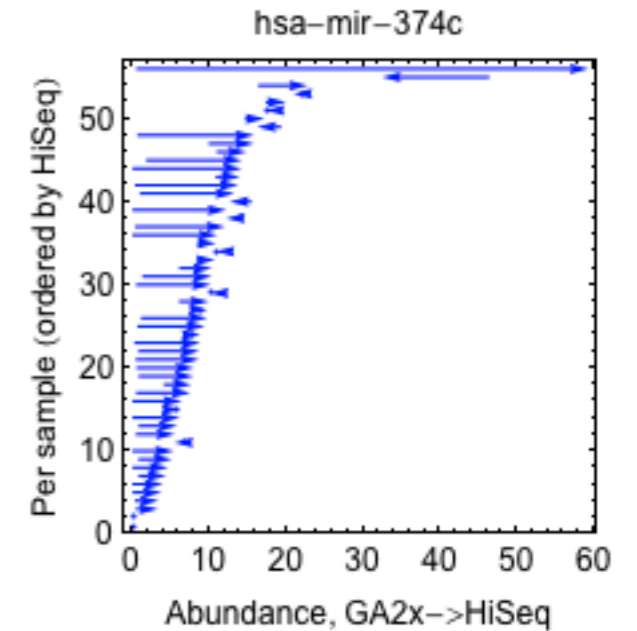
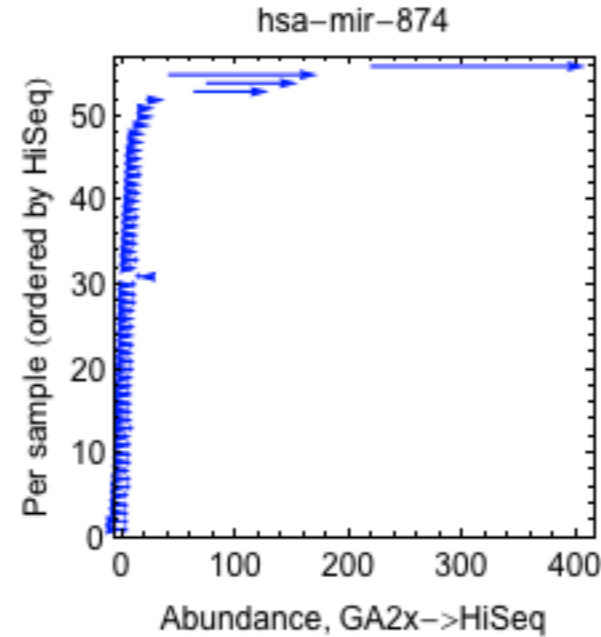
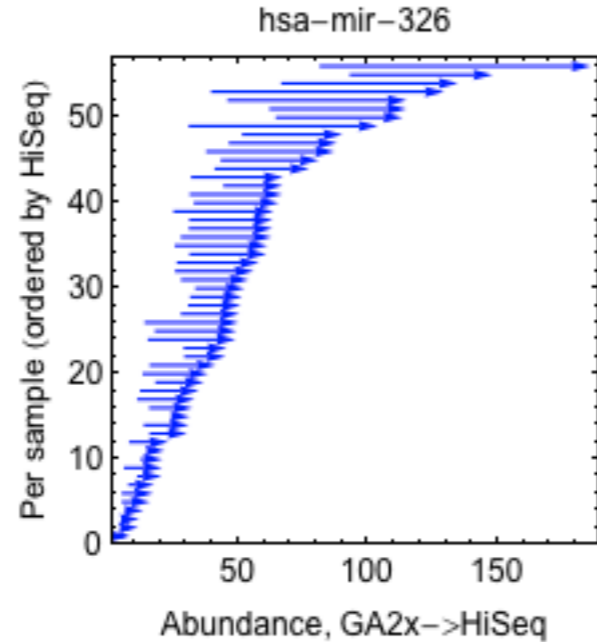
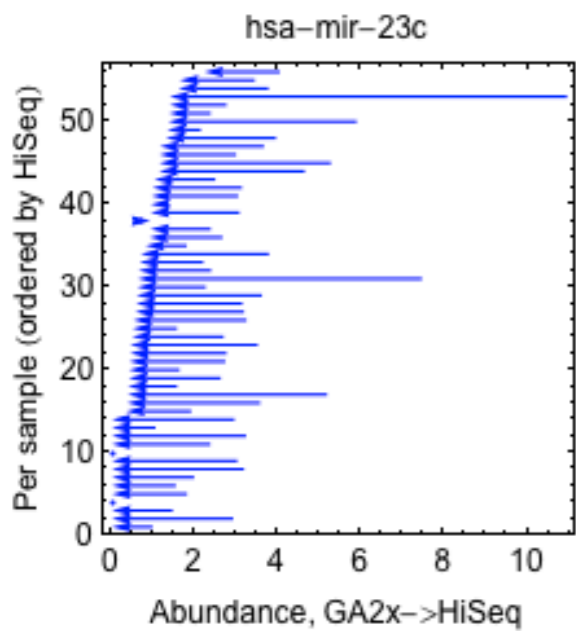
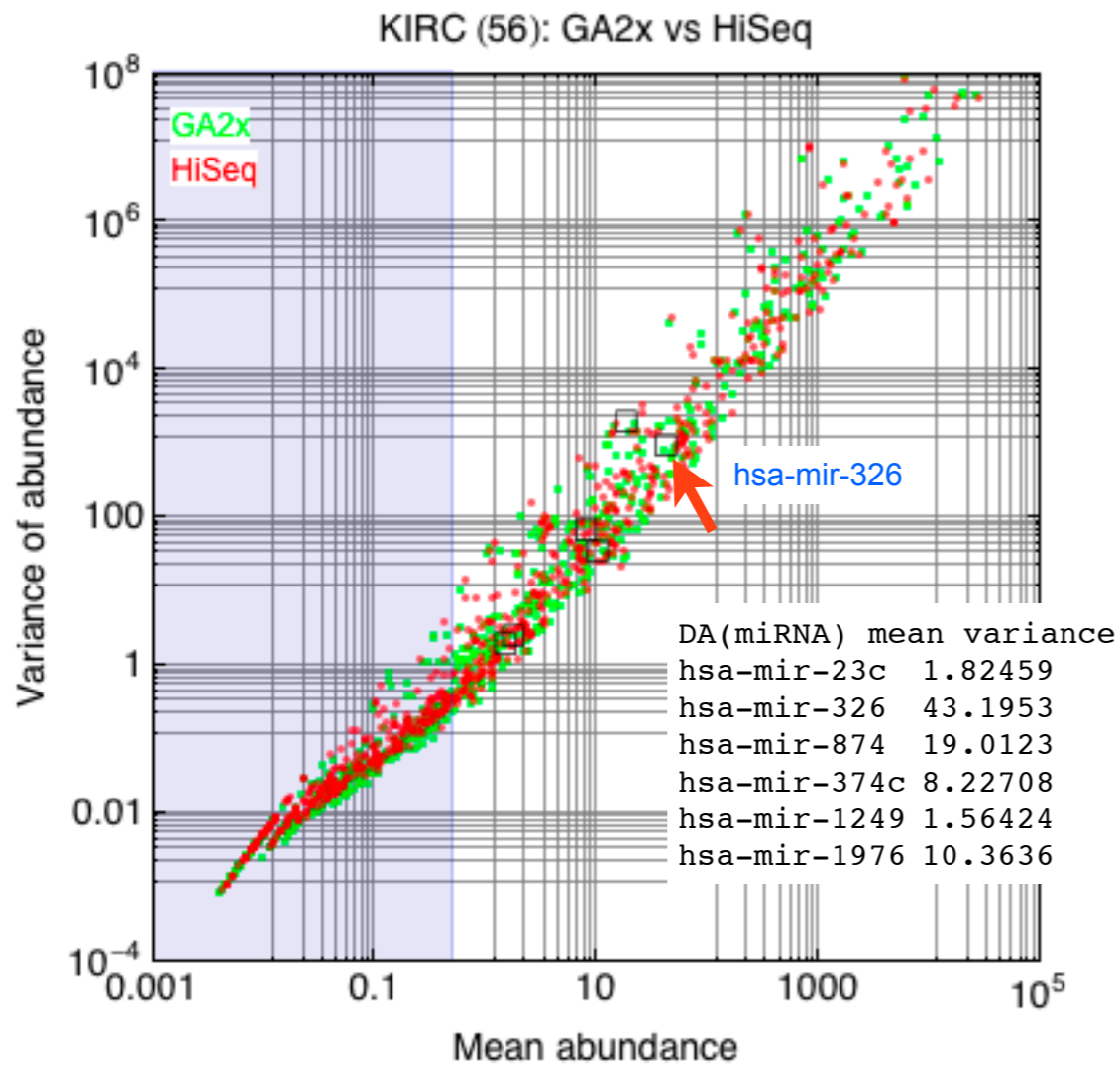
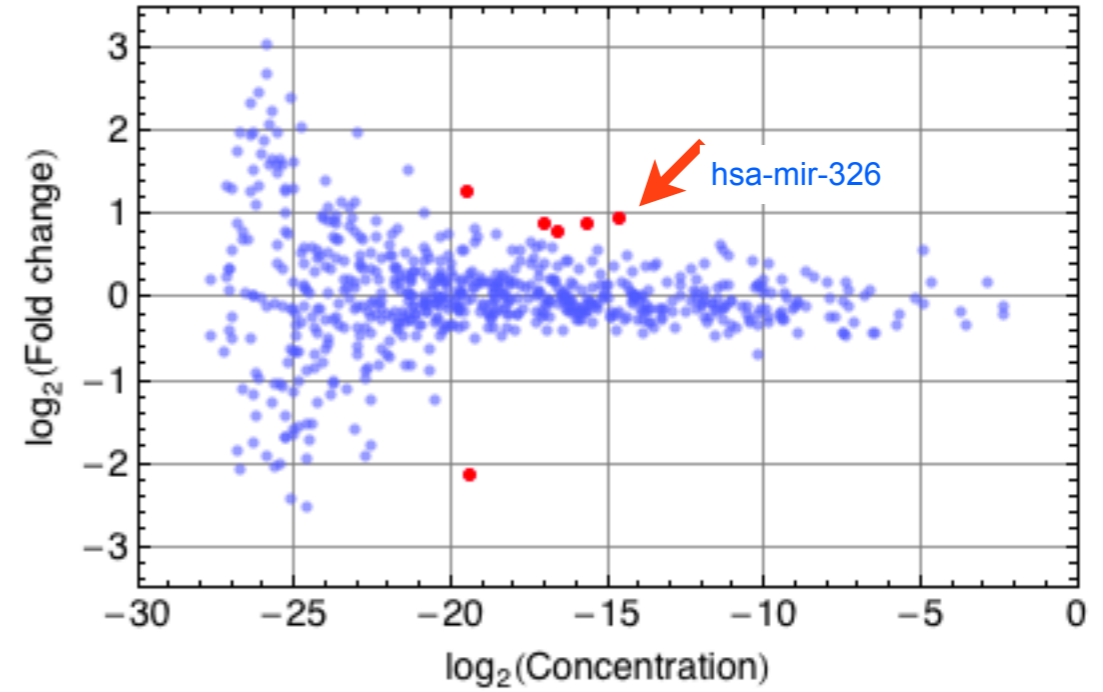
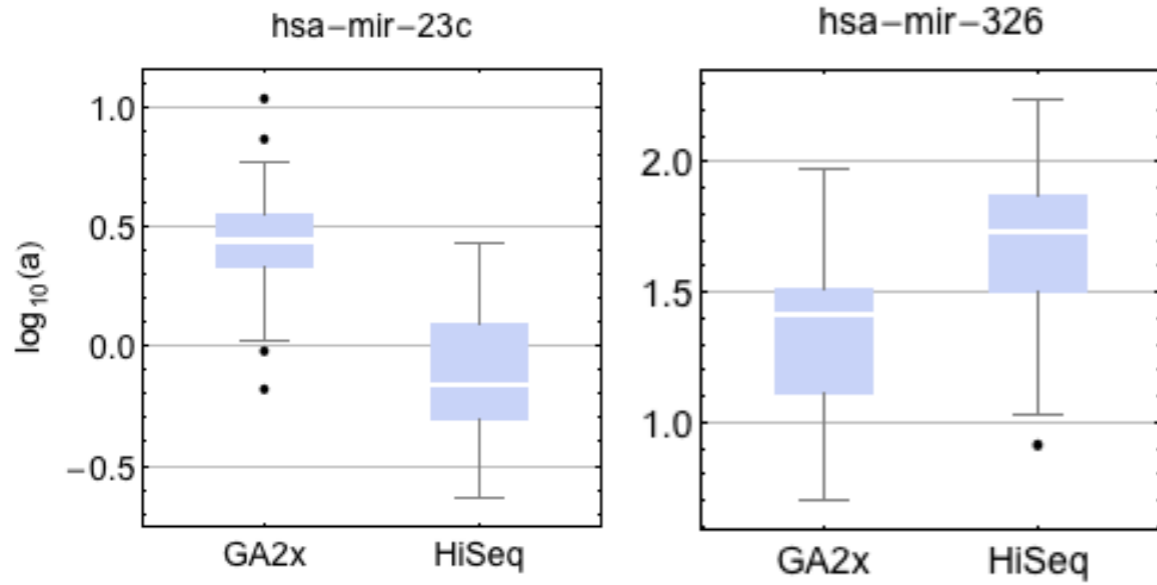


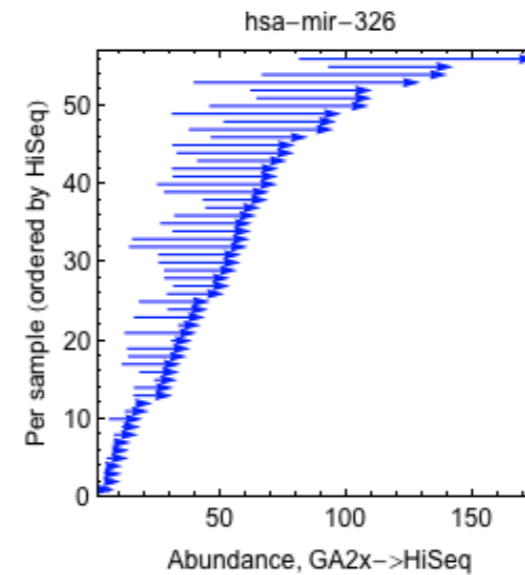
logConc	logFC	P.Value	adj.P.Val
hsa-mir-23c	-19.46	-2.278	2.19e-12 1.604e-09
hsa-mir-326	-14.65	0.944	6.76e-06 0.00194
hsa-mir-874	-15.65	0.964	7.95e-06 0.0019
hsa-mir-374c	-17.00	0.939	3.33e-05 0.0061
hsa-mir-3156-2	-24.36	5.884	4.54e-05 0.0066
hsa-mir-1249	-19.49	1.247	8.14e-05 0.0099
...			



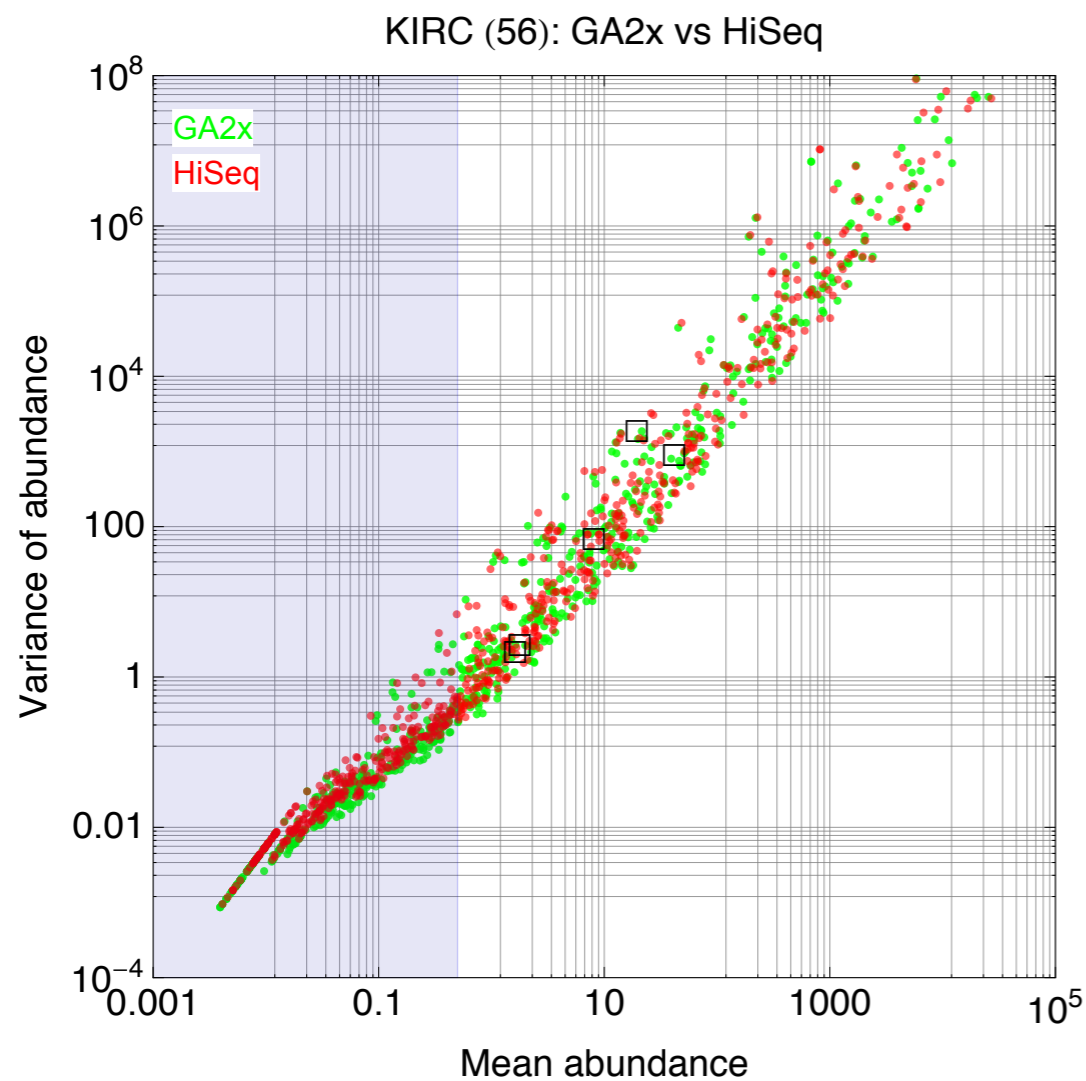
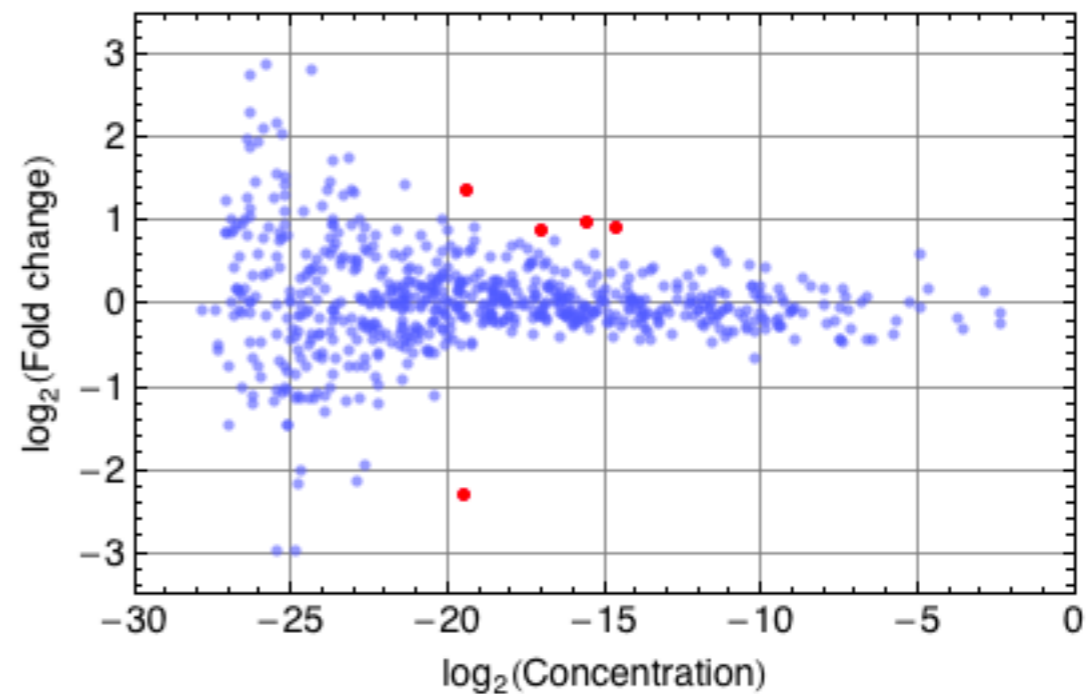
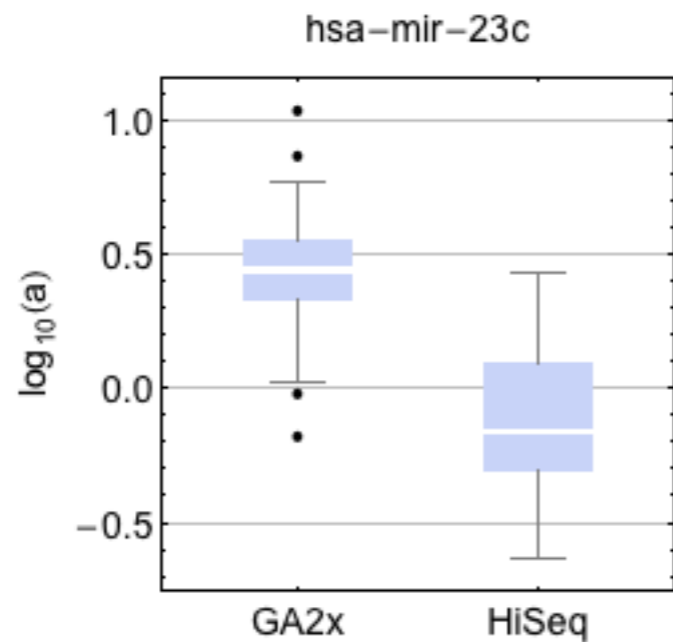
KIRC/P GA2x vs HiSeq, subsample 2, 735 miRNAs



gene	logConc	logFC	P.Value	adj.P.Val
hsa-mir-23c	-19.40	-2.133	1.69e-11	1.240e-08
hsa-mir-326	-14.65	0.975	3.10e-06	0.00114
hsa-mir-874	-15.701	0.906	2.55e-05	0.00625
hsa-mir-374c	-17.033	0.911	5.31e-05	0.00813
hsa-mir-1249	-19.485	1.280	5.53e-05	0.00813
hsa-mir-1976	-16.611	0.797	0.00037	0.0450
...				



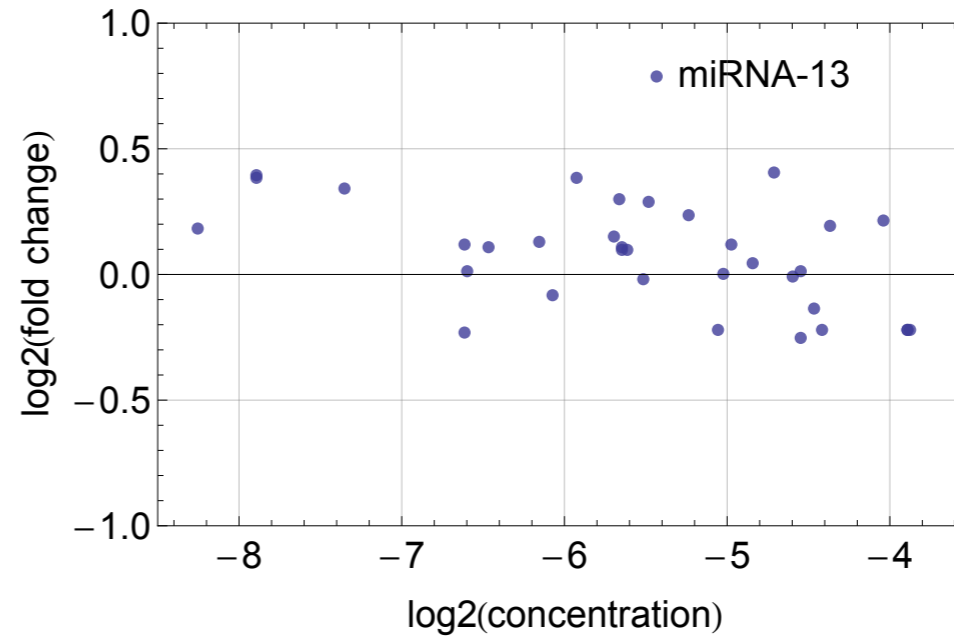
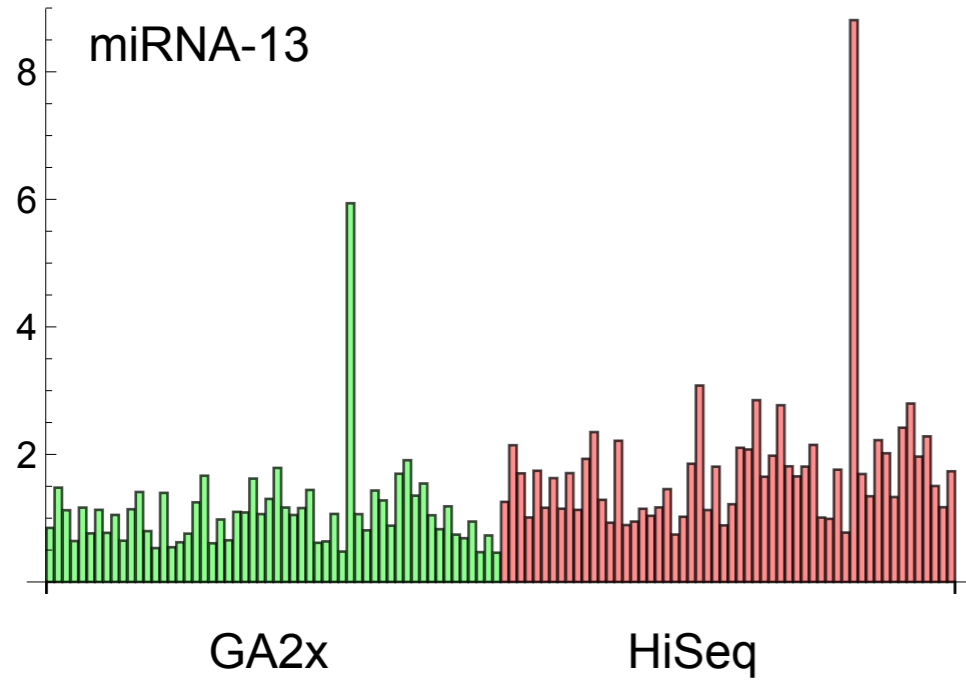
KIRC/P GA2x vs HiSeq, subsample 1, 735 miRNAs



gene	logConc	logFC	P.Value	adj.P.Val
hsa-mir-23c	-19.477	-2.29	2.88e-12	2.12e-09
hsa-mir-874	-15.620	0.984	5.62e-06	0.0021
hsa-mir-326	-14.679	0.923	1.13e-05	0.0024
hsa-mir-1249	-19.440	1.376	1.32e-05	0.0024
hsa-mir-374c	-17.047	0.884	0.000101	0.0148

KIRC/P GA2x vs HiSeq, subsample 5, 35 miRNAs

Differential abundance analysis, edgeR v1.5.1



gene	logConc	logFC	P.Value	adj.P.Val
mi-13	-5.4255	0.783499	0.000945101	0.0330785
mi-23	-4.70622	0.406441	0.0291534	0.510185
mi-1	-3.89152	-0.221841	0.120596	0.751885
mi-2	-3.89345	-0.220216	0.120596	0.751885
mi-3	-3.87952	-0.220564	0.122239	0.751885
mi-34	-4.04362	0.211961	0.152072	0.751885
...				