NEO GENOMICS

TSO 500 HT

Comprehensive tissue profiling

Powered by TruSight™ Oncology 500 High-Throughput

TSO 500 HT assay is a comprehensive genomic profiling (CGP) assay that provides clinically actionable insights through broad DNA and RNA sequencing of solid tumor tissue.

With coverage of over 500 cancer-related genes, TSO 500 HT empowers biopharmaceutical partners with deep molecular insights for biomarker identification, target analysis, and resistance detection – advancing precision oncology at every stage.

517-gene panel covering all major variant classes by DNA and RNA NGS

SNVs | InDels | CNVs | Fusions | MSI & TMB status

Results available within 10 days

Reduced sample input: As few as 10 slides

Analysis report Standard and custom options

TSO 500 HT validation performance data

Variant class	Analytical sensitivity	Specificity	Accuracy
SNVs	95.2%	>99.9%	99.9%
InDels	92.4%	>99.9%	99.9%
CNVs	100.0%	99.6%	99.7%
Fusions	94.4%	99.9%	99.7%
Technical assay			
Limit of detection (LOD)	5% VAF for small variants CNV reporting cutoff is 2.2x fold-change		

Multimodal comprehensive menu: Complement your genomic data with our extensive portfolio of assays spanning IHC, ISH, FISH, Cytogenetics, Flow, and Spatial testing.

CNV = copy number variant; FFPE = formalin-fixed paraffin-embedded
FNAs = fine needle aspirations; H&E = hematoxylin and eosin
IHC = immunohistochemistry; InDels = insertions/deletions; MSI = microsatellite instability
NGS = next-generation sequencing; SNVs = single-nucleotide variants; TMB = tumor mutation burden
VAF = variant allele frequency

Batch testing TAT based on sample size
Clinically annotated report available upon request

TSO 500 HT specimen requirements

BLOCK

FFPE tissue: ≥5 mm^2 of tissue surface area and ≥20% tumor (~500 tumor cells). *(Additional 100 neoplastic cells for PD-L1.)*

PRE-CUT SLIDES

5-micron unstained slides: 10 unstained slides *(2 sections per slide preferred)* plus 1 additional unstained slide for H&E.

For cell block, FNAs, small needle core biopsies: 20 unstained slides *(2 sections per slide preferred)* plus 1 additional unstained slide for H&E; 3 unstained slides are required per IHC clone ordered *(e.g., PD-L1)*.

TSO 500 HT gene list

DNA: Detection of SNVs, InDels, and CNVs

ABL1	BCL2L2	CDKN2C	EIF4A2	**FGF1**	GNA13	IGF1R	MALT1	NCOA3	PHOX2B	RAC1	SH2D1A	TERC
ABL2	BCL6	CEBPA	EIF4E	**FGF2**	GNAQ	IGF2	MAP2K1	NCOR1	PIK3C2B	RAD21	SHQ1	TERT
ABRAXAS1	BCOR	CENPA	ELOC	**FGF3**	GNAS	IKBKE	MAP2K2	NEGR1	PIK3C2G	RAD50	SLIT2	TET1
ACVR1	BCORL1	CHD2	EML4	**FGF4**	GPS2	IKZF1	MAP2K4	NF1	PIK3C3	RAD51	SLX4	TET2
ACVR1B	BCR	CHD4	EMSY	**FGF5**	GREM1	IL10	MAP3K1	NF2	**PIK3CA**	RAD51B	SMAD2	TFE3
ADGRA2	BIRC3	**CHEK1**	EP300	**FGF6**	GRIN2A	IL7R	MAP3K4	NFE2L2	**PIK3CB**	RAD51C	SMAD3	**TFRC**
AKT1	BLM	**CHEK2**	EPCAM	**FGF7**	GRM3	INHA	MAP3K13	NFKBIA	PIK3CD	RAD51D	SMAD4	TGFBR1
AKT2	BMPR1A	CIC	EPHA3	**FGF8**	GSK3B	INHBA	MAP3K14	NKX2-1	PIK3CG	RAD52	SMARCA4	TGFBR2
AKT3	**BRAF**	COP1	EPHA5	**FGF9**	H1-2	INPP4A	MAPK1	NKX3-1	PIK3R1	RAD54L	SMARCB1	TMEM127
ALK	**BRCA1**	CREBBP	EPHA7	**FGF10**	H2BC5	INPP4B	MAPK3	NOTCH1	PIK3R2	**RAF1**	SMARCD1	TMPRSS2
ALOX12B	**BRCA2**	CRKL	EPHB1	**FGF14**	H3-5	INSR	MAX	NOTCH2	PIK3R3	RANBP2	SMC1A	TNFAIP3
AMER1	BRD4	CRLF2	**ERBB2**	**FGF19**	H3-3A	IRF2	MCL1	NOTCH3	PIM1	RARA	SMC3	TNFRSF14
ANKRD11	BRIP1	CSF1R	**ERBB3**	**FGF23**	H3-3B	IRF4	MDC1	NOTCH4	PLCG2	RASA1	SMO	TOP1
ANKRD26	BTG1	CSF3R	ERBB4	**FGFR1**	H3-4	IRS1	**MDM2**	NPM1	PLK2	RB1	SNCAIP	TOP2A
APC	BTK	CSNK1A1	**ERCC1**	**FGFR2**	H3C1	IRS2	**MDM4**	**NRAS**	PMAIP1	RBM10	SOCS1	TP53
AR	CALR	CTCF	**ERCC2**	**FGFR3**	H3C2	JAK1	MED12	**NRG1**	PMS1	RECQL4	SOX2	TP63
ARAF	CARD11	CTLA4	ERCC3	**FGFR4**	H3C3	**JAK2**	MEF2B	NSD1	PMS2	REL	SOX9	TRAF2
ARFRP1	CASP8	CTNNA1	ERCC4	FH	H3C4	JAK3	MEN1	NTRK1	PNRC1	**RET**	SOX10	TRAF7
ARID1A	CBFB	CTNNB1	ERCC5	FLCN	H3C6	JUN	**MET**	NTRK2	POLD1	RHEB	SOX17	TSC1
ARID1B	CBL	CUL3	ERG	FLI1	H3C7	KAT6A	MGA	NTRK3	POLE	RHOA	SPEN	TSC2
ARID2	CCN6	CUX1	ERRFI1	FLT1	H3C8	KDM5A	MITF	NUP93	PPARG	**RICTOR**	SPOP	TSHR
ARID5B	**CCND1**	CXCR4	**ESR1**	FLT3	H3C10	KDM5C	MLH1	NUTM1	PPM1D	RIT1	SPTA1	U2AF1
ASXL1	CCND2	CYLD	ETS1	FLT4	H3C11	KDM6A	MLLT3	PAK1	PPP2R1A	RNF43	SRC	VEGFA
ASXL2	**CCND3**	DAXX	ETV1	FOXA1	H3C12	KDR	MPL	PAK3	PPP2R2A	ROS1	SRSF2	VHL
ATM	**CCNE1**	DCUN1D1	ETV4	FOXL2	H3C13	KEAP1	MRE11A	PAK5	PPP6C	RPS6KA4	STAG1	VTCN1
ATR	CD274	DDR2	ETV5	FOXO1	H3C14	KEL	MSH2	PALB2	PRDM1	**RPS6KB1**	STAG2	WT1
ATRX	CD276	DDX41	ETV6	FOXP1	H3C15	KIF5B	MSH3	PARP1	PREX2	RPS6KB2	STAT3	XIAP
AURKA	CD74	DHX15	EWSR1	FRS2	HGF	**KIT**	MSH6	PAX3	PRKAR1A	RPTOR	STAT4	XPO1
AURKB	CD79A	DICER1	EZH2	FUBP1	HNF1A	KLF4	MST1	PAX5	PRKCI	RUNX1	STAT5A	XRCC2
AXIN1	CD79B	DIS3	FANCA	FYN	HNRNPK	KLHL6	MST1R	PAX7	PRKDC	RUNX1T1	STAT5B	YAP1
AXIN2	CDC73	DNAJB1	FANCC	GABRA6	HOXB13	KMT2A	MTOR	PAX8	PRKN	RYBP	STK11	YES1
AXL	CDH1	DNMT1	FANCD2	GATA1	HRAS	**KRAS**	MUTYH	PBRM1	PRSS8	SDHA	STK40	ZBTB2
B2M	CDK12	DNMT3A	FANCE	GATA2	HSD3B1	**LAMP1**	MYB	PDCD1	PTCH1	SDHAF2	SUFU	ZBTB7A
BAP1	**CDK4**	DNMT3B	FANCF	GATA3	HSP90AA1	LATS1	**MYC**	PDCD1LG2	**PTEN**	SDHB	SUZ12	ZFHX3
BARD1	**CDK6**	DOT1L	FANCG	GATA4	ICOSLG	LATS2	**MYCL**	**PDGFRA**	PTPN11	SDHC	SYK	ZNF217
BBC3	CDK8	E2F3	FANCI	GATA6	ID3	LMO1	**MYCN**	**PDGFRB**	PTPRD	SDHD	TAF1	ZNF703
BCL10	CDKN1A	EED	FANCL	GEN1	IDH1	LRP1B	MYD88	PDK1	PTPRS	SETBP1	TBX3	ZRSR2
BCL2	CDKN1B	EGFL7	FAS	GID4	IDH2	LYN	MYOD1	PDPK1	PTPRT	SETD2	TCF3	
BCL2L1	CDKN2A	**EGFR**	FAT1	GLI1	IFNGR1	LZTR1	NAB2	PGR	QKI	SF3B1	TCF7L2	
BCL2L11	CDKN2B	EIF1AX	FBXW7	GNA11	IGF1	MAGI2	NBN	PHF6	RAB35	SH2B3	TENT5C	

Shaded content is analyzed for CNV detection in addition to SNVs and InDels.

RNA: Detection of fusions and splice variants

ABL1	AXL	BRCA2	EML4	ETS1	EWSR1	FGFR4	JAK2	KMT2A	MYC	NRG1	PAX3	PIK3CA	ROS1
AKT3	BCL2	CDK4	ERBB2	ETV1	FGFR1	FLI1	KDR	**MET**	NOTCH1	NTRK1	PAX5	PPARG	RPS6KB1
ALK	BRAF	CSF1R	ERG	ETV4	FGFR2	FLT1	KIF5B	MLLT3	NOTCH2	NTRK2	PDGFRA	RAF1	TMPRSS2
AR	BRCA1	**EGFR**	ESR1	ETV5	FGFR3	FLT3	KIT	MSH2	NOTCH3	NTRK3	PDGFRB	RET	

All genes listed are assessed for known and novel fusions; shaded content is analyzed for splice variants.

Genomic signatures: MSI, TMB

MSI-high is defined as ≥20% of loci showing instability; microsatellite-stable (MSS) is defined as <20% of loci showing instability.

TMB-high is defined as ≥10.0 mutations per megabase (mut/Mb); TMB-low is defined as <10.0 mut/Mb

For more information on TSO 500 HT, call us at 866.776.5907, option 3, or email us at ContactPharma@NeoGenomics.com.

NeoGenomics, Inc. is a premier cancer diagnostics company specializing in cancer genetics testing and oncology data solutions. We offer one of the most comprehensive oncology-focused testing menus across the cancer continuum, serving oncologists, pathologists, hospital systems, academic centers, and pharmaceutical firms with innovative diagnostic and predictive testing to help them diagnose and treat cancer. Headquartered in Fort Myers, FL, NeoGenomics operates a network of CAP-accredited and CLIA-certified laboratories for full-service sample processing and analysis services throughout the US and a CAP-accredited full-service, sample-processing laboratory in Cambridge, England, United Kingdom.

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