

P value adjustment method: bonferroni

biotype	sample_group	mean_nsites	median_nsites
five_prime_utr	SCR	604	615
five_prime_utr	shRNA33	678	681
five_prime_utr	shRNA37	740	754
intron	SCR	1960.33333	1986
intron	shRNA33	1859	1867
intron	shRNA37	1917.33333	1886
CDS	SCR	7776	7823
CDS	shRNA33	8035.33333	8059
CDS	shRNA37	9685	9765
three_prime_utr	SCR	10044.6667	10114
three_prime_utr	shRNA33	8942.33333	8846
three_prime_utr	shRNA37	10775	10826

Pairwise comparisons
using t tests with pooled SD

5'UTR:
KD-37 vs Control p= 0.0049 *

CDS:
KD-37 vs Control p=3.5e-05 *
KD-37 vs KD-33 p= 8.2e-05 *

3' UTR:
KD-37 vs KD-33 p=0.00011 *
KD-33 vs Control p=0.00194 *
KD-37 vs Control p=0.01551 *

biotype	sample_group	mean_nsites	median_nsites
five_prime_utr	SCR	604	615
five_prime_utr	shRNA	709	686.5
intron	SCR	1960.33333	1986
intron	shRNA	1888.16667	1878.5
CDS	SCR	7776	7823
CDS	shRNA	8860.16667	8725
three_prime_utr	SCR	10044.6667	10114
three_prime_utr	shRNA	9858.66667	9943.5

P value adjustment method:
bonferroni

Pairwise comparisons
using t tests with non-pooled SD

5'UTR: p=0.0037 *
Intro: p=0.17
CDS: p=0.035 *

3'UTR:p=0.68

