

Transcriptome-based screening of ion channels and transporters in a migratory chondroprogenitor cell line isolated from late-stage osteoarthritic cartilage

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TaqMan Array 96 - Well FAST Plate P/N: 4413255
 Production Order: 2541818
 Plate Name: Custom Config.1X96

Assay IDs

	1	2	3	4	5	6	7	8	9	10	11	12
A	Hs99999901_s1	Hs99999908_m1	Hs99999905_m1	Hs99999909_m1	Hs04194521_s1	Hs00240655_m1	Hs00609480_m1	Hs00167753_m1	Hs00167789_m1	Hs00193172_m1	Hs00367969_m1	Hs00234934_m1
B	Hs00184168_m1	Hs00163885_m1	Hs00167681_m1	Hs00704965_s1	Hs04176264_s1	Hs00267404_s1	Hs00366312_m1	Hs01038858_m1	Hs01851693_s1	Hs03043902_s1	Hs01848195_s1	Hs00175686_m1
C	Hs00247255_m1	Hs00175689_m1	Hs00175706_m1	Hs01112471_m1	Hs01003997_m1	Hs00175721_m1	Hs00218912_m1	Hs00901640_m1	Hs00376854_m1	Hs01099348_m1	Hs00219765_m1	Hs00367960_m1
D	Hs00608195_m1	Hs00162985_m1	Hs00211805_m1	Hs00202960_m1	Hs00175753_m1	Hs03046013_m1	Hs00259863_m1	Hs00743683_s1	Hs00963373_m1	Hs00957788_m1	Hs00181881_m1	Hs00181916_m1
E	Hs00609908_m1	Hs00166991_m1	Hs00181461_m1	Hs00168821_m1	Hs01092295_m1	Hs00544877_m1	Hs00193090_m1	Hs00155949_m1	Hs01090453_m1	Hs00222625_m1	Hs00608066_m1	Hs00253432_m1
F	Hs00392875_m1	Hs01567972_m1	Hs00168906_m1	Hs00165722_m1	Hs00161595_m1	Hs00168918_m1	Hs00163961_m1	Hs00189078_m1	Hs00156541_m1	Hs00163986_m1	Hs00154518_m1	Hs00241850_m1
G	Hs00427895_g1	Hs00426158_g1	Hs00559461_m1	Hs00362166_g1	Hs00749895_s1	Hs00213494_m1	Hs00401339_m1	Hs00976287_m1	Hs00998916_m1	Hs00185016_m1	Hs00266938_m1	Hs00188073_m1
H	Hs00175772_m1	Hs00205246_m1	Hs00205704_m1	Hs00158457_m1	Hs01030641_m1	Hs01546821_m1	Hs00158470_m1	Hs01028916_m1	Hs00292214_s1	Hs01105469_g1	Hs00242342_m1	Hs00175573_m1

Gene Symbols

	1	2	3	4	5	6	7	8	9	10	11	12
A	18S	GUSB	GAPDH	HPRT1	PPIA	CACNA1A	CACNA1B	CACNA1D	CACNA1E	CACNA1F	CACNA1G	CACNA1H
B	CACNA1I	CACNA1S	CACNA1C	P2RY1	P2RY2	P2RY4	P2RY6	P2RY11	P2RY12	P2RY13	P2RY14	P2RX1
C	P2RX2	P2RX3	P2RX4	P2RX5	P2RX6	P2RX7	TRPV1	TRPV2	TRPV3	TRPV4	TRPV5	TRPV6
D	TRPC1	TRPC3	TRPC4	TRPC5	TRPC6	ORAI1	ORAI2	ORAI3	STIM1	STIM2	ITPR1	ITPR2
E	ITPR3	RYR1	RYR2	RYR3	ATP2A1	ATP2A2	ATP2A3	ATP2B1	ATP2B2	ATP2B3	ATP2B4	SLC8A1
F	SLC8A2	SLC8A3	SCNN1A	SCNN1B	SCNN1D	SCNN1G	CLCN1	CLCN2	CLCN4	CLCN5	CLCN6	CLCN7
G	CLCNKA	CLCNKB	CLIC1	CLIC3	CLIC4	CLIC5	CLIC6	CLCA1	CLCA2	CLCA3P	KCNMA1	KCNMB1
H	KCNMB2	KCNMB3	KCNMB4	KCNN1	KCNN2	KCNN3	KCNN4	AQP1	AQP2	AQP3	AQP4	AQP9

Table S1. Details (assay numbers, gene symbols, plate layout) of the custom configured TaqMan 96-Well Fast Gene Expression Array plate (Design ID: PP00XUF; Thermo Fisher Scientific).

<i>Primer</i>	<i>GenBank Accession Number</i>	<i>Sequence</i>	<i>Amplicon Size (bp)</i>
KCNMA1_F	NM_001322829.2	TGGATGCGCTCATCATCCCG	197
KCNMA1_R		AATCTTCTGGGCCTCCTTCGTC	
KCNMB1_F	NM_004137.4	GTACCACACGGAGGACACTC	179
KCNMB1_R		GCTGGAATAGGACGCTGGTT	
KCNMB2_F	NM_001278911.2	TGAATGCGTCCATCACGGAA	115
KCNMB2_R		TCCCCGGAAGAAGTCAGGTT	
KCNMB3_F	NM_001163677.2	CATCCCCGTGCAAATCACAC	184
KCNMB3_R		GAAGCCCATCATGGCAAACC	
KCNMB4_F	NM_014505.6	GATGAGATTGGTTCCCAGCCA	142
KCNMB4_R		GAACGCCACCACAAATGTC	
KCNN1_F	NM_001386974.1	GGTACCACGACAAGCAGGAA	374
KCNN1_R		GGCTTGGAGGAACCTACGCT	
KCNN3_F	NM_001204087.2	GGCGGATAGCCATGACCTAC	106
KCNN3_R		CGTGCCGTCCAGAAGAACTT	
KCNN4_F	NM_002250.3	AAGCTCCGGGAACAAGTGAAC	123
KCNN4_R		CGCCAGCGTGTCATCTGT	
RPS18_F	NM_022551.3	CACAGGAGGCCTACACGCCG	119
RPS18_R		AGGCTATTTTCCGCCGCCCA	
PPIA_F	NM_021130.5	GCGTCTCCTTTGAGCTGTTTG	368
PPIA_R		GGCCTCCACAATATTCATGCC	
HPRT1_F	NM_000194.2	GAACCTCTCGGCTTTCCCG	153
HPRT1_R		CATCACTAATCACGACGCCA	

Table S2. Sequences of primer pairs used for the validation of the microarray data.

<i>Protein class</i>	<i>Positive correlation (%)</i>
Transporters	64.6
Receptors	67.3
Enzymes	64.8
Extracellular matrix	50.8
Adhesion	67.1
Unclassified	60.1
Overall	64.1

Table S3. Correlation analysis between up and down regulation patterns of proteins identified in the surfaceome of CPCs and MSCs using quantitative proteomics analysis (C. Matta et al., 2019; PMID: 31227739 PMID: PMC6588563 DOI: 10.1038/s41598-019-44957-y), and their transcripts using Affymetrix analysis.

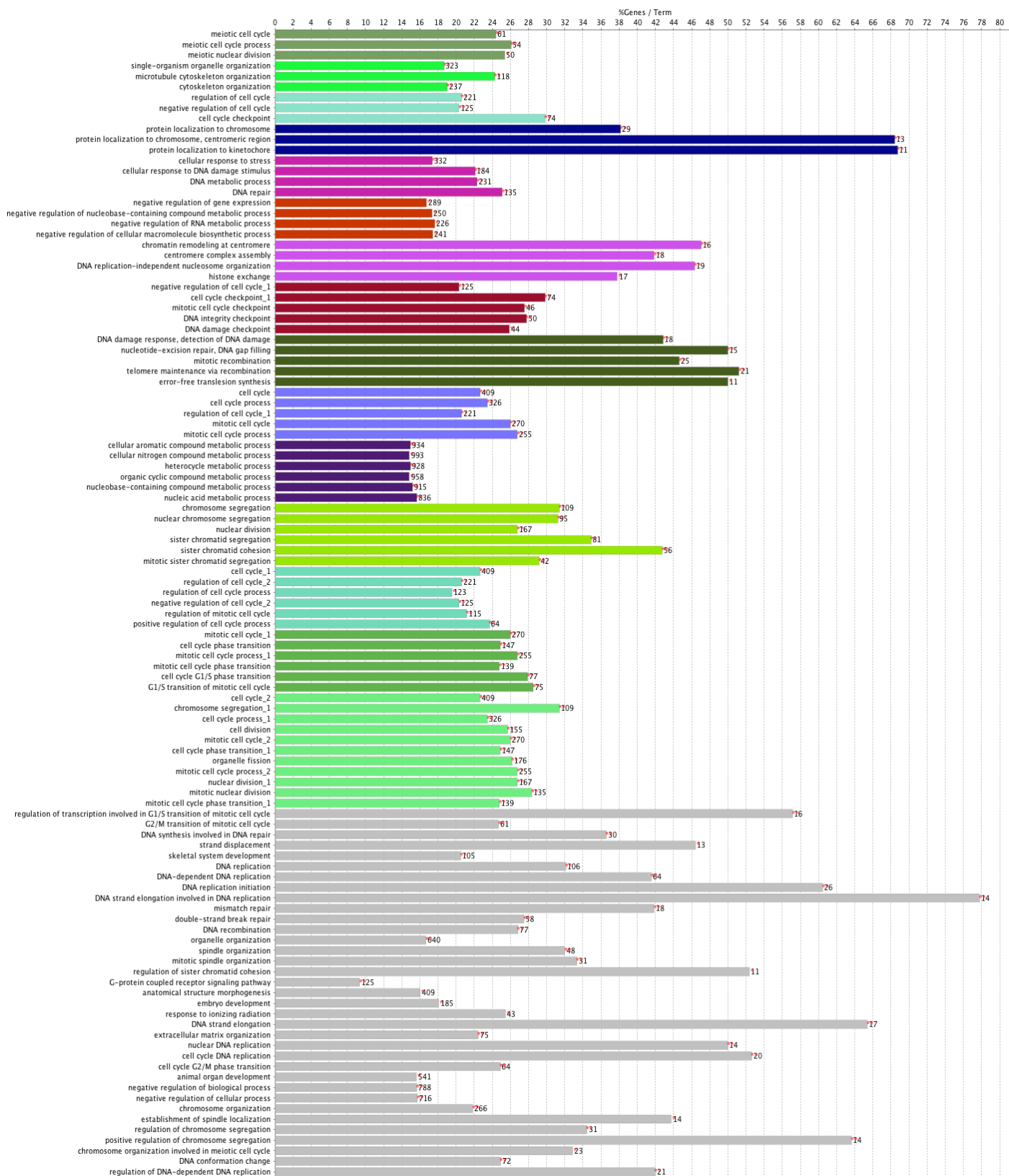


Figure S1. Boxplot summarising the overrepresented Gene ontology pathways in CPCs vs MSCs analysed by Cytospace CluGO. Coloured bars indicate significantly overrepresented pathways (cut-off value: $P < 0.05$).