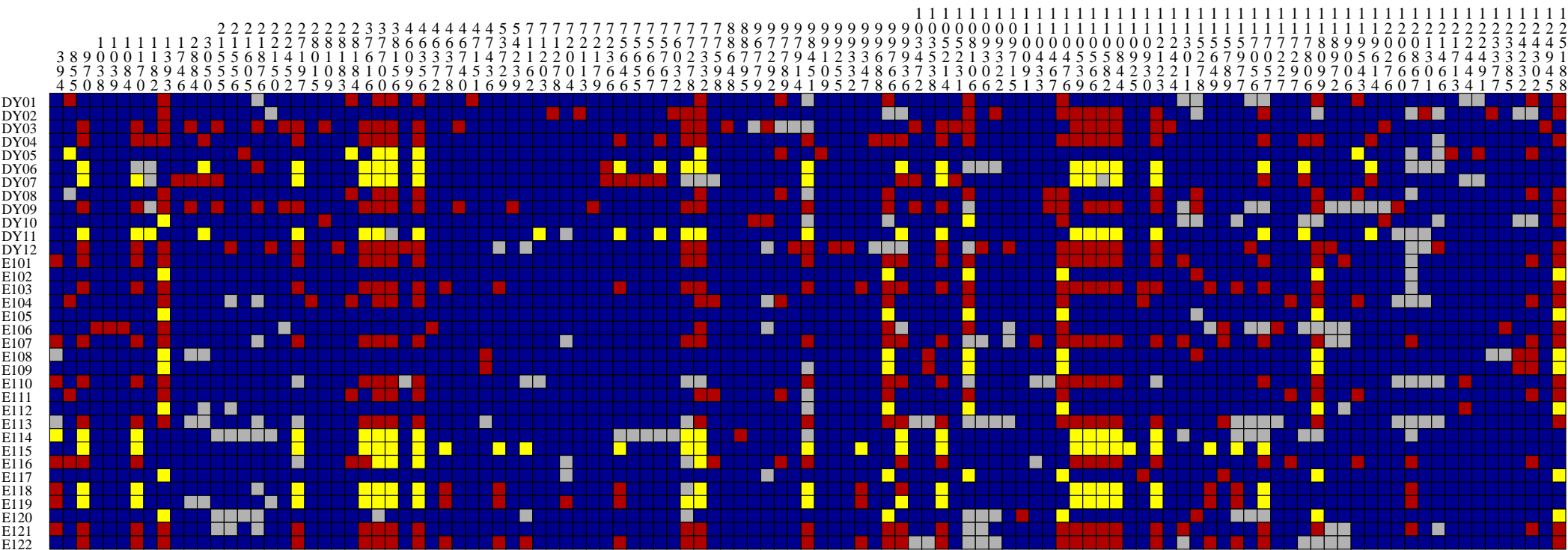


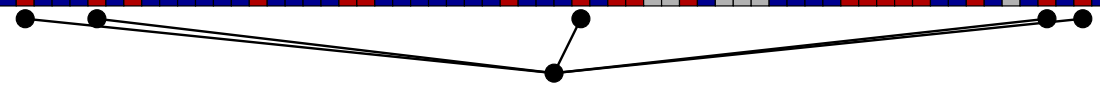




abl2, p-value: 0.045



- Homozygote-Common allele
- Heterozygote
- Homozygote-Rare allele
- Missing data



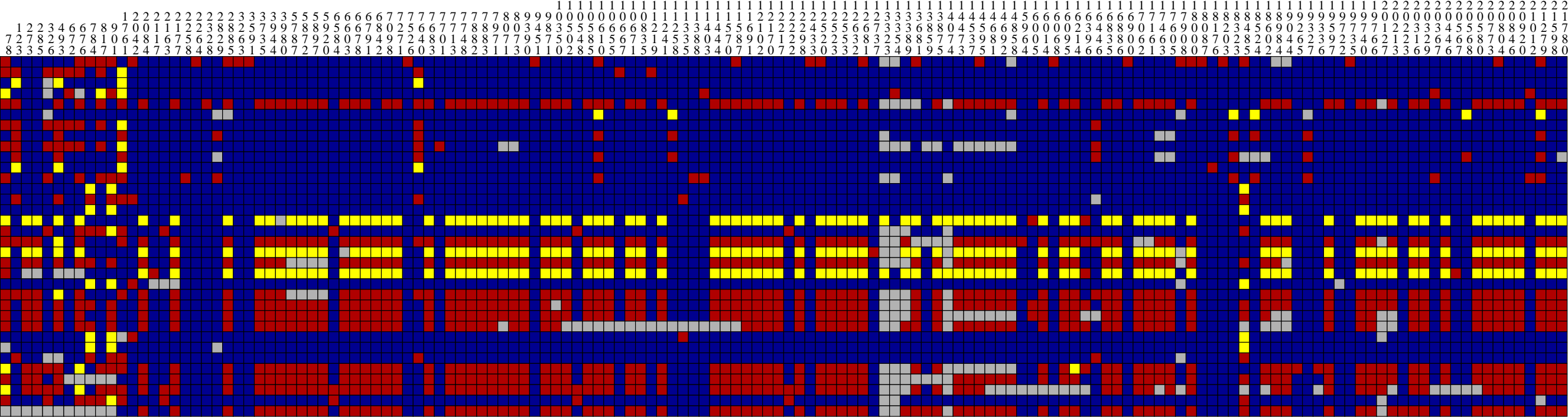








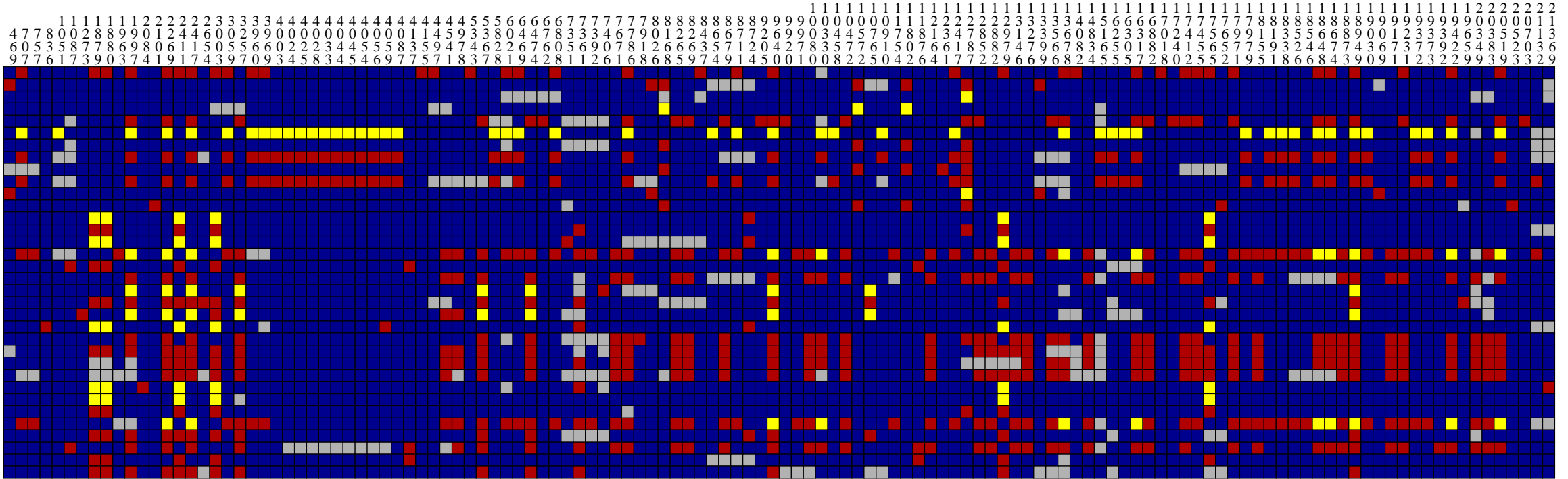
adh4, p-value: 0.3554



- Homozygote-Common allele
- Heterozygote
- Homozygote-Rare allele
- Missing data



adh5, p-value: 0.0404

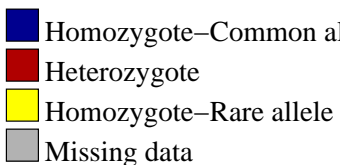
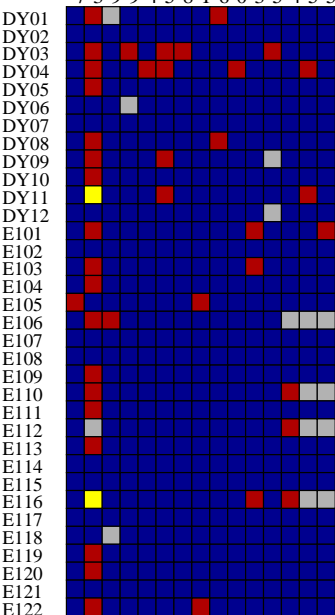


- Homozygote-Common allele
- Heterozygote
- Homozygote-Rare allele
- Missing data

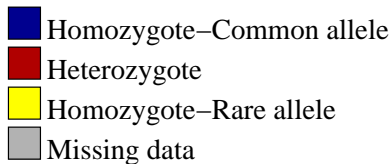
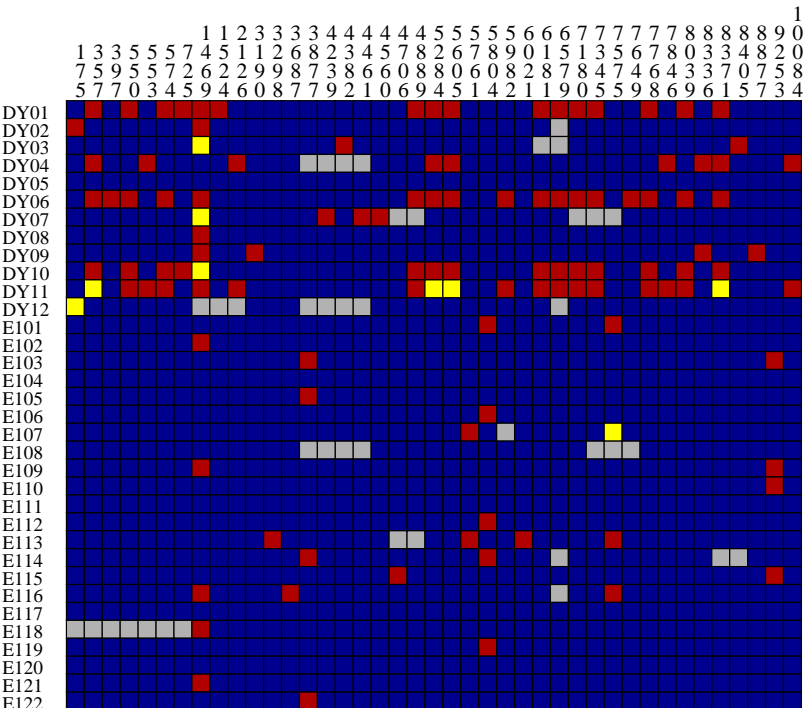


adm, p-value: 0.4336

1 2 2 2 3 4 4 4 4 5 5 5 5  
6 6 8 1 3 8 0 0 2 5 0 3 7 7  
0 3 2 4 1 5 2 5 7 4 5 4 5 6 8  
7 3 9 9 4 5 8 1 6 0 3 5 4 5 5

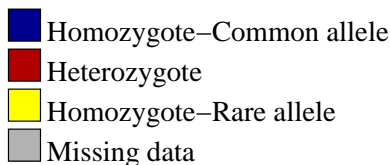
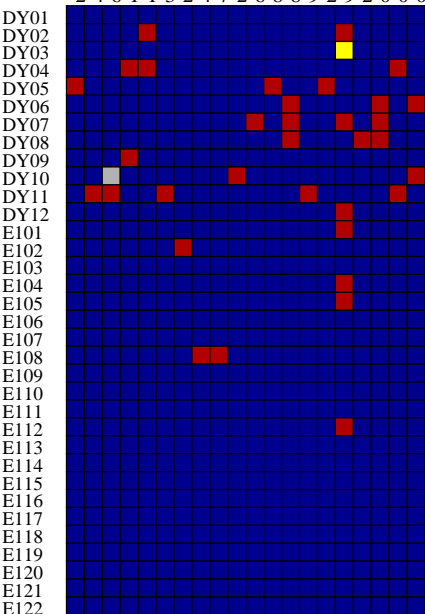


angptl7, p-value: 0.5992

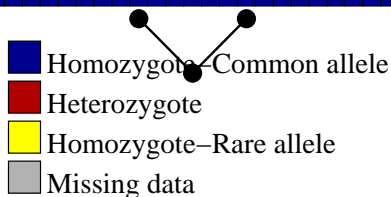
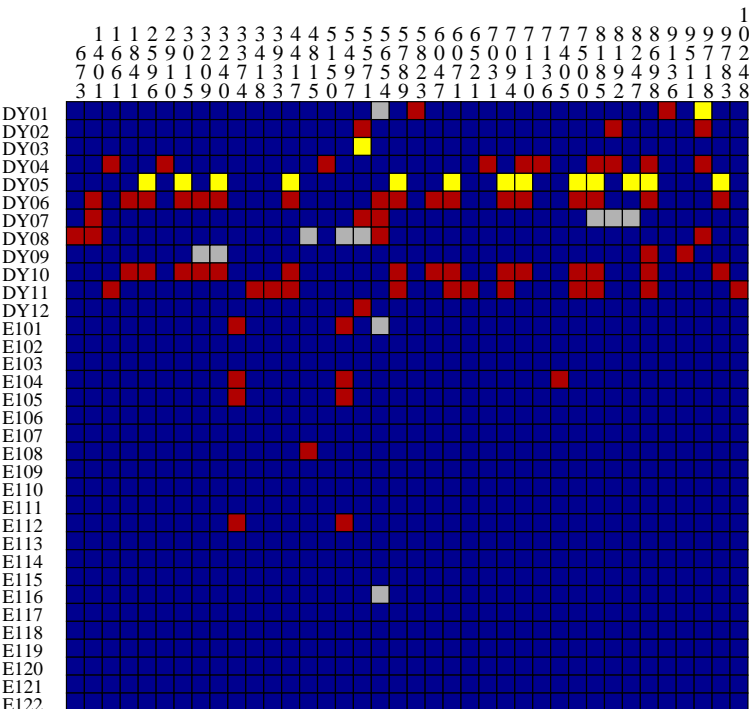


aoc2, p-value: 0.4684

1 1 1 1 2 2 2 3 3 3 4 4 4 4 7 8 8 8  
6 9 3 4 5 9 0 0 8 8 8 9 1 3 4 6 2 0 2 4  
3 9 2 3 7 6 0 5 0 1 4 0 3 6 5 4 8 1 7 5  
2 4 6 1 1 3 2 4 7 2 6 8 8 9 2 9 2 0 0 0



aoc3, p-value: 0.2806



























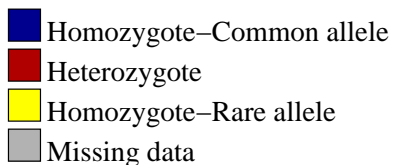
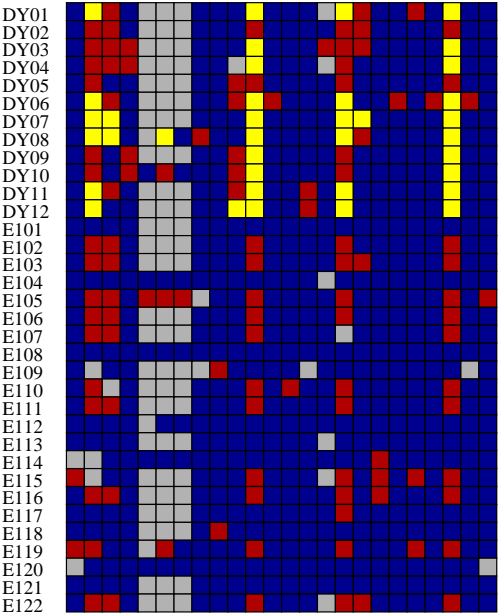






ces2, p-value: 0.4752

|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|   |   |   |   |   |   |   |   |   |   |   | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |   |   |   |   |
|   | 2 | 3 | 4 | 4 | 4 | 5 | 5 | 6 | 7 | 7 | 7 | 8 | 9 | 0 | 0 | 1 | 1 | 1 | 2 | 2 | 3 | 3 |   |
| 4 | 7 | 8 | 2 | 2 | 6 | 9 | 0 | 4 | 2 | 0 | 0 | 5 | 4 | 5 | 7 | 7 | 0 | 5 | 6 | 4 | 9 | 1 | 8 |
| 5 | 3 | 3 | 4 | 1 | 2 | 1 | 5 | 3 | 0 | 3 | 6 | 2 | 8 | 5 | 4 | 6 | 8 | 4 | 5 | 3 | 7 | 5 | 7 |
| 3 | 8 | 0 | 6 | 5 | 9 | 1 | 5 | 4 | 0 | 5 | 0 | 9 | 5 | 9 | 8 | 9 | 8 | 9 | 1 | 5 | 7 | 9 | 3 |











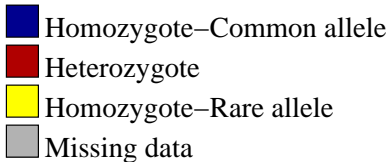
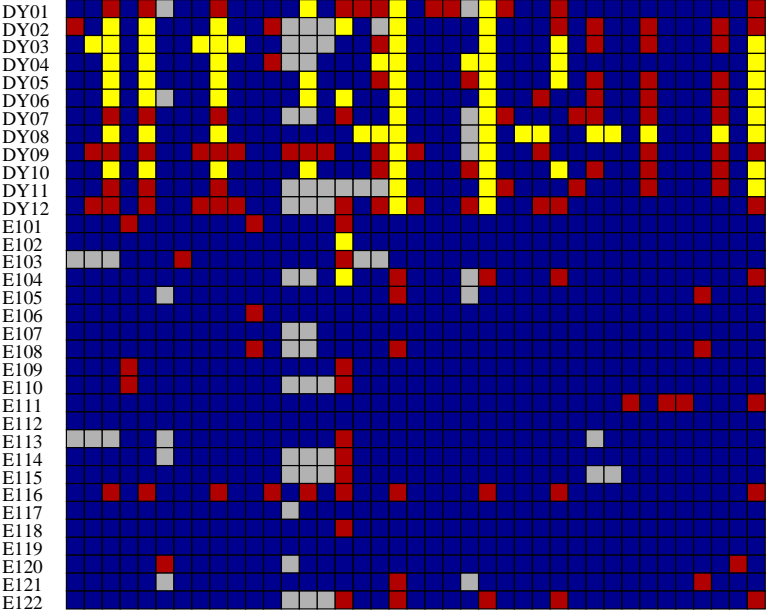






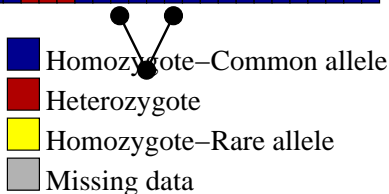
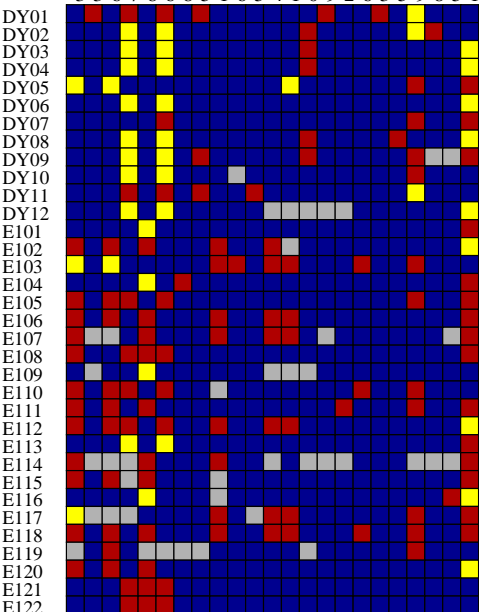
cyp3a4, p-value: 0.5744

1 1 1 1 1 1 1 1 1 1 1 2  
1 1 2 3 5 6 6 5 7 7 7 7 8 8 8 8 9 9 9 0 2 2 3 4 4 4 5 6 7 7 7 8 8 9 9 9  
7 7 7 2 6 2 7 1 7 8 0 0 6 7 8 0 1 2 6 0 2 3 5 2 8 0 4 5 5 1 7 2 4 5 6 9 4 4 6  
5 6 8 8 3 6 1 5 8 2 3 2 6 9 4 1 7 8 5 6 2 2 8 6 6 1 9 8 9 1 8 9 1 4 6 2 3 8 2  
0 1 6 0 5 8 0 5 5 5 4 4 5 0 1 4 9 2 0 1 3 9 2 7 3 2 0 2 8 9 5 7 0 6 1 6 5 2 0



dclre1b, p-value: 0.1512

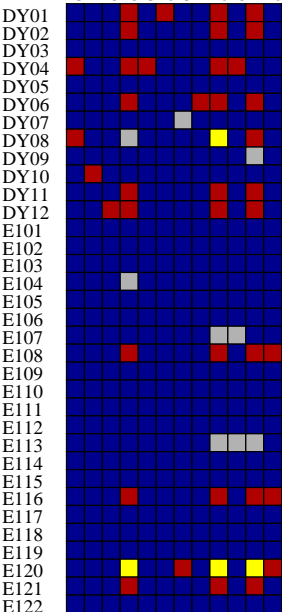
1 1 1  
 1 1 1 1 1 2 2 3 3 3 4 4 4 4 9 9 9 0 0 1  
 2 9 9 5 7 8 9 9 3 5 1 6 7 1 3 4 9 0 7 8 2 5 7  
 9 0 8 1 2 6 4 5 4 4 9 1 8 3 6 3 1 2 3 5 6 9 2  
 3 3 6 7 8 6 8 5 1 6 5 4 1 0 9 2 6 3 5 9 8 5 1





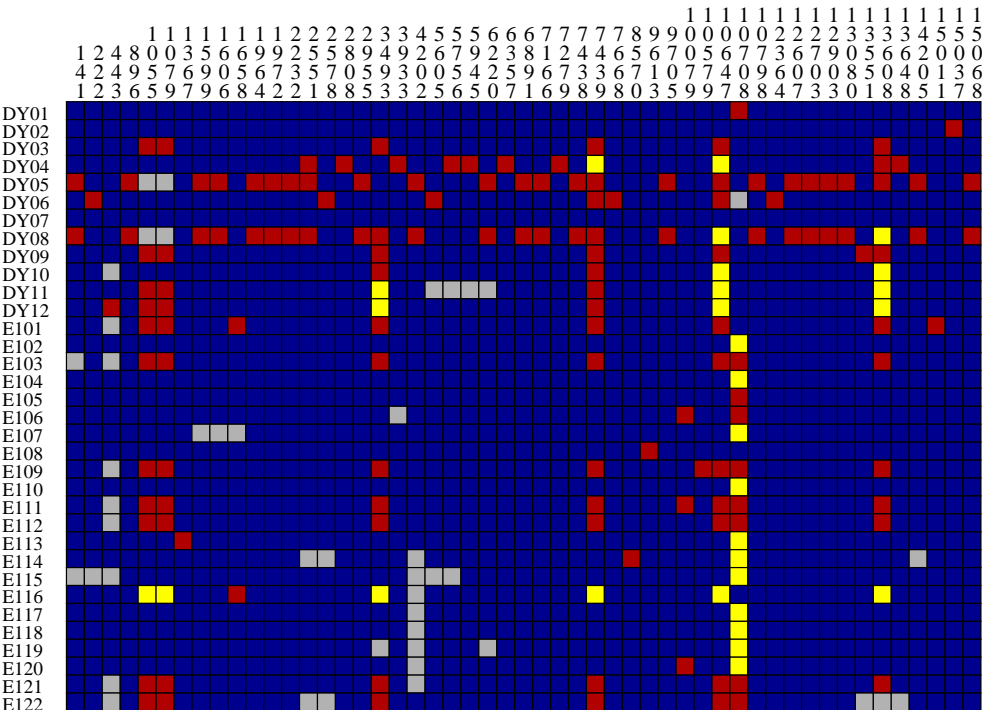
ddit3, p-value: 0.4





|   |   |   |   |   |   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|---|---|---|---|---|
|   | 1 | 1 | 2 | 3 | 3 | 3 | 3 | 4 | 4 | 4 | 6 |
| 1 | 2 | 2 | 9 | 4 | 7 | 7 | 8 | 0 | 2 | 3 | 0 |
| 7 | 0 | 4 | 5 | 7 | 7 | 9 | 1 | 4 | 6 | 5 | 0 |
| 3 | 4 | 5 | 8 | 3 | 6 | 3 | 4 | 6 | 8 | 4 | 0 |



■ Homozygote-Common  
■ Heterozygote  
■ Homozygote-Rare allele  
■ Missing data

dut, p-value: 0.6572

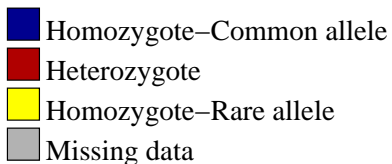
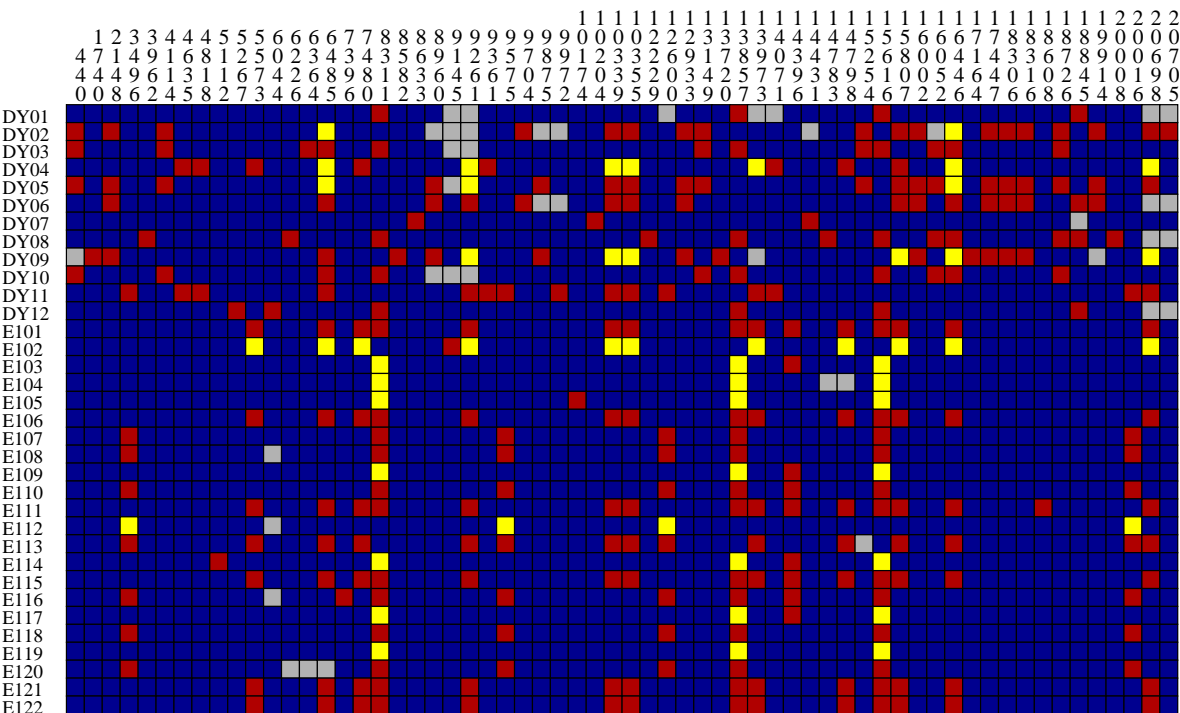


-  Homozygote-Common allele
-  Heterozygote
-  Homozygote-Rare allele
-  Missing data

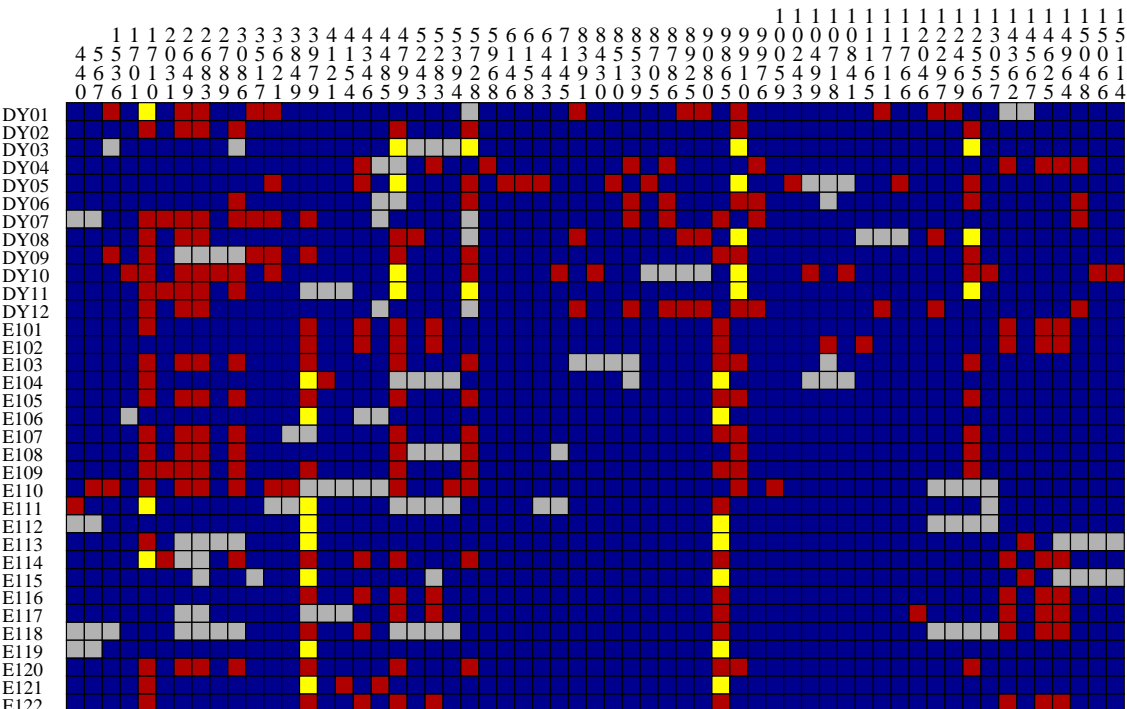




eno1, p-value: 0.7168



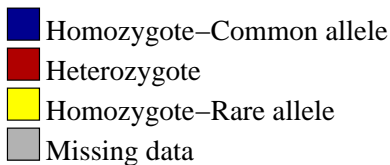
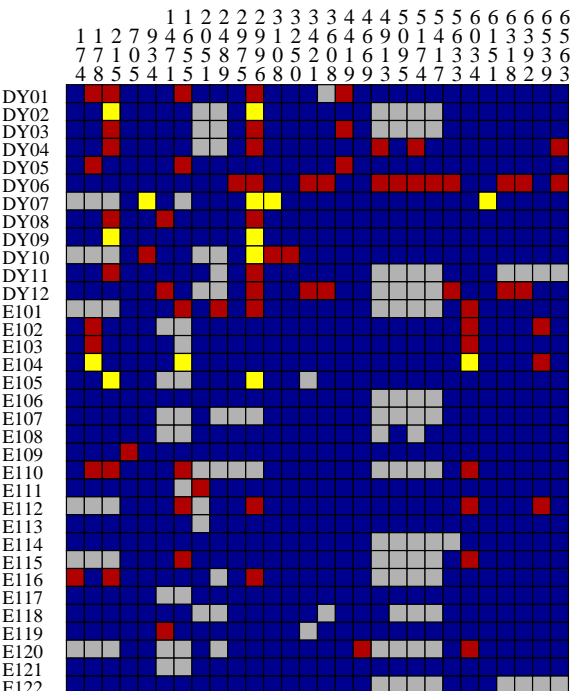
epx, p-value: 0.6962



- Homozygote–Common allele
- Heterozygote
- Homozygote–Rare allele
- Missing data



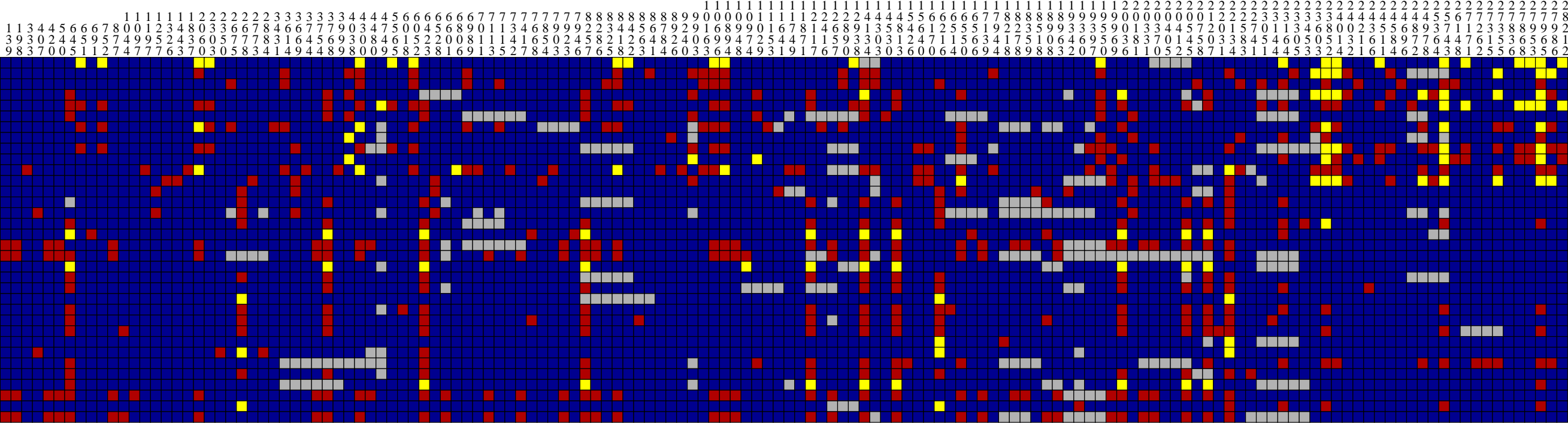
fancf, p-value: 0.4934







fgf5, p-value: 0.0332



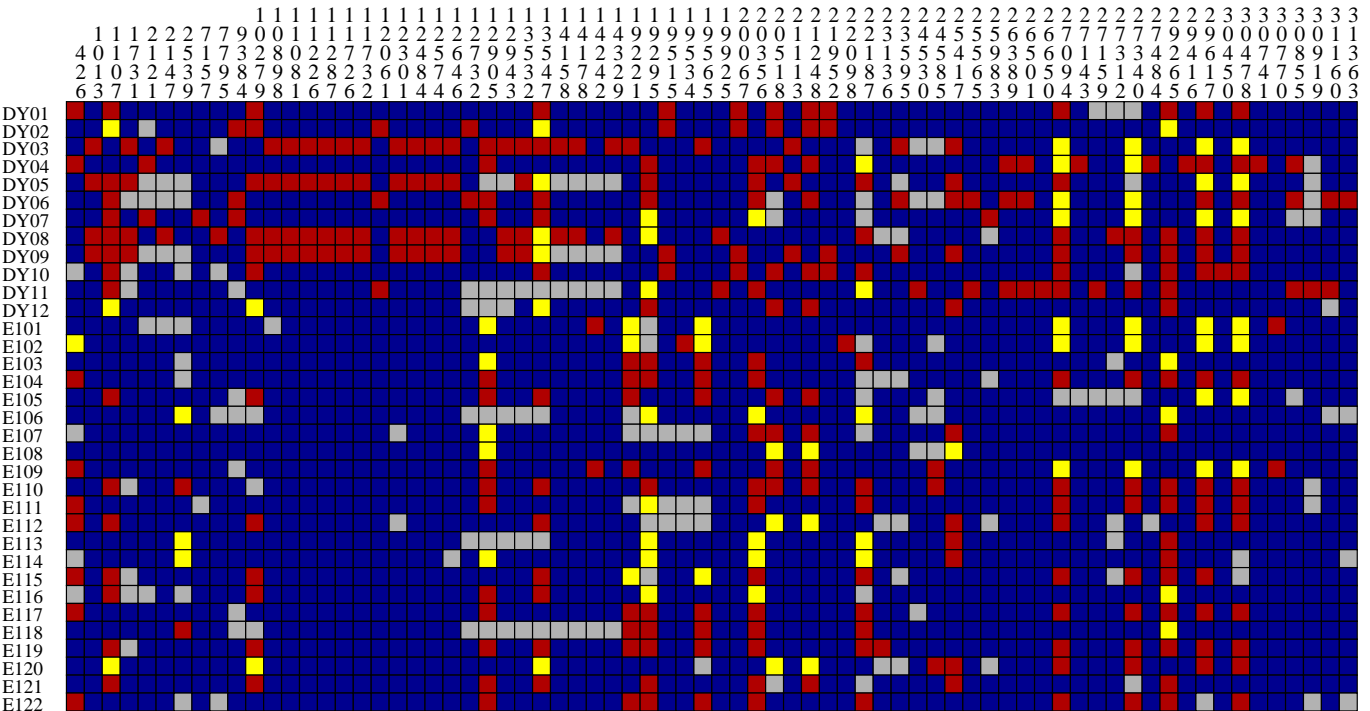
- Homozygote-Common allele
- Heterozygote
- Homozygote-Rare allele
- Missing data



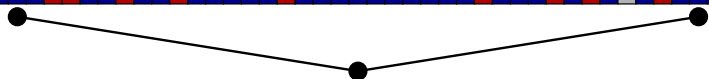




fmo4, p-value: 0.3032

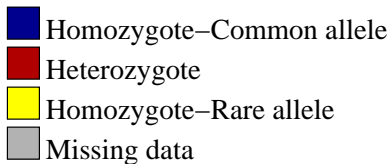
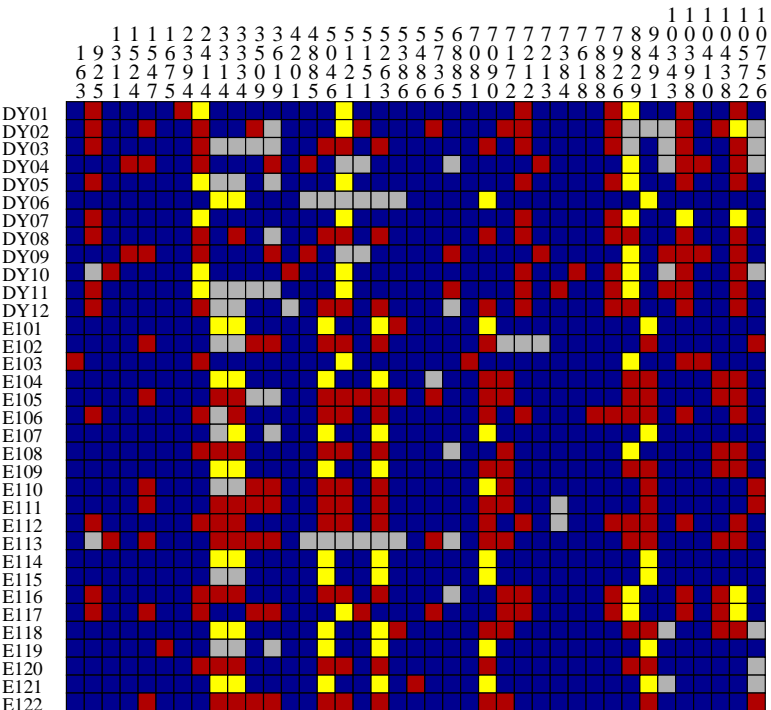


- Homozygote–Common allele
- Heterozygote
- Homozygote–Rare allele
- Missing data





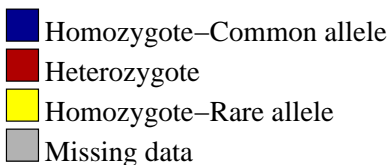
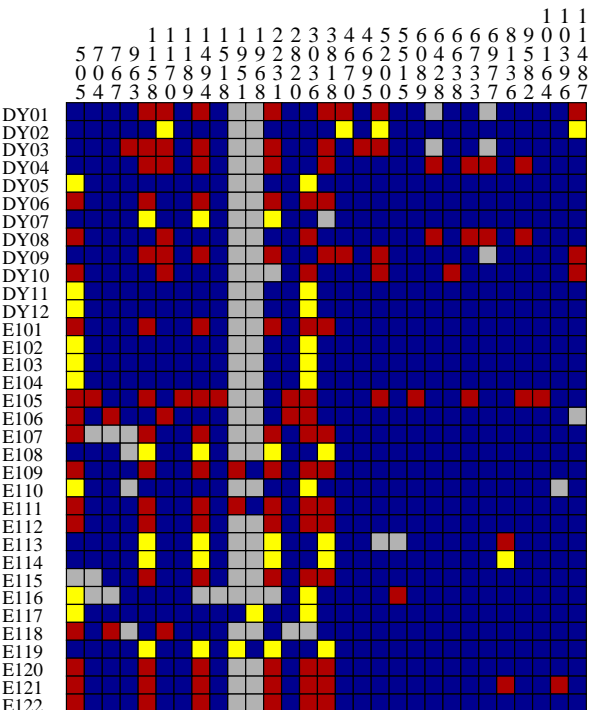
fosb, p-value: 0.5878







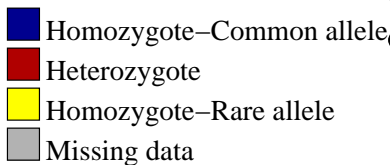
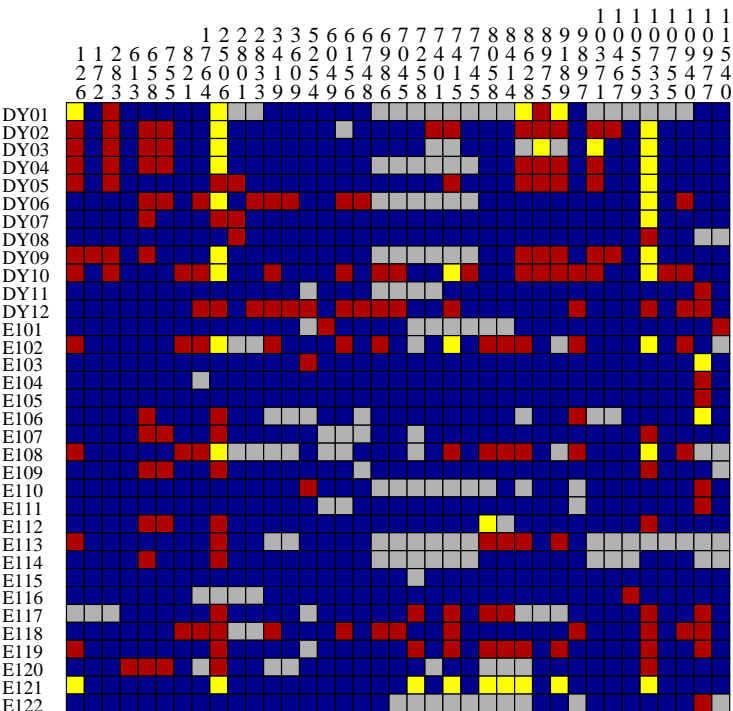
glrx2, p-value: 0.5046





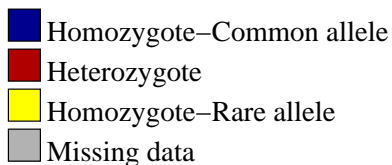
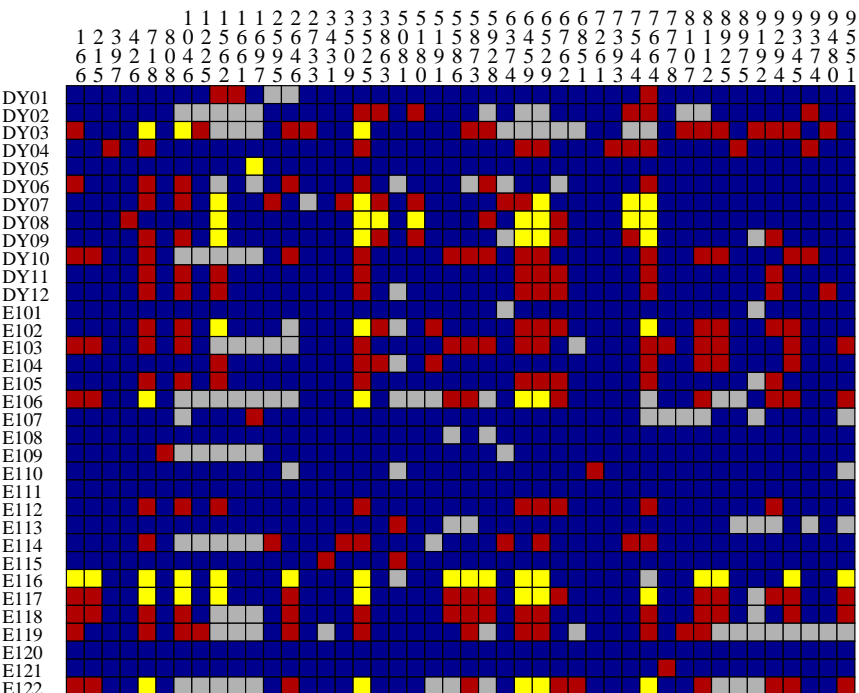


gpx5, p-value: 0.2898

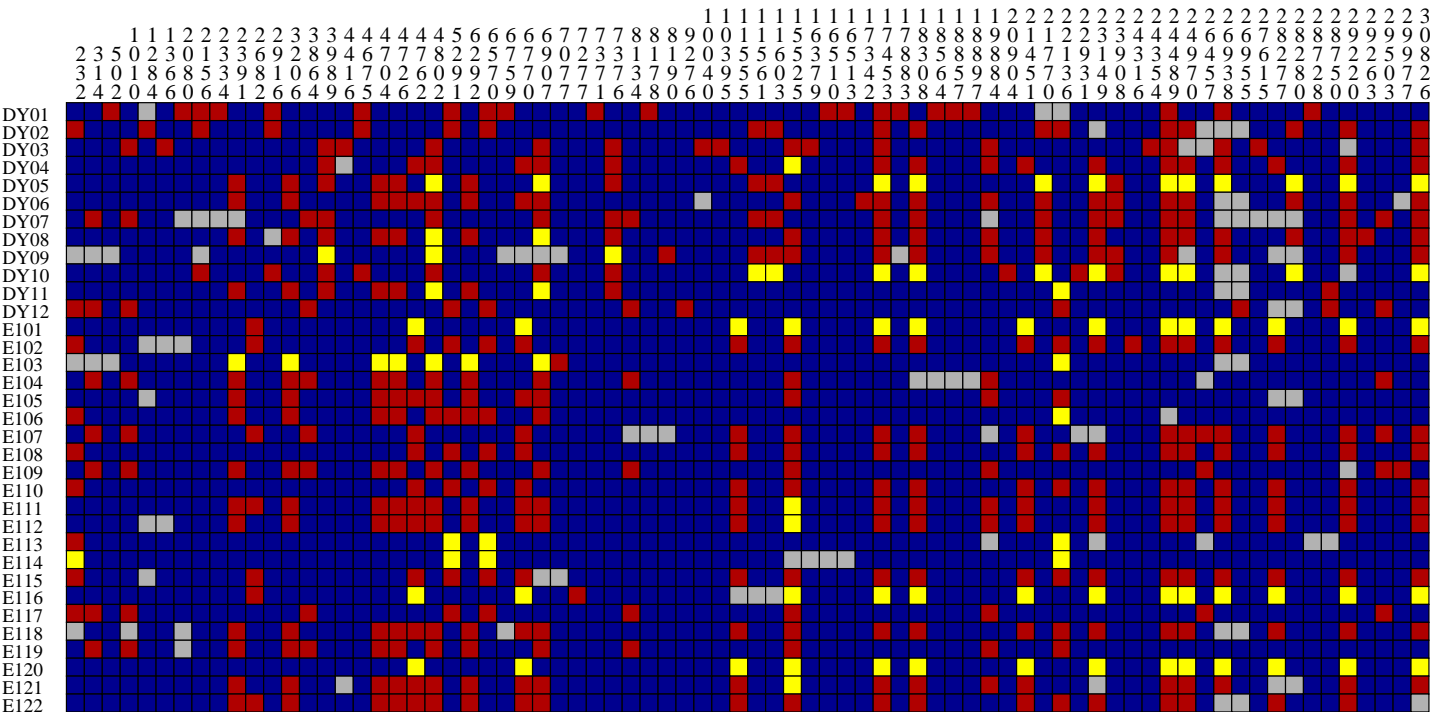




gpx7, p-value: 0.6112



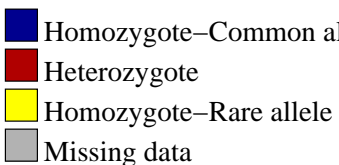
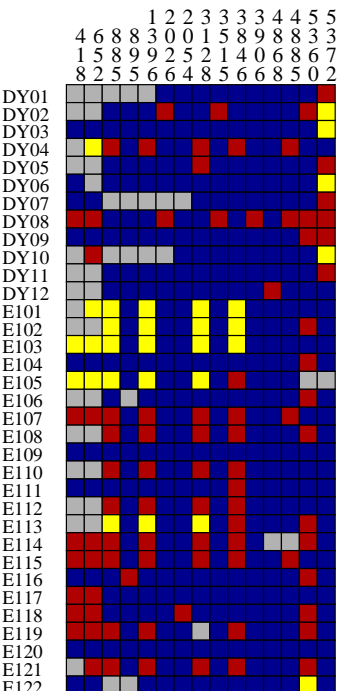
gss, p-value: 0.7926



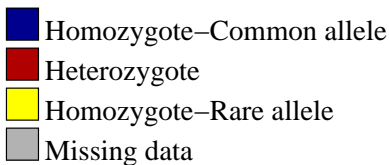
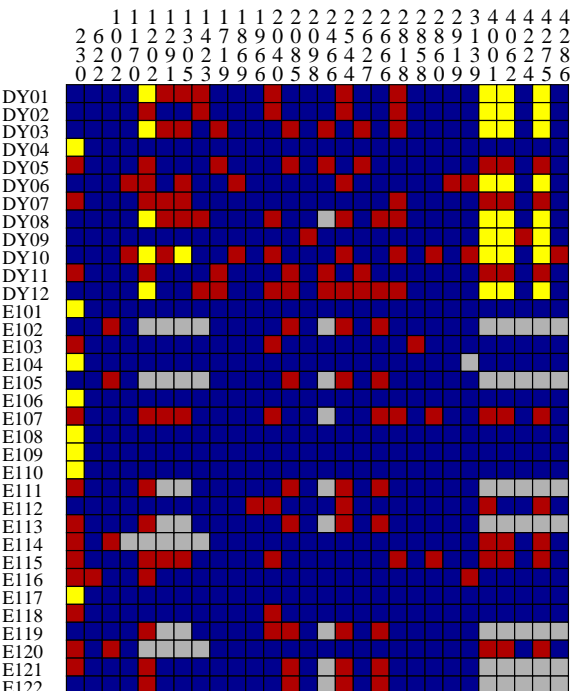
- Homozygote–Common allele
- Heterozygote
- Homozygote–Rare allele
- Missing data



$h^2_{afx}$ , p-value: 0.428



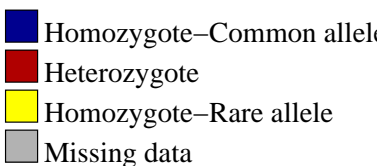
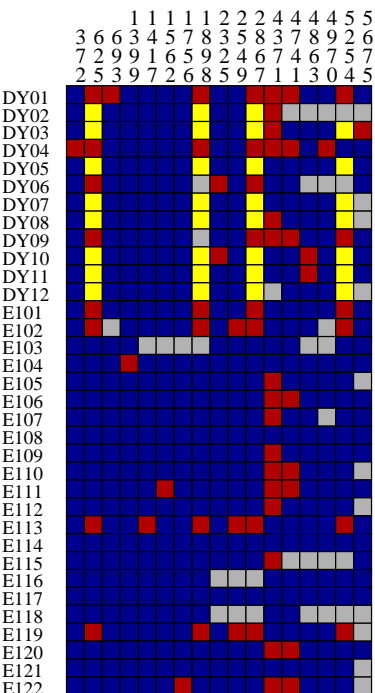
ifna1, p-value: 0.5156



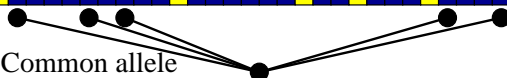
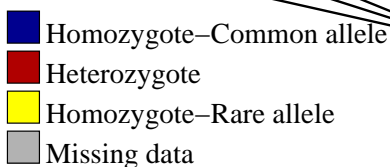
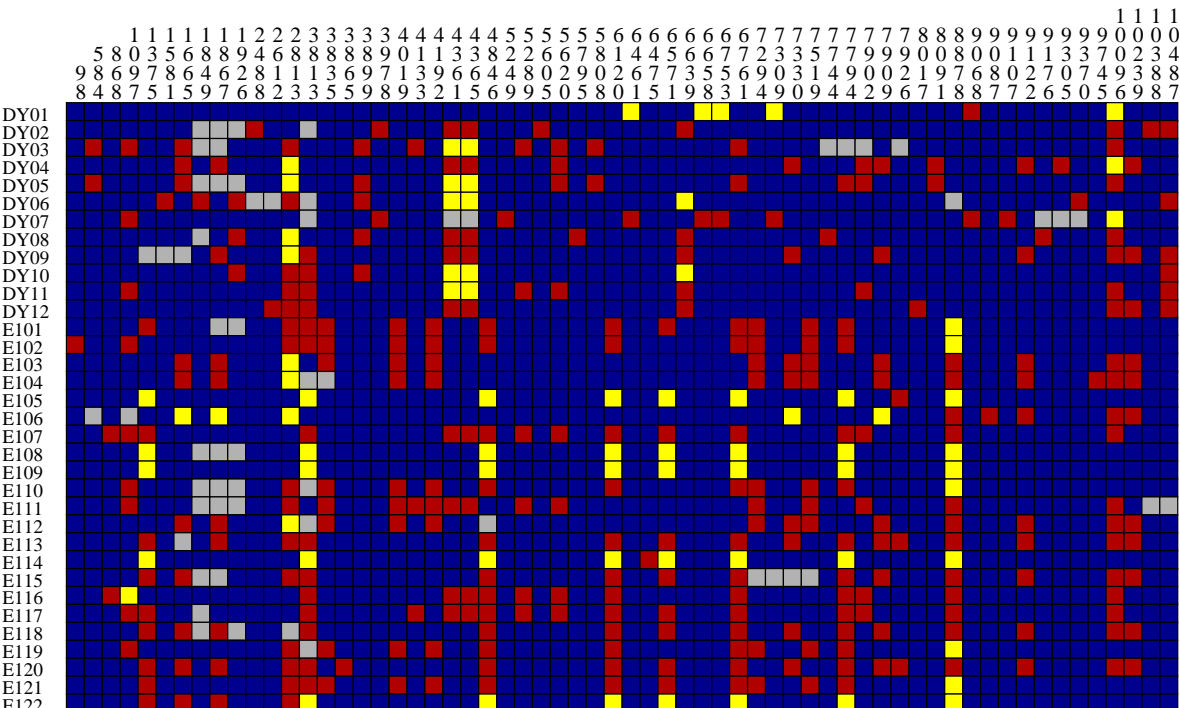




lcmt2, p-value: 0.4486



mad212, p-value: 0.0736

















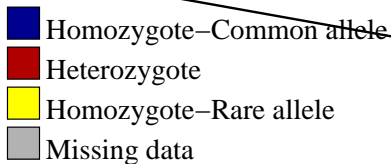
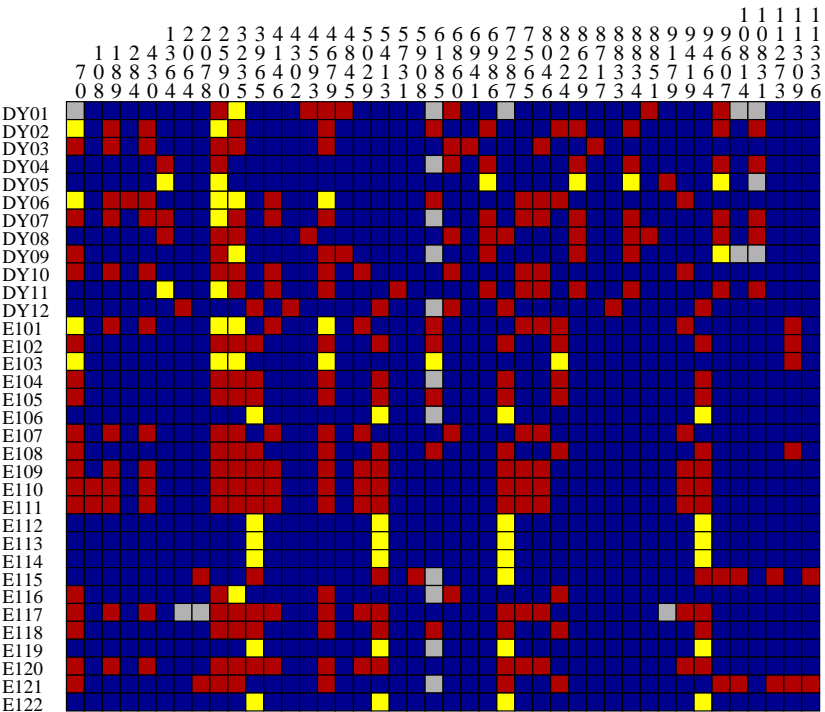








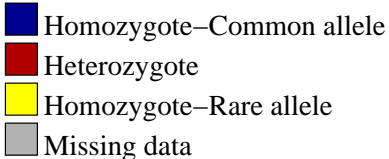
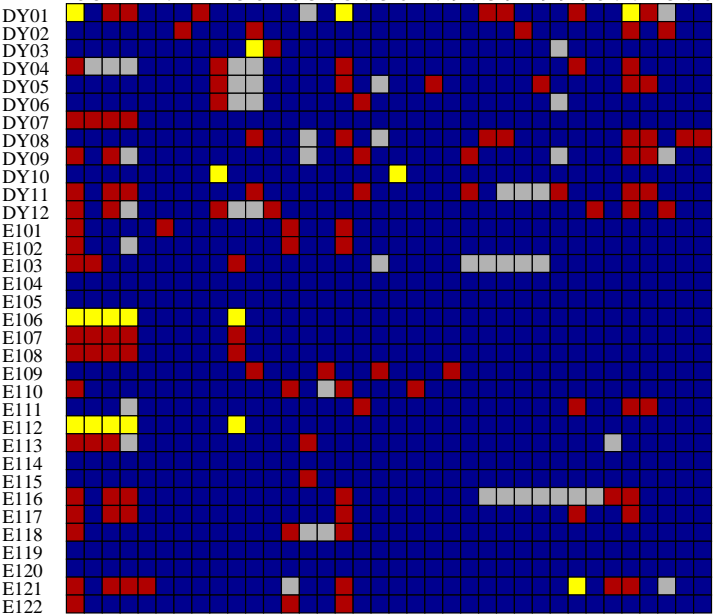
mmp9, p-value: 0.0422





mpo, p-value: 0.581

1 1 1 1 1 1 1 2 2 2 4 5 5 5 6 6 7 7 9 9 9 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1  
1 3 4 5 8 8 8 9 1 4 4 3 2 4 6 7 8 4 8 1 2 7 9 9 0 2 2 6 0 0 2 8 0 2 4 5  
7 5 1 3 3 6 7 2 1 6 7 2 6 7 5 0 6 1 3 4 7 9 2 7 8 9 9 3 6 8 4 2 0 6 8 7  
8 5 2 4 4 7 1 4 2 3 8 1 0 3 6 5 7 3 6 2 7 9 7 3 9 2 9 9 6 8 7 7 1 3 7 0



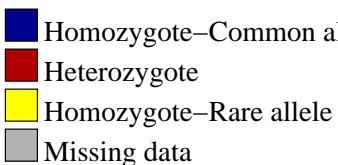
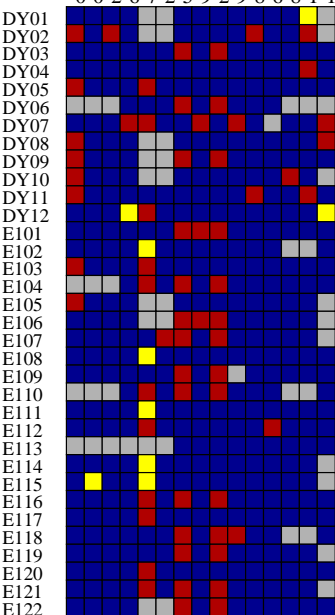






ngb, p-value: 0.4216

2 2 5 5 5 5 6 7 8 8 9  
 2 3 4 8 5 9 0 1 3 7 0 3 1 3 0  
 7 2 3 0 2 3 3 5 7 5 4 4 5 1 6  
 0 0 2 6 7 2 5 9 2 9 8 6 8 1 1









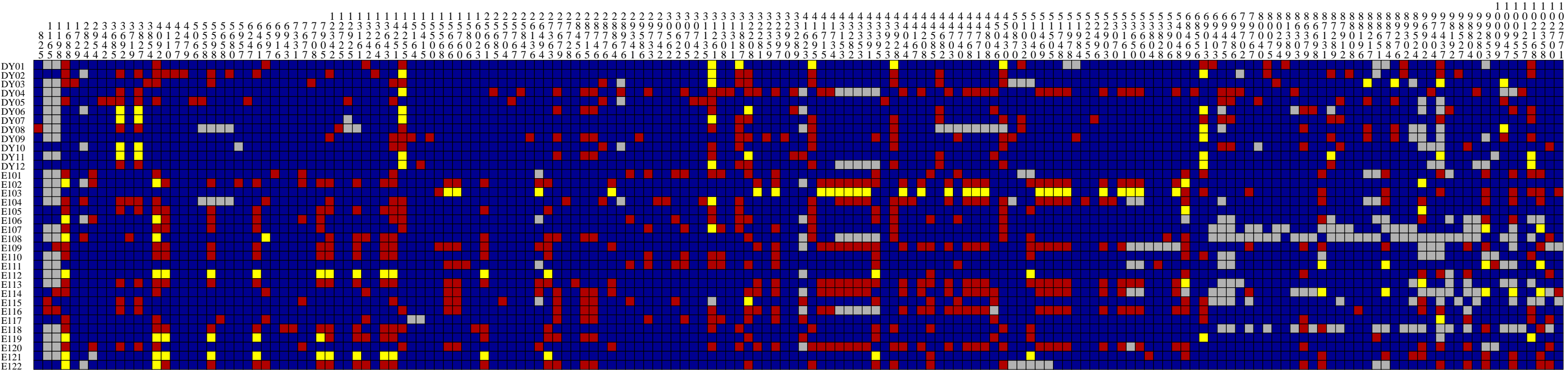






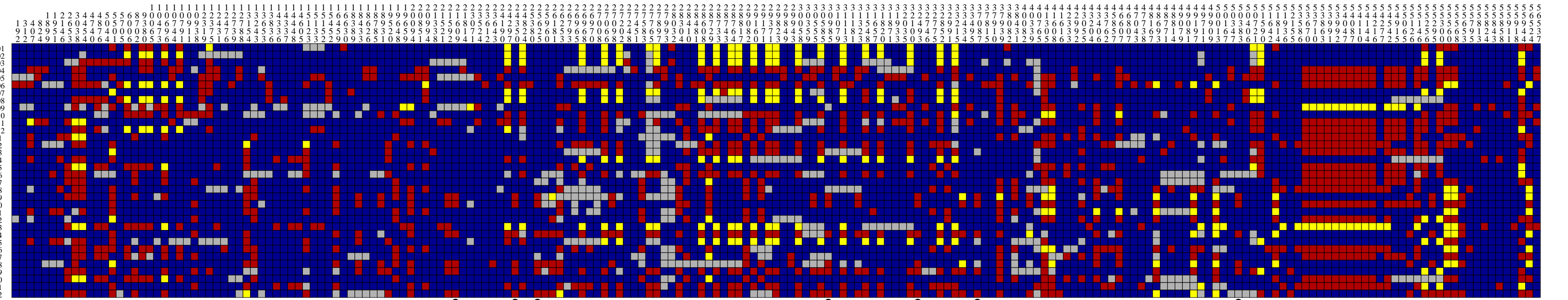


pax3, p-value: 0.1876



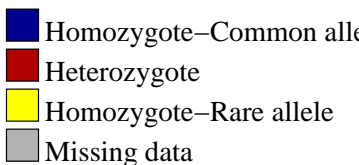
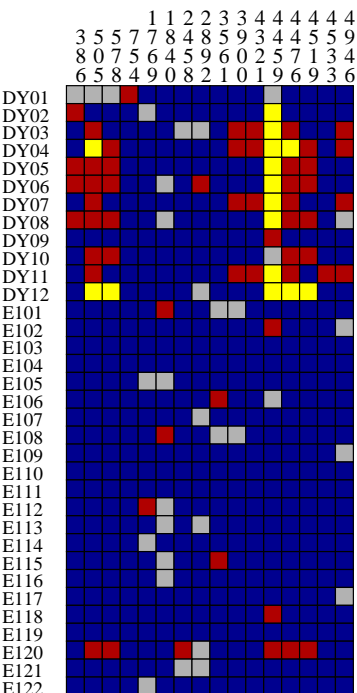
- Homozygote–Common allele
- Heterozygote
- Homozygote–Rare allele
- Missing data

pdlim1, p-value: 0.2652



Legend:  
■ Homozygote-Common allele  
■ Heterozygote  
■ Homozygote-Rare allele  
■ Missing data

pold4, p-value: 0.4422





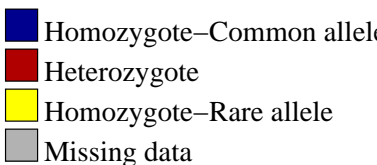
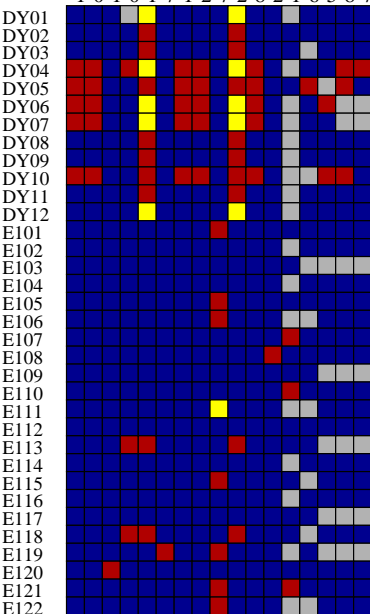






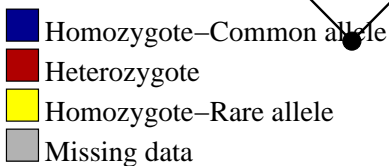
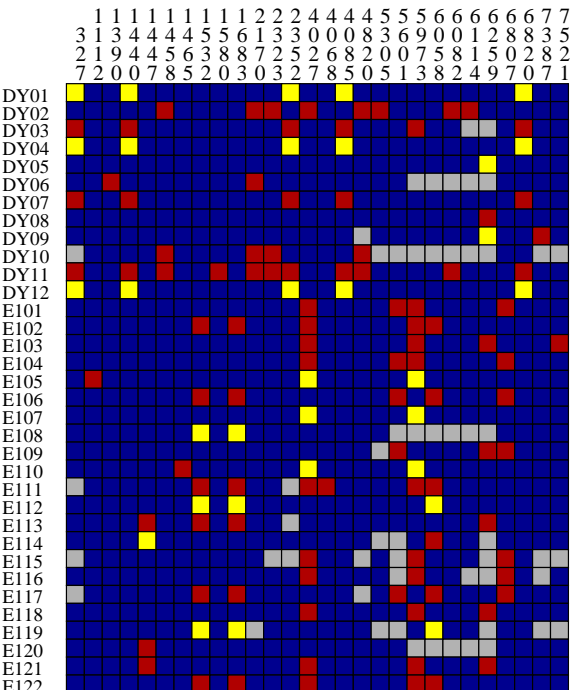
prdx2, p-value: 0.4446

1 1 1 1 2 2 2 3 3 3 3 3 4 6 7 7 7  
0 0 3 7 0 3 5 0 0 1 4 7 5 3 1 6 6  
8 9 0 1 4 3 1 1 9 5 5 1 3 4 0 4 6  
1 0 1 0 1 7 1 2 7 2 8 2 1 6 5 8 7





prdx5, p-value: 0.1878

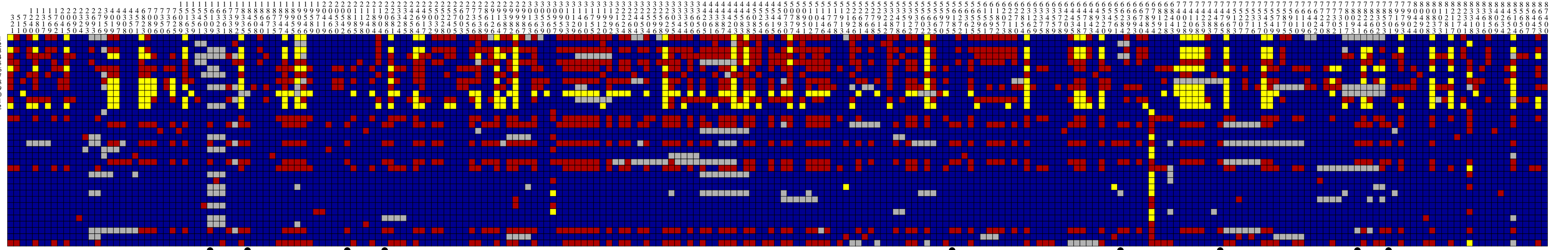








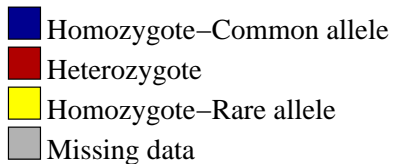
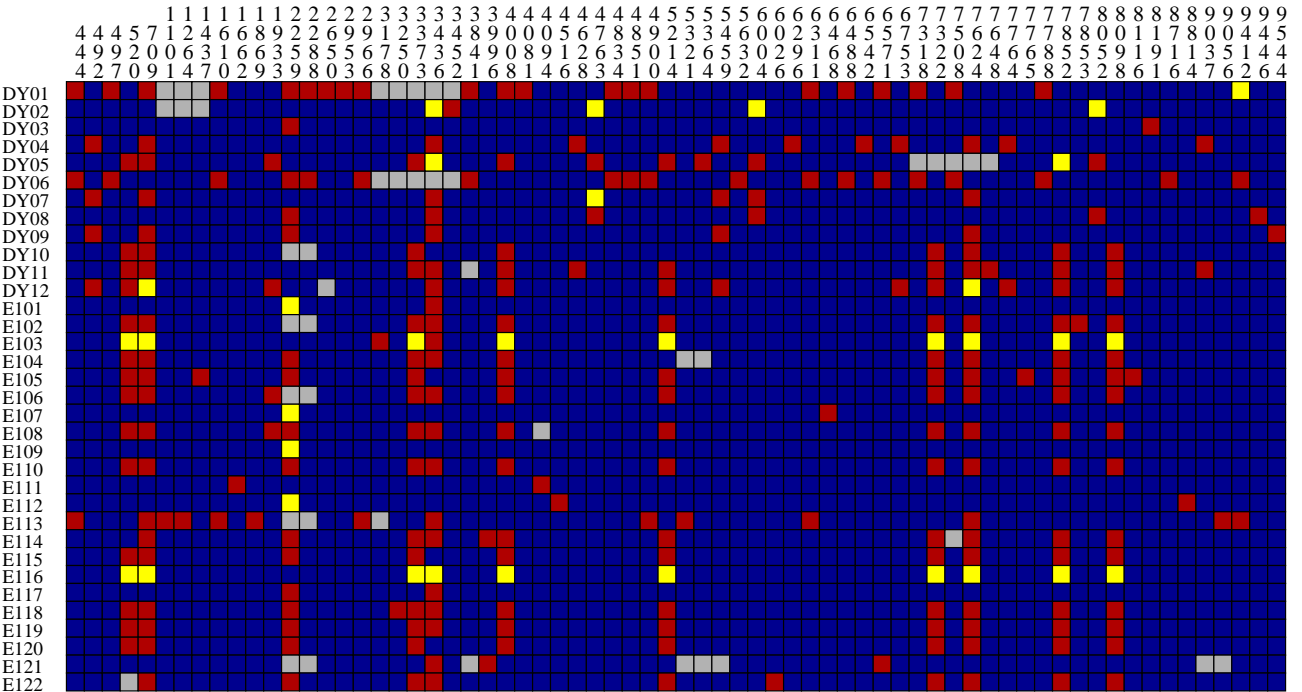
rad18, p-value: 0.0362



■ Homozygote-Common allele  
■ Heterozygote  
■ Homozygote-Rare allele  
■ Missing data



recql4, p-value: 0.7632

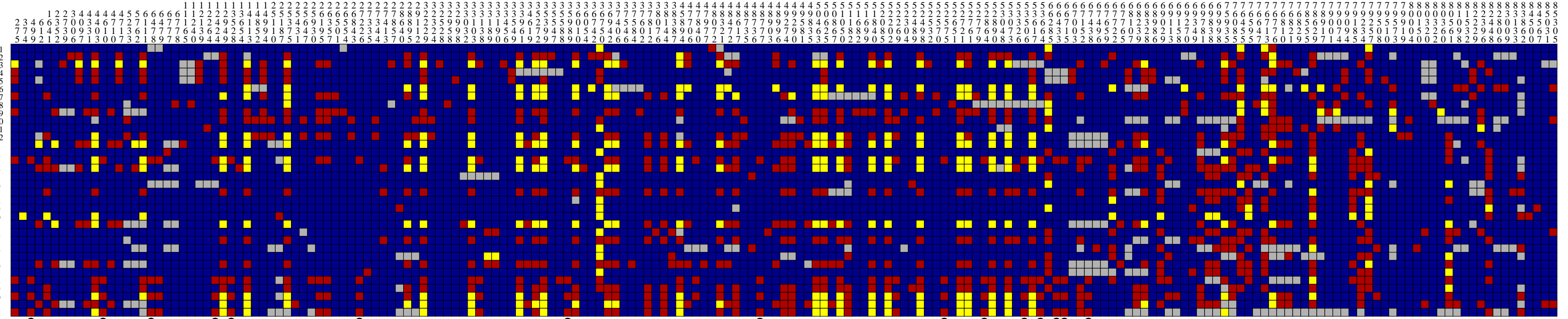








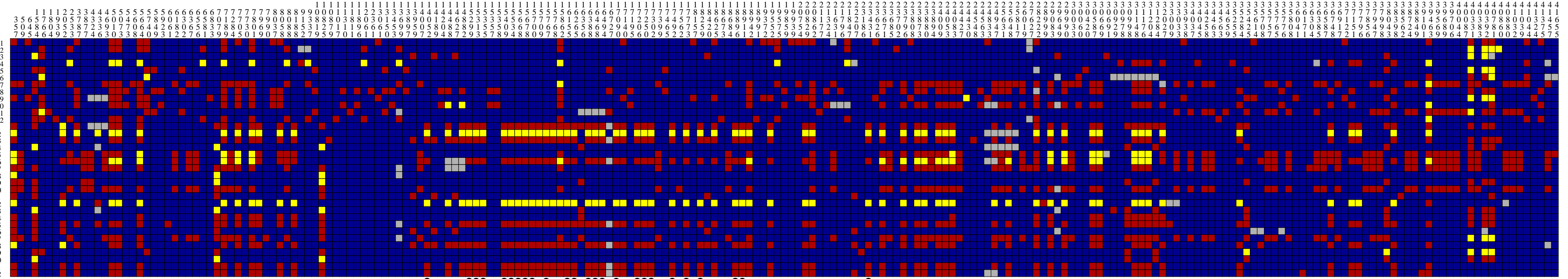
rpa3, p-value: 0.0052



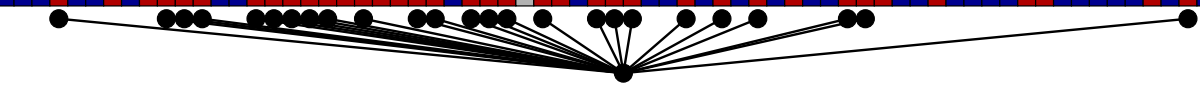
- Homozygote-Common allele
- Heterozygote
- Homozygote-Rare allele
- Missing data



scara3, p-value: 0.0322



■ Homozygote-Common allele  
■ Heterozygote  
■ Homozygote-Rare allele  
■ Missing data







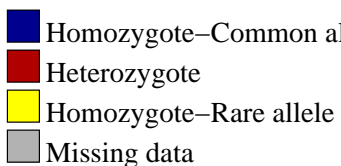
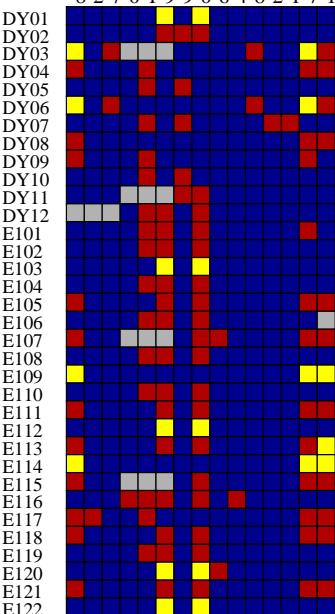




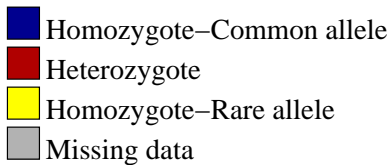
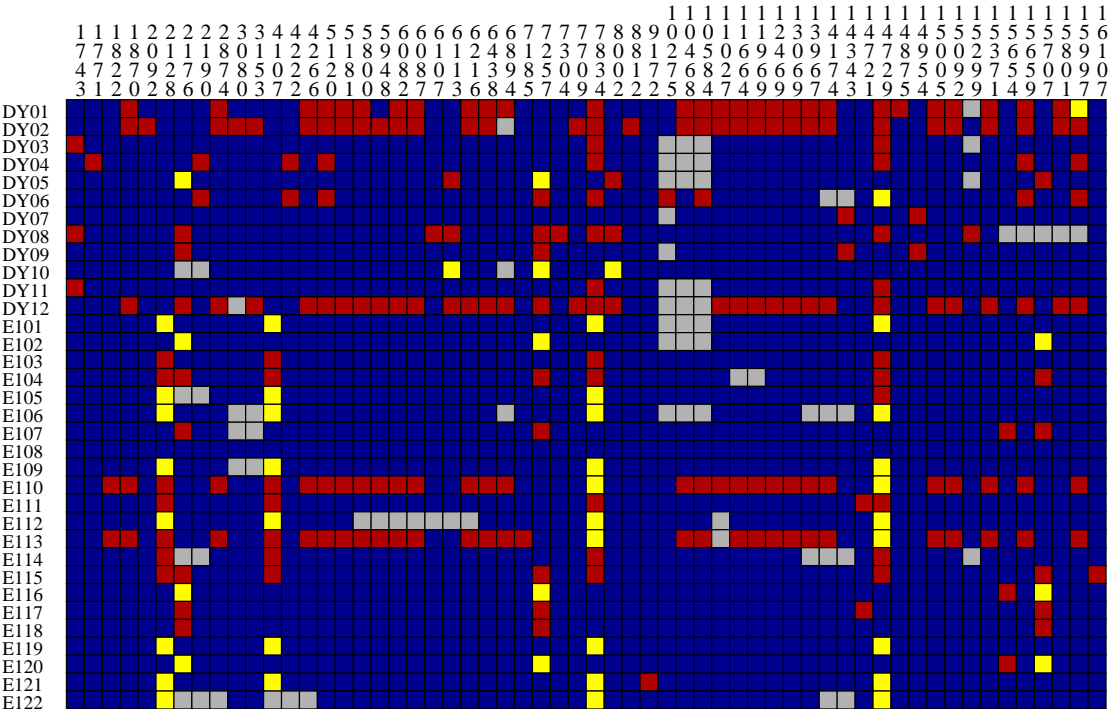


sphar, p-value: 0.438

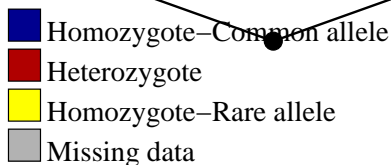
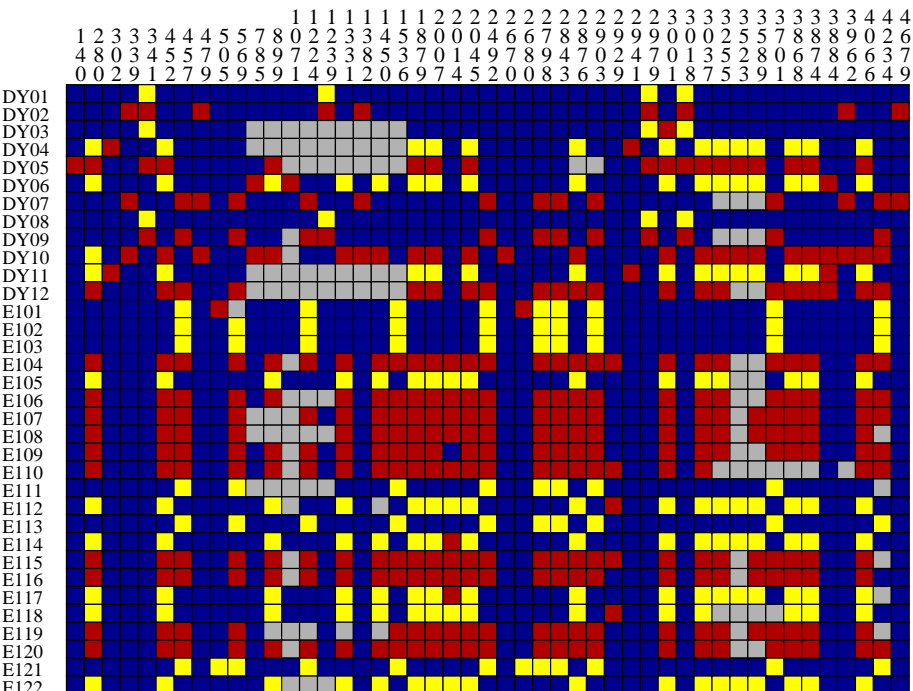
1 1 1 1 1 1 3 3 3 3 4 4  
5 9 9 1 2 3 6 8 9 0 3 6 6 7 8  
1 3 8 6 7 2 2 8 7 5 3 5 6 6 3  
8 2 7 0 1 9 9 0 6 4 8 2 1 7 1



spo11, p-value: 0.689

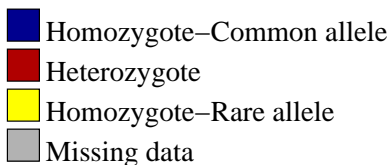
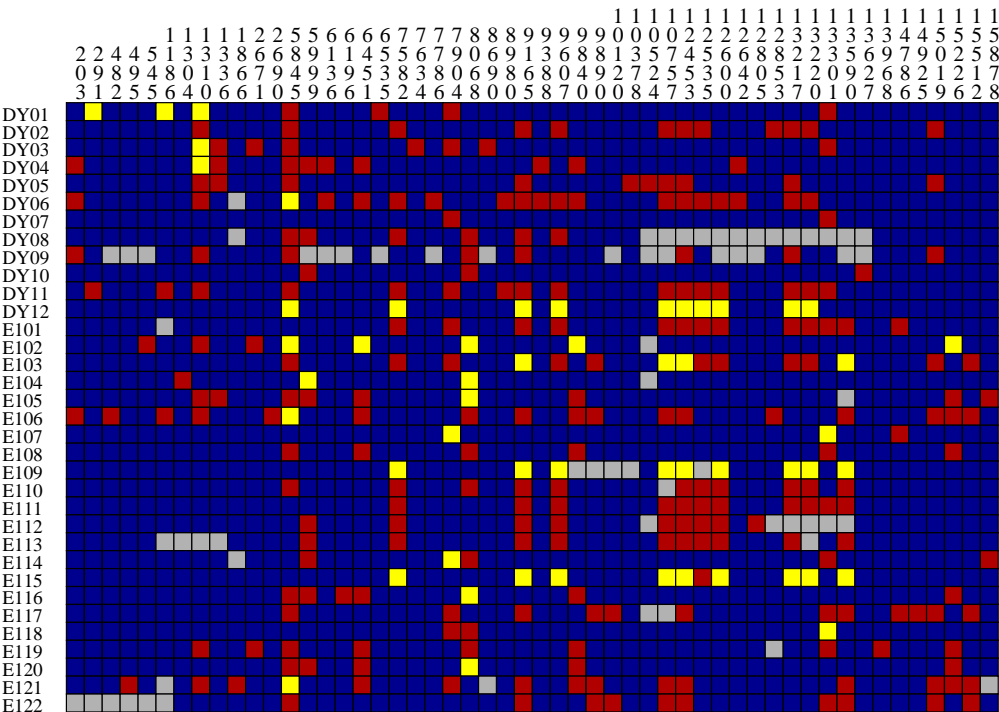


spr3, p-value: 0.2414

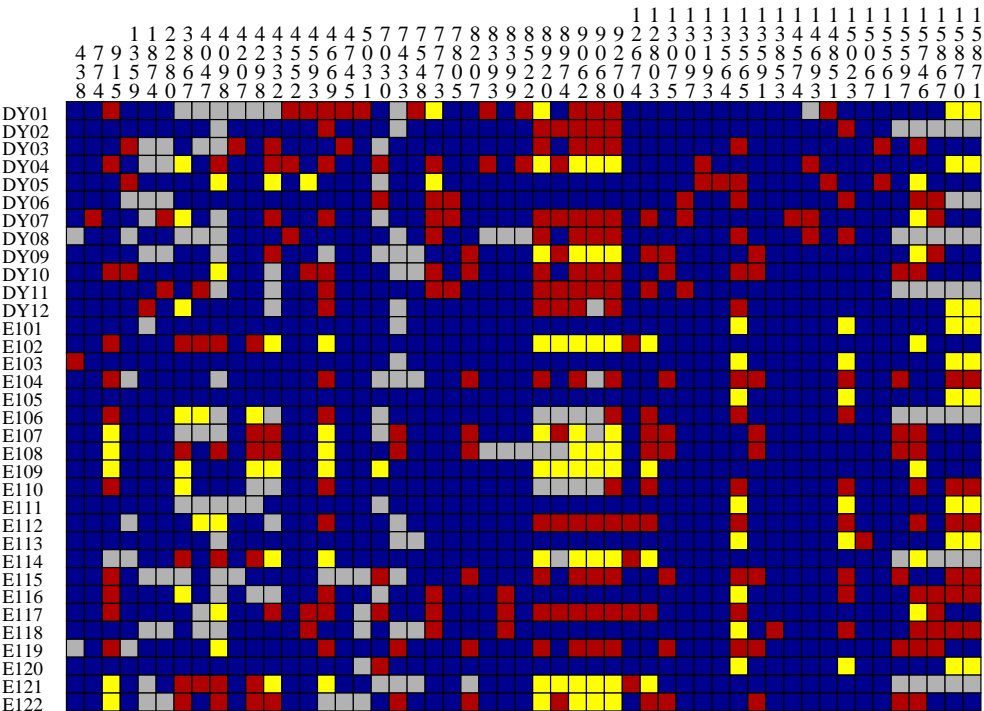




stk25, p-value: 0.333



tbxa2r, p-value: 0.6176



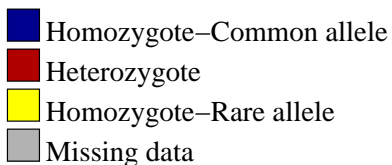
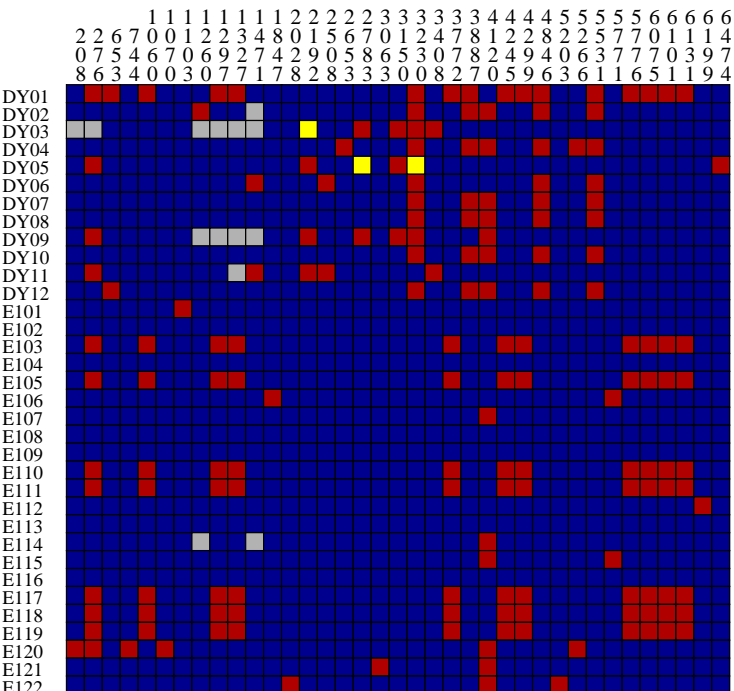
- Homozygote–Common allele
- Heterozygote
- Homozygote–Rare allele
- Missing data





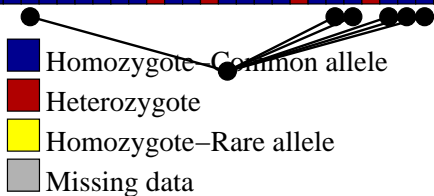
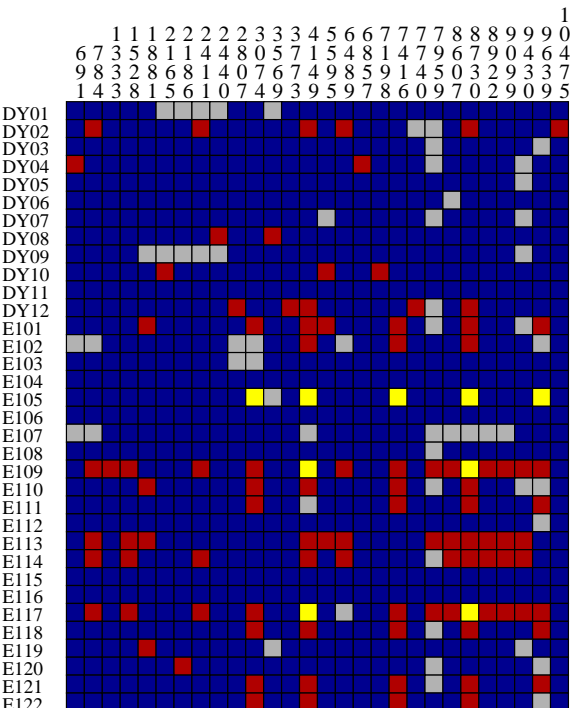


tnfrsf4, p-value: 0.5824





# tp53i3, p-value: 0.0132

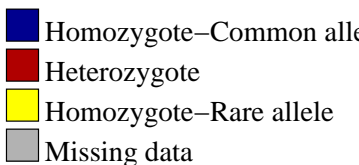
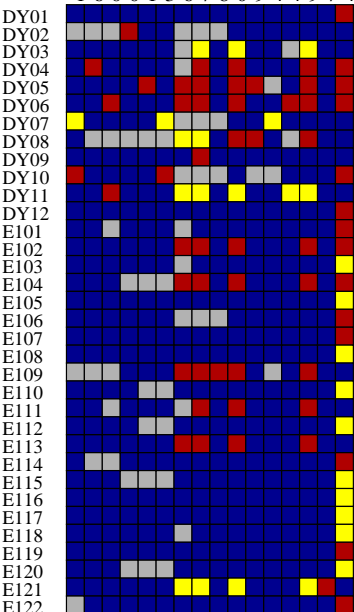






tuba1, p-value: 0.4312

1 1 1 1 2 2 3 3 3 3 4 7 7  
 1 5 8 2 5 6 8 1 1 1 3 3 5 1 2 2  
 7 8 4 8 3 6 5 0 5 8 6 7 9 2 4 5  
 1 6 0 0 1 3 6 7 8 0 9 4 4 9 7 4



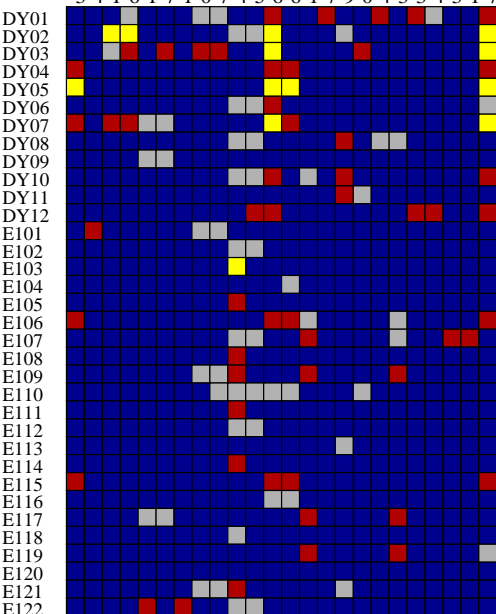






ube2v2, p-value: 0.1038

|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|   |   |   |   |   |   | 1 | 1 | 1 | 2 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 4 | 4 | 4 | 5 | 5 |   |   |
|   |   |   |   |   |   | 1 | 2 | 5 | 5 | 6 | 2 | 2 | 4 | 4 | 5 | 1 | 1 | 5 | 6 | 6 | 2 | 3 | 3 | 0 | 4 |
| 1 | 1 | 2 | 5 | 9 | 0 | 3 | 8 | 1 | 8 | 9 | 6 | 8 | 2 | 7 | 9 | 6 | 0 | 7 | 9 | 4 | 5 | 1 | 1 |   |   |
| 2 | 4 | 5 | 2 | 6 | 3 | 9 | 6 | 1 | 5 | 0 | 3 | 3 | 0 | 7 | 4 | 2 | 4 | 1 | 2 | 3 | 6 | 7 | 9 |   |   |
| 3 | 4 | 1 | 6 | 1 | 7 | 1 | 0 | 7 | 4 | 5 | 6 | 6 | 1 | 7 | 9 | 0 | 4 | 3 | 3 | 4 | 3 | 1 | 7 |   |   |



- Homozygote-Common allele
- Heterozygote
- Homozygote-Rare allele
- Missing data











