

Treatments	S	R	T	Reponse Rate (S/T)
BGJ398	14	24	38	0.37
BKM120	30	8	38	0.79
BYL719	24	14	38	0.63
BYL719 + LJM716	33	5	38	0.87
CGM097	12	26	38	0.32
CLR457	27	11	38	0.71
HDM201	14	24	38	0.37
INC424	14	23	37	0.38
LEE011	23	15	38	0.61
LKA136	12	26	38	0.32
LLM871	23	15	38	0.61
binimetinib	22	16	38	0.58
paclitaxel	26	12	38	0.68

Legend

S	Number of Sensitive PDXs for the corresponding treatment
R	Number of Resistant PDXs for the corresponding treatment
T	Total number of PDXs tested against the corresponding treatment (i.e. S + R)

Treatments	S	R	T	Reponse Rate (S/T)
BKM120	25	14	39	0.36
BYL719	26	15	41	0.37
BYL719 + LJM716	27	12	39	0.31
CGM097	11	25	36	0.69
CLR457	28	12	40	0.3
HDM201	12	27	39	0.69
LEE011	24	17	41	0.41
LKA136	14	25	39	0.64
binimetinib	27	14	41	0.34
cetuximab	16	24	40	0.6
CKX620	29	9	38	0.24
encorafenib	12	28	40	0.7
LFW527 + binimetinib	16	15	31	0.48

Legend

S	Number of Sensitive PDXs for the corresponding treatment
R	Number of Resistant PDXs for the corresponding treatment
T	Total number of PDXs tested against the corresponding treatment (i.e. S + R)

ID	Treatment_Name	S	T	Reponse Rate (S/T)	MCC	PR	RC	NPredResp	Marker gene	p-value	Effect size (Φ)	#Mutated	Mutation prevalence
BRCA													
1	BGJ398	14	38	0.37	0.48	0.61	0.79	18	KIF20B	6.28E-03	0.48	18	0.47
2	BKM120	30	38	0.79	-0.78	0.22	0.07	9*	CCDC66	1.64E-01	0.27	8	0.21
3	BYL719	24	38	0.63	-0.10	0.57	0.33	14*	KIF20B	2.05E-02	0.40	18	0.47
5	BYL719 + LJM716	33	38	0.87	0.04	0.88	0.45	17*	ANKRD36	4.63E-02	0.39	19	0.50
6	CGM097	12	38	0.32	-0.11	0.00	0.00	1*	VWF	6.71E-03	0.50	4	0.11
7	CLR457	27	38	0.71	-0.68	0.00	0.00	6	AVEN	1.54E-01	0.28	6	0.16
8	HDM201	14	38	0.37	0.31	1.00	0.14	2*	ADAMTS7	3.99E-03	0.51	5	0.13
9	INC424	14	37	0.38	0.06	0.50	0.07	2*	PCDHB7	4.59E-03	0.51	5	0.14
10	LEE011	23	38	0.61	-0.48	0.00	0.00	5*	MUC6	6.34E-02	0.35	6	0.16
15	LKA136	12	38	0.32	0.22	0.67	0.17	3*	TLK2	1.97E-03	0.55	7	0.18
16	LLM871	23	38	0.61	0.38	1.00	0.30	7	EP400	2.91E-02	0.38	7	0.18
17	binimetinib	22	38	0.58	0.24	0.68	0.68	22*	PABPC3	2.01E-02	0.43	19	0.50
18	paclitaxel	26	38	0.68	-0.82	0.00	0.00	9*	HYDIN	3.85E-02	0.35	8	0.21
CRC													
2	BKM120	25	39	0.64	-0.22	0.44	0.16	9*	PIEZO1	3.78E-02	0.37	15	0.38
3	BYL719	26	41	0.63	0.43	0.80	0.77	25	TMEM184A	8.82E-03	0.43	25	0.61
5	BYL719 + LJM716	27	39	0.69	0.24	0.74	0.93	34*	LSR	6.01E-02	0.33	33	0.85
6	CGM097	11	36	0.31	-0.13	0.17	0.09	6*	USP19	5.60E-03	0.53	4	0.11
7	CLR457	28	40	0.70	-0.02	0.69	0.64	26*	CTSA	2.13E-02	0.40	28	0.70
8	HDM201	12	39	0.31	-0.23	0.00	0.00	4*	WDR33	5.63E-03	0.49	8	0.21
10	LEE011	24	41	0.59	-0.70	0.08	0.04	13*	LOC728888	2.81E-02	0.36	10	0.24
15	LKA136	14	39	0.36	-0.22	0.00	0.00	3*	ANKRD36C	1.22E-02	0.45	4	0.10
17	binimetinib	27	41	0.66	0.40	0.88	0.56	17	CEACAM3	1.83E-02	0.40	17	0.41
29	cetuximab	16	40	0.40	0.59	0.90	0.56	10	ACR	3.33E-04	0.59	10	0.25
31	CKX620	29	38	0.76	-0.37	0.59	0.34	17*	CDC42EP1	1.30E-01	0.28	18	0.47
32	encorafenib	12	40	0.30	-0.10	0.00	0.00	1*	IGSF3	5.42E-03	0.51	4	0.10
34	LFW527 + binimetinib	16	31	0.52	0.47	1.00	0.38	6	KAT6B	1.77E-02	0.47	6	0.19

* cases that have number of predicted responsive in all folds different to the number of PDXs have mutated marker gene → the marker gene is not stable among all folds, in some certain folds the gene with lowest p-value is a different gene

NB: MCC, PR, RC and Nresp are calculated by LOOCV as explained in the Methods section of the paper

Legend

BRCA	Breast Cancer
CRC	ColorRectal Cancer
S	Number of Sensitive PDXs for the corresponding treatment
T	Total number of PDXs tested against the corresponding treatment
MCC	Matthews Correlation Coefficient
PR	Precision
RC	Recall
NPredResp	Number of PDXs that are predicted responsive for the corresponding treatment using the single-gene marker

ID	Treatment_Name	S	T	Reponse Rate (S/T)	RF-OMC MCC	RF-all MCC	RF-OMC PR	RF-all PR	RF-OMC RC	RF-all RC	RF-OMC BestProf	RF-all BestProf	RF-OMC #features	RF-all #features	Selected features
BRCA															
1	BGJ398	14	38	0.37	0.41	0.06	0.59	0.20	0.71	0.07	SNV	GEX	2	22665	KIF20B, SIPA1L3
2	BKM120	30	38	0.79	0.13	0.00	0.82	0.79	0.73	1.00	SNV	CN	3	23853	FOXC1, IGSF3, TLR6
3	BYL719	24	38	0.63	0.38	0.19	0.75	0.63	0.83	0.77	GEX	SNV	6	15232	PPP1R13B, NEK6, EHD1, HIP1R, CCDC85C, CCNK
5	BYL719 + LJM716	33	38	0.87	-0.06	0.00	0.86	0.86	0.73	0.73	SNV	SNV	2	15232	NCOA3, ZFXH3
6	CGM097	12	38	0.32	0.19	0.24	0.45	0.42	0.42	0.08	CN	GEX	8	22665	OR1D4, LOC728392, ADCYAP1R1, C7orf41, JAZF1, MIS12, SMG6, CRHR2
7	CLR457	27	38	0.71	0.38	0.00	0.80	0.74	0.89	0.96	CNA	GEX	2	22665	NUDT11, TBP
8	HDM201	14	38	0.37	0.21	0.40	0.59	0.59	0.29	0.29	SNV	SNV	2	15232	ADAMTS7, RPS17L
9	INC424	14	37	0.38	0.41	0.18	0.61	0.40	0.71	0.29	SNV	GEX	10	22665	NR1H2, PCDHB7, EP400, NBPF9, GOLGB1, MAGI1, SF3B3, VWF, KIF20B, ARID1A
10	LEE011	23	38	0.61	0.28	0.01	0.68	0.35	0.87	0.26	SNV	CNA	9	21534	VWA1, GSTM1, NUDT11, HUWE1, POTEF, STAG3, VPS13A, POLR2J2, AMH
15	LKA136	12	38	0.32	0.48	0.00	0.75	0.00	0.50	0.00	SNV	GEX	3	22665	NR1H2, TLK2, CTSA
16	LLM871	23	38	0.61	0.19	0.25	0.66	0.66	0.78	0.78	CN	CN	23853	23853	All available genes
17	binimetinib	22	38	0.58	0.60	0.56	0.78	0.78	0.93	0.93	GEX	GEX	14	22665	CRB3, NDUFA1, MPG, ECI1, ING2, KIF9, TSTD1, FAM100A, TCEAL3, HAGH, PEX11G, SNORA72, SNORA70, PIN1
18	paclitaxel	26	38	0.68	0.49	0.18	0.82	0.71	0.88	0.77	SNV	CN	2	23853	MUC20, UPK3BL
CRC															
2	BKM120	25	39	0.64	-0.07	0.19	0.63	0.59	0.80	0.72	GEX	CN	8	23853	BDKRB2, ZNF607, CDK1, EXT2, TMPO, RPL4, GNB2L1, ZNF808
3	BYL719	26	41	0.63	0.24	0.16	0.73	0.73	0.69	0.69	CN	CN	14	23853	HIBADH, TAX1BP1, CBX3, HNRNPA2B1, NFE2L3, SNX10, NPVF, RNU6.16, CYCS, MIR148A, C7orf31, OSBPL3, IRF6, C1orf74
5	BYL719 + LJM716	27	39	0.69	0.38	0.18	0.80	0.68	0.81	0.85	CNA	CN	2	23853	AQR, FLNC
6	CGM097	11	36	0.31	0.43	0.37	0.80	0.80	0.36	0.36	GEX	GEX	3	22665	NONO, RBBP7, CDK4
7	CLR457	28	40	0.70	0.17	0.24	0.74	0.70	0.82	0.93	CN	GEX	19	22665	RAP1GDS1, PDLIM5, ANK1, ARSJ, HPGDS, SMARCAD1, BMPR1B, FAM13A.AS1, ANK2, C4orf37, C4orf22, AP3M2, PLAT, DKK2, ALPK1, AP1AR, C4orf21, C4orf32, LARP7
8	HDM201	12	39	0.31	0.23	0.00	0.54	0.27	0.25	0.33	SNV	CN	6	23853	WDR33, CEACAM7, NEMF, POLDIP2, BMP2K, PER1
10	LEE011	24	41	0.59	0.30	0.25	0.66	0.63	0.88	0.65	SNV	CN	4	23853	ANKRD12, BCL9, ABCB8, HERC1
15	LKA136	14	39	0.36	0.15	0.28	0.46	0.46	0.43	0.43	CN	CN	2	23853	MICALCL, OR52E8
17	binimetinib	27	41	0.66	-0.05	0.00	0.64	0.27	0.67	0.13	CN	SNV	2	15232	POLR2J2, UPK3BL
29	cetuximab	16	40	0.40	0.47	0.39	0.62	0.43	0.81	0.44	SNV	CN	4	23853	ACR, DENND4B, NOTCH1, RPL22
31	CKX620	29	38	0.76	0.07	0.00	0.77	0.60	0.93	0.43	CN	SNV	6	15232	LIMS3.1, PP1AL4A, PP1AL4C.1, PP1AL4B, FAM91A2, LOC728855
32	encorafenib	12	40	0.30	0.01	0.17	0.31	0.14	0.17	0.17	CN	SNV	7	15232	MIR4493, BSX, C11orf63, CRTAM, UBASH3B, ME3, CCDC15
34	LFW527 + binimetinib	16	31	0.52	0.17	0.23	0.57	0.58	0.81	0.44	SNV	CN	4	23853	ASXL1, DHX16, KIAA1199, SLC28A2

Note 1: MCC, PR and RC are median values calculated 10 LOOCV runs as explained in the Methods section of the paper. MCCs are shown in Figure 2.

Note 2: Figures 3-5 show the results for one of the 10 runs and hence might not necessarily display exactly the same MCC as above.

Legend

BRCA	Breast Cancer
CRC	ColorRectal Cancer
S	Number of Sensitive PDXs
T	Total number of PDXs tested against the corresponding treatment
RF	Random Forest
RF-OMC	Random Forest with Optimal Model Complexity
RF-all	Random Forest using all available features
MCC	Matthews Correlation Coefficient
PR	Precision
RC	Recall
BestProf	The best profile for that method (either RF-OMC or RF-all)
SNV	Single Nucleotide Variants
CNA	Copy Number Alterations
CN	Copy Number (real values)
GEX	Gene expression levels