

Supplementary Table 1. Overview of RNA-seq methods to study bacterial RNA biology on a genome scale

Process of interest	Method	Description	Key reference
Transcript annotation/identification	Capp-Switch sequencing	Detection of transcript 5' ends	(Boutard et al., 2016)
	Cappable-seq		(Ettwiller et al., 2016)
	dRNA-seq		(Sharma et al., 2010)
	Term-seq	Detection of transcript 3' ends	(Dar et al., 2016)
	Iso-seq	Full-length transcriptome sequencing	Neither technique has been applied to bacteria, yet
	Nanopore (direct) RNA-seq		
RNA modification	Bisulfite-seq	Detection of m ⁵ C modifications	(Edelheit et al., 2013)
	NAD captureSeq	Detection of 5' NAD caps	(Cahová et al., 2015)
	PA-m ⁶ A-seq	Detection of m ⁶ A modifications	(Deng et al., 2015)
RNA structure	DMS-seq	Analysis of RNA secondary structures	(Burkhardt et al., 2017)
	PARS		(Del Campo et al., 2015)
Translational control	Ribosome profiling	Analysis of translation rates	(Li et al., 2014)
RNA decay	RNA-seq after inhibition of transcription	Global analysis of RNA decay rates	(Chen et al., 2015)
	RNA-seq of RNase knockout and wildtype strains	Analysis of the effect of an RNase on steady state RNA levels	(Lasa et al., 2011)
	RNA-seq of specifically enriched RNAs from RNase knockout and wildtype strains	Analysis of the influence of an RNase on a specific RNA pool	(Lybecker et al., 2014)

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Supplementary Table 1. Continued

Process of interest	Method	Description	Key reference
	RNA-seq of RNase knockout and wildtype strains with 5' end-mapping	Identification of the targets and cleavage motif of an RNase	(Linder et al., 2014)
	TIER-seq		(Chao et al., 2017)
sRNA targetome (RNA-centric)	Pulse-expression	Identification of direct and indirect sRNA targets	(Westermann et al., 2016)
	GRIL-seq	Identification of direct sRNA targets	(Han et al., 2016)
	MAPS		(Lalaouna et al., 2015)
sRNA-mediated transcriptional regulation	RNA-seq after inhibition of Rho in sRNA knockout and wildtype strains	Analysis of the regulation of Rho by sRNAs	(Sedlyarova et al., 2016)
RBP targetome	RIP-seq	Identification of RBP targets	(Sittka et al., 2008)
	CLIP-seq	Identification of RBP targets and its binding motif	(Holmqvist et al., 2016)
sRNA targetome (protein-centric)	CLASH	Identification of sRNA-target interactions facilitated by an RBP	(Waters et al., 2017)
	RIL-seq		(Melamed et al., 2016)
Pathogen-host interaction	Dual RNA-seq	Simultaneous analysis of host and pathogen transcriptomes during infection	(Westermann et al., 2016)
Single cell transcriptomics	RNA-seq of single bacterial cells	Analysis of the transcriptome of a single bacterial cell	(Wang et al., 2015)

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