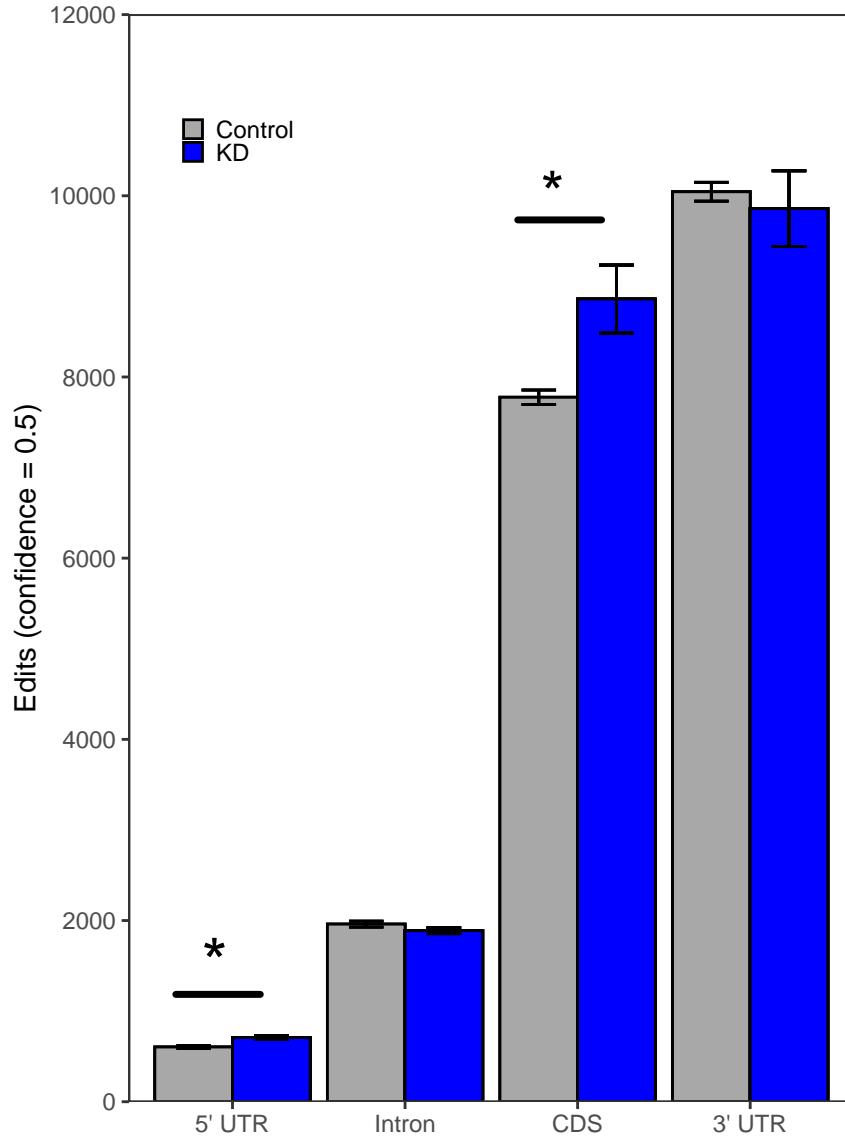


biotype	sample_group	mean_nsites	median_nsites
five_prime_utr	SCR	604	615
five_prime_utr	shRNA	709	686.5
intron	SCR	1960.33333	1986
intron	shRNA	1888.16667	1878.5
CDS	SCR	7776	7823
CDS	shRNA	8860.16667	8725
three_prime_utr	SCR	10044.66667	10114
three_prime_utr	shRNA	9858.66667	9943.5

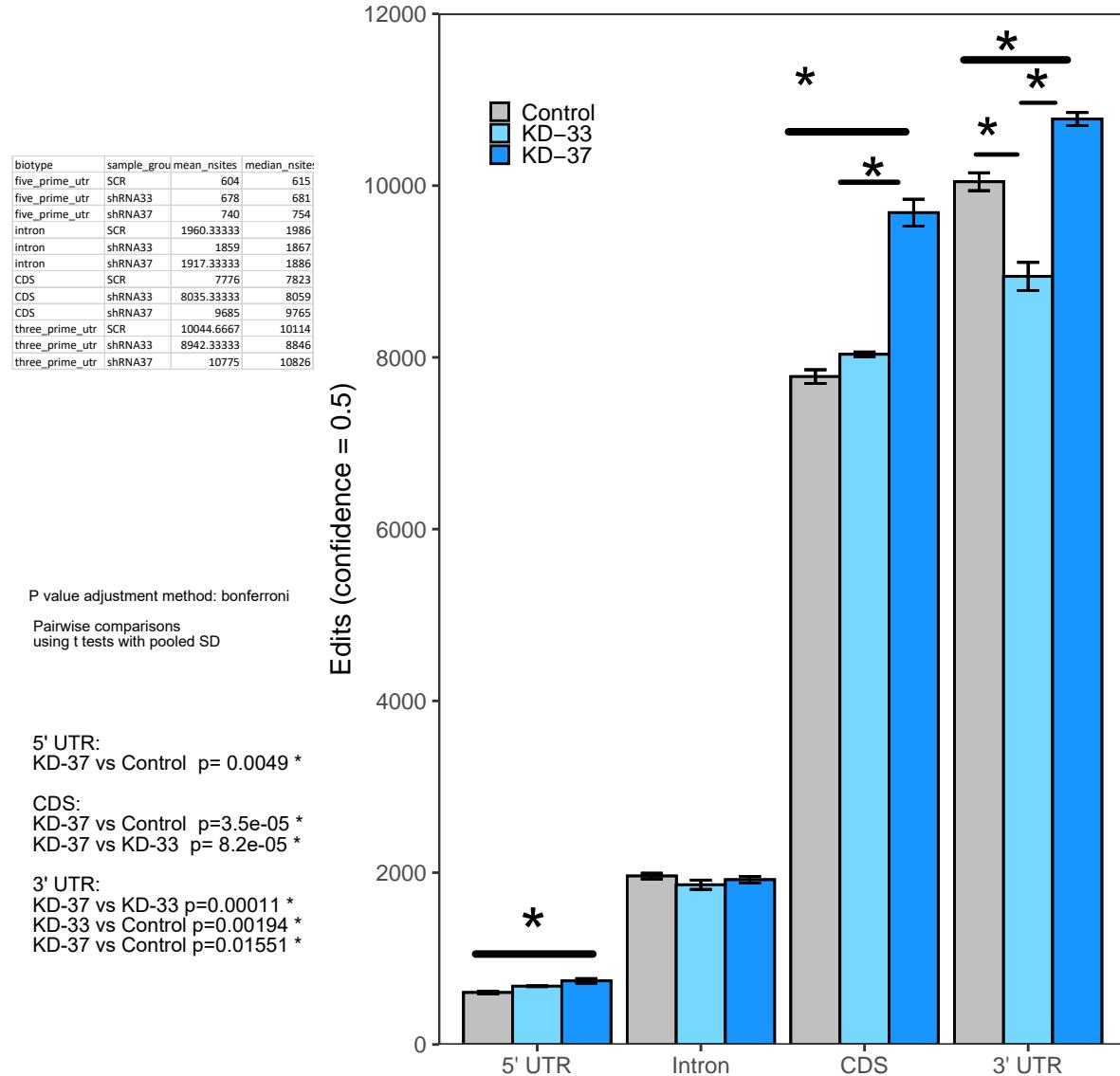


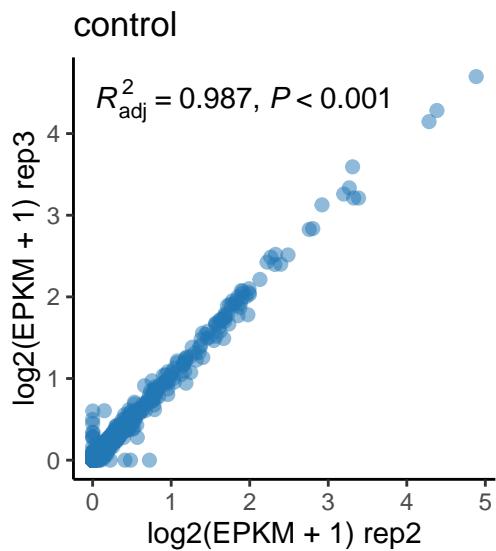
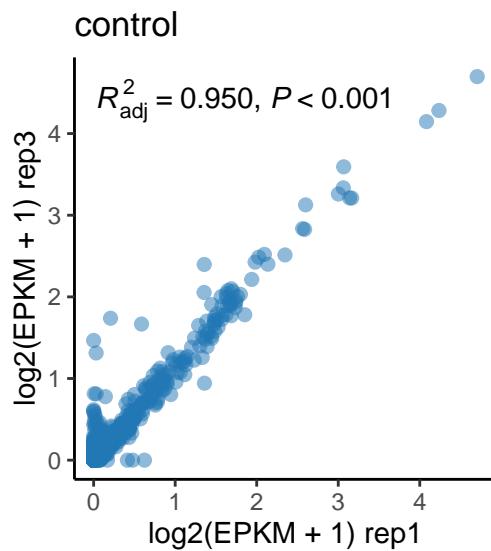
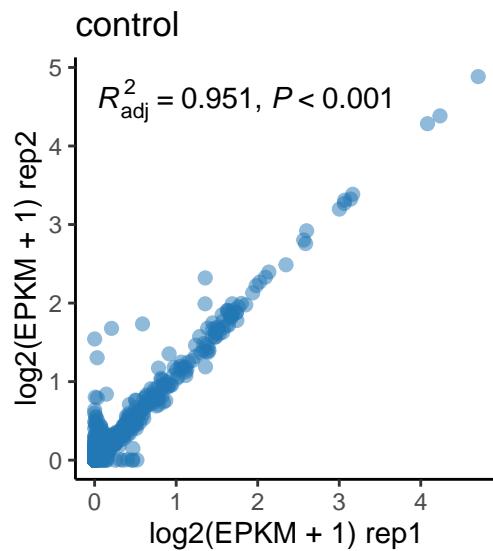
P value adjustment method:
bonferroni

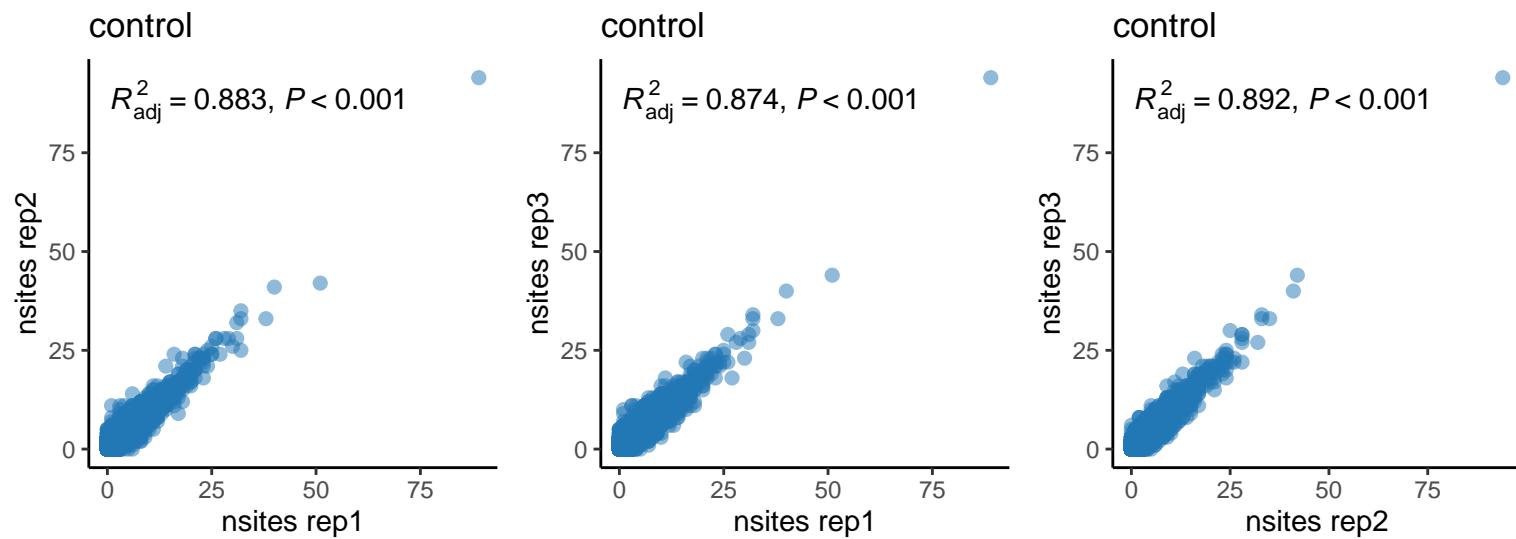
Pairwise comparisons
using t tests with non-pooled SD

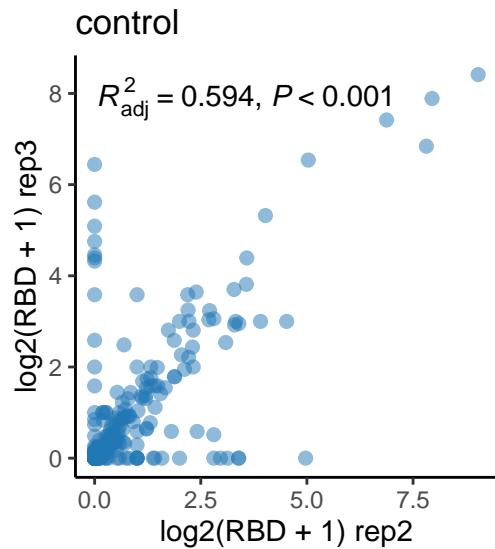
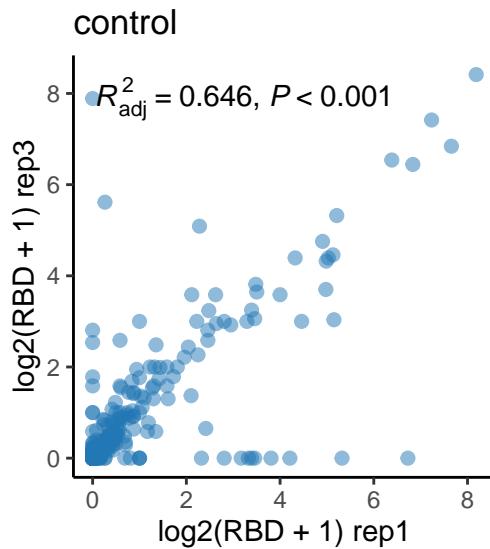
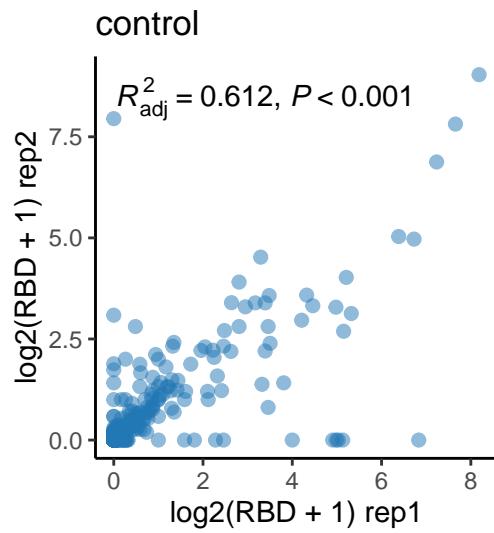
5'UTR: p=0.0037 *
Intro: p=0.17
CDS: p=0.035 *

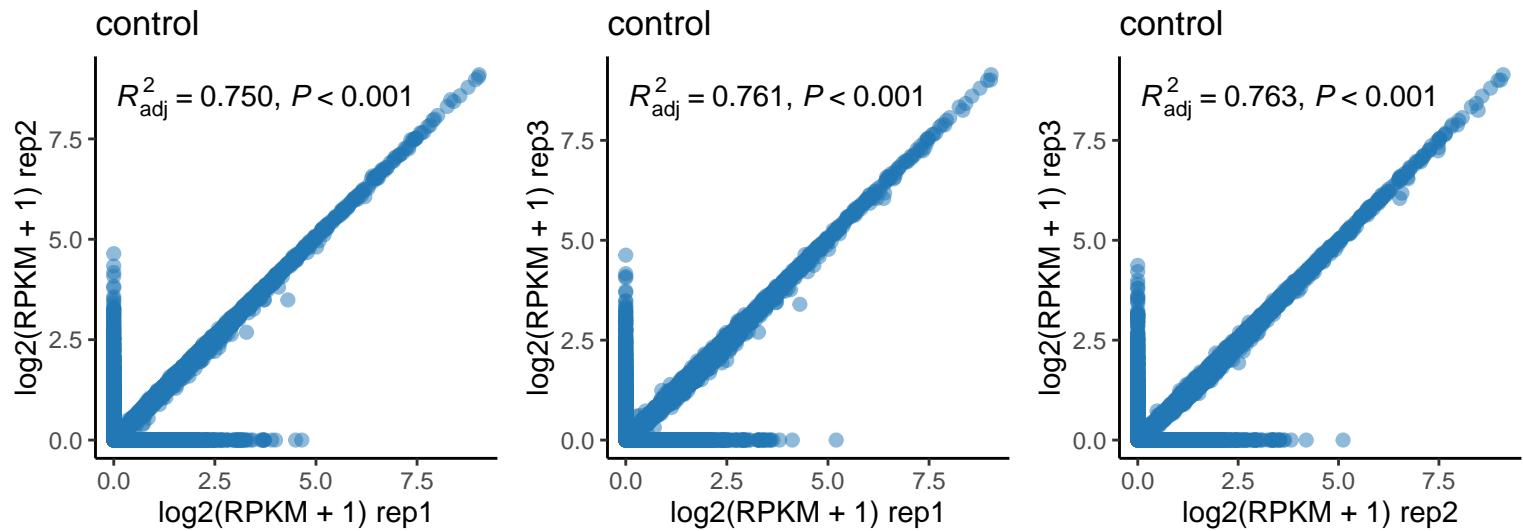
3'UTR:p=0.68

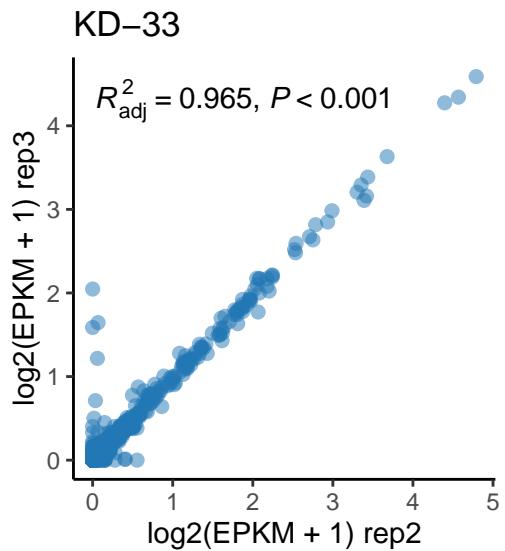
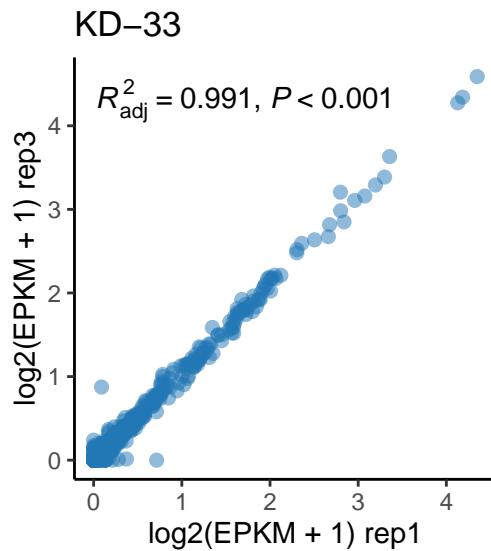
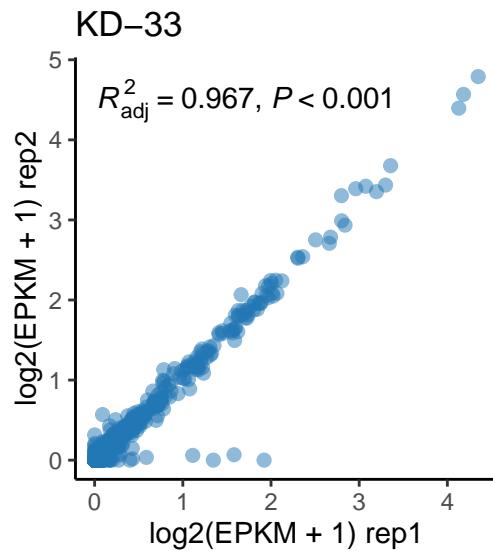


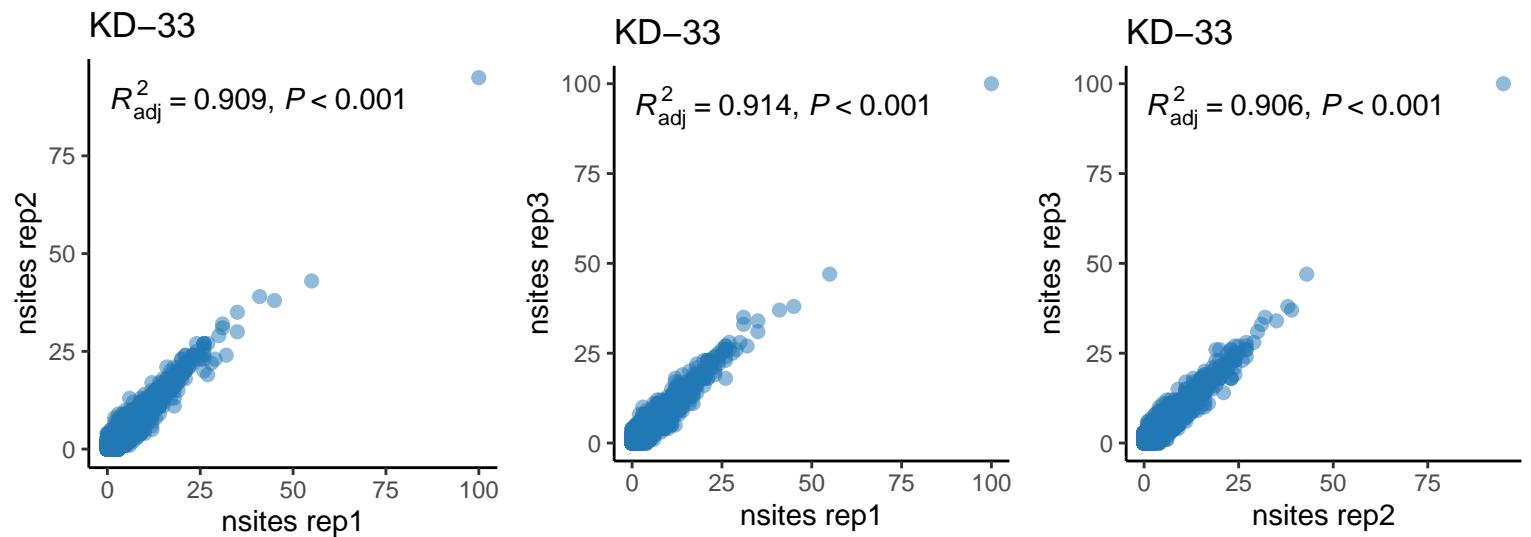


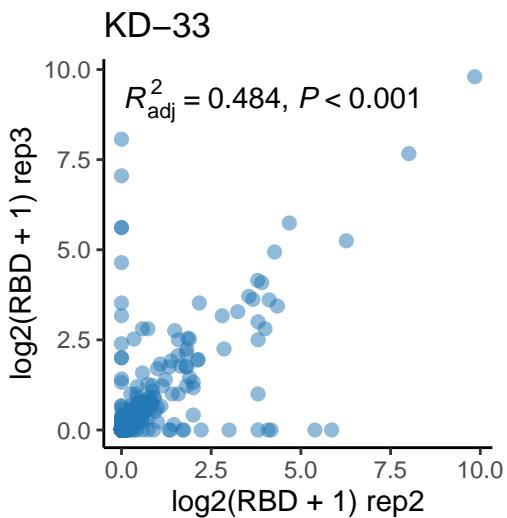
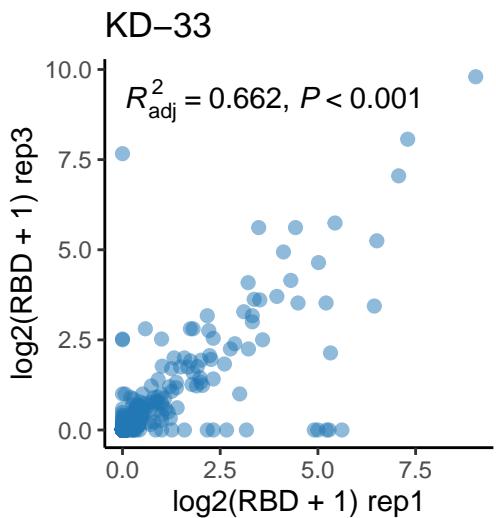
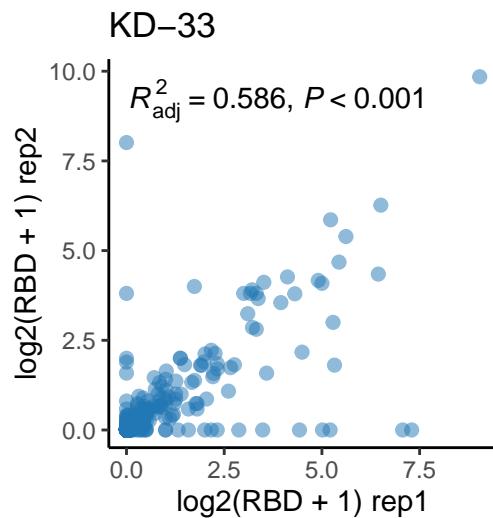


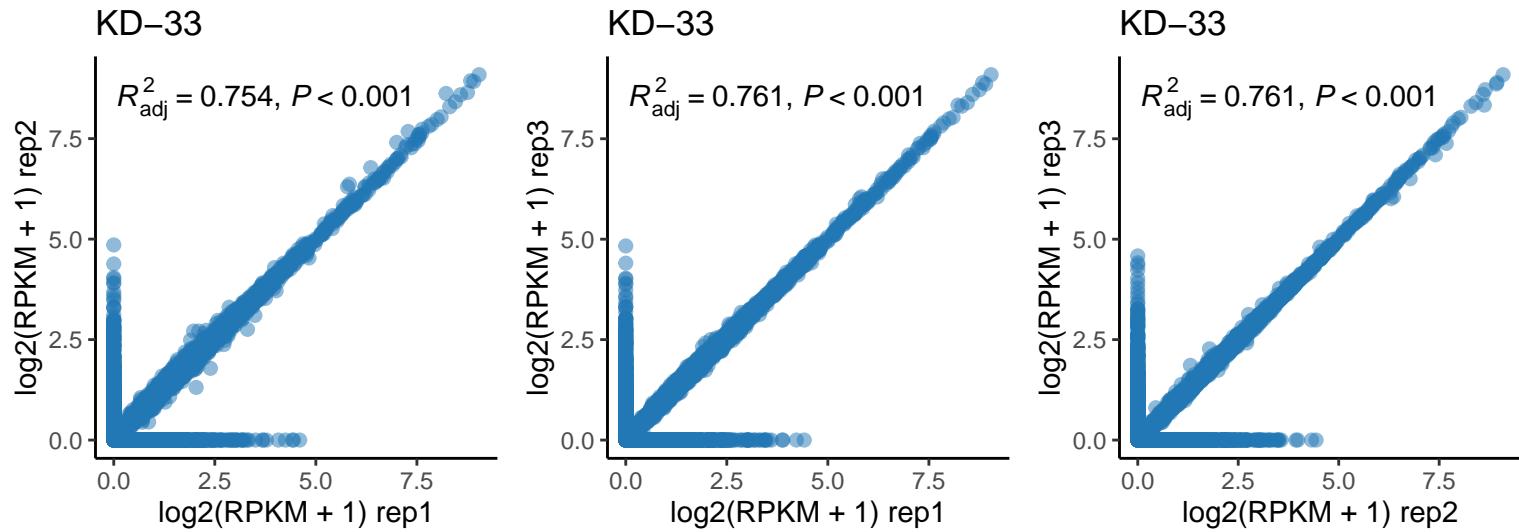


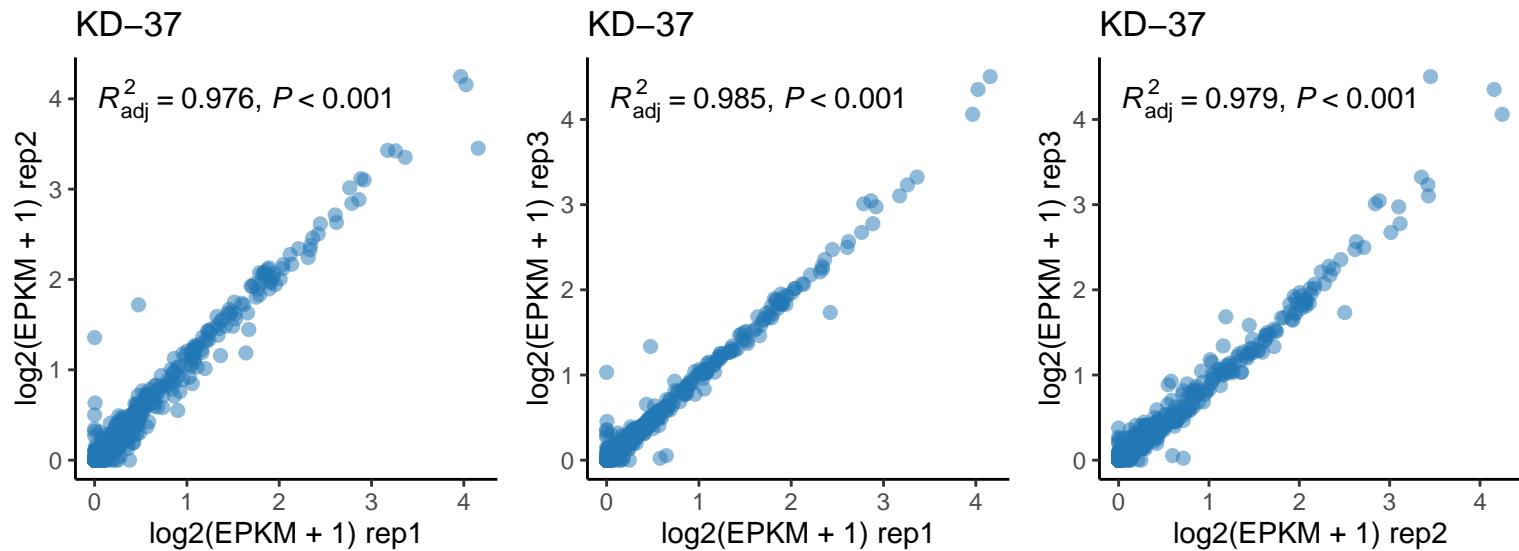


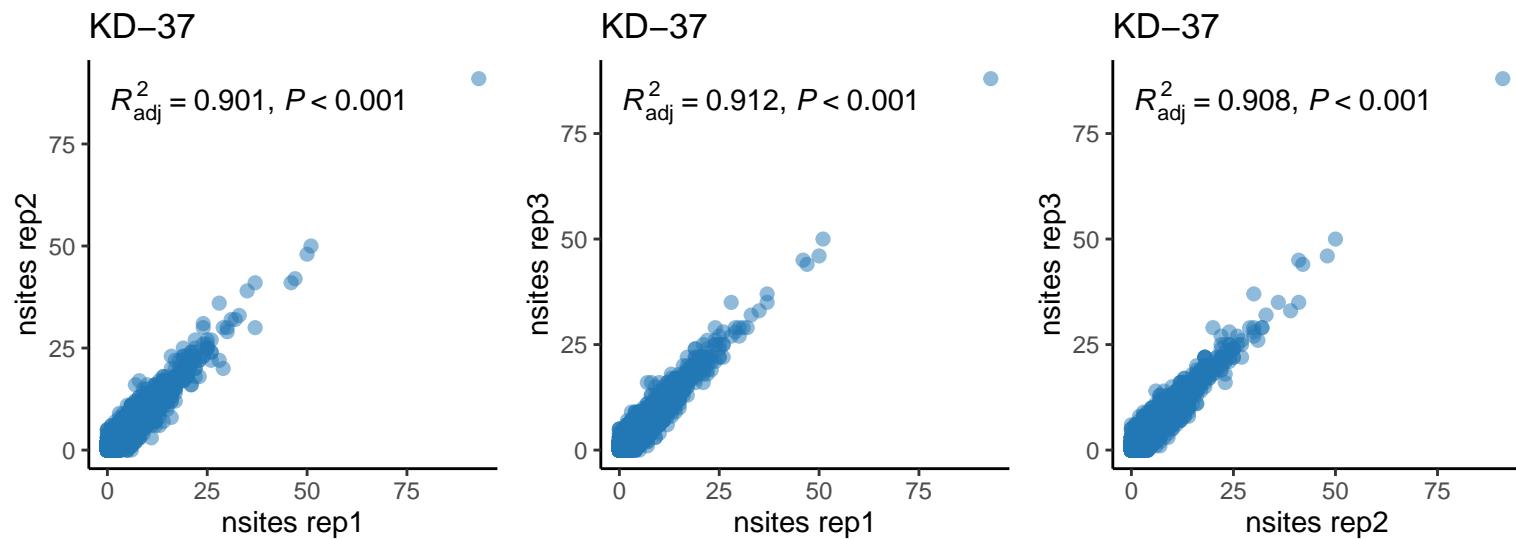


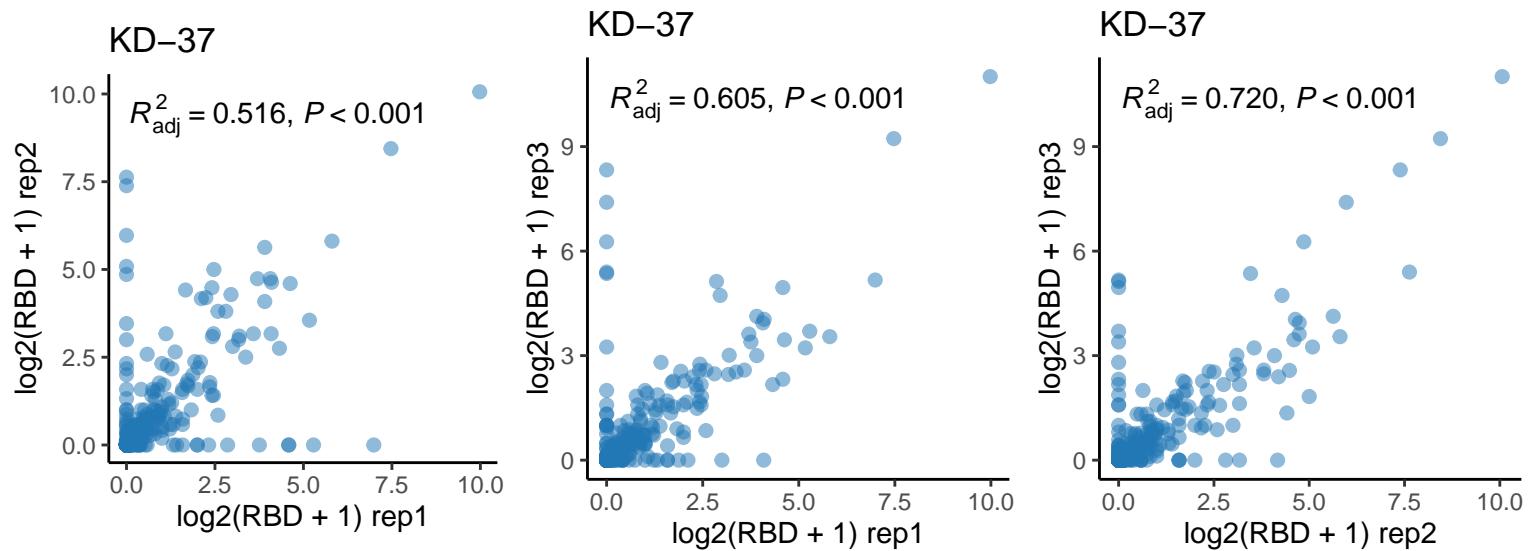


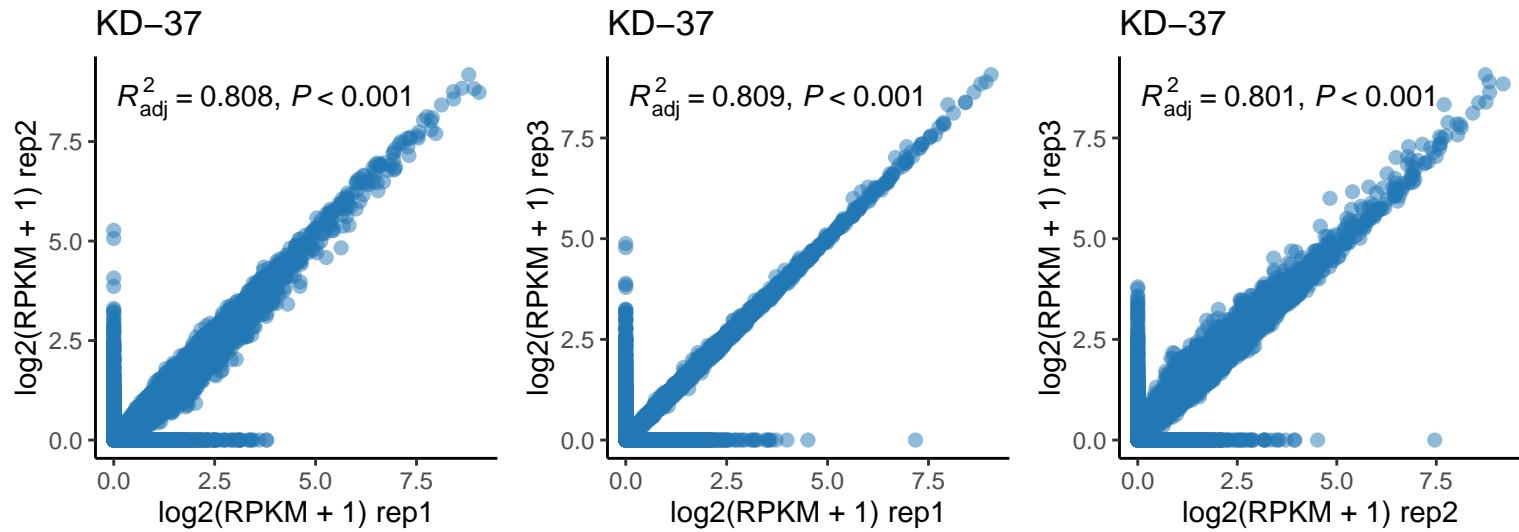


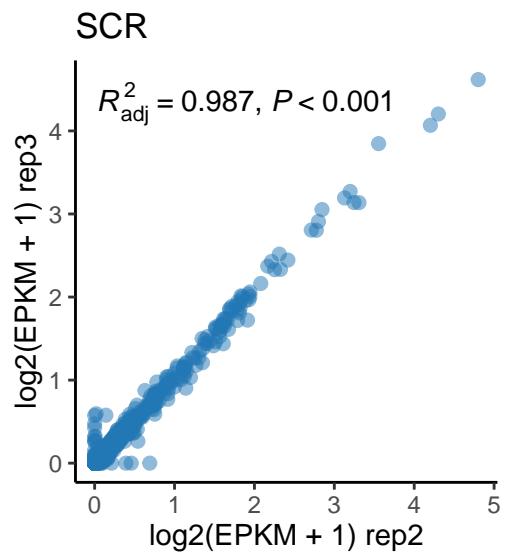
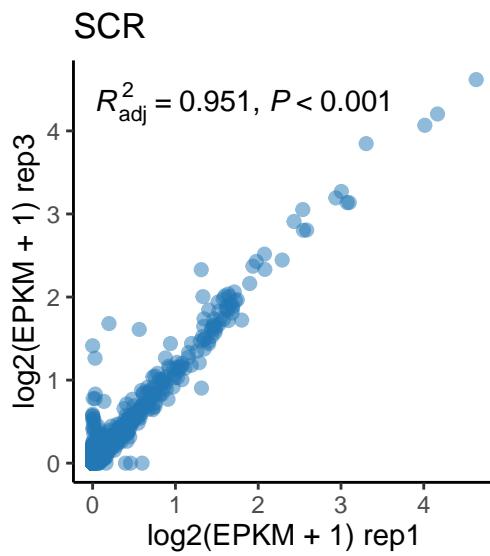
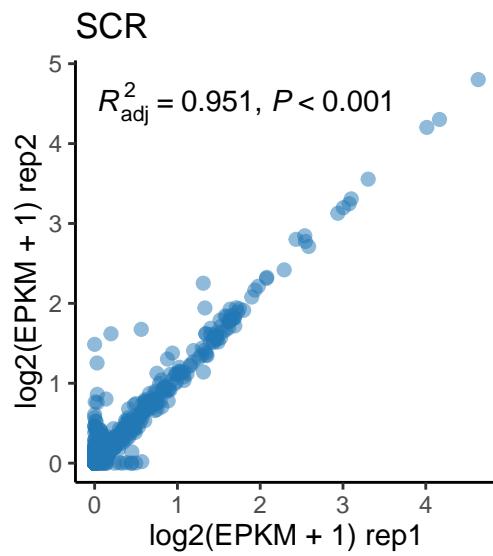










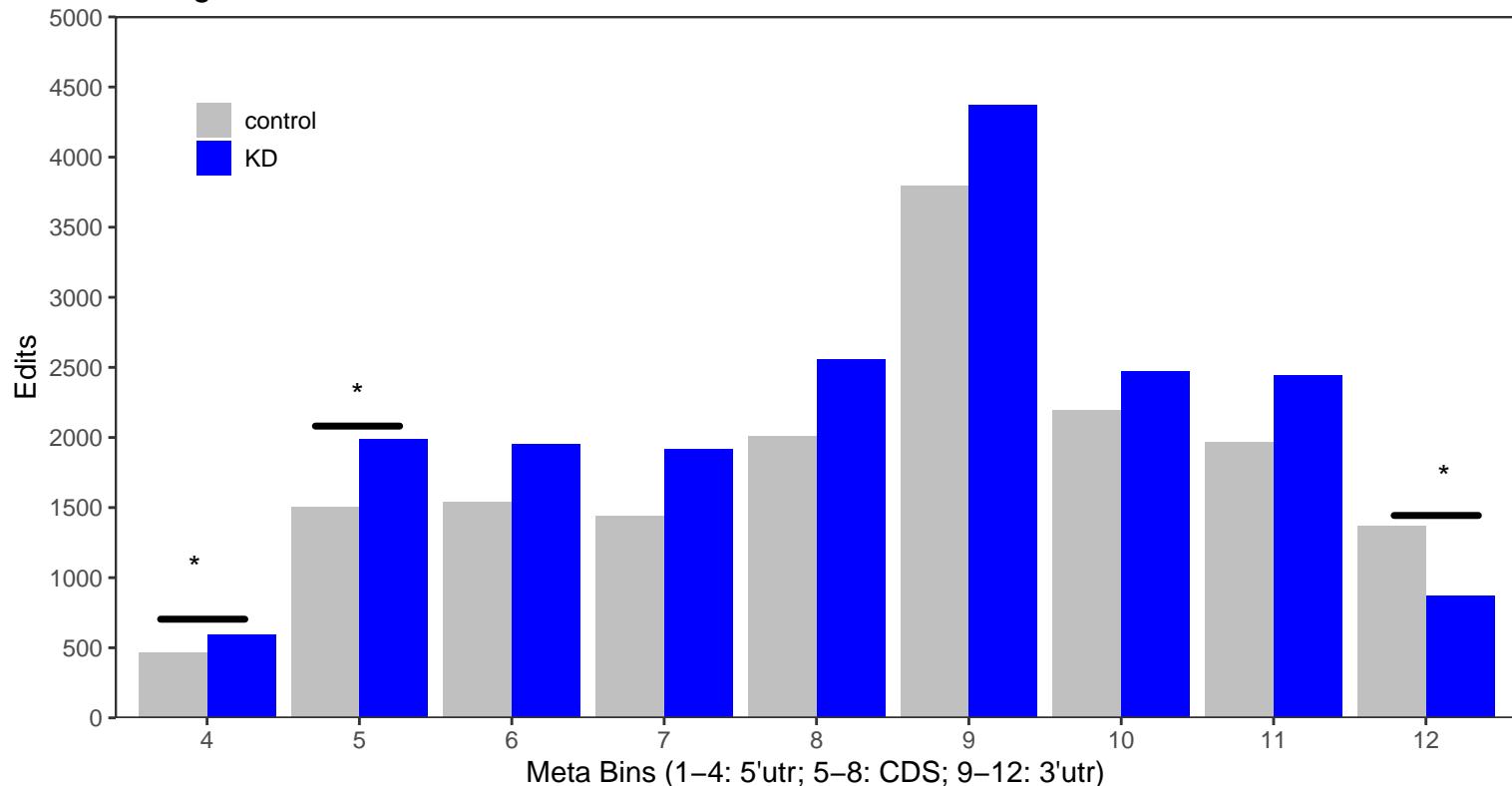


bin 4: KD vs control p= *

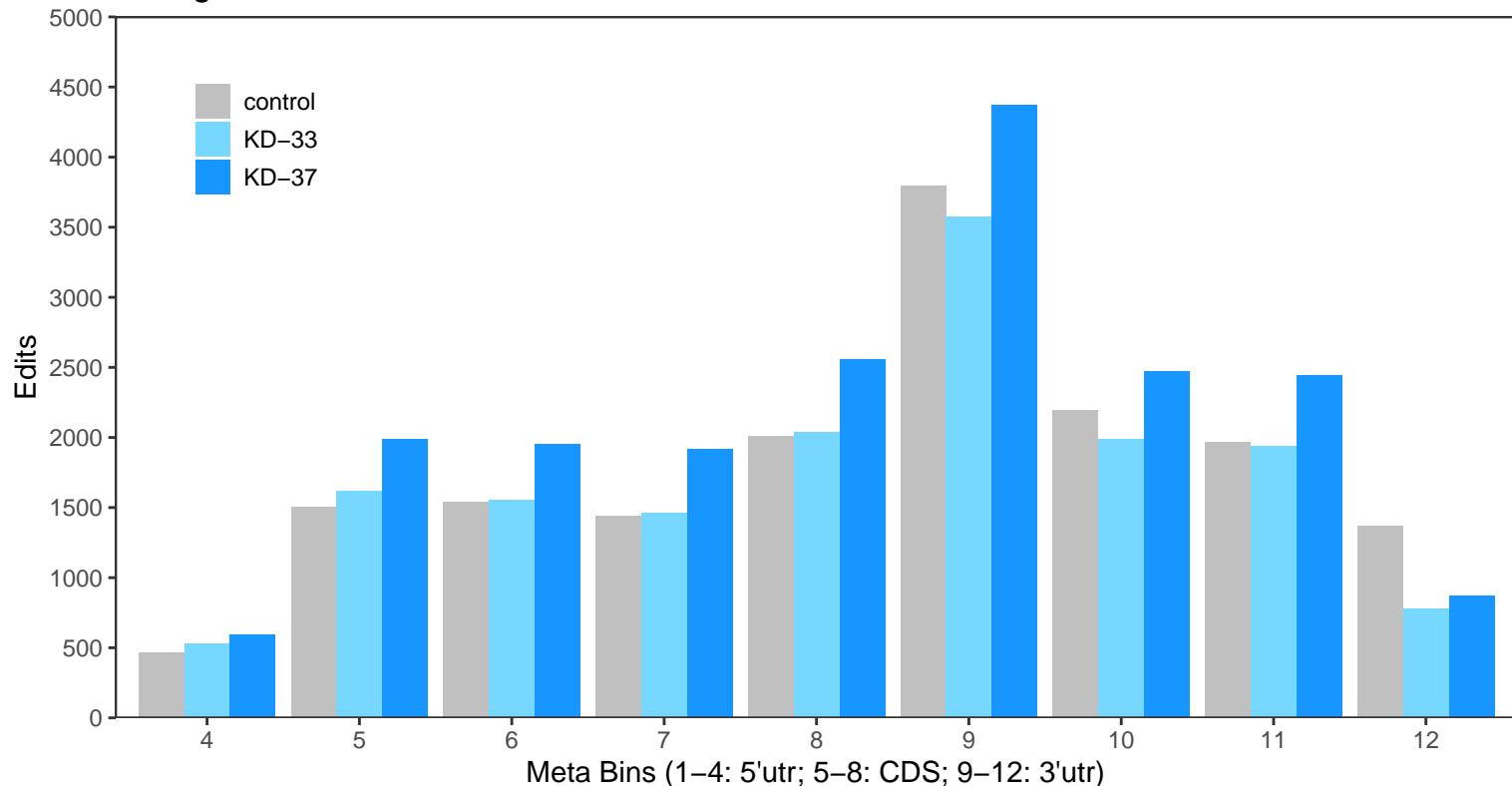
bin 5: KD vs control p=

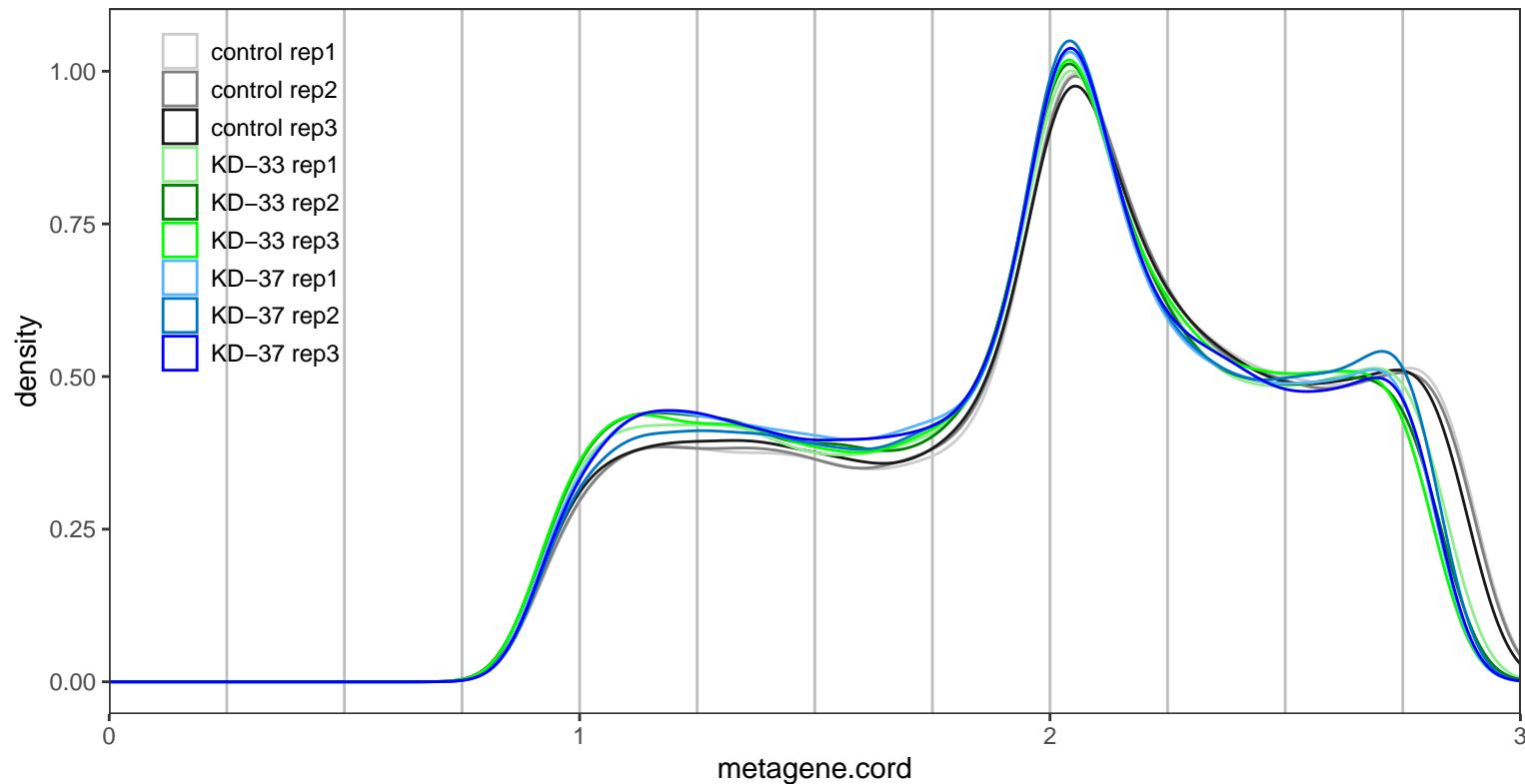
bin 12:KD vs control p

Metagene Bar Plot

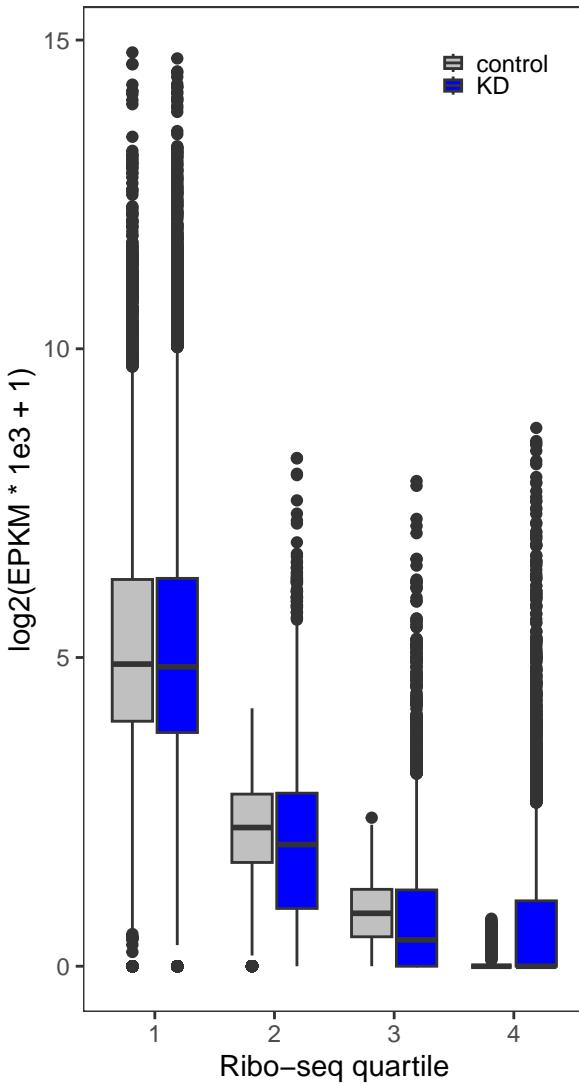


Metagene Bar Plot





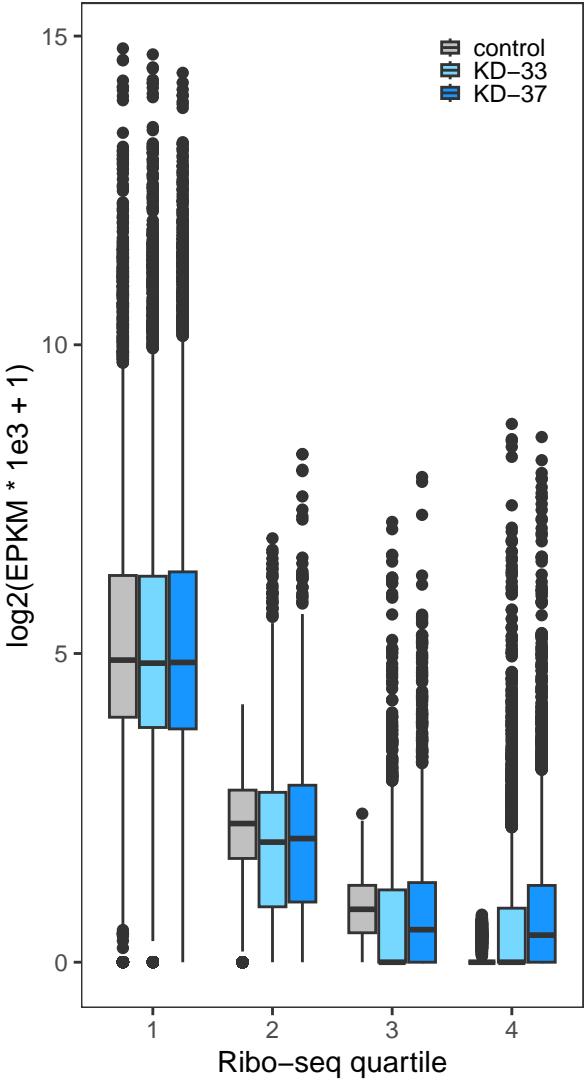
Rank by control EPKM value



bin	group1	group2	p.adj	p.adj.signif
1	SCR	shRNA	3.16E-05	****
2	SCR	shRNA	1.18E-45	****
3	SCR	shRNA	3.18E-97	****
4	SCR	shRNA	0	****

bin	combined_group	mean_EPKM	median_EPKM
1	SCR	209.115521	28.7211561
1	shRNA	220.32946	27.8296628
2	SCR	4.267667	3.74355546
2	shRNA	4.67087634	2.9221731
3	SCR	0.92210751	0.81159089
3	shRNA	1.2651697	0.34381469
4	SCR	0.0352692	0
4	shRNA	1.82307446	0

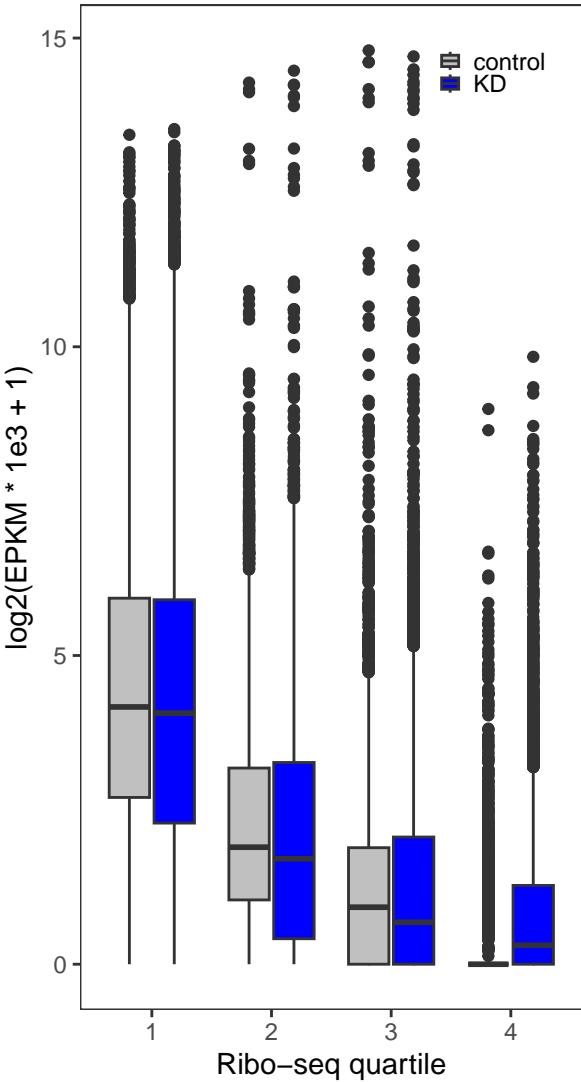
Rank by control EPKM value



bin	group1	group2	p.adj	p.adj.signif
1	SCR	shRNA33	0.001	**
1	SCR	shRNA37	0.00072	***
2	SCR	shRNA33	2.4E-47	****
2	SCR	shRNA37	3.7E-23	****
2	shRNA33	shRNA37	0.00019	***
3	SCR	shRNA33	1E-102	****
3	SCR	shRNA37	2.2E-46	****
3	shRNA33	shRNA37	3.4E-10	****
4	SCR	shRNA33	0	****
4	SCR	shRNA37	0	****
4	shRNA33	shRNA37	2.6E-49	****

bin	sample_group	mean_EPKM	median_EPKM
1	SCR	209.1155214	28.7211561
1	shRNA33	226.3052048	27.3103542
1	shRNA37	214.13537151	27.9336983
2	SCR	4.267666999	3.74355546
2	shRNA33	4.287526467	2.85075594
2	shRNA37	5.054226212	3.00777181
3	SCR	0.92210751	0.81159089
3	shRNA33	1.144735549	0
3	shRNA37	1.38560386	0.44128227
4	SCR	0.035269202	0
4	shRNA33	1.577129213	0
4	shRNA37	2.069019701	0.3556724

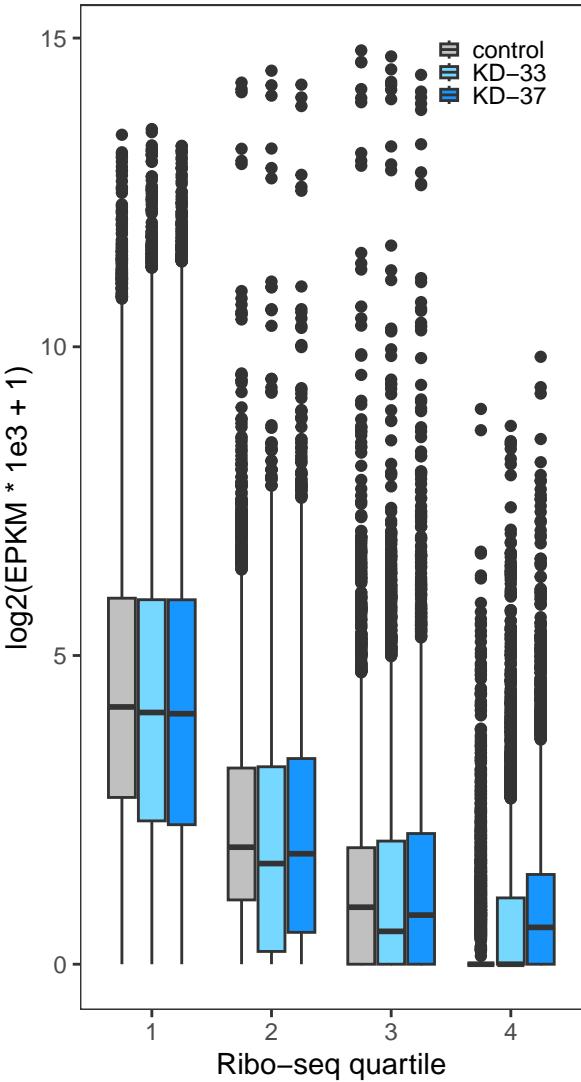
Rank by control nsites value



bin	group1	group2	p.adj	p.adj.signif
1	SCR	shRNA	3.99E-09	****
2	SCR	shRNA	1.04E-32	****
3	SCR	shRNA	1.24E-26	****
4	SCR	shRNA	0	****

bin	combined_group	mean_EPKM	median_EPKM
1	SCR	154.06647	16.9594773
1	shRNA	170.093152	15.7520645
2	SCR	26.7828349	2.7201037
2	shRNA	25.9625116	2.26829746
3	SCR	32.9207959	0.89662995
3	shRNA	29.5491392	0.60086734
4	SCR	0.57046449	0
4	shRNA	2.48377775	0.23674702

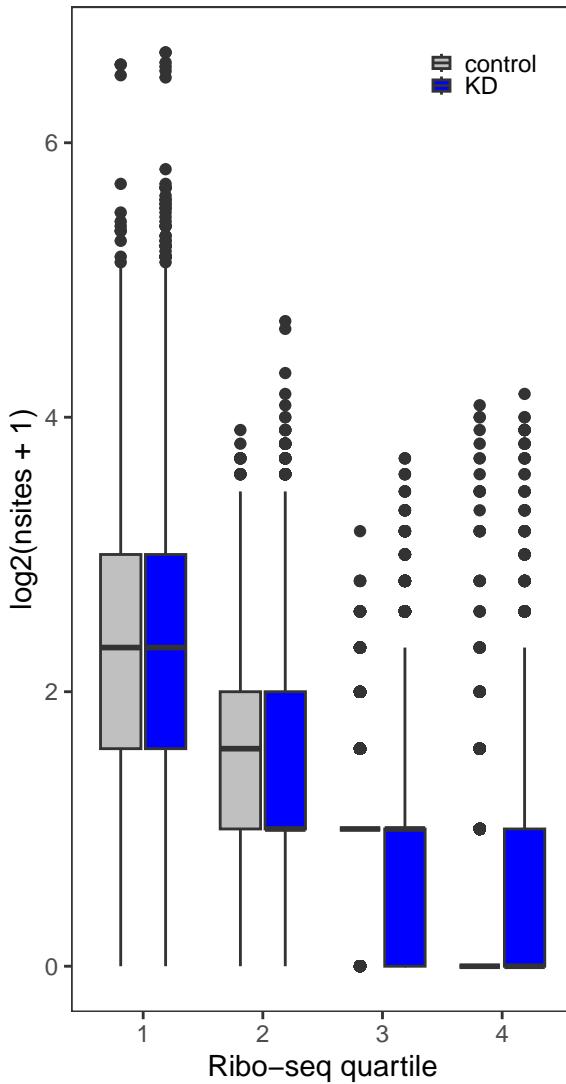
Rank by control nsites value



bin	group1	group2	p.adj	p.adj.signif
1	SCR	shRNA33	0.00000918	****
1	SCR	shRNA37	9.9E-08	****
2	SCR	shRNA33	4.62E-35	****
2	SCR	shRNA37	9.6E-16	****
2	shRNA33	shRNA37	0.000312	***
3	SCR	shRNA33	1.28E-34	****
3	SCR	shRNA37	4.56E-09	****
3	shRNA33	shRNA37	2.53E-08	****
4	SCR	shRNA33	0	***
4	SCR	shRNA37	0	***
4	shRNA33	shRNA37	4.41E-46	****

bin	sample_group	mean_EPKM	median_EPKM
1	SCR	154.06647	16.9594773
1	shRNA33	172.786499	15.8765002
1	shRNA37	167.399805	15.6476622
2	SCR	26.7828349	2.7201037
2	shRNA33	26.5215935	2.09582635
2	shRNA37	25.4034296	2.45572002
3	SCR	32.9207959	0.89662995
3	shRNA33	31.9050094	0.44634198
3	shRNA37	27.193269	0.73609541
4	SCR	0.57046449	0
4	shRNA33	2.10149378	0
4	shRNA37	2.86606171	0.51230889

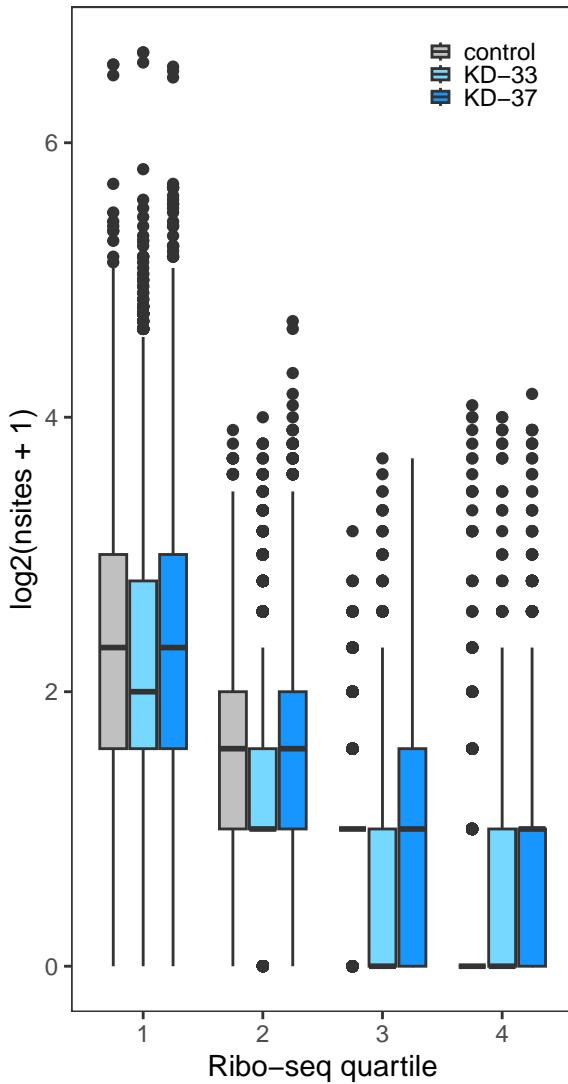
Rank by control EPKM value



bin	group1	group2	p.adj	p.adj.signif
2	SCR	shRNA	2.6E-39	****
3	SCR	shRNA	2.63E-111	****
4	SCR	shRNA	0	****

bin	combined_gr	mean_nsites	median_nsites
1	SCR	5.27929688	4
1	shRNA	5.47281901	4
2	SCR	2.18335776	2
2	shRNA	2.00464094	1
3	SCR	1.08272268	1
3	shRNA	0.93201433	1
4	SCR	0.15860609	0
4	shRNA	0.73400098	0

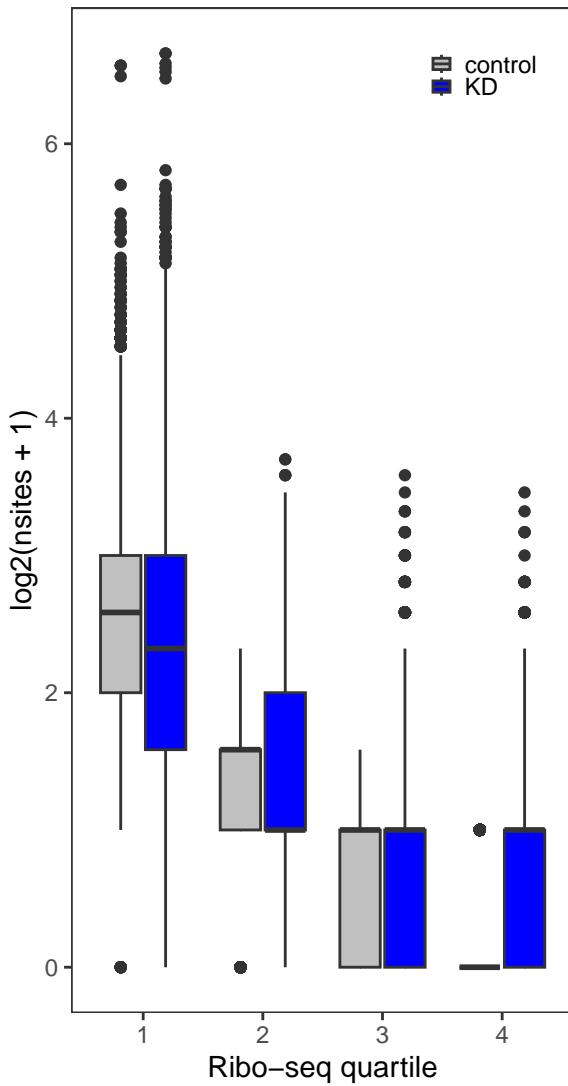
Rank by control EPKM value



bin	group1	group2	p.adj	p.adj.signif
1	SCR	shRNA33	4.59E-08	****
1	SCR	shRNA37	0.0000017	****
1	shRNA33	shRNA37	3.33E-24	****
2	SCR	shRNA33	1.91E-65	****
2	SCR	shRNA37	5.52E-08	****
2	shRNA33	shRNA37	8.85E-23	****
3	SCR	shRNA33	2.8E-135	****
3	SCR	shRNA37	5.22E-45	****
3	shRNA33	shRNA37	4.23E-17	****
4	SCR	shRNA33	0	****
4	SCR	shRNA37	0	****
4	shRNA33	shRNA37	3.87E-61	****

bin	sample_group	mean_nsites	median_nsites
1	SCR	5.27929688	4
1	shRNA33	5.07617188	3
1	shRNA37	5.86946615	4
2	SCR	2.18335776	2
2	shRNA33	1.80328937	1
2	shRNA37	2.20599251	2
3	SCR	1.08272268	1
3	shRNA33	0.82152744	0
3	shRNA37	1.04250122	1
4	SCR	0.15860609	0
4	shRNA33	0.59159746	0
4	shRNA37	0.87640449	1

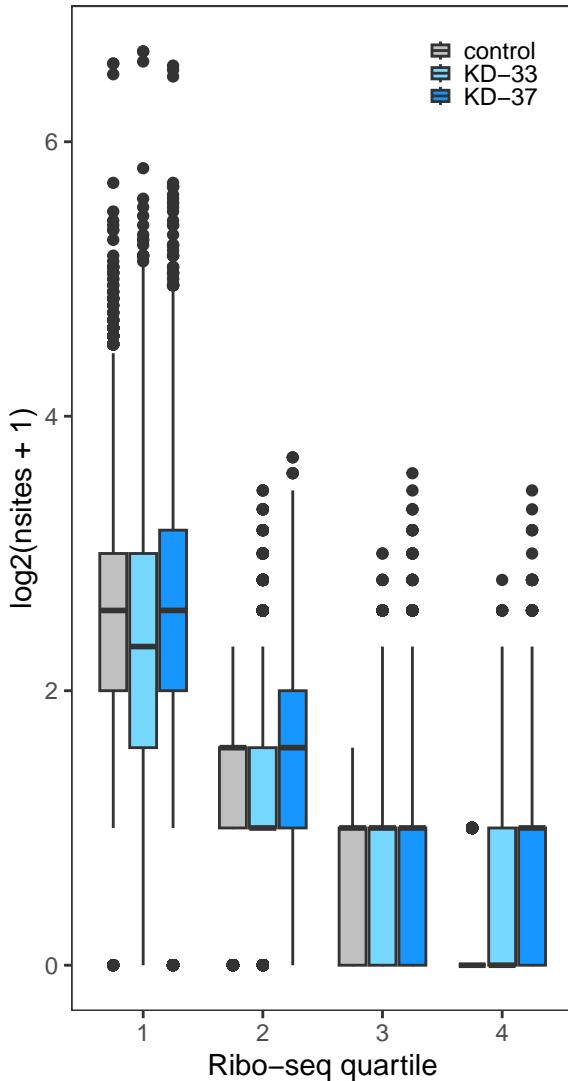
Rank by control nsites value



bin	group1	group2	p.adj	p.adj.signif
1	SCR	shRNA	4.79E-29	****
2	SCR	shRNA	4.58E-49	****
3	SCR	shRNA	1.07E-08	****
4	SCR	shRNA	0	****

bin	combined_grc	mean_nsites	median_nsites
1	SCR	6.06233724	5
1	shRNA	5.84822591	4
2	SCR	1.78798241	2
2	shRNA	1.72699886	1
3	SCR	0.76437062	1
3	shRNA	0.86940238	1
4	SCR	0.0889106	0
4	shRNA	0.69866471	1

Rank by control nsites value



bin	group1	group2	p.adj	p.adj.signif
1	SCR	shRNA33	2.65E-53	****
1	SCR	shRNA37	0.000231	***
1	shRNA33	shRNA37	7.8E-20	****
2	SCR	shRNA33	1.91E-103	****
2	SCR	shRNA37	0.000133	***
2	shRNA33	shRNA37	3.36E-38	****
3	SCR	shRNA33	5.25E-29	****
3	shRNA33	shRNA37	3.18E-21	****
4	SCR	shRNA33	0	****
4	SCR	shRNA37	0	****
4	shRNA33	shRNA37	4.83E-63	****

bin	sample_group	mean_nsites	median_nsites
1	SCR	6.06233724	5
1	shRNA33	5.45849609	4
1	shRNA37	6.23795573	5
2	SCR	1.78798241	2
2	shRNA33	1.51359713	1
2	shRNA37	1.94040059	2
3	SCR	0.76437062	1
3	shRNA33	0.76176518	1
3	shRNA37	0.97703957	1
4	SCR	0.0889106	0
4	shRNA33	0.55854095	0
4	shRNA37	0.83878847	1