RNA-seq of *Fisculla terrestris* provide evidence of meiotic genes

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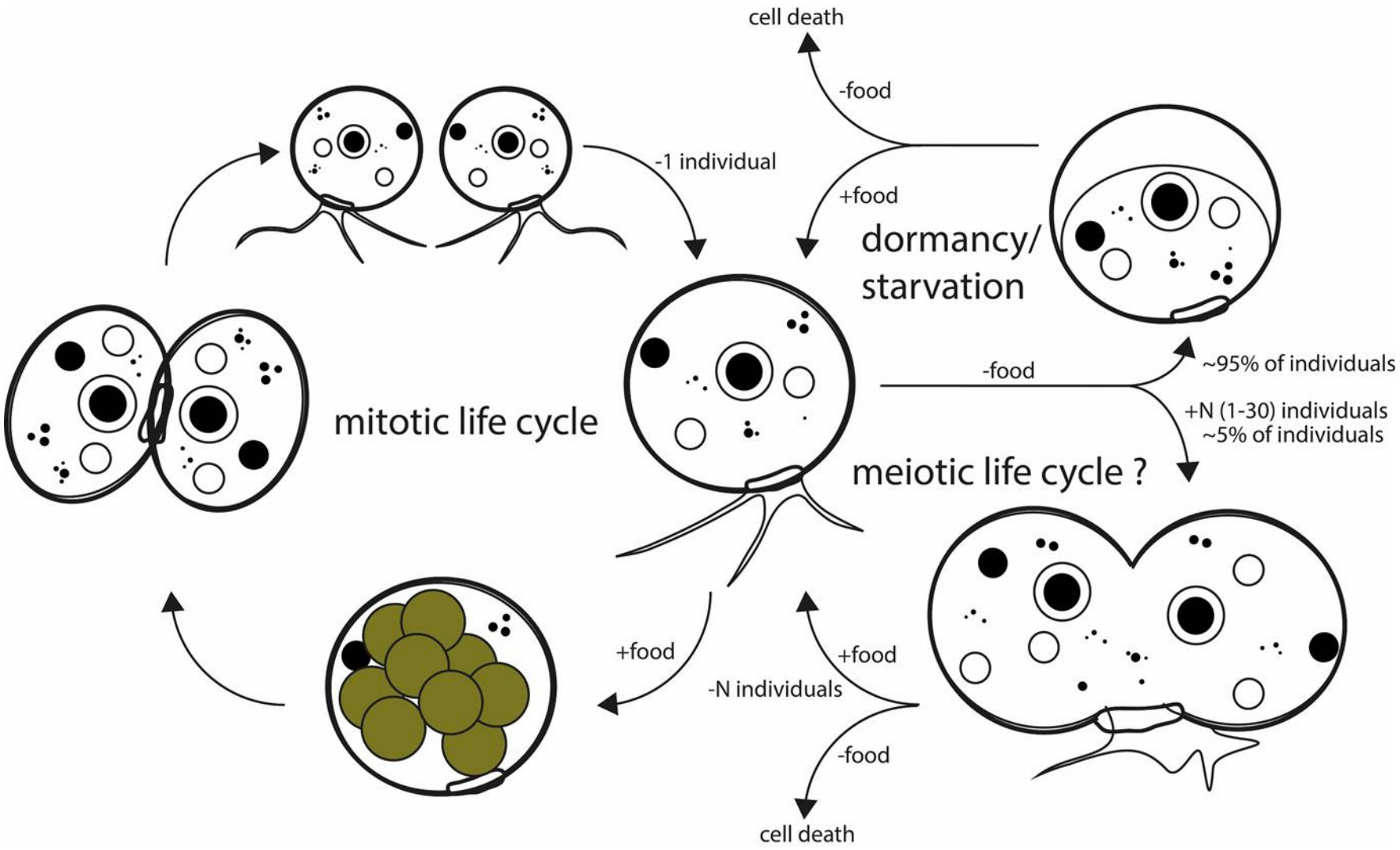
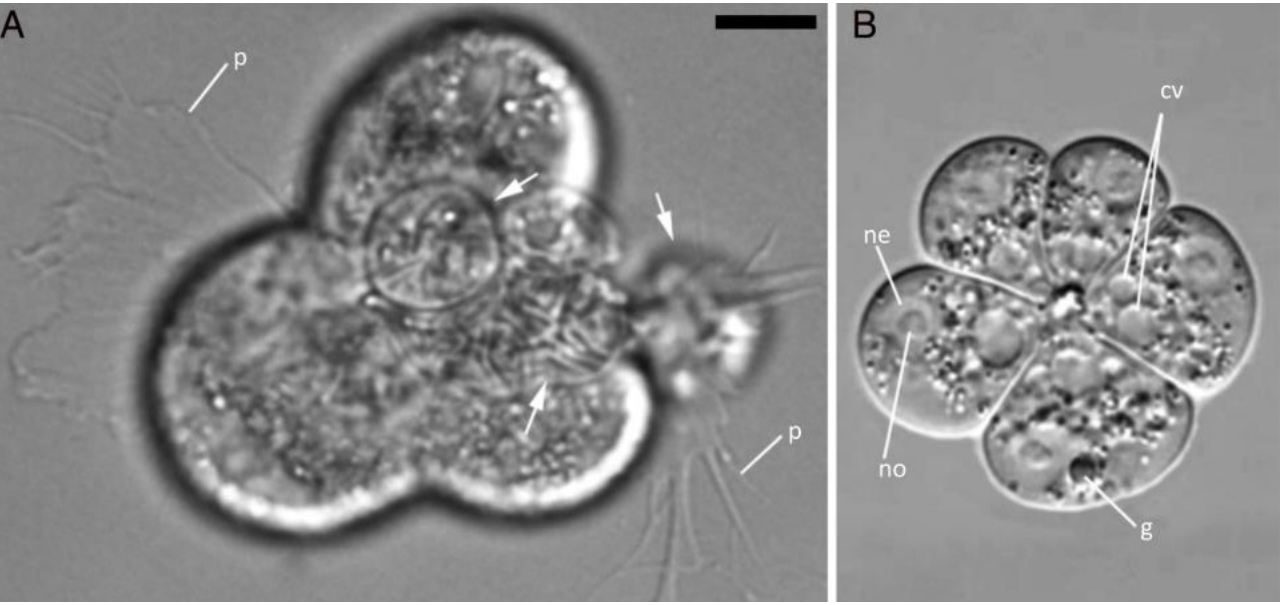
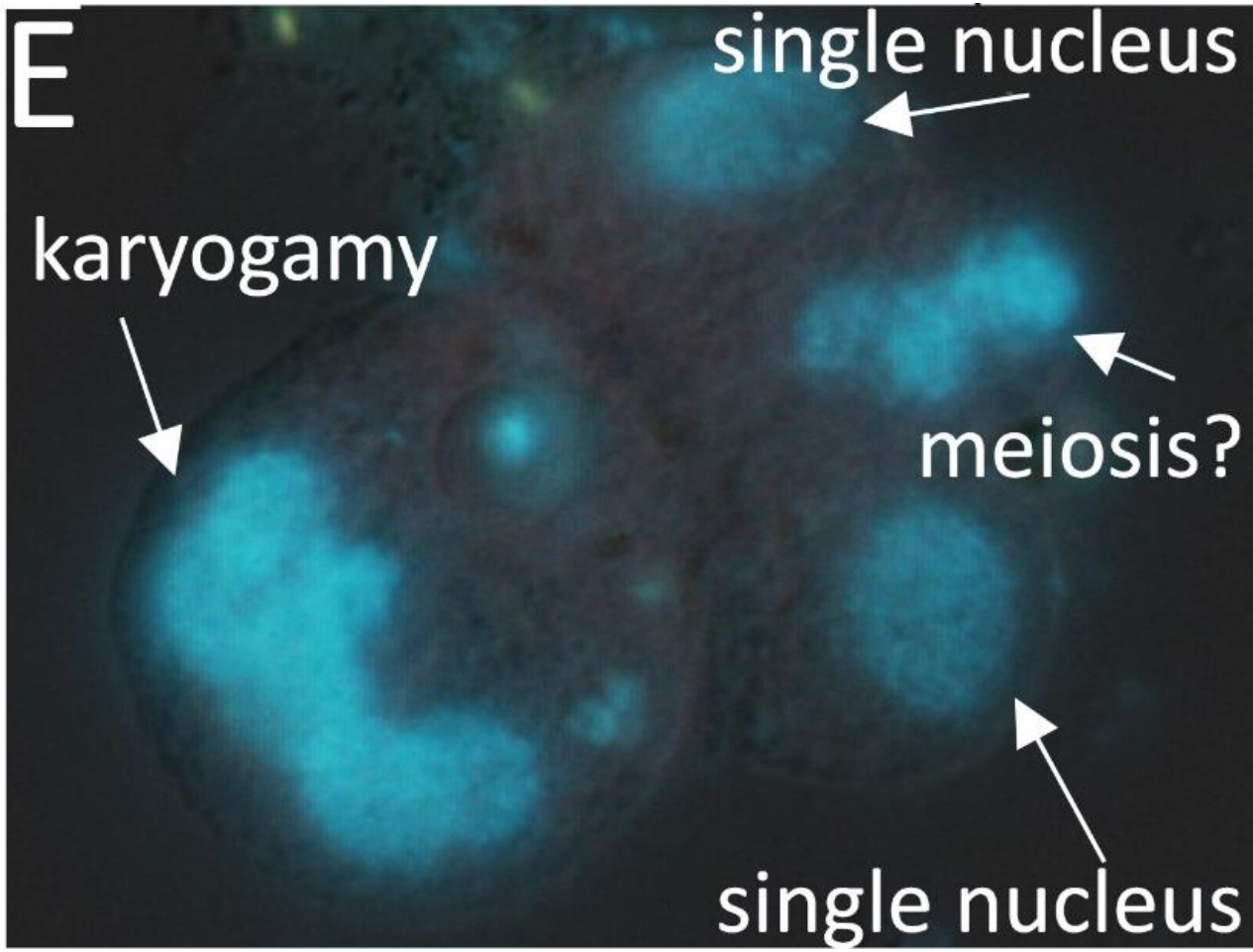
Life cycle of *Fisculla terrestris*



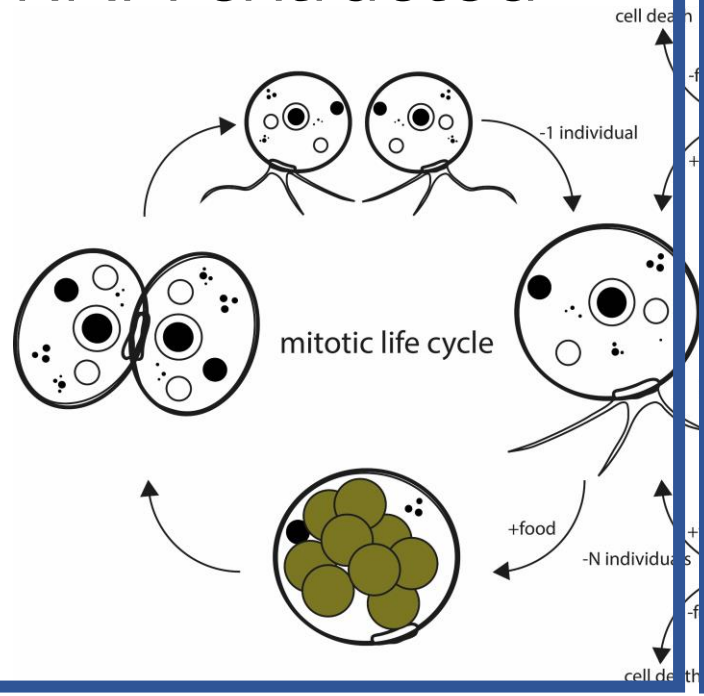
Nuclei fuse during cell aggregation



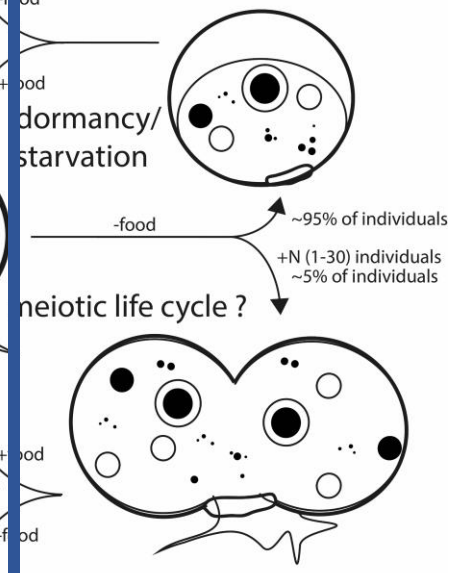


Differential expression experiment

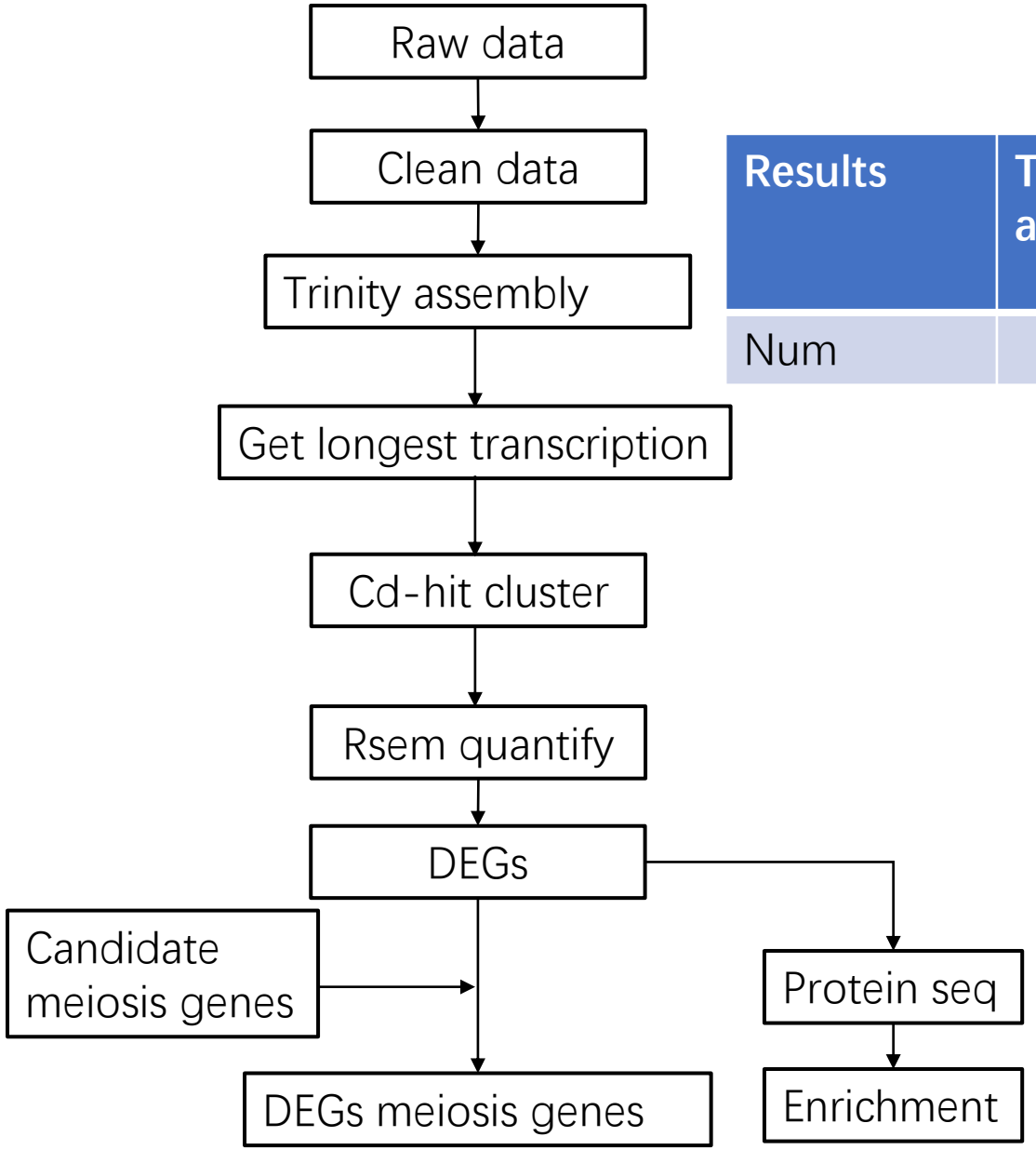
Treatment 1:
high mitotic growth
low putative meiosis
food present (*S. cerevisiae*)
five replicates – RNA extracted



Treatment 2:
Low mitotic growth
high putative meiosis
food absent/lowly abundant
five replicates – RNA extracted



Pipeline

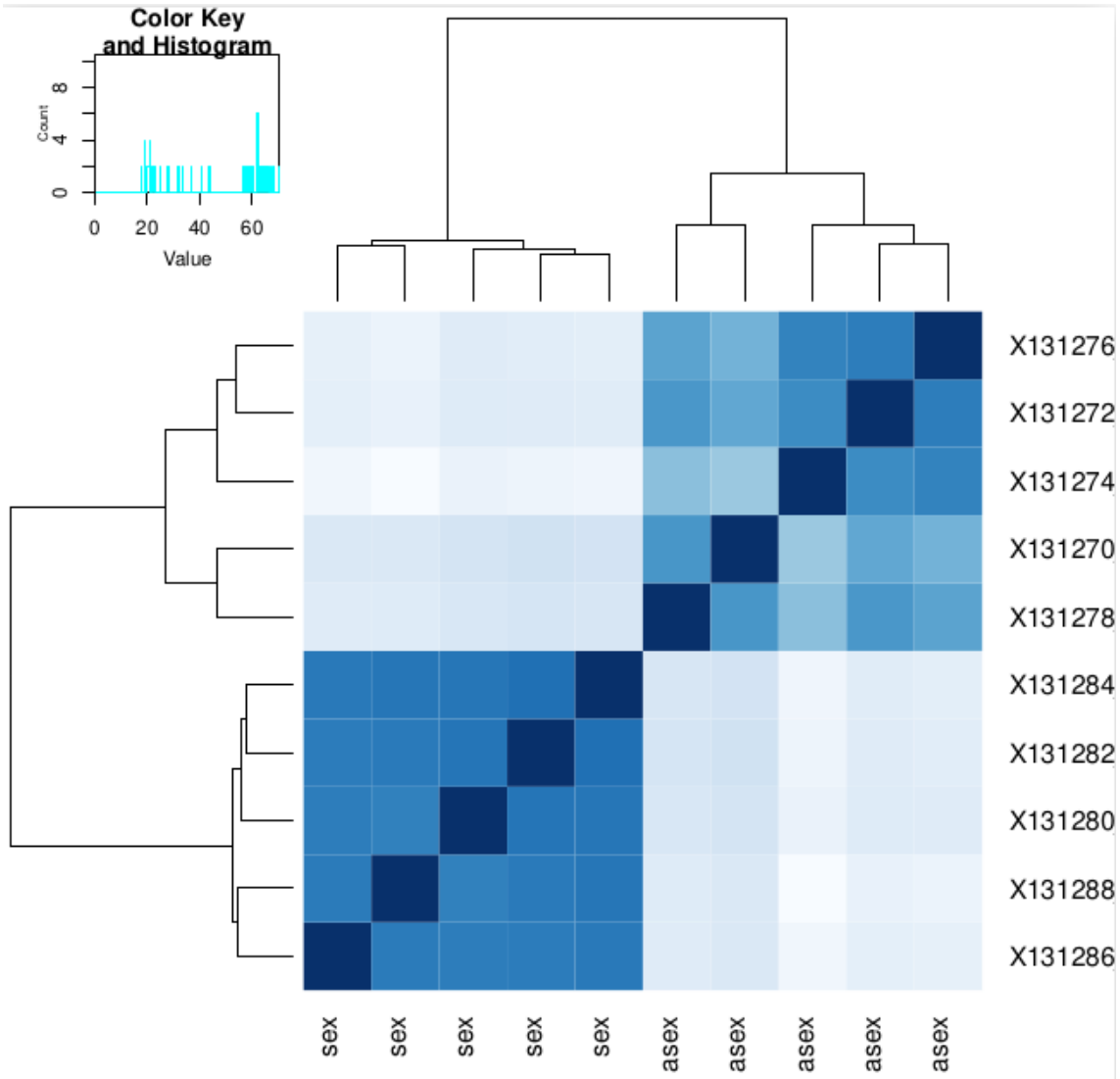


Results	Trinity assembly	Unigenes	Cd-hit transcriptions	Transdecoder to Protein	Protein cd-hit
Num	43531	40050	36525	26868	26580

Adjust-P value

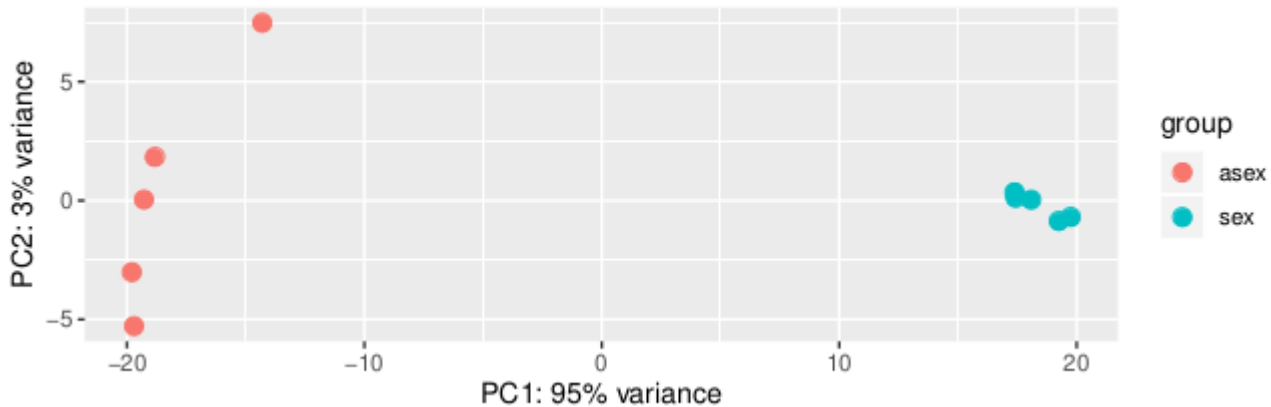
DEGs	Protein
16474	15327

sample_distances_plot

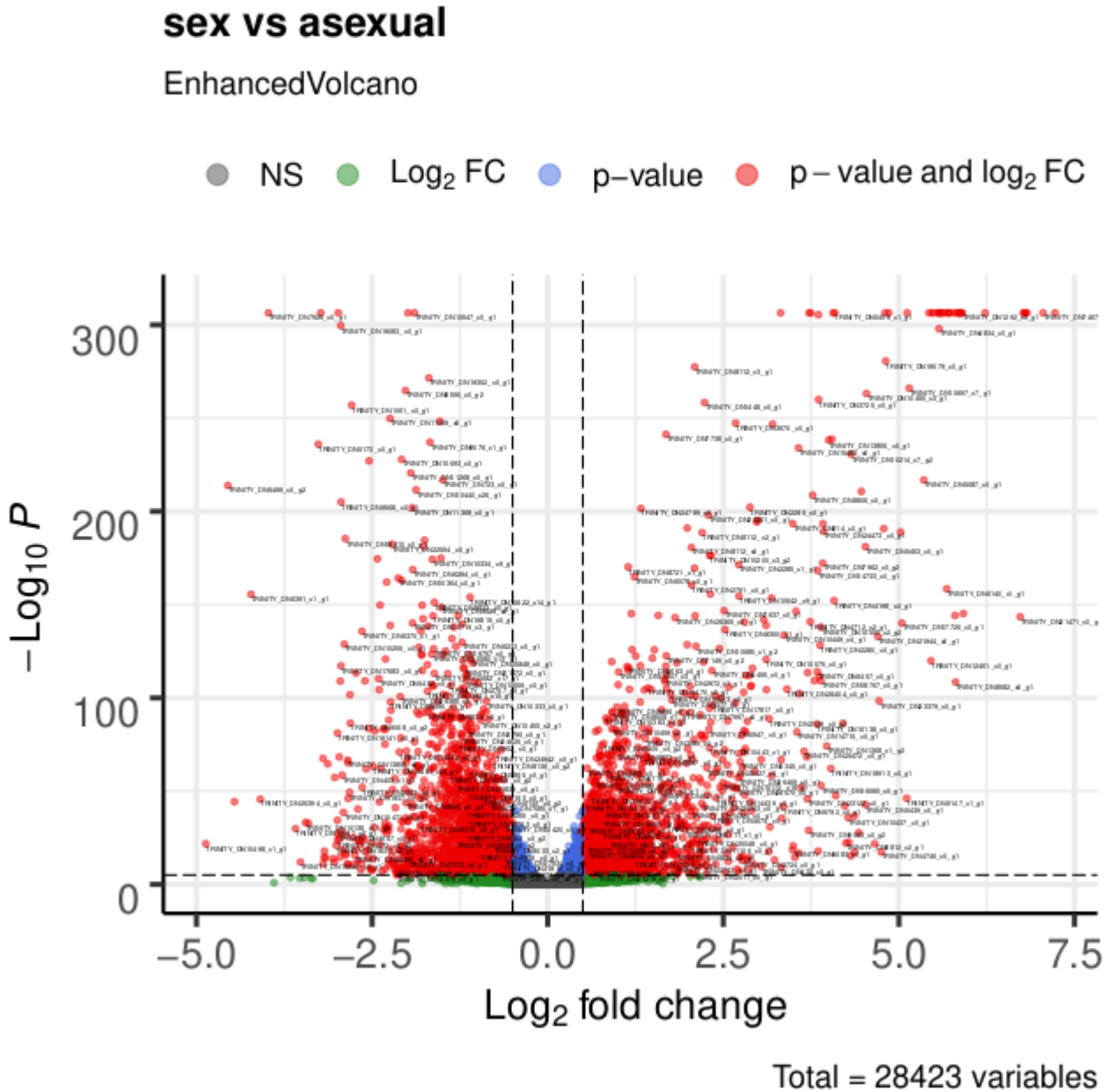


CCG Sample ID	Sample Name
131270	Fisculla_asex_1
131272	Fisculla_asex_2
131274	Fisculla_asex_3
131276	Fisculla_asex_4
131278	Fisculla_asex_5
131280	Fisculla_sex_6
131282	Fisculla_sex_7
131284	Fisculla_sex_8
131286	Fisculla_sex_9
131288	Fisculla_sex_10

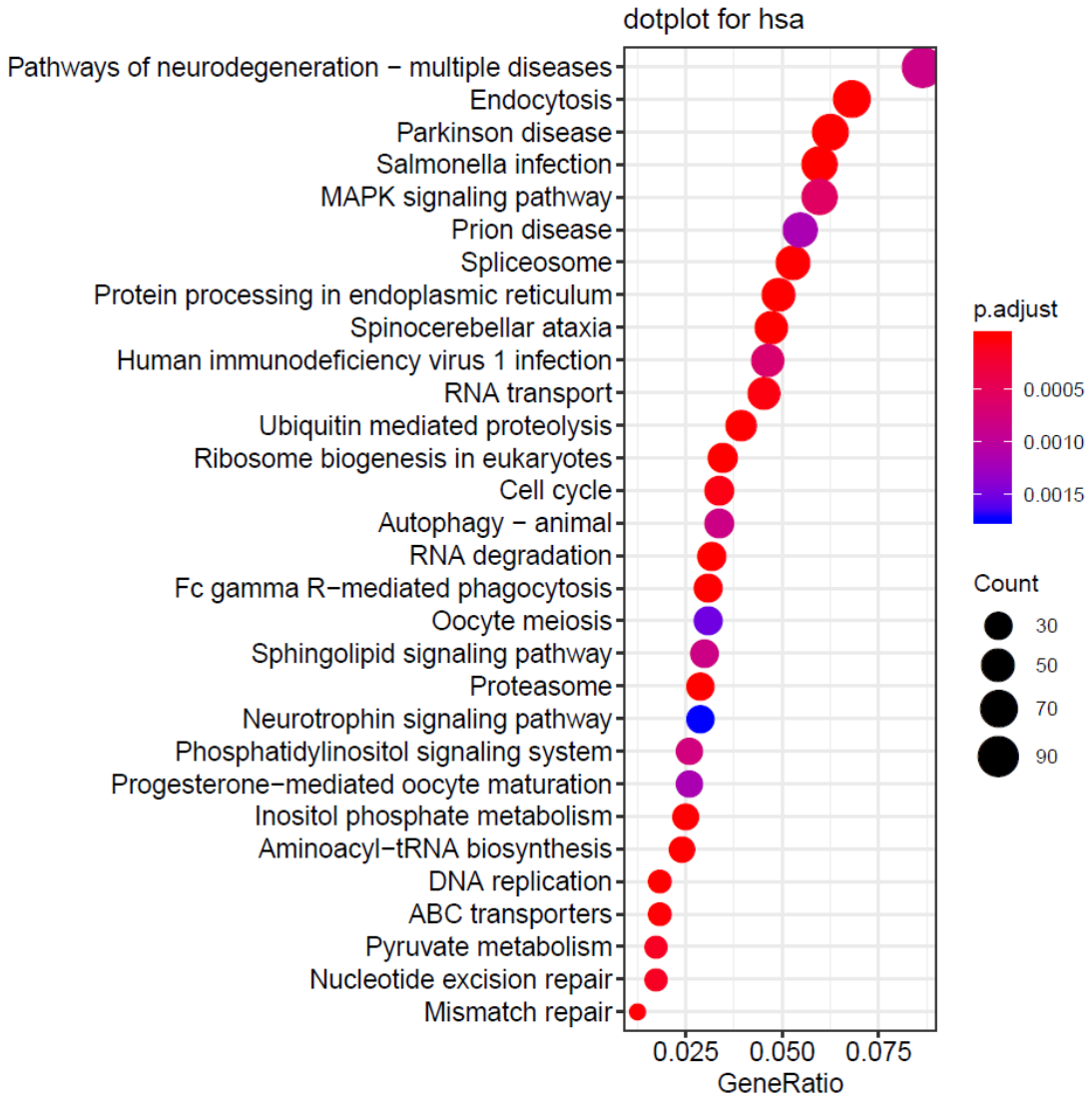
PCA_plot

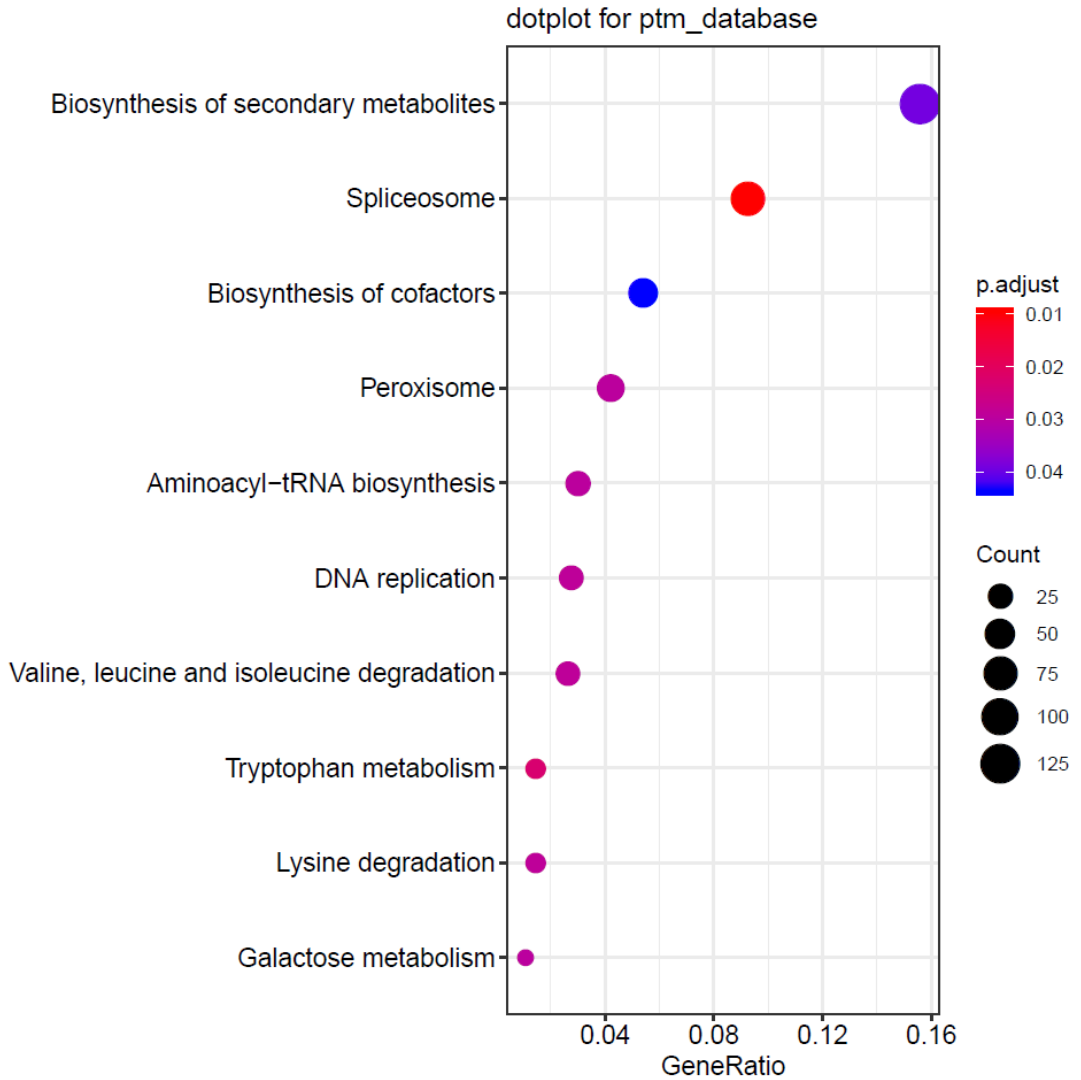


Volcano plot of all expressing genes



Enrichment of DEGS



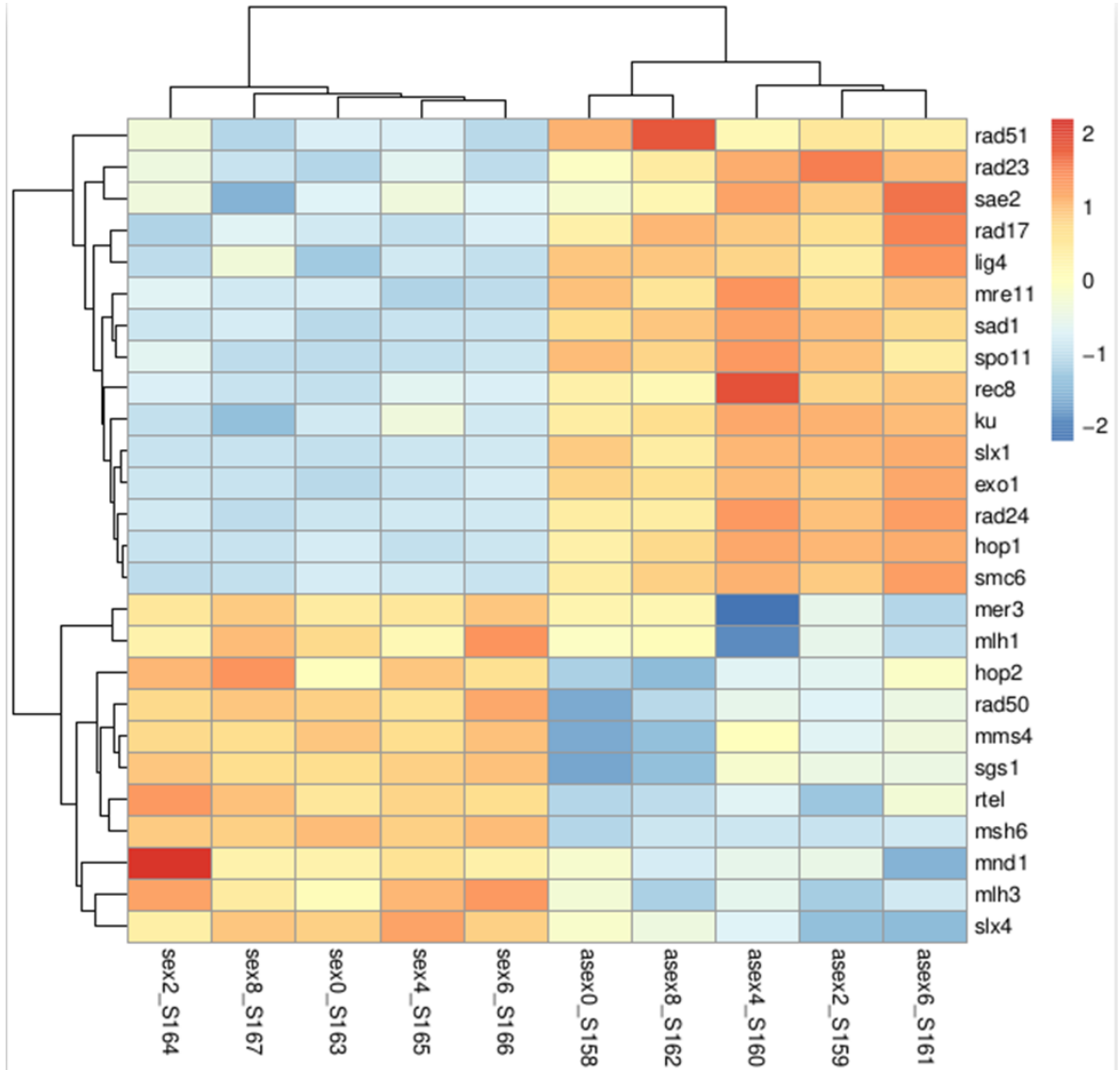


Candidate meiosis genes

Blast result show

found 36 of 39 genes, and 25 Different expressing

25 DEGs, 14 downregulate in sex group and 11 up



Next step:

1. eggnog-mapper annotation
2. Write method

Thank you!