

In vitro and in vivo rationale for the triple combination of panobinostat (LBH589) and dexamethasone with either bortezomib (PBD) or lenalidomide (PLD) in multiple myeloma

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Supplementary Table 1. Genes specifically deregulated by the triple combinations of PBD. MM1S cells were treated with panobinostat (7 nM), dexamethasone (0.9 μM) and bortezomib (3 nM) as single agents for 48 hours and in triple combinations for 24 hour, in order to obtain 20–25% apoptosis. After this period, cells were collected and changes in GEP were analyzed. A summary of the most relevant genes specifically deregulated by the triple combination, grouped by categories is shown.

Supp. table 1 Genes exclusively deregulated by panobinostat + dexamethasone + bortezomib

Probe set	Gene Symbol	MM1S FC	Description
Apoptosis			
201466_s_at	JUN	8.14	jun oncogene
204121_at	GADD45G	7.88	growth arrest and DNA-damage-inducible, gamma
209305_s_at	GADD45B	5.54	growth arrest and DNA-damage-inducible, beta
225606_at	BIM	3.46	BCL2-like 11 (apoptosis facilitator)
204859_s_at	APAF1	3.16	apoptotic peptidase activating factor 1
213373_s_at	CASP8	2.73	caspase 8, apoptosis-related cysteine peptidase
205467_at	CASP10	2.62	caspase 10, apoptosis-related cysteine peptidase
1729_at	TRADD	2.36	TNFRSF1A-associated via death domain
208906_at	CYCS	-2.54	cytochrome c, somatic
227143_s_at	BID	-2.76	BH3 interacting domain death agonist
204824_at	ENDO G	-3.55	endonuclease G
219366_at	AVEN	-5.14	apoptosis, caspase activation inhibitor
Cell cycle			
219534_x_at	CDKN1C	7.89	cyclin-dependent kinase inhibitor 1C (p57, Kip2)
213523_at	CCNE1	-2.34	cyclin E1
200951_s_at	CCND2	-2.63	cyclin D2
213226_at	CCNA2	-2.76	cyclin A2
228361_at	E2F2	-3.03	E2F transcription factor 2
155772_at	CDC25A	-3.87	cell division cycle 25 homolog A (S. pombe)
203967_at	CDC6	-4.23	cell division cycle 6 homolog (S. cerevisiae)
204947_at	E2F1	-4.92	E2F transcription factor 1
Chemokine			
205096_at	CCR1	-2.79	chemokine (C-C motif) receptor 1
207681_at	CXCR3	-33.2	chemokine (C-X-C motif) receptor 3

Supplementary Table 2. Genes specifically deregulated by the triple combinations of PLD. MM1S cells were treated with panobinostat (7 nM), dexamethasone (0.9 μM) and lenalidomide (1 μM) as single agents for 48 hours and in triple combinations for 26 hours, in order to obtain 20–25% apoptosis. After this period, cells were collected and changes in GEP were analyzed. A summary of the most relevant genes specifically deregulated by the triple combination, grouped by categories, is shown.

Supp. table 2 Genes exclusively deregulated by panobinostat + dexamethasone + lenalidomide

Probe set	Gene Symbol	MM1S FC	Description
Apoptosis			
203140_at	BCL6	24.02	B-cell CLL/lymphoma 6 (zinc finger protein 51)
213598_at	CASP4	4.78	caspase 4, apoptosis-related cysteine peptidase
1552703_s_at	CASP1	3.54	caspase 1, apoptosis-related cysteine peptidase
204859_s_at	APAF1	3.01	apoptotic peptidase activating factor 1
1729_at	TRADD	2.91	TNFRSF1A-associated via death domain
201473_at	JUNB	2.28	jun B proto-oncogene
220543_s_at	FAIM	-2.86	Fas apoptotic inhibitory molecule
201746_at	TP53	-2.87	tumor protein p53 (Li-Fraumeni syndrome)
210792_x_at	SIVA1	-2.91	SIVA1, apoptosis-inducing factor
204824_at	ENDO G	-3.04	endonuclease G
204493_at	BID	-3.18	BH3 interacting domain death agonist
208906_at	CYCS	-3.30	cytochrome c, somatic
219366_at	AVEN	-3.40	apoptosis, caspase activation inhibitor
Cell cycle			
216894_x_at	CDKN1C	3.17	cyclin-dependent kinase inhibitor 1C (p57, Kip2)
222156_x_at	CCPG1	2.85	cell cycle progression 1
217988_at	CCNB1IP1	2.65	cyclin B1 interacting protein 1
221427_s_at	CCNL2	2.65	cyclin L2
213523_at	CCNE1	-2.58	cyclin E1
202246_s_at	CDK4	-2.95	cyclin-dependent kinase 4
200951_s_at	CCND2	-4.29	cyclin D2
228361_at	E2F2	-4.49	E2F transcription factor 2
204126_s_at	CDC45L	-6.87	CDC45 cell division cycle 45-like (S. cerevisiae)
Chemokine			
204103_at	CCL4	3.84	chemokine (C-C motif) ligand 4
206978_at	CCR2	3.33	chemokine (C-C motif) receptor 2
207681_at	CXCR3	-7.06	chemokine (C-X-C motif) receptor 3