	Short name	Method	Software version	Input	Available from	Reference
■	BPSC	BPSC	BPSC 0.99.0/1	CPM	GitHub	[11]
■	D3E	D3E	D3E 1.0	raw counts	GitHub	[12]
■	DESeq2	DESeq2	DESeq2 1.14.1	raw counts	Bioconductor	[13]
■	DESeq2betapFALSE	DESeq2 without beta prior	DESeq2 1.14.1	raw counts	Bioconductor	[13]
■	DESeq2census	DESeq2	DESeq2 1.14.1	Census counts	Bioconductor	[13]
■	DESeq2nofilt	DESeq2 without the built-in independent filtering	DESeq2 1.14.1	raw counts	Bioconductor	[13]
■	DEsingle	DEsingle	DEsingle 0.1.0	raw counts	GitHub	[14]
■	edgeRLRT	edgeR/LRT	edgeR 3.19.1	raw counts	Bioconductor	[15–17]
■	edgeRLRTcensus	edgeR/LRT	edgeR 3.19.1	Census counts	Bioconductor	[15–17]
■	edgeRLRTdeconv	edgeR/LRT with deconvolution normalization	edgeR 3.19.1, scran 1.2.0	raw counts	Bioconductor	[15, 17, 18]
■	edgeRLRTrobust	edgeR/LRT with robust dispersion estimation	edgeR 3.19.1	raw counts	Bioconductor	[15–17, 19]
■	edgeRQLF	edgeR/QLF	edgeR 3.19.1	raw counts	Bioconductor	[15, 16, 20]
■	edgeRQLFDetRate	edgeR/QLF with cellular detection rate as covariate	edgeR 3.19.1	raw counts	Bioconductor	[15, 16, 20]
■	limmatrend	limma-trend	limma 3.30.13	log_2(CPM)	Bioconductor	[21, 22]
■	MASTcpm	MAST	MAST 1.0.5	log_2(CPM+1)	Bioconductor	[23]
■	MASTcpmDetRate	MAST with cellular detection rate as covariate	MAST 1.0.5	log_2(CPM+1)	Bioconductor	[23]
■	MASTtpm	MAST	MAST 1.0.5	log_2(TPM+1)	Bioconductor	[23]
■	MASTtpmDetRate	MAST with cellular detection rate as covariate	MAST 1.0.5	log_2(TPM+1)	Bioconductor	[23]
■	metagenomeSeq	metagenomeSeq	metagenomeSeq 1.16.0	raw counts	Bioconductor	[24]
■	monocle	monocle (tobit)	monocle 2.2.0	TPM	Bioconductor	[25]
■	monoclecensus	monocle (Negative Binomial)	monocle 2.2.0	Census counts	Bioconductor	[25, 26]
■	monoclecount	monocle (Negative Binomial)	monocle 2.2.0	raw counts	Bioconductor	[25]
■	NODES	NODES	NODES 0.0.0.9010	raw counts	Author-provided link	[27]
■	ROTScpm	ROTS	ROTS 1.2.0	CPM	Bioconductor	[28, 29]
■	ROTStpm	ROTS	ROTS 1.2.0	TPM	Bioconductor	[28, 29]
■	ROTSvoom	ROTS	ROTS 1.2.0	voom-transformed raw counts	Bioconductor	[28, 29]
■	SAMseq	SAMseq	samr 2.0	raw counts	CRAN	[30]
■	scDD	scDD	scDD 1.0.0	raw counts	Bioconductor	[31]
■	SCDE	SCDE	scde 2.2.0	raw counts	Bioconductor	[32]
■	SeuratBimod	Seurat (bimod test)	Seurat 1.4.0.7	raw counts	GitHub	[33, 34]
■	SeuratBimodnofilt	Seurat (bimod test) without the internal filtering	Seurat 1.4.0.7	raw counts	GitHub	[33, 34]
■	SeuratBimodIsExpr2	Seurat (bimod test) with internal expression threshold set to 2	Seurat 1.4.0.7	raw counts	GitHub	[33, 34]
■	SeuratTobit	Seurat (tobit test)	Seurat 1.4.0.7	TPM	GitHub	[25, 33]
■	ttest	t-test	stats (R v 3.3)	TMM-normalized TPM	CRAN	[16, 35]
■	voomlimma	voom-limma	limma 3.30.13	raw counts	Bioconductor	[21, 22]
■	Wilcoxon	Wilcoxon test	stats (R v 3.3)	TMM-normalized TPM	CRAN	[16, 36]