

Function	Package	Source	Purpose
useEnsembl	biomaRt	<a href="https://bioconductor.org/packages/release/bioc/html/biomaRt.html">https://bioconductor.org/packages/release/bioc/html/biomaRt.html</a>	Annotation of gene names
rpkm	edgeR	<a href="http://bioconductor.org/packages/release/bioc/html/edgeR.html">http://bioconductor.org/packages/release/bioc/html/edgeR.html</a>	Calculation of RPKM values
DGEList	edgeR	<a href="http://bioconductor.org/packages/release/bioc/html/edgeR.html">http://bioconductor.org/packages/release/bioc/html/edgeR.html</a>	Manipulation of read counts for DE analysis
ggplot	ggplot2	<a href="https://cran.r-project.org/web/packages/ggplot2/index.html">https://cran.r-project.org/web/packages/ggplot2/index.html</a>	Data visualisation
glmnet	glmnet	<a href="https://cran.r-project.org/web/packages/glmnet/index.html">https://cran.r-project.org/web/packages/glmnet/index.html</a>	LASSO logistic regression
cv.glmnet	glmnet	<a href="https://cran.r-project.org/web/packages/glmnet/index.html">https://cran.r-project.org/web/packages/glmnet/index.html</a>	LASSO cross-validation
predict	glmnet	<a href="https://cran.r-project.org/web/packages/glmnet/index.html">https://cran.r-project.org/web/packages/glmnet/index.html</a>	LASSO predictions
voom	limma	<a href="https://bioconductor.org/packages/release/bioc/html/limma.html">https://bioconductor.org/packages/release/bioc/html/limma.html</a>	Transformation of RNA-seq data for linear modelling
lmFit	limma	<a href="https://bioconductor.org/packages/release/bioc/html/limma.html">https://bioconductor.org/packages/release/bioc/html/limma.html</a>	Fitting linear models for RNA-seq data
eBayes	limma	<a href="https://bioconductor.org/packages/release/bioc/html/limma.html">https://bioconductor.org/packages/release/bioc/html/limma.html</a>	Empirical Bayes statistics for DE analysis
pheatmap	pheatmap	<a href="https://cran.r-project.org/web/packages/pheatmap/index.html">https://cran.r-project.org/web/packages/pheatmap/index.html</a>	Plotting heatmaps
featureCounts	Rsubread	<a href="https://bioconductor.org/packages/release/bioc/html/Rsubread.html">https://bioconductor.org/packages/release/bioc/html/Rsubread.html</a>	Assigning mapped sequencing reads to genomic features
cor/cor.test	stats	<a href="https://cran.r-project.org/web/packages/STAT/index.html">https://cran.r-project.org/web/packages/STAT/index.html</a>	Calculating correlation coefficients
survfit	survival	<a href="https://cran.r-project.org/web/packages/survival/index.html">https://cran.r-project.org/web/packages/survival/index.html</a>	Computing an estimate of a survival curve using the Kaplan-Meier method
coxph	survival	<a href="https://cran.r-project.org/web/packages/survival/index.html">https://cran.r-project.org/web/packages/survival/index.html</a>	Computing Cox proportional hazards models
draw.pairwise.venn	VennDiagram	<a href="https://cran.r-project.org/web/packages/VennDiagram/index.html">https://cran.r-project.org/web/packages/VennDiagram/index.html</a>	Plotting Venn diagrams
viridis	viridis	<a href="https://cran.r-project.org/web/packages/viridis/index.html">https://cran.r-project.org/web/packages/viridis/index.html</a>	Colour palettes
cpgDensityCalc	Repitools	<a href="https://bioconductor.org/packages/release/bioc/html/Repitools.html">https://bioconductor.org/packages/release/bioc/html/Repitools.html</a>	CpG density calculations