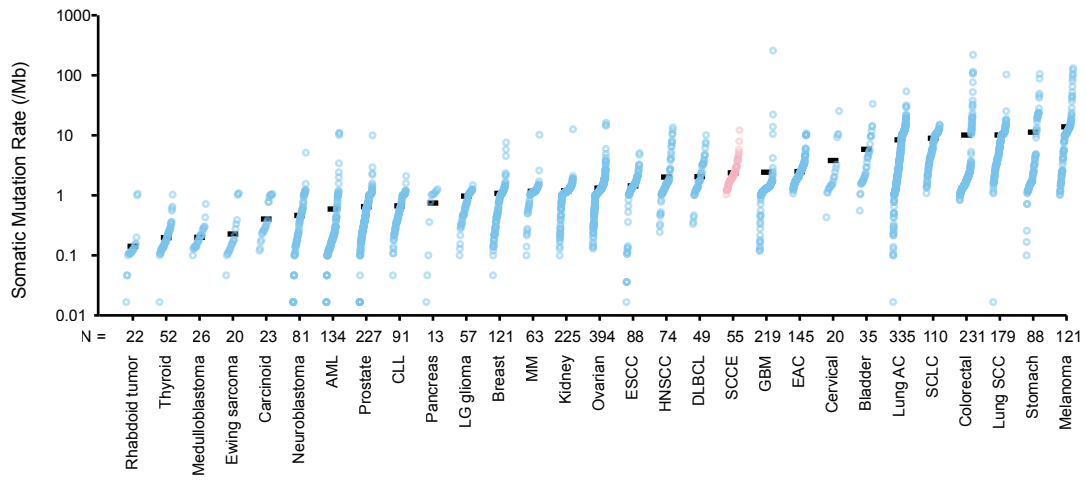


Figure S2



Supplementary information, Figure S2 Somatic mutation rates detected in exomes from SCCE and other human cancers. Each dot represents an examined tumor sample, and tumor types are ordered by their median somatic mutation rates (indicated by the black dash line). The number beneath X-axis indicates the number of examined cases of each cancer. Except SCCE, ESCC, HNSCC, EAC and SCLC, all of the other cancers were adopted from *Lin, D. C. et al*¹. CLL, chronic lymphocytic leukemia; MM, multiple myeloma; GBM, glioblastoma multiforme; DLBCL, diffuse large B-cell lymphoma; Lung AC, lung adenocarcinoma; Lung SCC, lung squamous cell carcinoma. WES denotes whole exome sequencing.

Reference

1. Lin DC, Hao JJ, Nagata Y *et al*. Genomic and molecular characterization of esophageal squamous cell carcinoma. *Nat Genet* 2014; **46**:467-473.