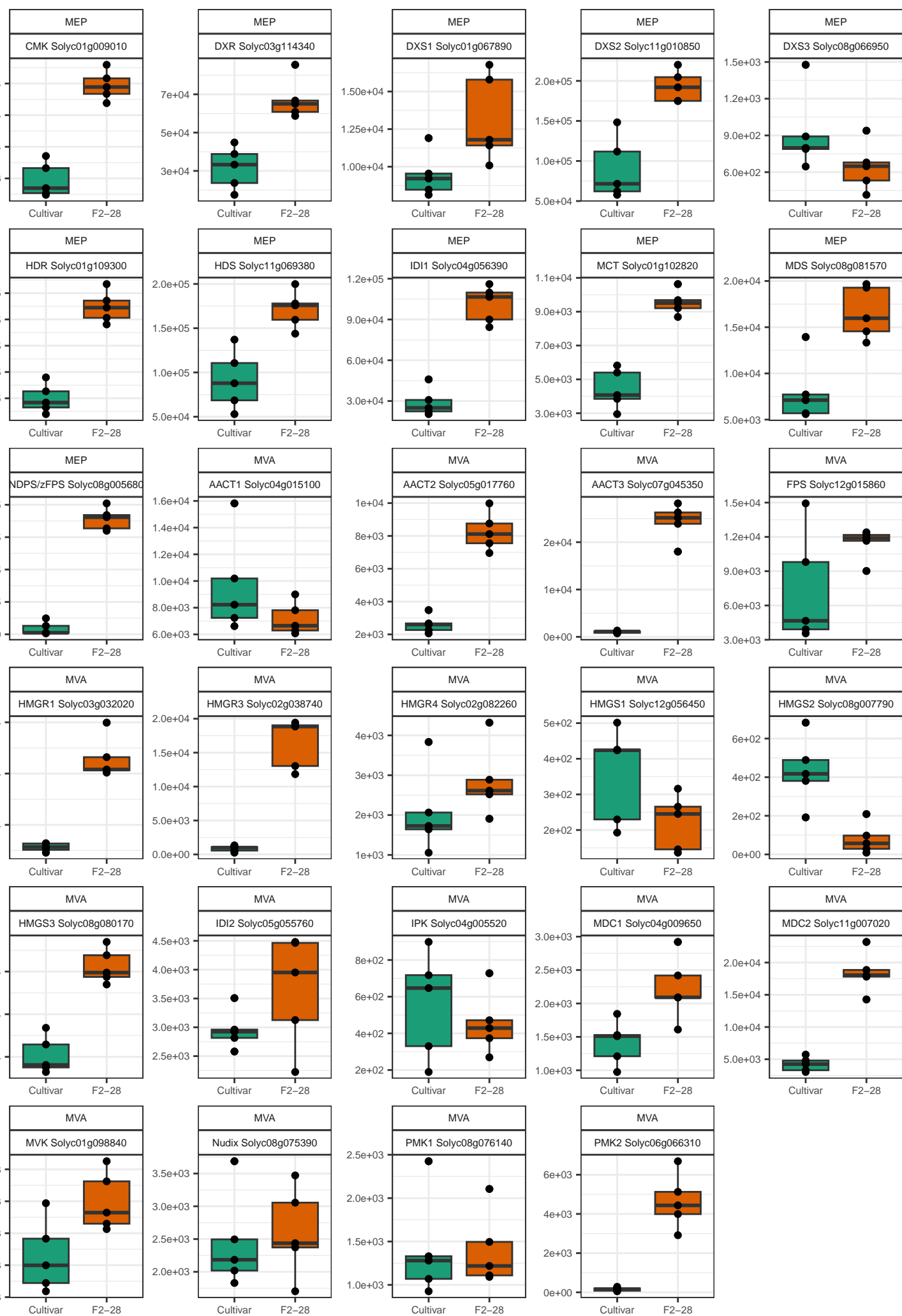


normalised_counts



genotype