

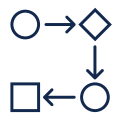
Transform Your Single-Cell Multiomics Data into Actionable Knowledge

BaseJumper Bioinformatics Platform



Comprehensive multiomic analysis platform

Explore single-cell multiomic data in a single platform.



No coding expertise required

Leverage pre-built and industry-standard bioinformatics workflows to accelerate the interpretation of large data sets.



Flexibility

Import and integrate multimodal analyses from different analytes, single-cell sequencing technologies, and sequencing platforms.



Available in three formats

BaseJumper is available as a **cloud-based platform**, command-line based **local installation**, or as **custom bioinformatics services** through ResolveServicesSM.



Generate publication-quality figures

Publication-quality figures are made possible with BaseJumper Services, available through ResolveServices.



Access



BaseJumper

Build



Compute



Discover



Export

Figure 1: Data analysis at your fingertips.

Users can access BaseJumper Cloud through the online portal or visit BioSkryb's website to download BaseJumper Local. They can build their datasets from multiomic analyses and select pre-designed bioinformatics workflows. Data are displayed in easy-to-interpret and ready-to-export formats. BaseJumper Services, available through ResolveServices, provides custom bioinformatics services.



Product Summary

- DNA/RNA pre-designed analysis workflows such as BJ-DNA-QC, BJ-WGS, BJ-WES, BJ-Expression, and BJ-Somatic-VariantCalling
- Quality control (QC) tools
- Data tables and graphs including, but not limited to examples in Figures 2–4
- Self-service or fee-for-service bioinformatics available

Selected Metrics

Selected metrics are subset of all metrics that provides overview of the sample quality assessment.

Copy table | Configure columns | Scatter plot | Violin plot | Showing 10 rows and 14 columns

sample_name	PreSeq Count	% chrM	% Chimeras	% Aligned	% Error	Insert Size	Total Reads	Adapter Trimmed Reads	Adapter Trimmed Bases	Gini coefficient	Average ploidy	Number of segments	Segment score of MAD
AAFTWFM5-A10-CT-D-SC-Detroit-DNAv2	440349118	0.17	12.69	99.85	0.25	516	5803160	22663	776456	0.03	2.00	14.0	0.325
AAFTWFM5-A10-CT-D-SC-Detroit-DNAv2-96	489690476	0.14	5.15	99.89	0.31	303	1804802	5022	465916	0.02	2.00	8.0	0.192
AAFTWFM5-A11-CT-D-SC-Detroit-DNAv2	4547791554	0.19	14.73	98.90	0.27	255	3610484	34323	1214817	0.04	2.00	27.0	0.227
AAFTWFM5-A11-CT-D-SC-Detroit-DNAv2-96	792239	0.39	22.17	98.75	0.38	283	6290	70	931	0.31	2.00	3.0	0.000
AAFTWFM5-A12-CT-D-SC-Detroit-DNAv2	3342370828	0.16	16.01	99.67	0.27	287	1883764	33796	1284766	0.04	2.00	53.0	1.132
AAFTWFM5-A12-CT-D-SC-Detroit-DNAv2-96	442656258	0.20	6.19	98.77	0.35	297	1413504	7630	86651	0.04	2.00	30.0	0.247
AAFTWFM5-A2-CT-D-SC-HG001-DNAv2	3800481890	0.97	19.05	98.95	0.25	275	1474800	13741	456251	0.03	2.00	18.0	0.752
AAFTWFM5-A2-CT-D-SC-HG001-DNAv2-96	4832953990	0.13	6.30	99.69	0.32	301	1966076	6514	66561	0.02	2.00	7.0	0.230
AAFTWFM5-A3-CT-D-SC-HG001-DNAv2	2562424174	0.81	16.78	99.84	0.27	275	1374002	14854	345169	0.06	2.00	52.0	1.817
AAFTWFM5-A3-CT-D-SC-HG001-DNAv2-96	4350660796	0.16	7.17	99.84	0.34	304	1737830	7080	78337	0.03	2.00	23.0	0.191
AAFTWFM5-A4-CT-D-SC-HG001-DNAv2	2221651848	0.83	16.78	99.81	0.28	264	1434330	20185	620591	0.06	2.00	50.0	3.005
AAFTWFM5-A4-CT-D-SC-HG001-DNAv2-96	762020117	1.73	14.42	99.72	0.45	292	947556	11866	142306	0.12	2.00	58.0	1.710
AAFTWFM5-A5-CT-D-SC-HG001-DNAv2	4085720401	0.28	14.83	99.92	0.25	267	1719030	13422	371653	0.03	2.00	21.0	0.681
AAFTWFM5-A5-CT-D-SC-HG001-DNAv2-96	4035207206	0.92	7.21	99.62	0.34	303	1581190	10251	257891	0.03	2.00	77.0	0.791
AAFTWFM5-A6-CT-D-SC-HG002-DNAv2	4262634285	0.64	14.26	99.94	0.25	249	1661242	17030	556453	0.03	2.00	18.0	0.441

Figure 2 (left): BaseJumper embedded QC metric table. Quickly evaluate data quality.

Figure 4 (below): BaseJumper embedded transcript coverage map. Assess full transcript coverage of RNA sequence data.

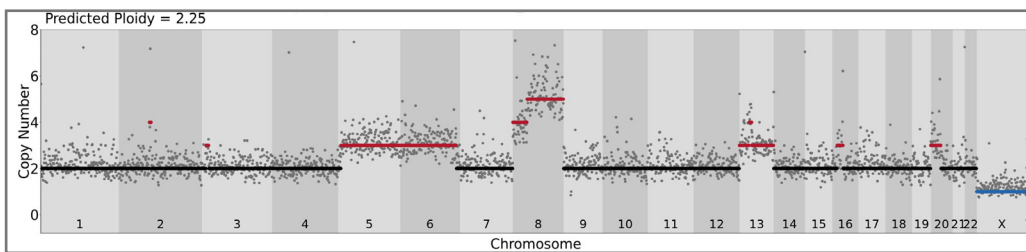
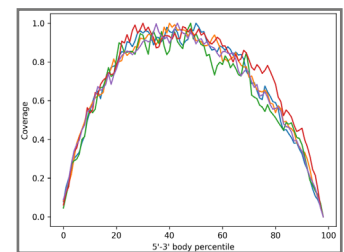


Figure 3: BaseJumper embedded copy number profiles. Visualize copy number gains and losses for each sample.



Products

Product	Description	Codes	Well Format
ResolveOME™ Whole Genome and Transcriptome Single-Cell Core Kit	PTA-based kit for whole genome and transcriptome amplification plus NGS library preparation from single cells.	100956	96
		100957	384
ResolveDNA® Whole Genome Single-Cell Core Kit	PTA-based kit for whole genome amplification plus NGS library preparation from single cells.	100954	96
		100955	384
ResolveDNA® Whole Genome Amplification Kit	PTA-based kit for whole genome amplification from as little as 4 pg input DNA.	100545	Up to 384*
BaseJumper® Bioinformatics Platform	A platform for multiomic data analysis.	100605	-
ResolveXOME™ Exome Capture Module	Exome capture module for use with ResolveDNA or ResolveOME Single-Cell Core Kits.	Early-Access	-

*Dependent on workflow option used

For a complete list of services, products, and pricing, email a member of our team, info@bioskryb.com



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