docs

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There are some files available.

```
[1] "/Library/Frameworks/R.framework/Resources/library/yeastRNASeq/reads/mut_1_f.fastq.bowti
[2] "/Library/Frameworks/R.framework/Resources/library/yeastRNASeq/reads/mut_2_f.fastq.bowti
[3] "/Library/Frameworks/R.framework/Resources/library/yeastRNASeq/reads/wt_1_f.fastq.bowtie
[4] "/Library/Frameworks/R.framework/Resources/library/yeastRNASeq/reads/wt_2_f.fastq.bowtie
```

Some have been aligned with bowtie. You can read these in using ShortRead.

```
> require(ShortRead)
> aligned <- lapply(files, function(f) readAligned(f, type = "Bowtie"))
> names(aligned) <- gsub(".fastq.bowtie", "", basename(files))

> sapply(aligned, function(a) table(chromosome(a)))
```
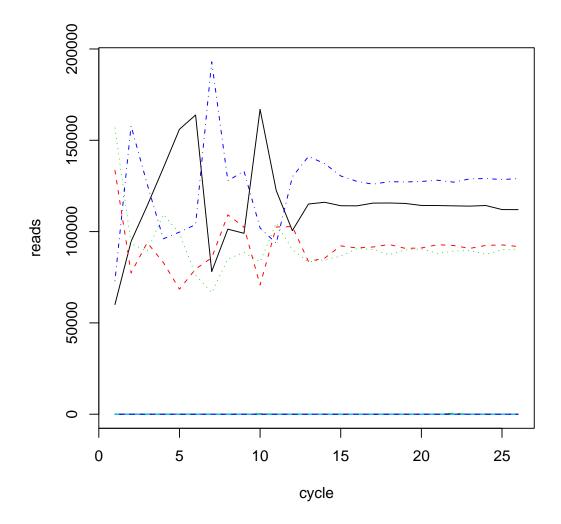
	mut_1_f	mut_2_f	wt_1_f	wt_2_f
Scchr01	6675	6730	9778	10320
Scchr02	24799	24573	26367	27478
Scchr03	10544	10369	16813	17602
Scchr04	55675	55226	60442	63251
Scchr05	21299	21462	18068	19028
Scchr06	12128	11962	11552	12085
Scchr07	45207	45233	38763	40899
Scchr08	19012	18848	22873	23904
Scchr09	11389	11217	11097	11803
Scchr10	23292	23252	17779	18725
Scchr11	23239	22977	24400	25425
Scchr12	38979	39003	33865	35507
Scchr13	33739	33397	33443	34907
Scchr14	23613	23657	20330	21169
Scchr15	41188	40409	37494	39322
Scchr16	31752	31708	27221	28765
Scmito	788	825	64	74

```
> a <- alphabetByCycle(sread(aligned[[1]]))
> matplot(t(a), ylab = "reads", xlab = "cycle", type = "l")
```