

Supplementary Information

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Table S2: RNA sequencing on human melanoma cell lines. Expression of Cell migration related genes in three melanoma cell lines, WM1862, WM983A and WM983B.

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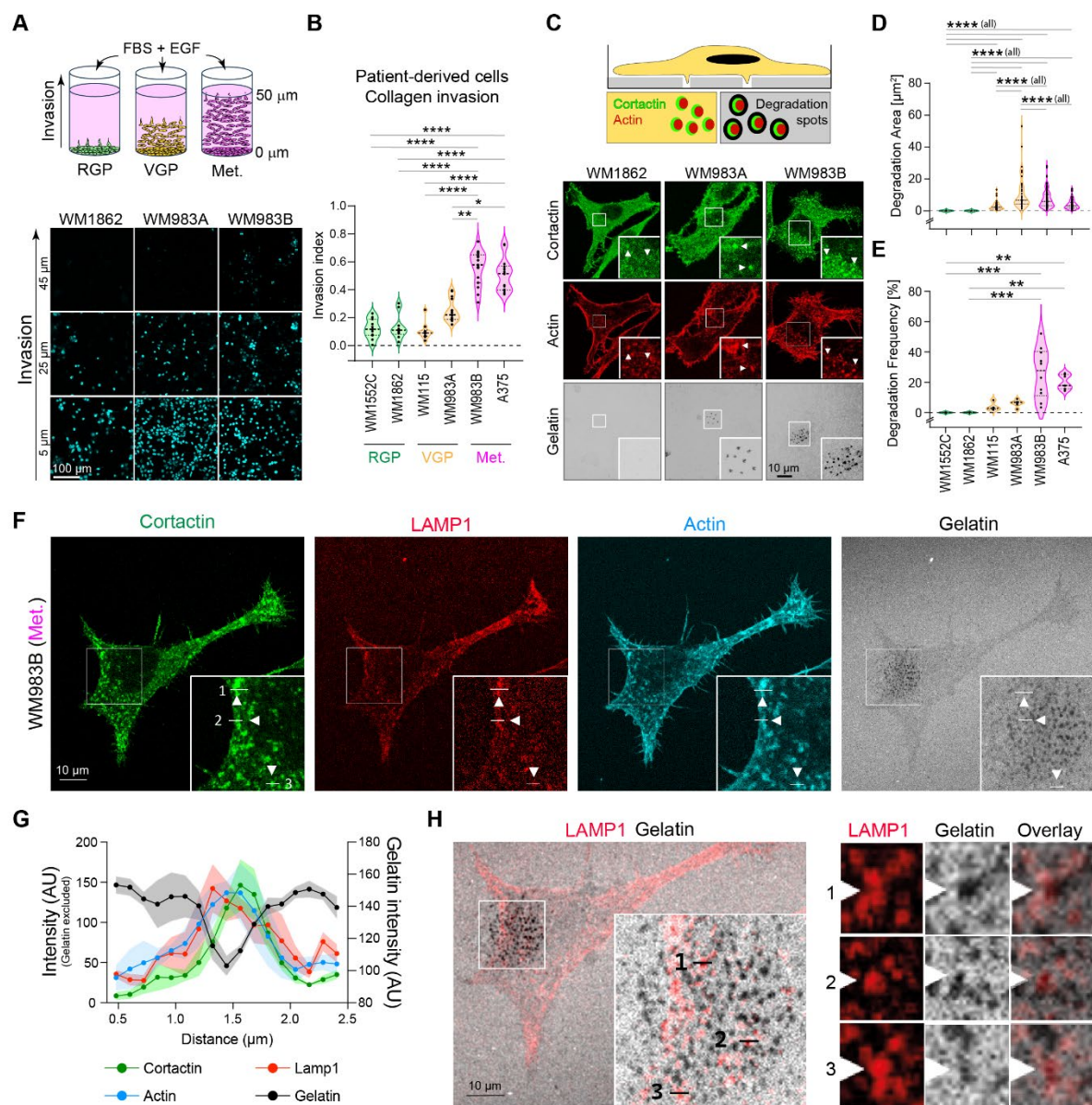


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Figure S1: Melanoma invasiveness correlates with matrix degradation.

A-B) Invasive potential of human melanoma cells (WM1552c, WM1862, WM115, WM983A, WM983B, A375) was analyzed using collagen invasion assay. **A)** Representative images showing cell invasion after 24 hours. Spreading distance was analyzed by confocal imaging. **B)** For each cell line, the invasion index equals the number of nuclei above 10 μm distance divided by the total number of cells, (Mean $\pm$ SD) = 0.1213 ± 0.070 , 0.1334 ± 0.089 , 0.2500 ± 0.080 , 0.1036 ± 0.060 , 0.5562 ± 0.125 , 0.5070 ± 0.117 , respectively, in triplicate, one dot represents 1 field of view. Kruskal-Wallis with Dunn's multiple comparison post-hoc test, p values (from top): <0.0001 , <0.0001 , <0.0001 , <0.0001 , <0.0001 , 0.0287 , 0.0050 . **C-E)** Degradation capacity of the melanoma cell lines was assessed using gelatin degradation assay allowing to visualize actin (red), cortactin (green) and degradation spots (black). **C)** Representative images of cells seeded on FITC-gelatin for 24 hours, stained with cortactin and phalloidin and imaged by TIRF microscopy. **D)** For cells displaying degradation activity, the degradation area (total area per cell) was quantified, (Mean $\pm$ SD) = 0.00 , 0.00 , 11.13 ± 11.00 , 3.19 ± 2.76 , 7.48 ± 5.59 , 3.99 ± 2.97 , respectively, in triplicate, one dot represents 1 cell, Kruskal-Wallis with Dunn's multiple comparison post-hoc test, p values <0.0001 . **E)** Degradation frequency was calculated as a percentage of cells displaying gelatin degradation activity, (Mean $\pm$ SD) = 0.00 , 0.00 , 6.19 ± 2.26 , 4.00 ± 2.94 , 26.08 ± 16.52 , 20.08 ± 4.79 , respectively, in triplicate, one dot represents 1 field of view. Kruskal-Wallis with Dunn's multiple comparison post-hoc test, p values (from top): 0.0012 , 0.0003 , 0.0012 , 0.0003 . **F-H)** WM983B cells were seeded on gelatin for 24 hours, fixed and stained with cortactin (green), LAMP1 antibody (red) and phalloidin (actin, cyan). **G)** The level of colocalization was quantified by line profiling in ImageJ. **H)** Zoom on partial colocalization between LAMP1 and gelatin degradation spots in three different regions. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; **** $p < 0.0001$. Source data are provided as a Source Data file.

Figure S2: Lysosome position, size and number changes along melanoma progression.

A-B) Lysosome positioning in non-constrained cells scales with metastatic potential in human melanoma cells. **A)** Representative images of LysoTracker staining, live cell imaging in RGP (WM1552c and WM1862), VGP (WM115 and WM983A) and metastatic (WM983B) patient-derived cells, n=60, n=51, n=107, n=40, n=108, respectively, in triplicate. Extended data for Figure 1B. **B)** Quantification of lysosome spreading index (Mean $\pm$ SD) = 2.294 ± 0.8067 , 3.390 ± 1.597 , 4.124 ± 1.036 , 4.477 ± 1.180 , 4.111 ± 1.225 , respectively. Kruskal-Wallis with Dunn's multiple comparison post-hoc test, p values (from top): <0.0001 , <0.0001 , <0.0001 , <0.0001 , 0.0130 , 0.0017 , 0.0075 . **C-D)** Lysosome distribution, number and volume in melanoma cells grown on micropatterns. **C)** 3D density maps of LAMP1 in WM1862, WM983A, WM983B cells, calculated in R software, displaying the smallest area that can be occupied by 25, 50 and 75% of all compartments, in triplicate. **D)** Graphs showing (left) lysosome number (Mean $\pm$ SD) = 405.9 ± 68 , 341.9 ± 74 , 479.7 ± 99 , respectively, and (right) volume (Mean $\pm$ SD) = 0.2211 ± 0.023 , 0.2035 ± 0.021 , 0.2071 ± 0.034 , respectively, in cells grown on micropatterns. One dot represents one cell, Kruskal-Wallis with Dunn's multiple comparison post-hoc test, p value <0.0001 in all significant comparisons. **E)** Graphs showing normalized fluorescence of lysosome mass with LysoTracker (top) (Mean $\pm$ SD) = 1.21 ± 0.18 , 1.02 ± 0.08 , 0.77 ± 0.16 , respectively, (middle) lysosome acidity with LysoSensor (Mean $\pm$ SD) = 1.06 ± 0.08 , 0.95 ± 0.08 , 0.98 ± 0.15 respectively and (bottom) cathepsin B degradative activity with Magic Red, (Mean $\pm$ SD) = 1.007 ± 0.25 , 1.03 ± 0.19 , 0.96 ± 0.06 respectively, analyzed by flow cytometry. One dot represents the average of one experiment. One-way ANOVA. No comparison is statistically different. With LysoTracker, WM1862 Vs WM983B, $p=0.0512$. Right: Gating strategy used for each dye. Source data are provided as a Source Data file.

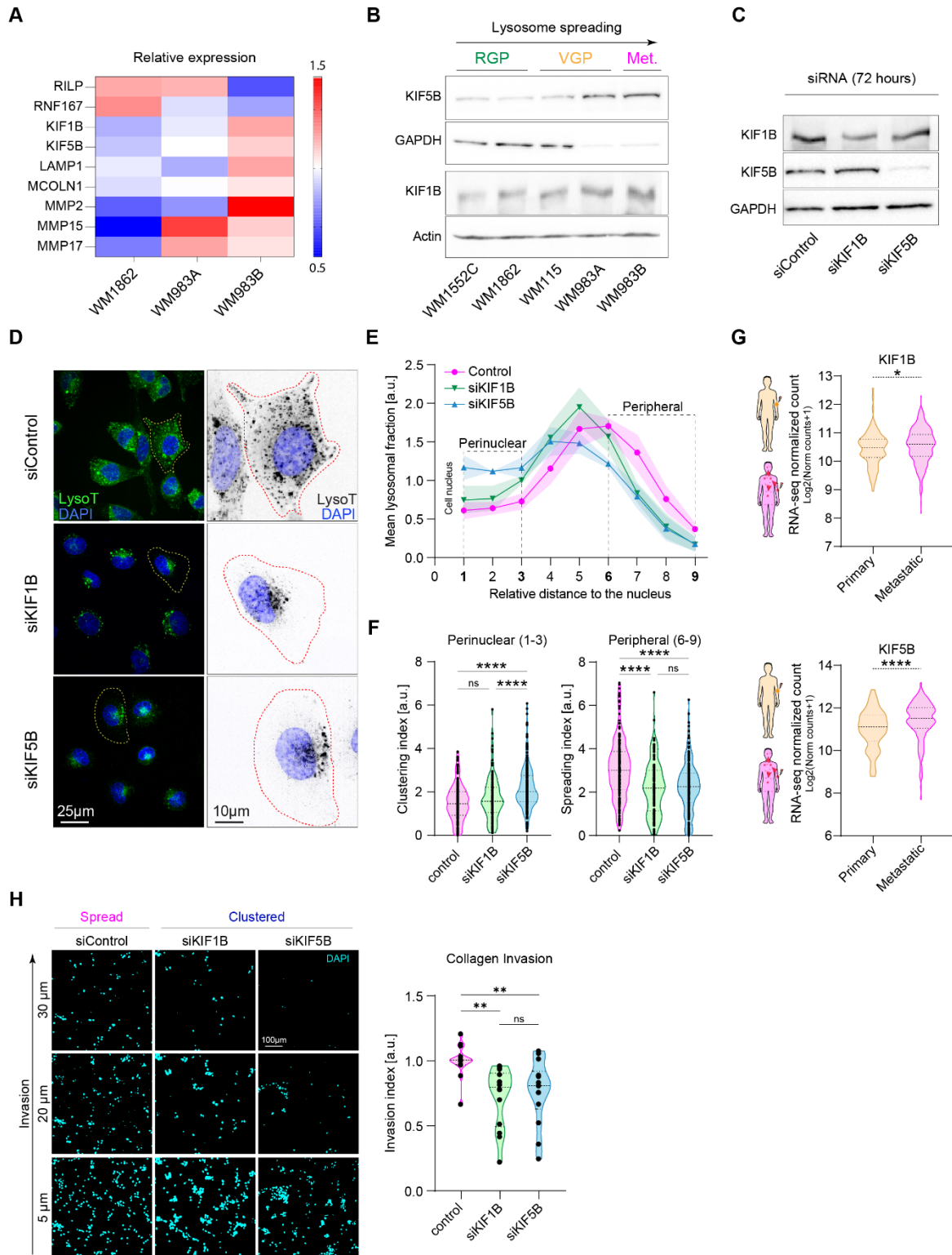


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Figure S3: In human melanoma, KIF5B and KIF1B are overexpressed and promote lysosome spreading to cell periphery.

A-B) KIF1B and KIF5B expression is increased in metastatic melanoma cells, as shown by RNA sequencing. **A)** Selection of differentially regulated genes, color code indicates relative expression levels (red= high, blue= low). All genes show a statistically significant difference between WM1862 and WM983B with $p_{Adj} < 0.0001$, except for MCOLN1 where $p_{Adj} = 0.026$. **B)** Western blot analysis of KIF5B, KIF1B expression in patient-derived cell lines. **C-F)** KIF1B and KIF5B promote lysosome spreading in metastatic melanoma cells. **C)** Expression of KIFs upon siRNA treatment, western blot. **D)** Representative images of WM983B cells treated with control, KIF1B or KIF5B siRNAs. Live cell imaging with lysotracker (LysoT). **E)** Lysosome positioning relative to the nucleus shows an increase of lysosomes in the perinuclear area and a decrease in the peripheral region upon KIF1B or KIF5B depletion. **F)** Quantification of (left) Perinuclear index (Mean $\pm$ SD) = 1.505 ± 0.830 , 1.696 ± 0.983 , 2.198 ± 0.9996 and (right) Peripheral index (Mean $\pm$ SD) = 3.051 ± 1.358 , 2.185 ± 1.210 , 2.222 ± 1.128 , 2.294 ± 0.8067 , respectively. One dot represents one cell, Kruskal-Wallis with Dunn's multiple comparison post-hoc test, p values < 0.0001 when significant. **G)** Analysis of sequencing data from tumors of melanoma patients. KIF1B (top) and KIF5B (bottom) show increased expression in metastatic cohort compared to primary melanoma TCGA cohort, Mann-Whitney test, two-tailed, p values: 0.0380, < 0.0001 , respectively. **H)** Representative images showing collagen invasion (24 hours) upon KIFs depletion by siRNA (72 hours). Spreading distance was analyzed by confocal imaging. For each condition, the invasion index equals the number of nuclei above 15 μm distance divided by the total number of cells, (Mean $\pm$ SD) = 1.0 ± 0.124 , 0.7199 ± 0.2307 , 0.7623 ± 0.2456 , respectively. Kruskal-Wallis with Dunn's multiple comparison post-hoc test, p values (from top): 0.0093, 0.0011, > 0.9999 , in triplicate, one dot represents 1 field of view. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; **** $p < 0.0001$. Source data are provided as a Source Data file.

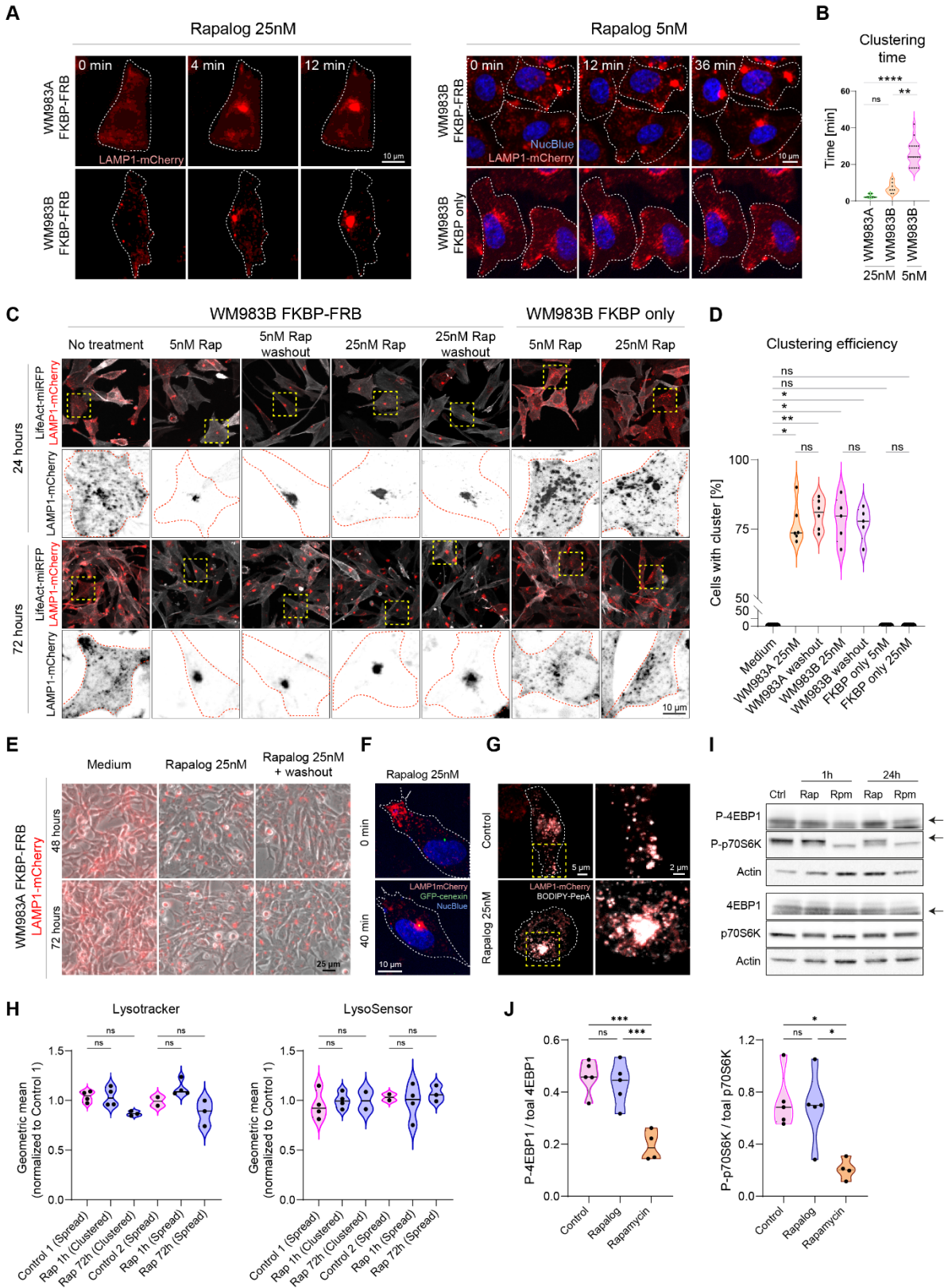


Figure S4 Jerabkova-Roda et al.

Figure S4: Fast and stable Rapalog-induced lysosome perinuclear clustering.

A) Rapalog induces fast perinuclear lysosome clustering. Representative images of WM983A and WM983B cells expressing two heterodimerizing domains (FKBP-FRB) and WM983B cells expressing only one heterodimerizing domain (FKBP only) extracted from a 1-hour time-lapse. After acquiring the first time-frame, cells were treated with 25 nM Rapalog (left) or with 5 nM Rapalog (right). **B)** Graph showing clustering timing at different Rapalog concentrations. Cluster formation was quantified as the time needed until a visible cluster appeared. Time [min] = 2.6 ± 1.0 , 7.0 ± 2.8 , 25.7 ± 6.8 , respectively. One dot represents 1 cell, Kruskal-Wallis with Dunn's multiple comparison post-hoc test, p values (from top): <0.0001 , 0.0034 , 0.4805 , in duplicate. **C-E)** Rapalog treatment induces stable perinuclear lysosome clustering. Representative images of **C)** WM983B and **E)** WM983A (FKBP-FRB) cells treated with 5nM or 25 nM Rapalog and imaged at 48 hours and 72 hours timepoints. Washout condition – cells were treated for 1 hour with Rapalog, washed 3x in PBS and cultured in normal growth medium for the duration of the experiment. **D)** Analysis of C, E showing percentage of cells with a lysosome cluster at 72h timepoint, Kruskal-Wallis test with Dunn's multiple comparison post-hoc test, p values (from top): >0.9999 , >0.9999 , 0.0244 , 0.0181 , 0.0038 , 0.0338 , >0.9999 , >0.9999 , >0.9999 . **F)** Rapalog induces lysosome clustering (LAMP1-mCherry= red) around the microtubule organizing center (cenexin-GFP= green), nucleus= blue. **G)** Cargo delivery to lysosomes is not perturbed by Rapalog treatment. WM983B (FKBP-FRB) cells expressing LAMP1-mCherry (red) were cultured in medium or in medium with 25 nM Rapalog for 1 hour and then treated with PepstatinA-BODIPY (white) probe for 45 minutes, live cell imaging, spinning disk. **H)** Lysosome mass (lysotracker), (Mean $\pm$ SD) = 1.04 ± 0.06 , 1.04 ± 0.09 , 0.87 ± 0.02 , 0.99 ± 0.06 , 1.12 ± 0.08 , 0.88 ± 0.13 and lysosome acidity (lysosensor), (Mean $\pm$ SD) = 0.95 ± 0.14 , 1.00 ± 0.08 , 1.00 ± 0.12 , 1.03 ± 0.04 , 0.98 ± 0.18 , 1.07 ± 0.08 are not affected by Rapalog-induced lysosome clustering, measured by cytometry. No statistical differences found, Kruskal-Wallis with Dunn's multiple comparison post-hoc test, in triplicate. **I)** Western blot analysis of phosphorylated (top) and total (bottom) forms of mTORC1 targets p70S6K and 4EBP1 (arrow) on extracts from WM983B cells treated with Rapalog (Rap) or Rapamycin (Rpm) (5nM each) for 1h or 24h and **J)** Quantification of phosphorylated over total forms at 24h, Control, Rapalog: n=5, Rapamycin: n=4 biological replicates, (Mean $\pm$ SD) = 0.4568 ± 0.064 , 0.4319 ± 0.082 , 0.1942 ± 0.057 and 0.7277 ± 0.213 , 0.6845 ± 0.273 , 0.2073 ± 0.079 , 4EBP1 and p70S6K, respectively, one dot represents one experiment, One way ANOVA with Holm-Sidak's comparison test, p values (from top, left): 0.0004 , 0.5551 , 0.0007 and 0.0113 , 0.7539 , 0.0128 , respectively. * $p<0.05$; ** $p<0.01$; *** $p<0.001$; **** $p<0.0001$. Source data are provided as a Source Data file.

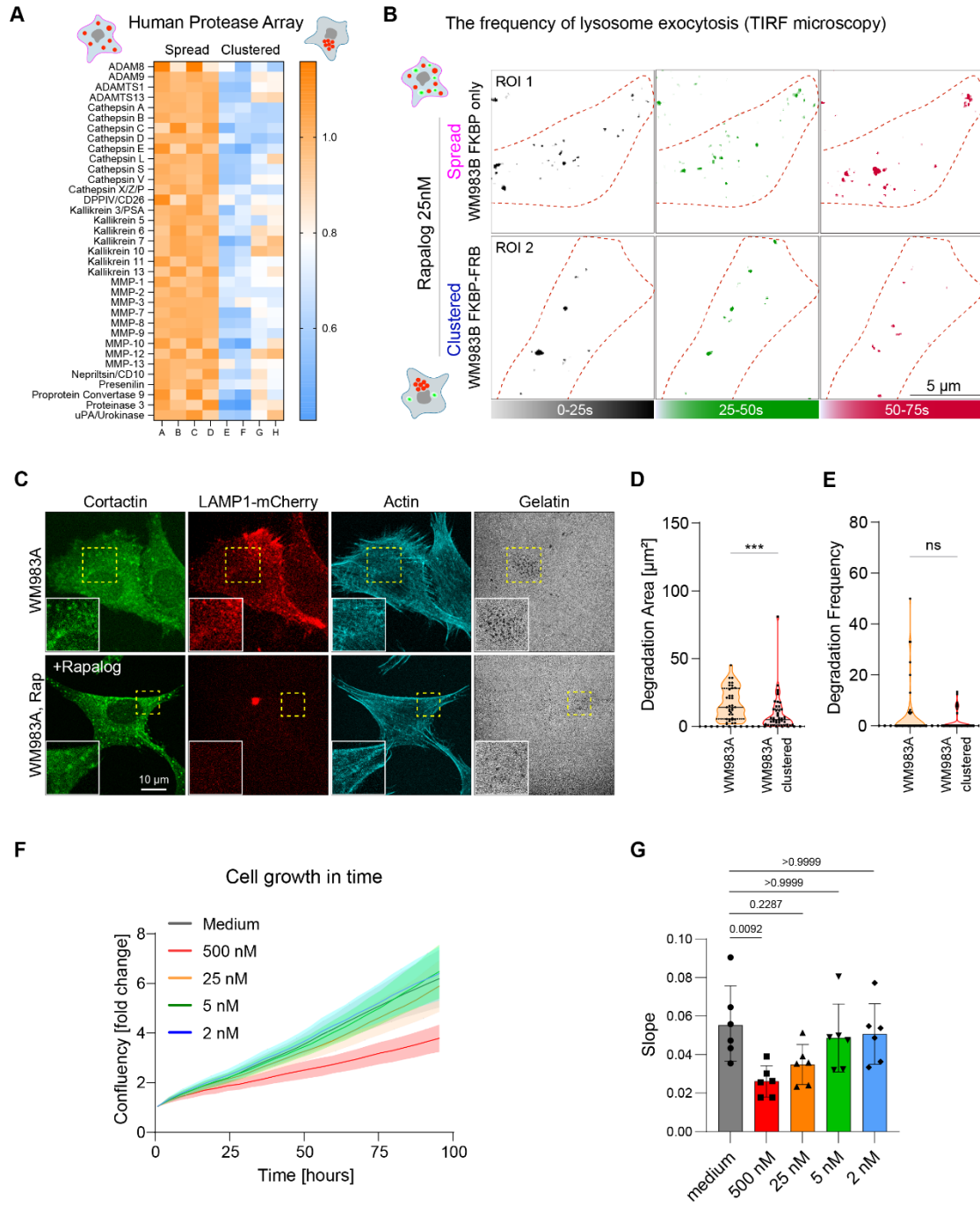


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Figure S5: Peripheral lysosomes promote secretion of proteases.

A) Lysosome clustering impairs secretion of proteases, quantified from conditioned medium by Human protease array. Color code indicates relative secretion levels. **B)** Quantification of cell secretion by TIRF microscopy showing the number of secretion events over time. **C-E)** Lysosome clustering impairs gelatin degradation. **C)** Representative immunofluorescence images of WM983A cells. **D)** Degradation Area (Mean $\pm$ SD) = 16.94 ± 11.71 n= 36 cells, 9.38 ± 13.47 n= 45 cells, in triplicate, Mann-Whitney test, two-tailed, p value= 0.0002. **E)** Degradation frequency (Mean $\pm$ SD) = 3.62 ± 9.73 n= 57 cells, 1.49 ± 3.44 n= 58 cells, in triplicate, Mann-Whitney test, two-tailed, p value= 0.5765. **F)** Proliferation rate of WM983B cells treated with increasing concentrations of Rapalog was analyzed using incucyte. Cell confluency was quantified for each time-point, all values were normalized to time 0 and the growth curves were plotted. Colored lines depict different culture conditions: medium (black), 2 nM (blue), 5 nM (green), 25 nM (orange), 500 nM Rapalog (red) and are representing average value of three experiments $\pm$ SD. **G)** Slopes were calculated for the different growth conditions. Slope (Mean $\pm$ SD) = 0.0552 ± 0.02 , 0.0261 ± 0.01 , 0.0348 ± 0.01 , 0.0486 ± 0.02 , 0.0507 ± 0.02 , respectively. Kruskal-Wallis test with Dunn's multiple comparison post-hoc test, respective p-values are shown in the graph. One dot represents one experiment (performed in technical triplicate), n= 6 biological replicates. *p<0.05; ** p<0.01; *** p<0.001; **** p<0.0001. Source data are provided as a Source Data file.

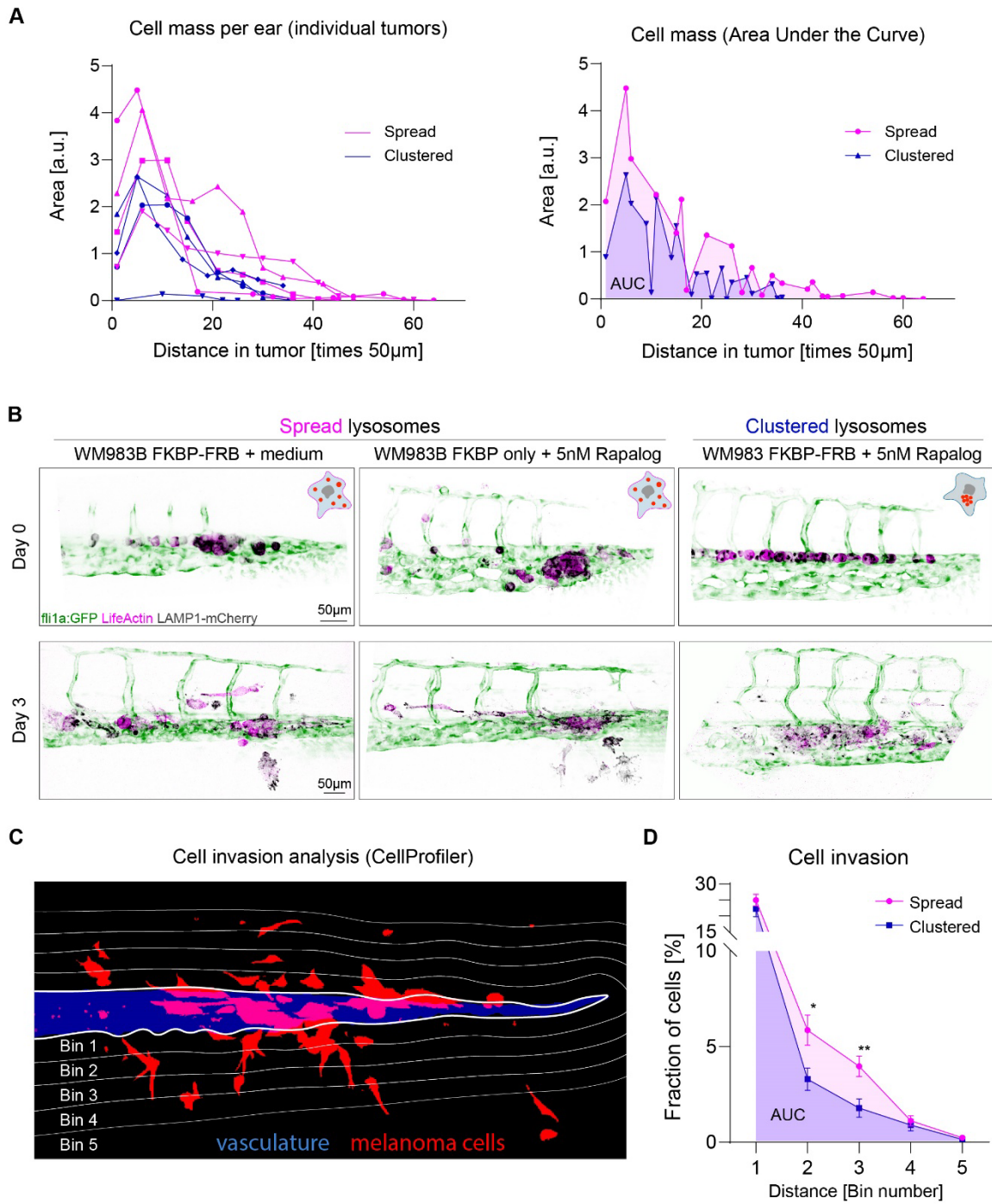


Figure S6 Jerabkova-Roda et al.

Figure S6: Monitoring cell invasion *in vivo*.

A) Lysosome clustering prevents tumor invasion in mice, magenta = spread lysosomes $n=4$ (FKBP only, 5nM Rap), blue = clustered lysosomes $n=4$ (FKBP-FRB, 5nM Rap). (left) Cell mass in the individual ears, plotted over distance, normalized to mean of each experiment, AUC = 48.95, 76.60, 45.32, 49.37 and 1.872, 33.13, 35.49, 39.72 in spread and clustered condition, respectively. (right) Mean cell mass per condition (spread, clustered), AUC (Mean $\pm$ SD) = 56.93 ± 5.98 , 30.48 ± 1.61 , respectively. **B)** Representative immunofluorescence images: day 0, day 3 post-injection in zebrafish embryos, green= Fli1a:GFP (vasculature), black= LAMP1-mCherry (lysosomes), magenta= LifeAct-miRFP670 (melanoma cells). **C)** Schematics of the quantification strategy for post-extravasation invasion potential (day 3, 72 hours). Representative example of the segmented image. Z-projections of vasculature (blue) and WM983B melanoma cells (red) were segmented using ImageJ. Segmented images were further analyzed in CellProfiler: Image was divided into five regions (bins) with increasing distance from the vasculature region and the total cell area in each region was quantified. **D)** Percentage of tumor cells in each bin (cell area per bin / total cell area) is plotted for both conditions. Magenta = cells with spread lysosomes, blue= cells with clustered lysosomes. Each line represents mean value from three independent experiments $\pm$ SD. Percentage (spread) = 24.9 ± 10.9 , 5.9 ± 4.7 , 3.9 ± 3.2 , 1.1 ± 1.6 , 0.2 ± 0.6 , respectively, $n=35$ embryos. Percentage (clustered) = 22.2 ± 9.5 , 3.3 ± 2.3 , 1.8 ± 1.9 , 0.9 ± 1.2 , 0.1 ± 0.3 , respectively, $n=15$ embryos, p values (from left) = 0.3768, 0.0121, 0.0043, 0.5767, 0.5771, multiple unpaired t -tests with Welch correction. * $p<0.05$; ** $p<0.01$; *** $p<0.001$; **** $p<0.0001$. Source data are provided as a Source Data file.

Table 1: Lysosome genes differentially expressed (refers to Figure 1A)

Gene	GeneSymbol	Average	WM1862	WM1862	WM1862	WM1862	WM983A	WM983A	WM983A	WM983A	WM983B	WM983B	WM983B
ENS00000011986	ABCD1	2606.597931	1.70984909	1.698634074	2.165143828	1.865820678	0.470239199	0.619388744	0.661886886	0.412210243	0.621293358	0.676469725	0.561573056
ENS000000157766	ACAN	79.82246872	1.362753019	0.851552102	2.71846108	1.807085612	0.540699128	1.069125149	1.166533055	1.793663063	0.132210469	0.20820505	0.160680829
ENS000000102575	ACPS	1927.866114	2.197409265	2.155628998	2.285839264	1.642360738	0.555199858	0.545654325	0.645212426	0.393813401	0.300881179	0.268763968	0.566155225
ENS000000196839	ADA	478.26861545	1.478605243	1.284341113	1.37148154	1.145110869	0.835255933	0.928327236	0.659424789	0.942267634	0.705275078	0.943400102	0.794409187
ENS000000038002	AGA	450.6861845	1.731679416	1.350083426	1.486486167	1.510961127	0.499755206	0.75496154	0.86617889	0.532341542	0.825742499	0.725608597	0.892319946
ENS000000151150	ANKK	60.30011197	1.102413111	1.370036056	1.859262028	2.069790946	1.083837671	0.563214871	0.39333445	2.613982342	0.134193302	0.316947075	0.316678112
ENS000000106357	AP1S1	2971.060627	1.672654271	1.380444973	1.664611327	1.320844996	0.543293643	0.717216813	0.349707134	0.886721693	0.940013368	0.868680356	0.953599745
ENS000000162257	AP1S2	4022.719991	1.615698843	1.466943107	1.435353619	1.324196832	0.697646272	0.706574519	0.72062691	0.587749439	0.837592589	0.829979107	0.821693322
ENS000000006187	AP2B1	4057.403923	1.426394459	1.098181515	1.371271607	1.214592242	0.700559493	0.792043652	0.899715506	0.775828718	0.859178404	1.021265447	0.900552348
ENS000000005370	AP5M1	1034.824471	1.440501045	1.15303364	1.432894418	1.481922782	0.76025979	0.80616965	0.921697086	0.780634871	0.772283268	0.76055282	0.81054866
ENS000000066650	ATP1A1	3368.65902	1.73512103	1.124925541	1.580992586	1.694441687	0.844436736	0.60566085	0.48338175	1.21236672	0.69680989	0.743454337	0.597212647
ENS000000033627	ATP6V0A1	3201.369985	1.086373778	0.79262795	0.984096444	1.025779337	0.402262679	0.947153684	0.703830127	1.826254335	0.76778465	0.7158721	0.652627372
ENS000000147614	ATP6V0D2	513.3890994	2.607335387	2.446354534	2.182034962	2.258702107	0.369896802	0.522434329	0.586899615	0.319817998	0.175662892	0.187753649	0.239184476
ENS000000100554	ATP6V1D	1811.678397	1.246686624	1.337997648	1.262631003	1.194866344	0.56536598	0.719562165	0.839329141	0.807136662	0.890724094	0.898910765	0.891508877
ENS000000186318	BACE1	282.400746	1.689124811	1.145680579	1.557956581	1.432728546	0.786975194	0.725567022	1.308120277	0.419144797	0.734740728	0.945723349	0.509566243
ENS000000105327	BBC3	867.9969728	1.745211952	1.838481852	1.562216656	1.388391195	1.324048411	0.615995848	0.384575599	1.607110832	0.553755216	0.296770354	0.352919518
ENS000000132692	BCL2	70.9108321	2.738915775	1.960449311	2.554109143	2.152851229	0.41717079	0.365286469	0.48679879	0.260490297	0.265544477	0.323609665	0.155715416
ENS000000196072	BLOC1S2	1209.945552	1.153761269	1.221235327	1.153768033	0.988401634	1.29534727	0.858622454	0.779748941	0.283758425	0.632587	0.901287771	0.814034503
ENS000000165714	BORCS5	221.1130456	2.004272938	1.962712798	1.962745111	1.952463191	0.685957542	0.535614304	0.397248422	0.427718123	0.551045765	0.60804255	0.497735475
ENS000000164713	BRI3	5269.460744	1.153149738	1.328044975	1.044417551	1.022349649	1.325918675	0.874543204	0.628313373	1.815447351	0.79349639	0.681068973	0.734842676
ENS000000185127	C6orf120	597.0031538	2.014402511	1.334754428	1.599279337	1.542235355	0.681622333	0.600936666	0.551786387	0.836077418	0.682964141	0.737694402	0.58939209
ENS000000121691	CAT1	1862.731881	1.6145742	1.386097456	1.449360712	1.568183779	0.980417832	0.708722921	0.755489623	1.334872507	0.683064663	0.583937452	0.553430876
ENS00000019582	CD74	8498.83459	0.895114641	1.06138538	1.053843158	0.896717123	1.833976261	1.397906551	1.214492478	0.337319581	0.446914494	0.192921745	0.282951879
ENS000000089486	CDIP1	587.1083793	1.79088533	1.726409126	1.760587165	1.577903665	0.517141828	0.544220779	0.48274166	0.737654994	0.502909043	0.694512693	0.777428314
ENS000000255112	CHMP1B	2530.874789	0.910948208	1.17801164	0.809160324	0.948696266	1.674616489	0.830948485	0.494607325	2.487056616	0.723271734	0.511204872	0.680689293
ENS000000130724	CHMP2A	2969.459463	1.141708576	1.372737374	0.993824691	1.03767735	0.882077303	0.707028368	1.427892943	0.709824474	0.583732582	0.67491878	0.77844508
ENS000000176108	CHMP6	436.0028738	1.051091678	1.004957499	0.95597959	1.076981156	1.145439518	1.310213629	1.629954605	0.979114611	0.607320645	0.850007701	0.680525652
ENS000000073464	CLCN4	265.2627459	1.541588015	1.182682084	1.526999116	1.076929959	0.302008333	1.43132367	1.311400257	1.629142821	0.256791357	0.142518	0.7284341579
ENS000000093137	CMTME	5773.925662	0.94529316	1.108960546	0.943145525	1.160348842	1.692098543	0.8687182	0.472853014	2.148217863	0.807040314	0.45592249	0.646661992
ENS000000142156	COL6A1	1379.4202102	1.377112302	1.07954843	1.217844567	1.010857407	0.783719231	1.152756328	1.376832617	1.008427311	0.584929368	0.650593775	0.610378489
ENS000000143162	CREG1	1558.884942	1.420143331	1.318841108	1.434323413	1.426035822	0.952398967	0.756925015	0.793423268	0.803005206	0.757604081	0.793702352	0.684836156
ENS000000117984	CTSD	1822.1489	1.15340186	1.375779194	1.370833252	0.905052894	1.626580899	1.162526089	0.966508204	1.174655903	0.662751798	0.611337230	0.750778759
ENS000000103811	CTSH	1595.141442	2.808925804	2.39679016	2.462629695	2.342800159	0.398120482	0.286067619	0.288192175	0.437255061	0.178029031	0.14185632	0.137418791
ENS000000143387	CTSL	4572.732114	1.949773658	1.483997171	1.701620133	1.345465093	0.423852095	0.440481323	0.463356617	0.200214967	0.854270523	0.98924217	0.827763323
ENS000000135047	CTSM	6074.285072	2.096874776	2.098814246	1.988279865	1.452103657	0.551367402	0.484133695	0.489098745	0.337989504	0.64036369	0.682885241	0.645206139
ENS000000102580	DNAJC3	1888.247004	1.170311576	0.990785608	1.717223598	1.265621782	0.955426186	0.79877107	0.709932728	1.290416064	0.944547981	0.686221294	0.92398781
ENS000000137976	DNAJB2B	30.21236038	3.067056127	1.488350003	2.184616638	1.724712869	0.285706338	0.115293005	0.581516014	0.130429587	0.110105117	0.212500915	0.099787385
ENS000000149927	DOCA2	107.023	3.538582105	2.68706763	2.931496549	2.407476888	0.202304408	0.06509393	0.06564283	0.135006927	0.026893198	0.062114057	0.009569792
ENS000000176978	DPP7	4219.542168	1.463711104	1.613608995	1.37028925	1.201574584	0.784374487	0.705191831	0.786109408	0.450757283	0.068056713	0.136048929	0.899875507
ENS000000136048	DRAM1	847.86498	0.937278939	1.126074448	1.158084265	1.087133463	1.118423112	1.216053354	1.138642354	1.145986198	0.712873	0.663497059	0.69339183
ENS000000101210	EFT1A2	220.1970516	3.627272978	2.664246389	2.808546608	2.778270037	0.01120018	0.070909447	0.011968124	0.047721931	0.0107547368	0.012195602	0.028212336
ENS000000138798	EGF	107.8495662	1.326137312	1.212033531	1.643140507	1.489244554	0.651722844	1.243454629	1.645315945	1.778172852	0.329140736	0.246552044	0.127561694
ENS000000115363	EVA1A	684.3817733	1.287859637	0.161271328	1.297444503	1.02703072	1.414549254	1.306892899	1.648250779	0.602711437	0.658584038	0.689425467	0.455688706
ENS000000157295	FNH1	1359.824219	1.49322873	0.702024012	1.423544404	1.426853772	0.613920897	0.935610523	1.066548648	0.864529494	0.797955488	0.834116937	0.727087072
ENS000000167996	FTP2	2002.64179	1.372883832	1.426450565	1.481366121	1.105003199	1.262037122	0.710165536	0.61549259	1.766493021	0.648644658	0.443691689	0.517886314
ENS000000087066	FTL	60070.32334	1.571951435	1.657887589	1.36910597	1.237071091	1.367200733	0.770004065	0.539408681	1.527725867	0.555399499	0.444914956	0.549430189
ENS000000179163	FUCA1	200.202226	1.937655202	1.525844501	1.687764578	1.574192239	0.703986785	0.702944059	0.720766138	0.664437382	0.55169617	0.646493567	0.524824683
ENS000000171298	GAA	1795.864962	1.310140023	1.216431861	1.117677042	1.03506111	1.311493615	0.946043172	1.017433416	1.359706691	0.631455474	0.659810656	0.658814965
ENS000000102393	GLA	1300.97157	1.283616447	1.205720034	1.289873734	1.218845513	0.78761664	0.703321866	0.869014615	0.657283461	1.028737843	0.991929214	0.875890434
ENS000000170266	GLB1	2048.021645	1.21570161	1.684499155	1.641590847	1.607445541	0.576214107	0.507263398	0.535727865	0.59646907	0.55839308	0.604309999	0.596933661
ENS000000166105	GLB1L3	16.6791568	1.811613222	1.630129273	2.873019522	1.104035276	1.18291121	0.210669665	2.047568993	0	0.548018716	0.10993731	0.482056813
ENS000000196743	GM2A	274.589033	2.118953038	1.795752432	1.945492501	1.563661471	0.53511146	0.585079042	0.697428305	0.55660267	0.50267027	0.618847901	0.450467344
ENS000000127955	GNAI1	571.8396963	1.46657483	1.238047959	1.658587153	1.339961635	0.776613121	0.941678359	0.633978281	0.661028694	0.680007797	0.694608129	0.7161020291
ENS000000063660	GPC1	70.7442442	1.806430855	1.269154314	1.563571974	1.187722371	0.875636687	0.960464674	1.265355286	0.368837077	0.546565833	0.796465731	0.683468044
ENS000000147257	GPC3	5.248042646	3.454567655	1.793362888	1.7826258	1.949339195	0	0.49779614	0	2.00231386	0	0.158336002	0
ENS000000076119	GPC4	65.55993913	3.1648092										

ENSG00000167705	RILP	206.6893982	1.1792767	1.533018698	1.233581765	1.128499619	1.563110143	0.985882782	0.561011895	1.849329555	0.645200825	0.313583666	0.599049885	0.408454467
ENSG00000108523	RNF167	2889.434313	1.374461261	1.300733337	1.372751231	1.364177725	0.958524939	0.665748988	0.820552548	1.209228384	0.754718376	0.687900113	0.751016253	0.740186845
ENSG00000205039	RRAGD	2247.481767	1.126198292	1.10925935	1.029463948	0.931309907	1.376061505	1.08334957	1.10495851	1.36292479	0.808930763	0.683255004	0.557444897	0.826843465
ENSG00000115884	SDC1	258.040156	2.603497056	2.455886844	3.710613306	2.164662122	0.205488561	0.182235964	0.289366312	0.142531304	0.022308084	0.083726528	0.046206543	0.093477375
ENSG00000169439	SDC2	355.1003635	1.80678663	1.540187506	1.555704567	1.24168354	1.257082974	1.495913024	1.244323226	0.843379911	0.27287803	0.184864281	0.240203457	0.316992853
ENSG00000133661	SFTPD	3.300209038	0.610389563	1.267481316	1.095861262	2.789881974	0	0	0.266179675	5.97020621	0	0	0	0
ENSG00000110013	SIAE	195.4401672	2.107793375	1.503541842	1.905989148	1.627913536	0.378568013	0.739642551	0.943890921	0.470461118	0.51543486	0.590987107	0.567830827	0.647946702
ENSG00000149577	SIDT2	489.6824045	1.404833184	1.161735939	1.384789614	1.380930212	1.115567152	0.851821583	0.870048733	1.40021758	0.664176513	0.643134404	0.556274782	0.566470303
ENSG00000181045	SLC26A11	655.4103486	1.303170111	1.281224619	1.045665897	1.145691092	0.950133377	1.114746947	1.29339256	0.941941835	0.750935067	0.797470052	0.654907525	0.720720919
ENSG00000198246	SLC29A3	50.6729866	1.729264013	2.043062803	1.998382207	1.816982642	0.267684161	0.910808328	0.20802766	1.607143699	0.549060006	0.508349293	0.162897129	0.198338061
ENSG00000115194	SLC30A3	27.7919986	2.754307127	2.633912146	2.309806519	2.76074475	0.044369722	0	0	0.945256644	0.172603079	0.089697122	0	0.28930289
ENSG00000104154	SLC30A4	220.9983353	0.91606356	0.809152038	1.039158388	0.893414666	1.026680495	1.598585799	1.709211448	1.468072397	0.677226448	0.624160265	0.622514796	0.618489698
ENSG00000123699	SLC35F6	1370.121775	1.202659493	1.032670218	1.191118777	1.084157101	0.897309944	1.082388338	1.402628203	1.028679477	0.777952722	0.767199636	0.789227225	0.743808866
ENSG00000123643	SLC36A1	945.0731627	1.137149415	0.854230128	1.213083923	1.271912389	0.899001203	0.825600971	0.999215964	1.655334794	0.821261372	0.76318762	0.821987839	0.738034363
ENSG00000138821	SLC39A8	614.396202	1.684456968	1.35340537	1.557610853	1.311443333	0.676827933	0.867186962	1.055998477	0.70967002	0.593735529	0.741780996	0.666704503	0.781178955
ENSG00000168003	SLC3A2	7085.796555	1.688533791	1.669303668	1.610430997	1.357426548	0.71734124	0.706039469	0.717680606	0.578184198	0.727082884	0.767182862	0.76833857	0.692455167
ENSG00000103257	SLC7A5	16366.79842	1.960742621	1.629568882	2.080895747	1.759366026	0.209279964	0.363462179	0.480341189	0.232964072	0.827788435	0.955733446	0.793872993	0.705876445
ENSG00000145335	SNCA	2703.218446	1.373013801	1.282405626	1.349248006	1.156151756	0.63635514	0.872358793	0.949544689	0.538391432	0.951511379	0.961529545	0.812251319	1.117238514
ENSG00000208528	SNX1	3277.933227	1.023819608	0.962175422	1.11406565	1.036150288	1.185748536	1.165188394	1.17084197	0.079936424	0.815416178	0.874319417	0.812256669	0.760079446
ENSG00000129515	SNX8	1757.915965	1.087468411	1.140373264	1.064655908	1.085921179	0.709784037	0.885721179	0.71258677	0.901046652	0.714238712	0.849905022	0.954203028	0.984203028
ENSG00000008294	SPAG9	6798.71896	1.109913752	0.948571088	1.163638273	1.206640492	1.222473063	0.059140385	1.105244841	1.721626254	0.69992725	0.547779706	0.582914152	0.632110744
ENSG00000104133	SPG11	1970.009134	1.134508137	0.990527241	0.958295145	0.953430867	1.260659257	1.043209152	0.879336318	1.969616952	0.79196403	0.690911926	0.631770044	0.695870931
ENSG000000063176	SPHK2	536.0046668	1.272150961	1.279847701	1.561994315	1.555513586	0.821308157	0.984536176	0.947273978	0.44355709	0.737440456	0.998376449	0.732356634	0.665644498
ENSG00000131748	STARD3	1678.630219	1.110031349	1.185514241	1.122482841	1.090894531	1.300978186	0.83780918	0.628498593	1.431192955	0.843014991	0.782625266	0.842513286	0.82444458
ENSG00000101846	STS	299.6053665	1.398499435	1.183240794	1.614511814	1.673136073	0.674995303	1.002760301	1.307680387	0.868070753	0.438701676	0.535284604	0.648983559	0.654135302
ENSG00000166900	STX3	5596.04403	1.004138899	1.171494277	1.016264034	1.191017295	1.533018413	0.893219909	0.593528932	1.963470337	0.786232952	0.51822855	0.639191374	0.690195027
ENSG00000170310	STX8	379.7209591	1.816956605	1.867188435	1.21196547	1.031855719	0.798871686	0.786605858	0.809691937	0.629573357	0.613959917	0.680570079	0.850208644	0.902552293
ENSG00000198203	SULT1C2	54.33973251	2.539344501	2.444045287	2.079838197	1.506111975	0.068078542	0.689094184	0.678966167	1.474524051	0.158899792	0.091750996	0.084391738	0.184954571
ENSG00000100321	SYNGR1	1347.182041	1.855641366	1.62001557	2.084549441	1.7146774	0.804579719	0.756934388	0.959185771	0.405608052	0.336847378	0.552660921	0.398269648	0.511030535
ENSG000000011347	SYT7	13.10039217	1.99897611	1.037724523	2.070490771	1.093272715	1.223673475	0	0	3.208523346	0.219702638	0.317148556	0.140020982	0.690463582
ENSG00000185339	TCN2	155.7673749	1.939828369	1.382973134	2.19407936	1.300389517	0.894557854	0.486374029	0.817726064	0.303574663	0.51736983	0.666822958	0.612356398	0.883947823
ENSG00000205356	TECPR1	1677.279908	1.17337699	1.139084722	1.074326282	1.147276299	1.191746708	1.005142031	0.748939666	1.358730914	0.821385836	0.818925398	0.728906841	0.792151912
ENSG00000164342	TLR3	126.9742124	1.911701441	1.358912334	2.043635331	1.45024624	0.41759897	0.59666081	0.940891879	0.868966993	0.619578928	0.608617523	0.621198424	0.561985856
ENSG00000204405	TMEM199	371.5305229	1.309396527	1.362303546	1.496641041	1.3134352	0.740145077	0.799259845	0.799168838	0.72476779	0.854735633	0.881208656	0.891169111	0.827769637
ENSG00000164841	TMEM74	26.01579777	2.20676588	1.849028937	2.29373806	2.477354587	0.142197054	0.401672152	0.168829835	0.252448258	0.516284637	0.479105485	0.246779065	0.96579605
ENSG00000175348	TMEM98	854.7614803	1.279860049	1.317630942	1.277788647	1.199243987	1.058906485	0.895812305	0.95988294	0.58395338	0.853035223	0.88562622	0.866259436	0.832474385
ENSG00000162341	TPC2	3215.668596	1.883695465	1.571045551	2.166398728	1.798107447	0.411466923	0.553524989	0.608093296	0.295329299	0.587462991	0.817344113	0.533356686	0.794174512
ENSG00000170043	TRAPP1	1343.441904	1.35924413	1.317835164	1.336587474	1.044768311	0.871071516	0.750615095	0.774846721	0.721567549	0.876955973	0.999538432	0.925055578	1.021914057
ENSG00000113595	TRIM23	619.3007726	1.16284806	0.866241064	1.040393188	1.116682846	1.089161284	1.098188869	1.048236206	1.493174483	0.878374565	0.762120678	0.731598403	0.712435354
ENSG00000142185	TRPM2	172.8549104	0.70505855	0.963686784	0.881270552	0.979012115	1.901232715	0.910519334	0.420329275	3.561661863	0.527071512	0.18407575	0.511997111	0.45418447
ENSG00000103197	TSC2	2794.597615	1.400561116	1.098276891	1.348704277	0.848528611	0.799274045	0.804705595	0.998451348	0.815347313	0.81716868	0.819167509	0.729342012	0.819167509
ENSG00000077498	TYR	6937.863625	2.125076344	1.606471337	1.707714079	1.456411387	0.450388551	0.509221667	0.735515717	0.311822438	0.668327529	0.890496559	0.582460067	0.956094326
ENSG00000221983	UBA52	11861.3658	1.339192736	1.568515029	1.336925361	1.077671336	1.118519858	0.735485226	0.704751605	0.676068172	0.833107108	0.774884055	0.891387809	0.943491705
ENSG00000114316	USP4	2636.455817	1.023077722	1.065786446	1.028130314	0.978609338	1.358726763	0.916579448	0.800959923	1.75920618	0.875170958	0.686458693	0.772289088	0.734969127
ENSG00000111667	USP5	2432.122313	1.694606101	1.453726753	1.815629692	1.549597761	0.610953456	0.638759045	0.768242656	0.396955158	0.673753088	0.810412823	0.891475643	0.695887827
ENSG00000129204	USP6	27.22461404	1.294866114	1.766929104	1.726945553	0.901849941	0.860594092	0.511783024	0.709867493	1.881665393	0.634320998	0.457832437	0.404265738	0.849080113
ENSG00000160695	VPS11	966.1609263	1.142561635	1.004434291	1.191285806	1.042969316	0.860234622	1.103213514	1.502933357	1.137929904	0.66729538	0.839416264	0.755633318	0.752092732
ENSG00000104142	VPS18	2498.331746	1.079236979	1.100432742	1.171103933	1.092088113	1.164845663	1.058576651	0.965180595	1.138275311	0.78991889	0.845478311	0.736791637	0.858071175
ENSG00000069329	VPS35	3590.873679	1.375526263	1.121783829	1.250132824	1.354960046	0.76089504	0.76608529	0.843986125	0.812067947	0.934316071	0.936505017	0.931500425	0.912151123
ENSG00000127580	WDR24	360.128809	1.507472691	1.356069787	1.295474504	1.110717625	0.75672991	0.916450411	0.970826331	0.554402583	0.916429145	1.091390848	0.870995092	0.653041163
ENSG00000164253	WDR41	1060.293006	1.205464091	1.103639444	1.144362591	1.055543646	1.018790063	0.081651865	1.256000013	0.875856665	0.818881381	0.801727477	0.849440506	0.788642166
ENSG00000114742	WDR48	1905.194986	1.911117655	1.343677385	1.968504224	1.943810445	0.599346602	0.536606949	0.48597902	0.871459415	0.64809315	0.572231073	0.580570948	0.538603134
ENSG00000186187	ZNRF1	418.6767393	1.14751428	1.051541185	1.15									

Table 2: Positive Regulation of cell migration genes differentially expressed (refers to Figure 1A)

Gene	GeneSymbol	Average	WM1862	WM1862	WM1862	WM1862	WM983A	WM983A	WM983A	WM983A	WM983B	WM983B	WM983B
ENS000000127387	AAMP	3560.206653	0.858056265	0.843297603	0.841870651	0.797105914	0.804600882	0.950506793	1.118723237	0.526118837	1.209416714	1.361191882	1.332388088
ENS000000143322	ABL2	3645.55694	0.862373907	0.511726655	0.101668573	0.865031525	0.506042021	0.10685731	0.89554996	0.596088992	1.259873154	1.565088794	1.7360019
ENS000000137845	ADAM10	7478.350113	0.685293164	0.810765839	0.886086175	0.872609549	0.969564741	1.032170824	0.976806649	1.321195414	1.090974746	0.98647567	1.151860309
ENS000000151694	ADAM17	1147.517213	0.658295077	0.554073519	0.675240754	0.762339897	0.901590325	1.12677141	1.193447269	1.540725864	1.0517675	1.170197535	1.280414915
ENS000000168615	ADAM9	2738.891445	0.664142816	0.461227442	0.615660159	0.596898369	0.582593919	0.86811436	1.017360095	0.698274331	1.524797494	1.6735029	1.798905652
ENS000000154734	ADAMTS1	1138.655277	0.683765996	0.235109798	0.352555702	0.380043122	0.597796417	1.195723697	1.195723697	0.672536433	1.782878378	1.528863801	1.7747494807
ENS000000135744	AGT	17.35607673	0.696602631	0	0.885872594	0.294805558	0.710708979	0.200759031	0.354048973	0.984165611	1.38237881	1.619893356	2.027383558
ENS000000131016	AKAP12	5310.314013	0.788647326	0.550604794	0.823555587	0.707043559	0.690904361	1.139540419	1.324046436	0.676513784	1.194026219	1.6430324	1.15531314
ENS000000126016	AMOT	492.4582976	0.734257353	0.380111805	0.618731514	0.535969134	0.485784355	0.938882394	1.204080201	0.698837833	1.229314421	1.829117549	1.555013396
ENS000000135046	ANKA1	2705.859771	0.333147303	0.345373374	0.463455679	0.37320174	1.201742263	1.42656552	1.561550846	0.983013006	2.480606554	1.021395618	1.95373703
ENS000000138772	ANKA3	243.1858912	0.13253487	0.348312987	0.156152143	0.222957592	1.211897854	0.777050034	0.617694948	1.652808636	1.633278633	1.906658242	1.538754052
ENS000000142192	APP	22269.0729	0.770520233	0.561126295	0.715257006	0.57203671	0.803640008	1.295020002	1.240763327	0.642104502	1.188891751	1.474721018	1.219628857
ENS000000137135	ARHGEF39	440.3677585	0.812590048	0.786023451	1.090224757	0.836318602	0.46483526	0.654545896	1.095148895	0.653233009	2.59246169	1.651085529	1.305148525
ENS000000168874	ATOH8	457.7686909	0.292633545	0.269562171	0.481924662	0.18118809	1.27158374	1.862366556	2.153084988	0.880910551	1.035330049	1.472149107	0.897592778
ENS000000124406	ATP9A1	707.6517005	0.480092191	0.55252038	0.350754451	0.56997675	1.877358708	1.177600416	0.74608194	2.8686022	1.567807619	1.130195633	1.247307352
ENS000000156735	BAG4	680.5558177	0.822866901	0.76387465	0.948889098	0.12010809	0.677663886	0.60481811	1.02480171	1.22141518	1.117208899	1.124251742	1.042457382
ENS000000141376	BCAS3	5226.632594	0.18195754	0.104361067	0.95887046	0.801915785	0.732645928	0.715764122	0.72438865	0.349578472	1.3015037	1.480146627	1.290297973
ENS000000171791	BCL2	953.053291	0.716524499	0.50583291	0.849068767	0.702613126	1.279200202	1.388110722	1.237652308	1.02909148	1.26946638	1.260746666	1.110365511
ENS000000142871	CCN1	894.1550064	0.95471076	0.901223097	0.176954768	0.0457484	0.468819968	1.485199028	1.325303092	0.794737992	1.420605484	1.461816776	1.307226726
ENS000000177697	CD151	4208.380626	0.0738443097	0.881928098	0.958833107	0.72229628	1.77292283	0.76047498	1.160724433	0.488979127	1.196573609	1.326958503	1.568343058
ENS000000196776	CD47	2828.684112	0.686144863	0.814428701	0.620726674	0.714639898	1.54495471	1.160913085	1.136628816	1.55328516	0.927263181	0.8254817	0.927642907
ENS000000020586	CD9	5179.731882	0.551055105	0.541672038	0.527153017	0.400737088	1.257946062	1.169109075	0.015355249	0.47700292	1.404666403	1.514083144	1.414598447
ENS000000165043	CIB1	1903.519456	0.793581982	0.808285832	0.684303644	0.69635802	1.657428248	0.832290839	1.177683825	1.035365637	1.130195633	1.247307352	1.026498735
ENS000000163347	CLDN1	640.0037869	0	0	0.01395274	0.004736183	0.239772555	0.468472698	0.501580354	0.383110258	2.305204088	2.71212597	1.287159399
ENS000000085719	CPNE3	2303.740272	0.861293015	0.713578427	0.883385753	0.869488024	0.971514454	1.096240977	1.188555013	0.956748136	1.096100424	1.235389099	1.369736268
ENS000000099942	CRKL	3080.834821	0.843103778	0.741424794	0.673699575	0.825779897	0.987713974	1.02283024	1.023737492	1.137592295	1.100763806	1.19155938	1.09035824
ENS000000138061	CYP1B1	698.6828002	0.155485765	0.334399075	0.20936321	0.180488194	0.802236742	0.948913242	1.061668036	1.477351168	1.819578545	1.493511881	2.922734125
ENS000000162733	DDR2	2514.921336	0.997225774	0.538062711	0.996260001	0.739120576	0.553008414	1.128117405	1.224976338	0.69095089	1.164282684	1.464375242	1.377796159
ENS000000198171	DRGRK1	2488.349066	0.619296578	0.58877567	0.556292224	0.656270933	1.222047987	1.384739362	1.14870132	0.673036169	1.18840125	1.255272216	1.32325635
ENS000000087470	DNM1L	131.593811	0.987605277	0.76878847	1.041903357	0.10340903	0.59911666	0.865818089	1.20132369	0.588507192	1.181068749	1.3043906	1.286672728
ENS000000116641	DOCK7	2884.552089	0.57488791	0.34109387	0.498872351	0.547114034	1.064821503	1.14677585	0.753071864	1.375435532	1.777724033	1.62708017	1.488247642
ENS000000146648	EGRF	32.9892489	0.519038188	0.09509036	1.0952981	0.217077419	0.6728385	0.475151351	0.673743483	1.02572275	1.19237915	1.158868512	1.278901484
ENS000000134014	ELP3	1185.23113	0.68833606	0.515267584	0.64940467	0.73825923	0.78238638	0.90591542	1.194012338	0.739200592	1.421274824	1.49893141	1.521345609
ENS000000161671	EMC10	1058.882039	0.60411586	0.366394843	0.420955677	0.427997188	0.597415208	0.92796717	0.842044028	1.614040674	1.702463327	2.168254891	1.820675515
ENS000000136960	ENP22	306.6319567	0.104898332	0.103405645	0.0133784	0.014627853	0.738258249	1.10926146	1.23849198	0.652826669	1.811262993	2.407651393	1.362439129
ENS000000142627	EPHA2	428.8721874	0.609388372	0.376534352	0.603609301	0.392509229	0.225641994	0.72467712	0.469263379	0.345025567	1.707402821	1.954596434	3.064189343
ENS000000134954	ETS1	5141.540396	0.708395499	0.550576953	0.793965325	0.742367638	0.6739374	0.901382755	1.13395261	0.805253236	1.300582303	1.378582656	1.412260506
ENS000000181904	F2R	1755.809267	0.804712431	0.275161493	0.541065655	0.230729229	1.241684982	1.593532807	1.833135056	0.929145603	1.034359688	1.021768082	1.864825916
ENS000000117525	F3	131.133006	0.399401673	0.486452951	0.682599455	0.553899655	0.507794782	1.201791536	1.179008486	1.322213042	1.26507423	1.425763632	1.664609473
ENS000000108921	FAM83H	1060.108513	0.98780758	0.69316594	0.978058259	0.856926859	0.556013887	0.845321687	1.044123167	0.455972275	1.194136829	1.487136829	1.131634713
ENS000000112029	FBX05	873.8368683	0.64427571	0.882651674	0.867516514	0.88771024	0.447308499	0.80714961	1.562098708	0.67365712	1.315214323	1.387310651	1.737979756
ENS000000077782	FGFR1	871.0851462	0.706327083	0.502894915	0.663927975	0.647303562	0.780242708	1.221363472	1.638453012	0.726625511	0.86107297	1.405457634	1.496270989
ENS000000174951	FIT1	7.102292594	0.14165473	0	0	0.151031704	0	0.122472943	0.247092101	0.554208655	3.50818752	2.192849738	1.97886917
ENS000000196371	FUT4	253.8295847	0.10316912	0.201872391	0.167414363	0.21763881	0.728711416	0.778773735	1.315096917	1.754272453	1.734877535	1.607371808	1.830041782
ENS000000179348	GATA2	136.8323853	0.472241766	0.482764734	0.55456066	0.420622123	1.245279995	1.913620291	1.004333322	1.03407578	1.174804463	1.054064038	1.081029648
ENS000000111846	GCNT2	127.76885	0.145056997	0.116785965	0.149231949	0.127690056	1.035883331	1.402277413	1.275343932	0.936241671	1.774107737	1.858715218	1.422682861
ENS000000104522	GFUS	1651.193102	0.824262641	0.867652306	0.887062422	0.853141062	0.899902943	0.96931927	0.627651628	1.06689886	1.339637255	1.47252157	1.17510833
ENS000000136235	GNMB	24554.61229	0.970223308	0.69316594	0.978058259	0.856926859	0.67490136	1.00404517	1.203981875	0.550348005	1.162625357	1.302203966	1.205313019
ENS000000170961	HAS2	440.539005	0.381235994	0.40591447	0.332481427	0.327430571	1.648682878	1.879851245	2.261229887	0.983940426	1.80113351	1.004070771	1.434989834
ENS000000113070	HBEF	336.732292	0.4995155	0.593157924	0.63094717	0.519511094	1.00705486	1.24143589	0.635830082	1.37043151	1.332553751	1.922941479	1.098359038
ENS000000094631	HDAC6	1092.22261	0.930461818	0.775526925	0.836078863	0.821434996	0.876106796	1.147300694	1.368073688	0.642198987	1.07783956	1.239329972	1.141490833
ENS000000048052	HDAC9	94.4758456	0.380131758	0.199401982	0.29705289	0.341909893	0.856554649	1.422357601	1.844375242	1.230303044	1.170734172	0.846210391	1.979473534
ENS000000090339	ICAM1	303.124062	0.61295922	0.733540627	0.625184565	0.660651633	1.06815039	0.944667129	0.806876432	1.55843933	1.197530997	1.200725075	1.361118206
ENS000000157368	IL34	154.2798177	0	0.054225647	0.101720481	0.066530961	0.575480636	0.812796357	0.854081522	0.544272557	2.089437184	2.256746522	2.488500555
ENS000000115232	ITGA4	2385.545359	0.245045738	0.300175012	0.2238541	0.522083762	0.974655657	0.892240793	0.920636346	1.902268325	1.994182238	2.241061622	1.589877447
ENS000000091449	ITGA6	3655.286289	0.613645153	0.471976417	0.828155957	0.67197844	0.55895751	1.1					

Table 3: Proteomic analysis of cell medium, list of hits corresponding to Figure 2D)

protein_set_id	accession	Clustered Vs Spread log Fold Change	Clustered Vs Spread pValue
19314	sp P04908 H2A1B_HUMAN	6,342191451	0,000204616
19395	sp P53634 CATC_HUMAN	-0,781580636	0,004082027
20188	sp Q96KG7 MEG10_HUMAN	-1,351320057	0,004085503
19592	sp Q07954 LRP1_HUMAN	-1,102509205	0,004949343
20455	sp P06280 AGAL_HUMAN	-0,823936279	0,005930019
20320	sp P98155 VLDLR_HUMAN	-1,642686833	0,010427447
20016	sp P01130 LDLR_HUMAN	-0,799216732	0,010513742
20193	sp P02786 TFR1_HUMAN	-0,954069546	0,012939708
20447	sp Q99519 NEUR1_HUMAN	-0,960603563	0,014698715
19462	sp P53041 PPP5_HUMAN	0,660528097	0,01525975
19856	sp P54578 UBP14_HUMAN	0,770161562	0,017425941
20487	sp O75054 IGSF3_HUMAN	-0,587333651	0,024072151
20291	sp Q5VU97 CAHD1_HUMAN	1,024205139	0,02457342
19904	sp P24752 THIL_HUMAN	-1,508107986	0,024917899
19862	sp P25774 CAT5_HUMAN	-1,121522126	0,025834738
19874	sp Q68BL7 OLM2A_HUMAN	1,209553813	0,026552665
19808	sp P28062 PSB8_HUMAN	0,561182673	0,02768074
20068	sp Q92484 ASM3A_HUMAN	-0,898032715	0,031112035
19901	sp Q8NHP8 PLBL2_HUMAN	-0,795350697	0,031819803
19650	sp O43237 DC1L2_HUMAN	-0,539174655	0,033622041
20492	sp P00390 GSHR_HUMAN	1,121204278	0,033653576
19764	sp P10155 RO60_HUMAN	0,962255171	0,041429745
20477	sp P30048 PRDX3_HUMAN	-1,325967988	0,046757674
19403	sp Q13510 ASA1_HUMAN	-0,861434931	0,048969694
19496	sp P43235 CATK_HUMAN	-1,246452127	0,050948014
19974	sp P61163 ACTZ_HUMAN	0,637810883	0,051177857
20267	sp O00462 MANBA_HUMAN	-0,840116856	0,055797238
19479	sp O00584 RNT2_HUMAN	-0,426035275	0,056138492
19729	sp P13686 PPA5_HUMAN	-0,917029322	0,056954602
20111	sp O14979 HNRDL_HUMAN	-1,103315758	0,058053677
19770	sp P07686 HEXB_HUMAN	-0,578173086	0,060057885
20031	sp O95834 EMAL2_HUMAN	0,664530063	0,066556922
19680	sp P62263 RS14_HUMAN	1,692340296	0,067359269
19785	sp Q92820 GGH_HUMAN	-0,53056449	0,080189891
19887	sp Q13332 PTPRS_HUMAN	-0,693339196	0,086579212
20268	sp Q14956 GPNMB_HUMAN	-0,509313945	0,087543759
19685	sp Q00688 FKBP3_HUMAN	0,496418166	0,087682207
20029	sp P07339 CATD_HUMAN	-0,474418939	0,0905938
19504	sp Q13740 CD166_HUMAN	0,960462512	0,093384
19916	sp Q9Y646 CBPQ_HUMAN	-0,775399816	0,094158689
19568	sp O15031 PLXB2_HUMAN	-0,641130383	0,09484923
19594	sp P52888 THOP1_HUMAN	0,637383658	0,09906184
19360	sp P00505 AATM_HUMAN	0,604862976	0,101569501
20198	sp P23396 RS3_HUMAN	0,495583805	0,101653404
19918	sp O75828 CBR3_HUMAN	0,366402824	0,101719989
20452	sp O00469 PLOD2_HUMAN	-0,406758182	0,102630827
19636	sp P67809 YBOX1_HUMAN	0,577354666	0,104428002
19381	sp P07858 CATB_HUMAN	-0,641357707	0,104730356
20191	sp Q16719 KYNU_HUMAN	0,58085926	0,109296523
20363	sp Q9H1B5 XYLT2_HUMAN	-0,462439383	0,112307675
20394	sp Q07021 C1QBP_HUMAN	0,564248429	0,114980943
19580	sp P38571 LICH_HUMAN	-0,813616093	0,116565321
19996	sp P08581 MET_HUMAN	-1,01237578	0,117613183
20204	sp Q9GZZ1 NAA50_HUMAN	0,584853366	0,117811787
19669	sp P60900 PSA6_HUMAN	0,51233974	0,122745949
19753	sp P05556 ITB1_HUMAN	-0,318060155	0,126986356
20396	sp P51580 TPMT_HUMAN	0,332468195	0,131667075
20485	sp O95831 AIFM1_HUMAN	0,603768164	0,133724764
20212	sp P11279 LAMP1_HUMAN	-0,471238093	0,136141487
19440	sp P07602 SAP_HUMAN	-0,845667279	0,138931415
20048	sp Q5JRX3 PREP_HUMAN	0,53407336	0,140466216
20073	sp O00115 DNS2A_HUMAN	-0,593579123	0,145879496
20345	sp Q8NOV5 GNT2A_HUMAN	-0,984637537	0,14652591
19749	sp O00560 SDCB1_HUMAN	-0,386052389	0,149287619
19551	sp Q9NSE4 SYIM_HUMAN	0,765166743	0,149405932
20127	sp P42785 PCP_HUMAN	-0,948774743	0,149809019
19494	sp P15586 GNS_HUMAN	-0,469025844	0,152350736
19524	sp Q9UHL4 DPP2_HUMAN	-0,875986087	0,153997026
19955	sp P11717 MPRI_HUMAN	-0,434947732	0,155188993
20229	sp P20042 IF2B_HUMAN	0,559429653	0,1608213
20223	sp Q9UBG0 MRC2_HUMAN	-0,467522369	0,161186314
19882	sp Q9UBR2 CATZ_HUMAN	-0,764769746	0,162214039
19418	sp Q99733 NP1L4_HUMAN	-0,688828784	0,162573606
20202	sp Q8IZQ5 SELH_HUMAN	-0,497119433	0,16338948
19979	sp O95166 GBRAP_HUMAN	0,352088108	0,164250139
19829	sp Q00577 PURA_HUMAN	0,324374895	0,169310137

19477	sp A0A0B4J2D5 GAL3B_HUMAN	1,004289476	0,169671131
20232	sp P10619 PPGB_HUMAN	-0,623265608	0,170424446
19844	sp Q9NXG2 THUM1_HUMAN	0,793238817	0,170971405
19626	sp P62820 RAB1A_HUMAN	-0,410350392	0,172315869
19796	sp P06276 CHLE_HUMAN	-0,325520478	0,175348472
19899	sp Q8NCW5 NNRE_HUMAN	0,447412713	0,177393391
20261	sp P12955 PEPD_HUMAN	0,499488701	0,17998212
20051	sp P13798 ACPH_HUMAN	1,079106286	0,180941087
19647	sp Q9BTY2 FUCO2_HUMAN	-0,469939138	0,191530237
19526	sp P48723 HSP13_HUMAN	-0,504639277	0,193047605
20182	sp P31150 GDIA_HUMAN	0,325726543	0,194609506
20005	sp P00750 TPA_HUMAN	-0,540550672	0,196408905
19880	sp P07996 TSP1_HUMAN	0,531063323	0,197405966
19489	sp P13796 PLSL_HUMAN	0,502689524	0,199807522
19845	sp P25789 PSA4_HUMAN	0,380824277	0,200913619
19365	sp Q08431 MFGM_HUMAN	-0,76248342	0,203396907
20258	sp P07585 PGS2_HUMAN	-0,660025086	0,204794629
19715	sp P40306 PSB10_HUMAN	0,492184997	0,205226774
20177	sp P18206 VINC_HUMAN	0,33217295	0,208752527
20315	sp P29401 TKT_HUMAN	0,29848633	0,210753982
20311	sp Q96019 ACL6A_HUMAN	0,715911253	0,212629013
19835	sp Q99436 PSB7_HUMAN	0,376456244	0,215424742
19633	sp P37802 TAGL2_HUMAN	-0,401612701	0,215479609
20393	sp P43007 SATT_HUMAN	-0,362918302	0,221404547
19991	sp O00410 IPO5_HUMAN	0,711052926	0,222191197
20094	sp P06865 HEXA_HUMAN	-0,65148129	0,22489233
20422	sp P06858 LIPL_HUMAN	-1,216557785	0,225318257
19967	sp Q14240 IF4A2_HUMAN	0,787257513	0,23097056
19857	sp P40926 MDHM_HUMAN	0,470975023	0,232535684
20163	sp P41271 NBL1_HUMAN	-0,477395541	0,232970055
19570	sp Q9UHD1 CHRD1_HUMAN	0,335863415	0,234447478
19548	sp Q9GZL7 WDR12_HUMAN	0,633702155	0,235440771
20161	sp Q7Z739 YTHD3_HUMAN	-0,506569863	0,235952264
20331	sp Q14103 HNRPD_HUMAN	0,857458699	0,236685532
20361	sp P84090 ERH_HUMAN	0,683821421	0,238653728
19926	sp P41091 IF2G_HUMAN	0,378368966	0,238863433
19693	sp Q92598 HS105_HUMAN	0,333712968	0,239281462
19742	sp P52907 CAZA1_HUMAN	0,298947829	0,240038359
20080	sp Q9NQR4 NIT2_HUMAN	-0,756872854	0,24021154
19696	sp P12273 PIP_HUMAN	-0,846677275	0,242244284
20066	sp Q96G03 PGM2_HUMAN	1,056244984	0,245086628
20276	sp Q06481 APLP2_HUMAN	-0,399594017	0,249748529
20178	sp Q9NPH2 INO1_HUMAN	0,46110533	0,24976896
19376	sp Q02790 FKBP4_HUMAN	0,247093463	0,25093351
20356	sp P07711 CATL1_HUMAN	-0,267649734	0,253534499
20460	sp P07311 ACYP1_HUMAN	-0,515183466	0,254661747
19851	sp P36957 ODO2_HUMAN	-0,423040511	0,258802263
20471	sp P62241 RS8_HUMAN	0,284921894	0,259191643
20116	sp P04083 ANXA1_HUMAN	-0,388432066	0,260945237
20303	sp P02100 HBE_HUMAN	-0,522487496	0,263374959
20289	sp P28066 PSA5_HUMAN	0,27220948	0,263952296
20036	sp Q14773 TPP1_HUMAN	-0,735515739	0,264531862
19363	sp Q9NR28 DBLOH_HUMAN	-0,781042887	0,265844898
19488	sp Q32M24 LRRF1_HUMAN	0,537467186	0,266544076
20137	sp P23284 PPIB_HUMAN	-0,365385521	0,270376025
19561	sp Q02809 PLOD1_HUMAN	-0,327214183	0,271353944
20466	sp P30740 ILEU_HUMAN	0,293917016	0,273626305
20364	sp P17931 LEG3_HUMAN	-0,383901954	0,277633438
19919	sp Q9BY44 EIF2A_HUMAN	0,313042035	0,279149419
19826	sp Q16658 FSCN1_HUMAN	-0,237963485	0,281666807
19413	sp P82970 HMG5_HUMAN	0,295511673	0,283802561
19574	sp P13987 CD59_HUMAN	-0,360296483	0,283868638
20486	sp Q14974 IMB1_HUMAN	0,226410018	0,28496871
20446	sp O00499 BIN1_HUMAN	0,269174544	0,286274895
19303	sp P62081 RS7_HUMAN	0,251613728	0,286686275
19797	sp P25786 PSA1_HUMAN	0,378418414	0,296182902
20334	sp Q8WUM4 PDC6I_HUMAN	-0,338845939	0,296606239
19550	sp Q13011 ECH1_HUMAN	0,359272255	0,299190854
20184	sp O15240 VGF_HUMAN	-0,805603238	0,29976068
19831	sp A6NMY6 AXA2L_HUMAN	-0,402825138	0,300793725
20386	sp P61916 NPC2_HUMAN	-0,469919617	0,301020064
20427	sp P25787 PSA2_HUMAN	0,317971201	0,301220171
20298	sp Q9BTT0 AN32E_HUMAN	0,270103221	0,302961979
19834	sp P46782 RS5_HUMAN	0,218009863	0,303499236
19728	sp P14324 FPP5_HUMAN	0,24624998	0,304138138
19353	sp P41250 GARS_HUMAN	-0,348846905	0,305471437
19921	sp Q9H4A4 JAMPB_HUMAN	0,278740279	0,306151176
20366	sp Q02750 MP2K1_HUMAN	1,119124164	0,307540369

20310	sp P15104 GLNA_HUMAN	0,527444117	0,307732418
19840	sp P43034 LIS1_HUMAN	0,280767194	0,308098792
19690	sp P00491 PNPH_HUMAN	0,25614642	0,308308433
19430	sp P04075 ALDOA_HUMAN	0,262915447	0,308751646
19983	sp Q02880 TOP2B_HUMAN	0,315303863	0,309451844
19535	sp O43324 MCA3_HUMAN	0,389831133	0,309954394
19646	sp P50281 MMP14_HUMAN	-0,318451573	0,310412973
20153	sp O15143 ARC1B_HUMAN	0,238616777	0,311550014
20426	sp Q9HC38 GLOD4_HUMAN	0,290828233	0,315700332
20170	sp P61247 RS3A_HUMAN	0,33203745	0,319114313
20207	sp P62495 ERF1_HUMAN	0,774176785	0,320257122
19827	sp P62826 RAN_HUMAN	0,252786338	0,324009143
20101	sp P09622 DLDH_HUMAN	0,313579981	0,325249625
20279	sp Q04446 GLGB_HUMAN	0,459706233	0,328272099
20290	sp P27105 STOM_HUMAN	-0,426220807	0,328548555
19861	sp P14543 NID1_HUMAN	-0,405712727	0,334091107
20371	sp Q8WVY7 UBCP1_HUMAN	0,80531858	0,340428516
19746	sp P49746 TSP3_HUMAN	-0,253277127	0,340719915
20392	sp Q9NPJ3 ACO13_HUMAN	0,453306505	0,340799762
20179	sp Q15819 UB2V2_HUMAN	0,593043169	0,342293536
20375	sp Q96JB1 DYH8_HUMAN	-0,859712674	0,342746166
20012	sp P42677 RS27_HUMAN	0,567640039	0,343879813
19676	sp P06733 ENOA_HUMAN	0,371027832	0,345682624
19814	sp Q9Y617 SERC_HUMAN	0,262086052	0,345753093
19295	sp P05023 AT1A1_HUMAN	-0,374863793	0,345934339
20217	sp Q9UJ70 NAGK_HUMAN	-0,456503319	0,347011457
19932	sp P07954 FUMH_HUMAN	0,29177074	0,347733271
19755	sp Q14152 EIF3A_HUMAN	-0,470343335	0,351307419
19471	sp P12109 CO6A1_HUMAN	-0,58826246	0,352691549
19708	sp Q9GZT8 NIF3L_HUMAN	0,299702551	0,352695102
19930	sp P61224 RAP1B_HUMAN	-0,303869904	0,353147389
19817	sp P10451 OSTP_HUMAN	-0,343967625	0,353224253
19460	sp P36551 HEM6_HUMAN	0,320729472	0,353585017
19359	sp Q9Y256 TMA7_HUMAN	0,271430675	0,353869311
19947	sp Q09328 MGT5A_HUMAN	-0,634912753	0,354910654
20272	sp P19021 AMD_HUMAN	-0,68111263	0,358737672
20445	sp O00625 PIR_HUMAN	-0,232570958	0,359674582
20135	sp P55786 PSA_HUMAN	0,256557237	0,360984958
19705	sp P30084 ECHM_HUMAN	0,704511585	0,361505528
20186	sp Q13214 SEM3B_HUMAN	-0,386984986	0,362299301
20023	sp P52292 IMA1_HUMAN	0,319994707	0,362695104
19394	sp P09871 C1S_HUMAN	-0,275109807	0,363835005
19497	sp O60911 CATL2_HUMAN	-0,283414952	0,366933387
20401	sp P49207 RL34_HUMAN	-0,946935444	0,36737357
19564	sp P28838 AMPL_HUMAN	0,703287294	0,369439243
19928	sp P17174 AATC_HUMAN	0,622082151	0,372152457
20297	sp Q53H82 LACB2_HUMAN	0,244433984	0,373232733
19317	sp Q16610 ECM1_HUMAN	-0,407886656	0,376249239
19900	sp Q16363 LAMA4_HUMAN	-0,348789302	0,377927834
20389	sp P51884 LUM_HUMAN	-0,340810966	0,378678368
20349	sp P20827 EFNA1_HUMAN	-0,236023884	0,385923324
19630	sp P00736 C1R_HUMAN	-0,312529355	0,386240806
20360	sp P32004 L1CAM_HUMAN	-0,282876782	0,389028702
19684	sp O43396 TXNL1_HUMAN	0,221146795	0,393126241
20167	sp P30153 2AAA_HUMAN	0,23241594	0,394235873
20155	sp Q99598 TSNAX_HUMAN	0,528885425	0,395147505
20123	sp P62750 RL23A_HUMAN	0,354708813	0,395265109
19385	sp P09341 GROA_HUMAN	-0,333489397	0,397373594
19800	sp Q12841 FSTL1_HUMAN	-0,297622112	0,398547726
20026	sp P78504 JAG1_HUMAN	-0,568500212	0,399331957
20417	sp P50552 VASP_HUMAN	0,211669817	0,399912075
19389	sp P30566 PUR8_HUMAN	0,200888755	0,400832882
20254	sp Q9NRG0 CHRC1_HUMAN	0,281690816	0,40283903
20302	sp O95782 AP2A1_HUMAN	-0,320154899	0,405151966
20156	sp P61158 ARP3_HUMAN	0,210183748	0,405505536
19370	sp Q13685 AAMP_HUMAN	0,215095992	0,406782972
20200	sp P05067 A4_HUMAN	-0,342046781	0,406847239
19472	sp P63313 TYB10_HUMAN	0,294349918	0,40688756
20425	sp Q15758 AAAT_HUMAN	-0,236383955	0,407765019
20183	sp P50395 GDIB_HUMAN	0,195756879	0,411103044
20173	sp P31949 S10AB_HUMAN	0,179666919	0,414650389
19436	sp O00533 NCHL1_HUMAN	-0,455595002	0,414910195
19556	sp Q8NBJ4 GOLM1_HUMAN	-0,427709133	0,415813187
20374	sp P04062 GLCM_HUMAN	-0,47242389	0,416016098
20072	sp P62888 RL30_HUMAN	0,191345155	0,417156152
20064	sp P34932 HSP74_HUMAN	0,173128513	0,418042313
19956	sp Q8N475 FSTL5_HUMAN	-0,487444587	0,419435088
20476	sp Q9NZU0 FLRT3_HUMAN	-0,205304703	0,419882512

19923	sp P46777 RL5_HUMAN	0,320362163	0,421235073
19279	sp P30050 RL12_HUMAN	0,228321055	0,421370372
19954	sp P49773 HINT1_HUMAN	-0,469164132	0,422703697
20097	sp P84098 RL19_HUMAN	0,221868179	0,422990964
19740	sp O43175 SERA_HUMAN	0,63075972	0,423020031
19571	sp P13693 TCTP_HUMAN	0,22181904	0,423035971
20475	sp Q14008 CKAP5_HUMAN	0,39995356	0,423854754
20018	sp O60568 PLOD3_HUMAN	-0,31227536	0,424815451
20493	sp Q9Y376 CAB39_HUMAN	0,295693059	0,430223795
20192	sp Q9UKZ9 PCOC2_HUMAN	-0,262973503	0,431501324
19841	sp P61201 CSN2_HUMAN	0,220429746	0,432338099
19396	sp O95373 IPO7_HUMAN	0,21539174	0,432782245
19456	sp P49458 SRP09_HUMAN	0,232734567	0,434065319
20019	sp Q9BX55 AP1M1_HUMAN	0,43388456	0,434352622
20353	sp P62269 RS18_HUMAN	0,229809677	0,436467691
20037	sp P06756 ITAV_HUMAN	-0,296989736	0,437687964
20317	sp P30520 PURA2_HUMAN	0,28157813	0,439983376
19518	sp O75347 TBCA_HUMAN	1,331816615	0,442251909
19536	sp O76003 GLRX3_HUMAN	-0,447766238	0,44289622
19508	sp O75083 WDR1_HUMAN	-0,265053443	0,444779343
19323	sp P11021 BIP_HUMAN	0,185227315	0,447309911
19422	sp O95336 6PGL_HUMAN	-0,459658815	0,447343865
19612	sp P36871 PGM1_HUMAN	0,190119432	0,449367034
19474	sp Q16531 DDB1_HUMAN	0,260629774	0,450437478
20464	sp P48681 NEST_HUMAN	-0,469302568	0,45176519
19725	sp Q92499 DDX1_HUMAN	0,644099121	0,451935044
19623	sp P62273 RS29_HUMAN	0,253839865	0,46242427
19585	sp Q08380 LG3BP_HUMAN	-0,243549845	0,465153771
20352	sp Q9H1E3 NUCK5_HUMAN	0,294631736	0,466078211
19619	sp A0A1B0GUS4 UB2L5_HUMAN	0,261055128	0,466078403
20039	sp P10809 CH60_HUMAN	0,186010065	0,466910752
20318	sp O43278 SPIT1_HUMAN	-0,191231956	0,467759962
19498	sp P00367 DHE3_HUMAN	-0,294946432	0,471540102
20122	sp P08195 4F2_HUMAN	-0,238765397	0,473490173
20388	sp Q15370 ELO8_HUMAN	0,237771353	0,473846964
20206	sp P39019 RS19_HUMAN	0,18079449	0,476248855
19300	sp P00558 PGK1_HUMAN	0,163949882	0,476560652
19896	sp Q9UQ80 PAZG4_HUMAN	0,177883838	0,478134433
20350	sp P62258 I433E_HUMAN	0,206828365	0,47848502
20408	sp P11387 TOP1_HUMAN	0,321469356	0,480084091
20369	sp Q06323 PSME1_HUMAN	0,592122532	0,480945491
19280	sp Q96RW7 HMCN1_HUMAN	-0,266127904	0,484125263
19652	sp P26038 MOE5_HUMAN	0,151997415	0,485178127
20286	sp Q5T6V5 QSPP_HUMAN	-0,602660378	0,485542595
19378	sp P21399 ACOC_HUMAN	0,183002914	0,48608378
19820	sp P09382 LEG1_HUMAN	-0,180993509	0,486514124
20113	sp Q9BWS9 CHID1_HUMAN	-0,330924456	0,487202944
19980	sp Q00796 DHSO_HUMAN	0,192445611	0,48799794
20380	sp P55809 SCOT1_HUMAN	0,249386605	0,488119933
19682	sp Q13310 PABP4_HUMAN	-0,319181473	0,489394183
19905	sp Q16851 UGPA_HUMAN	0,161313014	0,49052627
19691	sp Q6YHK3 CD109_HUMAN	-0,164612187	0,493916897
19544	sp O15347 HMGGB3_HUMAN	0,543273937	0,494747513
20130	sp O60462 NRP2_HUMAN	-0,263154555	0,497857037
20228	sp Q99497 PARK7_HUMAN	0,237555049	0,498286035
20084	sp P27695 APEX1_HUMAN	0,209787966	0,499741699
19815	sp P08603 CFAH_HUMAN	-0,482359523	0,49988689
19978	sp P01034 CYTC_HUMAN	-0,306370319	0,501244768
20413	sp Q86TI2 DPP9_HUMAN	0,178015696	0,501494417
19324	sp P0DMV9 HS71B_HUMAN	0,139333215	0,50156207
19294	sp P61981 I433G_HUMAN	0,183454231	0,502066909
19557	sp P01023 A2MG_HUMAN	-0,434360015	0,502604552
20336	sp Q08945 SSRP1_HUMAN	-0,577202299	0,503375534
19842	sp P62328 TYB4_HUMAN	0,196059528	0,503771303
19373	sp P18124 RL7_HUMAN	0,342596233	0,504079847
19435	sp P46940 IQGA1_HUMAN	0,157342699	0,507356214
20075	sp Q9UBT2 SAE2_HUMAN	0,24559222	0,508786447
19912	sp Q13616 CUL1_HUMAN	0,209756986	0,509394546
20007	sp P52565 GDIR1_HUMAN	0,18371615	0,509740269
19283	sp P33176 KINH_HUMAN	0,319985678	0,510366291
20175	sp P49189 AL9A1_HUMAN	0,189034833	0,511582692
19670	sp P11216 PYGB_HUMAN	0,141915713	0,514712724
19604	sp P22090 RS4Y1_HUMAN	-0,338194441	0,515781732
19402	sp P62906 RL10A_HUMAN	0,152660603	0,516743745
19399	sp Q9UJJ9 GNPTG_HUMAN	-0,329491428	0,517603823
19783	sp P30086 PEBP1_HUMAN	0,170392315	0,517915922
19466	sp P07195 LDHB_HUMAN	0,171751445	0,517988407
20245	sp P18669 PGAM1_HUMAN	0,222967393	0,51841158

20461	sp Q9NR30 DDX21_HUMAN	0,382889574	0,519696578
20210	sp P46781 RS9_HUMAN	0,277552729	0,520103277
20410	sp Q9NY33 DPP3_HUMAN	0,168934318	0,520373784
19500	sp P02649 APOE_HUMAN	-0,734480883	0,521143537
20244	sp P98160 PGBM_HUMAN	-0,180923718	0,521673126
19738	sp P28482 MK01_HUMAN	-0,214650345	0,522094165
19481	sp B2RXH8 HNRC2_HUMAN	-0,212550878	0,522562729
20257	sp Q9ULV4 COR1C_HUMAN	0,154883944	0,522849179
19897	sp P40925 MDHC_HUMAN	0,149116541	0,523072926
19892	sp P61160 ARP2_HUMAN	-0,168301123	0,52511151
19336	sp P60981 DEST_HUMAN	0,203706131	0,527455181
20351	sp Q13263 TIF1B_HUMAN	0,467808731	0,528122882
19992	sp P05455 LA_HUMAN	0,209267371	0,529213479
20081	sp P23381 SYWC_HUMAN	0,212306548	0,530367557
19653	sp P15311 EZRI_HUMAN	0,136059634	0,532003336
19813	sp P09132 SRP19_HUMAN	0,141439967	0,532495867
20474	sp P11047 LAMC1_HUMAN	-0,317307702	0,535945466
19709	sp O75368 SH3L1_HUMAN	0,36068671	0,537664579
19600	sp P01024 CO3_HUMAN	-0,17849424	0,537860512
19995	sp O75144 ICOSL_HUMAN	0,15991439	0,539595462
20242	sp P07942 LAMB1_HUMAN	-0,314910272	0,540481986
19701	sp P09486 SPRC_HUMAN	-0,219546696	0,540861586
20038	sp O00468 AGRIN_HUMAN	-0,446476219	0,541314046
19538	sp Q9NPH3 IL1AP_HUMAN	-0,168907538	0,542387428
20189	sp P16035 TIMP2_HUMAN	-0,236800388	0,543096588
19605	sp Q96KP4 CNDP2_HUMAN	0,187460221	0,544465143
20470	sp O75326 SEM7A_HUMAN	-0,266510695	0,546456684
20333	sp Q9NY27 PP4R2_HUMAN	-0,294851409	0,546545739
20201	sp Q9UKM7 MA1B1_HUMAN	-0,233099777	0,549109317
19675	sp P09104 ENOG_HUMAN	0,347334921	0,549217336
19993	sp P08582 TRFM_HUMAN	-0,397939401	0,549310695
19674	sp Q9HB71 CYBP_HUMAN	0,201697063	0,550211042
20160	sp Q13867 BLMH_HUMAN	0,179122795	0,551407063
19616	sp Q9Y4L1 HYOU1_HUMAN	-0,182248226	0,551444165
19516	sp P51114 FXR1_HUMAN	0,272855141	0,552729722
19602	sp O00154 BACH_HUMAN	0,159813538	0,553232874
20227	sp P47914 RL29_HUMAN	0,155021015	0,553438144
20283	sp P54136 SYRC_HUMAN	0,329609773	0,558566661
19788	sp Q9P265 DIP2B_HUMAN	-0,339152102	0,558716494
19681	sp P11940 PABP1_HUMAN	0,214636326	0,559184244
19405	sp P26583 HMGB2_HUMAN	0,344750148	0,561377409
20047	sp Q9ULC4 MCTS1_HUMAN	-0,255357207	0,561696949
19380	sp P31153 METH2_HUMAN	0,368752682	0,561845217
19492	sp P15531 NDKA_HUMAN	0,238080838	0,562053264
19703	sp P60174 TPIS_HUMAN	0,184856431	0,562102982
19313	sp P17050 NAGAB_HUMAN	-0,316343554	0,562627623
19707	sp Q9BR76 COR1B_HUMAN	0,230639721	0,564942471
19442	sp P03950 ANGI_HUMAN	-0,348151987	0,565245522
20091	sp P08708 RS17_HUMAN	0,143882164	0,565819757
19629	sp P62851 RS25_HUMAN	0,142041478	0,569041874
19565	sp P09960 LKHA4_HUMAN	0,135520839	0,569281378
20002	sp P35268 RL22_HUMAN	0,180128631	0,56939491
19736	sp Q9UHD8 SEPT9_HUMAN	0,27342256	0,569961914
19486	sp Q92859 NEO1_HUMAN	0,154588873	0,571578853
20033	sp Q43583 DENR_HUMAN	0,292703721	0,571601558
19547	sp Q96C86 DCPS_HUMAN	-0,270107391	0,572269448
19464	sp P00338 LDHA_HUMAN	0,142498024	0,574318659
20041	sp P58215 LOXL3_HUMAN	0,226165039	0,574556512
20166	sp Q0VDG4 SCRN3_HUMAN	0,145085939	0,575414382
19319	sp Q96AG4 LRC59_HUMAN	0,266351306	0,575819055
19628	sp P04179 SODM_HUMAN	0,219176208	0,576791469
20098	sp Q9UHY7 ENOPH_HUMAN	0,140860947	0,576909516
20432	sp O00567 NOP56_HUMAN	-0,178082022	0,577501501
19866	sp Q01459 DIAC_HUMAN	-0,41727652	0,578587753
19775	sp P29966 MARCS_HUMAN	0,19202726	0,581536375
20022	sp Q969E4 TCAL3_HUMAN	0,275031451	0,581861044
19846	sp P62266 RS23_HUMAN	0,171618173	0,582041935
19951	sp Q9UNF0 PACN2_HUMAN	0,128067554	0,583884651
20174	sp Q14CX7 NAA25_HUMAN	0,192725138	0,583922271
19933	sp P43487 RANG_HUMAN	0,186726855	0,584291443
19863	sp P02545 LMNA_HUMAN	0,140688742	0,584330992
19455	sp Q9NQW7 XPP1_HUMAN	0,161860899	0,585142069
19514	sp P25398 RS12_HUMAN	0,135861138	0,585453525
20262	sp Q8WWM7 JTX2L_HUMAN	0,196931236	0,585790703
20157	sp P13667 PDIA4_HUMAN	0,140381658	0,586851281
20110	sp P07237 PDIA1_HUMAN	0,15006307	0,587051809
19732	sp P26012 ITB8_HUMAN	-0,321006405	0,588151523
19779	sp P69849 NOMO3_HUMAN	-0,12549977	0,589413493

20138	sp Q13822 ENPP2_HUMAN	-0,179545845	0,590014689
20083	sp Q86UD1 OAF_HUMAN	-0,276938741	0,590235753
19805	sp O15372 EIF3H_HUMAN	0,3514113	0,590280123
20059	sp P12270 TPR_HUMAN	0,322522145	0,591144258
20287	sp P25391 LAMA1_HUMAN	-0,240930278	0,59138679
20015	sp P62244 RS1F5A_HUMAN	0,177276122	0,592083386
20259	sp Q9BWD1 THIC_HUMAN	0,155474922	0,592539705
20222	sp P11362 FGFR1_HUMAN	-0,174244916	0,592566399
19318	sp P37108 SRP14_HUMAN	0,168766329	0,593601228
19572	sp Q969P0 IGSF8_HUMAN	-0,564340086	0,593841786
20154	sp P12956 XRCC6_HUMAN	0,199332575	0,594585057
20060	sp P41236 IPP2_HUMAN	0,209911973	0,595145194
19482	sp P32119 PRDX2_HUMAN	-0,260495497	0,595304528
20247	sp O43493 TGN02_HUMAN	-0,131080818	0,595815407
19869	sp Q15424 SAFB1_HUMAN	0,265249226	0,596449385
19945	sp Q14061 COX17_HUMAN	0,152310963	0,5966061
20004	sp P29218 IMPA1_HUMAN	-0,210134502	0,596960698
19292	sp P63104 1433Z_HUMAN	0,132496885	0,597439201
19519	sp P35052 GPC1_HUMAN	-0,142366913	0,604572432
19493	sp Q02818 NUCB1_HUMAN	-0,326785684	0,604826334
19491	sp P22392 NDKB_HUMAN	0,196301518	0,60486843
19608	sp Q14914 PTGR1_HUMAN	0,210967299	0,605499629
19644	sp P50990 TCPQ_HUMAN	0,144141339	0,607086526
19520	sp P16152 CBR1_HUMAN	0,115231591	0,607258777
19333	sp Q99832 TCPH_HUMAN	0,164067658	0,609086971
20014	sp P61956 SUMO2_HUMAN	0,230671576	0,609181105
20062	sp P62993 GRB2_HUMAN	-0,201739843	0,610478157
19390	sp P62917 RL8_HUMAN	0,160135142	0,612442066
19877	sp P36955 PEDF_HUMAN	-0,300877223	0,613379928
19778	sp Q08257 QOR_HUMAN	0,100968539	0,615546451
20124	sp Q04760 LGUL_HUMAN	0,167904401	0,615819782
19986	sp P06744 G6PI_HUMAN	0,16878753	0,616208461
20479	sp Q12904 AIMP1_HUMAN	0,133200327	0,619356385
19710	sp Q9H3G5 CPVL_HUMAN	-0,5982555	0,620177621
19969	sp P13497 BMP1_HUMAN	-0,136817848	0,621088742
19615	sp P30405 PIIF_HUMAN	0,338227464	0,626337499
20465	sp Q8IUX7 AEBP1_HUMAN	-0,327723956	0,627275379
19438	sp P07225 PROS_HUMAN	-0,206684625	0,628324214
20365	sp Q02878 RL6_HUMAN	0,122968365	0,630452816
19903	sp Q10471 GALT2_HUMAN	-0,156324349	0,63054904
20330	sp P13489 RINI_HUMAN	-0,22939552	0,631204444
19282	sp P00492 HPR1_HUMAN	0,119710876	0,632838154
19553	sp Q01581 HMC51_HUMAN	0,205751381	0,633637203
20282	sp P48745 CCN3_HUMAN	-0,136292589	0,633936994
20294	sp Q9Y2W1 TR150_HUMAN	-0,270098424	0,634466344
20376	sp Q15393 SF3B3_HUMAN	0,411047884	0,636341711
19321	sp P43251 BTD_HUMAN	-0,215831553	0,636991328
20453	sp O94985 CSTN1_HUMAN	-0,172751251	0,638307974
19907	sp P37837 TALDO_HUMAN	0,192072575	0,639546252
19743	sp P27797 CALR_HUMAN	0,105682377	0,640629979
19982	sp O75223 GGCT_HUMAN	0,106125451	0,64218029
19640	sp Q9UN22 NSF1C_HUMAN	0,242406397	0,64252958
20488	sp P62318 SMD3_HUMAN	-0,231437157	0,643257575
20056	sp O60832 DKC1_HUMAN	0,460948094	0,644483349
20280	sp P78417 GSTO1_HUMAN	0,119738666	0,645701731
19433	sp P08134 RHOC_HUMAN	-0,120156766	0,645949651
19635	sp Q8N1G4 LRC47_HUMAN	-0,152104535	0,646860471
19975	sp Q14764 MVP_HUMAN	0,276822125	0,647228992
19946	sp Q16836 HCDH_HUMAN	0,149838015	0,649984974
19375	sp Q9Y2V2 CHSP1_HUMAN	0,213846045	0,650457488
19790	sp P01033 TIMP1_HUMAN	-0,253418939	0,650775611
19849	sp P40429 RL13A_HUMAN	0,1256786	0,653108579
19925	sp P49589 SYCC_HUMAN	0,165033567	0,653723059
19531	sp P30101 PDIA3_HUMAN	0,115294636	0,65384479
20424	sp P62316 SMD2_HUMAN	-0,154510601	0,654309483
20211	sp O95433 AHS1_HUMAN	0,099810335	0,655801077
19965	sp Q9Y266 NUDC_HUMAN	0,106839153	0,657563476
20256	sp P48444 COPD_HUMAN	-0,268044783	0,658413657
20322	sp Q16666 IF16_HUMAN	0,13053873	0,65985706
19286	sp P05120 PAI2_HUMAN	0,325779346	0,660159843
19424	sp Q15149 PLEC_HUMAN	0,346595498	0,662573251
20082	sp P53999 TCP4_HUMAN	0,368996411	0,663733742
20011	sp O75937 DNJC8_HUMAN	0,204031015	0,66549075
19902	sp Q15185 TEBP_HUMAN	0,174643467	0,667341333
19802	sp P58546 MTPN_HUMAN	-0,096891142	0,667717247
20415	sp P43490 NAMPT_HUMAN	0,107196904	0,667810205
20450	sp O95861 BPNT1_HUMAN	0,089674238	0,66880144
20221	sp Q99523 SORT_HUMAN	-0,165686431	0,669032945

20434	sp P22234 PUR6_HUMAN	0,215815756	0,670302048
19505	sp O14602 IF1AY_HUMAN	0,14367384	0,671010261
20181	sp O15145 ARPC3_HUMAN	0,089283121	0,673898339
19741	sp P27824 CALX_HUMAN	-0,105063017	0,674041237
19698	sp P0C055 H2AZ_HUMAN	0,20951596	0,674154608
20383	sp Q9UN86 G3BP2_HUMAN	0,143652168	0,675443517
19512	sp P51858 HDGF_HUMAN	0,129643974	0,676360206
20085	sp P19823 ITI2_HUMAN	-0,420496661	0,678879787
20077	sp P39748 FEN1_HUMAN	0,162785122	0,679074857
20118	sp P13500 CCL2_HUMAN	0,1477292	0,679922792
20266	sp P11233 RALA_HUMAN	-0,145460042	0,680598591
20104	sp O75116 ROCK2_HUMAN	-0,335348214	0,68253711
19312	sp P50579 MAP2_HUMAN	0,258001558	0,682829242
20195	sp P17987 TCPA_HUMAN	-0,117603606	0,683050854
19473	sp P52209 6PGD_HUMAN	0,101683026	0,683878053
20034	sp Q16881 TRXR1_HUMAN	0,160299003	0,684977597
19959	sp P46821 MAP1B_HUMAN	0,249794321	0,68650658
19864	sp Q14847 LASP1_HUMAN	0,167797006	0,688682612
19429	sp P39023 RL3_HUMAN	0,11767073	0,688814742
20055	sp Q8NBS9 TXND5_HUMAN	0,123814631	0,689836977
19521	sp Q8NE71 ABCF1_HUMAN	0,195710074	0,690016201
20165	sp P27816 MAP4_HUMAN	-0,160201342	0,691139604
20402	sp Q92520 FAM3C_HUMAN	-0,174839643	0,691195524
19499	sp Q8NC51 PAIRB_HUMAN	-0,149007627	0,693114632
20323	sp Q9NYU2 UGGG1_HUMAN	-0,243893705	0,693605979
19427	sp O43399 TPD54_HUMAN	0,332412686	0,694318843
20252	sp Q16543 CDC37_HUMAN	0,205666207	0,694366619
19654	sp P35241 RADI_HUMAN	0,104170148	0,694802455
19745	sp P48643 TCPE_HUMAN	0,141644149	0,695518745
19386	sp Q9NY97 B3GN2_HUMAN	-0,126372335	0,699594329
19534	sp P32455 GBP1_HUMAN	0,249771177	0,700577789
20354	sp P09661 RU2A_HUMAN	0,220900963	0,70088412
19621	sp P14314 GLU2B_HUMAN	0,101462566	0,701025357
19458	sp P07108 ACBP_HUMAN	0,116990749	0,703860135
20187	sp P61254 RL26_HUMAN	-0,119834359	0,706209729
20472	sp Q9Y6E2 BZW2_HUMAN	0,216033575	0,707780815
20274	sp P04792 HSPB1_HUMAN	0,167235014	0,7086699
19843	sp P61313 RL15_HUMAN	0,099486249	0,708700826
20231	sp P07814 SYEP_HUMAN	0,127915832	0,709092903
19789	sp P09417 DHPR_HUMAN	0,088593865	0,710230383
19724	sp Q9H354 YJ001_HUMAN	-0,077838235	0,7109772
19397	sp Q9NPF2 CHSTB_HUMAN	-0,307458878	0,712786121
20442	sp P35520 CBS_HUMAN	0,104167487	0,712955237
19484	sp Q99470 SDF2_HUMAN	0,20763224	0,713428694
19411	sp P67936 TPM4_HUMAN	0,219165095	0,715146121
19664	sp Q12906 ILF3_HUMAN	0,205533543	0,715239472
19495	sp P50502 F10A1_HUMAN	-0,111649799	0,715275291
19288	sp P02795 MT2_HUMAN	0,176895767	0,716033253
20069	sp Q15046 SYK_HUMAN	0,125083868	0,716971094
19441	sp P07737 PROF1_HUMAN	0,107387008	0,717752688
19824	sp Q15274 NADC_HUMAN	0,113761273	0,718800231
20128	sp Q04637 IF4G1_HUMAN	0,136052186	0,720852992
20344	sp P15880 RS2_HUMAN	0,109670711	0,722172936
20197	sp P43121 MUC18_HUMAN	-0,162248423	0,722352222
20391	sp Q86UP2 KTN1_HUMAN	0,092627527	0,722410213
20131	sp P09543 CN37_HUMAN	-0,204425478	0,72244989
19751	sp P07093 GDN_HUMAN	-0,086406793	0,722866303
19388	sp P06899 H2B1J_HUMAN	0,116332642	0,723313467
20299	sp Q02543 RL18A_HUMAN	0,108478044	0,724394447
19342	sp Q14517 FAT1_HUMAN	-0,163911173	0,724754455
20484	sp P49354 FNTA_HUMAN	0,097930873	0,727196647
20489	sp O75882 ATR_N_HUMAN	-0,125170416	0,727755278
19795	sp P08253 MMP2_HUMAN	0,101121591	0,727920425
19747	sp Q9NRX4 PHP14_HUMAN	0,176972551	0,728883984
20338	sp P04181 OAT_HUMAN	-0,11502061	0,730436216
20378	sp P23526 SAHH_HUMAN	0,080800095	0,730933558
20316	sp Q96P70 IPO9_HUMAN	0,069553568	0,731547132
20319	sp O00244 ATOX1_HUMAN	0,08814097	0,73291285
20430	sp P01036 CYTS_HUMAN	-0,338286982	0,733115058
20441	sp Q9NSD9 SYFB_HUMAN	0,228415181	0,735713876
19392	sp P38159 RBMX_HUMAN	0,152400288	0,736530508
20385	sp Q9NQX1 PRDM5_HUMAN	0,099146121	0,737016592
19949	sp P35659 DEK_HUMAN	0,216445796	0,738399416
20042	sp P62280 RS11_HUMAN	0,118648061	0,739009569
20132	sp P52788 SPSY_HUMAN	-0,118107304	0,739284391
19511	sp P60660 MYL6_HUMAN	-0,107184178	0,740227229
19434	sp P78539 SRPX_HUMAN	-0,19132219	0,740881185
20218	sp Q6UW49 SPESP_HUMAN	0,307087816	0,74107562

19767	sp P31939 PUR9_HUMAN	0,099997485	0,741212331
20423	sp Q13449 LSAMP_HUMAN	-0,085082264	0,741401031
19476	sp P43243 MATR3_HUMAN	-0,18934623	0,743086544
19798	sp Q4J6C6 PPCEL_HUMAN	-0,243394713	0,745565666
19906	sp P63165 SUMO1_HUMAN	0,296064083	0,746373157
19968	sp P22455 FGFR4_HUMAN	-0,140996351	0,747796427
19281	sp P24534 EF1B_HUMAN	-0,110266728	0,748298755
20078	sp Q15084 PDIA6_HUMAN	-0,099670861	0,749942872
19964	sp P17405 ASM_HUMAN	0,123232582	0,750255882
19549	sp P53004 BIEA_HUMAN	-0,129018183	0,751130707
19867	sp Q99536 VAT1_HUMAN	0,073694119	0,75118358
20185	sp P05362 ICAM1_HUMAN	0,0906635	0,751201086
20285	sp Q9BKK5 B2L13_HUMAN	0,110016621	0,75148441
20203	sp P63167 DYL1_HUMAN	0,084692265	0,752094425
19838	sp P35270 SPRE_HUMAN	-0,137549382	0,753037572
19787	sp P29692 EF1D_HUMAN	-0,131260506	0,753729505
19963	sp Q01082 SPTB2_HUMAN	-0,141641177	0,753940105
20387	sp Q9Y4K0 LOXL2_HUMAN	-0,121837915	0,755444991
19914	sp P61088 UBE2N_HUMAN	0,106725476	0,755810297
19614	sp P50991 TCPD_HUMAN	-0,070741336	0,760111631
19727	sp P48147 PPCE_HUMAN	0,109813434	0,762270598
19702	sp Q9Y383 LC7L2_HUMAN	0,160669416	0,762673448
19560	sp Q9NZU5 LMCD1_HUMAN	0,167938621	0,763266441
20196	sp Q01844 EWS_HUMAN	-0,183465605	0,763279204
19352	sp P54727 RD23B_HUMAN	0,082201726	0,765089601
19450	sp Q03252 LMNB2_HUMAN	-0,153821125	0,765324335
20151	sp Q95881 TXD12_HUMAN	0,196427369	0,768541578
19832	sp P54819 KAD2_HUMAN	-0,151554747	0,769321376
19850	sp P35237 SPB6_HUMAN	-0,09132654	0,769424076
20339	sp P60033 CD81_HUMAN	0,294081224	0,769932373
20046	sp P17096 HMGAI_HUMAN	0,29432657	0,771761782
19461	sp P21291 CSR1_HUMAN	0,075530272	0,773382466
19297	sp Q43768 ENSA_HUMAN	-0,168251599	0,775448626
19768	sp P15121 ALDR_HUMAN	-0,057233587	0,777731206
19818	sp P11413 G6PD_HUMAN	0,095776972	0,778181303
20403	sp Q9Y315 DEOC_HUMAN	0,109823733	0,778202769
20102	sp Q6ZMJ2 SCAR5_HUMAN	0,148576168	0,780405426
20065	sp P68104 EF1A1_HUMAN	-0,096057516	0,780456797
20341	sp Q02952 AKA12_HUMAN	-0,085860022	0,782853023
19958	sp Q00839 HNRPU_HUMAN	0,127494815	0,782963438
20199	sp Q00391 QSOX1_HUMAN	-0,171183087	0,783588245
19302	sp P60709 ACTB_HUMAN	0,065272542	0,78428877
19546	sp Q9ULB5 CADH7_HUMAN	0,110258625	0,784555285
20429	sp Q060869 EDF1_HUMAN	0,158820346	0,785703202
19997	sp Q99075 HBEGF_HUMAN	-0,082927591	0,787660802
20168	sp P02751 FINC_HUMAN	-0,09213635	0,788462581
20348	sp P08579 RU2B_HUMAN	0,11900899	0,788510659
20292	sp P55010 IF5_HUMAN	0,099578112	0,788894682
20121	sp P63208 SKP1_HUMAN	-0,07648748	0,788905776
19470	sp P08238 HS90B_HUMAN	0,064652573	0,789096693
19731	sp Q6UVY6 MOXD1_HUMAN	-0,118217169	0,79480301
19613	sp P23588 IF4B_HUMAN	0,07435878	0,800004112
19624	sp Q16831 UPP1_HUMAN	0,061828166	0,80030385
19750	sp P63220 RS21_HUMAN	-0,122772362	0,800440595
20301	sp P62913 RL11_HUMAN	0,089534278	0,800485254
20398	sp Q9Y5B9 SP16H_HUMAN	0,146780771	0,80048659
19586	sp Q9NUQ9 CYRIB_HUMAN	0,092942368	0,801458279
19671	sp P06737 PYGL_HUMAN	-0,058652386	0,803540669
20076	sp Q05682 CALD1_HUMAN	0,085915763	0,805059264
20120	sp O75874 IDHC_HUMAN	0,060947873	0,805954098
20237	sp Q00299 CLIC1_HUMAN	0,060762795	0,807084157
20025	sp P51572 BAP31_HUMAN	0,116715606	0,807169551
20089	sp Q7KZF4 SND1_HUMAN	0,089600457	0,807513315
19688	sp Q9BRK5 CAB45_HUMAN	-0,091161051	0,807949728
19506	sp Q92823 NRCAM_HUMAN	0,10209871	0,811091094
19981	sp P46063 RECQ1_HUMAN	-0,132148235	0,814391314
20335	sp Q96FW1 OTUB1_HUMAN	-0,152100964	0,814990236
19335	sp P23528 COF1_HUMAN	0,062667222	0,816144901
19733	sp P62854 RS26_HUMAN	0,090220572	0,816217374
20248	sp P62277 RS13_HUMAN	0,146160137	0,816645173
20420	sp Q9UNW1 MINP1_HUMAN	-0,103347959	0,816935235
20491	sp P38919 IFA43_HUMAN	0,067463465	0,817032775
19898	sp O15067 PUR4_HUMAN	0,062589642	0,817496413
19941	sp P19338 NUCL_HUMAN	0,085483318	0,81954043
19517	sp Q01105 SET_HUMAN	0,069041698	0,820416303
20463	sp Q13813 SPTN1_HUMAN	0,074940797	0,823125077
19940	sp Q15121 PEA15_HUMAN	-0,081156562	0,82320187
20115	sp P61970 NTF2_HUMAN	0,075672806	0,824530206

19645	sp O76021 RL1D1_HUMAN	0,056323256	0,826049433
20234	sp Q86UE4 LYRIC_HUMAN	0,064706137	0,826818769
19343	sp O95394 AGM1_HUMAN	0,097015575	0,829117622
19966	sp P60842 IF4A1_HUMAN	0,058693303	0,829157954
19475	sp P40121 CAPG_HUMAN	0,073617423	0,829591063
19786	sp B5ME19 EIFCL_HUMAN	0,082096604	0,830439284
19819	sp Q9BRA2 TXD17_HUMAN	0,07923581	0,830950848
19962	sp Q13126 MTAP_HUMAN	0,050521365	0,831571449
19309	sp P16401 H15_HUMAN	0,132814286	0,832098468
19315	sp P16104 H2AX_HUMAN	0,16414675	0,833759649
20150	sp O43847 NRDC_HUMAN	0,069727434	0,835635313
20043	sp P14618 KPYP_HUMAN	0,044897988	0,835722497
20340	sp P04406 G3P_HUMAN	-0,09828121	0,838430375
19957	sp Q9Y6N7 ROBO1_HUMAN	0,04369401	0,839066555
19804	sp P31948 STIP1_HUMAN	0,078561448	0,84187179
19922	sp P30085 KCY_HUMAN	0,045793396	0,842155221
20454	sp Q13564 ULA1_HUMAN	-0,047334123	0,84221938
19537	sp O00339 MATN2_HUMAN	0,090846823	0,842670264
19637	sp P11766 ADHX_HUMAN	0,06293872	0,843085812
19791	sp Q9H2E6 SEM6A_HUMAN	-0,10659633	0,844309722
20045	sp P30041 PRDX6_HUMAN	0,063699152	0,847234559
20250	sp Q9P2E9 RRBP1_HUMAN	-0,094880669	0,848013796
20053	sp P05114 HMGN1_HUMAN	0,081425537	0,848326176
19595	sp P26641 EF1G_HUMAN	0,050415962	0,849021931
20281	sp O00622 CCN1_HUMAN	-0,062228097	0,849293689
19943	sp P80303 NUCB2_HUMAN	-0,099653463	0,851040006
20251	sp Q12905 ILF2_HUMAN	-0,084428181	0,851057479
20313	sp Q9Y3FA STRAP_HUMAN	0,090639323	0,851888534
19803	sp Q15113 PCOC1_HUMAN	-0,062975822	0,852473602
19871	sp P49915 GUAA_HUMAN	0,095902368	0,853678405
19533	sp P62805 H4_HUMAN	0,065729676	0,854660409
19700	sp P26358 DNMT1_HUMAN	0,088066803	0,85527165
19777	sp Q14738 2ASD_HUMAN	-0,042983562	0,856522765
19780	sp P10768 ESTD_HUMAN	0,04946613	0,859274517
20008	sp Q9UHB6 LIMA1_HUMAN	0,053560359	0,862844514
19523	sp Q13428 TCOF_HUMAN	0,111805515	0,863684459
20418	sp Q16270 IBP7_HUMAN	0,057022216	0,8645794
20467	sp P26373 RL13_HUMAN	0,05504476	0,866597646
19328	sp P35579 MYH9_HUMAN	-0,075245995	0,869479085
20421	sp P61604 CH10_HUMAN	-0,05853422	0,871259096
19603	sp O75390 CISY_HUMAN	-0,051841743	0,872066682
19771	sp Q15459 SF3A1_HUMAN	0,092496022	0,872266816
19935	sp P49588 SYAC_HUMAN	0,144204216	0,872493998
19936	sp P49327 FAS_HUMAN	0,056480561	0,873292703
19284	sp Q9NR45 SIAS_HUMAN	0,128967483	0,875823169
19759	sp Q14204 DYHC1_HUMAN	-0,071252354	0,875838367
19354	sp P39687 AN32A_HUMAN	0,052908357	0,87616171
19469	sp P07900 HS90A_HUMAN	0,035495179	0,876308484
19970	sp P14866 HNRPL_HUMAN	-0,049608554	0,876880633
20225	sp P24821 TENA_HUMAN	-0,046205478	0,880750119
19407	sp O43707 ACTN4_HUMAN	0,039690948	0,884894012
20209	sp P27694 RFA1_HUMAN	0,043280543	0,886415606
19734	sp P53396 ACLY_HUMAN	-0,038940722	0,887106807
20063	sp Q13185 CBX3_HUMAN	-0,04616719	0,888258396
19762	sp P55145 MANF_HUMAN	-0,066161793	0,888279686
19416	sp P30040 ERP29_HUMAN	0,038173212	0,897681607
19999	sp Q9BY32 ITPA_HUMAN	-0,039972619	0,89861719
19938	sp A6NN14 ZN729_HUMAN	0,046775968	0,898987672
20468	sp P46778 RL21_HUMAN	0,03863363	0,899404383
19587	sp P36578 RL4_HUMAN	-0,035296226	0,899427496
19687	sp P14550 AK1A1_HUMAN	0,0546711	0,899566894
19735	sp O15394 NCAM2_HUMAN	-0,052588359	0,900582755
20087	sp O15305 PMM2_HUMAN	0,056963753	0,902617648
19891	sp P62857 RS28_HUMAN	0,030583583	0,902940532
19837	sp P40123 CAP2_HUMAN	0,044229832	0,906767314
20444	sp P61086 UBE2K_HUMAN	0,03481839	0,907868908
20049	sp Q15642 CIP4_HUMAN	-0,023119385	0,909432258
20000	sp P16949 STMN1_HUMAN	-0,053485583	0,909530228
20134	sp Q9UKX7 NUP50_HUMAN	-0,05256768	0,910425504
20370	sp Q14978 NOLC1_HUMAN	-0,08112567	0,912638978
20146	sp Q07955 SRSF1_HUMAN	0,036286887	0,913599615
19910	sp Q9GZNR CT027_HUMAN	0,074363453	0,915760564
19668	sp P09874 PARP1_HUMAN	0,061816211	0,916949638
20213	sp P35998 PRS7_HUMAN	-0,070505134	0,9169601
19853	sp P54577 SYCY_HUMAN	0,049067742	0,918442413
19692	sp P55884 EIF3B_HUMAN	0,059729426	0,918849223
19924	sp Q13907 IDI1_HUMAN	-0,020869641	0,923049268
19502	sp Q9Y490 TLN1_HUMAN	0,037523837	0,927674742

19683	sp Q13435 SF3B2_HUMAN	-0,034458268	0,929006005
19822	sp Q13433 S39A6_HUMAN	-0,02896282	0,929035038
19760	sp Q15075 EEA1_HUMAN	0,034118595	0,93406648
19420	sp P19022 CADH2_HUMAN	-0,01765922	0,935047549
19776	sp P49321 NASP_HUMAN	0,036523493	0,935863817
19382	sp P13010 XRCC5_HUMAN	0,038042496	0,935895228
19364	sp Q01469 FABP5_HUMAN	0,016197087	0,938243807
20208	sp Q9P1F3 ABRAL_HUMAN	-0,028238421	0,941171698
20440	sp P62249 RS16_HUMAN	-0,021802188	0,94170526
20327	sp Q15942 ZYX_HUMAN	0,039183527	0,943125594
19793	sp P31431 SDC4_HUMAN	0,019416297	0,943627496
20437	sp P63244 RACK1_HUMAN	-0,023613326	0,945374722
19657	sp P22314 UBA1_HUMAN	-0,036905233	0,949065704
19870	sp O60841 IF2P_HUMAN	-0,044881967	0,949085454
20296	sp Q9UKK9 NUDT5_HUMAN	-0,019842334	0,949282746
19875	sp Q9ULF5 S39AA_HUMAN	0,038555525	0,949495095
20384	sp P23246 SFPQ_HUMAN	-0,023950568	0,949664546
19344	sp P68363 TBA1B_HUMAN	-0,040904838	0,950417975
19697	sp P43686 PRSF6_HUMAN	0,01922973	0,951071783
19555	sp Q14247 SRC8_HUMAN	0,035264659	0,951100299
20307	sp O75369 FLNB_HUMAN	-0,03526509	0,951659283
19563	sp P60953 CDC42_HUMAN	-0,016668211	0,951726003
19576	sp P14625 ENPL_HUMAN	-0,013749834	0,952527211
20147	sp P15018 LIF_HUMAN	-0,046762468	0,953720657
19799	sp P04080 CYTB_HUMAN	0,013268802	0,956660355
19656	sp P60866 RS20_HUMAN	-0,017022637	0,956678202
20372	sp O14974 MYPT1_HUMAN	0,017689732	0,95686358
20328	sp P49368 TCPG_HUMAN	0,015139055	0,957684105
19412	sp P63241 IF5A1_HUMAN	0,011054097	0,958030286
19686	sp P78371 TCPB_HUMAN	0,011798644	0,958686771
19895	sp Q14118 DAG1_HUMAN	0,018243209	0,960195504
20136	sp Q9UBQ7 GRHPR_HUMAN	-0,015033516	0,960701422
20275	sp Q969H8 MYDGF_HUMAN	0,011113187	0,960811636
19414	sp Q16181 SEP7_HUMAN	0,023677126	0,961134788
20129	sp P26368 U2AF2_HUMAN	0,037497777	0,961405056
19730	sp Q9BXJ9 NAA15_HUMAN	-0,022547903	0,961742113
19756	sp P06748 NPM_HUMAN	-0,012377665	0,962205914
19971	sp O94973 AP2A2_HUMAN	-0,017014444	0,962786897
20103	sp Q5VY80 ULBP6_HUMAN	-0,024799323	0,963240299
19806	sp Q01813 PFKAP_HUMAN	0,020755565	0,963641505
20480	sp O15540 FABP7_HUMAN	0,032131779	0,963979773
20106	sp P14780 MMP9_HUMAN	0,016849947	0,965400857
20431	sp Q9UKY7 CDV3_HUMAN	-0,041667428	0,965666066
20093	sp O75475 PSIP1_HUMAN	-0,021024028	0,965795305
20241	sp P48507 GSHO_HUMAN	-0,013277274	0,966144216
20100	sp P46060 RAGP1_HUMAN	-0,019872713	0,966412342
19661	sp Q99715 COCA1_HUMAN	-0,02896038	0,971233644
19748	sp P26639 SYTC_HUMAN	-0,008788629	0,971849996
20009	sp Q14697 GANAB_HUMAN	-0,012755415	0,973388225
19539	sp Q86VP6 CAND1_HUMAN	0,00943536	0,978315277
20265	sp P11234 RALB_HUMAN	0,007441367	0,978983931
20044	sp P42167 LAP2B_HUMAN	-0,010249105	0,979736569
19723	sp Q09028 RBBP4_HUMAN	0,013337261	0,980058823
19510	sp Q15181 IPYR_HUMAN	-0,010901045	0,9804951
19828	sp P13591 NCAM1_HUMAN	-0,004534065	0,980778008
20052	sp Q9H299 SH3L3_HUMAN	-0,008618776	0,981173778
19423	sp P30044 PRDX5_HUMAN	0,014234992	0,983044383
19792	sp Q99798 ACON_HUMAN	0,005137053	0,983232486
20143	sp Q15293 RCN1_HUMAN	-0,007632568	0,983800008
19334	sp Q9Y281 COF2_HUMAN	0,006656281	0,983898302
20342	sp P13612 ITA4_HUMAN	0,005431193	0,985083396
19720	sp Q16555 DPYL2_HUMAN	-0,009342097	0,985888705
19931	sp P82979 SARNP_HUMAN	0,013168358	0,985980987
19848	sp Q865Q4 AGRG6_HUMAN	0,005663472	0,987380681
19532	sp P40227 TCPZ_HUMAN	-0,006910311	0,987824984
19401	sp P13639 EF2_HUMAN	-0,004254428	0,988684385
19836	sp Q01518 CAP1_HUMAN	-0,003123745	0,991824623
20010	sp P18621 RL17_HUMAN	0,002482544	0,992406506
19431	sp P09972 ALDOC_HUMAN	0,002532922	0,992622531
19293	sp P27348 I433T_HUMAN	-0,003093108	0,992898037
20293	sp P83731 RL24_HUMAN	-0,002603466	0,99457974
20473	sp Q7L1Q6 BWZ1_HUMAN	0,000935706	0,99852905
19356	sp Q60907 TBL1X_HUMAN	0,000561688	0,999082641

Table 4: Human Protease Array (corresponding to Figure S4A)

	Control	Control	Control	Control	Rapalog 5nM	Rapalog 5nM	Rapalog 5nM	Rapalog 5nM	Control [%]	Rapalog [% of control]
ADAM8	1.147717	0.852283	1.15873	0.84127	0.774411	0.533206	0.746363	0.587302	100	66.0
ADAM9	1.027607	0.972393	1.024194	0.975806	0.620266	0.592668	0.839214	0.808132	100	71.5
ADAMTS1	1.023897	0.976103	0.992701	1.007299	0.556102	0.547179	0.792214	0.810219	100	67.6
ADAMTS13	1.004161	0.995839	0.974874	1.025126	0.583189	0.587307	0.875419	0.89866	100	73.6
Cathepsin A	0.997188	1.002812	0.970847	1.029153	0.651642	0.689132	0.606976	0.61868	100	64.2
Cathepsin B	1.02308	0.97692	0.983442	1.016558	0.690258	0.642286	0.62038	0.617672	100	64.3
Cathepsin C	0.896558	1.103442	0.930233	1.069767	0.516407	0.625453	0.624862	0.665836	100	60.8
Cathepsin D	0.999935	1.000065	0.985497	1.014503	0.731973	0.623161	0.562947	0.60059	100	63.0
Cathepsin E	1.094293	0.905707	1.057143	0.942857	0.541856	0.47676	0.63869	0.697421	100	58.9
Cathepsin L	0.99064	1.00936	0.972477	1.027523	0.58572	0.590158	0.742546	0.912271	100	70.8
Cathepsin S	1.020089	0.979911	0.971026	1.028974	0.571797	0.596897	0.692362	0.7153	100	64.4
Cathepsin V	1.006443	0.993557	0.954325	1.045675	0.566174	0.584872	0.800049	0.791059	100	68.6
Cathepsin X/Z/P	0.966757	1.033243	0.971185	1.028815	0.701833	0.730565	0.644144	0.654838	100	68.3
DPPIV/CD26	1.117334	0.882666	1.042017	0.957983	0.801751	0.659795	0.796744	0.757878	100	75.4
Kallikrein 3/PSA	0.985857	1.014143	1.054054	0.945946	0.551682	0.72544	0.833334	0.822917	100	73.3
Kallikrein 5	0.974425	1.025575	1	1	0.670176	0.718398	0.639628	0.811835	100	71.0
Kallikrein 6	0.942437	1.057563	0.965986	1.034014	0.706947	0.676587	0.89144	0.839002	100	77.8
Kallikrein 7	0.961601	1.038399	1.008772	0.991228	0.497709	0.556055	0.872259	0.966923	100	72.3
Kallikrein 10	0.961426	1.038574	1.019355	0.980645	0.600281	0.659802	0.974731	0.944893	100	79.5
Kallikrein 11	1.056922	0.943078	1.034965	0.965035	0.59863	0.684269	0.776224	0.765443	100	70.6
Kallikrein 13	0.943741	1.056259	0.944724	1.055276	0.641374	0.736734	0.774707	0.852178	100	75.1
MMP-1	1.045864	0.954136	0.990291	1.009709	0.732064	0.699026	0.778317	0.785801	100	74.9
MMP-2	0.977902	1.022098	0.967157	1.032843	0.696487	0.70715	0.700996	0.701869	100	70.2
MMP-3	1.002066	0.997934	1.0033	0.9967	0.679249	0.815638	0.778465	0.717409	100	74.8
MMP-7	0.981057	1.018943	1.001368	0.998632	0.549956	0.554512	0.795087	0.76767	100	66.7
MMP-8	1.004194	0.995806	1.007722	0.992278	0.589924	0.604858	0.732143	0.761905	100	67.2
MMP-9	0.987	1.013	1.017751	0.982249	0.648874	0.66088	0.723701	0.675049	100	67.7
MMP-10	1.0573	0.9427	1.063291	0.936709	0.508022	0.449979	0.731804	0.868407	100	64.0
MMP-12	0.956382	1.043618	0.93007	1.06993	0.603263	0.645063	0.927156	0.981061	100	78.9
MMP-13	1.017502	0.982498	1	1	0.824547	0.658938	0.79974	0.790104	100	76.8
Neprilisin/CD10	1.020975	0.979025	0.938547	1.061453	0.638855	0.614965	0.861266	0.766527	100	72.0
Presenilin	1.031023	0.968977	1.035294	0.964706	0.695308	0.721402	0.825245	0.761765	100	75.1
Proprotein Convertase 9	1.088068	0.911932	1.100324	0.899676	0.577882	0.473507	0.893069	0.708468	100	66.3
Proteinase 3	1.044048	0.955952	0.907692	1.092308	0.433047	0.407147	0.830128	0.853846	100	63.1
uPA/Urokinase	1.002609	0.997391	1.078125	0.921875	0.582279	0.564111	0.794922	0.963542	100	72.6

Left : Human protease array, levels of secretion in cells with spread and clustered lysosomes (control, 5nM Rapalog, respectively).
Right : Secretion levels are shown as percentage from the control.