Supplemental Materials

Baseline Genomic Features in *BRAFV600*-Mutated Metastatic Melanoma Patients Treated with BRAF Inhibitor + MEK Inhibitor in Routine Care

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Table S1. List of studied genes.

Mutation analysis (Next Generation Sequencing)			DNA Copy number analysis	mRNA expression analysis
AKT1	GRIN2A	RAF1	NRAS	RAF1
AKT2	GRM3	RASA2	MAP2K1	ARAF
AKT3	HOXD8	RET	MET	PDGFRB
ALK	HRAS	RPS27	CDKN2A	IGF1R
ARAF	IDH1	SERPINB3	CDK4	MET
BRAF	IGF1R	SNX31	CDK6	HGF
BTK	JAK2	STAT3	CCND1	KIT
CCND1	KDR	STK11	CCND2	EGFR
CDK4	KIT	STK19	CCND3	ERBB2
CDKN2A	KRAS	TACC1	RB1	MAP3K8
CD274	MAP2K1	TERT	CTNNB1	MKI67
CTNNB1	MAP2K2	TRRAP		E2F2
CXCR4	MDM2	WT1		RB1
DDR1	MET			CDK2
DDR2	MITF			CDK4
DDX3X	MRPS31			CDK6
DUSP4	NOTCH1			CCND1
<i>EGFR</i>	NOTCH2			RRM2
ERBB2	NRAS			BCL2
ERBB3	PDGFRA			BCL2L1
ERBB4	PDGFRB			BCL2L11
EZH2	PHLPP1			BMF
FBXW7	PIK3CA			MCL1
FERMT3	PIK3CG			BAD
FGFR1	PIK3R1			PTEN
FGFR2	PIK3R2			CDKN1A
FGFR3	PLCG2			CDKN1B
FLT3	PPP6C			CDKN2A
GNA11	PTPN11			

Table S2. Mutations detected by Next Generation Sequencing (Panel of 74 genes) on the 24 baseline samples.

Patient ID	Mutation	
1	KDR:NM_002253:exon11:c.1416A>T:p.Q472H 48%	
1	DUSP4:NM_001394:exon4:c.983T>C :p.L328P 3.7%	
1	BRAF :NM_004333:exon15:c.1799T>A:p.V600E 41%	
2	BRAF:NM_004333:exon15:c.1799T>A:p.V600E 6%	
2	CDKN2A:NM_001195132:exon3:c.465C>G:p.I155M 10.5%	
2	CTNNB1:NM_001904:exon3:c.131_133del:p.S45del3.8%	
3	NOTCH2:NM_024408:exon34:c.6956C>T:p.A2319V 47%	
3	DDR2:NM_006182:exon12:c.1323G>A:p.M441I 35%	
3	RAC1:NM_006908:exon2:c.85C>T:p.P29S 50%	
3	MET:NM_000245:exon2:c.1124A>G:p.N375S 7%	
3	BRAF :NM_004333:exon15:c.1799T>A:p.V600E 85%	
3	AKT1:NM_005163:exon3:c.49G>A:p.E17K 27%	
4	DDR2:NM_001014796:exon13:c.1323G>A:p.M441I 49.7%	
4	BRAF:NM_004333:exon15:c.1798_1799delinsAA:p.V600K 57.8%	
4	NOTCH1:NM_017617:exon33:c.6149A>G:p.N2050S 63%	
4	MAP2K1:NM_002755:exon3:c.371C>T:p.P124L 37.6%	
5	BRAF:NM_004333:exon15: c.1798_1799delinsAA:p.V600K 48.8%	
5	IDH1:NM_005896:exon4:c.394C>T:p.R132C 19.5%	
5	GRIN2A:NM_001134407:exon13:c.2714C>T:p.S905F 18.8%	
5	CTNNB1:NM_001904:exon3:c.131_133del:p.S45del 2.9%	
6	BRAF:NM_004333:exon15:c.1799T>A:p.V600E 26%	
7	BRAF:NM_004333:exon15:c.1799T>A:p.V600E 25%	
7	NOTCH2:NM_024408:exon34:c.6562G>A:p.A2188T 48%	
8	BRAF:NM_004333:exon15:c.1799T>A:p.V600E 32,8%	
8	EGFR-AS1 52.8%	
9	CDKN2A NM_000077:exon2:c.457+1G>A 8%	
9	BRAF:NM_004333:exon15:c.1799T>A:p.V600E 71%	
10	BRAF:NM_004333:exon15:c.1799T>A:p.V600E 51%	
10	BRAF:NM_004333:exon15:c.1798_1799delinsAA:p.V600K 5.2%	
10	NOTCH1:NM_017617:exon33:c.6149A>G:p.N2050S 6%	
10	MAP2K1:NM_002755:exon3:c.371C>T:p.P124L 4%	
11	BRAF:NM_004333:exon15:c.1799T>A:p.V600E 52.9%	
12	BRAF:NM_004333:exon15:c.1799T>A:p.V600E 35.5%	
12	SERPINB3:NM_006919:exon4:c.284C>T:p.S95F 35.6%	
13	BRAF:NM_004333:exon15:c.1799T>A:p.V600E 19.8%	
13	AKT1:NM_005163:exon3:c.138C>A:p.D46E 52.3%	
14	BRAF :NM_004333:exon15:c.1799T>A:p.V600E 31%	
14	MET NM_001127500:exon2:c.11C>T:p.P4L 6%	
15	NOTCH2:NM_024408:exon34:c.6094C>A:p.H2032N 50%	
15	BRAF:NM_004333:exon15:c.1799T>A:p.V600E 58%	
16	BRAF:NM_004333:exon15:c.1799T>A:p.V600E 33.5%	
17	BRAF:NM_004333:exon15:c.1798_1799delinsAG:p.V600R 30%	
17	FGFR3:NM_000142:exon7:c.905G>A:p.G302D 19%	
18	PI3KCA:NM_006218.3:exon7:c.1173A>G:p.I391M 39%	
18	BRAF :NM_004333:exon15:c.1799T>A:p.V600E 70%	
19	BRAF:NM_004333:exon15:c.1799T>A:p.V600E 70%	
20	BRAF:NM_004333:exon15:c.179717A.p. v600E 36 % BRAF:NM_004333:exon15:c.1798_1799delinsAA:p.V600K 18.6%	
20	NOTCH2:NM_024408:exon34:c.7223T>A:p.L2408H 46.2%	
21	BRAF:NM_004333:exon15:c.1799T>A:p.V600E 30%	
22	BRAF:NM_004333:exon15:c.1799T>A:p.V600E 30 %	
23	BRAF:NM_004333:exon15:c.1799T>A:p.V600E 11 %	
24	BRAF:NM_004333:exon15:c.1799T>A:p.V600E 32 %	
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