

LG length in bp

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August 9, 2018

Get contig names to find them in fasta.fai file and add the 2nd column of the .fai file which contains contig lengths.

Script below: run for L.1 to L.7 and record Linkage group lengths.

```
cat OM_geneticmap.bed | grep "L.1" | cut -f 1 | sort | uniq > search.txt
grep -w -f search.txt /home/exserta/Documents/master_project_noelle/data/optical_mapping_raw/P.exserta.
rm search.txt
```

```
## cat: OM_geneticmap.bed: No such file or directory
## 0
```

```
lens <- c(46083570, 34179769, 61776312, 58184792, 48860405, 50202786, 48388317)
lensMbp <- lens / 1000000
pdf("figures/length_of_LGs_omgenome.pdf")
barplot(lensMbp, ylim = c(0, 70), names.arg = paste("L",seq(1,7), sep=""), sub=paste("Length of linkage
dev.off()
```

```
## pdf
## 2
```

Question : why are the linkage groups shorted if I search them on the OM genome? Because I didn't find all Contigs? (subsequences..)?