

**Supplementary Table S1: List of tools & packages and their usage in CSI NGS Portal**

All the tools and packages are regularly updated to the latest stable versions (unless version number is explicitly specified).  
An exhaustive list of dependencies are omitted.

Tool/package	Bioinformatics Pipeline	Usage	Link
<b>Website Development</b>			
Apache2	NA	Web server	<a href="https://httpd.apache.org/">https://httpd.apache.org/</a>
PHP	NA	Website interface and functionality	<a href="https://www.php.net/">https://www.php.net/</a>
HTML5	NA	Website interface and functionality	<a href="https://www.w3.org/TR/html5/">https://www.w3.org/TR/html5/</a>
CSS	NA	Website styling	<a href="https://www.w3.org/Style/CSS/">https://www.w3.org/Style/CSS/</a>
Bootstrap v3.3.6	NA	Interactive tables and responsive design	<a href="https://getbootstrap.com/">https://getbootstrap.com/</a>
JavaScript	NA	Dynamic features	<a href="https://developer.mozilla.org/en-US/docs/Web/JavaScript">https://developer.mozilla.org/en-US/docs/Web/JavaScript</a>
jQuery v1.12.1	NA	Dynamic features	<a href="https://jquery.com/">https://jquery.com/</a>
jQuery File Upload	NA	Data upload interface	<a href="https://github.com/blueimp/jQuery-File-Upload">https://github.com/blueimp/jQuery-File-Upload</a>
<b>Database</b>			
MariaDB	NA	Data storage	<a href="https://mariadb.org/">https://mariadb.org/</a>
<b>Programming Languages</b>			
Bash	All	Wrapper scripts for pipeline development	<a href="https://www.gnu.org/software/bash/">https://www.gnu.org/software/bash/</a>
Python	All	Running of packages in conda environment	<a href="https://www.python.org/">https://www.python.org/</a> , <a href="https://anaconda.com">https://anaconda.com</a>
Perl	All	Running of in-house and external pipelines	<a href="https://www.perl.org/">https://www.perl.org/</a>
R	Diff4C-Seq, Diff-Exp, Pathway-Enrichment	Running CRAN and Bioconductor packages	<a href="https://www.r-project.org/">https://www.r-project.org/</a>
<b>Anaconda2 Packages</b>			
FastQC	All	Quality control	<a href="https://www.bioinformatics.babraham.ac.uk/projects/fastqc/">https://www.bioinformatics.babraham.ac.uk/projects/fastqc/</a>
Trimmomatic	All	Adapter removal and read trimming	<a href="http://www.usadellab.org/cms/?page=trimmomatic">http://www.usadellab.org/cms/?page=trimmomatic</a>
bedtools	All	Genome arithmetic	<a href="https://bedtools.readthedocs.io">https://bedtools.readthedocs.io</a>
Samtools	All	Manipulation of HTS files	<a href="https://github.com/samtools/samtools">https://github.com/samtools/samtools</a>
Picard	DNA-Seq, RIP-Seq	Manipulation of HTS files	<a href="https://github.com/broadinstitute/picard">https://github.com/broadinstitute/picard</a>
BWA (mem)	DNA-Seq, RNA-Editing, 4C-Seq	Read mapping	<a href="https://github.com/lh3/bwa">https://github.com/lh3/bwa</a>
Bowtie2	SHAPE-Seq, Bisulfite-Seq, ngsplot-deepTools	Read mapping	<a href="http://bowtie-bio.sourceforge.net/bowtie2/index.shtml">http://bowtie-bio.sourceforge.net/bowtie2/index.shtml</a>
NovoAlign	smallRNA	Read mapping	<a href="http://www.novocraft.com/products/novoalign/">http://www.novocraft.com/products/novoalign/</a>
STAR	RNA-Seq, RIP-Seq, rMATs, circRNA, eCLIP-Seq, ngsplot-deepTools	RNA-Seq read alignment	<a href="https://github.com/alexdobin/STAR">https://github.com/alexdobin/STAR</a>
GATK4 (Mutect2)	DNA-Seq	Genome analysis toolkit (Mutation calling)	<a href="https://software.broadinstitute.org/gatk/documentation/article?id=11136">https://software.broadinstitute.org/gatk/documentation/article?id=11136</a>
HTSeq (count)	RNA-Seq	Gene expression quantification	<a href="https://htseq.readthedocs.io/en/master/count.html">https://htseq.readthedocs.io/en/master/count.html</a>
Salmon	RNA-Seq	Isoform expression quantification	<a href="https://salmon.readthedocs.io/en/latest/salmon.html">https://salmon.readthedocs.io/en/latest/salmon.html</a>
MACS2	ChIP-Seq, RIP-Seq	Identification of transcription factor binding sites	<a href="https://github.com/taoliu/MACS">https://github.com/taoliu/MACS</a>
Homer	ChIP-Seq	Motif enrichment analysis	<a href="http://homer.ucsd.edu/homer/motif/">http://homer.ucsd.edu/homer/motif/</a>
ViennaRNA (RNAfold)	SHAPE-Seq	RNA secondary structure prediction	<a href="https://www.tbi.univie.ac.at/RNA/RNAfold.1.html">https://www.tbi.univie.ac.at/RNA/RNAfold.1.html</a>
TrimGalore/Cutadapt	RIP-Seq, Bisulfite-Seq	Adapter removal and read trimming	<a href="https://github.com/FelixKrueger/TrimGalore">https://github.com/FelixKrueger/TrimGalore</a>
Singularity	eCLIP-Seq	Running eCLIP container	<a href="https://www.sylabs.io/guides/2.6/user-guide/">https://www.sylabs.io/guides/2.6/user-guide/</a>
Bismark	Bisulfite-Seq	Methylation calling of bisulfite treated sequencing reads	<a href="https://www.bioinformatics.babraham.ac.uk/projects/bismark/">https://www.bioinformatics.babraham.ac.uk/projects/bismark/</a>
metilene	Bisulfite-Seq	Identification of differentially methylated regions	<a href="https://www.bioinf.uni-leipzig.de/Software/metilene/">https://www.bioinf.uni-leipzig.de/Software/metilene/</a>
<b>R CRAN Packages</b>			
R ggplot2	Diff-Exp, Pathway-Enrichment	Generation of plots and data visualisation	<a href="https://cran.r-project.org/web/packages/ggplot2/index.html">https://cran.r-project.org/web/packages/ggplot2/index.html</a>
R tidyverse	4C-Seq, Diff-Exp, Pathway-Enrichment	Data manipulation	<a href="https://www.tidyverse.org/">https://www.tidyverse.org/</a>
R RMySQL	Diff-Exp	Database connection	<a href="https://cran.r-project.org/web/packages/RMySQL/index.html">https://cran.r-project.org/web/packages/RMySQL/index.html</a>
<b>R Bioconductor Packages</b>			
R Bioconductor r3Cseq	4C-Seq	Identification of 4C interactions	<a href="https://www.bioconductor.org/packages/release/bioc/html/r3Cseq.html">https://www.bioconductor.org/packages/release/bioc/html/r3Cseq.html</a>
R Bioconductor BSgenome	4C-Seq	Reference genome annotations	<a href="https://bioconductor.org/packages/release/bioc/html/BSgenome.html">https://bioconductor.org/packages/release/bioc/html/BSgenome.html</a>
R Bioconductor org.Hs.eg.db	Diff-Exp	Reference genome annotations	<a href="https://bioconductor.org/packages/release/data/annotation/html/org.Hs.eg.db.html">https://bioconductor.org/packages/release/data/annotation/html/org.Hs.eg.db.html</a>
R Bioconductor DESeq2	Diff-Exp	Differential gene expression analysis	<a href="https://www.bioconductor.org/packages/release/bioc/html/DESeq2.html">https://www.bioconductor.org/packages/release/bioc/html/DESeq2.html</a>
R Bioconductor DEXSeq	Diff-Exp	Differential exon usage analysis	<a href="https://bioconductor.org/packages/release/bioc/html/DEXSeq.html">https://bioconductor.org/packages/release/bioc/html/DEXSeq.html</a>
R Bioconductor regionReport	Diff-Exp	Generation of interactive report for DESeq2 results	<a href="https://www.bioconductor.org/packages/release/bioc/html/regionReport.html">https://www.bioconductor.org/packages/release/bioc/html/regionReport.html</a>
R Bioconductor biomaRt	Diff-Exp	ID mapping and conversion	<a href="https://www.bioconductor.org/packages/release/bioc/html/biomaRt.html">https://www.bioconductor.org/packages/release/bioc/html/biomaRt.html</a>
R Bioconductor ReactomePA	Diff-Exp, Pathway-Enrichment	Pathway enrichment analysis	<a href="https://www.bioconductor.org/packages/release/bioc/html/ReactomePA.html">https://www.bioconductor.org/packages/release/bioc/html/ReactomePA.html</a>
R Bioconductor enrichplot	Diff-Exp, Pathway-Enrichment	Visualisation of pathway enrichment results	<a href="https://bioconductor.org/packages/release/bioc/html/enrichplot.html">https://bioconductor.org/packages/release/bioc/html/enrichplot.html</a>
R Bioconductor DOSE	Diff-Exp, Pathway-Enrichment	Visualisation of pathway enrichment results	<a href="https://bioconductor.org/packages/release/bioc/html/DOSE.html">https://bioconductor.org/packages/release/bioc/html/DOSE.html</a>
<b>Standalone Software</b>			
ANNOVAR	DNA-Seq, RNA-Editing, eCLIP-Seq	Annotation of variants and peaks	<a href="http://annovar.openbioinformatics.org">http://annovar.openbioinformatics.org</a>
GSEA	Diff-Exp	Gene set enrichment analysis	<a href="https://www.gsea-msigdb.org/gsea/index.jsp">https://www.gsea-msigdb.org/gsea/index.jsp</a>
icSHAPE	SHAPE-Seq	SHAPE reactivity calculation	<a href="https://github.com/qczhang/icSHAPE">https://github.com/qczhang/icSHAPE</a>
rMATs	rMATs	Identification of differential alternative splicing events	<a href="http://rnaseq-mats.sourceforge.net/">http://rnaseq-mats.sourceforge.net/</a>
eCLIP	eCLIP-Seq	Identification of genomic locations of RNA-bound proteins	<a href="https://github.com/Yeolab/edli">https://github.com/Yeolab/edli</a>
Cell Ranger	scRNA-Seq	Single cell gene expression analysis	<a href="https://support.10xgenomics.com/single-cell-gene-expression/software/pipelines/latest">https://support.10xgenomics.com/single-cell-gene-expression/software/pipelines/latest</a>
ngsplot	ngsplot-deepTools	Visual exploration at functional genomic regions	<a href="https://github.com/shenlab-sinai/ngsplot">https://github.com/shenlab-sinai/ngsplot</a>
deepTools	ngsplot-deepTools	Visual exploration at functional genomic regions	<a href="https://github.com/deeptools/deeptools">https://github.com/deeptools/deeptools</a>