Pipeline fq dir: pathlib.Path outdir: pathlib.Path required mods: list sample sheet: list init (self, args) check dirs(self) prepare_samplesheet(self, ss=None) setup workdir(self) prepare_qsub(self) BulkRNASeqPipeline pipe_name: str init (self, args) summarize fastqc(self) summarize_counts(self) SCRNASeqPipeline pipe name: str init (self, args)

SampleSheet Sample samples: list name: str r1: str r2: str tech: str trim_opt: str hisat_opt: str init (self, args) write sheet(self) _init__(self, args) parse_umgc(self, u) resolve_options(self) build_from_dir(self, d) sanitize_paths(self)