CinCSeq Comprehensive Cancer Panel

The CinCSeq Comprehensive Cancer Panel is designed to interrogate for single nucleotide variants (SNV), multi-nucleotide variants (MNV), and insertion and deletion (Indel) variants across 388 cancer-related genes, and copy number variations (CNV) across 531 cancer-related genes (Table 1) from genomic DNA. The DNA portion covers approximately 95% of coding exons of sequenced genes. The RNA portion is designed to identify gene fusions and select structural variants (SV) involving 184 cancer-related genes (Table 2). It can identify known fusion partners as well as ~98% of novel fusion partners of driver oncogenes.

Sequencing is performed using the GOAL consortium (https://www.goalabs.org/) hybrid capture probe set with custom modifications for pediatric and young adult cancer on high-throughput Illumina sequencing platforms. Analytic sensitivity is 3-5% variant allele fraction (VAF) with at least 300x sequencing depth for detection of SNV, MNV, and small Indels (<10bp) and 5-10% VAF with a minimum of 200x sequencing depth for larger indels (>10bp) and SV, including internal tandem duplication (ITD) variants. Genomic regions with lower coverage are specified in the report. A minimum of 5 unique spanning reads supporting a gene fusion call is required. Orthogonal confirmation for one or more genomic alterations may be performed if appropriate. For more information about the test, call the lab at 513-636-9820.

Reporting Units:

CinCSeq is a qualitative NGS assay that reports clinically actionable and potentially clinically actionable sequence variants with interpretation text. Variants of uncertain significance (VUS) are listed in the report without any associated interpretation text. Benign or likely benign variants are not included in the report.

Acceptable Specimens:

- 3-5 mL whole blood in EDTA tube
- 3-5 mL bone marrow in EDTA tube
- Fresh/frozen tissue
- FFPE tissue: 1 H&E slide and 6 unstained slides at 5 microns each; fix in 10% neutral buffered formalin
- Paraffin block (block will be returned upon completion of test)
- A minimum of 20% viable tumor cells is required for DNA mutation and gene fusion identification. For reliable copy number variation (CNV) detection, at least 50% viable tumor cells are required.

Unacceptable Specimens:

- Decalcified tissue
- Frozen whole blood or bone marrow
- Sample collected in heparin

Shipping Conditions:

- Blood and bone marrow samples collected within the institution must be delivered to the lab within 6 hours of collection. Do NOT freeze.
- Blood and bone marrow samples collected outside the institution must be shipped at 4°C in an insulated container by **overnight** courier. Do NOT freeze.
- Tissue, slides, or blocks at ambient temperature.
- **For all samples, ship for delivery on Monday through Friday. Receiving docks are CLOSED on weekends and holidays; do NOT ship if delivery will occur on those days.**

Testing Schedule:

CinCSeq testing is performed Mon-Fri. For testing outside of this schedule, call the lab at 513-636-9820.
TAT: 7-10 business days (maximum 14 business days)

CPT Codes:

88363 – Tissue review & selection
81455 – Targeted genome analysis
G0452 – Physician interpretation

Clinical Lab Index:

CinCSeq Comprehensive Panel:
https://www.testmenu.com/cincinnatichildrens/Tests/1169861

Contact Information:

Cincinnati Children's Division of Pathology
Molecular and Genomic Pathology Services (MGPS)
Phone: 513-636-9820
Fax: 513-517-7099
Email: pathology@cchmc.org
Website: cincinnatichildrens.org/pathology

For pricing or billing questions, call 513-636-4261.

Shipping Address:

Cincinnati Children's Hospital Medical Center
Attn: Molecular and Genomic Pathology Services (MGPS)
240 Albert Sabin Way, R2.001
Cincinnati, OH 45229

References:
1. Cancer Genome Atlas Research Network. *Cell*. 2017; 171:950-965.e28.
2. Li M, et al. *J Mol Diagn.* 2017; 19:4-23.

Table 1: DNA gene list (SNV, MNV, Indels - 388 genes) (CNV – 531 genes)

* - Only CNV analysis or ^ - Internal Tandem Duplication (ITD) interrogated; $ - Exon 1 region not entirely sequenced

ABL1	ABL2	ABRAXAS1*	ACVR1	ACVR1B*	ADGRA2*	AKT1	AKT2	AKT3	ALK
AMER1	APC	AR	ARAF	ARFRP1*	ARID1A	ARID1B$	ARID2	ASXL1	ATM
ATR	ATRX	AURKA	AURKB	AXIN1	AXIN2	AXL	B2M	BAP1	BARD1
BCL10*	BCL11B*	BCL2	BCL2L1*	BCL2L2*	BCL6	BCL7A	BCOR^	BCORL1	BIRC3
BLM	BMPR1A	BRAF	BRCA1	BRCA2	BRCC3*	BRD3*	BRD4	BRINP3*	BRIP1
BTG1	BTK	BUB1B*	C19MC	CALR	CARD11	CASP8*	CBFB	CBL	CBLB
CBLC	CCN6	CCND1	CCND2	CCND3	CCNE1	CD19*	CD274	CD28*	CD40*
CD58	CD79A	CD79B	CDC73	CDH1	CDK12	CDK4	CDK6	CDK8	CDKN1A
CDKN1B	CDKN2A	CDKN2B	CDKN2C	CEBPA	CHD2	CHD4	CHEK1	CHEK2	CIC
CIITA*	COL1A1	CREBBP	CRKL	CRLF2	CSF1R	CSF3R	CSNK1A1*	CTCF	CTLA4*
CTNNA1*	CTNNB1	CUL3	CUX1	CXCR4	CYLD	DAXX	DDR2	DDX3X	DDX41
DGCR8	DICER1	DNM2	DNMT3A	DOT1L	DROSHA	EBF1	EED	EFNB2*	EGFR
EGR2*	EIF1AX	ELOC	EMSY*	EP300	EPCAM	EPHA3	EPHA5	EPHA7*	EPHB1
EPHB4*	ERBB2	ERBB3	ERBB4	ERCC1*	ERCC2	ERCC3*	ERCC4*	ERCC5*	ERG*
ERRFI1*	ESR1	ETNK1	ETS1*	ETV1*	ETV4*	ETV5*	ETV6	EWSR1*	EXT1
EZH2	FANCA	FANCC	FANCD2*	FANCE*	FANCF*	FANCG*	FANCL*	FANCM*	FAS
FAT1	FAT3*	FBXO11	FBXW7	FGF10*	FGF14*	FGF19	FGF23*	FGF3	FGF4
FGF6*	FGFR1	FGFR2	FGFR3	FGFR4	FH	FLCN	FLT1	FLT3^	FLT4
FOXA1	FOXL2	FOXO1*	FOXP1	FOXR2*	FRK	FRS2*	FUBP1	FUS*	GABRA6*
GATA1	GATA2	GATA3	GATA4*	GATA6*	GEN1*	GID4*	GLI1	GLI2	GNA11
GNA13	GNA14	GNAQ	GNAS	GNB1	GPC3*	GREM1*	GRIN2A	GRM3*	GSK3B
H1-4	H3-3A	H3-3B	H3C2	H3C3	HDAC4	HDAC9	HGF	HIF1A	HMGA2*
HNF1A	HOXB13*	HRAS	HSD3B1	HSP90AA1*	ID3	IDH1	IDH2	IGF1R	IGF2*
IKBKE	IKZF1	IKZF2	IKZF3	IL2RG*	IL6ST	IL7R	INHBA*	INPP4B	IRF2
IRF4	IRF8*	IRS2*	ITK*	ITPKB*	JAK1	JAK2	JAK3	JAZF1*	JUN*
KAT6A*	KBTBD4	KCNJ5	KDM4C	KDM5A	KDM5C	KDM6A	KDR	KEAP1	KEL*
KIF1B*	KIF5B*	KIT	KLF2	KLF4	KLHL6*	KMT2A	KMT2B	KMT2C	KMT2D
KRAS	LEF1	LIFR*	LMO1	LRP1B*	LYN*	LYST*	LZTR1	MAGI2*	MAML2*
MAP2K1	MAP2K2	MAP2K4	MAP3K1	MAP3K14	MAP3K3*	MAP3K7*	MAPK1	MAPK3	MAX
MCL1	MDM2	MDM4	MECOM	MED12	MEF2B	MEN1	MET	MITF	MLH1
MLH3	MLLT1	MN1	MPL	MRE11	MSH2	MSH3	MSH6	MTOR	MUTYH
MYB	MYBL1	MYC	MYCL*	MYCN	MYD88	MYH9*	MYOD1	NBN	NCOA2*
NCOR1	NCOR2	NF1	NF2	NFE2	NFE2L2	NFKBIA	NFKBIE	NKX2-1	NOTCH1
NOTCH2	NOTCH3	NPM1	NRAS	NSD1	NSD2	NT5C2	NTHL1	NTRK1	NTRK2
NTRK3	NUP214*	NUP93*	NUTM1*	OTX2	PAK3	PALB2	PAX3*	PAX5	PAX7*
PAX8*	PBRM1	PDCD1	PDCD1LG2*	PDGFB*	PDGFRA	PDGFRB	PDK1*	PHF6	PHOX2B
PIGA	PIK3C2B*	PIK3CA	PIK3CB	PIK3CD	PIK3CG	PIK3R1	PIK3R2	PIM1	PLAG1*
PLCG1	PLCG2	PML*	PMS1	PMS2	POLD1*	POLE	POLR2A	POT1	PPARG*
PPM1D	PPP2R1A	PRDM1	PREX2	PRKAR1A	PRKCA	PRKCI*	PRKDC	PRKN	PRPF40B
PRPF8	PRSS8*	PTCH1	PTEN	PTPN11	PTPRD	PTPRT	QKI*	RAB35*	RAC1
RAD21	RAD50	RAD51	RAD51B	RAD51C	RAD51D	RAF1	RANBP2*	RARA*	RASA1
RB1	RBM10	RECQL*	RECQL4*	REL*	RELA*	RET	RHOA	RICTOR	RINT1*
RIT1	RNF43	ROS1*	RPS15	RPS20*	RPS6KA3	RPTOR	RRAGC	RSPO2*	RSPO3*
RUNX1	RUNX1T1*	SAMD9	SAMD9L	SBDS*	SDHA	SDHB	SDHC	SDHD	SETBP1
SETD2	SF1	SF3A1	SF3B1	SGK1	SH2B3	SIX1	SIX2	SLIT2*	SLX4
SMAD2	SMAD3	SMAD4	SMARCA4	SMARCB1	SMC1A	SMC3	SMO	SNCAIP*	SOCS1
SOS1	SOX10*	SOX2	SOX9*	SPEN	SPOP	SPTA1	SRC	SRSF2	SS18*
STAG2	STAT3	STAT4*	STAT5B	STAT6	STK11	SUFU	SUZ12	SYK*	TAF1
TBL1XR1	TBX3	TBXT*	TCF12	TCF3	TCF7L2	TEK	TENT5C*	TERC	TERT
TET1*	TET2	TFE3*	TFEB*	TGFBR2	TMPRSS2*	TNFAIP3	TNFRSF14	TOP1	TOP2A*
TP53	TP63	TPMT*	TRAF3	TRAF7	TRRAP	TSC1	TSC2	TSHR	TYK2
U2AF1	U2AF2	USP6*	USP7	VAV1	VEGFA	VHL	WRN	WT1	XPC*
XPO1	XRCC2*	YAP1*	YWHAE*	ZBTB2*	ZFTA*	ZMYM3	ZNF217*	ZNF703*	ZNF750
ZRSR2									

Table 2: RNA gene list (184 genes)

* - CTNNB1 exon-level (large) deletions, ^ - EGFRvIII, and $ - MET exon 14 skipping variant interrogated in addition to gene fusion

ABL1	ABL2	AKT3	ALK	ARHGAP26	AXL	BCL10	BCL11B	BCL2	BCL6
BCOR	BCORL1	BCR	BIRC3	BRAF	BRD3	BRD4	BTG1	C11ORF95	CAMTA1
CARD11	CBFB	CBL	CCND1	CCND3	CDK6	CHIC2	CIC	CIITA	COL1A1
CREBBP	CRLF2	CSF1R	CTNNB1*	DEK	DNAJB1	DUSP22	EBF1	EGFR^	EP300
EPC1	EPOR	ERBB2	ERG	ESR1	ETV1	ETV4	ETV5	ETV6	EWSR1
FER	FGFR1	FGFR2	FGFR3	FGR	FLT3	FOS	FOSB	FOXO1	FOXP1
FOXR2	FUS	GLI1	GLI2	GLIS2	HLF	HMGA2	HTRA1	IKZF1	IKZF2
IKZF3	IRF4	ITK	JAK1	JAK2	JAK3	JAZF1	KAT6A	KIF5B	KLF2
KMT2A	LMO1	LYN	MALT1	MAML2	MAST1	MAST2	MEAF6	MECOM	MEF2D
MET$	MKL1	MKL2	MLLT10	MLLT4	MN1	MSMB	MYB	MYBL1	MYC
MYH11	MYH9	NCOA1	NCOA2	NCOA3	NF1	NF2	NFKB2	NOTCH1	NOTCH2
NPM1	NR4A3	NRG1	NSD1	NTRK1	NTRK2	NTRK3	NUMBL	NUP214	NUP98
NUTM1	PAG1	PAX3	PAX5	PAX7	PAX8	PDCD1LG2	PDGFB	PDGFRA	PDGFRB
PHF1	PIK3CA	PKN1	PLAG1	PML	PPARG	PRDM1	PRDM16	PRKACA	PRKCA
PRKCB	PTCH1	PTK2B	PVT1	QKI	RAF1	RARA	RELA	RET	ROS1
RSPO2	RSPO3	RUNX1	RUNX1T1	SETD2	SS18	SSX1	SSX2	SSX4	STAT6
SUZ12	SYK	TAF15	TAL1	TBL1XR1	TCF12	TCF3	TERT	TET1	TFE3
TFEB	TFG	THADA	TMPRSS2	TOP1	TP63	TYK2	USP6	VGLL2	WHSC1
YAP1	YWHAE	ZCCHC7	ZNF384						