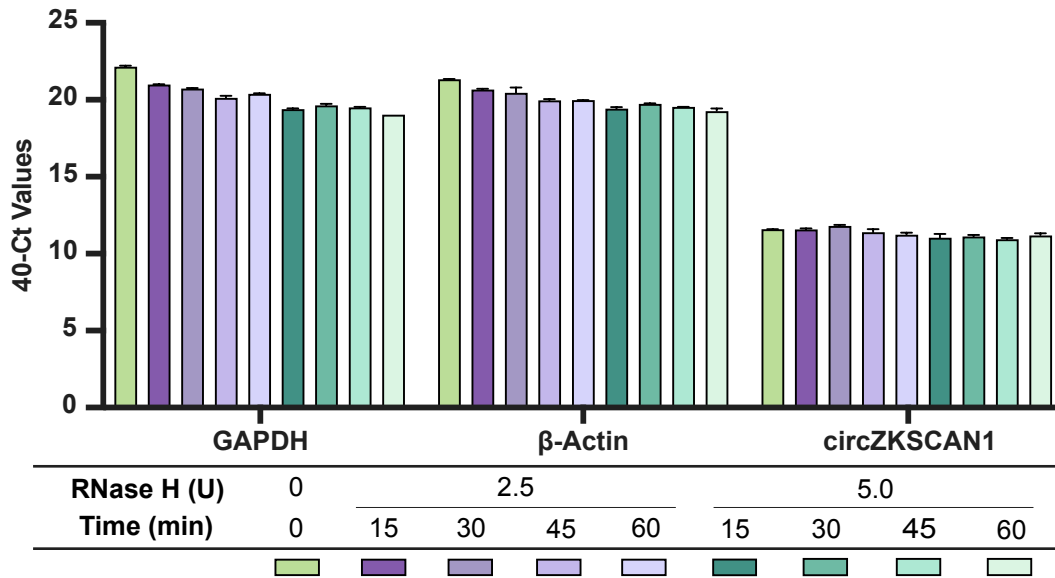
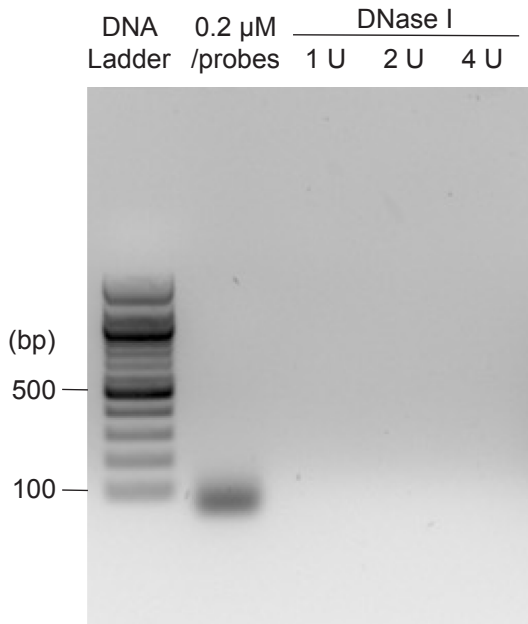


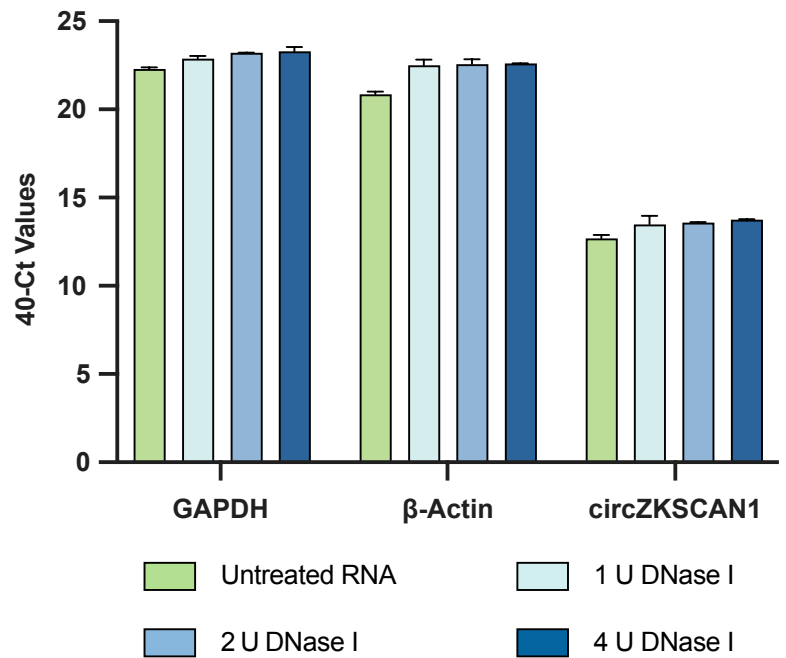
A



B

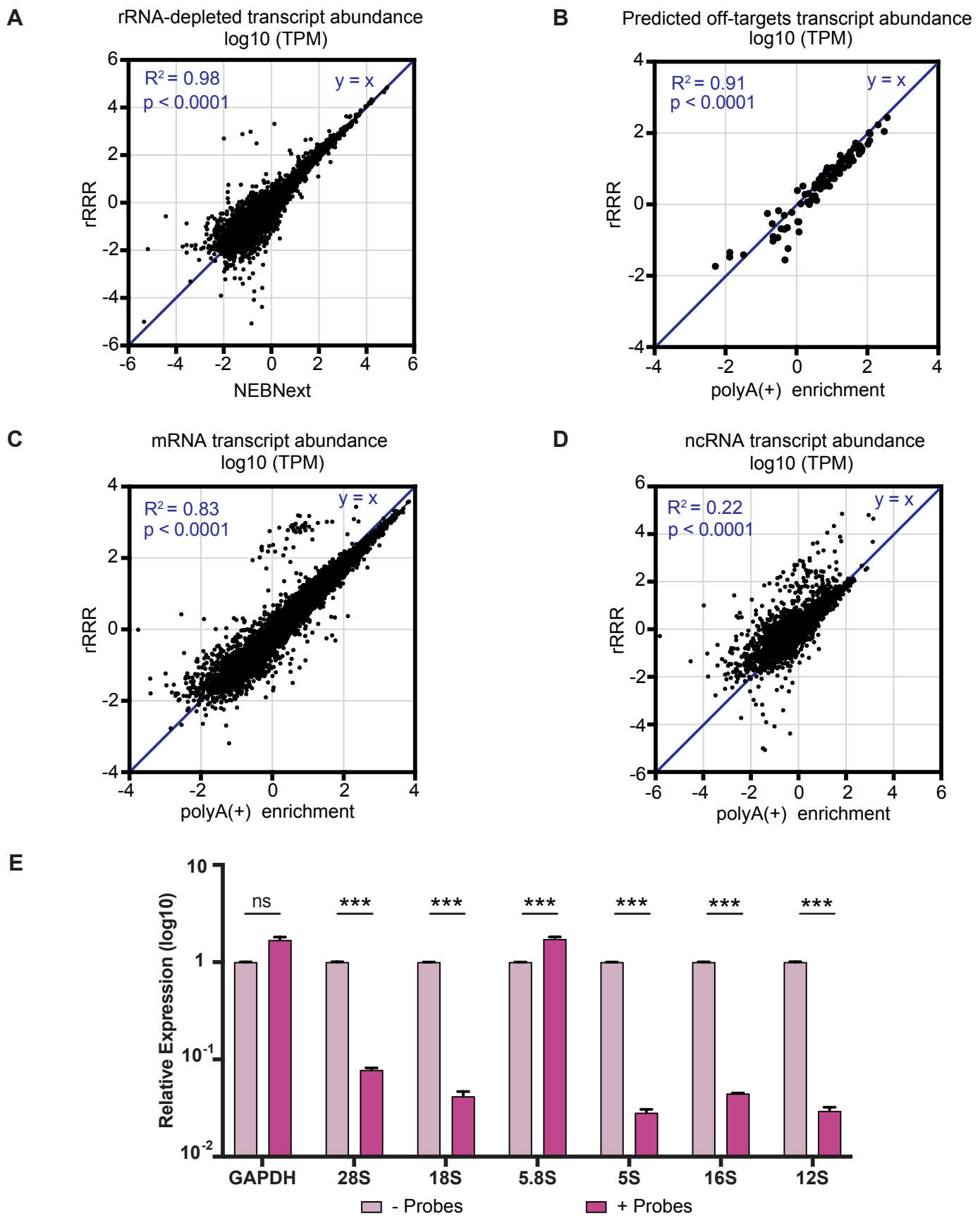


C



**Supplemental Figure 1.** Optimization of rRRR for removal of excess of probes and efficient rRNA depletion.

- A) Total HeLa RNA was incubated with 0, 2.5, or 5.0 U of RNase H for 0, 15, 30, 45, or 60 minutes. RT-qPCR of the RNA after the incubations showed the effects of the enzyme on non-rRNAs (GAPDH,  $\beta$ -Actin, and circZKSCAN1) to determine an optimal condition that does not cause unwanted degradation of non-rRNA genes.
- B) 0.2  $\mu$ M probes were incubated with increasing units of DNase I to find optimum unit needed for removing the probes.
- C) RT-qPCR of GAPDH,  $\beta$ -Actin, and cZKSCAN1 after treatment with 1 U, 2 U, or 4 U of DNase I (Mean of n = 3 technical replicates with SEM).



**Supplemental Figure 2.** rRRR in comparison to other commercial methods.

A) Analysis of rRNA-depleted RNA transcripts between rRRR and NEBNext treated RNA depicted  $R^2 = 0.98$ .

B) Predicted off-targets transcripts between rRRR treated RNA and polyA RNA had  $R^2 = 0.91$ .

C) Scatter plots for mRNA and (D) ncRNA between rRRR-treated RNA and polyA(+) RNA showed  $R^2 = 0.83$  and  $0.22$  respectively. RNA-seq was performed in duplicate. TPM: Transcripts Per Million,  $R^2$ : Coefficient of determination.

E) Relative expression of transcripts in “- Probes” and “+ Probes” from HeLa RNA depleted for rRNAs using RiboMinus Kit. Representative data is shown as mean of  $n = 3$  biological replicates with SEM.

ns:  $p > 0.05$ , \* :  $p \leq 0.05$ , \*\* :  $p \leq 0.01$ , \*\*\* :  $p \leq 0.001$  (unpaired t-test).

## A. Probes Hybridization

RNA Amount	Volume ( $\mu\text{L}$ )	46.6 $\mu\text{M}$ Probes ( $\mu\text{L}$ )	1M Tris-Cl (pH 7.4) ( $\mu\text{L}$ )	5M NaCl ( $\mu\text{L}$ )	H <sub>2</sub> O
1 $\mu\text{g}$	x	2.0	1.0	0.4	up to 10 $\mu\text{L}$
10 $\mu\text{g}$	x	20.0	3.0	1.2	up to 30 $\mu\text{L}$
20 $\mu\text{g}$	x	40.0	6.0	2.4	up to 60 $\mu\text{L}$

Incubation: 95 °C for 2 minutes, TD from 95 °C to 22 °C 0.1C/sec, and hold at 22 °C for 5 minutes

## B. RNase H Reaction

RNA Amount	Vol. From Previous Reaction ( $\mu\text{L}$ )	RNase H ( $\mu\text{L}$ )	10X RNase H Buffer ( $\mu\text{L}$ )	H <sub>2</sub> O
1 $\mu\text{g}$	10.0	0.5	1.5	up to 15 $\mu\text{L}$
10 $\mu\text{g}$	30.0	5.0	4.0	up to 40 $\mu\text{L}$
20 $\mu\text{g}$	60.0	10.0	8.0	up to 80 $\mu\text{L}$

Incubation: 37 °C for 30 minutes

## C. DNase I Reaction

RNA Amount	Vol. From Previous Reaction ( $\mu\text{L}$ )	DNase I ( $\mu\text{L}$ )	10X DNase I Buffer ( $\mu\text{L}$ )	H <sub>2</sub> O
1 $\mu\text{g}$	15.0	1.0	2.0	up to 20 $\mu\text{L}$
10 $\mu\text{g}$	40.0	10.0	6.0	up to 60 $\mu\text{L}$
20 $\mu\text{g}$	80.0	20.0	12.0	up to 120 $\mu\text{L}$

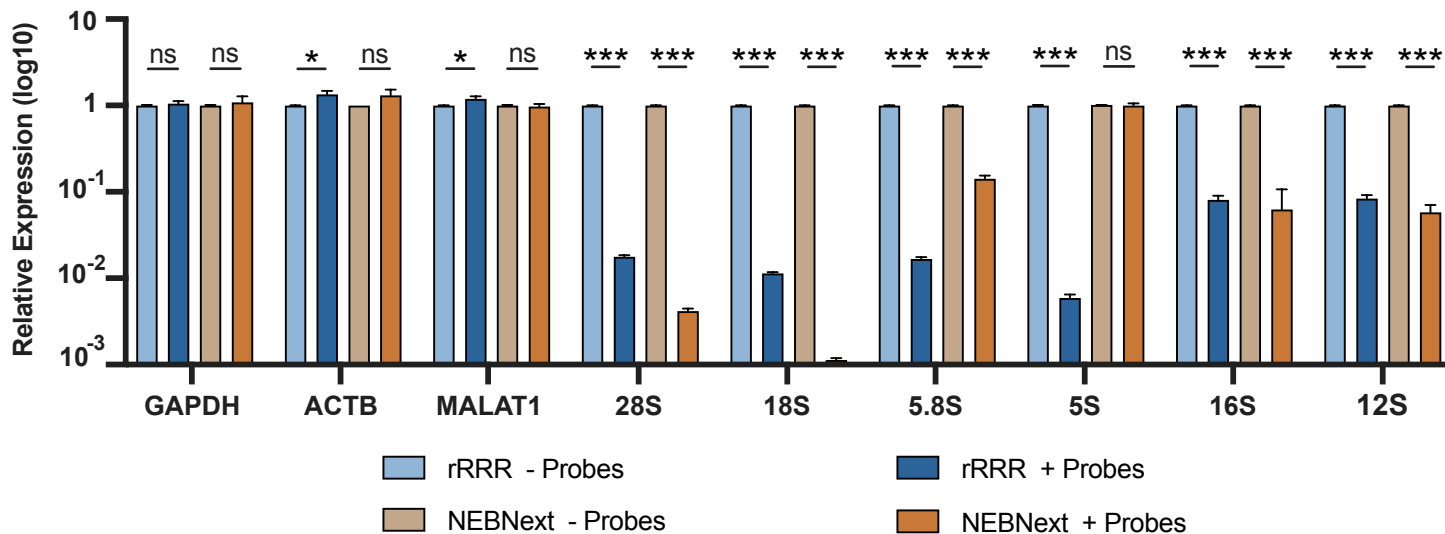
Incubation: 37 °C for 30 minutes

## D. Bead Purification

RNA Amount	Volume of Previous Reaction	Beads ( $\mu\text{L}$ )
1 $\mu\text{g}$	20.0	36.0
10 $\mu\text{g}$	60.0	108.0
20 $\mu\text{g}$	110.0	198.0

Followed manufacturer's protocol

**Supplemental Figure 3.** Reactions volumes used for rRNA depletions with 1  $\mu\text{g}$ , 10  $\mu\text{g}$ , and 20  $\mu\text{g}$  of starting input RNA.



**Supplemental Figure 4.** Relative expression of transcripts in “- Probes” and “+ Probes” extracted from human lymph node FFPE cores was subjected to rRNA depletion using rRRR and NEBNext.

Representative data is shown as mean of n = 3 biological replicates with SEM.

ns:  $p > 0.05$ , \* :  $p \leq 0.05$ , \*\* :  $p \leq 0.01$ , \*\*\* :  $p \leq 0.001$  (unpaired t-test).

A

Procedure	Reagent	Catalog #	$\mu\text{L}$ per ug reaction	Cost per 1 $\mu\text{g}$ Reaction
<b>Baldwin et. al.</b>	25 nmole DNA Oligo 50-mer (n = 195 probes), 100 $\mu\text{M}$	Sigma	3.3	\$0.24
	Lucigen Thermostable RNase H, 5 U/ $\mu\text{l}$	H39500	2.0	\$8.84
	Turbo DNase, 2 U/ $\mu\text{l}$	AM2238	7.5	\$2.28
	Beckman Coulter Agencourt RNAClean XP Beads	A63987	176.0	\$4.00
	<b>Total Cost</b>			<b>\$15.40</b>

B

Procedure	Reagent	Catalog #	$\mu\text{L}$ per ug reaction	Cost per 1 $\mu\text{g}$ Reaction
<b>RTR2D</b>	25 nmole DNA Oligo 35-mer (n = 30 probes), 50 $\mu\text{M}$	Sigma	6.0	\$0.15
	NEB M-MuLV Reverse Transcriptase, 200 U/ $\mu\text{l}$	M0253S	1.0	\$1.74
	NEB RNase Inhibitor, 2 U/ $\mu\text{l}$	M0314S	2.0	\$0.45
	NEB Exonuclease I, 2 U/ $\mu\text{l}$	M0293S	2.0	\$2.16
	NEB RNase H, 2 U/ $\mu\text{l}$	M0297S	2.0	\$1.05
	NEB DNase I, 2 U/ $\mu\text{l}$	M0303S	2.0	\$3.28
	NEB dNTPs, 10 mM	N0447S	2.0	\$0.31
	Thermo Phenol Chloroform based purifications	15593031	600	\$1.00
<b>Total Cost</b>			<b>\$10.14</b>	

**Supplemental Figure 5.** Cost breakdown of other non-commercial RNase-H based rRNA depletion methods

A) Cost of reagents for RNase H based rRNA depletion method by Baldwin et. al. (9) was calculated. The cost for depleting rRNAs from 1  $\mu\text{g}$  of total RNA amounted to \$15.4.

B) Cost calculations of RTR2D (10), totaled to \$10.14 for depleting rRNAs from 1  $\mu\text{g}$  of total RNA.