Human angiogenin is a potent cytotoxin in the absence of ribonuclease inhibitor

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TABLE OF CONTENTS

TABLE S1. tRFs with differential levels

			Δ*RNH1*		WT	
tRF Type	Precursor tRNA	Length	A/R	A/U	A/R	A/U
tRF-1	tRNA-Ile-AAT-2-1	17	-	-	-	-2.06
tRF-1	tRNA-Ile-AAT-5-2	17	-3.13	-1.75	-1.60	-1.83
tRF-1	tRNA-Val-TAC-3-1	17	-	-	-	-2.26
tRF-3	tRNA-Ala-TGC-4-1	18	-	-	-	-1.65
tRF-3	tRNA-Gly-TCC-1-1	22	-	-	-2.71	-1.62
tRF-3	tRNA-Gly-TCC-2-2	22	-	-	-2.71	-1.62
tRF-3	tRNA-Gly-TCC-3-1	22	-	-	-2.71	-1.62
tRF-3	tRNA-Pro-TGG-1-1	22	-2.81	-	-	-
tRF-3	tRNA-Pro-TGG-3-1	22	-2.81	-	-	-
tRF-3	tRNA-Ser-TGA-4-1	18	-3.04	-1.66	-	-
tRF-3	tRNA-Tyr-GTA-2-1	17	-	-	-2.36	-
tRF-3	tRNA-Tyr-GTA-5-2	17	-	-	-2.36	-
tRF-3	tRNA-Tyr-GTA-7-1	17	-	-	-2.43	-
tRF-3	tRNA-Val-AAC-2-1	17	-3.81	-2.30	-	-1.28
tRF-3	tRNA-Val-AAC-chr6-84	17	-3.84	-2.25	-	-1.27
tRF-5	nm-tRNA-Tyr-GTA-chr1-125	32	-	-	-	-2.80
tRF-5	nm-tRNA-Tyr-GTA-chr14-8	32	-	-	-	-2.80
tRF-5	tRNA-Gly-GCC-1-4	32	2.66	1.28	2.37	2.80
tRF-5	tRNA-iMet-CAT-1-2	31	-	-0.98	-	-
tRF-5	tRNA-iMet-CAT-2-1	31	-	-0.98	-	-
tRF-5	tRNA-Leu-CAG-1-7	26	-3.02	-2.78	-1.19	-
tRF-5	tRNA-Leu-CAG-2-2	26	-3.02	-2.78	-1.19	-
tRF-5	tRNA-Lys-CTT-2-4	32	-1.73	-1.69	-	-
tRF-5	tRNA-Lys-CTT-3-1	32	-2.43	-2.95	-	-
tRF-5	tRNA-Lys-TTT-3-3	32	-	-2.16	-	-
tRF-5	tRNA-Lys-TTT-5-1	32	-	-2.16	-	-
tRF-5	tRNA-Val-AAC-1-5	32	-	-1.25	1.81	-
tRF-5	tRNA-Val-AAC-3-1	32	-	-1.25	1.81	-
tRF-5	tRNA-Val-AAC-4-1	32	-	-1.25	1.81	-
tRF-5	tRNA-Val-AAC-5-1	23	-2.68	-1.75	-1.28	-
tRF-5	tRNA-Val-CAC-1-6	32	-	-1.14	1.84	-
tRF-5	tRNA-Val-CAC-4-1	32	-	-1.14	1.84	-
tRF-5	tRNA-Val-CAC-5-1	32	-	-1.14	1.84	-
tRF-novel	tRNA-Gln-TTG-1-1	19	-3.07	-2.26	-1.38	-
tRF-novel	tRNA-Gln-TTG-3-1	19	-2.69	-1.87	-1.46	-

Values are for $\log_2$(fold change) in tRF levels as calculated with NOISeqBIO. Treatments: A/R, $\log_2$(ANG/RNase 1); A/U, $\log_2$(ANG/untreated). All values of $\log_2$(fold change) have $p \leq 0.05$. Each tRF was measured in 2 of 3 biological replicates in both conditions.

TABLE S2. Average tRF Expression

			Δ*RNH1* (%)			WT (%)		
Type	Precursor tRNA	Length	A	R	U	A	R	U
tRF-1	tRNA-Ala-CGC-2-1	18	-	-	0.34	0.18	0.41	0.29
tRF-1	tRNA-Arg-ACG-1-2	19	-	-	0.32	0.12	0.42	0.30
tRF-1	tRNA-Arg-CCT-2-1	30	-	-	-	-	0.12	0.18
tRF-1	tRNA-Arg-TCG-2-1	29	-	-	-	-	0.19	0.20
tRF-1	tRNA-Cys-GCA-2-4	23	-	-	0.39	0.16	0.24	0.24
tRF-1	tRNA-Glu-CTC-2-1	22	-	0.10	-	-	0.14	0.22
tRF-1	tRNA-Gly-GCC-1-4	17	-	-	-	-	-	0.20
tRF-1	tRNA-Gly-GCC-4-1	17	-	-	-	-	-	0.20
tRF-1	tRNA-Ile-AAT-2-1	17	-	0.26	0.43	0.16	0.45	0.43
tRF-1	tRNA-Ile-AAT-5-2	17	0.16	0.53	1.39	0.61	1.23	1.44
tRF-1	tRNA-Leu-TAG-3-1	21	-	-	-	-	-	0.10
tRF-1	tRNA-Ser-TGA-1-1	20	-	-	-	0.24	0.44	0.39
tRF-1	tRNA-Thr-AGT-1-3	28	-	-	-	-	0.22	0.21
tRF-1	tRNA-Thr-CGT-3-1	17	-	-	0.40	0.16	-	-
tRF-1	tRNA-Thr-CGT-3-1	18	-	-	-	-	-	0.40
tRF-1	tRNA-Val-TAC-3-1	17	-	-	0.71	0.24	0.39	0.76
tRF-1	tRNA-Val-TAC-3-1	18	-	0.21	-	-	-	-
tRF-3	tRNA-Ala-AGC-1-1	22	-	-	-	0.16	-	0.16
tRF-3	tRNA-Ala-AGC-2-1	17	0.11	-	-	-	-	-
tRF-3	tRNA-Ala-AGC-2-1	18	-	0.49	0.97	0.55	1.05	0.94
tRF-3	tRNA-Ala-AGC-3-1	17	0.11	-	-	-	-	-
tRF-3	tRNA-Ala-AGC-3-1	18	-	0.48	0.97	0.55	1.04	0.92
tRF-3	tRNA-Ala-CGC-1-1	22	-	0.35	0.60	0.43	0.71	0.68
tRF-3	tRNA-Ala-CGC-2-1	22	-	0.35	0.63	0.43	0.71	0.67
tRF-3	tRNA-Ala-CGC-3-1	17	-	0.29	-	-	-	-
tRF-3	tRNA-Ala-CGC-3-1	18	-	-	0.45	0.25	0.57	0.50
tRF-3	tRNA-Ala-TGC-1-1	17	0.09	-	-	-	-	-
tRF-3	tRNA-Ala-TGC-1-1	18	-	0.41	0.90	0.53	0.91	0.91
tRF-3	tRNA-Ala-TGC-2-1	22	-	0.35	0.60	0.43	0.71	0.68
tRF-3	tRNA-Ala-TGC-3-1	22	-	0.35	0.63	0.43	0.71	0.67
tRF-3	tRNA-Ala-TGC-4-1	17	-	0.30	-	-	-	-
tRF-3	tRNA-Ala-TGC-4-1	18	-	-	0.46	0.25	0.56	0.52
tRF-3	tRNA-Ala-TGC-6-1	17	0.09	-	-	-	-	-
tRF-3	tRNA-Ala-TGC-6-1	18	-	0.41	0.90	0.53	0.91	0.89
tRF-3	tRNA-Asp-GTC-2-7	22	-	-	-	-	0.94	-
tRF-3	tRNA-Asp-GTC-3-1	22	-	0.27	-	-	0.82	-
tRF-3	tRNA-Cys-GCA-11-	17	-	-	-	-	0.38	0.34
tRF-3	tRNA-Cys-GCA-14-	17	-	-	-	-	0.38	0.34
tRF-3	tRNA-Cys-GCA-2-1	17	-	-	-	-	0.38	0.34
tRF-3	tRNA-Cys-GCA-4-1	17	-	-	-	-	0.38	0.34
tRF-3	tRNA-Cys-GCA-5-1	17	-	-	-	-	0.38	0.34

tRF-3	tRNA-Cys-GCA-7-1	17	-	-	-	-	0.38	0.34
tRF-3	tRNA-Cys-GCA-8-1	17	-	-	-	-	0.38	0.34
tRF-3	tRNA-Gln-CTG-5-1	17	-	0.10	-	-	0.26	0.24
tRF-3	tRNA-Gln-TTG-1-1	17	-	-	-	-	-	0.38
tRF-3	tRNA-Gln-TTG-1-1	18	-	-	0.39	-	-	-
tRF-3	tRNA-Gln-TTG-2-1	17	-	0.13	-	-	0.20	0.30
tRF-3	tRNA-Gln-TTG-2-1	18	-	-	0.40	-	-	-
tRF-3	tRNA-Gln-TTG-3-1	17	-	-	-	-	-	0.38
tRF-3	tRNA-Gln-TTG-3-1	18	-	-	0.39	-	-	-
tRF-3	tRNA-Glu-TTC-4-2	26	-	-	0.29	-	0.33	0.43
tRF-3	tRNA-Gly-CCC-2-1	22	-	-	-	0.13	0.41	0.15
tRF-3	tRNA-Gly-TCC-1-1	22	-	0.26	0.48	0.29	1.29	0.60
tRF-3	tRNA-Gly-TCC-2-2	22	-	0.26	0.48	0.29	1.29	0.61
tRF-3	tRNA-Gly-TCC-3-1	22	-	0.26	0.48	0.29	1.29	0.60
tRF-3	tRNA-Leu-AAG-1-2	18	-	0.19	0.40	0.29	0.67	0.34
tRF-3	tRNA-Leu-AAG-2-2	18	-	0.19	0.40	0.29	0.67	0.34
tRF-3	tRNA-Leu-AAG-3-1	18	-	0.18	0.38	0.28	0.64	0.32
tRF-3	tRNA-Leu-AAG-4-1	18	-	0.18	0.38	0.28	0.64	0.33
tRF-3	tRNA-Leu-CAA-1-2	22	-	0.14	-	0.15	0.21	0.17
tRF-3	tRNA-Leu-CAA-2-1	22	-	0.14	-	0.15	0.21	0.17
tRF-3	tRNA-Leu-CAA-3-1	22	-	0.14	-	0.15	0.21	0.17
tRF-3	tRNA-Leu-CAA-4-1	22	-	0.14	-	0.15	0.23	0.16
tRF-3	tRNA-Leu-CAG-2-2	22	-	-	-	0.15	0.20	-
tRF-3	tRNA-Leu-TAG-1-1	18	-	0.19	0.40	0.29	0.67	0.34
tRF-3	tRNA-Leu-TAG-3-1	18	-	0.19	0.40	0.30	0.67	0.35
tRF-3	tRNA-Pro-AGG-1-1	22	-	0.19	0.43	0.24	0.29	0.40
tRF-3	tRNA-Pro-AGG-2-3	22	-	0.19	0.43	0.24	0.29	0.40
tRF-3	tRNA-Pro-AGG-3-1	22	-	0.19	0.43	0.24	0.29	0.40
tRF-3	tRNA-Pro-CGG-1-1	22	-	0.19	0.44	0.24	0.29	0.31
tRF-3	tRNA-Pro-CGG-2-1	22	-	0.19	0.43	0.24	0.29	0.40
tRF-3	tRNA-Pro-TGG-1-1	22	0.08	0.24	0.56	0.27	0.36	0.33
tRF-3	tRNA-Pro-TGG-2-1	22	-	0.19	0.43	0.24	0.29	0.40
tRF-3	tRNA-Pro-TGG-3-1	22	0.08	0.24	0.56	0.27	0.36	0.33
tRF-3	tRNA-Ser-AGA-1-1	18	-	-	-	-	-	0.17
tRF-3	tRNA-Ser-AGA-2-5	18	-	-	-	-	-	0.17
tRF-3	tRNA-Ser-AGA-3-1	18	-	-	-	-	-	0.17
tRF-3	tRNA-Ser-AGA-4-1	18	-	-	-	-	-	0.17
tRF-3	tRNA-Ser-GCT-3-1	18	-	-	-	-	-	0.42
tRF-3	tRNA-Ser-GCT-3-1	22	-	0.18	0.30	0.15	0.34	-
tRF-3	tRNA-Ser-GCT-4-1	18	-	-	-	-	-	0.42
tRF-3	tRNA-Ser-GCT-4-1	22	-	0.18	0.30	0.15	0.34	-
tRF-3	tRNA-Ser-GCT-5-1	18	-	-	-	-	-	0.41
tRF-3	tRNA-Ser-GCT-5-1	22	-	0.17	0.29	0.14	0.34	-
tRF-3	tRNA-Ser-TGA-2-1	18	-	-	-	-	-	0.17
tRF-3	tRNA-Ser-TGA-3-1	18	-	-	-	-	-	0.17

tRF-3	tRNA-Ser-TGA-4-1	18	0.08	0.26	0.68	0.29	0.49	0.54
tRF-3	tRNA-Tyr-GTA-1-1	17	-	0.12	0.32	-	0.65	0.51
tRF-3	tRNA-Tyr-GTA-2-1	17	-	0.43	1.18	0.67	2.28	1.36
tRF-3	tRNA-Tyr-GTA-3-1	17	-	-	-	-	0.58	0.17
tRF-3	tRNA-Tyr-GTA-5-2	17	-	0.43	1.18	0.67	2.28	1.36
tRF-3	tRNA-Tyr-GTA-6-1	17	-	-	-	-	0.58	0.17
tRF-3	tRNA-Tyr-GTA-7-1	17	-	0.33	0.98	0.57	2.05	0.88
tRF-3	tRNA-Tyr-GTA-8-1	17	-	0.12	0.32	-	0.65	0.51
tRF-3	tRNA-Val-AAC-1-5	17	-	-	2.39	-	1.91	2.79
tRF-3	tRNA-Val-AAC-2-1	17	0.18	0.86	2.46	1.77	2.01	2.86
tRF-3	tRNA-Val-AAC-4-1	17	-	-	2.39	-	1.91	2.79
tRF-3	tRNA-Val-AAC-chr6-84	17	0.16	0.75	2.24	1.63	1.69	2.64
tRF-3	tRNA-Val-CAC-1-6	17	-	-	2.38	-	1.91	2.79
tRF-3	tRNA-Val-CAC-2-1	17	-	-	-	-	0.26	0.27
tRF-3	tRNA-Val-CAC-5-1	17	-	-	2.38	-	1.91	2.79
tRF-3	tRNA-Val-TAC-1-2	22	-	-	0.42	0.36	0.38	0.58
tRF-3	tRNA-Val-TAC-2-1	22	-	-	0.42	0.36	0.38	0.58
tRF-5	tRNA-Tyr-GTA-chr1-125	32	-	0.17	0.33	0.10	0.16	0.44
tRF-5	tRNA-Tyr-GTA-chr14-8	32	-	0.17	0.33	0.10	0.16	0.44
tRF-5	tRNA-Ala-AGC-4-1	22	-	-	-	-	-	0.16
tRF-5	tRNA-Ala-CGC-1-1	22	-	-	-	-	-	0.17
tRF-5	tRNA-Ala-CGC-2-1	22	-	-	-	-	-	0.17
tRF-5	tRNA-Ala-CGC-3-1	22	-	-	-	-	-	0.15
tRF-5	tRNA-Ala-TGC-2-1	22	-	-	-	-	-	0.17
tRF-5	tRNA-Ala-TGC-3-1	22	-	-	-	-	-	0.17
tRF-5	tRNA-Ala-TGC-4-1	22	-	-	-	-	-	0.15
tRF-5	tRNA-Asp-GTC-2-7	32	0.08	-	-	-	-	-
tRF-5	tRNA-Gln-CTG-1-3	32	0.18	-	-	-	-	-
tRF-5	tRNA-Gln-CTG-2-1	32	0.18	-	-	-	-	-
tRF-5	tRNA-Gln-CTG-5-1	32	0.17	-	-	-	-	-
tRF-5	tRNA-Gln-TTG-1-1	32	0.08	-	-	-	-	-
tRF-5	tRNA-Gln-TTG-2-1	32	0.08	-	-	-	-	-
tRF-5	tRNA-Glu-CTC-1-7	32	5.51	5.00	-	9.44	-	-
tRF-5	tRNA-Glu-CTC-2-1	32	5.51	5.00	-	9.44	-	-
tRF-5	tRNA-Glu-TTC-1-1	30	-	-	-	0.08	-	0.15
tRF-5	tRNA-Glu-TTC-1-1	32	0.06	-	-	-	-	-
tRF-5	tRNA-Glu-TTC-2-2	32	0.27	-	-	-	-	-
tRF-5	tRNA-Glu-TTC-3-1	32	0.65	0.45	-	-	-	-
tRF-5	tRNA-Glu-TTC-4-2	32	0.65	0.45	-	-	-	-
tRF-5	tRNA-Glu-TTC-8-1	32	0.65	0.44	-	0.36	-	0.27
tRF-5	tRNA-Gly-GCC-1-4	32	66.88	27.58	10.57	24.30	4.69	3.48
tRF-5	tRNA-His-GTG-1-6	29	-	1.42	1.98	4.70	3.87	1.66
tRF-5	tRNA-iMet-CAT-1-2	31	1.06	2.10	0.59	-	-	-
tRF-5	tRNA-iMet-CAT-2-1	31	1.06	2.10	0.59	-	-	-

tRF-5	tRNA-Leu-AAG-1-2	26	-	-	-	-	0.13	0.15
tRF-5	tRNA-Leu-AAG-2-2	26	-	-	-	-	0.13	0.15
tRF-5	tRNA-Leu-AAG-3-1	26	-	-	-	-	0.13	0.15
tRF-5	tRNA-Leu-CAG-1-7	26	0.15	1.00	1.18	0.57	0.87	0.85
tRF-5	tRNA-Leu-CAG-2-2	26	0.15	1.00	1.18	0.57	0.87	0.85
tRF-5	tRNA-Leu-TAG-1-1	26	-	-	-	-	0.13	0.15
tRF-5	tRNA-Lys-CTT-2-4	32	0.13	0.41	0.42	-	0.33	0.27
tRF-5	tRNA-Lys-CTT-3-1	32	0.07	0.35	0.36	0.27	0.26	0.20
tRF-5	tRNA-Lys-CTT-4-1	32	-	0.48	-	-	-	-
tRF-5	tRNA-Lys-TTT-3-3	32	0.57	1.70	-	-	-	-
tRF-5	tRNA-Lys-TTT-5-1	32	0.57	1.70	-	-	-	-
tRF-5	tRNA-Ser-AGA-1-1	23	-	-	-	-	0.13	0.26
tRF-5	tRNA-Ser-AGA-1-1	24	-	0.20	-	-	-	-
tRF-5	tRNA-Ser-AGA-2-5	23	-	-	-	-	0.13	0.26
tRF-5	tRNA-Ser-AGA-2-5	24	-	0.20	-	-	-	-
tRF-5	tRNA-Ser-AGA-3-1	23	-	-	-	-	0.13	0.26
tRF-5	tRNA-Ser-AGA-3-1	24	-	0.20	-	-	-	-
tRF-5	tRNA-Ser-AGA-4-1	23	-	-	-	-	-	0.23
tRF-5	tRNA-Ser-AGA-4-1	24	-	0.18	-	-	-	-
tRF-5	tRNA-Ser-TGA-2-1	23	-	-	-	-	0.13	0.25
tRF-5	tRNA-Ser-TGA-2-1	24	-	0.20	-	-	-	-
tRF-5	tRNA-Ser-TGA-3-1	23	-	-	-	-	0.13	0.25
tRF-5	tRNA-Ser-TGA-3-1	24	-	0.20	-	-	-	-
tRF-5	tRNA-Ser-TGA-4-1	23	-	-	-	-	0.13	0.25
tRF-5	tRNA-Ser-TGA-4-1	24	-	0.20	-	-	-	-
tRF-5	tRNA-Val-AAC-1-5	32	1.56	3.72	2.28	4.23	1.81	2.36
tRF-5	tRNA-Val-AAC-2-1	23	-	-	0.32	-	-	-
tRF-5	tRNA-Val-AAC-3-1	32	1.56	3.72	2.28	4.23	1.81	2.36
tRF-5	tRNA-Val-AAC-4-1	32	1.56	3.72	2.28	4.23	1.81	2.36
tRF-5	tRNA-Val-AAC-5-1	23	0.16	0.54	1.03	0.62	1.00	0.83
tRF-5	tRNA-Val-CAC-1-6	32	1.71	3.75	2.32	4.36	1.83	2.39
tRF-5	tRNA-Val-CAC-2-1	32	0.35	0.41	-	-	-	-
tRF-5	tRNA-Val-CAC-4-1	32	1.71	3.75	2.32	4.36	1.83	2.39
tRF-5	tRNA-Val-CAC-5-1	32	1.70	3.75	2.32	4.36	1.83	2.39
tRF-5	tRNA-Val-TAC-1-2	31	-	0.14	-	-	-	-
tRF-novel	tRNA-Asp-GTC-1-1	22	-	0.15	-	-	0.36	-
tRF-novel	tRNA-Asp-GTC-4-1	22	-	0.15	-	-	0.35	-
tRF-novel	tRNA-Asp-GTC-5-1	19	-	-	-	0.08	-	-
tRF-novel	tRNA-Gln-CTG-1-3	20	-	1.16	2.25	-	2.37	1.66
tRF-novel	tRNA-Gln-CTG-2-1	20	-	1.16	2.24	-	2.38	1.66
tRF-novel	tRNA-Gln-CTG-3-2	19	0.18	-	-	-	-	-
tRF-novel	tRNA-Gln-CTG-3-2	20	-	0.96	1.72	-	1.94	1.21
tRF-novel	tRNA-Gln-CTG-4-1	19	0.18	-	-	-	-	-
tRF-novel	tRNA-Gln-CTG-4-1	20	-	0.96	1.69	-	1.94	1.20
tRF-novel	tRNA-Gln-CTG-5-1	23	-	-	0.41	-	-	-

tRF-novel	tRNA-Gln-CTG-5-1	26	-	-	-	-	-	0.21
tRF-novel	tRNA-Gln-CTG-6-1	19	0.19	-	-	-	-	-
tRF-novel	tRNA-Gln-CTG-6-1	20	-	1.01	1.77	-	1.96	1.22
tRF-novel	tRNA-Gln-TTG-1-1	19	0.21	0.68	1.19	0.68	1.18	-
tRF-novel	tRNA-Gln-TTG-1-1	22	-	-	-	-	-	0.61
tRF-novel	tRNA-Gln-TTG-2-1	18	-	0.19	0.39	-	-	0.38
tRF-novel	tRNA-Gln-TTG-2-1	22	-	-	-	-	0.25	-
tRF-novel	tRNA-Gln-TTG-3-1	19	0.18	0.67	1.18	0.64	1.17	-
tRF-novel	tRNA-Gln-TTG-3-1	22	-	-	-	-	-	0.61
tRF-novel	tRNA-Glu-CTC-1-7	32	-	-	2.04	-	2.15	1.51
tRF-novel	tRNA-Glu-CTC-2-1	32	-	-	2.04	-	2.37	1.54
tRF-novel	tRNA-Gly-GCC-2-3	20	-	-	1.00	-	1.24	0.98
tRF-novel	tRNA-Gly-GCC-2-3	22	-	0.64	-	-	-	-
tRF-novel	tRNA-Gly-GCC-2-3	24	0.13	-	-	-	-	-
tRF-novel	tRNA-Gly-GCC-3-1	20	-	-	1.01	-	1.24	0.98
tRF-novel	tRNA-Gly-GCC-3-1	22	-	0.64	-	-	-	-
tRF-novel	tRNA-Gly-GCC-3-1	24	0.13	-	-	-	-	-
tRF-novel	tRNA-Gly-GCC-5-1	20	-	-	-	-	-	0.29
tRF-novel	tRNA-Gly-GCC-5-1	21	-	-	-	0.42	-	-
tRF-novel	tRNA-Gly-GCC-5-1	22	-	0.33	-	-	-	-
tRF-novel	tRNA-Gly-GCC-5-1	24	0.13	-	-	-	-	-
tRF-novel	tRNA-iMet-CAT-1-2	18	-	-	-	-	0.75	-
tRF-novel	tRNA-iMet-CAT-1-2	31	-	-	-	-	-	0.33
tRF-novel	tRNA-iMet-CAT-2-1	18	-	-	-	-	0.73	-
tRF-novel	tRNA-iMet-CAT-2-1	31	-	-	-	-	-	0.33
tRF-novel	tRNA-Lys-CTT-1-2	32	-	0.57	0.53	0.41	0.51	0.35
tRF-novel	tRNA-Lys-CTT-4-1	32	-	-	0.48	0.37	0.45	0.31
tRF-novel	tRNA-Lys-CTT-6-1	17	-	0.33	0.54	-	0.54	0.36
tRF-novel	tRNA-Lys-CTT-6-1	21	0.13	-	-	-	-	-
tRF-novel	tRNA-Lys-TTT-3-3	20	-	-	0.75	-	-	0.77
tRF-novel	tRNA-Lys-TTT-3-3	32	-	-	-	-	0.58	-
tRF-novel	tRNA-Lys-TTT-4-1	20	-	0.42	0.53	0.51	0.59	0.54
tRF-novel	tRNA-Lys-TTT-4-1	21	0.33	-	-	-	-	-
tRF-novel	tRNA-Lys-TTT-5-1	20	-	-	0.75	-	-	0.78
tRF-novel	tRNA-Lys-TTT-5-1	32	-	-	-	-	0.59	-
tRF-novel	tRNA-Lys-TTT-6-1	20	-	0.37	0.48	0.47	0.55	0.47
tRF-novel	tRNA-Lys-TTT-6-1	21	0.32	-	-	-	-	-
tRF-novel	tRNA-Met-CAT-2-1	21	-	-	-	-	0.21	0.12
tRF-novel	tRNA-Met-CAT-3-2	21	-	-	-	-	0.22	0.12
tRF-novel	tRNA-Met-CAT-4-3	21	-	-	-	-	0.21	0.12
tRF-novel	tRNA-Met-CAT-5-1	21	-	-	-	-	0.20	0.12
tRF-novel	tRNA-Thr-CGT-6-1	18	-	-	-	-	0.30	0.20
tRF-novel	tRNA-Val-CAC-2-1	18	-	-	0.61	-	-	0.33
tRF-novel	tRNA-Val-CAC-6-1	18	-	0.14	0.43	-	0.20	0.20
tRF-novel	tRNA-Val-CAC-6-1	20	0.22	-	-	0.33	-	-

tRF-novel	tRNA-Val-TAC-1-2	21	0.34	-	-	-	-	-
tRF-novel	tRNA-Val-TAC-2-1	17	0.08	-	-	-	-	-

Values are for percent average expression in tRF levels as calculated with tRF2Cancer. Treatments: A, ANG; R, RNase 1; U, Untreated. All tRFs were identified in at least 2 of 3 biological replicates.

TABLE S3. tRNAs with differential levels

tRNA Name	Δ*RNH1* A/R	Δ*RNH1* A/U	WT A/R	WT A/U
Tyr-GTA-chr10-3	-	-	-	-4.87133
Tyr-GTA-chr1-125	-2.84739	-5.87496	-2.7248	-2.92902
Tyr-GTA-chr14-8	-2.88621	-5.91918	-2.74293	-2.94326
Tyr-GTA-chr21-2	-2.84739	-5.87496	-2.7248	-2.92902
Tyr-GTA-chr2-12	-	-	-5.33511	-
Tyr-GTA-chr9-10	-	-6.21221	-	-
Tyr-GTA-chr9-4	-	-4.9163	-6.25643	-5.54804
Gln-TTG-6-1	-4.03757	-5.81164	-2.97997	-2.52093
Gln-TTG-9-1	-	0	-	-6.5197
Leu-TAA-1-1	-	-5.83236	-	-
Leu-TAA-4-1	-3.3889	-6.27025	-	-1.74909
Ala-AGC-1-1	-	-	-	-5.4994
Ala-AGC-4-1	-	-	-	-3.75695
Ala-AGC-8-1	-3.16365	-	-	-
Ala-AGC-8-2	-3.16365	-	-	-
Ala-CGC-3-1	-	-3.70617	-2.81208	-
Ala-CGC-4-1	-	-	-	-3.91345
Ala-CGC-5-1	-	0	-	-4.80576
Ala-TGC-3-1	-	-	-	-4.88762
Ala-TGC-3-2	-	-	-	-4.88762
Ala-TGC-4-1	-	-2.8163	-3.84068	-5.38585
Ala-TGC-5-1	-	-	-	-3.64791
Ala-TGC-6-1	-	-3.18095	-3.80565	-5.40732
Ala-TGC-7-1	-	-	-	-3.64791
Arg-ACG-1-1	-2.74799	-4.94213	-3.85961	-2.70908
Arg-ACG-1-2	-2.74799	-4.94213	-3.85961	-2.70908
Arg-ACG-1-3	-2.74799	-4.94213	-3.85961	-2.70908
Arg-ACG-2-1	-1.66102	-4.02698	-	-
Arg-ACG-2-2	-1.66102	-4.02698	-	-
Arg-ACG-2-3	-1.66102	-4.02698	-	-
Arg-ACG-2-4	-1.66102	-4.02698	-	-
Arg-CCG-1-1	-	-	-6.49877	-6.04571
Arg-CCG-1-2	-	-	-6.49877	-6.04571
Arg-CCG-1-3	-	-	-6.49877	-6.04571
Arg-CCG-2-1	-3.57593	-2.71029	-	-
Arg-CCT-1-1	-2.97442	-3.38158	-4.2399	-5.01787
Arg-CCT-2-1	-2.90074	-2.93241	-4.08597	-5.27897
Arg-CCT-3-1	-2.72708	-4.7063	-4.7801	-3.63992
Arg-CCT-4-1	-2.914	-3.7982	-4.92207	-3.64284
Arg-TCT-2-1	-1.353	-	-	-
Arg-TCT-3-1	-2.30423	-3.98003	-2.38368	-2.46517
Arg-TCT-5-1	-2.83725	-4.02529	-2.69144	-2.52392

Asn-GTT-10-1	-3.38862	-5.21624	-	-
Asn-GTT-1-1	-2.38239	-4.33996	-	-
Asn-GTT-17-1	-	-4.01939	0	0
Asn-GTT-2-1	-3.14037	-4.63759	-2.94271	-2.83827
Asn-GTT-2-2	-3.14037	-4.63759	-2.94271	-2.83827
Asn-GTT-2-3	-3.14037	-4.63759	-2.94271	-2.83827
Asn-GTT-2-4	-3.14037	-4.63759	-2.94271	-2.83827
Asn-GTT-2-5	-3.14037	-4.63759	-2.94271	-2.83827
Asn-GTT-2-6	-3.14037	-4.63759	-2.94271	-2.83827
Asn-GTT-3-1	-2.41427	-4.53507	-2.49934	-
Asn-GTT-3-2	-2.41427	-4.53507	-2.49934	-
Asn-GTT-4-1	-	-3.86388	-	-
Asn-GTT-6-1	-3.93791	-5.12842	-	-2.84623
Asp-GTC-3-1	-	-	-2.87834	-2.28779
Cys-GCA-1-1	2.087495	-	-	-
Cys-GCA-11-1	-	-4.87899	-	-
Cys-GCA-17-1	-	-5.23799	-	-
Cys-GCA-20-1	-	0	-	-4.14926
Cys-GCA-2-1	-1.01681	-	-	-
Cys-GCA-21-1	-	-5.89673	-	-
Cys-GCA-2-2	-1.01681	-	-	-
Cys-GCA-2-3	-1.01681	-	-	-
Cys-GCA-23-1	-	-5.43444	-	-
Cys-GCA-2-4	-1.01681	-	-	-
Cys-GCA-24-1	-	-5.6477	-	-
Cys-GCA-25-1	-	-5.94361	-	-
Cys-GCA-4-1	-0.99468	-	-	-
Cys-GCA-5-1	-1.89197	-2.60543	-	-
Cys-GCA-7-1	-	-3.99027	-	-
Cys-GCA-8-1	-	-2.42271	-	-
Gln-CTG-1-1	-	-2.47142	-1.72353	-1.57616
Gln-CTG-1-2	-	-2.47142	-1.72353	-1.57616
Gln-CTG-1-3	-	-2.47142	-1.72353	-1.57616
Gln-CTG-1-4	-	-2.47142	-1.72353	-1.57616
Gln-CTG-1-5	-	-2.47142	-1.72353	-1.57616
Gln-CTG-2-1	-	-2.47849	-1.72093	-1.56977
Gln-CTG-3-1	-4.1867	-6.77468	-2.70031	-2.8208
Gln-CTG-3-2	-4.1867	-6.77468	-2.70031	-2.8208
Gln-CTG-4-1	-1.77264	-4.5221	-2.449	-2.59942
Gln-CTG-4-2	-1.77264	-4.5221	-2.449	-2.59942
Gln-CTG-6-1	-3.94191	-6.56684	-2.50382	-2.70527
Gln-CTG-7-1	3.807028	-	-	-
Gln-CTG-chr19-4	-	-5.8547	-	-5.24018
Gln-TTG-1-1	-	-3.4299	-2.23288	-2.21515
Gln-TTG-2-1	-	-2.48766	-2.47785	-2.54207

Gln-TTG-3-1	-2.50934	-5.41082	-2.22001	-2.24104
Gln-TTG-3-2	-2.50934	-5.41082	-2.22001	-2.24104
Gln-TTG-3-3	-2.50934	-5.41082	-2.22001	-2.24104
Glu-CTC-1-1	0.526727	-	-0.55372	-0.63347
Glu-CTC-1-2	0.526727	-	-0.55372	-0.63347
Glu-CTC-1-3	0.526727	-	-0.55372	-0.63347
Glu-CTC-1-4	0.526727	-	-0.55372	-0.63347
Glu-CTC-1-5	0.526727	-	-0.55372	-0.63347
Glu-CTC-1-6	0.526727	-	-0.55372	-0.63347
Glu-CTC-1-7	0.526727	-	-0.55372	-0.63347
Glu-CTC-2-1	0.527545	-	-0.54934	-0.62824
Glu-CTC-5-1	-	-	-4.56486	-4.73422
Glu-TTC-10-1	-	-2.90076	-3.23469	-2.61027
Glu-TTC-1-1	-	-	-1.80243	-
Glu-TTC-1-2	-	-	-1.80243	-
Glu-TTC-2-1	1.405875	-	-	-
Glu-TTC-2-2	1.405875	-	-	-
Glu-TTC-3-1	1.734595	1.528142	-	-
Glu-TTC-4-1	1.715924	1.474512	-	-
Glu-TTC-4-2	1.715924	1.474512	-	-
Glu-TTC-8-1	1.751555	1.573552	-	-
Glu-TTC-9-1	-	-	-3.61911	-2.70689
Gly-CCC-1-1	-	-	-0.711	-
Gly-CCC-1-2	-	-	-0.711	-
Gly-CCC-2-1	-1.57105	-2.30654	-	-
Gly-CCC-2-2	-1.57105	-2.30654	-	-
Gly-CCC-5-1	-	-	-2.61238	-
Gly-CCC-6-1	-4.52526	-7.67051	-2.64083	-2.14447
Gly-CCC-7-1	-	-4.26859	-	-4.3871
Gly-GCC-1-1	0.595762	-	-	-
Gly-GCC-1-2	0.595762	-	-	-
Gly-GCC-1-3	0.595762	-	-	-
Gly-GCC-1-4	0.595762	-	-	-
Gly-GCC-1-5	0.595762	-	-	-
Gly-GCC-2-1	-	-0.29743	-	-
Gly-GCC-2-2	-	-0.29743	-	-
Gly-GCC-2-3	-	-0.29743	-	-
Gly-GCC-2-4	-	-0.29743	-	-
Gly-GCC-2-5	-	-0.29743	-	-
Gly-GCC-2-6	-	-0.29743	-	-
Gly-GCC-3-1	-	-0.29507	-	-
Gly-GCC-5-1	-	-	0.411541	-
Gly-TCC-1-1	-	-	-2.45662	-
Gly-TCC-2-1	-1.05364	-3.0875	-2.2854	-2.43261
Gly-TCC-2-2	-1.05364	-3.0875	-2.2854	-2.43261

Gly-TCC-2-3	-1.05364	-3.0875	-2.2854	-2.43261
Gly-TCC-2-4	-1.05364	-3.0875	-2.2854	-2.43261
Gly-TCC-2-5	-1.05364	-3.0875	-2.2854	-2.43261
Gly-TCC-2-6	-1.05364	-3.0875	-2.2854	-2.43261
Gly-TCC-3-1	-	-1.87289	-	-
Gly-TCC-4-1	-	-5.67056	-	-
His-GTG-1-1	-	-	-0.9771	-
His-GTG-1-2	-	-	-0.9771	-
His-GTG-1-3	-	-	-0.9771	-
His-GTG-1-4	-	-	-0.9771	-
His-GTG-1-5	-	-	-0.9771	-
His-GTG-1-6	-	-	-0.9771	-
His-GTG-1-7	-	-	-0.9771	-
His-GTG-1-8	-	-	-0.9771	-
His-GTG-1-9	-	-	-0.9771	-
His-GTG-2-1	-	-3.05468	-	-
Ile-AAT-2-1	-	-5.6513	-	-
Ile-AAT-3-1	-	-5.6513	-	-
Ile-AAT-4-1	-	-4.78252	-3.73081	-5.04677
Ile-AAT-5-1	-	-5.78252	-	-
Ile-AAT-5-2	-	-5.78252	-	-
Ile-AAT-5-3	-	-5.78252	-	-
Ile-AAT-5-4	-	-5.78252	-	-
Ile-AAT-5-5	-	-5.78252	-	-
Ile-AAT-6-1	-	0	-4.77731	-5.31357
Ile-AAT-8-1	-3.03752	-5.42197	-	-
Ile-AAT-9-1	-	-	-	-4.56285
Ile-TAT-1-1	-	-3.53551	-	0
Ile-TAT-2-3	-	-3.53551	-	0
Leu-AAG-1-1	-1.97216	-	-	-
Leu-AAG-1-2	-1.97216	-	-	-
Leu-AAG-1-3	-1.97216	-	-	-
Leu-AAG-2-1	-1.96557	-	-	-
Leu-AAG-2-2	-1.96557	-	-	-
Leu-AAG-2-3	-1.96557	-	-	-
Leu-AAG-2-4	-1.96557	-	-	-
Leu-AAG-3-1	-1.96557	-	-	-
Leu-CAA-1-1	-2.08231	-3.8873	-3.56686	-4.32631
Leu-CAA-1-2	-2.12699	-3.94946	-3.16643	-4.1876
Leu-CAA-2-1	-2.13368	-4.01688	-2.49639	-3.90116
Leu-CAA-3-1	-2.06275	-3.83784	-	-3.45589
Leu-CAA-4-1	-2.00092	-4.06073	-3.2061	-4.31379
Leu-TAA-1-1	1.534311	-	-	-
Leu-TAA-3-1	-	-3.54277	-4.3062	-5.48883
Leu-TAA-4-1	1.892357	-	0	0

Leu-TAG-1-1	-1.90925	-	-	-
Leu-TAG-2-1	1.184648	-	-	-
Leu-TAG-3-1	-	-	-3.39643	-3.49197
Lys-CTT-10-1	-	-	-4.77731	-
Lys-CTT-1-1	-	-0.9831	1.494161	1.715847
Lys-CTT-11-1	-3.73159	-6.07767	-4.64839	-4.39485
Lys-CTT-1-2	-	-0.9831	1.494161	1.715847
Lys-CTT-2-1	-	-1.16184	2.685364	2.172222
Lys-CTT-2-2	-	-1.16184	2.685364	2.172222
Lys-CTT-2-3	-	-1.16184	2.685364	2.172222
Lys-CTT-2-4	-	-1.16184	2.685364	2.172222
Lys-CTT-2-5	-	-1.16184	2.685364	2.172222
Lys-CTT-3-1	-2.99274	-3.27634	-2.29151	-
Lys-CTT-4-1	-	-0.92587	1.747432	1.943258
Lys-CTT-5-1	-	-2.53749	-	-
Lys-CTT-6-1	-4.34442	-7.53133	-3.95648	-4.23472
Lys-CTT-7-1	-	-2.73505	-	-
Lys-CTT-8-1	-	-2.16739	-	-
Lys-CTT-chr15-5	0	0	-5.87359	-4.64518
Lys-CTT-chr7-30	-	-5.40885	-8.55701	-7.28096
Lys-TTT-1-1	-	-3.06257	-	-
Lys-TTT-14-1	-	-	-7.00079	-6.16658
Lys-TTT-2-1	-	-3.06928	-	-
Lys-TTT-3-1	-1.1947	-	-	-
Lys-TTT-3-2	-1.1947	-	-	-
Lys-TTT-3-3	-1.1947	-	-	-
Lys-TTT-3-4	-1.1947	-	-	-
Lys-TTT-3-5	-1.1947	-	-	-
Lys-TTT-4-1	-1.20819	-2.152	-2.50242	-3.01758
Lys-TTT-5-1	-1.20138	-	-	-
Lys-TTT-6-1	-	-	-2.56562	-2.48742
Lys-TTT-7-1	-1.59498	-	-2.76709	-4.59281
Lys-TTT-8-1	1.527709	-	-	-
Lys-TTT-9-1	-	-4.67056	-7.11426	-7.00816
Met-CAT-1-1	-2.39592	-3.52847	-2.68089	-2.72254
Met-CAT-2-1	-	-	-	-4.02769
Met-CAT-4-1	-	-	-	-4.02769
Met-CAT-4-2	-	-	-	-4.02769
Met-CAT-4-3	-	-	-	-4.02769
Met-CAT-5-1	-	-	-	-3.99376
Met-CAT-6-1	-2.30853	-3.21335	-	-
Phe-GAA-1-1	-2.9256	-4.97001	-	-2.92443
Phe-GAA-1-2	-2.9256	-4.97001	-	-2.92443
Phe-GAA-1-3	-2.9256	-4.97001	-	-2.92443
Phe-GAA-1-4	-2.9256	-4.97001	-	-2.92443

Phe-GAA-1-5	-2.9256	-4.97001	-	-2.92443
Phe-GAA-1-6	-2.9256	-4.97001	-	-2.92443
Phe-GAA-2-1	-2.89596	-5.13445	-	-2.95498
Phe-GAA-3-1	-	-4.64224	-3.2557	-3.29209
Phe-GAA-5-1	-	-5.77334	-5.16742	-6.47032
Pro-AGG-2-1	-	-	-2.25965	-
Pro-AGG-2-2	-	-	-2.25965	-
Pro-AGG-2-3	-	-	-2.25965	-
Pro-AGG-2-4	-	-	-2.25965	-
Pro-AGG-2-5	-	-	-2.25965	-
Pro-AGG-2-6	-	-	-2.25965	-
Pro-AGG-2-7	-	-	-2.25965	-
Pro-AGG-2-8	-	-	-2.25965	-
Pro-TGG-1-1	-3.96671	-5.46154	-3.06563	-2.98239
Pro-TGG-3-1	-	-	-2.26255	-
Pro-TGG-3-2	-	-	-2.26255	-
Pro-TGG-3-3	-	-	-2.26255	-
Pro-TGG-3-4	-	-	-2.26255	-
Pro-TGG-3-5	-	-	-2.26255	-
SeC-TCA-2-1	-	-	-	-3.04198
Ser-AGA-4-1	-2.55139	-4.37715	-3.73567	-4.61312
Ser-CGA-1-1	3.287595	-	-	-
Ser-CGA-2-1	3.285537	-	-	-
Ser-CGA-3-1	4.411013	-	-	-
Ser-CGA-4-1	-	-	-3.69289	-3.38046
Ser-GCT-1-1	3.896844	-	-	-
Ser-GCT-2-1	3.897154	-	-	-
Ser-GCT-3-1	3.789298	-	-	-
Ser-GCT-4-1	3.743573	-	-	-
Ser-GCT-4-2	3.743573	-	-	-
Ser-GCT-4-3	3.743573	-	-	-
Ser-GCT-5-1	3.934759	-	-	-
Ser-GCT-6-1	-2.00766	-4.93301	-	-
Ser-TGA-1-1	-	-	-3.77731	-3.96542
Sup-TTA-1-1	-2.56782	-5.51812	-	-
Thr-AGT-2-1	-	-5.45035	-4.88888	-4.6536
Thr-AGT-2-2	-	-5.45035	-4.88888	-4.6536
Thr-AGT-3-1	-	-4.57914	-4.52735	-4.19873
Thr-AGT-4-1	-	-	-5.70601	-6.29743
Thr-AGT-5-1	-	-	-6.8131	-6.08453
Thr-AGT-6-1	-	-5.45035	-4.77174	-4.6536
Thr-CGT-3-1	-	-5.45035	-4.28061	-4.12851
Thr-TGT-2-1	-	-	-3.19235	-
Thr-TGT-3-1	-	-	-	-3.96542
Thr-TGT-4-1	-	-2.89558	-	-

Thr-TGT-5-1	-2.27964	-3.31719	-	-
Thr-TGT-6-1	-	-2.24326	-	-
Trp-CCA-1-1	-	-	-	-4.33418
Trp-CCA-3-1	-	-	-	-3.59722
Trp-CCA-3-2	-	-	-	-3.59722
Trp-CCA-3-3	-	-	-	-3.59722
Tyr-GTA-1-1	-	-6.46733	-7.23661	-6.54804
Tyr-GTA-3-1	-5.74764	-7.63914	-5.16308	-5.93971
Tyr-GTA-4-1	-	-	-5.37052	-3.67405
Tyr-GTA-5-1	-	-2.78282	-5.33387	-4.22301
Tyr-GTA-5-2	-	-4.65906	-	-
Tyr-GTA-5-3	-	-2.87439	-5.24219	-
Tyr-GTA-5-4	-	-2.87439	-4.66195	-
Tyr-GTA-5-5	-	-2.87439	-5.03428	-4.93234
Tyr-GTA-6-1	-	-2.50943	-4.95075	-4.662
Tyr-GTA-7-1	-	-	-5.37052	-3.30521
Tyr-GTA-8-1	-	-3.53551	-4.83117	-5.61011
Val-AAC-1-1	-0.5647	0.604749	-0.6896	-0.8064
Val-AAC-1-2	-0.5647	0.604749	-0.6896	-0.8064
Val-AAC-1-3	-0.5647	0.604749	-0.6896	-0.8064
Val-AAC-1-4	-0.5647	0.604749	-0.6896	-0.8064
Val-AAC-1-5	-0.5647	0.604749	-0.6896	-0.8064
Val-AAC-2-1	-1.52364	-	-1.33314	-
Val-AAC-3-1	-0.5647	0.605364	-0.6891	-0.80594
Val-AAC-4-1	-0.56466	0.606216	-0.68901	-0.80599
Val-CAC-10-1	-	-	-4.83456	-4.14926
Val-CAC-1-1	-0.35309	-	0.339328	-
Val-CAC-11-1	-	-	-	-4.73422
Val-CAC-11-2	-	-	-	-4.73422
Val-CAC-1-2	-0.35309	-	0.339328	-
Val-CAC-1-3	-0.35309	-	0.339328	-
Val-CAC-1-4	-0.35309	-	0.339328	-
Val-CAC-1-5	-0.35309	-	0.339328	-
Val-CAC-1-6	-0.35309	-	0.339328	-
Val-CAC-2-1	-	0.956561	-	-
Val-CAC-4-1	-0.35309	-	0.339975	-
Val-CAC-5-1	-0.35217	-	0.358185	-
Val-TAC-2-1	-1.28588	-3.23338	-2.32199	-2.43273

Values are for log$_2$(fold change) in tRNA levels as calculated with NOISeqBIO. Treatments: A/R, log$_2$(ANG/RNase 1); A/U, log$_2$(ANG/untreated). All values of log$_2$(fold change) have $p \leq 0.05$.

TABLE S4. miRNA with differential levels

miRNA Name	Δ*RNH1* A/R	Δ*RNH1* A/U	WT A/R	WT A/U
hsa-miR-92b-3p	0.637961	-	0.917395	-
hsa-miR-21-5p	0.23454	0.391549	-0.28297	-
hsa-miR-1246	-3.48241	-	-	-
hsa-miR-181b-5p	0.398107	0.309214	-	-
hsa-miR-192-5p	-0.34387	-	-	-
hsa-let-7i-5p	-0.56144	-	-0.72627	-
hsa-miR-196a-5p	-0.81072	-	-	-
hsa-miR-183-5p	-	-	-1.52403	-
hsa-miR-16-5p	-	-	-0.55057	-
hsa-miR-423-3p	0.46394	-	-	-
hsa-miR-98-5p	-0.70656	-	-0.54702	-
hsa-miR-10a-5p	-	-0.56752	-	-
hsa-let-7b-5p	-0.44477	-	-0.55481	-
hsa-miR-92a-3p	0.696078	-	0.685252	-
hsa-miR-191-5p	-0.61775	-0.58719	-0.6549	-
hsa-let-7c-5p	-0.88866	-	-0.76867	-
hsa-miR-27b-3p	-	-0.38275	-	-
hsa-miR-148b-3p	-	-0.358	-	-
hsa-miR-30a-5p	-	0.377059	-	-
hsa-miR-93-5p	-0.31718	-	-0.78504	-
hsa-miR-99b-5p	-	-1.48949	-	-
hsa-miR-100-5p	-	-0.94423	-	-
hsa-miR-21-3p	-	-0.53326	-	-
hsa-miR-24-3p	-	-	-1.15176	-
hsa-miR-320a	-0.67418	-	-0.79949	-
hsa-miR-99a-5p	-	-1.06808	-	-
hsa-miR-22-3p	-	-0.26951	-	-
hsa-miR-30d-5p	-	0.303704	-	-
hsa-miR-423-5p	0.306335	-	-	-
hsa-miR-186-5p	-0.35832	-	-	-
hsa-miR-193b-3p	-1.1136	-	-1.49097	-
hsa-miR-17-5p	-	-	-0.78964	-
hsa-miR-148a-3p	-	-0.39106	-0.40573	-
hsa-miR-374a-3p	-	-0.86105	-	-
hsa-miR-181a-5p	-	0.36722	-	-
hsa-miR-27a-3p	-	-0.26946	-	-
hsa-miR-106b-3p	-	0.848428	-	-
hsa-miR-126-5p	-	-1.2177	-	-
hsa-miR-30c-5p	-	-0.41851	-	-
hsa-let-7e-5p	-	-0.39318	-	-
hsa-miR-30a-3p	-	-0.39102	-	-
hsa-miR-182-5p	-	0.630049	-	-

hsa-miR-20a-5p	-	-	-0.54094	-
hsa-miR-331-3p	-	-1.33843	-	-
hsa-miR-484	-	-0.81671	-	-
hsa-miR-31-5p	-	-	-0.51893	-
hsa-miR-221-3p	-	-	-0.66057	-
hsa-miR-103a-3p	-	-	-0.27398	-

Values are for $\log_2$(fold change) in tRNA levels as calculated with NOISeqBIO. Treatments: A/R, $\log_2$(ANG/RNase 1); A/U, $\log_2$(ANG/untreated). All values of $\log_2$(fold change) have $p \leq 0.05$.

Table S5. Enriched GO terms for miRNAs

Upregulated miRNAs	Downregulated miRNAs
hsa-miR-181b-5p, hsa-miR-423-3p, hsa-miR-92b-3p, hsa-miR-92a-3p, hsa-miR-181a-5p	hsa-miR-192-5p, hsa-miR-98-5p, hsa-miR-196a-5p, hsa-let-7c-5p, hsa-let-7i-5p, hsa-let-7b-5p, hsa-miR-193b-3p, hsa-miR-320a, hsa-miR-22-3p, hsa-miR-103a-3p, hsa-miR-93-5p, hsa-miR-183-5p, hsa-miR-31-5p, hsa-miR-17-5p, hsa-miR-20a-5p hsa-miR-24-3p, hsa-miR-221-3p, hsa-miR-192-5p

Unique enriched GO terms in miRNAs upregulated after ANG treatment

Name	Log size
U6 snRNA binding	3.114
RNA polymerase II repressing transcription factor binding	2.976
6-phosphofructo-2-kinase activity	3.356
glutathione transferase activity	3.671
microtubule binding	4.557
NADP binding	4.917
protein binding involved in protein folding	3.250
hydrogen ion transmembrane transporter activity	5.115
axon guidance receptor activity	2.220
modified amino acid binding	4.368
calcium-dependent phospholipase A2 activity	1.908
deacetylase activity	4.212
polyubiquitin binding	3.321
translation initiation factor activity	4.762
NAD$^+$ ADP-ribosyltransferase activity	3.663
steroid hormone receptor activity	3.829
cyclin-dependent protein serine/threonine kinase inhibitor activity	3.104
phosphatidylinositol-3-phosphatase activity	2.768
protein deacetylase activity	3.833
lyase activity	5.704
transcription coactivator activity	4.105
centromeric DNA binding	2.906
eukaryotic translation initiation factor 2α kinase activity	2.639
NADPH binding	3.704
single-stranded RNA binding	3.899
MAP kinase activity	3.725
ATP-dependent DNA helicase activity	4.659
phosphotyrosine binding	3.104
poly(A) binding	3.024
MHC class I receptor activity	1.771
signal recognition particle binding	3.274
fructose binding	2.053
Y-form DNA binding	2.377

acetyltransferase activity	5.239
methyltransferase activity	5.593
transferase activity	6.472
fructose-2,6-bisphosphate 2-phosphatase activity	2.413
S-methyl-5-thioribose-1-phosphate isomerase activity	3.355
bisphosphoglycerate 2-phosphatase activity	1.708
bisphosphoglycerate mutase activity	2.468
transferase activity, transferring acyl groups	5.610
LRR domain binding	2.515
scavenger receptor activity	3.761
insulin receptor substrate binding	2.528
translation initiation factor binding	3.625
insulin-like growth factor binding	3.297
protein homodimerization activity	4.493
α-2A adrenergic receptor binding	2.004
threonine-type endopeptidase activity	4.253
androgen receptor binding	2.808
insulin-like growth factor-activated receptor activity	1.505
peroxiredoxin activity	4.348

Unique enriched GO terms in miRNAs downregulated after ANG treatment

Name	Log size
cofactor binding	5.897
protein disulfide oxidoreductase activity	4.634
peroxidase activity	4.725
cyclin binding	3.226
hydrolase activity	6.497
chemoattractant activity	2.815
cell adhesion molecule binding	4.095
protein serine/threonine/tyrosine kinase activity	3.596
protein tyrosine kinase activity	4.288
non-membrane spanning protein tyrosine kinase activity	3.768
electron carrier activity	5.254
NAD binding	5.129
L-ascorbic acid binding	3.938
Hsp90 protein binding	2.934
protein self-association	3.279
translation factor activity, RNA binding	5.107
protein tyrosine phosphatase activity	4.515
transcription factor activity, protein binding	5.074
phosphatidylinositol 3-kinase binding	2.873
Wnt-protein binding	3.083
sequence-specific DNA binding	5.495
oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	4.399
thiol-dependent ubiquitin-specific protease activity	4.040

protein transporter activity	4.863
growth factor binding	3.677
peptide binding	4.098
calcium-dependent protein binding	3.176
DNA-directed DNA polymerase activity	4.808
catalytic activity	6.967
helicase activity	5.236
microtubule motor activity	4.487
histone acetyltransferase activity	3.966
manganese ion binding	4.557
4 iron, 4 sulfur cluster binding	5.152
PDZ domain binding	3.259
peptidase activity	5.756
transcription corepressor activity	3.847
protein kinase inhibitor activity	3.627
RNA binding	5.871
core promoter binding	3.798
receptor activity	5.579
mRNA 3'-UTR binding	3.365
double-stranded RNA binding	4.071
DNA binding	6.247
p53 binding	3.276
ion channel binding	3.388
chaperone binding	4.155
histone-lysine *N*-methyltransferase activity	3.995
single-stranded DNA binding	4.490
vitamin D receptor binding	2.217
methylated histone binding	3.331
transforming growth factor β-activated receptor activity	2.529
lamin binding	2.493
transforming growth factor β binding	2.667
RNA polymerase II carboxy-terminal domain kinase activity	3.175

Enriched Molecular Function GO terms for miRNAs up- or downregulated after ANG treatment. Lists of differentially regulated miRNAs were chosen from hierarchical clusters of fold-change data generated with NOISeqBIO (see: Table S3). The GO terms listed are semantically reduced, and then analyzed for uniqueness using network analysis (see: Materials and Methods section). “Log size” refers to the extent of enrichment for a particular term.

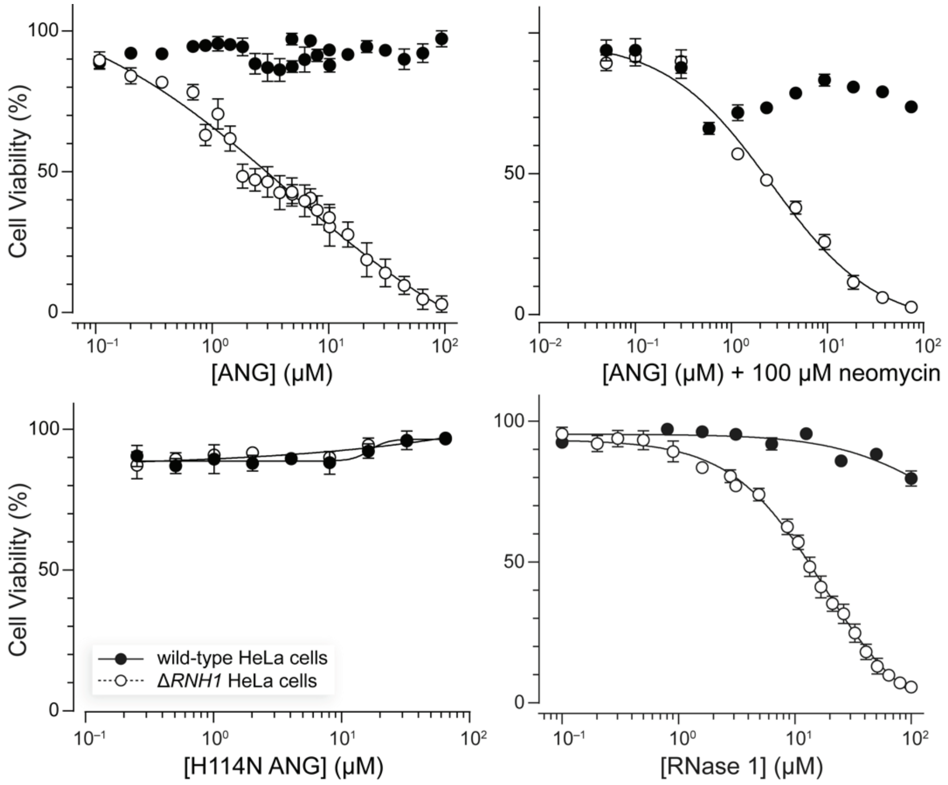

Figure S1. Toxicity of ANG and related proteins for wild-type and Δ*RNH1* HeLa cells. Ribonucleases were incubated with cells for 48 h at 37 °C and 5% CO_2. Data points are the average of at least three biological replicates as measured with a tetrazolium dye-based assay for metabolic activity. Values of EC_{50} were calculated by fitting the data to Eq. 1 and are listed in Table 1.