

Supplementary Data

Supplementary Methods and Materials

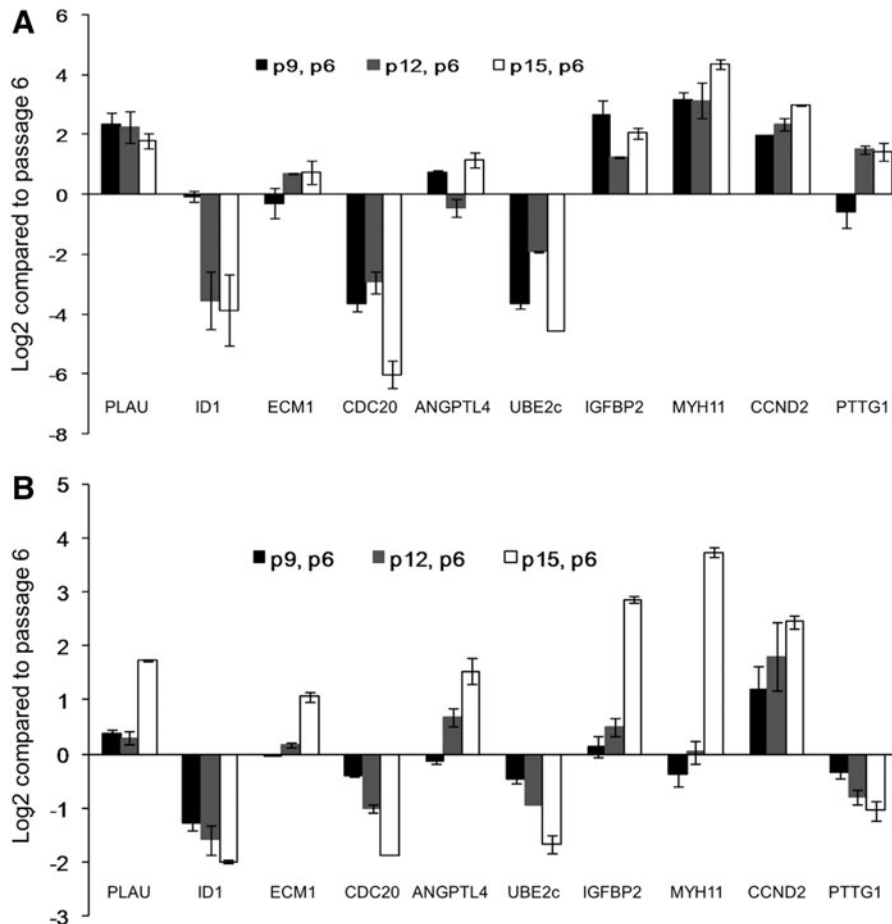
CSCs isolation methods

Explants culture. Briefly, samples were washed twice with PBS⁻ and 10% penicillin/streptomycin (Gibco; 15070-063) to remove the blood clots. Samples then were cut into 1–2 mm³ pieces and treated once with 2 mg/mL trypsin (Gibco, 27250-018) and 1 mg/mL collagenase IV (Gibco; 17104-019) for 5 min. The supernatant was removed and pieces were cultured as explants on plates coated with 1 mg/mL fibronectin (Sigma-Aldrich; F0635) in cardiac explants medium [IMDM (Sigma-Aldrich; 13390), 10% FBS (Gibco; 10270-106), 100 U/mL penicillin, 100 µg/mL streptomycin, 2 mM L-glutamine (Gibco; 25030-024), and 0.1 mM 2-mercaptoethanol (Sigma-Aldrich; M7522)]. After 3 weeks, small phase-bright cells that had migrated over a layer of fibroblast-like cells were collected by light enzymatic digestion using trypsin/EDTA (Gibco; 15400) 0.025% at room temperature. Cells were cultured to form cardiospheres on poly D-lysine

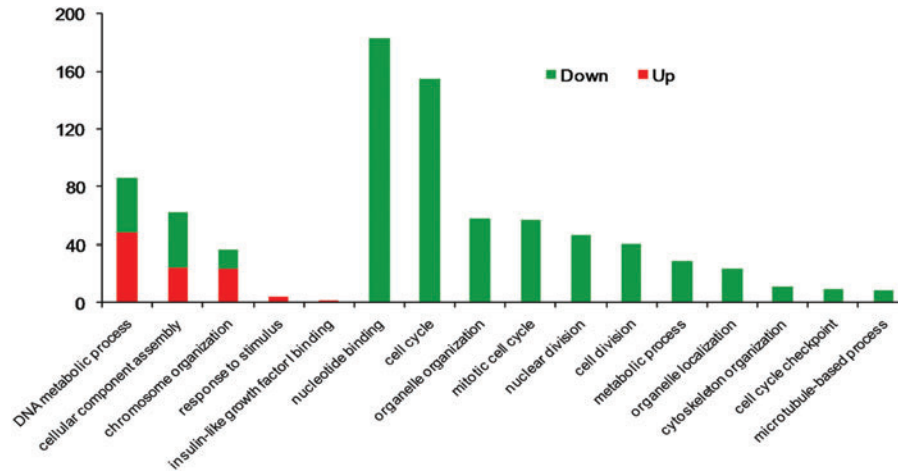
(Sigma-Aldrich; P0899)-coated plates in cardiosphere medium that contained 35% IMDM/65% DMEM-Ham's F12, 2% B27, 0.1 mM 2-mercaptoethanol, 10 ng/mL EGF, 20 ng/mL bFGF, 40 nM cardiostrophin 1 (R&D Systems; 612-CD), 40 nM thrombin (Sigma-Aldrich; T7572), 100 U/mL penicillin, 100 µg/mL streptomycin, and 2 mM L-glutamine. Cardiospheres were plated on fibronectin-coated plates in CEM medium after 3–5 days to enable adherent growth.

Clonogenic expansion culture. For clonogenic expansion, the cell suspension was cultured in tissue culture flasks to remove the fibroblasts and cardiomyocytes. After 75 min the medium was collected, centrifuged, suspended in culture medium, and counted. The cells were diluted to a concentration of 10 cells/mL and 100 µL of suspension was added to one well of a fibronectin-coated 96-well plate. After 1–2 week(s) cells with clonogenic potential grew in the wells.

Cell sorting. In the third protocol, cells were sorted by their c-KIT surface antigen using an anti-human c-KIT microbead-conjugated antibody (MiltenyiBiotec; 130-091-



SUPPLEMENTARY FIG. S1. Confirmation of microarray data. Reproducibility of microarray data was performed using quantitative real-time (qRT-PCR) for six up- and four downregulated genes between four passages (passage 6: p6, passage 9: p9, passage 12: p12 and passage 15: p15). Real-time reverse transcriptase-PCR (RT-PCR) data (A) confirms microarray data (B) in all reactions except for one case *PTTG1* in which downregulation in p15 compared to p6 that was observed in microarray data was not visualized in real-time analysis. Analysis of real time data was performed by the $2^{-\Delta\Delta Ct}$ method.



SUPPLEMENTARY FIG. S2. Gene ontology analysis of two distinct expression clusters. BINGO software was used to classify significantly changed transcripts.

332) according to the manufacturer's protocol. Cells were washed once with PBS⁻, centrifuged, and then suspended in Clni MACS buffer (MiltenyiBiotec; 700-25). Anti-human c-KIT microbead-conjugated antibody (MiltenyiBiotec; 130-091-332) was added and cells were allowed to incubate for 15 min. Cells were washed with PBS⁻ to remove excess antibody and then were moved through a MACS column. c-KIT⁺ cells were collected by flushing out the buffer with a plunger. Purity of the sorted cells was measured with anti-human CD117 antibody (MiltenyiBiotec; 130-091-734).

MACS buffer was removed after centrifugation and cells were cultured on fibronectin-coated plates in IMDM that contained 10% FBS, 1% penicillin/streptomycin, and 1% L-glutamine at 37°C. bFGF (10 ng/mL; Royan Institute) was used to induce cell growth.

Flow cytometry

We analyzed the cell surface antigens with the intent to identify the cell type and characteristics of the isolated cells. Surface marker candidates for flow cytometry analysis included CD90 (Dako; F7274), CD117 (MiltenyiBiotec; 130-091-734), CD105 (R&D Systems FAB10971P), CD133 (MiltenyiBiotec 293C3), CD34 (BD Pharmingen; 550619), CD45 (Dako; F0861), Sca-1 (eBioscience 12-5981-81), and CD31 (BD Pharmingen; 555445). For each test, we incubated 10⁵ cells for 30 min with antibodies according to the manufacturer's instructions. Flow cytometry was performed with a BD FACScalibur (BD Biosciences) system and data were analyzed by WinMDI2.9 software.

Population doubling time

Isolated cells in passages 3–6 were plated at 10⁴ cells per well in six-well culture plates. Cell count was performed daily for 6 days (cells were trypsinized and we used trypan blue to count viable cells). Population doubling time (PDT) was calculated using the following formula:

$$N = N_0 2^{T/PDT}$$

N = Cell count at the end of each day
 N_0 = Initial cell count
 T = PDT

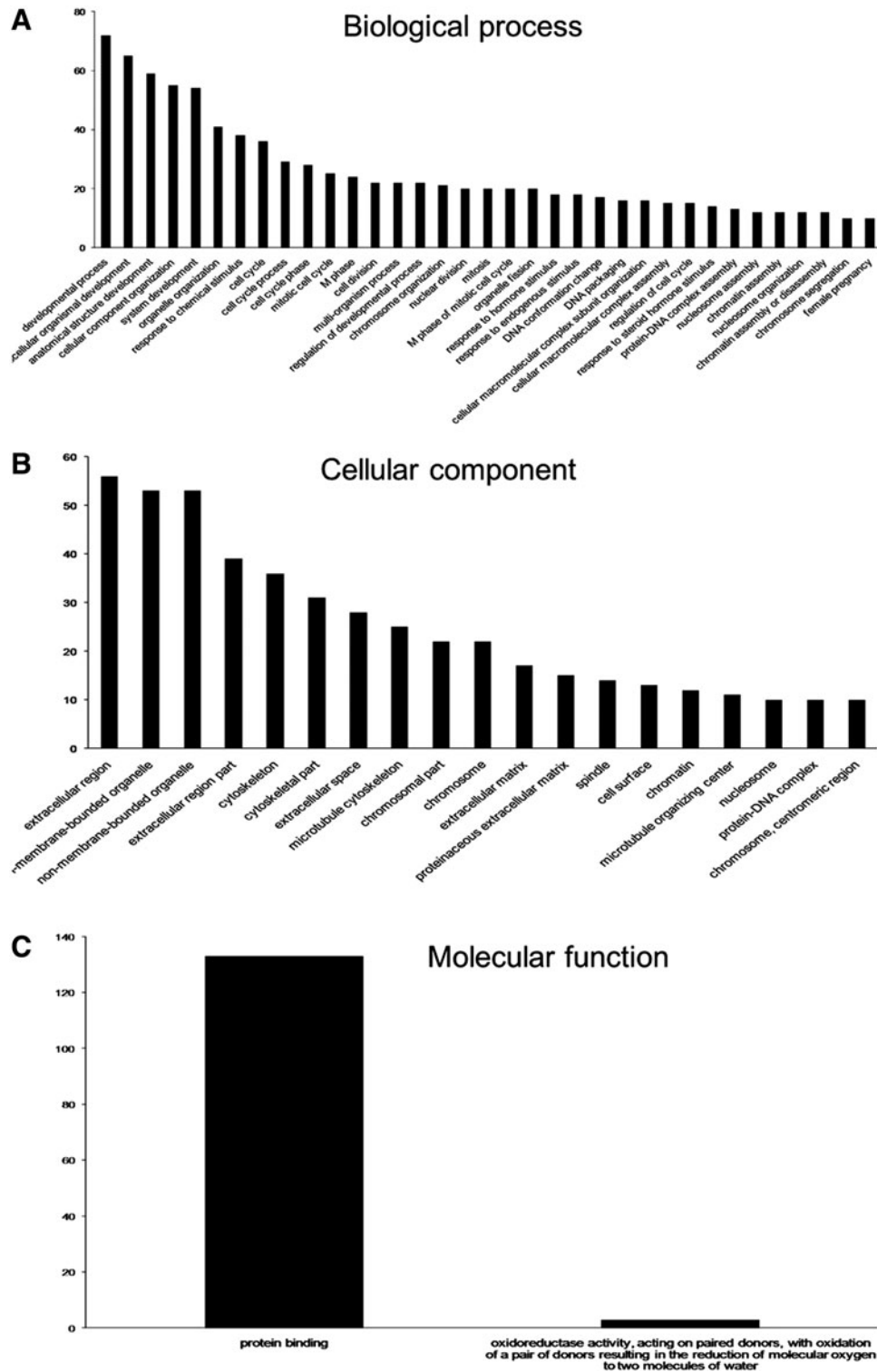
Reverse transcriptase-PCR and quantitative real-time PCR

For molecular analysis, total RNA was manually isolated. Briefly, the cell pellet was first washed with PBS after which 1 mL of RNX-plus buffer (CinnaGen; MR7713C) was added and the sample vortexed to dissolve the clumps. Next, 100 μ L of chloroform was added, vortexed, and centrifuged at 12,000 g for 15 min. The upper phase contained RNA and DNA, which was transferred to another RNase- and DNase-free tube, where an equal volume of isopropanol was added. Samples were incubated at 4°C for 15 min and then centrifuged at 12,000 g for 15 min. The pellet was washed in 200 μ L of 70% ethanol and centrifuged at 7,500 g for 8 min. This pellet was dissolved in 50 μ L DEPS treated water. RNA concentration was determined by OD value and DNA contamination was removed using a DNase1 kit (Fermentaz; en0521). First strand cDNA synthesis was performed using 3 μ g of RNA according to a PrimeScript 1st strand cDNA synthesis kit (TaKaRa; 6110A) protocol and the PCR reaction carried out with 1 μ g of synthesized cDNA and candidate gene primers using Ex Taq kits (TaKaRa; RR001A) according to the manufacturer's instructions.

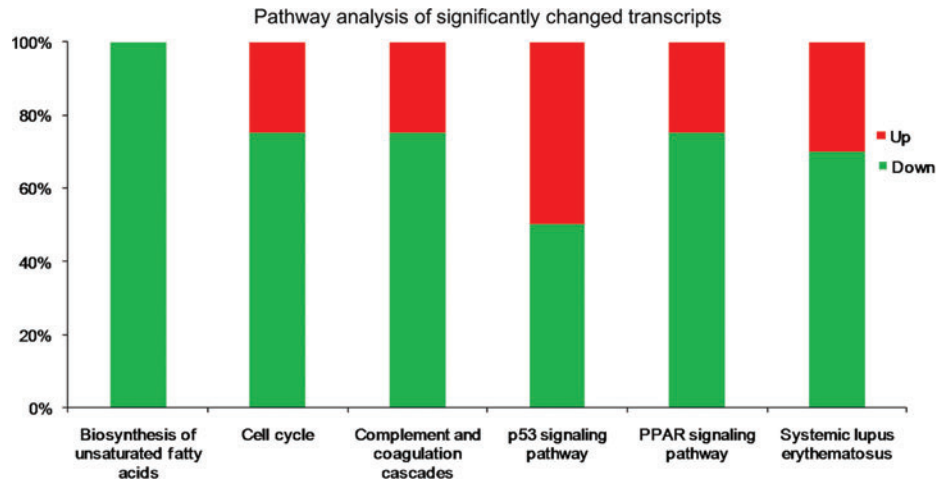
For real-time PCR, 3 μ g of total RNA was used for cDNA synthesis according to a cDNA synthesis for a real-time kit (TaKaRa; RR037A) protocol. The real-time PCR was undertaken by a Rotor Gene Corbett System (R080873) using a SYBR premix Ex Taq kit (TaKaRa; RR041A). Quantitative gene expression analysis was performed by the 2^{- $\Delta\Delta$ ct} formula and target genes were normalized by the house-keeping gene *GAPDH*. The primers are presented in Supplementary Tables S3, S5, and S6.

Immunocytochemistry

Cells cultured in four-well plates were fixed with 4% paraformaldehyde and permeabilized with 0.2% (v/v) Triton X-100. Cells were incubated overnight with primary antibodies, CONNEXIN43 (GJA1) (1:200, Abcam; Ab62689), cardiac Troponin T (cTnT) (1:200, Abcam; Ab64623), and MHC (1:200, Abcam; Ab15) according to the manufacturer's instructions. FITC-conjugated antibodies, goat anti-



SUPPLEMENTARY FIG. S3. Functional classification of differentially expressed genes. Gene ontologies are shown in biological process (A), cellular component (B) and molecular function (C) clusters.



SUPPLEMENTARY FIG. S4. Pathway analysis of significantly changed transcripts. KEGG data base was used to find significant pathways including our differentially expressed transcripts. The percentage of *up*- (red) and *down*regulated (green) transcripts involved in each pathway is shown in the graph.

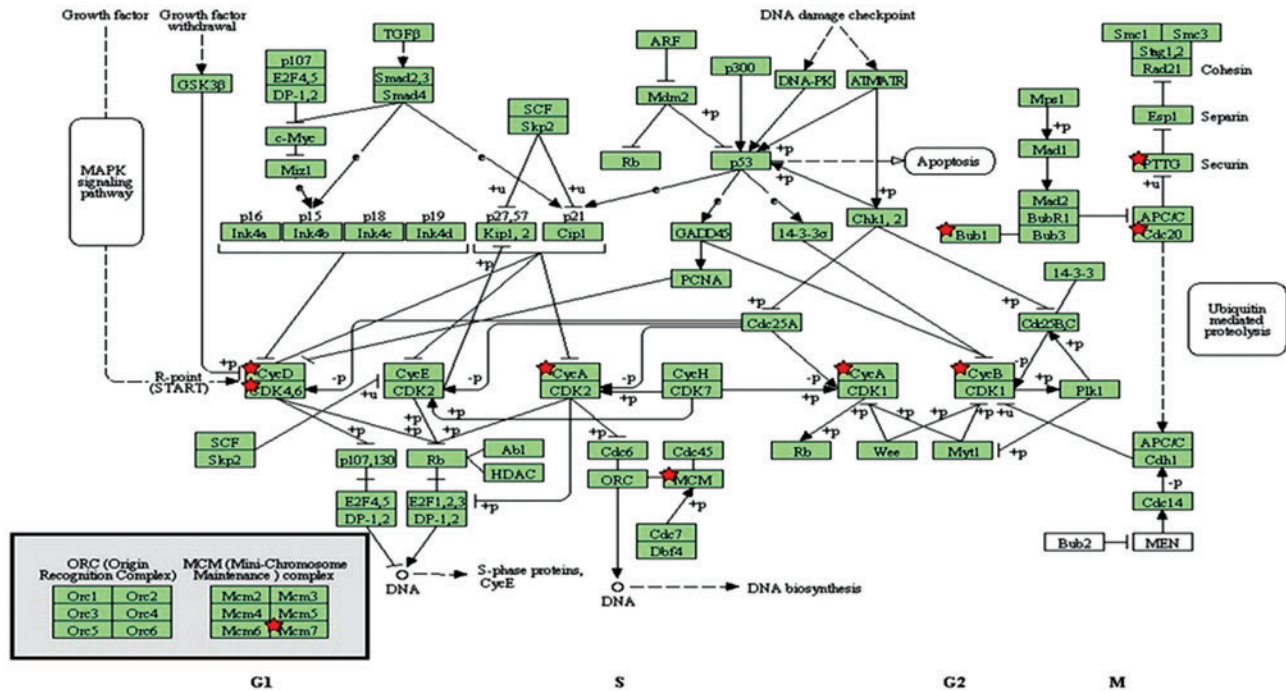
rabbit IgG FITC (1:200, Sigma-Aldrich; F1262), rabbit anti-goat IgG FITC (1:200, Sigma-Aldrich, F7367), and goat anti-mouse IgG FITC (1:200, Sigma-Aldrich, F9006) were used as secondary antibodies. DAPI (Sigma-Aldrich; D8417) was used as a counterstain. Cells were analyzed under a fluorescent microscope (Olympus; IX71).

Ultra-structure analysis

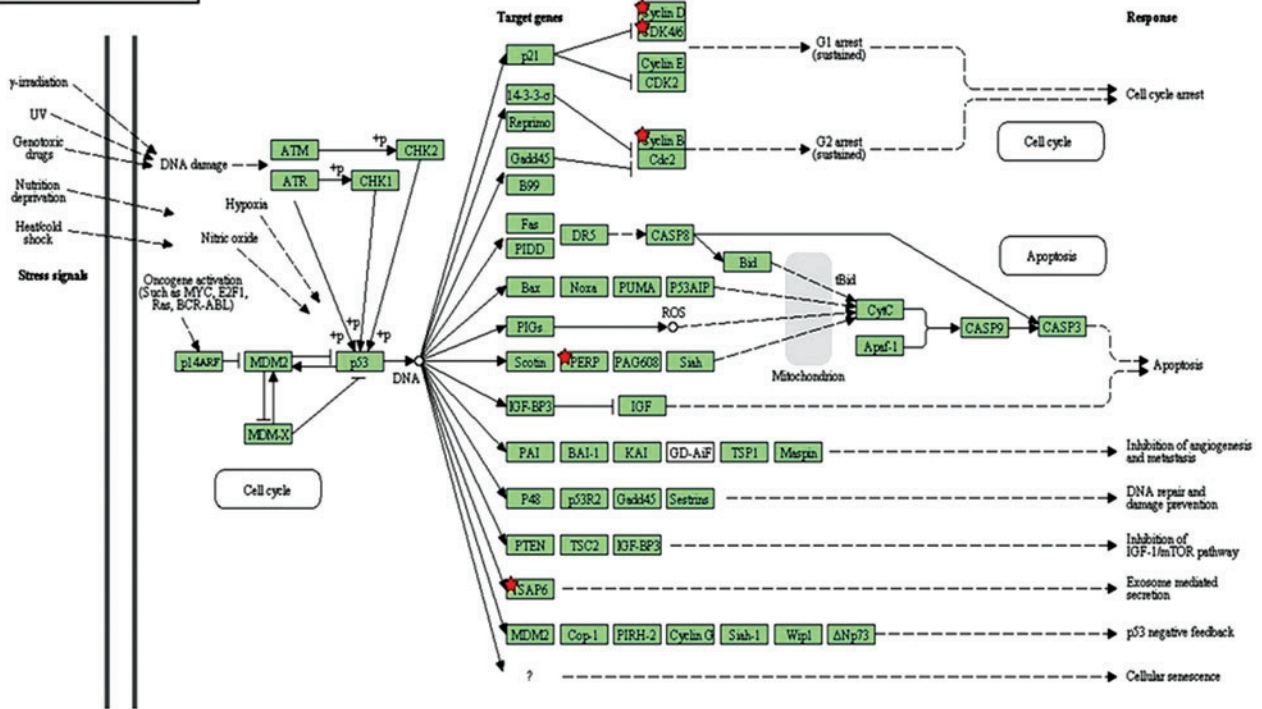
At 5–6 weeks after initiation of myogenic differentiation, cells were scraped and fixed with 2% glutaraldehyde in 0.1 M PBS for 2 h. Samples were washed thrice (2× for 2 h and 1× for 3 h), then fixed with 1% osmium tetroxide for 3 h. The

samples were washed twice with water (30 min each) and dehydrated in an increasing acetone series of 30%, 50%, 70%, and 90%, each for 1 h followed by three times (1 h each) in 100% acetone. Infiltration into Spurr's resin was achieved by an acetone/resin series initially at a 3:1 ratio for 3 h, a 1:1 ratio for 4 h, and finally at a 1:3 ratio for 6 h, followed by fresh resin (15 h). The samples were then embedded in molds that contained 100% resin and polymerized at 65°C for 2 days. After polymerization, the sections were randomly cut at ~70 nm and stained with lead citrate (50 min) and uranyl acetate (1 h). Micrographs of transverse sections of the cells were taken on plate films by a Zeiss EM900 transmission electron microscope.

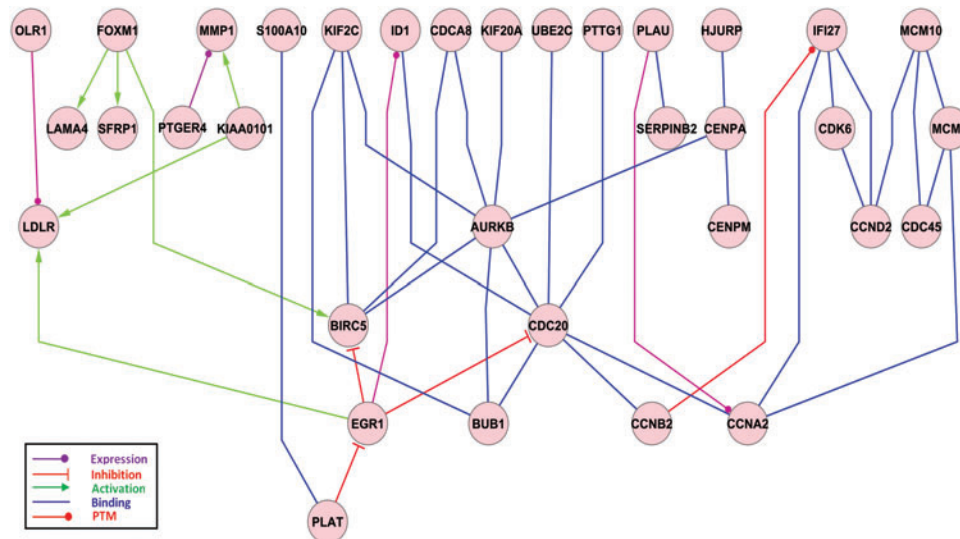
A CELL CYCLE



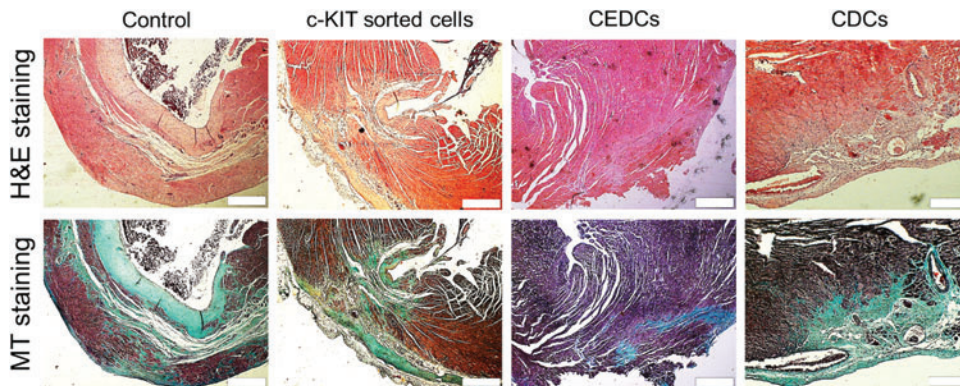
B P53 SIGNALING PATHWAY



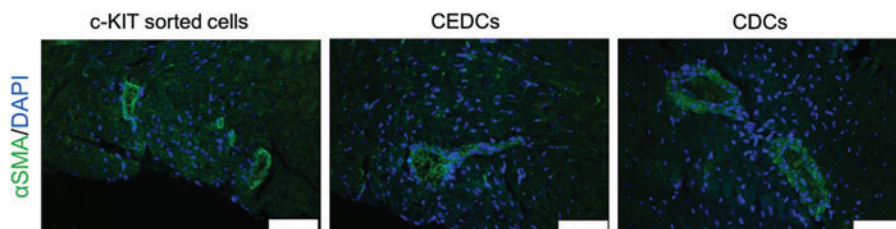
SUPPLEMENTARY FIG. S5. The main important pathways with significantly changed transcripts. Cell cycle (A) and p53 signaling (B) pathways exist among the significantly changed pathways.



SUPPLEMENTARY FIG. S6. Gene regulatory network of differentially expressed transcripts. String data base was used for creating an interaction regulatory network for genes expressed differentially in three stages. *Green arrows* indicate an activation mode, *red arrows* indicate an inhibitory mode, *purple edges* indicate an expression mode, and *blue lines* represent protein bindings. *Red edges* represent posttranslational modification of source or target genes.



SUPPLEMENTARY FIG. S7. Infarction area in transplanted rat hearts 8 weeks after infarction. Hematoxylin and eosin (H&E) and Masson trichrome (MT) staining of infarcted rat hearts 8 weeks after transplantation showed attenuation of infarction area in cardiac stem cells (CSCs) transplanted groups compared to vehicle group.



SUPPLEMENTARY FIG. S8. Blood vessels staining of infarcted rat heart tissues. Anti alpha smooth muscle actin (α SMA) antibody was used to visualize rat heart vessels. Nuclei were counterstained with DAPI. Scale bar=200 μ m.

SUPPLEMENTARY TABLE S1. CHARACTERISTICS OF CARDIAC TISSUE BIOPSIES OBTAINED DURING ROUTINE SURGERIES OF PATIENTS WITH TETRALOGY OF FALLOT

Demographic characteristics (<i>n</i> = 35)	
Sex, male	25 (71.4%)
Age, years	5.8 (4.8)
Race, Iranian	35 (100%)
Cardiac hypertrophic tissue	35 (100%)
Tissue place	32 (91.4%)
Right atrium	35 (100%)
Right ventricle	

Data are shown as *n* (%) or mean (SD).

SUPPLEMENTARY TABLE S2. FLOW CYTOMETRY RESULTS (MEAN ± STANDARD DEVIATION) FOR ALL THREE GROUPS

Surface markers	<i>c-KIT</i> ⁺ (Passages 3–6)	CEDCs (Passages 3–6)	CDCs (Passages 3–6)
CD90	20.1 ± 1.5	68.9 ± 17.0	30.4 ± 5.2
CD117	89.0 ± 2.0	7.8 ± 4.2	7.2 ± 1.2
Sca-1	7.8 ± 3.8	21.0 ± 2.7	7.9 ± 0.7
CD105	88.7 ± 1.2	92.3 ± 2.1	84.8 ± 1.5
CD133	2.2 ± 0.02	2.0 ± 0.3	5.4 ± 1.4
CD34-CD45	2.0 ± 1.3	2.1 ± 1.8	1.6 ± 1.7
CD31	3.0 ± 0.7	2.6 ± 2.1	4.1 ± 1.0

CEDC, clonogenic expansion-derived cell; CDC, cardiosphere-derived cell.

SUPPLEMENTARY TABLE S3. GENE CANDIDATES AND THEIR PRIMER SEQUENCES USED FOR REVERSE TRANSCRIPTASE-POLYMERASE CHAIN REACTION ANALYSIS

Gene	Primers	Annealing temperature (°C)
SOX2	F: 5' GGC AGC TAC AGC ATG ATG CAG 3' R: 5' GCT CTG GTA GTG CTG GGA CAT G 3'	65
<i>c-KIT</i>	F: 5' ATT GTT CTG TGG ACC AGG AG 3' R: 5' GGT TGT TGT GAC ATT TGC TG 3'	62
ABCG2	F: 5' CTA AGC AGG GAC GAA CAA TCA TC 3' R: 5' TGA CAG AAG GAG GTG GTG TAG C 3'	62
Isl-1	F: 5' CAC CAT GGG AGA CAT GGG AGA TC 3' R: 5' TCA GCG TCT TCT GCG TCT TCT TC 3'	60
Nkx2.5	F: 5' TCT ATC CAC GTG CCT ACA G 3' R: 5' CCT CTG TCT TCT CCA GCT C 3'	62
GATA4	F: 5' GCC TGT CAT CTC ACT ACG G 3' R: 5' GAA GTC TCC AAC TCA CAG G 3'	60
MEF-2c	F: 5' ACA CCT ACA TAA CAT GCC ACC 3' R: 5' ATC ATG TTG CCC ATC CTT CAG 3'	62
α-MHC	F: 5' GAG TGG AAG CAG AAG TAT GAG G 3' R: 5' CTT GAT CTG GTT GAA CTC TAG C 3'	61
β-MHC	F: 5' GTG AAG AAG AAG ATG GAA GGA G 3' R: 5' GCT CAC TAG TCT CAA TCA GCT C 3'	62
MLC-2v	F: 5' TGT GGG TCA CCT GAG GCT GTG GTT CAG 3' R: 5' GAA GGC TGA CTA TGT CCG GGA GAT GC 3'	62

SUPPLEMENTARY TABLE S4. mRNA EXPRESSION IN ISOLATED CELLS FROM DIFFERENT METHODS

Genes	<i>Stemness markers</i>			<i>Cardiac transcription factors</i>				<i>Cardiac structural genes</i>		
	SOX2	c-KIT	ABCG	is11	MEF-2c	GATA4	Nkx2.5	aMHC	bMHC	Mlc-2v
c-KIT ⁺ cells	+	+	+	-	+	+	-	-	-	-
CEDCs	+	+/-	+	-	+	+	-	-	-	-
CDCs	+	+	+	-	+	+	-	-	-	-
Before culture	+	+	+	-	+	+	-	+	+	+

SUPPLEMENTARY TABLE S5. GENE CANDIDATES AND THEIR PRIMER SEQUENCES USED FOR REAL-TIME REVERSE TRANSCRIPTASE-POLYMERASE CHAIN REACTION ANALYSIS OF CARDIOMYOGENIC DIFFERENTIATION EFFICIENCY

<i>Gene</i>	<i>Primers</i>	<i>Annealing temperature</i>
α -MHC	F: 5' GAG TGG AAG CAG AAG TAT GAG G 3' R: 5' CTT GAT CTG GTT GAA CTC TAG C 3'	60
Cardiac troponin T	F: 5' ATG ATG CAT TTT GGG GGT TA 3' R: 5' CAG CAC CTT CCT CCT CTC AG 3'	60
CONNEXIN 43 (GJA1)	F: 5' GCT ATG ACA AGT CTT TCC CA 3' R: 5' CAG TTT CTC TTC CTT TCG CA 3'	60
GATA4	F: 5' CCT GTC ATC TCA CTA CGG 3' R: 5' GCT GTT CCA AGA GTC CTG 3'	60
MEF2C	F: 5' TCC GAG TTC TTA TTC CAC C 3' R: 5' ATC CTC CCA TTC CTT GTC 3'	60

SUPPLEMENTARY TABLE S6. GENE CANDIDATES AND THEIR PRIMER SEQUENCES USED FOR QUANTITATIVE REAL-TIME POLYMERASE CHAIN REACTION

<i>Gene</i>	<i>Primers</i>	<i>Annealing temperature (°C)</i>
CyclinD2	F: 5' ACG TTG GTC CTG ACG GTA CT 3' R: 5' TGA GCT GCT GGC TAA GAT CA 3'	60
PLAU	F: 5' CCA GCT CAC AAT TCC AGT CA 3' R: 5' GTC ACC ACC AAA ATG CTG TG 3'	60
Angptl4	F: 5' GGA ACA GCT CCT GGC AAT C 3' R: 5' GCA CCT AGA CCA TGA GGT GG 3'	60
CDC20	F: 5' TGT AAT GGG GAG ACC AGA GG 3' R: 5' ATT CGC ATC TGG AAT GTG TG 3'	60
ID1	F: 5' GAC ACA AGA TGC GAT CGT CC 3' R: 5' AGT TGG AGC TGA ACT CGG AA 3'	60
UBE2C	F: 5' TTG TAA GGG TAG CCA CTG GG 3' R: 5' GAT GTC TGG CGA TAA AGG GA 3'	60
ECM1	F: 5' AGC TGC GTA GCC AAC TTC TT 3' R: 5' ATT TGG CTG TTG CTT CTG CT 3'	60
MYH11	F: 5' TAG AAT GGA CTG GTC CTC CC 3' R: 5' ACC CCT ATA AAC ACC TGC CC 3'	60
IGFBP2	F: 5' CAA CAT GTT CAT GGT GCT GTC 3' R: 5' GCG AGG GCA CTT GTG AGA 3'	60
PTTG1	F: 5' CAA TCT GGT GCT CTT CAG GC 3' R: 5' CAA AAA GCT CTG TTC CTG CC 3'	60

SUPPLEMENTARY TABLE S7. LIST OF THE FIRST 35 TRANSCRIPTS WITH THE HIGHEST EXPRESSION IN PASSAGE 15 COMPARED TO PASSAGE 6 ($p \leq 0.05$)

<i>Gene name</i>	<i>Probe ID</i>	<i>Fold change 15 vs. 6</i>	<i>Regulation 15 vs. 6</i>	<i>Gene ontology</i>
MYH11	ILMN_1660086	13.29004	Up	61061: muscle structure development, 31033: myosin filament assembly or disassembly
IGFBP2	ILMN_1725193	7.285891	Up	5520: insulin-like growth factor binding, 7165: signal transduction, 32502: developmental process
LOC728285	ILMN_1660067	6.250169	Up	
LRRN3	ILMN_2048591	6.2097874	Up	10646: regulation of cell communication, 7165: signal transduction
LRRN3	ILMN_1773650	6.1623387	Up	10646: regulation of cell communication, 7165: signal transduction
IGFBP5	ILMN_2132982	5.7907147	Up	61061: muscle structure development, 10646: regulation of cell communication, 48514: blood vessel morphogenesis, 14910: regulation of smooth muscle cell migration, 5520: insulin-like growth factor binding, 7165: signal transduction
CCND2	ILMN_1667081	5.4573216	Up	60284: regulation of cell development, 32355: response to estradiol stimulus
IGFBP5	ILMN_1750324	5.427988	Up	61061: muscle structure development, 10646: regulation of cell communication, 48514: blood vessel morphogenesis, 14910: regulation of smooth muscle cell migration, 5520: insulin-like growth factor binding, 7165: signal transduction
KRTAP2-1	ILMN_1658448	4.9025908	Up	
LOC728934	ILMN_3248758	4.8879204	Up	
VIPR1	ILMN_2199389	4.8161716	Up	7165: signal transduction
LOC644350	ILMN_3248701	4.6565723	Up	
CCND2	ILMN_2067656	4.2120514	Up	60284: regulation of cell development, 32355: response to estradiol stimulus
THY1	ILMN_1779875	3.96656	Up	32502: developmental process, 10646: regulation of cell communication, 1944: vasculature development, 23052: signaling, 30334: regulation of cell migration
LOC284998	ILMN_1680902	3.9538634	Up	
CYP26B1	ILMN_1812297	3.781622	Up	32502: developmental process, 10646: regulation of cell communication, 1709: cell fate determination, 34653: retinoic acid catabolic process
SERPINB2	ILMN_2150851	3.6596315	Up	44421: extracellular region part
RGS5	ILMN_2082273	3.5997288	Up	10646: regulation of cell communication, 35466: regulation of signaling pathway
TMEM16A	ILMN_2091310	3.5267606	Up	32502: developmental process
MIR1974	ILMN_3308961	3.51614	Up	
SERPINB2	ILMN_2150856	3.5036848	Up	44421: extracellular region part
ITGA7	ILMN_1791409	3.3850226	Up	32502: developmental process, 61061: muscle structure development, 1944: vasculature development, 23052: signaling
PLAU	ILMN_1656057	3.3158271	Up	32502: developmental process, 10646: regulation of cell communication, 14910: regulation of smooth muscle cell migration, 1944: vasculature development, 70482: response to oxygen levels, 7165: signal transduction
LOXL4	ILMN_2179083	3.3125908	Up	44421: extracellular region part
SYNPO2L	ILMN_1690253	3.2738929	Up	
RGS5	ILMN_1651554	3.219241	Up	10646: regulation of cell communication, 35466: regulation of signaling pathway
MYH3	ILMN_1795119	3.17207	Up	32502: developmental process, 61061: muscle structure development

(continued)

SUPPLEMENTARY TABLE S7. (CONTINUED)

<i>Gene name</i>	<i>Probe ID</i>	<i>Fold change 15 vs. 6</i>	<i>Regulation 15 vs. 6</i>	<i>Gene ontology</i>
C21ORF7	ILMN_1699071	3.1382837	Up	
HIST1H2BK	ILMN_1813314	3.0989647	Up	
RCAN2	ILMN_2120210	3.0838456	Up	32502: developmental process, 7165: signal transduction
PLAT	ILMN_1738742	3.0226436	Up	32502: developmental process, 10646: regulation of cell communication, 44421: extracellular region part, 1944: vasculature development, 70482: response to oxygen levels, 14909: smooth muscle cell migration
HIST1H2BK	ILMN_1796179	2.9314847	Up	
NTF3	ILMN_1809364	2.917006	Up	32502: developmental process, 61061: muscle structure development, 10646: regulation of cell communication, 19838: growth factor binding, 1709: cell fate determination, 7165: signal transduction
ANGPTL4	ILMN_2386444	2.90783	Up	32502: developmental process, 7165: signal transduction, 70482: response to oxygen levels, 44421: extracellular region part
CCDC81	ILMN_1794534	2.8979778	Up	

SUPPLEMENTARY TABLE S8. LIST OF THE FIRST 35 TRANSCRIPTS WITH THE LOWEST EXPRESSION IN PASSAGE 15 COMPARED TO PASSAGE 6 ($P \leq 0.05$)

<i>Gene name</i>	<i>Probe ID</i>	<i>Fold change 15 vs. 6</i>	<i>Regulation 15 vs. 6</i>	<i>Gene ontology</i>
TMEM119	ILMN_1738116	-4.2157	Down	
SCRG1	ILMN_1726204	-4.15577	Down	44421: extracellular region part
ID1	ILMN_1665832	-3.94933	Down	16043: cellular component organization
CXCR7	ILMN_1798360	-3.82689	Down	
CECR1	ILMN_1751851	-3.73055	Down	44421: extracellular region part
CDC20	ILMN_1663390	-3.6461	Down	278: mitotic cell cycle, 51301: cell division, 280: nuclear division, 7049: cell cycle, 6996: organelle organization
UBE2C	ILMN_2301083	-3.44567	Down	278: mitotic cell cycle, 51301: cell division, 280: nuclear division, 7049: cell cycle, 6996: organelle organization, 7096: regulation of exit from mitosis
INHBE	ILMN_1811767	-3.38487	Down	5576: extracellular region
SUSD2	ILMN_1693270	-3.3524	Down	
TOP2A	ILMN_1686097	-3.34535	Down	7059: chromosome segregation, 6996: organelle organization
C1R	ILMN_1677198	-3.34412	Down	5576: extracellular region
SCD	ILMN_1689329	-3.29973	Down	
PTGS1	ILMN_2339835	-3.24931	Down	
MAMDC2	ILMN_1679391	-3.20696	Down	44421: extracellular region part
UBE2C	ILMN_1714730	-3.18636	Down	278: mitotic cell cycle, 51301: cell division, 280: nuclear division, 7049: cell cycle, 6996: organelle organization, 7096: regulation of exit from mitosis
CXCR7	ILMN_2371458	-3.08501	Down	
KCNG1	ILMN_1673769	-2.99953	Down	
CXCL2	ILMN_1682636	-2.95528	Down	5576: extracellular region
CDC45L	ILMN_1670238	-2.91041	Down	7049: cell cycle, 15630: microtubule cytoskeleton
C20ORF100	ILMN_2082209	-2.88561	Down	
TNNT2	ILMN_1664071	-2.84906	Down	6996: organelle organization, 44430: cytoskeletal part
PCOLCE	ILMN_1707070	-2.82506	Down	5576: extracellular region
PRC1	ILMN_1728934	-2.79546	Down	278: mitotic cell cycle, 51301: cell division, 280: nuclear division, 7049: cell cycle, 6996: organelle organization, 7096: regulation of exit from mitosis, 7017: microtubule-based process
KIAA0101	ILMN_2285996	-2.79169	Down	
LDLR	ILMN_2053415	-2.77714	Down	5576: extracellular region
EMILIN2	ILMN_1697268	-2.77374	Down	5576: extracellular region
PIM1	ILMN_1815023	-2.74218	Down	278: mitotic cell cycle, 7049: cell cycle, 6996: organelle organization
KIF20A	ILMN_1695658	-2.73614	Down	7017: microtubule-based process, 15630: microtubule cytoskeleton
NUSAP1	ILMN_1726720	-2.72233	Down	278: mitotic cell cycle, 51301: cell division, 280: nuclear division, 7049: cell cycle, 6996: organelle organization, 7017: microtubule-based process, 7059: chromosome segregation, 7017: microtubule-based process, 15630: microtubule cytoskeleton
KIFC1	ILMN_2222008	-2.70518	Down	278: mitotic cell cycle, 51301: cell division, 280: nuclear division, 7049: cell cycle, 6996: organelle organization, 7017: microtubule-based process, 7059: chromosome segregation, 7017: microtubule-based process, 15630: microtubule cytoskeleton
BIRC5	ILMN_2349459	-2.70271	Down	278: mitotic cell cycle, 51301: cell division, 280: nuclear division, 7049: cell cycle, 6996: organelle organization, 7017: microtubule-based process, 7059: chromosome segregation, 7017: microtubule-based process, 15630: microtubule cytoskeleton, 7096: regulation of exit from mitosis
FBLN2	ILMN_2390919	-2.70269	Down	5576: extracellular region
FBLN1	ILMN_1700541	-2.69215	Down	5576: extracellular region
CRLF1	ILMN_1681515	-2.67243	Down	5576: extracellular region
CEP55	ILMN_1747016	-2.64866	Down	278: mitotic cell cycle, 51301: cell division, 280: nuclear division, 7049: cell cycle, 6996: organelle organization, 7017: microtubule-based process, 7059: chromosome segregation, 7017: microtubule-based process, 15630: microtubule cytoskeleton

SUPPLEMENTARY TABLE S9. TOTAL SIGNIFICANT GENE ONTOLOGY OF UPREGULATED TRANSCRIPTS OBTAINED FROM BINGO SOFTWARE WITH THE LIST OF INCLUDED TRANSCRIPTS

<i>Gene ontology</i>	<i>GO ID</i>	<i>Genes</i>
Nucleosome	786	HIST2H2AA4 HIST1H4H HIST1H2AC HIST2H2AA3 HIST1H1C HIST2H2BE HIST1H2BD HIST1H2BK
Nucleosome assembly	6334	HIST2H2AA4 HIST1H4H HIST1H2AC HIST2H2AA3 HIST1H1C HIST2H2BE HIST1H2BD HIST1H2BK
Chromatin assembly	31497	HIST2H2AA4 HIST1H4H HIST1H2AC HIST2H2AA3 HIST1H1C HIST2H2BE HIST1H2BD HIST1H2BK
Protein-DNA complex assembly	65004	HIST2H2AA4 HIST1H4H HIST1H2AC HIST2H2AA3 HIST1H1C HIST2H2BE HIST1H2BD HIST1H2BK
Nucleosome organization	34728	HIST2H2AA4 HIST1H4H HIST1H2AC HIST2H2AA3 HIST1H1C HIST2H2BE HIST1H2BD HIST1H2BK
Protein-DNA complex	32993	HIST2H2AA4 HIST1H4H HIST1H2AC HIST2H2AA3 HIST1H1C HIST2H2BE HIST1H2BD HIST1H2BK
DNA packaging	6323	HIST2H2AA4 HIST1H4H HIST1H2AC HIST2H2AA3 HIST1H1C HIST2H2BE HIST1H2BD HIST1H2BK
Chromatin assembly or disassembly	6333	HIST2H2AA4 HIST1H4H HIST1H2AC HIST2H2AA3 HIST1H1C HIST2H2BE HIST1H2BD HIST1H2BK
DNA conformation change	71103	HIST2H2AA4 HIST1H4H HIST1H2AC HIST2H2AA3 HIST1H1C HIST2H2BE HIST1H2BD HIST1H2BK
Chromatin	785	HIST2H2AA4 HIST1H4H HIST1H2AC HIST2H2AA3 HIST1H1C HIST2H2BE HIST1H2BD HIST1H2BK
Chromosomal part	44427	DYNC1I1 HIST2H2AA4 HIST1H4H HIST1H2AC HIST2H2AA3 HIST1H1C HIST2H2BE HIST1H2BD HIST1H2BK
Cellular macromolecular complex assembly	34622	HIST2H2AA4 HIST1H4H HIST1H2AC HIST2H2AA3 HIST1H1C HIST2H2BE HIST1H2BD HIST1H2BK
Chromosome	5694	DYNC1I1 HIST2H2AA4 HIST1H4H HIST1H2AC HIST2H2AA3 HIST1H1C HIST2H2BE HIST1H2BD HIST1H2BK
Cellular macromolecular complex subunit organization	34621	HIST2H2AA4 HIST1H4H HIST1H2AC HIST2H2AA3 HIST1H1C HIST2H2BE HIST1H2BD HIST1H2BK
Chromatin organization	6325	HIST2H2AA4 HIST1H4H HIST1H2AC HIST2H2AA3 HIST1H1C HIST2H2BE HIST1H2BD HIST1H2BK
Insulin-like growth factor I binding	31994	IGFBP2 IGFBP5
Chromosome organization	51276	HIST2H2AA4 HIST1H4H HIST1H2AC HIST2H2AA3 HIST1H1C HIST2H2BE HIST1H2BD HIST1H2BK
Macromolecular complex assembly	65003	ANGPTL4 HIST2H2AA4 HIST1H4H HIST1H2AC HIST2H2AA3 HIST1H1C HIST2H2BE HIST1H2BD HIST1H2BK
Extracellular region part	44421	ANGPTL4 GAS6 IGFBP2 LOXL4 CCL20 SERPINB2 ADAMTSL4 IGFBP5 CFH ECM1 GPC4
Response to estrogen stimulus	43627	OXTR IGFBP2 KRT19 CCND2
Macromolecular complex subunit organization	43933	ANGPTL4 HIST2H2AA4 HIST1H4H HIST1H2AC HIST2H2AA3 HIST1H1C HIST2H2BE HIST1H2BD HIST1H2BK
Cyclin-dependent protein kinase holoenzyme complex	307	CDK6 CCND2
Regulation of insulin-like growth factor receptor signaling pathway	43567	IGFBP2 IGFBP5

SUPPLEMENTARY TABLE S10. TOTAL SIGNIFICANT GENE ONTOLOGY OF DOWN-REGULATED TRANSCRIPTS OBTAINED FROM BINGO SOFTWARE WITH THE LIST OF INCLUDED TRANSCRIPTS

<i>Gene ontology</i>	<i>GO ID</i>	<i>Genes</i>
Mitotic cell cycle	278	ASPM UBE2C BIRC5 CCNA2 KIF2C CDCA8 FAM83D DLGAP5 CENPF NCAPG PRC1 BUB1 CENPA AURKB CDCA5 CDC20 NUSAP1 CEP55 TPD52L1 CCNB2 CDCA3 PTTG1 PIM1 KIFC1
Mitosis	7067	ASPM UBE2C BIRC5 CCNA2 KIF2C CDCA8 FAM83D DLGAP5 CENPF NCAPG BUB1 AURKB CDCA5 CDC20 NUSAP1 CEP55 CDCA3 CCNB2 PTTG1 KIFC1
Nuclear division	280	ASPM UBE2C BIRC5 CCNA2 KIF2C CDCA8 FAM83D DLGAP5 CENPF NCAPG BUB1 AURKB CDCA5 CDC20 NUSAP1 CEP55 CDCA3 CCNB2 PTTG1 KIFC1
Cell cycle	7049	TRIP13 CCNA2 KIF2C FAM83D DLGAP5 CENPF NCAPG PRC1 BUB1 STEAP3 AURKB CDC20 MCM7 NUSAP1 TPD52L1 CCNB2 TACC3 PIM1 UHRF1 HJURP UBE2C ASPM BIRC5 FOXM1 CDCA8 CENPA CDCA5 CEP55 CDCA3 PTTG1 KIFC1 CDC45L
Cell cycle phase	22403	TRIP13 CCNA2 KIF2C FAM83D CENPF DLGAP5 PRC1 NCAPG BUB1 AURKB CDC20 NUSAP1 TPD52L1 CCNB2 TACC3 PIM1 UBE2C ASPM BIRC5 CDCA8 CDCA5 CEP55 CDCA3 PTTG1 KIFC1
M phase	279	TRIP13 ASPM UBE2C BIRC5 CCNA2 KIF2C CDCA8 FAM83D DLGAP5 CENPF NCAPG PRC1 BUB1 AURKB CDCA5 CDC20 NUSAP1 CEP55 CCNB2 PTTG1 KIFC1
M phase of mitotic cell cycle	87	ASPM UBE2C BIRC5 CCNA2 KIF2C CDCA8 FAM83D DLGAP5 CENPF NCAPG BUB1 AURKB CDCA5 CDC20 NUSAP1 CEP55 CDCA3 CCNB2 PTTG1 KIFC1
Organelle fission	48285	ASPM UBE2C BIRC5 CCNA2 KIF2C CDCA8 FAM83D DLGAP5 CENPF NCAPG BUB1 AURKB CDCA5 CDC20 NUSAP1 CEP55 CDCA3 CCNB2 PTTG1 KIFC1
Cell cycle process	22402	TRIP13 CCNA2 KIF2C FAM83D CENPF DLGAP5 PRC1 NCAPG BUB1 AURKB CDC20 NUSAP1 TPD52L1 CCNB2 TACC3 PIM1 UBE2C ASPM BIRC5 CDCA8 CENPA CDCA5 CEP55 CDCA3 PTTG1 KIFC1
Cell division	51301	ASPM UBE2C BIRC5 CCNA2 KIF2C CDCA8 FAM83D DLGAP5 CENPF NCAPG PRC1 BUB1 AURKB CDCA5 CDC20 NUSAP1 CEP55 CCNB2 CDCA3 PTTG1 KIFC1
Spindle	5819	KIF4A CDC20 ASPM NUSAP1 BIRC5 CDCA8 FAM83D DLGAP5 CENPF PRC1 BUB1 KIFC1 AURKB
Chromosome segregation	7059	NUSAP1 HJURP BIRC5 PTTG1 DLGAP5 CENPF NCAPG KIFC1 TOP2A CDCA5
Microtubule cytoskeleton	15630	KIF4A ASPM BIRC5 KIF2C CDCA8 FAM83D DLGAP5 CENPF PRC1 BUB1 AURKB CDC20 G6PD NUSAP1 CEP55 CCNB2 NDN TACC3 KIFC1 KIF20A CDC45L
Organelle organization	6996	KIF4A CCNA2 KIF2C FAM83D DLGAP5 CENPF NCAPG PRC1 BUB1 AURKB TOP2A CDC20 NUSAP1 CCNB2 TACC3 PIM1 HJURP UBE2C ASPM BIRC5 MYH11 CDCA8 HIST1H4C CENPA CDCA5 CEP55 CDCA3 PTTG1 TNNT2 ASF1B KIFC1
Chromosome, centromeric region	775	HJURP BIRC5 KIF2C CDCA8 CENPF BUB1 CENPA CENPM AURKB
Organelle localization	51640	ASPM NUSAP1 BIRC5 DLGAP5 CENPF CENPA TACC3 CDCA5
Chromosome passenger complex	32133	BIRC5 CDCA8 AURKB
DNA conformation change	71103	MCM7 NUSAP1 HJURP HIST1H4C ASF1B NCAPG CENPA TOP2A CDCA5
Cytoskeletal part	44430	KIF4A ASPM BIRC5 MYH11 KIF2C CDCA8 FAM83D DLGAP5 CENPF PRC1 BUB1 AURKB CDC20 G6PD NUSAP1 CEP55 TNNT2 NDN TACC3 KIFC1 KIF20A CDC45L
Condensed chromosome, centromeric region	779	HJURP KIF2C CENPF BUB1 CENPA CENPM AURKB
DNA packaging	6323	NUSAP1 HJURP HIST1H4C ASF1B NCAPG CENPA TOP2A CDCA5
Spindle pole	922	ASPM FAM83D DLGAP5 CENPF PRC1 BUB1
Chromosomal part	44427	MCM7 HJURP BIRC5 KIF2C CDCA8 HIST1H4C CENPF ASF1B NCAPG BUB1 CENPA CENPM AURKB
Condensed chromosome	793	HJURP KIF2C CENPF NCAPG BUB1 CENPA CENPM AURKB

(continued)

SUPPLEMENTARY TABLE S10. (CONTINUED)

<i>Gene ontology</i>	<i>GO ID</i>	<i>Genes</i>
Cellular component organization	16043	KIF4A CCNA2 KIF2C FAM83D DLGAP5 CENPF NCAPG PRC1 BUB1 AURKB TOP2A TEK COL12A1 CDC20 NUSAP1 TPD52L1 CCNB2 TACC3 PIM1 ASPM UBE2C HJURP BIRC5 MYH11 ID1 LDLR CDCA8 HIST1H4C CENPA CDCA3 CEP55 CDCA3 PTTG1 TNNT2 NDN ASF1B KIFC1
Mitotic sister chromatid segregation	70	NUSAP1 DLGAP5 NCAPG KIFC1 CDCA5
Chromosome localization	50000	BIRC5 DLGAP5 CENPF CDCA5
Establishment of chromosome localization	51303	BIRC5 DLGAP5 CENPF CDCA5
Sister chromatid segregation	819	NUSAP1 DLGAP5 NCAPG KIFC1 CDCA5
Oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water	16717	FADS2 SCD FADS1
Condensed chromosome kinetochore	777	HJURP KIF2C CENPF BUB1 CENPA CENPM
Establishment of organelle localization	51656	NUSAP1 BIRC5 DLGAP5 CENPF CENPA CDCA5
Extracellular region part	44421	SFRP1 PCOLCE SULF1 LDLR CXCL12 IL32 MAMDC2 COL16A1 COL12A1 CECR1 EMILIN2 FLT3LG CRLF1 FBLN2 SCRG1 CXCL2 FBLN1 HAPLN1 LAMA4 TIMP3
DNA metabolic process	6259	MCM10 MCM7 TRIP13 UHRF1 GINS2 TPD52L1 PTTG1 CENPF NYNRIN PIM1 TYMS TK1 TOP2A CDC45L
Centromere complex assembly	34508	HJURP CENPF CENPA
Centrosome	5813	CDC20 G6PD BIRC5 CEP55 DLGAP5 NDN TACC3 CDC45L
Chromosome	5694	MCM7 HJURP BIRC5 KIF2C CDCA8 HIST1H4C CENPF ASF1B NCAPG BUB1 CENPA CENPM AURKB
Microtubule organizing center	5815	CDC20 G6PD BIRC5 CEP55 DLGAP5 NDN BUB1 TACC3 KIFC1 CDC45L
Cellular process	9987	SLC40A1 EGR1 TRIP13 CIS CXCL12 NCAPG MAMDC2 STEAP3 COL12A1 TOP2A AURKB TEK CECR1 NQO1 PTGS1 CDC20 EMILIN2 PCK2 MARCKSL1 KCNG1 CCNB2 TACC3 TYMS KIF20A TK1 FADS2 ASPM UBE2C HJURP MYH11 FOXM1 CDCA8 HIST1H4C SLC7A5 NYNRIN CENPA PP1R13L CDCA5 CACNA1H CDCA3 TNNT2 ASF1B NDN LAMA4 KIFC1 CHAC1 CDC45L KIF4A SFRP1 CCNA2 GINS2 KIF2C FAM83D DLGAP5 CENPF PRC1 BUB1 PHGDH MCM10 WISP1 MCM7 G6PD NUSAP1 MELK TPD52L1 HAPLN1 PIM1 STXBP6 TROAP UHRF1 BIRC5 ID1 TRIB3 SULF1 LDLR SCD GSDMD IL32 MTHFD2 COL16A1 ASNS FADS1 TNFAIP6 CEP55 PTTG1 PSAT1 SLC40A1 SLC6A9 CIS CFB NCAPG STEAP3 AURKB TOP2A PTGS1 NQO1 EMILIN2 CDC20 FLT3LG PCK2 SIP1L2 MARCKSL1 KCNG1 SCRG1 TACC3 HJURP PCOLCE FOXM1 CDCA8 NYNRIN CENPA PPP1R13L CACNA1H CDCA3 TNNT2 NDN ASF1B LAMA4 KIFC1 CHAC1 SFRP1 CCNA2 FAM83D TMEM119 CENPF PRC1 CDCA7 SPANXA2 WISP1 NUSAP1 CRLF1 GPR124 ADHI1A SORBS2 PIM1 C20ORF100 ID1 LDLR SCD IL32 COL16A1 CXCR7 FADS1 CXCL2 PTTG1 CIR SPANXA1 EGR1 TRIP13 CXCL12 SHISA2 MAMDC2 TEK COL12A1 CECR1 FBLN1 CCNB2 TYMS RAB33A TK1 KIF20A S100A10 FADS2 UBE2C ASPM MYH11 INHBE HIST1H4C SLC7A5 SUSD2 CDCA5 TIMP3 CDC45L KIF4A GINS2 KIF2C DLGAP5 BUB1 PHGDH MCM10 G6PD MCM7 MELK TPD52L1 HAPLN1 STXBP6 TROAP UHRF1 BIRC5 TRIB3 SULF1 GSDMD MTHFD2 ASNS TNFAIP6 OLFML3 CEP55 CRIP1 PSAT1
Biological_process	8150	SLC40A1 EGR1 TRIP13 CIS CXCL12 NCAPG MAMDC2 STEAP3 COL12A1 TOP2A AURKB TEK CECR1 NQO1 PTGS1 CDC20 EMILIN2 PCK2 MARCKSL1 KCNG1 CCNB2 TACC3 TYMS KIF20A TK1 FADS2 ASPM UBE2C HJURP MYH11 FOXM1 CDCA8 HIST1H4C SLC7A5 NYNRIN CENPA PP1R13L CDCA5 CACNA1H CDCA3 TNNT2 ASF1B NDN LAMA4 KIFC1 CHAC1 CDC45L KIF4A SFRP1 CCNA2 GINS2 KIF2C FAM83D DLGAP5 CENPF PRC1 BUB1 PHGDH MCM10 WISP1 MCM7 G6PD NUSAP1 MELK TPD52L1 HAPLN1 PIM1 STXBP6 TROAP UHRF1 BIRC5 ID1 TRIB3 SULF1 LDLR SCD GSDMD IL32 MTHFD2 COL16A1 ASNS FADS1 TNFAIP6 CEP55 PTTG1 PSAT1 SLC40A1 SLC6A9 CIS CFB NCAPG STEAP3 AURKB TOP2A PTGS1 NQO1 EMILIN2 CDC20 FLT3LG PCK2 SIP1L2 MARCKSL1 KCNG1 SCRG1 TACC3 HJURP PCOLCE FOXM1 CDCA8 NYNRIN CENPA PPP1R13L CACNA1H CDCA3 TNNT2 NDN ASF1B LAMA4 KIFC1 CHAC1 SFRP1 CCNA2 FAM83D TMEM119 CENPF PRC1 CDCA7 SPANXA2 WISP1 NUSAP1 CRLF1 GPR124 ADHI1A SORBS2 PIM1 C20ORF100 ID1 LDLR SCD IL32 COL16A1 CXCR7 FADS1 CXCL2 PTTG1 CIR SPANXA1 EGR1 TRIP13 CXCL12 SHISA2 MAMDC2 TEK COL12A1 CECR1 FBLN1 CCNB2 TYMS RAB33A TK1 KIF20A S100A10 FADS2 UBE2C ASPM MYH11 INHBE HIST1H4C SLC7A5 SUSD2 CDCA5 TIMP3 CDC45L KIF4A GINS2 KIF2C DLGAP5 BUB1 PHGDH MCM10 G6PD MCM7 MELK TPD52L1 HAPLN1 STXBP6 TROAP UHRF1 BIRC5 TRIB3 SULF1 GSDMD MTHFD2 ASNS TNFAIP6 OLFML3 CEP55 CRIP1 PSAT1

(continued)

SUPPLEMENTARY TABLE S10. (CONTINUED)

<i>Gene ontology</i>	<i>GO ID</i>	<i>Genes</i>
Cytoskeleton	5856	KIF4A ASPM BIRC5 MYH11 KIF2C CDCA8 FAM83D DLGAP5 CENPF PRC1 BUB1 AURKB CDC20 G6PD NUSAP1 CEP55 CCNB2 TNNT2 SORBS2 NDN TACC3 KIFC1 KIF20A CDC45L
Kinetochore	776	HJURP KIF2C CENPF BUB1 CENPA CENPM
Regulation of mitotic cell cycle	7346	UBE2C NUSAP1 BIRC5 CCNA2 DLGAP5 CENPF BUB1 ASNS
Chromosome condensation	30261	NUSAP1 NCAPG TOP2A CDCA5
Protein binding	5515	EGRI TRIP13 CFB CXCL12 NCAPG TOP2A AURKB TEK CECR1 CDC20 EMILIN2 FLT3LG SIPA1L2 MARCKSL1 KCNG1 FBLN1 CCNB2 TACC3 RAB33A SI00A10 KIF20A ASPM UBE2C HJURP MYH11 PCOLCE FOXM1 INHBE CDCA8 HIST1H4C CENPA PPP1R13L CDCA5 SUSD2 TNNT2 NDN ASF1B LAMA4 CHAC1 CDC45L TIMP3 KIF4A SFRP1 CCNA2 GINS2 KIF2C DLGAP5 CENPF PRC1 BUB1 MCM10 WISP1 MCM7 G6PD NUSAP1 CRLF1 MELK GPR124 TPD52L1 SORBS2 ADH1A PIM1 UHRF1 BIRC5 ID1 TRIB3 LDLR IL32 MTHFD2 COL16A1 ASNS CXCR7 FADS1 CXCL2 CRIP1 PTTG1 FAM64A
DNA replication	6260	MCM10 MCM7 GINS2 CENPF TYMS TK1 TOP2A CDC45L
Regulation of cell cycle process	10564	UBE2C NUSAP1 BIRC5 FOXM1 DLGAP5 CENPF BUB1
Microtubule-based process	7017	KIF4A UBE2C NUSAP1 KIF2C PRC1 CENPA TACC3 KIFC1 KIF20A
Nonmembrane-bounded organelle	43228	KIF4A KIF2C FAM83D DLGAP5 CENPF NCAPG PRC1 BUB1 AURKB CDC20 MCM7 G6PD NUSAP1 CCNB2 SORBS2 TACC3 PIM1 CENPM KIF20A HJURP ASPM BIRC5 MYH11 CDCA8 HIST1H4C CENPA CEP55 TNNT2 NDN ASF1B FAM64A KIFC1 CDC45L
Intracellular nonmembrane-bounded organelle	43232	KIF4A KIF2C FAM83D DLGAP5 CENPF NCAPG PRC1 BUB1 AURKB CDC20 MCM7 G6PD NUSAP1 CCNB2 TNNT2 NDN ASF1B FAM64A KIFC1 CDC45L
Regulation of cell cycle	51726	UBE2C NUSAP1 BIRC5 CCNA2 FOXM1 DLGAP5 CENPF BUB1 PIM1 TACC3 ASNS CDC45L
Spindle microtubule	5876	KIF4A NUSAP1 BIRC5 PRC1
Chromosome organization	51276	HJURP CDCA8 HIST1H4C DLGAP5 CENPF NCAPG CENPA TOP2A CDCA5 NUSAP1 PTTG1 ASF1B KIFC1
Mitotic chromosome condensation	7076	NUSAP1 NCAPG CDCA5
Condensed nuclear chromosome, centromeric region	780	BUB1 CENPA AURKB
Extracellular matrix	31012	EMILIN2 SFRP1 FBLN2 FBLN1 HAPLN1 MAMDC2 COL16A1 LAMA4 COL12A1 TIMP3
Spindle checkpoint	31577	BIRC5 CENPF BUB1
Positive regulation of cell cycle	45787	NUSAP1 BIRC5 DLGAP5 PIM1 ASNS
Organic acid biosynthetic process	16053	FADS2 SCD PSAT1 ASNS PHGDH FADS1 PTGS1
Carboxylic acid biosynthetic process	46394	FADS2 SCD PSAT1 ASNS PHGDH FADS1 PTGS1
L-serine biosynthetic process	6564	PSAT1 PHGDH
Stearoyl-CoA 9-desaturase activity	4768	FADS2 SCD

(continued)

SUPPLEMENTARY TABLE S10. (CONTINUED)

<i>Gene ontology</i>	<i>GO ID</i>	<i>Genes</i>
Positive regulation of cell cycle process	90068	UBE2C NUSAP1 BIRC5 DLGAP5
Small molecule biosynthetic process	44283	FADS2 G6PD PCK2 SCD PSAT1 ASNS TYMS PHGDH FADS1 CECR1 PTGS1
Extracellular matrix structural constituent	5201	EMILIN2 FBLN2 FBLN1 LAMA4 COL12A1
Proteinaceous extracellular matrix	5578	EMILIN2 FBLN2 FBLN1 HAPLN1 MAMDC2 COL16A1 LAMA4 COL12A1 TIMP3
Positive regulation of exit from mitosis	31536	UBE2C BIRC5
Kinetochores assembly	51382	CENPF CENPA
Cytokinesis	910	NUSAP1 BIRC5 PRC1 AURKB
Cofactor binding	48037	G6PD BIRC5 PSAT1 STEAP3 ASNS TYMS PHGDH NQO1
Cellular biosynthetic process	44249	FADS2 TRIP13 GINS2 FOXMI1 LDLR SCD MTHFD2 CENPF ASNS PHGDH TOP2A FADS1 NQO1 PTGS1 CECR1 MCM10 MCM7 G6PD PCK2 PTTG1 PSAT1 TYMS TK1 CDC45L
Protein-DNA complex assembly	65004	HJURP HIST1H4C CENPF ASF1B CENPA
Microtubule associated complex	5875	BIRC5 KIF2C CDCA8 KIFC1 AURKB
Regulation of mitotic metaphase/anaphase transition	30071	DLGAP5 CENPF BUB1
Kinetochores organization	51383	CENPF CENPA
Microtubule cytoskeleton organization	226	UBE2C NUSAP1 KIF2C PRC1 CENPA TACC3
Interphase of mitotic cell cycle	51329	BIRC5 TPD52L1 CENPF PIM1 CDCA5
Nucleus	5634	SPANXA1 EGR1 TRIP13 KIAA0101 NCAPG TOP2A AURKB PTGS1 CDC20 CCNB2 CENPM KIF20A HJURP UBE2C ASPM FOXMI1 CDCA8 HIST1H4C CENPA PPP1R13L CDCA5 CACNA1H NDN ASF1B KIFC1 CDC45L KIF4A CCNA2 GINS2 KIF2C CENPF DLGAP5 PRC1 CDCA7 BUB1 SPANXA2 MCM10 MCM7 NUSAP1 SORBS2 PIM1 C20ORF100 UHRF1 BIRC5 IDI1 TRIB3 SCD FADS1 HCFC1R1 SPANXE PTTG1 FAM64A COL16A1 COL12A1
FACIT collagen	5593	COL16A1 COL12A1
Regulation of mitosis	7088	NUSAP1 DLGAP5 CENPF BUB1
Regulation of nuclear division	51783	NUSAP1 DLGAP5 CENPF BUB1
Midbody	30496	BIRC5 CENPF AURKB
Interphase	51325	BIRC5 TPD52L1 CENPF PIM1 CDCA5
Cell cycle checkpoint	75	BIRC5 CCNA2 CENPF BUB1 CDC45L
Biosynthetic process	9058	FADS2 TRIP13 GINS2 FOXMI1 LDLR SCD MTHFD2 CENPF ASNS PHGDH TOP2A FADS1 NQO1 PTGS1 CECR1 MCM10 MCM7 G6PD PCK2 PTTG1 PSAT1 TYMS TK1 CDC45L
Extracellular region	5576	SFRP1 C1S CFB CXCL12 MAMDC2 COL12A1 CECR1 WISPI FLT3LG EMILIN2 CRLF1 SCRG1 FBLN1 HAPLN1 PCOLCE SULF1 LDLR INHBE IL32 COL16A1 OLFML3 FBLN2 CXCL2 LAMA4 C1R TIMP3 PSAT1 PHGDH
L-serine metabolic process	6563	PSAT1 PHGDH
Anchoring collagen	30934	COL16A1 COL12A1

(continued)

SUPPLEMENTARY TABLE S10. (CONTINUED)

<i>Gene ontology</i>	<i>GO ID</i>	<i>Genes</i>
Establishment of mitotic spindle localization	40001	NUSAP1 CENPA
Extracellular space	5615	SFRP1 PCOLCE SULF1 LDLR CXCL12 IL32 COL12A1 CECR1 FLT3LG CRLF1 SCRG1 CXCL2 FBLN1
Response to stress	6950	TRIP13 UHRF1 CCNA2 TRIB3 C1S CFB IL32 ASNS TOP2A FADS1 NQO1 PTGS1 TNFAIP6 MCM7 G6PD CXCL2 PTTG1 CIR TACC3 PIM1 TYMS CHAC1 TIMP3
Microtubule motor activity	3777	KIF4A KIF2C KIFC1 KIF20A
Binding	5488	EGR1 TRIP13 C1S CXCL12 CFB MAMDC2 NCAPG STEAP3 TEK TOP2A AURKB CECR1 NQO1 PTGS1 CDC20 EMILIN2 FLT3LG SIPA1L2 PCK2 MARCKSL1 KCNG1 FBLN1 CCNB2 TACC3 RAB33A TYMS SI00A10 KIF20A TKI FADS2 ASPM UBE2C HJURP MYH11 PCOLCE FOXMI1 INHBE CDCA8 HIST1H4C SLC7A5 NYNRIN CENPA PPP1R13L CDCA5 SUSD2 TNNT2 ASF1B NDN LAMA4 KIFC1 CHAC1 CDC45L TIMP3 KIF4A SFRP1 CCNA2 GINS2 KIF2C DLGAP5 CENPF PRC1 BUB1 PHGDH MCM10 WISP1 MCM7 G6PD NUSAP1 CRLF1 MELK GPR124 TPD52L1 HAPLN1 SORBS2 ADH1A PIM1 C20ORF100 UHRF1 BIRC5 ID1 TRIB3 SULF1 LDLR SCD IL32 MTHFD2 COL16A1 ASNS CXCR7 FADS1 TNFAIP6 FBLN2 CXCL2 CRIP1 PTTG1 PSAT1 CIR FAM64A
Unsaturated fatty acid	6636	FADS2 FADS1 PTGS1
biosynthetic process		
Response to chemical stimulus	42221	EGR1 CCNA2 ID1 TRIB3 C1S LDLR CXCL12 CENPF ASNS FADS1 NQO1 PTGS1 G6PD PCK2 CXCL2 TNNT2 PIM1 TYMS CHAC1 TIMP3
Mitotic cell cycle spindle assembly checkpoint	7094	CENPF BUB1
Regulation of chromosome segregation	51983	KIF2C BUB1
Developmental process	32502	SLC40A1 EGR1 TRIP13 SFRP1 CCNA2 C1S SHISA2 CENPF BUB1 PHGDH COL12A1 CECR1 PTGS1 CDC20 G6PD CRLF1 SCRG1 CCNB2 TACC3 PIM1 ASPM MYH11 PCOLCE ID1 FOXMI1 SLC7A5 ASNS FADS1 OLFML3 CACNA1H TNNT2 NDN ASF1B LAMA4 TIMP3
Arachidonic acid metabolic process	19369	FADS1 PTGS1
Negative regulation of mitotic metaphase/anaphase transition	45841	CENPF BUB1
Spindle localization	51653	NUSAP1 CENPA
Establishment of spindle localization	51293	NUSAP1 CENPA
Mitotic cell cycle spindle checkpoint	71174	CENPF BUB1
Serine family amino acid biosynthetic process	9070	PSAT1 PHGDH
Nucleosome assembly	6334	HJURP HIST1H4C ASF1B CENPA
Complement activation	6956	C1S CFB CIR
Phosphoinositide-mediated signaling	48015	UBE2C HIST1H4C TYMS TOP2A
Cellular response to stimulus	51716	EGR1 TRIP13 UHRF1 CCNA2 TRIB3 GSDMD ASNS TOP2A FADS1 NQO1 G6PD MCM7 PTTG1 PIM1 TYMS

(continued)

SUPPLEMENTARY TABLE S10. (CONTINUED)

<i>Gene ontology</i>	<i>GO ID</i>	<i>Genes</i>
Activation of plasma proteins involved in acute inflammatory response	2541	C1S CFB C1R
Motor activity	3774	KIF4A MYH11 KIF2C KIFC1 KIF20A
Cell proliferation	8283	MCM7 UHRF1 ASPM KIF2C CRIP1 DLGAP5 CENPF PIM1 TACC3
Fatty acid biosynthetic process	6633	FADS2 SCD FADS1 PTGS1
Chromatin assembly	31497	HJURP HIST1H4C ASF1B CENPA
Regulation of exit from mitosis	7096	UBE2C BIRC5
Spindle assembly checkpoint	71173	CENPF BUB1
Cellular macromolecular complex subunit organization	34621	UBE2C HJURP MYH11 KIF2C HIST1H4C CENPF ASF1B CENPA
Response to hormone stimulus	9725	EGR1 PCK2 CCNA2 TRIB3 LDLR ASNS FADS1 TIMP3 PTGS1
Cytoplasm	5737	SPANXA1 SLC40A1 EGR1 KIAA0101 SHISA2 NCAPG MAMDC2 STEAP3 TOP2A AURKB NQO1 PTGS1 CDC20 PCK2 CCNB2 TACC3 CENPM TK1 KIF20A FADS2 HJURP UBE2C ASPM MYH11 CDCA8 SLC7A5 PPP1R13L CDCA5 CACNA1H CDCA3 TNNT2 NDN KIFC1 CHAC1 CDC45L TIMP3 KIF4A CCNA2 KIF2C FAM83D DLGAP5 CENPF PRC1 BUB1 SPANXA2 MCM7 G6PD NUSAP1 MELK TPD52L1 SORBS2 ADH1A PIM1 STXBP6 TROAP BIRC5 SULF1 LDLR SCD MTHFD2 ASNS FADS1 HCFC1R1 CEP55 SPANXE CRIP1 PTTG1
Cellular response to stress	33554	MCM7 G6PD TRIP13 UHRF1 CCNA2 PTTG1 PIM1 ASNS TYMS FADS1 TOP2A
Metaphase plate congression	51310	CENPF CDCA5