

Cancer	AVG-DIS-CLS	Z_c-DIS
ACC	0.0318	0.001
BLCA	0.0104	0.016
BRCA	0.0246	0.002
GBMLGG	0.1544	0.207
HNSC	0.0231	0.154
KIPAN	0.2858	0.227
KIRC	0.0839	0.21
KIRP	0.2190	0.004
LGG	0.1072	0.141
LIHC	0.0585	0.025
LUAD	0.1717	0.062
LUSC	0.0169	0.010
MESO	0.0498	0.090
PAAD	0.0253	0.080
THYM	0.0416	0.020
UCEC	0.0274	0.270
UVM	0.0265	0.019

The names of 17 cancer types with positive random bias properties are listed in the first column of the table above. The average distance between each cluster proportion of the SSAR gene sets and 0.05 is displayed in the second column. For each cancer type, we used the following formula to determine this value:

$$\frac{\sum_{i=0}^n SSAR_{CL}(i) - 0.05}{n}$$

The second column represents the distance of proportion of SSAR gene sets after removing the effect of corresponding fixed-point set from 0.05.