SUPPLEMENTARY APPENDIX

The kinesin spindle protein inhibitor filanesib enhances the activity of pomalidomide and dexamethasone in multiple myeloma

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MATERIAL AND METHODS

Reagents and drugs. Filanesib (F) was provided by Array BioPharma Inc. (Boulder, CO, USA). Thalidomide (T), lenalidomide (L) and pomalidomide (P) were purchased from Selleckchem (Houston, TX, USA), dexamethasone (D) from Sigma-Aldrich (St Louis, MO, USA) and bortezomib from LC Laboratories (Woburn, MA, USA). Generic chemicals were acquired from Sigma Chemical Co., Roche Biochemicals (Mannheim, Germany), Merck & Co., Inc. (Darmstadt, Germany).

MM cell lines, patient samples and cultures. Origin, authentication and *in vitro* growth conditions of human MM cell lines have already been characterized (17, 18). The study of drug activity in the presence of IL-6, IGF-1 or in co-culture with primary bone marrow mesenchymal stromal cells (BMSCs) or the human mesenchymal stromal cell line (hMSC–TERT) was performed as described previously (19, 20).

Cell viability, cell cycle and apoptosis assays. Cell viability of MM cells after exposure to drugs was evaluated by the MTT assay (21). The half-maximal inhibitory concentration (IC_{50}) of the drug or drug combination was calculated using SigmaPlot graphing software. The cell cycle profile, apoptosis induction and mitochondrial membrane potential were evaluated using the Annexin V-FITC / Propidium iodide kit provided by Immunostep (Salamanca, Spain), Draq5 from Biostatus (Leicestershire, UK) and tetramethylrhodamine ethyl ester (TMRE) from Invitrogen (Thermofisher Scientific, Waltham MA, USA), following the manufacturers' instructions. Cell acquisition and data analysis were performed as previously described (20).

Quantification of *in vitro* synergism. Synergism was evaluated using Calcusyn software (22) (Biosoft, Ferguson, MO, USA), which calculates a combination index (CI) with the following interpretation: CI > 1: antagonistic effect, CI = 1: additive effect and CI < 1: synergistic effect.

Immunofluorescence study to quantify monopolar spindles *in vitro*. MM.1S cells were plated on poly-L-lysine-coated coverslips, allowed to recover overnight and then treated with PD, F or PDF or control vehicle for 24 h. After fixation in cold methanol for 5 min, cells were blocked and permeabilized in a 5% bovine serum albumin (BSA) 0.01% Tween 20 containing solution, and incubated overnight with a monoclonal primary anti-α-tubulin antibody (Sigma). Coverslips were washed before staining with Alexa Fluor 488 conjugated anti-mouse IgG secondary antibody (Life Technologies, Thermo Fisher Scientific, Waltham, MA, USA). Finally, coverslips were briefly incubated in a DAPI solution (Sigma) to identify nuclei, and mounted in Vectashield medium. The number of monopolar spindles was evaluated in at least 10 randomly selected fields with the 63x objective. At least 100 cells were counted for each treatment.

Western blot. Isolation of total protein or nuclear, cytosolic and mitochondrial protein fractions, as well as western blot procedures were performed as described (23). Primary antibodies used in western blot were purchased from Santa Cruz Biotechnology (anti-Mcl-1; Santa Cruz, CA, USA), Calbiochem (anti-cytochrome C; Billerica, MA, USA). All other antibodies were purchased from Cell Signaling Technology (Boston, MA, USA). Horseradish peroxidase-conjugated secondary antibodies were acquired from GE Healthcare (Little Chalfont, UK).

Gene silencing with siRNA. MM.1S cells were transiently transfected with either 100 nM non-targeting control short interfering RNA (NT-siRNA) or 100 nM ON

TARGET plus SMART pool siRNA targeting human BAX (Bax-siRNA; Dharmacon, Lafayette, CO, USA) using the Nucleofector II system (Lonza, Allendale, NJ, USA). After 24-48 h of siRNA transfection, diminished Bax expression was confirmed by western blot.

Animal models. In the human subcutaneous plasmacytoma model, CB17- SCID mice (The Jackson Laboratory, Bar Harbor, ME, USA) were subcutaneously injected into the right flank with $3x10^6$ MM.1S cells that had been resuspended in 100 µL of RPMI-1640 medium and 100 µL of Matrigel (BD Biosciences, San Jose, CA, USA). When tumors became palpable, mice were randomized to the control group (receiving the vehicle alone-PBS) or the different treatment groups. Tumor volume was measured with calipers, and changes in volume and clinical signs in the mice were monitored as previously described (20, 24). Animal experiments were conducted according to institutional guidelines for the use of Laboratory Animals and after acquiring permission from the local Ethical Committee for Animal Experimentation of the University of Salamanca.

Histological and immunohistochemistry (IHC) analyses. Representative tumor fractions were fixed in formalin, paraffin-embedded, cut into 3-µm sections, and either stained with hematoxylin and eosin or prepared for IHC, which was performed as previously described (24). For Bax staining, a primary anti-Bax antibody was used (Cell Signaling, Boston, MA, USA), together with the EnVision anti-mouse/rabbit peroxidase complexes (Dako, Glostrup, Denmark). Peroxidase activity was identified using the 3,3′-diaminobenzidine MAPO system (Ventana Medical Systems, Roche, Tucson, AZ, USA). Finally, sections were subsequently counterstained with hematoxylin and analyzed by standard light microscopy.

TUNEL (Terminal deoxynucleotidyl transferase dUTP nick end labeling) was performed using the In Situ Cell Death Detection Kit (Roche, Mannheim, Germany). Sections were counterstained with DAPI and data were visualized by confocal laser microscopy (Leica TCS SP2). The number of TUNEL$^+$ cells were evaluated in 10 randomly selected fields with the 60x objective for each experimental condition. These procedures were carried out by independent personnel of the Comparative Pathology Unit of our center. Disagreements between measurements were resolved by consensus.

RNA isolation, cDNA synthesis and microarray hybridization and analysis. Tumors and MM1.S cells (n=3 for each treatment) were homogenized in RLT Plus buffer (Qiagen). Total RNA was isolated using an RNeasy Plus Mini Kit (Qiagen), column-purified (Qiagen, RNeasy mini kit) and processed for hybridization of Human Gene 2.0 ST arrays (Affymetrix) following the manufacturer's instructions. The raw intensity data were preprocessed using the RMA algorithm (25) implemented in the Affymetrix Expression Console, version 1.4.1.46. Differentially expressed genes were identified using the significance analysis of microarrays (SAM) algorithm (26), version 4.01, selecting all genes with a value of $q < 0.05$. Data were mined to identify ontological categories (GO, Gene Ontology) that were significantly altered with respect to control at biological process level 5 in samples treated with PD, F and PDF using the DAVID Database (https://david.ncifcrf.gov/). Microarray data are available through the GEO repository database (Accession number GSE94341).

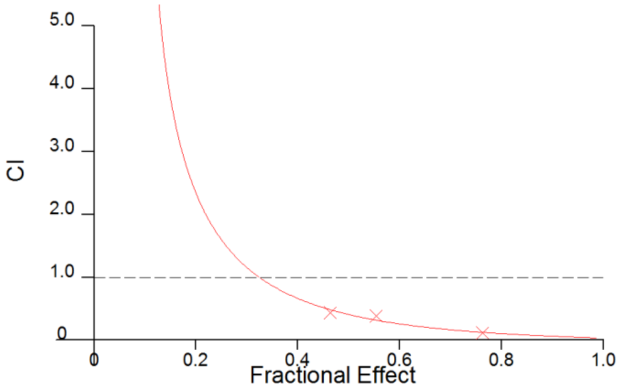
Statistical analyses. Statistical analyses were performed with IBM SPSS Statistics v.21.0 (IBM Corp., Armonk, NY, USA).

Supplementary Figure 1

Thalidomide + Dexamethasone + Filanesib

CI For experimental values

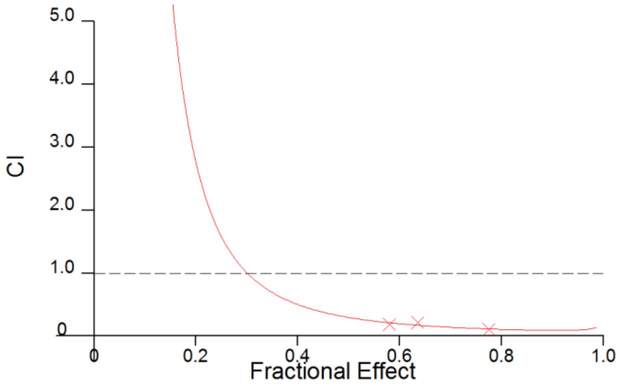
T (nM)	D (nM)	F (nM)	Fa	CI
25000	2.5	0.2	0.464092	0.435
50000	5	0.4	0.554807	0.390
100000	10	0.8	0.763846	0.112



Lenalidomide + Dexamethasone + Filanesib

CI For experimental values

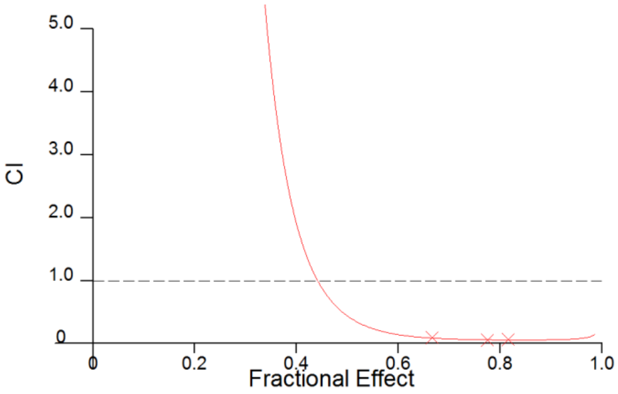
L (nM)	D (nM)	F (nM)	Fa	CI
125	2.5	0.2	0.580561	0.189
250	5	0.4	0.636008	0.217
500	10	0.8	0.775603	0.103



Pomalidomide + Dexamethasone + Filanesib

CI For experimental values

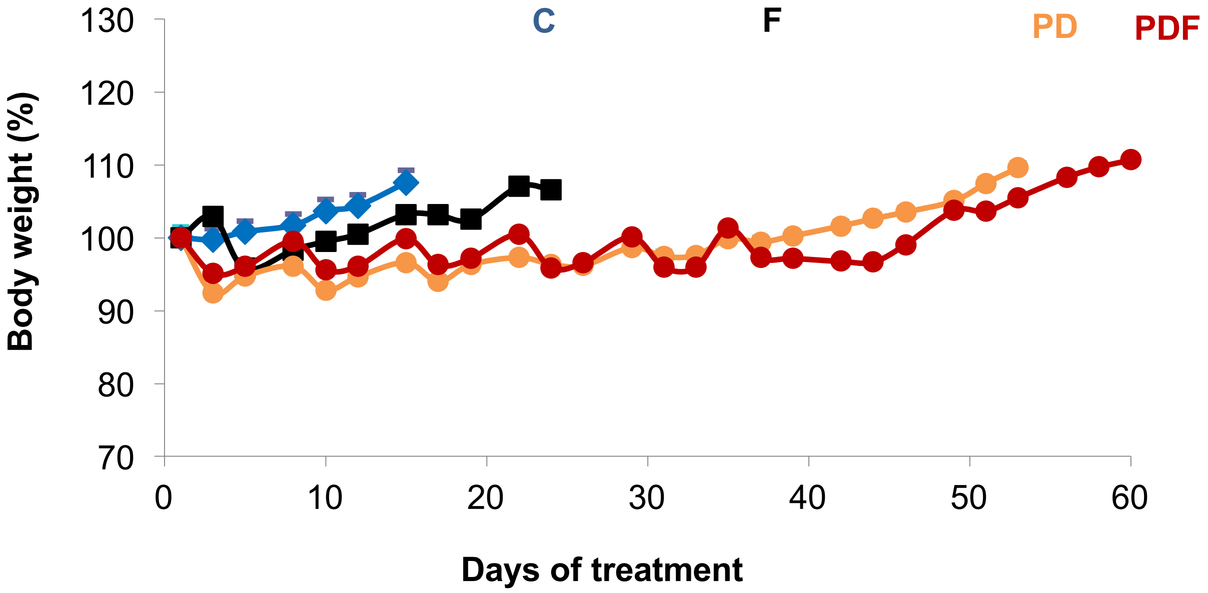
P (nM)	D (nM)	F (nM)	Fa	CI
125	2.5	0.2	0.666667	0.095
250	5	0.4	0.775603	0.051
500	10	0.8	0.816699	0.063



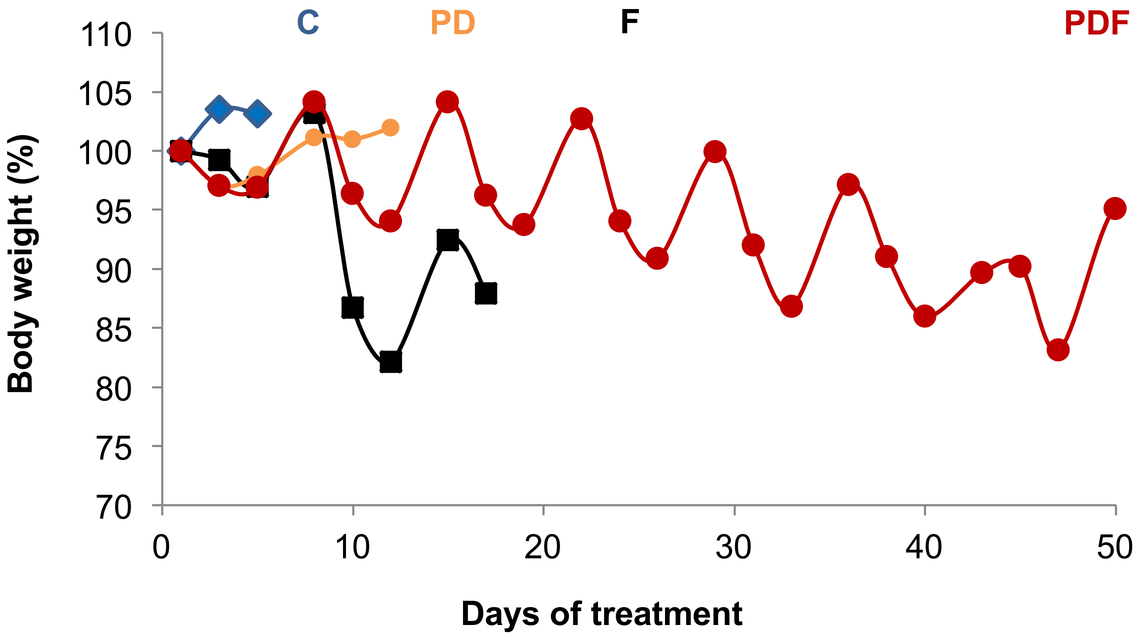
Synergism analysis of the triple combinations TDF, LDF and PDF on the MM.1S cell line using a constant ratio combination design. In the left panel, doses and units used for each drug, together with the obtained fractional effect or fraction of cells affected (Fa) and the combination indexes (CI) calculated by the Calcusyn software for each combination data point is given. For the PDF and LDF combinations, a constant ratio of 62.5 : 1.25 : 0.1 was used; for the TDF combination, the constant ratio between drugs was 12500 : 1.25 : 0.1. On the right panel, the Fa-CI plot is shown for each triple combination, since the Calcusyn program allows an algebraic estimation of the CIs along the Fa when using the constant ratio drug combination design. In these Fa-CI plots, CIs obtained for experimental data points are shown.

Supplementary Figure 2

A



B

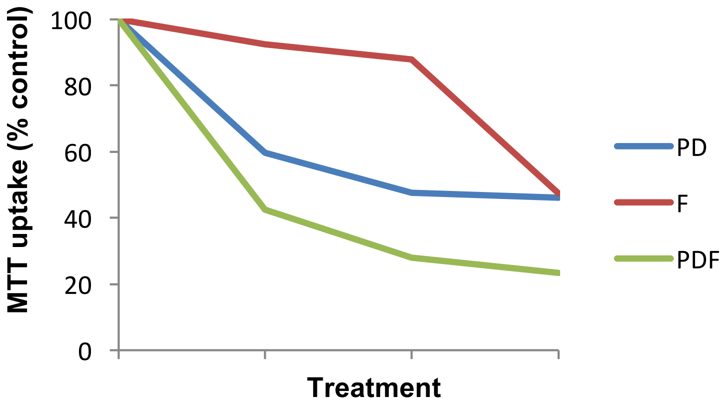


Effect of intraperitoneal administration of PDF on body weight in xenograft mouse models of MM. A & B) Average body weight of mice with small (mean volume around 125 mm3) (A) or large (mean volume around 2500 mm3) (B) plasmacytomas monitored over the treatment period. The percentage weight at each day of treatment was calculated considering day 1 for control mice (C) as 100%. Data are expressed as the mean ± SEM.

Supplementary Figure 3

A

MM144

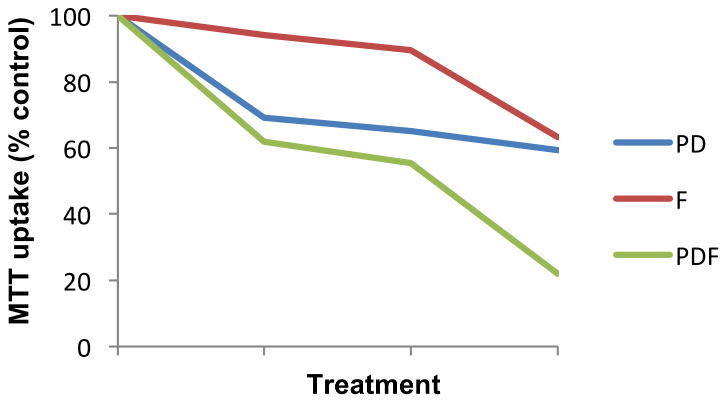


CI For experimental values

P (nM)	D (nM)	F (nM)	Fa	CI
62.5	1.25	0.15	0.57395	0.220
125	2.5	0.3	0.72003	0.293
250	5	0.3	0.76631	0.511

B

JJN3

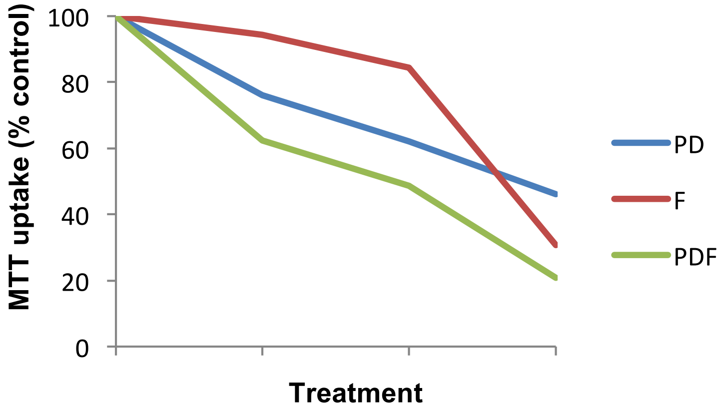


CI For experimental values

P (nM)	D (nM)	F (nM)	Fa	CI
62.5	1.25	0.15	0.37984	201.485
125	2.5	0.3	0.44550	17.610
250	5	0.3	0.78000	0.452

C

RPMI8226-LR5

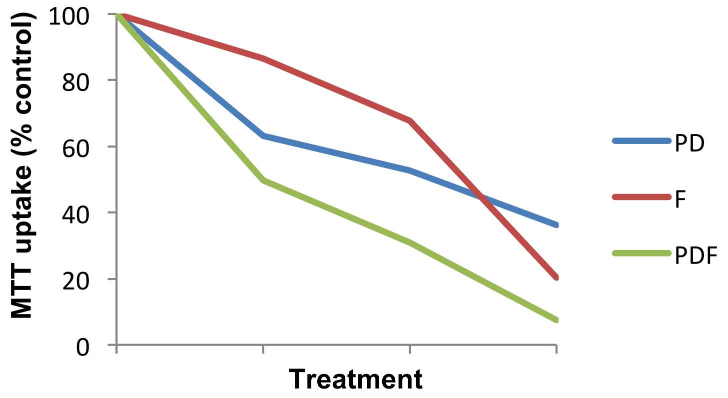


CI For experimental values

P (nM)	D (nM)	F (nM)	Fa	CI
62.5	1.25	0.15	0.37681	0.392
125	2.5	0.3	0.51206	0.606
250	5	0.3	0.79188	0.684

D

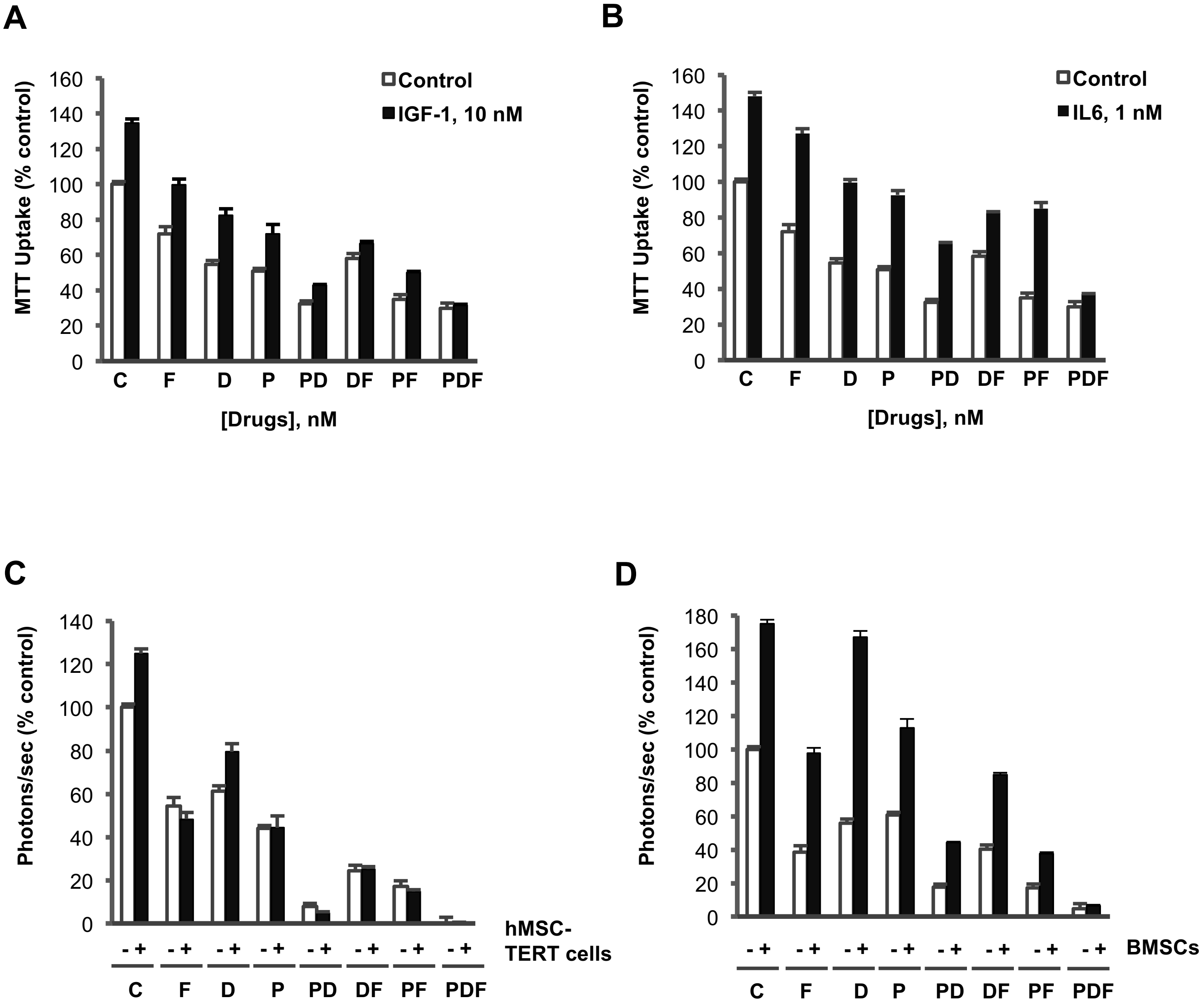
OPM-2



CI For experimental values

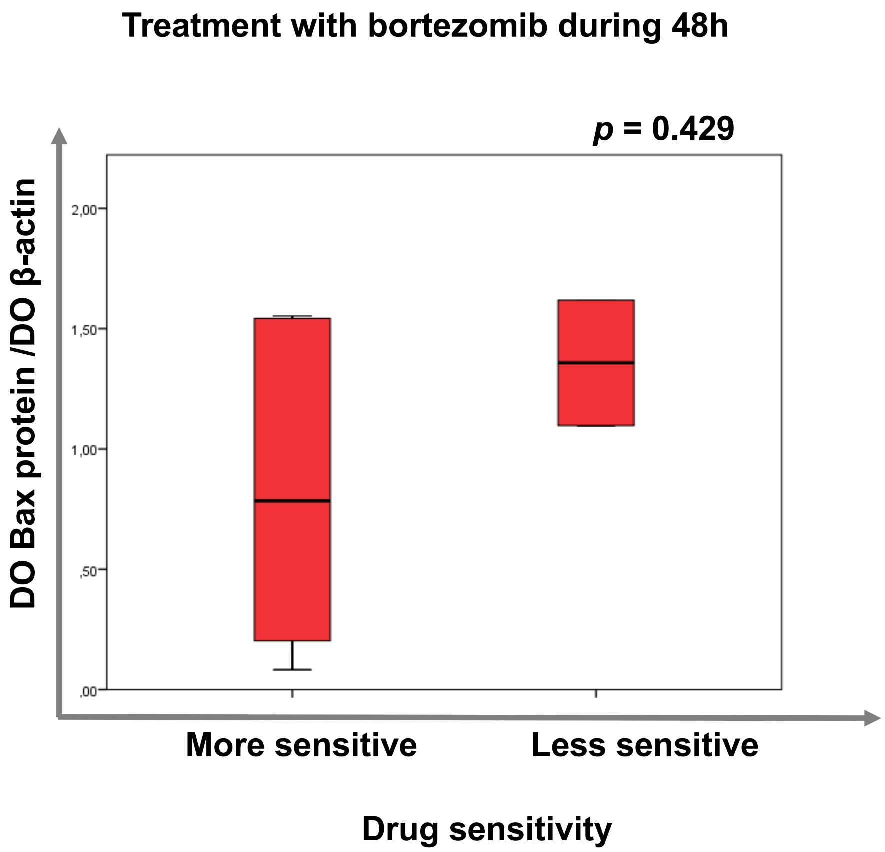
P (nM)	D (nM)	F (nM)	Fa	CI
62.5	1.25	0.15	0.50241	0.376
125	2.5	0.3	0.69024	0.469
250	5	0.3	0.92516	0.356

Supplementary Figure 3. Activity and synergism analysis of the PDF combination on the MM144 (A), JJN3 (B), RPMI8226-LR5 (C) and OPM-2 (D) cell lines. For each cell line, the activity of the triple combination with the indicated doses the drugs for each data point as assessed by MTT assay after 48 hours of culture is shown in the left handside. Note that a constant ratio drug combination design of 62.5 : 1.25 : 0.15 is maintained for the PDF combination. On the right handside, the correspondent CI values calculated by the Calcusyn program for each data point are also shown.



PDF overcomes the protective effects of growth factors and stroma. A & B) Cell viability was analyzed by MTT metabolization in MM.1S cells preincubated with 10 nM IGF-1 (A) or 1 nM IL-6 (B) and then cultured with the indicated conditions for 48 h. C & D) Bioluminescence signal of MM.1S-Luc cells treated for 48 h at indicated conditions in the presence or absence of either hMSC–TERT cells (C) or BMSCs (D) determined by bioluminescence after luciferin addition. Data are summarized as the mean ± SD (n=4). Results are shown as a percentage of control.

Supplementary Figure 5



Treatment with bortezomib during 48h

Bortezomib efficacy was not dependent on basal Bax protein levels. Relation between basal levels of Bax protein (determined by densitometry of bands using imageJ software and using levels of β-actin as loading control) and drug sensitivity to bortezomib was estimated according to IC50 for 48 h with $p < 0.05$ (Mann-Whitney U test).

Supplementary Tables

Supplementary Table 1. List of the most (top 100) differentially deregulated genes for the PDF treatment *in vitro vs* the control condition ordered by q-value. Gene identification and fold change with respect to control are given (78/100 genes were upregulated -red- and 22/100 were downregulated -green-).

Position (by q-value)	Affimetrix probe set	Gene Symbol	Gene Title	Fold Change
1	16705961	DDIT4	DNA-damage-inducible transcript 4	24,5686
2	17010760	NT5E	5'-nucleotidase, ecto (CD73)	5,2666
3	17113362	CAPN6	calpain 6	5,6308
4	16889636	BMPR2	bone morphogenetic protein receptor, type II (serine/threonine kinase)	5,5188
5	16749583	FAR2	fatty acyl CoA reductase 2	5,4656
6	16947173	MME	membrane metallo-endopeptidase	4,2176
7	17010354	CD109	CD109 molecule	5,5590
8	17018497	FKBP5	FK506 binding protein 5	3,2047
9	16874339	RRAS	related RAS viral (r-ras) oncogene homolog	6,4109
10	16676693	PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	3,6761
11	16904425	GRB14	growth factor receptor-bound protein 14	3,2670
12	16833327	SLFN5	schlafen family member 5	4,3888
13	16712086	ITGA8	integrin, alpha 8	-3,3440
14	16705011	DKK1	dickkopf WNT signaling pathway inhibitor 1	4,5034
15	17112349	CYSLTR1	cysteinyl leukotriene receptor 1	5,3958
16	16662623	ZC3H12A	zinc finger CCCH-type containing 12A	3,2980
17	16897026	ZFP36L2	ZFP36 ring finger protein-like 2	3,0419
18	16947715	SERPINI1	serpin peptidase inhibitor, clade I (neuroserpin), member 1	4,2268
19	16676183	ATP2B4	ATPase, Ca++ transporting, plasma membrane 4	4,5334
20	16927283	USP41	ubiquitin specific peptidase 41	3,4967
21	17012804	MYB	v-myb myeloblastosis viral oncogene homolog (avian)	-2,8656
22	16807324	BMF	Bcl2 modifying factor	4,0062
23	16998850	EPB41L4A	erythrocyte membrane protein band 4.1 like 4A	3,2604
24	16830577	CD68 /// SNORA67	CD68 molecule /// small nucleolar RNA, H/ACA box 67	2,7473
25	17024079	MAP3K5	mitogen-activated protein kinase kinase kinase 5	3,0983
26	17004167	IRF4	interferon regulatory factor 4	-2,5559
27	16673191	PBX1	pre-B-cell leukemia homeobox 1	2,6468
28	17022529	WASF1	WAS protein family, member 1	5,6603
29	16855898	CBLN2	cerebellin 2 precursor	-5,6554

30	17066083	PDGFRL	platelet-derived growth factor receptor-like	3,1682
31	16694617	IQGAP3	IQ motif containing GTPase activating protein 3	3,2017
32	16799357	EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4	2,3497
33	16881031	ANTXR1	anthrax toxin receptor 1	3,4873
34	16843602	CCL3L3	chemokine (C-C motif) ligand 3-like 3	-2,9111
35	17087588	MSANTD3 /// TMEFF1	Myb/SANT-like DNA-binding domain containing 3 /// transmembrane protein with EGF-like and two follistatin-like domains 1	-2,5071
36	16881069	ANXA4	annexin A4	2,8551
37	16804490	ISG20	interferon stimulated exonuclease gene 20kDa	2,6911
38	17062280	AASS	aminoadipate-semialdehyde synthase	2,9670
39	16715361	P4HA1	prolyl 4-hydroxylase, alpha polypeptide I	2,8670
40	16851427	CABLES1	Cdk5 and Abl enzyme substrate 1	-2,4560
41	16849349	TMC6 /// TNRC6C-AS1	transmembrane channel-like 6 /// TNRC6C antisense RNA 1	2,9446
42	16961806	GNB4	guanine nucleotide binding protein (G protein), beta polypeptide 4	2,4425
43	16963241	TFRC	transferrin receptor (p90, CD71)	-2,2769
44	17078558	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	2,1537
45	16873007	ETHE1	ethylmalonic encephalopathy 1	2,5653
46	16683445	FUCA1	fucosidase, alpha-L- 1, tissue	2,6554
47	17113147	TSC22D3	TSC22 domain family, member 3	3,1506
48	16688339	WLS	wntless homolog (Drosophila)	2,1945
49	16718719	KIAA1598	KIAA1598	2,4298
50	16781168	LOC440149	uncharacterized LOC440149	2,9906
51	16933398	CRYBB1	crystallin, beta B1	-2,1842
52	16977052	CXCL10	chemokine (C-X-C motif) ligand 10	-4,4776
53	16706200	VCL	vinculin	2,7055
54	16982147	CCDC110	coiled-coil domain containing 110	-2,7509
55	16743091	FZD4	frizzled family receptor 4	2,9608
56	16843578	CCL3	chemokine (C-C motif) ligand 3 /// c-C motif chemokine 3-like	-2,4436
57	16690566	SORT1	sortilin 1	2,2137
58	16676343	MDM4	Mdm4 p53 binding protein homolog (mouse)	3,5764
59	16773662	ALOX5AP	arachidonate 5-lipoxygenase-activating protein	2,9648
60	16732386	OAF	OAF homolog (Drosophila)	-1,9394
61	17085760	MAMDC2	MAM domain containing 2	2,2349
62	16938562	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)	2,3666
63	17086193	PSAT1	phosphoserine aminotransferase 1	-2,5800
64	16663033	SMAP2	small ArfGAP2	2,1630
65	16849238	RHBDF2	rhomboid 5 homolog 2 (Drosophila)	2,4000
66	16944665	DTX3L	deltex 3-like (Drosophila)	2,3204
67	16749398	STK38L	serine/threonine kinase 38 like	-2,2405
68	16834766	GRN	granulin	2,2726

69	16862118	LGALS17A	Charcot-Leyden crystal protein pseudogene	-3,1969
70	16836214	TOM1L1	target of myb1 (chicken)-like 1	2,5848
71	16833876	GRB7	growth factor receptor-bound protein 7	2,0959
72	16729128	SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, collagen binding protein 1	2,5906
73	16987531	ERAP2	endoplasmic reticulum aminopeptidase 2	2,0616
74	16668582	CD53	CD53 molecule	2,1044
75	16929529	TOM1	target of myb1 (chicken)	2,2001
76	16879721	EPAS1	endothelial PAS domain protein 1	2,3965
77	16869643	GIPC1	GIPC PDZ domain containing family, member 1	2,1892
78	16836528	YPEL2	yippee-like 2 (Drosophila)	2,2656
79	16836697	BCAS3	breast carcinoma amplified sequence 3	2,0897
80	16903140	CXCR4	chemokine (C-X-C motif) receptor 4	2,0658
81	16999245	PPIC	peptidylprolyl isomerase C (cyclophilin C)	2,1949
82	16692918	FAM63A	family with sequence similarity 63, member A	2,0728
83	16934045	PIK3IP1	phosphoinositide-3-kinase interacting protein 1	2,9113
84	16849379	TK1	thymidine kinase 1, soluble	2,0123
85	16834395	TUBG2	tubulin, gamma 2	2,4750
86	16801557	CCNB2	cyclin B2	1,9254
87	16716918	BLNK	B-cell linker	2,0808
88	16987125	POLR3G	polymerase (RNA) III (DNA directed) polypeptide G (32kD)	-2,5603
89	16825154	ARHGAP17	Rho GTPase activating protein 17	2,2649
90	16769144	SYCP3	synaptonemal complex protein 3	-2,4411
91	17023658	MOXD1	monooxygenase, DBH-like 1	2,5144
92	16903090	MCM6	minichromosome maintenance complex component 6	-2,0534
93	16687352	LRP8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	-2,2047
94	16841852	FLCN /// PLD6	folliculin /// phospholipase D family, member 6	-2,0191
95	16968735	HERC6	HECT and RLD domain containing E3 ubiquitin protein ligase family member 6	2,2178
96	16674973	C1orf21	chromosome 1 open reading frame 21	2,0368
97	16669796	TXNIP	thioredoxin interacting protein /// thioredoxin-interacting protein-like	2,3283
98	16875297	TMC4	transmembrane channel-like 4	1,9228
99	16949759	HES1	hairy and enhancer of split 1, (Drosophila)	-2,3674
100	16886564	FMNL2	formin-like 2	2,3134

Supplementary Table 2. List of the most differentially deregulated genes for the PDF treatment in mouse turmors with respect to control tumors ordered by q-value. Gene identification and fold change with respect to control are given (44/100 genes were upregulated -red- and 56/100 were downregulated -green-).

Position (by q-value)	Affimetrix probe set	Gene Symbol	Gene Title	Fold change
1	17061881	DOCK4	dedicator of cytokinesis 4	2,4679
2	16797421	IGHG1 /// IGHD2-21	immunoglobulin heavy constant gamma 1 (G1m marker)	-3,5417
3	16830202	XAF1	XIAP associated factor 1	3,1376
4	16687618	DHCR24	24-dehydrocholesterol reductase	-2,4940
5	17104939	LOC100506745	protein shisa-5-like	1,6968
6	16944695	PARP14	poly (ADP-ribose) polymerase family, member 14	2,5951
7	17053892	INSIG1	insulin induced gene 1	-2,0825
8	16764758	GALNT6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)	-1,6764
9	16691245	AMPD1	adenosine monophosphate deaminase 1	-2,6988
10	16761269	CLEC7A	C-type lectin domain family 7, member A	1,5083
11	16798919	ARHGAP11A	Rho GTPase activating protein 11A	1,7493
12	16785483	FUT8 /// FUT8-AS1	fucosyltransferase 8 (alpha (1,6) fucosyltransferase) /// FUT8 antisense RNA 1	1,4881
13	16693187	TDRKH	tudor and KH domain containing	1,7296
14	16966285	UCHL1 /	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase) /// ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	-1,7271
15	16800962	SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	-2,2404
16	16697695	KIF14	kinesin family member 14	1,7671
17	16815918	TNFRSF17	tumor necrosis factor receptor superfamily, member 17	-1,5686
18	16814183	ARHGDIG	Rho GDP dissociation inhibitor (GDI) gamma	2,5266
19	16741501	DHCR7	7-dehydrocholesterol reductase	-1,8235
20	16911493	SPTLC3	serine palmitoyltransferase, long chain base subunit 3	1,8228
21	16927790	IGLC1 /// IGLV3-25	immunoglobulin lambda constant 1 (Mcg marker)	-1,6779
22	16698529	NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	1,5015
23	16799492	LOC100505573	uncharacterized LOC100505573	1,9582
24	16927787	IGLV3-27	immunoglobulin lambda variable 3-27	-2,1462
25	16891107	WNT10A	wingless-type MMTV integration site family, member 10A	-1,4580
26	16799577	CHST14	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 14	-1,8400
27	17093245	AQP3	aquaporin 3 (Gill blood group)	-1,6772
28	16797378	IGHG1	immunoglobulin heavy constant gamma 1 (G1m marker)	-2,2145
29	16793885	RAB15	RAB15, member RAS oncogene family	-1,8380

30	16940593	P4HTM	prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)	-1,4433
31	16708249	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	-1,9709
32	16844046	SNORA21 /// RPL23	small nucleolar RNA, H/ACA box 21 /// ribosomal protein L23	1,8872
33	17059932	PON2	paraoxonase 2	1,5843
34	16924147	TPTE	transmembrane phosphatase with tensin homology	2,0554
35	16698984	NEK2	NIMA-related kinase 2	1,6285
36	16896442	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	1,6539
37	16844312	TOP2A	topoisomerase (DNA) II alpha 170kDa	1,5883
38	17046094	RNU1-14P	RNA, U1 small nuclear 14, pseudogene	2,5165
39	16943184	ST3GAL6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	1,7729
40	17005368	ALDH5A1	aldehyde dehydrogenase 5 family, member A1	-1,7486
41	16949759	HES1	hairy and enhancer of split 1, (Drosophila)	-2,1112
42	16727570	C11orf80	chromosome 11 open reading frame 80	-1,6450
43	16770789	C12orf49	chromosome 12 open reading frame 49	-1,5616
44	16833488	MRM1	mitochondrial rRNA methyltransferase 1 homolog (S. cerevisiae)	-1,4732
45	16855898	CBLN2	cerebellin 2 precursor	-2,0109
46	17042984	CHST12	carbohydrate (chondroitin 4) sulfotransferase 12	-1,5928
47	16986249	HMGCR	3-hydroxy-3-methylglutaryl-CoA reductase	-1,4571
48	16972950	ANKRD37	ankyrin repeat domain 37	-1,4140
49	17017935	HLA-DOB /// TAP2	major histocompatibility complex, class II, DO beta	-1,5440
50	16733989	MIR210	microRNA 210	-1,6391
51	17064135	PDIA4	protein disulfide isomerase family A, member 4	-1,3672
52	17104049	MAGED2 /// SNORA11	melanoma antigen family D, 2 /// small nucleolar RNA, H/ACA box 11	-2,2135
53	16811638	SEMA7A	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)	-1,5388
54	16835672	ITGA3	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	-1,6387
55	16830577	CD68 /// SNORA67	CD68 molecule /// small nucleolar RNA, H/ACA box 67	1,9670
56	16677425	CENPF	centromere protein F, 350/400kDa	1,7347
57	16748620	ATF7IP	activating transcription factor 7 interacting protein	1,4339
58	16675673	CAMSAP2	calmodulin regulated spectrin-associated protein family, member 2	1,6086
59	16659140	PLOD1	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	-1,7806
60	16812517	LOC388152	golgin A2 pseudogene	-1,3278
61	16837226	SNORA38B	small nucleolar RNA, H/ACA box 38B	-1,9131
62	16711464	ANKRD16	ankyrin repeat domain 16	-1,3960
63	16740524	RNASEH2C	ribonuclease H2, subunit C	-1,4251
64	16734092	CEND1	cell cycle exit and neuronal differentiation 1	-1,4207
65	16825779	SEPT1	septin 1	-1,5320
66	16662623	ZC3H12A	zinc finger CCCH-type containing 12A	-1,4665
67	16844099	CACNB1	calcium channel, voltage-dependent, beta 1 subunit	-1,3520
68	16710906	ZNF511	zinc finger protein 511	-1,5987
69	16842850	DHRS13	dehydrogenase/reductase (SDR family) member 13	-1,6364
70	16695268	IGSF8	immunoglobulin superfamily, member 8	-1,4159

71	16799690	SPINT1	serine peptidase inhibitor, Kunitz type 1	-1,6686
72	16826019	C16orf58	chromosome 16 open reading frame 58	-1,5785
73	17086496	DAPK1	death-associated protein kinase 1	-1,5807
74	16686010	LEPRE1	leucine proline-enriched proteoglycan (leprecan) 1	-1,4417
75	16661314	SFN	stratifin	-1,4721
76	16906534	STAT1	signal transducer and activator of transcription 1, 91kDa	1,7165
77	16803006	LOC729739	peptidylprolyl isomerase A (cyclophilin A) pseudogene	2,0813
78	17102689	USP9X	ubiquitin specific peptidase 9, X-linked	1,3614
79	16911283	PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	1,4544
80	16798801	ARHGAP11B	Rho GTPase activating protein 11B	1,8806
81	17023484	ARHGAP18	Rho GTPase activating protein 18	1,3925
82	17045555	BLVRA	biliverdin reductase A	1,8577
83	16958124	PARP9	poly (ADP-ribose) polymerase family, member 9	2,3008
84	16961806	GNB4	guanine nucleotide binding protein (G protein), beta polypeptide 4	1,9562
85	16692452	NBPF14 /// NBPF8	neuroblastoma breakpoint family, member 14	1,9937
86	16759469	SNORA49	small nucleolar RNA, H/ACA box 49	1,9804
87	17012163	RNU1-18P	RNA, U1 small nuclear 18, pseudogene	2,2760
88	16923031	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	1,9884
89	16811994	PEAK1	NKF3 kinase family member	1,6269
90	16765513	CBX5	chromobox homolog 5	1,3674
91	17021122	IBTK	inhibitor of Bruton agammaglobulinemia tyrosine kinase	1,4665
92	17050797	CPED1	cadherin-like and PC-esterase domain containing 1	1,5166
93	16718800	RAB11FIP2	RAB11 family interacting protein 2 (class I)	1,3790
94	17076346	PPAPDC1B	phosphatidic acid phosphatase type 2 domain containing 1B /// NULL	-1,3170
95	16803959	LOC388152	golgin A2 pseudogene /// chondroitin sulfate proteoglycan 4 pseudogene 8	-1,2939
96	16825810	LOC100506928	uncharacterized LOC100506928	-1,7497
97	16960647	DHX36	DEAH (Asp-Glu-Ala-His) box polypeptide 36	1,4335
98	16985518	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	1,4323
99	16858386	LDLR	low density lipoprotein receptor	-1,6679
100	16745236	H2AFX	H2A histone family, member X	-1,4897

Supplementary Table 3. List of the differentially deregulated genes after PDF treatment *in vitro* involved in mitotic and cell cycle processes. Genes are ordered by the number of "GO Biological processes" in which the genes are involved. Shaded genes are potential candidates mediating PDF effects *in vitro*.

Position by number of mitotic functions	Affimetrix probe set	Gene symbol	Gene Title	Fold Change
1	16985599	CCNB1	cyclin B1	1,4632
2	16730845	ATM /// NPAT	ataxia telangiectasia mutated /// nuclear protein, ataxia-telangiectasia locus	1,2661
3	17000439	CDC25C	cell division cycle 25C	1,4680
4	16916958	PCNA	proliferating cell nuclear antigen	-1,6766
5	16931384	GTSE1	G-2 and S-phase expressed 1	1,3133
6	16777502	CENPJ	centromere protein J	-1,2262
7	16840732	TP53	tumor protein p53	-1,1606
8	16753853	MDM2	MDM2 oncogene, E3 ubiquitin protein ligase	-1,1677
9	16918445	E2F1	E2F transcription factor 1	-2,0685
10	16864244	PRMT1	protein arginine methyltransferase 1	-1,6228
11	16890915	RQCD1	RCD1 required for cell differentiation1 homolog (S. pombe)	-1,3821
12	17052776	CASP2	caspase 2, apoptosis-related cysteine peptidase	-1,4116
13	16802918	PML	promyelocytic leukemia	1,3334
14	16676150	BTG2	BTG family, member 2	1,2570
15	16856315	ARID3A	AT rich interactive domain 3A (BRIGHT-like)	-1,2818
16	16818980	RBL2	retinoblastoma-like 2 (p130)	1,2404
17	16858321	CARM1	coactivator-associated arginine methyltransferase 1	-1,2243
18	16776905	TFDP1	transcription factor Dp-1	-1,2753
19	16977196	CNOT6L	CCR4-NOT transcription complex, subunit 6-like	-1,1786
20	16665932	GADD45A	growth arrest and DNA-damage-inducible, alpha	-1,1798
21	16728261	CCND1	cyclin D1	-1,6265
22	16658192	TP73	tumor protein p73	-1,7339
23	17076867	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	-1,3638
24	16684089	RPA2	replication protein A2, 32kDa	-1,2865
25	17104578	FOXO4	forkhead box O4	1,1740
26	16968697	PKD2	polycystic kidney disease 2 (autosomal dominant)	-1,2382
27	16850517	NDC80	NDC80 kinetochore complex component	1,3460
28	16834056	CDC6	cell division cycle 6	-1,9952
29	16877473	GEN1	GEN1 Holliday junction 5' flap endonuclease	1,2656
30	16766683	CDK4	cyclin-dependent kinase 4	-1,4386
31	16872551	TGFB1	transforming growth factor, beta 1	1,5768
32	16677425	CENPF	centromere protein F, 350/400kDa	1,6572

33	16799426	BUB1B /// PAK6	BUB1 mitotic checkpoint serine/threonine kinase B /// p21 protein (Cdc42/Rac)-activated kinase 6	1,1930
34	16855697	VPS4B	vacuolar protein sorting 4 homolog B (S. cerevisiae)	1,2360
35	16927052	CDC45	cell division cycle 45	-1,4873
36	16697695	KIF14	kinesin family member 14	1,3877
37	16802152	RAB11A	RAB11A, member RAS oncogene family	1,3172
38	16683644	SYF2	SYF2 homolog, RNA splicing factor (S. cerevisiae)	1,2579
39	16804902	BLM	Bloom syndrome, RecQ helicase-like	-1,2068
40	16959325	TOPBP1	topoisomerase (DNA) II binding protein 1	-1,1830
41	16924068	PRMT2	protein arginine methyltransferase 2	1,5107
42	16939023	CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	1,5173
43	16766767	CTDSP2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	1,3865
44	17010552	TTK	TTK protein kinase	1,3546
45	16685165	CLSPN	claspin	-1,4069
46	16827170	NAE1	NEDD8 activating enzyme E1 subunit 1	-1,2329
47	16868847	KANK2	KN motif and ankyrin repeat domains 2	-1,2421
48	16667037	CDC7	cell division cycle 7	-1,2438
49	16901755	BUB1	BUB1 mitotic checkpoint serine/threonine kinase	1,2082
50	16817182	LCMT1	leucine carboxyl methyltransferase 1	1,1895
51	16682425	RCC2	regulator of chromosome condensation 2	-1,4513
52	17113744	CUL4B	cullin 4B	1,3571
53	16781516	APEX1	APEX nuclease (multifunctional DNA repair enzyme) 1 /// APEX nuclease (multifunctional DNA repair enzyme) 1	-1,3733
54	16746992	CCND2	cyclin D2	-1,3807
55	16948909	EIF4G1	eukaryotic translation initiation factor 4 gamma, 1	-1,2739
56	16834812	DBF4B	DBF4 homolog B (S. cerevisiae)	1,2511
57	16760649	PHB2	prohibitin 2	-1,1737
58	16673191	PBX1	pre-B-cell leukemia homeobox 1 /// uncharacterized LOC100131938	2,6468
59	16834486	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki) /// proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	-1,4365
60	16793225	DLGAP5	discs, large (Drosophila) homolog-associated protein 5	1,4023
61	17053019	CUL1	cullin 1	-1,3893
62	16733104	CHEK1	checkpoint kinase 1	-1,1916
63	16897026	ZFP36L2	ZFP36 ring finger protein-like 2	3,0419
64	16810933	TIPIN	TIMELESS interacting protein	-2,1573
65	16698984	NEK2	NIMA-related kinase 2	1,6175
66	16663514	CDC20	cell division cycle 20	1,5784
67	16927198	RANBP1	RAN binding protein 1 /// RAN binding protein 1	-1,4861
68	16912871	CHMP4B	charged multivesicular body protein 4B	-1,2450
69	16843131	CRLF3	cytokine receptor-like factor 3	-1,2154
70	17088929	NEK6	NIMA-related kinase 6	-1,2410
71	16869570	PRKACA	protein kinase, cAMP-dependent, catalytic, alpha	1,2121
72	16949214	SENP2	SUMO1/sentrin/SMT3 specific peptidase 2	-1,1819
73	17070331	CHMP4C	charged multivesicular body protein 4C	2,3538

74	16879883	MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)	-1,7236
75	16911040	CDC25B	cell division cycle 25B	1,4458
76	16856959	FZR1	fizzy/cell division cycle 20 related 1 (Drosophila)	1,3170
77	16978568	CENPE	centromere protein E, 312kDa	1,4784
78	16932008	BID	BH3 interacting domain death agonist	-1,3007
79	16707221	KIF20B	kinesin family member 20B	1,2419
80	16846568	PPP1R9B	protein phosphatase 1, regulatory subunit 9B /// protein phosphatase 1, regulatory subunit 9B	1,3048
81	16872089	SIRT2	sirtuin 2	1,2545
82	16734475	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	-1,2842
83	16840902	AURKB	aurora kinase B	1,1459
84	16912379	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)	1,3027
85	16708468	BTRC	beta-transducin repeat containing E3 ubiquitin protein ligase	1,3250
86	17045198	ANLN	anillin, actin binding protein	1,2004
87	16799793	NUSAP1	nucleolar and spindle associated protein 1	1,1957
88	16845263	BECN1	beclin 1, autophagy related /// beclin 1, autophagy related	1,2025
89	16661589	RCC1 /// SNHG3	regulator of chromosome condensation 1 /// small nucleolar RNA host gene 3 (non-protein coding) /// regulator of chromosome condensation 1 /// small nucleolar RNA, H/ACA box 73A	-1,1816
90	16821869	CDT1	chromatin licensing and DNA replication factor 1	-1,1822
91	16705942	ANAPC16	anaphase promoting complex subunit 16	1,5602
92	16851022	CHMP1B	charged multivesicular body protein 1B	1,3508
93	16964000	TACC3	transforming, acidic coiled-coil containing protein 3	1,3577
94	16770040	ANAPC7	anaphase promoting complex subunit 7	-1,1713
95	16760048	FOXM1	forkhead box M1	1,1660
96	16802519	KIF23	kinesin family member 23	1,1471
97	16836214	TOM1L1	target of myb1 (chicken)-like 1	2,5848
98	16769250	IGF1	insulin-like growth factor 1 (somatomedin C)	1,8607
99	16867915	INSR	insulin receptor	1,8113
100	16953279	CDC25A	cell division cycle 25A	-1,6930
101	16844312	TOP2A	topoisomerase (DNA) II alpha 170kDa	1,4734
102	17117724	PSMD3	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 /// uncharacterized LOC100505620	1,6826
103	16898788	TGFA	transforming growth factor, alpha	1,5199
104	16821021	PSMD7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	-1,4781
105	16892039	PSMD1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	-1,3538
106	16935228	PDGFB	platelet-derived growth factor beta polypeptide	1,3652
107	16848032	PSMD12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	-1,3750
108	16833139	PSMD11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	-1,4914
109	16814825	EME2 /	essential meiotic endonuclease 1 homolog 2 (S. pombe)	-1,3249
110	16714504	ZWINT	ZW10 interacting kinetochore protein	-1,2939
111	16841982	TOM1L2	target of myb1-like 2 (chicken)	1,2654
112	16709140	SMC3	structural maintenance of chromosomes 3	-1,2786

113	16690594	PSMA5	proteasome (prosome, macropain) subunit, alpha type, 5	-1,2968
114	16905322	ATF2	activating transcription factor 2	1,2576
115	16835797	EME1	essential meiotic endonuclease 1 homolog 1 (S. pombe)	1,2923
116	16886919	PSMD14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14 /// proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	-1,2337
117	16889807	CD28	CD28 molecule	-1,2173
118	16948871	PSMD2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	-1,2342
119	17007307	PSMB9	proteasome (prosome, macropain) subunit, beta type, 9	1,2180
120	17049965	PSMC2	proteasome (prosome, macropain) 26S subunit, ATPase, 2	-1,2353
121	17090373	ABL1	c-abl oncogene 1, non-receptor tyrosine kinase	1,2422
122	16862145	PSMC4	proteasome (prosome, macropain) 26S subunit, ATPase, 4	-1,1954
123	16738023	PSMC3	proteasome (prosome, macropain) 26S subunit, ATPase, 3	-1,2191
124	16784642	PSMA3	proteasome (prosome, macropain) subunit, alpha type, 3	-1,2128
125	17067963	EIF4EBP1	eukaryotic translation initiation factor 4E binding protein 1	-1,2605
126	16670850	PSMB4	proteasome (prosome, macropain) subunit, beta type, 4	-1,1502
127	16829885	PSMB6	proteasome (prosome, macropain) subunit, beta type, 6	-1,1718
128	16803540	PSMA4	proteasome (prosome, macropain) subunit, alpha type, 4	-1,1959
129	16727802	RAD9A	RAD9 homolog A (S. pombe) /// uncharacterized LOC100130987	-1,1552
130	17079293	CCNE2	cyclin E2	-1,7937
131	17101622	OFD1	oral-facial-digital syndrome 1	1,5815
132	16984032	SKP2	S-phase kinase-associated protein 2, E3 ubiquitin protein ligase	-1,3950
133	16784299	CDKN3	cyclin-dependent kinase inhibitor 3	1,4047
134	17115077	CETN2	centrin, EF-hand protein, 2	1,2935
135	16832852	ATAD5	ATPase family, AAA domain containing 5	-1,2622
136	16733952	HRAS /// HRAS	v-Ha-ras Harvey rat sarcoma viral oncogene homolog	-1,2267
137	16801557	CCNB2	cyclin B2	1,9254
138	16860418	CCNE1	cyclin E1	-1,7116
139	16840018	MYBBP1A	MYB binding protein (P160) 1a	-1,6200
140	16736638	E2F8	E2F transcription factor 8	-1,3603
141	17102230	POLA1	polymerase (DNA directed), alpha 1, catalytic subunit	-1,3197
142	17019287	CUL7	cullin 7	1,3046
143	16766590	DCTN2	dynactin 2 (p50)	1,2546
144	16744684	ZNF259	zinc finger protein 259	-1,1865
145	16992096	SPDL1	spindle apparatus coiled-coil protein 1	1,2281
146	16877007	KLF11	Kruppel-like factor 11	-1,9137
147	16823512	TFAP4	transcription factor AP-4 (activating enhancer binding protein 4)	-1,4977
148	16687188	ORC1	origin recognition complex, subunit 1	-1,5622
149	17104484	KIF4A	kinesin family member 4A	1,5053
150	16908373	USP37	ubiquitin specific peptidase 37	-1,4526

151	16766318	PRIM1	primase, DNA, polypeptide 1 (49kDa)	-1,5116
152	16661117	CEP85	centrosomal protein 85kDa	-1,3700
153	16815090	CCNF	cyclin F	1,2950
154	16726790	POLA2	polymerase (DNA directed), alpha 2, accessory subunit	-1,3007
155	16983412	FBXL7	F-box and leucine-rich repeat protein 7	1,4379
156	17093480	DCTN3	dynactin 3 (p22)	1,3297
157	17038792	KIFC1	kinesin family member C1	1,3246
158	17007459	KIFC1	kinesin family member C1 /// kinesin family member C1	1,3267
159	17041352	KIFC1 /// RPL12P1	kinesin family member C1	1,3267
160	16666896	PKN2	protein kinase N2	1,3515
161	17092688	HAUS6	HAUS augmin-like complex, subunit 6	-1,4165
162	16835272	KPNB1	karyopherin (importin) beta 1	-1,3019
163	16852206	HAUS1	HAUS augmin-like complex, subunit 1	1,3068
164	16858774	CALR	calreticulin	-1,1904
165	16850477	TYMS	thymidylate synthetase	-1,2265
166	16744078	NPAT	nuclear protein, ataxia-telangiectasia locus	-1,2213
167	16809506	ARPP19	cAMP-regulated phosphoprotein, 19kDa	-1,1773
168	17086634	CKS2	CDC28 protein kinase regulatory subunit 2	1,2489
169	16772625	POLE	polymerase (DNA directed), epsilon, catalytic subunit	-1,2252
170	17008867	CUL9	cullin 9	1,2387
171	16800108	HAUS2	HAUS augmin-like complex, subunit 2	-1,1776
172	16829764	GSG2	germ cell associated 2 (haspin)	1,1824
173	16912625	MAPRE1	microtubule-associated protein, RP/EB family, member 1	-1,1615
174	16676183	ATP2B4	ATPase, Ca++ transporting, plasma membrane 4	4,5334
175	16694617	IQGAP3	IQ motif containing GTPase activating protein 3	3,2017
176	16903090	MCM6	minichromosome maintenance complex component 6	-2,0534
177	16959668	CEP70	centrosomal protein 70kDa	1,9416
178	17020019	MCM3	minichromosome maintenance complex component 3	-1,5997
179	16702547	OPTN	optineurin	1,5317
180	16702571	MCM10	minichromosome maintenance complex component 10	-1,6061
181	17068782	MCM4	minichromosome maintenance complex component 4	-1,6929
182	16945101	MCM2	minichromosome maintenance complex component 2	-1,6040
183	16976158	PPAT	phosphoribosyl pyrophosphate amidotransferase	-1,6920
184	16707551	CEP55	centrosomal protein 55kDa	1,4996
185	16818600	ORC6	origin recognition complex, subunit 6	-1,4150
186	17060412	MCM7	minichromosome maintenance complex component 7	-1,5393
187	16929573	MCM5	minichromosome maintenance complex component 5	-1,5156
188	16799598	CASC5	cancer susceptibility candidate 5	1,5386
189	16897797	PNPT1	polyribonucleotide nucleotidyltransferase 1	-1,5687
190	17058905	YWHAG	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	-1,3809
191	16911212	MCM8	minichromosome maintenance complex component 8	-1,4598
192	16991859	HMMR	hyaluronan-mediated motility receptor (RHAMM)	1,4882
193	16730540	BIRC2	baculoviral IAP repeat containing 2	1,4471

194	16850189	CSNK1D	casein kinase 1, delta /// casein kinase 1, delta	1,2736
195	16994170	NSUN2	NOP2/Sun RNA methyltransferase family, member 2	-1,3563
196	16887601	DYNC1I2	dynein, cytoplasmic 1, intermediate chain 2 /// dynein, cytoplasmic 1, intermediate chain 2 pseudogene 1	1,3217
197	16869841	AKAP8	A kinase (PRKA) anchor protein 8	-1,3131
198	16913957	MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	-1,2653
199	16903427	ORC4	origin recognition complex, subunit 4	1,2915
200	17108546	BRCC3	BRCA1/BRCA2-containing complex, subunit 3	-1,2005
201	17089667	ODF2	outer dense fiber of sperm tails 2	1,2027
202	17066118	PCM1	pericentriolar material 1	1,2752
203	17050154	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	-1,2736
204	16978387	PPP3CA	protein phosphatase 3, catalytic subunit, alpha isozyme	-1,2282
205	16824004	GSPT1	G1 to S phase transition 1	-1,1956
206	17088589	CNTRL	centriolin	-1,3191
207	16869860	AKAP8L	A kinase (PRKA) anchor protein 8-like	1,1707
208	16762573	ASUN	asunder spermatogenesis regulator	-1,2162
209	17065292	MCPH1	microcephalin 1	1,1874
210	16757255	PTPN11	protein tyrosine phosphatase, non-receptor type 11	-1,1684
211	16859454	BABAM1	BRISC and BRCA1 A complex member 1 /// BRISC and BRCA1 A complex member 1	1,1937
212	17074571	PINX1 /// SOX7	PIN2/TERF1 interacting, telomerase inhibitor 1 /// PIN2/TERF1 interacting, telomerase inhibitor 1 /// SRY (sex determining region Y)-box 7 ///	-1,7907
213	17069545	RRS1	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	-1,8081
214	16851121	SEH1L	SEH1-like (S. cerevisiae)	-1,6177
215	16736891	KIF18A	kinesin family member 18A	1,4470
216	16813342	PRC1	protein regulator of cytokinesis 1	1,4497
217	16658664	SLC25A33	solute carrier family 25 (pyrimidine nucleotide carrier), member 33	-1,5337
218	16662648	CDCA8	cell division cycle associated 8	1,3750
219	16877956	CENPA /// SLC35F6	centromere protein A /// solute carrier family 35, member F6	1,2900
220	16800209	TUBGCP4	tubulin, gamma complex associated protein 4	-1,3765
221	16681210	KLHL21	kelch-like family member 21	-1,3355
222	16702503	CDC123	cell division cycle 123	-1,2633
223	16663958	KIF2C	kinesin family member 2C	1,3087
224	16725735	FEN1	flap structure-specific endonuclease 1	-1,3229
225	16838359	BIRC5	baculoviral IAP repeat containing 5	1,2458
226	17110058	DYNLT3	dynein, light chain, Tctex-type 3	1,3286
227	16779720	MZT1	mitotic spindle organizing protein 1	-1,2812
228	16995140	RAD1	RAD1 homolog (S. pombe)	-1,2788
229	17098808	GOLGA2	golgin A2	1,2481
230	16902411	BIN1	bridging integrator 1	1,1726
231	16781136	TUBGCP3	tubulin, gamma complex associated protein 3	-1,1926
232	16686796	STIL	SCL/TAL1 interrupting locus	1,1698
233	16730522	BIRC3	baculoviral IAP repeat containing 3	1,2017

234	16869643	GIPC1	GIPC PDZ domain containing family, member 1	2,1892
235	16949759	HES1	hairy and enhancer of split 1, (Drosophila)	-2,3674
236	16945664	NUDT16	nudix (nucleoside diphosphate linked moiety X)-type motif 16	2,2200
237	16843376	NLE1	notchless homolog 1 (Drosophila)	-1,4643
238	16957568	NAA50	N(alpha)-acetyltransferase 50, NatE catalytic subunit	-1,3816
239	16697544	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	1,5645
240	16658449	PHF13	PHD finger protein 13	-1,3156
241	16845794	KIF18B	kinesin family member 18B	1,2869
242	16746379	NCAPD3	non-SMC condensin II complex, subunit D3	-1,3057
243	17067410	FZD3	frizzled family receptor 3	-1,3675
244	16991839	CCNG1	cyclin G1	1,3014
245	16886757	PKP4	plakophilin 4	1,2731
246	16924305	BTG3	BTG family, member 3	-1,2838
247	16747287	NCAPD2	non-SMC condensin I complex, subunit D2	1,2419
248	16984083	NIPBL	Nipped-B homolog (Drosophila)	1,2540
249	17013072	HECA	headcase homolog (Drosophila)	1,2521
250	16766137	TIMELESS	timeless circadian clock	-1,1973
251	17080595	DSCC1	DNA replication and sister chromatid cohesion 1	-1,2818
252	16799357	EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4	2,3497
253	16828886	GINS2	GINS complex subunit 2 (Psf2 homolog)	-1,9489
254	16802190	MAP2K1	mitogen-activated protein kinase kinase 1	1,7290
255	17072669	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	-1,7808
256	16668079	GPSM2	G-protein signaling modulator 2	1,7670
257	16708552	NOLC1	nucleolar and coiled-body phosphoprotein 1	-1,7005
258	16687618	DHCR24	24-dehydrocholesterol reductase	-1,5488
259	16721479	ILK	integrin-linked kinase	1,6867
260	16707695	HELLS	helicase, lymphoid-specific	-1,9358
261	16850063	STRA13	stimulated by retinoic acid 13	-1,4507
262	16781285	GAS6	growth arrest-specific 6	1,5051
263	16936408	MAPK12	mitogen-activated protein kinase 12	-1,4710
264	16958812	RUVBL1	RuvB-like 1 (E. coli)	-1,3470
265	16818755	PAPD5	PAP associated domain containing 5	-1,5775
266	16950569	TADA3	transcriptional adaptor 3	1,3184
267	17067102	CDCA2	cell division cycle associated 2	1,3876
268	16987008	RASA1	RAS p21 protein activator (GTPase activating protein) 1	1,3267
269	16950146	LMLN	leishmanolysin-like (metallopeptidase M8 family)	1,4166
270	16880122	SPTBN1	spectrin, beta, non-erythrocytic 1	1,4163
271	16685596	RRAGC	Ras-related GTP binding C	1,3558
272	16718983	MCMBP	minichromosome maintenance complex binding protein	-1,3547
273	16895848	PPM1G	protein phosphatase, Mg2+/Mn2+ dependent, 1G	-1,3294
274	16856153	TXNL4A	thioredoxin-like 4A /// thioredoxin-like 4A	-1,4108
275	16856463	STK11	serine/threonine kinase 11	1,2680
276	16814927	TSC2	tuberous sclerosis 2 /// tuberous sclerosis 2	1,3353

277	16989636	KIF20A	kinesin family member 20A	1,3497
278	16775014	CKAP2	cytoskeleton associated protein 2	1,2746
279	16671889	LAMTOR2	late endosomal/lysosomal adaptor, MAPK and MTOR activator 2	1,2901
280	16959465	ANAPC13	anaphase promoting complex subunit 13	-1,2918
281	16947904	SKIL	SKI-like oncogene	1,3348
282	16863243	MARK4	MAP/microtubule affinity-regulating kinase 4	1,2753
283	17070381	LRRCC1	leucine rich repeat and coiled-coil centrosomal protein 1	1,3623
284	16847771	ERN1	endoplasmic reticulum to nucleus signaling 1	1,2941
285	16953241	MAP4	microtubule-associated protein 4	1,2887
286	16840262	NUP88	nucleoporin 88kDa	-1,2444
287	16868838	SPC24	SPC24, NDC80 kinetochore complex component	1,2866
288	16760621	CDCA3	cell division cycle associated 3 /// cell division cycle associated 3	1,2463
289	16673154	NUF2	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)	1,2743
290	16800991	USP8	ubiquitin specific peptidase 8	1,2105
291	16697985	ARL8A	ADP-ribosylation factor-like 8A	-1,2657
292	17099361	TSC1	tuberous sclerosis 1	1,2335
293	17092852	KLHL9	kelch-like family member 9	1,2663
294	16938271	KAT2B	K(lysine) acetyltransferase 2B	1,2097
295	16807605	OIP5	Opa interacting protein 5	1,2784
296	17021596	RRAGD	Ras-related GTP binding D	-1,2248
297	16760546	ING4	inhibitor of growth family, member 4	1,3025
298	16951485	SGOL1	shugoshin-like 1 (S. pombe)	1,2402
299	16726925	SSSCA1	Sjogren syndrome/scleroderma autoantigen 1	-1,2542
300	16847432	BRIP1	BRCA1 interacting protein C-terminal helicase 1	-1,2150
301	16692297	PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit /// 5'-AMP-activated protein kinase subunit beta-2-like	1,2324
302	16830839	CNTROB	centrobin, centrosomal BRCA2 interacting protein	1,1995
303	17057433	TBRG4 /// SNORA5B	transforming growth factor beta regulator 4 /// small nucleolar RNA, H/ACA box 5B	-1,2898
304	16939960	KIF15	kinesin family member 15	1,2007
305	16659171	MFN2	mitofusin 2	-1,2024
306	16879408	EML4	echinoderm microtubule associated protein like 4	1,2201
307	16673043	UHMK1	U2AF homology motif (UHM) kinase 1	-1,1728
308	16935142	SUN2	Sad1 and UNC84 domain containing 2	1,2095
309	16911132	PRNP	prion protein	-1,1875
310	16912192	GINS1	GINS complex subunit 1 (Psf1 homolog)	-1,1576
311	16691668	NOTCH2	notch 2	1,2558
312	16794898	NEK9	NIMA-related kinase 9	1,2026
313	16661323	NUDC	nuclear distribution C homolog (A. nidulans)	-1,1763
314	16851900	MAPRE2	microtubule-associated protein, RP/EB family, member 2	-1,1507
315	16800355	WDR76	WD repeat domain 76	-1,4609
316	16677201	DTL	denticleless E3 ubiquitin protein ligase homolog (Drosophila)	-1,5166
317	16773348	NUPL1	nucleoporin like 1	-1,3900
318	17084796	TMEM8B	transmembrane protein 8B	1,4079

319	16878556	WDR43	WD repeat domain 43	-1,3830
320	16666835	SH3GLB1	SH3-domain GRB2-like endophilin B1	1,3543
321	17101815	TXLNG	taxilin gamma	-1,3422
322	16995409	NUP155	nucleoporin 155kDa	-1,3460
323	17089898	NUP188	nucleoporin 188kDa	-1,3945
324	17015889	NUP153	nucleoporin 153kDa	-1,2870
325	17096091	PTCH1	patched 1	1,3830
326	17078134	EYA1	eyes absent homolog 1 (Drosophila)	1,2446
327	16856699	DOT1L	DOT1-like histone H3K79 methyltransferase	-1,3382
328	16833518	AATF	apoptosis antagonizing transcription factor	-1,3220
329	16950932	NUP210	nucleoporin 210kDa	-1,2437
330	16931590	PIM3	pim-3 oncogene	-1,1965
331	17064679	XRCC2	X-ray repair complementing defective repair in Chinese hamster cells 2	-1,2808
332	16802408	FEM1B	fem-1 homolog b (C. elegans)	1,1824
333	16738869	PRPF19	pre-mRNA processing factor 19	-1,1841
334	16852098	PIK3C3	phosphatidylinositol 3-kinase, catalytic subunit type 3	1,2416
335	16765284	AAAS	achalasia, adrenocortical insufficiency, alacrimia	-1,1772
336	16702351	GATA3	GATA binding protein 3	1,8809
337	16666616	PRKACB	protein kinase, cAMP-dependent, catalytic, beta	-1,6132
338	16909551	NPPC	natriuretic peptide C	-1,7371
339	16973578	SLBP	stem-loop binding protein	-1,3883
340	17008036	C6orf89	chromosome 6 open reading frame 89	1,3555
341	17023414	PTPRK	protein tyrosine phosphatase, receptor type, K	1,5075
342	16873313	ERCC1	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)	1,3571
343	16881786	HTRA2	HtrA serine peptidase 2	-1,2968
344	16683624	RUNX3	runt-related transcription factor 3	-1,4499
345	17005396	GMNN	geminin, DNA replication inhibitor	-1,3148
346	16734762	TRIM21	tripartite motif containing 21	1,2879
347	16834071	RARA	retinoic acid receptor, alpha	1,3030
348	16680284	CCNL2	cyclin L2	1,2381
349	16938899	MLH1	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)	-1,1777
350	16925239	DONSON	downstream neighbor of SON	-1,1777
351	17012804	MYB	v-myb myeloblastosis viral oncogene homolog (avian)	-2,8656
352	16851427	CABLES1	Cdk5 and Abl enzyme substrate 1	-2,4560
353	16769144	SYCP3	synaptonemal complex protein 3	-2,4411
354	16841852	FLCN /// PLD6	folliculin /// phospholipase D family, member 6 ///	-2,0191
355	16845126	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	1,8218
356	16693187	TDRKH	tudor and KH domain containing	1,9796
357	16930707	MEI1	meiosis inhibitor 1	2,3181
358	16885118	RALB	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	1,5882
359	16701748	GTPBP4	GTP binding protein 4	-1,6100
360	16836492	PRR11	proline rich 11	1,5534
361	16669389	PHGDH	phosphoglycerate dehydrogenase	-1,5170

362	17080946	KIAA0196	KIAA0196	1,4631
363	16661567	PHACTR4	phosphatase and actin regulator 4	1,5002
364	16662134	RBBP4	retinoblastoma binding protein 4 /// retinoblastoma binding protein 4 pseudogene 1	-1,4231
365	16908604	CNPPD1	cyclin Pas1/PHO80 domain containing 1	1,5461
366	16829369	FANCA	Fanconi anemia, complementation group A	-1,4768
367	16861200	LIN37	lin-37 homolog (C. elegans)	1,6304
368	16722217	ARNTL	aryl hydrocarbon receptor nuclear translocator-like	1,4248
369	16662430	AGO4	argonaute RISC catalytic component 4	1,5187
370	17022588	CDK19	cyclin-dependent kinase 19	1,4895
371	16813286	CIB1	calcium and integrin binding 1 (calmyrin)	1,4220
372	16909958	PER2	period circadian clock 2	-1,4313
373	16694804	ARHGEF11	Rho guanine nucleotide exchange factor (GEF) 11	1,4254
374	16879923	MSH6	mutS homolog 6 (E. coli)	-1,5196
375	16872443	SERTAD1	SERTA domain containing 1	1,4736
376	16968765	HERC5	HECT and RLD domain containing E3 ubiquitin protein ligase 5	-1,3810
377	16800173	CCNDBP1	cyclin D-type binding-protein 1	1,4003
378	17086784	CENPP /// IPPK	centromere protein P /// inositol 1,3,4,5,6-pentakisphosphate 2-kinase	-1,2919
379	17009482	CENPQ	centromere protein Q	-1,4359
380	16683358	E2F2	E2F transcription factor 2	-1,3198
381	17008595	UBR2	ubiquitin protein ligase E3 component n-recognin 2	1,3182
382	16701440	AHCTF1	AT hook containing transcription factor 1 /// AT hook containing transcription factor 1 pseudogene 1	-1,3381
383	16982635	TRIP13	thyroid hormone receptor interactor 13	-1,2976
384	16674998	RNF2	ring finger protein 2	-1,3069
385	16921036	CABLES2	Cdk5 and Abl enzyme substrate 2	-1,3217
386	16839606	MNT	MNT, MAX dimerization protein	-1,2791
387	17076103	TEX15	testis expressed 15	-1,4106
388	16842070	TOP3A	topoisomerase (DNA) III alpha	-1,2903
389	16742454	PAK1	p21 protein (Cdc42/Rac)-activated kinase 1	1,2194
390	16979400	PRDM5	PR domain containing 5	1,2678
391	16986748	MSH3	mutS homolog 3 (E. coli)	-1,1882
392	16985614	CENPH	centromere protein H	-1,2111
393	17105401	CENPI	centromere protein I	1,2265
394	17067890	ZNF703	zinc finger protein 703	1,2442
395	16919044	RBL1	retinoblastoma-like 1 (p107)	-1,2598
396	16721126	RRM1	ribonucleotide reductase M1	-1,2163
397	16935517	CENPM	centromere protein M	-1,2661
398	16724516	MADD	MAP-kinase activating death domain	1,2190
399	16800117	STARD9	StAR-related lipid transfer (START) domain containing 9	1,3175
400	16950017	PAK2	p21 protein (Cdc42/Rac)-activated kinase 2	-1,1876
401	16768857	CDK17	cyclin-dependent kinase 17	1,1862
402	16933931	PES1	pescadillo ribosomal biogenesis factor 1	-1,2236
403	16937505	FANCD2	Fanconi anemia, complementation group D2	1,1798
404	16669796	TXNIP	thioredoxin interacting protein /// thioredoxin-interacting protein-like	2,3283

405	16801179	MAPK6	mitogen-activated protein kinase 6	-1,6958
406	16664118	NASP	nuclear autoantigenic sperm protein (histone-binding) /// nuclear autoantigenic sperm protein (histone-binding)	-1,6875
407	16740956	POLD4	polymerase (DNA-directed), delta 4, accessory subunit	1,6832
408	17008092	PIM1	pim-1 oncogene	-1,6148
409	16922584	CHAF1B	chromatin assembly factor 1, subunit B (p60)	-1,6991
410	16860737	PDCD2L	programmed cell death 2-like	-1,7191
411	16857258	UHRF1	ubiquitin-like with PHD and ring finger domains 1 /// ubiquitin-like with PHD and ring finger domains 1	-1,5932
412	16962493	RFC4	replication factor C (activator 1) 4, 37kDa	-1,3639
413	16713230	PARD3	par-3 partitioning defective 3 homolog (C. elegans)	1,3869
414	16857192	CHAF1A	chromatin assembly factor 1, subunit A (p150)	-1,4802
415	17058617	RFC2	replication factor C (activator 1) 2, 40kDa	-1,4019
416	17002777	STK10	serine/threonine kinase 10	1,4566
417	16884956	STEAP3	STEAP family member 3, metalloreductase	-1,4579
418	16856980	HMG20B	high mobility group 20B	1,3061
419	16679411	EXO1	exonuclease 1	-1,3441
420	16794256	ERH	enhancer of rudimentary homolog (Drosophila)	-1,3507
421	16985353	ERBB2IP	erbb2 interacting protein	1,3285
422	17005234	E2F3	E2F transcription factor 3	1,2681
423	16833263	LIG3	ligase III, DNA, ATP-dependent /// ligase III, DNA, ATP-dependent	1,2552
424	16845172	PSMC3IP	PSMC3 interacting protein	-1,3339
425	17007910	MAPK13	mitogen-activated protein kinase 13	1,2889
426	17068093	TACC1	transforming, acidic coiled-coil containing protein 1	-1,3935
427	16716027	ANXA11	annexin A11	1,2534
428	17046041	IKZF1	IKAROS family zinc finger 1 (Ikaros)	1,2886
429	17104082	APEX2	APEX nuclease (apurinic/apyrimidinic endonuclease) 2	-1,2737
430	16828153	TXNL4B	thioredoxin-like 4B	-1,3035
431	16901593	sep-01	septin 10	1,3109
432	16969414	TET2	tet methylcytosine dioxygenase 2	1,2227
433	16773946	RFC3	replication factor C (activator 1) 3, 38kDa	-1,3430
434	16702685	SUV39H2	suppressor of variegation 3-9 homolog 2 (Drosophila)	-1,2245
435	16886503	RIF1	RAP1 interacting factor homolog (yeast)	-1,3189
436	17009918	PTP4A1	protein tyrosine phosphatase type IVA, member 1	-1,1934
437	17109716	RPS6KA3	ribosomal protein S6 kinase, 90kDa, polypeptide 3	-1,2300
438	17057174	POLD2	polymerase (DNA directed), delta 2, accessory subunit	-1,1924
439	16960517	SIAH2	siah E3 ubiquitin protein ligase 2	-1,2119
440	16916901	RASSF2	Ras association (RalGDS/AF-6) domain family member 2	-1,1804
441	16937035	ARL8B /	ADP-ribosylation factor-like 8B	-1,2276
442	17077135	RB1CC1	RB1-inducible coiled-coil 1	1,2178
443	16704320	RASSF4	Ras association (RalGDS/AF-6) domain family member 4	1,1767
444	16757687	RFC5	replication factor C (activator 1) 5, 36.5kDa	-1,2192
445	17098932	C9orf114	chromosome 9 open reading frame 114	-1,1867
446	16882304	USP39	ubiquitin specific peptidase 39	-1,1906
447	16915173	RBM38	RNA binding motif protein 38	-1,1508