

<b>Package</b>	<b>Category</b>	<b>Capability</b>	<b>Support</b>
Partek Flow	NGS core	Raw read QC	Yes
Partek Flow	NGS core	Trimming	Yes
Partek Flow	NGS core	Read mapping to reference	Yes
Partek Flow	NGS core	De novo assembly	No
Partek Flow	NGS core	Long-read support	Yes
Partek Flow	DNA variation	Variant calling (germline/somatic/other)	Yes
Partek Flow	DNA variation	Variant annotation / consequence prediction	Yes
Partek Flow	Transcriptomics	Bulk RNA-seq (counts/DE workflows)	Yes
Partek Flow	Transcriptomics	Single-cell RNA-seq	Yes
Partek Flow	Transcriptomics	Spatial transcriptomics	Yes
Partek Flow	Transcriptomics	CITE-seq / multi-omic single-cell	Yes
Partek Flow	Transcriptomics	miRNA-seq	Yes
Partek Flow	Epigenomics	ChIP-seq	Yes
Partek Flow	Epigenomics	ATAC-seq	Yes
Partek Flow	Epigenomics	Bisulfite / methylation-seq	No
Partek Flow	Microbial	Metagenomics	Yes
Partek Flow	Biological interpretation	Pathway analysis / enrichment	Yes
Partek Flow	Biological interpretation	Gene set enrichment (GSEA)	Yes
Partek Flow	Visualization	Genome browser	Yes
Partek Flow	Visualization	PCA / dimensionality reduction	Yes
Partek Flow	Visualization	t-SNE	Yes
Partek Flow	Visualization	UMAP	Yes
Partek Flow	Visualization	Heatmaps + clustering	Yes
Partek Flow	Visualization	Volcano plots	Yes
Partek Flow	Operational	Workflow/pipeline builder	Yes
QIAGEN CLC Genomics Workbench	NGS core	Raw read QC	Yes

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QIAGEN CLC Genomics Workbench	NGS core	Trimming	Yes
QIAGEN CLC Genomics Workbench	NGS core	Demultiplexing	Yes
QIAGEN CLC Genomics Workbench	NGS core	Read mapping to reference	Yes
QIAGEN CLC Genomics Workbench	NGS core	De novo assembly	Yes
QIAGEN CLC Genomics Workbench	NGS core	Long-read support	Yes
QIAGEN CLC Genomics Workbench	DNA variation	Variant calling (germline/somatic/other)	Yes
QIAGEN CLC Genomics Workbench	DNA variation	Variant annotation / consequence prediction	Yes
QIAGEN CLC Genomics Workbench	Transcriptomics	Bulk RNA-seq (counts/DE workflows)	Yes
QIAGEN CLC Genomics Workbench	Transcriptomics	Single-cell RNA-seq	Yes (plugin available)
QIAGEN CLC Genomics Workbench	Transcriptomics	CITE-seq / multi-omic single-cell	No
QIAGEN CLC Genomics Workbench	Transcriptomics	miRNA-seq	Yes
QIAGEN CLC Genomics Workbench	Epigenomics	ChIP-seq	Yes

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QIAGEN CLC Genomics Workbench	Epigenomics	ATAC-seq	Yes
QIAGEN CLC Genomics Workbench	Epigenomics	Bisulfite / methylation-seq	Yes
QIAGEN CLC Genomics Workbench	Microbial	Microbial genomics	Yes (plugin available)
QIAGEN CLC Genomics Workbench	Biological interpretation	Gene set enrichment (GSEA)	Yes
QIAGEN CLC Genomics Workbench	Biological interpretation	Gene ontology (GO) enrichment	Yes
QIAGEN CLC Genomics Workbench	Visualization	Genome browser	Yes
QIAGEN CLC Genomics Workbench	Visualization	PCA / dimensionality reduction	Yes
QIAGEN CLC Genomics Workbench	Visualization	Heatmaps + clustering	Yes
QIAGEN CLC Genomics Workbench	Visualization	Volcano plots	Yes
QIAGEN CLC Genomics Workbench	Sequence & molecular biology	Sanger analysis	Yes
QIAGEN CLC Genomics Workbench	Sequence & molecular biology	BLAST	Yes
QIAGEN CLC Genomics Workbench	Sequence & molecular biology	Multiple sequence alignment	Yes

<b>Package</b>	<b>Category</b>	<b>Capability</b>	<b>Support</b>
QIAGEN CLC Genomics Workbench	Sequence & molecular biology	Phylogenetic trees	Yes
QIAGEN CLC Genomics Workbench	Sequence & molecular biology	Primer design	Yes
QIAGEN CLC Genomics Workbench	Sequence & molecular biology	Cloning tools	No
QIAGEN CLC Genomics Workbench	Sequence & molecular biology	CRISPR tools	No
QIAGEN CLC Genomics Workbench	Operational	Workflow/pipeline builder	Yes
Qlucore Omics Explorer	NGS core	Raw read QC	No
Qlucore Omics Explorer	NGS core	Trimming	No
Qlucore Omics Explorer	NGS core	Demultiplexing	No
Qlucore Omics Explorer	NGS core	Read mapping to reference	No
Qlucore Omics Explorer	NGS core	De novo assembly	No
Qlucore Omics Explorer	NGS core	Long-read support	No
Qlucore Omics Explorer	DNA variation	Variant calling (germline/somatic/other)	No
Qlucore Omics Explorer	DNA variation	Variant annotation / consequence prediction	No
Qlucore Omics Explorer	Transcriptomics	Bulk RNA-seq (counts/DE workflows)	Partial
Qlucore Omics Explorer	Transcriptomics	Single-cell RNA-seq (counts/DE workflows/visualization)	Partial
Qlucore Omics Explorer	Transcriptomics	CITE-seq / multi-omic single-cell	Partial

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Qlucore Omics Explorer	Transcriptomics	miRNA-seq	Partial
Qlucore Omics Explorer	Epigenomics	ChIP-seq	Partial
Qlucore Omics Explorer	Epigenomics	ATAC-seq	Partial
Qlucore Omics Explorer	Epigenomics	Bisulfite / methylation-seq	Partial
Qlucore Omics Explorer	Microbial	Metagenomics	Partial
Qlucore Omics Explorer	Biological interpretation	Pathway analysis / enrichment	Partial
Qlucore Omics Explorer	Biological interpretation	Gene set enrichment (GSEA)	Yes
Qlucore Omics Explorer	Biological interpretation	Gene ontology (GO) browsing	Yes
Qlucore Omics Explorer	Visualization	Genome browser	No
Qlucore Omics Explorer	Visualization	PCA / dimensionality reduction	Yes
Qlucore Omics Explorer	Visualization	t-SNE / embedding plots	Yes
Qlucore Omics Explorer	Visualization	Heatmaps + clustering	Yes
Qlucore Omics Explorer	Visualization	Volcano plots	Yes
Qlucore Omics Explorer	Machine learning	Built-in ML classification (SVM/kNN/trees/boosting)	Yes
Geneious Prime	NGS core	Raw read QC	Yes
Geneious Prime	NGS core	Ttrimming	Yes
Geneious Prime	NGS core	Demultiplexing	Yes
Geneious Prime	NGS core	Read mapping to reference	Yes
Geneious Prime	NGS core	De novo assembly	Yes
Geneious Prime	NGS core	Long-read support	No

<b>Package</b>	<b>Category</b>	<b>Capability</b>	<b>Support</b>
Geneious Prime	DNA variation	Variant calling (germline/somatic/other)	Partial
Geneious Prime	DNA variation	Variant annotation / consequence prediction	No
Geneious Prime	Transcriptomics	Bulk RNA-seq (counts/DE workflows)	Yes
Geneious Prime	Transcriptomics	Single-cell RNA-seq	No
Geneious Prime	Transcriptomics	CITE-seq / multi-omic single-cell	No
Geneious Prime	Transcriptomics	miRNA-seq	No
Geneious Prime	Epigenomics	ChIP-seq	No
Geneious Prime	Epigenomics	ATAC-seq	No
Geneious Prime	Epigenomics	Bisulfite / methylation-seq	No
Geneious Prime	Microbial	Metagenomics	No
Geneious Prime	Biological interpretation	Pathway analysis / enrichment	No
Geneious Prime	Biological interpretation	Gene set enrichment (GSEA)	No
Geneious Prime	Biological interpretation	Gene ontology (GO) browsing	No
Geneious Prime	Visualization	Genome browser	Yes
Geneious Prime	Visualization	PCA / dimensionality reduction	Yes
Geneious Prime	Visualization	t-SNE / embedding plots	No
Geneious Prime	Visualization	Heatmaps + clustering	No
Geneious Prime	Visualization	Volcano plots	Yes
Geneious Prime	Machine learning	Built-in ML classification (SVM/kNN/trees/boosting)	No
Geneious Prime	Sequence & molecular biology	Multiple sequence alignment	Yes
Geneious Prime	Sequence & molecular biology	Phylogenetic trees	Yes
Geneious Prime	Sequence & molecular biology	Primer design	Yes

<b>Package</b>	<b>Category</b>	<b>Capability</b>	<b>Support</b>
Geneious Prime	Sequence & molecular biology	Cloning tools	Yes
Geneious Prime	Sequence & molecular biology	CRISPR tools	Yes
Geneious Prime	Sequence & molecular biology	BLAST	Yes
Biodiscovery Nexus Copy Number	DNA variation	Copy number variation (CNV) detection from aCGH/ SNP array/ NGS data	Yes
Biodiscovery Nexus Copy Number	DNA variation	Allele-specific copy number/ LOH/ and mosaicism analysis	Yes
Biodiscovery Nexus Copy Number	Clinical genomics	Visualization/ annotation/ interpretation of CNVs with gene/ disease/ pathway context	Yes
Qiagen IPA	Functional genomics	Pathway/ network/ upstream regulator analysis for gene expression and omics data	Yes
Qiagen IPA	Multi-omics	Integration and interpretation of transcriptomics/ proteomics/ metabolomics/ and variant data	Yes
Qiagen IPA	Biological interpretation	Causal analysis/ disease/function prediction/ literature-backed biological insights	Yes
SnapGene	Molecular biology	Plasmid and DNA sequence visualization/ annotation/ and editing	Yes
SnapGene	Molecular cloning	In silico cloning/ restriction enzyme analysis/ primer design	Yes
SnapGene	Sequence analysis	Simulation of PCR/ Gibson Assembly/ other cloning workflows	Yes
Easy Panel	Flow cytometry	Design of flow cytometry panels	Yes