OmniSeq®

Genomic Profiling

OmniSeq's genomic profiling panel is a comprehensive genomic profiling test that uses next generation DNA sequencing of the full exonic coding region of 523 genes to detect small variants (single and multinucleotide substitutions, insertions, deletions and indels), and copy number alterations (gains and losses), and includes calculation of microsatellite instability (MSI) and tumor mutational burden (TMB) genomic signatures.

523 Genes (full-coding) interrogated for single nucleotide variants (SNVs), insertions and deletions (Indels)
59 Genes associated with copy number alterations detected by DNA-seq
55 Genes with reportable fusions (rearrangements) and splice variants detected by RNA-seq
HRD Genes associated with Homologous Recombination Deficiency are detected by DNA-seq
PHV Genes with potential hereditary variants (PHVs) are detected by DNA-seq
TMB Tumor mutational burden is reported
MSI Microsatellite instability status is reported

DNA-Sequencing of 523 genes (full coding exonic regions) for the detection of substitutions, indels, MSI and TMB														
ABL1	ABL2	ACVR1	ACVR1B	AKT1	AKT2	AKT3	ALK	ALOX12B	AMER1	ANKRD11	ANKRD26	APC	AR	ARAF
ARFRP1	ARID1A	ARID1B	ARID2	ARID5B	ASXL1	ASXL2	ATM	ATR	ATRX	AURKA	AURKB	AXIN1	AXIN2	AXL
B2M	BAP1	BARD1	BBC3	BCL10	BCL2	BCL2L1	BCL2L11	BCL2L2	BCL6	BCOR	BCORL1	BCR	BIRC3	BLM
BMPR1A	BRAF	BRCA1	BRCA2	BRD4	BRIP1	BTG1	BTK	C11ORF30	CALR	CARD11	CASP8	CBFB	CBL	CCND1
CCND2	CCND3	CCNE1	CD274	CD276	CD74	CD79A	CD79B	CDC73	CDH1	CDK12	CDK4	CDK6	CDK8	CDKN1A
CDKN1B	CDKN2A	CDKN2B	CDKN2C	CEBPA	CENPA	CHD2	CHD4	CHEK1	CHEK2	chrY	CIC	CREBBP	CRKL	CRLF2
CSF1R	CSF3R	CSNK1A1	CTCF	CTLA4	CTNNA1	CTNNB1	CUL3	CUX1	CXCR4	CYLD	DAXX	DCUN1D1	DDR2	DDX41
DHX15	DICER1	DIS3	DNAJB1	DNMT1	DNMT3A	DNMT3B	DOT1L	E2F3	EED	EGFL7	EGFR	EIF1AX	EIF4A2	EIF4E
EML4	EP300	EPCAM	EPHA3	EPHA5	EPHA7	EPHB1	ERBB2	ERBB3	ERBB4	ERCC1	ERCC2	ERCC3	ERCC4	ERCC5
ERG	ERRFI1	ESR1	ETS1	ETV1	ETV4	ETV5	ETV6	EWSR1	EZH2	FAM175A	FAM46C	FANCA	FANCC	FANCD2
FANCE	FANCF	FANCG	FANCI	FANCL	FAS	FAT1	FBXW7	FGF1	FGF10	FGF14	FGF19	FGF2	FGF23	FGF3
FGF4	FGF5	FGF6	FGF7	FGF8	FGF9	FGFR1	FGFR2	FGFR3	FGFR4	FH	FLCN	FLI1	FLT1	FLT3
FLT4	FOXA1	FOXL2	FOXO1	FOXP1	FRS2	FUBP1	FYN	GABRA6	GATA1	GATA2	GATA3	GATA4	GATA6	GEN1
GID4	GLI1	GNA11	GNA13	GNAQ	GNAS	GPR124	GPS2	GREM1	GRIN2A	GRM3	GSK3B	H3F3A	H3F3B	H3F3C
HGF	HIST1H1C	HIST1H2BD	HIST1H3A	HIST1H3B	HIST1H3C	HIST1H3D	HIST1H3E	HIST1H3F	HIST1H3G	HIST1H3H	HIST1H3I	HIST1H3J	HIST2H3A	HIST2H3D
HIST3H3	HLA-A	HNF1A	HNRNPK	HOXB13	HRAS	HSD3B1	HSP90AA1	ICOSLG	ID3	IDH1	IDH2	IFNGR1	IGF1	IGF1R
IGF2	IKBKE	IKZF1	IL10	IL7R	INHA	INHBA	INPP4A	INPP4B	INSR	IRF2	IRF4	IRS1	IRS2	JAK1
JAK2	JAK3	JUN	KAT6A	KDM5A	KDM5C	KDM6A	KDR	KEAP1	KEL	KIF5B	KIT	KLF4	KLHL6	KMTA
KMT2B	KMT2C	KMT2D	KRAS	LAMP1	LATS1	LATS2	LMO1	LRP1B	LYN	LZTR1	MAGI2	MALT1	MAP2K1	MAP2K2
MAP3K1	MAP3K13	MAP3K14	MAP3K4	MAPK1	MAPK3	MAX	MCL1	MDC1	MDM2	MDM4	MED12	MEF2B	MEN1	MET
MAP2K4	MGA	MITF	MLH1	MLLT3	MPL	MRE11A	MSH2	MSH3	MSH6	MST1	MST1R	MTOR	MUTYH	MYB
MYC	MYCL	MYCN	MYD88	MYOD1	NAB2	NBN	NCOA3	NCOR1	NEGR1	NF1	NF2	NFE2L2	NFKBIA	NKX2-1
NKX3-1	NOTCH1	NOTCH2	NOTCH3	NOTCH4	NPM1	NRAS	NRG1	NSD1	NTRK1	NTRK2	NTRK3	NUP93	NUTM1	PAK1
PAK3	PAK7	PALB2	PARK2	PARP1	PAX3	PAX5	PAX7	PAX8	PBRM1	PDCD1	PDCD1LG2	PDGFRA	PDGFRB	PDK1
PDPK1	PGR	PHF6	PHOX2B	PIK3C2B	PIK3C2G	PIK3C3	PIK3CA	PIK3CB	PIK3CD	PIK3CG	PIK3R1	PIK3R2	PIK3R3	PIM1
PLCG2	PLK2	PMAIP1	PMS1	PMS2	PNRC1	POLD1	POLE	PPARG	PPM1D	PPP2R1A	PPP2R2A	PPP6C	PRDM1	PREX2
PRKAR1A	PRKCI	PRKDC	PRSS8	PTCH1	PTEN	PTPN11	PTPRD	PTPRS	PTPRT	QKI	RAB35	RAC1	RAD21	RAD50
RAD51	RAD51B	RAD51C	RAD51D	RAD52	RAD54L	RAF1	RANBP2	RARA	RASA1	RB1	RBM10	RECQL4	REL	RET
RFWD2	RHEB	RHOA	RICTOR	RIT1	RNF43	ROS1	RPS6KA4	RPS6KB1	RPS6KB2	RPTOR	RUNX1	RUNX1T1	RYBP	SDHA
SDHAF2	SDHB	SDHC	SDHD	SETBP1	SETD2	SF3B1	SH2B3	SH2D1A	SHQ1	SLIT2	SLX4	SMAD2	SMAD3	SMAD4
SMARCA4	SMARCB1	SMARCD1	SMC1A	SMC3	SMO	SNCAIP	SOCS1	SOX10	SOX17	SOX2	SOX9	SPEN	SPOP	SPTA1
SRC	SRSF2	STAG1	STAG2	STAT3	STAT4	STAT5A	STAT5B	STK11	STK40	SUFU	SUZ12	SYK	TAF1	TBX3
TCEB1	TCF3	TCF7L2	TERC	TERT	TET1	TET2	TFE3	TFRC	TGFBR1	TGFBR2	TMEM127	TMPRSS2	TNFAIP3	TNFRSF14
TOP1	TOP2A	TP53	TP63	TRAF2	TRAF7	TSC1	TSC2	TSHR	U2AF1	VEGFA	VHL	VTCN1	WISP3	WT1
XIAP	XPO1	XRCC2	YAP1	YES1	ZBTB2	ZBTB7A	ZFHX3	ZNF217	ZNF703	ZRSR2				
DNA-Sequencing of 59 genes for the detection of copy gain and copy loss in ATM, BRCA1, BRCA2, and PTEN														
AKT2	ALK	AR	ATM	BRAF	BRCA1	BRCA2	CCND1	CCND3	CCNE1	CDK4	CDK6	CHEK1	CHEK2	EGFR
ERBB2	ERBB3	ERCC1	ERCC2	ESR1	FGF1	FGF10	FGF14	FGF19	FGF2	FGF23	FGF3	FGF4	FGF5	FGF6
FGF7	FGF8	FGF9	FGFR1	FGFR2	FGFR3	FGFR4	JAK2	KIT	KRAS	LAMP1	MDM2	MDM4	MET	MYC
MYCL1	MYCN	NRAS	NRG1	PDGFRA	PDGFRB	PIK3CA	PIK3CB	PTEN	RAF1	RET	RICTOR	RPS6KB1	TFRC	
RNA-Sequencing of 55 genes for the detection of fusions and skipping mutations (splice variants) in MET and EGFR														
ABL1	AKT3	ALK	AR	AXL	BCL2	BRAF	BRCA1	BRCA2	CDK4	CSF1R	EGFR	EML4	ERBB2	ERG
ESR1	ETS1	ETV1	ETV4	ETV5	EWSR1	FGFR1	FGFR2	FGFR3	FGFR4	FLI1	FLT1	FLT3	JAK2	KDR
KIF5B	KIT	MET	MLL	MLLT3	MSH2	MYC	NOTCH1	NOTCH2	NOTCH3	NRG1	NTRK1	NTRK2	NTRK3	PAX3
PAX7	PDGFRA	PDGFRB	PIK3CA	PPARG	RAF1	RET	ROS1	RPS6KB1	TMPRSS2	TP53				
Microsatellite Instability (MSI)														
Tumor Mutational Burden (TMB)														

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