

RMH Panels Gene lists

RMH200 Version 2 panel

This custom capture panel is property of the Royal Marsden NHS trust and has been clinically validated to cover the following regions as part of the RMH200v2 panel. Analysis is performed using DNA capture and targeted sequencing using the RMH200 panel. Detection of variants is dependent on the percentage of tumour infiltration, DNA input concentration and DNA quality. This panel is capable of detecting gene amplifications (>2 copies) and deletions (<0.5 copies). Structural variant analysis is undergoing validation and calls are advisory only. Where no paired germline control is available, variants of germline origin cannot be excluded. Analysis is performed based on genome build hg19.

Please note that some rare mutations in the genes analysed may not be detected. Alterations outside the specified regions analysed cannot be detected. The limit of detection of these methods needs to be considered together with the level of tumour involvement and the quantity and quality. Some mutations may be present below the level of detection.

ABL1	CCNE1	FANCI	KRAS	PDCD1LG2	SETD2
ACVR1	CCNE2	FANCL	LIN28B	PDGFRA	SF3B1
AKT1	CD79B	FAT1	LZTR1	PHOX2B	SH2B3
AKT2	CDH1	FBXW7	MAP2K1	PIK3CA	SMAD2
AKT3	CDK12	FGF10	MAP2K2	PIK3CD	SMAD3
ALK	CDK2	FGFR1	MAP2K4	PIK3R1	SMAD4
AMER1	CDK4	FGFR2	MAP3K1	PIN1	SMARCA4
ANTRX2	CDK6	FGFR3	MAPK1	PMS1	SMARCB1
APC	CDKN1A	FGFR4	MCL1	PMS2	SMARCE1
AR	CDKN1B	FH	MDM2	POLD1	SMO
ARAF	CDKN2A	FLT3	MDM4	POLE	SOX2
ARID1A	CDKN2B	FOXL2	MEN1	POT1	SRSF2
ARID1B	CDKN2C	FOXO1	MET	PPM1D	STAG2
ARID2	CEBPA	GATA1	MLH1	PPP2R2A	STK11
ASXL1	CHEK1	GATA3	MN1	PRKAR1A	SUFU
ATM	CHEK2	GNA11	MPL	PTCH1	TCEB1
ATR	CIC	GNAQ	MRE11A	PTCH2	TCF3
ATRX	CKS1B	GNAS	MSH2	PTEN	TERT
AURKA	CREBBP	GPR161	MSH6	PTPN11	TET2
AXIN1	CRLF1	H3F3A	MTOR	RAD21	TFE3
AXIN2	CTNNB1	HIST1H3B	MYC	RAD50	TP53
B2M	CXCR4	HIST1H3C	MYCL	RAD51B	TP63

BAP1	DAXX	HIST2H3A	MYCN	RAD51C	TSC1
BARD1	DDR2	HIST2H3C	MYD88	RAD51D	TSC2
BBC3	DDX3X	HRAS	NF1	RAD54L	U2AF1
BCL2	DICER1	IDH1	NF2	RAF1	VHL
BCOR	DROSHA	IDH2	NFE2	RB1	WT1
BCORL1	EGFR	IGF1R	NFE2L2	RBM10	YAP1
BIRC3	ELP1	IRF4	NOTCH1	RET	DPYD
BRAF	EMSY	IRS2	NOTCH2	RhoA	EBF1
BRCA1	EP300	JAK2	NOTCH3	RICTOR	IL3RA
BRCA2	EPHB2	KBTBD4	NPM1	RIT1	KIAA1549
BRIP1	ERBB2	KDM6A	NRAS	RNF43	MYOD1
BTG1	ERBB3	KDR	NTRK1	ROS1	TG
BTK	ESR1	KEAP1	NTRK2	RUNX1	YES1
CALR	ETV6	KIT	NTRK3	SDHA	YWHAE
CASP8	EZH2	KLF2	OTX1	SDHB	H3F3B
CBL	F2R	KMT2A	PALB2	SDHC	ID3
CCND1	FADD	KMT2C	PAX5	SDHD	NA
CCND2	FAM46C	KMT2D	PBRM1	SETBP1	NA

HaemOnc panel

This custom capture panel is property of the Royal Marsden NHS trust and has been clinically validated to cover the following regions as part of the HaemOnc panel. Analysis is performed using DNA capture and targeted sequencing using the HaemOnc panel. Detection of variants is dependent on the percentage of tumour infiltration, DNA input concentration and DNA quality. Where no paired germline control is available, variants of germline origin cannot be excluded. Analysis is performed based on genome build hg19.

Please note that some rare mutations in the genes analysed may not be detected. Alterations outside the specified regions analysed cannot be detected. The limit of detection of these methods needs to be considered together with the level of tumour involvement and the quantity and quality. Some mutations may be present below the level of detection.

ABCA1	CCND3	ERBB3	KLF2	NTRK2	SAMD9L
ABL1	CD274	ETNK1	KMT2A	NTRK3	SAMHD1
ACD	CD79B	ETV6	KMT2C	NUDT15	SBDS
AKT1	CDKN2A	EZH2	KMT2D	NUP98	SETBP1
ANKRD26	CDKN2B	FAM46C	KMT2E	PALB2	SF1
ARAF	CDKN2C	FANCL	KRAS	PAX5	SF3B1
ARID1A	CEBPA	FBXW7	LAMB4	PDGFRA	SH2B3
ASXL1	CHEK2	FLT3	LMO1	PDS5B	SMC1A
ATM	CKS1B	FOXO1	LMO2	PHF6	SMC3
ATR	CREBBP	G6PC3	LUC7L2	PIGA	SRSF2
ATRX	CRLF2	GATA1	MAP2K1	PIK3CA	STAG2
BCL11B	CSF2RA	GATA2	MAP3K1	PIK3CD	STAT3
BCL2	CSF3R	GFI1	MECOM	PIK3R1	STAT5B
BCL2	CSNK1A1	GNAS	MEF2B	PLCG2	SUZ12
BCL6	CTC1	GNB1	MET	PMS1	TAL1
BCOR	CTCF	GPRC5A	MPL	PMS2	TERC
BCORL1	CUX1	HAX1	MYB	PPM1D	TERT
BCR	CXCR4	HRAS	MYC	PRPF8	TET1
BIRC3	DCLRE1C	IDH1	MYCN	PTEN	TET2
BOD1L1	DDX41	IDH2	MYD88	PTPN11	TINF2
BRAF	DIS3	IKZF1	NCOR1	PTPRT	TP53
BRCA1	DKC1	IL3RA	NCOR2	RAD21	TPMT
BRCA2	DNAJC21	IL7R	NF1	RAD50	TRAF2
BRCC3	DNM2	IRF1	NFE2	RAD51C	U2AF1
BTG1	DNMT3A	IRF4	NOTCH1	RAD51D	U2AF2

BTK	DNMT3B	JAGN1	NOTCH2	RB1	USP7
CALR	DUSP22	JAK1	NPM1	RHOA	VPS45
CARD11	DYPD	JAK2	NRAS	RIT1	WAS
CBL	EBF1	JAK3	NRD1	RPL10	WT1
CBLB	EED	KDM5A	NSD1	RPL5	XPO1
CCND1	ELANE	KDM6A	NT5C2	RUNX1	XRCC2
CCND2	EP300	KIT	NTRK1	SAMD9	ZRSR2

RNA Pan-Cancer panel

The [Illumina Pan Cancer Gene fusion panel](#) targets 1,385 cancer-associated genes and 21,043 exons.

This target enrichment design consists of coding regions including 160 bp of the 5' and 3' UTR of every targeted gene, to ensure full gene coverage. Enrichment was performed with 21,283 probes targeting 1385 genes associated with gene fusions, following manufacturer's protocols. Bioinformatic analysis was performed using the RNA-Seq Alignment App v2.0.1 (BaseSpace Sequencing Hub) using STAR aligner (to RefSeq Homo Sapiens/ hg19 genome) and Manta for gene fusion calling with default parameters.

High confidence fusion calls have a fusion score of >0.6 and ≥ 3 fusion supporting reads. Detection of fusions is currently undergoing validation, therefore any variants should be subject to confirmation by an orthogonal method. The method is not currently suitable for detection of STIL-TAL1 fusions.

The sensitivity of this assay is 100% (95%CI: 66.37% to 100%) with a specificity of 100% (95%:78.20% to 100%); The level of detection (LOD) is under validation. Detection of fusions is dependent on the percentage of tumour infiltration, RNA input concentration and RNA quality. Some fusions may be present below the level of detection, depending on the level of tumour infiltration and the size of the sample sent.