

GopherPipelines

User Bash Shell

```
gopher_pipelines.py  
brnaseq(args)  
main()
```

ArgHandling

```
args.py  
usage()  
pipeline_args()
```

```
bulk_rnaseq_args.py  
add_args(parser)
```

```
sc_rnaseq_args.py  
add_args(parser)
```

```
set_verbosity.py  
verb(level, name)
```

FileOps

```
default_dirs.py  
default_output(pipeline)
```

```
dir_funcs.py  
dir_exists(d)  
dir_writeable(d)  
dir_empty(d)
```

Pipelines

```
Pipeline.py  
class Pipeline(object)
```

```
DieGracefully.py  
general_error()  
bad_outdir()  
bad_workdir()  
bad_resources()  
brnaseq_inc()  
brnaseq_conflict()  
bad_hisat2()  
bad_fastq()  
empty_fastq()  
diegracefully()
```

```
BulkRNASeq.py  
class BulkRNASeqPipeline(Pipeline)
```

SampleSheet

```
Samplesheet.py  
class Samplesheet(object)
```

```
BulkRNASeqSampleSheet.py  
class BulkRNASeqSampleSheet(SampleSheet.Samplesheet)
```

single_sample.template.pbs

subread.r

tpm.r

prep.r

Sample sheet file

