TEMPUS | ONCOLOGY

xT + xR

BROAD MOLECULAR PROFILING FOR SOLID TUMORS

xT Solid Tumor + Normal Match DNA Sequencing
xR RNA Whole Transcriptome Sequencing

xT Solid Tumor/Normal DNA seq + xR RNA seq

- **648 gene panel by DNA seq**
- **Incidental germline findings through DNA seq**
- **Microsatellite instability (MSI) Status and Tumor Mutational Burden (TMB) through DNA seq**
- **Results typically expected within 10 days of specimen retrieval**
- **Whole transcriptome RNA seq with validated fusion detection**
- **Altered splicing for MET Exon 14 and EGFRvIII through RNA seq**

ADD-ON TESTS

- **Algorithmic testing options with no additional tissue required**

  Homologous Recombination Deficiency (HRD)* / Tumor Origin (TO)† / DPYD** / UGT1A1** / PurIST℠†

  **xT solid tumor + normal match DNA seq required for breast and ovarian cancer HRD testing; all other cancers require xR RNA seq*

  †xR RNA seq required

  ***xT solid tumor + normal match DNA seq required*

- **Immunohistochemistry (IHC) Options: PD-L1 and MMR**

Ordering Options

Our comprehensive platform allows for easy ordering options:

- Flexible ordering options via online ordering through the Tempus Hub, paper requisition, or EHR integration
- Solid tumor and liquid biopsy available as ordered separately or in combination
- Automatic conversion option from xT Solid Tumor/Normal Match DNA seq to xF liquid biopsy panel, in the event of insufficient tumor tissue
- Receive secure access to patient results on the go by downloading the Tempus Hub Mobile App

See requisition for more details

What is xT Solid Tumor + Normal Match?

Solid tumor + normal matched testing is DNA sequencing of a solid tumor biopsy and a normal sample (blood or saliva) simultaneously.

Through our tumor/normal match approach, there is a 28% reduction in somatic false-positive calls and improving variant accuracy compared to a tumor-only analysis.[1]

Tumor/normal match sequencing may additionally detect incidental germline findings in a limited set of genes, for which a validated germline panel may be indicated for confirmatory testing.[2]

The Benefits of Combined Molecular and Clinical Data For Patients[1]

As published in *Nature Biotechnology* Journal

Results from our retrospective, 500 de-identified patient cohort illustrates:

- Potential value of integrated clinical and molecular data
- High rates of patients matched to targeted therapies and clinical trials with paired tumor/normal DNA sequencing and whole transcriptome RNA sequencing

Increase in therapy matching for cancer patients

29.6%

of patients with DNA sequencing alone are matched to targeted therapies

43.4%

of patients with combined DNA sequencing, RNA sequencing, and immune biomarker assessment are matched to targeted therapies

Increase in clinically relevant fusion detection via RNA sequencing

Out of the 32 total oncogenic gene fusions within the study, whole transcriptome RNA sequencing discovered **4 that would have been missed** using DNA sequencing alone.

Increase in clinical trial matching

96.2%

of patients were matched to a clinical trial through integrated clinical and molecular data analysis

We help provide access to our tests for patients in financial need.

Patients can complete the application online at **access.tempus.com** or call **800-739-4137** to speak to a member of our team.

If you have any questions on our comprehensive portfolio please contact your Tempus Representative or email **support@tempus.com**.

xT DNA seq Gene Panel

Average coverage ~500x

ABCB1	BCL7A	CDKN1B	DOT1L	FANCG	GATA4	HNF1B
ABCC3	BCLAF1	CDKN1C	DPYD	FANCI	GATA6	HOXA11
ABL1	BCOR	CDKN2A**	DYNC2H1	FANCL	GEN1	HOXB13
ABL2	BCORL1	CDKN2B	EBF1	FANCM	GLI1	HRAS
ABRAXAS1	BCR	CDKN2C	ECT2L	FAS	GLI2	HSD11B2
ACTA2	BIRC3	CEBPA**	EGF	FAT1	GNA11	HSD3B1
ACVR1	BLM**	CEP57	EGFR**	FBXO11	GNA13	HSD3B2
(ALK2)	BMPR1A**	CFTR	EGLN1	FBXW7	GNAQ	HSP90AA1
ACVR1B	BRAF	CHD2	EIF1AX	FCGR2A	GNAS	HSPH1
AGO1	BRCA1**	CHD4	ELF3	FCGR3A	GPC3	IDH1
AJUBA	BRCA2**	CHD7	ELOC	FDPS	GPS2	IDH2
AKT1	BRD4	CHEK1	(TCEB1)	FGF1	GREM1	IDO1
AKT2	BRIP1**	CHEK2**	EMSY	FGF10	GRIN2A	IFIT1
AKT3	BTG1	CIC	ENG	FGF14	GRM3	IFIT2
ALK	BTK	CIITA	EP300	FGF2	GSTP1	IFIT3
AMER1	BUB1B	CKS1B	EPCAM**	FGF23	H19	IFNAR1
APC**	C11orf65	CREBBP	EPHA2	FGF3	H3F3A	IFNAR2
APLNR	C3orf70	CRKL	EPHA7	FGF4	HAS3	IFNGR1
APOB	C8orf34	CRLF2	EPHB1	FGF5	HAVCR2	IFNGR2
AR	CALR	CSF1R	EPHB2	FGF6	HDAC1	IFNL3
ARAF	CARD11	CSF3R	EPOR	FGF7	HDAC2	IKBKE
ARHGAP26	CARM1	CTC1	ERBB2	FGF8	HDAC4	IKZF1
ARHGAP35	CASP8	CTCF	(HER2)	FGF9	HGF	IL10RA
ARID1A	CASR	CTLA4	ERBB3	FGFR1	HIF1A	IL15
ARID1B	CBFB	CTNNA1	ERBB4	FGFR2	HIST1H1E	IL2RA
ARID2	CBL	CTNNB1	ERCC1	FGFR3	HIST1H3B	IL6R
ARID5B	CBLB	CTRC	ERCC2	FGFR4	HIST1H4E	IL7R
ASNS	CBLC	CUL1	ERCC3	FH**	HLA-A	ING1
ASPSCR1	CBR3	CUL3	ERCC4	FHIT	HLA-B	INPP4B
ASXL1	CCDC6	CUL4A	ERCC5	FLCN**	HLA-C	IRF1
ATIC	CCND1	CUL4B	ERCC6	FLT1	HLA-DMA	IRF2
ATM**	CCND2	CUX1	ERG	FLT3	HLA-DMB	IRF4
ATP7B	CCND3	CXCR4	ERRFI1	FLT4	HLA-DOA	IRS2
ATR	CCNE1	CYLD	ESR1	FNTB	HLA-DOB	ITPKB
ATRX	CD19	CYP1B1	ETS1	FOXA1	HLA-DPA1	JAK1
AURKA	CD22	CYP2D6	ETS2	FOXL2	HLA-DPB1	JAK2
AURKB	CD274 (PD-	CYP3A5	ETV1	FOXO1	HLA-DPB2	JAK3
AXIN1	L1)	CYSLTR2	ETV4	FOXO3	HLA-DQA1	JUN
AXIN2**	CD40	DAXX	ETV5	FOXP1	HLA-DQA2	KAT6A
AXL	CD70	DDB2	ETV6**	FOXQ1	HLA-DQB1	KDM5A
B2M	CD79A	DDR2	EWSR1	FRS2	HLA-DQB2	KDM5C
BAP1**	CD79B	DDX3X	EZH2	FUBP1	HLA-DRA	KDM5D
BARD1**	CDC73	DICER1**	FAM46C	FUS	HLA-DRB1	KDM6A
BCL10	CDH1**	DIRC2	FANCA	G6PD	HLA-DRB5	KDR
BCL11B	CDK12	DIS3	FANCB	GABRA6	HLA-DRB6	KEAP1
BCL2	CDK4**	DIS3L2	FANCC	GALNT12	HLA-E	KEL
BCL2L1	CDK6	DKC1	FANCD2	GATA1	HLA-F	KIF1B
BCL2L11	CDK8	DNM2	FANCE	GATA2**	HLA-G	KIT**
BCL6	CDKN1A	DNMT3A	FANCF	GATA3	HNF1A	KLF4

***Genes in which incidental germline findings are reported*

KLHL6	MSH2**	PAX7	PTCH1**	SEMA3C	TBC1D12	XPA
KLLN	MSH3**	PAX8	PTCH2	SETBP1	TBL1XR1	XPC
KMT2A	MSH6**	PBRM1	PTEN**	SETD2	TBX3	XPO1
KMT2B	MTAP	PCBP1	PTPN11	SF3B1	TCF3	XRCC1
KMT2C	MTHFD2	PDCD1	PTPN13	SGK1	TCF7L2	XRCC2
KMT2D	MTHFR	PDCD1LG2	PTPN22	SH2B3	TCL1A	XRCC3
KRAS	MTOR	PDGFRA**	PTPRD	SHH	TERT*	YEATS4
L2HGDH	MTRR	PDGFRB	PTPRT	SLC26A3	TET2	ZFHX3
LAG3	MUTYH**	PDK1	QKI	SLC47A2	TFE3	ZMYM3
LATS1	MYB	PHF6	RAC1	SLC9A3R1	TFEB	ZNF217
LCK	MYC	PHGDH	RAD21	SLIT2	TFEC	ZNF471
LDLR	MYCL	PHLPP1	RAD50	SLX4	TGFBR1	ZNF620
LEF1	MYCN	PHLPP2	RAD51	SMAD2	TGFBR2	ZNF750
LMNA	MYD88	PHOX2B**	RAD51B	SMAD3	TIGIT	ZNRF3
LMO1	MYH11	PIAS4	RAD51C**	SMAD4**	TMEM127**	ZRSR2
LRP1B	NBN**	PIK3C2B	RAD51D**	SMARCA1	TMEM173	
LYN	NCOR1	PIK3CA	RAD54L	SMARCA4**	TMPRSS2	
LZTR1	NCOR2	PIK3CB	RAF1	SMARCB1**	TNF	
MAD2L2	NF1**	PIK3CD	RANBP2	SMARCE1	TNFAIP3	
MAF	NF2**	PIK3CG	RARA	SMC1A	TNFRSF14	
MAFB	NFE2L2	PIK3R1	RASA1	SMC3	TNFRSF17	
MAGI2	NFKBIA	PIK3R2	RB1**	SMO	TNFRSF9	
MALT1	NHP2	PIM1	RBM10	SOCS1	TOP1	
MAP2K1	NKX2-1	PLCG1	RECQL4	SOD2	TOP2A	
MAP2K2	NOP10	PLCG2	RET**	SOX10	TP53**	
MAP2K4	NOTCH1	PML	RHEB	SOX2	TP63	
MAP3K1	NOTCH2	PMS1	RHOA	SOX9	TPM1	
MAP3K7	NOTCH3	PMS2**	RICTOR	SPEN	TPMT	
MAPK1	NOTCH4	POLD1**	RINT1	SPINK1	TRAF3	
MAX**	NPM1	POLE**	RIT1	SPOP	TRAF7	
MC1R	NQO1	POLH	RNF139	SPRED1	TSC1**	
MCL1	NRAS	POLQ	RNF43	SRC	TSC2**	
MDM2	NRG1	POT1	ROS1	SRSF2	TSHR	
MDM4	NSD1	POU2F2	RPL5	STAG2	TUSC3	
MED12	NSD2	PPARA	RPS15	STAT3	TYMS	
MEF2B	NT5C2	PPARD	RPS6KB1	STAT4	U2AF1	
MEN1**	NTHL1**	PPARG	RPTOR	STAT5A	UBE2T	
MET**	NTRK1	PPM1D	RRM1	STAT5B	UGT1A1	
MGMT	NTRK2	PPP1R15A	RSF1	STAT6	UGT1A9	
MIB1	NTRK3	PPP2R1A	RUNX1**	STK11**	UMPS	
MITF	NUDT15	PPP2R2A	RUNX1T1	SUFU**	VEGFA	
MKI67	NUP98	PPP6C	RXRA	SUZ12	VEGFB	
MLH1**	OLIG2	PRCC	SCG5	SYK	VHL**	
MLH3	P2RY8	PRDM1	SDHA**	SYNE1	VSIR	
MLLT3	PAK1	PREX2	SDHAF2**	TAF1	WEE1	
MN1	PALB2**	PRKAR1A**	SDHB **	TANC1	WNK1	
MPL	PALLD	PRKDC	SDHC**	TAP1	WNK2	
MRE11	PAX3	PRKN	SDHD**	TAP2	WRN	
MS4A1	PAX5	PRSS1	SEC23B	TARBP2	WT1**	

Specimen Requirements

FFPE solid tumor tissue

Tempus will request tissue from pathology department

10% formalin fixation (neutral buffered) for 6–72 hours, paraffin embedded

EDTA is the only accepted method of decalcification

Tumor required to be at least 20% of the sample by ratio of tumor nuclei to benign nuclei[3]

Normal match sample

2 x 8.5mL Streck (preferred) or EDTA tubes filled with peripheral blood; or saliva from patient

LEARN MORE

Visit tempus.com/oncology/

xT DNA + xR RNA Performance Specifications

DNA PERFORMANCE SPECIFICATIONS—CHICAGO LAB

Variant Type	Limit of Detection	Analytical Sensitivity	Negative Percentage Agreement (PA)
SNVs	5%	98.2%	>99%
Indels (≤40bp)	10.1%	91.1%	>99%
Copy Number Alterations	*Gain:* 30% Tumor Purity *Loss:* 40% Tumor Purity	91.4%	>99%
Microsatellite Instability	30% Tumor Purity	90.5%	98.4%
Fusions	30% Tumor Purity	90.9%	>99%

RNA PERFORMANCE SPECIFICATIONS—CHICAGO LAB

Variant Type	Limit of Detection	Positive PA	Negative PA
Rearrangements / Fusions	20% Tumor Purity	100.0% PPA (targeted) 97.0% PPA (untargeted)	99.9% NPA (targeted) 99.9% NPA (untargeted)
Altered Splicing (MET Exon 14)	20% Tumor Purity	100.0% PPA	100.0% NPA
Altered Splicing (EGFRvIII)	20% Tumor Purity	95.5% PPA	91.3% NPA

Please visit our website for complete performance specifications across all Tempus labs.

References

1 Based on a retrospective study involving a cohort of randomly selected patients with tumor types including brain, breast, colorectal, lung, ovarian, endometrial, pancreatic and prostate cancer. Beaubier N, Bontrager M, Huether R, et al. Integrated genomic profiling expands clinical options for patients with cancer. Nat Biotechnol. 2019;37(11):1351-1360.

2 Yap TA, Ashok A, Stoll J, et al. Prevalence of germline findings among tumors from cancer types lacking hereditary testing guidelines. JAMA Network Open. 2022;5(5).

3 Required to be at least 40% for xE panel