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| **ES metric abbr.** | **ES metric name** | ***ESw* scale** | ***ESw* interpretation** | **Reference** |
| GES | Gene Enrichment Score | $$R\_{\geq 0}$$ | <1: *g* depleted in *c* 1: *g* no enrichment>1: *g* enriched in *c* | Zeisel (*Cell*, 2018) |
| EP | Expression Proportion | [0, 1] |  0: *g* not expressed in *c*0.5: *c* makes up 50% of *g* total mean expression. 1: *g* uniquely expressed in *c* | Skene (*Nature Genetics*, 2018) |
| NSI | Normalized Specificity Index | [0, 1] | 0: *g* not expressed in *c*0.5: *g*’s mean expression fold-change (focal cell type compared to other cell types) is on average within the top 50% of all genes1: *g*’s mean expression fold-change is the largest fold-change observed over all genes. | Modified from Dougherty (*Bioinformatics*, 2010) |
| DET | Differential Expression T-statistic | $$R$$ | <0: *g’s* mean expression lower in *c*>0: *g’s* mean expression higher in *c* | - |