

## SUPPLEMENTARY INFORMATION

### **A role for FOXO1 in BCR-ABL1-independent tyrosine kinase inhibitor resistance in chronic myeloid leukemia**

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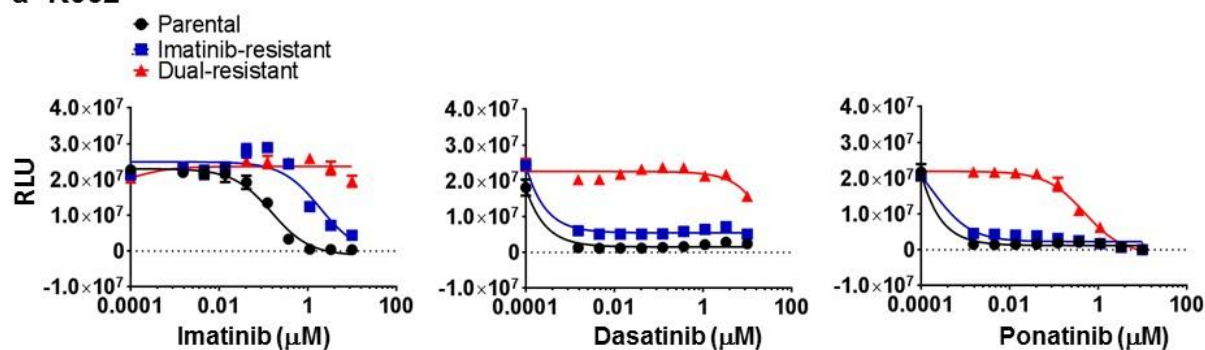
Running Title: Elevated FOXO1 in BCR-ABL1-independent resistance

Key Words: Chronic myeloid leukemia, FOXO1, tyrosine kinase inhibitors

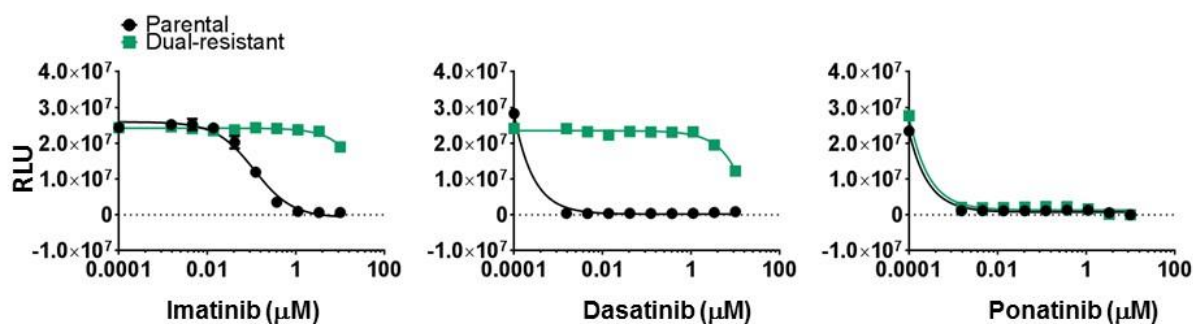
Conflict of Interest: Some of the authors are employees of Roche/Genentech. We used our in-house molecules, GDC-0941 and GDC-0973, as representative PI3K and MEK kinase inhibitors, respectively. These molecules have been published and are available from commercial sources. Furthermore, our findings should be applicable to similar inhibitors from other sources.

## Supplementary Figures

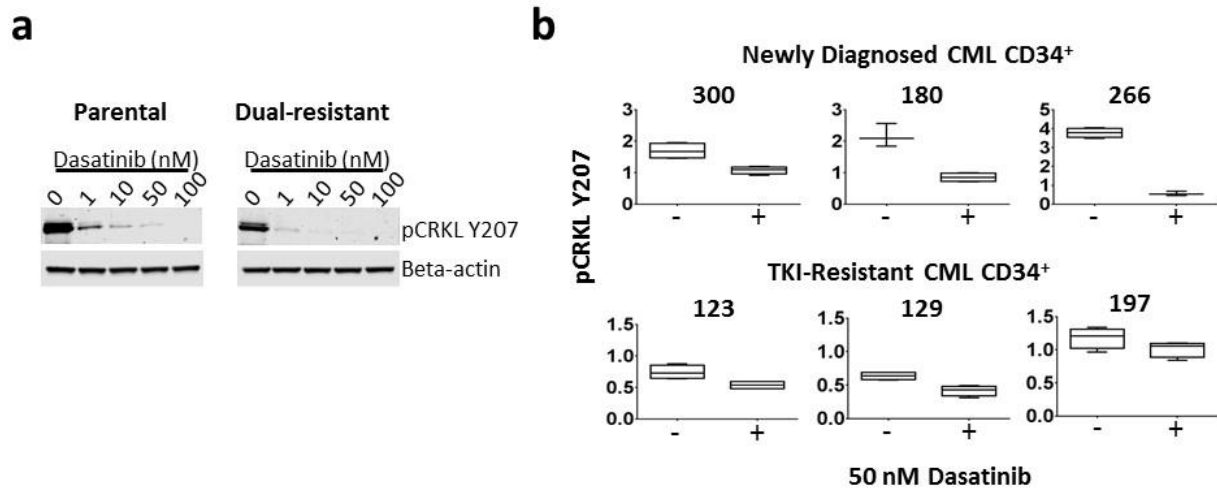
### a K562



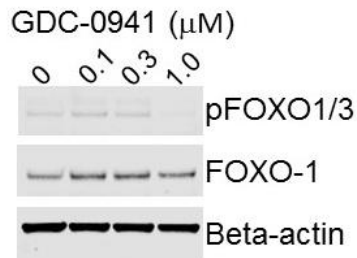
### b KCL-22



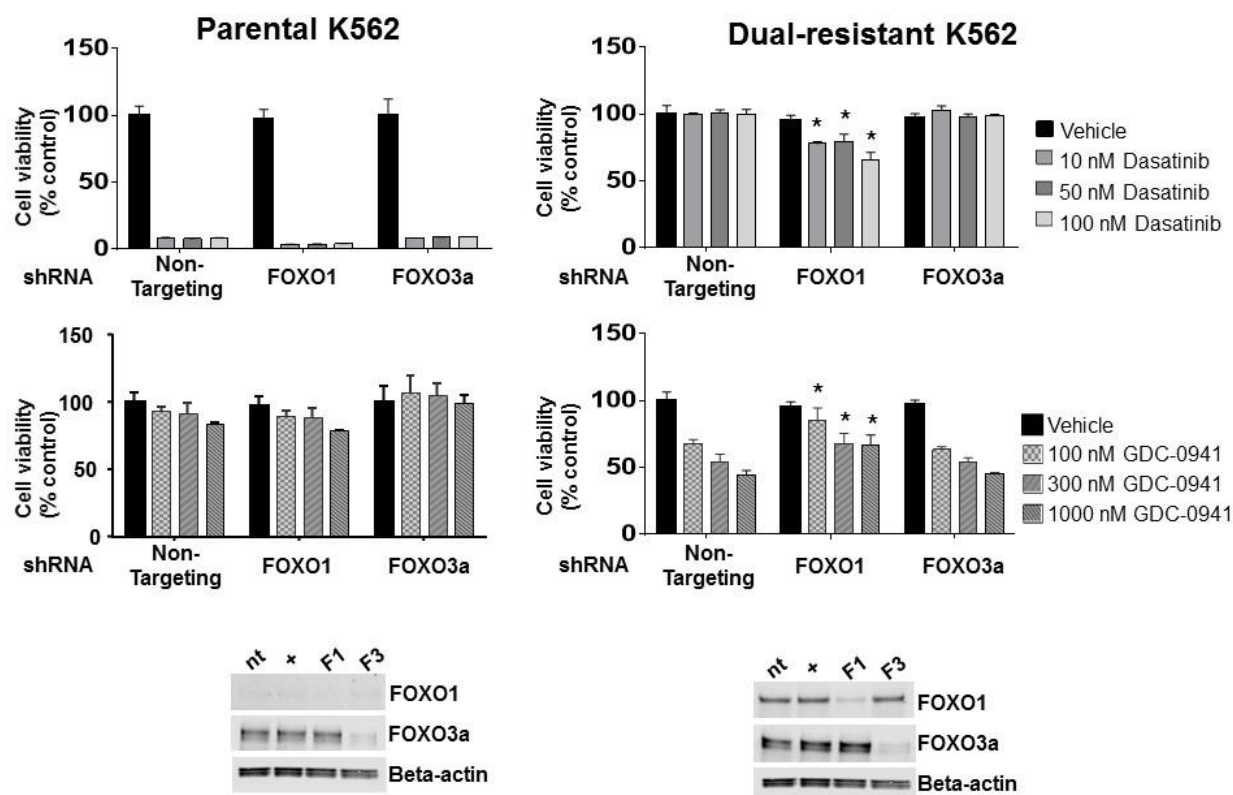
**Supplementary Figure S1. Imatinib and dual-resistant K562 cells are resistant to all three ABL-TKI therapies, whereas the KCL-22 cells are highly sensitive to ponatinib.** Graphs represent raw cell viability data corresponding to all K562 (a) and KCL-22 (b) cell line data prior to being normalized to d0 as shown in Figure 1. Data is shown as relative light units (RLU).



**Supplementary Figure S2. Effect of dasatinib on CRKL phosphorylation in parental and dual-resistant K562 cell lines and primary CML CD34<sup>+</sup> cells.** (a) Parental and dual-resistant cells were treated with 0-100 nM dasatinib for 4 h and analyzed for pCRKL Y207 levels by immunoblot analysis. (b) Primary CML CD34<sup>+</sup> cells were treated with 50 nM dasatinib for 4 h and assessed for pCRKL Y207 levels by reverse phase protein arrays. Data was normalized to total protein and log2 transformed.



**Supplementary Figure S3. Effect of GDC-0941 on FOXO1 phosphorylation in the dual-resistant K562 cell line.** Dual-resistant K562 cells were treated with 0.1, 0.3 or 1  $\mu\text{M}$  GDC-0941 for 1 h and assessed for pFOXO1 by immunoblot analysis. Similar experiments were performed on the parental cell line, but expression of both FOXO1 and pFOXO1 were too low to detect (data not shown).



**Supplementary Figure S4. Knockdown of FOXO1 sensitizes dual-resistant K562 cells to dasatinib and attenuates sensitivity to GDC-0941.** Parental (*left*) and dual-resistant (*right*) K562 cells were lentivirally transduced with shRNA targeting either FOXO1 (F1) or FOXO3a (F3) or a non-targeting (nt) or GAPDH (+) control. Resulting cells were treated with dasatinib or GDC-0941 for 72 h at the indicated concentrations. Data represents the mean % of vehicle-treated, non-targeting control cells. Error bars represent standard deviation. \* $p < 0.05$ .

## Supplementary Tables

**Supplementary Table S1.** Primary samples used in this study

Patient ID	Diagnosis	Previous ABL-TKI Therapy	BCR-ABL Mutation Status
<b>Newly Diagnosed patients</b>			
180	CP-CML	None	None
266	CP-CML	None	None
300	CP-CML	None	None
<b>Relapsed with no BCR-ABL mutations</b>			
109	AP-CML	Nilotinib only	None
113	CP-CML	Imatinib/Dasatinib/Nilotinib	None
123	AP-CML	Imatinib/Dasatinib/Nilotinib	None
124	CP-CML	Imatinib/Dasatinib/Nilotinib	None
128	CP-CML	Imatinib/Dasatinib/Nilotinib	None
129	CP-CML	Imatinib/Dasatinib	None
131	CP-CML	Imatinib/Dasatinib/Nilotinib/Ponatinib	None
137	CP-CML	Imatinib/Dasatinib/Nilotinib	None
142	CP-CML	Imatinib/Dasatinib/Nilotinib	None
151	CP-CML	Imatinib/Dasatinib	None
159	CP-CML	Imatinib/Dasatinib/Nilotinib	None
185	CP-CML	Imatinib/Dasatinib/Nilotinib	None
186	CP-CML	Imatinib/Dasatinib/Nilotinib	None
197	AP-CML	Nilotinib only	None
<b>Relapsed with BCR-ABL kinase mutations</b>			
77	BP-CML	Dasatinib/Nilotinib	T315I
252	CP-CML	Imatinib/Nilotinib	E255K

Abbreviations are as follows: AP-CML, accelerated phase CML; CP-CML, chronic phase CML; BP-CML, blastic phase CML.

**Supplementary Table S2.** Validated antibodies used in RPPA or immunoblot analyses

Protein Name	Antibody specificity	modified residue	Vendor	Catalog number
4EBP1	Phospho-serine	S65	Cell Signaling	9452
Aceyl-coA carboxylase	Phospho-serine	S79	Cell Signaling	3661
Akt	Phospho-threonine	T308	Cell Signaling	9275
Arrestin 1 beta	Phospho-serine	S412	Cell Signaling	2416
ATP citrate Lyase	Phospho-serine	S455	Cell Signaling	4331
Bcl-2	Total		Epitomics	1017-1
Beta-catenin	Phospho-serine	S552	Cell Signaling	9566
b-Raf	Phospho-threonine	T401	Epitomics	2298-1
c-Abl	Phospho-tyrosine	Y245	Cell Signaling	2861
Cofilin	Phospho-serine	S3	Cell Signaling	3313
CRKL	Phospho-tyrosine	Y207	Cell Signaling	3181
cPLA2	Phospho-serine	S505	Cell Signaling	2831
c-Raf	Phospho-serine	S259	Cell Signaling	9421
eIF4G	Phospho-serine	S1108	Cell Signaling	2441
ERK1/2	Phospho-threonine/tyrosine	T202/Y204	Cell Signaling	9101
FAK	Phospho-tyrosine	Y397	BD Biosciences	611806
FGFR3	Phospho-tyrosine	Y724	Santa Cruz	SC-33041
FOXO-1	Total		Cell Signaling	2880
FOXO-1/3	Phospho-threonine	T24/32	Cell Signaling	9464
FOXO-3	Total		Cell Signaling	12829
FOXO-4	Total		Cell Signaling	9472
mTOR	Phospho-serine	S2448	Cell Signaling	2971
p38 MAPK	Phospho-threonine/tyrosine	T180/Y182	Cell Signaling	4511
p70S6 Kinase	Phospho-threonine	T389	Cell Signaling	9205
PKC pan beta II	Phospho-serine	S660	Cell Signaling	9371
PTEN	Total		Cell Signaling	9188
S6 Riboprotein	Phospho-serine	S240/244	Cell Signaling	5364
Shc	Phospho-tyrosine	Y317	Upstate	07-206
Smad 1/5/8	Phospho-serine	S463/465;S463/465;S426/428	Cell Signaling	9511
Src	Phospho-tyrosine	Y416	Cell Signaling	2101

**Supplementary Table S3.** shRNA sequences purchased from Dharmacon GE Lifesciences

shRNA	Vector	Sequence
Non-targeting	pSMART hCMV/TurboGFP	TGGTTTACATGTTGTGTGA
GAPDH	pSMART hCMV/TurboGFP	GTGTGAACCATGAGAAGTA
FOXO1	pSMART hCMV/TurboGFP	CGAGTTTAGTAACAGTGCA
FOXO3a	pSMART hCMV/TurboGFP	CTATGTGTCTGGTCACTTA

**Supplementary Table S4a.** Genotyping data of parental K562 and KCL-22 cell lines compared to their respective resistant cells and clones

Identity of resistant cells and clones harboring mutation	Gene affected by mutation	Chromosome	Position	amino acid change type	Variant Depth	% Variant frequency
None (including T315I)	ABL1	chr9	133748283	nonsynonymous SNV	0	0
K562: clone 12	APC	chr5	112163632	nonsynonymous SNV	118	16.21
K562: clone 13	BAG2	chr6	57048734	nonsynonymous SNV	26	100
K562: dual-resistant cells	BCL2	chr18	60985559	nonsynonymous SNV	39	19.21
K562: clone 12	BRCA2	chr13	32912090	nonsynonymous SNV	260	12.98
K562: dual-resistant cells	FGFR3	chr4	1803628	nonsynonymous SNV	12	14.29
K562: clone 4	FURIN	chr15	91419743	frameshift deletion	35	97.22
K562:clone 12	NF2	chr22	30051608	nonsynonymous SNV	838	16.05
K562:clone 12	NOTCH3	chr19	15297997	nonsynonymous SNV	45	15.41
K562:clone 11	PCBP2	chr12	53858617	nonsynonymous SNV	26	21.14
K562:clone 11	PIK3R2	chr19	18273935	nonsynonymous SNV	74	23.87
K562:clone 12	PTEN	chr10	89653819	nonsynonymous SNV	634	23.84
K562:clone 13	SMARCA4	chr19	11129641	nonsynonymous SNV	352	12.1
K562:clone 17	SMARCA4	chr19	11129641	nonsynonymous SNV	386	11.93
K562:clone 12	SMARCA4	chr19	11129641	nonsynonymous SNV	375	13.35
	<b>Gene</b>	<b>chromosome</b>	<b>position</b>	<b>amino acid change type</b>	<b>Variant Depth</b>	<b>% Variant frequency</b>
KCL-22 resistant pool	ABL1 (T315I)	chr9	133748283	nonsynonymous SNV	487	39.31
KCL-22 resistant pool	BRCA2	chr13	32914046	nonsynonymous SNV	1184	52.23
KCL-22 resistant pool	SMARCA4	chr19	11129641	nonsynonymous SNV	388	11.3

**Supplementary Table S4b.** Common copy number changes found in all K562 resistant and dual-resistant clones

Region	Cytoband Location	Event	Region Length
chr1:156,033,119-156,121,675	q22	CN Gain	88556
chr1:156,769,763-156,785,486	q23.1	CN Gain	15723
chr1:156,855,043-156,874,778	q23.1	CN Gain	19735
chr3:10,152,338-10,172,022	p25.3	LOH	19684
chr6:43,376,408-43,731,249	p21.1	LOH	354841
chr6:45,356,858-45,846,458	p21.1	LOH	489600
chr6:135,915,090-136,239,693	q23.3	Allelic Imbalance	324603
chr6:137,305,405-137,865,120	q23.3	Allelic Imbalance	559715
chr6:138,102,669-141,710,518	q23.3 - q24.1	Allelic Imbalance	3607849
chr6:142,046,810-143,089,945	q24.1 - q24.2	Allelic Imbalance	1043135
chr6:143,840,188-145,626,680	q24.2 - q24.3	Allelic Imbalance	1786492
chr6:146,671,014-152,308,419	q24.3 - q25.1	Allelic Imbalance	5637405
chr6:152,488,203-154,335,788	q25.1 - q25.2	Allelic Imbalance	1847585
chr6:154,505,013-156,879,238	q25.2 - q25.3	Allelic Imbalance	2374225
chr6:157,661,869-159,994,563	q25.3	Allelic Imbalance	2332694
chr6:160,464,613-160,733,977	q25.3	Allelic Imbalance	269364
chr6:160,877,340-161,405,220	q25.3 - q26	Allelic Imbalance	527880
chr6:161,671,955-169,630,783	q26 - q27	Allelic Imbalance	7958828
chr6:170,313,770-171,115,067	q27	Allelic Imbalance	801297
chr8:488,787-1,241,469	p23.3	CN Gain	752682
chr8:89,846,131-90,229,522	q21.3	LOH	383391
chr17:27,580,998-28,883,543	q11.2	LOH	1302545
chr17:37,172,086-37,717,570	q12	LOH	545484
chr19:41,423,017-42,181,729	q13.2	LOH	758712
chr19:42,882,567-42,912,442	q13.2	CN Gain	29875
chr20:26,139,727-26,309,255	p11.1	LOH	169528
chr20:30,028,437-30,151,385	q11.21	LOH	122948
chr20:31,766,814-32,324,030	q11.21 - q11.22	LOH	557216
chr20:34,962,918-35,996,604	q11.23	LOH	1033686



**Supplementary Table S4c.** Genes known to be present in the regions with copy number changes

Gene Symbol	Chromosome	Length	Name	Aberration
RAB25	chr1	9331	RAB25, member RAS oncogene family	CN Gain
MEX3A	chr1	9987	mex-3 homolog A	CN Gain
LMNA	chr1	57513	lamin A/C	CN Gain
SEMA4A	chr1	27809	semaphorin 4A	CN Gain
PRCC	chr1	33337	papillary renal cell carcinoma (translocation-associated)	CN Gain
SH2D2A	chr1	10607	SH2 domain containing 2A	CN Gain
PEAR1	chr1	22705	platelet endothelial aggregation receptor 1	CN Gain
BRK1	chr3	11543	BRICK1, SCAR/WAVE actin-nucleating complex subunit	LOH
ABCC10	chr6	22873	ATP-binding cassette, sub-family C (CFTR/MRP), member 10	LOH
DLK2	chr6	5698	delta-like 2 homolog (Drosophila)	LOH
TJAP1	chr6	29035	tight junction associated protein 1 (peripheral)	LOH
LRRC73	chr6	3380	leucine rich repeat containing 73	LOH
YIPF3	chr6	5165	Yip1 domain family, member 3	LOH
POLR1C	chr6	4471	polymerase (RNA) I polypeptide C	LOH
POLH	chr6	44384	polymerase (DNA directed), eta	LOH
GTPBP2	chr6	8720	GTP binding protein 2	LOH
MAD2L1BP	chr6	11411	MAD2L1 binding protein	LOH
RSPH9	chr6	25983	radial spoke head 9 homolog	LOH
MRPS18A	chr6	16617	mitochondrial ribosomal protein S18A	LOH
RUNX2	chr6	222767	runt-related transcription factor 2	LOH
LINC00271	chr6	193039	long intergenic non-protein coding RNA 271	allelic imbalance
PDE7B	chr6	343877	phosphodiesterase 7B	allelic imbalance
NHEG1	chr6	11074	neuroblastoma highly expressed 1	allelic imbalance
IL20RA	chr6	45192	interleukin 20 receptor, alpha	allelic imbalance
IL22RA2	chr6	29830	interleukin 22 receptor, alpha 2	allelic imbalance
IFNGR1	chr6	21948	interferon gamma receptor 1	allelic imbalance
OLIG3	chr6	2197	oligodendrocyte transcription factor 3	allelic imbalance
LOC100130476	chr6	44565	uncharacterized LOC100130476	allelic imbalance
TNFAIP3	chr6	16128	tumor necrosis factor, alpha-induced protein 3	allelic imbalance
PERP	chr6	19020	PERP, TP53 apoptosis effector	allelic imbalance
PBOV1	chr6	2502	prostate and breast cancer overexpressed 1	allelic imbalance
KIAA1244	chr6	182749	KIAA1244	allelic imbalance
HEBP2	chr6	9248	heme binding protein 2	allelic imbalance
MIR3145	chr6	83	microRNA 3145	allelic imbalance
NHSL1	chr6	150489	NHS-like 1	allelic imbalance
FLJ46906	chr6	5622	uncharacterized LOC441172	allelic imbalance
LOC100507462	chr6	48470	uncharacterized LOC100507462	allelic imbalance
CCDC28A	chr6	19801	coiled-coil domain containing 28A	allelic imbalance
ECT2L	chr6	107961	epithelial cell transforming sequence 2 oncogene-like	allelic imbalance
REPS1	chr6	83780	RALBP1 associated Eps domain containing 1	allelic imbalance
ABRACL	chr6	14622	ABRA C-terminal like	allelic imbalance
HECA	chr6	45699	headcase homolog (Drosophila)	allelic imbalance
TXLNB	chr6	52011	taxilin beta	allelic imbalance
CITED2	chr6	2397	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	allelic imbalance
LOC645434	chr6	5603	uncharacterized LOC645434	allelic imbalance
LOC100132735	chr6	89400	uncharacterized LOC100132735	allelic imbalance
MIR3668	chr6	76	microRNA 3668	allelic imbalance
MIR4465	chr6	71	microRNA 4465	allelic imbalance
NMBR	chr6	13193	neuromedin B receptor	allelic imbalance
VTA1	chr6	73677	Vps20-associated 1 homolog (S. cerevisiae)	allelic imbalance
GPR126	chr6	144349	G protein-coupled receptor 126	allelic imbalance
LOC153910	chr6	111436	uncharacterized LOC153910	allelic imbalance
HIVEP2	chr6	193736	human immunodeficiency virus type I enhancer binding protein 2	allelic imbalance
LOC285740	chr6	15011	uncharacterized LOC285740	allelic imbalance
PHACTR2	chr6	223007	phosphatase and actin regulator 2	allelic imbalance
LTV1	chr6	20437	LTV1 homolog (S. cerevisiae)	allelic imbalance
ZC2HC1B	chr6	73912	zinc finger, C2HC-type containing 1B	allelic imbalance
PLAGL1	chr6	124300	pleiomorphic adenoma gene-like 1	allelic imbalance
HYMAI	chr6	5835	hydatidiform mole associated and imprinted (non-protein coding)	allelic imbalance
SF3B5	chr6	738	splicing factor 3b, subunit 5, 10kDa	allelic imbalance
STX11	chr6	41424	syntaxin 11	allelic imbalance
UTRN	chr6	561299	utrophin	allelic imbalance
GRM1	chr6	409951	glutamate receptor, metabotropic 1	allelic imbalance
RAB32	chr6	11260	RAB32, member RAS oncogene family	allelic imbalance
ADGB	chr6	216463	androglobin	allelic imbalance
LOC729176	chr6	2157	katanin p80 subunit B-like 1 pseudogene	allelic imbalance
STXBPS-AS1	chr6	363227	STXBPS antisense RNA 1	allelic imbalance



Gene Symbol	Chromosome	Length	Name	Aberration
TCP10	chr6	11423	t-complex 10	allelic imbalance
C6orf123	chr6	12322	chromosome 6 open reading frame 123	allelic imbalance
MLLT4-AS1	chr6	2908	MLLT4 antisense RNA 1 (head to head)	allelic imbalance
MLLT4	chr6	145031	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4	allelic imbalance
HGC6.3	chr6	1017	uncharacterized LOC100128124	allelic imbalance
KIF25	chr6	27218	kinesin family member 25	allelic imbalance
FRMD1	chr6	23377	FERM domain containing 1	allelic imbalance
DACT2	chr6	12820	dapper, antagonist of beta-catenin, homolog 2 (Xenopus laevis)	allelic imbalance
SMOC2	chr6	226845	SPARC related modular calcium binding 2	allelic imbalance
THBS2	chr6	38264	thrombospondin 2	allelic imbalance
LOC154449	chr6	8237	uncharacterized LOC154449	allelic imbalance
DLL1	chr6	8405	delta-like 1 (Drosophila)	allelic imbalance
MIR4644	chr6	85	microRNA 4644	allelic imbalance
FAM120B	chr6	98395	family with sequence similarity 120B	allelic imbalance
PSMB1	chr6	18215	proteasome (prosome, macropain) subunit, beta type, 1	allelic imbalance
TBP	chr6	18539	TATA box binding protein	allelic imbalance
PDCD2	chr6	9122	programmed cell death 2	allelic imbalance
C8orf42	chr8	55993	chromosome 8 open reading frame 42	CN gain
ERICH1	chr8	67028	glutamate-rich 1	CN gain
ERICH1-AS1	chr8	400192	ERICH1 antisense RNA 1	CN gain
CRYBA1	chr17	7629	crystallin, beta A1	LOH
NUFIP2	chr17	38314	nuclear fragile X mental retardation protein interacting protein 2	LOH
MIR4523	chr17	70	microRNA 4523	LOH
TAOK1	chr17	160980	TAO kinase 1	LOH
ABHD15	chr17	6355	abhydrolase domain containing 15	LOH
TP53I13	chr17	4438	tumor protein p53 inducible protein 13	LOH
GIT1	chr17	16125	G protein-coupled receptor kinase interacting ArfGAP 1	LOH
ANKRD13B	chr17	21254	ankyrin repeat domain 13B	LOH
CORO6	chr17	6669	coronin 6	LOH
SSH2	chr17	304055	slingshot protein phosphatase 2	LOH
EFCAB5	chr17	178598	EF-hand calcium binding domain 5	LOH
MIR3184	chr17	76	microRNA 3184	LOH
MIR423	chr17	95	microRNA 423	LOH
NSRP1	chr17	69670	nuclear speckle splicing regulatory protein 1	LOH
SLC6A4	chr17	41651	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	LOH
BLMH	chr17	43973	bleomycin hydrolase	LOH
TMIGD1	chr17	17701	transmembrane and immunoglobulin domain containing 1	LOH
CPD	chr17	90735	carboxypeptidase D	LOH
GOSR1	chr17	49408	golgi SNAP receptor complex member 1	LOH
LRR37A11P	chr17	23301	leucine rich repeat containing 37, member A11, pseudogene	LOH
LOC100131347	chr17	24434	RAD52 motif 1 pseudogene	LOH
PLXDC1	chr17	88348	plexin domain containing 1	LOH
ARL5C	chr17	9269	ADP-ribosylation factor-like 5C	LOH
CACNB1	chr17	24249	calcium channel, voltage-dependent, beta 1 subunit	LOH
RPL19	chr17	4446	ribosomal protein L19	LOH
STAC2	chr17	15253	SH3 and cysteine rich domain 2	LOH
FBXL20	chr17	149014	F-box and leucine-rich repeat protein 20	LOH
MED1	chr17	46991	mediator complex subunit 1	LOH
CDK12	chr17	73063	cyclin-dependent kinase 12	LOH
CYP2B7P1	chr19	26397	cytochrome P450, family 2, subfamily B, polypeptide 7 pseudogene 1	LOH
CYP2B6	chr19	27099	cytochrome P450, family 2, subfamily B, polypeptide 6	LOH
CYP2A13	chr19	7746	cytochrome P450, family 2, subfamily A, polypeptide 13	LOH
CYP2F1	chr19	13930	cytochrome P450, family 2, subfamily F, polypeptide 1	LOH
CYP2S1	chr19	14331	cytochrome P450, family 2, subfamily S, polypeptide 1	LOH
AXL	chr19	42565	AXL receptor tyrosine kinase	LOH
HNRNPUL1	chr19	45422	heterogeneous nuclear ribonucleoprotein U-like 1	LOH
CCDC97	chr19	14696	coiled-coil domain containing 97	LOH
TGFB1	chr19	23021	transforming growth factor, beta 1	LOH
B9D2	chr19	9758	B9 protein domain 2	LOH
TMEM91	chr19	20118	transmembrane protein 91	LOH
EXOSC5	chr19	10982	exosome component 5	LOH
BCKDHA	chr19	27218	branched chain keto acid dehydrogenase E1, alpha polypeptide	LOH
B3GNT8	chr19	3373	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8	LOH
ATP5SL	chr19	8622	ATP5S-like	LOH
C19orf69	chr19	1609	chromosome 19 open reading frame 69	LOH
LOC100505495	chr19	46482	uncharacterized LOC100505495	LOH
CEACAM21	chr19	10668	carcinoembryonic antigen-related cell adhesion molecule 21	CN gain
CEACAM4	chr19	8100	carcinoembryonic antigen-related cell adhesion molecule 4	CN gain
CEACAM7	chr19	14863	carcinoembryonic antigen-related cell adhesion molecule 7	CN gain
MEGF8	chr19	53162	multiple EGF-like-domains 8	CN gain
CNFN	chr19	3275	cornifelin	CN gain
LIPE	chr19	25914	lipase, hormone-sensitive	CN gain
LOC100996307	chr19	255209	uncharacterized LOC100996307	CN gain

Gene Symbol	Chromosome	Length	Name	Aberration
LOC284801	chr20	22216	uncharacterized LOC284801	LOH
MIR663A	chr20	94	microRNA 663a	LOH
DEFB123	chr20	9651	defensin, beta 123	LOH
DEFB124	chr20	7509	defensin, beta 124	LOH
REM1	chr20	9605	RAS (RAD and GEM)-like GTP-binding 1	LOH
LINC00028	chr20	1798	long intergenic non-protein coding RNA 28	LOH
HM13	chr20	55131	histocompatibility (minor) 13	LOH
PSIMCT-1	chr20	836	malignant T cell amplified sequence 1 pseudogene	LOH
BPIFA2	chr20	13265	BPI fold containing family A, member 2	LOH
BPIFA4P	chr20	16859	BPI fold containing family A, member 4, pseudogene	LOH
BPIFA3	chr20	10426	BPI fold containing family A, member 3	LOH
BPIFA1	chr20	7315	BPI fold containing family A, member 1	LOH
BPIFB1	chr20	26745	BPI fold containing family B, member 1	LOH
CDK5RAP1	chr20	42694	CDK5 regulatory subunit associated protein 1	LOH
SNTA1	chr20	35937	syntrophin, alpha 1	LOH
CBFA2T2	chr20	159911	core-binding factor, runt domain, alpha subunit 2; translocated to, 2	LOH
C20orf144	chr20	1631	chromosome 20 open reading frame 144	LOH
NECAB3	chr20	17373	N-terminal EF-hand calcium binding protein 3	LOH
ACTL10	chr20	2029	actin-like 10	LOH
E2F1	chr20	10920	E2F transcription factor 1	LOH
PXMP4	chr20	17588	peroxisomal membrane protein 4, 24kDa	LOH
ZNF341	chr20	60269	zinc finger protein 341	LOH
DLGAP4	chr20	161598	discs, large (Drosophila) homolog-associated protein 4	LOH
MYL9	chr20	8341	myosin, light chain 9, regulatory	LOH
TGIF2	chr20	20481	TGFB-induced factor homeobox 2	LOH
TGIF2-C20orf24	chr20	38005	TGIF2-C20orf24 readthrough	LOH
C20orf24	chr20	6825	chromosome 20 open reading frame 24	LOH
SLA2	chr20	33697	Src-like-adaptor 2	LOH
NDRG3	chr20	94374	NDRG family member 3	LOH
DSN1	chr20	22038	DSN1, MIND kinetochore complex component, homolog (S. cerevisiae)	LOH
SOGA1	chr20	86244	suppressor of glucose, autophagy associated 1	LOH
C20orf118	chr20	18064	chromosome 20 open reading frame 118	LOH
SAMHD1	chr20	60021	SAM domain and HD domain 1	LOH
RBL1	chr20	98234	retinoblastoma-like 1 (p107)	LOH
MROH8	chr20	78347	maestro heat-like repeat family member 8	LOH
RPN2	chr20	62571	ribophorin II	LOH
GHRH	chr20	5811	growth hormone releasing hormone	LOH
MANBAL	chr20	27614	mannosidase, beta A, lysosomal-like	LOH
SRC	chr20	60735	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	LOH