I have copied an Excel file (“41467\_2020\_16293\_MOESM4\_ESM.xlxs”) which has ~1500 genes involved in Hallmark of Cancer pathways. Can you please extract P/LP variants in these genes and create a binary variable (carrier/no-carrier)? Please create 2 variables – one including P/LP based on CliniVar and LOF only; and another further including P/LP variants classified by MetaSVM. In the final model for each outcome, we should also include this genetic variable, along with P/LP carrier status based on Zhaoming’s paper (cancer susceptibility genes) and Qin’s paper (DNA repair genes)

Na Qin 392 variants of which 386 were found in our data,