SOPHiA GENETICS™

MSK-IMPACT® Flex powered with SOPHiA DDM™

Elevate your comprehensive genomic profiling

Optimize lab efficiency with a complete sample-to-report CGP solution.
The modular design allows you to add analysis options – DNA, RNA, and/or HRD – at a sample level, supporting greater agility and cost-effectiveness in your research.

CURATED

Targets **533 DNA genes** and **140 RNA genes curated** from **guidelines, databases** (incl. OncoKB™), and **clinical trial evidence.** The DNA content is based on **MSK-IMPACT®**, curated by clinical genomics experts at MSK.

COMPREHENSIVE

Combines **DNA** and **RNA** analysis to cover **SNVs/Indels, CNVs** (whole gene amplifications/deletions and exon-level CNVs), **partner-agnostic fusions, gene expression, exon skipping, MSI, TMB,** and **HRD.**

AGILE

Optimizes lab efficiency and costs through **sample-level modularity**, enabling flexible addition of RNA and HRD analysis, **wide sequencer platform compatibility**, and **seamless automation options.**

A modular approach for agile analysis

EXPERTLY DESIGNED CONTENT

505 genes based on MSK-IMPACT® *DNA* + **28 genes based on guidelines and trials** *DNA*

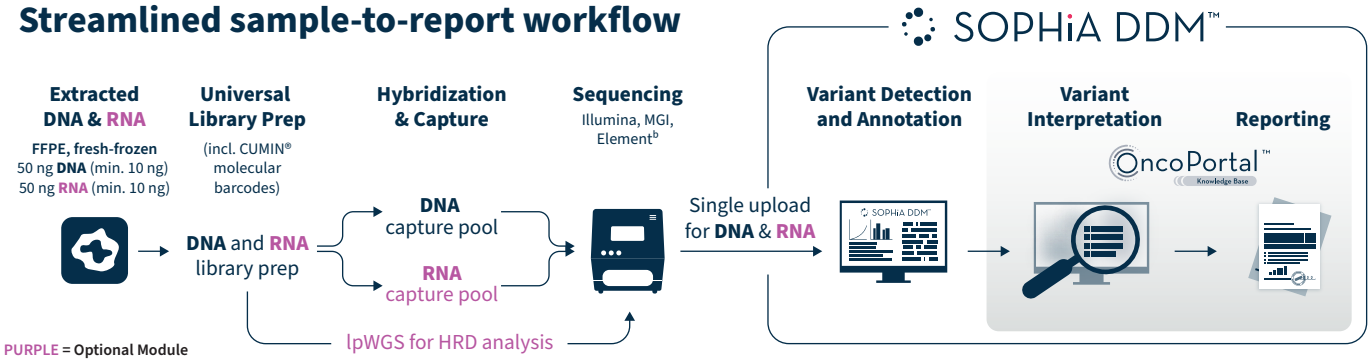
OPTIONAL MODULES

140 genes for RNA analysis[a] *RNA* + **Genomic instability for HRD assessment** *lpWGS*

MSK-IMPACT® Flex powered with **SOPHiA DDM™**

Comprehensive analysis with sample-level modularity of DNA, RNA, and HRD results

Streamlined sample-to-report workflow



Ready-to-sequence libraries in **1.5 (DNA)** or **2.5 (DNA + RNA)** days • **Automation** scripts available • Flexible sample **multiplexing capability** • **<5 day** turnaround[c]

[a]Powered by SOPHiA DDM™ RNAtarget PanCancer Solution. 140 genes in total, 135 for fusion detection. [b]Pipelines available for Illumina sequencers. MGI and Element pipelines will require a MaxCare Program for verification. [c]For indicative purposes only; actual duration may be subject to change depending on the number of samples, server load, and other technical limitations.

Discover the new generation of SOPHiA DDM™

- **Advanced secondary analysis** leveraging noise suppression algorithms for accurate variant detection
- **Enhanced variant annotation** including ClinGen/CGC/VICC Oncogenicity pre-classification, extended catalogs (including spicing predictors), and cross application variant frequency
- **Simplified interpretation** with OncoPortal™ Knowledge Base, compiling all relevant clinical insights in one place

Launching on the new generation platform in late 2025.

Detect key variants and biomarkers

From DNA (533 genes)

SNVs/Indels in 533 genes (all genes of the panel): *ABL1, ABRAXAS1, ACVR1, AGO1, AGO2, AKT1, AKT2, AKT3, ALB, ALK, ALOX12B, AMER1, ANKRD11, APC, APLNR, AR, ARAF, ARHGAP35, ARID1A, ARID1B, ARID2, ARID5B,* ***ASS1****, ASXL1, ASXL2, ATM, ATR, ATRX, ATXN7, AURKA, AURKB, AXIN1, AXIN2, AXL, B2M, BABAM1, BAP1, BARD1, BBC3, BCL10, BCL2, BCL2L1, BCL2L11, BCL6, BCOR,* ***BCORL1****, BIRC3, BLM, BMPR1A, BRAF, BRCA1, BRCA2, BRD4, BRIP1, BTK,* ***C11orf95****, CALR, CARD11, CARM1, CASP8, CBFB, CBL, CCND1, CCND2, CCND3, CCNE1, CCNQ, CD274, CD276,* ***CD58****, CD79A, CD79B, CDC42, CDC73, CDH1, CDK12, CDK4, CDK6, CDK8, CDKN1A, CDKN1B, CDKN2A, CDKN2B, CDKN2C, CEBPA, CENPA, CHEK1, CHEK2, CIC, CMTR2, COP1, CREBBP, CRKL, CRLF2, CSDE1, CSF1R, CSF3R, CTCF, CTLA4, CTNNB1, CTR9, CUL3, CXCR4, CXorf67, CYLD, CYP19A1, CYSLTR2, DAXX, DCUN1D1,* ***DDR1****, DDR2, DICER1, DIS3, DNAJB1, DNMT1, DNMT3A, DNMT3B, DOT1L,* ***DPYD****, DROSHA, DUSP4, E2F3, EED, EGFL7, EGFR, EIF1AX, EIF4A2, EIF4E, ELF3, ELOC, EP300, EPAS1, EPCAM, EPHA3, EPHA5, EPHA7, EPHB1, ERBB2, ERBB3, ERBB4, ERCC2, ERCC3, ERCC4, ERCC5, ERF, ERG, ERRFI1, ESR1, ETAA1, ETV1, ETV6, EZH1, EZH2, FANCA,* ***FANCB****, FANCC,* ***FANCD2, FANCE, FANCF, FANCG, FANCI, FANCL, FANCM, FAS****, FAT1, FBXW7, FGF19,* ***FGF23****, FGF3, FGF4, FGFR1, FGFR2, FGFR3, FGFR4, FH, FLCN, FLT1, FLT3, FLT4, FOXA1, FOXF1, FOXL2, FOXO1, FOXP1, FUBP1, FYN, GAB1, GAB2, GATA1, GATA2, GATA3,* ***GEN1****, GLI1, GNA11,* ***GNA13****, GNAQ, GNAS, GNB1, GPS2, GREM1, GRIN2A, GSK3B, H3F3A, H3F3B, H3F3C,* ***HDAC2****, HGF, HIST1H1C, HIST1H2BD, HIST1H3A, HIST1H3B, HIST1H3C, HIST1H3D, HIST1H3E, HIST1H3F, HIST1H3G, HIST1H3H, HIST1H3I, HIST1H3J, HIST2H3C, HIST2H3D, HIST3H3, HLA-A, HLA-B, HLA-C, HNF1A, HOXB13, HRAS, ICOSLG, ID3, IDH1, IDH2,* ***IDO2****, IFNGR1, IGF1, IGF1R, IGF2, IKBKE, IKZF1, IL10, IL7R, INHA, INHBA, INPP4A, INPP4B, INPPL1, INSR, IRF4, IRS1, IRS2, JAK1, JAK2, JAK3, JUN, KBTBD4, KDM5A, KDM5C, KDM6A, KDR, KEAP1, KIT, KLF4, KLF5, KMT2A, KMT2B, KMT2C, KMT2D, KMT5A, KNSTRN, KRAS, LATS1, LATS2,* ***LDB1****, LMO1, LYN, LZTR1, MAD2L2, MALT1, MAP2K1, MAP2K2, MAP2K4, MAP3K1, MAP3K13, MAP3K14, MAPK1, MAPK3, MAPKAP1, MAX, MCL1, MDC1, MDM2, MDM4, MED12, MEF2B, MEN1, MET, MGA, MITF, MLH1, MLLT1, MPL, MRE11, MSH2, MSH3, MSH6, MSI1, MSI2, MST1, MST1R, MTAP, MTOR, MUTYH, MYC, MYCL, MYCN, MYD88, MYOD1, NADK, NBN, NCOA3, NCOR1, NEGR1, NF1, NF2, NFE2L2, NFKBIA, NKX2-1, NKX3-1, NOTCH1, NOTCH2, NOTCH3, NOTCH4, NPM1, NRAS, NSD1, NSD2, NSD3, NTHL1, NTRK1, NTRK2, NTRK3, NUF2, NUP93, PAK1, PAK5, PALB2, PARP1, PAX5, PBRM1, PDCD1, PDCD1LG2, PDGFRA, PDGFRB, PDPK1, PGBD5, PGR, PHF6, PHOX2B, PIK3C2G, PIK3C3, PIK3CA, PIK3CB, PIK3CD, PIK3CG, PIK3R1, PIK3R2, PIK3R3, PIM1, PLCG2, PLK2, PMAIP1,* ***PML****, PMS1, PMS2, PNRC1, POLD1, POLE, POT1, PPARG, PPM1D, PPP2R1A,* ***PPP2R2A****, PPP4R2, PPP6C, PRDM1, PRDM14, PREX2, PRKAR1A, PRKCI, PRKD1, PRKN,* ***PRPF8****, PTCH1, PTEN, PTP4A1, PTPN11, PTPRD, PTPRS, PTPRT, RAB35, RAC1, RAC2, RAD21, RAD50, RAD51, RAD51B, RAD51C, RAD51D, RAD52, RAD54L, RAF1, RARA, RASA1, RB1, RBM10, RECQL, RECQL4, REL, REST, RET, RHEB, RHOA, RICTOR, RIT1, RNF43, ROS1, RPS6KA4, RPS6KB2, RPTOR, RRAGC, RRAS, RRAS2, RTEL1, RUNX1, RXRA, RYBP, SCG5, SDHA, SDHAF2, SDHB, SDHC, SDHD, SERPINB3, SERPINB4, SESN1, SESN2, SESN3, SETD2, SETDB1, SF3B1, SH2B3, SH2D1A, SHOC2, SHQ1, SLFN11, SLX4, SMAD2, SMAD3, SMAD4, SMARCA2, SMARCA4, SMARCB1, SMARCD1, SMARCE1, SMO, SMYD3, SOCS1, SOS1, SOX17, SOX2, SOX9, SPEN, SPOP, SPRED1, SPRTN, SRC, SRSF2, STAG2, STAT3, STAT5A, STAT5B,* ***STAT6****, STK11, STK19, STK40, SUFU, SUZ12, SYK, TAP1, TAP2, TBX3, TCF3, TCF7L2, TEK, TENT5C, TERT, TET1, TET2,* ***TFE3****, TGFBR1, TGFBR2, TMEM127, TMPRSS2, TNFAIP3, TNFRSF14, TOP1, TP53, TP53BP1, TP63, TRAF2, TRAF7, TRIP13, TSC1, TSC2, TSHR, U2AF1,* ***UGT1A1****, UPF1,* ***USH2A****, USP8, VEGFA, VHL, VTCN1, WT1, WWTR1, XIAP, XPO1, XRCC2, YAP1, YES1, ZFHX3, ZNRF3, ZRSR2*

Note: DNA genes in bold are additional genes compared to the MSK-IMPACT® powered with SOPHiA DDM™ panel.

Whole gene amplifications and deletions In 520 genes: *All genes of the panel EXCEPT for HIST2H3D, HIST2H3C, HIST1H3A, HIST1H3D, HIST1H3E, HIST1H3F, HIST1H3G, HIST1H3H, HIST1H3I, HIST1H3J, HLA-A, HLA-C, H3F3B*

Gene-level and exon-level CNVs in 49 genes: *APC, ARID1A, ATM, BAP1, BARD1, BRCA1, BRCA2, BRIP1, CDH1, CDK12, CHEK1, CHEK2, DICER1, EGFR, EPCAM, FANCA, FANCD2, FANCL, FH, FLCN, MET, MLH1, MRE11, MSH2, MSH6, NBN, NF1, NF2, PALB2, PMS2, PPP2R2A, PTCH1, PTEN, RAD51B, RAD51C, RAD51D, RAD54L, RB1, SDHA, SDHB, SDHC, SMARCA4, SMARCB1, STK11, SUFU, TP53, TSC1, TSC2, WT1*

Other biomarkers: *MSI, TMB, TERT promoter, HRD. Additional information*: DNA fusions in 23 genes and MET exon 14 skipping from DNA*

*Results available on SOPHiA DDM™ when activated.

From RNA (140 genes)

Fusions (partner-agnostic) in 135 genes: *ACVR2A, AKT1, AKT2, AKT3, ALK, ARHGA-P26, ARHGA-P6, AR, AXL, BCOR, BRAF, BRD3, BRD4, CAMTA1, CCNB3, CCND1, CHMP2A, CIC, CRTC1, CSF1, CSF1R, CTNNB1, DNAJB1, EGF, EGFR, EPC1, ERBB2, ERBB4, ERG, ESR1, ESRRA, ETV1, ETV4, ETV5, ETV6, EWSR1, FGF1, FGFR1, FGFR2, FGFR3, FGR, FOSB, FOS, FOXO1, FOXO4, FUS, GLI1, GRB7, GREB1, HMGA2, IGF1R, INSR, JAK2, JAK3, JAZF1, KANSL1, KIT, KRAS, MAML2, MAP2K1, MAP3K8, MAST1, MAST2, MBTD1, MDM2, MEAF6, MET, MGEA5, MKL2, MN1, MSMB, MUSK, MYBL1, MYB, MYC, MYOD1, NCOA1, NCOA2, NCOA3, NFATC2, NFE2L2, NFIB, NOTCH1, NOTCH2, NR4A3, NRG1, NTRK1, NTRK2, NTRK3, NUMBL, NUTM1, PAX3, PAX8, PDGFB, PDGFD, PDGFRA, PDGFRB, PHF1, PHKB, PIK3CA, PKN1, PLAG1, PPARG, PRDM10, PRKACA, PRKACB, PRKCA, PRKCB, PRKCD, PRKD1, PRKD2, PRKD3, RAD51B, RAF1, RELA, RET, ROS1, RSPO2, RSPO3, SS18L1, SS18, STAT6, TAF15, TCF12, TERT, TFE3, TFEB, TFG, THADA, TMPRSS2, USP6, VGLL2, WWTR1, YAP1, YWHAE*

Exon skipping in 9 genes: *ALK (ex2-17, ex2-3), ARvII (ex4-8), BRAF (ex2-10, ex4-10, ex2-8, ex3-8, ex4-8), EGFRvIII (ex2-7), ERBB2 (ex16), MET (ex14, ex15), NFE2L2 (ex2, ex3), NOTCH1 (ex2-27, ex3-27, ex3-28, ex21-27), PDGFRA (ex8-9). ITD of kinase domain: BRAF (ex10–18), EGFRvIII (ex18-25)*

Gene expression in 56 genes: *AKT1, AKT3, ALK, ALPK1, ARHGA-P26, BCOR, BRAF, CSF1, CTNNB1, DICER1, EGFR, ERBB2, ERG, ESR1, ETV1, ETV4, FGFR1, FGFR2, FGFR3, FUS, HMGA2, HRAS, JAK2, JAK3, KRAS, MAP2K1, MDM2, MET, MYBL1, MYOD1, NCOA1, NFE2L2, NFIB, NOTCH1, NRAS, NRG1, NTRK1, NTRK2, NTRK3, PDGFRA, PIK3CA, PKN1, PRKACA, PRKACB, PRKCD, RAD51B, RAF1, RET, ROS1, SS18L1, SS18, STAT6, TCF12, TFE3, THADA, YAP1*

Specifications

Sample type	FFPE, fresh-frozen	
Starting material	50 ng DNA (10 ng minimum)	50 ng RNA (10 ng minimum)
Sequencer compatibility	• Illumina NextSeq® 550, NextSeq® 1000/2000, NovaSeq™ 6000, NovaSeq™ X • For other sequencer types, including Element and MGI, SOPHiA DDM™ MaxCare Program is recommended to optimize performance.	
Recommended paired-end reads	• DNA – 51 million • RNA – 11 million • lpWGS (for genomic instability) – 20 million	
Wet lab time	1.5 days for DNA	2.5 days for DNA + RNA
Limit of detection at 95% (LOD95)	5%	
Product codes	BS0132ILLRSMY13 (DNA) - kit size 16, 32, 48, 96 CS2517ILLRSRY16 (RNA) - kit size: 16, 32, 48	CS2517ILBRSRY16 (RNA) – kit size 96 DL0121ILLRSM (GIInger™) – dry lab only

HRD, homologous recombination deficiency; lpWGS, low-pass whole genome sequencing; MSI, microsatellite instability; TMB, tumor mutational burden.