

Name	Inferred metadata					Input	Output	Availability	License
	Source organism	Read length statistics	Library type	Read orientation	3' adapter sequence				
<b>Sequence Taxonomic Analysis Tool (STAT)</b>	Yes	No	No	No	No	FASTA/Q	TXT	<a href="#">GitHub</a>	Public Domain (US, with exceptions)
<b>GUESSmyLT</b>	No	No	Yes	Yes	No	FASTQ	TXT	<a href="#">GitHub</a> , <a href="#">Bioconda</a> , <a href="#">BioContainers</a>	GPL-3.0
<b>Salmon</b>	No	No	Yes	Yes	No	FASTA/Q	JSON	<a href="#">GitHub</a> , <a href="#">Bioconda</a> , <a href="#">BioContainers</a>	GPL-3.0
<b>HTSinfer</b>	Yes	Yes	Yes	Yes	Yes	FASTQ	JSON	<a href="#">GitHub</a> , <a href="#">Bioconda</a> , <a href="#">BioContainers</a>	Apache-2.0

**Supplementary table 1:** Comparison of available metadata inference tools.