SUPPLEMENTAL MATERIALS AND METHODS

Drugs and antibodies

Quizartinib (LC-Laboratories; Q-4799), gilteritinib (ChemieTek, Indianapolis, IN; CT-GILT), midostaurin (Sigma-Aldrich; M1323), sorafenib (LKT Laboratories, St Paul, MN; S5868), dexamethasone 21-acetate (Sigma-Aldrich; D1881), prednisolone (Sigma-Aldrich; P6004), triamcinolone (Sigma-Aldrich; T6376), MIK665 (ChemieTek; CT-MIK665), CHIR99021 (LC-laboratories; C-6556), and bortezomib (LC-laboratories; B-1408) were dissolved in DMSO. Antibodies were obtained from the following sources: MCL-1[1] ; BCL-2[1] ; Phospho-FLT3 (#3464), FLT3 (#3462), Phospho-STAT5 (#4322), Phospho-p42/44 MAPK (#4370), p42/44 MAPK (#4695), β-Catenin (#8480), Glucocorticoid Receptor (#3660) and BCL-XL (#2764) from Cell Signaling Technology (Danvers, MA); BIM (B7929), β-Actin (A5441) and α-Tubulin (T5168) from Sigma-Aldrich.

Cell viability and apoptosis assays

Dose response curves were performed by seeding 50000 cells/well in a 96-well plate and adding serially-diluted drugs or vehicle to each well, while maintaining a final DMSO concentration of 0.01%. Cell viability was measured using the CellTiter-Glo (Promega; Cat# G7570) assay according to the manufacturer's instruction. Single cell clones used for the dose response analysis shown in Supplemental Figure 1C were isolated using FACS sorter where single MV4-11 cells were sorted into each well of a 96-well plate and grown from a single cell.

Cell viability assessed by flow cytometry was performed by seeding 300000 cells/well in a 48-well plate, adding drug or vehicle to 500µl of media in each well, and incubated for the indicated durations of time. For combination matrix experiments, 60000 cells/well were seeded in a 96 well plate and treated with serial dilutions of drugs (DMSO concentration was kept below 0.01%) for 48h. Cells were stained with APC-Annexin V and 7-AAD (BioLegend, San Diego, CA) according to the manufacturer's protocol. FACSCanto 10 (BD) and FlowJo were used to run and analyze the stained cells.

Caspase-3/7 activity assay was done by seeding 60000 cells/well in a 96-well plate treated with 5µM Caspase-3/7 Green Detection Reagent (ThermoFisher Scientific; C10423) and

monitored using IncuCyte Live-Cell Analysis system (Sartorius, Göttingen, Germany) over a 24h period.

Immunoblotting

An equal number of cells treated as described in the figure legends were flash frozen and lysed in 62.5 mM Tris-HCl (pH 6.8), 2% (w/v) SDS, 10% glycerol, 0.01% (w/v) bromophenol blue, and 41.7 mM dithiothreitol (Cell Signaling; #7722), sonicated on ice for 10 seconds and boiled at 100^{o}C for 5 minutes. Lysates were subjected to electrophoresis followed by transfer to PVDF membrane and an overnight incubation with primary antibodies, followed by 1h incubation with fluorescent secondary antibodies (LI-COR, Lincoln, NE; #925-32210/11). Blots were scanned using a LI-COR Odyssey CLx Imager.

RNA sequencing and analysis

MV4-11 cells were treated with DMSO for 48h, dexamethasone for 48h, quizartinib for 48h or 5d, and quizartinib plus dexamethasone for 48h or 5d (in which dexamethasone was added on day 3). RNA was extracted using the mirVana™ miRNA Isolation Kit (Thermo Fisher Scientific, Waltham, MA). cDNA libraries were prepared using the NEXTflex™ Illumina Rapid Directional RNA-Seq Library Prep Kit (BioO Scientific, Austin, TX) per the manufacturer's instructions and run on an Illumina HiSeq 2500. Reads that passed the Illumina CASAVA pipeline were aligned to the human reference genome (GRCh38) using STAR (v2.7.3)[2], and gene and transcript quantifications are performed by RSEM against a gene annotation file, which contains by default GENCODE annotations (gencodeV24pri). Read counts were extracted, and used for differential expression analysis through edgeR[2] and DESEQ2[3] packages. Genes were first filtered by edgeR to remove non expressed genes in both DTPs and parental cells, then a significant false discovery rate of adjusted P value ($p < 0.05$) were used for differential expression analysis from DESEQ2. Genes with 1.5-fold upregulation or downregulation in drug treated cells relative to DMSO control treated cells were used for core analysis with Ingenuity Pathway Analysis (IPA) software, Gene Ontology pathway analysis (using metascape[4]) and Protein-Protein Interaction (PPI) analysis to generate differential expression results for canonical pathways, upstream regulators, pathway analysis and drug-target prediction.

In vivo models of AML

NOD-scid IL2rγnull (NSG) mice were purchased from The Jackson Laboratory (Bar Harbor, ME) and maintained in compliance with guidelines and protocols approved by Penn State College of Medicine IACUC. Luciferase expressing MOLM13 cells (300,000 cells) were injected intravenously in to 6-week old male NSG mice. On day 12 (Figure 4C) or day 7 (Supplemental Figure 5B) post injection, engraftment was confirmed using IVIS Spectrum imaging system (PerkinElmer, Waltham, MA) and once daily oral treatment with vehicle (22% 2-Hydroxypropyl-β-cyclodextrin; Sigma-Aldrich; C0926), quizartinib (2mg/kg; LC-Laboratories, Woburn, MA; Q-4799) or dexamethasone 21-phosphate disodium salt dissolved first in saline then in 22% 2-Hydroxypropyl-β-cyclodextrin (10mg/kg; Sigma-Aldrich; D1159) (Figure 4C) or with vehicle, quizartinib (2 mg/kg) or dexamethasone 21 phosphate disodium salt (3 mg/kg) (Supplemental Figure 5B) alone or in combination was started and continued until the indicated end point. No bone marrow conditioning was performed prior to engraftment of MOLM13 cells.

Alternatively, MOLM13 cells (500,000 cells) were transplanted with Matrigel subcutaneously into the flank of 6-week old female NSG mice. Once palpable tumor grew in 10 days, treatment with vehicle (22% 2-Hydroxypropyl-β-cyclodextrin; Sigma-Aldrich; C0926) and saline, quizartinib (oral 2mg/kg; LC-Laboratories, Woburn, MA; Q-4799) or dexamethasone 21-phosphate disodium salt dissolved in saline (IP 10mg/kg; Sigma-Aldrich; D1159) alone or in combination was initiated. Once daily treatment continued for a total of 20 days. On day 30 after cell injection, all mice were euthanized and tumor weight and volume measured.

CRISPR/Cas9 genome editing and MCL-1 overexpression

Single guide RNA (gRNA) targeting GR (5′- AACCAAAAGTCTTCGCTGCT -3′) or BIM (5′-AGGTAGACAATTGCAGCCTG -3′) was sub-cloned into pLenti-CRISPR-V2 (Addgene, Watertown, MA; Plasmid #52961). The retroviral vector pMSCV-puro-Flag-mMcl-1^{KR} was obtained through Addgene (Plasmid #32983). Lentiviral and retroviral packaging, transduction and puromycin selection were performed as described previously.[5] Single clones were isolated and screened for gene disruption by immunoblotting.

Supplemental References

1. Krajewski S, Bodrug S, Gascoyne R, Berean K, Krajewska M, Reed JC.

Immunohistochemical analysis of Mcl-1 and Bcl-2 proteins in normal and neoplastic lymph nodes. *Am J Pathol*. 1994;145(3):515-525.

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5. Tang Z, Takahashi Y, Chen C, et al. Atg2A/B deficiency switches cytoprotective autophagy to non-canonical caspase-8 activation and apoptosis. *Cell Death Differ*. 2017;24(12):2127-2138. doi:10.1038/cdd.2017.133

SUPPLEMENTAL TABLES AND FIGURES

Supplemental Table 1. Compounds predicted to kill DTPs based on PPI analysis.

PubChem CID	Targeted Genes
3843095	H2BFS, HIST1H2AC, IGF1, LSP1, SH3TC, TF
7217946	CX3CR1, H2BFS, HIST1H2AC, LGALS2, LSP1, SORL1, TF
60857	CX3CR1, HIST1H2AC, IGF1, KIT, LGALS2, SORL1
11201705	CX3CR1, H2BFS, HIST1H2AC, MYOM1, TF
2662 (Celecoxib)	CX3CR1, H2BFS, HIST1H2AC, SLC14A1, SORL1
5702028	HCC515, HIST1H2AC, IGF1, SLC14A1, SORL1
6604780	CX3CR1, H2BFS, HIST1H2AC, PRUNE2, SORL1
5283389 (N-Arachidonoylglycine)	H2BFS, HIST1H2AC, SORL1, TF, ZNF467
2733526 (Tamoxifen)	CX3CR1, H2BFS, HIST1H2AC, IGF1, SORL1
3136844	H2BFS, HIST1H2AC, IGF1, PRUNE2, SORL1

Supplemental Table 2. Top 20 chemicals predicted to regulate DTPs based on IPA analysis.

	Upstream Regulator	Molecule Type	Predicted Activation State	p-value of overlap
1	fluticasone propionate	chemical drug		5.14E-09
2	filgrastim	biologic drug	Inhibited	6.23E-09
3	dexamethasone	chemical drug		9.24E-08
4	salmonella minnesota R595 lipopolysaccharides	chemical - endogenous non-mammalian	Activated	5.7E-06
5	lipopolysaccharide	chemical drug	Activated	1.55E-05
6	17-alpha-ethinylestradiol	chemical drug		8.02E-05
7	tretinoin	chemical - endogenous mammalian	Activated	9.36E-05
8	eicosapentenoic acid	chemical drug		0.000406
9	prostaglandin D2	chemical - endogenous mammalian	Activated	0.000622
10	interferon beta-1a	biologic drug		0.000628
11	genistein	chemical drug	Activated	0.000673
12	ATP-gamma-S	chemical reagent		0.000989
13	urea	chemical - endogenous mammalian		0.00138
14	cholesterol	chemical - endogenous mammalian		0.00149
15	adalimumab	biologic drug		0.00163
16	phloretin	chemical - endogenous non-mammalian		0.00163
17	C20-D3-vitamin A	chemical drug		0.00163
18	mimosine	chemical drug		0.00186
19	2-aminopurine	chemical reagent		0.00189
20	cholecalciferol	chemical - endogenous mammalian		0.00192

Supplemental Table 3. Top 50 drugs that kill DTPs but not parental cells based on drug screening.

	Drug	**Therapeutic Effect**
1	Fludrocortisone acetate	Anti-inflammatory
2	Prednisolone	Anti-inflammatory
3	Isoflupredone acetate	Anti-inflammatory
4	6-alpha-Methylprednisolone	Anti-inflammatory
5	Amodiaquine dihydrochloride dihydrate	Anti-inflammatory
6	Triamcinolone	Anti-inflammatory
7	Dexamethasone acetate	Anti-inflammatory
8	Betamethasone	Anti-inflammatory
9	Mometasone furoate	Anti-inflammatory
10	Budesonide	Anti-inflammatory
11	Diflorasone Diacetate	Anti-inflammatory
12	Cortisol acetate	Anti-inflammatory
13	Alclometasone dipropionate	Anti-inflammatory
14	Clobetasol propionate	Anti-inflammatory
15	(R)-Naproxen sodium salt	Anti-inflammatory
16	Flunisolide	Anti-inflammatory
17	Flurandrenolide	Anti-inflammatory
18	Flumethasone	Anti-inflammatory
19	Fluocinonide	Anti-inflammatory
20	Halcinonide	Anti-inflammatory
21	Beclomethasone dipropionate	Anti-inflammatory
22	Deflazacort	Anti-inflammatory
23	Fluorometholone	Anti-inflammatory
24	Prednicarbate	Anti-Inflammatory
25	Amcinonide	Anti-inflammatory
26	Clocortolone pivalate	Anti-inflammatory
27	Rimexolone	Anti-inflammatory
28	Fluticasone propionate	Anti-inflammatory
29	Fluocinolone acetonide	Anti-inflammatory
30	Fulvestrant	Antineoplastic
31	Dipyridamole	Anticoagulant
32	Flunarizine dihydrochloride	Anticonvulsant
33	Tolnaftate	Antifungal
34	Fluphenazine dihydrochloride	Antipsychotic
35	Pimethixene maleate	Antihistaminic
36	Dilazep dihydrochloride	Antiplatelet
37	Thioridazine hydrochloride	Antipsychotic
38	Mizolastine	Antihistaminic

39	Vatalanib	Antineoplastic
40	Amiodarone hydrochloride	Antianginal
41	Sertindole	Antipsychotic
42	Butoconazole nitrate	Antibacterial
43	Raloxifene hydrochloride	Antisteoporotic
44	(±)-Metoprolol (+)-tartrate salt	Antiarrhythmic
45	Estrone	Antimenopausal
46	Fluspirilen	Antipsychotic
47	Megestrol acetate	Antineoplastic
48	Aprepitant	Antiemetic
49	Folinic acid calcium salt	Antianemic
50	Proadifen hydrochloride	Local anesthetic

Supplemental Table 4. Top 20 transcription regulators predicted to be upstream regulators of the up-regulated genes in quizartinib treated cells based on IPA analysis.

	Upstream Regulator	**Molecule Type**	**Predicted Activation State**	**p-value of overlap**
1	CIITA	transcription regulator	Activated	2.482
2	MAFB	transcription regulator	Activated	2.713
3	BCOR	transcription regulator		
4	TYROBP	transmembrane receptor	Activated	2.213
5	STAT1	transcription regulator	Activated	3.165
6	IRF8	transcription regulator		1.733
7	IKZF1	transcription regulator		-0.97
8	CD2	transmembrane receptor	Activated	2.646
9	RFX5	transcription regulator		
10	BTNL2	transmembrane receptor	Activated	2.828
11	RAD21	transcription regulator	Activated	2
12	PRDM1	transcription regulator		-1.267
13	IKZF3	transcription regulator	Inhibited	-2.449
14	IRF1	transcription regulator	Activated	2.359
15	ZBTB16	transcription regulator		-0.936
16	ZBTB32	transcription regulator		
17	CEBPD	transcription regulator		0.4
18	STAT6	transcription regulator		-0.522
19	STAT3	transcription regulator		0.572
20	SPI1	transcription regulator	Activated	2.428

Supplemental Table 5. Top 20 cytokines and complex predicted to be upstream regulators of the up-regulated genes in quizartinib treated cells based on IPA analysis.

	Upstream Regulator	**Molecule Type**	**Predicted Activation State**	**p-value of overlap**
1	EBI3	cytokine	Activated	6.47E-07
2	IL27	cytokine	Activated	1.94E-06
3	IFNG	cytokine		2.88E-06
4	IL10	cytokine	Activated	7.45E-06
5	TNF	cytokine	Activated	1.12E-05
6	IL13	cytokine		7.89E-05
7	Ige	complex	Activated	0.000131
8	IL15	cytokine		0.000144
9	IL12 (complex)	complex	Activated	0.00396
10	IL18	cytokine	Activated	0.00402
11	IFNA1/IFNA13	cytokine	Activated	0.0101
12	IL1B	cytokine		0.00101
13	IL21	cytokine	Activated	0.00103
14	IL2	cytokine	Activated	0.00115
15	BCR (complex)	complex		0.00137
16	NFkB (complex)	complex	Activated	0.00141
17	IL4	cytokine		0.00152
18	IL6	cytokine		0.00182
19	Inflammasome	complex		0.0465
20	CSF1	cytokine		0.00207

Supplemental Table 6. Top 20 transcription regulators predicted to be upstream regulators of the down-regulated genes in quizartinib plus dexamethasone treated cells based on IPA analysis.

	Upstream Regulator	**Molecule Type**	**Predicted Activation State**	**p-value of overlap**
1	CIITA	transcription regulator	Inhibited	1.77E-15
2	RFX5	transcription regulator		7.25E-08
3	STAT3	transcription regulator		8E-08
4	CTCF	transcription regulator	Inhibited	2.01E-07
5	RAD21	transcription regulator	Inhibited	2.09E-06
6	PRDM1	transcription regulator		3.45E-06
7	SPI1	transcription regulator		9.17E-06
8	CEBPE	transcription regulator		1.44E-05
9	BCOR	transcription regulator		2.63E-05
10	STAT1	transcription regulator		6.76E-05
11	NFKB2	transcription regulator	Inhibited	6.98E-05
12	TCL1A	transcription regulator		0.000111
13	HOXA10	transcription regulator	Activated	0.000149
14	NKX2-1	transcription regulator		0.000157
15	RFXAP	transcription regulator		0.000271
16	ZEB2	transcription regulator		0.00046
17	ZBTB32	transcription regulator		0.000494
18	IRF8	transcription regulator		0.000645
19	SIRT1	transcription regulator		0.00094
20	TBX21	transcription regulator		0.000943

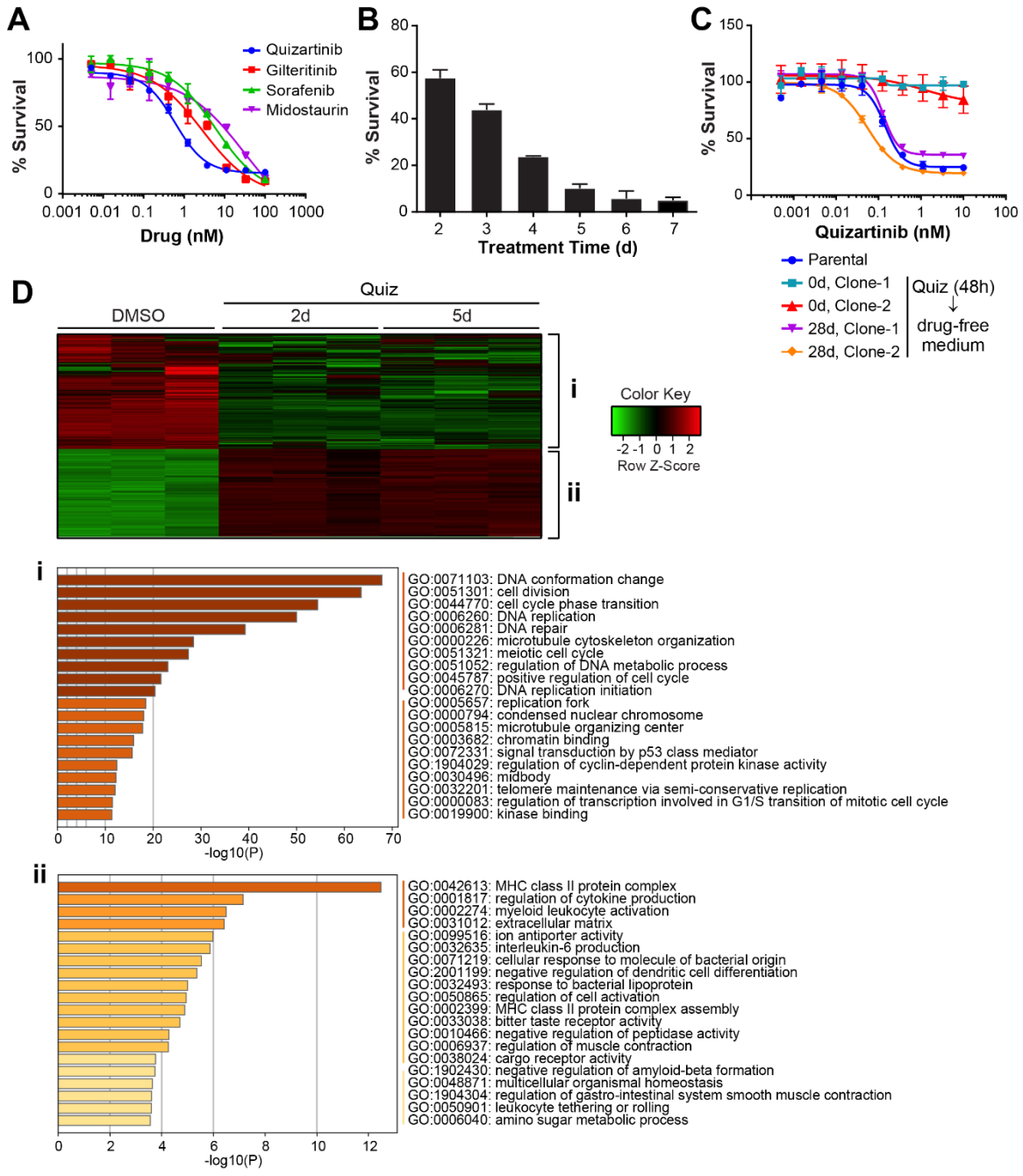
Supplemental Table 7. Top 20 cytokines and complex predicted to be upstream regulators of the down-regulated genes in quizartinib plus dexamethasone treated cells based on IPA analysis.

	Upstream Regulator	**Molecule Type**	**Predicted Activation State**	**p-value of overlap**
1	Ige	complex		-1.633
2	NFkB (complex)	complex	Inhibited	-2.2
3	BCR (complex)	complex		-1.982
4	CREB-NFkB	complex		
5	HLA-B27	complex		
6	Immunoglobulin	complex		0.277
7	IL12 (complex)	complex		
8	IgG	complex		
9	Bcl9-Cbp/p300-Ctnnb1-Lef/Tcf	complex		
10	Ifn gamma	complex		
11	CD3	complex		
12	LDL	complex		
13	Iga	complex		
14	IL6	cytokine		-0.877
15	CSF3	cytokine		1.569
16	IL27	cytokine	Inhibited	-2.951
17	IFNG	cytokine	Inhibited	-2.88
18	EBI3	cytokine	Inhibited	-2.425
19	IL4	cytokine	Inhibited	-2.586
20	TNFSF13B	cytokine		

Supplemental Table 8. Clinical characteristics of AML patients used in the study.

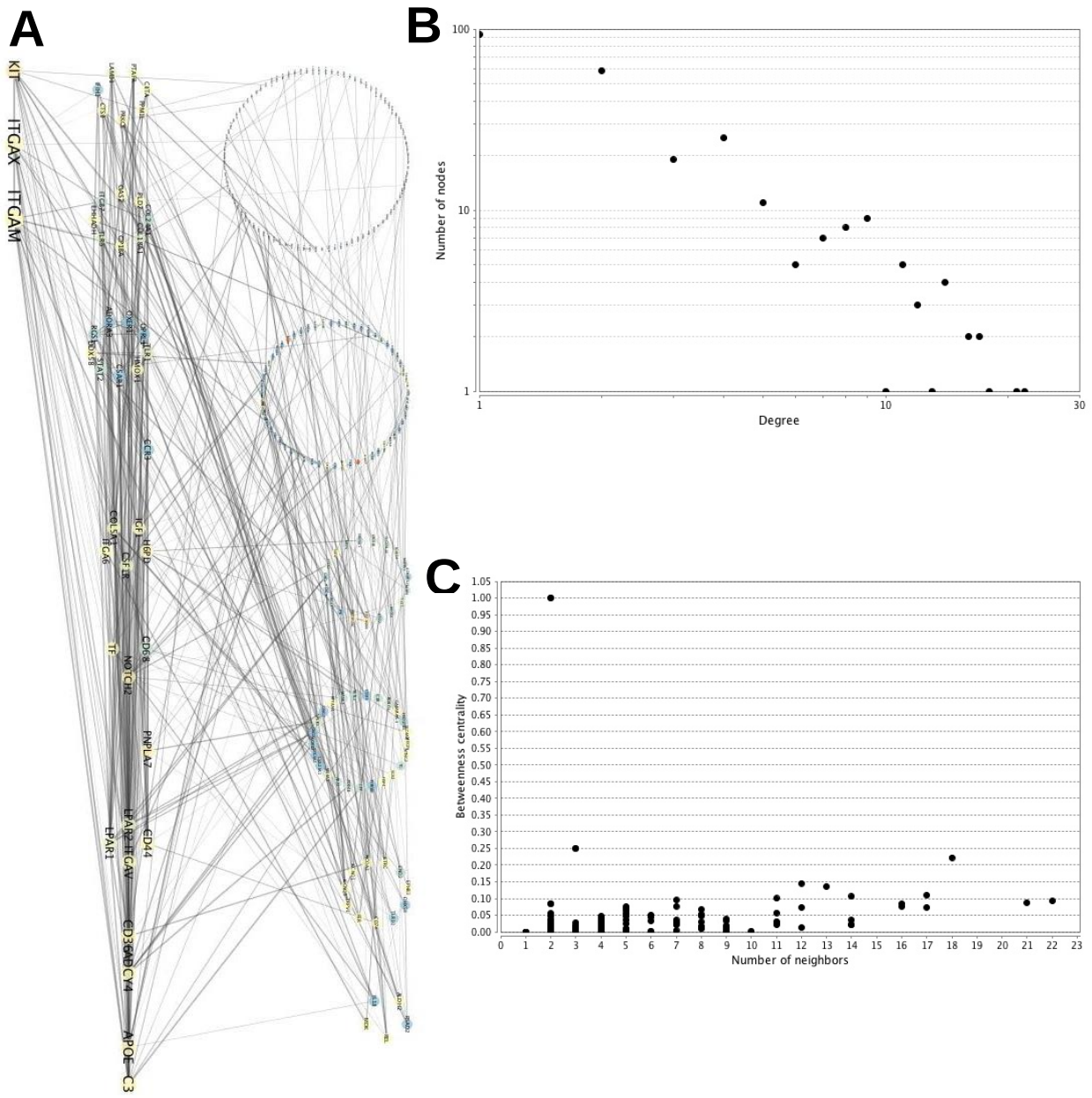
Code	Gender	Stage	Diagnosis	Cytogenetics	NPM1	FLT3	% Blast	RES
765	M	Dx	AML	t(16;16)	N/A	ITD	77.0	Yes
791	M	Dx	AML	Normal	Mut	D835mut	64.0	Yes
801	M	Dx	AML	Normal	N/A	ITD	22.4	Yes
1224	F	Rel	AML	N/A	Mut	ITD	66.0	Yes
1244	M	Dx	AML	t(3;5)	WT	ITD	63.5	Yes
1259	F	Rel	AML	Complex	N/A	WT	N/A	No
1335	F	Dx	AML	Normal	N/A	WT	34.0	No
1340	F	Dx	AML	Normal	N/A	WT	N/A	No
1342	M	Dx	AML	N/A	WT	WT	N/A	No
939	F	Dx	AML	Normal	WT	ITD	93.8	No
1032	F	Rel	AML	Normal	N/A	ITD	74.5	No
1172	F	Dx	AML	Normal	WT	ITD	96.0	No
1265	M	Dx	AML	N/A	N/A	ITD	96.0	No

Dx: Diagnosis; Rel: Relapse; N/A: Not Available; Mut: Mutant; WT: Wild-type; RES: Response to quizartinib plus dexamethasone



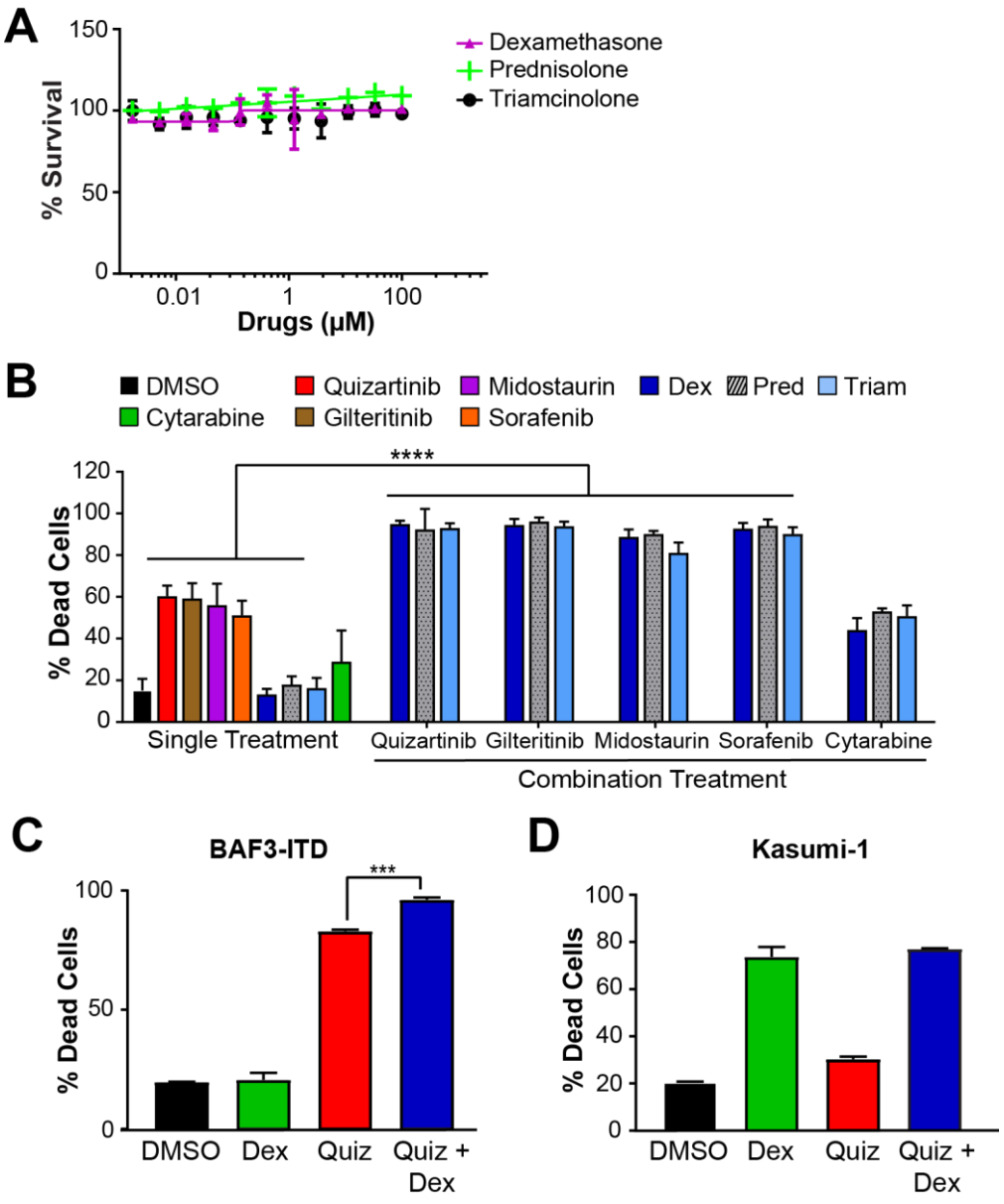
Supplemental Figure 1. (A) Survival curve showing the viability of MV4-11 cells treated with the indicated concentrations of FLT3 inhibitors for 48h using CellTiter-Glo assay. **(B)** MV4-11 cells were treated with 100nM quizartinib for the indicated durations of time, stained with APC-Annexin V and 7-AAD, and analyzed by FACS for detection of viable cells. **(C)** Single clone derived MV4-11 cells (isolated using the FACS sorter) were used to generate DTPs (quizartinib treatment for 48h). DTPs were subsequently used for survival curve analysis either immediately

following generation (0d) or after 28d culture in drug-free media. **(D)** A heat-map of differentially expressed genes (Green, down-regulated; Red, up-regulated) in MV4-11 cells treated with either DMSO or quizartinib (Quiz; 10nM) for either 2d or 5d. The surviving cells were isolated by Ficoll centrifugation before RNA-sequencing. RNA-seq was conducted in three biological replicates. Pathway analysis of down-regulated **(D-i)** and up-regulated **(D-ii)** genes.

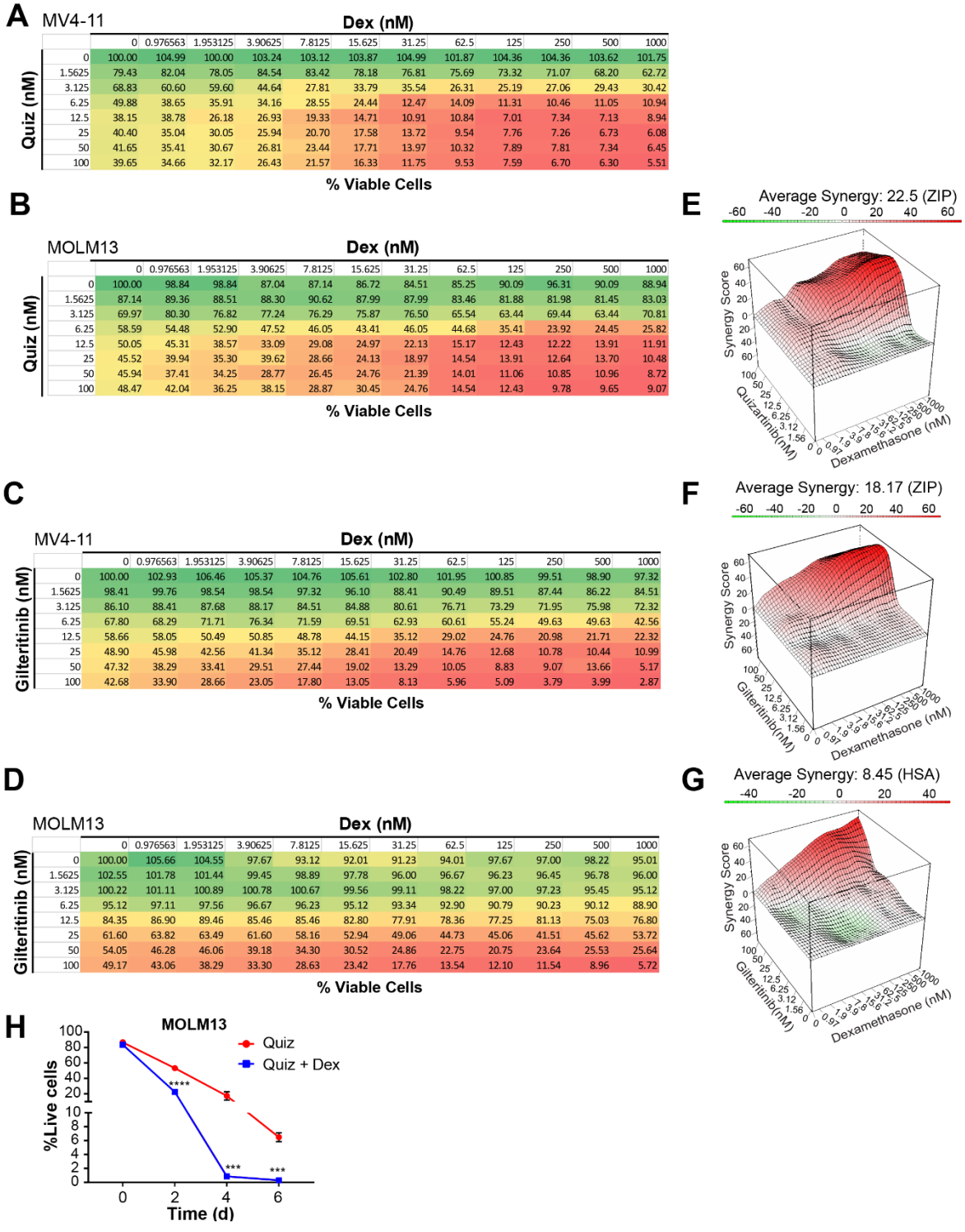


Supplemental Figure 2. (A) Protein-protein interaction network. Nodes are grouped based on node degree. The node size is mapped to the node degree (low values to small sizes). The node color is mapped to the betweenness centrality (low values to dark colors). The edge size is mapped to the combined interaction score (low values to small size). **(B)** Network hubs. Nodes with high node degree (the number of interactions that a node has). List of nodes with high node degree (>=10) in the PPI network: ITGAM (22), ITGAX (21), KIT (18), C3 (17), APOE (17), ADCY4 (16), CD36 (16), ITGAV (14), LPAR1 (14), LPAR2 (14), CD44 (14), PNPLA7 (13), NOTCH2

(12), TF (12), CD68 (12), CSF1R (11), ITGA6 (11), COL5A1 (11), IGF1 (11), H6PD (11), CCR3 (10). **(C)** Network bottlenecks. Nodes with high betweenness centrality (an indicator of a node's centrality in a network). List of nodes with high betweenness centrality in the PPI network: BAIAP2 (1), GNS (1), HIST1H2BK (0.25), HIST1H2AC (0.25), KIT (0.22), NOTCH2 (0.15), PNPLA7 (0.14), C3 (0.11), CD44 (0.11), H6PD (0.1), PRKCE (0.095), ITGAM (0.093), ITGAX (0.087), CD36 (0.084), HIST2H2BE (0.083), HIST1H2AG (0.083).

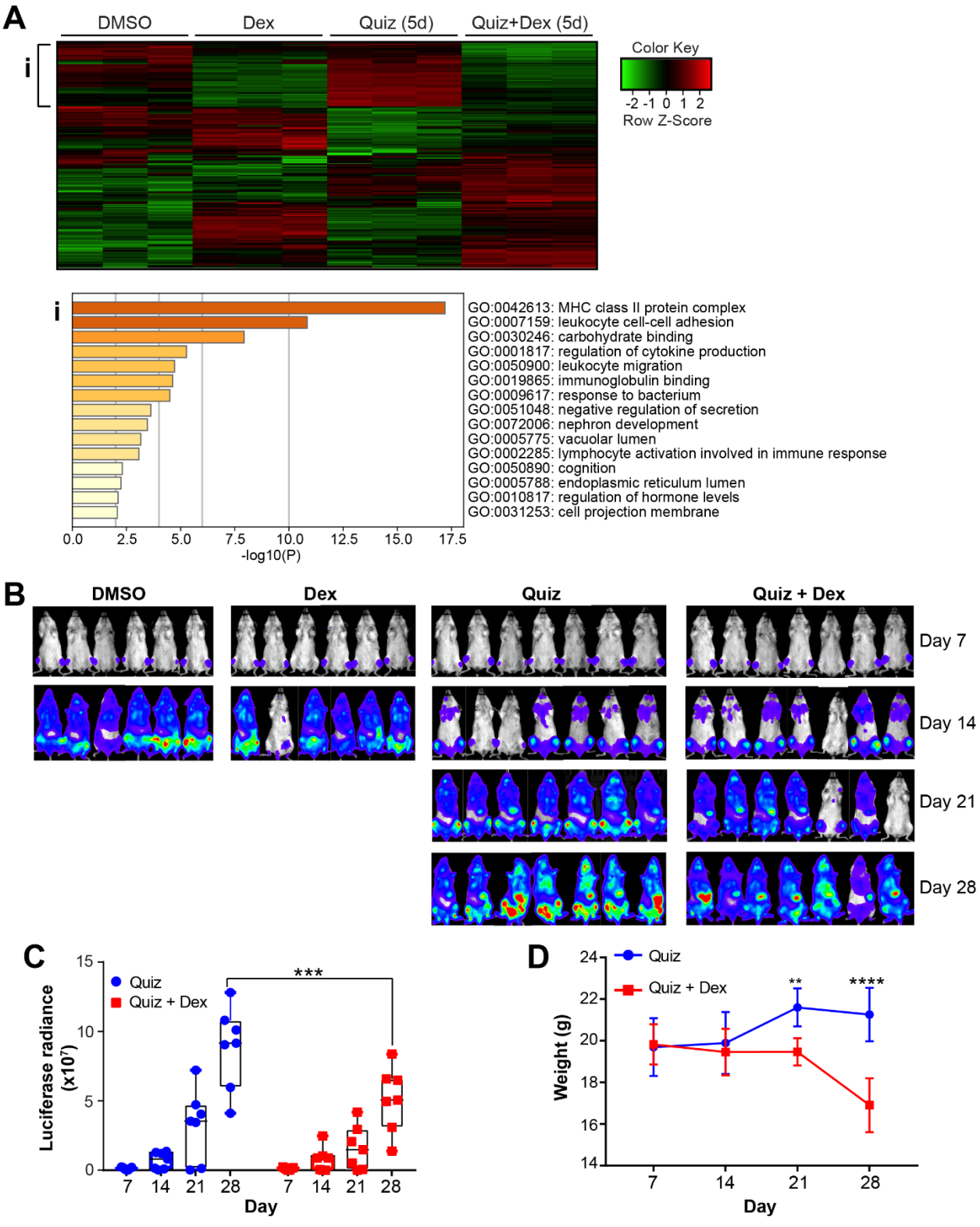


Supplemental Figure 3. (A) Survival curve showing the viability of MV4-11 cells treated with the indicated concentrations of anti-inflammatory GCs. **(B)** FACS analysis of replicate experiments to quantify dead cells (Annexin V and 7-AAD positive) for the indicated drug combinations (100nM FLT3 inhibitors, 1μM cytarabine and 50μM GCs) in MOLM13 cells **(C)**, FACS analysis of BAF3-FLT3-ITD **(C)** and Kasumi-1 **(D)** cell viability following treatment with quizartinib (Quiz; 100nM) alone or in combination with dexamethasone (Dex; 50μM) for 48h.



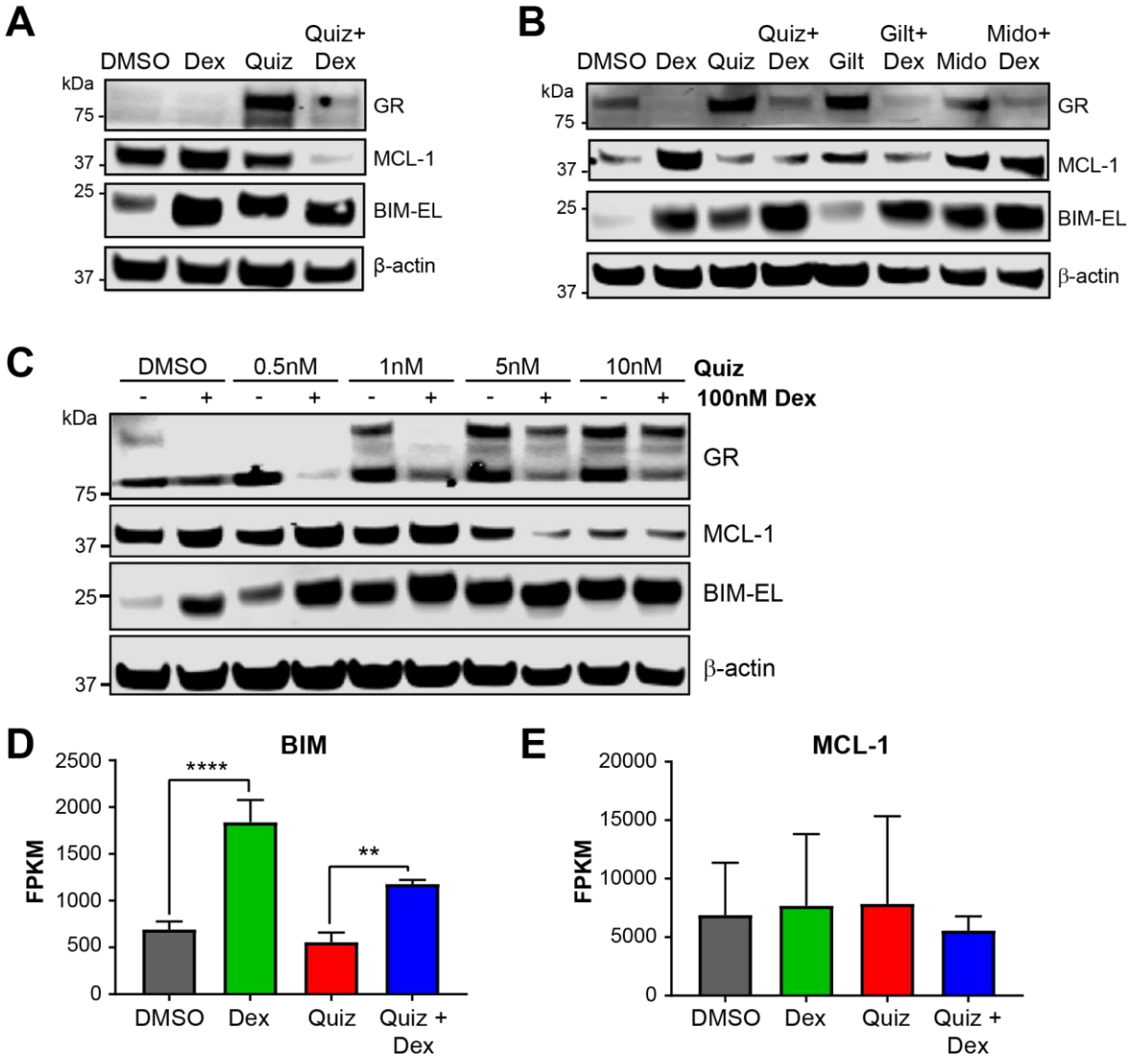
Supplemental Figure 4. Table showing the drug combination matrix of serially diluted quizartinib and dexamethasone in MV4-11 **(A)** and MOLM13 **(B)** cells. Table showing the drug combination matrix of serially diluted gilteritinib and dexamethasone in MV4-11 **(C)** and MOLM13 **(D)** cells.

(E) Three-dimensional graph showing the synergy score of quizartinib and dexamethasone combination in MOLM13 cells. Three-dimensional graph showing the synergy score of gilteritinib and dexamethasone combination in MV4-11 **(F)** and MOLM13 **(G)** cells. **(H)** Quantification of viable MOLM13 cells (Annexin V and 7-AAD negative) using FACS analysis for the indicated time points after quizartinib (Quiz; 10nM) ± dexamethasone (100nM) treatment.



Supplemental Figure 5. A heat-map of differentially expressed genes (Green, down-regulated; Red, up-regulated) in MV4-11 cells treated with 10nM quizartinib (Quiz) for 5d and 100nM

dexamethasone for 2d (Dex). For the combination treatment, cells were treated with 10nM quizartinib for 5d and 100nM dexamethasone was added on day 3. **(A-i)** Pathway analysis of genes up-regulated in quizartinib treated cells and down-regulated in cells treated with the combination of quizartinib and dexamethasone. RNA-seq was conducted in 3 biological replicates. **(B)** *In vivo* bioluminescence imaging, **(C)** Luciferase signal quantification, and **(D)** Body weight tracking were performed at the indicated time points on NSG mice xenografted with MOLM13-Luc cells and treated with vehicle or the indicated drugs (2mg/kg quizartinib; 3mg/kg dexamethasone).



Supplemental Figure 6. (A) A representative immunoblot showing the expression of GR, MCL-1 and BIM following treatment of MOLM13 cells with indicated drugs for 48h: 10nM quizartinib (Quiz), 100nM dexamethasone (Dex). **(B)** A representative immunoblot showing the expression of GR, MCL-1 and BIM following treatment of MV4-11 cells with indicated drugs: 10nM quizartinib, 50nM gilteritinib (Gilt), 100nM midostaurin (Mido) and 100nM dexamethasone for 48h. **(C)** A representative immunoblot showing the expression of GR, MCL-1 and BIM following treatment of MV4-11 cells with indicated drugs and concentration for 48h. Bar graph showing the gene expression (FPKM from RNA-seq in Figure 3D) of BIM **(D)** and MCL-1 **(E)**.

MV4-11

Quiz (nM) \ MIK-665 (nM)	0	0.009766	0.019531	0.039063	0.078125	0.15625	0.3125	0.625	1.25	2.5	5	10
0	100.00	105.01	104.40	101.71	100.49	95.60	94.99	82.76	68.09	46.82	25.18	7.93
1.5625	88.75	82.40	75.67	69.68	69.93	61.00	48.66	26.16	14.30	9.71	5.73	3.53
3.125	69.56	62.35	61.98	56.97	55.01	43.28	34.72	11.71	12.47	6.45	4.34	4.41
6.25	54.52	56.60	52.44	48.78	43.15	35.94	32.40	15.16	8.69	4.56	3.69	2.16
12.5	58.07	49.27	53.67	52.93	40.59	25.92	33.25	13.33	7.86	4.27	3.03	3.17
25	62.59	68.46	49.63	51.83	46.21	32.52	32.76	11.17	7.16	4.89	4.65	2.05
50	51.71	63.20	58.92	65.28	48.04	34.72	20.54	8.09	6.32	2.71	5.11	2.62
100	69.19	69.80	53.91	46.21	47.07	30.68	27.38	8.56	6.14	4.43	4.54	4.13

% Viable Cells

Supplemental Figure 7. The drug combination matrix following FACS cell viability analysis of MV4-11 cells treated with serially diluted quizartinib (Quiz) and MIK-665 for 48 h.