

Abbreviations

AID	activation-induced cytidine deaminase pathway
ANOVA	analysis of variance
ATP	adenosine-5'-triphosphate
BER	base-excision repair
CAP	circular a posteriori projection
cDNA	complementary DNA
CEL-Seq	single-cell RNA-Seq by multiplexed linear amplification
CHD	chromodomain-helicase-DNA-binding protein
ChIP	chromatin immunoprecipitation
circRNA	circular RNA
CRISPR	clustered regularly interspaced short palindromic repeats
CRISPRi	CRISPR interference
CV	coefficient of variation
DM	distance to the median
DMEM	Dulbecco modified Eagle's minimal essential medium
EC	embryonic carcinoma
EDTA	ethylenediaminetetraacetic acid
EMT	endothelial to mesenchymal transition
EpiSC	epiblast stem cells
ERCC	external RNA controls consortium
ESCAPE	embryonic stem cell atlas from pluripotency evidence
FACS	fluorescence-activated cell sorting
FDR	false discovery rate

FISH	fluorescence in situ hybridization
FISSEQ	fluorescent in situ sequencing
FWER	family-wise error rate
GDP	guanosine-5'-diphosphate
GFP	green fluorescent protein
GO	gene ontology
gRNA	guide RNA
GSNAP	genomic short-read nucleotide alignment program
GTF	general transfer format
GTP	guanosine-5'-triphosphate
HDAC	histone deacetylase
hESC	human embryonic stem cells
HSC	hematopoietic stem cell
ICA	independent component analysis
IFC	integrated fluidic circuit
iPSC	induced-pluripotent stem cells
IVT	in vitro transcription
JAK	janus-associated kinase
KRAB	Krüppel associated box
KS test	Kolmogorov–Smirnov test
LB	Luria-Bertani broth
LCM	laser capture microdissection
LIF	leukaemia inhibitory factor
lncRNA	long non-coding RNA
LTR	long terminal repeat
MAPK	mitogen-activated protein kinase
MAP2K	mitogen-activated protein kinase kinase
MAP3K	mitogen-activated protein kinase kinase kinase
MARS-Seq	massively parallel single-cell RNA-sequencing
MEF	mouse embryonic fibroblast
mESCs	mouse embryonic stem cells
mRNA	messenger RNA
MST	minimal spanning tree
MuERV-L	murine endogenous retrovirus L
NFAT	nuclear factor of activated T-cells

NPC	neuronal progenitor cell
NURD	nucleosome remodelling and histone deacetylase complex
NURF	nucleosome remodelling factor
PAM	protospacer Adjacent Motif
PC	principal component
PCA	principal component analysis
PLA	proximity ligation assay
PI3K	phosphoinositide 3-kinase
PRC1	polycomb-group repressive complex 1
PRC2	polycomb-group repressive complex 2
qPCR	quantitative real-time polymerase chain reaction
RNA	ribonucleic acid
RPM	reads per million
rRNA	ribosomal RNA
SC3-seq	single-cell mRNA 3-prime end sequencing
scRNA-seq	single cell RNA sequencing
SCUBA	single-cell clustering using bifurcation analysis
SH2	src homology 2 domain
SOM	self-organizing map
SNN	shared nearest neighbour
SRF	serum response factor
SRY-box	sex determining region Y box
STAT	signal transducers and activators of transcription
STO	Sandos Inbred Mice Thioguanine/Ouabain-resistant mouse fibroblast cell line
STRT-Seq	single-cell tagged reverse transcription sequencing
TIVA	transcriptome in vivo analysis
tSNE	t-distributed stochastic neighbour embedding
UMI	unique molecular identifier
WGCNA	weighted gene co-expression network analysis
ZGA	zygote genome activation
ZIFA	zero inflated factor analysis