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SUPPLEMENTARY INFORMATION

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RNA sequencing: the teenage years

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Application	Method	Ref	Year	PubMed	GEO (datasets)	SRA
RNA-Seq	RNA-Seq	1	2008	16799	90584	1327346
	RNASeq	2	2008	1981	38174	134841
	mRNA-Seq	3	2008	382	4930	62475
Single-cell	Various	4	2009	5529	60378	424058
Spatialomics	Various	5,6	2016, 2019	188	130	3397
Nascent RNA	GRO-Seq	7	2008	76	1335	606
	4sU/SLAM-Seq	8	2017	28	77	452
	PRO-Seq	9	2013	21	193	89
	NET-Seq	10	2015	15	135	122
	mNET-Seq	11	2015	11	94	81
Translatome	Polysome profiling	12	2011	143	149	110
	Ribo-Seq	13	2009	84	573	636
Structurome	SHAPE-MaP	14	2014	32	69	306
	SHAPE-Seq	15	2011	22	4	42
	PARS	16	2010	15	1	0
	Structure-Seq	17	2014	13	40	23
Interactome (R-P)	CLIP-Seq	18	2008	199	435	724
	PAR-CLIP	19	2010	150	710	907
	iCLIP	20	2010	101	611	1891
	eCLIP	21	2016	27	874	1077
Interactome (R-R)	CLASH	22	2011	95	12	18

Supplementary table 1 | Relative use of RNA-Seq methods. The major methods discussed in this review are listed here alongside PubMed, GEO, and SRA search results to demonstrate the variety of "RNA-Seq" methods and their relative use. Applications, and their methods, are listed in the order they appear in the manuscript (methods with very low citation counts are not included). The terms "RNA-Seq", "RNASeq" and "mRNA-Seq" have all been used to describe the same DGE methodology, users should be cautious of searching for a single term as only a subset of results will be found[23]. Additionally, the method used to deplete rRNAs has a significant impact on results but the terms "oligo-dT, Ribozero/Ribominus, RNaseH depletion" do not return large numbers of citations/hits highlighting the requirement for clear reporting of experimental procedures in a searchable manner. Individual search terms are included in each hyperlink, for each search the same format was used where possible within each database (PubMed, GEO and SRA, queried April 2019). R-P: RNA-protein interaction, R-R: RNA-RNA interaction.

Platform	RNA-Seq samples on SRA	%age of SRA RNA-Seq
Illumina	1,444,514	97.2%
Ion Torrent	11,709	0.8%
ABI SOLiD	10,504	0.7%
Roche 454	7,690	0.5%
BGI Seq	4,416	0.3%
Pacific Biosciences	3,283	0.2%
Helicos	3,091	0.2%
Oxford Nanopore	450	<0.1%
Capillary	420	<0.1%
Complete Genomics	95	<0.1%

Supplementary table 2 | Relative use of sequencing technologies for RNA-Seq. Analysis of Short Read Archive RNA-Seq datasets generated on various sequencing platforms confirms the (current) dominance of Illumina short-read methods. SRA queried June 2019 for "("transcriptomic"[Source]) AND "xxx"[Platform]".

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