

Table S1. 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

Table S2. 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

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	UND	0.38	0.46	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	UND	1.99	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	UND	0.39	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	UND	0.56	UND	UND	UND	UND	UND	UND
ahy-miR156b-5p	UND	UND	UND	0.69	UND	UND	UND	UND	UND	UND
hsa-miR-4661-5p	UND	UND	UND	0.69	UND	UND	UND	UND	UND	UND
gso-miR3522a	UND	UND	UND	0.45	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	UND	0.61	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	UND	0.18	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	UND	0.11	UND	UND	UND	UND	UND	UND
bta-miR-374a	UND	UND	UND	UND	UND	UND	UND	0.25	UND	UND
hsa-miR-6803-3p	UND	UND	0.09	0.08	UND	UND	UND	UND	UND	UND
aly-miR172c-3p	UND	UND	UND	0.11	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	UND	0.12	UND	UND
asu-miR-44a-3p	UND	UND	UND	UND	UND	UND	UND	0.12	UND	UND
cin-let-7b-5p	UND	UND	0.09	UND	UND	UND	UND	UND	UND	UND
aae-miR-71-5p	UND	0.07	UND	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	UND	0.13	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	UND	0.07	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
cfa-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	UND	0.07	UND	UND	UND	UND	UND	UND	UND	UND
oha-miR-221-5p	UND	UND	UND	UND	UND	UND	UND	0.09	UND	UND
pma-miR-30d	UND	UND	UND	UND	UND	UND	UND	UND	0.06	UND
vvi-miR156e	0.12	UND	UND	UND	UND	UND	UND	UND	UND	UND
xtr-miR-106	UND	UND	UND	UND	UND	UND	UND	0.07	UND	UND
xtr-miR-215	UND	UND	UND	UND	UND	UND	UND	0.07	UND	UND

Table S4. Non-host tDRs (RPM)

Name	APOB		Bile		HDL		Liver		Urine	
	SRBIKO	WT	SRBIKO	WT	SRBIKO	WT	SRBIKO	WT	SRBIKO	WT
<i>Azotobacter_chroococcum_NCIMB_8003_tRNA-fMet-CAT-1-1</i>	406.59	1883.53	3.81	1.65	470.97	896.65	0.24	0.28	1.91	2.36
<i>Bacillus_anthraxis_2000031021_tRNA-fMet-CAT-1-1</i>	342.82	1600.84	2.81	1.02	371.22	746.21	0.14	0.21	1.66	2.52
<i>Marinomonas_mediterranea_MMB-1_tRNA-fMet-CAT-1-1</i>	372.40	667.50	2.78	0.95	508.11	757.97	0.22	0.18	0.52	1.38
<i>Azotobacter_chroococcum_NCIMB_8003_tRNA-Asp-GTC-1-1</i>	289.05	259.24	16.91	10.29	755.71	486.88	0.69	0.48	10.09	130.03
<i>Azotobacter_chroococcum_NCIMB_8003_tRNA-Glu-TTC-1-1</i>	199.88	527.80	1.86	1.51	425.53	562.52	0.34	0.22	4.92	103.80
<i>Alteromonas_australis_DE170_tRNA-fMet-CAT-1-1</i>	183.01	394.68	2.15	1.18	281.00	429.81	0.11	0.17	0.33	0.40
<i>Azotobacter_chroococcum_NCIMB_8003_tRNA-Ile-GAT-1-1</i>	123.26	37.56	5.05	1.28	411.82	554.90	0.16	0.17	0.85	3.70
<i>Escherichia_coli_ETEC_H10407_tRNA-fMet-CAT-1-1</i>	135.34	596.56	1.06	0.28	143.47	278.48	0.08	0.09	0.61	0.91
<i>Candidatus_Hamiltonella_defensa_5AT_Acyrtosiphon_pisum_1</i>	152.19	326.84	1.41	0.43	238.12	355.25	0.09	0.10	0.14	0.29
<i>Propionibacterium_acidipropionici_ATCC_4875_tRNA-Asn-GTT-</i>	259.00	181.66	12.41	6.24	267.05	339.82	0.55	0.21	34.81	115.59
<i>Pseudomonas_alkylphenolia_KL28_tRNA-Leu-CAA-1-1</i>	69.34	93.13	1.15	0.10	530.75	337.68	0.23	0.13	0.21	0.07
<i>Pseudomonas_alkylphenolia_KL28_tRNA-Tyr-GTA-1-1</i>	157.71	205.15	3.94	1.49	403.56	222.46	0.22	0.12	13.56	1.15
<i>Pseudomonas_brassicacearum_DF41_tRNA-Asn-GTT-1-1</i>	15.93	49.97	0.26	0.22	242.56	441.83	0.19	0.17	0.63	0.14
<i>Dyella_japonica_A8_tRNA-Asn-GTT-1-1</i>	109.52	436.12	0.83	0.89	165.33	243.29	0.24	0.19	27.37	21.66
<i>Hahella_chejuensis_KCTC_2396_tRNA-fMet-CAT-1-1</i>	82.18	391.77	1.18	0.31	91.82	179.39	0.03	0.05	0.40	0.59
<i>Macropus_eugenii_GL115445.trna6-GluTTC</i>	24.81	36.50	65.61	59.95	14.42	3.02	1.19	0.84	109.03	266.09
<i>Dasyus_novemcinctus_AAGV03074463.trna2-GluCTC</i>	5.75	33.95	79.77	93.69	40.01	8.82	1.64	5.77	80.70	76.79
<i>gamma_proteobacterium_HdN1_tRNA-Val-TAC-1-1</i>	14.02	27.68	6.25	0.15	431.46	230.91	0.32	0.13	0.07	0.04
<i>Bacteroides_dorei_tRNA-Glu-TTC-1-1</i>	153.69	309.08	40.20	5.31	81.87	123.04	0.26	0.14	5.72	1.93
<i>Pseudomonas_cichorii_JBC1_tRNA-Ser-CGA-1-1</i>	136.35	87.36	2.42	0.89	194.80	158.98	0.15	0.19	0.11	0.07
<i>Pseudomonas_fluorescens_A506_tRNA-Ala-GGC-1-1</i>	42.13	34.35	6.23	2.39	204.33	193.41	0.13	0.35	2.95	3.18
<i>Pseudomonas_alkylphenolia_KL28_tRNA-Pro-TGG-1-1</i>	55.02	14.76	1.86	0.34	252.17	181.89	0.06	0.11	0.08	1.41
<i>Lactobacillus_brevis_ATCC_367_tRNA-fMet-CAT-1-1</i>	70.38	152.01	0.13	0.18	105.29	165.25	0.04	0.04	0.06	0.11
<i>Acinetobacter_baumannii_1656-2_tRNA-Val-TAC-1-1</i>	160.05	99.78	23.10	4.69	160.03	158.83	0.36	0.41	13.31	3.75
<i>Acidovorax_avenae_subsp_avenae_ATCC_19860_tRNA-Ala-TC</i>	145.64	162.84	27.09	11.46	66.40	115.29	0.15	0.22	5.74	25.54
<i>Acinetobacter_baumannii_1656-2_tRNA-Glu-TTC-1-1</i>	119.24	125.54	22.14	2.25	125.24	240.95	0.35	0.21	2.74	43.12
<i>Pseudomonas_brassicacearum_DF41_tRNA-Arg-ACG-1-1</i>	95.13	51.10	1.18	1.24	134.26	350.77	0.13	0.17	6.53	3.83
<i>Rhodocyclaceae_bacterium_PG1-Ca6_tRNA-Met-CAT-3-1</i>	182.94	190.75	1.89	0.45	67.33	78.56	0.23	0.17	8.39	1.72
<i>Lachnoclostridium_phytofermentans_ISDg_tRNA-Asn-GTT-1-1</i>	UND	0.10	0.46	1.88	0.11	UND	0.14	0.92	80.97	6.73
<i>Acinetobacter_baumannii_1656-2_tRNA-Arg-ACG-1-1</i>	173.84	73.25	11.69	4.50	157.20	92.22	0.24	0.31	8.53	63.57

<i>Micrococcus_luteus_NCTC_2665_tRNA-Lys-CTT-1-1</i>	114.27	268.40	5.11	3.29	48.08	99.15	0.12	0.13	3.33	4.40
<i>Pseudomonas_brassicacearum_DF41_tRNA-Ala-TGC-2-1</i>	27.34	35.41	1.95	3.34	112.24	114.62	0.14	0.08	0.23	222.81
<i>Stenotrophomonas_maltophilia_13637_tRNA-Thr-GGT-1-1</i>	82.39	7.79	0.22	0.39	155.81	175.85	0.11	UND	0.02	0.14
<i>Geobacter_bemidjiensis_Bem_tRNA-fMet-CAT-1-1</i>	42.39	189.99	0.46	0.17	44.72	88.70	0.02	0.02	0.23	0.30
<i>Geobacter_daltonii_FRC-32_tRNA-fMet-CAT-1-1</i>	40.58	190.11	0.33	0.08	43.61	88.40	0.05	0.03	0.19	0.29
<i>Acidovorax_avenae_subsp_avenae_ATCC_19860_tRNA-Asp-G</i>	25.65	72.40	9.44	1.86	70.33	63.00	0.12	0.08	4.06	338.92
<i>Trichechus_manatus_latirostris_JH594675.trna156-ArgTCT</i>	6.65	32.29	68.29	45.93	0.16	0.57	4.51	10.14	82.88	49.63
<i>Agrobacterium_fabrum_str_C58_tRNA-Asp-GTC-1-1</i>	127.87	186.24	0.72	0.94	43.70	32.52	0.20	0.09	1.09	0.94
<i>Pseudomonas_fluorescens_A506_tRNA-His-GTG-1-1</i>	55.91	31.70	0.41	0.31	166.40	104.79	0.13	0.08	0.14	0.07
<i>Pseudomonas_alkylphenolia_KL28_tRNA-Gly-TCC-1-1</i>	29.84	68.01	0.51	0.23	85.47	157.78	0.09	0.12	0.66	1.66
<i>Arabidopsis_thaliana_TAIR10_Feb_2011_tRNA-Glu-TTC-4-1</i>	242.46	141.97	1.13	3.29	34.37	74.63	0.24	0.26	1.91	15.21
<i>Tursiops_truncatus_JH472793.trna26-GluTTC</i>	1.91	11.04	51.15	60.24	2.87	2.11	0.31	0.94	35.92	41.22
<i>Aeromonas_hydrophila_4AK4_tRNA-Phe-GAA-1-1</i>	19.38	9.22	1.71	1.41	54.18	189.26	0.04	0.08	1.31	UND
<i>Pseudomonas_fluorescens_A506_tRNA-Leu-CAG-1-1</i>	11.24	2.31	3.20	0.25	91.28	144.68	0.08	0.04	6.83	0.76
<i>Acinetobacter_baumannii_1656-2_tRNA-Asp-GTC-1-1</i>	48.80	146.11	1.93	1.46	54.43	42.94	0.10	0.24	0.94	4.97
<i>Alcanivorax_borkumensis_SK2_tRNA-Val-TAC-1-1</i>	117.11	296.54	4.07	0.15	88.98	31.72	0.08	0.18	UND	0.05
<i>Acinetobacter_baumannii_1656-2_tRNA-Leu-CAA-1-1</i>	89.96	70.53	8.47	5.13	95.97	62.39	0.17	0.13	1.58	10.64
<i>Dyella_japonica_A8_tRNA-Glu-TTC-1-1</i>	107.87	68.10	0.58	0.26	42.22	66.77	0.12	0.06	3.93	109.03
<i>Pseudomonas_alkylphenolia_KL28_tRNA-Thr-GGT-1-1</i>	2.48	20.33	0.04	0.23	121.43	116.05	0.08	UND	0.74	0.08
<i>Aeromonas_hydrophila_4AK4_tRNA-Tyr-GTA-1-1</i>	31.53	39.06	2.25	0.09	106.16	87.54	0.08	UND	2.43	0.03
<i>Bacillus_cellulosilyticus_DSM_2522_tRNA-fMet-CAT-1-1</i>	28.98	135.57	0.24	0.07	31.39	63.14	0.01	0.02	0.14	0.21
<i>Alcanivorax_pacificus_W11-5_tRNA-Ala-TGC-1-1</i>	8.92	125.55	1.19	2.28	38.07	251.98	0.06	0.08	0.23	0.02
<i>Dyella_japonica_A8_tRNA-Tyr-GTA-1-1</i>	83.16	238.11	0.14	0.10	77.24	46.13	UND	UND	0.18	UND
<i>Arthrobacter_arilaitensis_Re117_tRNA-Arg-ACG-1-1</i>	118.62	59.86	5.42	0.95	85.66	84.61	0.21	0.11	4.94	8.05
<i>Mycobacterium_africanum_GM041182_tRNA-Met-CAT-2-1</i>	58.35	66.96	5.14	4.62	54.79	87.95	0.18	0.08	2.68	3.52
<i>Marinomonas_posidonica_IVIA-Po-181_tRNA-fMet-CAT-2-1</i>	31.99	69.10	0.06	0.79	47.95	75.13	0.02	0.02	0.03	0.06
<i>Acinetobacter_baumannii_1656-2_tRNA-Ala-TGC-1-1</i>	41.43	122.47	17.63	3.14	82.37	122.84	0.29	0.40	0.40	25.93
<i>Azotobacter_chroococcum_NCIMB_8003_tRNA-Gln-TTG-1-1</i>	30.59	3.88	1.37	0.68	122.77	70.02	0.14	0.20	1.75	3.39
<i>Propionibacterium_acnes_266_tRNA-Met-CAT-1-1</i>	49.27	108.00	5.93	0.87	66.82	54.93	0.22	0.16	1.56	0.07
<i>Acinetobacter_baumannii_1656-2_tRNA-Pro-TGG-1-1</i>	76.29	35.42	5.77	2.35	120.00	64.44	0.48	0.31	1.76	3.08
<i>Pseudomonas_fluorescens_A506_tRNA-Ser-TGA-1-1</i>	0.22	32.09	0.07	0.06	159.29	58.65	0.23	0.07	UND	UND
<i>Burkholderia_ambifaria_AMMD_tRNA-fMet-CAT-1-1</i>	51.46	87.79	9.41	2.72	39.29	42.60	0.12	0.12	5.69	4.10
<i>Methylophaga_frappieri_JAM7_tRNA-Asp-GTC-2-1</i>	90.28	74.98	1.55	1.58	26.90	83.97	0.15	0.05	0.72	0.37
<i>Erwinia_amylovora_ATCC_49946_tRNA-Glu-TTC-1-1</i>	36.32	149.16	5.74	1.01	40.20	65.23	0.27	0.37	6.51	34.86
<i>Pseudomonas_chlororaphis_PA23_tRNA-Cys-GCA-1-1</i>	52.02	36.94	1.53	0.55	137.90	58.71	0.06	0.19	0.25	0.07

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
Agrobacterium_radiobacter_K84_tRNA-Gly-GCC-1-1	67.59	121.09	3.65	1.63	38.70	25.10	0.12	0.19	3.53	4.39
Acinetobacter_baumannii_1656-2_tRNA-Gln-TTG-1-1	113.35	43.44	3.34	2.44	84.65	31.42	0.13	0.10	6.17	4.02
Methylobacterium_extorquens_AM1_tRNA-Glu-CTC-1-1	9.43	215.32	6.41	0.23	40.93	42.93	0.10	0.12	5.17	385.65
Acetobacter_pasteurianus_386B_tRNA-fMet-CAT-1-1	99.83	92.87	4.26	1.37	44.01	6.34	0.28	0.19	0.94	30.38
Acinetobacter_baumannii_1656-2_tRNA-Asn-GTT-2-1	71.11	55.01	17.62	3.04	79.53	29.62	0.21	0.24	9.25	11.53
Erwinia_amylovora_ATCC_49946_tRNA-fMet-CAT-2-1	26.26	25.41	2.91	1.58	84.46	57.74	0.10	0.07	0.40	1.98
Stenotrophomonas_maltophilia_13637_tRNA-Gln-CTG-1-1	251.99	45.93	0.22	0.17	17.88	21.57	UND	0.25	0.06	2.44
Pseudomonas_fluorescens_A506_tRNA-Leu-TAA-1-1	4.75	18.39	0.15	0.08	140.93	56.46	0.26	0.12	0.41	0.06
Bacteroides_thetaiotaomicron_VPI-5482_tRNA-Thr-TGT-1-1	41.39	58.99	28.38	4.59	65.49	41.11	0.42	0.19	3.64	8.54
Collimonas_arenae_Cal35_tRNA-Pro-TGG-1-1	47.85	54.20	8.37	3.12	50.94	45.30	0.08	0.18	2.65	3.25
Pseudoxanthomonas_suwonensis_11-1_tRNA-Ser-CGA-1-1	17.85	164.90	0.05	1.84	55.28	14.72	UND	0.12	0.09	0.01
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
Bradyrhizobium_diazoeficiens_USDA_110_USDA110_tRNA-Glu	24.47	22.81	0.08	0.86	108.76	142.01	0.21	UND	0.06	0.11
Aeromonas_hydrophila_4AK4_tRNA-Asp-GTC-1-1	24.19	71.59	16.87	3.07	61.00	13.79	0.12	0.14	11.53	26.22
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
Acinetobacter_baumannii_1656-2_tRNA-Thr-TGT-1-1	98.26	59.13	6.22	2.49	37.33	48.78	0.44	0.40	4.33	45.19
Acidovorax_avenae_subsp_avenae_ATCC_19860_tRNA-Ser-GC	82.94	39.79	6.37	5.70	36.13	104.11	0.14	0.08	0.67	24.14
Moraxella_catarrhalis_25239_tRNA-Leu-TAG-1-1	123.71	105.37	2.86	1.48	62.66	38.88	UND	0.08	1.00	1.52
Actinobacillus_equuli_subsp_equuli_19392_tRNA-Glu-TTC-1-1	65.50	67.50	2.41	2.81	26.16	11.17	0.02	0.13	6.71	29.86
Flavobacterium_johnsoniae_UW101_ATCC_17061_tRNA-Ser-T	65.04	154.73	9.18	3.44	36.52	33.75	0.32	UND	11.61	29.16
Janthinobacterium_agaricidamnosum_NBRC_102515_DSM_962	23.94	59.16	0.11	0.34	98.93	29.57	UND	UND	5.47	88.47
Bradyrhizobium_diazoeficiens_USDA_110_USDA110_tRNA-Glu	51.05	44.88	0.64	1.12	47.65	131.10	UND	0.07	0.03	0.58
Pseudomonas_alkylphenolia_KL28_tRNA-Trp-CCA-1-1	27.94	25.93	6.18	UND	71.11	43.78	0.09	0.16	1.24	UND
Pseudomonas_aeruginosa_19BR_tRNA-Thr-TGT-1-1	27.69	50.25	0.90	0.87	47.51	50.97	0.09	0.09	0.79	3.23
Collimonas_fungivorans_Ter331_tRNA-Gly-GCC-1-1	19.43	74.52	25.89	5.69	19.27	65.72	0.08	0.22	2.13	1.60
Buchnera_aphidicola_str_Tuc7_Acyrtosiphon_pisum_tRNA-fMe	17.94	81.36	0.20	0.06	19.88	38.80	0.01	0.01	0.08	0.10
Oleispira_antarctica_RB-8_tRNA-fMet-CAT-1-1	17.46	81.34	0.14	0.14	19.88	38.80	0.01	0.01	0.08	0.10
Bacillus_clausii_KSM-K16_tRNA-fMet-CAT-1-1	17.39	81.34	0.14	0.03	19.24	37.89	0.01	0.01	0.08	0.12
Bdellovibrio_bacteriovorus_109J_tRNA-fMet-CAT-1-1	17.40	81.37	0.16	0.03	18.72	37.89	0.01	0.01	0.08	0.13
Candidatus_Portiera_aleyrodidarum_BT-B-HRs_tRNA-Met-CAT-	17.39	81.34	0.14	0.03	18.69	37.97	0.01	0.01	0.08	0.12
Bradyrhizobium_diazoeficiens_USDA_110_USDA110_tRNA-Ala	25.40	62.38	0.36	0.51	78.09	108.15	0.15	0.02	0.07	0.19
Caenorhabditis_remanei_tRNA-Met-CAT-3-1	32.38	49.47	23.39	1.79	26.16	39.50	0.24	0.12	1.92	7.30
Pseudoxanthomonas_suwonensis_11-1_tRNA-Gly-GCC-1-1	139.33	71.15	0.31	1.41	65.44	8.73	0.28	0.12	1.33	0.07
Corynebacterium_atypicum_R2070_tRNA-Arg-ACG-1-1	104.74	83.77	14.16	3.20	37.35	41.93	0.10	UND	1.48	14.21

Table S5. Non-host rDRs (RPM)

Taxon	APOB		Bile		HDL		Liver		Urine	
	SRBIKO	WT	SRBIKO	WT	SRBIKO	WT	SRBIKO	WT	SRBIKO	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

Table S6. Mean HMB genome counts (RPM).

Tissue/Fluid Genotype	APOB		Bile		HDL		Liver		Urine	
	SRBIKO	WT	SRBIKO	WT	SRBIKO	WT	SRBIKO	WT	SRBIKO	WT
<i>Pseudomonas</i> 2 1 26 uid40037	6857.88	7230.43	501.42	122.62	15120.46	16703.68	11.35	12.62	246.22	800.27
<i>Micrococcus luteus</i> SK58 uid34071	9218.81	10506.32	821.54	180.63	10096.96	6536.87	5.85	4.09	483.87	1851.52
<i>Acinetobacter</i> ATCC 27244 uid30949	6782.46	7926.32	878.12	215.31	7823.02	6409.50	28.64	32.01	445.36	1172.43
<i>Propionibacterium</i> 409 HC1 uid64685	6756.75	8603.30	735.71	179.80	7264.35	6293.69	3.77	3.71	524.87	1865.46
<i>Acinetobacter baumannii</i>	5963.21	6577.97	713.88	176.36	7173.29	5969.11	20.72	23.07	360.68	959.91
<i>Enhydrobacter aerosaccus</i> SK60 uid31335	3919.44	4040.57	384.40	86.75	4459.11	3880.14	5.48	5.70	184.02	707.78
<i>Massilia timonae</i> CCUG 45783 uid52185	3341.42	5274.94	735.89	168.06	4213.81	3195.46	7.05	5.93	296.12	884.87
<i>Pelomonas</i> sp.	2117.13	2631.60	468.28	118.16	4347.53	2156.21	4.11	3.15	185.67	1003.14
<i>Plesiomonas shigelloides</i>	538.83	1078.63	62.42	19.75	1260.35	2062.57	1.72	1.50	33.17	76.04
<i>Moraxella catarrhalis</i>	2195.09	2233.18	241.63	53.91	2549.17	2054.93	7.20	8.02	139.96	435.16
<i>Aeromonas</i> sp.	841.10	765.62	101.73	21.51	1380.05	1933.28	1.48	1.71	39.34	48.56
<i>Psychrobacter</i> 1501 2011 uid65121	1574.10	1518.02	215.57	58.45	1779.47	1644.02	4.79	5.34	97.96	304.58
<i>Desulfovibrio</i> 3 1 syn3 uid42529	181.79	146.13	89.15	31.71	422.27	1228.60	0.90	0.82	18.69	33.21
<i>Faecalibacterium prausnitzii</i> M21 2 uid18203	581.60	2090.80	81.69	20.19	598.97	1205.08	0.37	0.72	16.38	19.14
<i>Bilophila</i> 4 1 30 uid41961	244.83	314.34	155.07	49.17	389.01	1135.94	16.70	22.51	13.37	21.08
<i>Ralstonia</i> 5 2 56FAA uid39391	778.97	648.97	149.56	43.77	1041.40	1023.25	1.77	1.41	61.83	130.77
<i>Listeria innocua</i> ATCC 33091 uid65129	653.08	2008.88	21.91	8.19	556.80	991.41	0.32	0.42	10.69	14.98
<i>Anaerostipes</i> 3 2 56FAA uid39999	472.59	1946.91	17.67	9.89	486.55	985.15	0.26	0.29	16.55	12.25
<i>Porphyromonas asaccharolytica</i> PR426713P I uid	107.89	98.99	48.77	12.42	471.03	823.65	0.58	0.42	8.07	12.10
<i>Afipia broomeae</i> ATCC 49717 uid52155	724.93	935.07	114.09	32.33	801.40	798.12	1.71	1.92	74.80	194.12
<i>Oxalobacter formigenes</i> OXCC13 uid32499	539.45	703.07	147.52	34.07	2058.70	745.03	1.55	1.48	40.40	84.08
<i>Sphingobium yanoikuyae</i> 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 uid4197	390.50	398.47	47.66	14.20	513.32	673.23	1.11	1.25	25.25	131.29
<i>Proteus mirabilis</i> ATCC 29906 uid31523	346.15	502.28	32.60	9.99	530.84	672.96	0.84	0.87	12.62	54.15
<i>Enterobacter cancerogenus</i> ATCC 35316 uid2866	398.65	505.20	64.06	16.12	556.74	661.65	1.97	2.32	43.71	104.13
<i>Sphingomonas</i> sp.	730.76	659.58	122.12	27.45	798.82	660.73	2.72	2.26	59.16	101.06
<i>Catenibacterium mitsuokai</i> DSM 15897 uid19923	422.77	1090.11	15.59	6.82	553.52	657.12	0.45	0.45	27.43	12.00
<i>Oligella urethralis</i>	875.65	1123.23	202.71	51.47	1023.37	654.82	0.97	0.60	79.01	264.72
<i>Brevundimonas diminuta</i> 470 4 uid67195	2482.32	2142.71	97.79	25.12	822.09	637.94	2.47	2.58	44.16	56.49
<i>Achromobacter piechaudii</i> ATCC 43553 uid46343	1015.63	557.09	201.70	37.84	925.84	625.33	1.51	1.28	65.46	321.57
<i>Cardiobacterium hominis</i> 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 morganii	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 ornithinolytica	310.39	325.82	45.73	13.77	450.26	508.36	1.18	1.44	26.40	76.54
Klebsiella pneumoniae rhinoscleromatis ATCC 13	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
Methylobacterium 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 47FAA 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 uid5	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 cinnamea	489.54	476.70	57.42	15.27	342.85	387.44	0.71	0.58	27.75	25.59
Microbacterium ginsengisoli	493.18	658.63	91.83	19.54	524.29	369.24	0.85	0.79	30.08	81.12
Neisseria 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	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 uid67	202.77	174.74	29.19	9.73	281.61	327.40	0.56	0.72	13.52	50.83

Coprobacillus 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	36.84	290.84	296.89	0.94	0.72	28.50	89.80
Actinobacillus ureae 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 27758 uid20525	212.87	333.72	14.57	7.30	242.29	296.43	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 hippei YIT 12066 uid48507	211.63	245.30	23.13	6.61	303.48	263.46	0.34	0.38	11.94	25.21
Dermabacter hominis	326.18	327.86	29.72	9.01	362.29	257.67	0.46	0.31	27.18	35.01
Myroides odoratimimus CIP 103059 uid52197	245.63	279.61	70.70	19.40	265.97	239.53	0.70	0.43	17.84	92.33
Arcobacter butzleri JV22 uid53195	178.61	221.68	53.17	13.41	173.04	235.08	0.37	0.23	5.56	76.14
Bacillus 2 A 57 CT2 uid40003	264.21	228.02	28.25	11.76	226.87	216.78	0.31	0.29	15.97	24.76
Holdemania filiformis DSM 12042 uid30361	45.48	58.73	11.09	4.01	156.79	211.67	0.19	0.13	3.21	48.20
Anaerobaculum hydrogeniformans ATCC BAA 18	88.88	83.80	257.99	96.45	146.73	209.65	59.93	54.24	45.95	49.80
Aeromicrobium marinum DSM 15272 uid34545	223.49	304.39	36.11	11.06	275.35	209.38	0.69	0.45	28.68	39.51
Enterococcus faecalis ATCC 29200 uid31459	261.74	235.08	24.80	9.61	164.61	207.46	0.34	0.40	13.21	11.86
Subdoligranulum variabile DSM 15176 uid18181	141.03	155.59	40.47	10.96	190.85	201.79	0.35	0.37	22.97	61.70
Olsenella oral taxon 809 F0356 uid39743	36.45	26.37	14.22	4.36	131.23	189.73	0.17	0.15	3.66	5.39
Hafnia alvei ATCC 51873 uid65123	126.69	135.12	13.93	4.83	177.61	186.90	0.33	0.43	7.40	17.30
Propionimicrobium lymphophilum	197.66	150.58	19.60	8.04	217.58	184.11	0.19	0.25	11.18	9.06
Actinomyces oral taxon 170 F0386 uid48493	270.27	203.96	27.01	8.78	244.06	183.40	0.43	0.26	14.83	172.59
Bergeyella zoohelcum ATCC 43767 uid52163	116.28	195.52	43.82	9.21	195.84	177.71	0.79	0.50	9.99	15.40
Chryseobacterium gleum ATCC 35910 uid30953	210.38	187.94	47.64	10.12	266.47	168.58	0.94	1.05	13.35	43.99

<i>Brevibacterium mcbrellneri</i> ATCC 49030 uid34583	177.30	165.84	32.85	6.64	252.31	156.90	0.27	0.34	13.33	43.37
<i>Sphingobacterium spiritivorum</i> ATCC 33300 uid31	143.82	63.80	29.97	11.48	81.31	155.15	0.34	0.57	8.06	14.77
<i>Atopobium rimae</i> ATCC 49626 uid30999	29.20	108.78	19.10	4.17	164.21	155.02	0.20	0.17	3.62	8.26
<i>Turicella otitidis</i> ATCC 51513 uid52203	280.34	172.02	40.35	7.06	179.54	153.55	0.29	0.30	10.09	12.30
<i>Capnocytophaga gingivalis</i> ATCC 33624 uid3138	164.53	146.20	31.26	8.52	218.75	151.45	0.34	0.50	13.71	28.69
<i>Helicobacter pylori</i>	39.54	72.21	30.93	6.66	108.48	146.64	0.16	0.24	4.20	4.69
<i>Megamonas funiformis</i> YIT 11815 uid46421	77.83	130.74	23.10	6.79	66.46	145.94	0.19	0.20	12.66	8.02
<i>Granulicatella adiacens</i> ATCC 49175 uid37271	89.30	170.92	16.88	5.72	148.40	143.99	0.17	0.20	13.73	20.37
<i>Flavobacteria bacterium</i>	162.67	139.49	32.68	6.83	142.53	143.29	0.39	0.53	5.52	51.62
<i>Segniliparus rugosus</i> ATCC BAA 974 uid40685	175.81	128.13	20.93	9.19	151.57	137.91	0.30	0.22	9.17	18.53
<i>Desulfitobacterium hafniense</i> DP7 uid30023	160.21	141.34	18.20	6.21	168.81	134.49	0.23	0.21	6.44	9.20
<i>Anaerotruncus colihominis</i> DSM 17241 uid19659	71.89	102.51	26.22	6.21	93.72	131.27	0.15	0.16	10.73	7.86
<i>Dorea formicigenerans</i> 4 6 53AFAA uid46407	115.76	55.10	34.09	9.29	100.77	128.70	0.51	0.38	10.16	13.77
<i>Gemella haemolysans</i> ATCC 10379 uid30487	202.59	96.48	27.49	5.79	143.32	126.01	0.29	0.23	6.21	12.94
<i>Trueperella pyogenes</i>	135.39	124.67	24.27	8.06	151.90	121.05	0.36	0.23	12.28	16.91
<i>Clostridiales bacterium 1 7 47FAA</i> uid30067	104.40	99.44	47.64	30.44	107.41	117.99	1.29	1.79	24.46	40.94
<i>Flavonifractor plautii</i> ATCC 29863 uid18189	163.73	71.31	30.87	5.85	57.80	117.73	0.11	0.26	31.45	12.68
<i>Aneurinibacillus migulanus?</i>	93.63	134.74	19.08	5.42	121.63	117.32	0.15	0.12	8.16	7.35
<i>Arcanobacterium</i> sp.	155.69	249.78	39.54	6.20	150.26	115.63	0.23	0.13	13.72	44.62
<i>Phascolarctobacterium succinatutens</i> YIT 12067	52.89	26.12	11.12	3.59	58.00	112.42	0.09	0.10	2.78	10.84
<i>Desmospora</i> 8437 uid64725	228.51	155.68	18.46	8.43	138.65	111.05	0.09	0.17	5.18	7.32
<i>Paraprevotella clara</i> YIT 11840 uid48501	94.23	139.00	48.75	9.60	133.66	109.04	0.27	0.18	9.91	29.33
<i>Treponema denticola</i> AL 2 uid64903	40.13	14.62	8.67	3.11	54.32	106.53	0.09	0.13	3.42	2.11
<i>Fingoldia magna</i> ACS 171 V Col3 uid49435	58.54	169.12	20.30	5.41	180.12	106.10	0.18	0.26	9.03	6.71
<i>Blautia hansenii</i> DSM 20583 uid30021	113.15	75.70	35.36	7.59	136.99	105.27	0.35	0.29	13.11	91.43
<i>Akkermansia muciniphila</i>	100.15	57.21	29.47	7.48	138.74	105.18	0.17	0.21	2.00	7.10
<i>Alistipes</i> HGB5 uid54031	62.67	48.54	14.11	4.87	74.60	104.80	0.22	0.14	6.44	6.74
<i>Actinobaculum massiliae</i> ACS 171 V Col2 uid520	118.84	191.36	24.62	6.71	158.82	104.66	0.27	0.15	15.73	53.62
<i>Bifidobacterium</i> 12 1 47BFAA uid41959	116.84	256.68	14.64	12.26	121.32	103.78	0.18	0.20	6.94	5.62
<i>Veillonella</i> 3 1 44 uid41975	80.80	105.46	20.37	4.21	70.56	103.55	0.19	0.12	7.63	8.74
<i>Alloscardovia omnicolens</i>	49.04	112.52	18.14	7.38	57.51	101.49	0.22	0.16	5.66	8.16
<i>Abiotrophia defectiva</i>	75.87	102.78	18.91	6.46	116.83	100.11	0.22	0.11	9.48	10.13
<i>Parabacteroides</i> D13 uid38359	46.57	62.08	15.61	6.24	73.17	98.32	0.13	0.23	2.22	7.49
<i>Roseburia intestinalis</i> L1 82 uid30005	119.26	167.75	19.23	8.61	100.07	97.71	0.15	0.15	14.90	61.25
<i>Campylobacter</i> 10 1 50 uid40015	79.15	61.72	23.19	5.23	70.06	97.45	0.26	0.23	5.63	10.36

<i>Sporosarcina newyorkensis</i> uid64749	215.66	88.37	16.48	7.38	78.80	96.62	0.20	0.29	10.41	51.31
<i>Erysipelothrix rhusiopathiae</i> ATCC 19414 uid3146	58.88	67.41	8.93	2.65	142.18	94.89	0.14	0.16	1.78	4.70
<i>Weissella paramesenteroides</i> ATCC 33313 uid341	49.63	282.88	25.68	5.47	83.42	93.48	0.14	0.23	3.85	11.77
<i>Aerococcus urinae</i>	61.82	134.24	28.78	7.08	71.93	91.11	0.06	0.15	5.15	6.82
<i>Anaerofustis stercorihominis</i> DSM 17244 uid1965	44.69	30.82	11.47	3.03	56.46	88.33	0.15	0.16	6.21	3.61
<i>Tissierellia bacterium</i>	79.27	69.99	18.42	5.44	116.40	87.61	0.11	0.10	12.12	10.01
<i>Leuconostoc mesenteroides cremoris</i> ATCC 1925	99.81	30.47	23.02	3.63	61.39	85.76	0.18	0.24	4.93	13.49
<i>Weeksella virosa</i>	98.13	100.54	14.54	3.43	89.57	85.30	0.27	0.23	8.10	10.37
<i>Pseudoflavonifractor capillosus</i> ATCC 29799 uid1	118.41	66.42	16.81	6.32	69.05	82.16	0.16	0.07	8.31	9.97
Ruminococcaceae bacterium D16 uid42541	75.84	51.66	9.75	4.91	54.44	80.80	0.08	0.09	5.81	7.39
Lachnospiraceae bacterium 1 1 57FAA uid39377	63.27	77.20	26.29	8.72	76.67	79.80	0.20	0.10	23.15	14.59
<i>Johnsonella ignava</i> ATCC 51276 uid40693	74.36	68.34	12.43	3.16	73.88	79.73	0.10	0.08	7.00	9.77
<i>Butyricoccus pullicaecorum</i>	68.19	47.82	10.10	4.78	51.56	78.47	0.10	0.06	10.23	9.54
<i>Clostridium</i> 7 2 43FAA uid32457	103.28	91.49	20.83	7.54	78.37	78.05	0.17	0.32	8.05	15.65
<i>Facklamia hominis</i>	60.58	72.82	11.72	5.31	74.93	74.63	0.14	0.16	4.76	10.57
<i>Mitsuokella multacida</i> DSM 20544 uid28653	45.80	112.67	16.87	4.82	118.14	72.86	0.12	0.16	5.17	7.37
<i>Odoribacter laneus</i> YIT 12061 uid46423	55.38	48.62	20.31	6.93	61.75	71.59	2.69	2.92	3.30	24.91
<i>Dolosigranulum pigrum</i> ATCC 51524 uid52171	55.00	97.13	12.09	4.58	116.63	70.86	0.22	0.17	7.47	143.93
<i>Shuttleworthia satelles</i> DSM 14600 uid33169	65.14	23.91	13.50	5.62	56.04	70.79	0.11	0.11	5.60	7.64
<i>Catabacter hongkongensis</i>	55.62	37.73	8.68	4.40	48.13	70.74	0.09	0.06	5.47	2.93
<i>Butyrivibrio crossotus</i> DSM 2876 uid28999	64.73	65.75	22.71	5.63	96.27	70.68	0.18	0.19	13.61	9.91
<i>Selenomonas F0473</i> uid64897	33.27	41.21	8.53	2.72	68.90	70.19	0.07	0.09	3.98	8.24
<i>Eubacterium</i> 3 1 31 uid39375	58.23	83.69	5.38	2.70	88.56	66.88	0.11	0.28	2.41	44.83
<i>Anaeroglobus geminatus</i> F0357 uid50397	35.13	16.83	9.59	2.58	53.19	66.74	0.08	0.08	2.99	7.52
<i>Gardnerella vaginalis</i>	59.47	151.07	10.17	5.02	56.43	65.82	0.12	0.10	7.76	7.00
<i>Dysgonomonas mossii</i> DSM 22836 uid46411	40.50	40.14	13.34	2.92	64.04	64.65	0.16	0.09	1.70	5.49
<i>Peptoniphilus oral</i> taxon 836 F0141 uid49437	34.93	19.26	14.21	3.04	33.35	64.38	0.12	0.09	2.70	4.32
<i>Parascardovia denticolen</i>	59.84	88.24	9.04	5.11	59.04	63.61	0.10	0.08	4.07	4.15
<i>Eggerthella</i> 1 3 56FAA uid40023	67.86	48.73	18.27	4.47	43.18	60.99	0.29	0.15	3.48	3.42
<i>Mobiluncus curtisii</i> ATCC 35241 uid34631	100.56	161.69	21.77	5.25	75.42	59.76	0.19	0.14	4.50	6.65
<i>Dialister invisus</i> DSM 15470 uid33143	44.75	55.61	13.91	4.07	43.82	59.48	0.11	0.06	3.47	6.40
<i>Lachnoanaerobaculum</i> sp.	74.58	48.70	11.32	4.96	57.08	59.44	0.13	0.08	6.39	8.13
Erysipelotrichaceae bacterium 21 3 uid39369	59.27	86.09	6.01	2.81	65.91	59.39	0.15	0.14	8.32	43.52
<i>Fusobacterium periodonticum</i>	57.73	51.40	5.44	2.97	55.94	59.03	0.08	0.10	4.52	6.37
<i>Barnesiella intestinihominis</i> YIT 11860 uid46375	41.74	66.86	11.39	3.26	93.23	58.95	0.14	0.14	3.34	16.74

Megasphaera UPII 135 E uid64691	51.21	24.13	6.78	4.42	62.26	58.59	0.11	0.13	3.08	6.10
Streptomyces sp.	34.29	51.04	6.33	4.48	53.54	58.32	0.12	0.13	1.61	39.03
Eremococcus coleocola ACS 139 V Col8 uid5402	71.07	55.90	8.06	5.17	101.23	57.97	0.09	0.12	4.96	8.09
Stomatobaculum longum uid49875	36.66	40.90	7.92	4.05	42.09	51.39	0.08	0.06	24.48	3.82
Bacteroidetes oral taxon 274 F0058 uid41957	45.52	29.48	10.87	2.90	45.32	50.14	0.12	0.10	8.35	17.03
Cetobacterium somerae	56.03	67.15	4.61	3.61	69.16	50.07	0.07	0.13	2.07	5.97
Marvinbryantia formatexigens DSM 14469 uid210	75.76	48.42	16.98	6.30	74.26	49.70	0.15	0.09	10.44	16.12
Anaerococcus hydrogenalis ACS 025 V Sch4 uid5	70.95	57.84	16.97	7.86	109.42	48.00	0.19	0.09	8.70	16.54
Acidaminococcus D21 uid34117	35.61	28.46	5.47	3.32	46.34	47.77	0.09	0.07	2.59	7.26
Paenibacillus HGF5 uid54029	44.89	38.37	10.99	3.38	41.72	46.80	0.44	0.17	2.46	8.98
Helcococcus kunzii ATCC 51366 uid52183	26.91	33.76	6.60	2.41	41.06	46.66	0.06	0.13	2.36	2.23
Tannerella 6 1 58FAA CT1 uid40043	58.81	42.92	17.20	5.00	54.96	45.71	0.17	0.15	8.37	34.76
Gordonibacter pamelaee	49.02	59.20	12.26	4.00	39.92	45.23	0.12	0.11	3.32	4.60
Paenisporosarcina sp.	133.64	167.94	29.99	3.75	84.43	44.71	0.25	0.22	4.38	11.26
Jonquetella anthropi E3 33 E1 uid33111	23.10	20.69	8.25	2.22	42.04	40.73	0.11	0.08	1.97	2.71
Alloiococcus otitis ATCC 51267 uid52161	29.59	29.96	8.76	2.56	37.03	40.21	0.08	0.19	3.19	5.94
Catonella morbi	36.87	35.12	9.47	2.82	68.22	39.72	0.09	0.07	7.73	7.58
Adlercreutzia equolifaciens	23.65	27.92	6.62	3.82	29.36	38.01	0.10	0.09	2.13	2.86
Slackia exigua ATCC 700122 uid38335	46.71	17.96	7.44	3.26	29.98	37.62	0.08	0.08	3.99	3.90
Scardovia inopinata F0304 uid41979	52.07	89.05	7.80	3.58	47.93	36.79	0.08	0.07	3.26	3.43
Bulleidia extracta W1219 uid40673	33.37	24.05	6.19	2.50	42.26	35.75	0.14	0.11	2.24	2.09
Solobacterium moorei F0204 uid43121	31.54	28.78	3.38	1.99	31.73	35.13	0.05	0.06	1.65	1.40
Mollicutes bacterium	25.68	33.24	11.08	2.86	32.03	35.10	0.09	0.09	1.85	7.29
Leptotrichia goodfellowii F0264 uid34093	62.85	26.16	7.78	6.73	65.26	33.27	0.13	0.12	3.57	3.29
Collinsella intestinalis DSM 13280 uid29307	55.37	59.77	8.60	3.95	39.78	32.95	0.15	0.05	3.50	5.17
Parvimonas oral taxon 393 F0440 uid61837	17.89	21.84	11.37	3.97	43.33	32.81	0.09	0.15	2.56	2.41
Mogibacterium timidum	29.66	25.41	9.07	3.35	41.40	32.32	0.09	0.06	2.10	1.82
Filifactor alocis	35.73	22.64	6.78	1.97	33.63	32.07	0.07	0.04	3.62	2.23
Peptostreptococcus anaerobius 653 L uid34105	48.62	48.17	28.90	11.35	64.33	31.37	0.19	0.31	1.16	0.70
Centipeda periodontii DSM 2778 uid53025	31.37	27.17	6.23	2.45	32.74	31.28	0.05	0.06	2.60	1.70
Sneathia amnii	35.32	37.34	2.84	1.76	49.52	31.02	0.17	0.79	1.55	1.20
Pyramidobacter piscolens W5455 uid34581	25.91	20.82	5.79	1.87	33.16	30.76	0.10	0.06	2.03	3.91
Parasutterella excrementihominis YIT 11859 uid41	6.64	0.20	0.56	0.32	6.32	9.84	0.00	0.02	0.02	4.87
Turicibacter HGF1 uid59523	30.39	2.84	1.89	0.77	12.27	9.06	0.01	0.07	0.68	0.82
Methanobrevibacter smithii DSM 2375 uid27821	4.15	46.95	2.86	1.37	11.89	7.51	0.07	0.00	0.50	44.80

Table S7. Mean ENV genome counts (RPM).

Genome	APOB		Bile		HDL		Liver		Urine	
	SRBIKO	WT	SRBIKO	WT	SRBIKO	WT	SRBIKO	WT	SRBIKO	WT
<i>Pseudomonas fluorescens</i>	10441.38	10024.31	432.1253	97.12528	20366.48	20816.99	13.62704	12.8481	270.8596	554.289
<i>Propionibacterium acnes</i>	7656.893	9636.294	835.5112	210.4637	8000.842	6990.82	4.563057	4.37897	576.4113	1995.311
<i>Stenotrophomonas maltophilia</i>	6529.635	7948.452	97.98898	42.14445	3159.071	2793.012	3.73041	3.392313	130.2848	304.0579
<i>Janthinobacterium lividum</i>	3683.407	5134.163	830.4949	161.7239	4857.424	3418.197	6.585493	5.299056	382.1809	1010.644
<i>Pseudomonas putida</i>	4501.4	4717.613	325.7505	77.98935	7190.048	7177.258	8.701397	9.057773	228.9784	517.7027
<i>Azotobacter chroococcum</i>	2599.03	2862.043	189.3168	47.38598	4625.87	4670.863	3.260278	3.457399	78.40823	241.2425
<i>Polaromonas JS666</i>	1346.545	1469.561	343.7328	75.94224	1646.013	1298.179	2.200749	2.209759	141.4844	254.4039
<i>Pseudoxanthomonas suwonensis</i>	947.3923	1467.529	54.86566	19.0609	886.5587	674.1928	1.199115	1.178846	34.92674	79.24461
<i>Delftia Cs1</i>	1093.846	1299.49	239.2626	110.3036	1458.172	991.6503	2.334398	2.698764	127.7165	376.9643
<i>Herbiconiux solani</i>	1404.343	1279.012	200.8481	54.42156	1427.246	1164.91	2.086304	1.651819	89.26375	276.1174
<i>Exiguobacterium pavilionensis</i>	766.4804	1166.143	68.67924	23.95607	859.9169	844.8524	0.697847	0.430292	18.68669	87.29716
<i>Variovorax paradoxus</i>	1068.752	1116.084	261.1077	60.60062	1480.889	1111.862	2.251618	1.986077	106.3545	295.4005
<i>Promicromonospora kroppenstedtii</i>	1108.58	1083.767	130.2406	43.86181	1081.35	799.8351	1.761075	1.259411	62.19459	175.8732
<i>Agrobacterium rhizogenes</i>	993.7832	993.4637	108.0025	36.00345	664.6669	1090.517	2.269609	2.167087	49.39837	107.2077
<i>Xanthomonas campestris</i>	744.152	966.0134	52.0048	15.66691	760.242	634.3616	1.328536	1.320348	34.39339	51.60496
<i>Acidovorax citrulli</i>	853.028	954.5343	179.7138	47.84181	1130.495	1009.688	1.642454	1.316959	56.54211	284.9429
<i>Pseudogulbenkiania ferrooxidans</i>	409.1255	810.539	59.15257	15.43259	489.8613	640.5181	0.705132	0.958561	27.04178	74.13109
<i>Ottowia sp.</i>	718.0789	788.4567	148.6644	40.74772	786.8431	567.7971	0.925874	0.773961	50.80191	209.8105
<i>Bdellovibrio bacteriovorus</i>	406.7283	787.631	56.18508	26.87837	383.3648	553.9836	1.111532	1.011987	7.367683	71.45819
<i>Idiomarina sp.</i>	333.3445	749.5147	60.02028	14.36038	431.8333	715.7446	1.094226	1.070005	14.34664	37.24749
<i>Hydrogenophaga intermedia</i>	651.095	709.3008	127.2422	33.41409	774.707	561.4605	0.991181	0.92772	40.03114	178.9253
<i>Alteromonas stellipolaris</i>	445.637	707.6104	33.15154	6.07707	516.2865	481.6106	0.591998	0.552357	11.2988	66.48717
<i>Hahella chejuensis</i>	361.5045	701.2834	32.97849	8.369949	530.1275	605.7584	0.793548	0.926262	19.51384	26.37383
<i>Roseateles depolymerans</i>	578.5676	678.5981	122.3405	28.10377	1122.76	487.516	1.116486	0.923779	36.87846	180.6249
<i>Mitsuaria chitosanitabida</i>	556.2251	669.4874	142.8594	32.07325	1286.691	551.2016	1.334608	1.034209	41.74907	217.1919
<i>Lentibacillus amyloliquefaciens</i>	261.7095	659.3515	43.14242	13.6252	295.0606	378.7194	0.448864	0.335742	11.69156	17.78298
<i>Herbaspirillum seropedicae</i>	406.4414	623.9266	145.564	31.3967	591.6393	596.8376	0.93325	1.086263	40.99828	71.60012
<i>Paucibacter sp. KCTC 42545</i>	636.0493	608.6945	145.1993	32.63311	1283.284	644.5413	1.317221	0.94171	43.41095	274.8806
<i>Xylella fastidiosa</i>	504.4232	607.9902	32.28361	10.27471	529.6159	510.7631	0.982018	0.876577	22.64891	37.59586
<i>Buchnera aphidicola</i>	226.9688	602.7541	14.22334	4.663113	263.5578	363.467	0.534957	0.453095	7.347262	12.25628

Luteimonas sp.	416.9737	601.3897	27.02228	10.40061	431.2457	371.5225	0.764856	0.77735	20.21138	49.77451
Fulvimarina pelagi	427.4679	599.1399	74.41894	22.39872	316.5728	593.3546	1.120087	1.059009	30.94709	69.43499
Bradyrhizobium japonicum	611.9741	572.7009	100.0407	28.25619	685.8175	758.7973	1.464851	1.573108	73.84585	112.9321
Geobacter sp.	196.6993	565.8524	33.18379	8.463917	219.7991	361.9384	0.355556	0.309814	10.23814	41.17091
Lysobacter antibioticus	474.0963	545.3474	25.05775	10.36693	484.4214	391.3472	0.936366	0.793868	24.61282	37.09617
Marinomonas posidonica	463.9697	544.296	60.21436	14.6113	747.4472	827.9886	1.781436	2.332674	22.41403	53.14949
Conexibacter woesei	219.44	533.9238	23.20098	4.82012	218.1889	329.5759	0.366185	0.206847	9.300989	14.66925
Altererythrobacter marensis	492.5742	509.6933	71.68676	25.2052	520.3992	479.8471	2.125161	1.886118	52.82933	94.71501
Rubrobacter radiotolerans	138.8074	505.8889	11.45694	4.406084	134.9337	278.1492	0.158871	0.173017	2.963657	5.148828
Leclercia adecarboxylata	460.6076	502.7068	57.29557	14.90717	400.5295	520.0615	2.151574	2.609011	57.40451	119.2087
Thalassolituus oleivorans	381.1674	487.4053	41.60274	11.09921	723.5377	781.562	0.827657	0.784046	14.79542	54.13833
Cellvibrio japonicus	399.0403	466.1564	70.62875	17.12221	747.7012	760.922	1.104063	1.055594	28.63851	84.41938
Azoarcus sp.	506.3229	464.9243	102.7927	27.57284	797.58	612.0585	2.002427	2.785801	38.17085	174.7745
Dokdonella koreensis	245.4924	410.1087	22.20514	6.763321	357.9259	357.5346	0.432595	0.508189	10.61735	21.23581
Methylophaga nitratreducenticresce	449.1192	407.6307	30.21872	9.22521	525.2705	426.4514	1.03855	1.298812	17.1171	184.3781
Simidiua agarivorans	463.525	406.6065	44.26062	15.48194	968.0857	905.9255	1.323023	1.410238	33.02685	88.80472
Anabaena cylindrica	771.7591	405.4073	115.806	63.02321	558.2063	452.488	1.537615	1.915333	38.98246	332.8714
Aeromonas hydrophila	410.2102	400.927	57.41643	11.35604	509.9103	1182.336	0.893268	0.874321	24.1268	25.17777
Agarivorans gilvus	250.3169	398.4339	21.13642	5.610868	442.0943	627.593	0.451528	0.45901	9.22288	39.51801
Sedimenticola sp.	386.2565	393.6201	53.51225	20.98447	432.3609	539.1899	1.725238	1.873661	28.44446	115.7815
Alcanivorax sp.	382.5755	391.7832	65.07286	15.23708	668.1428	661.2582	1.900559	2.183832	26.03338	45.60215
Beggiatoa leptomitiformis	276.3699	382.1842	53.87702	19.15934	402.1794	338.7334	0.668741	0.744287	17.38898	50.62043
Ruegeria mobilis	305.3837	381.2449	41.89156	14.89292	299.5074	210.546	0.520676	0.666246	23.54356	13.91239
Cupriavidus basilensis	430.9501	365.759	140.755	32.11816	626.0929	1083.105	1.311996	1.113834	43.80719	132.326
Rheinheimera sp.	209.9996	365.4183	34.51624	7.764514	360.0366	511.0622	0.953843	0.946888	11.5912	23.03758
Arenimonas composti	269.7948	353.6708	21.09448	7.477562	314.4053	324.6709	0.526653	0.538587	11.66634	25.47214
Thiobacillus denitrificans	232.4086	352.2435	56.3364	18.57576	317.347	409.4075	0.849149	0.843687	20.72628	119.7342
Piscirickettsia salmonis	338.7834	336.6118	78.43621	13.29305	431.3856	437.3996	1.024326	0.976072	16.70555	31.11805
Rhizobiales bacterium	396.3646	333.8277	50.42599	13.18938	293.0361	258.6617	0.698865	0.841272	24.02617	103.6776
Lactococcus lactis	373.2051	328.892	38.11403	16.92999	315.8467	282.4018	0.473595	0.656189	24.77407	75.23486
Gyнуella sunshinyii	228.5759	323.7937	30.40356	10.19299	439.7043	574.7726	0.578694	0.597341	23.31951	38.8163
Marinobacterium sp.	316.0837	320.608	37.0683	10.14057	584.4037	770.0642	0.732387	0.844493	12.75057	31.99795
Sulfuricella denitrificans	234.1344	320.0867	85.41548	19.30219	301.4038	320.4118	0.788369	1.133266	23.19302	84.54007
Paraburkholderia sacchari	380.1396	319.9322	71.1986	25.85214	482.5494	340.0967	0.829124	0.634352	28.49235	98.2642
Regiella insecticola	219.8747	319.7289	21.60082	5.093694	296.9253	423.2644	0.351253	0.413024	5.91624	14.09222

<i>Lelliottia amnigena</i>	258.7648	318.0992	33.19136	10.7953	294.9124	320.8761	1.273433	1.332551	21.8019	83.06232
<i>Frateuria aurantia</i>	232.7953	314.9316	24.81153	7.277664	303.146	328.8893	0.532935	0.536015	12.40043	164.607
<i>Devosia epidermidihirudinis</i>	316.7116	314.7651	38.4024	10.97663	267.3566	179.514	0.534367	0.356286	19.91411	36.97635
<i>Methylomonas methanica</i>	194.3251	313.5727	37.76628	7.363892	481.616	549.2883	0.862936	0.625438	12.29421	56.50546
<i>Pandoraea pulmonicola</i>	294.2725	304.6453	69.23851	21.69251	495.5126	385.5412	0.756411	0.762184	25.58162	83.33051
<i>Grimontia hollisae</i>	190.2332	292.4094	15.91758	4.303807	279.6068	395.2888	0.375609	0.385357	7.293496	22.42073
<i>Legionella hackeliae</i>	370.1487	292.2562	29.1073	11.49398	408.7625	439.3981	0.591686	0.665423	11.30481	44.40526
<i>Kluyvera intermedia</i>	209.0351	289.1098	27.52926	7.912556	298.4683	265.5744	0.961972	0.922334	20.21131	61.25892
<i>Thioploca ingrca</i>	171.6426	285.4721	36.13252	8.369331	262.8974	320.1903	0.52762	0.770577	9.516249	24.85427
<i>Wohlfahrtiimonas chitiniclastica</i>	179.4397	281.7602	39.64594	8.219989	280.7668	380.9208	0.412139	0.506119	8.022656	26.16077
<i>Rhodanobacter denitrificans</i>	259.6764	280.7288	27.27677	7.887663	347.4895	348.0885	0.537041	0.486191	14.45887	31.80953
<i>Halomonas huangheensis</i>	225.2677	271.807	25.4621	6.969989	343.1934	498.0301	0.652001	0.70434	9.418355	42.0879
<i>Gluconacetobacter diazotrophicus</i>	200.7771	271.6153	20.62506	6.637129	143.0947	188.8033	0.454825	0.449086	12.51902	11.41458
<i>Rhodovulum sp.</i>	255.9759	268.6854	60.98933	13.16889	276.7633	240.8068	0.773496	0.716131	10.20826	35.58599
<i>Glaciecola sp.</i>	172.2331	268.4822	15.21733	4.359944	279.5657	355.3605	0.409391	0.436968	6.650497	31.88698
<i>Kosakonia sacchari</i>	226.4069	268.407	32.96202	10.40013	282.2313	294.1908	1.104916	1.134661	24.96021	73.06236
<i>Obesumbacterium proteus</i>	288.8497	264.4978	26.55582	8.803611	340.2857	400.959	0.704957	0.803811	17.43746	47.6961
<i>Bordetella pertussis</i>	472.6704	259.6044	75.17948	15.93212	333.7846	293.8678	0.582902	0.51514	33.41223	166.2093
<i>Bosea sp.</i>	212.2434	251.1976	37.41301	9.755237	246.8488	222.6381	0.784077	0.835581	17.47898	59.90762
<i>Tatlockia micdadei</i>	258.9251	248.5667	22.23595	7.312068	294.325	361.0225	0.404713	0.526965	8.754795	28.2851
<i>Chromohalobacter salexigens</i>	200.43	245.9837	28.27805	6.912285	345.4733	464.4003	0.62244	0.530402	11.10473	45.62403
<i>Pluralibacter gergoviae</i>	254.7777	242.6707	38.00243	8.610576	368.0774	319.3993	1.049416	1.084601	25.5599	85.04676
<i>Cronobacter malonaticus</i>	264.544	242.6647	129.714	32.10406	477.4362	1460.791	1.45711	2.555776	23.12334	39.7258
<i>Congregibacter litoralis</i>	197.0061	239.9668	29.3336	6.869261	416.8896	508.5715	0.703672	0.686165	11.13555	19.60334
<i>Advenella kashmirensis</i>	282.3127	239.393	78.19218	12.57443	285.1339	205.4204	0.582241	0.474247	20.89149	148.2792
<i>Teredinibacter turnerae</i>	255.665	239.2822	33.55065	8.318976	519.0748	713.754	0.619129	0.677823	18.01455	20.51051
<i>Marinobacter sp.</i>	270.0234	239.1845	47.91138	10.53921	406.6838	502.3498	0.801472	0.917204	19.46777	29.28131
<i>Polynucleobacter necessarius</i>	226.1456	238.099	60.96176	12.9617	279.8777	303.5984	0.59217	0.522565	21.62823	37.96527
<i>Geobacillus sp. C56-T3</i>	464.5293	236.9002	33.21662	16.79789	272.1758	176.4512	0.365932	0.473957	29.02463	51.99107
<i>Asaia sp.</i>	158.1339	236.1001	14.21518	5.483526	126.3281	111.6217	0.336022	0.372202	8.00574	10.80414
<i>Dyella japonica</i>	228.2852	235.6251	24.22726	6.743156	293.2486	294.4791	0.47971	0.520854	9.995061	30.44624
<i>Rahnella aquatilis</i>	228.6261	229.1685	21.64398	7.577426	289.4702	281.1593	0.920697	0.818007	14.49921	50.28125
<i>Francisella tularensis</i>	156.8996	227.9289	26.26666	6.322891	287.8565	194.0877	0.716306	0.525002	9.650619	30.31689
<i>Thiomargarita nelsonii</i>	142.2054	224.725	75.35003	17.64852	246.5609	301.5837	10.00831	12.22915	26.10261	27.54192
<i>Spongiibacter sp.</i>	149.3703	221.8525	21.4719	6.216727	276.5439	330.4934	0.426089	0.627091	7.666492	26.36652

<i>Cedecea neteri</i>	199.9469	217.5554	31.94359	8.492872	252.759	285.6909	0.857275	0.963983	16.05844	97.48335
<i>Erwinia</i> sp.	166.7546	216.5566	22.62432	7.111393	234.1574	281.297	0.774381	0.809546	27.14354	28.69702
<i>Magnetospirillum caucaseum</i>	218.0301	214.7092	26.67452	9.295813	187.0291	143.8204	1.639128	1.72282	8.32587	65.83966
<i>Nitrincola lacisaponensis</i>	209.5847	213.3837	22.26553	5.489059	401.2331	622.9672	0.485294	0.669043	7.636723	27.94545
<i>Thiolapillus brandeum</i>	166.8506	213.0346	19.28958	5.493216	370.2313	517.6774	0.531281	0.477753	16.31044	29.66265
<i>Gluconobacter frateurii</i>	183.9387	211.5848	16.80669	5.879363	136.3357	126.6651	0.333424	0.325546	9.292285	10.69341
<i>Halothiobacillus</i> sp.	188.3745	211.1746	22.89738	11.70267	335.9647	327.4715	0.415291	0.406082	11.35959	33.99216
<i>Colwellia</i> sp.	144.9103	208.2122	25.04039	14.62222	202.7823	170.7612	1.096641	1.226419	11.95275	86.66621
<i>Raoultella ornithinolytica</i>	192.9396	206.4033	30.75758	8.234869	305.8459	319.6459	0.86856	0.985197	18.74698	62.45569
<i>Yersinia pestis</i>	157.3819	206.3709	20.24333	7.276157	239.8168	271.0651	0.631683	0.613708	11.23502	36.17314
<i>Tolumonas auensis</i>	185.6699	202.3293	31.87825	8.220521	280.225	364.3345	0.616825	0.842445	17.30222	20.71064
<i>Pseudoalteromonas rubra</i>	164.8341	194.2418	16.48166	5.269675	268.7468	291.2171	0.460238	0.482585	5.643791	43.14328
<i>Acetobacter pasteurianus</i>	184.7329	194.1477	18.24313	6.077088	120.3885	155.9784	0.343889	0.409077	14.80447	10.25243
<i>Thiocystis violascens</i>	167.7017	192.8027	22.74109	6.370258	225.7902	249.1659	0.317917	0.401054	8.68537	10.541
<i>Oceanimonas</i> sp.	171.5575	192.3399	31.51247	10.13371	241.2256	340.6094	0.912848	1.010097	13.69591	25.12677
<i>Alkalilimnicola ehrlichii</i>	154.4169	189.9013	22.58282	8.432882	213.2341	201.6856	0.283945	0.273192	8.469742	11.73947
<i>Methylococcus capsulatus</i>	204.3305	176.5421	27.83449	8.461987	403.4917	471.0205	0.490383	0.496147	9.168309	17.09194
<i>Pantoea</i> sp.	179.7284	172.1101	26.34749	6.705928	217.863	256.9422	0.601919	0.722807	13.73379	40.03797
<i>Kangiella geojedonensis</i>	197.6183	171.0126	48.764	20.27445	238.5103	266.1377	0.59275	0.952817	13.84088	19.38033
<i>Ferrimonas balearica</i>	133.0402	170.2048	20.96064	4.932878	246.5668	346.668	0.389002	0.425321	8.362801	26.4786
<i>Pectobacterium atrosepticum</i>	146.8172	167.4896	20.72616	7.062507	216.2087	270.8002	0.55416	0.573526	11.55581	40.3691
<i>Methylomicrobium alcaliphilum</i>	190.8816	165.9973	38.45785	16.1	206.1048	248.2859	0.461247	0.3958	12.95358	17.52659
<i>Beggiatoa alba</i>	167.3089	161.9805	41.23946	12.94974	242.2603	241.185	0.549572	0.62241	13.51766	32.57867
<i>Chania multitudinisentens</i>	181.1857	159.055	18.67967	6.942991	197.907	240.0692	0.589942	0.631717	14.05399	38.3434
<i>Nitrosococcus halophilus</i>	187.6587	157.9446	38.09326	15.57816	236.8717	171.7641	0.863156	0.994857	21.23143	15.56046
<i>Shewanella denitrificans</i>	205.804	153.6972	21.94211	6.658744	194.7101	288.2692	0.394448	0.403214	6.526254	11.24818
<i>Halorhodospira halochloris</i>	133.0359	150.1264	32.00049	7.657684	208.3238	241.7782	0.419464	0.448014	10.32229	17.52257
<i>Ectothiorhodospira</i> sp.	134.5812	150.1131	19.09029	5.014308	189.9032	211.2008	0.33289	0.327894	6.930134	11.81158
<i>Wenzhouxiangella marina</i>	140.3352	149.3583	35.05365	9.972459	210.7498	238.1013	0.405251	0.394313	9.817677	28.45221
<i>Bibersteinia trehalosi</i>	146.5834	148.6663	26.68911	9.091092	253.2054	204.693	0.615427	0.669958	47.045	142.0828
<i>Mannheimia haemolytica</i>	165.9174	148.5888	45.43097	12.61928	271.0509	253.8708	2.881753	3.041731	42.7066	140.1543
<i>Deinococcus proteolyticus</i>	112.1604	147.7897	13.79125	6.478176	119.376	94.65438	0.238118	0.256452	12.85711	7.897247
<i>Xenorhabdus bovienii</i>	126.7567	144.4526	19.21663	5.51151	212.3529	229.6558	0.492683	0.520002	7.438009	27.17506
<i>Dickeya zeae</i>	153.3648	143.7989	19.02507	6.238198	224.3553	269.0945	0.550654	0.563013	17.96845	40.218
<i>Listonella anguillarum</i>	128.9319	138.4727	20.5449	5.47501	163.4835	216.1068	0.318041	0.835781	7.328942	14.28581

<i>Spiribacter salinus</i>	167.509	136.2409	27.90694	13.33594	218.5575	208.2121	0.284331	0.294303	10.43957	15.99944
<i>Lacimicrobium alkaliphilum</i>	91.65045	132.7747	13.76818	4.318919	158.3831	168.0168	0.260648	0.280912	6.191122	13.42969
<i>Pragia fontium</i>	141.7952	129.3702	17.85431	6.315188	200.5452	239.7729	0.535594	0.576864	10.41122	39.25187
<i>Chloracidobacterium thermophilum</i>	64.15936	128.2831	43.5445	7.213011	83.38445	77.42582	0.123379	0.237289	4.702831	7.78926
<i>Gilliamella apicola</i>	121.616	128.2367	19.70854	6.001709	138.4239	155.4507	0.472854	0.452911	9.460817	17.07726
<i>Photorhabdus temperata</i>	148.5263	125.1626	15.94687	7.45147	213.6534	244.4526	0.421318	0.462636	8.376569	37.13934
<i>Leptolyngbya</i> sp.	269.8816	123.5723	48.25567	22.63192	233.8575	242.5238	0.503472	0.362871	15.41211	134.2898
<i>Komagataeibacter hansenii</i>	114.6184	123.2756	8.564105	2.055454	81.10793	70.24852	0.143129	0.205535	2.78258	3.805995
<i>Paenibacillus polymyxa</i>	142.1162	118.2868	38.57964	11.87721	153.0586	215.545	0.509855	0.377535	10.69817	18.44662
<i>Gallibacterium anatis</i>	94.90886	113.1708	24.56221	5.945699	138.324	149.7782	0.542892	0.584075	9.488958	71.53635
<i>Coxiella burnetii</i>	108.5306	111.9496	14.12108	5.687017	133.3855	171.796	0.25506	0.221439	7.398202	25.6359
<i>Thioalkalivibrio nitratireducens</i>	140.1971	111.1298	27.879	6.700901	201.0197	207.1219	0.407215	0.407066	9.742063	12.93485
<i>Frischella perrara</i>	138.0919	111.1279	19.37762	6.668561	204.5651	209.82	0.405617	0.438127	6.773002	17.09165
<i>Sodalis praecaptivus</i>	120.0669	110.6676	34.87089	7.468402	217.8755	254.4911	0.601707	0.669572	14.2432	25.97558
<i>Allochromatium vinosum</i>	112.1534	108.5869	18.16106	5.743975	152.7956	166.8409	0.330975	0.317947	7.166518	10.57845
<i>Hirschia baltica</i>	158.4651	107.6926	17.22007	8.369306	81.84456	82.58893	0.330113	0.254109	7.153668	13.02778
<i>Photobacterium gaetbulicola</i>	93.89624	106.0413	21.2387	4.568386	162.7576	171.0517	0.292581	0.327881	7.482451	32.96256
<i>Acidithiobacillus caldus</i>	88.14772	103.1929	22.79434	5.68636	151.2856	181.9892	0.345587	0.343863	8.863366	35.19844
<i>Desulfuromonas acetoxidans</i>	120.6258	101.3656	17.21858	9.747111	127.415	101.5319	0.329834	0.342367	12.49019	9.875502
<i>Chlamydia pneumoniae</i>	17.9511	99.87121	11.43318	2.704182	29.27507	49.50767	0.178832	0.12538	2.083267	3.506039
<i>Thioglobus singularis</i>	126.6161	95.22582	23.45935	7.338815	159.0141	137.3068	0.38901	0.418999	7.918388	17.32868
<i>Aliivibrio fischeri</i>	108.3175	94.39655	15.95828	4.23705	163.5544	154.9262	0.271425	0.326664	6.478396	24.60609
<i>Brevibacillus brevis</i>	174.9304	93.45914	23.7501	9.681565	184.3818	122.3781	0.301544	0.494532	10.79865	164.9132
<i>Vibrio parahaemolyticus</i>	83.88364	88.25431	15.55993	4.17371	146.7175	173.3918	0.302353	0.388992	8.282254	16.34723
<i>Wolbachia</i> sp.	60.06514	84.88766	12.25614	3.038059	89.2012	84.87114	0.194687	0.167056	3.944208	30.50286
<i>Spiroplasma chrysopicola</i>	30.61493	83.54839	14.79116	4.987894	50.75013	54.69668	0.1042	0.415616	3.784546	10.53832
<i>Moritella viscosa</i>	83.47383	79.74315	47.74029	8.902042	175.0154	358.4786	0.690775	0.890174	5.856067	9.464623
<i>Blochmannia floridanus</i>	108.813	73.26956	15.86576	5.349133	155.5488	109.5259	0.528254	0.530337	7.454899	9.709125
<i>Zymobacter palmae</i>	25.75706	46.75405	6.007197	6.328609	50.64746	87.16747	0.176731	0.117548	2.841429	15.16828
<i>Fictibacillus enclensis</i>	115.229	28.05671	19.00742	5.59833	102.9794	43.59651	0.094577	0.090513	4.13531	4.963443
<i>Ureaplasma urealyticum</i>	31.12494	14.60557	3.860481	1.796922	34.60964	38.17884	0.06388	0.262154	2.532755	1.529974
<i>Mycoplasma pneumoniae</i>	24.17954	10.56967	9.346498	2.994747	19.49569	51.7848	0.057306	0.112335	1.511789	1.610068

Table S8. Fungi genome counts (RPM).

Genome	APOB		Bile		HDL		Liver		Urine	
	SRBIKO	WT	SRBIKO	WT	SRBIKO	WT	SRBIKO	WT	SRBIKO	WT
<i>Fusarium oxysporum</i>	15697.31	13445.86	1985.136	484.9474	15232.19	12801.52	55.62051	64.8901	625.1118	2035.879
<i>Histoplasma capsulatum</i>	11619.72	8980.506	1758.056	462.0398	11951.41	12543.87	55.49659	62.33399	666.7751	1353.75
<i>Cryptococcus neoformans</i>	6092.292	4555.517	715.6396	189.9308	4101.027	4807.551	31.26217	32.0238	411.0778	890.6091
<i>Aspergillus niger</i>	4590.692	2946.055	655.305	163.1871	3249.87	3510.839	24.91059	31.28647	219.9401	428.964
<i>Saccharomyces cerevisiae</i>	5242.123	3677.244	703.679	182.3832	4508.991	3477.469	15.09392	17.24365	236.9088	657.8845
<i>Candida albicans</i>	4112.733	2637.751	560.1879	138.9744	2775.145	3253.018	17.48146	21.20442	162.018	378.0827
<i>Candida glabrata</i>	4061.288	2621.49	480.7519	119.1226	2970.4	2787.326	11.1336	12.12618	156.3034	365.2643
<i>Penicillium chrysogenum</i>	2112.639	1827.062	500.0876	146.1811	2069.625	2620.234	14.7705	18.35836	175.0293	283.3209

Table S9. 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

Table S10. Multivariate analysis of class-independent sRNA profiles compared to liver .

Group	Class level Comparison	F _{version}	p _{version}	F _{anova}	p _{anova}
APOB	Independent APOB vs. L	16.83	1.47E-03	19.56	2.00E-03
Bile	Independent Bile vs. Liv	2.76	1.22E-01	49.74	3.00E-03
HDL	Independent HDL vs. Li	80.90	1.11E-06	15.71	1.00E-03
Urine	Independent Urine vs. L	7.02	2.44E-02	22.07	2.00E-03
APOB	Independent APOB vs E	4.19	6.31E-02	10.08	2.00E-03
APOB	Independent APOB vs f	0.92	3.58E-01	2.62	2.00E-03
APOB	Independent APOB vs l	0.06	8.16E-01	5.83	2.00E-03
Bile	Independent Bile vs HD	14.51	2.49E-03	11.18	1.00E-03
Bile	Independent Bile vs Uri	1.75	2.16E-01	8.01	2.00E-03

Table S11. 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	Genome/Database	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
lncDR	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	RPMmicrona
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

Table S13. Comparisons to other pipelines

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	11839204.29	15418341.00	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 > 10RPM	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

Table S14. 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

Table S15. DEseq2 comparison of sRNA changes at the fragment level in SR-BI KO vs. WT mice

Group	Class	Sequence	Length	FoldChange	pvalue
HDL	miRNA	TGAGATGAAGCACTGTAGCTC	21	0.19	1.03E-06
HDL	miRNA	AAAGCTGGGTGAGAGGGC	19	0.05	1.38E-06
HDL	miRNA	TAAGTCACTAGTGGTCCGTT	21	0.06	4.21E-06
HDL	miRNA	TGAGATGAAGTACTGTAGCTC	21	0.09	1.46E-05
HDL	miRNA	TGAGATGAAGCACTGTAGCTCA	22	0.12	1.90E-05
HDL	miRNA	AGAGATGAAGCACTGTAGCTC	21	0.16	4.84E-05
HDL	miRNA	TTGGTCCCTTCAACCAGCT	20	0.13	7.73E-05
HDL	miRNA	TCAGATGAAGCACTGTAGCTC	21	0.15	8.39E-05
HDL	miRNA	TTCACAGTGGCTAAGTTCTGC	21	0.12	8.94E-05
HDL	miRNA	TGAGGTAGTAGATTGTATA	19	0.08	9.06E-05
HDL	miRNA	TGAGGTAGTAGTTGTGCT	19	0.08	1.19E-04
HDL	miRNA	TGACATGAAGCACTGTAGCTC	21	0.19	1.85E-04
HDL	miRNA	TGAGATGAAGCACTGTGGCTC	21	0.18	3.09E-04
HDL	miRNA	GAGATGAAGCACTGTAGCTC	20	0.09	3.34E-04
HDL	miRNA	TAGCTTATCAGACTGATGTT	20	0.14	4.05E-04
HDL	miRNA	TGAGATGAAGCACTGTAGC	19	0.16	4.67E-04
HDL	miRNA	TTCACAGTGGCTAAGTT	17	0.10	4.89E-04
HDL	miRNA	TGAGATGAAGCACCGTAGCTC	21	0.18	7.76E-04
HDL	miRNA	TTGTTCTGCTCGCTCGCGTGA	21	0.11	9.42E-04
HDL	miRNA	TGAGATGAAGAACTGTAGCTC	21	0.21	1.10E-03
HDL	miRNA	TGAGATGAAGCACTGTATCTC	21	0.23	1.32E-03
HDL	miRNA	GCACTGAGATGGGAGTGGTG	20	8.24	1.38E-03
APOB	miRNA	AGAGGTAGTAGTTGCATA	19	9.93	2.06E-05
APOB	miRNA	ATCACATTGCCAGGGATTACCA	22	9.41	1.01E-04
Bile	miRNA	ATCACATTGCCAGGGATTACCA	22	0.08	1.49E-04
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	7.22	2.08E-06
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	6.26	8.01E-06
HDL	snDR	GCGGGAAACTCGGCTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	5.70	1.70E-05
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	5.21	1.85E-05
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCATTGCGCTCTCCCCTG	59	6.75	5.99E-05
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	4.21	2.12E-04
HDL	snDR	ACGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	4.51	2.38E-04
HDL	snDR	GCGGGAAACTCGACTGCACAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	5.64	2.43E-04
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	4.29	2.69E-04
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGATAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	4.92	3.03E-04
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	4.14	3.83E-04
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGCTGCGTTCGCGCTCTCCCCTG	59	5.84	3.92E-04
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGAGGACTGCGTTCGCGCTCTCCCCTG	59	4.31	6.02E-04
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	3.84	6.33E-04
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTGGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	3.61	7.57E-04
HDL	snDR	GCGGGAAACTCGACCGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	5.15	7.93E-04
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGTGTTGCGCTCTCCCCTG	59	4.20	8.26E-04
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGTGTTGCGCTCTCCCCTG	59	4.37	9.41E-04
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCACTCTCCCCTG	59	3.92	9.62E-04
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGCTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	3.55	1.15E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	4.19	1.60E-03
HDL	snDR	GCGGGAAACTCACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	3.76	1.61E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	3.94	1.64E-03
HDL	snDR	GCGGGAAACCCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	3.58	1.66E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCACTCCCCTG	59	4.00	1.66E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTTATGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	3.88	1.71E-03
HDL	snDR	GGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	57	3.12	1.80E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	3.29	1.85E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTAGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	3.17	1.94E-03
HDL	snDR	ATAATTTGTGGTAGTGGGG	19	6.58	2.23E-03
HDL	snDR	GCTGGAACCTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	4.01	2.29E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	3.67	2.72E-03
HDL	snDR	GNGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	4.14	3.23E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	3.53	5.80E-03
HDL	snDR	GCGGGAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	3.12	6.18E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCTCTG	59	3.48	6.21E-03
HDL	snDR	GTGGGAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	2.87	6.28E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTATCCCCTG	59	2.71	6.46E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCG	59	4.34	6.57E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCACCCCTG	59	2.96	6.75E-03
HDL	snDR	GCAGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	4.32	7.32E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	3.42	7.47E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGTGACTGCGTTCGCGCTCTCCCCTG	59	2.98	8.85E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCTCTCCCCTG	59	3.27	8.90E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGCTGCGTTCGCGCTCTCCCCTG	59	2.78	9.00E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	4.07	9.41E-03
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	2.65	1.01E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	2.87	1.04E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCAG	59	2.63	1.19E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTC	59	2.74	1.20E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCT	58	5.57	1.21E-02
HDL	snDR	GCGGGAAACTCGCTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	2.88	1.37E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	2.60	1.45E-02

HDL	snDR	GGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTAGCGCTCTCCCCTG	57	2.36	1.46E-02
HDL	snDR	GCGGGAGACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	2.61	1.54E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGAGGGGGACTGCGTTCGCGCTCTCCCCTG	59	2.58	1.60E-02
HDL	snDR	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	59	2.72	1.62E-02
APOB	snDR	AGTCGGCATTGGCAATTTTGACAGTCTCTACGGAGACTG	40	28.09	2.59E-03
Liver	snDR	AGTGGGGGACTGCGTTCGCGCTCTCCCCTG	30	0.11	1.38E-05
Liver	snDR	TTTTGAGGCCTTGTCTTGACAAGGCT	27	0.13	6.82E-05
Liver	snDR	AATTTTTGAGGCCTTGTCTTGACAAGGCT	30	0.17	2.48E-04
Liver	snDR	AATTTTTGAGGTCCTGCTCGTGCAAGGCT	30	0.17	3.01E-04
Liver	snDR	CAATTTTTGAGGCCTTGTCTTGACAAGGCT	31	0.16	3.72E-04
Liver	snDR	CAATTTTTGAGGTCCTGCTCGTGCAAGGCT	31	0.19	4.34E-04
Liver	snDR	TTTTGAGGTCCTGCTCGTGCAAGGCT	27	0.18	4.64E-04
Liver	snDR	GTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	35	0.21	7.07E-04
Liver	snDR	TTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTA	37	0.22	1.08E-03
Liver	snDR	GTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	32	0.23	1.39E-03
Liver	snDR	AATTTTTGAGGCCTTGTTCGCAAGGCT	30	0.22	1.39E-03
Liver	snDR	TAAACCAATTTTTGAGGCCTTGTTCGCAAGGCT	37	0.23	1.77E-03
Liver	snDR	ACCCGCCTACTTTCGCGGATGCTGGGTGACGCGATCTGCCCG	43	0.23	2.21E-03
Liver	snDR	TTTTGAGGCCTTGTTCGCAAGGCT	27	0.17	2.24E-03
Urine	snDR	ATGCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG	61	0.03	1.20E-03
HDL	rDR	TCCCCGCGGGGCCCGCTCGTCCCCGCGCTCGTCCGCACTCTCTTCCCCCTCCT	55	12.97	1.15E-04
HDL	rDR	TCCCCGCGGGGCCCGCTCGTCCCCGCGCTCGTCCGCACTCTCTTCCCCCTCCT	56	15.82	5.52E-04
HDL	rDR	CTCGTGCATCTATTGAAAGTCAGCCCTCGACACAAGGGTTGT	45	4.15	1.11E-03
HDL	rDR	TCCCCGCGGGGCCCGCTCGTCCCCGCGCTCGTCCGCACTCTCTTCCCCCTCC	54	8.80	1.83E-03
HDL	rDR	CCCCGCGGGGCCCGCTCGTCCCCGCGCTCGTCCGCACTCTCTTCCCCCTCC	53	13.05	1.86E-03
HDL	rDR	GGGTCCGTCGGGCTGGGGCGCAAGCGGGGCTGGGGCGCGCCGCGGCT	49	10.28	1.94E-03
HDL	rDR	GCCGGGAGGTGGAGCACGACGCGTACGCGTTAGGACCCGAAAGA	44	16.14	2.29E-03
HDL	rDR	CCCCGCGGGGCCCGCTCGTCCCCGCGCTCGTCCGCACTCTCTTCCC	47	5.48	2.38E-03
APOB	rDR	GACTCTTAGCGGTGGATCACTCGGCTCGTGCG	32	0.02	1.79E-05
APOB	rDR	CCGCGGGGCCCGCTCGTCCCCGCGCTCGTCCGCACTCTCTTCCCCCT	39	47.91	2.96E-05
APOB	rDR	TTCCCCGCGGGGCCCGCTCGTCCCCGCGCTCGTCCGCACTCTCTTCCC	48	0.01	4.28E-05
APOB	rDR	CCGCGGGGCCCGCTCGTCCCCGCGCTCGTCCGCACTCTCTTCCCCCT	49	30.23	7.00E-04
Liver	rDR	CGCGTCGCGGCTGGGAAATGTGGCGTACGGAAGAC	35	0.15	4.21E-06
Liver	rDR	CGCGTCGCGGCTGGGAAATGTGGCGTACGGAAGACC	37	0.17	5.08E-06
Liver	rDR	CGCGTCGCGGCTGGGAAATGTGGCGTACGGAAGAC	36	0.19	2.92E-05
Liver	rDR	GTCCCCGCGCTCGTCCGCACTCTCTTCCCCCTCCTT	39	0.18	3.13E-05
Liver	rDR	CGCGTCGCGGCTGGGAAATGTGGCGTACGGAAGACCCACTCCCCGCGCC	51	0.20	3.71E-05
Liver	rDR	GCGCGTCGCGGCTGGGAAATGTGGCGTACGGAAGACC	38	0.19	3.80E-05
Liver	rDR	AGTCTGGCACGGTGAAGAGACATGAGAGGTGTAGAATAAGTGGGAGGCC	50	0.19	4.01E-05
Liver	rDR	CGCGTCGCGGCTGGGAAATGTGGCGTACGGAAGACCC	38	0.20	5.04E-05
Liver	rDR	ACCGATTGGATGGTTTGTAGTGGCCCTCGGATCGCCCGCGGGGCT	48	0.20	7.09E-05
Liver	rDR	TCTCTACTTGGATAACTGTGGTAATTCTAGAGCTAATACATGCCGACGGGCGGTGACC	59	0.22	7.10E-05
Liver	rDR	AGTTAAAAGCTCGTAGTTGGATCTTGGGAGCGGGCGGGCTCC	45	0.24	8.23E-05
Liver	rDR	GGGGGCCGCGGGCGGGCGGACTCTGGACGCGAGCC	36	0.22	8.46E-05
Liver	rDR	ACATGAGAGGTGTAGAATAAGTGGGAGGCC	32	0.21	8.51E-05
Liver	rDR	CGGGCGGGCGGGTCCAACCCGCGGGGTTCCGGAGCGGGAGGAACCA	48	0.23	1.51E-04
Liver	rDR	ACGTAGCAGAGCAGCTCCCTCGTGGATCTATTGAAAGTCAGCCCTCGACACAAGGGTTTGT	63	0.23	1.78E-04
Liver	rDR	AAGGGCTGGTTCGGTTCGGGCTGGGGCGCAAGCGGGGCT	39	0.22	2.07E-04
Urine	rDR	GACTCTAGTCTGGCACGGTGAAGAGACATGAGAGGTGTAGAATAAGTGGGAGGCC	56	0.02	2.49E-05
Urine	rDR	GCGCGGGGAGGTGGAGCACGAGCGTACGCGTTAGGACCCGAAAGAT	47	0.02	3.32E-05
APOB	tDR	TCTCTGGTGGTCTAGTGGTTAGGATTCGGGCT	33	0.16	2.90E-05
Liver	tDR	GCCTGTACGCGGGAGACCGGGTTCGATCCCCGACGGGGAGCC	45	0.17	3.91E-06
Liver	tDR	GCATTGGTAGTTCAATGGTGAATTTCTCCCTCCACGCGGGTGACCCGGGTT	53	4.80	1.87E-05
Bile	tDR	GTTTCCGTAGTGTAGTGGTTATCAGCTCGCCT	33	5.92	5.00E-07
Bile	tDR	GACCTCGTGGCGCAATGGTAGCGCTTCTGACT	32	8.64	3.02E-06
HDL	snoDR	GCCCATGATGGTATGAGAGTAGTGGACAGAAGGGATTTCTGAAAAACATTTTCTGAGG	59	24.64	2.64E-05
HDL	snoDR	AGTAATGATGATTTCTGGTATTCTGAGTGTCTCGCTGACGCCATACCCGACGCGCTGACC	63	11.19	1.65E-03
APOB	miscRNA	TTCGAGACCCGCGGGGCTCCCTGGCCCTT	30	25.70	7.05E-05
APOB	miscRNA	TTCGAGACCCGCGGGGCTCCCTGGCCCTT	31	12.52	5.15E-03
APOB	miscRNA	TACCTAACCCGTGAGTGGTTGGTTCGAGACCCGCGGGGCTCCCTGGCCCTT	53	10.07	1.59E-02

Table S16. Significantly altered exogenous genome counts in SR-BI KO mice compared to WT mice.

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

Table S17. DEseq2 comparison of non-host bacterial sRNA changes in SR-BI KO vs. WT mice

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

Table S19. Candidate sRNA sequences used for real-time PCR validation.

Name	Sequence
exo_rDR_Pflo23S	AGAGAACTCGGGTGAAGGAACT
exo_rDR_Vsp	TGGGTGTGACGGGGAAGCAGG
exo_rDR_Jliv	GACCAGGACGTTGATAGGCTGGGTGTGGAAGTG
miscRNA_Rpph1	CGGGCCTCATAACCCAATTCAGACTACTCTCCCCCGCCCTC
snDR_Gm26232	GCGGGAAACTCGACTGCATAATTTGTGGTAGTGGGGGACTGCGTTCGCGCTCTCCCCTG
snDR_Gm22866	ATAATTTGTGGTAGTGGGG
tDR-GluCTC	TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTC
tDR-GlyGCC	GCATTGGTGGTTCAGTGGTAGAATTCTCGC