



**S1 Fig.** Distribution of cumC ( $C$ ) for the 553 pan-cancer essential genes identified by CRISPR-Cas9 screenings in 324 cancer cell lines compared to non-essential genes. The red line is the average value of the  $cumC$  for the essential genes and the shadow represent the distribution of the average  $cumC$  of the non-essential genes by 10,000 times random sampling. The number of genes for each random sample is equal to the pan-cancer essential genes.