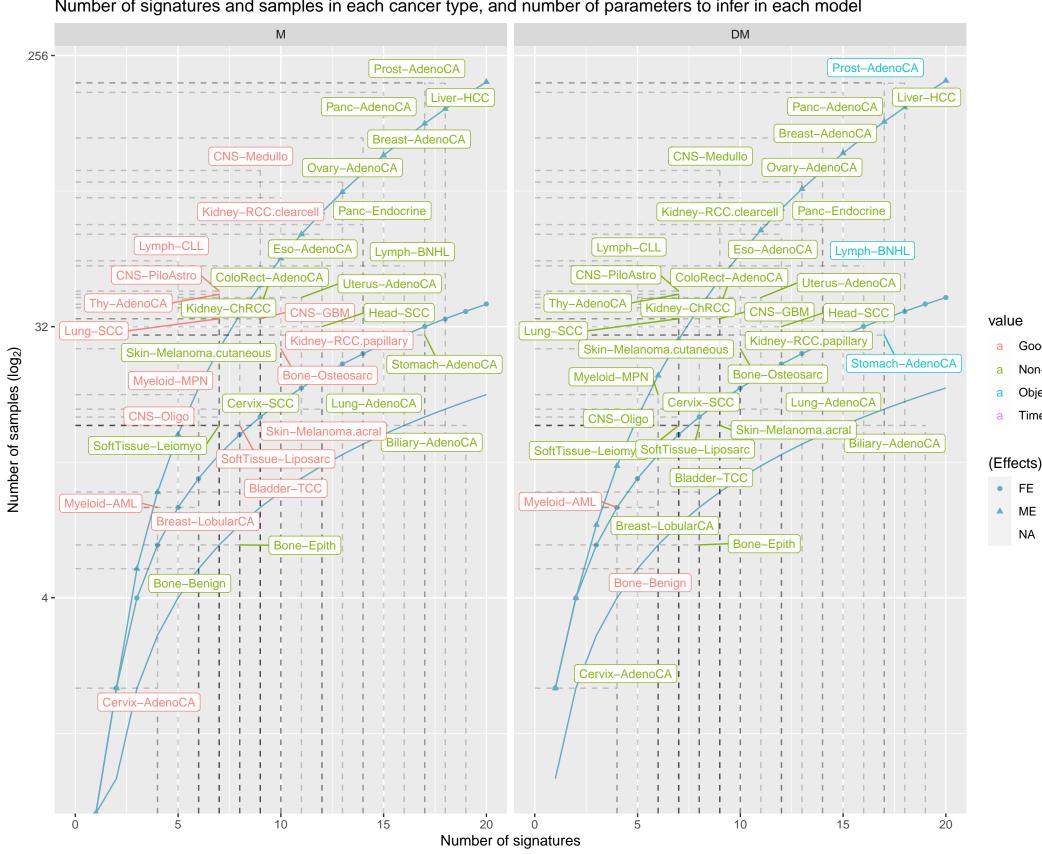Number of signatures and samples in each cancer type, and number of parameters to infer in each model