```
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_counts(self)
                                 SCRNASeqPipeline
                        pipe_name: str
```

init (self, args)

```
name: str
r1: pathlib.Path
r2: pathlib.Path
run_id: str

__init__(self, args)
```