Step	Description	TMM (edgeR)	RLE (DESeq2)
I	Pre-normalization by library size	$Y_{gkr} = \frac{X_{gkr}}{N_{kr}}$	
II	Reference sample, or *pseudo-reference sample* (DESeq2)	$Y_g^{\text{TMM}} = Y_{g11}$	$Y_g^{\text{RLE}} = \sqrt[KR]{\prod_{k=1}^{K}\prod_{r=1}^{R} X_{gkr}}$
III	Relative sizes of transcriptomes and reference sample, or *relative scaling factors* (edgeR), or *size factors* (DESeq2)	$\tau_{kr}^{\text{TMM}} = \frac{1}{\#\boldsymbol{\mathcal{G}}_{kr}^{*}} \sum_{g \in \boldsymbol{\mathcal{G}}_{kr}^{*}} \frac{Y_{gkr}}{Y_g^{\text{TMM}}}$ *where* $\boldsymbol{\mathcal{G}}_{kr}^{*}$ represents the set of not trimmed genes	$\tau_{kr}^{\text{RLE}} = \underset{g}{\text{median}} \left(\frac{X_{gkr}}{Y_g^{\text{LRE}}} \right)$
IV	*Relative scaling factors* adjusted to multiply to 1 (edgeR)	$\tilde{\tau}_{kr}^{\text{TMM}} = \frac{\tau_{kr}^{\text{TMM}}}{\tilde{\tau}^{\text{TMM}}}$ where $\tilde{\tau}^{\text{TMM}} = \sqrt[KR]{\prod_{k=1}^{K}\prod_{r=1}^{R} \tau_{kr}^{\text{TMM}}}$	
V	Taking into account both the relative size and the library size, or *effective library size* (edgeR)	$e_{kr}^{\text{TMM}} = \tilde{\tau}_{kr}^{\text{TMM}} N_{kr}$	
VI	Normalization factors, or *relative normalization factors* (edgeR), or *size factors* (DESeq2)	$f_{kr}^{\text{TMM}} = \tilde{\tau}_{kr}^{\text{TMM}}$	$f_{kr}^{\text{RLE}} = \tau_{kr}^{\text{RLE}}$
VII	Normalization of counts, or *counts-per-million* (edgeR)	$Z_{gkr}^{\text{TMM}} = \frac{X_{gkr}}{e_{kr}^{\text{TMM}}} 10^6$	$Z_{gkr}^{\text{RLE}} = \frac{X_{gkr}}{f_{kr}^{\text{RLE}}}$