S5 Text: Gene ontology enrichment analysis of highly (and lowly) variable genes among the analysed mouse ESC dataset.
BASiCS: Bayesian Analysis of Single-Cell Sequencing Data

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Table S2: Gene ontology (GO) enrichment analysis of genes detected as highly (or lowly) variably by BASiCS and the methods described in [1] and [2]. Only the 5 GO categories with smallest p-values are displayed in each case.

Method	GO term	Annotated	Significant	Expected	p-value
BASiCS (LVG)	Translation	340	101	25.87	1.8×10^{-19}
	ATP synthesis coupled proton transport	14	11	1.07	1.3×10^{-10}
	Translational initiation	68	26	5.17	4.9×10^{-10}
	Binding of sperm to zona pellucida	10	8	0.76	4.2×10^{-8}
	Translational elongation	33	13	2.51	3.4×10^{-7}
BASiCS (HVG)	Cell differentiation	1017	25	12.43	1.2×10^{-3}
	Regulation of epidermis development	19	3	0.23	1.5×10^{-3}
	Brown fat cell differentiation	8	2	0.1	3.9×10^{-3}
	Pyrimidine nucleobase metabolic process	8	2	0.1	3.9×10^{-3}
	Pyrimidine-containing compound catabolic process	8	2	0.1	3.9×10^{-3}
Islam (HVG)	Negative regulation of cell proliferation	204	16	3.15	1.3×10^{-6}
	Nitric oxide mediated signal transduction	5	3	0.08	3.5×10^{-5}
	Cellular response to metal ion	21	4	0.32	2.6×10^{-4}
	Positive regulation of blood pressure	9	3	0.14	2.8×10^{-4}
	Regulation of cell growth	114	8	1.76	3.5×10^{-4}
Brennecke (HVG)	Lung development	75	25	10.04	7.1×10^{-6}
	Anterior/posterior axis specification	26	12	3.48	4.9×10^{-5}
	Somitogenesis	24	11	3.21	1.1×10^{-4}
	Regulation of cell migration	165	47	22.08	1.5×10^{-4}
	Regulation of embryonic development	33	13	4.42	1.7×10^{-4}

References

[1] Islam S, Zeisel A, Joost S, La Manno G, Zajac P, et al. (2014) Quantitative single-cell RNA-seq with unique molecular identifiers. Nature Methods 11: 163-166.

[2] Brennecke P, Anders S, Kim JK, Kołodziejczyk AA, Zhang X, et al. (2013) Accounting for technical noise in single-cell RNA-seq experiments. Nature Methods 10: 1093-1095.