

Figure 1-Figure Supplement 1. Distribution of cholesterol, protein, and triglycerides across size-exclusion fractions. (A-C) Colorimetric assays for (A) total cholesterol, (B) total protein, and (C) triglycerides.). Wild-type, WT (blue); Scavenger receptor BI Knockout mice (*Scarb1^{-/-}*), SR-BI KO (red). Size-exclusion chromatography fractions used to isolate HDL and APOB particles. mg, milligrams. HDL WT, N=7; HDL SR-BI KO N=7; APOB WT, N=7, APOB SR-BI KO N=7; Liver WT, N=7; Liver SR-BI KO, N=7; Bile WT, N=7; Bile SR-BI KO, N=6; Urine WT, N=5; Urine SR-BI KO, N=6.

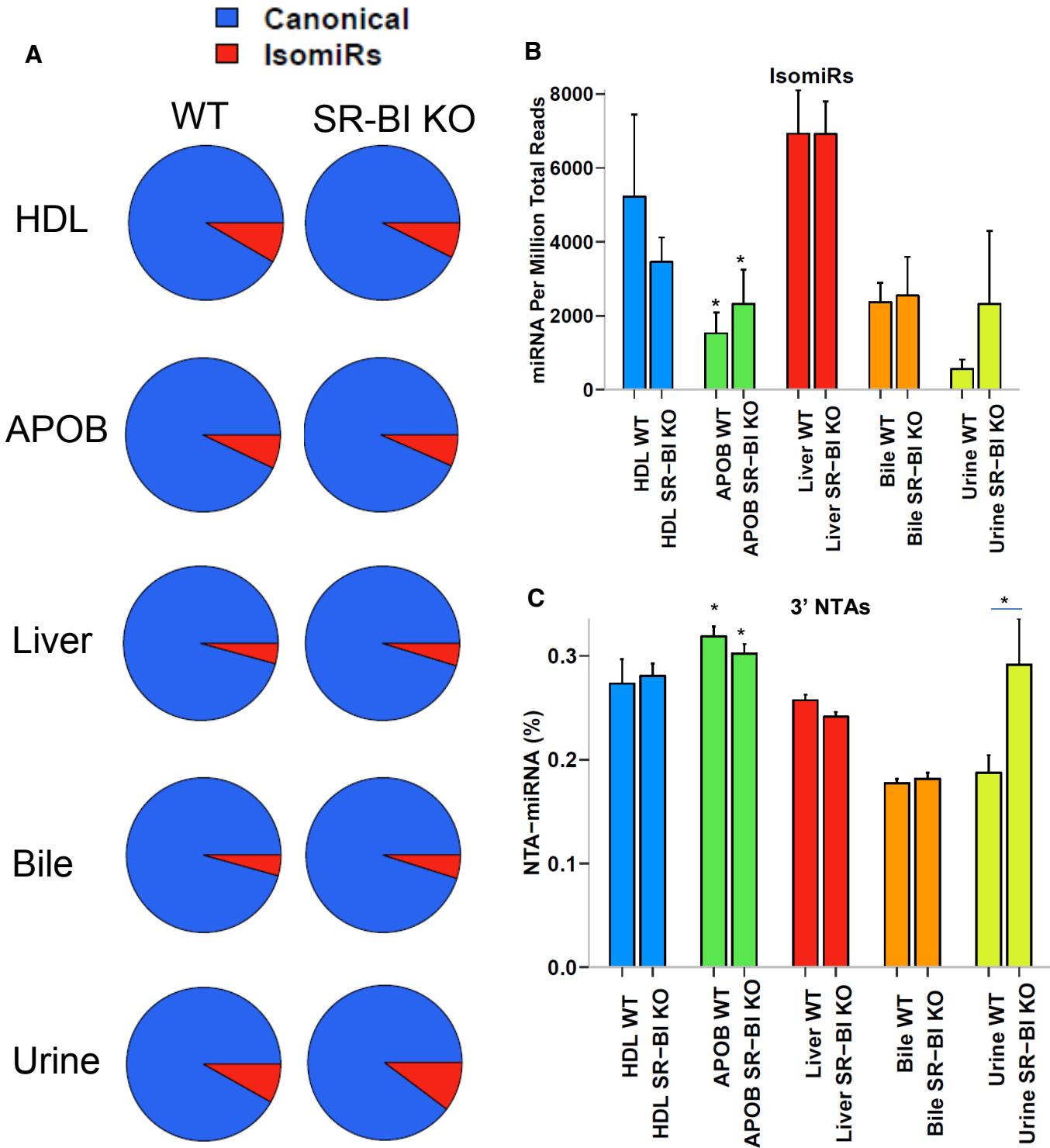


Figure 2-Figure Supplement 1. Expression of miRNA 5' isomiRs and 3' NTAs across sample types. WT, wild-type mice; SR-BI KO, Scavenger receptor BI Knockout mice (*Scarb1^{-/-}*). **(A)** Pie charts illustrating the fraction of miRNA 5' isomiRs (red) per total miRNA reads. **(B-C)** sRNA-seq analysis of miRNA **(B)** 5' isomiRs and **(C)** 3' non-templated additions (NTA). Mean \pm S.E.M. Student's t-tests.
 * $p<0.05$. Unless noted, groups are compared to liver. HDL WT, N=7; HDL SR-BI KO N=7; APOB WT, N=7, APOB SR-BI KO N=7; Liver WT, N=7; Liver SR-BI KO, N=7; Bile WT, N=7; Bile SR-BI KO, N=6; Urine WT, N=5; Urine SR-BI KO, N=6.

Figure 2 - Source Data 1. HDL-miRNA levels (mean) by real-time PCR TaqMan assays, as reported by relative quantitative values (RQV).

	miR-181a	miR-10b	miR-26a	miR-146a	miR-338-5p	miR-92a	miR-223	miR-375	miR-451
WT	0.10	0.07	0.49	7.51	5.74	13.14	11.77	1.25	76.91
SR-BI KO	0.09	0.08	0.39	7.81	5.47	20.54	13.09	2.12	102.21

Figure 2 - Source Data 2. Multivariate analysis of sRNA profiles compared to liver profiles (WT only).

Group	Class	Level	Dispersion_Fvalue	Dispersion_pvalue	Permanova_Fvalue	Permanova_pvalue
APOB	All_host	Parent	39.59	7.33E-12	9.82	1.00E-03
HDL	All_host	Parent	32.11	4.43E-10	8.71	1.00E-03
Bile	All_host	Parent	41.74	2.87E-12	12.53	1.00E-03
Urine	All_host	Parent	30.31	6.01E-10	7.03	1.00E-03
APOB	lincRNA	Parent	7.72	1.01E-03	9.24	1.00E-03
HDL	lincRNA	Parent	7.95	8.33E-04	7.48	1.00E-03
Bile	lincRNA	Parent	16.21	2.10E-06	9.23	1.00E-03
Urine	lincRNA	Parent	8.37	5.99E-04	9.50	1.00E-03
APOB	miRNA	Parent	31.03	4.18E-10	9.57	1.00E-03
HDL	miRNA	Parent	23.20	2.82E-08	7.11	1.00E-03
Bile	miRNA	Parent	17.09	1.78E-06	5.56	1.00E-03
Urine	miRNA	Parent	15.47	3.42E-06	8.42	1.00E-03
APOB	miscRNA	Parent	15.91	2.55E-06	7.05	1.00E-03
HDL	miscRNA	Parent	7.85	9.07E-04	6.44	1.00E-03
Bile	miscRNA	Parent	18.50	4.77E-07	9.17	1.00E-03
Urine	miscRNA	Parent	11.66	4.91E-05	7.47	1.00E-03
APOB	rRNA	Parent	12.03	3.75E-05	17.19	1.00E-03
HDL	rRNA	Parent	7.20	1.53E-03	15.67	1.00E-03
Bile	rRNA	Parent	10.48	1.18E-04	15.39	1.00E-03
Urine	rRNA	Parent	5.40	6.85E-03	5.47	1.00E-03
APOB	snoRNA	Parent	27.03	3.34E-09	7.70	1.00E-03
HDL	snoRNA	Parent	28.49	1.54E-09	8.05	1.00E-03
Bile	snoRNA	Parent	34.82	6.53E-11	9.36	1.00E-03
Urine	snoRNA	Parent	23.99	1.80E-08	6.96	1.00E-03
APOB	snRNA	Parent	10.01	1.68E-04	2.85	2.70E-02
HDL	snRNA	Parent	15.64	3.06E-06	8.91	1.00E-03
Bile	snRNA	Parent	14.68	5.83E-06	3.58	1.00E-02
Urine	snRNA	Parent	10.15	1.51E-04	2.94	2.80E-02
APOB	tRNA	Parent	42.41	2.15E-12	3.50	3.40E-02
HDL	tRNA	Parent	34.77	6.68E-11	0.74	4.95E-01
Bile	tRNA	Parent	29.00	1.18E-09	14.42	1.00E-03
Urine	tRNA	Parent	20.52	1.37E-07	9.50	1.00E-03
APOB	All_host	Fragment	78.26	<2.2e-16	7.81	1.00E-03
HDL	All_host	Fragment	79.02	<2.2e-16	7.29	1.00E-03
Bile	All_host	Fragment	68.60	<2.2e-16	8.88	1.00E-03
Urine	All_host	Fragment	50.33	<2.2e-16	7.77	1.00E-03
APOB	miRNA	Fragment	35.96	3.82E-11	8.85	1.00E-03
HDL	miRNA	Fragment	29.30	1.01E-09	7.12	1.00E-03
Bile	miRNA	Fragment	22.15	5.19E-08	5.42	1.00E-03
Urine	miRNA	Fragment	20.13	1.74E-07	7.65	1.00E-03
APOB	miscRNA	Fragment	146.61	<2.2e-16	4.32	1.00E-03
HDL	miscRNA	Fragment	123.10	<2.2e-16	5.89	1.00E-03
Bile	miscRNA	Fragment	79.49	<2.2e-16	5.66	1.00E-03
Urine	miscRNA	Fragment	137.23	<2.2e-16	4.23	1.00E-03
APOB	rDR	Fragment	379.50	<2.2e-16	6.27	1.00E-03
HDL	rDR	Fragment	335.62	<2.2e-16	6.67	1.00E-03
Bile	rDR	Fragment	209.64	<2.2e-16	8.07	1.00E-03
Urine	rDR	Fragment	243.10	<2.2e-16	7.26	1.00E-03
APOB	snoDR	Fragment	95.54	<2.2e-16	5.76	1.00E-03
HDL	snoDR	Fragment	97.85	<2.2e-16	6.45	1.00E-03
Bile	snoDR	Fragment	71.98	<2.2e-16	7.26	1.00E-03
Urine	snoDR	Fragment	82.83	<2.2e-16	5.64	1.00E-03
APOB	snDR	Fragment	56.19	9.85E-15	4.73	1.00E-03
HDL	snDR	Fragment	68.87	<2.2e-16	5.72	1.00E-03
Bile	snDR	Fragment	37.79	1.64E-11	4.89	1.00E-03
Urine	snDR	Fragment	50.18	9.25E-14	3.44	1.00E-03
APOB	tDR	Fragment	41.70	2.92E-12	5.32	1.00E-03
HDL	tDR	Fragment	33.55	1.20E-10	2.94	1.40E-02
Bile	tDR	Fragment	22.95	3.15E-08	10.22	1.00E-03
Urine	tDR	Fragment	16.27	2.01E-06	7.08	1.00E-03

tDRs

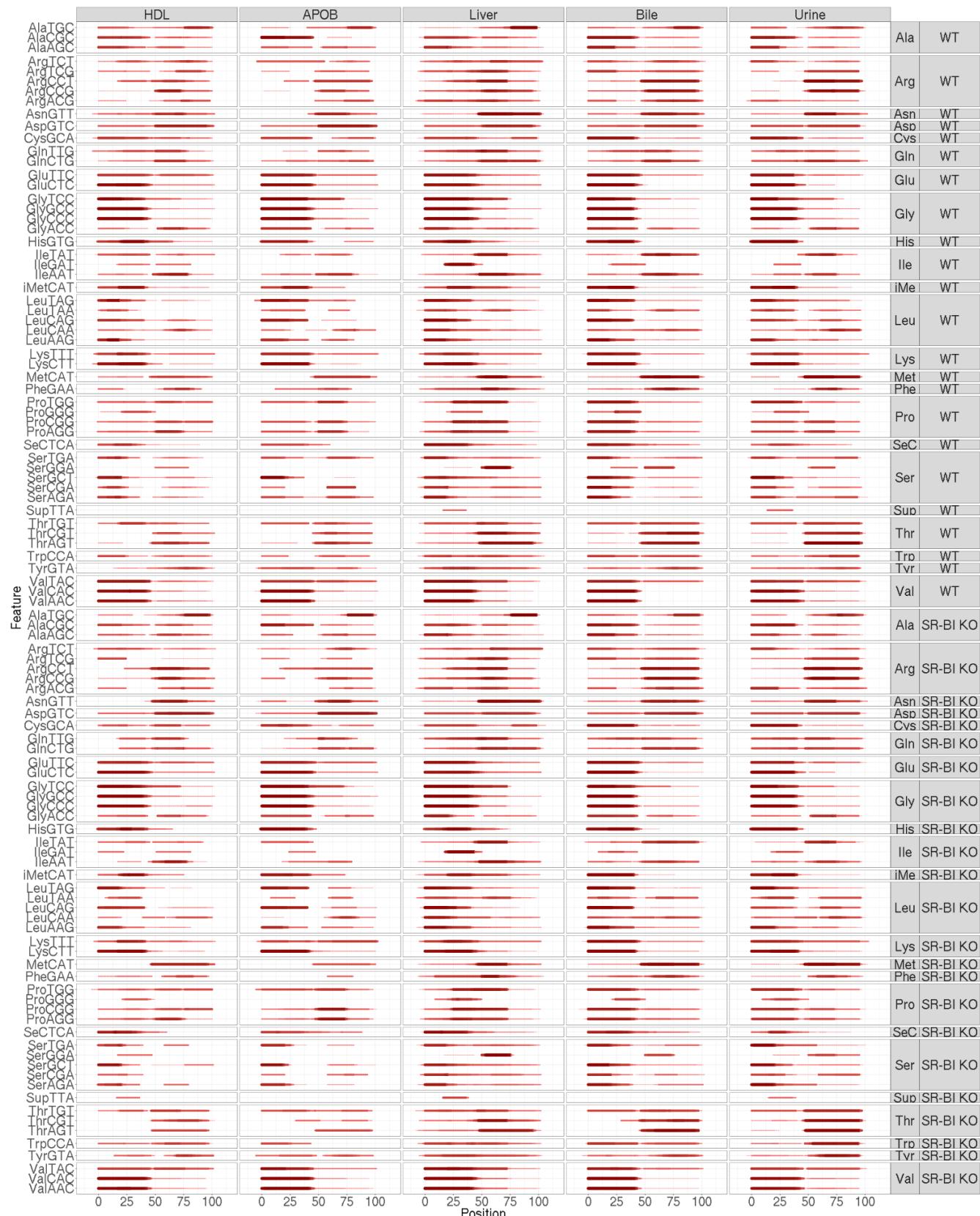
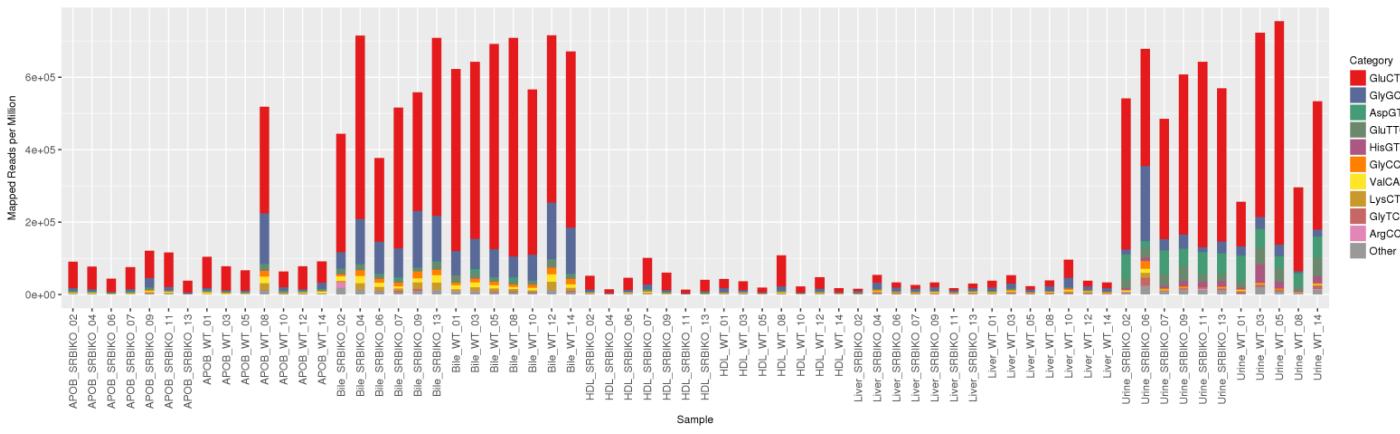


Figure 4-Figure Supplement 1. Positional coverage analysis of host tDRs based on parent tRNA amino acid anticodons. Signal (red) represents mean coverage percentage across parent length. WT, wild-type mice; SR-BI KO, Scavenger receptor BI Knockout mice (*Scarb1^{-/-}*). HDL WT, N=7; HDL SR-BI KO N=7; APOB WT, N=7, APOB SR-BI KO N=7; Liver WT, N=7; Liver SR-BI KO, N=7; Bile WT, N=7; Bile SR-BI KO, N=6; Urine WT, N=5; Urine SR-BI KO, N=6.

A**B**

Category

	GluCTC		AspGTC		GlyCCC		Other
	GlyGCC		GluTTC		ValCAC		

HDL

APOB

Liver

Bile

Urine

WT

SR-BI KO

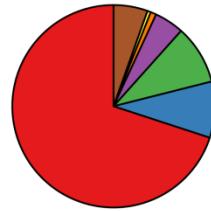
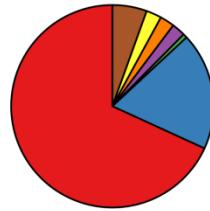
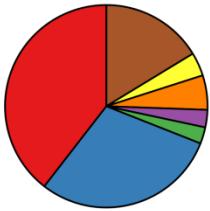
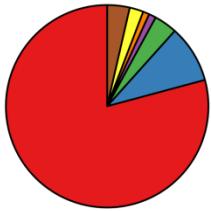
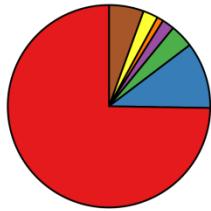
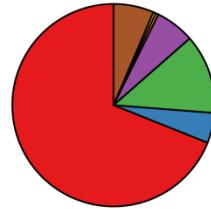
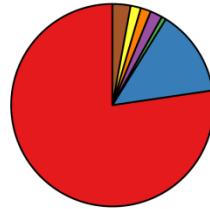
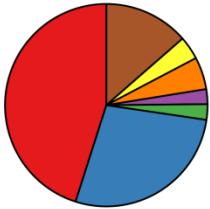
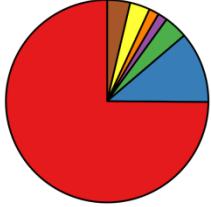
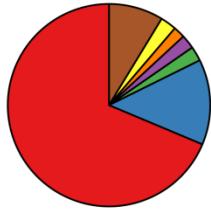


Figure 4-Figure Supplement 2. Classification of host tDRs based on parent tRNA amino acid anticodons. WT, wild-type mice; SR-BI KO, Scavenger receptor BI Knockout mice (*Scarb1^{-/-}*). (A) Normalized read counts for host tDRs (per million total reads) based parent tRNA amino acid anticodons. (B) Pie charts illustrating the percent of host tDRs per total tDR counts for parent tRNA amino acid anticodons. HDL WT, N=7; HDL SR-BI KO N=7; APOB WT, N=7, APOB SR-BI KO N=7; Liver WT, N=7; Liver SR-BI KO, N=7; Bile WT, N=7; Bile SR-BI KO, N=6; Urine WT, N=5; Urine SR-BI KO, N=6.

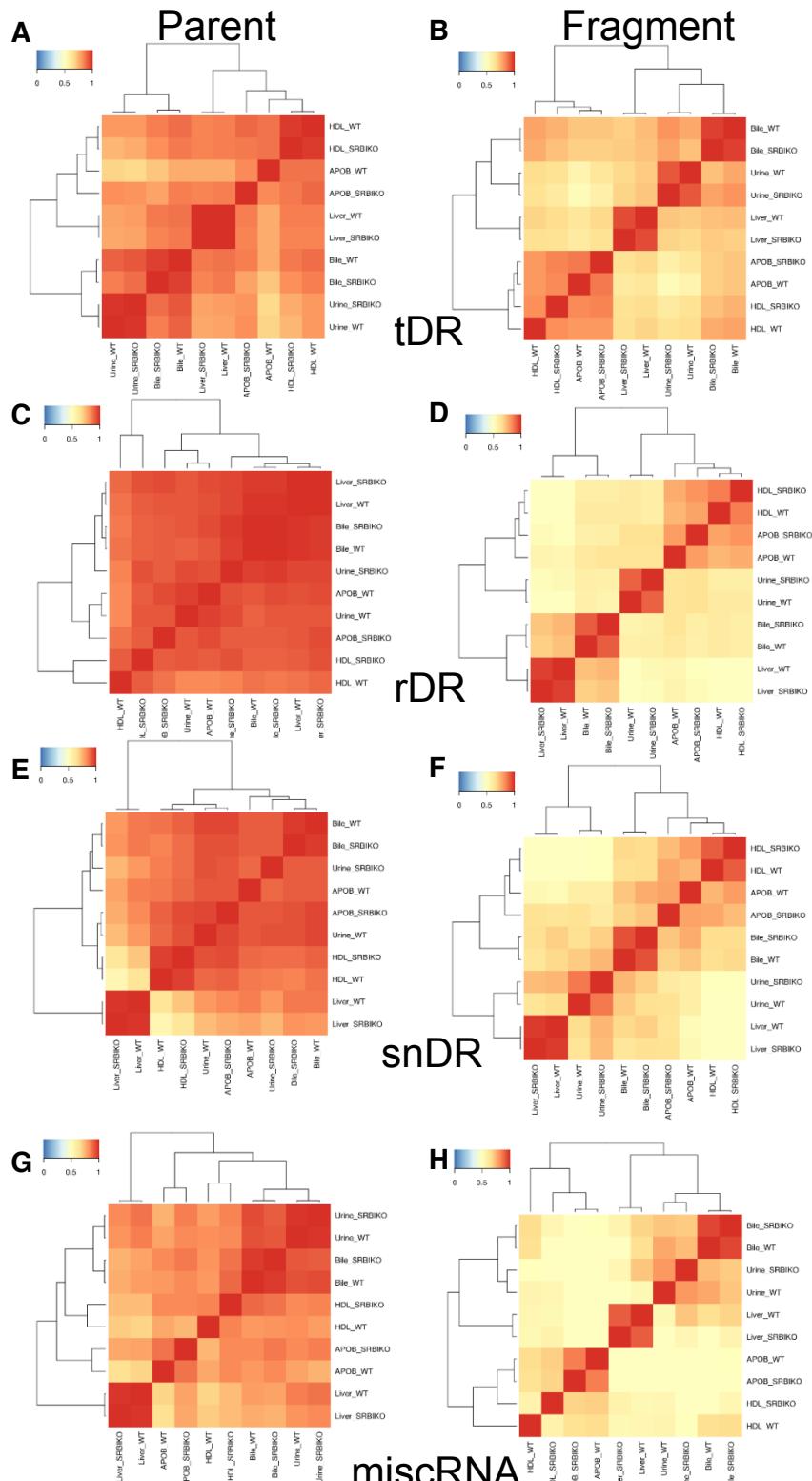
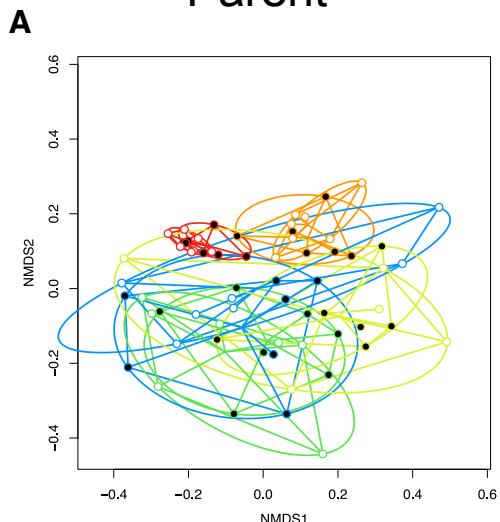


Figure 4-Figure Supplement 3. Groups are defined by the profile of individual fragments, not parent RNAs. (A-H) Heatmap of hierarchical clustered pairwise correlation (Spearman, R) coefficients between group means for host sRNAs. (A) Parent tDR (B) Fragment tDR (C) Parent rDR (D) Fragment rDR (E) Parent snDR (F) Fragment snDR (G) Parent miscRNA (H) Fragment miscRNA. WT, wild-type mice; SR-BI KO, Scavenger receptor BI Knockout mice (*Scarb1^{-/-}*). HDL WT, N=7; HDL SR-BI KO N=7; APOB WT, N=7, APOB SR-BI KO N=7; Liver WT, N=7; Liver SR-BI KO, N=7; Bile WT, N=7; Bile SR-BI KO, N=6; Urine WT, N=5; Urine SR-BI KO, N=6.

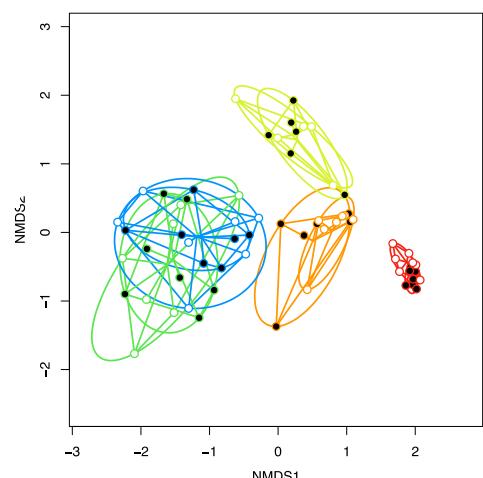
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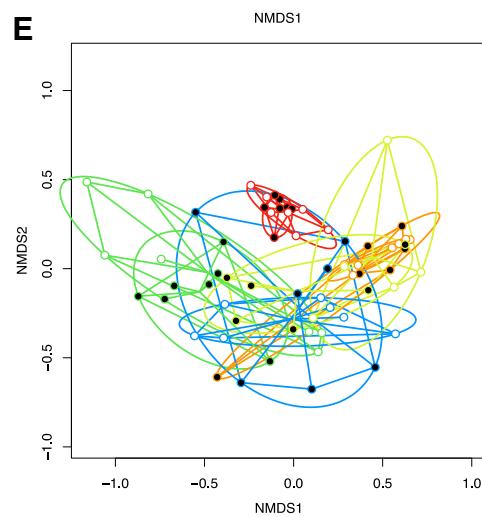
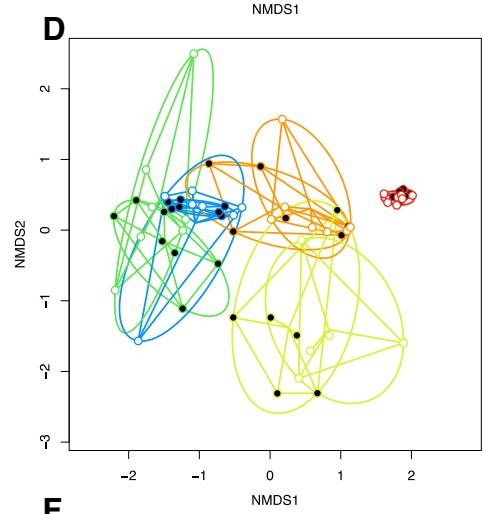
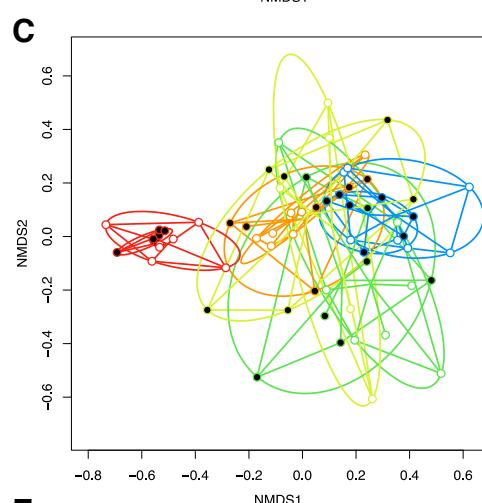
rDR

- WT
- SR-BI KO
- APOB
- Bile
- HDL
- Liver
- Urine

Fragment



snDR



miscRNA

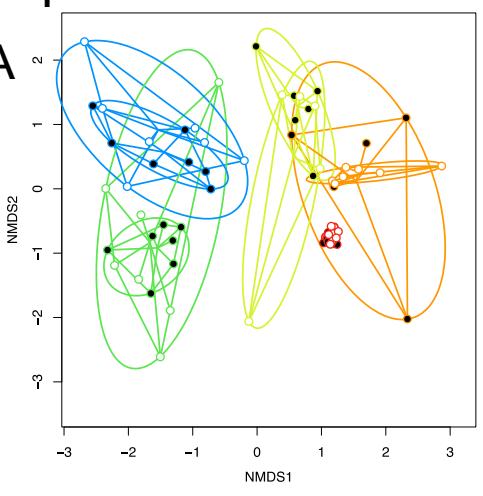
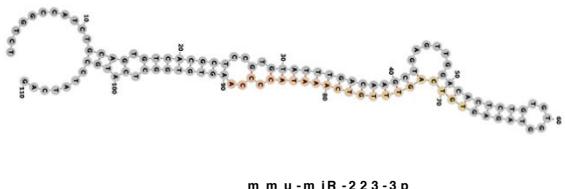
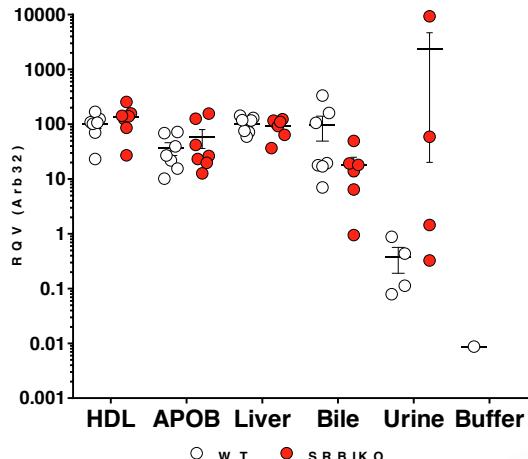
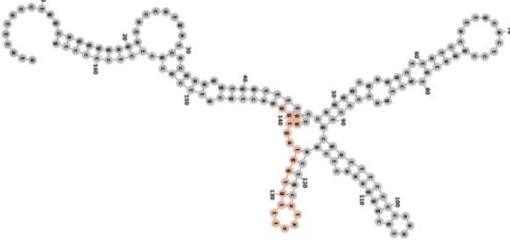


Figure 4-Figure Supplement 4. Lipoprotein host sRNA profiles are distinct from liver and biofluids.

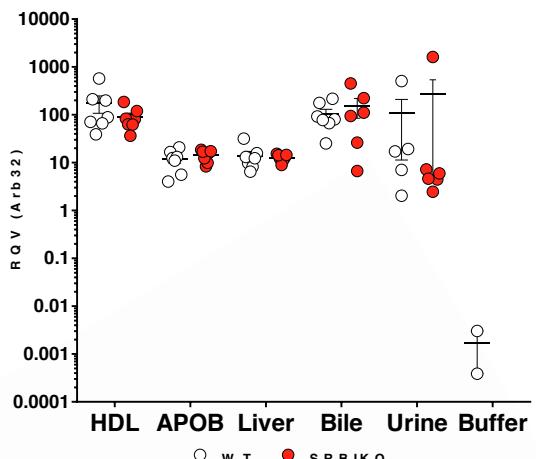
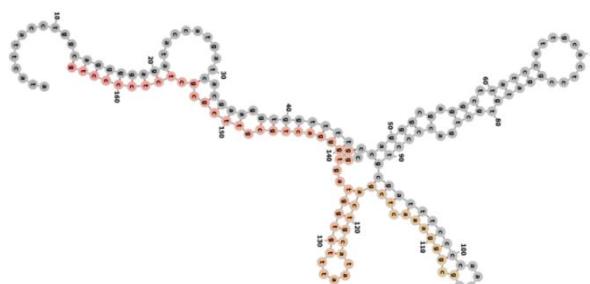
(A-F) Principal Coordinate Analysis (PCoA) of host sRNA profiles based on **(A)** parent rRNAs, **(B)** individual fragment rDRs, **(C)** parent snRNAs, **(D)** individual fragment snDRs, **(E)** parent miscellaneous RNAs (miscRNA), and **(F)** individual fragment miscRNAs for samples from WT (empty circles) and SR-BI KO (filled circles) mice. NMDS1, Non-metric multidimensional scaling. WT, wild-type mice; SR-BI KO, Scavenger receptor BI Knockout mice (*Scarb1*^{-/-}). HDL WT, N=7; HDL SR-BI KO N=7; APOB WT, N=7; APOB SR-BI KO N=7; Liver WT, N=7; Liver SR-BI KO, N=7; Bile WT, N=7; Bile SR-BI KO, N=6; Urine WT, N=5; Urine SR-BI KO, N=6.

A

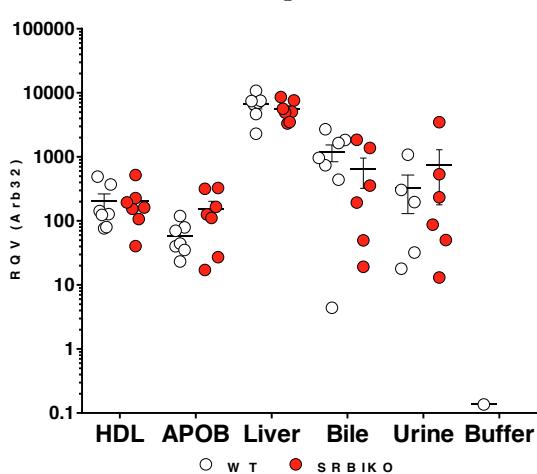
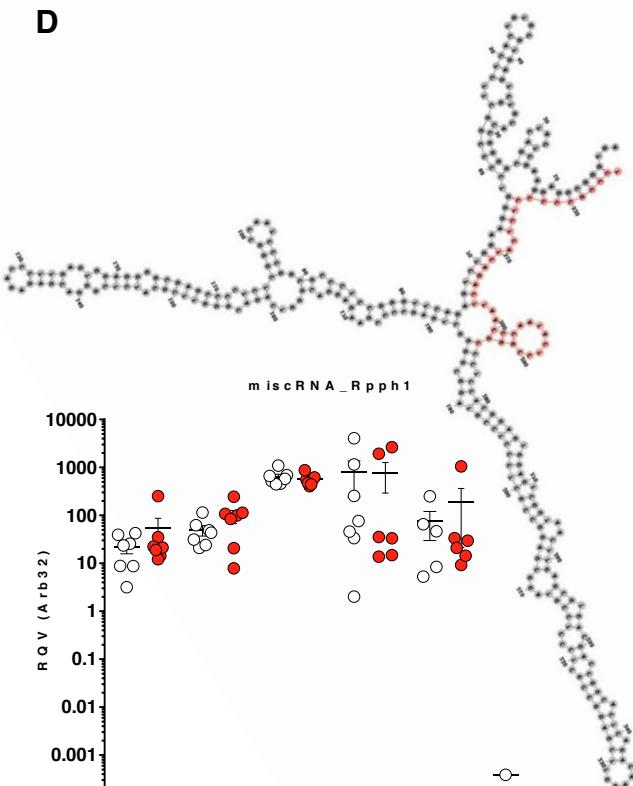
mmu-miR-223-3p

**B**

snDR_Gm26232

**C**

snDR_Gm22866

**D**

miscRNA_Rpph1

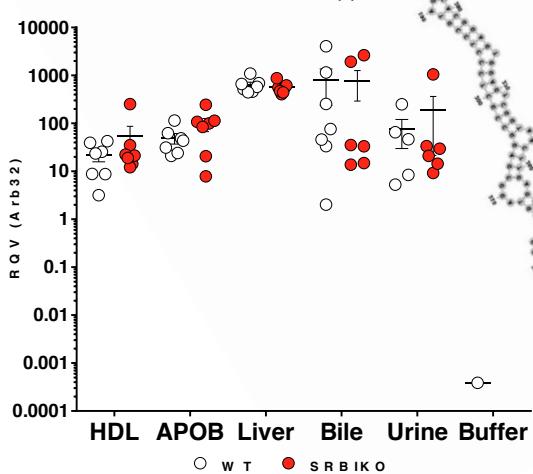


Figure 4-Figure Supplement 5. Lipoproteins transport multiple classes of host sRNAs (A-D) Real-time PCR analysis of candidate sRNAs with predicted folding structures of parent RNAs for (A) mmu-miR-223-3p, (B) snDR_Gm26232, (C) snDR_Gm22866, and (D) miscellaneous RNA (miscRNA) Rpph1. WT (white circles), wild-type mice; SR-BI KO (red circles), Scavenger receptor BI Knockout mice (*Scarb1*^{-/-}). HDL WT, N=7; HDL SR-BI KO N=7; APOB WT, N=7, APOB SR-BI KO N=7; Liver WT, N=7; Liver SR-BI KO, N=7; Bile WT, N=7; Bile SR-BI KO, N=6; Urine WT, N=5; Urine SR-BI KO, N=6.

snDRs

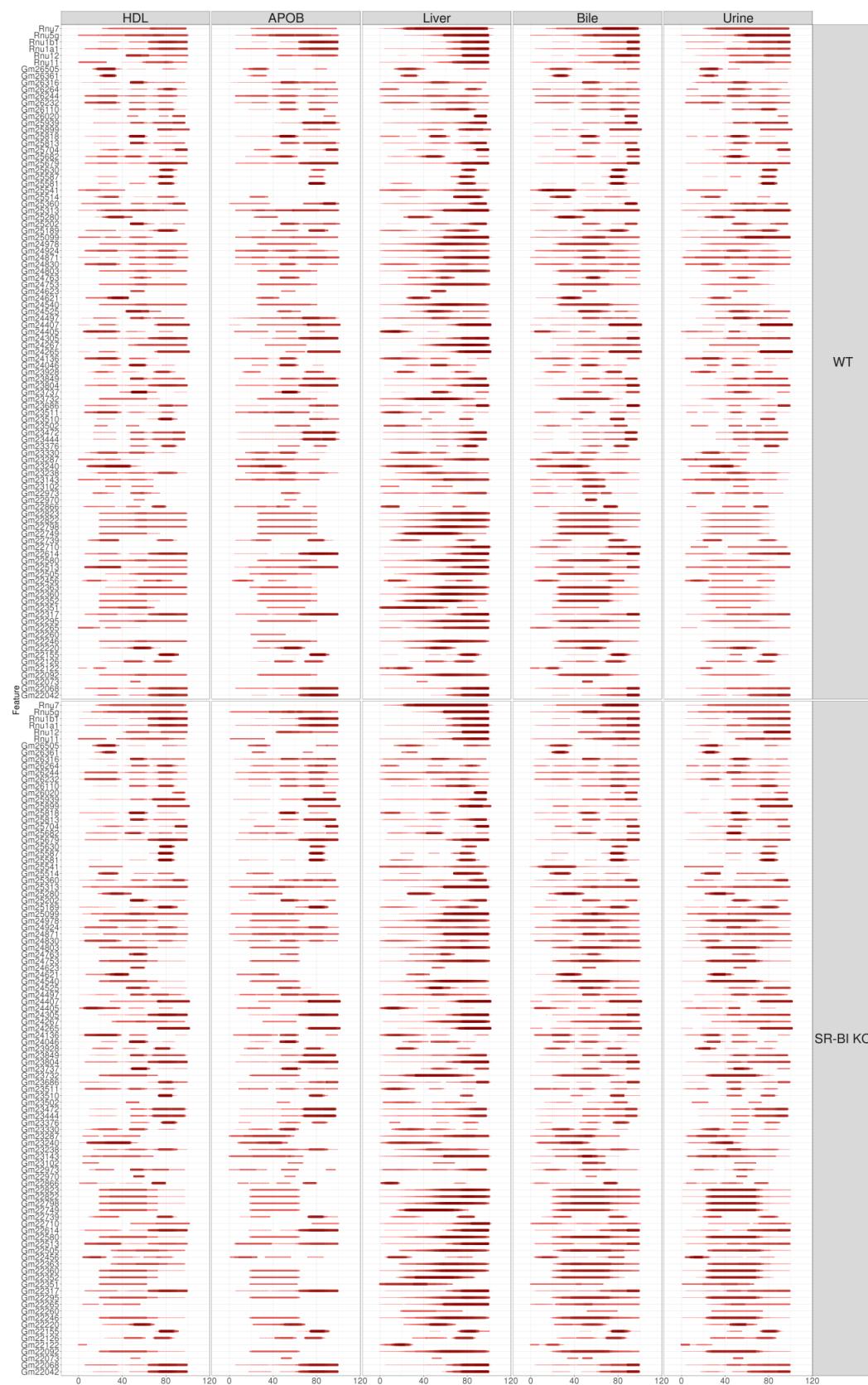


Figure 4-Figure Supplement 6. Positional coverage analysis of host snDRs based on parent snRNAs.

Signal (red) represents mean coverage percentage across parent length. WT, wild-type mice; SR-BI KO, Scavenger receptor BI Knockout mice (*Scarb1*^{-/-}). HDL WT, N=7; HDL SR-BI KO N=7; APOB WT, N=7, APOB SR-BI KO N=7; Liver WT, N=7; Liver SR-BI KO, N=7; Bile WT, N=7; Bile SR-BI KO, N=6; Urine WT, N=5; Urine SR-BI KO, N=6.

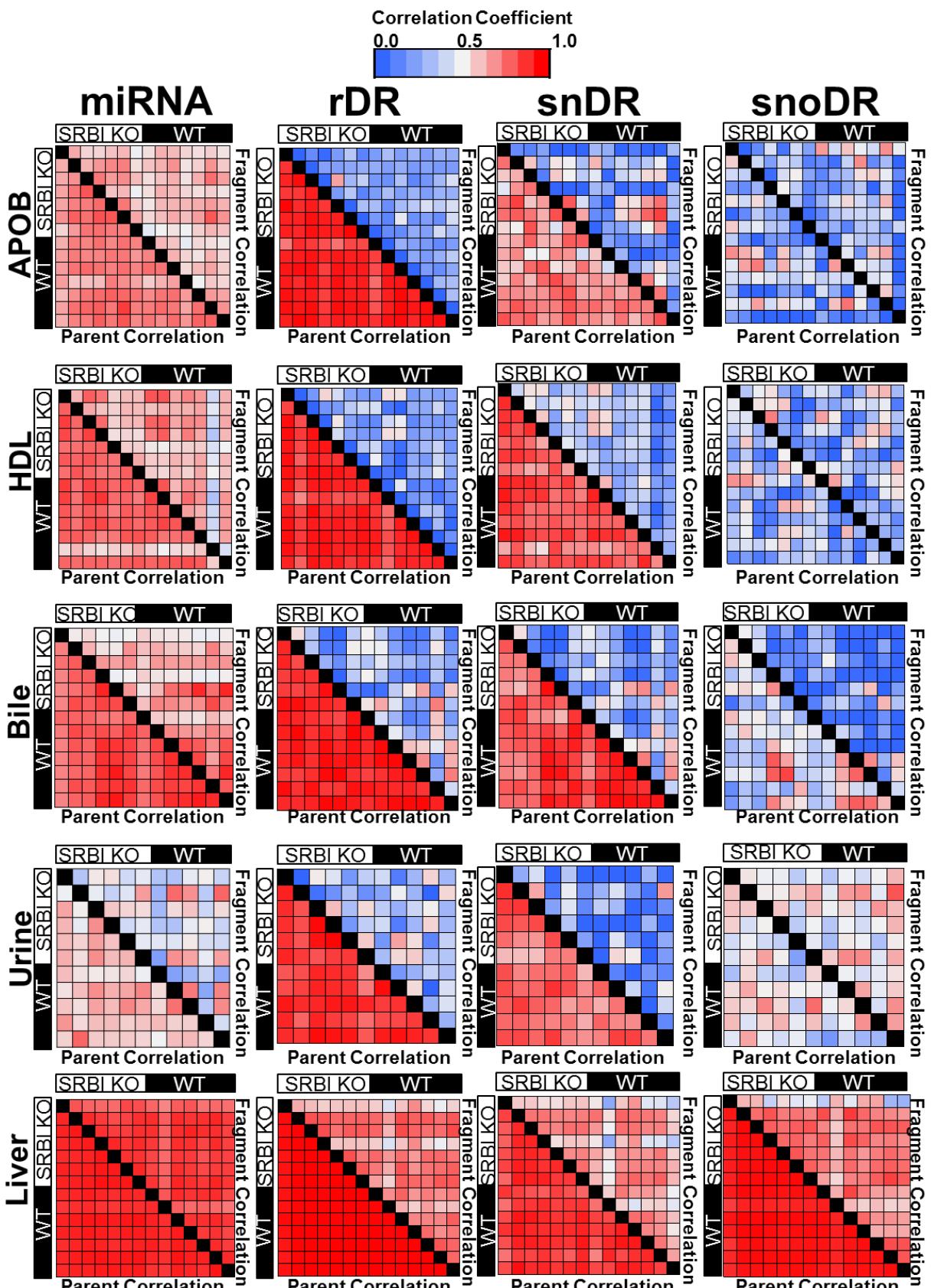


Figure 4-Figure Supplement 7. Lipoprotein sRNA profiles are highly-correlated for parent RNAs and lowly-correlated for individual sRNAs fragments. Heatmaps of correlation coefficients (Spearman, R) for host sRNA parents and individual fragments across samples within each group for miRNAs, rDRs, snDRs, and snoDRs. WT, wild-type mice; SR-BI KO, Scavenger receptor BI Knockout mice (*Scarb1^{-/-}*). HDL WT, N=7; HDL SR-BI KO N=7; APOB WT, N=7, APOB SR-BI KO N=7; Liver WT, N=7; Liver SR-BI KO, N=7; Bile WT, N=7; Bile SR-BI KO, N=6; Urine WT, N=5; Urine SR-BI KO, N=6.

A

Non-Host tDRs

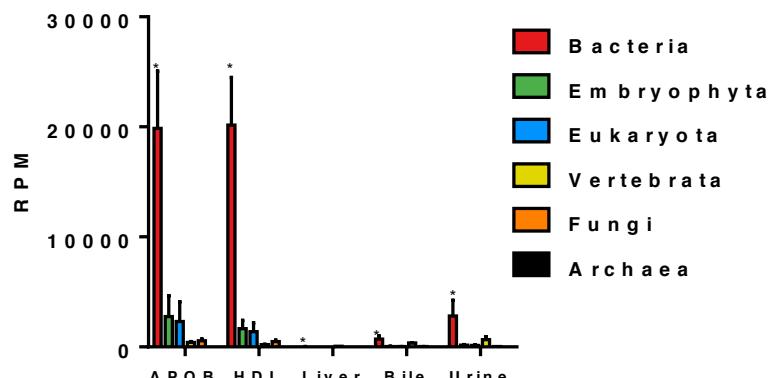
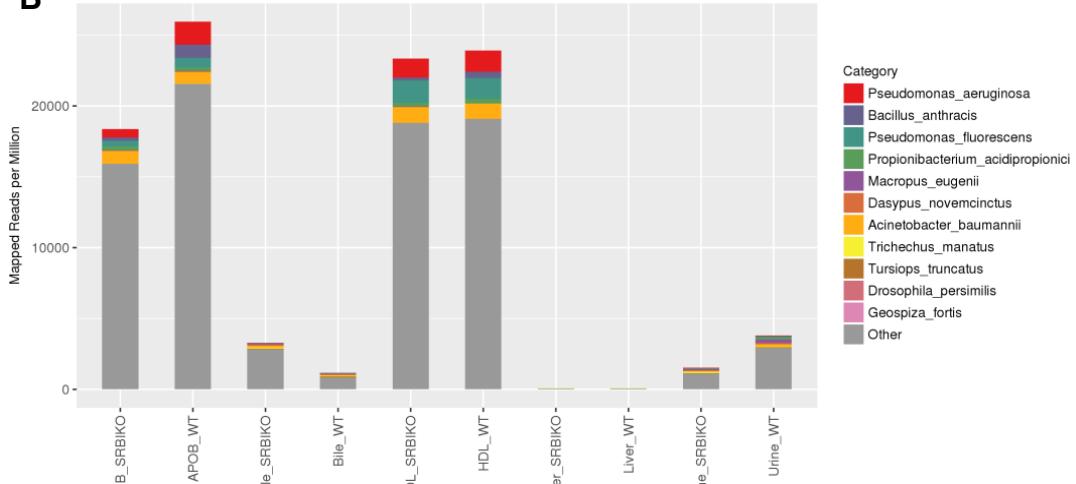
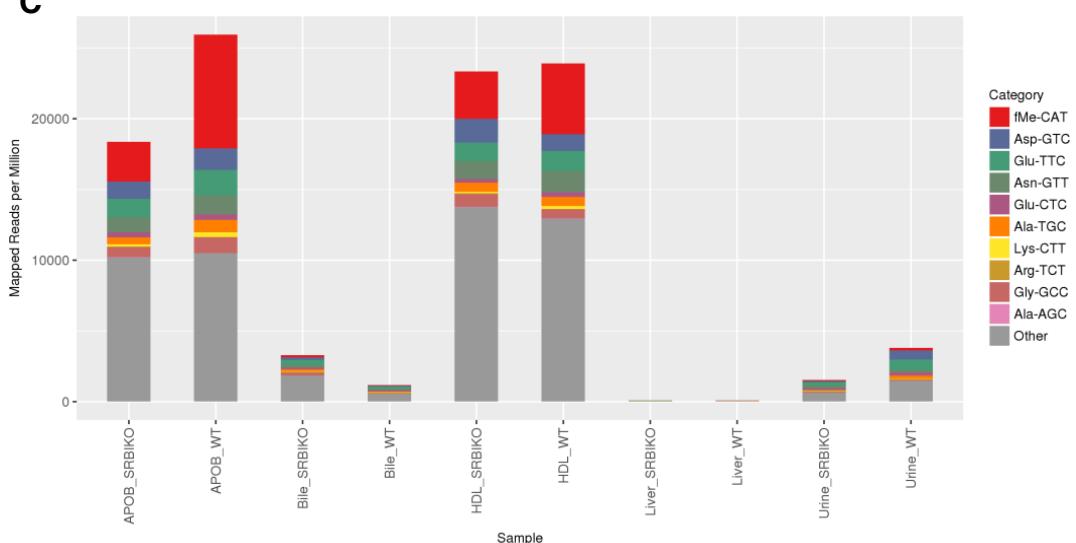
**B****C**

Figure 5-Figure Supplement 1. Lipoproteins transport non-host bacterial tDRs. (A) Abundance of non-host tDRs based on parent tRNA transcripts (database) across kingdoms and higher organizations, as reported as Reads Per Million total reads (RPM). Two-way ANOVA Tukey's multiple comparisons test. *p<0.05. (B-C) Stacked bar plots of non-host tDRs aligned to parent rRNAs across kingdoms and higher organizations, as reported as mapped reads per million total reads for (B) bacterial species and (C) parent tRNA amino acid anti-codons. WT, wild-type mice; SR-BI KO, Scavenger receptor BI Knockout mice (*Scarb1^{-/-}*). HDL WT, N=7; HDL SR-BI KO N=7; APOB WT, N=7, APOB SR-BI KO N=7; Liver WT, N=7; Liver SR-BI KO, N=7; Bile WT, N=7; Bile SR-BI KO, N=6; Urine WT, N=5; Urine SR-BI KO, N=6.

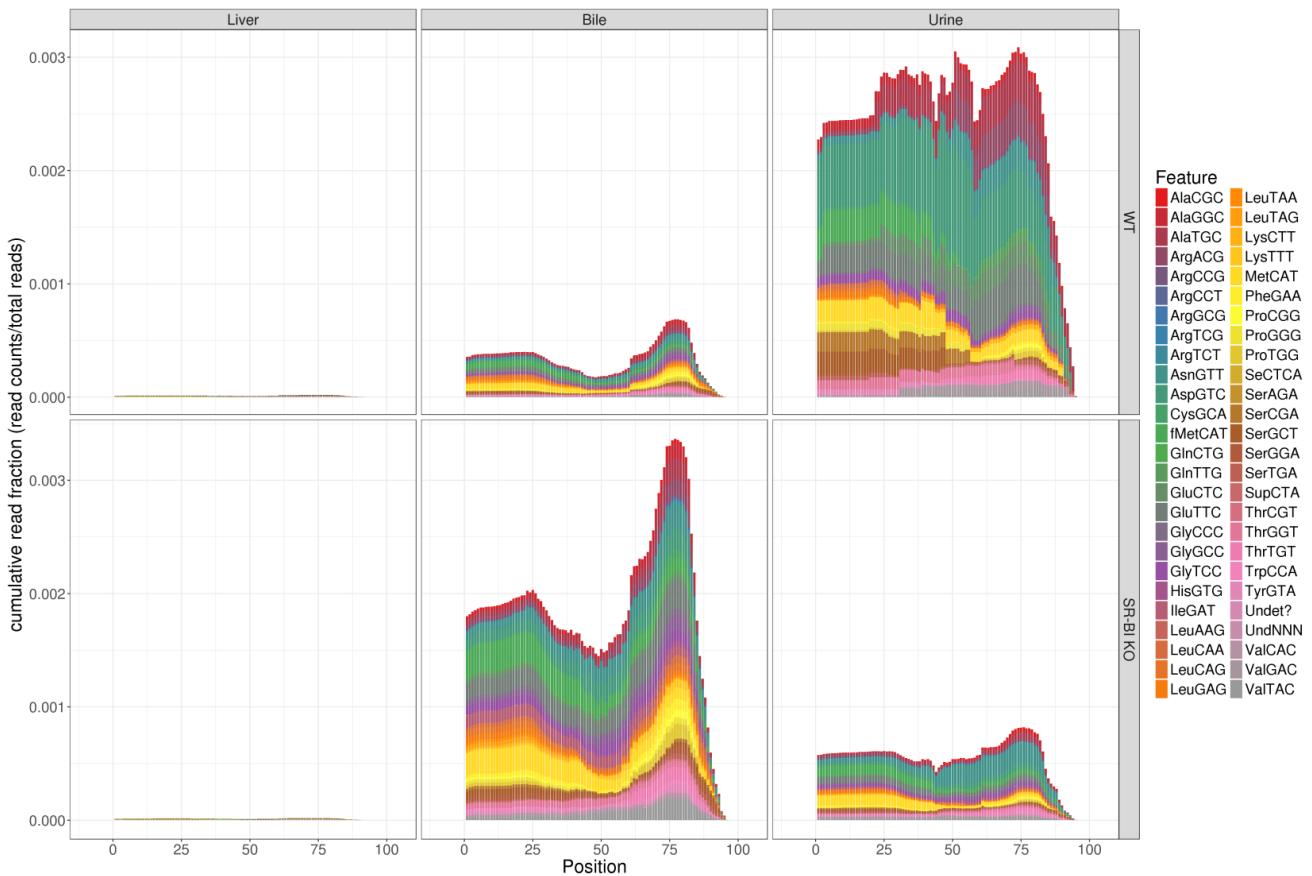


Figure 5-Figure Supplement 2. Bile and urine contain non-host tDRs. Positional coverage maps of non-host tDRs for parent tRNA amino acid anti-codons, as reported as mean cumulative read fractions (read counts / total counts) for liver, bile, and urine. WT, wild-type mice; SR-BI KO, Scavenger receptor BI Knockout mice (*Scarb1*^{-/-}). HDL WT, N=7; HDL SR-BI KO N=7; APOB WT, N=7, APOB SR-BI KO N=7; Liver WT, N=7; Liver SR-BI KO, N=7; Bile WT, N=7; Bile SR-BI KO, N=6; Urine WT, N=5; Urine SR-BI KO, N=6.

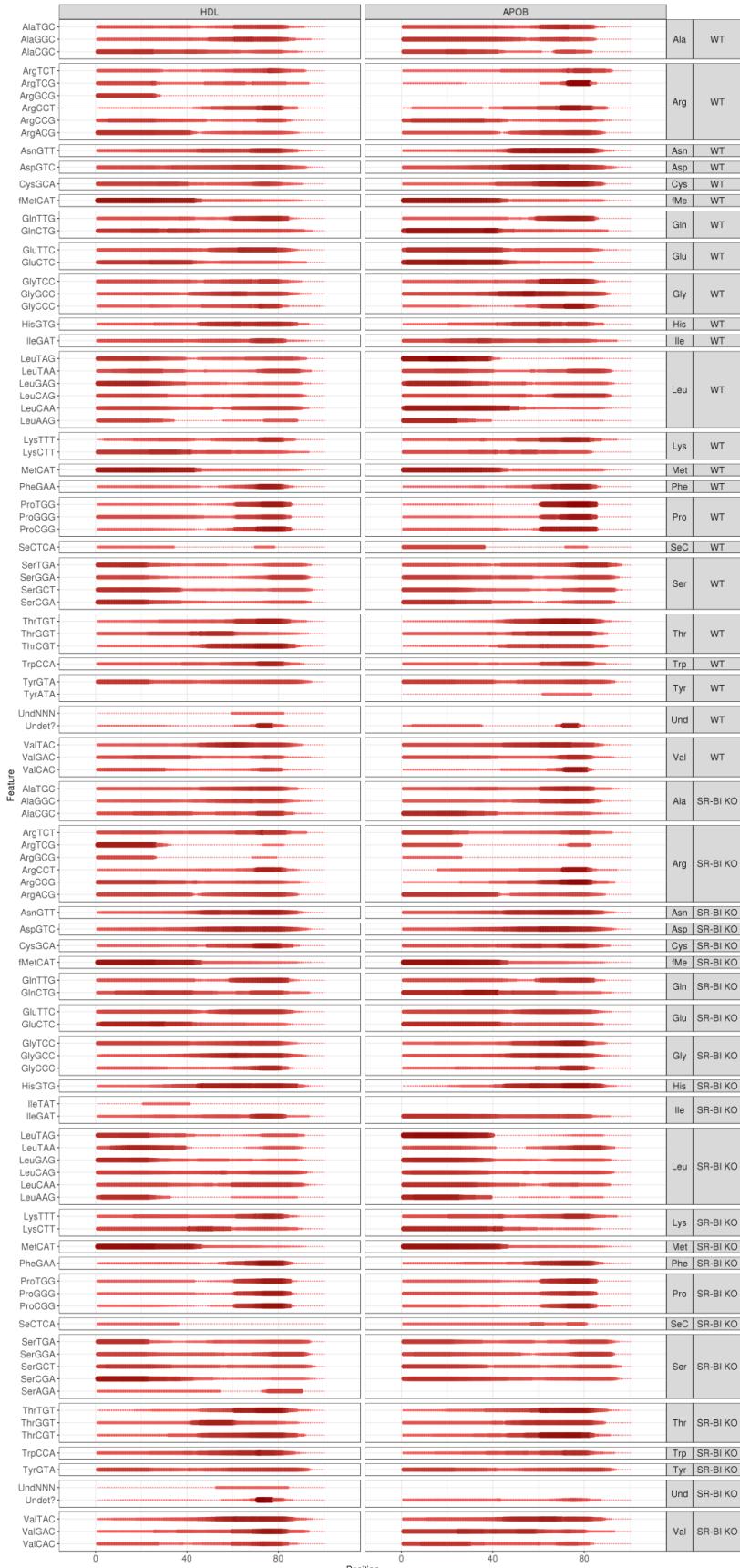


Figure 5-Figure Supplement 3. Positional coverage analysis of non-host tDRs based on parent tRNA amino acid anticodons. Signal (red) represents mean coverage percentage across parent length. WT, wild-type mice; SR-BI KO, Scavenger receptor BI Knockout mice (*Scarb1*^{-/-}). HDL WT, N=7; HDL SR-BI KO N=7; APOB WT, N=7; APOB SR-BI KO N=7; Liver WT, N=7; Liver SR-BI KO, N=7; Bile WT, N=7; Bile SR-BI KO, N=6; Urine WT, N=5; Urine SR-BI KO, N=6.

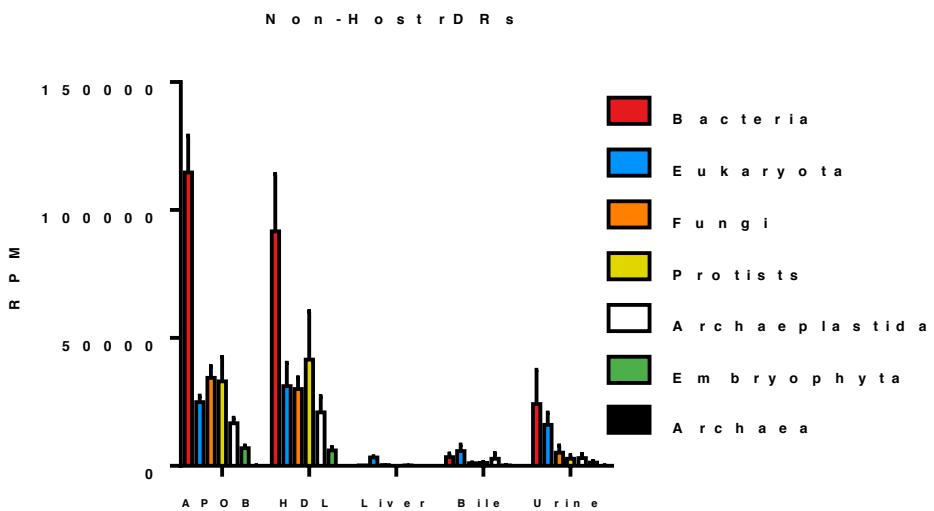


Figure 5-Figure Supplement 4. Lipoproteins transport non-host rDRs. (A) Abundance of non-host rDRs based on parent rRNA transcripts (database) across kingdoms and higher organizations, as reported as Reads Per Million total reads (RPM).

Figure 5-Source Data 1. Non-host miRNAs (Mean RPM)

Name	APOB_SRBIKO	APOB_WT	Bile_SRBIKO	Bile_WT	HDL_SRBIKO	HDL_WT	Liver_SRBIKO	Liver_WT	Urine_SRBIKO	Urine_WT
bta-miR-574	35.22	16.46	42.78	58.56	52.88	65.38	5.24	5.70	6.97	16.50
ahy-miR159	10.56	UND	82.14	0.52	1.91	13.23	UND	0.12	4.22	UND
api-miR-71	UND	4.69	4.12	UND	UND	11.02	UND	UND	UND	UND
aly-miR164a-5p	UND	UND	UND	UND	UND	9.93	UND	UND	UND	UND
aly-miR166a-3p	12.35	UND	0.06	1.08	15.29	8.90	UND	UND	0.36	UND
tae-miR9662a-3p	UND	UND	UND	UND	UND	8.59	UND	0.12	UND	1.73
chi-miR-1307-3p	UND	UND	UND	UND	UND	4.37	UND	UND	UND	UND
bdi-miR159b-3p.1	0.79	UND	0.15	0.37	UND	4.07	UND	UND	UND	UND
aae-miR-14	UND	11.16	1.54	UND	8.59	3.22	UND	0.12	1.87	4.12
ata-miR528-5p	UND	UND	UND	UND	UND	2.60	UND	UND	UND	UND
cme-miR156j	12.80	0.68	6.40	0.92	2.32	2.51	UND	UND	UND	UND
hsa-miR-1284	UND	UND	UND	UND	UND	2.48	UND	UND	UND	UND
pde-miR947	UND	UND	UND	UND	UND	2.25	UND	UND	UND	UND
aga-miR-276-3p	UND	24.52	15.76	UND	UND	2.19	UND	UND	UND	UND
hsa-miR-1304-3p	UND	UND	UND	UND	UND	1.09	UND	UND	UND	UND
ssa-miR-125b-5p	0.30	0.15	0.33	0.42	0.26	0.40	0.20	0.27	0.10	0.11
ggo-miR-584	UND	UND	UND	UND	UND	0.17	UND	0.15	UND	UND
efu-miR-660	UND	UND	UND	UND	0.10	0.11	UND	UND	UND	UND
cfa-miR-329b	UND	UND	UND	UND	UND	0.11	UND	UND	UND	UND
age-miR-197	11.61	UND	UND	0.47	2.91	0.11	UND	UND	UND	UND
ahy-miR156c	17.06	2.22	UND	1.92	4.68	0.06	UND	UND	UND	0.16
lgi-miR-71	UND	UND	UND	UND	UND	0.06	UND	UND	UND	UND
asu-miR-71-5p	10.20	3.13	25.89	UND	0.06	UND	UND	0.09	0.02	UND
hsa-miR-1908-5p	8.48	10.15	0.13	UND	7.03	UND	UND	UND	UND	UND
ppc-miR-228-5p	8.05	UND	15.29	UND	UND	UND	UND	UND	0.01	UND
hsa-miR-92a-1-5p	UND	UND	UND	0.34	11.52	UND	UND	UND	UND	UND
str-miR-8366a-3p	UND	UND	15.30	UND	UND	UND	UND	UND	UND	UND
asu-miR-50-5p	UND	9.84	2.20	UND	UND	UND	UND	UND	UND	UND
cbn-miR-46	UND	UND	12.88	UND	UND	UND	UND	UND	UND	UND
bta-miR-424-3p	9.20	UND	UND	UND	UND	UND	UND	UND	UND	UND
pab-miR951	UND	UND	UND	6.55	UND	UND	UND	UND	UND	UND
hsa-miR-3614-5p	UND	UND	UND	UND	4.78	UND	UND	UND	UND	UND
hsa-miR-489-3p	UND	UND	UND	UND	UND	UND	UND	UND	0.30	2.80
mdm-miR482a-5p	UND	UND	UND	UND	4.06	UND	UND	UND	UND	UND
aau-miR396	UND	UND	UND	UND	1.82	UND	UND	UND	UND	UND
oha-miR-122-5p	UND	UND	UND	UND	UND	0.38	0.46	UND	UND	UND
aae-miR-278-3p	UND	UND	3.41	UND	UND	UND	UND	UND	UND	UND
aly-miR166a-5p	UND	UND	UND	UND	3.18	UND	UND	UND	UND	UND
aga-miR-277	UND	UND	3.21	UND	UND	UND	UND	UND	UND	UND
cte-miR-750	UND	UND	3.07	UND	UND	UND	UND	UND	UND	UND
hsa-miR-937-3p	UND	UND	4.50	UND	UND	UND	UND	UND	UND	UND
ggo-miR-589	3.78	UND	UND	UND	UND	UND	UND	UND	UND	UND
aly-miR168a-5p	UND	UND	UND	0.74	UND	UND	0.15	UND	UND	UND
gma-miR482b-3p	3.04	UND	UND	UND	UND	UND	UND	UND	UND	UND
sme-miR-31b-5p	UND	UND	UND	UND	UND	UND	UND	1.99	UND	UND
api-miR-2a	UND	UND	1.94	UND	UND	UND	UND	UND	UND	UND
sme-lin-4-5p	UND	UND	2.45	UND	UND	UND	UND	UND	UND	UND
aly-miR403a-3p	UND	UND	UND	1.02	UND	UND	UND	UND	UND	UND
sme-bantam-a	UND	UND	1.57	UND	UND	UND	UND	UND	UND	UND
aae-miR-8-3p	UND	UND	1.14	UND	UND	UND	UND	UND	UND	UND
hsa-miR-629-5p	UND	UND	0.96	UND	UND	UND	UND	UND	UND	UND
asu-miR-86-5p	UND	UND	1.22	UND	UND	UND	UND	UND	UND	UND
ata-miR396e-3p	UND	UND	0.82	UND	UND	UND	UND	UND	UND	UND
aau-miR162	UND	UND	0.39	UND	UND	UND	UND	UND	UND	UND
aae-miR-34-5p	UND	UND	0.87	UND	UND	UND	UND	UND	UND	UND
ipu-miR-99b	UND	UND	0.12	0.34	UND	UND	0.14	0.09	UND	UND
lva-miR-183-5p	UND	UND	0.07	0.06	UND	UND	UND	UND	0.36	UND
gma-miR171k-3p	UND	UND	0.56	UND	UND	UND	UND	UND	UND	UND
ahy-miR156b-5p	UND	UND	0.69	UND	UND	UND	UND	UND	UND	UND
hsa-miR-4661-5p	UND	UND	0.69	UND	UND	UND	UND	UND	UND	UND
gso-miR3522a	UND	UND	0.45	UND	UND	UND	UND	UND	UND	UND
hsa-miR-3605-3p	UND	UND	0.70	UND	UND	UND	UND	UND	UND	UND
hsa-miR-942-5p	UND	UND	0.61	UND	UND	UND	UND	UND	UND	UND
asu-miR-100a-5p	UND	UND	0.42	UND	UND	UND	UND	UND	UND	UND
osa-miR159f	0.12	UND	0.41	UND	UND	UND	UND	UND	UND	UND
bta-miR-3613a	UND	UND	0.24	UND	UND	UND	UND	UND	UND	UND
aqc-miR159	UND	UND	0.41	UND	UND	UND	UND	UND	UND	UND
pma-miR-194-5p	UND	UND	UND	UND	UND	UND	0.12	UND	UND	UND
aae-miR-13-3p	UND	UND	UND	UND	UND	UND	UND	0.18	UND	UND
hsa-miR-1269b	UND	UND	0.18	UND	UND	UND	UND	UND	UND	UND
pde-miR159	UND	UND	0.31	UND	UND	UND	UND	UND	UND	UND
bbe-miR-183-5p	UND	UND	0.11	UND	UND	UND	UND	UND	UND	UND
bta-miR-374a	UND	UND	UND	UND	UND	UND	0.25	UND	UND	UND
hsa-miR-6803-3p	UND	UND	0.09	0.08	UND	UND	UND	UND	UND	UND
aly-miR172c-3p	UND	UND	0.11	UND	UND	UND	UND	UND	UND	UND
bma-miR-57	UND	UND	UND	UND	0.06	UND	UND	UND	UND	UND
cbn-miR-81	UND	UND	UND	UND	UND	UND	0.12	UND	UND	UND
asu-miR-44a-3p	UND	UND	UND	UND	UND	UND	0.12	UND	UND	UND
cin-let-7b-5p	UND	UND	0.09	UND	UND	UND	UND	UND	UND	UND
aae-miR-71-5p	UND	UND	0.07	UND	UND	UND	UND	UND	UND	UND
cte-miR-100	UND	UND	0.06	UND	UND	UND	UND	UND	UND	UND
aae-miR-10	UND	UND	UND	UND	UND	UND	0.13	UND	UND	UND
dvi-miR-310-3p	UND	UND	UND	UND	0.07	UND	UND	UND	UND	UND
aga-miR-275	UND	UND	UND	UND	UND	UND	0.07	UND	UND	UND
efu-miR-23a	UND	UND	UND	0.08	UND	UND	UND	UND	UND	UND
hsa-miR-181a-2-3p	UND	UND	UND	0.08	UND	UND	UND	UND	UND	UND
hsa-miR-4433a-3p	UND	UND	UND	0.07	UND	UND	UND	UND	UND	UND
cta-miR-590	UND	UND	0.06	UND	UND	UND	UND	UND	UND	UND
hsa-miR-625-3p	UND	UND	UND	UND	0.07	UND	UND	UND	UND	UND
mml-miR-133a	0.07	UND	UND	UND	UND	UND	UND	UND	UND	UND
oha-miR-221-5p	UND	UND	UND	UND	UND	UND	0.09	UND	UND	UND
pma-miR-30d	UND	UND	UND	UND	UND	UND	UND	0.06	UND	UND
vvi-miR156e	0.12	UND	UND	UND	UND	UND	UND	UND	UND	UND
xtr-miR-106	UND	UND	UND	UND	UND	UND	0.07	UND	UND	UND
xtr-miR-215	UND	UND	UND	UND	UND	UND	0.07	UND	UND	UND

Figure 5-Source Data 2. Top 100 (WT HDL) Non-host tDRs (RPM)

Name	APOB_SRBIKO	APOB_WT	Bile_SRBIKO	Bile_WT	SRBIKO	HDL_SRBIKO	HDL_WT	Liver_SRBIKO	Liver_WT	Urine_SRBIKO	Urine_WT
Azotobacter_chroococcum_NCIMB_8003_tRNA-fMet-CAT-1-1	406.59	1883.53	3.81	1.65	470.97	896.65	0.24	0.28	1.91	2.36	
Marinomonas_mediterranea_MMB-1_tRNA-fMet-CAT-1-1	372.40	667.50	2.78	0.95	508.11	757.97	0.22	0.18	0.52	1.38	
Bacillus_anthraxis_2000031021_tRNA-fMet-CAT-1-1	342.82	1600.84	2.81	1.02	371.22	746.21	0.14	0.21	1.66	2.52	
Azotobacter_chroococcum_NCIMB_8003_tRNA-Glu-TTC-1-1	199.88	527.80	1.86	1.51	425.53	562.52	0.34	0.22	4.92	103.80	
Azotobacter_chroococcum_NCIMB_8003_tRNA-Ile-GAT-1-1	123.26	37.56	5.05	1.28	411.82	554.90	0.16	0.17	0.85	3.70	
Azotobacter_chroococcum_NCIMB_8003_tRNA-Asp-GTC-1-1	289.05	259.24	16.91	10.29	755.71	486.88	0.69	0.48	10.09	130.03	
Pseudomonas_brasicacearum_DF41_tRNA-Asn-GTT-1-1	15.93	49.97	0.26	0.22	242.56	441.83	0.19	0.17	0.63	0.14	
Alteromonas_australica_DE170_tRNA-fMet-CAT-1-1	183.01	394.68	2.15	1.18	281.00	429.81	0.11	0.17	0.33	0.40	
Candidatus_hamiltonella_defensa_5AT_Acythosiphon_pisum_T5A_tRNA-fMet-CAT-1-1	152.19	326.84	1.41	0.43	238.12	355.25	0.09	0.10	0.14	0.29	
Pseudomonas_brasicacearum_DF41_tRNA-Arg-ACG-1-1	95.13	51.10	1.18	1.24	134.26	350.77	0.13	0.17	6.53	3.83	
Propionibacterium_acidipropionici_ATCC_4875_tRNA-Asn-GTT-1-1	259.00	181.66	12.41	6.24	267.05	339.82	0.55	0.21	34.81	115.59	
Pseudomonas_alkylphenolia_KL28_tRNA-Leu-CAA-1-1	69.34	93.13	1.15	0.10	530.75	337.68	0.23	0.13	0.21	0.07	
Blochmannia_endosymbiont_of_Polyrhachis_Hedomyrma_turneri_675_tRNA-Val-TAC-1-1	UND	UND	UND	UND	314.99	UND	UND	UND	UND	UND	
Brachypodium_distachyon_chr1.tma146-GluCTC	0.12	UND	0.16	0.69	8.82	289.78	UND	0.13	15.02	11.26	
Escherichia_coli_ETEC_H10407_tRNA-fMet-CAT-1-1	135.34	596.56	1.06	0.28	143.47	278.48	0.08	0.09	0.61	0.91	
Acinetobacter_baumannii_1656-2_tRNA-Ile-GAT-1-1	4.18	3.29	7.30	0.60	26.74	276.52	0.15	0.15	2.74	3.95	
Alcanivorax_pacificus_W11-5_tRNA-Ala-TGC-1-1	8.92	125.55	1.19	2.28	38.07	251.98	0.08	0.08	0.23	0.02	
Dyella_japonica_A_tRNA-Asn-GTT-1-1	109.52	436.12	0.83	0.89	165.33	243.29	0.24	0.19	27.37	21.66	
Acinetobacter_baumannii_1656-2_tRNA-Glu-TTC-1-1	119.24	125.54	22.14	2.25	125.24	240.95	0.35	0.21	2.74	43.12	
gamma_proteobacterium_HdN1_tRNA-Val-TAC-1-1	14.02	27.68	6.25	0.15	431.46	230.91	0.32	0.13	0.07	0.04	
Pseudomonas_alkylphenolia_KL28_tRNA-Tyr-GTA-1-1	157.71	205.15	3.94	1.49	403.56	222.46	0.22	0.12	13.56	1.15	
Ruminococcus_champannensis_18P13_JCM_17042_tRNA-Ile-GAT-1-1	UND	84.78	0.00	0.00	0.03	213.04	UND	0.12	0.01	UND	
Pseudomonas_fluorescens_A506_tRNA-Ala-GGC-1-1	42.13	34.35	6.23	2.39	204.33	193.41	0.13	0.35	2.95	3.18	
Aeromonas_hyphrophila_4AK4_tRNA-Phe-GAA-1-1	19.38	9.22	1.71	1.41	54.18	189.26	0.04	0.08	1.31	UND	
Pseudomonas_alkylphenolia_KL28_tRNA-Pro-TGG-1-1	55.02	14.76	1.86	0.34	252.17	181.89	0.06	0.11	0.08	1.41	
Haemlea_chejuensis_KCTC_2396_tRNA-fMet-CAT-1-1	82.18	391.77	1.18	0.31	91.82	179.39	0.03	0.05	0.40	0.59	
Bacillus_sp_X12014_tRNA-Gln-TTG-1-1	UND	UND	0.53	UND	178.25	UND	UND	0.30	UND	UND	
Stenotrophomonas_maltophilia_13637_tRNA-Thr-GGT-1-1	82.39	7.79	0.22	0.39	155.81	175.85	0.11	UND	0.02	0.14	
Lactobacillus_brevis_ATCC_367_tRNA-fMet-CAT-1-1	70.38	152.01	0.13	0.18	105.29	165.25	0.04	0.04	0.06	0.11	
Dechloromonas_aromatica_RC8_tRNA-Thr-CGT-1-1	UND	UND	1.40	UND	5.58	163.22	0.13	UND	0.02	3.36	
Pseudomonas_cichorii_JBC1_tRNA-Ser-CGA-1-1	136.35	87.36	2.42	0.89	194.80	158.98	0.15	0.19	0.11	0.07	
Acinetobacter_baumannii_1656-2_tRNA-Val-TAC-1-1	160.05	99.78	23.10	4.69	160.03	158.83	0.36	0.41	13.31	3.75	
Pseudomonas_alkylphenolia_KL28_tRNA-Gly-TCC-1-1	29.84	68.01	0.51	0.23	85.47	157.78	0.09	0.12	0.66	1.66	
Streptomyces_lividans_TK24_tRNA-Asn-GTT-1-1	UND	UND	1.40	UND	150.40	UND	UND	0.12	UND	UND	
Propionibacterium_acnes_266_tRNA-Arg-CGG-1-1	UND	UND	0.40	UND	148.41	UND	UND	UND	UND	UND	
Aerococcus_urinae_ACS-120-V-Cd10a_tRNA-Asn-GTT-1-1	UND	UND	0.29	UND	147.92	UND	UND	UND	UND	UND	
Pseudomonas_fluorescens_A506_tRNA-Leu-CAG-1-1	11.24	2.31	3.20	0.25	91.28	144.68	0.08	0.04	6.63	0.76	
Megamonas_hypermegale_ART12/1_tRNA-Leu-TAA-1-1	UND	0.01	0.01	0.01	0.10	144.40	UND	UND	0.01	UND	
Mycelopithora_thermophila_ATCC_42464_tRNA-Gln-CTG-4-1	UND	71.68	0.21	0.13	142.61	0.15	UND	0.06	UND	UND	
Bradyrhizobium_diazoefficiens_USDA_110_USDA110_tRNA-Glu-CTC-1-1	24.47	22.81	0.08	0.86	108.76	142.01	0.21	UND	0.06	0.11	
Microbacterium_testaceum_STL037_tRNA-Ala-CGC-1-1	UND	UND	0.53	UND	140.75	UND	UND	UND	UND	UND	
Anabaena_cylindrica_PCC_7122_tRNA-Met-CAT-1-1	151.53	0.07	0.23	1.32	12.21	139.06	UND	UND	0.04	UND	
Fimbrimonas_ginsengisoli_Gsoil_348_tRNA-Met-CAT-2-1	1.08	UND	UND	UND	135.81	UND	UND	UND	UND	UND	
Alcanivorax_pacificus_W11-5_tRNA-Glu-TTC-1-1	UND	UND	0.00	0.53	0.00	135.44	UND	UND	1.54	UND	
Micrococcus_luteus_NCTC_2665_tRNA-Pro-GGG-1-1	UND	UND	2.41	0.16	135.33	UND	UND	UND	UND	UND	
Cellulomonas_flavigena_DSM_20109_tRNA-Leu-CAG-1-1	1.02	135.59	0.20	1.52	10.50	133.46	UND	UND	7.60	UND	
Bradyrhizobium_diazoefficiens_USDA_110_USDA110_tRNA-Gln-CTC-1-1	51.05	44.88	0.64	1.12	47.65	131.10	UND	0.07	0.03	0.58	
Rhodoluna_laccolitica_MWH-Ta8_tRNA-Gln-CTG-1-1	UND	0.20	0.37	0.71	19.11	130.99	UND	UND	0.01	UND	
Janthinobacterium_agaricidamnumos_NBRC_102515_DSM_9628_tRNA-Arg-CCT-1-1	UND	UND	UND	UND	17.77	129.26	UND	UND	UND	UND	
Fusarium_graminearum_CS3005_tRNA-Gly-GCC-1-1	12.91	104.40	2.77	0.64	36.86	128.13	0.21	0.29	0.40	UND	
Pelusinus_fermentans_JBW45_tRNA-Arg-TCG-1-1	UND	UND	UND	UND	127.41	UND	UND	UND	UND	UND	
Propionibacterium_acnes_266_tRNA-Ser-TGA-1-1	46.40	0.10	UND	0.86	5.19	123.28	0.14	UND	0.28	UND	
Bacteroides_dorei_tRNA-Glu-TTC-1-1	153.69	309.08	40.20	5.31	81.87	123.04	0.26	0.14	5.72	1.93	
Acinetobacter_baumannii_1656-2_tRNA-Ala-TGC-1-1	41.43	122.47	17.63	3.14	82.37	122.84	0.29	0.40	0.40	25.93	
Propionibacterium_avidum_44067_tRNA-Lys-TTT-1-1	UND	212.34	7.23	UND	0.06	122.09	UND	UND	UND	UND	
Sideroxydans_llithotrophicus_ES-1_tRNA-Gln-TTG-1-1	UND	133.37	0.85	UND	0.06	116.73	UND	0.07	UND	UND	
Exiguobacterium_sp_AT1b_chr1.tma23-SerGGA	UND	UND	UND	UND	116.16	UND	UND	UND	UND	UND	
Propionibacterium_acnes_266_tRNA-Ser-TGA-1-1	UND	UND	0.06	UND	0.10	116.15	UND	0.01	UND	UND	
Pseudomonas_alkylphenolia_KL28_tRNA-Thr-GGT-1-1	2.48	20.33	0.04	0.23	121.43	116.05	0.08	UND	0.74	0.08	
Acidovorax_avenae_subsp_avenae_ATCC_19860_tRNA-Ser-GCT-1-1	145.64	162.84	27.09	11.46	66.40	115.29	0.15	0.22	5.74	25.54	
Pseudomonas_basicacearum_DF41_tRNA-Ala-TGC-2-1	27.34	35.41	1.95	3.34	112.24	114.62	0.14	0.08	0.23	222.81	
Bacillus_amylolyticus_CC178_tRNA-Met-CAT-1-1	UND	UND	UND	UND	114.28	UND	UND	0.65	UND	UND	
Mycobacterium_neoaurum_VKM_Ac-1815D_tRNA-Gln-CTG-1-1	UND	0.41	0.02	UND	0.29	111.34	UND	UND	0.02	UND	
Bradyrhizobium_diazoefficiens_USDA_110_USDA110_tRNA-Ala-GCG-1-1	25.40	62.38	0.36	0.51	78.09	108.15	0.15	0.02	0.07	0.19	
Pseudomonas_fluorescens_A506_tRNA-Leu-TAG-1-1	1.47	43.44	1.14	0.10	45.76	106.20	0.08	UND	0.19	UND	
Pseudomonas_fluorescens_A506_tRNA-His-GTG-1-1	55.91	31.70	0.41	0.31	166.40	104.79	0.13	0.08	0.14	0.07	
Acidovorax_avenae_subsp_avenae_ATCC_19860_tRNA-Ser-GCT-1-1	82.94	39.79	6.37	5.70	36.13	104.11	0.14	0.08	0.67	24.14	
Bacteroides_xylanisolvens_XB1A_tRNA-His-GTG-1-1	UND	UND	0.17	0.07	100.89	UND	UND	UND	UND	UND	
Ruminococcus_oebeum_BM-162_tRNA-Pro-GGG-1-1	UND	UND	0.34	6.69	100.76	0.13	UND	UND	UND	UND	
Barnetella_australis_AustNH1_tRNA-Thr-TGT-1-1	92.40	6.87	UND	UND	100.10	UND	UND	UND	UND	UND	
Micrococcus_luteus_NCTC_2665_tRNA-Lys-CTT-1-1	114.27	268.40	5.11	3.29	48.08	99.15	0.12	0.13	3.33	4.40	
Acinetobacter_baumannii_1656-2_tRNA-Arg-ACG-1-1	173.84	73.25	11.69	4.50	157.20	92.22	0.24	0.31	8.53	63.57	
Geobacter_benedictiensis_Bam_tRNA-fMet-CAT-1-1	42.39	189.99	0.46	0.17	44.72	88.70	0.02	0.02	0.23	0.30	
Geobacter_daltonii_FRC-32_tRNA-fMet-CAT-1-1	40.58	190.11	0.33	0.08	43.61	88.40	0.05	0.03	0.19	0.29	
Mycobacterium_africanum_GM041182_tRNA-Met-CAT-2-1	58.35	66.96	5.14	4.62	54.79	87.95	0.18	0.08	2.68	3.52	
Aeromonas_hyphrophila_4AK4_tRNA-Tyr-GTA-1-1	31.53	39.06	2.25	0.09	106.16	87.54	0.08	UND	2.43	0.03	
Catenulopspora_acidiphila_DSM_44928_tRNA-Gln-CTG-1-1	UND	1.43	0.23	0.06	1.03	87.00	UND	0.26	1.51	UND	
Elusimicrobium_minutum_Pei191_tRNA-Ser-GCT-1-1	0.06	4.73	0.04	0.07	0.95	86.68	UND	UND	0.17	UND	
Acinetobacter_baumannii_6411_tRNA-Trp-CCA-2-1	27.20	UND	1.80	0.46	47.15	85.60	0.13	0.40	3.51	1.05	
Arthrobacter_aralitensis_Re117_tRNA-Arg-ACG-1-1	118.62	59.86	5.42	0.95	85.66	84.61	0.21	0.11	4.94	8.05	
Brachypodium_distachyon_chr5.tma4-SerGCT	UND	208.23	0.10	0.87	19.36	84.20	0.13	UND	0.18	UND	
Verrucimonas_spinosum_DSM_4136_JCM_18804_tRNA-Cys-GCA-1-1	UND	69.27	UND	UND	84.01	0.14	UND	UND	UND	UND	
Methylphaga_frapplieri_JAM7_tRNA-Asp-GTC-2-1	90.28	74.98	1.55	1.58	26.90	83.97	0.15	0.05	0.72	0.37	
Acinetobacter_baumannii_1656-2_tRNA-Leu-TAG-1-1	135.20	88.41	2.46	0.40	20.59	83.38	0.27	UND	0.01	4.09	
Sulfuricurvum_kujinense_DSM_16994_tRNA-Glu-TTC-2-1	UND	UND	UND	UND	82.92	UND	UND	UND	UND	UND	
Psychrobacter_arcticus_273-4_tRNA-Val-TAC-1-1	122.81	93.17	4.36	1.04	13.39	82.89	0.14	0.53	0.57	70.07	
Faecalibacterium_prausnitzii_L2-6_L26_tRNA-Val-GAC-1-1	1.15	45.91	2.95	1.44	1.58	81.92	UND	UND	UND	UND	
Rhodocyclaceae_bacterium_PG1-Cab_tRNA-Met-CAT-3-1	182.94	190.75	1.89	0.45	67.33	78.56	0.23	0.17	8.39	1.72	
Pantoea_ananatis_AJ13355_tRNA-Val-TAC-1-1	0.21	UND	0.24	UND	0.09	78.42	UND	UND	0.24	UND	
Flavobacterium_branchiophilum_FL-15_tRNA-Val-TAC-1-1	0.09	4.43	2.34	0.08	2.77	78.15	0.02	UND	0.28	UND	
Pseudomonas_chlororaphis_PA23_tRNA-Thr-CGT-1-1</td											

Figure 5-Source Data 3. Non-host rDRs (RPM)

Name	APOB_SRBIKO	APOB_WT	Bile_SRBIKO	Bile_WT	HDL_SRBIKO	HDL_WT	Liver_SRBIKO	Liver_WT	Urine_SRJKO	Urine_WT
Bacteria	104478.09	114730.23	14291.84	3421.66	115759.51	91728.06	183.83	179.03	6799.78	24244.83
Eukaryota	28441.08	24937.70	10932.99	5757.57	26842.12	31188.21	2449.16	3312.43	10555.64	16042.07
Fungi	49869.36	34405.14	4707.79	1006.22	41715.80	30034.45	231.77	254.22	2355.37	5241.13
Protists	23129.74	33023.18	4782.32	1215.89	18249.65	41609.68	79.35	70.98	1821.22	2813.75
Archaeplastida	34829.30	16663.40	7711.99	2775.75	17734.88	20892.10	108.43	128.65	1268.66	3120.96
Embryophyta	9430.06	6939.73	1022.50	216.15	6597.24	6100.84	41.54	46.83	521.24	1288.62
Archaea	21.59	89.19	15.87	5.46	72.70	37.15	0.14	0.20	13.44	82.41

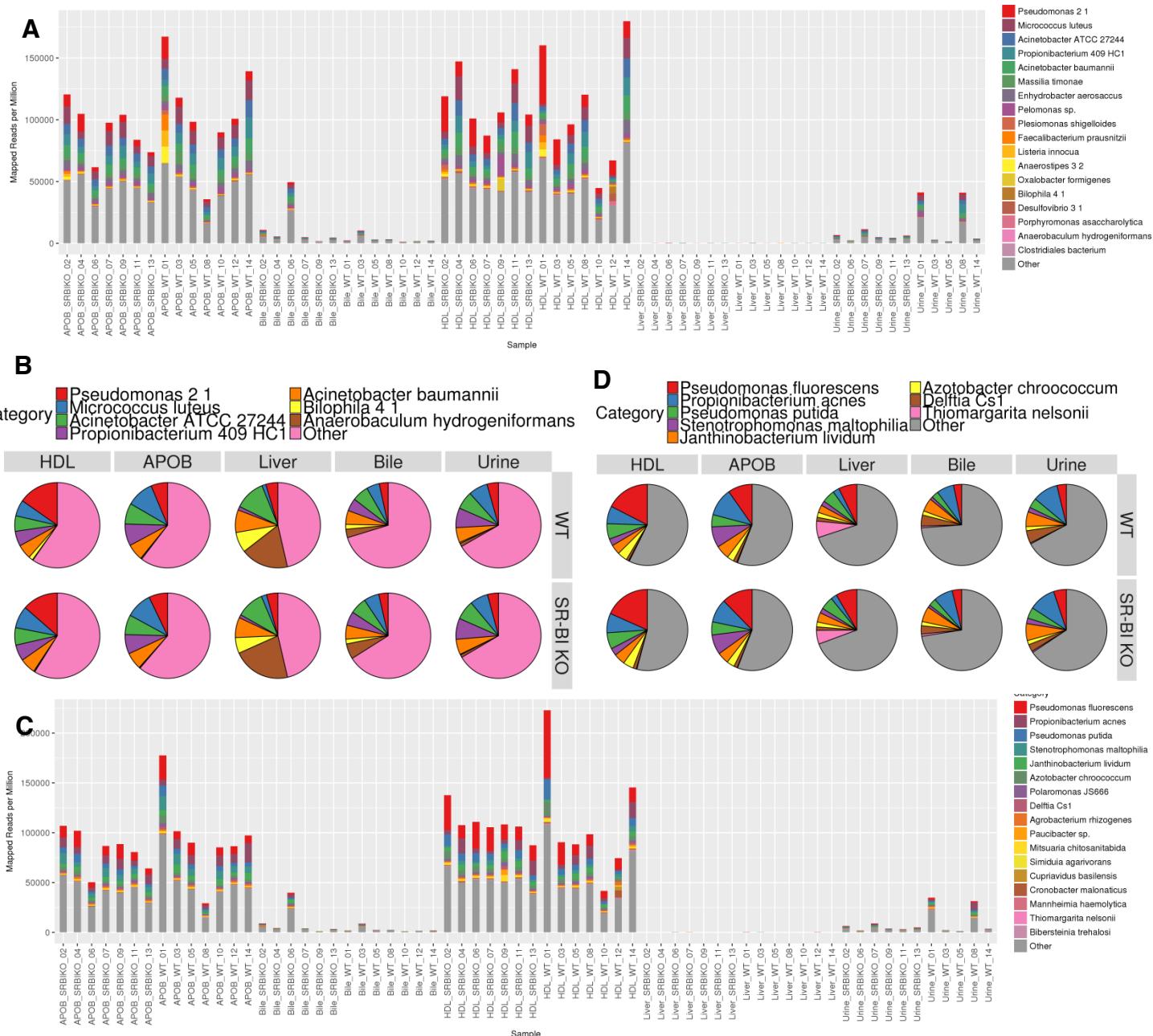


Figure 6-Figure Supplement 1. Lipoproteins transport non-host bacterial sRNAs. WT, wild-type mice; SR-BI KO, Scavenger receptor BI Knockout mice (*Scarb1*^{-/-}). **(A)** Stacked bar plots of non-host sRNAs aligned to bacterial genomes in the human microbiome project (HMB), as reported as mapped reads per million total reads. **(B-C)** Pie charts illustrating the distribution of genome counts per total bacterial reads for species in the **(C)** HMB and **(C)** environment (ENV). **(D)** Stacked bar plots of non-host sDRs aligned to ENV bacterial genomes, as reported as mapped reads per million total reads. HDL WT, N=7; HDL SR-BI KO N=7; APOB WT, N=7, APOB SR-BI KO N=7; Liver WT, N=7; Liver SR-BI KO, N=7; Bile WT, N=7; Bile SR-BI KO, N=6; Urine WT, N=5; Urine SR-BI KO, N=6.

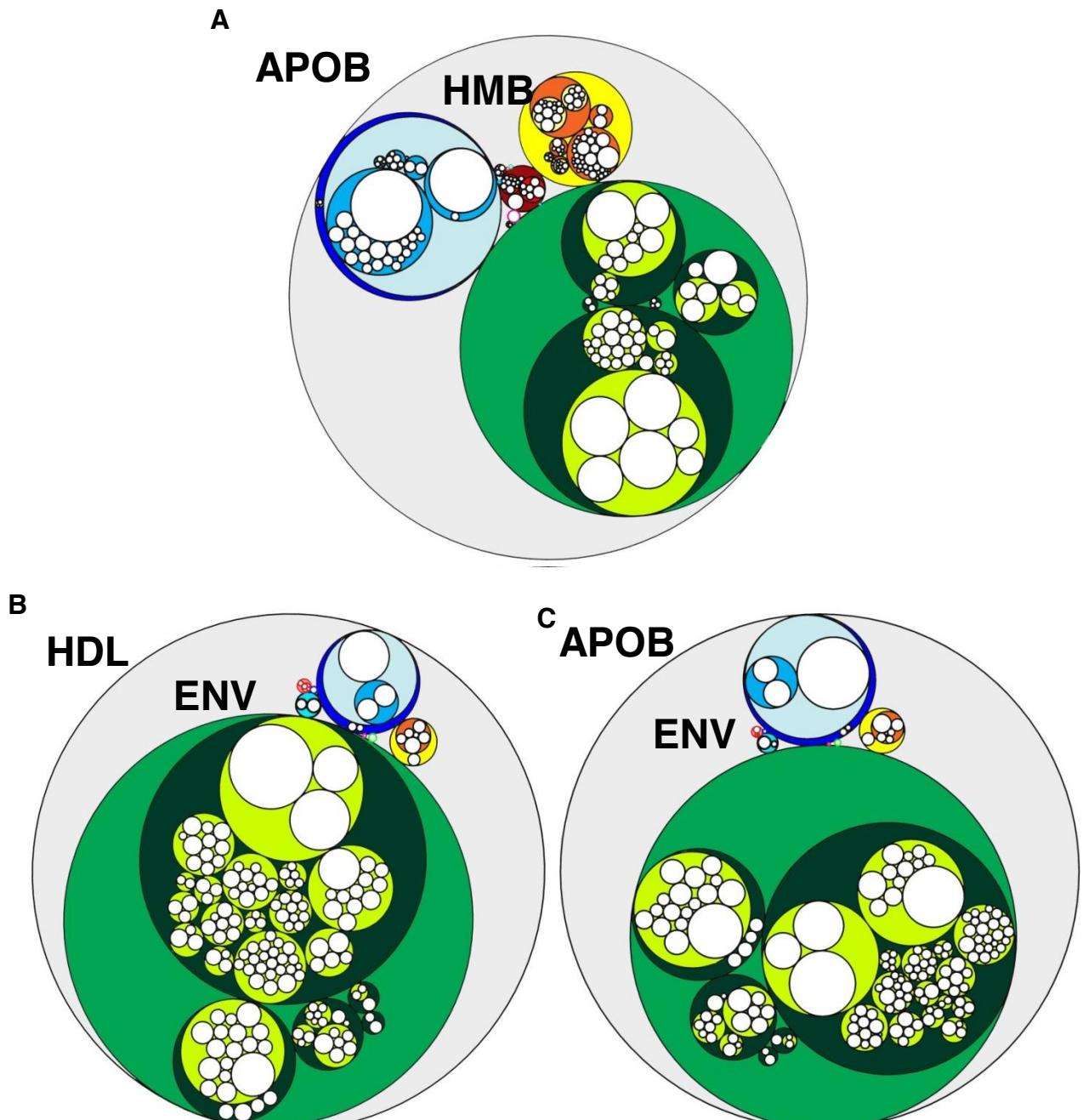
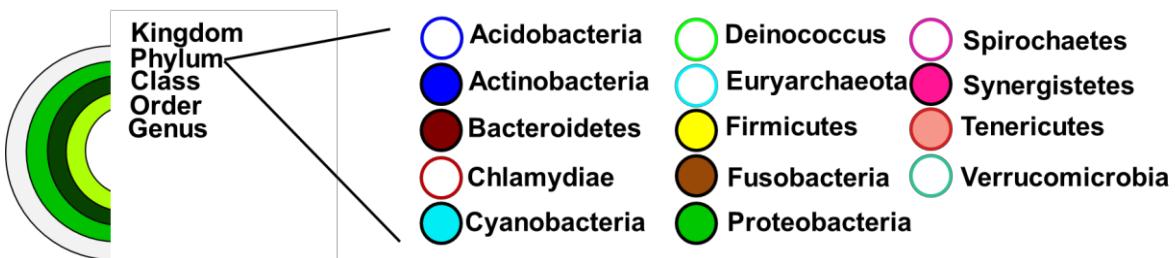


Figure 6-Figure Supplement 2. Lipoproteins are enriched for proteobacteria sRNAs. WT, wild-type mice; SR-BI KO, Scavenger receptor BI Knockout mice (*Scarb1^{-/-}*). **(A-C)** Circular tree maps for non-host bacterial sRNAs on lipoproteins from WT mice, as organized by taxonomy – proteobacteria, green; actinobacteria, blue; firmicutes, yellow; bacteroidetes, red. Maps were generated from bacterial counts organized by species within the human microbiome project (HMB) on **(A)** APOB particles and bacterial species in the environment (ENV) on **(B)** HDL and **(C)** APOB particles. Diameter is proportional to the mean number of reads at the genome level (counts). HDL WT, N=7; APOB WT, N=7

Category ■ BothCategories ■ MicrobiomeOnly ■ EnvironmentOnly

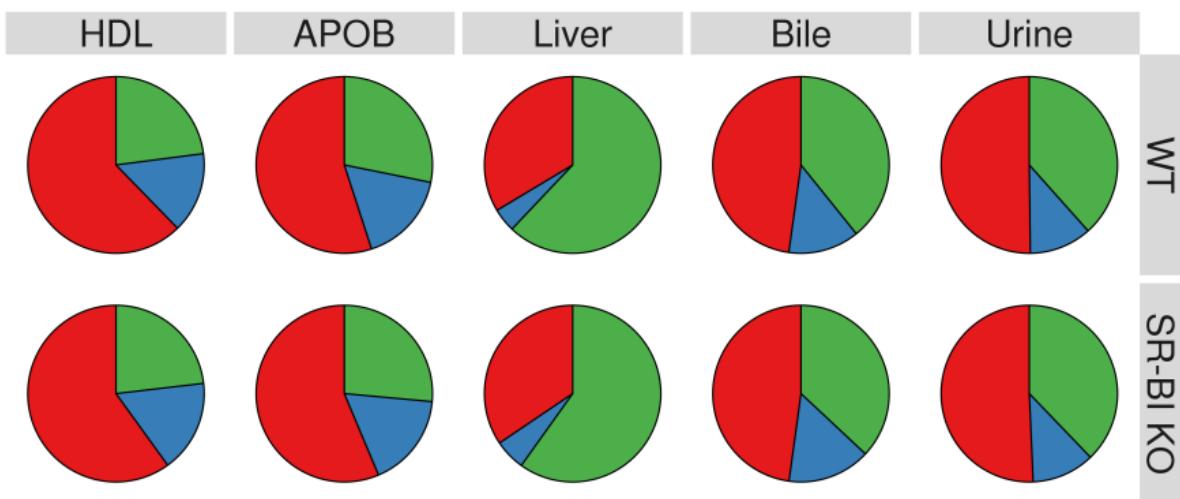


Figure 6-Figure Supplement 3. Lipoproteins transport non-host sRNAs from bacteria species specific for the microbiome or environment. Pie charts illustrating alignment overlap for non-host bacterial genome reads between species in the human microbiome project or environment. HDL WT, N=7; HDL SR-BI KO N=7; APOB WT, N=7, APOB SR-BI KO N=7; Liver WT, N=7; Liver SR-BI KO, N=7; Bile WT, N=7; Bile SR-BI KO, N=6; Urine WT, N=5; Urine SR-BI KO, N=6.

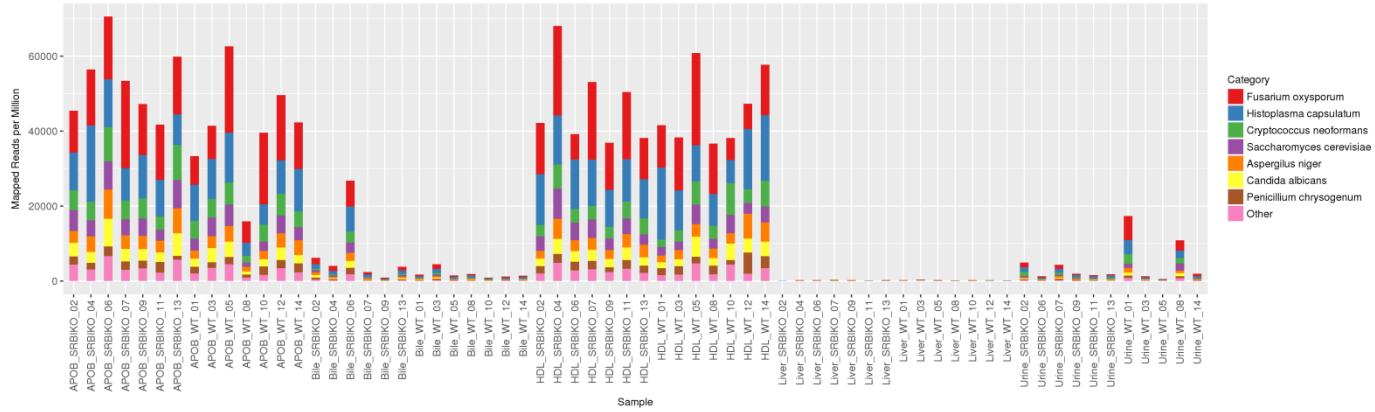
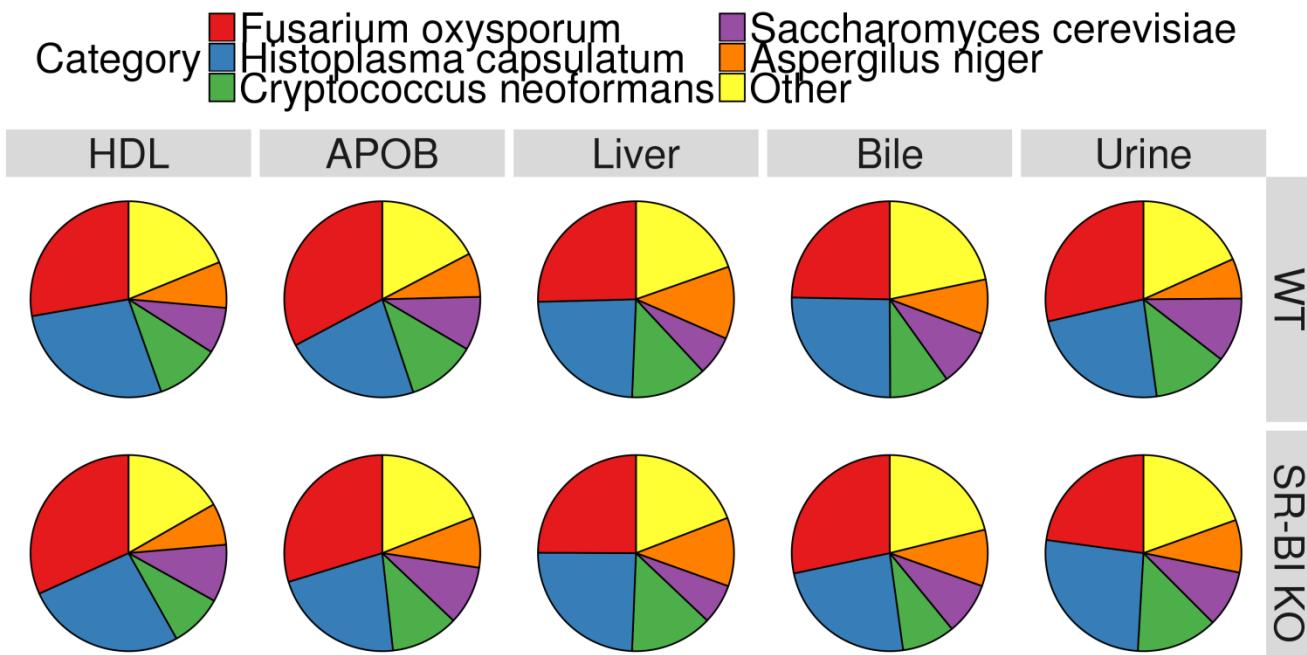
A**B**

Figure 6-Figure Supplement 4. Lipoproteins transport non-host fungal sRNAs. WT, wild-type mice; SR-BI KO, Scavenger receptor BI Knockout mice (*Scarb1^{-/-}*). (A) Stacked bar plots of non-host sRNAs aligned to fungal genomes, as reported as mapped reads per million total reads. (B) Pie charts illustrating the distribution of genome counts per total fungal reads. HDL WT, N=7; HDL SR-BI KO N=7; APOB WT, N=7, APOB SR-BI KO N=7; Liver WT, N=7; Liver SR-BI KO, N=7; Bile WT, N=7; Bile SR-BI KO, N=6; Urine WT, N=5; Urine SR-BI KO, N=6.

Fungal sRNAs

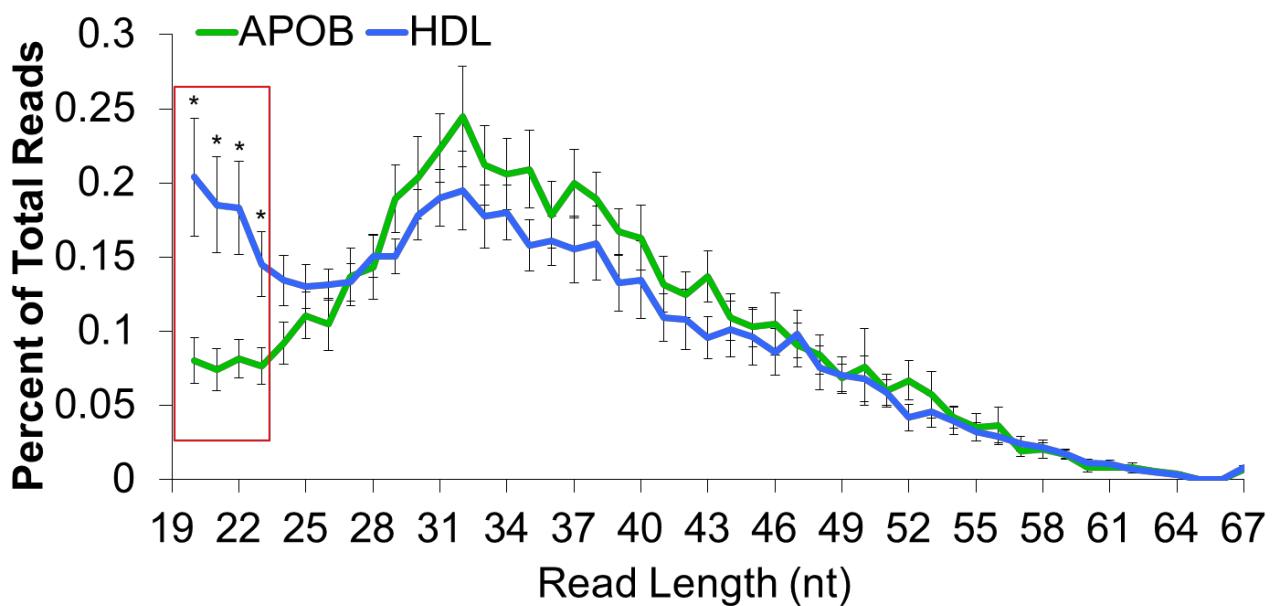


Figure 6-Figure Supplement 5. HDL transport short fungal sRNAs. Distribution of read lengths, as reported as percent of total reads, for non-host fungal sRNAs. Two-tailed Student's t-tests. * $p < 0.05$. HDL WT, N=7; HDL SR-BI KO N=7; APOB WT, N=7, APOB SR-BI KO N=7; Liver WT, N=7; Liver SR-BI KO, N=7; Bile WT, N=7; Bile SR-BI KO, N=6; Urine WT, N=5; Urine SR-BI KO, N=6.

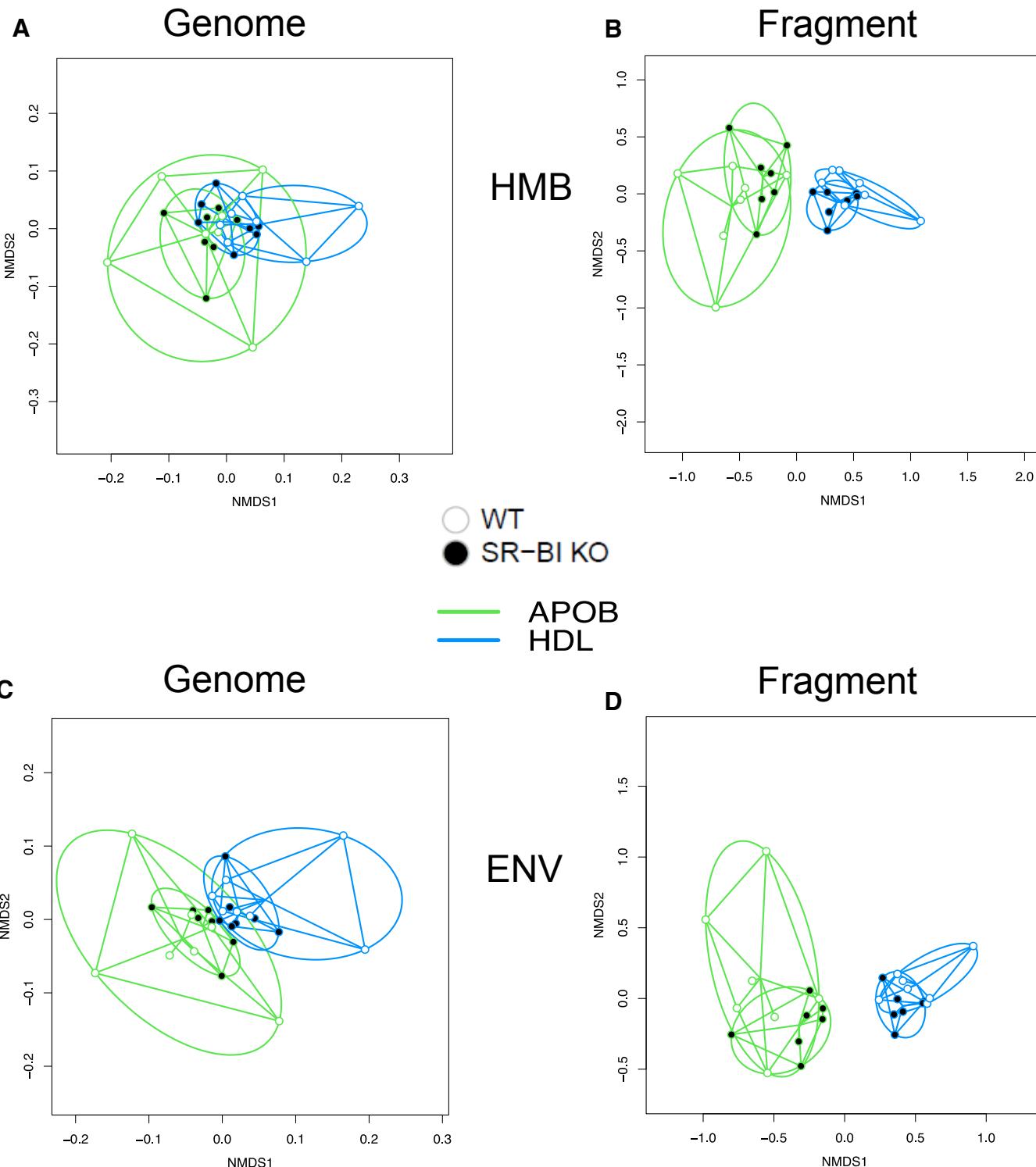


Figure 6-Figure Supplement 6. HDL and APOB sRNA profiles are distinct. (A-D) Principal Coordinate Analysis (PCoA) of non-host bacterial sRNA profiles based on (A) genome counts for species in the human microbiome project (HMB), (B) individual fragment counts for HMB, (C) genome counts for species in the environment (ENV), (D) individual fragment counts for ENV. NMDS1, Non-metric multidimensional scaling. WT (empty circles), wild-type mice; SR-BI KO (filled circles), Scavenger receptor BI Knockout mice (*Scarb1*^{-/-}). HDL WT, N=7; HDL SR-BI KO N=7; APOB WT, N=7, APOB SR-BI KO N=7.

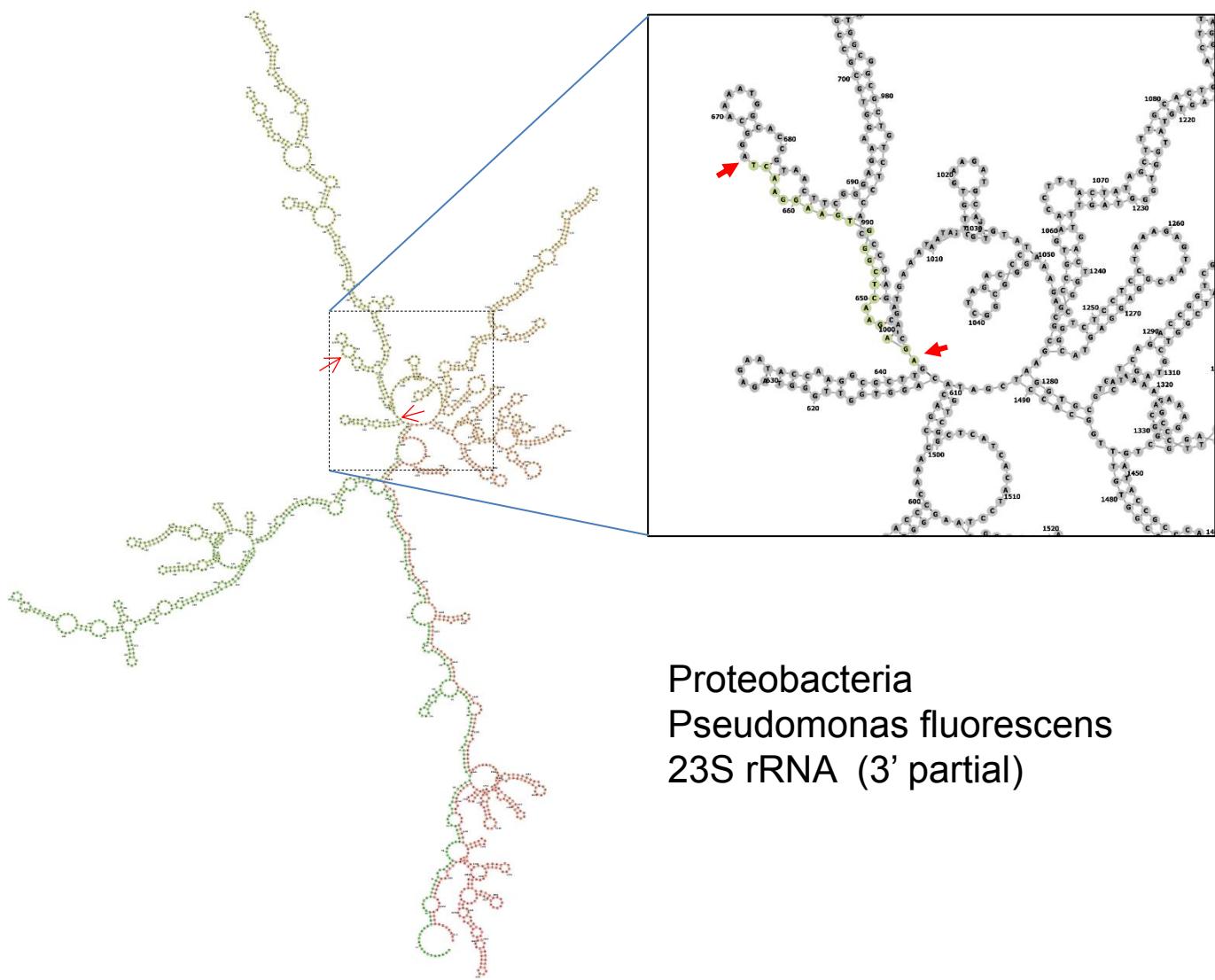


Figure 6-Figure Supplement 7. Alignment of candidate (bacterial) sRNA to *Pseudomonas fluorescens* 23S rRNA.

Proteobacteria
Janthinobacterium lividum
23S rRNA (3' partial)

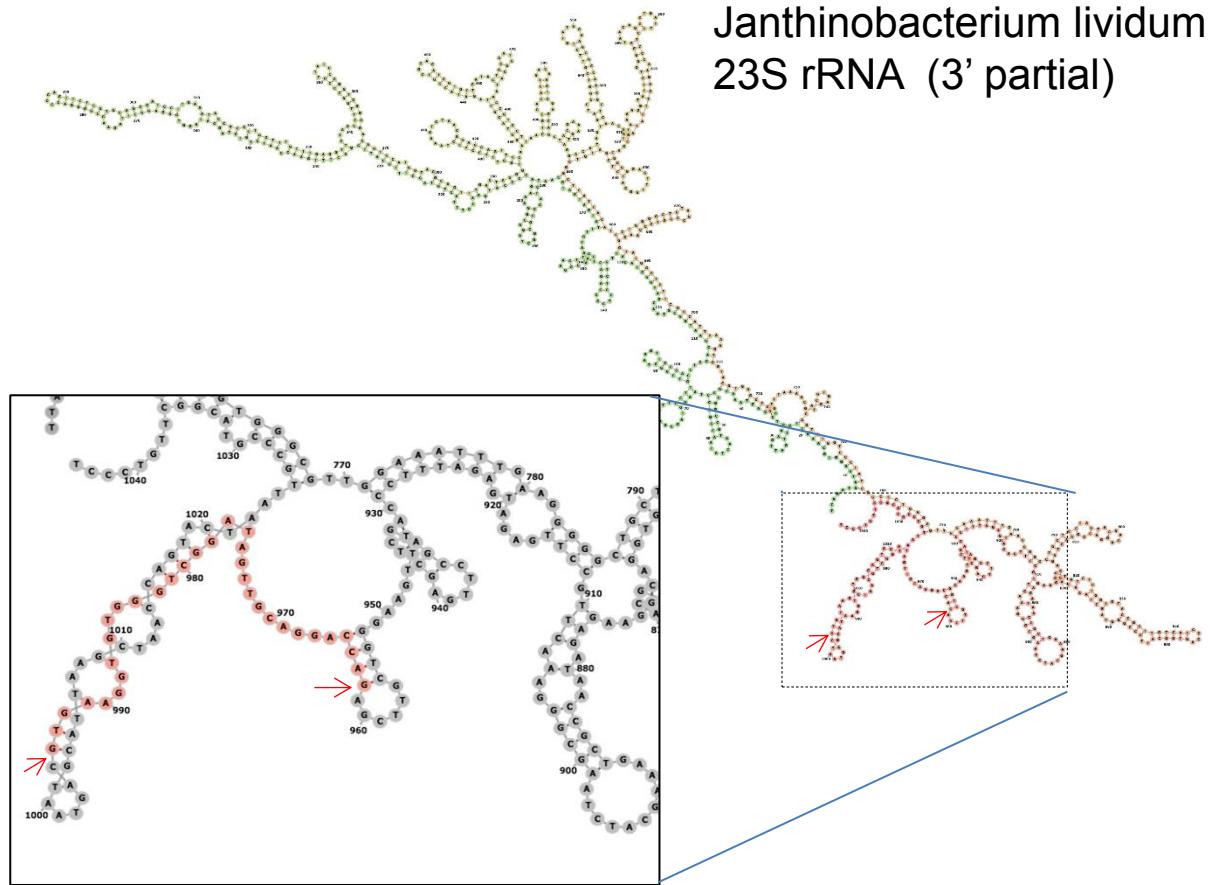
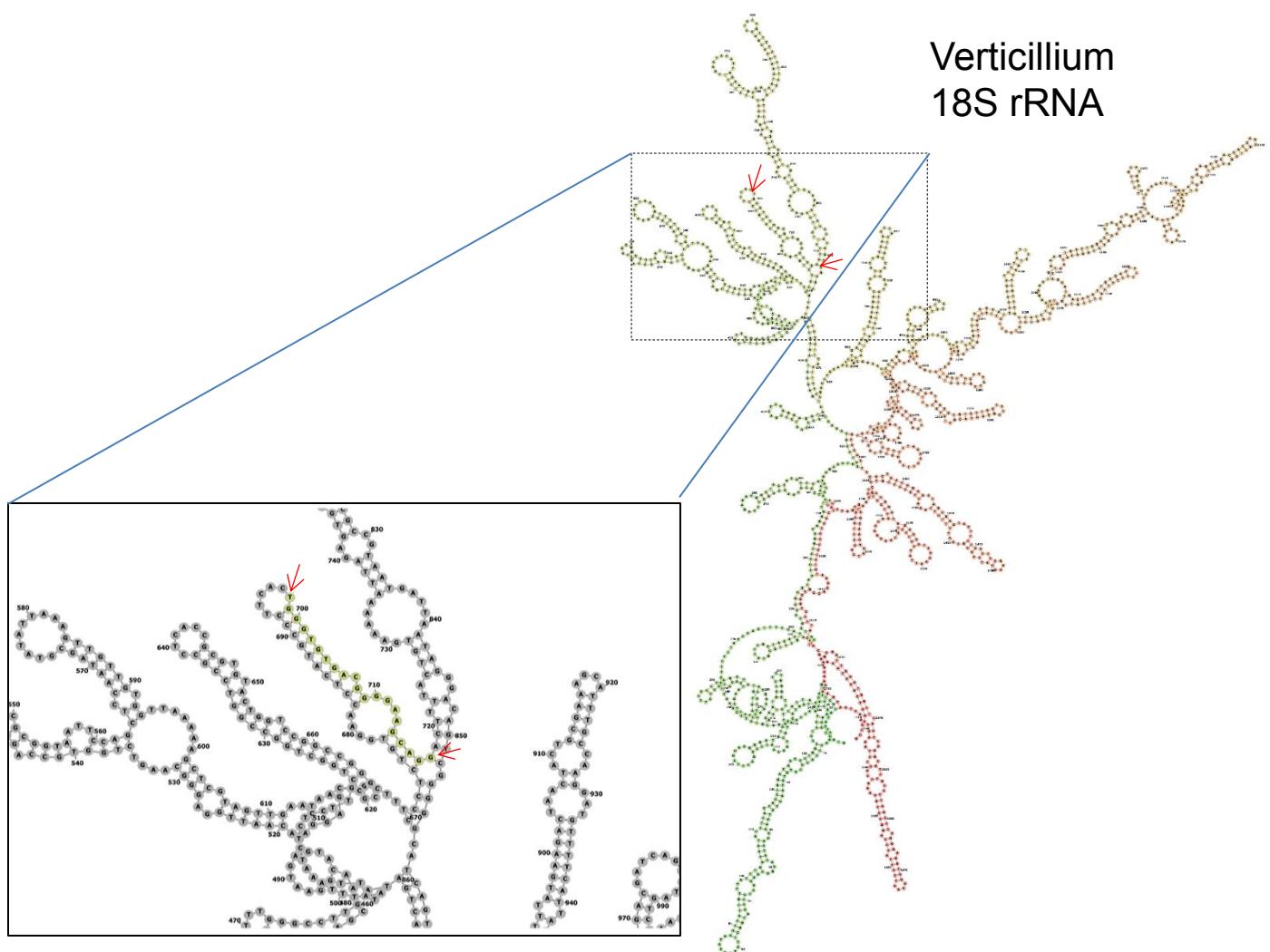


Figure 6-Figure Supplement 8. Alignment of candidate (bacterial) sRNA to *Janthinobacterium lividum* 23S rRNA.

Verticillium 18S rRNA



exo_rDR_Vsp

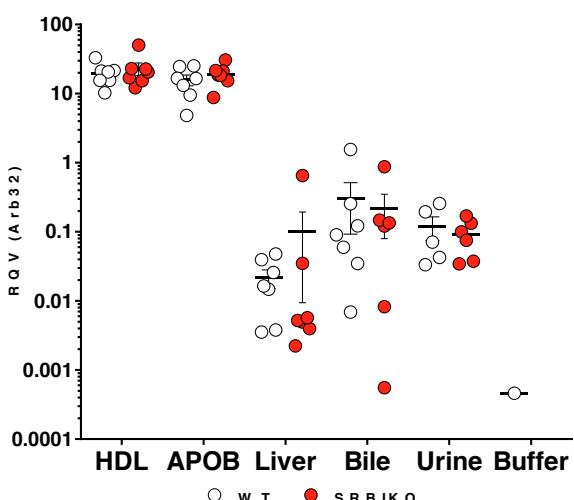


Figure 6-Figure Supplement 9. HDL and APOB particles transport a non-host fungal sRNA.

Alignment of candidate (fungal) sRNA to *Verticillium* 18S rRNA. Real-time PCR analysis of candidate non-host fungal sRNA for exogenous rDR *Verticillium* (exo_rDR_Vsp). WT (white circles), wild-type mice; SR-BI KO (red circles), Scavenger receptor BI Knockout mice (*Scarb1*^{-/-}). HDL WT, N=7; HDL SR-BI KO N=7; APOB WT, N=7, APOB SR-BI KO N=7; Liver WT, N=7; Liver SR-BI KO, N=7; Bile WT, N=7; Bile SR-BI KO, N=6; Urine WT, N=5; Urine SR-BI KO, N=6.

Figure 6-Source Data 1. Top 100 (WT HDL) mean HMB genome counts (RPM).

Name	APOB_SRBIKO	APOB_WT	Bile_SRBIKO	Bile_WT	HDL_SRBIKO	HDL_WT	Liver_SRBIKO	Liver_WT	Urine_SRBIKO	Urine_WT
Pseudomonas 2 1 26 uid40037	6857.88	7230.43	501.42	122.62	15120.46	16703.68	11.35	12.62	246.22	800.27
Micrococcus luteus SK58 uid34071	9218.81	10506.32	821.54	180.63	10096.96	6536.87	5.85	4.09	483.87	1851.52
Acinetobacter ATCC 27244 uid30949	6782.46	7926.32	878.12	215.31	7823.02	6409.50	28.64	32.01	445.36	1172.43
Propionibacterium 409 HC1 uid64685	6756.75	8603.30	735.71	179.80	7264.35	6293.69	3.77	3.71	524.87	1865.46
Acinetobacter baumannii	5963.21	6577.97	713.88	176.36	7173.29	5969.11	20.72	23.07	360.68	959.91
Enhydrobacter aerosaccus SK60 uid31335	3919.44	4040.57	384.40	86.75	4459.11	3880.14	5.48	5.70	184.02	707.78
Massilia timorae CCUG 45783 uid52185	3341.42	5274.94	735.89	168.06	4213.81	3195.46	7.05	5.93	296.12	884.87
Pelomonas sp.	2117.13	2631.60	468.28	118.16	4347.53	2156.21	4.11	3.15	185.67	1003.14
Plesiomonas shigelloides	538.83	1076.63	62.42	19.75	1260.35	2062.57	1.72	1.50	33.17	76.04
Moraxella catarrhalis	2195.09	2233.18	241.63	53.91	2549.17	2054.93	7.20	8.02	139.96	435.16
Aeromonas sp.	841.10	765.62	101.73	21.51	1380.05	1933.28	1.48	1.71	39.34	48.56
Psychrobacter 1501 2011 uid65121	1574.10	1518.02	215.57	58.45	1779.47	1644.02	4.79	5.34	97.96	304.58
Desulfovibrio 3 1 syn3 uid42529	181.79	146.13	89.15	31.71	422.27	1228.60	0.90	0.82	18.69	33.21
Faecalibacterium prausnitzii M21 2 uid18203	581.60	2090.80	81.69	20.19	598.97	1205.08	0.37	0.72	16.38	19.14
Bilophila 4 1 30 uid41961	244.83	314.34	155.07	49.17	389.01	1135.94	16.70	22.51	13.37	21.08
Ralstonia 5 2 56FAA uid39391	778.97	648.97	149.56	43.77	1041.40	1023.25	1.77	1.41	61.83	130.77
Listeria innocua ATCC 33091 uid65129	653.08	2008.88	21.91	8.19	556.80	991.41	0.32	0.42	10.69	14.98
Anaerostipes 3 2 56FAA uid39999	472.59	1946.91	17.67	9.89	486.55	985.15	0.26	0.29	16.55	12.25
Porphyromonas asaccharolytica PR426713P 1 uid59515	107.89	98.99	48.77	12.42	471.03	823.65	0.58	0.42	8.07	12.10
Afipia bromoeae ATCC 49717 uid52155	724.93	935.07	114.09	32.33	801.40	798.12	1.71	1.92	74.80	194.12
Oxalobacter formigenes OCXX13 uid32499	539.45	703.07	147.52	34.07	2058.70	745.03	1.55	1.48	40.40	84.08
Sphingobium yanoikuya ATCC 51230 uid52201	602.40	743.90	108.21	24.55	729.44	694.74	3.10	3.00	62.30	141.78
Enterobacteriaceae bacterium 9 2 54FAA uid41973	390.50	398.47	47.66	14.20	513.32	673.23	1.11	1.25	25.25	131.29
Proteus mirabilis ATCC 29906 uid31523	346.15	502.28	32.60	9.99	530.84	672.96	0.84	0.87	12.62	54.15
Enterobacter cancerogenus ATCC 35316 uid28663	398.65	505.20	64.06	16.12	556.74	661.65	1.97	2.32	43.71	104.13
Sphingomonas sp.	730.76	659.58	122.12	27.45	798.82	660.73	2.72	2.26	59.16	101.06
Catenibacterium mitsuokai DSM 15897 uid19923	422.77	1090.11	15.59	6.82	553.52	657.12	0.45	0.45	27.43	12.00
Oligella urethralis	875.65	1123.23	202.71	51.47	1023.37	654.82	0.97	0.60	79.01	264.72
Brevundimonas diminuta 470 4 uid67195	2482.32	2142.71	97.79	25.12	822.09	637.94	2.47	2.58	44.16	56.49
Achromobacter piechaudii ATCC 43553 uid46343	1015.63	557.09	201.70	37.84	925.84	625.33	1.51	1.28	65.46	321.57
Cardiobacterium hominis ATCC 15826 uid37269	470.06	525.20	35.27	15.50	644.09	610.77	1.03	1.07	22.07	35.42
Rhizobium sp.	982.38	1178.60	56.53	21.19	823.91	603.03	2.06	1.94	51.10	124.46
Kocuria sp.	630.63	615.03	43.87	17.51	904.07	562.60	0.49	0.46	38.03	74.67
Arthrobacter sp.	646.33	448.00	54.96	22.17	616.61	554.35	0.75	0.58	39.76	79.12
Citrobacter 30 2 uid32453	396.75	363.88	46.12	12.93	470.23	540.03	1.22	1.41	34.21	70.34
Synergistes 3 1 syn1 uid39419	86.52	73.84	41.38	11.79	184.57	539.53	0.40	0.61	5.75	11.16
Morganella morgani	295.71	289.64	45.10	11.88	445.83	522.60	0.98	0.99	18.32	61.22
Bacteroides vulgatus CL09T03C04 uid64837	394.63	524.29	135.18	23.47	469.45	519.39	0.66	0.74	27.02	31.88
Edwardsiella tarda ATCC 23685 uid28661	313.96	304.79	69.72	16.23	492.38	518.47	1.19	1.44	26.91	58.96
Salmonella enterica	368.13	336.42	53.63	15.71	459.56	512.00	1.44	1.43	31.94	90.15
Raoultella ornithinotlica	310.39	325.82	45.73	13.77	450.26	508.36	1.18	1.44	26.40	76.54
Klebsiella pneumoniae rhinoscleromatis ATCC 13884 uid40	313.89	314.69	46.85	12.90	430.68	495.49	1.34	1.30	25.74	81.79
Cedecea neteri	313.15	322.28	44.91	13.82	410.47	494.38	1.28	1.39	22.62	96.70
Serratia odorifera DSM 4582 uid40087	293.11	242.01	35.05	12.62	402.69	489.50	1.04	1.06	22.37	50.56
Escherichia 1 1 43 uid32463	434.19	365.54	62.09	17.24	454.54	481.26	2.00	1.89	32.77	90.10
Providencia stuartii ATCC 25827 uid20553	237.69	248.46	38.49	10.96	406.71	478.52	0.73	0.83	15.65	50.48
Shigella	363.16	350.27	55.25	16.37	419.66	476.67	1.73	1.96	31.30	97.18
Dermacoccus Ellin185 uid34079	566.60	532.86	56.45	19.99	550.25	469.09	0.70	0.73	41.82	173.50
Lautropia mirabilis ATCC 51599 uid52989	445.91	509.06	91.23	22.05	664.29	456.38	1.04	1.07	26.10	89.53
Methyllobacterium sp.	571.96	932.88	100.78	25.71	514.98	455.48	1.46	1.68	23.60	55.27
Kluyvera intermedia	309.86	403.90	42.78	12.80	444.28	444.76	1.31	1.25	27.91	75.42
Rhodococcus erythropolis SK121 uid34067	502.82	475.99	60.37	15.92	371.60	441.55	0.90	0.79	37.16	130.73
Lactobacillus 7 1 47FBA uid40031	346.49	395.41	21.47	5.20	293.09	439.50	0.33	0.30	10.62	17.13
Corynebacterium accolens ATCC 49725 uid31443	651.67	722.84	53.44	19.72	585.79	426.45	0.57	0.70	33.63	111.56
Staphylococcus epidermidis 14 1 R1 SE uid64683	455.32	426.75	79.89	16.71	488.70	408.93	0.88	0.54	56.66	127.24
Pseudoramibacter alactolyticus ATCC 23263 uid52995	398.65	602.08	32.61	10.01	501.17	403.99	0.27	0.35	23.02	98.19
Prevotella C561 uid41971	163.74	165.74	68.99	15.03	224.27	401.90	0.64	0.52	5.81	19.06
Ruminococcus 5 1 39BFAA uid32503	386.70	606.62	92.32	37.46	466.90	398.99	0.74	0.58	36.13	132.30
Dietzia cinnamaea	489.54	476.70	57.42	15.27	342.85	387.44	0.71	0.58	27.75	25.59
Microbacterium ginsengisoli	493.18	656.63	91.83	19.54	524.29	369.24	0.85	0.79	30.08	81.12
Nisseria GT4A CT1 uid40033	238.57	360.01	56.37	16.39	335.69	364.85	0.78	0.95	19.80	58.13
Pasteurella dagmatis ATCC 43325 uid40085	150.46	156.54	27.14	8.50	272.78	360.25	0.66	0.77	41.89	117.38
Haemophilus oral taxon 851 F0397 uid48495	208.45	168.12	29.95	8.44	335.50	355.47	0.77	0.85	41.84	112.99
Mycobacterium parascrofulaceum ATCC BAA 614 uid31521	310.49	244.70	58.40	16.27	214.25	342.54	0.64	0.44	19.19	30.56
Rothia dentocariosa	449.95	445.25	53.25	15.54	567.77	338.92	0.48	0.25	17.61	162.00
Aggregatibacter actinomycetemcomitans Y4 uid67199	202.77	174.74	29.19	9.73	281.61	327.40	0.56	0.72	13.52	50.83
Coprococcus D7 uid32495	253.40	299.47	26.59	5.29	228.54	323.60	0.29	0.27	5.57	5.76
Leifsonia sp.	497.15	416.55	63.46	21.56	495.55	322.24	0.73	0.68	23.86	77.36
Eikenella corrodens ATCC 23834 uid30493	225.66	310.04	44.93	14.54	344.31	322.00	0.63	0.79	19.67	68.80
Roseomonas cervicalis ATCC 49957 uid31527	439.53	531.31	56.12	13.07	365.28	317.41	0.86	0.95	20.92	94.65
Streptococcus 2 1 36FAA uid37947	469.28	407.18	60.37	13.50	465.07	314.42	0.41	0.43	25.93	103.10
Staphylococcus aureus ATCC 51811 uid48445	310.83	313.03	49.77	10.90	308.92	314.16	0.48	0.29	17.42	64.73
Oscillibacter sp.	164.76	118.08	74.09	12.86	165.15	312.75	0.64	0.96	41.42	16.47
Kytococcus sedentarius	670.50	303.32	41.33	11.37	389.11	311.24	0.56	0.43	20.70	41.41
Simonsiella muelleri ATCC 29453 uid41981	248.65	231.30	46.59	15.98	287.67	309.93	0.67	1.18	22.17	63.63
Kingella denitrificans ATCC 33394 uid53051	221.95	241.72	44.33	13.78	312.50	304.51	0.77	1.09	27.12	70.98
Pediococcus acidilactici 7 4 uid40051	220.78	296.20	17.14	5.13	232.85	304.31	0.23	0.27	7.68	9.90
Brachybacterium faecium	305.74	315.54	55.05	12.57	321.40	300.22	0.40	0.69	21.42	53.76
Sutterella parvirubra YIT 11816 uid48499	261.75	252.91	55.32	14.06	356.73	299.70	0.60	0.69	15.20	141.88
Cyanobacterium stanieri	376.87	261.86	69.91	16.84	290.84	296.89	0.94	0.72	28.50	89.80
Actinobacillus ureas ATCC 25976 uid52977	171.01	211.20	32.61	8.96	259.13	296.66	0.75	0.76	12.78	60.77
Coprococcus comes ATCC 27785 uid20525	212.87	333.72	14.57	7.30	242.29	294.63	0.18	0.18	10.49	16.08
Yokenella regensburgei ATCC 43003 uid65133	142.00	178.07	20.25	6.18	216.08	286.04	0.59	0.52	10.43	41.94
Burkholderiales bacterium 1 1 47 uid41965	241.12	250.14	60.33	14.86	389.03	274.85	0.55	0.49	15.19	159.17
Oribacterium ACB1 uid49877	175.34	243.45	9.60	3.90	194.12	266.73	0.15	0.13	15.33	5.27
Succinatimonas hippel YIT 12066 uid48507	211.63	245.30	23.13	6.61	303.48</					

Figure 6-Source Data 2. Top 100 (WT HDL) mean ENV genome counts (RPM).

Name	APOB_SRBIKO	APOB_WT	Bile_SRBIKO	Bile_WT	HDL_SRBIKO	HDL_WT	Liver_SRBIKO	Liver_WT	Urine_SRBIKO	Urine_WT
Pseudomonas fluorescens	10441.38	10024.31	432.13	97.13	20366.48	20816.99	13.63	12.85	270.86	554.29
Propionibacterium acnes	7656.89	9636.29	835.51	210.46	8000.84	6990.82	4.56	4.38	576.41	1995.31
Stenotrophomonas maltophilia	6529.63	7948.45	97.99	42.14	3159.07	2793.01	3.73	3.39	130.28	304.06
Janthinobacterium lividum	3683.41	5134.16	830.49	161.72	4857.42	3418.20	6.59	5.30	382.18	1010.64
Pseudomonas putida	4501.40	4717.61	325.75	77.99	7190.05	7177.26	8.70	9.06	228.98	517.70
Azotobacter chroococcum	2599.03	2862.04	189.32	47.39	4625.87	4670.86	3.26	3.46	78.41	241.24
Polaromonas JS666	1346.54	1469.56	343.73	75.94	1646.01	1298.18	2.20	2.21	141.48	254.40
Pseudoxanthomonas suwonense	947.39	1467.53	54.87	19.06	886.56	674.19	1.20	1.18	34.93	79.24
Delftia Cs1	1093.85	1299.49	239.26	110.30	1458.17	991.65	2.33	2.70	127.72	376.96
Herbicoulix solani	1404.34	1279.01	200.85	54.42	1427.25	1164.91	2.09	1.65	89.26	276.12
Exiguobacterium pavilionensis	766.48	1166.14	68.68	23.96	859.92	844.85	0.70	0.43	18.69	87.30
Variovorax paradoxus	1068.75	1116.08	261.11	60.60	1480.89	1111.86	2.25	1.99	106.35	295.40
Promicromonospora kroppenst	1108.58	1083.77	130.24	43.86	1081.35	799.84	1.76	1.26	62.19	175.87
Agrobacterium rhizogenes	993.78	993.46	108.00	36.00	664.67	1090.52	2.27	2.17	49.40	107.21
Xanthomonas campestris	744.15	966.01	52.00	15.67	760.24	634.36	1.33	1.32	34.39	51.60
Acidovorax citrulli	853.03	954.53	179.71	47.84	1130.50	1009.69	1.64	1.32	56.54	284.94
Pseudogulbenkiania ferrooxida	409.13	810.54	59.15	15.43	489.86	640.52	0.71	0.96	27.04	74.13
Ottowia sp.	718.08	788.46	148.66	40.75	786.84	567.80	0.93	0.77	50.80	209.81
Bdellovibrio bacteriovorus	406.73	787.63	56.19	26.88	383.36	553.98	1.11	1.01	7.37	71.46
Idiomarina sp.	333.34	749.51	60.02	14.36	431.83	715.74	1.09	1.07	14.35	37.25
Hydrogenophaga intermedia	651.09	709.30	127.24	33.41	774.71	561.46	0.99	0.93	40.03	178.93
Alteromonas stellipolaris	445.64	707.61	33.15	6.08	516.29	481.61	0.59	0.55	11.30	66.49
Hahella chejuensis	361.50	701.28	32.98	8.37	530.13	605.76	0.79	0.93	19.51	26.37
Roseateles depolymerans	578.57	678.60	122.34	28.10	1122.76	487.52	1.12	0.92	36.88	180.62
Mitsunaria chitosanitabida	556.23	669.49	142.86	32.07	1286.69	551.20	1.33	1.03	41.75	217.19
Lentibacillus amyloliquefaciens	261.71	659.35	43.14	13.63	295.06	378.72	0.45	0.34	11.69	17.78
Herbaspirillum seropedicae	406.44	623.93	145.56	31.40	591.64	596.84	0.93	1.09	41.00	71.60
Pauibacter sp. KCTC 42545	636.05	608.69	145.20	32.63	1283.28	644.54	1.32	0.94	43.41	274.88
Xylella fastidiosa	504.42	607.99	32.28	10.27	529.62	510.76	0.98	0.88	22.65	37.60
Buchnera aphidicola	226.97	602.75	14.22	4.66	263.56	363.47	0.53	0.45	7.35	12.26
Luteimonas sp.	416.97	601.39	27.02	10.40	431.25	371.52	0.76	0.78	20.21	49.77
Fulvimonas pelagi	427.47	599.14	74.42	22.40	316.57	593.35	1.12	1.06	30.95	69.43
Bradyrhizobium japonicum	611.97	572.70	100.04	28.26	685.82	758.80	1.46	1.57	73.85	112.93
Geobacter sp.	196.70	565.85	33.18	8.46	219.80	361.94	0.36	0.31	10.24	41.17
Lysobacter antibioticus	474.10	545.35	25.06	10.37	484.42	391.35	0.94	0.79	24.61	37.10
Marinomonas posidonica	463.97	544.30	60.21	14.61	747.45	827.99	1.78	2.33	22.41	53.15
Coneixabacter woeseli	219.44	533.92	23.20	4.82	218.19	329.58	0.37	0.21	9.30	14.67
Altererythrobacter marenensis	492.57	509.69	71.69	25.21	520.40	479.85	2.13	1.89	52.83	94.72
Rubrobacter radiotolerans	138.81	505.89	11.46	4.41	134.93	278.15	0.16	0.17	2.96	5.15
Leclercia adecarboxylata	460.61	502.71	57.30	14.91	400.53	520.06	2.15	2.61	57.40	119.21
Thalassolitus oleivorus	381.17	487.41	41.60	11.10	723.54	781.56	0.83	0.78	14.80	54.14
Celvibrio japonicus	399.04	466.16	70.63	17.12	747.70	760.92	1.10	1.06	28.64	84.42
Azoarcus sp.	506.32	464.92	102.79	27.57	797.58	612.06	2.00	2.79	38.17	174.77
Dokdonella koreensis	245.49	410.11	22.21	6.76	357.93	357.53	0.43	0.51	10.62	21.24
Methylomonas nitratireducens	449.12	407.63	30.22	9.23	525.27	426.45	1.04	1.30	17.12	184.38
Simiduia agarivorans	463.53	406.61	44.26	15.48	968.09	905.93	1.32	1.41	33.03	88.80
Anabaena cylindrica	771.76	405.41	115.81	63.02	558.21	452.49	1.54	1.92	38.98	332.87
Aeromonas hydrophila	410.21	400.93	57.42	11.36	509.91	1182.34	0.89	0.87	24.13	25.18
Agarivorans gilvus	250.32	398.43	21.14	5.61	442.09	627.59	0.45	0.46	9.22	39.52
Sedimenticola sp.	386.26	393.62	53.51	20.98	432.36	539.19	1.73	1.87	28.44	115.78
Alcanivorax sp.	382.58	391.78	65.07	15.24	668.14	661.26	1.90	2.18	26.03	45.60
Beggiaiotia leptomitiformis	276.37	382.18	53.88	19.16	402.18	338.73	0.67	0.74	17.39	50.62
Ruegeria mobilis	305.38	381.24	41.89	14.89	299.51	210.55	0.52	0.67	23.54	13.91
Cupriavidus basilensis	430.95	365.76	140.75	32.12	626.09	1083.10	1.31	1.11	43.81	132.33
Rheinheimera sp.	210.00	365.42	34.52	7.76	360.04	511.06	0.95	0.95	11.59	23.04
Arenimonas composti	269.79	353.67	21.09	7.48	314.41	324.67	0.53	0.54	11.67	25.47
Thiobacillus denitrificans	232.41	352.24	56.34	18.58	317.35	409.41	0.85	0.84	20.73	119.73
Piscirickettsia salmonis	338.78	336.61	78.44	13.29	431.39	437.40	1.02	0.98	16.71	31.12
Rhizobiales bacterium	396.36	333.83	50.43	13.19	293.04	258.66	0.70	0.84	24.03	103.68
Lactococcus lactis	373.21	328.89	38.11	16.93	315.85	282.40	0.47	0.66	24.77	75.23
Gynuella sunshinyii	228.58	323.79	30.40	10.19	439.70	574.77	0.58	0.60	23.32	38.82
Marinobacterium sp.	316.08	320.61	37.07	10.14	584.40	770.06	0.73	0.84	12.75	32.00
Sulfuricella denitrificans	234.13	320.09	85.42	19.30	301.40	320.41	0.79	1.13	23.19	84.54
Paraburkholderia sacchari	380.14	319.93	71.20	25.85	482.55	340.10	0.83	0.63	28.49	98.26
Regiella insecticola	219.87	319.73	21.60	5.09	296.93	423.26	0.35	0.41	5.92	14.09
Lelliottia ammigena	258.76	318.10	33.19	10.80	294.91	320.88	1.27	1.33	21.80	83.06
Fraterula aurantiaca	232.80	314.93	24.81	7.28	303.15	328.89	0.53	0.54	12.40	164.61
Devosia epidermidihirudinis	316.71	314.77	38.40	10.98	267.36	179.51	0.53	0.36	19.91	36.98
Methylomonas methanica	194.33	313.57	37.77	7.36	481.62	549.29	0.86	0.63	12.29	56.51
Pandoraea palmonicola	294.27	304.65	69.24	21.69	495.51	385.54	0.76	0.76	25.58	83.33
Grimontia hollisae	190.23	292.41	15.92	4.30	279.61	395.29	0.38	0.39	7.29	22.42
Legionella hakeeliae	370.15	292.26	29.11	11.49	408.76	439.40	0.59	0.67	11.30	44.41
Kluyvera intermedia	209.04	289.11	27.53	7.91	298.47	265.57	0.96	0.92	20.21	61.26
Thioploca ingrica	171.64	285.47	36.13	8.37	262.90	320.19	0.53	0.77	9.52	24.85
Wohlfahrtimonas chitiniclasticus	179.44	281.76	39.65	8.22	280.77	380.92	0.41	0.51	8.02	26.16
Rhodanobacter denitrificans	259.68	280.73	27.28	7.89	347.49	348.09	0.54	0.49	14.46	31.81
Halomonas huangheensis	225.27	271.81	25.46	6.97	343.19	498.03	0.65	0.70	9.42	42.09
Gluconacetobacter diazotrophicus	200.78	271.62	20.63	6.64	143.09	188.80	0.45	0.45	12.52	11.41
Rhodovulum sp.	255.98	268.69	60.99	13.17	276.76	240.81	0.77	0.72	10.21	35.59
Glaciecola sp.	172.23	268.48	15.22	4.36	279.57	355.36	0.41	0.44	6.65	31.89
Kosakonia sacchari	226.41	268.41	32.96	10.40	282.23	294.19	1.10	1.13	24.96	73.06
Obesumbacterium proteus	288.85	264.50	26.56	8.80	340.29	400.96	0.70	0.80	17.44	47.70
Bordetella pertussis	472.67	259.60	75.18	15.93	333.78	293.87	0.58	0.52	33.41	166.21
Bosea sp.	212.24	251.20	37.41	9.76	246.85	222.64	0.78	0.84	17.48	59.91
Tallockia micidae	258.93	248.57	22.24	7.31	294.32	361.02	0.40	0.53	8.75	28.29
Chromohalobacter salexigens	200.43	245.98	28.28	6.91	345.47	464.40	0.62	0.53	11.10	45.62
Pluralibacter gergoviae	254.78	242.67	38.00	8.61	368.08	319.40	1.05	1.08	25.56	85.05
Cronobacter malonicus	264.54	242.66	129.71	32.10	477.44	1460.79	1.46	2.56	23.12	39.73
Congregibacter litoralis	197.01	239.97	29.33	6.87	416.89	508.57	0.70	0.69	11.14	19.60
Advenella kashmirensis	282.31	239.39	78.19	12.57	285.13	205.42	0.58	0.47	20.89	148.28
Teredinibacter tumerae	255.67	239.28	33.55	8.32	519.07	713.75	0.62	0.68	18.01	20.51
Marinobacter sp.	270.02	239.18	47.91	10.54	406.68	502.35	0.80	0.		

Figure 6-Source Data 3. Fungi genome counts (RPM).

Name	APOB_SRBIKO	APOB_WT	Bile_SRBIKO	Bile_WT	HDL_SRBIKO	HDL_WT	Liver_SRBIKO	Liver_WT	Urine_SRBIKO	Urine_WT
Fusarium oxysporum	15697.31	13445.86	1985.14	484.95	15232.19	12801.52	55.62	64.89	625.11	2035.88
Histoplasma capsulatum	11619.72	8980.51	1758.06	462.04	11951.41	12543.87	55.50	62.33	666.78	1353.75
Cryptococcus neoformans	6092.29	4555.52	715.64	189.93	4101.03	4807.55	31.26	32.02	411.08	890.61
Aspergilus niger	4590.69	2946.05	655.30	163.19	3249.87	3510.84	24.91	31.29	219.94	428.96
Saccharomyces cerevisiae	5242.12	3677.24	703.68	182.38	4508.99	3477.47	15.09	17.24	236.91	657.88
Candida albicans	4112.73	2637.75	560.19	138.97	2775.14	3253.02	17.48	21.20	162.02	378.08
Candida glabrata	4061.29	2621.49	480.75	119.12	2970.40	2787.33	11.13	12.13	156.30	365.26
Penicillium chrysogenum	2112.64	1827.06	500.09	146.18	2069.63	2620.23	14.77	18.36	175.03	283.32

Figure 6-Source Data 4. Multivariate analysis of non-host sRNA profiles (WT only).

Comparison	Class	Level	Dispersion_Fvalue	Dispersion_pvalue	Permanova_Fvalue	Permanova_pvalue
APOB vs HDL	Microbiome	Parent	62.30	1.18E-15	0.46	7.49E-01
APOB vs HDL	Environment	Parent	59.02	3.68E-15	0.37	7.87E-01
APOB vs HDL	Fungi	Parent	54.10	2.11E-14	0.09	9.78E-01
APOB vs HDL	Microbiome	fragment	27.46	2.66E-09	1.52	9.40E-02
APOB vs HDL	Environment	fragment	32.39	2.11E-10	1.70	4.80E-02
APOB vs HDL	Fungi	fragment	30.00	7.03E-10	1.42	1.10E-01

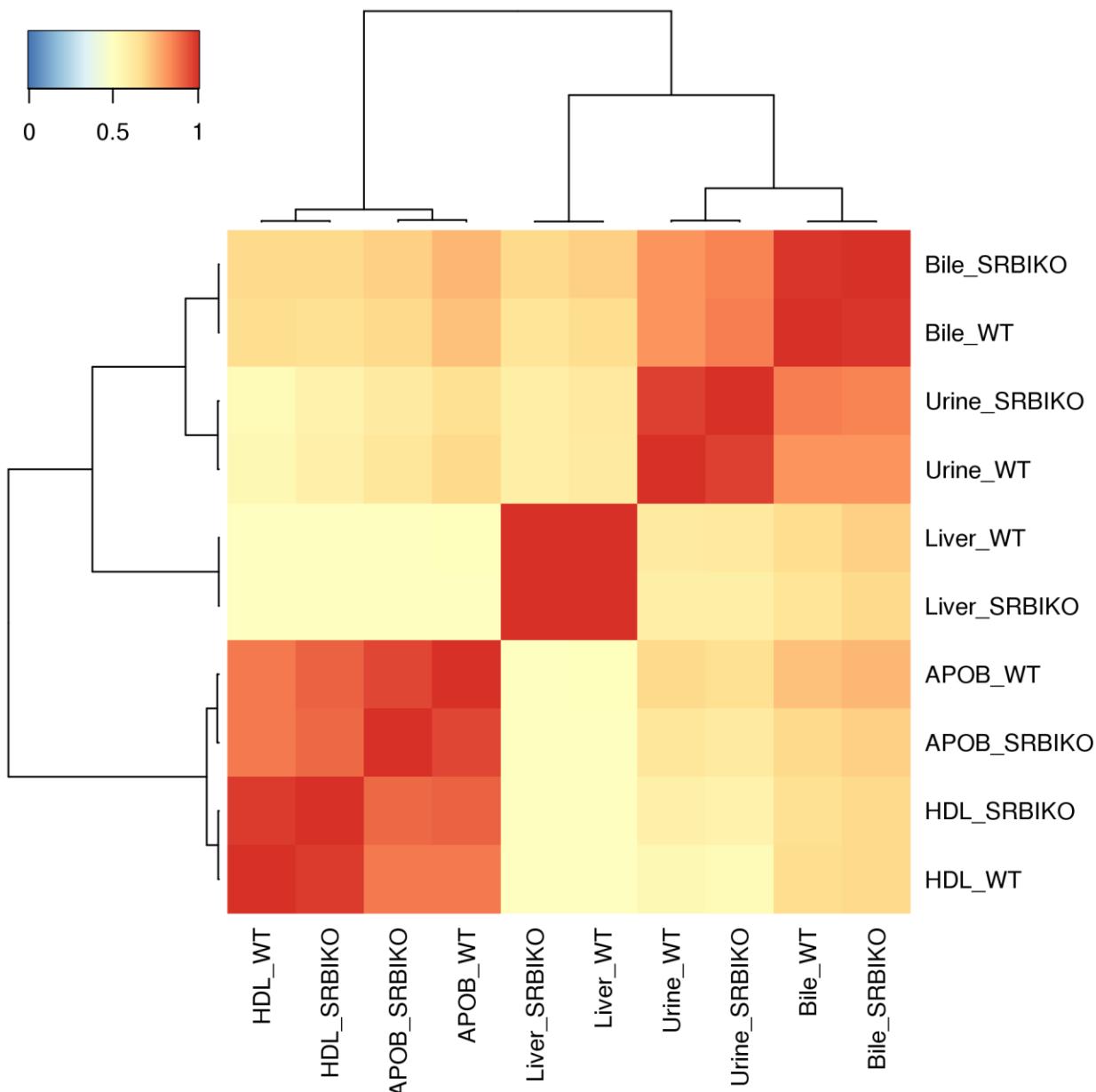


Figure 7-Figure Supplement 1. Correlation of sample types based on the most abundant sRNAs.

Heatmap of hierarchical clustered pairwise correlation (Spearman, R) coefficients between group means for the top ranked (collective top 100 non-redundant) sRNAs for each group. WT, wild-type mice; SR-BI KO, Scavenger receptor BI Knockout mice (*Scarb1*^{-/-}). HDL WT, N=7; HDL SR-BI KO N=7; APOB WT, N=7, APOB SR-BI KO N=7; Liver WT, N=7; Liver SR-BI KO, N=7; Bile WT, N=7; Bile SR-BI KO, N=6; Urine WT, N=5; Urine SR-BI KO, N=6.

Figure 7-Source Data 1. Multivariate analysis of class-independent sRNA profiles compared to liver .

Group	Class_level	Comparison	Dispersion_Fvalue	Dispersion_pvalue	Permanova_Fvalue	Permanova_pvalue
APOB	Independent	APOB vs. Liver	16.83	1.47E-03	19.56	2.00E-03
Bile	Independent	Bile vs. Liver	2.76	1.22E-01	49.74	3.00E-03
HDL	Independent	HDL vs. Liver	80.90	1.11E-06	15.71	1.00E-03
Urine	Independent	Urine vs. Liver	7.02	2.44E-02	22.07	2.00E-03
APOB	Independent	APOB vs Bile	4.19	6.31E-02	10.08	2.00E-03
APOB	Independent	APOB vs HDL	0.92	3.58E-01	2.62	2.00E-03
APOB	Independent	APOB vs Urine	0.06	8.16E-01	5.83	2.00E-03
Bile	Independent	Bile vs HDL	14.51	2.49E-03	11.18	1.00E-03
Bile	Independent	Bile vs Urine	1.75	2.16E-01	8.01	2.00E-03

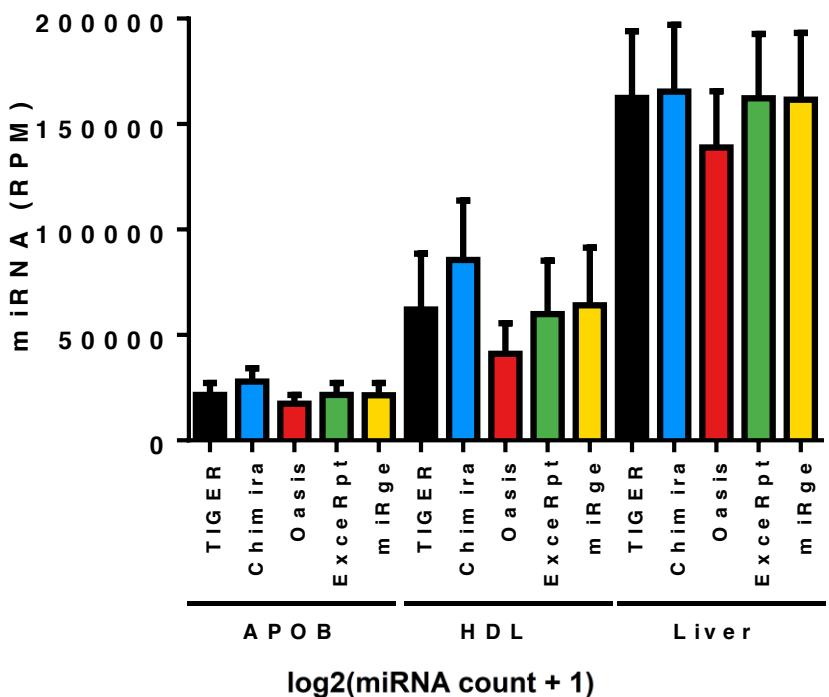
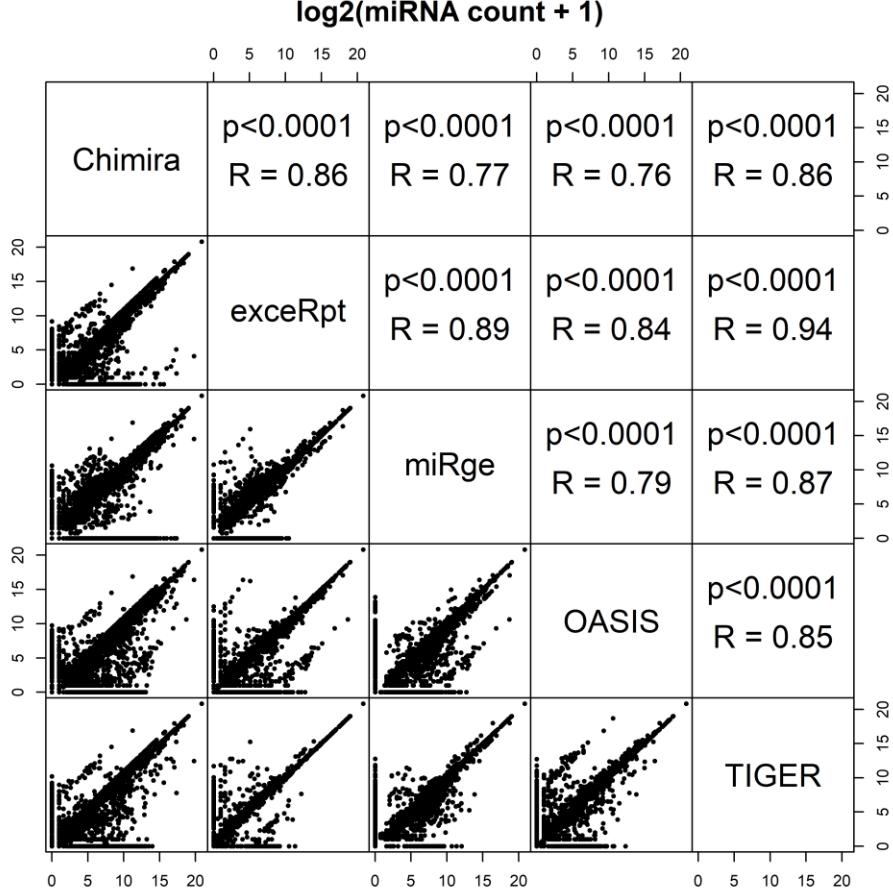
A**B**

Figure 8-Figure Supplement 1. TIGER pipeline comparison for canonical miRNA analysis. (A) sRNA-seq analysis of canonical miRNAs for different pipelines, as reported as miRNAs Reads Per Million (RPM) total reads, for WT HDL, APOB, and liver samples. (B) Correlations between different analysis pipelines for canonical miRNAs in WT HDL, APOB, and liver samples. Spearman correlation. HDL WT, N=7; APOB WT, N=7, Liver WT, N=7.

Figure 8-Source Data 1. TIGER comparisons to other pipelines

Feature	TIGER	Chimira	Oasis	ExceRpt	miRge
Web frontend	N	Y	Y	Y	N
Alignment tool	Bowtie	BLASTn	STAR	Bowtie	Bowtie
Alignment Strategy	ome/Datal ome/Datal	Database	Database	Genome/Database	Database
Host miRNAs	Y	Y	Y	Y	Y
Novel miRNAs	N	N	Y	N	N
isomiRs	Y	Y	N	N	Y
NTAs	Y	Y	N	N	Y
miRNA SNPs and Editing	N	Y	N	N	Y
Non-host miRNAs	Y	N	Y	Y	Y
tDR	Y	N	N	Y	Y
IncDR	Y	N	N	Y	Y
snoDR	Y	N	Y	Y	Y
snDR	Y	N	Y	Y	Y
miscRNA	Y	N	N	Y	Y
piRNA	N	N	Y	Y	N
rDR	Y	N	Y	Y	Y
circRNA	N	N	N	Y	N
Bacteria	Y	N	Y	Y	N
Archaea	N	N	Y	Y	N
Virus	N	N	Y	Y	N
Fungi	Y	N	N	Y	N
Non-host tDR	Y	N	N	N	N
Non-host rDR	Y	N	N	Y	N
Normalization	DESeq2	DEseq2	DESeq2	N	RPMmicrorna
DE	DEseq2	DEseq2	DESeq2	N	N
DE 2 groups	Y	Y	N	N	N
DE Multivariate	N	N	Y	N	N
Classification	N	N	Y	N	N
GO	N	N	N	N	N
Pathway	N	N	N	N	N
Data Vizualization	Y	Y	Y	Y	Y
batch	Y	Y	Y	Y	Y

Figure 8-Source Data 2. TIGER summary output table

	APOB_SRBIKO	APOB_WT	Bile_SRBIKO	Bile_WT	HDL_SRBIKO	HDL_WT	Liver_SRBIKO	Liver_WT	Urine_SRBIKO	Urine_WT
Total Reads	10196709.57	10426434.00	12611515.50	14416869.43	11002029.43	11839204.29	7838441.86	9019201.29	41206902.67	13495370.20
Total Host	2003891.42	2671368.58	9685697.66	12028412.90	2550703.46	2896888.46	6857275.57	7841642.73	33782075.02	10371862.86
Total Non-Host	3713751.43	3630707.71	614156.00	244993.57	3757938.29	3856228.71	26809.14	39649.00	1060624.00	803242.20
Too Short	349226.43	185342.29	516190.00	405730.86	993402.29	1714684.14	33616.14	46629.57	1227994.33	333724.00
Unmapped	4129840.29	3939015.43	1795471.83	1737732.14	3699985.43	3371403.00	920741.00	1091280.00	5136209.33	1986541.20
Total Assigned	6066869.28	6487418.58	10816043.66	12679137.33	7302044.03	8467801.32	6917700.86	7927921.30	36070693.35	11508829.06
%assigned	0.5950	0.6222	0.8576	0.8795	0.6637	0.7152	0.8825	0.8790	0.8754	0.8528
Host										
Host Total sRNA	1914365.56	2567869.58	9142975.49	11749523.62	2340102.46	2599891.46	6338489.14	7151785.44	33549187.02	10208411.06
Host_genome_miRNAs	351802.34	238748.81	721278.22	818896.40	592698.41	953958.69	1094634.13	1604115.51	421902.32	103311.80
Host_genome_rDRs	667283.73	797402.51	1064988.10	1238583.41	1005522.01	990735.86	3475737.93	3947849.40	7595901.73	2628239.78
Host_genome_snoDRs	13087.47	22021.84	35746.53	24456.91	20199.77	15443.81	1483539.89	1113488.01	55134.10	60582.94
Host_genome_snDRs	26653.61	25355.51	65127.00	66221.54	124622.37	107456.56	13723.73	22817.17	22426.18	20723.36
Host_genome_tDRs	810224.36	1455182.47	7212599.28	9563855.07	567157.56	486575.10	235225.47	402458.97	25360776.53	7343478.26
Host_genome_lincDRs	4192.43	7784.57	15092.00	11871.14	5238.71	9543.43	3963.43	5166.43	43599.17	12545.40
Host_genome_yDRs	5947.14	5402.00	10053.67	11279.57	10069.71	7292.29	2582.00	4789.57	36221.33	30091.40
Host_genome_misc_RNA	35174.86	15971.86	18090.33	14360.29	14593.00	28885.29	29082.57	51100.00	13224.83	9438.40
Host_genome_non-sRNA	89525.86	103499.00	542722.17	278889.29	210601.00	296997.00	518786.43	689857.29	232888.00	163451.80
Non-Host										
Non-Host_Genome Total										
Bacteria_HMB	941383.69	1148866.43	135118.65	47241.43	1241479.42	1272444.32	2071.43	2521.45	206615.46	202763.60
Bacteria_ENV	845390.42	1010546.86	107792.36	38850.68	1228060.12	1359575.02	1299.42	1622.86	159180.67	164687.40
Fungus	542475.86	422503.86	78347.00	25885.57	516255.72	530335.14	1686.72	2375.29	83798.34	74262.19
Non-Host_Library Total										
Non_Host_genome_xenomiRs	574.86	279.14	1524.83	916.57	767.43	1135.29	43.86	64.14	201.67	86.20
Non_Host_genome_rDRs	2577912.00	2441756.15	458196.00	185914.86	2364865.00	2361221.00	23720.01	35672.72	832834.67	611805.40
Non_Host_genome_tDRs	189318.57	279545.43	35602.67	16303.14	278360.86	307671.71	634.14	886.14	59774.00	45919.59

Figure 8-Source Data 3. Comparisons to other

Feature	APOB				HDL				Liver							
	Chimira	Excerptr	miRge	Tiger	Oasis	Chimera	Excerptr	miRge	Tiger	Oasis	Chimera	Excerptr	miRge	Tiger	Oasis	
Total Reads	10426434.00	10426434.00	10426434.00	10426434.00	10968327.86	11839204.29	11839204.29	11839204.29	15418341.00	9019201.29	9019201.29	9019201.29	9019201.29	9019201.29	10019001.71	
Host Reads	NA	2107747.14	NA	2671368.57	227035.29	NA	2122452.29	NA	2896888.43	992068.71	NA	4205631.57	NA	7841642.71	1596410.14	
Host smallRNA reads	NA	NA	NA	2567869.57	NA	NA	NA	NA	2599891.43	NA	NA	NA	NA	7151785.43	NA	
miRNA total reads	311143.29	238433.51	237243.86	238748.86	203566.14	1210229.43	919625.98	987899.29	953958.71	826859.00	1631118.71	1597330.10	1596855.29	1604115.57	1514686.29	
miRNA > 10RPMM	106.29	88.14	87.86	91.57	89.14	163.71	133.29	149.71	139.00	135.00	178.57	159.57	163.86	163.14	150.14	
miRNA > 100RPMM	138.71	120.00	112.29	124.00	168.57	179.43	158.29	162.00	162.86	249.86	154.29	139.00	142.71	143.71	355.57	
miR-22-3p RPM	43.11	42.52	43.09	43.11	41.40	276.24	264.33	276.97	271.74	207.36	328.99	307.15	318.58	317.81	279.86	
miR-22-3p RPMM	1043.15	1339.40	1359.56	1350.37	42408.36	3070.00	3877.86	3912.65	3854.52	93608.02	2197.62	2061.37	2179.87	2163.78	58113.52	
miR-92a-3p RPM	1345.89	1291.03	1348.61	1317.49	1236.91	2979.72	2874.46	3032.06	2939.68	2284.63	1864.67	1777.16	1773.96	1818.32	1474.35	
miR-92a-3p RPMM	44542.21	55360.51	59004.65	57211.06	1229114.81	43031.09	56916.75	56626.52	55908.95	1059615.05	11493.81	11117.11	11211.06	11394.13	341504.14	
lncDR total reads	NA	3902.90	NA	7784.57	NA	NA	8537.44	NA	9543.43	NA	NA	13335.29	NA	5166.43	NA	
snoDR total reads	NA	16173.78	NA	22021.71	870.29	NA	11267.87	NA	15443.86	5718.57	NA	602487.35	NA	1113487.71	3194.14	
snDR total reads	NA	25489.81	NA	25355.57	1017.86	NA	106257.72	NA	107456.71	8121.00	NA	21608.42	NA	22817.43	421.29	
snDR > 100 RPMsnDR	NA	NA	NA	53.71	NA	NA	NA	NA	58.86	NA	NA	NA	NA	96.43	NA	
tDR total reads	NA	1621821.29	NA	1455182.43	NA	NA	535736.00	NA	486575.00	NA	NA	517326.14	NA	402458.86	NA	
tDR > 100 RPMtDR	NA	11.86	NA	18.57	NA	NA	17.00	NA	33.86	NA	NA	22.00	NA	41.71	NA	
rDR total reads	NA	1026293.14	NA	797402.57	531.86	NA	1394877.86	NA	990736.14	3347.86	NA	4365498.71	NA	3947849.86	994.14	
rDR > 100 RPMrDR	NA	NA	NA	17.43	NA	NA	NA	NA	18.71	NA	NA	NA	NA	13.43	NA	
piRNA total reads	NA	2281.14	NA	NA	10572.86	NA	5655.00	NA	NA	65242.43	NA	40670.86	NA	NA	7888.57	
misc_RNA total reads	NA	20073.65	NA	15971.86	NA	NA	23336.43	NA	28885.29	NA	NA	33462.51	NA	51100.00	NA	
other ncRNA total reads	NA	NA	1117470.71	NA	NA	NA	NA	2162839.43	NA	NA	NA	NA	5609577.14	NA	NA	
mRNA total reads	NA	NA	14140.71	NA	NA	NA	NA	76421.29	NA	NA	NA	NA	150147.71	NA	NA	
Nonhost reads	NA	NA	NA	3630707.71	NA	NA	NA	NA	3856228.71	NA	NA	NA	NA	39649.00	NA	
% assigned	0.03	0.21	0.13	0.60	0.02	0.09	0.17	0.24	0.57	0.05	0.16	0.46	0.81	0.87	0.15	

\log_{10} Base Mean • 2 • 4 • 6

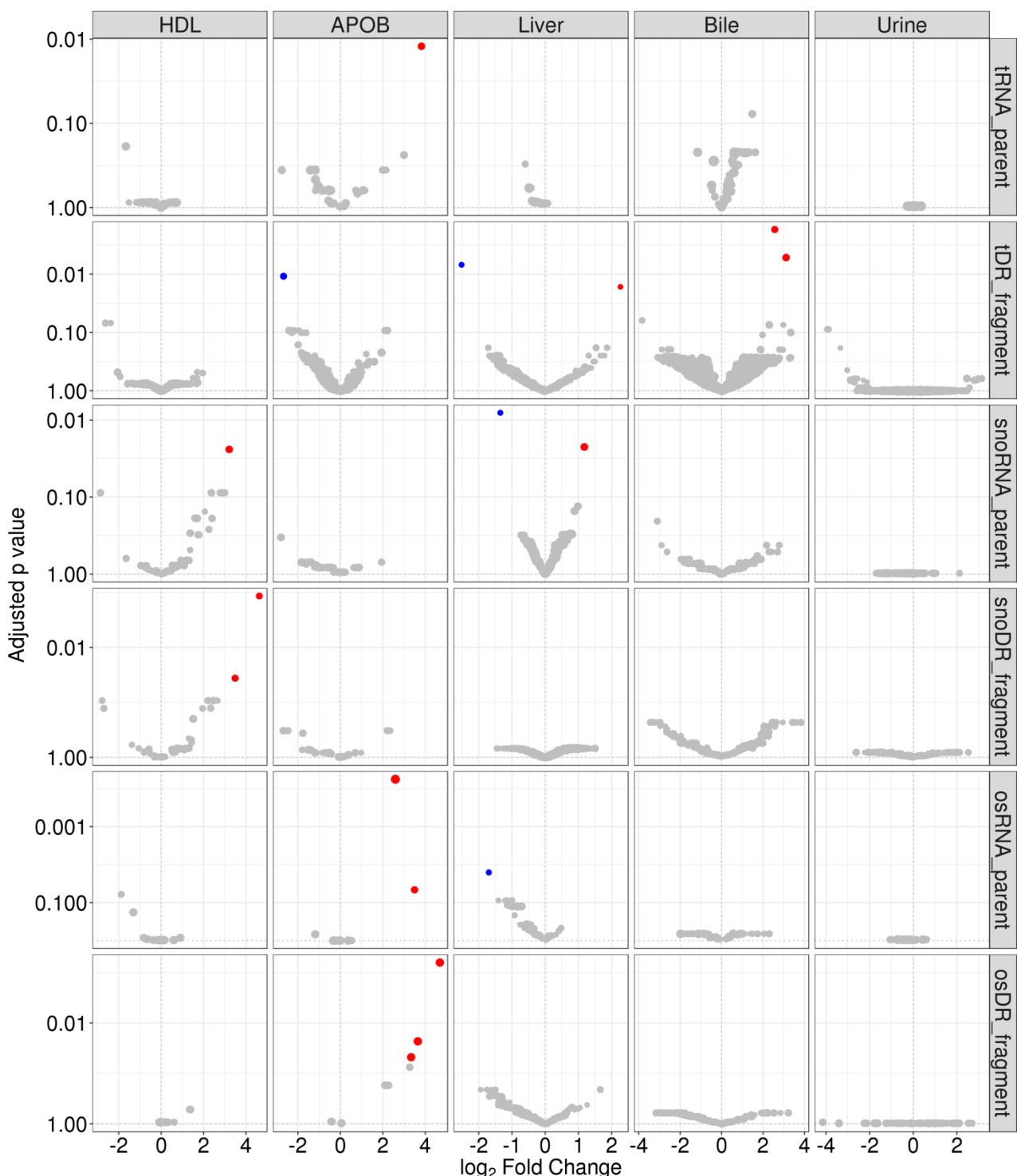


Figure 9-Figure Supplement 1. SR-BI does not regulate lipoprotein tDRs or snoDRs. Differential expression analysis by DEseq2. Volcano plots of demonstrating significant (adjusted $p > 0.05$) differential (>1.5 -absolute fold change) abundances for tDR, snoDRs, and other sRNAs (osDRs a.k.a. miscellaneous RNAs) at the parent and individual fragment levels - red, increased; blue, decreased. WT, wild-type mice; SR-BI KO, Scavenger receptor BI Knockout mice (*Scarb1^{-/-}*). HDL WT, N=7; HDL SR-BI KO N=7; APOB WT, N=7, APOB SR-BI KO N=7; Liver WT, N=7; Liver SR-BI KO, N=7; Bile WT, N=7; Bile SR-BI KO, N=6; Urine WT, N=5; Urine SR-BI KO, N=6.

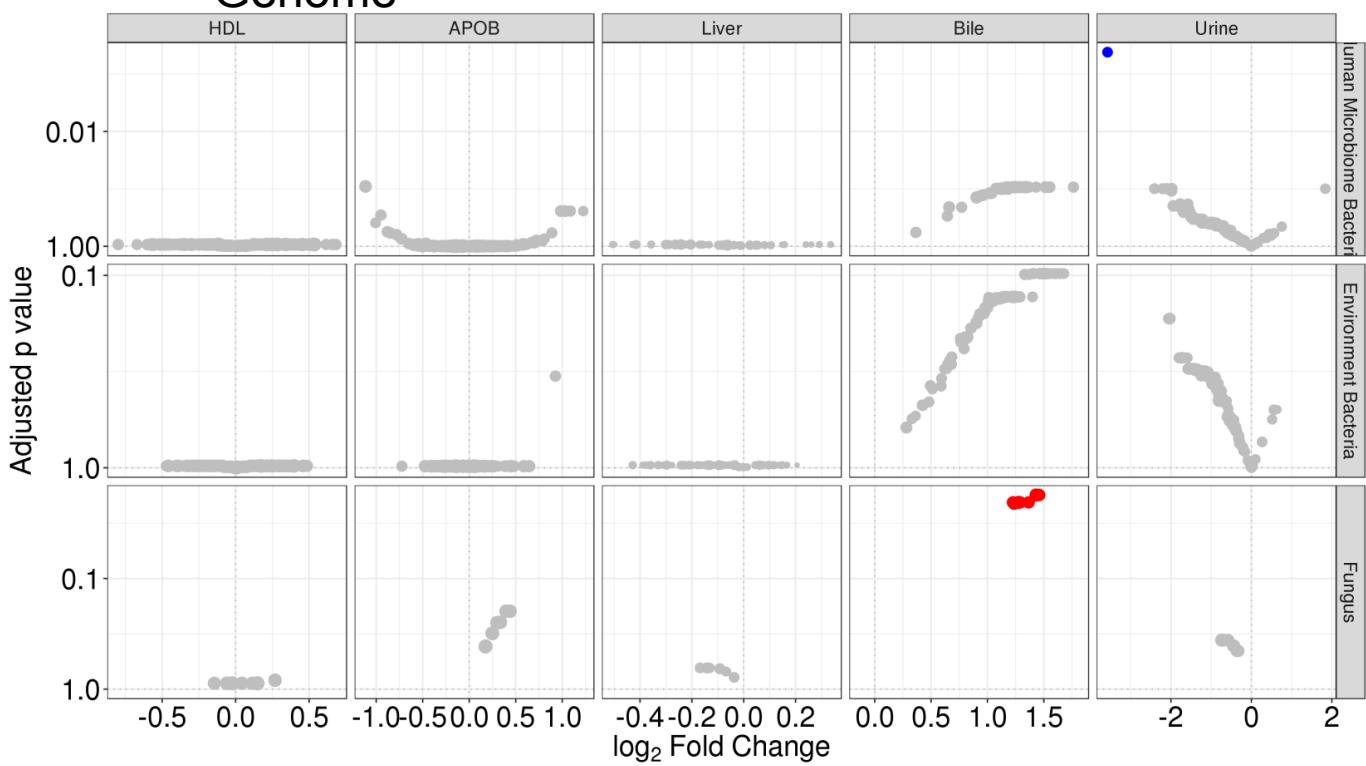
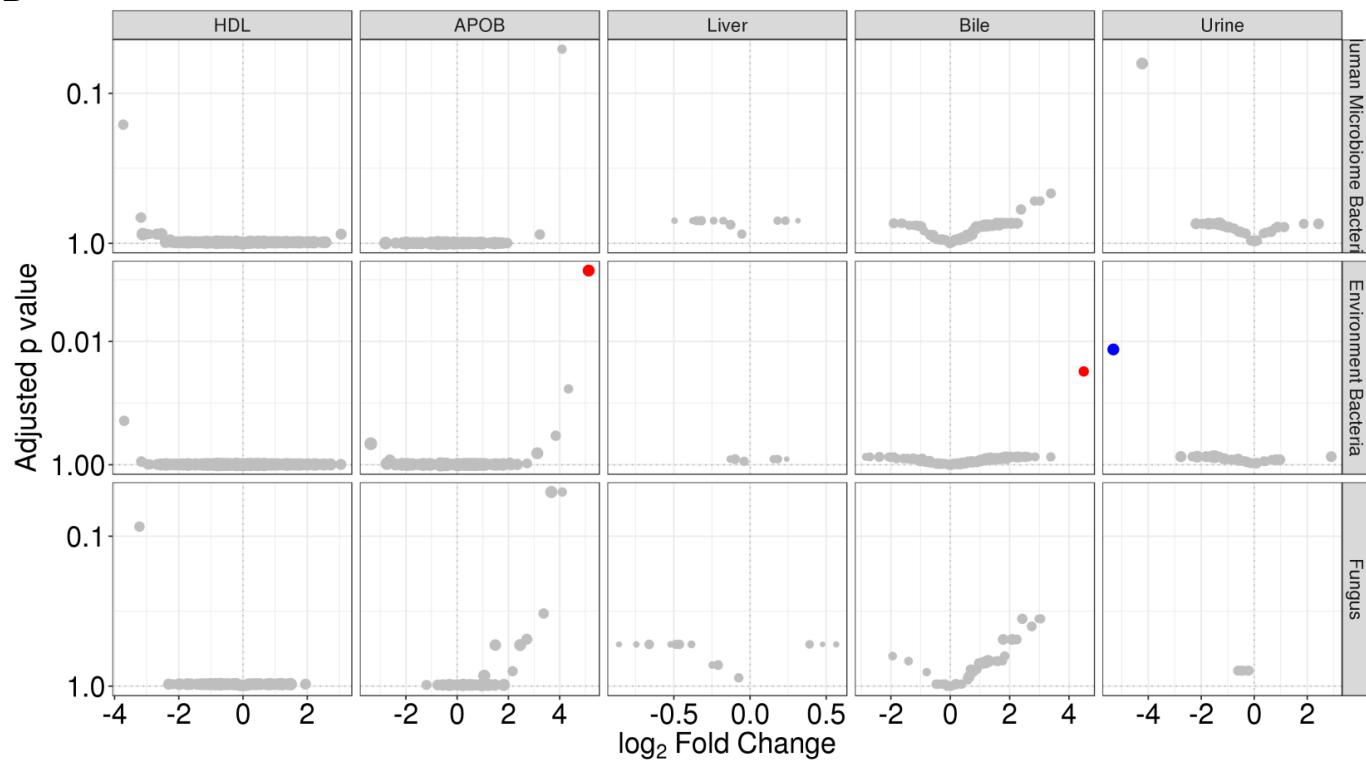
A**Genome** \log_{10} Base Mean • 1 • 2 • 3 • 4 • 5**B****Fragment** \log_{10} Base Mean • 1 • 2 • 3 • 4

Figure 9-Figure Supplement 2. SR-BI regulates fungal sRNAs in bile. Differential expression analysis by DEseq2. Volcano plots demonstrating significant (adjusted $p > 0.05$) differential (> 1.5 -absolute fold change) abundances for non-host bacterial and fungal sRNAs at the (A) genome and (B) individual fragment levels - red, increased; blue, decreased. WT, wild-type mice; SR-BI KO, Scavenger receptor BI Knockout mice (*Scarb1^{-/-}*). HDL WT, N=7; HDL SR-BI KO N=7; APOB WT, N=7; APOB SR-BI KO N=7; Liver WT, N=7; Liver SR-BI KO, N=7; Bile WT, N=7; Bile SR-BI KO, N=6; Urine WT, N=5; Urine SR-BI KO, N=6.

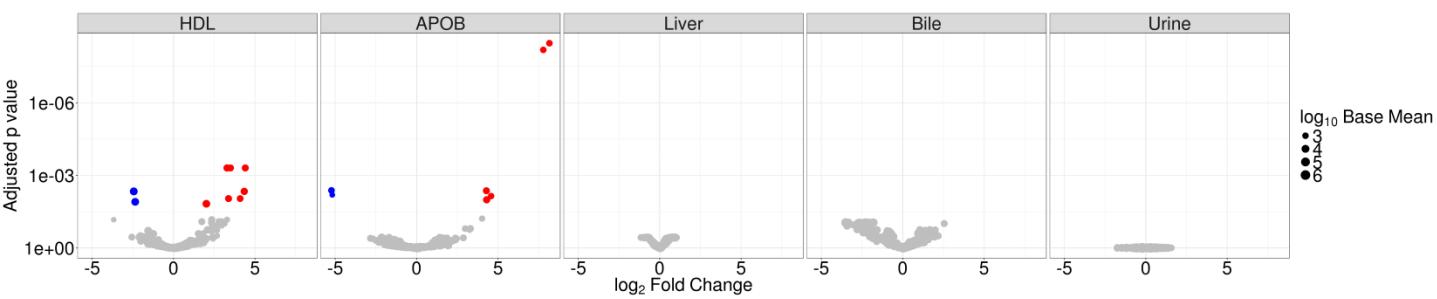


Figure 9-Figure Supplement 3. SR-BI regulates the top most abundant sRNAs on lipoproteins.

Differential expression analysis by DEseq2. Volcano plots of demonstrating significant (adjusted $p>0.05$) differential (>1.5 -absolute fold change) abundances for the top most abundant (collective top 100 non-redundant) sRNAs at the independent of class and contributing species between wild-type (WT) and Scavenger receptor BI Knockout mice (*Scarb1^{-/-}*) (SR-BI KO) mice - red, increased; blue, decreased. HDL WT, N=7; HDL SR-BI KO N=7; APOB WT, N=7, APOB SR-BI KO N=7; Liver WT, N=7; Liver SR-BI KO, N=7; Bile WT, N=7; Bile SR-BI KO, N=6; Urine WT, N=5; Urine SR-BI KO, N=6.

Figure 9-Source Data 1. DEseq2 comparison of sRNA changes at the parent level in SR-BI KO vs. WT mice

Group	Class	Gene	FoldChange	pvalue	padj	ENSEMBL
APOB	osRNA	misc_RNA:Vaultrc5	6.02	5.18E-06	5.70E-05	ENSMUSG00000065145.1
APOB	osRNA	lincRNA:Malat1	11.25	8.39E-03	4.61E-02	ENSMUSG00000092341.2
APOB	tDR	AsnGTT	14.09	3.92E-04	1.22E-02	
Bile	snDR	Gm24621	4.95	4.04E-04	2.99E-02	ENSMUSG00000064613.1
HDL	miRNA	mmu-miR-143-3p	0.20	2.60E-06	4.26E-04	
HDL	snDR	Gm25587	3.54	9.03E-04	2.92E-02	ENSMUSG00000064432.1
HDL	snDR	Gm22866	3.81	9.28E-04	2.92E-02	ENSMUSG00000065881.1
HDL	snoDR	Snord22	9.23	3.53E-04	2.40E-02	ENSMUSG00000065087.1
Liver	osRNA	lincRNA:Gm26904	0.31	3.04E-04	1.61E-02	ENSMUSG00000097560.1
Liver	snDR	Gm23686	0.43	4.33E-04	2.38E-02	ENSMUSG00000096391.1
Liver	snoDR	Gm22270	0.39	2.71E-05	8.04E-03	ENSMUSG00000077222.1
Liver	snoDR	Snord64	2.26	1.50E-04	2.23E-02	ENSMUSG00000077191.1
Urine	rDR	n-R5s2	0.19	8.88E-04	3.28E-02	ENSMUSG00000075918.1

Figure 9-Source Data 2. DEseq2 comparison of sRNA changes at the fragment level in SR-BI KO vs. WT mice

Group	Class	Sequence	Length	FoldChange	pvalue	padj
HDL	miRNA	TGAGATGAAGCACTGTAGCTC	21	0.19	1.03E-06	4.71E-04
HDL	miRNA	AAAGCTGGTTGAGAGGGC	19	0.05	1.38E-06	4.71E-04
HDL	miRNA	TAAGTCACTAGTGGTCCCGTT	21	0.06	4.21E-06	9.62E-04
HDL	miRNA	TGAGATGAAGACTGTAGCTC	21	0.09	1.46E-05	2.51E-03
HDL	miRNA	TGAGATGAAGCACTGTAGCTA	22	0.12	1.90E-05	2.61E-03
HDL	miRNA	AGAGATGAAGCACTGTAGCTC	21	0.16	4.84E-05	5.53E-03
HDL	miRNA	TTGGTCCCCTCAACCCAGCT	20	0.13	7.73E-05	6.21E-03
HDL	miRNA	TCAGATGAAGCACTGTAGCTC	21	0.15	8.39E-05	6.21E-03
HDL	miRNA	TTCACAGTGGCTAACATTCTGC	21	0.12	8.94E-05	6.21E-03
HDL	miRNA	TGAGGTAAGATTGTATA	19	0.08	9.06E-05	6.21E-03
HDL	miRNA	TGAGGTAAGTAGTTTGCT	19	0.08	1.19E-04	7.43E-03
HDL	miRNA	TGACATGAAGCACTGTAGCTC	21	0.19	1.85E-04	1.06E-02
HDL	miRNA	TGAGATGAAGCACTGTGGCTC	21	0.18	3.09E-04	1.63E-02
HDL	miRNA	GAGATGAAGCACTGTAGCTC	20	0.09	3.34E-04	1.63E-02
HDL	miRNA	TAGCTTATCAGACTGTATGTT	20	0.14	4.05E-04	1.85E-02
HDL	miRNA	TGAGATGAAGCACTGTAGC	19	0.16	4.67E-04	1.97E-02
HDL	miRNA	TCACAGTGGCTAACATT	17	0.10	4.89E-04	1.97E-02
HDL	miRNA	TGAGATGAAGCACCGTAGCTC	21	0.18	7.76E-04	2.95E-02
HDL	miRNA	TTGTCGTTGGCTCGCGTG	21	0.11	9.42E-04	3.40E-02
HDL	miRNA	TGAGATGAAGAACTGTAGCTC	21	0.21	1.10E-03	3.77E-02
HDL	miRNA	TGAGATGAAGCACTGTATCTC	21	0.23	1.32E-03	4.31E-02
HDL	miRNA	GCACTGAGATGGGAGTGGTG	20	8.24	1.38E-03	4.31E-02
APOB	miRNA	AGAGGTAAGTAGGTTGCATA	19	9.93	2.06E-05	8.02E-03
APOB	miRNA	ATCACATTGCCAGGGATTACCA	22	9.41	1.01E-04	1.97E-02
Bile	miRNA	ATCACATTGCCAGGGATTACCA	22	0.08	1.49E-04	3.32E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACCGCGTTCCGCGCTCTCCCTG	59	7.22	2.08E-06	3.56E-04
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	6.26	8.01E-06	6.84E-04
HDL	snDR	GCGGGAAACTCGCGCTAACATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	5.70	1.70E-05	7.92E-04
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGCAGGGGACTCGCGTTCCGCGCTCTCCCTG	59	5.21	1.85E-05	7.92E-04
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	6.75	9.59E-05	3.28E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	4.21	2.12E-04	5.12E-03
HDL	snDR	ACGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	4.51	2.38E-04	5.12E-03
HDL	snDR	GCGGGAAACTCGACTGCACAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	5.64	2.43E-04	5.12E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	4.29	2.69E-04	5.12E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGATAAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	4.92	3.03E-04	5.19E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTGCGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	4.14	3.83E-04	5.58E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	5.84	3.92E-04	5.58E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	4.31	6.02E-04	7.74E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	3.84	6.33E-04	7.74E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	3.61	7.57E-04	8.31E-03
HDL	snDR	GCGGGAAACTCGACCGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	5.15	7.93E-04	8.31E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	4.20	8.26E-04	8.31E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	4.37	9.41E-04	8.66E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	3.92	9.62E-04	8.66E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGCGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	3.55	1.15E-03	9.82E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGCGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	4.19	1.60E-03	1.12E-02
HDL	snDR	GCGGGAAACTCAACTGCATAATTGTGCGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	3.76	1.61E-03	1.12E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGCGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	3.94	1.64E-03	1.12E-02
HDL	snDR	GCGGGAAACTCCGACTGCATAATTGTGCGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	3.58	1.66E-03	1.12E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGCGTAGTGGGACTCGCGTTCCGCGACTCCCTG	59	4.00	1.66E-03	1.12E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGCGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	3.88	1.71E-03	1.12E-02
HDL	snDR	GGGAAACTCGACTGCATAATTGTGCGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	57	3.12	1.80E-03	1.13E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGCGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	3.29	1.85E-03	1.13E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGCGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	3.17	1.94E-03	1.15E-02
HDL	snDR	ATAATTGTGGTAGTGGGG	19	6.58	2.23E-03	1.26E-02
HDL	snDR	GCTGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	4.01	2.29E-03	1.26E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	3.67	2.72E-03	1.45E-02
HDL	snDR	GNNGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	4.14	3.23E-03	1.67E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	3.53	5.80E-03	2.88E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	3.12	6.18E-03	2.88E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	3.48	6.21E-03	2.88E-02
HDL	snDR	GTGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	2.87	6.28E-03	2.88E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTATCCCTG	59	2.71	6.46E-03	2.88E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	4.34	6.57E-03	2.88E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCCCCCTG	59	2.96	6.75E-03	2.89E-02
HDL	snDR	GCAGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	4.32	7.32E-03	3.04E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	3.42	7.47E-03	3.04E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	2.98	8.85E-03	3.42E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	3.27	8.90E-03	3.42E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	2.78	9.00E-03	3.42E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	4.07	9.41E-03	3.50E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	2.65	1.01E-02	3.66E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	2.87	1.04E-02	3.70E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCCCCAG	59	2.63	1.19E-02	4.07E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTC	59	2.74	1.20E-02	4.07E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCT	58	5.57	1.21E-02	4.07E-02
HDL	snDR	GCGGGAAACTCGCTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	2.88	1.37E-02	4.49E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGTGGGACTCGCGTTCCGCGCTCTCCCTG	59	2.60	1.45E-02	4.61E-02

HDL	snDR	GGGAAACTCGACTGCATAATTGTGGTAGTGGGGACTCGCTAGCGCTCTCCCTG	57	2.36	1.46E-02	4.61E-02
HDL	snDR	GCGGGAGACTCGACTGCATAATTGTGGTAGTGGGGACTCGCTAGCGCTCTCCCTG	59	2.61	1.54E-02	4.79E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGAGGGGGACTCGCTAGCGCTCTCCCTG	59	2.58	1.60E-02	4.85E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTGTGGTAGGGGGACTCGCTAGCGCTCTCCCATG	59	2.72	1.62E-02	4.85E-02
APOB	snDR	AGTCGGCATTGGCAATTGGACAGTCTACGGAGACTG	40	28.09	2.59E-03	2.85E-02
Liver	snDR	AGTGGGGACTCGCTCGCGCTCTCCCTG	30	0.11	1.38E-05	4.16E-03
Liver	snDR	TTTTGAGGCCCTGTCTTGACAAGGCT	27	0.13	6.82E-05	1.03E-02
Liver	snDR	AATTTTGAGGCCCTGTCTTGACAAGGCT	30	0.17	2.48E-04	2.00E-02
Liver	snDR	AATTTTGAGGCCCTGTCTCGCAGGGCT	30	0.17	3.01E-04	2.00E-02
Liver	snDR	CAATTTTGAGGCCCTGTCTCGCAGGGCT	31	0.16	3.72E-04	2.00E-02
Liver	snDR	CAATTTTGAGGCCCTGTCTCGCAGGGCT	31	0.19	4.34E-04	2.00E-02
Liver	snDR	TTTTGAGGTCTCGCTGTGCAGGGCT	27	0.18	4.64E-04	2.00E-02
Liver	snDR	GTGGTAGTGGGGACTCGCTCGCGCTCTCCCTG	35	0.21	7.07E-04	2.67E-02
Liver	snDR	TTGTGGTAGTGGGGACTCGCTCGCGCTCTCCCTA	37	0.22	1.08E-03	3.61E-02
Liver	snDR	GTAGTGGGGACTCGCTCGCGCTCTCCCTG	32	0.23	1.39E-03	3.82E-02
Liver	snDR	AATTTTGAGGCCCTGTCTCGCAGGGCT	30	0.22	1.39E-03	3.82E-02
Liver	snDR	TTAAACCAATTGGAGGCCCTGTCTCGGCAAGGCT	37	0.23	1.77E-03	4.45E-02
Liver	snDR	ACCCGCCACTTGGGGACTCGCTGGGTGACGCGATCTGCCCG	43	0.23	2.21E-03	4.84E-02
Liver	snDR	TTTTGAGGCCCTGTCTCGCAAGGCT	27	0.17	2.24E-03	4.84E-02
Urine	snDR	ATGCGGGAAACTCGACTGCATAATTGTGGTAGTGGGGACTCGCTCGCGCTCTCCCTG	61	0.03	1.20E-03	2.17E-02
HDL	rDR	TCCCCGCGGGGCCCGTCGTCCCCCGCGTCGTCCCCCGCGTCGTCCCCCGTCCT	55	12.97	1.15E-04	1.80E-02
HDL	rDR	TCCCCGCGGGGCCCGTCGTCCCCCGCGTCGTCCCCCGCGTCGTCCCCCGTCCT	56	15.82	5.52E-04	4.34E-02
HDL	rDR	CTCGCTCGATCTATTGAAAGTCAGGCCCTCGACACAAGGGTTGT	45	4.15	1.11E-03	4.67E-02
HDL	rDR	TCCCCGCGGGGCCCGTCGTCCCCCGCGTCGTCCCCCGCGTCCTTCCCCCTCC	54	8.80	1.83E-03	4.67E-02
HDL	rDR	CCCCCGCGGGGCCCGTCGTCCCCCGCGTCGTCCCCCGCGTCGTCCCCCTCC	53	13.05	1.86E-03	4.67E-02
HDL	rDR	GGGTGGTGGGGCTGGGGCGGAAGGGGGCTGGGGCGCGCCGCGGCT	49	10.28	1.94E-03	4.67E-02
HDL	rDR	GCGGGGAGGTGGAGCACGAGCGTACCGTTAGGACCGAAAGA	44	16.14	2.29E-03	4.67E-02
HDL	rDR	CCCCCGCGGGGCCCGTCGTCCCCCGCGTCGTGCCACCTCTTCCCC	47	5.48	2.38E-03	4.67E-02
APOB	rDR	GACTCTAGCGGTGGATCACTCGGCTCGCG	32	0.02	1.79E-05	3.47E-03
APOB	rDR	CCCGGGGGCCCGTCGTCCCCCGCGTCGTCCCCACCTCT	39	47.91	2.96E-05	3.47E-03
APOB	rDR	TTCCCCGGCGGGGCCCGTCGTCCCCCGCGTCGTGCCACCTCTTCCC	48	0.01	4.28E-05	3.47E-03
APOB	rDR	CCCGGGGGCCCGTCGTCCCCCGCGTCGTGCCACCTCTTCCCC	49	30.23	7.00E-04	4.25E-02
Liver	rDR	CGCGTCGCGGGCTGGAAATGTGGCGTACCGAAG	35	0.15	4.21E-06	9.74E-03
Liver	rDR	CGCGTCGCGGGCTGGAAATGTGGCGTACCGAAGACC	37	0.17	5.08E-06	9.74E-03
Liver	rDR	CGCGTCGCGGGCTGGAAATGTGGCGTACCGAAGAC	36	0.19	2.92E-05	2.20E-02
Liver	rDR	GTCCCCCGCGTCGTGCCACCTCTTCCCCCTCTTC	39	0.18	3.13E-05	2.20E-02
Liver	rDR	CGCGTCGCGGGCTGGAAATGTGGCGTACCGAAGACCCACTCCCCGGCGCC	51	0.20	3.71E-05	2.20E-02
Liver	rDR	GCGCGTCGCGGGCTGGAAATGTGGCGTACCGAAGACCC	38	0.19	3.80E-05	2.20E-02
Liver	rDR	AGTCTGGCACGGTGAAGAGACATGAGGGTAGAATAAGTGGGAGGCC	50	0.19	4.01E-05	2.20E-02
Liver	rDR	CGCGTCGCGGGCTGGAAATGTGGCGTACCGAAGACCC	38	0.20	5.04E-05	2.42E-02
Liver	rDR	ACCGATTGGATGGTTAGTGGAGGCCCTCGGATCGGCCCGGGGGTC	48	0.20	7.09E-05	2.51E-02
Liver	rDR	TCTCTACTTGATAACTGTGTAATTCTAGAGCTAATACATGCCGACGGGGCGCTGACC	59	0.22	7.10E-05	2.51E-02
Liver	rDR	AGTTAAAAGCTGTAGTTGGATCTGGGAGCGGGGGCGGT	45	0.24	8.23E-05	2.51E-02
Liver	rDR	GGGGGCCGGCGGCCGGCGACTCTGGACCGCGAGCC	36	0.22	8.46E-05	2.51E-02
Liver	rDR	ACATGAGAGGTGAGAATAAGTGGAGGCC	32	0.21	8.51E-05	2.51E-02
Liver	rDR	CGGGGCCGGCGGGTCAACCCCGCGGGGGTCCGGAGCGGGAGGAACCA	48	0.23	1.51E-04	4.12E-02
Liver	rDR	ACGTAGCAGAGCAGCTCCCTCGCTCGGATCTATTGAAAGTCAGCCCTCGACACAAGGGTTGT	63	0.23	1.78E-04	4.54E-02
Liver	rDR	AAGGGCTGGGTGGCTGGGCTGGGCGGAAGCGGGG	39	0.22	2.07E-04	4.95E-02
Urine	rDR	GACTCTAGTGGCACGGTGAAGAGACATGAGGGTAGAATAAGTGGGAGGCC	56	0.02	2.49E-05	4.59E-02
Urine	rDR	GCGCCGGGGAGGGTGGAGCACGAGCGTACCGCTTAGGACCGGAAAGAT	47	0.02	3.32E-05	4.59E-02
APOB	tDR	TCTCTGGTGGCTAGTGGTAGGATTGGCGCT	33	0.16	2.90E-05	1.09E-02
Liver	tDR	GCCTGTCACGGGGAGACGGGGGTTGATTCGGGCGACGGGGGAGCC	45	0.17	3.91E-06	6.92E-03
Liver	tDR	GCATTGGTAGTTCAATGGTAGAATTCTGGCTCCACGGGGTGACCCGGGTT	53	4.80	1.87E-05	1.66E-02
Bile	tDR	GTTCCTGAGTGTAGTGGTATCACGCTCGCCT	33	5.92	5.00E-07	1.72E-03
Bile	tDR	GACCTCGGGCGCAATGGTAGGCGCTTCTGACT	32	8.64	3.02E-06	5.22E-03
HDL	snoDR	GCCCCATGATGGTAGAGAGTAGTGGAGACAGAAGGGGATTCTGAAAAACACTTTCTGAGG	59	24.64	2.64E-05	1.16E-03
HDL	snoDR	AGTAATGATGATTCTGGTAGGTTGCTCGCTGACGCCATACCGCAGCGCGCTGACC	63	11.19	1.65E-03	3.64E-02
APOB	miscRNA	TCGAGACCCGGGGCGCTCCCTGGCCCTT	30	25.70	7.05E-05	6.35E-04
APOB	miscRNA	TCGAGACCCGGGGCGCTCCCTGGCCCTT	31	12.52	5.15E-03	2.32E-02
APOB	miscRNA	TTACCTAACCGTGAGTTGGTCAGAGACCCGGGGCGCTCCCTGGCCCTT	53	10.07	1.59E-02	4.78E-02

Figure 9-Source Data 3. Significantly altered exogenous genome counts in SR-BI KO mice compared to WT mice.

	Genome	Group	FoldChange	pvalue	padj
HMB	Streptomyces sp.	Urine	0.08	3.24E-06	4.17E-04
Fungi	Aspergilus niger	Bile	2.75	5.23E-03	1.76E-02
Fungi	Candida albicans	Bile	2.73	5.58E-03	1.76E-02
Fungi	Fusarium oxysporum	Bile	2.70	6.60E-03	1.76E-02
Fungi	Candida glabrata	Bile	2.58	1.03E-02	2.05E-02
Fungi	Histoplasma capsulatum	Bile	2.42	1.44E-02	2.05E-02
Fungi	Saccharomyces cerevisiae	Bile	2.44	1.73E-02	2.05E-02
Fungi	Penicillium chrysogenum	Bile	2.34	1.79E-02	2.05E-02
Fungi	Cryptococcus neoformans	Bile	2.36	2.10E-02	2.10E-02

Figure 9-Source Data 4. DEseq2 comparison of non-host bacterial sRNA changes in SR-BI KO vs. WT mice

Collection	Group	Sequence	Length	FoldChange	pvalue	padj
ENV	APOB	TCGACGACATCAGCTGCCATAAGTTCCCACAC	34	35.06	6.02E-06	7.11E-04
ENV	Bile	TTCAGCGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGG	58	22.55	1.44E-04	3.07E-02
ENV	Urine	GATAGTCGGATTCCCGTGTGAAAGTAGGTCATCGTCAGGCT	42	0.03	3.55E-04	1.35E-02

Figure 9-Source Data 5. DESeq2 comparison of sRNA changes at the class-ind level (Top 100) in SR-BI KO vs. WT mice