Tool name	Alignment and/or assembly	Quantification	Normalization	Differential expression	Ref.
TopHat	Reference genome + annotation	NA	NA	NA	[112]
STAR		NA	NA	NA	[113]
HISAT		NA	NA	NA	[114]
SOAPdenovo-Trans	De novo assembly	NA	NA	NA	[117]
StringTie	De novo assembly	Transcript estimates	NA	NA	[116]
Kallisto	Alignment-free assembly	Transcript estimates	NA	NA	[119]
Salmon		Transcript estimates	NA	NA	[120]
Cufflinks	Transcript assembly	Transcript estimates	NA	NA	[131]
RSEM	NA	Transcript estimates	NA	NA	[105]
MMSeq	NA	Transcript estimates	NA	NA	[132]
HTSeq	NA	Read counts from non-overlapping annotated features	NA	NA	[133]
featureCounts	NA	Read counts from non-overlapping annotated features	NA	NA	[134]
tximport	NA	Transcript estimates converted to read counts	NA	NA	[130]
edgeR	NA	NA	TMM	Negative binomial distribution + GLM	[143]
limma+voom	NA	NA	TMM	Mean–variance transform + GLM	[156]
DESeq2	NA	NA	Various	Negative binomial distribution + GLM	[155]
Ballgown	NA	NA	NA	Input from StringTie, RSEM or alignment-free quantification, + GLM	[157]
CuffDiff	NA	NA	NA	DE from Cufflinks estimates	[131]