TruSight Tumor 15

Research common somatic variants in solid tumor samples.

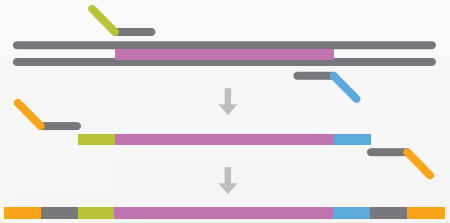
The TruSight Tumor 15 workflow provides a comprehensive assessment of 15 genes that are commonly mutated in solid tumors. It accurately analyzes low-frequency variants from 20 ng of starting DNA and is optimized for formalin-fixed, paraffin-embedded (FFPE) tumor tissue. Featuring a rapid workflow that can be easily integrated into lab procedures, it offers a single assay for accurate, economical, and rapid analysis of solid tumors.

Genes included

AKT1, BRAF, EGFR, ERBB2, FOXL2, GNA11, GNAQ, KIT, KRAS, MET, NRAS, PDGFRA, PIK3CA, RET, TP53

Highlights

- Discover a complete workflow with detailed QC steps and simple, predefined variant report.
- Experience rapid turnaround—3.5 hours of hands-on time; DNA to data in approximately 36 hours.
- Utilize somatic variants selected from relevant industry guidelines, key opinion leaders, and pharmaceutical researchers.
- Achieve accurate somatic variant analysis of 5% allele frequency with as little as 20 ng DNA from FFPE tissue samples.



TruSight Tumor 15 Kit

On System: Local Run Manager—TruSight Tumor 15
On Cloud: BaseSpace® Platform—TruSight Tumor 15
On Site: BaseSpace® Platform—TruSight Tumor 15

Prepare library → Sequence → Analyze data

Solid tumor profiling

TruSight Myeloid

Screen key genes in myeloid malignancies.

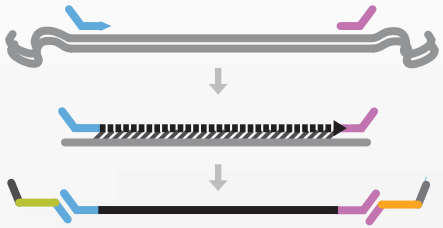
The TruSight Myeloid workflow covers 15 full genes (exons only) and key oncogenic hotspots of 39 additional genes, providing a comprehensive assessment of the key genes involved in myeloid malignancies in a single test. The result is an accurate, cost-effective solution for profiling common myeloid neoplasms.

Genes included

ABL1, ASXL1, ATRX, BCOR, BCORL1, BRAF, CALR, CBL, CBLB, CBLC, CDKN2A, CEBPA, CSF3R, CUX1, DNMT3A, ETV6/TEL, EZH2, FBXW7, FLT3, GATA1, GATA2, GNAS, HRAS, IDH1, IDH2, IKZF1, JAK2, JAK3, KDM6A, KIT, KRAS, MLL, MPL, MYD88, NOTCH1, NPM1, NRAS, PDGFRA, PHF6, PTEN, PTPN11, RAD21, RUNX1, SETBP1, SF3B1, SMC1A, SMC3, SRSF2, STAG2, TET2, TP53, U2AF1, WT1, ZRSR2

Highlights

- Leverage expert consortia-selected content targeting 54 genes mutated frequently in myeloid malignancies.
- Benefit from a single workflow that includes library preparation, sequencing, data analysis, and data annotation.
- Assess multiple genes simultaneously with high accuracy and sensitivity—efficiently and cost effectively.



TruSight Myeloid

On System: Local Run Manager—Amplicon
On Cloud: BaseSpace Platform—TruSeq Amplicon
On Site: BaseSpace Platform—TruSeq Amplicon
VariantStudio

Prepare library → Sequence → Analyze data

Hematological cancer profiling

TruSight Cancer

Broadly screen for variants linked to cancer.

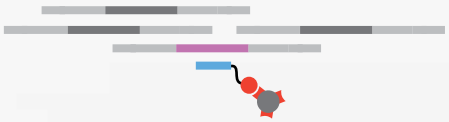
The TruSight Cancer workflow targets 94 genes associated with both common (eg, breast, colorectal) and rare cancers and 284 single nucleotide polymorphisms (SNPs) found to correlate with cancer through genome-wide association studies (GWAS). Conduct comprehensive evaluation of genes that contain genetic variants linked to a predisposition for cancer.

Genes included

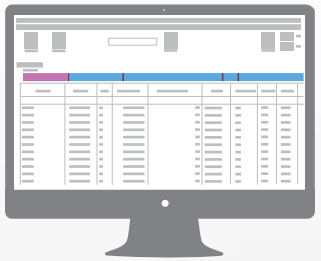
AIP, ALK, APC, ATM, BAP1, BLM, BMPR1A, BRCA1, BRCA2, BRIP1, BUB1B, CDC73, CDH1, CDK4, CDKN1C, CDKN2A, CEBPA, CEP57, CHEK2, CYLD, DDB2, DICER1, DIS3L2, EGFR, EPCAM, ERCC2, ERCC3, ERCC4, ERCC5, EXT1, EXT2, EZH2, FANCA, FANCB, FANCC, FANCD2, FANCE, FANCF, FANCG, FANCI, FANCL, FANCM, FH, FLCN, GATA2, GPC3, HNF1A, HRAS, KIT, MAX, MEN1, MET, MLH1, MSH2, MSH6, MUTYH, NBN, NF1, NF2, NSD1, PALB2, PHOX2B, PMS1, PMS2, PRF1, PRKAR1A, PTCH1, PTEN, RAD51C, RAD51D, RB1, RECQL4, RET, RHBDF2, RUNX1, SBDS, SDHAF2, SDHB, SDHC, SDHD, SLX4, SMAD4, SMARCB1, STK11, SUFU, TMEM127, TP53, TSC1, TSC2, VHL, WRN, WT1, XPA, XPC

Highlights

- Capture genes associated with a predisposition for cancer with content selected by the Institute of Cancer Research, London.
- Preserve precious samples, achieving data quality with as little as 50 ng of DNA.
- Benefit from a fast, simple workflow compatible with TruSight Rapid Capture Kits that enables library prep and enrichment in 1.5 days.



TruSight Cancer



On System: Local Run Manager—DNA Enrichment
On Cloud: BaseSpace Platform—Isaac/BWA Enrichment
On Site: BaseSpace Platform—Isaac/BWA Enrichment
VariantStudio

Prepare library → Sequence → Analyze data

Germline testing

TruSight RNA Pan-Cancer

Screen both solid and hematological cancers.

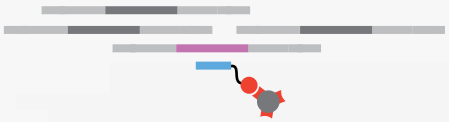
The TruSight RNA Pan-Cancer workflow enables analysis of gene fusions, variants, and gene expression changes in 1385 genes, providing a comprehensive view of the known functionally relevant changes occurring in cancer. It provides a sensitive, reproducible, and economical solution for studies of expression dynamics and functional mechanisms in cancer.

Genes included

ABCC3, ABI1, ABL1, ABL2, ABLIM, ACACA, ACE, ACER, ACKR3, ACSBG1, ACSL3, ACSL6, ACVR1B, ACVR1C, ACVR2A, ADD3, ADM, AFF1, AFF3, AFF4, AGR3, AHCYL1, AHI1, AHR, AHRR, AIP, AK2, AK5, AKAP12, AKAP6, AKAP9, AKR1C3, AKT1, AKT2, AKT, ALDH1A1, ALDH2, ALDOC, ALK, AMER1, AMH, ANGPT1, ANKRD28, ANLN, APC, APH1A, APLP2, APOD. For a complete list, visit www.illumina.com/products/trusight-rna-pan-cancer-panel.

Highlights

- Access gene expression information and fusion discovery with known and novel gene fusion partners.
- Streamline your workflow with an optimized, low-input protocol for a wide range of sample types including FFPE.



TruSight RNA Pan-Cancer

On Cloud: BaseSpace Platform—RNA Core
On Site: BaseSpace Platform—RNA Core
VariantStudio

Prepare library → Sequence → Analyze data