

Thesis SNV Filtering

Max Barclay

2023-01-30

```
#Reads the SNP csv files for each strains snippy
#Filters these to omit NAs and hypothetical proteins
Y1_1 <- read.csv(file="R_data/Y1.1.csv", header=TRUE) %>% filter(FTYPE != "" & PRODUCT != "hypothetical")
Y1_2 <- read.csv(file="R_data/Y1.2.csv", header=TRUE) %>% filter(FTYPE != "" & PRODUCT != "hypothetical")
Y1_3 <- read.csv(file="R_data/Y1.3.csv", header=TRUE) %>% filter(FTYPE != "" & PRODUCT != "hypothetical")

#Puts strain csv's into data frames
Y1_1Df <- data.frame(Y1_1)
Y1_2Df <- data.frame(Y1_2)
Y1_3Df <- data.frame(Y1_3)

#Filters the data frames into appropriate tables
Y1_1Df_filter <- subset(Y1_1Df, select = c("LOCUS_TAG", "PRODUCT"))
Y1_2Df_filter <- subset(Y1_2Df, select = c("LOCUS_TAG", "PRODUCT"))
Y1_3Df_filter <- subset(Y1_3Df, select = c("LOCUS_TAG", "PRODUCT"))
```

Anything hypothetical or unidentified by resequencing was filtered out here, while strains .csv files were put into data frames to allow for them to be converted to tables that only used the columns for locus tag and product to ensure no repeats and clarity for what the loci were linked to.

```
#Merged table for appendix
merged_tables <- rbind.fill(Y1_1Df_filter, Y1_2Df_filter, Y1_3Df_filter)
print(merged_tables)
```

##	LOCUS_TAG	PRODUCT
## 1	SC02962	bifunctional transferase/deacetylase
## 2	SC04127	ATP/GTP-binding protein
## 3	SC04594	2-oxoglutarate ferredoxin oxidoreductase subunit beta
## 4	SC04594	2-oxoglutarate ferredoxin oxidoreductase subunit beta
## 5	SC04595	oxidoreductase
## 6	SC04654	DNA-directed RNA polymerase subunit beta
## 7	SC04659	30S ribosomal protein S12
## 8	SC04659	30S ribosomal protein S12
## 9	SC05065	transcriptional regulator
## 10	SC06167	proline rich protein membrane protein
## 11	SC07350	membrane efflux protein
## 12	SC02962	bifunctional transferase/deacetylase
## 13	SC04127	ATP/GTP-binding protein
## 14	SC04594	2-oxoglutarate ferredoxin oxidoreductase subunit beta
## 15	SC04594	2-oxoglutarate ferredoxin oxidoreductase subunit beta
## 16	SC04595	oxidoreductase
## 17	SC04654	DNA-directed RNA polymerase subunit beta
## 18	SC04659	30S ribosomal protein S12
## 19	SC04659	30S ribosomal protein S12

```

## 20 SC05065 transcriptional regulator
## 21 SC06167 proline rich protein membrane protein
## 22 SC07015 glycosyl hydrolase
## 23 SC07350 membrane efflux protein
## 24 SC02962 bifunctional transferase/deacetylase
## 25 SC04127 ATP/GTP-binding protein
## 26 SC04594 2-oxoglutarate ferredoxin oxidoreductase subunit beta
## 27 SC04594 2-oxoglutarate ferredoxin oxidoreductase subunit beta
## 28 SC04595 oxidoreductase
## 29 SC04654 DNA-directed RNA polymerase subunit beta
## 30 SC04659 30S ribosomal protein S12
## 31 SC04659 30S ribosomal protein S12
## 32 SC05065 transcriptional regulator
## 33 SC05090 actinorhodin polyketide synthase bifunctional cyclase/dehydratase
## 34 SC06167 proline rich protein membrane protein
## 35 SC07350 membrane efflux protein

```

```

#Gives excel output of filtered tables in environment for external use
write.xlsx(Y1_1Df_filter, "Y1.1_Table.xlsx", colNames = TRUE, rowNames = TRUE)
write.xlsx(Y1_2Df_filter, "Y1.2_Table.xlsx", colNames = TRUE, rowNames = TRUE)
write.xlsx(Y1_3Df_filter, "Y1.3_Table.xlsx", colNames = TRUE, rowNames = TRUE)

```

rbind was used to give a full non-segregated table for all three strains. The individual filtered tables from before were exported to excel to allow for any modifications and use as figures in presentation etc.