

S6 Table. The average gravitation score of CRF CGC genes, non-CRF CGC genes and non-CGC CRF genes.

Cancer type	Average gravitation score \pm standard deviation			Adjusted p-value (q)		
	CRF CGC genes	Non-CRF CGC genes	Non-CGC CRF genes	I	II	III
BRCA	0.57 \pm 0.13	0.33 \pm 0.02	0.39 \pm 0.04	0.03	0.46	0.08
COAD	0.70 \pm 0.15	0.44 \pm 0.03	0.52 \pm 0.05	0.04	0.48	0.17
GBM	1.1 \pm 0.20	0.58 \pm 0.04	0.76 \pm 0.08	7.0 \times 10 ⁻⁴	0.13	0.06
HNSC	0.65 \pm 0.16	0.34 \pm 0.02	0.37 \pm 0.04	0.04	0.46	0.17
KIRC	1.9 \pm 0.64	0.53 \pm 0.04	0.74 \pm 0.08	6.8 \times 10 ⁻⁶	6.2 \times 10 ⁻³	0.04
LUAD	0.56 \pm 0.10	0.30 \pm 0.02	0.41 \pm 0.04	0.08	0.24	0.06
LUSC	0.39 \pm 0.07	0.23 \pm 0.02	0.29 \pm 0.03	0.03	0.46	0.09
OV	0.36 \pm 0.06	0.22 \pm 0.01	0.29 \pm 0.03	0.02	0.46	0.04
UCEC	0.82 \pm 0.28	0.42 \pm 0.03	0.47 \pm 0.05	0.04	0.46	0.06

The p-values in column **I** represent the Wilcoxon rank-sum test of average gravitation score between CRF CGC genes versus non-CRF CGC genes. The p-values in column **II** represent the Wilcoxon rank-sum test of average gravitation score between CRF CGC genes versus non-CGC CRF genes. The p-values in column **III** represent the Wilcoxon rank-sum test of average gravitation score between non-CRF CGC genes and non-CGC CRF genes. CRF: chromatin regulation factor, CGC: cancer gene census.