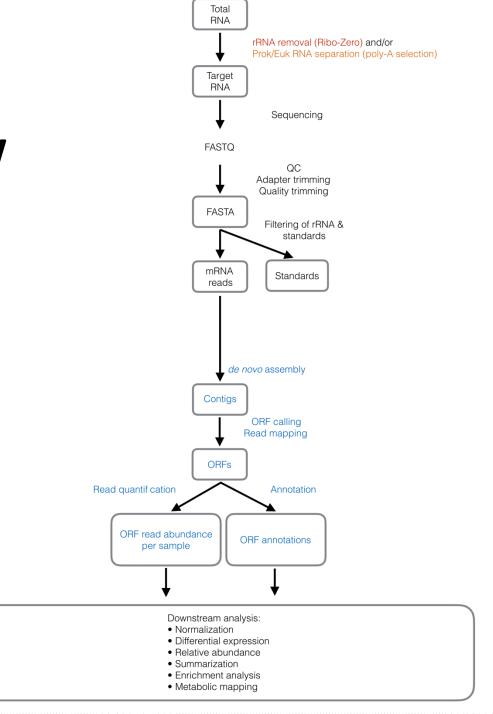
## General Workflow



## Additional Workflow Options

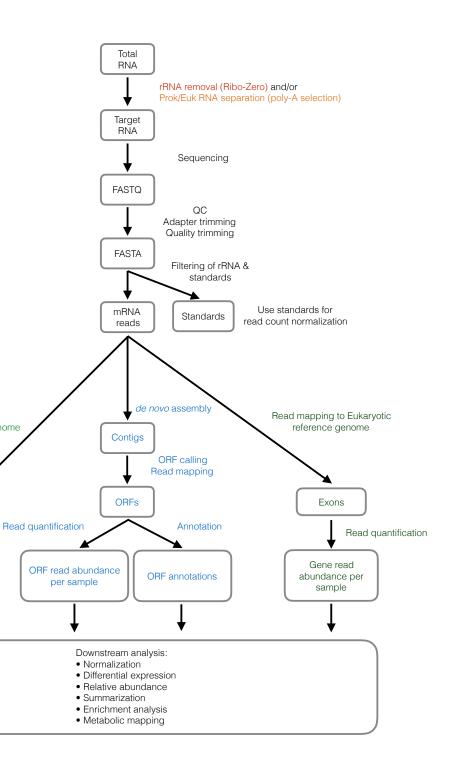
Read mapping to reference

transcriptome or Prokaryotic genome

Gene read

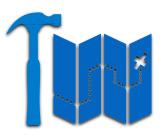
abundance per

sample





Map reads straight to reference



Assemble reads then map reads to assembly



Remove rRNA before sequencing (optional)



Remove non-target RNA before sequencing (optional)

		Reference genome	No reference genome
Microbe	Pure culture	*	
	Free-living community or mixed culture		
	Host-associated community		
Macrobe	Pure tissue		TWT
	Microbe-associated tissue		