

“Multi-Agent” Screening Improves Directed Enzyme Evolution by Identifying Epistatic Mutations

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Supplemental Figures

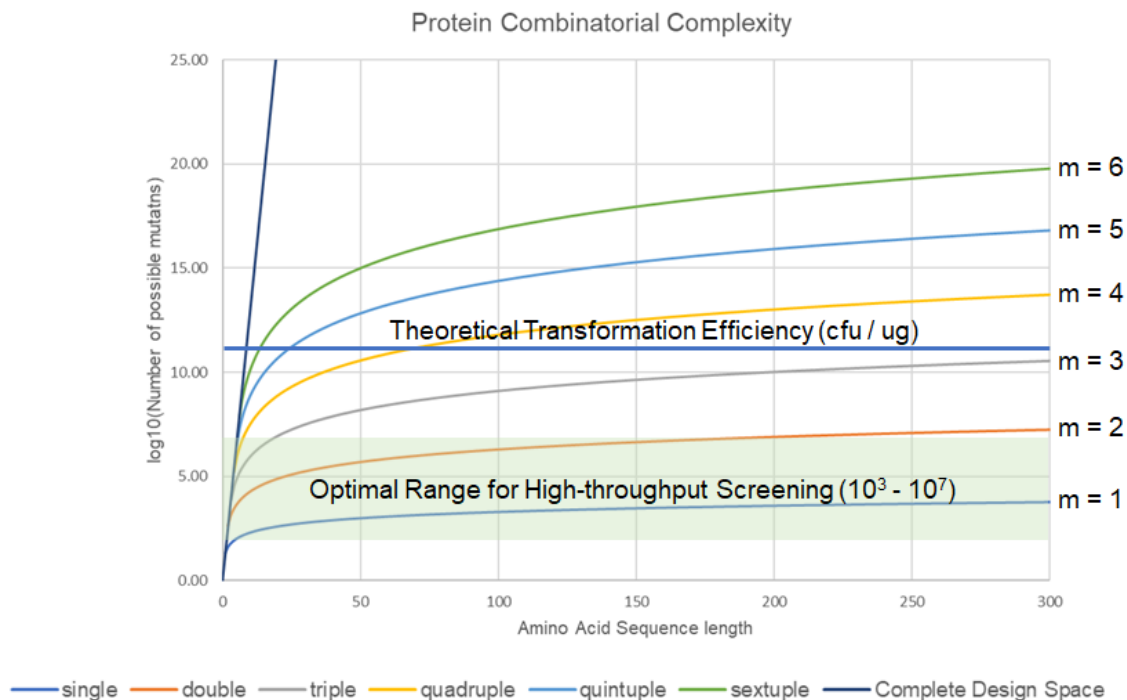


Figure S1: The Complexity of Protein Design Space with Different Criteria. The complexity of complete design space grows rapidly out of the range for high-throughput screening at very small sequence length. The curves designated with an m value represent the complexity of the m-mutant space at different sequence length, with only single- and double-mutant space manageable for the high-throughput screening capacity. The theoretical transformation efficiency is also labeled in the plot for reference.

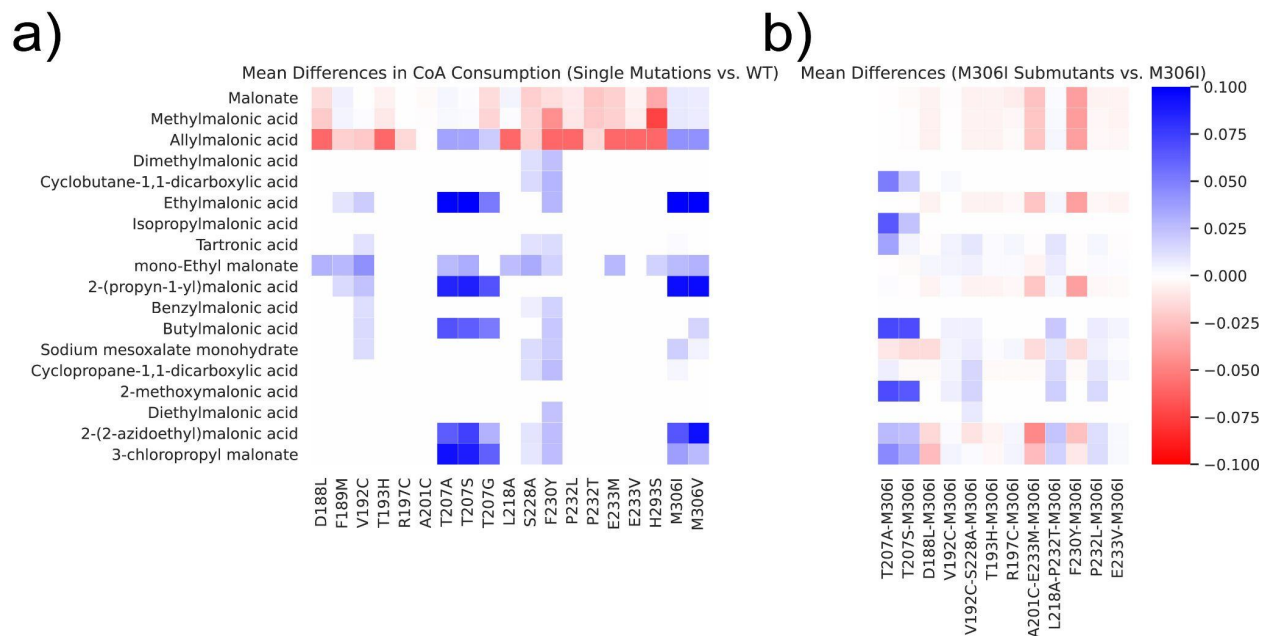


Figure S2. Mutation effects on different substrates given the **a)** WT sequence and **b)** M306I in the confirmatory activity assay. T207A/S/G all have a positive effect on some of the substrates given the WT sequence, and were missed in our initial screening, potentially due to sampling bias and/or assay variation. On average, 4.6 mutations would be found to have a positive effect given the WT sequence by screening only one substrate, ranging from 0 (for isopropylmalonic acid and 2-methoxymalonic acid) to 12 (for mono-ethyl malonate).

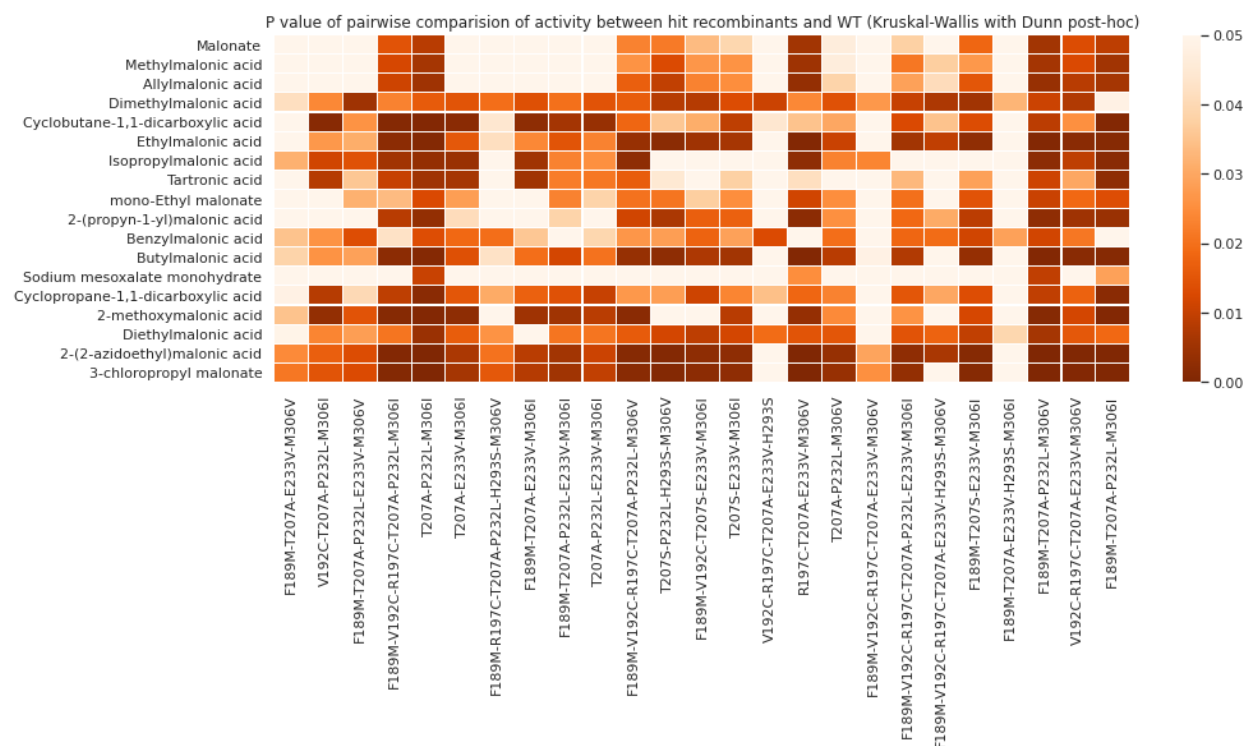


Figure S3. Statistical significance of comparison of activity between hit recombinants and WT. All hit recombinants show significantly improved activity on many substrates.

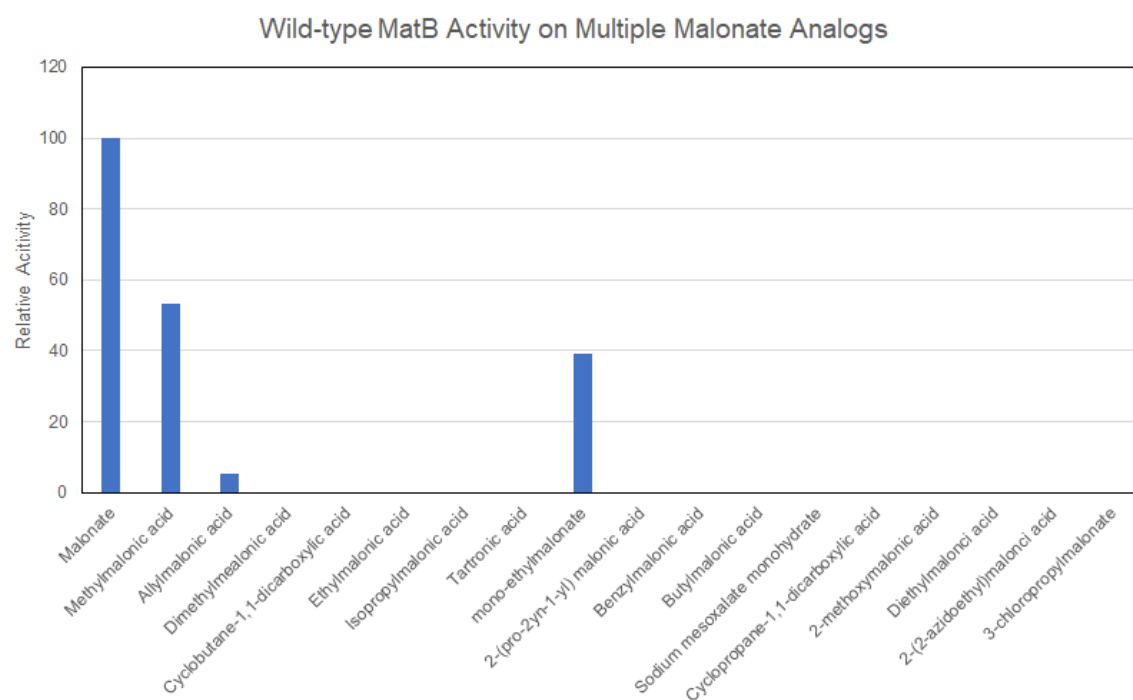


Figure S4. WT MatB Screening Activity Profile on the Selected Panel of Substrate Analogues.

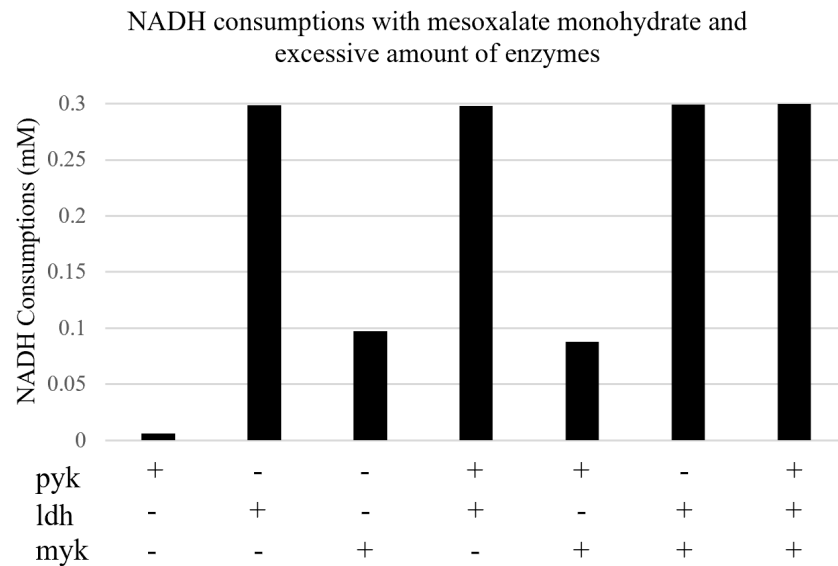
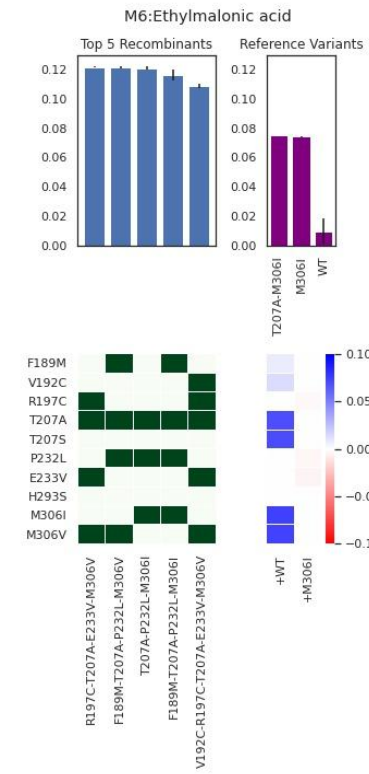
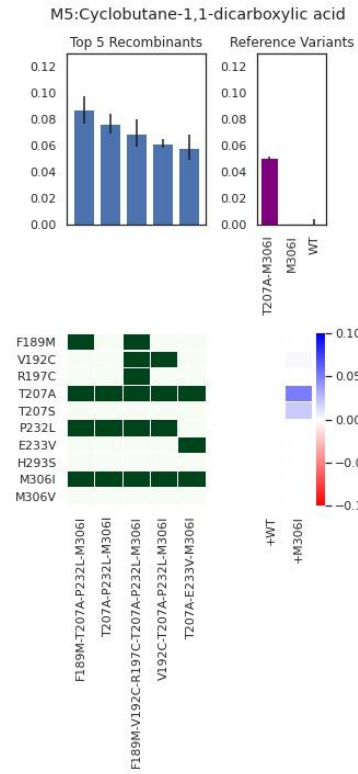
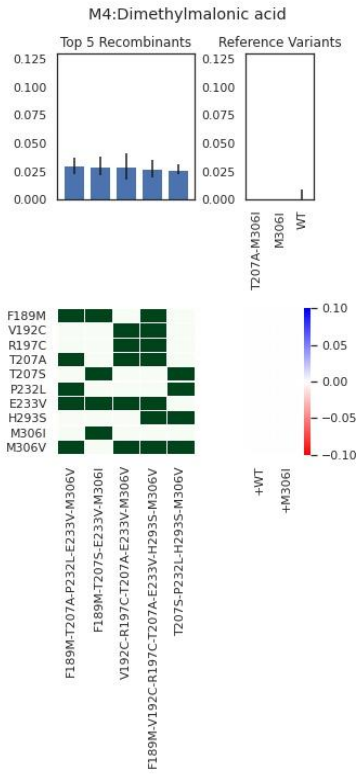
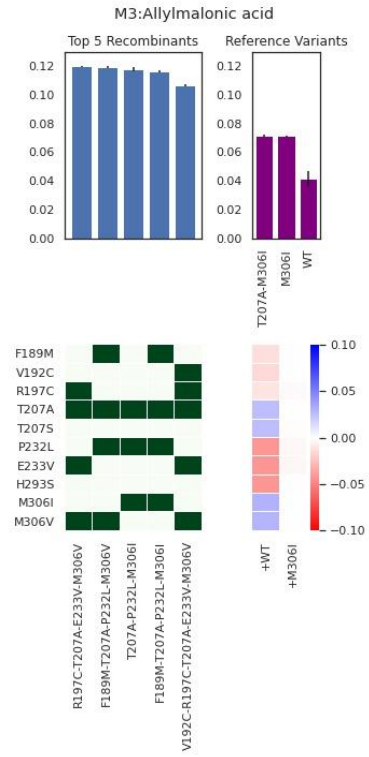
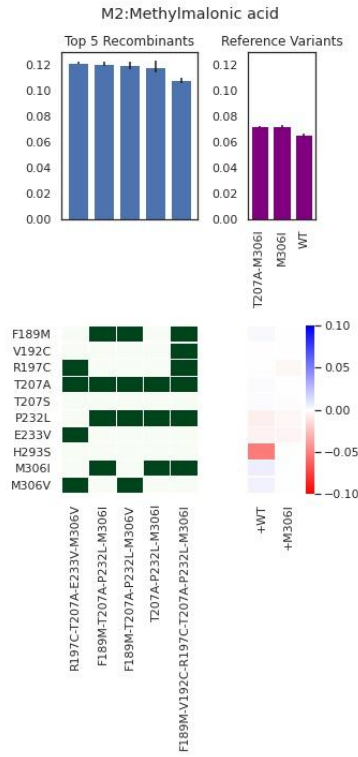
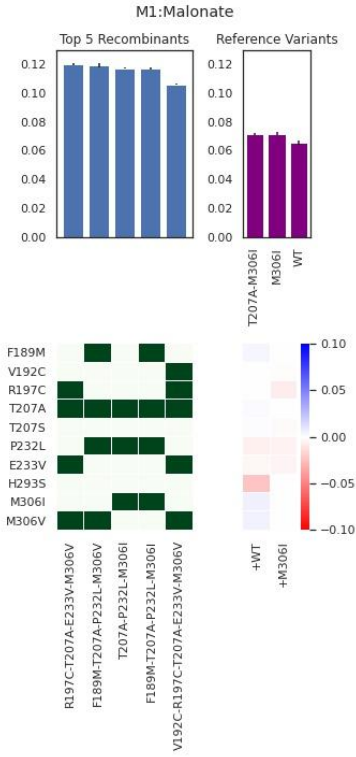
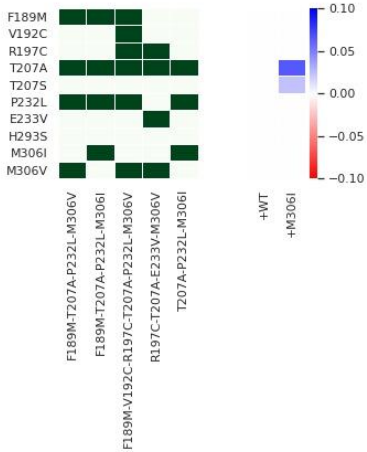
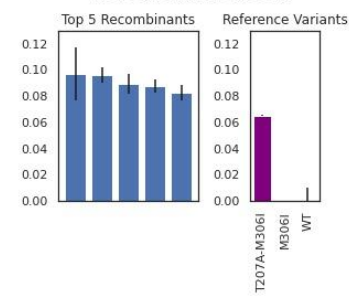


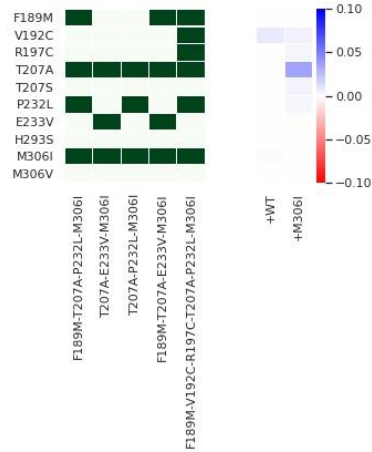
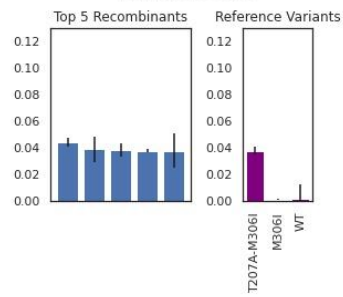
Figure S5: Reaction of Mesoxalic acid with NADH in the presence of coupling enzymes. The formation of AMP in the synthetase (matB) reaction is coupled to NADH oxidation by purified myokinase, pyruvate kinase, and lactate dehydrogenase, which can be monitored at 340 nm. Abbr.: pyk (pyruvate kinase), ldh (lactate dehydrogenase), myk (myokinase).



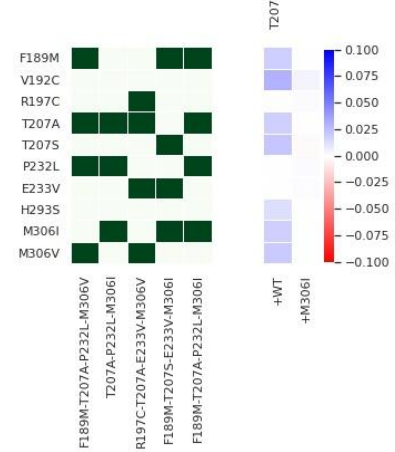
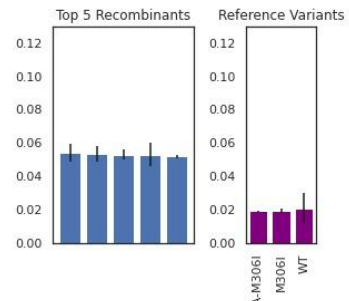
M7:isopropylmalonic acid



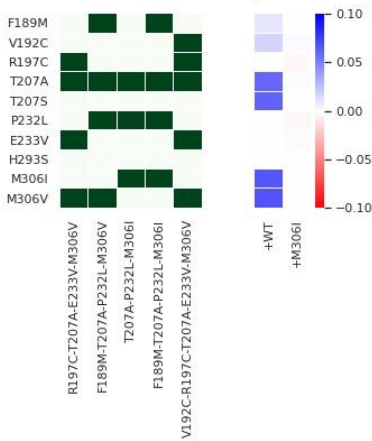
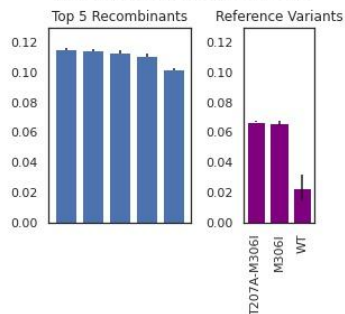
M8:Tartronic acid



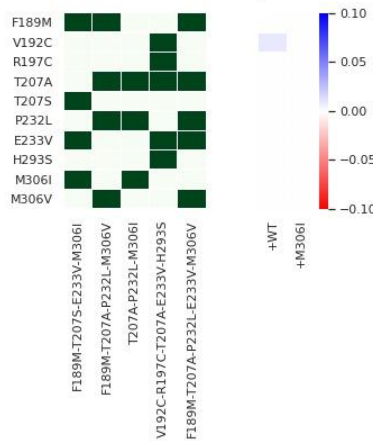
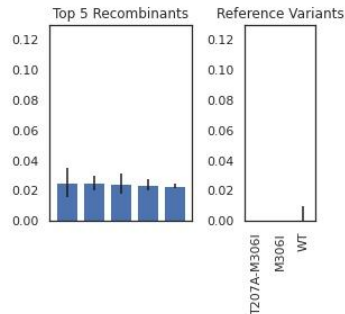
M9:mono-Ethyl malonate



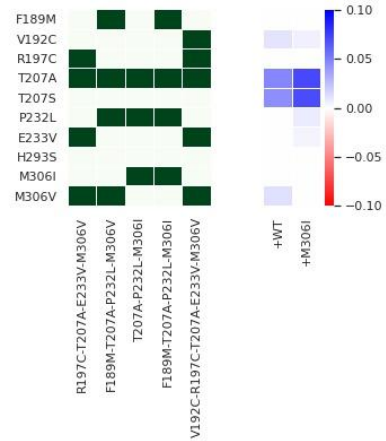
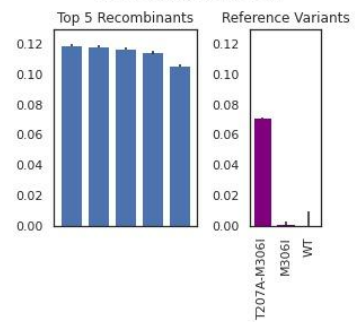
M10:2-(propyn-1-yl)malonic acid



M11:Benzymlalonic acid



M12:Butylmalonic acid



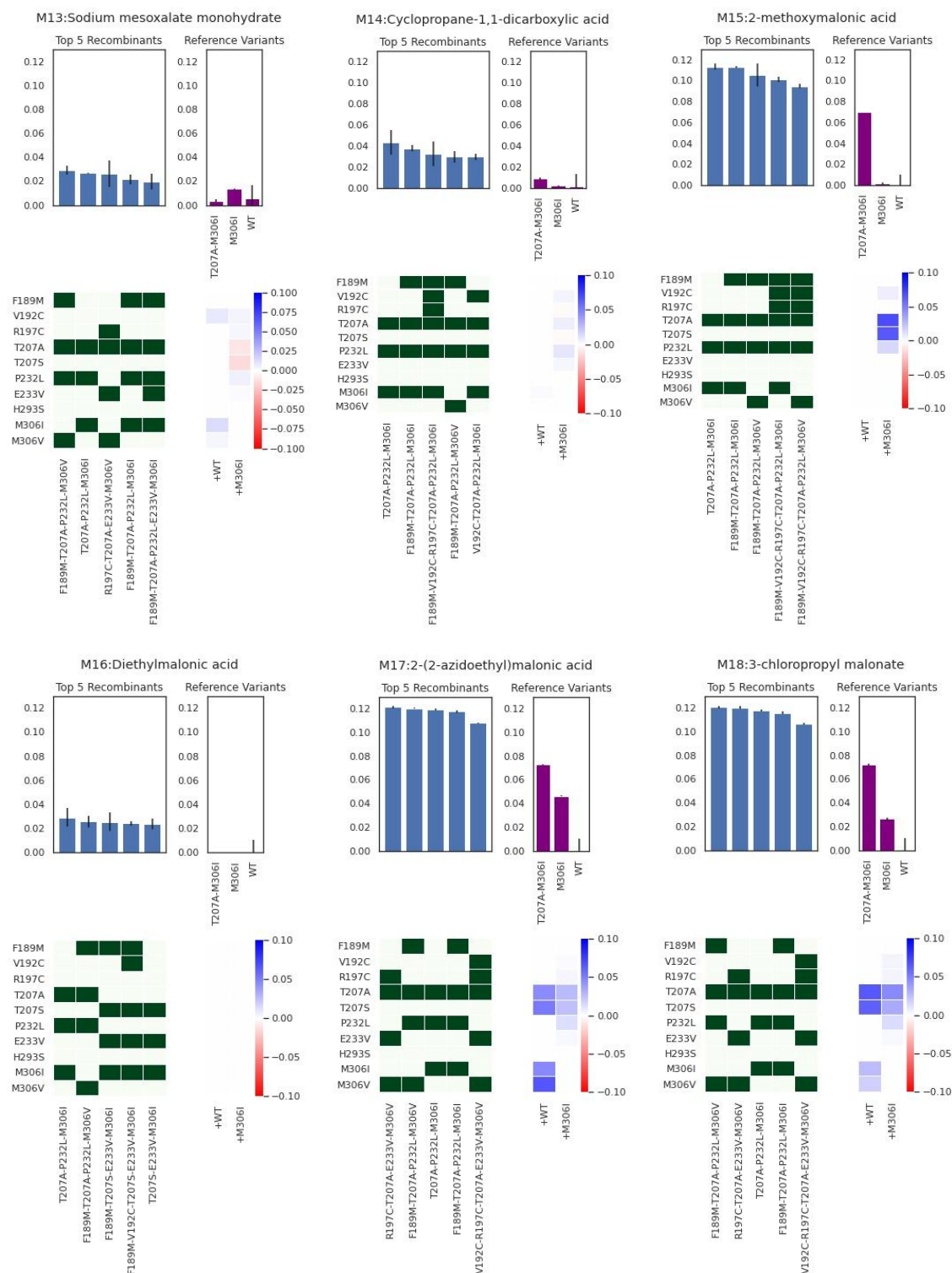
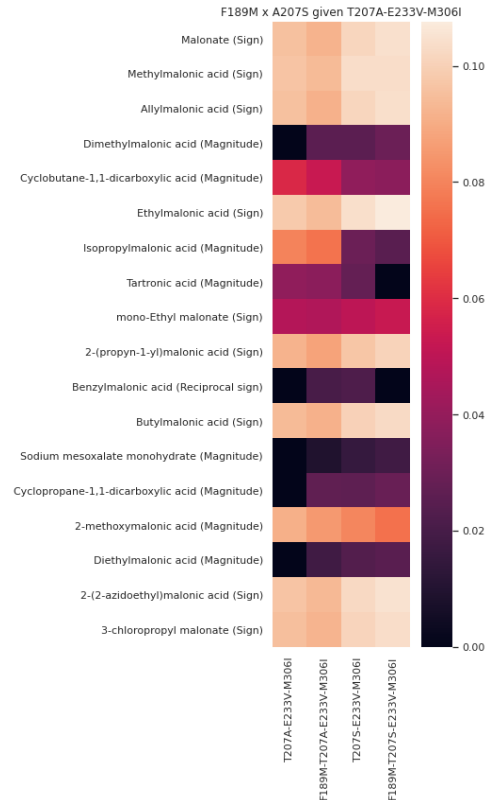
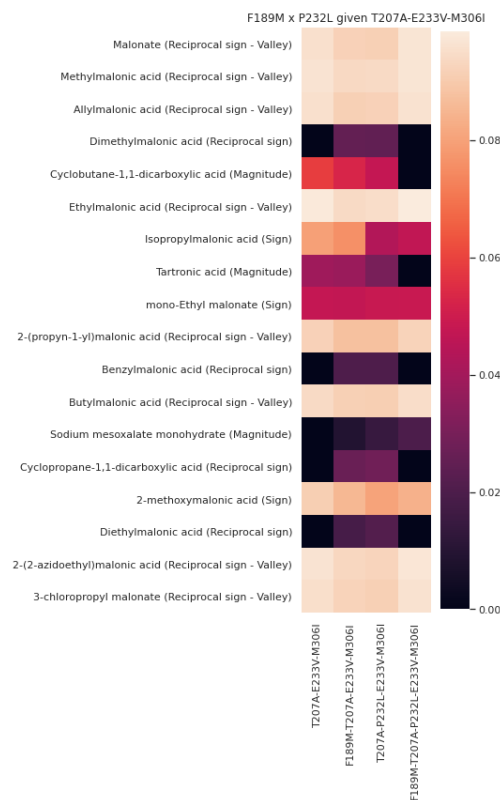
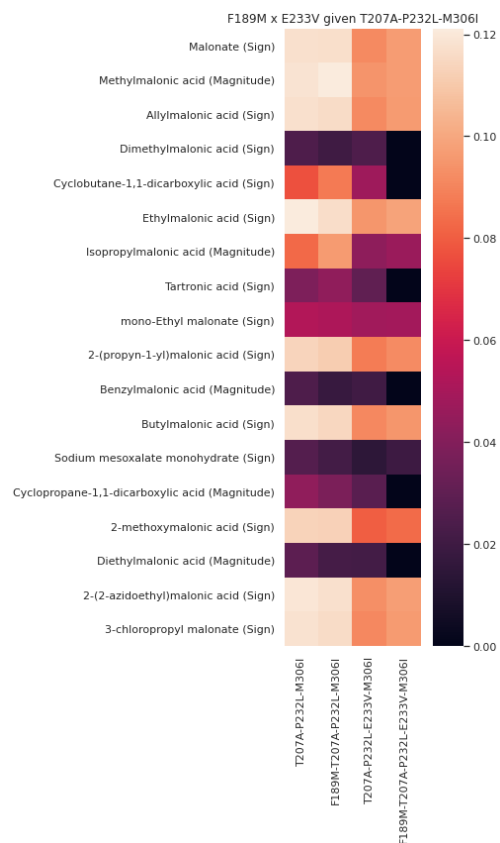
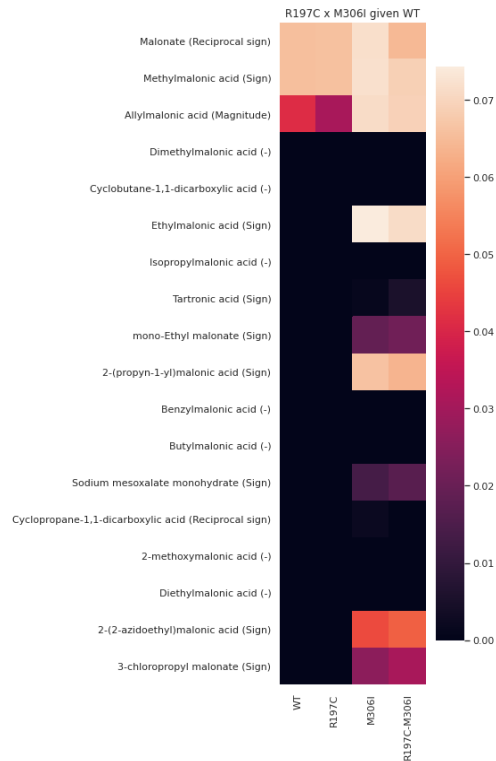
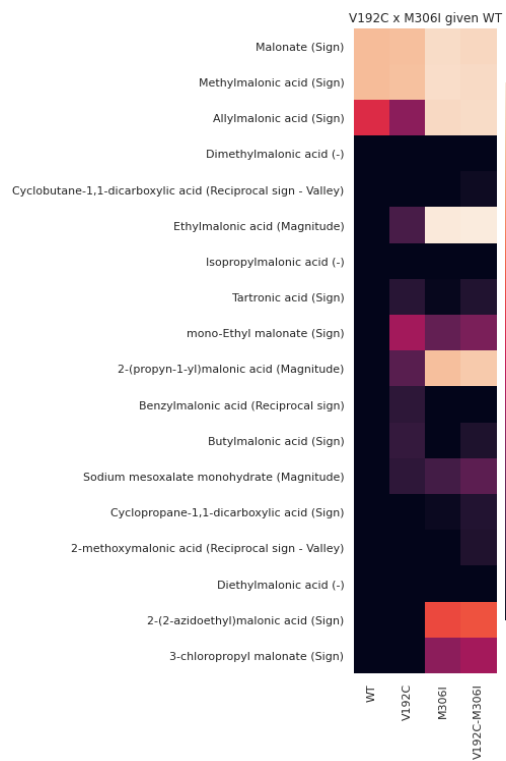
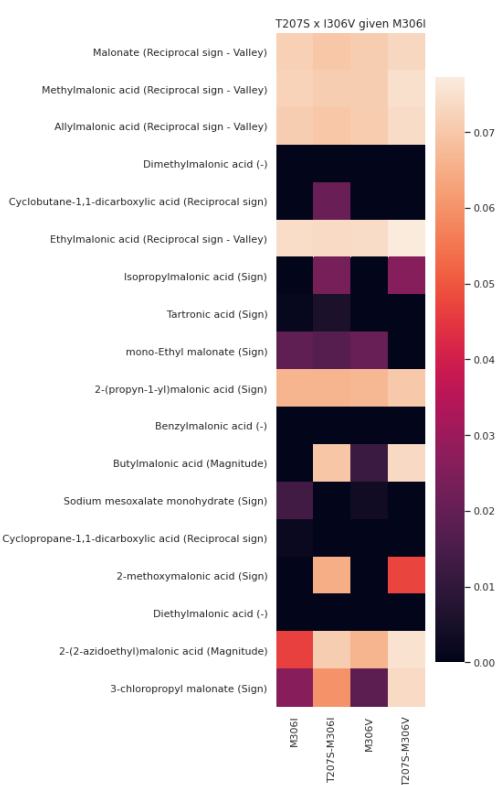
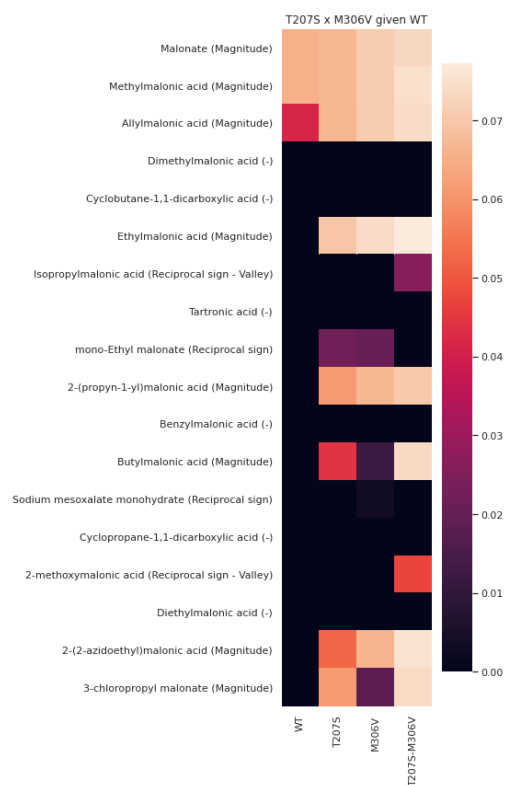
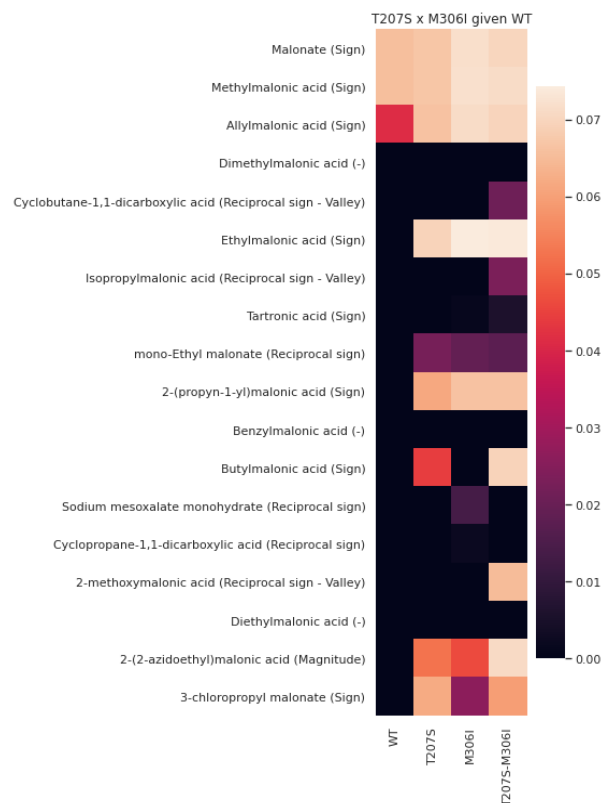
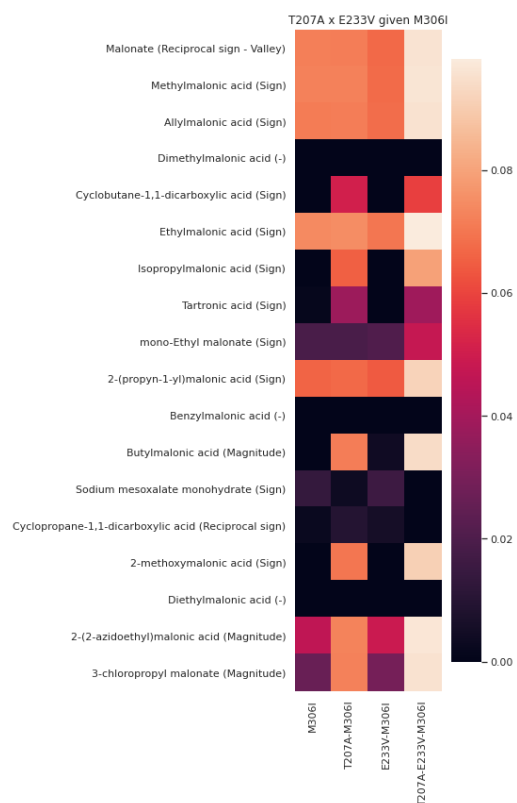
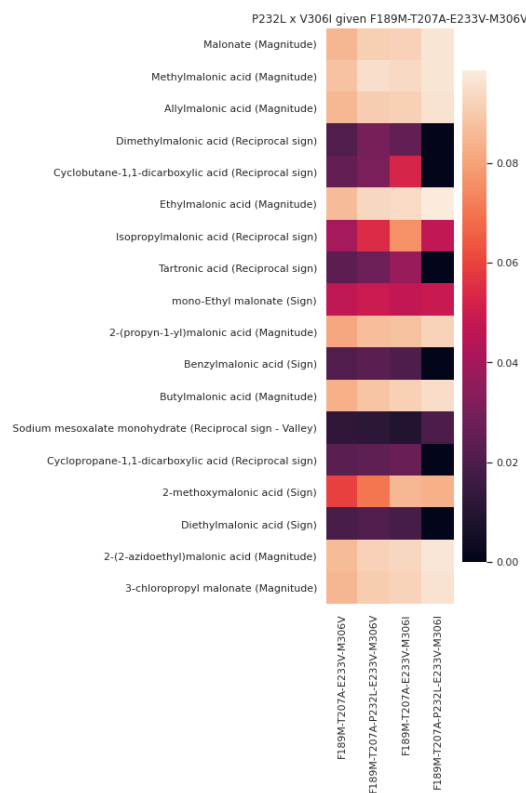
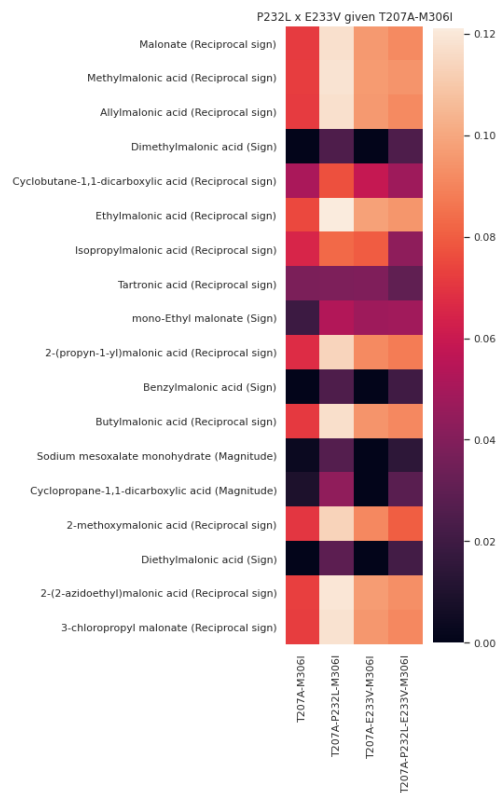
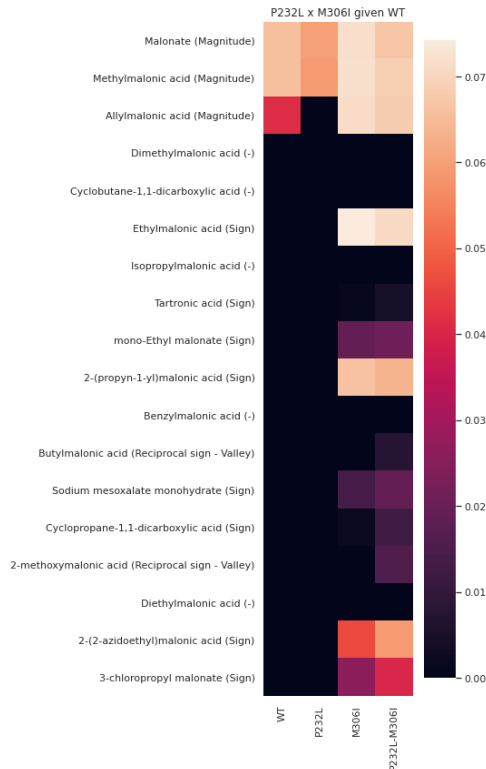
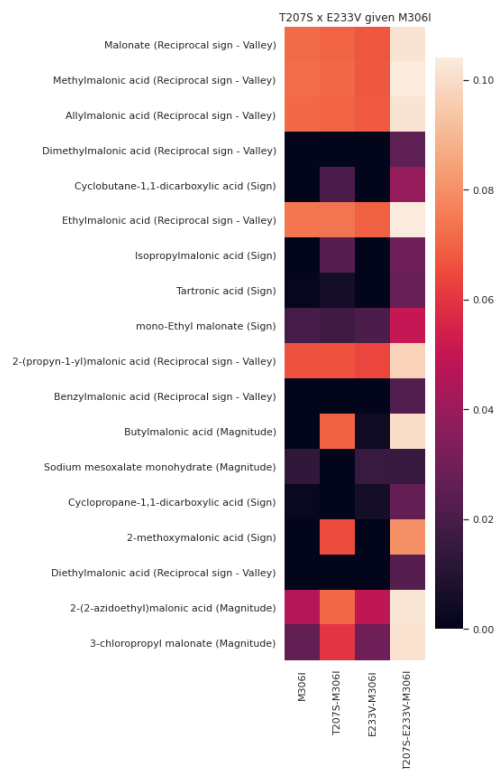


Figure S6. The top 5 active recombinants for all substrates contain mutations that are not directly beneficial given the WT or the M306I sequence.









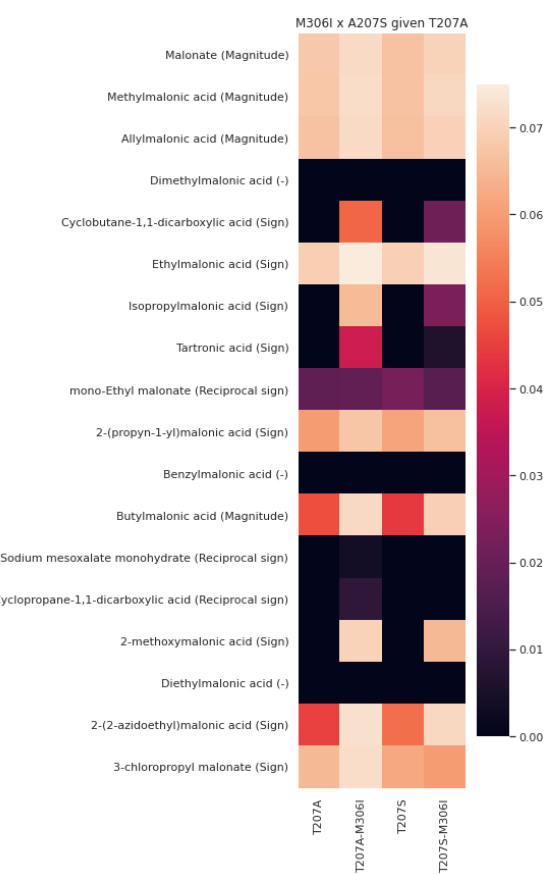
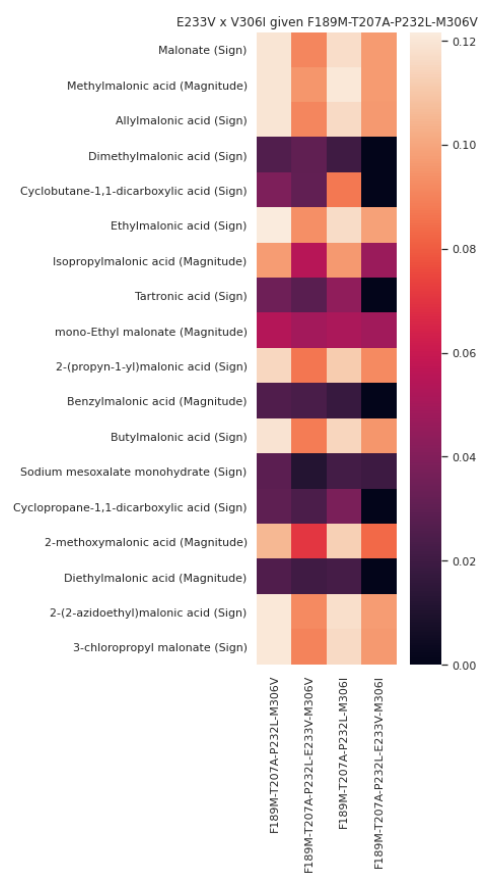
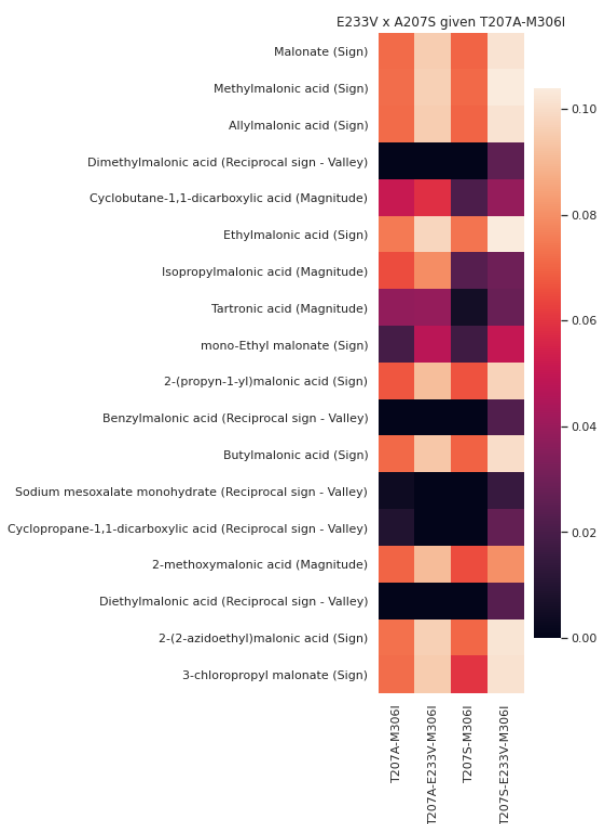
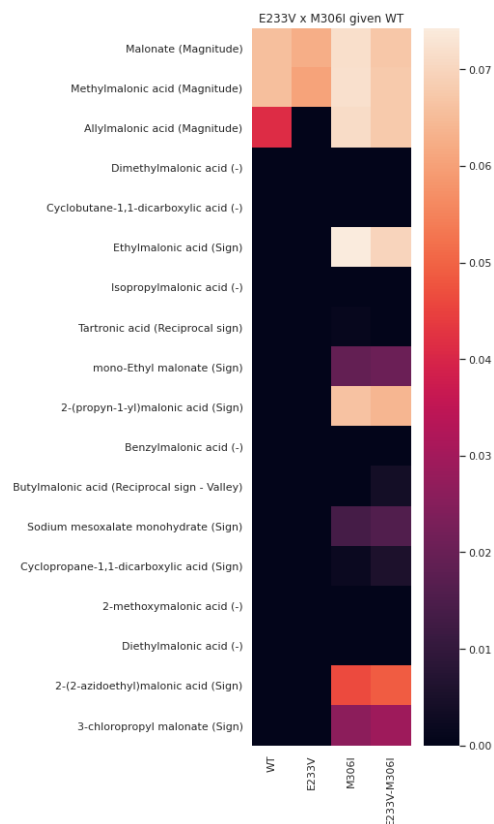


Figure S7. All possible pairwise epistasis in the sequence space of our assayed variants. Type of epistasis is widely substrate-dependent.

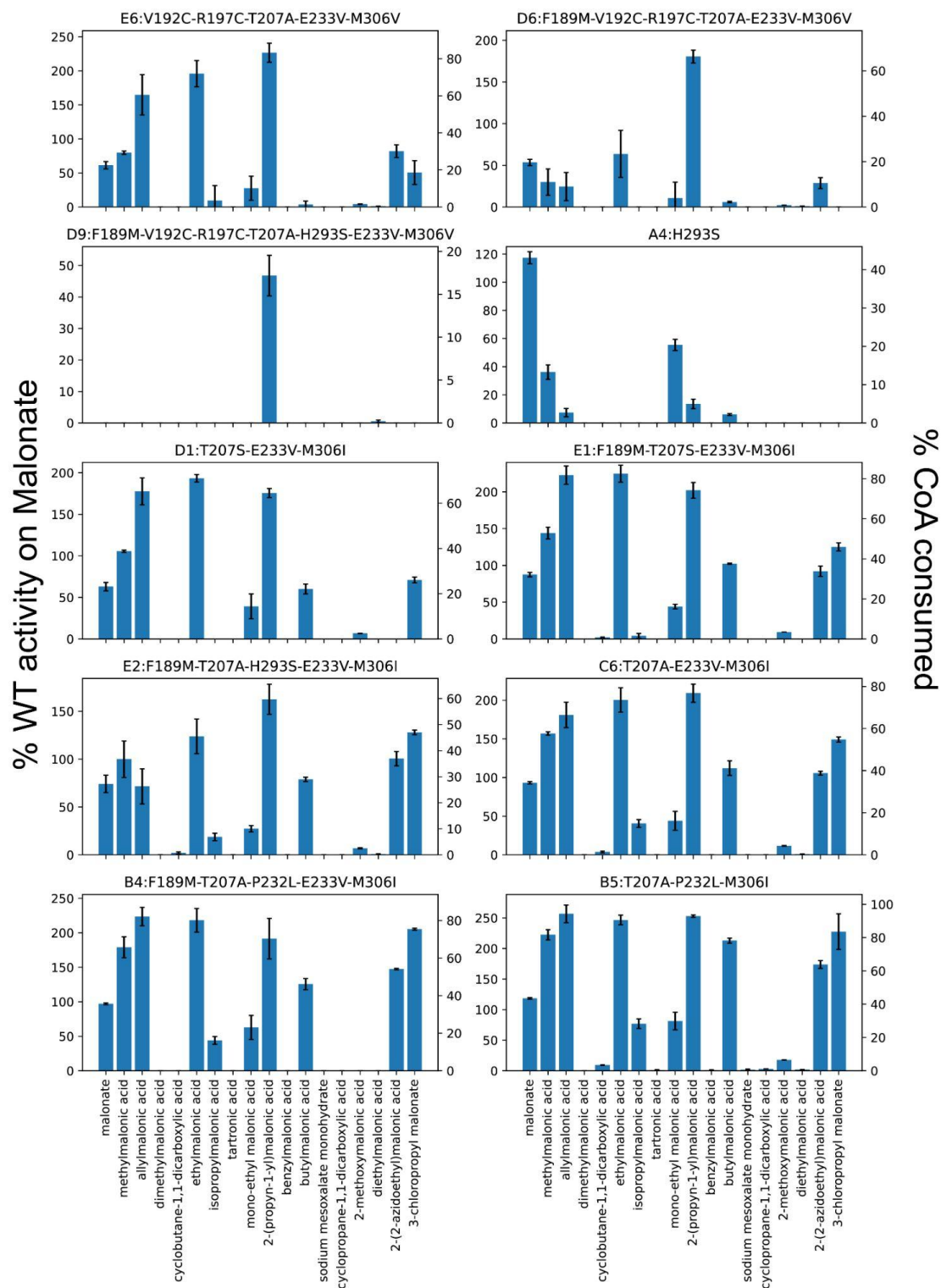


Figure S8. Complete specificity profile of 10 assayed purified recombinants.