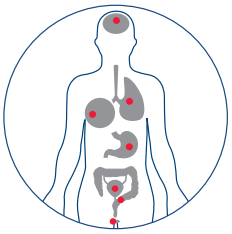
Single consolidated NGS workflow with DNA + RNA

QIAseq® Pan Cancer Multimodal cuts user interventions by 50%

Sample to Insight

QIAGEN



Challenges of pan cancer profiling

Pan cancer studies focus on profiling of relevant DNA and RNA alterations found across multiple cancers, as well as assessment of tumor mutational burden (TMB) and microsatellite instability (MSI) for solid tumors and heme malignancies. Recent advances in NGS chemistries, platforms and bioinformatics pipelines have empowered users to efficiently interrogate DNA and RNA alterations in biological samples. Current approaches, however, require the use of 2 separate workflows to prepare libraries from separate DNA and RNA isolates. Limitations of such approaches include:

- Precious samples must be split to extract DNA and RNA in separate sample prep protocols
- Large amounts of sample material are required to generate sufficient amounts of input DNA and RNA for multiple workflows
- Workflow has added complexity of deriving integrated insights from results of different technical approaches, each with its own innate bias
- Separate workflows result in inefficient use of resources and long turnaround times

Streamlined, consolidated one-day workflow

To overcome the limitations associated with current approaches, the QIAseq Pan Cancer Multimodal panel starts with total nucleic acids (or DNA + RNA) and prepares targeted DNA and RNA libraries containing Unique Molecular indices (UMIs) for Illumina® platforms using a one-day, consolidated workflow (see Figure 1).

The QIAseq Pan Cancer Multimodal panel delivers:

- The ONLY single consolidated workflow for DNA + RNA library prep using total nucleic acids as input
- Operational efficiency with a 50% reduction in user interventions
- Confident detection of low-frequency variants with UMIs
- Reduced index hopping with Unique Dual Indices (UDIs)
- Comprehensive coverage of known and novel fusions as well as all relevant alterations
- 523 DNA gene targets, 56 RNA fusion gene targets and 26 microsatellite instability MSI loci (Tables 1–3)

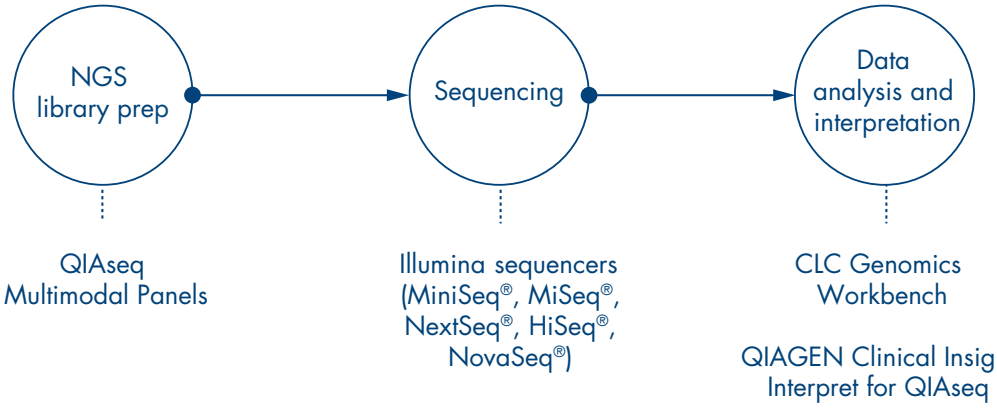


Figure 1. Extract more information, while reducing sample, time and cost with a simple, one-day workflow. This flexible solution enables the construction of libraries compatible with Illumina platforms from as little as 10 ng total nucleic acid isolated from a wide range of samples. The data analysis pipelines in CLC Genomics Workbench translate raw sequence data in FASTQ format to DNA and RNA variant files (VCFs), which can be further interpreted for biological significance through QCI® Interpret for QIAseq.

Confidently interpret NGS variants

Our software workflow makes it easy to extract, identify the variants of interest and deliver a comprehensive variant interpretation from your raw NGS data. The industry leading genomic analysis and interpretation software solutions, CLC Genomic Workbench and QCI Interpret for QIAseq, provide you with a comprehensive report to support your workflow, including variant classification, details on variant function, literature references, drug labels, drug interactions and relevant clinical trials. Accelerate your clinical research and go from raw NGS data to detailed and trusted insights in minutes – not hours.

Key differentiators

- The ONLY single consolidated workflow for DNA + RNA library prep using total nucleic acids as input
- Cuts user interventions by 50%
- Confident detection of low-frequency variants
- Detection of both known and novel fusions
- Increased target coverage of all relevant alterations

Table 1. 523 DNA gene targets (Part 1)

Genes targeted for SNP, InDel, and copy number variation (CNV) detection by DNA sequencing											
ABL1	*ASXL1*	*BCOR*	*CCND2*	*CENPA*	*DAXX*	*EP300*	*ETV5*	*FGF19*	*FOXA1*	*GPR124*	*HIST1H3I*
ABL2	*ASXL2*	*BCORL1*	*CCND3*	*CHD2*	*DCUN1D1*	*EPCAM*	*ETV6*	*FGF2*	*FOXL2*	*GPS2*	*HIST1H3J*
ACVR1	*ATM*	*BCR*	*CCNE1*	*CHD4*	*DDR2*	*EPHA3*	*EWSR1*	*FGF23*	*FOXO1*	*GREM1*	*HIST2H3A*
ACVR1B	*ATR*	*BIRC3*	*CD274*	*CHEK1*	*DDX41*	*EPHA5*	*EZH2*	*FGF3*	*FOXP1*	*GRIN2A*	*HIST2H3C*
AKT1	*ATRX*	*BLM*	*CD276*	*CHEK2*	*DHX15*	*EPHA7*	*FAM175A*	*FGF4*	*FRS2*	*GRM3*	*HIST2H3D*
AKT2	*AURKA*	*BMPR1A*	*CD74*	*CIC*	*DICER1*	*EPHB1*	*FAM46C*	*FGF5*	*FUBP1*	*GSK3B*	*HIST3H3*
AKT3	*AURKB*	*BRAF*	*CD79A*	*CREBBP*	*DIS3*	*ERBB2*	*FANCA*	*FGF6*	*FYN*	*H3F3A*	*HLA-A*
ALK	*AXIN1*	*BRCA1*	*CD79B*	*CRKL*	*DNAJB1*	*ERBB3*	*FANCC*	*FGF7*	*GABRA6*	*H3F3B*	*HLA-B*
ALOX12B	*AXIN2*	*BRCA2*	*CDC73*	*CRLF2*	*DNMT1*	*ERBB4*	*FANCD2*	*FGF8*	*GATA1*	*H3F3C*	*HLA-C*
AMER1	*AXL*	*BRD4*	*CDH1*	*CSF1R*	*DNMT3A*	*ERCC1*	*FANCE*	*FGF9*	*GATA2*	*HGF*	*HNF1A*
ANKRD11	*B2M*	*BRIP1*	*CDK12*	*CSF3R*	*DNMT3B*	*ERCC2*	*FANCF*	*FGFR1*	*GATA3*	*HIST1H1C*	*HNRNPK*
ANKRD26	*BAP1*	*BTG1*	*CDK4*	*CSNK1A1*	*DOT1L*	*ERCC3*	*FANCG*	*FGFR2*	*GATA4*	*HIST1H2BD*	*HOXB13*
APC	*BARD1*	*BTK*	*CDK6*	*CTCF*	*E2F3*	*ERCC4*	*FANCI*	*FGFR3*	*GATA6*	*HIST1H3A*	*HRAS*
AR	*BBC3*	*C11orf30*	*CDK8*	*CTLA4*	*EED*	*ERCC5*	*FANCL*	*FGFR4*	*GEN1*	*HIST1H3B*	*HSD3B1*
ARAF	*BCL10*	*CALR*	*CDKN1A*	*CTNNA1*	*EGFL7*	*ERG*	*FAS*	*FH*	*GID4*	*HIST1H3C*	*HSP90AA1*
ARFRP1	*BCL2*	*CARD11*	*CDKN1B*	*CTNNB1*	*EGFR*	*ERRFI1*	*FAT1*	*FLCN*	*GLI1*	*HIST1H3D*	*ICOSLG*
ARID1A	*BCL2L1*	*CASP8*	*CDKN2A*	*CUL3*	*EIF1AX*	*ESR1*	*FBXW7*	*FLI1*	*GNA11*	*HIST1H3E*	*ID3*
ARID1B	*BCL2L11*	*CBFB*	*CDKN2B*	*CUX1*	*EIF4A2*	*ETS1*	*FGF1*	*FLT1*	*GNA13*	*HIST1H3F*	*IDH1*
ARID2	*BCL2L2*	*CBL*	*CDKN2C*	*CXCR4*	*EIF4E*	*ETV1*	*FGF10*	*FLT3*	*GNAQ*	*HIST1H3G*	*IDH2*
ARID5B	*BCL6*	*CCND1*	*CEBPA*	*CYLD*	*EML4*	*ETV4*	*FGF14*	*FLT4*	*GNAS*	*HIST1H3H*	*IFNGR1*
IGF1	*KAT6A*	*LRP1B*	*MEF2B*	*MYD88*	*NSD1*	*PDGFRB*	*PMS1*	*PTPRS*	*REL*	*SDHD*	*SOX10*
IGF1R	*KDM5A*	*LYN*	*MEN1*	*MYOD1*	*NTRK1*	*PDK1*	*PMS2*	*PTPRT*	*RET*	*SETBP1*	*SOX17*

Table 2. 56 RNA fusion gene targets

Genes targeted for fusion, exon skipping, and alternatively spliced variant detection by RNA sequencing											
ABL1	*BCL2*	*CSF1R*	*ESR1*	*EWSR1*	*FLI1*	*KIF5B*	*MSH2*	*NRG1*	*PAX3*	*PIK3CA*	*ROS1*
AKT3	*BRAF*	*EGFR*	*ETS1*	*FGFR1*	*FLT1*	*KIT*	*MYC*	*NTRK1*	*PAX7*	*PPARG*	*RPS6KB1*
ALK	*BRCA1*	*EML4*	*ETV1*	*FGFR2*	*FLT3*	*KMT2A*	*NOTCH1*	*NTRK2*	*PDGFRA*	*RAF1*	*TMPRSS2*
AR	*BRCA2*	*ERBB2*	*ETV4*	*FGFR3*	*JAK2*	*MET*	*NOTCH2*	*NTRK3*	*PDGFRB*	*RET*	*TP53*
AXL	*CDK4*	*ERG*	*ETV5*	*FGFR4*	*KDR*	*MLLT3*	*NOTCH3*				

Table 1. 523 DNA gene targets (Part 2)

Genes targeted for SNP, InDel, and copy number variation (CNV) detection by DNA sequencing											
IGF2	*KDM5C*	*LZTR1*	*MET*	*NAB2*	*NTRK2*	*PDPK1*	*PNRC1*	*QKI*	*RFWD2*	*SETD2*	*SOX2*
IKBKE	*KDM6A*	*MAGI2*	*MGA*	*NBN*	*NTRK3*	*PGR*	*POLD1*	*RAB35*	*RHEB*	*SF3B1*	*SOX9*
IKZF1	*KDR*	*MALT1*	*MITF*	*NCOA3*	*NUP93*	*PHF6*	*POLE*	*RAC1*	*RHOA*	*SH2B3*	*SPEN*
IL10	*KEAP1*	*MAP2K1*	*MLH1*	*NCOR1*	*NUTM1*	*PHOX2B*	*PPARG*	*RAD21*	*RICTOR*	*SH2D1A*	*SPOP*
IL7R	*KEL*	*MAP2K2*	*MLLT3*	*NEGR1*	*PAK1*	*PIK3C2B*	*PPM1D*	*RAD50*	*RIT1*	*SHQ1*	*SPTA1*
INHA	*KIF5B*	*MAP2K4*	*MPL*	*NF1*	*PAK3*	*PIK3C2G*	*PPP2R1A*	*RAD51*	*RNF43*	*SLIT2*	*SRC*
INHBA	*KIT*	*MAP3K1*	*MRE11A*	*NF2*	*PAK7*	*PIK3C3*	*PPP2R2A*	*RAD51B*	*ROS1*	*SLX4*	*SRSF2*
INPP4A	*KLF4*	*MAP3K13*	*MSH2*	*NFE2L2*	*PALB2*	*PIK3CA*	*PPP6C*	*RAD51C*	*RPS6KA4*	*SMAD2*	*STAG1*
INPP4B	*KLHL6*	*MAP3K14*	*MSH3*	*NFKBIA*	*PARK2*	*PIK3CB*	*PRDM1*	*RAD51D*	*RPS6KB1*	*SMAD3*	*STAG2*
INSR	*KMT2A*	*MAP3K4*	*MSH6*	*NKX2-1*	*PARP1*	*PIK3CD*	*PREX2*	*RAD52*	*RPS6KB2*	*SMAD4*	*STAT3*
IRF2	*KMT2B*	*MAPK1*	*MST1*	*NKX3-1*	*PAX3*	*PIK3CG*	*PRKAR1A*	*RAD54L*	*RPTOR*	*SMARCA4*	*STAT4*
IRF4	*KMT2C*	*MAPK3*	*MST1R*	*NOTCH1*	*PAX5*	*PIK3R1*	*PRKCI*	*RAF1*	*RUNX1*	*SMARCB1*	*STAT5A*
IRS1	*KMT2D*	*MAX*	*MTOR*	*NOTCH2*	*PAX7*	*PIK3R2*	*PRKDC*	*RANBP2*	*RUNX1T1*	*SMARCD1*	*STAT5B*
IRS2	*KRAS*	*MCL1*	*MUTYH*	*NOTCH3*	*PAX8*	*PIK3R3*	*PRSS8*	*RARA*	*RYBP*	*SMC1A*	*STK11*
JAK1	*LAMP1*	*MDC1*	*MYB*	*NOTCH4*	*PBRM1*	*PIM1*	*PTCH1*	*RASA1*	*SDHA*	*SMC3*	*STK40*
JAK2	*LATS1*	*MDM2*	*MYC*	*NPM1*	*PDCD1*	*PLCG2*	*PTEN*	*RB1*	*SDHAF2*	*SMO*	*SUFU*
JAK3	*LATS2*	*MDM4*	*MYCL*	*NRAS*	*PDCD1LG2*	*PLK2*	*PTPN11*	*RBM10*	*SDHB*	*SNCAIP*	*SUZ12*
JUN	*LMO1*	*MED12*	*MYCN*	*NRG1*	*PDGFRA*	*PMAIP1*	*PTPRD*	*RECQL4*	*SDHC*	*SOCS1*	*SYK*
TAF1	*TCF7L2*	*TET2*	*TGFBR2*	*TNFRSF14*	*TP63*	*TSC2*	*VHL*	*WT1*	*XRCC2*	*ZBTB2*	*ZNF217*
TBX3	*TERC*	*TFE3*	*TMEM127*	*TOP1*	*TRAF2*	*TSHR*	*VTCN1*	*XIAP*	*YAP1*	*ZBTB7A*	*ZNF703*
TCEB1	*TERT*	*TFRC*	*TMPRSS2*	*TOP2A*	*TRAF7*	*U2AF1*	*WISP3*	*XPO1*	*YES1*	*ZFHX3*	*ZRSR2*
TCF3	*TET1*	*TGFBR1*	*TNFAIP3*	*TP53*	*TSC1*	*VEGFA*					

Table 3. 26 MSI loci

Genes targeted for microsatellite length detection by DNA sequencing											
BAT25	*BAT40*	*D17S250*	*D17S787*	*D18S61*	*D18S69*	*D2S123*	*D5S107*	*D7S519*	*NR21*	*NR24*	*D18S35*
BAT26	*D10S196*	*D17S588*	*D18S55*	*D18S64*	*D20S100*	*D3S1029*	*D5S346*	*D8S87*	*NR22*	*MONO-27*	*HSP110-T17*
BAT34C4	*D13S175*										

Ordering Information

Product	Contents	Number of samples	Panel variant number	Cat. no.
QIAseq Multimodal HC Panel; Pan Cancer Panel	Kit containing ALL reagents (except indexes) for multimodal (DNA and RNA) sequencing	12	UHS-5000Z-12	333942
		96	UHS-5000Z-96	333945
QIAseq Multimodal Index I Set A SW (96)	Box containing adapters, enough to process a total of 96 samples, for Multimodal panel sequencing on Illumina platforms using separate enrichment workflows; one of two sets required for multiplexing 96 samples	96	N/A	333985
QIAseq Multimodal Index I Set B SW (96)	Box containing adapters, enough to process a total of 96 samples, for Multimodal panel sequencing on Illumina platforms using separate enrichment workflows; two of two sets required for multiplexing 96 samples	96	N/A	333995

Visit **go.qiagen.com/QIAseqmultimodal** and discover how youcan double your NGS insights and free up half of your resources.

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