



**Figure 1 Distribution of chromosomal translocations in cancer genome.** Each dot represents a specific sample for different cancer types from pcawg database . The vertical axis shows translocation number per sample (log scaled) for each cancer type shown in the horizontal axis, and red lines are median number of translocations. 10 cancer types (SARC, BRCA, GBM, OV, LUSC, STAD, UCEC, HNSC, LIHC and SKCM) were selected for following analysis in this plot according to average translocation number and sample sizes.