Supplementary Table S1. Sensitivity to JQ1 of a Collection of Cancer Cell Lines

#	Cell_Line	Organ	Histology	MYCN Copy Number	LN_IC50	EMax
1	TGBC24TKB	Biliary tract	Gall bladder	0<cn<8	-1.436	0.049
2	ETK-1	Biliary tract	Adenocarcinoma	0<cn<8	-0.665	0.411
3	TGBC1TKB	Biliary tract	Gall bladder	0<cn<8	2.220	0.644
4	SW-1710	Bladder	Transitional cell carcinoma	0<cn<8	-2.839	0.112
5	BFTC-905	Bladder	Transitional cell carcinoma	0<cn<8	-1.794	0.252
6	SCaBER	Bladder	Squamous cell carcinoma	-	-1.650	0.209
7	HT-1197	Bladder	Transitional cell carcinoma	0<cn<8	-1.441	0.182
8	TCCSUP	Bladder	Transitional cell carcinoma	-	-1.262	0.269
9	647-V	Bladder	Transitional cell carcinoma	0<cn<8	-1.161	0.232
10	639-V	Bladder	Transitional cell carcinoma	0<cn<8	-1.119	0.175
11	EJ138	Bladder	Carcinoma	-	-1.053	0.201
12	DSH1	Bladder	Carcinoma	0<cn<8	-0.806	0.223
13	CAL-29	Bladder	Transitional cell carcinoma	-	-0.634	0.174
14	LB831-BLC	Bladder	Carcinoma	0<cn<8	-0.416	0.303
15	J82	Bladder	Transitional cell carcinoma	0<cn<8	-0.307	0.282
16	5637	Bladder	Carcinoma	-	-0.295	0.342
17	SW 780	Bladder	Transitional cell carcinoma	0<cn<8	0.431	0.531
18	RT-112	Bladder	Transitional cell carcinoma	0<cn<8	0.956	0.543
19	HT 1376	Bladder	Transitional cell carcinoma	0<cn<8	1.413	0.580
20	RT4	Bladder	Transitional cell carcinoma	0<cn<8	1.455	0.551
21	RT112/84	Bladder	Carcinoma	-	1.747	0.621
22	KU-19-19	Bladder	Transitional cell carcinoma	0<cn<8	2.353	0.739
23	UM-UC-3	Bladder	Transitional cell carcinoma	-	2.882	0.763
24	T24	Bladder	Transitional cell carcinoma	0<cn<8	4.372	0.886
25	MG-63	Bone	Sarcoma	0<cn<8	-2.587	0.248
26	Saos-2	Bone	Sarcoma	0<cn<8	-2.123	0.139
27	NOS-1	Bone	Sarcoma	-	-1.906	0.214
28	HuO9N2	Bone	Sarcoma	-	-1.808	0.204
29	U-2 OS	Bone	Sarcoma	0<cn<8	-1.577	0.206
30	SJSA-1	Bone	Sarcoma	0<cn<8	-1.561	0.278
31	CS1R	Bone	Unknown	-	-1.261	0.282
32	CAL-72	Bone	Sarcoma	-	-1.119	0.363
33	143B PML BK TK	Bone	Sarcoma	-	-0.576	0.330
34	G-292 Clone A141B1	Bone	Sarcoma	-	-0.524	0.431
35	HOS	Bone	Sarcoma	0<cn<8	-0.123	0.339
36	MHH-ES-1	Bone	Ewing's Sarcoma	-	0.016	0.374
37	KHOS-240S	Bone	Sarcoma	-	0.116	0.397
38	OSA 80	Bone	Sarcoma	-	0.162	0.459
39	CS1	Bone	Normal cells	-	0.386	0.461
40	KHOS-312H	Bone	Sarcoma	-	0.397	0.441
41	EW-16	Bone	Ewing's Sarcoma	0<cn<8	0.720	0.386
42	NY	Bone	Sarcoma	-	0.757	0.539
43	CHSA 0108	Bone	Sarcoma	-	1.036	0.577
44	143B	Bone	Sarcoma	0<cn<8	1.158	0.593
45	ES8	Bone	Ewing's Sarcoma	0<cn<8	1.212	0.175
46	Sarc9371	Bone	Sarcoma	-	1.703	0.648
47	ES4	Bone	Ewing's Sarcoma	0<cn<8	1.766	0.628
48	ES6	Bone	Ewing's Sarcoma	0<cn<8	1.970	0.621
49	CHSA8926	Bone	Sarcoma	-	2.745	0.665
50	CAL-85-1	Breast	Adenocarcinoma	0<cn<8	-2.723	0.059
51	CAMA-1	Breast	Adenocarcinoma	0<cn<8	-2.291	0.128
52	HCC1395	Breast	Ductal carcinoma	-	-1.830	0.158
53	HCC1428	Breast	Adenocarcinoma	-	-1.687	0.100
54	HCC1569	Breast	Metastatic Carcinoma	0<cn<8	-1.489	0.183
55	HCC38	Breast	Ductal carcinoma	-	-1.422	0.215
56	MDA-MB-330	Breast	Carcinoma	-	-1.404	0.082
57	MDA-MB-361	Breast	Adenocarcinoma	0<cn<8	-1.306	0.126
58	SK-BR-3	Breast	Carcinoma	-	-1.143	0.286
59	EFM-192B	Breast	Ductal carcinoma	-	-0.929	0.261
60	OCUB-M	Breast	Carcinoma	0<cn<8	-0.822	0.080

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61	ZR-75-30	Breast	Ductal carcinoma	0<cn<8	-0.810	0.349
62	MDA-MB-453	Breast	Metastatic Carcinoma	-	-0.798	0.140
63	BT-474	Breast	Ductal carcinoma	0<cn<8	-0.725	0.197
64	MDA-MB-468	Breast	Adenocarcinoma	0<cn<8	-0.673	0.232
65	HCC70	Breast	Ductal carcinoma	-	-0.557	0.101
66	HCC1419	Breast	Ductal carcinoma	0<cn<8	-0.496	0.264
67	MB 157	Breast	Carcinoma	-	-0.347	0.309
68	EFM-192A	Breast	Carcinoma	-	-0.178	0.377
69	BT-549	Breast	Ductal carcinoma	-	-0.124	0.341
70	EFM-19	Breast	Ductal carcinoma	0<cn<8	0.241	0.504
71	MCF7	Breast	Adenocarcinoma	0<cn<8	0.246	0.312
72	SW527	Breast	Carcinoma	-	0.437	0.473
73	JIMT-1	Breast	Carcinoma	-	0.509	0.471
74	CAL-120	Breast	Adenocarcinoma	-	0.896	0.501
75	ZR-75-1	Breast	Ductal carcinoma	-	1.135	0.463
76	AU565	Breast	Adenocarcinoma	0<cn<8	1.321	0.583
77	MDA-MB-415	Breast	Adenocarcinoma	0<cn<8	1.353	0.596
78	HCC1806	Breast	Ductal carcinoma	-	1.487	0.624
79	UACC-893	Breast	Ductal carcinoma	0<cn<8	1.574	0.629
80	MDA-MB-231	Breast	Adenocarcinoma	0<cn<8	1.720	0.604
81	EFM-192C	Breast	Carcinoma	-	1.742	0.532
82	MDA-MB-436	Breast	Adenocarcinoma	-	1.997	0.659
83	CAL-51	Breast	Carcinoma	0<cn<8	2.021	0.637
84	Hs 578T	Breast	Ductal carcinoma	0<cn<8	2.036	0.695
85	T47D	Breast	Carcinoma	-	2.102	0.692
86	KPL-1	Breast	Carcinoma	-	2.152	0.671
87	HCC1937	Breast	Ductal carcinoma	0<cn<8	2.188	0.647
88	HCC1143	Breast	Ductal carcinoma	-	2.391	0.603
89	MDA-MB-175-VII	Breast	Ductal carcinoma	0<cn<8	2.660	0.731
90	BT-20	Breast	Ductal carcinoma	0<cn<8	3.146	0.794
91	MT-3	Breast	Carcinoma	-	3.296	0.812
92	HDQ-P1	Breast	Carcinoma	-	3.523	0.779
93	HCC1954	Breast	Ductal carcinoma	0<cn<8	3.615	0.847
94	MDA-MB-435S	Breast	Ductal carcinoma	-	4.533	0.881
95	DoTc2 4510	Cervix	Carcinoma	0<cn<8	-2.133	0.177
96	Ca Ski	Cervix	Squamous cell carcinoma	-	-1.777	0.237
97	SISO	Cervix	Adenocarcinoma	-	-1.126	0.246
98	MS751	Cervix	Carcinoma	-	-0.936	0.239
99	HT-3	Cervix	Carcinoma	-	-0.735	0.296
100	C-4 II	Cervix	Carcinoma	0<cn<8	-0.402	0.329
101	CAL-39	Cervix	Squamous cell carcinoma	-	-0.186	0.392
102	C-4 I	Cervix	Carcinoma	-	0.022	0.424
103	ME-180	Cervix	Carcinoma	0<cn<8	0.324	0.449
104	SKG-IIIb	Cervix	Squamous cell carcinoma	-	0.830	0.530
105	C-33 A	Cervix	Carcinoma	-	0.856	0.531
106	HeLa	Cervix	Adenocarcinoma	-	0.986	0.557
107	SiHa	Cervix	Squamous cell carcinoma	-	1.288	0.512
108	SKG-IIIa	Cervix	Carcinoma	0<cn<8	1.491	0.595
109	SW756	Cervix	Squamous cell carcinoma	0<cn<8	1.647	0.650
110	Hs 588.T	Cervix	Adenocarcinoma	-	2.125	0.712
111	OMC-1	Cervix	Squamous cell carcinoma	-	2.347	0.667
112	BOKU	Cervix	Squamous cell carcinoma	0<cn<8	3.601	0.713
113	8-MG-BA	CNS	Glioblastoma	0<cn<8	-2.886	0.045
114	SVG p12	CNS	Glioblastoma	-	-2.224	0.145
115	GI-1	CNS	Glioblastoma	0<cn<8	-2.053	0.086
116	no-10	CNS	Glioblastoma	-	-1.867	0.120
117	D-566MG	CNS	Glioblastoma	0<cn<8	-1.821	0.172
118	SNB75	CNS	Glioblastoma	0<cn<8	-1.700	0.325
119	SK-MG-1	CNS	Glioblastoma	0<cn<8	-1.654	0.110
120	M059K	CNS	Glioblastoma	-	-1.621	0.220
121	M059J	CNS	Glioblastoma	0<cn<8	-1.597	0.096
122	MOG-G-CCM	CNS	Astrocytoma	0<cn<8	-1.459	0.114
123	H4	CNS	Glioblastoma	0<cn<8	-1.318	0.125
124	KS-1	CNS	Glioblastoma	0<cn<8	-1.309	0.363
125	no-11	CNS	Glioblastoma	-	-1.175	0.144

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126	Daoy	CNS	Medulloblastoma	0<cn<8	-0.992	0.174
127	MOG-G-UVW	CNS	Astrocytoma	0<cn<8	-0.917	0.310
128	ONS-76	CNS	Medulloblastoma	0<cn<8	-0.837	0.334
129	LN-18	CNS	Glioblastoma	-	-0.814	0.294
130	YKG-1	CNS	Glioblastoma	-	-0.809	0.315
131	U-138 MG	CNS	Glioblastoma	-	-0.774	0.289
132	1321N1	CNS	Astrocytoma	-	-0.754	0.302
133	SF-295	CNS	Glioblastoma	0<cn<8	-0.575	0.374
134	D-247MG	CNS	Glioblastoma	0<cn<8	-0.500	0.329
135	D-542MG	CNS	Glioblastoma	0<cn<8	-0.483	0.364
136	KALS-1	CNS	Glioblastoma	0<cn<8	-0.448	0.384
137	D-336MG	CNS	Glioblastoma	0<cn<8	-0.423	0.366
138	Hs 683	CNS	Glioblastoma	-	-0.205	0.437
139	B2-17	CNS	Glioblastoma	0<cn<8	-0.151	0.460
140	D-392MG	CNS	Glioblastoma	0<cn<8	-0.132	0.414
141	D-423MG	CNS	Glioblastoma	0<cn<8	-0.081	0.468
142	T98G	CNS	Glioblastoma	0<cn<8	0.046	0.424
143	LNZTA3WT4	CNS	Glioblastoma	-	0.050	0.383
144	GAMG	CNS	Glioblastoma	0<cn<8	0.070	0.451
145	U373 MG	CNS	Glioblastoma	-	0.270	0.237
146	DK-MG	CNS	Glioblastoma	0<cn<8	0.436	0.561
147	SW 1783	CNS	Astrocytoma	-	0.489	0.363
148	U-251 MG	CNS	Glioblastoma	-	0.581	0.479
149	KG-1-C	CNS	Glioblastoma	-	0.720	0.428
150	LNZTA3WT11	CNS	Glioblastoma	-	0.750	0.528
151	LN-229	CNS	Glioblastoma	-	0.859	0.559
152	SF126	CNS	Glioblastoma	0<cn<8	1.128	0.527
153	YH-13	CNS	Glioblastoma	0<cn<8	1.144	0.568
154	GB-1	CNS	Glioblastoma	-	1.406	0.492
155	DBTRG-05MG	CNS	Glioblastoma	0<cn<8	1.498	0.610
156	Becker	CNS	Glioblastoma	0<cn<8	1.518	0.608
157	U-118 MG	CNS	Glioblastoma	0<cn<8	1.659	0.594
158	A172	CNS	Glioblastoma	0<cn<8	1.661	0.636
159	LN-405	CNS	Astrocytoma	0<cn<8	1.691	0.582
160	42-MG-BA	CNS	Glioblastoma	-	1.866	0.620
161	SF268	CNS	Glioblastoma	0<cn<8	1.881	0.622
162	KNS-42	CNS	Glioblastoma	0<cn<8	2.122	0.694
163	GOS-3	CNS	Astrocytoma	-	2.953	0.769
164	SNB-19	CNS	Glioblastoma	0<cn<8	3.372	0.762
165	D-502MG	CNS	Glioblastoma	0<cn<8	3.391	0.798
166	KNS-81-FD	CNS	Glioblastoma	0<cn<8	3.531	0.835
167	CCF-STTG1	CNS	Astrocytoma	0<cn<8	3.806	0.752
168	GMS-10	CNS	Glioblastoma	-	4.065	0.898
169	KINGS-1	CNS	Glioblastoma	0<cn<8	4.171	0.902
170	SW 1088	CNS	Astrocytoma	0<cn<8	4.974	1.108
171	D-263MG	CNS	Glioblastoma	0<cn<8	4.995	1.025
172	KYSE-50	Esophagus	Squamous cell carcinoma	-	-2.620	0.057
173	KYSE-270	Esophagus	Squamous cell carcinoma	-	-2.267	0.138
174	KYSE-30	Esophagus	Squamous cell carcinoma	-	-1.807	0.126
175	KYSE-150	Esophagus	Squamous cell carcinoma	0<cn<8	-1.799	0.216
176	OE21	Esophagus	Squamous cell carcinoma	-	-1.756	0.283
177	T.T	Esophagus	Squamous cell carcinoma	-	-1.740	0.224
178	KYSE-410	Esophagus	Squamous cell carcinoma	0<cn<8	-1.605	0.345
179	KYSE-450	Esophagus	Squamous cell carcinoma	0<cn<8	-1.470	0.235
180	T.Tn	Esophagus	Squamous cell carcinoma	-	-1.205	0.227
181	TE-10	Esophagus	Squamous cell carcinoma	0<cn<8	-0.969	0.360
182	KYSE-510	Esophagus	Squamous cell carcinoma	-	-0.852	0.297
183	KYSE-220	Esophagus	Squamous cell carcinoma	-	-0.848	0.301
184	TE-15	Esophagus	Squamous cell carcinoma	-	-0.694	0.418
185	TE-5	Esophagus	Squamous cell carcinoma	0<cn<8	-0.318	0.400
186	KYSE-180	Esophagus	Squamous cell carcinoma	-	-0.176	0.432
187	TE7	Esophagus	Adenocarcinoma	-	-0.053	0.388
188	OE33	Esophagus	Adenocarcinoma	0<cn<8	-0.042	0.308
189	KYSE-140	Esophagus	Squamous cell carcinoma	0<cn<8	0.008	0.360
190	TE-11	Esophagus	Squamous cell carcinoma	-	0.194	0.399

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191	COLO-680N	Esophagus	Squamous cell carcinoma	0<cn<8	0.309	0.439
192	KYSE-520	Esophagus	Squamous cell carcinoma	-	0.361	0.512
193	OE19	Esophagus	Adenocarcinoma	0<cn<8	0.544	0.452
194	TE-9	Esophagus	Squamous cell carcinoma	0<cn<8	0.616	0.419
195	HCE7	Esophagus	Adenocarcinoma	-	0.799	0.494
196	KYSE-70	Esophagus	Squamous cell carcinoma	0<cn<8	1.028	0.558
197	TE-12	Esophagus	Squamous cell carcinoma	0<cn<8	1.600	0.633
198	TE-1	Esophagus	Squamous cell carcinoma	0<cn<8	2.378	0.669
199	HCE-4	Esophagus	Squamous cell carcinoma	0<cn<8	3.764	0.878
200	TE-8	Esophagus	Squamous cell carcinoma	-	4.146	0.908
201	PCI-4A	Head & Neck	Squamous cell carcinoma	-	-3.544	0.075
202	BB30-HNC	Head & Neck	Squamous cell carcinoma	-	-2.763	0.325
203	PCI-6A	Head & Neck	Squamous cell carcinoma	-	-2.195	0.074
204	Ca9-22	Head & Neck	Carcinoma	0<cn<8	-2.169	0.082
205	SCC-9	Head & Neck	Squamous cell carcinoma	0<cn<8	-2.154	0.380
206	HSC-2	Head & Neck	Squamous cell carcinoma	-	-1.874	0.214
207	PCI-4B	Head & Neck	Carcinoma	-	-1.628	0.241
208	H3118	Head & Neck	Carcinoma	-	-1.469	0.244
209	KOSC-2 cl3-43	Head & Neck	Squamous cell carcinoma	-	-1.445	0.177
210	HSC-3	Head & Neck	Squamous cell carcinoma	0<cn<8	-1.425	0.342
211	CAL-33	Head & Neck	Squamous cell carcinoma	0<cn<8	-1.270	0.327
212	LB771-HNC	Head & Neck	Squamous cell carcinoma	-	-1.214	0.286
213	RPMI 2650	Head & Neck	Squamous cell carcinoma	0<cn<8	-1.064	0.338
214	SCC-4	Head & Neck	Squamous cell carcinoma	-	-0.938	0.224
215	BICR 78	Head & Neck	Squamous cell carcinoma	-	-0.859	0.364
216	JHU-011	Head & Neck	Squamous cell carcinoma	-	-0.854	0.280
217	BHY	Head & Neck	Squamous cell carcinoma	0<cn<8	-0.802	0.340
218	SCC-15	Head & Neck	Squamous cell carcinoma	0<cn<8	-0.796	0.400
219	KON	Head & Neck	Squamous cell carcinoma	-	-0.328	0.298
220	Detroit 562	Head & Neck	Carcinoma	-	-0.234	0.373
221	OSC-19	Head & Neck	Squamous cell carcinoma	-	-0.230	0.232
222	PCI-15	Head & Neck	Squamous cell carcinoma	-	-0.152	0.447
223	JHU-029	Head & Neck	Squamous cell carcinoma	-	-0.136	0.308
224	ACCS	Head & Neck	Adenoid cystic carcinoma	-	-0.081	0.312
225	FaDu	Head & Neck	Squamous cell carcinoma	-	0.434	0.511
226	SCC-25	Head & Neck	Squamous cell carcinoma	0<cn<8	0.435	0.557
227	BICR 10	Head & Neck	Squamous cell carcinoma	-	0.545	0.670
228	OSC-20	Head & Neck	Squamous cell carcinoma	-	0.651	0.526
229	BICR 31	Head & Neck	Squamous cell carcinoma	-	1.026	0.551
230	DOK	Head & Neck	Dysplastic oral keratinocyte	-	1.123	0.571
231	A253	Head & Neck	Mucoepidermoid carcinoma	0<cn<8	1.126	0.473
232	SAT	Head & Neck	Squamous cell carcinoma	-	1.496	0.527
233	PCI-15A	Head & Neck	Squamous cell carcinoma	-	1.502	0.637
234	PCI-38	Head & Neck	Squamous cell carcinoma	-	1.606	0.621
235	HO-1-N-1	Head & Neck	Squamous cell carcinoma	-	1.623	0.567
236	SACC-83	Head & Neck	Adenoid cystic carcinoma	-	2.158	0.700
237	HO-1-u-1	Head & Neck	Squamous cell carcinoma	-	2.259	0.711
238	CAL 27	Head & Neck	Squamous cell carcinoma	0<cn<8	2.419	0.772
239	ACC3	Head & Neck	Adenoid cystic carcinoma	-	2.425	0.719
240	SAS	Head & Neck	Squamous cell carcinoma	0<cn<8	2.615	0.795
241	SKN-3	Head & Neck	Squamous cell carcinoma	-	2.980	0.742
242	BICR 22	Head & Neck	Squamous cell carcinoma	-	4.008	0.777
243	JHU-022	Head & Neck	Squamous cell carcinoma	-	4.042	0.896
244	RKO	Intestine	Carcinoma	0<cn<8	-3.170	0.089
245	Caco-2	Intestine	Adenocarcinoma	-	-2.844	0.061
246	COLO 205	Intestine	Adenocarcinoma	0<cn<8	-2.482	0.039
247	Gp2D	Intestine	Adenocarcinoma	0<cn<8	-2.183	0.161
248	C170	Intestine	Carcinoma	-	-2.084	0.155
249	LS-411N	Intestine	Adenocarcinoma	0<cn<8	-2.061	0.033
250	HT-29	Intestine	Adenocarcinoma	0<cn<8	-1.923	0.156
251	HCT 116	Intestine	Carcinoma	0<cn<8	-1.856	0.207
252	HRT-18	Intestine	Adenocarcinoma	-	-1.715	0.139
253	WiDr	Intestine	Adenocarcinoma	-	-1.691	0.199
254	Hs 257.T	Intestine	Adenocarcinoma	-	-1.593	0.162
255	GP5d	Intestine	Adenocarcinoma	0<cn<8	-1.121	0.291

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256	HCT-15	Intestine	Adenocarcinoma	0<cn<8	-1.075	0.191
257	COLO 201	Intestine	Adenocarcinoma	-	-0.949	0.301
258	NCI-H747	Intestine	Adenocarcinoma	0<cn<8	-0.659	0.285
259	LS174T	Intestine	Adenocarcinoma	0<cn<8	-0.293	0.287
260	LoVo	Intestine	Adenocarcinoma	-	-0.166	0.220
261	HCC2998	Intestine	Adenocarcinoma	0<cn<8	-0.143	0.213
262	SW 48	Intestine	Adenocarcinoma	0<cn<8	-0.012	0.432
263	HUTU-80	Intestine	Adenocarcinoma	0<cn<8	0.087	0.383
264	SNU-C2B	Intestine	Adenocarcinoma	0<cn<8	0.218	0.431
265	HCT-8	Intestine	Adenocarcinoma	-	0.753	0.412
266	HT115	Intestine	Carcinoma	-	0.785	0.479
267	RCM-1	Intestine	Adenocarcinoma	0<cn<8	0.838	0.496
268	SW620	Intestine	Adenocarcinoma	0<cn<8	0.884	0.506
269	COLO-678	Intestine	Carcinoma	-	1.075	0.603
270	SW 1463	Intestine	Adenocarcinoma	0<cn<8	1.350	0.572
271	SW837	Intestine	Adenocarcinoma	0<cn<8	1.427	0.629
272	CaR-1	Intestine	Adenocarcinoma	0<cn<8	1.812	0.639
273	COLO 741	Intestine	Carcinoma	0<cn<8	2.649	0.716
274	OUMS-23	Intestine	Carcinoma	-	2.784	0.777
275	LS-1034	Intestine	Adenocarcinoma	0<cn<8	2.958	0.783
276	HT55	Intestine	Carcinoma	0<cn<8	3.134	0.752
277	LS-123	Intestine	Adenocarcinoma	-	3.333	0.758
278	SK-CO-1	Intestine	Adenocarcinoma	0<cn<8	3.818	0.892
279	RCC10RGB	Kidney	Carcinoma	0<cn<8	-3.572	0.283
280	A498	Kidney	Carcinoma	0<cn<8	-2.912	0.081
281	786-O	Kidney	Clear cell renal cell adenocarcinoma	0<cn<8	-2.360	0.183
282	Caki-1	Kidney	Clear cell renal cell adenocarcinoma	0<cn<8	-2.005	0.317
283	UO-31	Kidney	Carcinoma	-	-1.758	0.356
284	G-402	Kidney	Leiomyoblastoma	0<cn<8	-1.699	0.140
285	VMRC-RCZ	Kidney	Carcinoma	0<cn<8	-1.618	0.230
286	769-P	Kidney	Clear cell renal cell adenocarcinoma	-	-1.206	0.221
287	OS-RC-2	Kidney	Carcinoma	0<cn<8	-0.232	0.434
288	BFTC-909	Kidney	Transitional cell carcinoma	0<cn<8	-0.040	0.391
289	TK10	Kidney	Carcinoma	-	0.015	0.445
290	ACHN	Kidney	Adenocarcinoma	0<cn<8	0.079	0.422
291	HA7-RCC	Kidney	Carcinoma	0<cn<8	0.526	0.372
292	LB996-RCC	Kidney	Carcinoma	0<cn<8	0.905	0.547
293	KMRC-1	Kidney	Carcinoma	-	1.146	0.529
294	SW 13	Kidney	Adrenal cortex adenocarcinoma	-	1.282	0.537
295	LB1047-RCC	Kidney	Carcinoma	0<cn<8	1.754	0.638
296	SN-12C	Kidney	Carcinoma	0<cn<8	1.800	0.571
297	G-401	Kidney	Rhabdoid tumor	0<cn<8	2.085	0.672
298	LB2241-RCC	Kidney	Carcinoma	0<cn<8	2.473	0.618
299	BB65-RCC	Kidney	Carcinoma	0<cn<8	2.737	0.674
300	RXF393	Kidney	Carcinoma	0<cn<8	3.902	0.768
301	A704	Kidney	Carcinoma	0<cn<8	5.386	0.929
302	SNU-398	Liver	Carcinoma	-	-1.812	0.233
303	SNU-387	Liver	Carcinoma	0<cn<8	-1.676	0.287
304	HuH-7	Liver	Carcinoma	0<cn<8	-1.669	0.098
305	HuCCT1	Liver	Extrahepatic cholangiocarcinoma	0<cn<8	-1.641	0.282
306	Hep 3B2.1-7	Liver	Carcinoma	-	-1.513	0.229
307	JHH-1	Liver	Carcinoma	-	-1.489	0.278
308	SNU-182	Liver	Carcinoma	-	-1.276	0.205
309	JHH-6	Liver	Carcinoma	-	-0.452	0.413
310	SNU-423	Liver	Carcinoma	0<cn<8	-0.303	0.345
311	HLE	Liver	Carcinoma	0<cn<8	-0.104	0.329
312	SK-HEP-1	Liver	Adenocarcinoma	0<cn<8	0.124	0.422
313	JHH-7	Liver	Carcinoma	-	0.218	0.429
314	C3A	Liver	Carcinoma	0<cn<8	0.317	0.493
315	SNU-449	Liver	Carcinoma	-	0.733	0.455
316	JHH-4	Liver	Carcinoma	-	1.137	0.547
317	Hep G2	Liver	Carcinoma	-	1.300	0.572
318	HLF	Liver	Carcinoma	-	1.308	0.600
319	EGI-1	Liver	Extrahepatic cholangiocarcinoma	0<cn<8	1.760	0.548
320	PLC/PRF/5	Liver	Carcinoma	0<cn<8	1.940	0.681

#	Cell_Line	Organ	Histology	MYCN Copy Number	LN_IC50	EMax
321	huH-1	Liver	Carcinoma	-	4.448	0.868
322	HOP-62	Lung	Adenocarcinoma	0<cn<8	-2.110	0.171
323	SBC-3	Lung	Small cell carcinoma	-	-2.005	0.093
324	IA-LM	Lung	Large cell carcinoma	0<cn<8	-1.831	0.230
325	NCI-H727	Lung	Carcinoma	0<cn<8	-1.584	0.351
326	UMC-11	Lung	Carcinoma	0<cn<8	-1.479	0.023
327	H2052	Lung	Mesothelioma	**cn ≥ 8**	-1.469	0.209
328	DMS 273	Lung	Small cell carcinoma	0<cn<8	-1.051	0.233
329	LC-2-ad	Lung	Adenocarcinoma	-	-0.857	0.358
330	H2731	Lung	Mesothelioma	-	-0.766	0.201
331	LXF-289	Lung	Adenocarcinoma	-	-0.219	0.316
332	SBC-5	Lung	Small cell carcinoma	0<cn<8	-0.211	0.305
333	NCI-H157	Lung	Squamous cell carcinoma	0<cn<8	-0.106	0.316
334	H2369	Lung	Mesothelioma	-	0.201	0.461
335	H2722	Lung	Mesothelioma	-	0.258	0.500
336	Lu-135	Lung	Small cell carcinoma	-	0.261	0.380
337	H2461	Lung	Mesothelioma	-	0.275	0.349
338	H2595	Lung	Mesothelioma	-	0.295	0.446
339	SW 1271	Lung	Carcinoma	-	0.339	0.416
340	H292	Lung	Pulmonary mucoepidermoid carcinoma	0<cn<8	0.517	0.455
341	H2804	Lung	Mesothelioma	-	0.577	0.475
342	H2803	Lung	Mesothelioma	-	0.626	0.528
343	H2596	Lung	Mesothelioma	-	0.673	0.456
344	NCI-H196	Lung	Small cell carcinoma	-	0.693	0.475
345	Calu-6	Lung	Adenocarcinoma	0<cn<8	0.699	0.441
346	H2591	Lung	Mesothelioma	-	0.749	0.488
347	NCI-H1355	Lung	Adenocarcinoma	0<cn<8	0.980	0.528
348	IST-MES1	Lung	Mesothelioma	-	1.031	0.506
349	H2795	Lung	Mesothelioma	-	1.254	0.575
350	NCI-H2126	Lung	Adenocarcinoma	0<cn<8	1.262	0.589
351	H2373	Lung	Mesothelioma	-	1.652	0.577
352	DMS 53	Lung	Small cell carcinoma	-	1.775	0.645
353	H28	Lung	Mesothelioma	0<cn<8	1.822	0.603
354	H290	Lung	Mesothelioma	-	1.901	0.620
355	NCI-H2452	Lung	Mesothelioma	0<cn<8	2.242	0.663
356	MPP-89	Lung	Mesothelioma	0<cn<8	2.426	0.707
357	EKVX	Lung	Adenocarcinoma	-	2.827	0.694
358	H2869	Lung	Mesothelioma	-	2.940	0.676
359	NCI-H841	Lung	Small cell carcinoma	-	3.137	0.782
360	NCI-H2286	Lung	Carcinoma	-	3.227	0.682
361	H513	Lung	Mesothelioma	-	3.650	0.861
362	COR-L 105	Lung:NSCLC	Adenocarcinoma	0<cn<8	-2.297	0.264
363	LCLC-97TM1	Lung:NSCLC	Large cell carcinoma	0<cn<8	-2.091	0.144
364	BEN	Lung:NSCLC	Carcinoma	0<cn<8	-1.965	0.071
365	VMRC-LCP	Lung:NSCLC	Squamous cell carcinoma	**cn ≥ 8**	-1.788	0.023
366	NCI-H650	Lung:NSCLC	Carcinoma	0<cn<8	-1.730	0.169
367	LU65A	Lung:NSCLC	Giant cell carcinoma	-	-1.578	0.134
368	HCC-44	Lung:NSCLC	Carcinoma	-	-1.470	0.227
369	LU99C	Lung:NSCLC	Giant cell carcinoma	-	-1.300	0.073
370	SK-MES-1	Lung:NSCLC	Squamous cell carcinoma	0<cn<8	-1.284	0.287
371	NCI-H2009	Lung:NSCLC	Adenocarcinoma	0<cn<8	-1.237	0.197
372	NCI-H1437	Lung:NSCLC	Adenocarcinoma	0<cn<8	-1.183	0.325
373	NCI-H522	Lung:NSCLC	Carcinoma	0<cn<8	-1.161	0.186
374	NCI-H810	Lung:NSCLC	Large cell carcinoma	-	-1.134	0.053
375	NCI-H2342	Lung:NSCLC	Adenocarcinoma	0<cn<8	-1.034	0.171
376	LU99B	Lung:NSCLC	Giant cell carcinoma	-	-0.934	0.268
377	NCI-H1944	Lung:NSCLC	Carcinoma	-	-0.884	0.405
378	LU65C	Lung:NSCLC	Giant cell carcinoma	-	-0.823	0.229
379	NCI-H2073	Lung:NSCLC	Adenocarcinoma	-	-0.796	0.355
380	LCLC-103H	Lung:NSCLC	Large cell carcinoma	0<cn<8	-0.627	0.353
381	NCI-H460	Lung:NSCLC	Large cell carcinoma	0<cn<8	-0.627	0.268
382	NCI-H596	Lung:NSCLC	Squamous cell carcinoma	0<cn<8	-0.550	0.431
383	273T	Lung:NSCLC	Squamous cell carcinoma	-	-0.484	0.366
384	NCI-H1299	Lung:NSCLC	Large cell carcinoma	0<cn<8	-0.415	0.323
385	NCI-H3122	Lung:NSCLC	Adenocarcinoma	-	-0.363	0.274

#	Cell_Line	Organ	Histology	MYCN Copy Number	LN_IC50	EMax
386	NCI-H1755	Lung:NSCLC	Adenocarcinoma	0<cn<8	-0.243	0.348
387	NCI-H2122	Lung:NSCLC	Adenocarcinoma	-	-0.214	0.283
388	NCI-H1650	Lung:NSCLC	Carcinoma	-	-0.145	0.423
389	NCI-H2030	Lung:NSCLC	Adenocarcinoma	0<cn<8	-0.130	0.450
390	ABC-1	Lung:NSCLC	Adenocarcinoma	0<cn<8	-0.047	0.403
391	201T	Lung:NSCLC	Adenocarcinoma	-	0.090	0.375
392	Calu-3	Lung:NSCLC	Adenocarcinoma	-	0.092	0.452
393	SK-LU-1	Lung:NSCLC	Adenocarcinoma	0<cn<8	0.186	0.376
394	NCI-H2347	Lung:NSCLC	Carcinoma	0<cn<8	0.236	0.469
395	NCI-H2085	Lung:NSCLC	Carcinoma	-	0.306	0.375
396	LC-1 sq	Lung:NSCLC	Squamous cell carcinoma	-	0.363	0.474
397	HCC-366	Lung:NSCLC	Carcinoma	-	0.397	0.278
398	NCI-H520	Lung:NSCLC	Squamous cell carcinoma	0<cn<8	0.442	0.356
399	NCI-H322	Lung:NSCLC	Carcinoma	-	0.450	0.483
400	NCI-H1693	Lung:NSCLC	Adenocarcinoma	0<cn<8	0.505	0.522
401	Calu-1	Lung:NSCLC	Carcinoma	0<cn<8	0.569	0.483
402	NCI-H2110	Lung:NSCLC	Carcinoma	-	0.578	0.491
403	LU99A	Lung:NSCLC	Giant cell carcinoma	0<cn<8	0.618	0.186
404	A549	Lung:NSCLC	Carcinoma	0<cn<8	0.679	0.477
405	NCI-H2023	Lung:NSCLC	Carcinoma	-	0.760	0.507
406	NCI-H1734	Lung:NSCLC	Adenocarcinoma	0<cn<8	0.783	0.466
407	NCI-H1568	Lung:NSCLC	Carcinoma	-	0.832	0.534
408	NCI-H1975	Lung:NSCLC	Adenocarcinoma	0<cn<8	0.938	0.545
409	NCI-H441	Lung:NSCLC	Carcinoma	0<cn<8	1.008	0.494
410	ChaGo-K-1	Lung:NSCLC	Carcinoma	-	1.009	0.526
411	HCC-15	Lung:NSCLC	Carcinoma	-	1.034	0.532
412	NCI-H2228	Lung:NSCLC	Adenocarcinoma	-	1.159	0.587
413	NCI-H358	Lung:NSCLC	Carcinoma	0<cn<8	1.174	0.554
414	HARA	Lung:NSCLC	Squamous cell carcinoma	-	1.187	0.587
415	NCI-H1915	Lung:NSCLC	Carcinoma	-	1.226	0.540
416	NCI-H2405	Lung:NSCLC	Adenocarcinoma	0<cn<8	1.240	0.493
417	DV-90	Lung:NSCLC	Adenocarcinoma	0<cn<8	1.388	0.593
418	NCI-H1651	Lung:NSCLC	Adenocarcinoma	-	1.503	0.528
419	NCI-H1648	Lung:NSCLC	Adenocarcinoma	0<cn<8	1.506	0.601
420	NCI-H838	Lung:NSCLC	Carcinoma	0<cn<8	1.578	0.514
421	NCI-H661	Lung:NSCLC	Large cell carcinoma	0<cn<8	1.595	0.626
422	PC-14	Lung:NSCLC	Adenocarcinoma	0<cn<8	1.637	0.606
423	COR-L23	Lung:NSCLC	Large cell carcinoma	0<cn<8	1.681	0.678
424	PC-3 [JPC-3]	Lung:NSCLC	Adenocarcinoma	-	1.723	0.596
425	NCI-H2172	Lung:NSCLC	Carcinoma	-	1.723	0.597
426	NCI-H1435	Lung:NSCLC	Carcinoma	-	1.830	0.638
427	NCI-H1993	Lung:NSCLC	Adenocarcinoma	0<cn<8	1.880	0.614
428	RERF-LC-MS	Lung:NSCLC	Adenocarcinoma	0<cn<8	1.917	0.643
429	NCI-H1793	Lung:NSCLC	Adenocarcinoma	0<cn<8	1.929	0.635
430	HOP92	Lung:NSCLC	Large cell carcinoma	0<cn<8	2.012	0.683
431	NCI-H2170	Lung:NSCLC	Squamous cell carcinoma	0<cn<8	2.091	0.590
432	NCI-H1703	Lung:NSCLC	Squamous cell carcinoma	0<cn<8	2.132	0.682
433	LK-2	Lung:NSCLC	Squamous cell carcinoma	-	2.140	0.628
434	SW 1573	Lung:NSCLC	Adenocarcinoma	0<cn<8	2.189	0.704
435	CAL-12T	Lung:NSCLC	Carcinoma	0<cn<8	2.205	0.722
436	NCI-H1792	Lung:NSCLC	Adenocarcinoma	0<cn<8	2.367	0.664
437	NCI-H1781	Lung:NSCLC	Adenocarcinoma	-	2.701	0.755
438	SW 900	Lung:NSCLC	Squamous cell carcinoma	-	2.920	0.789
439	HCC-827	Lung:NSCLC	Carcinoma	-	3.042	0.810
440	RERF-LC-Sq1	Lung:NSCLC	Squamous cell carcinoma	-	3.572	0.862
441	NCI-H1623	Lung:NSCLC	Adenocarcinoma	0<cn<8	3.821	0.867
442	NCI-H1563	Lung:NSCLC	Adenocarcinoma	-	4.073	0.919
443	SW982	Misc	Sarcoma	0<cn<8	-1.756	0.341
444	SK-LMS-1	Misc	Sarcoma	0<cn<8	-1.705	0.110
445	SW872	Misc	Liposarcoma	0<cn<8	-1.055	0.134
446	VA-ES-BJ	Misc	Sarcoma	0<cn<8	-0.395	0.368
447	SW684	Misc	Fibrosarcoma	0<cn<8	0.681	0.498
448	MFH-ino	Misc	Malignant fibrous histiocytoma	0<cn<8	1.731	0.644
449	BeWo	Miscellaneous	Choriocarcinoma	-	-1.480	0.093
450	Hs 633T	Miscellaneous	Fibrosarcoma	-	-1.375	0.181

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451	HT 1080	Miscellaneous	Fibrosarcoma	0<cn<8	0.584	0.462
452	GCT	Miscellaneous	Malignant fibrous histiocytoma	0<cn<8	0.840	0.505
453	SK-UT-1	Muscle	Leiomyosarcoma	-	-1.573	0.201
454	A-204	Muscle	Rhabdomyosarcoma	0<cn<8	-1.503	0.190
455	RH-30	Muscle	Rhabdomyosarcoma	-	-1.414	0.156
456	RD	Muscle	Rhabdomyosarcoma	0<cn<8	-0.344	0.227
457	OVTOKO	Ovary	Adenocarcinoma	-	-3.599	0.146
458	IGROV-1	Ovary	Carcinoma	0<cn<8	-3.390	0.078
459	FU-OV-1	Ovary	Carcinoma	-	-2.114	0.216
460	KGN	Ovary	Granulosa cell tumor	0<cn<8	-1.907	0.247
461	OC-314	Ovary	Carcinoma	-	-1.906	0.188
462	SK-OV-3	Ovary	Adenocarcinoma	0<cn<8	-1.344	0.337
463	OVMIU	Ovary	Adenocarcinoma	-	-1.213	0.159
464	PA-1	Ovary	Teratocarcinoma	0<cn<8	-0.812	0.037
465	EFO-27	Ovary	Adenocarcinoma	0<cn<8	-0.718	0.383
466	OVCAR-8	Ovary	Carcinoma	0<cn<8	-0.646	0.217
467	MDA-H2774	Ovary	Carcinoma	-	-0.475	0.252
468	KURAMOCHI	Ovary	Carcinoma	0<cn<8	-0.471	0.420
469	SW 626	Ovary	Adenocarcinoma	-	-0.444	0.406
470	RMG-I	Ovary	Mesonephroid adenocarcinoma	0<cn<8	-0.432	0.372
471	OVISE	Ovary	Adenocarcinoma	-	-0.419	0.329
472	EFO-21	Ovary	Carcinoma	-	-0.395	0.395
473	NCI/ADR-RES	Ovary	Carcinoma	0<cn<8	-0.036	0.399
474	NIH:OVCAR-3	Ovary	Adenocarcinoma	0<cn<8	0.027	0.301
475	OVCAR-4	Ovary	Carcinoma	0<cn<8	0.040	0.384
476	A2780cis	Ovary	Carcinoma	-	0.088	0.479
477	TOV-21G	Ovary	Adenocarcinoma	-	0.139	0.383
478	OV-90	Ovary	Adenocarcinoma	-	0.441	0.439
479	OAW42	Ovary	Carcinoma	0<cn<8	0.468	0.526
480	OVCAR-5	Ovary	Carcinoma	0<cn<8	0.865	0.542
481	OVSAYO	Ovary	Adenocarcinoma	-	1.119	0.505
482	RKN	Ovary	Myoma	-	1.205	0.579
483	MCAS	Ovary	Adenocarcinoma	-	1.314	0.552
484	TYK-nu	Ovary	Carcinoma	-	2.290	0.648
485	OAW28	Ovary	Carcinoma	-	2.338	0.698
486	A2780ADR	Ovary	Carcinoma	-	3.357	0.696
487	OVKATE	Ovary	Adenocarcinoma	-	3.664	0.887
488	SUIT-2	Pancreas	Adenocarcinoma	-	-2.202	0.184
489	BxPC-3	Pancreas	Adenocarcinoma	0<cn<8	-2.183	0.254
490	PL18	Pancreas	Carcinoma	-	-0.772	0.304
491	CFPAC-1	Pancreas	Adenocarcinoma	0<cn<8	-0.704	0.343
492	MZ1-PC	Pancreas	Carcinoma	-	-0.624	0.353
493	Panc 08.13	Pancreas	Adenocarcinoma	0<cn<8	-0.612	0.141
494	SU.86.86	Pancreas	Adenocarcinoma	-	-0.559	0.403
495	KP-1NL	Pancreas	Carcinoma	-	-0.549	0.300
496	PA-TU-8988T	Pancreas	Adenocarcinoma	-	-0.513	0.313
497	MIA PaCa-2	Pancreas	Adenocarcinoma	-	-0.424	0.262
498	Panc 02.03	Pancreas	Adenocarcinoma	-	-0.249	0.385
499	HUP-T4	Pancreas	Carcinoma	0<cn<8	-0.123	0.373
500	Panc 10.05	Pancreas	Adenocarcinoma	0<cn<8	-0.122	0.351
501	HPAF-II	Pancreas	Adenocarcinoma	0<cn<8	-0.043	0.504
502	KP-1N	Pancreas	Carcinoma	-	0.144	0.337
503	A13A	Pancreas	Carcinoma	-	0.338	0.400
504	Hs 766T	Pancreas	Adenocarcinoma	-	0.472	0.477
505	1108-MP2	Pancreas	Adenocarcinoma	-	0.800	0.543
506	617-MP17	Pancreas	Adenosquamous carcinoma	-	0.930	0.496
507	PL45	Pancreas	Adenocarcinoma	-	1.250	0.547
508	Panc 04.03	Pancreas	Adenocarcinoma	-	1.301	0.570
509	950-MP5	Pancreas	IPMN	-	1.391	0.639
510	609MP9	Pancreas	Adenocarcinoma	-	1.428	0.597
511	SW 1990	Pancreas	Adenocarcinoma	0<cn<8	1.454	0.576
512	HUP-T3	Pancreas	Carcinoma	0<cn<8	1.460	0.620
513	PL4	Pancreas	Carcinoma	-	1.957	0.732
514	PA-TU-8902	Pancreas	Adenocarcinoma	-	2.104	0.672
515	Panc 03.27	Pancreas	Adenocarcinoma	0<cn<8	2.222	0.728

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516	AsPC-1	Pancreas	Adenocarcinoma	0<cn<8	2.464	0.731
517	YAPC	Pancreas	Carcinoma	0<cn<8	2.550	0.747
518	PANC-1	Pancreas	Adenocarcinoma	-	2.595	0.603
519	DAN-G	Pancreas	Adenocarcinoma	-	2.798	0.782
520	Capan-2	Pancreas	Adenocarcinoma	0<cn<8	3.905	0.588
521	PSN1	Pancreas	Carcinoma	0<cn<8	5.655	1.118
522	NB69	PNS	Neuroblastoma	**cn ≥ 8**	-2.197	0.071
523	CHP-212	PNS	Neuroblastoma	**cn ≥ 8**	-2.079	0.056
524	ACN	PNS	Neuroblastoma	0<cn<8	-1.956	0.224
525	NB16	PNS	Neuroblastoma	0<cn<8	-1.256	0.170
526	BE(2)-C	PNS	Neuroblastoma	-	-1.092	0.075
527	MC-IXC	PNS	Neuroepithelia	0<cn<8	-1.021	0.029
528	SK-N-SH	PNS	Neuroblastoma	0<cn<8	-0.931	0.245
529	NB12	PNS	Neuroblastoma	0<cn<8	-0.342	0.266
530	GI-ME-N	PNS	Neuroblastoma	0<cn<8	0.281	0.459
531	SK-N-AS	PNS	Neuroblastoma	0<cn<8	1.485	0.598
532	BPH-1	Prostate	Benign	0<cn<8	-3.418	0.058
533	DU 145	Prostate	Adenocarcinoma	0<cn<8	-0.088	0.413
534	22RV1	Prostate	Adenocarcinoma	0<cn<8	0.030	0.545
535	PC-3	Prostate	Adenocarcinoma	0<cn<8	2.546	0.682
536	HCE-T	Sinus	Squamous cell carcinoma	0<cn<8	1.376	0.546
537	COLO-679	Skin	Melanoma	0<cn<8	-2.967	0.092
538	MEL-HO	Skin	Melanoma	0<cn<8	-2.461	0.131
539	MGH-ST-1	Skin	Melanoma	-	-2.235	0.084
540	WM35	Skin	Melanoma	-	-2.012	0.072
541	CHL-1	Skin	Melanoma	0<cn<8	-2.003	0.171
542	451Lu	Skin	Melanoma	-	-1.932	0.191
543	MGH-PO-1	Skin	Melanoma	-	-1.918	0.115
544	MGH-BO-1	Skin	Melanoma	-	-1.913	0.224
545	SK-MEL-24	Skin	Melanoma	0<cn<8	-1.913	0.202
546	MGH-TH-1	Skin	Melanoma	-	-1.834	0.322
547	SH-4	Skin	Melanoma	0<cn<8	-1.831	0.239
548	MM608	Skin	Melanoma	-	-1.767	0.043
549	SK-MEL-30	Skin	Melanoma	0<cn<8	-1.734	0.194
550	IPC-298	Skin	Melanoma	0<cn<8	-1.703	0.178
551	COLO 857	Skin	Melanoma	-	-1.657	0.087
552	MGH-SW-1	Skin	Melanoma	-	-1.628	0.062
553	WM1158	Skin	Melanoma	-	-1.581	0.081
554	WM793B	Skin	Melanoma	-	-1.501	0.311
555	K4	Skin	Melanoma	-	-1.437	0.141
556	M-14	Skin	Melanoma	0<cn<8	-1.402	0.088
557	MZ7-mel	Skin	Melanoma	0<cn<8	-1.383	0.079
558	WM164	Skin	Melanoma	-	-1.381	0.191
559	A373-C6	Skin	Melanoma	-	-1.327	0.253
560	A375.S2	Skin	Melanoma	-	-1.321	0.067
561	IGR-1	Skin	Melanoma	0<cn<8	-1.293	0.149
562	A101D	Skin	Melanoma	0<cn<8	-0.862	0.398
563	Hs 940.T	Skin	Melanoma	-	-0.861	0.343
564	WM278	Skin	Melanoma	-	-0.707	0.215
565	MGH-MC-1	Skin	Melanoma	-	-0.641	0.368
566	HT-144	Skin	Melanoma	0<cn<8	-0.575	0.381
567	MGH-BA-1	Skin	Melanoma	-	-0.372	0.226
568	IST-MEL1	Skin	Melanoma	-	-0.360	0.412
569	BU-ML	Skin	Melanoma	-	-0.342	0.358
570	UISO-MCC 1	Skin	Merkel cell carcinoma	-	-0.245	0.284
571	COLO-849	Skin	Melanoma	-	-0.217	0.381
572	COLO 853	Skin	Melanoma	-	-0.187	0.241
573	IGR-37	Skin	Melanoma	-	-0.077	0.370
574	Hs 939.T	Skin	Melanoma	-	0.067	0.535
575	1205Lu	Skin	Melanoma	-	0.175	0.430
576	IGR-39	Skin	Melanoma	-	0.230	0.449
577	NAE	Skin	Melanoma	-	0.239	0.413
578	WM1552C	Skin	Melanoma	-	0.305	0.430
579	K19	Skin	Melanoma	-	0.383	0.463
580	CP50-MEL-B	Skin	Melanoma	0<cn<8	0.384	0.479

#	Cell_Line	Organ	Histology	MYCN Copy Number	LN_IC50	EMax
581	UACC-62	Skin	Melanoma	0<cn<8	0.506	0.475
582	WM 266-4	Skin	Melanoma	-	0.515	0.476
583	RVH-421	Skin	Melanoma	0<cn<8	0.540	0.483
584	LB373-MEL-D	Skin	Melanoma	0<cn<8	0.578	0.491
585	SK-MEL-3	Skin	Melanoma	-	0.579	0.481
586	MEL-JUSO	Skin	Melanoma	0<cn<8	0.662	0.502
587	DJM-1	Skin	Malignant trichilemmal cyst	0<cn<8	0.664	0.450
588	COLO-829	Skin	Melanoma	0<cn<8	0.678	0.530
589	MM455	Skin	Melanoma	-	0.926	0.487
590	MMAC-SF	Skin	Melanoma	0<cn<8	0.931	0.509
591	MGH-MCC-1	Skin	Merkel cell carcinoma	-	1.029	0.527
592	UACC903	Skin	Melanoma	-	1.080	0.443
593	Hs 944.T	Skin	Melanoma	-	1.081	0.555
594	HMVII	Skin	Melanoma	0<cn<8	1.119	0.564
595	SK-MEL-5	Skin	Melanoma	0<cn<8	1.164	0.550
596	COLO-818	Skin	Melanoma	-	1.224	0.612
597	MCC13	Skin	Merkel cell carcinoma	-	1.306	0.608
598	SK-MEL-119	Skin	Melanoma	-	1.379	0.582
599	UACC-257	Skin	Melanoma	0<cn<8	1.502	0.575
600	SK-MEL-131	Skin	Melanoma	-	1.540	0.618
601	K2	Skin	Melanoma	-	1.566	0.580
602	A-375	Skin	Melanoma	0<cn<8	1.579	0.644
603	GAK	Skin	Melanoma	0<cn<8	1.805	0.647
604	MZ2-MEL.	Skin	Melanoma	0<cn<8	1.877	0.516
605	CP66-MEL	Skin	Melanoma	0<cn<8	1.878	0.623
606	A2058	Skin	Melanoma	0<cn<8	2.038	0.584
607	WM239A	Skin	Melanoma	-	2.117	0.659
608	WM902B	Skin	Melanoma	-	2.166	0.634
609	MCC26	Skin	Merkel cell carcinoma	-	2.417	0.691
610	LB2518-MEL	Skin	Melanoma	0<cn<8	2.598	0.735
611	SK-MEL-37	Skin	Melanoma	-	2.852	0.798
612	G-MEL	Skin	Melanoma	-	3.063	0.693
613	K8	Skin	Melanoma	-	3.101	0.785
614	MEWO	Skin	Melanoma	0<cn<8	3.395	0.878
615	SK-MEL-28	Skin	Melanoma	0<cn<8	3.478	0.768
616	WM-115	Skin	Melanoma	0<cn<8	4.281	0.872
617	COLO-800	Skin	Melanoma	-	4.496	0.948
618	C32	Skin	Melanoma	0<cn<8	5.438	1.139
619	HGC-27	Stomach	Adenocarcinoma	0<cn<8	-2.178	0.050
620	IM-95m	Stomach	Adenocarcinoma	-	-1.777	0.126
621	MKN74	Stomach	Adenocarcinoma	-	-1.756	0.215
622	IM-95	Stomach	Adenocarcinoma	-	-1.614	0.210
623	GT3TKB	Stomach	Adenocarcinoma	0<cn<8	-1.327	0.266
624	AGS	Stomach	Adenocarcinoma	0<cn<8	-0.400	0.298
625	MKN1	Stomach	Squamous cell carcinoma	0<cn<8	-0.250	0.325
626	ECC12	Stomach	Adenocarcinoma	-	-0.056	0.447
627	MKN45	Stomach	Adenocarcinoma	-	0.086	0.401
628	GCIY	Stomach	Adenocarcinoma	0<cn<8	0.342	0.456
629	MKN28	Stomach	Adenocarcinoma	0<cn<8	0.463	0.473
630	GTL-16	Stomach	Carcinoma	-	0.541	0.451
631	23132/87	Stomach	Adenocarcinoma	0<cn<8	1.021	0.484
632	TMK-1	Stomach	Adenocarcinoma	-	1.067	0.577
633	NUGC-3	Stomach	Carcinoma	0<cn<8	2.114	0.629
634	AZ-521	Stomach	Adenocarcinoma	-	3.396	0.783
635	NCI-N87	Stomach	Adenocarcinoma	0<cn<8	3.638	0.842
636	NUGC-4	Stomach	Adenocarcinoma	-	3.698	0.859
637	NTERA-S-cl-D1	Testes	Germ cell tumor	-	-2.660	0.065
638	CGTH-W-1	Thyroid	Follicular carcinoma	0<cn<8	-2.420	0.108
639	KMH-2	Thyroid	Anaplastic carcinoma	-	-1.796	0.125
640	CAL-62	Thyroid	Anaplastic carcinoma	0<cn<8	-1.456	0.113
641	TT2609-C02	Thyroid	Follicular carcinoma	-	-1.380	0.297
642	8305C	Thyroid	Anaplastic carcinoma	0<cn<8	-1.334	0.159
643	HTC-C3	Thyroid	Carcinoma	0<cn<8	-0.827	0.396
644	B-CPAP	Thyroid	Anaplastic carcinoma	0<cn<8	-0.729	0.211
645	FTC-238	Thyroid	Follicular carcinoma	-	-0.438	0.277

#	Cell_Line	Organ	Histology	MYCN Copy Number	LN_IC50	EMax
646	ML-1	Thyroid	Follicular carcinoma	-	-0.345	0.420
647	8505C	Thyroid	Anaplastic carcinoma	-	-0.274	0.314
648	ASH-3	Thyroid	Anaplastic carcinoma	-	0.071	0.364
649	BHT-101	Thyroid	Anaplastic carcinoma	0<cn<8	0.471	0.469
650	K5	Thyroid	Follicular carcinoma	0<cn<8	0.930	0.408
651	S-117	Thyroid	Sarcoma	-	1.478	0.482
652	RO82-W-1	Thyroid	Follicular carcinoma	-	2.323	0.667
653	FTC-133	Thyroid	Follicular carcinoma	-	2.658	0.762
654	TT	Thyroid	Medullary carcinoma	0<cn<8	4.383	0.919
655	A388	Unknown	Carcinoma	0<cn<8	-1.694	0.320
656	Ishikawa	Uterus	Adenocarcinoma	-	-1.636	0.090
657	KLE	Uterus	Adenocarcinoma	0<cn<8	-1.093	0.309
658	MFE-319	Uterus	Adenocarcinoma	-	-0.796	0.284
659	MES-SA	Uterus	Sarcoma	0<cn<8	-0.754	0.282
660	HEC-1	Uterus	Adenocarcinoma	-	-0.369	0.277
661	MES-SA/Dx-5	Uterus	Sarcoma	-	-0.231	0.267
662	SNG-M	Uterus	Adenocarcinoma	0<cn<8	0.017	0.359
663	JEG-3	Uterus	Choriocarcinoma	-	0.069	0.276
664	ESS-1	Uterus	Sarcoma	0<cn<8	0.147	0.451
665	RL95-2	Uterus	Squamous cell carcinoma	0<cn<8	0.484	0.431
666	MFE-296	Uterus	Adenocarcinoma	0<cn<8	0.614	0.494
667	Ishikawa (Heraklio) 02 ER-	Uterus	Adenocarcinoma	-	0.703	0.497
668	EFE-184	Uterus	Carcinoma	0<cn<8	1.142	0.451
669	MFE-280	Uterus	Adenocarcinoma	0<cn<8	1.687	0.601
670	AN3CA	Uterus	Adenocarcinoma	0<cn<8	3.827	0.759
671	EN	Uterus	Carcinoma	-	4.437	0.923
672	SW954	Vulva	Squamous cell carcinoma	0<cn<8	-0.359	0.452
673	SW962	Vulva	Squamous cell carcinoma	-	3.425	0.638

Supplementary Table S2. GI_{50} and E_{max} for multiple neuroblastoma cell lines treated with active or inactive BET inhibitors.

	BE(2)-C		Kelly		LAN-1		NGP		SH-SY5Y		SK-N-AS	
	GI_{50} (µM)	E_{max} (%)	GI_{50} (µM)	E_{max} (%)	GI_{50} (µM)	E_{max} (%)	GI_{50} (µM)	E_{max} (%)	GI_{50} (µM)	E_{max} (%)	GI_{50} (µM)	E_{max} (%)
JQ1R	ND	50	15.50	70	14.50	62	ND	44	ND	49	ND	41
JQ1S	0.43	87	0.56	96	0.59	93	ND	36	1.02	77	5.60	63
I-BET	0.78	82	3.71	68	1.78	75	ND	32	2.24	67	ND	41
I-BET151	1.95	83	5.62	72	4.37	75	ND	45	11.22	51	ND	24

Supplementary Table S3. Genes differentially expressed in JQ1 vs Vehicle treated neuroblastoma

#	JQ1_ vs_CT	GeneSymbol	GeneTitle	SNR	Pvalue	FDR (BH)	log2(Fold Change)	CT_ Mean	CT_ Std	JQ1_ Mean	JQ1_ Std
1	Down	GTF3C6	general transcription factor IIIC, polypeptide 6, alpha 35kDa	-4.08	1.2E-07	6.3E-04	-2.42	11.66	0.26	9.24	0.33
2	Down	HDAC9	histone deacetylase 9	-3.99	1.2E-07	6.3E-04	-2.89	8.46	0.33	5.57	0.40
3	Down	UTRN	utrophin	-3.90	1.1E-07	6.3E-04	-1.95	8.16	0.27	6.21	0.23
4	Down	TBL1XR1	transducin (beta)-like 1 X-linked receptor 1	-3.80	1.3E-07	6.3E-04	-0.79	11.55	0.11	10.76	0.10
5	Down	ZMYND8	zinc finger, MYND-type containing 8	-3.29	1.2E-05	8.1E-03	-1.64	10.46	0.16	8.83	0.34
6	Down	DLAT	dihydrolipoamide S-acetyltransferase	-3.15	7.1E-07	2.4E-03	-0.39	10.50	0.06	10.11	0.06
7	Down	BATF3	basic leucine zipper transcription factor, ATF-like 3	-3.07	3.3E-06	4.3E-03	-1.17	7.00	0.15	5.83	0.23
8	Down	FAM101A	family with sequence similarity 101, member A	-3.06	1.0E-06	2.8E-03	-0.79	5.28	0.14	4.49	0.12
9	Down	C14orf1	chromosome 14 open reading frame 1	-3.03	1.1E-05	8.0E-03	-0.89	9.57	0.19	8.68	0.10
10	Down	RAB7L1	RAB7, member RAS oncogene family-like 1	-3.01	3.9E-05	1.3E-02	-1.71	9.19	0.40	7.48	0.16
11	Down	LTV1	LTV1 homolog (S. cerevisiae)	-2.99	1.3E-06	2.8E-03	-0.71	9.94	0.13	9.23	0.11
12	Down	C18orf55	chromosome 18 open reading frame 55	-2.93	4.0E-06	5.0E-03	-0.80	10.26	0.11	9.46	0.16
13	Down	TH	tyrosine hydroxylase	-2.87	2.5E-05	1.1E-02	-1.69	9.31	0.19	7.61	0.40
14	Down	HOXC8	homeobox C8	-2.84	3.2E-06	4.3E-03	-2.81	8.98	0.43	6.17	0.56
15	Down	LOC100130776	hypothetical LOC100130776	-2.83	2.6E-05	1.1E-02	-0.89	6.12	0.21	5.23	0.10
16	Down	SULF2	sulfatase 2	-2.78	2.1E-05	1.1E-02	-1.12	10.00	0.14	8.87	0.26
17	Down	PA2G4	proliferation-associated 2G4, 38kDa	-2.77	3.4E-05	1.2E-02	-0.63	11.98	0.15	11.36	0.07
18	Down	RNF157	ring finger protein 157	-2.74	4.5E-05	1.4E-02	-1.31	8.41	0.33	7.10	0.15
19	Down	ASB13	ankyrin repeat and SOCS box-containing 13	-2.73	8.4E-06	7.8E-03	-0.92	8.18	0.20	7.26	0.13
20	Down	RAC3	ras-related C3 botulinum toxin substrate 3 (rho family, small GTP	-2.71	1.0E-04	1.8E-02	-0.80	8.67	0.08	7.87	0.22
21	Down	HEATR2	HEAT repeat containing 2	-2.65	3.6E-05	1.2E-02	-0.84	12.03	0.21	11.19	0.11
22	Down	SLC5A6	solute carrier family 5 (sodium-dependent vitamin transporter), m	-2.53	1.3E-04	2.1E-02	-0.90	11.02	0.10	10.12	0.26
23	Down	SORBS3	sorbin and SH3 domain containing 3	-2.48	8.6E-06	7.8E-03	-1.25	6.84	0.23	5.59	0.28
24	Down	ITPRIPL2	inositol 1,4,5-triphosphate receptor interacting protein-like 2	-2.48	8.0E-06	7.8E-03	-1.31	7.48	0.24	6.17	0.29
25	Down	PON2	paraoxonase 2	-2.47	3.0E-05	1.1E-02	-2.58	8.03	0.65	5.45	0.39
26	Down	RGS19	regulator of G-protein signaling 19	-2.47	2.5E-04	2.7E-02	-0.84	9.32	0.08	8.47	0.26
27	Down	TBL2	transducin (beta)-like 2	-2.45	8.3E-05	1.8E-02	-0.68	8.26	0.09	7.58	0.19
28	Down	SLC18A1	solute carrier family 18 (vesicular monoamine), member 1	-2.42	1.0E-05	7.8E-03	-2.14	7.98	0.48	5.84	0.40
29	Down	OAF	OAF homolog (Drosophila)	-2.39	3.1E-04	3.1E-02	-1.03	8.20	0.32	7.17	0.11
30	Down	C5orf43	chromosome 5 open reading frame 43	-2.39	2.2E-05	1.1E-02	-0.55	10.00	0.09	9.45	0.14
31	Down	ADORA2B	adenosine A2b receptor	-2.36	1.7E-04	2.3E-02	-2.33	7.17	0.70	4.84	0.29
32	Down	MAPK3	mitogen-activated protein kinase 3	-2.35	9.8E-05	1.8E-02	-1.05	8.20	0.15	7.15	0.30
33	Down	TOMM40L	translocase of outer mitochondrial membrane 40 homolog (yeast)	-2.35	1.0E-05	7.8E-03	-1.51	6.64	0.33	5.12	0.31
34	Down	LRP8	low density lipoprotein receptor-related protein 8, apolipoprotein e	-2.32	2.6E-05	1.1E-02	-0.71	8.54	0.18	7.84	0.12
35	Down	AEBP1	AE binding protein 1	-2.31	5.4E-05	1.5E-02	-0.77	8.45	0.21	7.68	0.12
36	Down	JAM2	junctional adhesion molecule 2	-2.29	3.0E-05	1.1E-02	-0.78	8.10	0.14	7.32	0.20
37	Down	CC2D2A	coiled-coil and C2 domain containing 2A	-2.29	2.1E-05	1.1E-02	-1.65	8.37	0.31	6.72	0.41
38	Down	MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1	-2.29	3.3E-05	1.2E-02	-1.56	10.31	0.27	8.75	0.41
39	Down	TFAP2B	transcription factor AP-2 beta (activating enhancer binding protein	-2.26	1.4E-05	9.0E-03	-1.10	11.28	0.24	10.18	0.25
40	Down	PLIN3	perilipin 3	-2.25	2.2E-05	1.1E-02	-0.77	8.11	0.15	7.34	0.19
41	Down	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	-2.24	4.7E-05	1.4E-02	-1.57	6.30	0.43	4.73	0.27
42	Down	RAB33A	RAB33A, member RAS oncogene family	-2.23	4.1E-04	3.6E-02	-1.80	8.94	0.21	7.14	0.60
43	Down	ARHGAP23	Rho GTPase activating protein 23	-2.23	1.6E-05	9.8E-03	-0.55	7.38	0.13	6.82	0.12
44	Down	MRPL15	mitochondrial ribosomal protein L15	-2.22	6.7E-05	1.7E-02	-1.13	11.27	0.19	10.14	0.32
45	Down	AS3MT	arsenic (+3 oxidation state) methyltransferase	-2.22	1.5E-04	2.2E-02	-1.07	7.63	0.33	6.56	0.16
46	Down	UBL4A	ubiquitin-like 4A	-2.22	4.3E-05	1.3E-02	-0.89	8.54	0.24	7.65	0.16
47	Down	MRPL11	mitochondrial ribosomal protein L11	-2.19	2.0E-05	1.1E-02	-0.78	10.84	0.19	10.06	0.17
48	Down	NOP16	NOP16 nucleolar protein homolog (yeast)	-2.17	2.3E-05	1.1E-02	-1.10	10.92	0.23	9.82	0.27
49	Down	CHRM1	cholinergic receptor, muscarinic 1	-2.17	9.7E-05	1.8E-02	-0.64	6.79	0.11	6.15	0.19
50	Down	C1orf31	chromosome 1 open reading frame 31	-2.16	2.3E-05	1.1E-02	-1.29	10.19	0.32	8.90	0.28
51	Down	MCHR1	melanin-concentrating hormone receptor 1	-2.15	2.2E-04	2.6E-02	-0.93	7.37	0.30	6.44	0.14
52	Down	C6orf192	chromosome 6 open reading frame 192	-2.14	1.6E-04	2.3E-02	-1.93	8.73	0.60	6.79	0.30
53	Down	AIFM2	apoptosis-inducing factor, mitochondrion-associated, 2	-2.14	2.4E-05	1.1E-02	-1.37	8.11	0.33	6.74	0.31
54	Down	C8orf38	chromosome 8 open reading frame 38	-2.13	9.4E-05	1.8E-02	-0.85	8.96	0.15	8.11	0.25
55	Down	ZC3H7B	zinc finger CCCH-type containing 7B	-2.11	3.8E-05	1.2E-02	-0.47	7.48	0.10	7.00	0.13
56	Down	CDK5RAP2	CDK5 regulatory subunit associated protein 2	-2.11	6.4E-05	1.7E-02	-0.71	8.31	0.20	7.61	0.13
57	Down	CDCA3	cell division cycle associated 3	-2.10	8.3E-05	1.8E-02	-0.85	8.42	0.25	7.57	0.15
58	Down	SENP3	SUMO1/sentrin/SMT3 specific peptidase 3	-2.09	2.8E-05	1.1E-02	-0.57	9.43	0.14	8.86	0.14
59	Down	BDH1	3-hydroxybutyrate dehydrogenase, type 1	-2.08	3.3E-05	1.2E-02	-1.00	7.64	0.26	6.64	0.22
60	Down	ZNF573	zinc finger protein 573	-2.08	1.3E-04	2.1E-02	-2.15	7.99	0.66	5.84	0.37
61	Down	L3MBTL2	l(3)mbt-like 2 (Drosophila)	-2.07	7.7E-05	1.8E-02	-0.72	8.22	0.21	7.50	0.14
62	Down	LOC653566	signal peptidase complex subunit 2 homolog pseudogen	-2.06	3.8E-04	3.4E-02	-0.51	11.72	0.07	11.20	0.18
63	Down	BIRC5	baculoviral IAP repeat-containing 5	-2.05	1.6E-04	2.3E-02	-0.60	11.11	0.10	10.51	0.19
64	Down	TXNDC15	thioredoxin domain containing 15	-2.05	1.0E-04	1.8E-02	-1.33	9.23	0.25	7.90	0.40
65	Down	LRRC34	leucine rich repeat containing 34	-2.04	3.5E-05	1.2E-02	-2.17	7.54	0.55	5.36	0.52

#	JQ1_ vs_CT	GeneSymbol	GeneTitle	SNR	Pvalue	FDR (BH)	log2(Fold Change)	CT_ Mean	CT_ Std	JQ1_ Mean	JQ1_ Std
66	Down	ZBTB2	zinc finger and BTB domain containing 2	-2.04	4.0E-05	1.3E-02	-1.06	7.57	0.28	6.51	0.24
67	Down	FDXACB1	ferredoxin-fold anticodon binding domain containing 1	-2.04	4.3E-05	1.3E-02	-1.15	7.01	0.26	5.86	0.31
68	Down	TRMT1	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	-2.02	1.6E-04	2.3E-02	-0.98	7.63	0.17	6.66	0.31
69	Down	KLHDC5	kelch domain containing 5	-2.02	7.6E-05	1.8E-02	-0.64	9.76	0.19	9.13	0.13
70	Down	HMP19	HMP19 protein	-2.00	5.4E-04	4.4E-02	-1.12	12.75	0.16	11.64	0.40
71	Down	IL12A	interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic ly	-2.00	1.2E-04	2.0E-02	-0.80	5.50	0.25	4.70	0.15
72	Down	GRWD1	glutamate-rich WD repeat containing 1	-1.99	9.9E-05	1.8E-02	-0.59	8.82	0.18	8.23	0.12
73	Down	MAGOHB	mago-nashi homolog B (Drosophila)	-1.98	7.3E-05	1.7E-02	-1.45	9.96	0.31	8.51	0.42
74	Down	GINS1	GINS complex subunit 1 (Psf1 homolog)	-1.97	1.4E-04	2.2E-02	-0.82	10.96	0.16	10.14	0.26
75	Down	FAM13A	family with sequence similarity 13, member A	-1.97	6.0E-05	1.6E-02	-0.99	7.37	0.28	6.38	0.23
76	Down	APBA2	amyloid beta (A4) precursor protein-binding, family A, member 2	-1.97	5.2E-05	1.5E-02	-0.67	8.64	0.16	7.96	0.18
77	Down	IMPDH1	IMP (inosine 5'-monophosphate) dehydrogenase 1	-1.96	8.1E-04	5.2E-02	-0.68	11.63	0.26	10.95	0.09
78	Down	CAB39L	calcium binding protein 39-like	-1.94	6.5E-05	1.7E-02	-1.91	8.07	0.54	6.15	0.45
79	Down	RNF112	ring finger protein 112	-1.92	6.5E-04	4.7E-02	-1.14	7.91	0.17	6.78	0.42
80	Down	BCAT1	branched chain amino-acid transaminase 1, cytosolic	-1.92	1.5E-04	2.3E-02	-1.12	11.99	0.36	10.87	0.22
81	Down	UROD	uroporphyrinogen decarboxylase	-1.92	1.4E-04	2.2E-02	-1.07	11.20	0.34	10.12	0.22
82	Down	TMEM100	transmembrane protein 100	-1.92	1.0E-04	1.8E-02	-0.83	7.72	0.25	6.90	0.18
83	Down	BRIX1	BRX1, biogenesis of ribosomes, homolog (S. cerevisiae)	-1.90	4.5E-04	3.8E-02	-0.93	11.69	0.33	10.76	0.15
84	Down	ADAT2	adenosine deaminase, tRNA-specific 2, TAD2 homolog (S. cerev	-1.90	2.9E-04	2.9E-02	-1.20	6.58	0.41	5.38	0.22
85	Down	ANKRD43	ankyrin repeat domain 43	-1.90	1.1E-04	1.9E-02	-1.62	6.78	0.36	5.16	0.49
86	Down	FAM35A	family with sequence similarity 35, member A	-1.90	6.4E-05	1.7E-02	-0.72	10.82	0.19	10.10	0.20
87	Down	MRPL3	mitochondrial ribosomal protein L3	-1.87	7.8E-05	1.8E-02	-0.75	12.07	0.22	11.32	0.19
88	Down	BCL2	B-cell CLL/lymphoma 2	-1.86	7.6E-05	1.8E-02	-0.79	6.74	0.22	5.95	0.20
89	Down	F12	coagulation factor XII (Hageman factor)	-1.86	1.9E-04	2.4E-02	-1.36	8.91	0.45	7.55	0.28
90	Down	SLITRK5	SLIT and NTRK-like family, member 5	-1.85	2.9E-04	2.9E-02	-2.09	7.89	0.72	5.80	0.41
91	Down	MAP2	microtubule-associated protein 2	-1.85	9.3E-05	1.8E-02	-0.72	11.14	0.18	10.42	0.21
92	Down	HEBP2	heme binding protein 2	-1.84	3.6E-04	3.4E-02	-0.97	9.76	0.18	8.79	0.34
93	Down	SEMA6D	sema domain, transmembrane domain (TM), and cytoplasmic do	-1.84	8.6E-05	1.8E-02	-1.25	6.20	0.36	4.95	0.32
94	Down	SERF1A	small EDRK-rich factor 1A (telomeric)	-1.84	8.6E-05	1.8E-02	-0.46	10.39	0.12	9.93	0.13
95	Down	MCPH1	microcephalin 1	-1.83	8.6E-05	1.8E-02	-1.35	6.10	0.37	4.75	0.37
96	Down	CNRIP1	cannabinoid receptor interacting protein 1	-1.82	3.4E-04	3.2E-02	-1.10	10.99	0.22	9.90	0.39
97	Down	NME1	non-metastatic cells 1	-1.81	1.7E-04	2.3E-02	-0.67	13.06	0.22	12.39	0.15
98	Down	DPP7	dipeptidyl-peptidase 7	-1.81	9.9E-05	1.8E-02	-1.14	9.63	0.33	8.48	0.30
99	Down	RASL10B	RAS-like, family 10, member B	-1.80	6.7E-04	4.7E-02	-1.09	8.99	0.42	7.90	0.19
100	Down	NOL12	nucleolar protein 12	-1.79	1.6E-04	2.3E-02	-0.56	9.55	0.18	8.99	0.13
101	Down	NUP205	nucleoporin 205kDa	-1.79	1.0E-04	1.8E-02	-0.68	11.51	0.20	10.84	0.18
102	Down	TRAF5	TNF receptor-associated factor 5	-1.79	1.0E-04	1.8E-02	-1.26	7.80	0.35	6.54	0.36
103	Down	EML3	echinoderm microtubule associated protein like 3	-1.79	1.0E-04	1.8E-02	-0.90	8.34	0.25	7.44	0.26
104	Down	PEMT	phosphatidylethanolamine N-methyltransferase	-1.78	2.3E-04	2.6E-02	-1.21	9.16	0.27	7.95	0.41
105	Down	HAX1	HCLS1 associated protein X-1	-1.78	2.4E-04	2.7E-02	-0.82	11.30	0.28	10.49	0.18
106	Down	BEND3	BEN domain containing 3	-1.78	2.5E-04	2.7E-02	-1.03	9.10	0.35	8.07	0.23
107	Down	EMILIN1	elastin microfibril interfacer 1	-1.77	4.1E-04	3.6E-02	-1.85	9.58	0.67	7.74	0.37
108	Down	OBFC2B	oligonucleotide/oligosaccharide-binding fold containing 2B	-1.76	1.2E-04	2.1E-02	-1.23	9.45	0.33	8.22	0.37
109	Down	TUB	tubby homolog (mouse)	-1.76	1.6E-04	2.3E-02	-1.07	10.19	0.27	9.12	0.34
110	Down	TCF7	transcription factor 7 (T-cell specific, HMG-box)	-1.76	1.4E-04	2.2E-02	-1.22	8.46	0.38	7.24	0.31
111	Down	ZFP36L2	zinc finger protein 36, C3H type-like 2	-1.75	1.4E-04	2.2E-02	-0.80	9.83	0.21	9.03	0.25
112	Down	LSM3	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)	-1.74	3.8E-04	3.5E-02	-0.48	11.47	0.17	10.99	0.10
113	Down	ALKBH8	alkB, alkylation repair homolog 8 (E. coli)	-1.73	3.6E-04	3.4E-02	-1.09	8.07	0.24	6.98	0.39
114	Down	E2F8	E2F transcription factor 8	-1.73	1.8E-04	2.4E-02	-1.22	7.23	0.40	6.01	0.31
115	Down	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	-1.72	1.7E-04	2.3E-02	-0.67	7.36	0.22	6.69	0.17
116	Down	DEDD	death effector domain containing	-1.71	2.7E-04	2.8E-02	-0.58	8.67	0.14	8.09	0.20
117	Down	PDE4B	phosphodiesterase 4B, cAMP-specific	-1.71	5.6E-04	4.4E-02	-2.46	7.64	0.94	5.18	0.50
118	Down	ARMC6	armadillo repeat containing 6	-1.71	2.8E-04	2.8E-02	-0.71	9.34	0.17	8.63	0.25
119	Down	SLC35F2	solute carrier family 35, member F2	-1.70	5.6E-04	4.4E-02	-1.13	7.57	0.43	6.44	0.23
120	Down	AURKA	aurora kinase A	-1.70	3.7E-04	3.4E-02	-0.77	10.73	0.28	9.96	0.17
121	Down	BAI3	brain-specific angiogenesis inhibitor 3	-1.70	2.1E-04	2.6E-02	-1.73	8.79	0.44	7.07	0.57
122	Down	DCLRE1A	DNA cross-link repair 1A	-1.69	1.7E-04	2.3E-02	-1.62	8.00	0.45	6.38	0.50
123	Down	WDR35	WD repeat domain 35	-1.69	2.0E-04	2.5E-02	-0.79	8.73	0.21	7.94	0.26
124	Down	DKK1	dickkopf homolog 1 (Xenopus laevis)	-1.68	2.2E-04	2.6E-02	-1.82	7.17	0.47	5.35	0.61
125	Down	PTPRU	protein tyrosine phosphatase, receptor type, U	-1.68	2.0E-04	2.4E-02	-0.60	7.67	0.16	7.07	0.19
126	Down	SLC3A2	solute carrier family 3 (activators of dibasic and neutral amino aci	-1.68	1.9E-04	2.4E-02	-0.62	9.60	0.20	8.98	0.17
127	Down	KCNMA1	potassium large conductance calcium-activated channel, subfami	-1.68	2.3E-04	2.6E-02	-1.58	8.54	0.41	6.95	0.53
128	Down	PPIL1	peptidylprolyl isomerase (cyclophilin)-like 1	-1.67	1.8E-04	2.4E-02	-0.91	10.62	0.28	9.72	0.26
129	Down	NPM3	nucleophosmin/nucleoplasmin 3	-1.67	7.2E-04	4.8E-02	-0.85	10.12	0.17	9.27	0.34
130	Down	KEAP1	kelch-like ECH-associated protein 1	-1.67	2.2E-04	2.6E-02	-0.61	9.85	0.16	9.25	0.20
131	Down	RNASEH2B	ribonuclease H2, subunit B	-1.66	1.9E-04	2.4E-02	-1.24	9.58	0.36	8.34	0.39
132	Down	APOBEC3C	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like	-1.65	5.4E-04	4.4E-02	-0.84	7.85	0.32	7.00	0.19
133	Down	SYN2	synapsin II	-1.65	2.5E-04	2.7E-02	-0.38	7.48	0.13	7.10	0.10
134	Down	SENP1	SUMO1/sentrin specific peptidase 1	-1.64	4.1E-04	3.6E-02	-1.52	8.00	0.56	6.48	0.37
135	Down	SPAG5	sperm associated antigen 5	-1.64	2.4E-04	2.7E-02	-0.52	9.89	0.14	9.37	0.17

#	JQ1_ vs_CT	GeneSymbol	GeneTitle	SNR	Pvalue	FDR (BH)	log2(Fold Change)	CT_ Mean	CT_ Std	JQ1_ Mean	JQ1_ Std
136	Down	DCTPP1	dCTP pyrophosphatase 1	-1.64	2.2E-04	2.6E-02	-0.82	11.35	0.26	10.53	0.24
137	Down	ATP5G1	ATP synthase, H+ transporting, mitochondrial Fo complex, subun	-1.63	6.0E-04	4.5E-02	-0.80	11.44	0.31	10.64	0.18
138	Down	INO80E	INO80 complex subunit E	-1.62	2.5E-04	2.7E-02	-0.40	8.13	0.11	7.73	0.13
139	Down	C1orf216	chromosome 1 open reading frame 216	-1.62	2.3E-04	2.6E-02	-1.39	8.30	0.44	6.91	0.42
140	Down	TTC27	tetratricopeptide repeat domain 27	-1.62	2.3E-04	2.6E-02	-1.23	9.61	0.39	8.39	0.37
141	Down	PRRT4	proline-rich transmembrane protein 4	-1.61	3.6E-04	3.4E-02	-1.66	9.62	0.60	7.96	0.43
142	Down	ADAM12	ADAM metallopeptidase domain 12	-1.61	2.9E-04	2.9E-02	-1.71	7.16	0.59	5.46	0.47
143	Down	KCNG3	potassium voltage-gated channel, subfamily G, member 3	-1.61	3.2E-04	3.1E-02	-0.63	5.27	0.17	4.65	0.22
144	Down	CCDC59	coiled-coil domain containing 59	-1.61	2.7E-04	2.8E-02	-0.75	9.24	0.21	8.50	0.25
145	Down	PCDH1	protocadherin 1	-1.61	2.4E-04	2.7E-02	-1.18	8.96	0.37	7.78	0.36
146	Down	ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	-1.60	2.7E-04	2.8E-02	-0.67	11.70	0.19	11.03	0.22
147	Down	LZTS2	leucine zipper, putative tumor suppressor 2	-1.60	2.7E-04	2.8E-02	-0.50	9.03	0.16	8.54	0.15
148	Down	NUDC	nuclear distribution gene C homolog (A. nidulans)	-1.59	4.2E-04	3.7E-02	-0.60	10.65	0.16	10.05	0.22
149	Down	DENND1B	DENN/MADD domain containing 1B	-1.58	5.6E-04	4.4E-02	-0.74	7.06	0.18	6.32	0.29
150	Down	DCAF4	DDB1 and CUL4 associated factor 4	-1.58	3.7E-04	3.4E-02	-1.00	8.84	0.36	7.85	0.27
151	Down	ABHD14A	abhydrolase domain containing 14A	-1.58	6.1E-04	4.6E-02	-0.77	7.45	0.19	6.68	0.30
152	Down	CAMK1D	calcium/calmodulin-dependent protein kinase ID	-1.57	4.3E-04	3.7E-02	-1.43	9.19	0.53	7.76	0.39
153	Down	TIMM13	translocase of inner mitochondrial membrane 13 homolog (yeast)	-1.56	4.5E-04	3.8E-02	-0.58	11.54	0.22	10.95	0.16
154	Down	EXOSC8	exosome component 8	-1.55	6.2E-04	4.6E-02	-0.66	10.95	0.26	10.29	0.17
155	Down	PLD6	phospholipase D family, member 6	-1.55	6.9E-04	4.7E-02	-1.70	9.01	0.42	7.31	0.68
156	Down	HSPC159	galectin-related protein	-1.55	5.2E-04	4.3E-02	-1.15	7.58	0.44	6.43	0.30
157	Down	DAZAP1	DAZ associated protein 1	-1.54	3.3E-04	3.2E-02	-0.79	11.31	0.25	10.52	0.26
158	Down	ZNF629	zinc finger protein 629	-1.54	5.0E-04	4.2E-02	-0.46	8.52	0.17	8.07	0.12
159	Down	SERTAD4	SERTA domain containing 4	-1.54	3.4E-04	3.2E-02	-1.42	7.59	0.45	6.17	0.47
160	Down	PSMD11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	-1.54	3.5E-04	3.4E-02	-0.41	11.58	0.13	11.17	0.14
161	Down	CUTA	cutA divalent cation tolerance homolog (E. coli)	-1.53	6.7E-04	4.7E-02	-0.86	11.55	0.22	10.69	0.34
162	Down	CAND2	cullin-associated and neddylation-dissociated 2 (putative)	-1.53	4.7E-04	4.0E-02	-0.77	7.21	0.29	6.44	0.22
163	Down	FAR2	fatty acyl CoA reductase 2	-1.53	4.0E-04	3.6E-02	-1.50	9.12	0.53	7.62	0.45
164	Down	ATF1	activating transcription factor 1	-1.52	3.7E-04	3.4E-02	-0.83	8.69	0.28	7.86	0.26
165	Down	APH1A	anterior pharynx defective 1 homolog A (C. elegans)	-1.52	3.7E-04	3.4E-02	-0.36	9.97	0.12	9.62	0.12
166	Down	AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elli	-1.51	5.2E-04	4.3E-02	-0.47	9.55	0.18	9.08	0.13
167	Down	GPR19	G protein-coupled receptor 19	-1.51	4.0E-04	3.6E-02	-1.79	8.71	0.62	6.92	0.56
168	Down	SEMA3E	sema domain, immunoglobulin domain (Ig), short basic domain, s	-1.50	5.9E-04	4.5E-02	-1.06	5.70	0.41	4.64	0.30
169	Down	PTRH2	peptidyl-tRNA hydrolase 2	-1.48	4.5E-04	3.8E-02	-0.44	10.06	0.15	9.62	0.15
170	Down	LDLR	low density lipoprotein receptor	-1.47	6.5E-04	4.7E-02	-0.55	10.44	0.21	9.89	0.16
171	Down	ELOVL6	ELOVL family member 6, elongation of long chain fatty acids (FE	-1.47	6.5E-04	4.7E-02	-0.81	9.27	0.23	8.46	0.32
172	Down	ITGB1BP1	integrin beta 1 binding protein 1	-1.47	6.2E-04	4.6E-02	-0.48	11.21	0.19	10.72	0.14
173	Down	TMEM33	transmembrane protein 33	-1.47	6.4E-04	4.6E-02	-0.59	9.90	0.23	9.31	0.17
174	Down	ABLIM1	actin binding LIM protein 1	-1.45	6.1E-04	4.6E-02	-1.39	10.54	0.53	9.15	0.43
175	Down	SLC7A5	solute carrier family 7 (cationic amino acid transporter, y+ system	-1.45	5.7E-04	4.4E-02	-0.70	9.00	0.22	8.30	0.26
176	Down	CARM1	coactivator-associated arginine methyltransferase 1	-1.45	6.1E-04	4.6E-02	-0.72	9.96	0.22	9.23	0.27
177	Down	ATPIF1	ATPase inhibitory factor 1	-1.44	6.9E-04	4.7E-02	-0.42	11.92	0.13	11.50	0.17
178	Down	RBMXL1	RNA binding motif protein, X-linked-like 1	-1.44	5.5E-04	4.4E-02	-0.95	7.95	0.31	7.00	0.34
179	Down	KCTD15	potassium channel tetramerisation domain containing 15	-1.44	5.6E-04	4.4E-02	-2.23	8.29	0.73	6.06	0.81
180	Down	CCDC58	coiled-coil domain containing 58	-1.44	5.4E-04	4.4E-02	-1.10	8.35	0.38	7.25	0.38
181	Down	CHD3	chromodomain helicase DNA binding protein 3	-1.44	5.6E-04	4.4E-02	-0.68	9.86	0.24	9.18	0.24
182	Down	FAM189B	family with sequence similarity 189, member B	-1.43	5.9E-04	4.5E-02	-0.70	9.60	0.25	8.91	0.24
183	Down	C1orf174	chromosome 1 open reading frame 174	-1.43	7.1E-04	4.8E-02	-0.80	9.13	0.25	8.33	0.31
184	Down	IGF2AS	insulin-like growth factor 2 antisense	-1.42	7.1E-04	4.8E-02	-0.71	6.69	0.22	5.98	0.28
185	Down	IPO8	importin 8	-1.42	8.1E-04	5.2E-02	-0.68	7.76	0.20	7.08	0.27
186	Down	MGST2	microsomal glutathione S-transferase 2	-1.42	7.6E-04	5.0E-02	-1.22	9.24	0.48	8.02	0.37
187	Down	CUL4A	cullin 4A	-1.41	6.5E-04	4.7E-02	-0.94	9.46	0.35	8.52	0.32
188	Down	TSEN2	tRNA splicing endonuclease 2 homolog (S. cerevisiae)	-1.41	8.0E-04	5.2E-02	-0.60	7.51	0.24	6.91	0.19
189	Down	CENPK	centromere protein K	-1.40	6.6E-04	4.7E-02	-0.41	9.85	0.14	9.45	0.15
190	Down	ERF	Ets2 repressor factor	-1.40	6.8E-04	4.7E-02	-0.61	7.27	0.22	6.66	0.21
191	Down	CNGB1	cyclic nucleotide gated channel beta 1	-1.40	6.9E-04	4.7E-02	-1.18	6.46	0.43	5.28	0.41
192	Down	PMP22	peripheral myelin protein 22	-1.37	7.9E-04	5.2E-02	-1.51	9.32	0.55	7.81	0.55
193	Down	MRPS18C	mitochondrial ribosomal protein S18C	-1.36	8.5E-04	5.4E-02	-0.57	10.33	0.22	9.76	0.20
194	Up	ADI1	acireductone dioxygenase 1	1.37	8.0E-04	5.2E-02	1.18	10.23	0.43	11.41	0.44
195	Up	OSTM1	osteopetrosis associated transmembrane protein 1	1.37	8.3E-04	5.3E-02	0.57	8.57	0.22	9.14	0.20
196	Up	PAPD5	PAP associated domain containing 5	1.38	7.4E-04	5.0E-02	0.62	10.02	0.23	10.63	0.22
197	Up	IFNAR2	interferon (alpha, beta and omega) receptor 2	1.40	7.6E-04	5.0E-02	0.63	6.91	0.25	7.54	0.20
198	Up	HEXDC	hexosaminidase (glycosyl hydrolase family 20, catalytic domain)	1.40	6.6E-04	4.7E-02	1.06	7.68	0.38	8.75	0.37
199	Up	FAM173A	family with sequence similarity 173, member A	1.41	6.8E-04	4.7E-02	0.85	8.89	0.32	9.74	0.28
200	Up	TUBB3	tubulin, beta 3	1.42	7.7E-04	5.0E-02	0.84	11.97	0.33	12.81	0.26
201	Up	RPGR	retinitis pigmentosa GTPase regulator	1.42	6.5E-04	4.7E-02	0.72	6.23	0.27	6.95	0.24
202	Up	EEF2	eukaryotic translation elongation factor 2	1.42	6.6E-04	4.7E-02	0.18	14.00	0.07	14.19	0.06
203	Up	DUSP14	dual specificity phosphatase 14	1.43	6.3E-04	4.6E-02	0.76	8.26	0.25	9.02	0.29
204	Up	SLC30A9	solute carrier family 30 (zinc transporter), member 9	1.43	6.5E-04	4.7E-02	0.41	10.09	0.16	10.50	0.13
205	Up	CCDC126	coiled-coil domain containing 126	1.43	5.8E-04	4.5E-02	0.86	7.91	0.29	8.77	0.31

#	JQ1_ vs_CT	GeneSymbol	GeneTitle	SNR	Pvalue	FDR (BH)	log2(Fold Change)	CT_ Mean	CT_ Std	JQ1_ Mean	JQ1_ Std
206	Up	CCNG2	cyclin G2	1.44	5.5E-04	4.4E-02	0.99	6.55	0.35	7.54	0.34
207	Up	ACTN4	actinin, alpha 4	1.44	6.1E-04	4.6E-02	0.28	9.36	0.10	9.64	0.09
208	Up	ZNF780B	zinc finger protein 780B	1.46	5.5E-04	4.4E-02	0.14	4.45	0.04	4.59	0.05
209	Up	B3GNTL1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-	1.46	5.2E-04	4.3E-02	0.81	5.63	0.26	6.44	0.30
210	Up	SPTAN1	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	1.47	5.8E-04	4.4E-02	1.22	7.80	0.37	9.03	0.46
211	Up	KIAA0247	KIAA0247	1.47	7.2E-04	4.8E-02	0.76	7.61	0.21	8.37	0.30
212	Up	MAPKBP1	mitogen-activated protein kinase binding protein 1	1.47	4.9E-04	4.1E-02	0.72	7.47	0.26	8.18	0.23
213	Up	ERRFI1	ERBB receptor feedback inhibitor 1	1.49	6.1E-04	4.6E-02	0.93	6.56	0.26	7.49	0.36
214	Up	JAK1	Janus kinase 1	1.51	6.2E-04	4.6E-02	1.10	8.82	0.43	9.92	0.30
215	Up	TPST1	tyrosylprotein sulfotransferase 1	1.52	7.0E-04	4.8E-02	0.81	8.77	0.32	9.58	0.21
216	Up	C14orf129	chromosome 14 open reading frame 129	1.55	6.3E-04	4.6E-02	0.60	9.27	0.15	9.88	0.24
217	Up	RABL2A	RAB, member of RAS oncogene family-like 2A	1.55	5.2E-04	4.3E-02	0.57	6.60	0.22	7.17	0.15
218	Up	BECN1	beclin 1, autophagy related	1.55	5.7E-04	4.4E-02	0.33	11.48	0.08	11.81	0.13
219	Up	PTMS	parathymosin	1.56	4.1E-04	3.6E-02	0.50	8.64	0.14	9.14	0.18
220	Up	RFESD	Rieske (Fe-S) domain containing	1.57	3.7E-04	3.4E-02	1.39	6.35	0.50	7.75	0.39
221	Up	CCNYL1	cyclin Y-like 1	1.57	3.1E-04	3.1E-02	1.36	7.20	0.46	8.56	0.41
222	Up	KLHL26	kelch-like 26 (Drosophila)	1.57	3.4E-04	3.2E-02	0.29	5.77	0.08	6.05	0.10
223	Up	C1orf123	chromosome 1 open reading frame 123	1.58	4.1E-04	3.6E-02	0.53	8.88	0.19	9.41	0.14
224	Up	VAMP8	vesicle-associated membrane protein 8 (endobrevin)	1.59	4.1E-04	3.6E-02	0.58	4.19	0.15	4.78	0.21
225	Up	BNIP3L	BCL2/adenovirus E1B 19kDa interacting protein 3-like	1.60	2.7E-04	2.8E-02	1.12	9.64	0.33	10.76	0.37
226	Up	CCS	copper chaperone for superoxide dismutase	1.60	3.1E-04	3.1E-02	0.80	8.16	0.28	8.96	0.22
227	Up	RPAIN	RPA interacting protein	1.60	6.8E-04	4.7E-02	0.33	11.24	0.13	11.57	0.07
228	Up	PCBP2	poly(rC) binding protein 2	1.61	2.4E-04	2.7E-02	0.27	13.14	0.09	13.40	0.08
229	Up	CTSS	cathepsin S	1.62	3.3E-04	3.2E-02	0.22	4.42	0.06	4.64	0.08
230	Up	ARSA	arylsulfatase A	1.63	2.3E-04	2.6E-02	0.70	6.13	0.23	6.83	0.20
231	Up	TM7SF2	transmembrane 7 superfamily member 2	1.63	7.6E-04	5.0E-02	1.19	7.32	0.48	8.50	0.25
232	Up	HIST1H2BC	histone cluster 1, H2bc	1.63	3.8E-04	3.4E-02	0.54	3.89	0.13	4.42	0.20
233	Up	GOLGA2	golgin A2	1.63	2.2E-04	2.6E-02	0.43	8.35	0.14	8.78	0.13
234	Up	ELL2	elongation factor, RNA polymerase II, 2	1.63	3.3E-04	3.2E-02	0.55	4.85	0.14	5.41	0.20
235	Up	ERLEC1	endoplasmic reticulum lectin 1	1.64	6.8E-04	4.7E-02	0.44	8.98	0.17	9.41	0.09
236	Up	RPS6KA2	ribosomal protein S6 kinase, 90kDa, polypeptide 2	1.65	4.5E-04	3.8E-02	0.43	6.90	0.10	7.32	0.16
237	Up	DNAL4	dynein, axonemal, light chain 4	1.66	4.9E-04	4.1E-02	0.35	7.64	0.08	7.99	0.13
238	Up	C17orf103	chromosome 17 open reading frame 103	1.66	1.9E-04	2.4E-02	1.61	4.80	0.47	6.42	0.50
239	Up	PYGB	phosphorylase, glycogen; brain	1.67	2.2E-04	2.6E-02	0.75	8.55	0.20	9.30	0.25
240	Up	HIST1H2BD	histone cluster 1, H2bd	1.67	1.9E-04	2.4E-02	2.54	9.08	0.70	11.63	0.82
241	Up	HIST1H2BG	histone cluster 1, H2bg	1.69	4.5E-04	3.8E-02	2.62	6.07	0.58	8.70	0.98
242	Up	C17orf91	chromosome 17 open reading frame 91	1.70	1.6E-04	2.3E-02	0.84	6.51	0.26	7.36	0.24
243	Up	CLGN	calmegin	1.70	2.7E-04	2.8E-02	1.63	7.25	0.57	8.88	0.39
244	Up	LRP5L	low density lipoprotein receptor-related protein 5-like	1.70	3.1E-04	3.1E-02	0.45	6.61	0.11	7.07	0.16
245	Up	CDK10	cyclin-dependent kinase 10	1.72	1.5E-03	5.3E-02	0.57	8.59	0.25	9.16	0.09
246	Up	PPDPF	pancreatic progenitor cell differentiation and proliferation factor h	1.72	1.1E-03	5.1E-02	0.54	8.72	0.22	9.27	0.09
247	Up	STX1A	syntaxin 1A (brain)	1.72	2.4E-04	2.6E-02	0.60	7.19	0.14	7.79	0.20
248	Up	VASN	vasorin	1.73	1.8E-04	2.4E-02	0.88	6.55	0.28	7.42	0.22
249	Up	ATOX1	ATX1 antioxidant protein 1 homolog (yeast)	1.74	1.9E-04	2.4E-02	0.38	10.22	0.10	10.61	0.13
250	Up	HNRPLL	heterogeneous nuclear ribonucleoprotein L-like	1.74	1.4E-04	2.2E-02	0.40	10.78	0.11	11.18	0.12
251	Up	APAF1	apoptotic peptidase activating factor 1	1.74	1.8E-04	2.4E-02	0.32	5.10	0.10	5.41	0.08
252	Up	TBC1D2	TBC1 domain family, member 2	1.74	1.4E-04	2.2E-02	0.42	5.83	0.13	6.25	0.11
253	Up	BAHCC1	BAH domain and coiled-coil containing 1	1.75	1.3E-04	2.1E-02	0.58	7.50	0.17	8.08	0.16
254	Up	UBL3	ubiquitin-like 3	1.75	8.3E-04	5.3E-02	0.66	7.99	0.11	8.65	0.26
255	Up	CPT2	carnitine palmitoyltransferase 2	1.77	1.4E-04	2.2E-02	0.53	6.92	0.17	7.45	0.13
256	Up	ITPR1	inositol 1,4,5-triphosphate receptor, type 1	1.78	1.2E-04	2.0E-02	0.93	9.17	0.28	10.10	0.24
257	Up	CDKN2D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	1.78	1.1E-04	1.9E-02	1.33	7.28	0.40	8.62	0.35
258	Up	SESN3	sestrin 3	1.80	7.7E-04	5.1E-02	1.10	5.55	0.43	6.65	0.18
259	Up	HIST3H2A	histone cluster 3, H2a	1.80	1.8E-04	2.4E-02	1.16	8.11	0.26	9.27	0.38
260	Up	EFHA1	EF-hand domain family, member A1	1.81	1.1E-04	1.8E-02	1.00	9.94	0.30	10.94	0.25
261	Up	CYB5R3	cytochrome b5 reductase 3	1.82	8.9E-05	1.8E-02	0.41	10.41	0.11	10.82	0.12
262	Up	BRD2	bromodomain containing 2	1.83	2.2E-04	2.6E-02	0.83	9.81	0.28	10.65	0.18
263	Up	HIST1H3D	histone cluster 1, H3d	1.84	1.8E-04	2.4E-02	1.62	6.84	0.35	8.45	0.53
264	Up	DNM1L	dynamin 1-like	1.85	1.2E-04	2.1E-02	0.50	11.55	0.15	12.04	0.11
265	Up	HIST1H2BF	histone cluster 1, H2bf	1.90	7.3E-05	1.7E-02	0.91	5.43	0.22	6.34	0.26
266	Up	PIM1	pim-1 oncogene	1.90	1.1E-04	1.9E-02	0.69	8.79	0.21	9.48	0.15
267	Up	RAB7B	RAB7B, member RAS oncogene family	1.91	8.2E-05	1.8E-02	0.18	4.75	0.05	4.94	0.04
268	Up	HIST1H2BC	histone cluster 1, H2bc	1.93	4.3E-04	3.7E-02	1.28	4.15	0.21	5.43	0.46
269	Up	PJA2	praja ring finger 2	1.94	7.0E-05	1.7E-02	0.60	9.88	0.14	10.48	0.17
270	Up	HEXIM1	hexamethylene bis-acetamide inducible 1	1.94	7.3E-04	4.9E-02	1.82	9.25	0.69	11.07	0.25
271	Up	SERTAD1	SERTA domain containing 1	1.94	1.2E-03	5.5E-02	1.14	6.71	0.13	7.85	0.46
272	Up	BBS4	Bardet-Biedl syndrome 4	1.95	1.7E-04	2.3E-02	0.72	8.28	0.14	9.00	0.23
273	Up	C5orf55	chromosome 5 open reading frame 55	1.96	7.2E-05	1.7E-02	0.46	7.44	0.10	7.90	0.13
274	Up	MYH9	myosin, heavy chain 9, non-muscle	1.97	9.3E-05	1.8E-02	0.42	9.89	0.09	10.31	0.12
275	Up	D2HGDH	D-2-hydroxyglutarate dehydrogenase	1.98	6.7E-05	1.7E-02	0.46	7.39	0.10	7.86	0.13

#	JQ1_ vs_CT	GeneSymbol	GeneTitle	SNR	Pvalue	FDR (BH)	log2(Fold Change)	CT_ Mean	CT_ Std	JQ1_ Mean	JQ1_ Std
276	Up	PPP3CB	protein phosphatase 3, catalytic subunit, beta isozyme	1.98	9.4E-05	1.8E-02	0.78	9.78	0.24	10.56	0.16
277	Up	KCTD21	potassium channel tetramerisation domain containing 21	2.00	7.3E-05	1.7E-02	0.73	6.36	0.15	7.09	0.21
278	Up	LOC729991	hypothetical protein LOC729991	2.00	6.1E-05	1.6E-02	0.96	7.16	0.21	8.12	0.27
279	Up	FAM164A	family with sequence similarity 164, member A	2.02	5.9E-05	1.6E-02	0.62	9.17	0.17	9.78	0.13
280	Up	ARL3	ADP-ribosylation factor-like 3	2.02	2.9E-04	2.9E-02	0.46	10.58	0.16	11.05	0.07
281	Up	LOC728392	hypothetical protein LOC728392	2.03	1.6E-03	5.4E-02	0.97	8.84	0.40	9.81	0.08
282	Up	DNAJC1	DnaJ (Hsp40) homolog, subfamily C, member 1	2.07	9.7E-05	1.8E-02	1.19	9.89	0.36	11.08	0.22
283	Up	SCARNA20	small Cajal body-specific RNA 20	2.07	9.2E-05	1.8E-02	2.44	7.44	0.73	9.89	0.45
284	Up	PCDH17	protocadherin 17	2.07	5.6E-05	1.6E-02	1.11	8.26	0.22	9.37	0.31
285	Up	C17orf108	chromosome 17 open reading frame 108	2.08	3.7E-05	1.2E-02	1.22	5.96	0.27	7.18	0.32
286	Up	C19orf63	chromosome 19 open reading frame 63	2.09	1.6E-04	2.3E-02	0.55	11.68	0.09	12.23	0.17
287	Up	AP1G2	adaptor-related protein complex 1, gamma 2 subunit	2.10	1.6E-04	2.3E-02	1.01	6.43	0.17	7.44	0.32
288	Up	RPL12	ribosomal protein L12	2.14	5.9E-05	1.6E-02	0.16	13.98	0.04	14.13	0.03
289	Up	FILIP1L	filamin A interacting protein 1-like	2.18	3.1E-05	1.2E-02	1.68	5.00	0.33	6.68	0.44
290	Up	POLG	polymerase (DNA directed), gamma	2.20	3.0E-04	3.0E-02	0.68	8.70	0.22	9.38	0.09
291	Up	HIST1H2AE	histone cluster 1, H2ae	2.21	1.7E-04	2.3E-02	2.43	7.05	0.35	9.48	0.75
292	Up	ZNF480	zinc finger protein 480	2.23	1.8E-05	1.1E-02	1.16	7.20	0.28	8.35	0.24
293	Up	RALGAPA1	Ral GTPase activating protein, alpha subunit 1 (catalytic)	2.24	2.1E-05	1.1E-02	0.88	9.11	0.18	10.00	0.22
294	Up	DCXR	dicarbonyl/L-xylulose reductase	2.25	3.0E-05	1.1E-02	1.69	10.50	0.44	12.19	0.31
295	Up	THAP8	THAP domain containing 8	2.26	1.5E-05	9.3E-03	1.39	8.02	0.29	9.40	0.32
296	Up	HIST1H2AC	histone cluster 1, H2ac	2.27	1.4E-05	9.0E-03	2.31	7.56	0.50	9.87	0.51
297	Up	TMEM8A	transmembrane protein 8A	2.29	8.0E-04	5.2E-02	1.27	6.75	0.10	8.02	0.46
298	Up	GCH1	GTP cyclohydrolase 1	2.32	2.0E-04	2.5E-02	1.21	7.70	0.37	8.91	0.15
299	Up	PCMTD1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain	2.35	2.9E-05	1.1E-02	0.46	7.64	0.12	8.11	0.08
300	Up	HIST2H2AA3	histone cluster 2, H2aa3	2.43	2.1E-04	2.6E-02	2.37	10.01	0.26	12.37	0.71
301	Up	C1orf63	chromosome 1 open reading frame 63	2.46	1.5E-04	2.2E-02	1.00	8.26	0.29	9.27	0.12
302	Up	SERPINI1	serpin peptidase inhibitor, clade I (neuroserpin), member 1	2.50	2.5E-05	1.1E-02	1.49	5.01	0.22	6.50	0.37
303	Up	PAG1	phosphoprotein associated with glycosphingolipid microdomains	2.52	9.1E-05	1.8E-02	1.66	8.18	0.46	9.84	0.20
304	Up	INPP4A	inositol polyphosphate-4-phosphatase, type I, 107kDa	2.64	5.6E-06	5.8E-03	0.71	9.08	0.15	9.79	0.12
305	Up	TMEFF2	transmembrane protein with EGF-like and two follistatin-like doma	2.65	1.9E-05	1.1E-02	1.38	7.68	0.33	9.06	0.19
306	Up	TUFT1	tuftelin 1	2.68	9.4E-06	7.8E-03	1.37	7.60	0.21	8.98	0.31
307	Up	OS9	osteosarcoma amplified 9, endoplasmic reticulum lectin	2.75	1.1E-05	8.1E-03	0.54	8.31	0.07	8.85	0.12
308	Up	GCLC	glutamate-cysteine ligase, catalytic subunit	2.78	5.2E-06	5.8E-03	0.81	8.74	0.17	9.55	0.12
309	Up	HIST1H2BK	histone cluster 1, H2bk	2.84	2.7E-06	4.1E-03	1.37	10.29	0.27	11.67	0.22
310	Up	HIST1H2AG	histone cluster 1, H2ag	2.95	9.7E-06	7.8E-03	2.48	6.61	0.31	9.09	0.53
311	Up	C19orf30	chromosome 19 open reading frame 30	2.97	4.8E-06	5.7E-03	2.55	4.81	0.34	7.36	0.52
312	Up	SDCBP	syndecan binding protein (syntenin)	3.01	1.1E-06	2.8E-03	1.04	9.81	0.18	10.85	0.17
313	Up	TAX1BP3	Tax1 (human T-cell leukemia virus type I) binding protein 3	3.85	2.1E-06	3.5E-03	1.54	9.32	0.14	10.85	0.26
314	Up	GDF11	growth differentiation factor 11	4.00	1.7E-06	3.1E-03	1.13	8.34	0.10	9.47	0.18
315	Up	HIST2H2BC	histone cluster 2, H2bc	4.20	2.0E-07	8.1E-04	1.69	5.33	0.16	7.02	0.24
316	Up	NEU1	sialidase 1 (lysosomal sialidase)	4.32	1.5E-06	3.1E-03	0.88	8.93	0.07	9.80	0.14

Supplementary Table S4. *MYCN* Amplification Upregulation Signature in Primary Neuroblastoma Tumors

#	ProbeID	GeneSymbol	SNR Score	P-Value	FDR(BH)	Q-Value	log2 (Fold Change)	*MYCN* NonAmpl Mean	*MYCN* NonAmpl Stdev	*MYCN* Ampl Mean	*MYCN* Ampl Stdev
1	213943_at	TWIST1	0.614	0.001	0.019	0.008	3.255	6.761	2.369	10.016	2.930
2	213418_at	HSPA6	0.924	0.000	0.011	0.006	3.250	3.980	1.555	7.229	1.962
3	209757_s_at	MYCN	1.031	0.000	0.011	0.006	3.052	9.270	1.372	12.322	1.587
4	205143_at	NCAN	0.534	0.003	0.023	0.010	2.928	3.645	2.535	6.572	2.946
5	233562_at	LOC84856	0.705	0.000	0.011	0.006	2.927	3.532	1.842	6.458	2.308
6	207028_at	MYCNOS	1.041	0.000	0.011	0.006	2.830	2.762	0.869	5.592	1.851
7	226884_at	LRRN1	0.773	0.000	0.011	0.006	2.685	3.560	1.301	6.245	2.174
8	201397_at	PHGDH	0.922	0.000	0.011	0.006	2.532	5.066	1.228	7.598	1.519
9	209988_s_at	ASCL1	0.445	0.014	0.049	0.020	2.504	5.450	2.709	7.955	2.923
10	229139_at	JPH1	0.815	0.000	0.011	0.006	2.449	3.172	1.164	5.622	1.842
11	229400_at	HOXD10	0.501	0.003	0.023	0.010	2.343	3.344	1.434	5.687	3.240
12	202934_at	HK2	0.753	0.000	0.011	0.006	2.315	5.244	1.476	7.559	1.596
13	204014_at	DUSP4	0.535	0.004	0.025	0.010	2.277	5.458	2.164	7.735	2.093
14	205394_at	CHEK1	0.649	0.000	0.014	0.006	2.231	3.851	1.466	6.082	1.971
15	204603_at	EXO1	0.643	0.001	0.016	0.007	2.179	4.454	1.569	6.632	1.818
16	203196_at	ABCC4	1.068	0.000	0.011	0.006	2.153	4.771	0.953	6.925	1.062
17	218984_at	PUS7	0.900	0.000	0.011	0.006	2.101	6.793	0.835	8.894	1.500
18	231882_at	FLJ39632	0.574	0.001	0.019	0.008	2.091	4.363	1.494	6.454	2.145
19	239413_at	CEP152	0.556	0.003	0.022	0.009	2.080	4.371	1.878	6.451	1.860
20	224428_s_at	CDCA7	0.475	0.011	0.044	0.018	2.057	5.978	2.241	8.035	2.093
21	207828_s_at	CENPF	0.496	0.010	0.040	0.016	1.996	7.104	2.195	9.099	1.828
22	225834_at	FAM72A	0.471	0.011	0.043	0.017	1.971	5.770	2.078	7.741	2.102
23	219867_at	CHODL	0.521	0.003	0.023	0.010	1.936	3.619	1.666	5.555	2.051
24	241224_x_at	DSCR8	0.524	0.003	0.023	0.010	1.925	2.524	0.946	4.448	2.725
25	204126_s_at	CDC45	0.515	0.004	0.025	0.011	1.895	5.040	1.926	6.935	1.752
26	223700_at	MND1	0.550	0.002	0.021	0.009	1.870	4.346	1.496	6.216	1.904
27	225687_at	FAM83D	0.494	0.008	0.036	0.015	1.861	5.296	1.962	7.157	1.802
28	213920_at	CUX2	0.451	0.011	0.043	0.018	1.844	6.555	2.029	8.399	2.057
29	205046_at	CENPE	0.510	0.006	0.030	0.013	1.834	4.042	1.778	5.876	1.821
30	202236_s_at	SLC16A1	0.793	0.000	0.014	0.006	1.816	5.529	1.016	7.345	1.274
31	204836_at	GLDC	0.791	0.000	0.011	0.006	1.814	2.559	0.343	4.373	1.949
32	228821_at	ST6GAL2	0.556	0.001	0.016	0.007	1.814	3.066	1.069	4.879	2.192
33	210448_s_at	P2RX5	0.671	0.000	0.014	0.006	1.811	5.081	1.357	6.892	1.342
34	218662_s_at	NCAPG	0.519	0.007	0.033	0.014	1.807	7.394	1.900	9.202	1.580
35	227243_s_at	EBF3	0.441	0.011	0.043	0.018	1.807	3.781	1.625	5.588	2.475
36	209642_at	BUB1	0.481	0.009	0.039	0.016	1.800	4.651	1.921	6.451	1.823
37	211696_x_at	HBB	0.488	0.009	0.039	0.016	1.800	12.053	2.400	13.853	1.292
38	209295_at	TNFRSF10B	0.473	0.006	0.031	0.013	1.782	6.033	1.559	7.815	2.209
39	223500_at	CPLX1	0.576	0.002	0.020	0.008	1.736	6.246	1.916	7.982	1.099
40	232034_at	LOC203274	0.591	0.002	0.020	0.009	1.728	6.995	1.413	8.723	1.510
41	218726_at	HJURP	0.448	0.013	0.048	0.020	1.721	4.791	1.974	6.512	1.871
42	210347_s_at	BCL11A	0.486	0.008	0.035	0.014	1.718	6.591	1.992	8.308	1.543
43	225081_s_at	CDCA7L	0.452	0.011	0.042	0.017	1.716	5.148	1.675	6.864	2.123
44	213707_s_at	DLX5	0.432	0.013	0.047	0.019	1.713	2.551	1.106	4.265	2.863
45	214710_s_at	CCNB1	0.515	0.006	0.030	0.013	1.712	6.925	1.949	8.637	1.378
46	200790_at	ODC1	0.660	0.001	0.016	0.007	1.699	10.671	0.783	12.369	1.792
47	223062_s_at	PSAT1	0.621	0.001	0.019	0.008	1.698	7.833	1.292	9.531	1.441
48	212282_at	TMEM97	1.036	0.000	0.011	0.006	1.680	9.155	0.962	10.835	0.659
49	206376_at	SLC6A15	0.692	0.000	0.011	0.006	1.663	6.781	1.717	8.444	0.688
50	225612_s_at	B3GNT5	0.491	0.005	0.028	0.011	1.654	4.918	1.511	6.572	1.856
51	227037_at	PLD6	0.948	0.000	0.011	0.006	1.648	6.932	0.924	8.580	0.815
52	231930_at	ELMOD1	0.804	0.000	0.011	0.006	1.647	2.313	0.267	3.959	1.781
53	235205_at	LOC346887	0.431	0.011	0.043	0.017	1.636	6.096	1.599	7.732	2.195
54	1562309_s_at	PHF21B	0.455	0.013	0.047	0.019	1.629	6.750	1.645	8.379	1.932
55	242560_at	FANCD2	0.450	0.014	0.050	0.020	1.628	5.438	1.933	7.065	1.682
56	202973_x_at	FAM13A	0.488	0.007	0.032	0.013	1.601	6.752	1.922	8.353	1.356
57	221580_s_at	TAF1D	1.025	0.000	0.011	0.006	1.589	9.058	0.650	10.647	0.901
58	220443_s_at	VAX2	0.951	0.000	0.011	0.006	1.586	2.347	0.282	3.932	1.385
59	216262_s_at	TGIF2	0.861	0.000	0.011	0.006	1.568	4.151	0.787	5.719	1.034
60	204798_at	MYB	0.499	0.004	0.026	0.011	1.565	3.338	1.268	4.903	1.870
61	231772_x_at	CENPH	0.542	0.003	0.023	0.010	1.561	4.843	1.353	6.405	1.526
62	224724_at	SULF2	0.661	0.000	0.011	0.006	1.557	7.024	1.522	8.581	0.832
63	224468_s_at	C19orf48	0.797	0.000	0.011	0.006	1.533	6.526	0.811	8.059	1.113
64	206510_at	SIX2	0.560	0.001	0.019	0.008	1.525	2.854	0.583	4.378	2.140
65	206023_at	NMU	0.405	0.014	0.049	0.020	1.503	2.997	1.368	4.500	2.344
66	217986_s_at	BAZ1A	0.550	0.002	0.020	0.009	1.497	5.995	1.321	7.492	1.400
67	210473_s_at	GPR125	0.662	0.000	0.014	0.006	1.493	7.665	0.992	9.158	1.263
68	201761_at	MTHFD2	0.978	0.000	0.011	0.006	1.489	9.931	0.749	11.419	0.773
69	202534_x_at	DHFR	0.586	0.002	0.021	0.009	1.486	8.778	1.288	10.264	1.249
70	213793_s_at	HOMER1	0.746	0.000	0.011	0.006	1.467	7.775	1.338	9.242	0.630
71	207035_at	SLC30A3	0.588	0.002	0.020	0.009	1.467	3.715	1.088	5.182	1.405
72	207404_s_at	HTR1E	0.416	0.011	0.043	0.018	1.458	2.641	1.174	4.099	2.333
73	242957_at	VWCE	0.689	0.000	0.014	0.006	1.444	3.518	0.976	4.962	1.120
74	224610_at	SNHG1	0.500	0.005	0.028	0.011	1.434	9.540	1.158	10.975	1.712
75	201774_s_at	NCAPD2	0.513	0.005	0.027	0.011	1.428	5.074	1.276	6.502	1.509
76	229276_at	IGSF9	0.554	0.003	0.022	0.009	1.426	3.907	1.181	5.334	1.396
77	1558139_at	FLJ39632	0.492	0.004	0.025	0.011	1.421	5.348	1.111	6.768	1.774
78	212414_s_at	GLYR1	0.607	0.001	0.016	0.007	1.416	7.194	1.303	8.610	1.031
79	202465_at	PCOLCE	0.578	0.001	0.019	0.008	1.413	9.030	0.951	10.443	1.493

#	ProbeID	GeneSymbol	SNR Score	P-Value	FDR(BH)	Q-Value	log2 (Fold Change)	*MYCN* NonAmpl Mean	*MYCN* NonAmpl Stdev	*MYCN* Ampl Mean	*MYCN* Ampl Stdev
80	223570_at	MCM10	0.495	0.006	0.031	0.013	1.412	5.072	1.451	6.485	1.403
81	207144_s_at	CITED1	0.557	0.002	0.020	0.008	1.399	4.464	1.079	5.863	1.432
82	224870_at	KIAA0114	0.696	0.001	0.018	0.008	1.398	8.171	0.969	9.569	1.041
83	223506_at	ZC3H8	0.733	0.000	0.011	0.006	1.396	5.738	0.860	7.135	1.046
84	212018_s_at	RSL1D1	0.755	0.000	0.011	0.006	1.396	8.668	1.077	10.064	0.773
85	201195_s_at	SLC7A5	0.763	0.000	0.011	0.006	1.378	7.139	0.749	8.517	1.057
86	237005_at	LOC442075	0.501	0.004	0.026	0.011	1.376	5.801	1.235	7.176	1.509
87	209975_at	CYP2E1	0.457	0.008	0.037	0.015	1.369	2.838	1.220	4.207	1.774
88	239106_at	CA5BP	0.457	0.010	0.040	0.017	1.367	5.936	1.419	7.302	1.570
89	225541_at	RPL22L1	0.618	0.001	0.018	0.008	1.366	9.140	0.958	10.506	1.252
90	223361_at	C6orf115	0.615	0.001	0.018	0.008	1.356	6.831	1.408	8.187	0.797
91	227228_s_at	CCDC88C	0.536	0.003	0.023	0.010	1.354	2.595	0.915	3.948	1.612
92	226455_at	CREB3L4	0.585	0.002	0.020	0.008	1.353	5.632	0.930	6.985	1.385
93	226661_at	CDCA2	0.438	0.013	0.048	0.020	1.352	4.884	1.535	6.236	1.556
94	217809_at	BZW2	0.732	0.000	0.011	0.006	1.352	10.405	0.879	11.757	0.969
95	200903_s_at	AHCY	0.790	0.000	0.011	0.006	1.351	8.632	0.710	9.982	1.000
96	219105_x_at	ORC6L	0.523	0.004	0.025	0.010	1.350	7.342	1.308	8.692	1.273
97	217988_at	CCNB1IP1	0.667	0.000	0.014	0.006	1.344	8.954	0.947	10.298	1.069
98	213713_s_at	GLB1L2	0.523	0.003	0.023	0.010	1.339	4.836	1.190	6.175	1.369
99	235572_at	SPC24	0.452	0.013	0.047	0.019	1.322	4.908	1.411	6.230	1.517
100	209760_at	KIAA0922	0.776	0.000	0.011	0.006	1.310	6.015	0.877	7.325	0.812
101	201797_s_at	VARS	0.967	0.000	0.014	0.006	1.307	6.963	0.680	8.270	0.672
102	203625_x_at	SKP2	0.502	0.006	0.030	0.013	1.292	7.936	1.157	9.228	1.415
103	242828_at	FIGN	0.443	0.010	0.040	0.016	1.289	6.965	1.357	8.255	1.555
104	219511_s_at	SNCAIP	0.476	0.006	0.031	0.013	1.287	4.544	1.104	5.831	1.598
105	228956_at	UGT8	0.483	0.006	0.030	0.012	1.285	2.569	0.735	3.853	1.922
106	201013_s_at	PAICS	0.854	0.000	0.011	0.006	1.278	9.562	0.738	10.841	0.758
107	1565786_x_at	FLJ45482	0.551	0.003	0.023	0.009	1.272	4.536	1.078	5.808	1.231
108	208117_s_at	LAS1L	0.775	0.000	0.011	0.006	1.266	6.531	0.823	7.796	0.809
109	205604_at	HOXD9	0.438	0.012	0.046	0.019	1.265	5.016	1.332	6.282	1.558
110	213338_at	TMEM158	0.410	0.011	0.043	0.018	1.261	3.026	1.054	4.287	2.024
111	233499_at	LRRC7	0.500	0.004	0.026	0.011	1.259	2.633	0.661	3.892	1.857
112	214096_s_at	SHMT2	0.734	0.000	0.011	0.006	1.256	9.492	0.828	10.748	0.883
113	1553972_a_at	CBS	0.578	0.001	0.019	0.008	1.249	7.171	1.106	8.420	1.055
114	219365_s_at	CAMKV	0.472	0.007	0.034	0.014	1.249	5.484	1.330	6.733	1.318
115	237737_at	LOC100289026	0.460	0.007	0.033	0.014	1.246	2.822	0.873	4.068	1.837
116	209434_s_at	PPAT	0.820	0.000	0.011	0.006	1.243	6.389	0.666	7.632	0.851
117	205768_s_at	SLC27A2	0.452	0.008	0.035	0.014	1.242	3.643	1.252	4.885	1.496
118	225520_at	MTHFD1L	1.035	0.000	0.011	0.006	1.235	7.532	0.579	8.767	0.615
119	235580_at	ZNF141	0.508	0.005	0.029	0.012	1.232	5.258	1.100	6.490	1.325
120	208758_at	ATIC	0.957	0.000	0.011	0.006	1.229	8.592	0.584	9.822	0.701
121	225398_at	RPUSD4	0.865	0.000	0.011	0.006	1.225	8.094	0.630	9.319	0.786
122	201746_at	TP53	0.598	0.001	0.019	0.008	1.219	3.553	0.915	4.772	1.124
123	204977_at	DDX10	0.821	0.000	0.011	0.006	1.209	7.119	0.705	8.328	0.769
124	210227_at	DLGAP2	0.499	0.005	0.028	0.012	1.204	5.942	1.402	7.146	1.012
125	209644_x_at	CDKN2A	0.426	0.013	0.047	0.020	1.197	5.275	1.106	6.472	1.705
126	208361_s_at	POLR3D	0.827	0.000	0.011	0.006	1.193	5.458	0.705	6.652	0.739
127	228503_at	RPS6KA6	0.615	0.001	0.018	0.008	1.183	6.190	0.805	7.373	1.118
128	229332_at	HPDL	0.564	0.001	0.019	0.008	1.179	2.449	0.770	3.628	1.322
129	203022_at	RNASEH2A	0.477	0.010	0.041	0.017	1.179	8.000	1.276	9.178	1.196
130	204170_s_at	CKS2	0.448	0.013	0.047	0.019	1.179	8.841	1.472	10.020	1.158
131	204947_at	E2F1	0.544	0.002	0.020	0.009	1.178	6.297	1.197	7.475	0.968
132	201391_at	TRAP1	1.003	0.000	0.011	0.006	1.168	8.961	0.511	10.129	0.653
133	213913_s_at	TBC1D30	0.472	0.013	0.048	0.020	1.166	6.979	1.353	8.145	1.118
134	214045_at	LIAS	0.595	0.001	0.016	0.007	1.163	2.873	0.652	4.035	1.303
135	203422_at	POLD1	0.497	0.009	0.039	0.016	1.162	6.089	1.242	7.251	1.097
136	229655_at	FAM19A5	0.573	0.001	0.018	0.008	1.162	6.486	1.028	7.648	1.000
137	204319_s_at	RGS10	0.482	0.006	0.030	0.012	1.161	8.172	1.467	9.333	0.941
138	205522_at	HOXD4	0.434	0.010	0.040	0.016	1.161	6.874	1.371	8.035	1.306
139	203693_s_at	E2F3	0.553	0.003	0.023	0.010	1.159	7.039	1.131	8.198	0.963
140	219122_s_at	THG1L	0.667	0.000	0.014	0.006	1.156	4.977	0.651	6.132	1.080
141	223157_at	C4orf14	0.890	0.000	0.011	0.006	1.153	7.987	0.569	9.140	0.727
142	206074_s_at	HMGA1	0.821	0.000	0.011	0.006	1.150	8.954	0.667	10.104	0.733
143	1558290_a_at	PVT1	0.589	0.002	0.020	0.008	1.146	6.241	1.077	7.387	0.868

Supplementary Table S5. Differential Expression of the *MYCN* Probes in JQ1 vs Vehicle Treated Neuroblastoma Cell Lines

#	ProbeID	GeneSymbol	SNR Score	P-Value	FDR(BH)	Q-Value	log2 (Fold Change)	Veh Mean	Veh Stdev	JQ1 Mean	JQ1 Stdev
1	11719868_a_at	MYCN	-1.9200	0.0022	0.0981	0.0761	0.7690	7.8005	0.1817	7.0315	0.2188
2	11750948_a_at	MYCN	-1.3858	0.0022	0.0981	0.0761	0.8998	12.6017	0.3386	11.7018	0.3107
3	11719870_s_at	MYCN	-0.9684	0.0118	0.2380	0.1814	0.3355	13.7185	0.1752	13.3830	0.1713
4	11719869_a_at	MYCN	-0.3207	0.3041	0.7907	0.6008	0.1855	13.5448	0.2614	13.3593	0.3171

Supplementary Table S6. GSEA Results for the Consensus JQ1 Downregulation Signature

#	GeneSet Name	Source	Size	NES	P-Value	FDR	Functional Cluster
1	WEI_MYCN_TARGETS_WITH_E_BOX	MSigDB v03	741	-1.567	0.000	0.001	A: MYC
2	JANOUEIX_LEROSEY_MYCN_AMPL_UP	GEO: GSE12460	152	-1.495	0.002	0.010	A: MYC
3	V$MYCMAX_01	MSigDB v03	185	-1.411	0.003	0.152	A: MYC
4	SCHUHMACHER_MYC_TARGETS_UP	MSigDB v03	67	-1.392	0.055	0.189	A: MYC
5	BILD_MYC_ONCOGENIC_SIGNATURE	MSigDB v03	182	-1.360	0.008	0.249	A: MYC
6	CACGTG_V$MYC_Q2	MSigDB v03	716	-1.271	0.000	0.036	A: MYC
7	V$NMYC_01	MSigDB v03	196	-1.271	0.045	0.249	A: MYC
8	BENPORATH_MYC_MAX_TARGETS	MSigDB v03	755	-1.155	0.043	0.249	A: MYC
9	DANG_BOUND_BY_MYC	MSigDB v03	1025	-1.153	0.023	0.237	A: MYC
10	WONG_MITOCHONDRIA_GENE_MODULE	MSigDB v03	207	-1.456	0.000	0.083	B: Metabolism
11	MOOTHA_MITOCHONDRIA	MSigDB v03	431	-1.398	0.000	0.181	B: Metabolism
12	REACTOME_METABOLISM_OF_RNA	MSigDB v03	93	-1.396	0.015	0.184	B: Metabolism
13	REACTOME_METABOLISM_OF_PROTEINS	MSigDB v03	213	-1.369	0.006	0.235	B: Metabolism
14	REACTOME_METABOLISM_OF_AMINO_ACIDS	MSigDB v03	161	-1.359	0.014	0.250	B: Metabolism
15	KEGG_PYRIMIDINE_METABOLISM	MSigDB v03	95	-1.341	0.026	0.246	B: Metabolism
16	KEGG_PURINE_METABOLISM	MSigDB v03	154	-1.328	0.023	0.233	B: Metabolism
17	REACTOME_PEPTIDE_CHAIN_ELONGATION	MSigDB v03	84	-1.501	0.001	0.045	C: Transcription/Translation
18	REACTOME_GTP_HYDROLYSIS_AND_JOINING_OF_THE_60S_RIBOSOMAL_SUBUNIT	MSigDB v03	105	-1.479	0.015	0.058	C: Transcription/Translation
19	REACTOME_VIRAL_MRNA_TRANSLATION	MSigDB v03	84	-1.477	0.001	0.057	C: Transcription/Translation
20	REACTOME_TRANSLATION	MSigDB v03	119	-1.475	0.012	0.060	C: Transcription/Translation
21	REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT	MSigDB v03	110	-1.466	0.008	0.073	C: Transcription/Translation
22	REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA_CELLS	MSigDB v03	98	-1.454	0.016	0.081	C: Transcription/Translation
23	REACTOME_FORMATION_OF_A_POOL_OF_FREE_40S_SUBUNITS	MSigDB v03	94	-1.450	0.025	0.086	C: Transcription/Translation
24	REACTOME_GENE_EXPRESSION	MSigDB v03	413	-1.438	0.000	0.104	C: Transcription/Translation
25	REACTOME_SYNTHESIS_OF_DNA	MSigDB v03	83	-1.402	0.033	0.174	C: Transcription/Translation
26	REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS	MSigDB v03	117	-1.341	0.038	0.228	C: Transcription/Translation
27	PUJANA_CHEK2_PCC_NETWORK	MSigDB v03	737	-1.555	0.000	0.002	D: Cell Cycle
28	REACTOME_MITOTIC_M_M_G1_PHASES	MSigDB v03	150	-1.446	0.001	0.093	D: Cell Cycle
29	REACTOME_CELL_CYCLE_CHECKPOINTS	MSigDB v03	104	-1.417	0.018	0.143	D: Cell Cycle
30	REACTOME_G1_S_TRANSITION	MSigDB v03	96	-1.413	0.026	0.148	D: Cell Cycle
31	REACTOME_CELL_CYCLE_MITOTIC	MSigDB v03	298	-1.410	0.000	0.153	D: Cell Cycle
32	REACTOME_S_PHASE	MSigDB v03	97	-1.393	0.022	0.191	D: Cell Cycle
33	REACTOME_MITOTIC_PROMETAPHASE	MSigDB v03	91	-1.373	0.019	0.230	D: Cell Cycle
34	REACTOME_ELONGATION_AND_PROCESSING_OF_CAPPED_TRANSCRIPTS	MSigDB v03	124	-1.351	0.026	0.247	D: Cell Cycle
35	PUJANA_BRCA2_PCC_NETWORK	MSigDB v03	407	-1.536	0.000	0.010	E: DNA Repair
36	PUJANA_XPRSS_INT_NETWORK	MSigDB v03	163	-1.501	0.000	0.042	E: DNA Repair
37	PUJANA_BRCA_CENTERED_NETWORK	MSigDB v03	92	-1.454	0.012	0.082	E: DNA Repair
38	V$E2F_Q6_01	MSigDB v03	161	-1.518	0.001	0.024	F: E2F
39	V$E2F_03	MSigDB v03	167	-1.486	0.001	0.057	F: E2F
40	V$E2F1_Q4_01	MSigDB v03	162	-1.482	0.001	0.062	F: E2F
41	V$E2F_Q4_01	MSigDB v03	165	-1.481	0.004	0.062	F: E2F
42	V$E2F_Q3_01	MSigDB v03	166	-1.470	0.001	0.065	F: E2F
43	V$E2F_02	MSigDB v03	164	-1.445	0.000	0.093	F: E2F
44	V$E2F1_Q6_01	MSigDB v03	172	-1.442	0.001	0.100	F: E2F
45	V$E2F_Q4	MSigDB v03	162	-1.438	0.001	0.103	F: E2F
46	V$E2F_Q6	MSigDB v03	161	-1.431	0.003	0.118	F: E2F
47	V$E2F_Q3	MSigDB v03	157	-1.422	0.011	0.135	F: E2F
48	V$E2F1_Q6	MSigDB v03	162	-1.420	0.003	0.138	F: E2F
49	V$E2F1_Q4	MSigDB v03	172	-1.400	0.008	0.177	F: E2F

Supplementary Table S7. Functional Enrichment Analysis for the neuroblastoma specific JQ1 downregulation signature.

Gene Set Name	# Genes in Gene Set (K)	# Genes in Overlap (k)	k/K	p value
LEE_NEURAL_CREST_STEM_CELL_UP	147	11	0.075	0.000
REACTOME_DOPAMINE_NEUROTRANSMITTER_RELEASE_CYCLE	14	3	0.214	0.001
V$LHX3_01	186	12	0.065	0.013
V$ZIC3_01	206	12	0.058	0.026
BIOCARTA_DEATH_PATHWAY	33	4	0.121	0.001
CONCANNON_APOPTOSIS_BY_EPOXOMICIN_DN	171	12	0.070	0.000
HOLLMAN_APOPTOSIS_VIA_CD40_DN	271	14	0.052	0.000
HAMAI_APOPTOSIS_VIA_TRAIL_DN	126	8	0.064	0.000
RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_DN	22	4	0.182	0.000
V$SRF_01	47	5	0.106	0.014
V$SRF_Q5_01	191	11	0.058	0.034
V$E47_01	205	14	0.068	0.004
RTAAACA_V$FREAC2_01	714	32	0.045	0.020
V$AR_Q2	99	7	0.071	0.033
V$EGR2_01	147	9	0.061	0.038
DOUGLAS_BMI1_TARGETS_UP	512	24	0.047	0.000
BENPORATH_SUZ12_TARGETS	1037	30	0.029	0.000
BENPORATH_EED_TARGETS	1062	29	0.027	0.000
BENPORATH_ES_WITH_H3K27ME3	1117	30	0.027	0.000
BENPORATH_PRC2_TARGETS	652	20	0.031	0.000
BENPORATH_OCT4_TARGETS	290	12	0.041	0.000
BENPORATH_NANOG_TARGETS	988	26	0.026	0.000
BENPORATH_SOX2_TARGETS	734	20	0.027	0.001

Supplementary Table S8. Statistical analysis of genotypes conferring sensitivity and resistance to JQ1

Gene	Sensitive (25%)	Resistant (75%)
MYCN	p = 0.015	NS
NOTCH1	p = 0.015	NS
GNAS	NS	p = 0.015
MDM2	NS	p = 0.026
NF2	NS	p = 0.02

Supplementary Table S9. shRNA Clone Information and Target Sequences

Designation	**Clone ID**	**Clone Name**	**Target Sequence**
shBRD4_2	TRCN0000195245	NM_058243.1-532s1c1	CCTATGGATATGGGAACAATA
shBRD4_3	TRCN0000021427	NM_058243.1-646s1c1	CCTGGAGATGACATAGTCTTA
shBRD4_4	TRCN0000021426	NM_058243.1-1485s1c1	CGTCCGATTGATGTTCTCCAA
shBRD4_10	TRCN0000199972	NM_058243.1-5005s1c1	CCAACCAAAGTCAGTTCCTTC
shMYCN_1	TRCN0000020694	NM_005378.3-2000s1c1	GCCAGTATTAGACTGGAAGTT
shMYCN_3	TRCN0000020696	NM_005378.3-230s1c1	CGGACGAAGATGACTTCTACT
shMYCN_5	TRCN0000020698	NM_005378.3-919s1c1	CTGAGCGATTCAGATGATGAA
shControl			CCTAAGGTTAAGTCGCCCTCGC