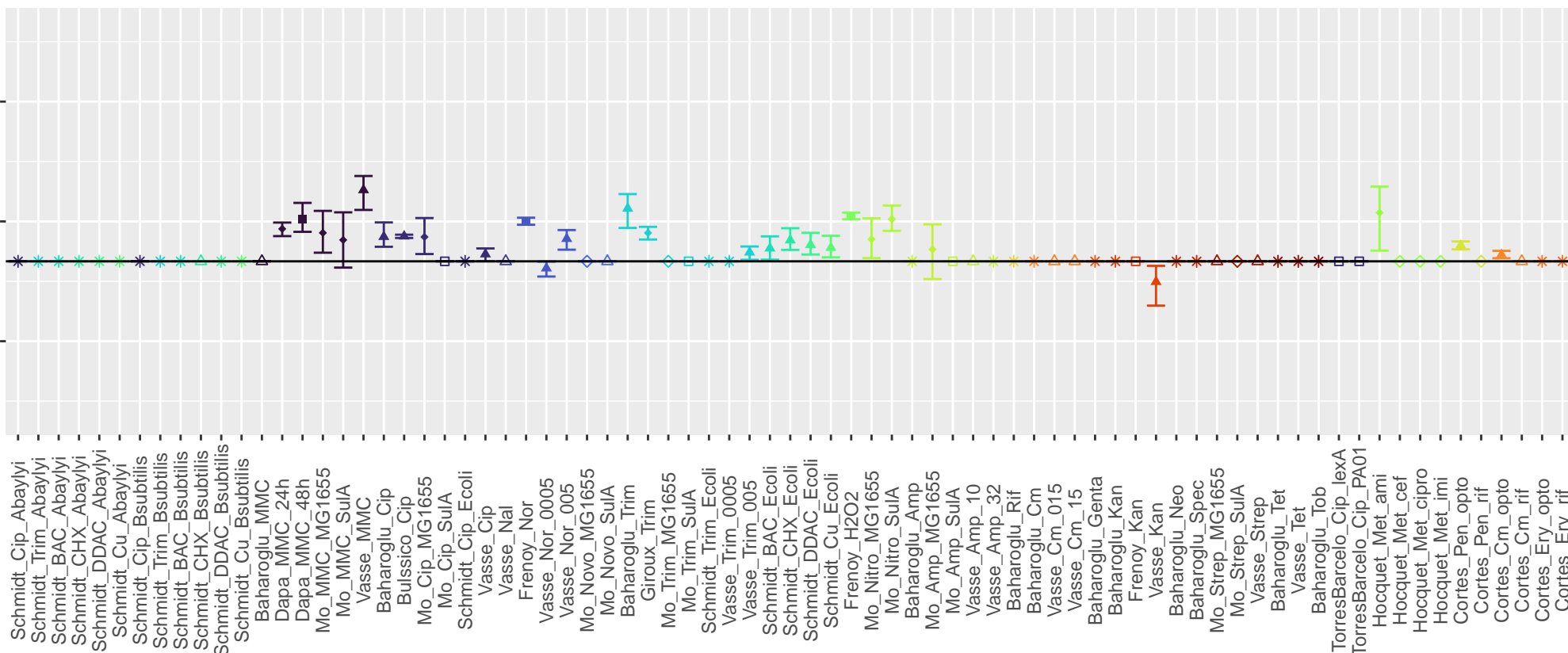


Fold-change population-wide mutation rate

Estimates from the homogeneous model with lowest AIC_c, if S significantly different from UT condition



Experiment ID

Selected model

- △ N0
- ◇ N1
- N2
- ▲ HOM0
- ◆ HOM1
- HOM2
- * S/UT not s. different