Electronic Supplementary Material (ESI) for Analytical Methods.

Supporting Information

Multiplexed microRNA Expression Profiling by Combined Asymmetric PCR and Label-Free Detection using Silicon Photonic Sensor Arrays

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Table S1. Summary of nucleic acid sequences

	Sequence (5′-3′)
hsa miRNA-let7f	UGAGGUAGUAGAUUGUAUAGUU
hsa miRNA-219	UGAUUGUCCAAACGCAAUUCU
hsa miRNA-10b	UACCCUGUAGAACCGAAUUUGUG
hsa miRNA-29a	UAGCACCAUCUGAAAUCGGUUA
hsa miRNA-335	UCAAGAGCAAUAACGAAAAAUGU
hsa miRNA-124a	UAAGGCACGCGGUGAAUGCC
hsa miRNA-222	AGCUACAUCUGGCUACUGGGUCUC
hsa miRNA-34a	UGGCAGUGUCUUAGCUGGUUGU
hsa miRNA-155	UUAAUGCUAAUCGUGAUAGGGGU
Conserved Stem Loop Primer	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGAT… miRNA specific overhang
miR-let7f SLP overhang	AACTATAC
miR-219 SLP overhang	AGAATTG
miR-10b SLP overhang	CACAAATTC
miR-29a SLP overhang	TAACCG
miR-335 SLP overhang	ACATTTTT
miR-124a SLP overhang	GGCATTC
miR-222 SLP overhang	GAGACCC
miR-34a SLP overhang	ACAACCA
miR-155 SLP overhang	ACCCCT
Conserved reverse primer	GTGCAGGGTCCGAGGT
miR-let7f forward primer	CGCGCTGAGGTAGTAGATT
miR-219 forward primer	CGCGTGATTGTCCAAACG
miR-10b forward primer	GCGTACCCTGGTAGAACC
miR-29a forward primer	CGCTAGCACCATCTGAAAT
miR-335 forward primer	CGCGTCAAGAGCAATAACG
miR-124a forward primer	CGTAAGGCACGCGGT
miR-222 forward primer	CGAGCTACATCTGGCTACT
miR-34a forward primer	GCGTGGCAGTGTCTTAGC
miR-155 forward primer	CGCGTTAATGCTAATCGTGAT

Table S2. Details on fluid flow conditions used in the assay

Step	Flow Rate (µL/min)	Duration (min)
Hybridization Buffer	20	5
RT-aPCR Product	20	15
Hybridization Buffer	20	5

Table S3. Research Subject Information

Subject	Gender	Age	Cancer type
A	M	62	Glioma – grade IV
B	M	42	Glioma – grade IV
C	M	47	Glioma – grade IV
D	F	52	Glioma – grade II
E	F	67	Glioma – grade IV
F	F	75	Glioma – grade IV
G	F	29	Glioma – grade III
H	F	48	Glioma – grade IV
I	F	37	Glioma – grade III
J	F	35	Glioma – grade III
K	M	26	Glioma – grade IV
L	M	38	Glioma – grade IV
M	F	67	Glioma – grade IV
N	M	25	Glioma – grade III
O	F	27	Glioma – grade II
P	M	30	Glioma – grade III
Q	M	51	Glioma – grade IV
R	F	63	Meningioma – grade I
S	F	69	Glioma – grade IV
T	F	74	Meningioma – grade I

Table S4. Fold Changes Presented in heat map (log 2)

Subject	let 7f	miR-10b	miR-29a	miR-34a	miR-124a	miR-155	miR-219	miR-222	miR-335
A	0.83	0.68	-0.92	-1.18	-2.76	-1.81	-1.19	-1.78	-1.27
B	0.73	0.55	0.09	0.05	0.12	-0.7	0.61	3.02	0.08
C	0.8	0.88	-0.14	-0.27	0.91	2.42	0.71	1.45	0.07
D	-0.03	0.7	-1.65	-2.97	-0.08	0.73	0.53	1.7	0.07
E	-3.1	-2.95	-2.63	-2.44	0.11	1.29	0.27	8.05	-6.21
F	-3.38	-3.72	-3.31	-2.62	-0.02	1.96	-0.01	1.87	0.07
G	-3.09	-1.35	-2.89	-2.51	-1.89	1.03	-0.3	0.04	0.1
H	-2.6	0.23	-2.22	-0.74	0.81	2.98	0.84	2.67	-0.03
I	-1.71	-0.43	-1.8	-2.85	-2.02	1.68	0.05	2.07	-2.25
J	1.21	1.43	1	1.66	1.51	3.6	2.86	4.32	-0.68
K	2.35	3.76	3.9	1.15	4.17	8.02	6.86	9.44	1.95
L	3.36	5.68	5.42	2.1	6.3	9.08	8.14	11.67	0.91
M	0.73	0.94	1.08	0.76	2.09	3.7	3.79	3.9	-2.51
N	0.69	1.46	1.38	0.88	2.23	3.14	1.54	3.15	-7.03
O	0.99	1.23	1.19	0.61	0.97	-0.38	-1.24	0.86	-6.44
P	2.73	5.46	1.97	0.32	6.23	8.51	3.54	6.45	5.05
Q	0.11	0.83	0.17	2.35	-0.51	3.73	4.32	7.05	-4.29
R	1.94	1.68	2.6	-1.37	-1.76	4.4	5.38	9.48	-1.73
S	1.33	0.98	1.16	-2.98	0.31	4.59	-0.13	6.27	-3.55
T	0.37	0.86	0.83	-1.21	-1.1	4.38	5.01	7.85	-1.36

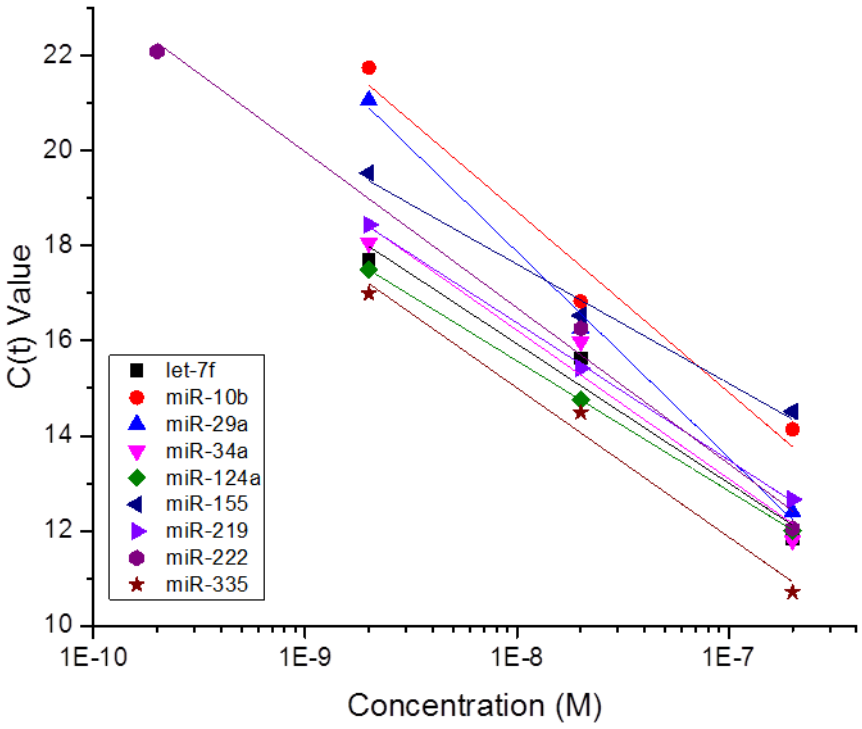

Figure S1. Amplification validation of miRNA targets. In order to prove linear amplification of all miRNA targets, samples of each target were subjected to the aPCR-microring assay at varying concentrations using a stem loop primer concentration of 200 µM. The results validated the designed primer sets by displaying log-linear amplification profiles.

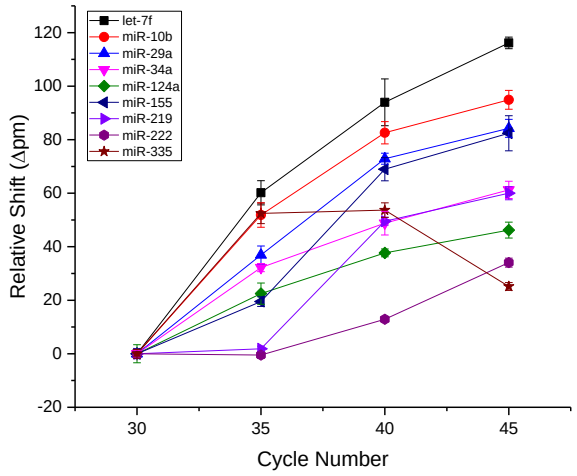

Figure S2. Amplification traces obtained using a 10 ng input for a pooled healthy RNA sample.

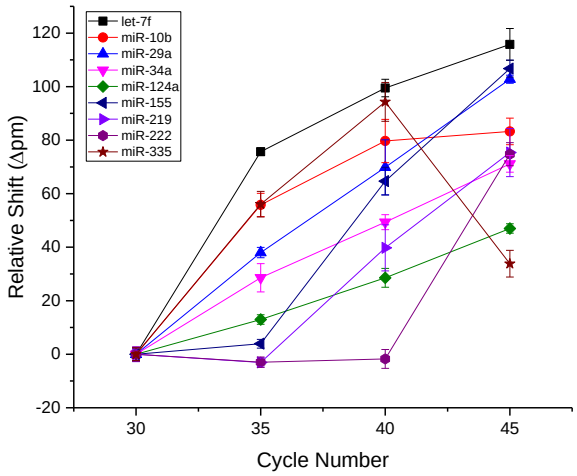

Figure S3. Amplification traces obtained using a 10 ng input for Subject A.

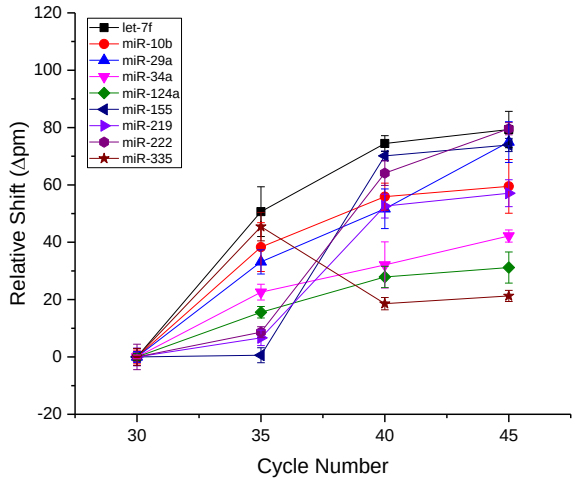

Figure S4. Amplification traces obtained using a 10 ng input for Subject B.

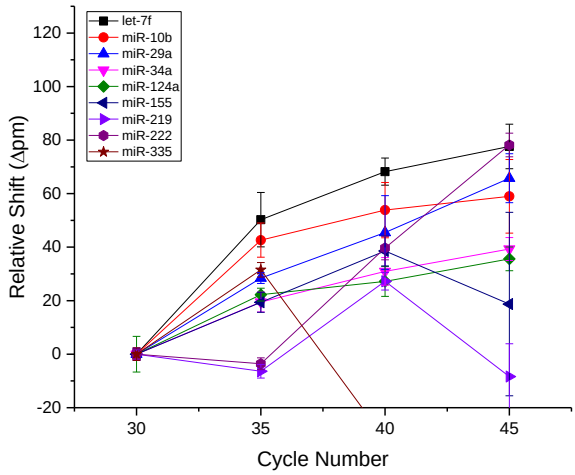

Figure S5. Amplification traces obtained using a 10 ng input for Subject C.

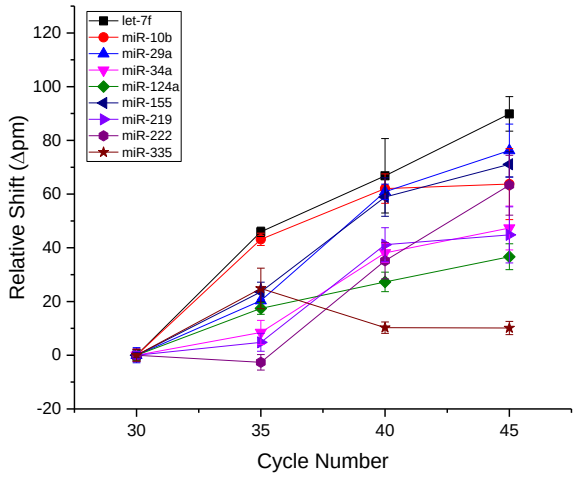

Figure S6. Amplification traces obtained using a 10 ng input for Subject D.

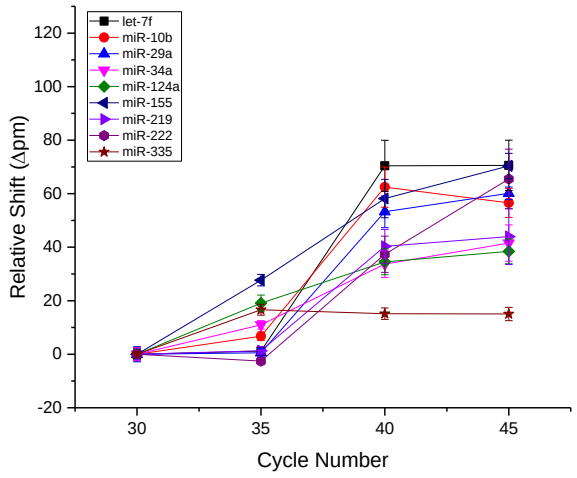

Figure S7. Amplification traces obtained using a 10 ng input for Subject E.

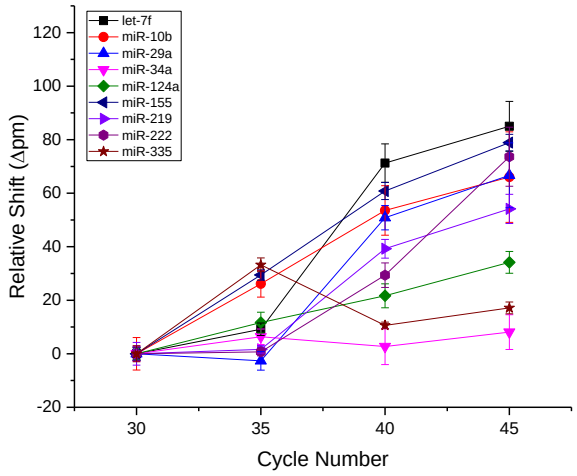

Figure S8. Amplification traces obtained using a 10 ng input for Subject F.

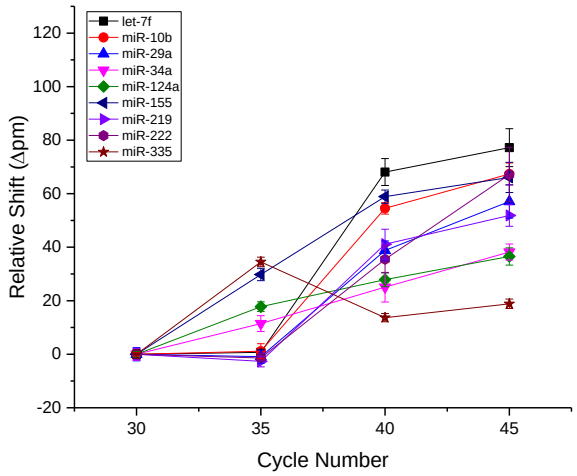

Figure S9. Amplification traces obtained using a 10 ng input for Subject G.

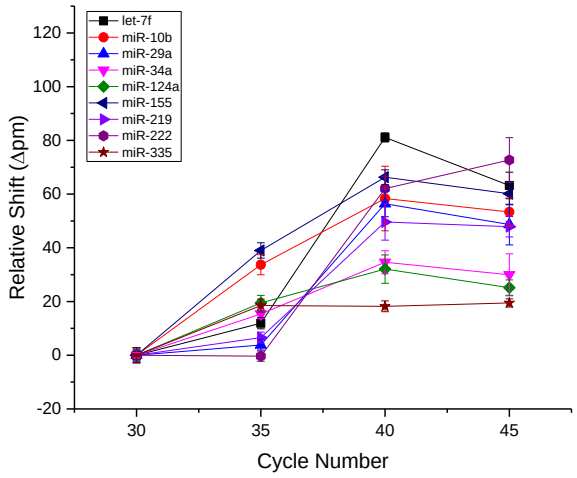

Figure S10. Amplification traces obtained using a 10 ng input for Subject H.

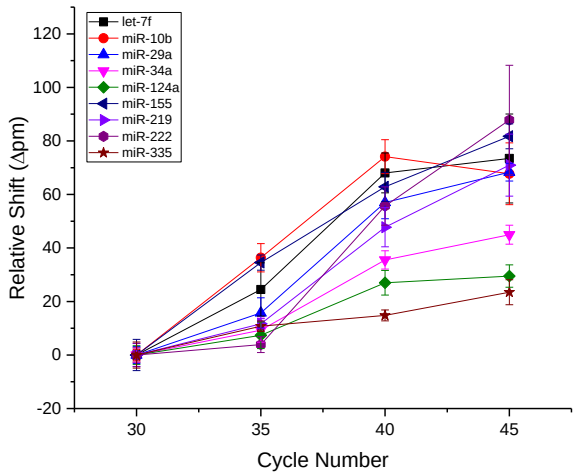

Figure S11. Amplification traces obtained using a 10 ng input for Subject I.

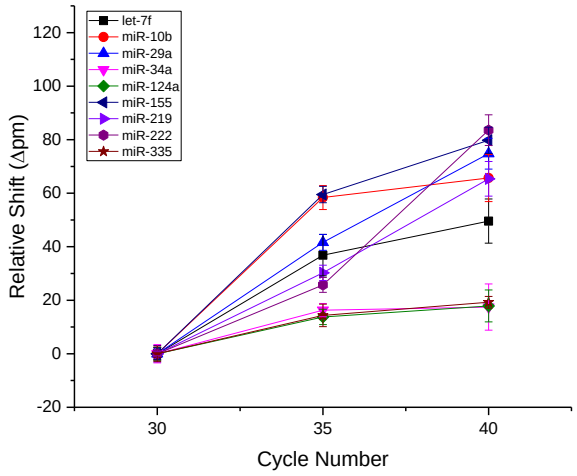

Figure S12. Amplification traces obtained using a 10 ng input for Subject J.

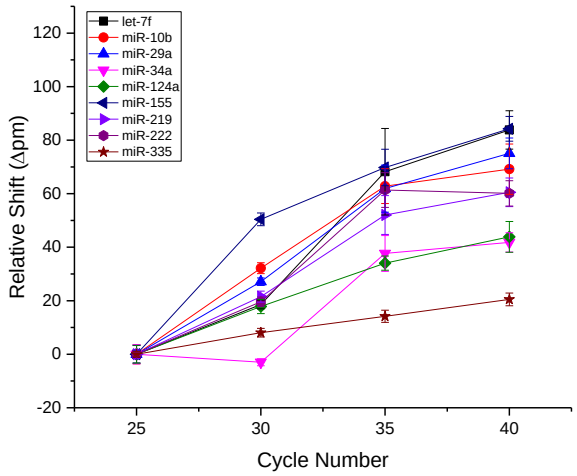

Figure S13. Amplification traces obtained using a 10 ng input for Subject K.

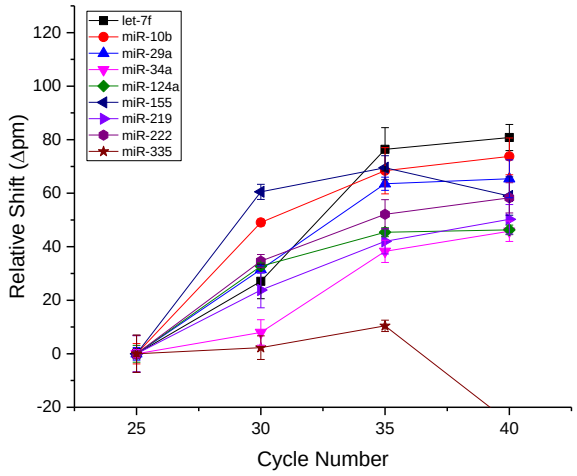

Figure S14. Amplification traces obtained using a 10 ng input for Subject L.

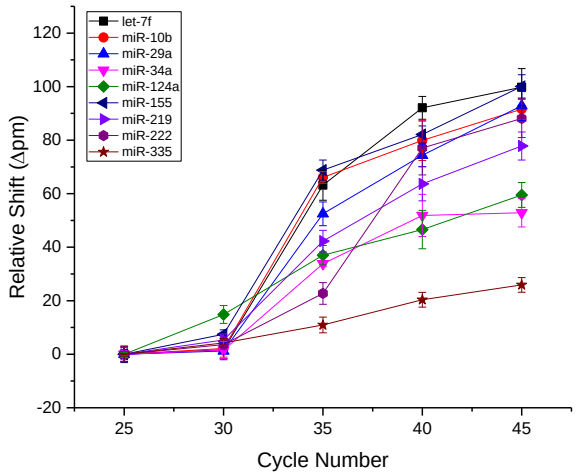

Figure S15. Amplification traces obtained using a 10 ng input for Subject M.

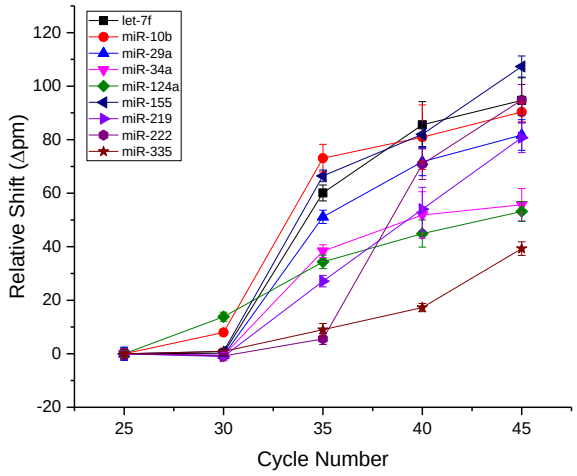

Figure S16. Amplification traces obtained using a 10 ng input for Subject N.

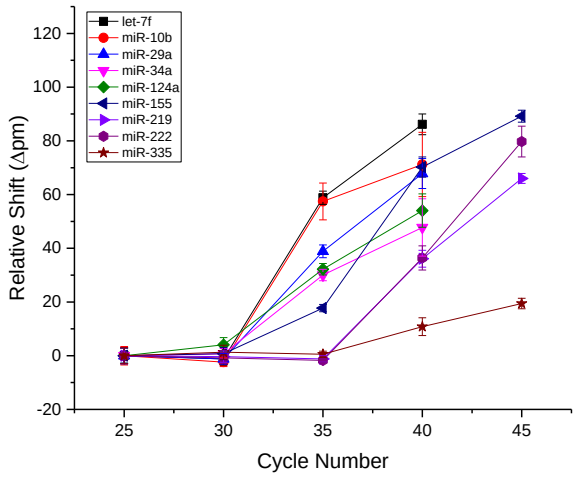

Figure S17. Amplification traces obtained using a 10 ng input for Subject O.

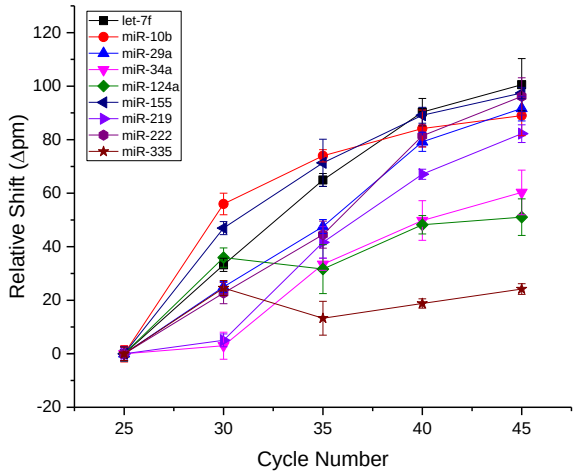

Figure S18. Amplification traces obtained using a 10 ng input for Subject P.

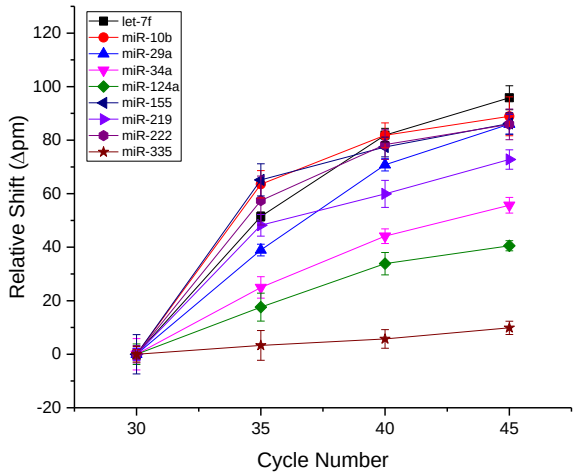

Figure S19. Amplification traces obtained using a 10 ng input for Subject Q.

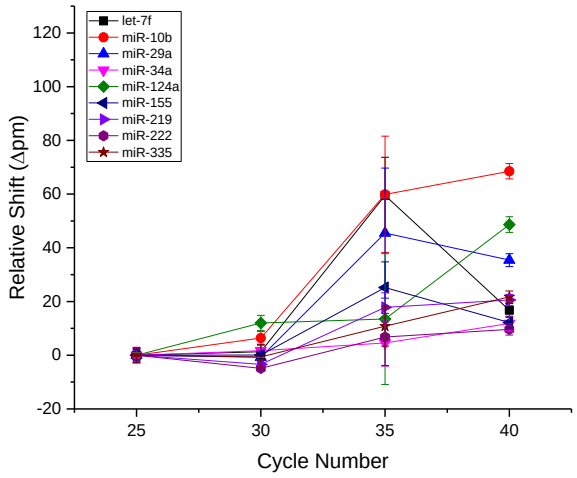

Figure S20. Amplification traces obtained using a 10 ng input for Subject R.

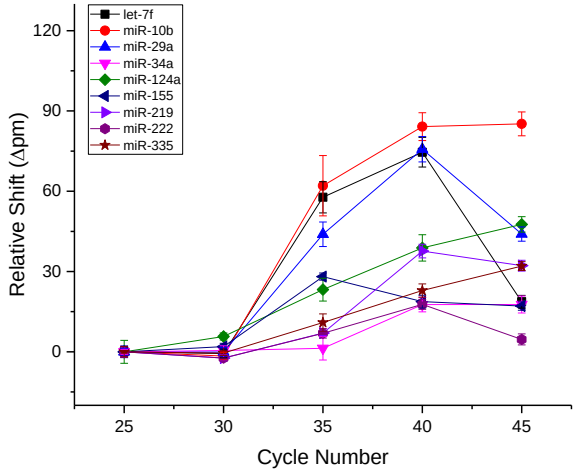

Figure S21. Amplification traces obtained using a 10 ng input for Subject S.

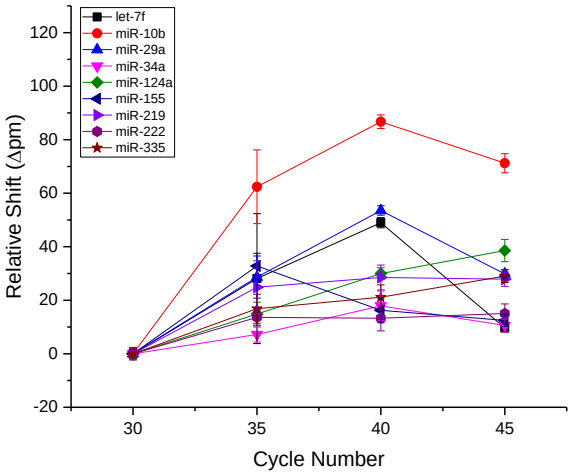

Figure S22. Amplification traces obtained using a 10 ng input for Subject T.