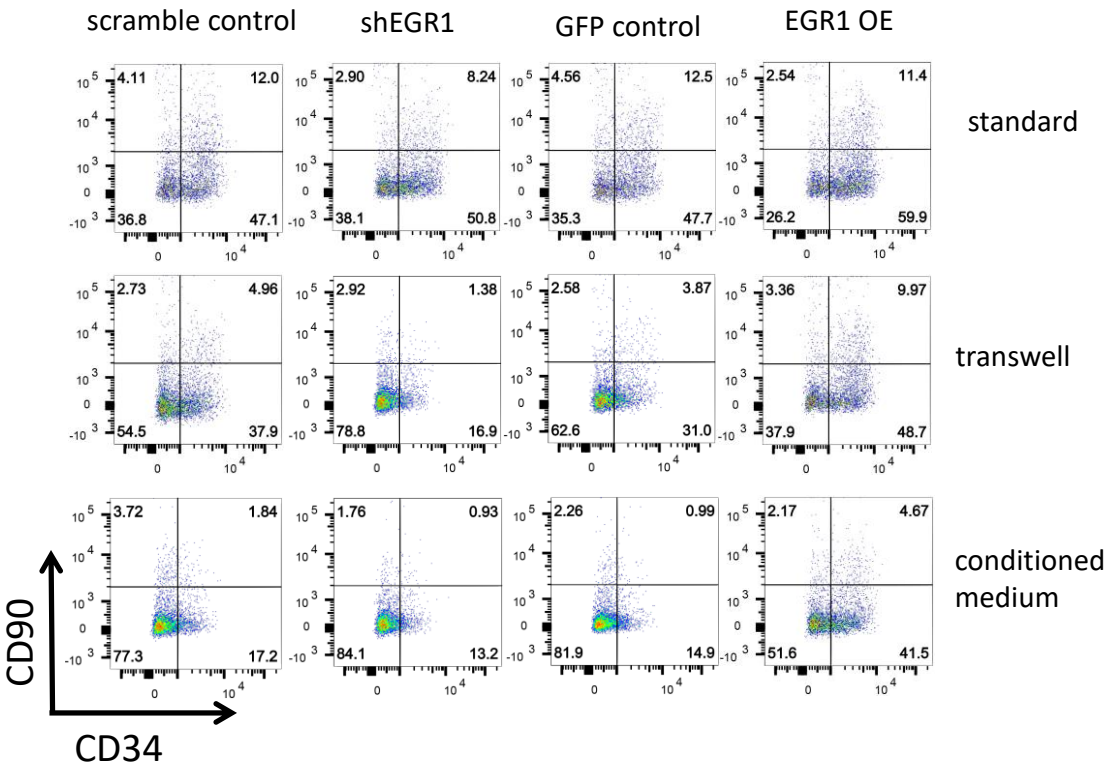

Figure S3

Five thousand cord blood CD34$^+$ cells were co-cultured for 4 days with 10,000 bone marrow derived feeder MSCs transfected with scramble control, shEGR1, GFP control and EGR1 overexpression plasmids, respectively, in SFEM supplemented with 25 ng/ml of SCF, TPO and Flt3L. Co-cultures were performed in either standard culture plates (standard) or transwell culture plates with the MSCs in the bottom well and CD34$^+$ cells in the insert (transwell). For conditioned medium cultures, 10,000 bone marrow derived MSCs transfected with scramble control, shEGR1, GFP control and EGR1 overexpression plasmids, respectively, were cultured with 200 µl SFEM supplemented with 25 ng/ml of SCF, TPO and Flt3L for four days. Conditioned media was collected and used to stimulate cultures with CB CD34$^+$ cells (without feeder cells). Representative FACS profiles of co-culture generated cells are shown.

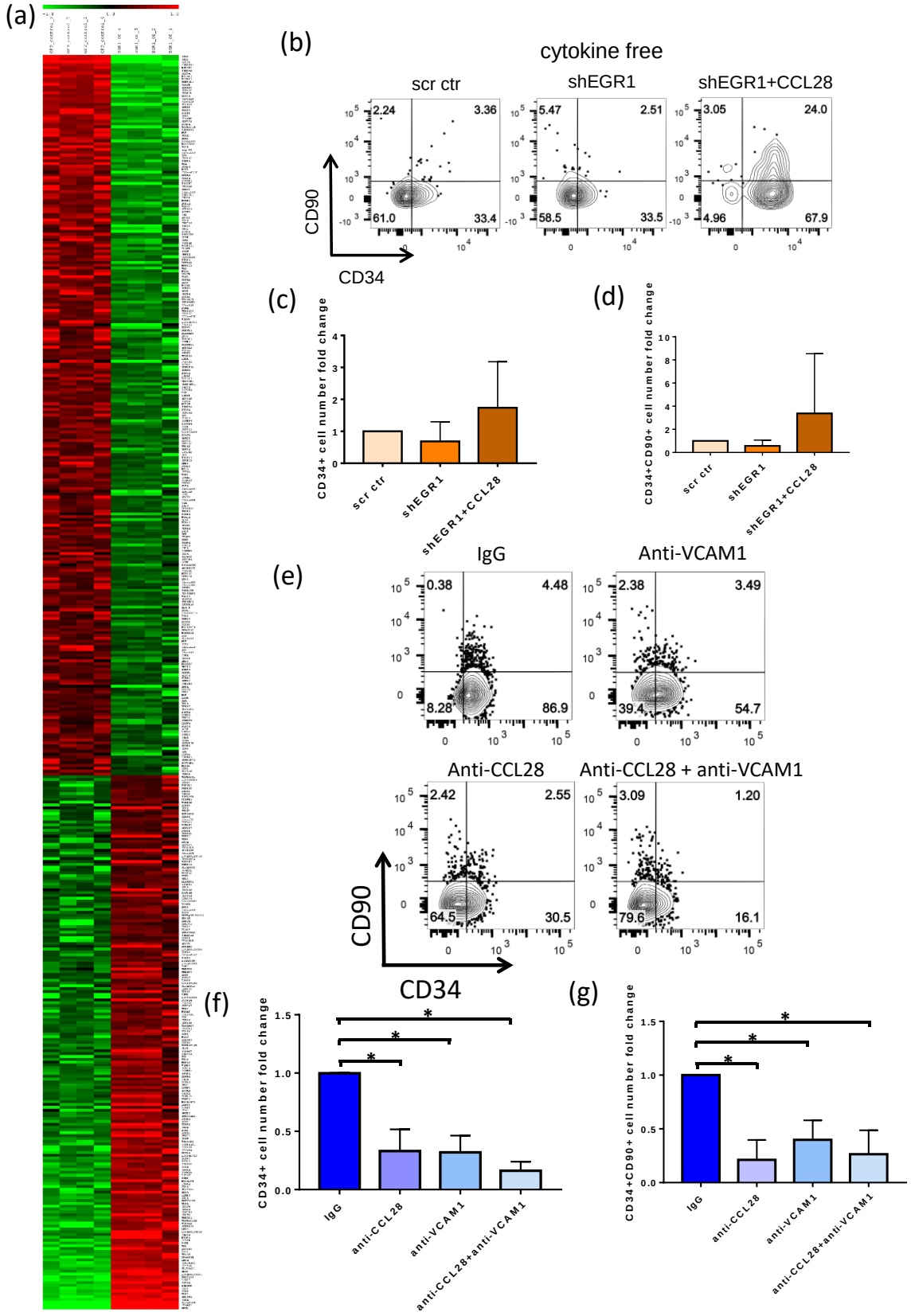
(a)
(b)
cytokine free
scr ctr
shEGR1
shEGR1+CCL28
2.24
3.36
61.0
33.4
5.47
2.51
58.5
33.5
3.05
24.0
4.96
67.9
CD90
CD34
(c)
CD34+ cell number fold change
scr ctr
shEGR1
shEGR1+CCL28
(d)
CD34+CD90+ cell number fold change
(e)
IgG
Anti-VCAM1
0.38
4.48
8.28
86.9
2.38
3.49
39.4
54.7
Anti-CCL28
Anti-CCL28 + anti-VCAM1
2.42
2.55
64.5
30.5
3.09
1.20
79.6
16.1
CD90
CD34
(f)
CD34+ cell number fold change
IgG
anti-CCL28
anti-VCAM1
anti-CCL28+anti-VCAM1
(g)
CD34+CD90+ cell number fold change

Figure S4

(a) Heatmap of significantly up- and down-regulated genes in EGR1 overexpressing cells versus controls. (b-d) 5,000 cord blood $CD34^+$ cells were co-cultured for 4 days with 10,000 bone marrow derived feeder stromal cells transfected with scramble control and shEGR1 plasmids, respectively, in cytokine-free culture condition supplemented with or without 100 ng/ml CCL28. (b) Representative FACS profiles of co-culture generated cells in cytokine-free culture. The type of feeder cells is indicated on top of the FACS plots in. (c,d) Fold change of total numbers of $CD34^+$ cells and $CD34^+CD90^+$ cells produced in cytokine-free cultures. (e-g) 5,000 cord blood $CD34^+$ cells were co-cultured for 4 days with 10,000 EGR1 overexpressing cells as feeder cells in cytokine-free culture condition supplemented with neutralizing antibody against CCL28, VCAM1 and IgG control (all at 100 ng/ml) for 4 days. (e) Representative FACS profiles of co-culture generated cells. Total number of $CD34^+$ cells (f) and $CD34^+CD90^+$ cells (g) produced in the co-cultures without/with neutralizing antibodies as indicated by the x-axis label. *:$p< 0.05$

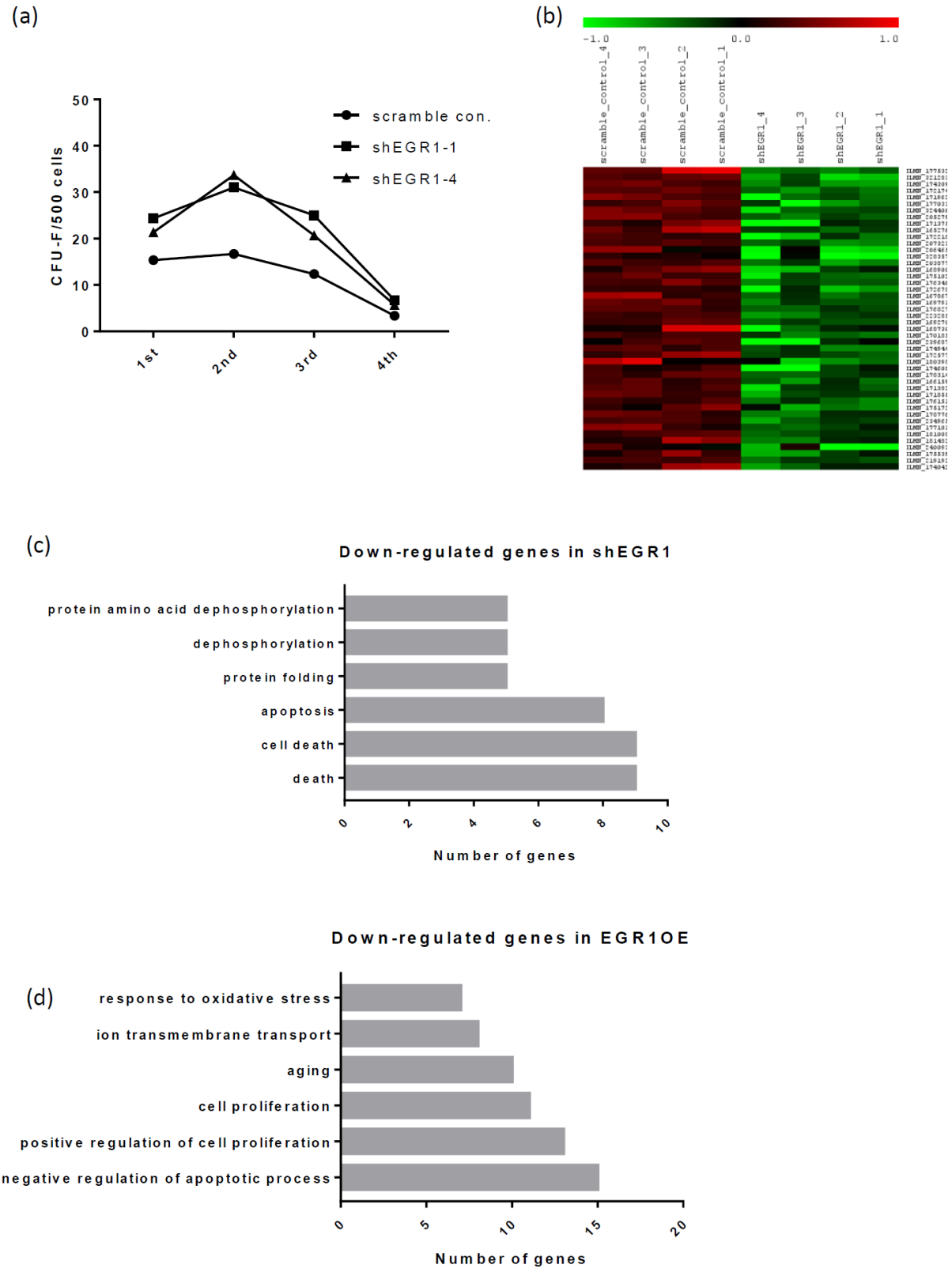
(a)
CFU-F/500 cells
50
40
30
20
10
0
1st
2nd
3rd
4th
scramble con.
shEGR1-1
shEGR1-4
(b)
-1.0
0.0
1.0
scramble_control_4
scramble_control_3
scramble_control_2
scramble_control_1
shEGR1_4
shEGR1_3
shEGR1_2
shEGR1_1
(c)
Down-regulated genes in shEGR1
protein amino acid dephosphorylation
dephosphorylation
protein folding
apoptosis
cell death
death
0
2
4
6
8
10
Number of genes
Down-regulated genes in EGR1OE
(d)
response to oxidative stress
ion transmembrane transport
aging
cell proliferation
positive regulation of cell proliferation
negative regulation of apoptotic process
0
5
10
15
20
Number of genes

Figure S5

(a) EGR1 knockdown cells were harvested after 14 days and replated for CFU-F assay for four times. Representative CFU-F frequencies of three different experiments are presented as mean ± SD. * $p<0.05$. (b) Heatmap of significantly down-regulated genes in EGR1 knockdown cells versus controls. (c) Biological process annotations for down-regulated proteins in EGR1 knockdown cells and (d) EGR1 overexpressing cells were identified using the DAVID Bioinformatics Resources 6.8.

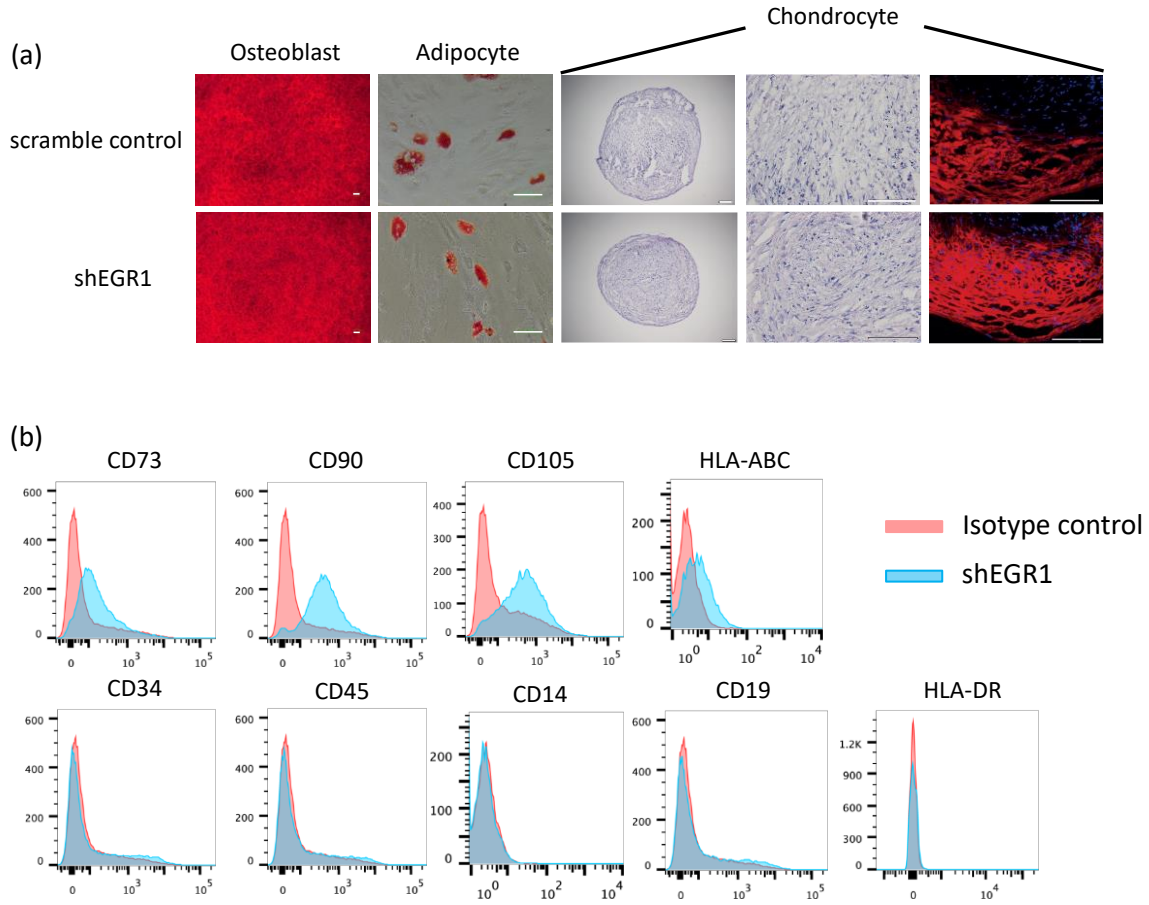

Figure S6

(a) Trilineage *in vitro* differentiation potential of EGR1 knockdown cells and controls. A representative set of pictures from a total of three replicates for each differentiation experiment is shown. Osteoblasts and adipocytes were stained with Alizarin red and oil-red-O, respectively. Chondrocyte pellets were stained with hematoxylin-eosin (HE) (left and middle panel) and antibodies against aggrecan (right panel). Scale bars represent 100 µm for all images. Differentiation capacity of EGR1 overexpressing cells could not be investigated due to insufficient cell numbers. (b) Typical BMSC surface marker profile of EGR1 knockdown cells; a representative set of data of a total of three experiments is shown. Blue: EGR1 knockdown cells; red: corresponding isotype control.

3. Supplemental Tables

Table S1. Up-regulated genes in EGR1 overexpressing cells

Gene name	Fold change*
HEYL	24.04682
LOXL4	5.469145
LOC100132805	5.333917
CRABP2	5.082554
FLJ40504	4.693288
CALCA	4.670778
ABLIM1	3.824112
HBA2	3.692209
SYN1	3.563409
SYT7	3.545673
GSTA1	3.504459
LOC646723	3.429366
TMEM130	3.394655
PDPN	3.379174
TUBA4A	3.363236
DLX3	3.342427
ANKRD38	3.334845
PRAGMIN	3.32348
CCL28	3.297285
RPUSD2	3.155637
MFAP4	3.100745
CRLF1	3.060728
COL8A2	3.015144
LOC100134259	3.014138
HES4	2.998961
SEPT5	2.925093
RAB40B	2.9152
PCNX	2.871909
CPA4	2.855123
CDK5RAP2	2.813803
LITAF	2.739239
FLJ20021	2.733041
TNC	2.722391
CPSF4	2.720022
MARCH6	2.71634
NRCAM	2.692568
MGC4294	2.668485
EXTL1	2.659776
FBXO2	2.639293
LMO4	2.637843

DUSP6	2.633063
SLC29A1	2.596552
LMO4	2.585314
CCT6B	2.559732
TNFRSF10D	2.525184
COL8A2	2.497526
DIO2	2.4887
CCDC80	2.481945
RBM15	2.478366
SH3PXD2A	2.456376
ENPP2	2.450576
HLX1	2.445158
ADSS	2.396962
CENTD3	2.341444
P2RX6	2.333991
TMEM91	2.333142
TNFRSF21	2.32309
LEMD3	2.32143
RIMKLB	2.314856
TNC	2.300494
CCNB1IP1	2.295839
GOLGA7	2.283916
TMEM99	2.268274
SPG3A	2.262277
CXCL16	2.255413
TACSTD2	2.254667
SPG3A	2.250582
ITPK1	2.24732
GOT1	2.231113
ATL1	2.224798
AFAP1	2.21616
UPP1	2.207567
MRPS6	2.196855
KLHL29	2.188431
JAG1	2.179362
TMEM126B	2.176408
GLDN	2.171981
RYBP	2.161275
PPP1R8	2.148596
DUSP14	2.130284
FSTL3	2.118973
ENPP2	2.115292
HAPLN1	2.108836
CAV1	2.105571

NCBP2	2.103025
PRKCD	2.095128
LFNG	2.091684
DCBLD2	2.082522
ATP6V1E2	2.071519
FLJ10916	2.062291
WDR19	2.05977
EDNRA	2.044538
COL22A1	2.024462
ERRFI1	2.011895
RAB22A	2.011799
MYH10	2.007465
LPHN2	2.006611
ROR2	2.005633
MGC15476	1.995416
CX3CL1	1.994451
MIZF	1.986694
LOC728006	1.973569
ABI2	1.969274
PTHR1	1.96808
AGPS	1.957946
ST3GAL5	1.956943
ALOX5AP	1.954736
HSPA12A	1.95364
C14ORF132	1.952735
SMYD3	1.949609
SC4MOL	1.947637
FLJ10986	1.944654
IGFBP2	1.936061
GLCE	1.930212
BHLHB3	1.928226
VASH1	1.927925
PRMT3	1.92763
BRPF1	1.926086
VDP	1.924077
TIMP3	1.90994
TNFRSF10B	1.907431
NPM3	1.903561
HSPB8	1.898188
LRRC32	1.897707
PRICKLE1	1.895564
RPL15	1.891342
TUBB2B	1.891338
LOC389662	1.884076

C16ORF80	1.878068
LRRC54	1.865839
SEC22A	1.861806
FBLN2	1.853324
LASS5	1.853191
KCNG1	1.851116
LOC402055	1.84924
LOC100129599	1.84588
NSMAF	1.844945
GCNT1	1.837608
PHLDA2	1.833745
TTC5	1.832985
ETS1	1.831743
TSPYL2	1.823639
ACVR1	1.821737
ATP6V0A2	1.819122
YRDC	1.817355
PHF13	1.810271
RWDD2A	1.809382
C6ORF64	1.801124
PTPLB	1.795147
ADCY3	1.793846
VCAM1	1.792743
LOC647150	1.790474
TEX2	1.788576
TMEM97	1.7878
INTS10	1.786562
FGGY	1.785374
C8ORF76	1.775816
CXXC5	1.774037
DAB2	1.771974
RRN3	1.766272
ZNF407	1.763096
THUMPD3	1.762694
EGFLAM	1.762673
PRPS2	1.75994
ATL1	1.757244
GNA12	1.75662
ZFAND5	1.740144
ZNF365	1.738365
FBLN2	1.733752
YWHAZ	1.726912
POLE3	1.726341
LOC100129759	1.725305

RDH13	1.721423
RPL9	1.721108
LOC730098	1.718807
UBL3	1.716626
DKFZP761P0423	1.716354
TRIP12	1.709918
PLAC9	1.705565
KIAA0649	1.69279
PRKAA1	1.688524
HNRPDL	1.679661
FAM131A	1.675193
BACE2	1.672757
NRCAM	1.666867
ZNF207	1.666276
PLEKHC1	1.663113
PLXNB1	1.630995
FAM119B	1.602944

Table S2. Down-regulated genes in EGR1 knockdown cells

Gene name	**Fold change***
MTG1	0.4651335
GLUD1	0.49536812
LOC728139	0.5112009
VCAN	0.51561624
CXorf40A	0.5266048
RABEP1	0.5286921
MCL1	0.53835016
RPAIN	0.54282737
IGFBP3	0.5483111
LOC647276	0.5512289
XRCC6	0.5516438
C2orf56	0.5568179
TNFRSF12A	0.560885
C9orf69	0.56164235
RNASEH1	0.5644487
LOC440589	0.56846654
ATPBD1B	0.57813084
SLC37A4	0.5794197
COL4A2	0.5830043
NONO	0.5833543
SERPINH1	0.5835326
NRP2	0.59852964
RPS9	0.6036461

TAGLN	0.6049642
DNAJC12	0.6092027
FTHL12	0.6101501
AMY1C	0.6101859
ALDH7A1	0.6108177
FTL	0.6123927
LOC649049	0.6131814
WHSC1L1	0.613947
LOC646294	0.61468005
LOC646723	0.61522424
M6PRBP1	0.6191784
PTGES	0.619627
AHSA1	0.6199522
ARL2BP	0.6229743
MIPEP	0.62435114
CAB39	0.627086
POLR2D	0.6271075
YWHAQ	0.62757957
C9orf50	0.62804794
PHF5A	0.6306418
CDS2	0.63101745
PARP12	0.6341547
TAF1C	0.6348977
PPP1CC	0.63563496
PTPRM	0.6360393
FAP	0.63685125
HEATR1	0.63895655
CXorf40B	0.6391185
MTMR4	0.63995576
DDIT4	0.64001524
TSPO	0.64432764
LSM12	0.64659804
ARPC1A	0.6480679
ILF2	0.6497163
EIF4G2	0.6502523
DCUN1D2	0.6505436
COBRA1	0.65230817
POP1	0.6526774
PTK2	0.6546412
RPS4Y1	0.6546739
HSPA8	0.65502083
WDR71	0.6567855
BFAR	0.65868634
PTP4A2	0.66107935

CSRP2BP	0.66213995
LOC91461	0.6639797
MOCOS	0.6648766
LOC441775	0.6654071
GOT2	0.6665561
ACLY	0.66721296
PEBP1	0.6686973
TIGD5	0.6689023
PTPRK	0.670189
SURF4	0.67073953
RGMB	0.6738465
MYC	0.6739198
ABCF3	0.674448
LOC653888	0.6751951
EIF3EIP	0.67540044
GLO1	0.675774
TBRG4	0.6768825
C9orf6	0.67795897
MAP3K4	0.6812834
LBH	0.6816504
LOC285176	0.6857253
GRN	0.68770385
LOC644029	0.68839926
EFCAB4A	0.69079137
MPDU1	0.6982763
PPIE	0.7070499

Table S3. Down-regulated genes in EGR1 overexpressing cells

Gene name	**Fold change***
CDC20	0.15815102
GAS6	0.24462053
MICAL1	0.2514341
CD24	0.27618173
SEPT4	0.28452358
FBLN1	0.28896004
FHOD3	0.33932027
CABLES1	0.34277028
SLC1A3	0.34325686
FEZ1	0.34732097
VEGFB	0.3489335
PODXL	0.36104074
GPRC5C	0.36204252
ITGA10	0.36207664

C10ORF116	0.366149
EHBP1L1	0.3680063
MAP4K2	0.36807543
TK1	0.36876675
TNFRSF14	0.3702543
RARRES3	0.37226787
ZNF34	0.3805235
NQO1	0.38100612
KIAA1199	0.38758293
S100A10	0.38770238
IL18BP	0.39480674
DDIT4	0.39773726
CKAP2L	0.3984352
ANKRD9	0.3992384
STC2	0.4000877
CRIP1	0.4026607
PRC1	0.40315002
ZNF775	0.40633786
FAM64A	0.4097832
IDH2	0.41060326
NUSAP1	0.4106741
MVP	0.41083208
GRK5	0.41301152
TCIRG1	0.41523704
ANXA11	0.41602263
ENG	0.41648003
TAGLN2	0.4168468
DDEFL1	0.41987488
ANPEP	0.42208642
MGC87042	0.42436945
UBE2C	0.4254324
COL8A1	0.42639893
DNAL4	0.43305585
PTTG1	0.43606496
CRISPLD2	0.4374978
SIDT2	0.4375223
TMEM158	0.4397441
FAM39DP	0.44066033
LOC649366	0.441047
AKR1C3	0.44206282
FARP1	0.44781372
NPR2	0.44874227
BCAS4	0.4491407
ARSD	0.44963104

TGFB1I1	0.45258313
PLK4	0.45277795
TKT	0.45310432
IFI30	0.45592034
RAB3IL1	0.46130627
MT1A	0.4619316
ARHGDIA	0.46426922
GPI	0.46708283
ATOH8	0.46718782
NUDT1	0.46728435
KCNMB1	0.46744573
MCM7	0.46810037
GPSM2	0.46980724
ACTN4	0.47453827
C17ORF68	0.4781475
EPDR1	0.48006555
CCNB2	0.4811842
CFD	0.48141733
RNF150	0.48448664
PLEKHH3	0.48503172
CHST14	0.48529178
EMP3	0.48589405
TRPV2	0.48595846
ADCY4	0.48602852
NT5C	0.48680586
PTGES	0.48859593
MOV10	0.4891507
SGSH	0.48998314
AURKA	0.49018893
SCNN1D	0.49079683
CLIC1	0.4909556
C11ORF80	0.49207956
MRPL23	0.49284706
P2RX4	0.49391636
TRPM4	0.4951819
CLTB	0.49571034
ATP6V0E2	0.49876997
C10ORF10	0.5009529
PRR6	0.5039548
PLAUR	0.5072452
ACSL5	0.5081115
MSRB2	0.5081497
MUTYH	0.51013297
WDR51A	0.5104153

GINS2	0.5131264
FADS1	0.5139733
DHRS3	0.51461667
C7ORF10	0.51580465
TBC1D2B	0.5166551
LARGE	0.5176216
ENO3	0.51925373
BCL2L1	0.5207038
STMN3	0.52117985
TFDP1	0.5216644
KIAA1644	0.5226889
SLC15A3	0.5227549
PEX16	0.52379847
CXCL12	0.5237991
BRI3	0.5244612
AXL	0.52471435
TBL1X	0.5251542
PLEKHQ1	0.5264136
SERPINF1	0.5277494
NME3	0.52857774
ALG9	0.5301495
SMPD1	0.53085303
PGD	0.53159475
IGFBP4	0.5320994
TALDO1	0.53260577
HCFC1R1	0.5333419
UNC93B1	0.53511024
ALDOA	0.5357041
FVT1	0.53790134
PUM1	0.5390357
IRAK1	0.5391665
TRIP13	0.5391793
PHF11	0.53965515
LOC644096	0.54054904
HNT	0.54165065
HLA-E	0.54217863
KRT81	0.5422072
EIF2B4	0.54266125
ICMT	0.54313856
LOC653210	0.54332876
FUCA1	0.54445845
C22ORF25	0.5446214
WDR71	0.5462399
TINF2	0.5463321

LTBR	0.54634225
TSPO	0.54718184
FHOD1	0.5475933
NINJ1	0.54775155
NRP1	0.5481697
PGLS	0.54995143
RRAS	0.5519728
ATP2A2	0.55233675
ARHGAP23	0.5541292
C9ORF142	0.5543595
CSTB	0.55454576
OGFR	0.55467445
CD320	0.5556943
SFXN5	0.5567052
C10ORF33	0.5568497
IFITM2	0.5569963
TUBB3	0.55735517
SORT1	0.5582776
FAM89A	0.5589613
LENG4	0.5607092
MGAT1	0.5610538
ISG15	0.56164014
WDR22	0.5651484
DTX3	0.56575805
MT2A	0.56733793
SCARA3	0.5676039
LAMA4	0.56816703
LRFN4	0.5692356
SIN3A	0.56927943
SECISBP2	0.5693249
CPT1A	0.5697325
CENTA1	0.5704499
RALY	0.5709072
ZNF341	0.5712033
CCDC16	0.5724743
CD99	0.5749912
CCT5	0.5762109
SEPX1	0.5763557
FXYD5	0.5769112
PLEC1	0.57705307
HMOX1	0.57863784
ABCC10	0.57867277
ATP2B4	0.57875115
CYB5R3	0.5794876

ECGF1	0.5807397
VIM	0.5823382
C20ORF55	0.5834289
FKSG30	0.58455724
ZFYVE19	0.584842
COMMD9	0.5849753
ACTB	0.5851506
IDE	0.58596903
PHF19	0.5877516
MRPL12	0.588378
CFL1	0.5883804
ADAM19	0.58854985
ANKS3	0.58895904
SLC7A6	0.5892533
ZSWIM4	0.58998704
RPS6KA2	0.5903171
CD44	0.59168845
NMB	0.5917483
PKM2	0.5934822
DCN	0.59394175
MOBKL2A	0.59471256
SLC35C1	0.5953934
FRAP1	0.59569556
ZBTB25	0.5968993
TUSC4	0.5973328
FAM129B	0.5978567
C1ORF102	0.59791
DNAJC12	0.5983575
IDH3G	0.59981424
HABP4	0.6004926
PAOX	0.6012136
EGFR	0.60265356
RC3H2	0.60266393
APOBEC3F	0.60370135
C6ORF47	0.60376835
SERINC3	0.604318
VEZF1	0.6046357
LRRC20	0.6047029
NBL1	0.60799634
ARHGDIB	0.6083563
MRGPRF	0.61021346
MGC16824	0.61232674
NRM	0.61590964
CALR	0.61610484

MVD	0.61764866
CIB1	0.6209554
RIPK1	0.62136376
TACC3	0.62401336
CAPNS1	0.62542814
FBXW5	0.62582606
PSMD4	0.6285216
DDX54	0.6328575
MED16	0.63317823

* Fold change represents the difference of the mean gene expression intensity in EGR1 overexpressing cells or EGR knock-down cells compared to control cells. Gene expression analysis was performed on sorted cells from four donors.

Table S4. Up-regulated proteins in EGR1 knockdown cells

Protein names	Gene names	Fold change (shEGR1/NT normalized)	Fold change (shEGR1/ scrambled normalized)
Acetyl-CoA acetyltransferase, cytosolic	ACAT2	11.795	7.088
Leucine-rich repeat-containing protein 15	LRRC15	4.592	5.321
Transmembrane protein 205	TMEM205	14.703	2.405
Protein kinase C iota type	PRKCI	6.053	2.442
Serine palmitoyltransferase 1	SPTLC1	5.248	2.572
DNA replication licensing factor MCM3	HCC5;MCM3	1.946	9.482
Insulin receptor substrate 1	IRS1	2.659	4.460
Serine/arginine-rich splicing factor 3	SRSF3;SFRS3	3.535	3.101
Eukaryotic translation initiation factor 1A, X-chromosomal; Eukaryotic translation initiation factor 1A, Y-chromosomal	EIF1AX; EIF1AY	10.586	1.791
Chondroitin sulfate proteoglycan 4	CSPG4	3.194	3.241
DNA replication licensing factor MCM5	MCM5	2.639	3.951
Pre-mRNA-processing factor 19	PRPF19	2.905	3.459
Condensin complex subunit 2	NCAPH	2.224	4.762
Secretory carrier-associated membrane protein 1	SCAMP1	3.133	2.938
	TPCN1	3.571	2.616
Transcription elongation factor B polypeptide 1	TCEB1	2.811	3.066
Hematological and neurological expressed 1-like protein	HN1L	2.962	2.626
DCC-interacting protein 13-beta	APPL2	2.725	2.845
SEC23-interacting protein	SEC23IP	8.377	1.590
	TPM4	2.929	2.423
Exocyst complex component 5	EXOC5	2.719	2.561
Protein FAM50B;Protein FAM50A	FAM50A;FAM 50B	2.909	2.386
High mobility group protein 20A	HMG20A	2.107	3.341
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 5	NDUFAF5	2.380	2.768
Survival of motor neuron-related-splicing factor 30	SMNDC1	2.312	2.732
N-terminal kinase-like protein	SCYL1	6.760	1.551
Guanine nucleotide-binding protein G(q) subunit alpha	GNAQ	3.964	1.837
Peptidyl-prolyl cis-trans isomerase;Peptidyl-prolyl cis-trans isomerase G	PPIG	2.507	2.458
Nucleolysin TIA-1 isoform p40	TIA1	2.130	2.740

E3 ubiquitin-protein ligase TRIP12	TRIP12	4.268	1.689
E3 ubiquitin-protein ligase;E3 ubiquitin-protein ligase Itchy homolog	ITCH	12.343	1.350
Breast cancer anti-estrogen resistance protein 1	BCAR1	3.332	1.863
Transformer-2 protein homolog beta	DKFZp686F18120;TRA2B	2.088	2.735
DnaJ homolog subfamily C member 7	DNAJC7	2.928	1.967
Replication factor C subunit 5	RFC5	2.429	2.148
Liprin-beta-1	PPFIBP1	2.679	1.982
Protein pelota homolog	PELO	2.283	2.235
Casein kinase II subunit beta	CSNK2B;CSNK2B-LY6G5B-1181;CSNK2B-LY6G5B--991	1.739	3.237
Cadherin-2	CDH2	2.427	2.079
Overexpressed in colon carcinoma 1 protein	OCC1;C12orf75	2.195	2.277
Transmembrane protein 119	TMEM119	1.798	2.946
28S ribosomal protein S35, mitochondrial	MRPS35	5.750	1.432
Sickle tail protein homolog	KIAA1217	2.099	2.329
NHS-like protein 1	NHSL1	1.743	3.089
WD repeat-containing protein 26	WDR26	1.847	2.703
Zinc finger MYM-type protein 3	ZMYM3	2.136	2.200
DNA replication licensing factor MCM7	MCM7	1.466	4.606
Serine/arginine-rich splicing factor 2	SRSF2;SFRS2	1.891	2.495
28S ribosomal protein S18b, mitochondrial	MRPS18B	2.508	1.884
Nuclear autoantigenic sperm protein	NASP	3.557	1.569
Sepiapterin reductase	SPR	1.603	3.348
40S ribosomal protein S27-like;40S ribosomal protein S27	RPS27L;RPS27;LOC392748	2.873	1.705
Discoidin domain-containing receptor 2	DKFZp686D1354;DDR2	2.532	1.828
Putative E3 ubiquitin-protein ligase UBR7	UBR7	2.375	1.900
DNA-directed RNA polymerase II subunit RPB1	POLR2A	1.378	5.520
Stathmin	STMN1	2.589	1.777
Protein ELYS	AHCTF1	1.397	4.959
Putative protein phosphatase inhibitor 2-like protein 3;Protein phosphatase inhibitor 2	PPP1R2;PPP1R2P3	1.949	2.215
Nucleolar transcription factor 1	UBTF	3.444	1.536
Huntingtin-interacting protein 1	HIP1	1.918	2.248
Syncoilin	SYNC	2.114	1.998
HEAT repeat-containing protein 5B	HEATR5B	1.894	2.247

Ubiquitin-associated protein 2	UBAP2	2.210	1.910
Talin-2	TLN2	2.156	1.946
Nuclear migration protein nudC	NUDC	2.050	2.027
Na(+)/H(+) exchange regulatory cofactor NHE-RF2	SLC9A3R2	1.896	2.210
CD2 antigen cytoplasmic tail-binding protein 2	CD2BP2	2.088	1.987
CLIP-associating protein 1	CLASP1	1.928	2.152
Urokinase plasminogen activator surface receptor	PLAUR	2.460	1.748
Lysine-specific demethylase 3B	JMJD1B;KDM3B	2.928	1.586
Structural maintenance of chromosomes protein 1A	SMC1A;DKFZp686L19178	2.093	1.950
Ras GTPase-activating protein nGAP	RASAL2	1.775	2.360
Breast cancer anti-estrogen resistance protein 3	BCAR3	2.987	1.568
Protein SON	SON	2.319	1.793
Stathmin;Stathmin-2	STMN2	1.953	2.082

Table S5. Down-regulated proteins in EGR1 knockdown cells

Protein names	**Gene names**	**Fold change (shEGR1/NT normalized)**	**Fold change (shEGR1/ scrambled normalized)**
Ras-related protein Rab-32	RAB32	0.214	0.114
Glutaminase kidney isoform, mitochondrial	GLS	0.186	0.152
NHP2-like protein 1;NHP2-like protein 1, N-terminally processed	NHP2L1	0.245	0.143
Ganglioside-induced differentiation-associated protein 2	GDAP2	0.043	0.448
Protein Niban	FAM129A	0.346	0.120
Eukaryotic translation initiation factor 4E	EIF4E	0.250	0.211
HLA class I histocompatibility antigen, alpha chain E	HLA- E; HLA-B	0.198	0.306
Mammalian ependymin-related protein 1	EPDR1; UCC1	0.308	0.210
Neuropathy target esterase	PNPLA6	0.131	0.406
Thioredoxin domain-containing protein 17	TXNDC17	0.276	0.289
Protein-glutamine gamma-glutamyltransferase 2	TGM2	0.386	0.205
Coatomer subunit zeta-2	COPZ2	0.357	0.239
Vinexin	SORBS3	0.266	0.346

Non-specific lipid-transfer protein	SCP2	0.333	0.279
72 kDa type IV collagenase;PEX	MMP2	0.330	0.288
Cytochrome P450 1B1	CYP1B1	0.170	0.460
Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannosidase	DKFZp434I213; MAN1B1	0.409	0.235
Uveal autoantigen with coiled-coil domains and ankyrin repeats	UACA	0.340	0.301
Chloride intracellular channel protein 4	CLIC4	0.386	0.265
Protein disulfide-isomerase A5	PDIA5	0.291	0.376
Bis(5-nucleosyl)-tetraphosphatase [asymmetrical]	NUDT2	0.138	0.545
Sorting nexin-3	SNX3	0.366	0.332
Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	0.417	0.286
Dynein light chain roadblock-type 1;Dynein light chain roadblock-type 2	DYNLRB1; DYNLRB2	0.554	0.162
WD repeat domain phosphoinositide-interacting protein 3	WDR45L; WDR45B	0.263	0.449
Glutathione S-transferase P	GSTP1	0.477	0.240
Transgelin	Q53GC9	0.309	0.408
Methylmalonyl-CoA mutase, mitochondrial	MUT	0.439	0.280
Fibronectin type-III domain-containing protein 3A	FNDC3A	0.299	0.423
Protein KIAA1199	KIAA1199	0.379	0.344
Sulfhydryl oxidase 1	QSOX1	0.583	0.148
Persulfide dioxygenase ETHE1, mitochondrial	ETHE1	0.303	0.429
Forkhead box protein P4	DKFZp762O213;FOXP4	0.498	0.238
Ragulator complex protein LAMTOR3	LAMTOR3	0.448	0.290
Prosaposin	PSAP	0.541	0.198
Prenylcysteine oxidase 1	PCYOX1	0.388	0.352
Metalloproteinase inhibitor 1	TIMP1	0.493	0.248
Translocon-associated protein subunit alpha	SSR1	0.456	0.292
Glutathione peroxidase; Glutathione peroxidase 1	GPX1	0.512	0.253
Phosphoglucomutase-1	PGM1	0.470	0.300
Beta-galactosidase	GLB1	0.434	0.336
SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLIRP	0.371	0.400
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	NDUFA8	0.447	0.328

Lactoylglutathione lyase	GLO1	0.449	0.336
Stromal interaction molecule 1	STIM1	0.186	0.599
SH2 domain-containing protein 4A	SH2D4A	0.260	0.531
Syntenin-1	SDCBP	0.451	0.345
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial	NDUFB5	0.491	0.305
ATP synthase-coupling factor 6, mitochondrial	ATP5J	0.393	0.411
Aspartyl aminopeptidase	DNPEP	0.317	0.491
Ras-related GTP-binding protein A;Ras-related GTP-binding protein B	RRAGB; RRAGA	0.334	0.475
Neurogenic locus notch homolog protein 3;Notch 3 extracellular truncation; Notch 3 intracellular domain	NOTCH3	0.488	0.322
ADP-ribosylation factor-like protein 8A;ADP-ribosylation factor-like protein 8B	ARL8A;ARL 8B	0.378	0.434
Integrin alpha-2	ITGA2	0.322	0.493
60S ribosomal protein L37a	RPL37A	0.554	0.267
ADP-ribose pyrophosphatase, mitochondrial	NUDT9	0.395	0.432
Copine-3	CPNE3	0.503	0.323
YTH domain family protein 1	YTHDF1	0.293	0.538
Phosphopantothenate--cysteine ligase	PPCS	0.349	0.497
ADP-ribosylation factor-like protein 3	ARL3	0.463	0.385
Bcl10-interacting CARD protein	C9orf89	0.502	0.348
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1	NDUFB1	0.360	0.496
Leucyl-cystinyl aminopeptidase;Leucyl-cystinyl aminopeptidase, pregnancy serum form	LNPEP	0.366	0.493
Transaldolase	TALDO1	0.523	0.337
Acylphosphatase-2	ACYP2	0.329	0.533
Galectin-3	LGALS3	0.519	0.350
26S proteasome non-ATPase regulatory subunit 6	PSMD6	0.612	0.248
ATP synthase subunit O, mitochondrial	ATP5O	0.396	0.485
Cytochrome c	CYCS	0.524	0.354
Histidine triad nucleotide-binding protein 1	HINT1	0.490	0.391
2,4-dienoyl-CoA reductase, mitochondrial	DECR1	0.485	0.397
Eukaryotic initiation factor 4A-III;	EIF4A3	0.458	0.427

Eukaryotic initiation factor 4A-III, N-terminally processed			
Estradiol 17-beta-dehydrogenase 11	HSD17B11	0.550	0.337
Protein phosphatase 1 regulatory subunit 12C	PPP1R12C	0.455	0.443
40S ribosomal protein S5;40S ribosomal protein S5, N-terminally processed	RPS5	0.532	0.363
Protein S100-A10	S100A10	0.583	0.309
Tyrosine-protein kinase SgK223	SGK223	0.568	0.328
60S acidic ribosomal protein P1	RPLP1	0.654	0.227
RalBP1-associated Eps domain-containing protein 1	REPS1	0.340	0.560
Ubiquitin-conjugating enzyme E2 K	UBE2K;HIP2	0.539	0.366
Fatty acid desaturase 3	FADS3	0.510	0.406
Epidermal growth factor receptor kinase substrate 8-like protein 2	EPS8L2	0.376	0.544
Peptidyl-prolyl cis-trans isomerase C;Peptidyl-prolyl cis-trans isomerase	PPIC	0.427	0.497
Heterochromatin protein 1-binding protein 3	HP1BP3	0.449	0.476
Peptidyl-prolyl cis-trans isomerase B	PPIB	0.605	0.306
Probable E3 ubiquitin-protein ligase HERC4	HERC4	0.438	0.489
WAS protein family homolog 6;Putative WAS protein family homolog 3;WAS protein family homolog 2;WAS protein family homolog 1;Putative WAS protein family homolog 4	FLJ00075;DKFZp434K1323;WASH;WASH6P;DKFZp686C24272;WASH3P;WASH2P;WASH1;WASH4P	0.593	0.334
Phosphoserine aminotransferase	PSAT1	0.657	0.255
Arylsulfatase A;Arylsulfatase A component B;Arylsulfatase A component C	ARSA;DKFZp686G12235	0.505	0.433
Dolichol-phosphate mannosyltransferase	DPM1	0.589	0.342
Survival motor neuron protein	SMN1;SMN2	0.324	0.605
S-formylglutathione hydrolase	ESD	0.526	0.416
Alkaline phosphatase, tissue-nonspecific isozyme;Alkaline phosphatase	ALPL	0.655	0.266
Secernin-1	SCRN1	0.394	0.551
Arylsulfatase B	ARSB	0.485	0.469

Laminin subunit beta-2	LAMB2	0.355	0.591
Ubiquitin-like modifier-activating enzyme ATG7	ATG7	0.486	0.476
Hydroxyacylglutathione hydrolase, mitochondrial	HAGH	0.469	0.494
Proteasome subunit beta type;Proteasome subunit beta type-1	PSMB1	0.641	0.304
Pentraxin-related protein PTX3	PTX3	0.367	0.590
Cartilage-associated protein	CRTAP	0.486	0.482
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	0.529	0.441
Trafficking protein particle complex subunit 8	TRAPPC8	0.450	0.521
Sulfurtransferase;3-mercaptopyruvate sulfurtransferase	MPST	0.670	0.276
EF-hand domain-containing protein D2	EFHD2	0.503	0.475
Nucleoporin Nup37	NUP37	0.405	0.570
Calpain-1 catalytic subunit	CAPN1	0.349	0.620
Copper transport protein ATOX1	ATOX1	0.671	0.288
A disintegrin and metalloproteinase with thrombospondin motifs 2	ADAMTS2	0.550	0.436
UPF0587 protein C1orf123	C1orf123	0.362	0.617
Vesicle-trafficking protein SEC22b	SEC22B	0.475	0.519
V-type proton ATPase 116 kDa subunit a isoform 1	ATP6V0A1; DKFZp686N0561	0.520	0.476
Up-regulated during skeletal muscle growth protein 5	USMG5	0.548	0.449

4. Supplemental References

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