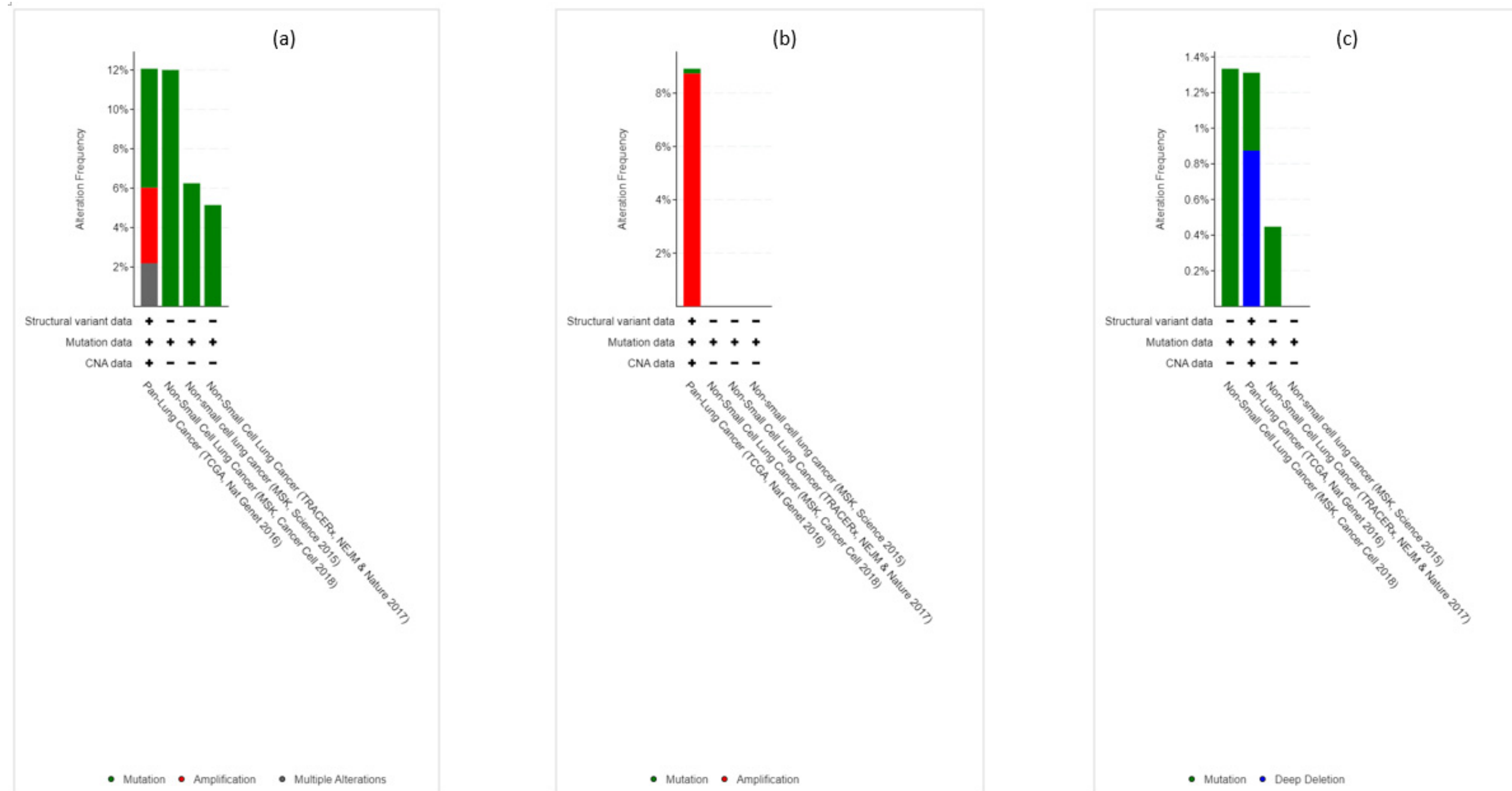


(A)



(B)

Figure S1. (A): The genomic alteration of the proposed 11 hub-DEGs among the NSCLC. The genomic mutations of the proposed genes are represented here where the infrared red color denotes the “inframe mutation”, infrared green color denotes “missense mutation” of known significance, infrared yellow color denotes “splice mutation”, infrared grey color denotes “Truncating mutation” of unknown significance, red color denotes “amplification” and blue color denotes “deep deletion” of unknown significance. (B) (a) EGFR (b) MYC and (c) CHEK1 alteration frequency over the four lung cancer studies.