

At a glance

Targeted genomic sequencing assay

for comprehensive molecular characterization of tumor specimens

Genomics technology is transforming oncology treatment and drug development. The tools are now available to better understand the relationship between biomarkers and patient responses.

Quintiles has developed the Quintiles Comprehensive Cancer Panel (QCCP), a targeted sequencing assay for simultaneous analysis of genomic variation which may be predictive of response to multiple therapies in clinical development.

Improve your probability of success with the QCCP

- Detects the most common actionable somatic alterations currently reported in cancer, including: point mutations, insertions, deletions and structural rearrangements
- Identifies pathways, markers of disease and unique variant types to select for patient populations likely to benefit from targeted therapies.
- Better predicts safety and efficacy based on a tumor's genetic make up

Technical specifications

Designed for both discovery and clinical applications, the QCCP – analytically validated CLIA standards – provides insight into most pathways associated with cancers.

Genes assessed	• Sequence variation assessed in 223 cancer, DNA repair & pharmacogenomic genes • Total target bases: 1.328 megabases • 206 genes assessed for coding sequence variation • 9 genes assessed for coding sequence and genomic rearrangements • 8 genes assessed for genomic rearrangements
Technology platforms	• Sequenced on Illumina sequencing platforms
Analytical specifications	• Analytically validated to CLIA standards • Sensitivity (SNVs/InDels): > 99% for SNVs present at $\geq 5\%$ allele frequency, > 99% for indels present at $\geq 10\%$ allele frequency • Specificity: > 99% for SNVs and indels present at $\geq 5\%$ allele frequency • Limit of detection: 4% for SNVs, 10% for indels



With over 90 publications, FDA collaborations and participation in standardization initiatives, EA|Quintiles continues its market position as a leading provider of genomics services in clinical trials and research.



Improve your probability
of success™

Comprehensive cancer panel content

The 223 gene cancer panel includes the genes most commonly associated with cancers and can be used to assess mutations, deletions, insertions and rearrangements.

ABL	BLM	CRLF2	ETV4	GNAS	MAP2K4	NFE2L2	PIK3R5	SF3B1	TP63
ABL2	BRAF	CTNNA1	ETV5	GRIN2A	MAP3K1	NOTCH1	PMS1	SMAD2	TP73
ACVR1B	BRCA1	CTNNB1	ETV6	H3F3A	MAPK1	NOTCH2	PMS2	SMAD3	TPMT
AKT1	BRCA2	CYP1A2	EWSR1	HNF1A	MDM2	NOTCH3	PPP2R1A	SMAD4	TRAF7
AKT2	BTK	CYP2C19	EZH2	HRAS	MDM4	NOTCH4	PRDM1	SMARCA4	TSC1
AKT3	CARD11	CYP2C9	FAM123B	IDH1	MED12	NPM1	PTCH1	SMARCB1	TSC2
ALK	CASP8	CYP2D6	FANCA	IDH2	MEN1	NRAS	PTCH2	SMO	TSHR
APC	CBL	DAXX	FBXW7	IGF1R	MET	NTRK1	PTEN	SOCS1	TYMS
AR	CCND1	DDR2	FGFR1	IGF2R	MITF	NTRK2	PTPN11	SRC	U2AF1
ARAF	CCND2	DNMT3A	FGFR2	IKZF1	MLH1	NTRK3	RAD50	SRSF2	UGT1A1
ARID1A	CCND3	DPYD	FGFR3	IL7R	MLL	PALB2	RAD51	STAG2	VHL
ARID1B	CCNE1	EGFR	FGFR4	INSR	MPL	PARP1	RAF1	STAT1	VKORC1
ASXL1	CDC73	EP300	FLT1	JAK1	MRE11A	PAX5	RARA	STAT3	WRN
ATM	CDH1	ERBB2	FLT3	JAK2	MSH2	PBRM1	RB1	STK11	WT1
ATR	CDK4	ERBB3	FLT4	JAK3	MSH6	PDGFRA	RET	SUFU	XPC
ATRX	CDK6	ERBB4	FOXL2	KDM6A	MTHFR	PDGFRB	RICTOR	TERT	XRCC1
AURKA	CDKN2A	ERCC1	G6PD	KDR	MTOR	PDK1	RNF43	TET2	
AURKB	CDKN2B	ERCC2	GATA1	KIT	MYC	PGR	ROS1	TGFBR2	
AXIN1	CEBPA	ERCC3	GATA2	KLF4	MYCN	PHF6	RPTOR	TMPRSS2	
BAP1	CHEK1	ERG	GATA3	KRAS	MYD88	PIK3CA	RSPO2	TNFAIP3	
BCL2	CHEK2	ERRF1	GLI1	MAML1	NBN	PIK3CG	RSPO3	TOP1	
BCOR	CREBBP	ESR1	GNA11	MAP2K1	NF1	PIK3R1	RUNX1	TOP2A	
BCR	CSF1R	ETV1	GNAQ	MAP2K2	NF2	PIK3R2	SETD2	TP53	

 Coding Sequence and Rearrangement Assessment (9 genes)

 Rearrangement Assessment Only (8 genes)



Tumor sample requirements:

Tumor samples should have $\geq 20\%$ tumor cellularity.

375 ng of tumor DNA
or 50 mg of fresh frozen tumor tissue
or 10 unstained FFPE slides (5-10 μm thick)



Turnaround time:

Standard TAT 3-4 weeks, expedited TAT available for prospective trials.

Unmatched genomic and bioinformatics expertise

Together, Expression Analysis (EAIQuintiles) and Quintiles provide comprehensive genomic technologies and valuable insight across the entire continuum of drug development.

- Unmatched experience in development of custom sequencing assays
- A variety of preconfigured CLIA LDTs
- Bioinformatics staff includes PhD-level scientists drawn from computer science, statistics and biology
- Other assays such as QPCR, RT-PCR, FISH, IHC, or 3rd generation sequencing also available
- Biological Pathway Analysis and Cohort Analysis

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