

Supplementary Information

**Exploring the microbial community (microflora)
associated with ovine *Haemonchus contortus*
(macroflora) field strains**

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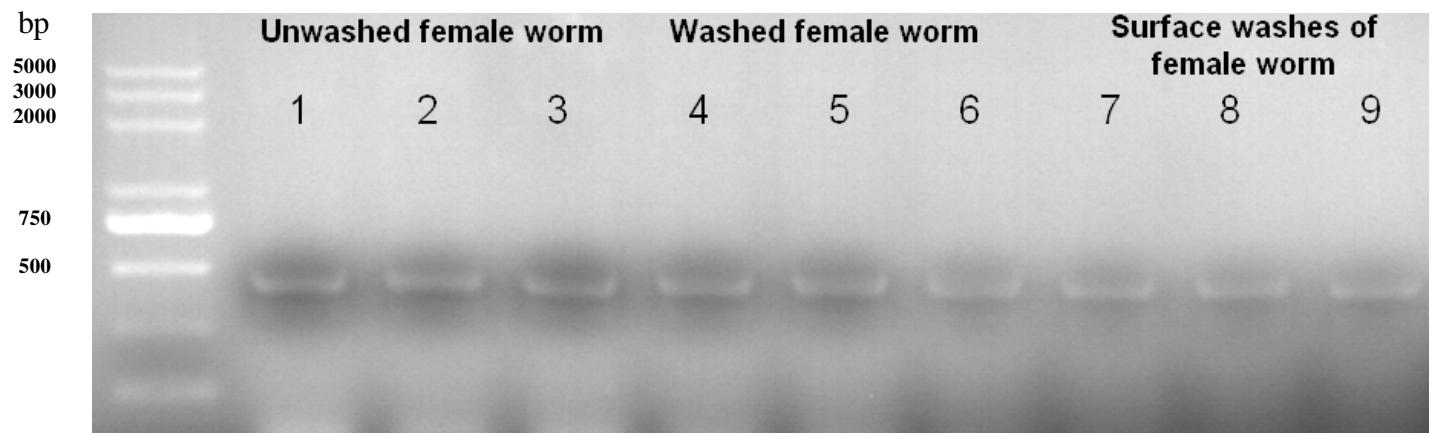
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Supplementary material for “Exploring the microbial community (microflora) associated with ovine *Haemonchus contortus* (macroflora) field strains”



Supplementary Figure S1: GoldView™ Nucleic Acid Stained 1.5% Agarose gel of V3-V4 region of 16S rRNA gene amplified product of unwashed an individual female worm (1, 2 and 3), washed an individual female worm (5, 6 and 7) and surface washes of an individual female worm (7, 8 and 9). Lane 1: Direct-load™ Star Marker Plus (D2000 Plus); GenStar Biosolutions Co. Ltd, Beijing, China.

Supplementary Table S1: An average bacterial composition associated with *H. contortus* adult female worms using amplification of V3-V4 hypervariable region of bacterial 16S rRNA gene sequence.

	V3-V4 region		
	Unwashed female worms ^a	Washed female Worms ^a	Washing solutions from female worms ^a
	(Average, ±SD)	(Average, ±SD)	(Average, ±SD)
<i>Anaerovibrio</i>	3.77E-03 ± 3.71E-04	0 ± 0	1.21E-03 ± 0.0003418
<i>Bacillus</i>	1.48E-03 ± 1.04E-04	0.00163131 ± 0.00015272	0.00E+00 ± 0
<i>Anaerotruncus</i>	2.57E-03 ± 2.56E-04	0 ± 0	8.24E-04 ± 0.000233
<i>Oribacterium</i>	5.21E-03 ± 5.17E-04	0 ± 0	1.67E-03 ± 0.0004729
<i>Ruminobacter</i>	2.36E-03 ± 2.36E-04	0 ± 0	7.57E-04 ± 0.0002131
<i>Mogibacterium</i>	2.36E-03 ± 2.36E-04	0 ± 0	7.57E-04 ± 0.0002131
<i>Acetitomaculum</i>	8.17E-03 ± 8.13E-04	0 ± 0	2.62E-03 ± 0.0007451
<i>Moryella</i>	1.45E-02 ± 1.46E-03	0 ± 0	4.64E-03 ± 0.001318
<i>Achromobacter</i>	2.52E-02 ± 1.77E-03	0.02773495 ± .002593656	0.00E+00 ± 0
<i>Kroppenstedtia</i>	7.41E-03 ± 5.20E-04	0.00815722 ± 0.00076303	0.00E+00 ± 0
<i>Stenotrophomonas</i>	4.44E-03 ± 3.12E-04	0.004894266 ± 0.0004577	0.00E+00 ± 0
<i>Butyrivibrio</i>	5.39E-02 ± 5.37E-03	0 ± 0	1.73E-02 ± 0.0049359
<i>Candidatus_Saccharimonas</i>	4.85E-03 ± 4.82E-04	0 ± 0	1.56E-03 ± 0.0004407
<i>Intestinimonas</i>	1.48E-03 ± 1.04E-04	0.00163131 ± 0.00015272	0.00E+00 ± 0
<i>Aeriscardovia</i>	2.22E-02 ± 1.56E-03	0.02447166 ± 0.00228877	0.00E+00 ± 0
<i>Saccharofermentans</i>	2.41E-02 ± 2.41E-03	0 ± 0	7.72E-03 ± 0.0021724
<i>Prevotella</i>	9.78E-01 ± 9.73E-02	0 ± 0	3.14E-01 ± 0.0888669
<i>Pseudomonas</i>	1.06E+00 ± 7.44E-02	1.16812319 ±	0.00E+00 ± 0

		0.10924532	
<i>Brevundimonas</i>	1.48E-03 ± 1.04E-04	0.00163131 ± 0.00015272	0.00E+00 ± 0
<i>Ochrobactrum</i>	1.54E+00 ± 1.08E-01	1.699978513 ± 0.1589851	0.00E+00 ± 0
<i>Rhizobium</i>	1.48E-03 ± 1.04E-04	0.00163131 ± 0.00015272	0.00E+00 ± 0
<i>Sphingomonas</i>	1.48E-03 ± 1.04E-04	0.00163131 ± 0.00015272	0.00E+00 ± 0
<i>Anaerosporobacter</i>	3.83E-03 ± 3.82E-04	0 ± 0	1.23E-03 ± 0.0003514
<i>Lentibacillus</i>	4.44E-03 ± 3.12E-04	0.004894266 ± 0.000458	0.00E+00 ± 0
<i>Atopobium</i>	4.44E-03 ± 3.12E-04	0.004894266 ± 0.0004577	0.00E+00 ± 0
<i>Luteibacter</i>	2.96E-03 ± 2.08E-04	0.003262955 ± 0.000305	0.00E+00 ± 0
<i>Ruminococcus</i>	1.76E-01 ± 1.24E-02	0.19414332 ± 0.01815669	0.00E+00 ± 0
<i>Selenomonas</i>	6.35E-03 ± 6.27E-04	0 ± 0	2.04E-03 ± 0.0005729
<i>Succinilasticum</i>	8.91E-02 ± 8.83E-03	0 ± 0	2.86E-02 ± 0.0080934
<i>Succinivibrio</i>	5.54E-02 ± 5.52E-03	0 ± 0	1.78E-02 ± 0.0050292
<i>Lactobacillus</i>	1.48E-03 ± 1.04E-04	0.00163131 ± 0.00015272	0.00E+00 ± 0
<i>Pyramidobacter</i>	4.43E-03 ± 4.41E-04	0 ± 0	1.42E-03 ± 0.0004029
<i>Delftia</i>	2.96E-03 ± 2.08E-04	0.003262955 ± 0.000305	0.00E+00 ± 0
<i>Acinetobacter</i>	4.44E-03 ± 3.12E-04	0.004894266 ± 0.0004577	0.00E+00 ± 0
<i>Bacteroides</i>	2.81E-02 ± 2.76E-03	0 ± 0	9.00E-03 ± 0.0025395
<i>Marinibryantia</i>	4.16E-03 ± 4.11E-04	0 ± 0	1.34E-03 ± 0.00038
<i>Coprococcus</i>	4.07E-03 ± 4.01E-04	0 ± 0	1.31E-03 ± 0.0003707
<i>Mycoplasma</i>	4.00E-02 ± 2.81E-03	0.044049058 ± 0.0041198	0.00E+00 ± 0
<i>Arthrobacter</i>	2.99E-05 ± 2.96E-06	0 ± 0	9.59E-06 ± 2.727E-06
<i>Pseudaminobacter</i>	1.48E-03 ± 1.04E-04	0.00163131 ± 0.00015272	0.00E+00 ± 0
<i>Flavonifractor</i>	4.44E-03 ± 3.12E-04	0.004894266 ± 0.0004577	0.00E+00 ± 0
<i>Blautia</i>	3.11E-03 ± 3.11E-04	0 ± 0	9.98E-04 ± 0.0002823
<i>Staphylococcus</i>	5.93E-03 ± 4.16E-04	0.00652591 ± 0.00061032	0.00E+00 ± 0
<i>Incertae_Sedis</i>	4.07E-02 ± 4.06E-03	0 ± 0	1.31E-02 ± 0.0037072
<i>Aquamicrobium</i>	1.48E-03 ± 1.04E-04	0.00163131 ± 0.00015272	0.00E+00 ± 0
<i>Syntrophococcus</i>	4.67E-03 ± 4.62E-04	0 ± 0	1.50E-03 ± 0.0004236
<i>Escherichia-Shigella</i>	2.67E+01 ± 1.87E+00	29.4119116 ± 2.75065773	0.00E+00 ± 0
<i>RC9_gut_group</i>	2.96E-03 ± 2.08E-04	0.003262955 ± 0.000305	0.00E+00 ± 0
<i>Desulfovibrio</i>	4.49E-03 ± 4.47E-04	0 ± 0	1.44E-03 ± 0.0004122
<i>Shinella</i>	2.96E-03 ± 2.08E-04	0.003262955 ± 0.000305	0.00E+00 ± 0
<i>Thalassospira</i>	1.20E-03 ± 1.20E-04	0 ± 0	3.84E-04 ± 0.0001087
<i>Shuttleworthia</i>	1.08E-02 ± 1.07E-03	0 ± 0	3.45E-03 ± 0.0009794
<i>Catonella</i>	8.98E-04 ± 8.93E-05	0 ± 0	2.88E-04 ± 8.15E-05

*Data represent an average value from three female adult worm (each worm come from different sheep on one farm) ± standard deviation (SD).

Supplementary Table S2: Alpha diversity analysis of *H. contortus* microbiome based on 16S rRNA gene sequence (V3-V4) of *H. contortus* life-cycle stages.

	Shannon Ave. \pm SD ^a	Chao1 Ave. \pm SD ^a	Good's coverage Ave. \pm SD ^a	PD whole tree Ave. \pm SD ^a	Observed species Ave. \pm SD ^a
Eggs	1.447 \pm 0.003	3.35 \pm 0.05	0.92 \pm 0.002	0.36 \pm 0.003	3.3 \pm 0.01
	1.776 \pm 0.002	24 \pm 0.1	0.982 \pm 0.001	4.077 \pm 0.007	13.6 \pm 0.3
	1.782 \pm 0.002	26.743 \pm 0.4	0.99 \pm 0.002	5.674 \pm 0.004	17.9 \pm 0.1
	1.807 \pm 0.007	25.752 \pm 0.5	0.994 \pm 0.004	5.723 \pm 0.003	19.8 \pm 0.2
	1.829 \pm 0.007	31.796 \pm 0.1	0.994 \pm 0.003	6.954 \pm 0.004	24.1 \pm 0.1
	1.828 \pm 0.006	36.465 \pm 0.6	0.995 \pm 0.002	7.45 \pm 0.05	26 \pm 0.2
	1.813 \pm 0.003	41.645 \pm 0.4	0.995 \pm 0.004	7.622 \pm 0.01	28.6 \pm 0.3
	1.811 \pm 0.001	38.813 \pm 0.1	0.997 \pm 0.002	7.64 \pm 0.04	27.8 \pm 0.3
	1.813 \pm 0.003	43.134 \pm 0.3	0.997 \pm 0.004	7.906 \pm 0.006	29.9 \pm 0.3
	1.803 \pm 0.003	39.61 \pm 0.1	0.997 \pm 0.006	7.858 \pm 0.008	30 \pm 0.7
	1.815 \pm 0.005	41.055 \pm 0.14	0.997 \pm 0.005	8.274 \pm 0.004	31.5 \pm 0.4
Larvae	2.839 \pm 0.006	24.1 \pm 0.02	0.31 \pm 0.001	3.06 \pm 0.06	3.3 \pm 0.01
	4.824 \pm 0.004	97.442 \pm 0.4	0.93 \pm 0.03	8.878 \pm 0.008	13.6 \pm 0.3
	4.986 \pm 0.005	109.46 \pm 0.6	0.966 \pm 0.02	10.251 \pm 0.01	17.9 \pm 0.1
	5.006 \pm 0.006	113.016 \pm 0.25	0.98 \pm 0.01	10.747 \pm 0.01	19.8 \pm 0.2
	5.03 \pm 0.03	114.136 \pm 0.3	0.987 \pm 0.002	11.12 \pm 0.01	24.1 \pm 0.1
	5.059 \pm 0.008	115.011 \pm 0.17	0.992 \pm 0.002	11.406 \pm 0.006	26 \pm 0.2
	5.07 \pm 0.07	112.606 \pm 0.6	0.995 \pm 0.003	11.562 \pm 0.01	28.6 \pm 0.3
	5.07 \pm 0.02	112.757 \pm 0.2	0.997 \pm 0.002	11.625 \pm 0.01	27.8 \pm 0.3
	5.074 \pm 0.004	112.1115 \pm 0.15	0.999 \pm 0.001	11.656 \pm 0.01	29.9 \pm 0.3
	5.065 \pm 0.001	112.186 \pm 0.18	0.999 \pm 0.001	11.683 \pm 0.01	30 \pm 0.7
Adults	5.07 \pm 0.02	112 \pm 0.1	1 \pm 0.001	11.683 \pm 0.01	31.5 \pm 0.4
	0.368 \pm 0.003	1.8 \pm 0.1	0.94 \pm 0.0001	0.315 \pm 0.004	1.8 \pm 0.01
	0.711 \pm 0.001	9.85 \pm 0.5	0.992 \pm 0.002	1.837 \pm 0.005	6.8 \pm 0.2
	0.766 \pm 0.003	18.975 \pm 0.5	0.992 \pm 0.001	5.001 \pm 0.008	11.5 \pm 0.4
	0.78 \pm 0.02	21.945 \pm 0.1	0.995 \pm 0.004	4.896 \pm 0.006	12.6 \pm 0.3
	0.765 \pm 0.004	26.013 \pm 0.1	0.995 \pm 0.003	6.387 \pm 0.007	15.7 \pm 0.2
	0.761 \pm 0.001	25.995 \pm 0.4	0.996 \pm 0.002	6.764 \pm 0.004	16.7 \pm 0.3
	0.772 \pm 0.002	29.268 \pm 0.1	0.996 \pm 0.001	6.964 \pm 0.003	18.5 \pm 0.4

	0.769±0.004	34.418±0.1	0.997±0.002	7.534±0.004	19.6±0.4
	0.767±0.005	33.54±0.4	0.997±0.001	8.405±0.005	21.2±0.2
	0.79±0.009	31.303±0.1	0.997±0.002	8.176±0.006	21.3±0.2
	0.788±0.003	39.218±0.1	0.997±0.0005	8.44±0.04	24.3±0.3

^aData represent average values from pooled populations (i.e from each sheep) of eggs/larvae/adults (male and female) come from three different sheep ± standard deviation (SD).

Supplementary Table S3: Alpha diversity analysis of *H. contortus* microbiome based on 16S rRNA gene sequence (V5-V7) of *H. contortus* life-cycle stages.

	Shannon Ave. ± SD ^a	Chao1 Average. ± SD ^a	Good's coverage Ave. ± SD ^a	PD whole tree Ave. ± SD ^a	Observed species Ave. ± SD ^a
Eggs	0.255±0.004	1.6±0.03	0.96±0.005	0.36±0.01	1.5±0.04
	0.543±0.003	10.95±0.01	0.997±0.0003	1.225±0.005	8.7±0.06
	0.519±0.003	17.783±0.007	0.997±0.0004	1.866±0.006	11.7±0.055
	0.52±0.005	25.483±0.008	0.997±0.0003	1.749±0.006	13.4±0.04
	0.507±0.004	20.868±0.009	0.998±0.0004	2.381±0.009	15.4±0.065
	0.52±0.004	27.928±0.009	0.998±0.0003	2.342±0.008	18.4±0.06
	0.528±0.0015	30.31±0.01	0.998±0.0003	2.631±0.009	19±0.07
	0.517±0.002	29.69±0.01	0.998±0.0003	2.584±0.007	20.2±0.02
	0.523±0.003	27.249±0.009	0.999±0.0005	3.097±0.01	21.5±0.04
	0.519±0.004	29.524±0.008	0.999±0.0004	2.65±0.08	22.2±0.01
	0.512±0.002	33.372±0.008	0.999±0.0002	3.108±0.008	22.4±0.03
Larvae	1.168±0.006				
		4.85±0.01	0.81±0.004	0.663±0.003	3.3±0.03
	2.031±0.009		41.501±0.001	0.987±0.0007	8.222±0.01
	2.058±0.009		43.685±0.012	0.995±0.0006	9.648±0.011
	2.067±0.005		44.309±0.004	0.997±0.0007	10.924±0.011
	2.086±0.006		46.844±0.014	0.998±0.0009	11.38±0.01
	2.094±0.004		48.76±0.01	0.998±0.0008	11.662±0.012
	2.073±0.013		49.176±0.009	0.999±0.0006	11.789±0.01
	2.081±0.009		47.145±0.011	0.999±0.0008	11.799±0.01
	2.078±0.008		48.098±0.011	0.999±0.0009	11.955±0.011
	2.082±0.008		47.537±0.012	1±0.001	11.953±0.009
	2.083±0.007		47.75±0.01	1±0.003	11.976±0.009
Adults	0.373±0.001	1.6±0.02	0.97±0.01	0.391±0.001	1.6±0.01
	0.709±0.002	16.883±0.01	0.994±0.004	3.464±0.003	9.1±0.07
	0.724±0.003	23.842±0.012	0.996±0.003	4.462±0.002	12.7±0.02
	0.723±0.003	23.01±0.01	0.997±0.002	5.929±0.005	15.3±0.04
	0.731±0.01	24.768±0.011	0.998±0.001	6.355±0.005	16.4±0.08
	0.746±0.013	28.73±0.01	0.998±0.001	7.444±0.004	20.6±0.07
	0.737±0.01	30.32±0.01	0.998±0.001	7.804±0.004	20.5±0.06
	0.737±0.011	32.829±0.011	0.998±0.001	8.216±0.006	22.1±0.08
	0.74±0.01	32.424±0.011	0.998±0.001	8.516±0.006	24.7±0.065
	0.741±0.011	39.875±0.012	0.999±0.0005	8.555±0.005	25.6±0.057
	0.736±0.007	39.86±0.01	0.999±0.0006	9.256±0.006	26.7±0.056

^aData represent average values from pooled populations (i.e from each sheep) of eggs/larvae/adults (male and female) come from three different sheep ± standard deviation (SD) (i.e. each cluster represents a sheep) ± standard deviation (SD)

Supplementary Table S4: Ovine abomasal microbiome composition at the genus level in the context of *Haemonchus* infection.

Genus	Control group ^a	7-day post-infection group ^a	50-day post-infection group ^a
<i>Achromobacter</i>	0	0.4862853±0.00103244	0
<i>Solobacterium</i>	0.2671057±0.000298942	0.6483818±0.001376589	0.3896459±0.000268505
<i>Desulfobulbus</i>	0	0.4862853±0.00103244	0.08646436±0.0000595825
<i>Delftia</i>	0	0.2161007±0.000458807	0
<i>Clostridium_sensu_stricto_1</i>	0	0.1080504±0.000229403	0
<i>Chryseobacterium</i>	0	8.266853±0.01755148	0
<i>Lysinimonas</i>	0	0.1080504±0.000229403	0
<i>Anaerotruncus</i>	1.468376±0.001643391	0.4322517±0.00091772	3.723269±0.0025657
<i>Kineococcus</i>	0	0.1080504±0.000229403	0
<i>Roseburia</i>	9.611181±0.01075673	5.673331±0.01204513	0.04323218±0.0000297912
<i>Flavonifractor</i>	70.748970±0.07918149	49.006770±0.104047	197.722900±0.1362506
<i>Oribacterium</i>	2.358299±0.002639383	3.187871±0.006768217	7.533127±0.005191069
<i>Ruminobacter</i>	6.095981±0.006822556	2.701586±0.005735777	3.420212±0.002356864
<i>Weissella</i>	0	3.187871±0.006768217	0.04323218±0.0000297912
<i>possible_genus_Sk003-Sk004</i>	0	0.1080504±0.000229403	0
<i>Mogibacterium</i>	6.985904±0.007818549	2.107238±0.004473908	5.931254±0.00408722
<i>Acetitomaculum</i>	2.936749±0.003286778	2.647552±0.005621058	11.819220±0.008144608
<i>Moryella</i>	2.002330±0.002240986	9.671676±0.02053408	20.910920±0.01440969
<i>Mucilaginibacter</i>	0	0.1080504±0.000229403	0
<i>Modestobacter</i>	0	0.1080504±0.000229403	0
<i>Myroides</i>	0.0444619±0.0000497613	0.3241511±0.00068821	0
<i>Syntrophomonas</i>	0.1333857±0.000149284	0	0.08646436±0.0000595825
<i>Sanguibacter</i>	0	0.3241511±0.00068821	0
<i>Bosea</i>	0	0.3781763±0.000802912	0
<i>Howardella</i>	0.4449633±0.000497998	0.1080504±0.000229403	0.5628193±0.000387838
<i>Clostridiales_bacterium_canine_ora_l_taxon_162</i>	0.1333857±0.000149284	0.05402518±0.000114702	0
<i>Butyrivibrio</i>	35.285490±0.03949115	151.775100±0.322236	77.928890±0.0537007
<i>Comamonas</i>	0.0444619±0.0000497613	19.451420±0.0412976	0
<i>Methylobacterium</i>	0	0.4862853±0.00103244	0
<i>Pseudoramibacter</i>	0	0.1620755±0.000344105	0
<i>Patulibacter</i>	0	0.7024111±0.0014913	0
<i>Brevibacillus</i>	0.0444619±0.0000497613	0.05402518±0.000114702	0
<i>Janthinobacterium</i>	0	0.7564447±0.001606019	0
<i>Campylobacter</i>	0.0889238±0.0000995226	0.3241511±0.00068821	0.04323218±0.0000297912
<i>Solibacillus</i>	0	0	0.2597282±0.000178978
<i>Wohlfahrtiimonas</i>	0.1778476±0.000199045	0	0.1300317±0.0000896047
<i>Stenotrophomonas</i>	0	6.807998±0.01445416	0.08646436±0.0000595825
<i>U29-B03</i>	2.091321±0.002340584	0.810474±0.00172073	11.646040±0.008025272
<i>Olsenella</i>	0	0.3781763±0.000802912	0.5628193±0.000387838
<i>Rhizobium</i>	0	5.295109±0.01124213	0
<i>Paenibacillus</i>	0.3559693±0.000398397	0.5943482±0.00126187	0.3463501±0.000238669
<i>Psychrobacter</i>	0	0.1080504±0.000229403	0
<i>Actinobaculum</i>	0.0444619±0.0000497613	0.2161007±0.000458807	0.04323218±0.0000297912
<i>Paraprevotella</i>	0.2671057±0.000298942	1.242730±0.002638459	0.2597282±0.000178978

<i>Gluconobacter</i>	0	0.2701259±0.000573508	0
<i>Bacillus</i>	0.4894587±0.000547797	1.945141±0.004129758	0.6494077±0.000447506
<i>Fibrobacter</i>	93.264050±0.1043801	18.208690±0.03865914	38.271740±0.02637301
<i>Candidatus_Captivus</i>	0.0444619±0.0000497613	0.05402518±0.000114702	0
<i>Candidatus_Saccharimonas</i>	11.391030±0.01274872	11.076500±0.02351669	7.013600±0.004833064
<i>Empedobacter</i>	0	9.887806±0.02099295	0
<i>Saccharofermentans</i>	21.224690±0.02375445	21.504620±0.04565679	34.894820±0.02404598
<i>Serratia</i>	0	0.7024111±0.0014913	0
<i>Kandleria</i>	0	27.880370±0.05919323	0
<i>Bordetella</i>	0	0.1080504±0.000229403	0
<i>Duganella</i>	0	0.2161007±0.000458807	0
<i>Citrobacter</i>	0.0444619±0.0000497613	14.210340±0.0301702	0
<i>Oscillibacter</i>	2.135819±0.002390386	5.511234±0.01170099	1.342108±0.000924845
<i>Megasphaera</i>	0	2.809649±0.005965207	0
<i>RC9_gut_group</i>	216.429600±0.2422256	93.691000±0.1989168	112.260900±0.07735885
<i>Victivallis</i>	11.702500±0.01309732	14.480500±0.03074377	0.5628193±0.000387838
<i>Sphingobium</i>	0	0.4862853±0.00103244	0
<i>dgA-11_gut_group</i>	0.0889238±0.0000995226	0	0
<i>Bifidobacterium</i>	0.6674433±0.000746995	0.1620755±0.000344105	0.04323218±0.0000297912
<i>Enterorhabdus</i>	4.983574±0.005577563	3.025774±0.006424067	4.156208±0.002864038
<i>Lactococcus</i>	0.0444619±0.0000497613	7.240250±0.01537188	0
<i>Hafnia</i>	0	0.3241511±0.00068821	0
<i>Ethanoligenens</i>	0.2671057±0.000298942	0	0
<i>Enterobacter</i>	0	9.023298±0.0191575	0
<i>Prevotella</i>	1288.966000±1.442597	2320.122000±4.925886	1415.318000±0.9752943
<i>Selenomonas</i>	1.201397±0.001344591	2.431426±0.005162198	9.178292±0.00632475
<i>Intestinimonas</i>	2.224810±0.002489983	1.404826±0.002982608	4.978789±0.003430877
<i>Succinibacter</i>	43.294810±0.04845509	39.010900±0.08282463	128.885700±0.088815
<i>Sharpea</i>	0	47.493880±0.100835	0.3029604±0.00020877
<i>Succinivibrio</i>	15.707160±0.01757929	27.069890±0.05747249	80.223460±0.05528189
<i>Arcobacter</i>	0	0.3781763±0.000802912	0
<i>SP3-e08</i>	0.9789173±0.001095594	0	0.08646436±0.0000595825
<i>Iamia</i>	0	0.1620755±0.000344105	0
<i>Solirubrobacter</i>	0	0.2161007±0.000458807	0
<i>Ochrobactrum</i>	0.0444619±0.0000497613	0.6483818±0.001376589	0.04323218±0.0000297912
<i>Pyramidobacter</i>	0.4894587±0.000547797	6.753964±0.01433944	6.407485±0.00441539
<i>Bacteroides</i>	15.707160±0.01757929	3.133842±0.006653506	40.652900±0.02801387
<i>Jatrophihabitans</i>	0	0.1080504±0.000229403	0
<i>Delta proteobacteria_bacterium_cani_ne_oral_taxon_266</i>	0	0.1080504±0.000229403	0
<i>Arthrobacter</i>	0	0.9185412±0.001950169	0.04323218±0.0000297912
<i>Treponema</i>	34.573550±0.03869435	33.661760±0.07146779	29.786150±0.0205256
<i>Alloprevotella</i>	1.201397±0.001344591	3.728190±0.007915376	0.3896459±0.000268505
<i>Microvirga</i>	0	0.1080504±0.000229403	0
<i>Sphingomonas</i>	0	7.240250±0.01537188	0
<i>Anaerovorax</i>	7.697843±0.008615343	3.512060±0.007456507	4.719027±0.003251876
<i>Elusimicrobium</i>	6.896913±0.007718951	11.184570±0.02374612	2.943981±0.002028694
<i>Mitsuokella</i>	0.1778476±0.000199045	0.2161007±0.000458807	2.814100±0.001939193
<i>Staphylococcus</i>	0.1333857±0.000149284	0	0.000000000000000

<i>Schwartzia</i>	$0.1333857 \pm 0.000149284$	0	3.117154 ± 0.002148027
<i>Mesorhizobium</i>	0	$0.3781763 \pm 0.000802912$	0
<i>Nocardiooides</i>	0	0.3241511 ± 0.00068821	0
<i>Aeromonas</i>	0	$0.9185412 \pm 0.001950169$	0
<i>Xanthomonas</i>	0	$0.7564447 \pm 0.001606019$	0
<i>Pseudobutyrivibrio</i>	15.484680 ± 0.01733029	12.157140 ± 0.025811	4.632439 ± 0.003192208
<i>Christensenella</i>	$0.8009326 \pm 0.000896395$	$0.2161007 \pm 0.000458807$	0.4762309 ± 0.00032817
<i>Actinotalea</i>	0	$0.1080504 \pm 0.000229403$	0
<i>Methanobrevibacter</i>	$0.2226438 \pm 0.000249181$	0	0
<i>Escherichia-Shigella</i>	0.000000000000000	0.1080504 ± 0.000229403	0
<i>Marvinbryantia</i>	2.135819 ± 0.002390386	$0.2701259 \pm 0.000573508$	6.017842 ± 0.004146888
<i>Anaerofustis</i>	$0.3115676 \pm 0.000348703$		$0.1300317 \pm 0.0000896047$
<i>probable_genus_10</i>	7.831332 ± 0.008764743	3.620127 ± 0.007685946	$0.9091694 \pm 0.000626508$
<i>Coprococcus</i>	1.957835 ± 0.002191188	$0.9185412 \pm 0.001950169$	5.887961 ± 0.004057387
<i>Deinococcus</i>	0	$0.1080504 \pm 0.000229403$	0
<i>Pseudomonas</i>	$0.2226438 \pm 0.000249181$	13.129710 ± 0.02787588	$0.08646436 \pm 0.0000595825$
<i>Papillibacter</i>	10.812580 ± 0.01210132	$0.1620755 \pm 0.000344105$	$0.3896459 \pm 0.000268505$
<i>Cellulomonas</i>	0	$0.1080504 \pm 0.000229403$	0
<i>Lapillicoccus</i>	0	$0.1620755 \pm 0.000344105$	0
<i>Defluviumonas</i>	0	$0.1620755 \pm 0.000344105$	0
<i>Streptococcus</i>	1.201397 ± 0.001344591	$0.1620755 \pm 0.000344105$	$0.1732638 \pm 0.000119396$
<i>Roseomonas</i>	0	$0.1080504 \pm 0.000229403$	0
<i>Ruminococcus</i>	107.324800 ± 0.1201168	67.269490 ± 0.1428209	96.069000 ± 0.06620103
<i>Denitrobacterium</i>	$0.1333857 \pm 0.000149284$	0	0
<i>Succinimonas</i>	$0.3115676 \pm 0.000348703$	0	$0.04323218 \pm 0.0000297912$
<i>Candidatus_Hepatincola</i>	$0.2671057 \pm 0.000298942$	0	$0.1732638 \pm 0.000119396$
<i>Nitrobacter</i>	0	$0.3781763 \pm 0.000802912$	0
<i>Variovorax</i>	0	0.4322517 ± 0.00091772	0
<i>Atopobium</i>	$0.8009326 \pm 0.000896395$	5.295109 ± 0.01124213	11.386280 ± 0.00784627
<i>Phocaeicola</i>	$0.3115676 \pm 0.000348703$	3.187871 ± 0.006768217	3.420212 ± 0.002356864
<i>Fretibacterium</i>	$0.3115676 \pm 0.000348703$	2.269334 ± 0.004818057	0.3029604 ± 0.00020877
<i>Quinella</i>	0	0	$0.2597282 \pm 0.000178978$
<i>Enhydrobacter</i>	0	1.674982 ± 0.003556179	0
<i>Stomatobaculum</i>	$0.2226438 \pm 0.000249181$	$0.3781763 \pm 0.000802912$	0
<i>Kocuria</i>	0	$0.1620755 \pm 0.000344105$	0
<i>Anaeroplasma</i>	24.917880 ± 0.02788782	4.484634 ± 0.009521395	$0.08646436 \pm 0.0000595825$
<i>Leuconostoc</i>	0	8.861202 ± 0.01881335	0
<i>Kurthia</i>	$0.0444619 \pm 0.0000497613$	$0.1080504 \pm 0.000229403$	0
<i>Soonwooa</i>	0	$0.2701259 \pm 0.000573508$	0
<i>Massilia</i>	0	$0.1620755 \pm 0.000344105$	0
<i>Oscillospira</i>	0	$0.3781763 \pm 0.000802912$	$0.5195268 \pm 0.000358005$
<i>Brevundimonas</i>	0	1.242730 ± 0.002638459	0
<i>Pedobacter</i>	0	$0.3781763 \pm 0.000802912$	0
<i>Sporobacter</i>	$0.3115676 \pm 0.000348703$	$0.1080504 \pm 0.000229403$	$0.2597282 \pm 0.000178978$
<i>Thalassospira</i>	5.829002 ± 0.006523757	11.346660 ± 0.02409027	1.731754 ± 0.001193349
<i>Acinetobacter</i>	$0.2671057 \pm 0.000298942$	54.193820 ± 0.1150597	1.125639 ± 0.000775676
<i>SRI_bacterium_canine_oral_taxon_380</i>	0	$0.6483818 \pm 0.001376589$	0
<i>AlysIELLA</i>	0	0	$0.08646436 \pm 0.0000595825$

<i>Lactobacillus</i>	0	7.726535±0.01640432	0.04323218±0.0000297912
<i>Shuttleworthia</i>	1.067908±0.001195191	0.1620755±0.000344105	15.585780±0.01074014
<i>Possible_genus_Sk018</i>	1.201397±0.001344591	1.026604±0.002179599	0
<i>Pantoea</i>	0	0.5943482±0.00126187	0
<i>Devosia</i>	0	0.6483818±0.001376589	0
<i>Curtobacterium</i>	0	2.701586±0.005735777	0
<i>Alkaliphilus</i>	0.0444619±0.0000497613	0.1080504±0.000229403	0.04323218±0.0000297912
<i>Collinsella</i>	0	0	0.08646436±0.0000595825
<i>Catonella</i>	0.1333857±0.000149284	0.2161007±0.000458807	1.298815±0.000895012
<i>Enterococcus</i>	0.1333857±0.000149284	1.945141±0.004129758	0.1732638±0.000119396
<i>Sphingobacterium</i>	0.0444619±0.0000497613	4.916886±0.01043911	0
<i>Aeromicrobium</i>	0	1.134667±0.002409029	0
<i>Anaerosporobacter</i>	0.1333857±0.000149284	0	5.541608±0.003818716
<i>Lachnospira</i>	0	0.1080504±0.000229403	0
<i>Desulfovibrio</i>	0.4004647±0.000448196	4.484634±0.009521395	6.494073±0.004475058
<i>Aeriscardovia</i>	0.1333857±0.000149284	0.6483818±0.001376589	0.6927001±0.000477339
<i>Wautersiella</i>	0	14.642600±0.03108792	0
<i>Hydrogenoanaerobacterium</i>	0.0444619±0.0000497613	0	0.1732638±0.000119396
<i>Spirochaeta</i>	1.112407±0.001244994	0.5943482±0.00126187	0.04323218±0.0000297912
<i>Vagococcus</i>	0	0.1620755±0.000344105	0
<i>Syntrophococcus</i>	3.515201±0.003934176	3.674156±0.007800657	6.753839±0.004654062
<i>Incertae_Sedis</i>	29.100520±0.03256899	30.473890±0.06469957	58.836310±0.04054403
<i>Acetobacter</i>	0	1.188696±0.002523739	0
<i>Anaerovibrio</i>	0.2671057±0.000298942	1.242730±0.002638459	5.455023±0.00375905
<i>Blautia</i>	7.475362±0.008366346	8.428950±0.01789563	4.502558±0.003102707

^aEach value is an average of three samples collected from three experimentally *H. contortus*-infected sheep (i.e. each sample represents a sheep) ± standard deviation (SD)

Supplementary Table S5: Ovine ruminal microbiome composition at the genus level in the context of *Haemonchus* infection.

Genus	Control group ^a	7-day post-infection group ^a	50-day post-infection group ^a
<i>Leuconostoc</i>	0	5.350628±0.03108216	0
<i>Denitrobacterium</i>	0.4538265±0.003355203	0	0
<i>Wohlfahrtiimonas</i>	0.2475418±0.001830111	0	0
<i>Bacteroides</i>	15.182560±0.1122468	0.5827417±0.003385186	1.778635±0.01738169
<i>Megasphaera</i>	0	0.3178591±0.001846465	0
<i>Lachnospira</i>	0	0.4238122±0.002461953	0.03176134±0.000310387
<i>Pseudobutyribrio</i>	40.514330±0.2995281	17.164390±0.09970912	5.113575±0.04997235
<i>Pyramidobacter</i>	0	0.9535774±0.005539395	0.285852±0.002793485
<i>Spirochaeta</i>	0.1650278±0.001220074	0.4238122±0.002461953	0.06352267±0.000620775
<i>Atopobium</i>	0.7838822±0.005795351	0.6357182±0.00369293	0.190568±0.001862324
<i>Elusimicrobium</i>	3.176786±0.02348642	0.105953±0.000615488	0.1270453±0.001241549
<i>Brevundimonas</i>	0	0.3708356±0.002154209	0
<i>Succinivibrio</i>	41.504500±0.3068486	5.138722±0.02985119	408.450800±3.991580
<i>Solobacterium</i>	0	0.4767887±0.002769698	0
<i>Sphingobium</i>	0	0.2648826±0.001538721	0
<i>Victivallis</i>	3.671869±0.02714664	16.104860±0.09355423	0.06352267±0.000620775
<i>Stenotrophomonas</i>	0	1.854178±0.01077105	0
<i>U29-B03</i>	1.155195±0.008540517	0.3708356±0.002154209	4.097213±0.04003996
<i>Pseudomonas</i>	0.2062848±0.001525092	1.748225±0.01015556	0
<i>Treponema</i>	43.484830±0.3214895	28.236480±0.1640276	38.304170±0.374327
<i>Wautersiella</i>	0.04125696±0.000305018	1.695249±0.009847814	0
<i>Paracoccus</i>	0	0.105953±0.000615488	0
<i>Candidatus_Saccharimonas</i>	19.885850±0.1470189	10.330420±0.06001012	1.111647±0.01086355
<i>Chryseobacterium</i>	0	0.5297652±0.003077442	0
<i>Papillibacter</i>	1.155195±0.008540517	1.695249±0.009847814	0
<i>Ruminobacter</i>	0	0	6.225222±0.0608359
<i>Acinetobacter</i>	0.2887987±0.002135129	12.555440±0.07293537	0
<i>Ochrobactrum</i>	0	0.1589296±0.000923233	0
<i>Oribacterium</i>	2.640445±0.01952118	7.204807±0.04185321	3.684315±0.03600492
<i>Klebsiella</i>	0	1.801202±0.0104633	0
<i>Microvirga</i>	0	0.105953±0.000615488	0
<i>Arthrobacter</i>	0	0.105953±0.000615488	0
<i>Enterorhabdus</i>	4.208210±0.03111188	11.813760±0.06862696	0.7305108±0.007138907
<i>RC9_gut_group</i>	188.503100±1.393629	56.049160±0.3255934	15.404250±0.1505378
<i>Succinilasticum</i>	60.317670±0.445937	34.752600±0.2018802	10.195390±0.09963431
<i>probable_genus_10</i>	5.280891±0.03904236	2.330967±0.01354074	0.09528401±0.000931162
<i>Photorhabdus</i>	0	0	0.1270453±0.001241549
<i>Marvinbryantia</i>	0.04125696±0.000305018	0.05297652±0.000307744	0
<i>Syntrophococcus</i>	0.990167±0.007320443	4.026216±0.02338856	0.2223294±0.002172711
<i>Sphingomonas</i>	0	2.119061±0.01230977	0

<i>Thalassospira</i>	0.6188544±0.004575277	1.059530±0.006154884	0.190568±0.001862324
<i>Empedobacter</i>	0	1.112507±0.006462628	0
<i>Desulfovibrio</i>	0.8663961±0.006405388	3.549427±0.02061886	1.619828±0.01582975
<i>Paenibacillus</i>	0.1650278±0.001220074	0.105953±0.000615488	0
<i>Incertae_Sedis</i>	12.995940±0.09608082	21.296560±0.1237132	3.684315±0.03600492
<i>Oscillibacter</i>	0.04125696±0.000305018	0.3178591±0.001846465	0.06352267±0.000620775
<i>Streptococcus</i>	2.021591±0.0149459	0.4238122±0.002461953	0
<i>Selenomonas</i>	10.561780±0.07808473	8.582196±0.04985456	24.487990±0.2393086
<i>Gluconobacter</i>	0	0.105953±0.000615488	0
<i>Bacillus</i>	0.4538265±0.003355203	0.2648826±0.001538721	0.03176134±0.000310387
<i>Enterococcus</i>	0.08251392±0.000610037	0.8476243±0.004923907	
<i>Succinimonas</i>	0	0	0.09528401±0.000931162
<i>Methylobacterium</i>	0	0.2119061±0.001230977	0
<i>Devsia</i>	0	1.112507±0.006462628	0
<i>Variovorax</i>	0	0.105953±0.000615488	0
<i>Pseudoxanthomonas</i>	0.08251392±0.000610037	0.105953±0.000615488	0
<i>Sphingobacterium</i>	0	0.9006009±0.005231651	0
<i>Blvii28_wastewater-sludge_group</i>	0.04125696±0.000305018	0	0.03176134±0.000310387
<i>possible_genus_Sk018</i>	0.6601114±0.004880295	2.489897±0.01446398	0.03176134±0.000310387
<i>Alloprevotella</i>	2.145362±0.01586096	0	0.1588067±0.001551936
<i>Schwartzia</i>	0.9489101±0.007015425	0	1.111647±0.01086355
<i>Enhydrobacter</i>	0	0.3708356±0.002154209	0
<i>Campylobacter</i>	0.2475418±0.001830111	0.05297652±0.000307744	0.06352267±0.000620775
<i>Anaerobiospirillum</i>	0.1237709±0.000915055	0	0.2223294±0.002172711
<i>Roseburia</i>	9.489100±0.07015425	3.072638±0.01784916	0
<i>Faecalibacterium</i>	0	0	0.1588067±0.001551936
<i>Intestinimonas</i>	0.2887987±0.002135129	6.516112±0.03785253	0.2223294±0.002172711
<i>Anaeroplasma</i>	2.062848±0.01525092	4.079192±0.0236963	0.03176134±0.000310387
<i>Comamonas</i>	0.08251392±0.000610037	2.225014±0.01292526	0
<i>Rhizobium</i>	0	0.4238122±0.002461953	0
<i>Anaerotruncus</i>	0.2062848±0.001525092	0.2119061±0.001230977	0
<i>Methanobrevibacter</i>	0.7013683±0.005185314	0	0.03176134±0.000310387
<i>Anaerovibrio</i>	3.094272±0.02287639	3.337521±0.01938788	7.559198±0.07387216
<i>Mogibacterium</i>	3.960668±0.02928177	1.589296±0.009232325	0.3811361±0.003724647
<i>Hafnia</i>	0	0.105953±0.000615488	0
<i>Weissella</i>	0	3.496450±0.02031112	0
<i>Acetitomaculum</i>	0.6188544±0.004575277	6.357183±0.0369293	0.285852±0.002793485
<i>Rhodopseudomonas</i>	0	0.105953±0.000615488	0
<i>Kandleria</i>	0	0.2648826±0.001538721	0
<i>Desulfobulbus</i>	0.08251392±0.000610037	0.3178591±0.001846465	0.1588067±0.001551936
<i>Butyrivibrio</i>	31.644090±0.2339492	101.609000±0.5902534	10.640050±0.1039797
<i>Saccharofermentans</i>	8.994017±0.06649403	21.296560±0.1237132	2.159771±0.02110633
<i>hoa5-07d05_gut_group</i>	0.08251392±0.000610037	0	0
<i>Enterobacter</i>	0	6.833971±0.039699	0

<i>Blautia</i>	2.929244 ± 0.02165631	17.111420 ± 0.09940137	$0.6669881 \pm 0.006518132$
<i>Bosea</i>	0	0.105953 ± 0.000615488	0
<i>Paraprevotella</i>	$0.04125696 \pm 0.000305018$	$0.9006009 \pm 0.005231651$	$0.1270453 \pm 0.001241549$
<i>Fretibacterium</i>	$0.7838822 \pm 0.005795351$	2.330967 ± 0.01354074	$0.2540907 \pm 0.002483098$
<i>Olsenella</i>	0	$0.1589296 \pm 0.000923233$	0
<i>Ruminococcus</i>	60.400190 ± 0.446547	74.537960 ± 0.4329961	22.201180 ± 0.2169607
<i>Curtobacterium</i>	0	$0.3178591 \pm 0.001846465$	0
<i>Lactobacillus</i>	0	7.204807 ± 0.04185321	0
<i>Alkaliphilus</i>	0	$0.05297652 \pm 0.000307744$	$0.03176134 \pm 0.000310387$
<i>Fibrobacter</i>	31.520320 ± 0.2330341	5.297652 ± 0.03077442	11.211750 ± 0.1095667
<i>Mesorhizobium</i>	0	0.105953 ± 0.000615488	0
<i>Anaerovorax</i>	$0.7013683 \pm 0.005185314$	1.907155 ± 0.01107879	$0.4128974 \pm 0.004035034$
<i>Flavonifractor</i>	3.176786 ± 0.02348642	5.456582 ± 0.03169765	4.573633 ± 0.04469576
<i>Lactococcus</i>	0	6.675042 ± 0.03877577	0
<i>Prevotella</i>	$2024.685000 \pm 14.968780$	1098.574000 ± 6.381691	$1833.995000 \pm 17.922690$
<i>Aeromicrobium</i>	0	$0.4238122 \pm 0.002461953$	0
<i>Moryella</i>	0	$0.1589296 \pm 0.000923233$	$0.1270453 \pm 0.001241549$
<i>Subdoligranulum</i>	0	0	$0.06352267 \pm 0.000620775$
<i>Howardella</i>	2.516675 ± 0.01860613	3.496450 ± 0.02031112	$0.4764201 \pm 0.004655809$
<i>Coprococcus</i>	$0.04125696 \pm 0.000305018$	$0.2119061 \pm 0.001230977$	$0.03176134 \pm 0.000310387$
<i>Shuttleworthia</i>	$0.4538265 \pm 0.003355203$	$0.3708356 \pm 0.002154209$	2.255055 ± 0.02203749
<i>Veillonella</i>	0	0	$0.06352267 \pm 0.000620775$
<i>Candidatus Hepatincola</i>	$0.2475418 \pm 0.001830111$	0	$0.03176134 \pm 0.000310387$
<i>SRI_bacterium_canine_oral_taxon_380</i>	0	$0.2648826 \pm 0.001538721$	0
<i>Quinella</i>	0	0	0.3493747 ± 0.00341426

^aEach value is an average of three samples collected from three experimentally *H. contortus*-infected sheep (i.e. each sample represents a sheep) ± standard deviation (SD)

Supplementary Table S6: An average composition of significantly different microbial taxa associated with *H. contortus* eggs, larvae and adults using 16S rRNA gene (V3-V4 region). *P*-values were calculated using Kruskal-Wallis test. The level of significance was determined at *P* < 0.05.

Phylum									
V3-V4 region	Eggs	Larvae	Adults	Eggs vs adults		Eggs vs larvae		Larvae vs adults	
	Median, IQR ^a	Median, IQR ^a	Median, IQR ^a	Chi-square	<i>p</i> -value	Chi-square	<i>p</i> -value	Chi-square	<i>p</i> -value
Planctomycetes	0	0.3256886, 0.00233	0	4.3548	0.0369	0	0	4.3548	0.0369
Elusimicrobia	0	0.1184322, 0.000847	0	4.3548	0.0369	0	0	4.3548	0.0369
Candidate_	0	0.1776483, 0.0012712	0	4.3548	0.0369	0	0	4.3548	0.0369
Firmicutes	0.607866, 0.00738	22.679767, 0.162288	0.153335, 0.0023912	3.8571	0.0495	3.8571	0.0495	3.8571	0.0495
Bacteroidetes	0.11323, 0.001375	6.0400424, 0.04322	0	3.8571	0.0495	4.3548	0.0369	4.3548	0.0369
Tenericutes	0	0	0.0537668, 0.0008384	0	0	4.3548	0.0369	4.3548	0.0369
Acidobacteria	0	0.4441208, 0.003178	0	4.3548	0.0369	0	0	4.3548	0.0369
Spirochaetae	0	0.2960805, 0.0021186	0	4.3548	0.0369	0	0	4.3548	0.0369
Proteobacteria	36.08457, 0.43828	66.23321, 0.47394	40.639736, 0.633758	3.8571	0.0495	3.8571	0.0495	3.8571	0.0495
Actinobacteria	0.119189, 0.001448	0	0.0358445, 0.000559	4.3548	0.0369	3.8571	0.0495	4.3548	0.0369

Class									
V3-V4 region	Eggs	Larvae	Adults	Eggs vs adults		Eggs vs larvae		Larvae vs adults	
	Median, IQR ^a	Median, IQR ^a	Median, IQR ^a	Chi-square	<i>p</i> -value	Chi-square	<i>p</i> -value	Chi-square	<i>p</i> -value
OM190	0	0.32568856, 0.00233	0	4.3548	0.0369	0	0	4.3548	0.0369
Acidobacteria	0	0.44412076, 0.00317796	0	4.3548	0.0369	0	0	4.3548	0.0369
Bacilli	0.238379, 0.002896	22.6797669, 0.1622882	0.047793, 0.0007453	3.8571	0.0495	3.8571	0.0495	3.8571	0.0495
Elusimicrobia	0	0.1184322, 0.00084746	0	4.3548	0.0369	0	0	4.3548	0.0369
Sphingobacteriia	0	4.02669492, 0.02881356	0	4.3548	0.0369	0	0	4.3548	0.0369
Deltaproteobacteria	0	0.29608051, 0.0021186	0	4.3548	0.0369	0	0	4.3548	0.0369
Coriobacteriia	0.047676, 0.000579	0	0.005974, 0.000093164	4.3548	0.0369	3.8571	0.0495	4.3548	0.0369
Spirochaetes	0	0.29608051, 0.0021186	0	4.3548	0.0369	0	0	4.3548	0.0369
Gammaproteobacteri a	28.64119, 0.34787	13.0571504, 0.0934322	38.50898, 0.60052987	3.8571	0.0495	3.8571	0.0495	3.8571	0.0495
Clostridia	0.369487, 0.004488	0	0.105542, 0.00164588	4.3548	0.0369	3.8571	0.0495	4.3548	0.0369
Flavobacteriia	0	0.65137712, 0.004661	0	4.3548	0.0369	0	0	4.3548	0.0369
Actinobacteria	0.071514, 0.000868	0	0.02987, 0.000465816	4.3548	0.0369	3.8571	0.0495	4.3548	0.0369
Betaproteobacteria	0.148987, 0.00181	44.5601165, 0.318856	0.04381, 0.0006832	3.8571	0.0495	3.8571	0.0495	3.8571	0.0495
Cytophagia	0	1.30275424, 0.009322	0	4.3548	0.0369	0	0	4.3548	0.0369
Bacteroidia	0.11323, 0.001375	0	1.5	4.3548	0.0369	4.3548	0.0369	0	0
Alphaproteobacteria	7.294386, 0.088595	8.31986229, 0.0595339	2.086948, 0.032545	3.8571	0.0495	3.8571	0.0495	3.8571	0.0495
Mollicutes	0	0	0.053767, 0.000838469	0	0	4.3548	0.0369	4.3548	0.0369

Order									
V3-V4	Eggs	Larvae	Adults	Eggs vs adults		Eggs vs larvae		Larvae vs adults	
	Median, IQR ^a	Median, IQR ^a	Median, IQR ^a	Chi-square	p-value	Chi-square	p-value	Chi-square	p-value
Rhodocyclales	0 0.069068	9.6522246, 0	0	4.3548	0.0369	0 0	0	4.3548 0.0369	
Clostridiales	0.369487, 0.004488	0 0.001646	0.105542, 4.3548	0.0369		3.8571 0.0495		4.3548 0.0369	
Myxococcales	0 0.0021186	0.2960805, 0	4.3548	0.0369	0 0	0		4.3548 0.0369	
Sphingobacteriales	0 0.0288136	4.0266949, 0	4.3548	0.0369	0 0	0		4.3548 0.0369	
Coriobacteriales	0.047676, 0.000579	0 0.000093	0.005974, 4.3548	0.0369	3.8571 0.0495	0.0495		4.3548 0.0369	
Cytophagales	0 0.009322	1.3027542, 0	4.3548	0.0369	0 0	0		4.3548 0.0369	
Flavobacteriales	0 0.00466	0.6513771, 0	4.3548	0.0369	0 0	0		4.3548 0.0369	
Caulobacterales	0.005959, 0.000073	0.7994174, 0.0057204	0.001991, 0.000031	3.8571	0.0495	3.8571 0.0495		3.8571 0.0495	
Subgroup_17	0 0.0006356	0.0888242, 0	4.3548	0.0369	0 0	0		4.3548 0.0369	
Bifidobacteriales	0.071514, 0.000868	0 0.000466	0.02987, 4.3548	0.0369	3.8571 0.0495	0.0495		4.3548 0.0369	
Spirochaetales	0 0.0021186	0.2960805, 0	4.3548	0.0369	0 0	0		4.3548 0.0369	
Hydrogenophilales	0 0.0057204	0.7994174, 0	4.3548	0.0369	0 0	0		4.3548 0.0369	
Xanthomonadales	0.035757, 0.000435	4.7076801, 0.0336864	0.007965, 0.000124	3.8571	0.0495	3.8571 0.0495		3.8571 0.0495	
Alteromonadales	0 0.0012712	0.1776483, 0	4.3548	0.0369	0 0	0		4.3548 0.0369	
Bacillales	0.095351, 0.001158	20.873676, 0.149365	0.039827, 0.000622	3.8571	0.0495	3.8571 0.0495		3.8571 0.0495	
Enterobacteriales	4.23718, 0.051464	1.0954979, 0.007839	35.90029, 0.5598	3.8571	0.0495	3.8571 0.0495		3.8571 0.0495	
MVP-88	0 0.000847	0.1184322, 0	4.3548	0.0369	0 0	0		4.3548 0.0369	
Rhodospirillales	0 0.0019068	0.2664725, 0	4.3548	0.0369	0 0	0		4.3548 0.0369	
Sphingomonadales	0.005959, 0.000073	0.1184322, 0.000847	0 3.8571	0.0495	4.3548 0.0369	0.0369		4.3548 0.0369	
Mycoplasmatales	0 0	0.053767, 0.000838	0 0	0	4.3548 0.0369	0.0369		4.3548 0.0369	
Burkholderiales	0.148987, 0.00181	33.960434, 0.243009	0.04381, 0.000684	3.8571	0.0495	3.8571 0.0495		3.8571 0.0495	
Pseudomonadales	24.36826, 0.29597	6.9875, 0.05	2.598729, 0.040526	3.8571	0.0495	3.8571 0.0495		3.8571 0.0495	
SC-I-84	0 0.0006356	0.0888242, 0	4.3548	0.0369	0 0	0		4.3548 0.0369	
Subgroup_6	0 0.0025424	0.3552966, 0	4.3548	0.0369	0 0	0		4.3548 0.0369	
Neisseriales	0 0.0004238	0.0592161, 0	4.3548	0.0369	0 0	0		4.3548 0.0369	
Lactobacillales	0.143027, 0.001737	1.8060911, 0.0129238	0.007965, 0.000124	3.8571	0.0495	3.8571 0.0495		3.8571 0.0495	
Rhizobiales	7.282467, 0.088451	7.1355403, 0.0510594	2.084957, 0.032514	3.8571	0.0495	3.8571 0.0495		3.8571 0.0495	
Bacteroidales	0.11323, 0.001375	0 0	4.3548	0.0369	4.3548 0.0369	0.0369	0	0	0

Family									
V3-V4	Eggs	Larvae	Adults	Eggs vs adults		Eggs vs larvae		Larvae vs adults	
	Median, IQR ^a	Median, IQR ^a	Median, IQR ^a	Chi-square	p-value	Chi-square	p-value	Chi-square	p-value
Caulobacteraceae	0.005959, 0.000073	0.7994174, 0.00572	0	3.8571	0.0495	4.3548	0.0369	4.3548	0.0369
Flavobacteriaceae	0	0.4441208, 0.003178	0	4.3548	0.0369	0	0	4.3548	0.0369
Leptospiraceae	0	0.2960805, 0.002119	0	4.3548	0.0369	0	0	4.3548	0.0369
Cytophagaceae	0	1.3027542, 0.00932	0	4.3548	0.0369	0	0	4.3548	0.0369
Neisseriaceae	0	0.0592161, 0.0004238	0	4.3548	0.0369	0	0	4.3548	0.0369
Family XIII	0.017878, 0.000217	0	0	4.3548	0.0369	4.3548	0.0369	0	0
Carnobacteriaceae	0.131108, 0.001592	0.1480403, 0.001059	0	3.8571	0.0495	4.3548	0.0369	4.3548	0.0369
Chitinophagaceae	0	1.9837394, 0.014195	0	4.3548	0.0369	0	0	4.3548	0.0369
KD3-93	0	0.1480403, 0.001059	0	4.3548	0.0369	0	0	4.3548	0.0369
Prevotellaceae	0.11323, 0.001375	0	0	4.3548	0.0369	4.3548	0.0369	0	0
Enterobacteriaceae	4.23718, 0.051464	1.0954979, 0.007839	35.9, 0.56	3.8571	0.0495	3.8571	0.0495	3.8571	0.0495
Polyangiaceae	0	0.0888242, 0.0006356	0	4.3548	0.0369	0	0	4.3548	0.0369
Alcaligenaceae	0.089392, 0.001086	29.904131, 0.213984	0.04, 0	3.8571	0.0495	4.3548	0.0369	4.3548	0.0369
Rhizobiaceae	0	0.2960805, 0.0021186	0.01, 0	4.3548	0.0369	5	0.0253	4.3548	0.0369
Env.OPS_17	0	0.2664725, 0.0019068	0	4.3548	0.0369	0	0	4.3548	0.0369
Lactobacillaceae	0	1.0658898, 0.0076272	0	4.3548	0.0369	0	0	4.3548	0.0369
AKYH767	0	1.0362818, 0.0074152	0	4.3548	0.0369	0	0	4.3548	0.0369
Pseudomonadaceae	24.36826, 0.29597	6.5433792, 0.04682	2.6, 0.05	3.8571	0.0495	3.8571	0.0495	3.8571	0.0495
Mycoplasmataceae	0	0	0.05, 0	0	0	5	0.0253	5	0.0253
LiUU-11-161	0	0.0888242, 0.0006356	0	4.3548	0.0369	0	0	4.3548	0.0369
Bifidobacteriaceae	0.071514, 0.000868	0	0.03, 0	4.3548	0.0369	4.3548	0.0369	5	0.0253
Staphylococcaceae	0	0.3552966, 0.0025424	0	4.3548	0.0369	0	0	4.3548	0.0369
Oxalobacteraceae	0	0.1184322, 0.000847	0	4.3548	0.0369	0	0	4.3548	0.0369
Moraxellaceae	0	0.4441208, 0.003178	0	4.3548	0.0369	0	0	4.3548	0.0369
Hydrogenophilaceae	0	0.7994174, 0.00572	0	4.3548	0.0369	0	0	4.3548	0.0369
Rhodocyclaceae	0	9.6522246, 0.069068	0	4.3548	0.0369	0	0	4.3548	0.0369
Thermoactinomycetaceae	0.023838, 0.000289	4.5892479, 0.032839	0.02, 0	3.8571	0.0495	4.3548	0.0369	4.3548	0.0369
Bacillaceae	0.071514, 0.000868	15.929131, 0.113984	0.02, 0	3.8571	0.0495	4.3548	0.0369	4.3548	0.0369
Brucellaceae	7.276508, 0.088379	4.7076801, 0.033686	2.08, 0.03	3.8571	0.0495	3.8571	0.0495	3.8571	0.0495
NS9_marine_group	0	0.2072564, 0.001483	0	4.3548	0.0369	0	0	4.3548	0.0369
Leuconostocaceae	0.011919,	0.592161,	0	3.8571	0.0495	4.3548	0.0369	4.3548	0.0369

	0.0001	0.0042						
PHOS-HE51	0	0.0592161, 0.0004238	0	4.3548	0.0369	0	0	4.3548 0.0369
Saprospiraceae	0	0.4441208, 0.003178	0	4.3548	0.0369	0	0	4.3548 0.0369
Burkholderiaceae	0.059595, 0.000724	0.7105932, 0.0050848	0	3.8571	0.0495	4.3548	0.0369	4.3548 0.0369
Bradyrhizobiaceae	0	0.8290254, 0.0059322	0	4.3548	0.0369	0	0	4.3548 0.0369
Comamonadaceae	0	3.2272775, 0.02309	0	4.3548	0.0369	5	0.0253	4.3548 0.0369
Alteromonadaceae	0	0.1776483, 0.0012712	0	4.3548	0.0369	0	0	4.3548 0.0369
Xanthomonadaceae	0.035757, 0.000435	4.4412076, 0.0317796	0.01, 0	3.8571	0.0495	4.3548	0.0369	4.3548 0.0369
Ruminococcaceae	0.351608, 0.004271	0	0.11, 0.01	4.3548	0.0369	3.9706	0.0463	4.5 0.0339
Phyllobacteriaceae	0.005959, 0.000073	1.3027542, 0.009322	0	3.8571	0.0495	4.3548	0.0369	4.3548 0.0369
Sphingomonadaceae	0.005959, 0.000073	0.1184322, 0.000847	0	3.8571	0.0495	4.3548	0.0369	4.3548 0.0369
Rhodospirillaceae	0	0.2664725, 0.0019068	0	4.3548	0.0369	0	0	4.3548 0.0369
Coriobacteriaceae	0.047676, 0.000579	0	0.01, 0	4.3548	0.0369	4.3548	0.0369	5 0.0253

Genus									
V3-V4 region	Eggs	Larvae	Adults	Eggs vs adults		Eggs vs larvae		Larvae vs adults	
	Median, IQR ^a	Median, IQR ^a	Median, IQR ^a	Chi-square	p-value	Chi-square	p-value	Chi-square	p-value
<i>Brevundimonas</i>	0.005959, 0.000073	0.7994174, 0.0057203	0.00199, 0.00003	3.8571	0.0495	3.8571	0.0495	3.8571	0.0495
<i>Trichococcus</i>	0	0.1480403, 0.0010593	0	4.3548	0.0369	0	0	4.3548	0.0369
<i>Turneriella</i>	0	0.2960805, 0.0021186	0	4.3548	0.0369	0	0	4.3548	0.0369
<i>Aeriscardovia</i>	0.071514, 0.000868	0	0.0299, 0.0005	4.3548	0.0369	3.8571	0.0495	4.3548	0.0369
<i>Acinetobacter</i>	0	0.4441208, 0.003178	0	4.3548	0.0369	0	0	4.3548	0.0369
<i>Lentibacillus</i>	0.023838, 0.000289	9.4449682, 0.0675848	0.00797, 0.00013	3.8571	0.0495	3.8571	0.0495	3.8571	0.0495
<i>Ruminococcus</i>	0.172825, 0.002099	0	0.0378, 0.0006	4.3548	0.0369	3.8571	0.0495	4.3548	0.0369
<i>Ralstonia</i>	0.059595, 0.000724	0.6513771, 0.004661	0	3.8571	0.0495	4.3548	0.0369	4.3548	0.0369
<i>Sphingopyxis</i>	0.005959, 0.000073	0.1184322, 0.0008475	0	3.8571	0.0495	4.3548	0.0369	4.3548	0.0369
<i>Dechloromonas</i>	0	1.0362818, 0.0074153	0	4.3548	0.0369	0	0	4.3548	0.0369
<i>Kroppenstedtia</i>	0.023838, 0.000289	4.5892479, 0.032839	0.0219, 0.0003	3.8571	0.0495	3.8571	0.0495	3.8571	0.0495
<i>Atopobium</i>	0.047676, 0.000579	0	0.00597, 0.00009	4.3548	0.0369	3.8571	0.0495	4.3548	0.0369
<i>Flavobacterium</i>	0	0.4441208, 0.003178	0	4.3548	0.0369	0	0	4.3548	0.0369
<i>Leuconostoc</i>	0.005959, 0.000073	0.2072564, 0.001483	0.00398, 0.00006	3.8571	0.0495	3.8571	0.0495	3.8571	0.0495
<i>Sorangium</i>	0	0.0888242, 0.0006	0	4.3548	0.0369	0	0	4.3548	0.0369
<i>Atopostipes</i>	0.131108, 0.001592	0	0	4.3548	0.0369	4.3548	0.0369	0	0
<i>Piscinibacter</i>	0	0.1480403, 0.001059	0	4.3548	0.0369	0	0	4.3548	0.0369
<i>Flavonifractor</i>	0.005959, 0.000073	0	0.00597, 0.00009	4.3548	0.0369	0.4286	0.5127	4.3548	0.0369
<i>Zoogloea</i>	0	0.7402013, 0.0052966	0	4.3548	0.0369	0	0	4.3548	0.0369
<i>Weissella</i>	0.005959, 0.000073	0.3849047, 0.0027542	0	3.8571	0.0495	4.3548	0.0369	4.3548	0.0369
<i>Herbaspirillum</i>	0	0.1184322, 0.0008475	0	4.3548	0.0369	0	0	4.3548	0.0369
<i>Rhizobium</i>	0	0.2960805, 0.0021186	0	4.3548	0.0369	4.3548	0.0369	3.8571	0.0495
<i>Pediococcus</i>	0	0.1184322, 0.0008475	0	4.3548	0.0369	0	0	4.3548	0.0369
<i>Luteibacter</i>	0.011919, 0.000145	0.0592161, 0.0004237	0.00398, 0.00006	3.8571	0.0495	3.8571	0.0495	3.8571	0.0495
<i>Achromobacter</i>	0.089392, 0.001086	29.815307, 0.2133475	0.0378, 0.0006	3.8571	0.0495	3.8571	0.0495	3.8571	0.0495
<i>Thermomonas</i>	0	0.2960805, 0.0021186	0	4.3548	0.0369	0	0	4.3548	0.0369
<i>Azotobacter</i>	2.294394, 0.027867	1.3027542, 0.009322	0.175, 0.002	3.8571	0.0495	3.8571	0.0495	3.8571	0.0495
<i>Intestinimonas</i>	0.005959, 0.000073	0	0.00199, 0.00003	4.3548	0.0369	3.8571	0.0495	4.3548	0.0369
<i>Thauera</i>	0	0.6513771, 0.00466	0	4.3548	0.0369	0	0	4.3548	0.0369
<i>Escherichia-</i>	4.23718,	1.0954979,	35.9,	3.8571	0.0495	3.8571	0.0495	3.8571	0.0495

<i>Shigella</i>	0.051464	0.00784	0.5						
<i>Delftia</i>	0	2.2798199,	0.00597,						
		0.0163	0.00009	4.3548	0.0369	4.3548	0.0369	3.8571	0.0495
<i>Prevotella</i>	0.083433,	0		4.3548	0.0369	4.3548	0.0369	0	0
	0.001013		0						
<i>Mycoplasma</i>	0	0	0.0538,		0	0	4.3548	0.0369	4.3548
			0.0008						
<i>Azospirillum</i>	0	0.2664725,			4.3548	0.0369	0		4.3548
		0.0019	0						
<i>Lautropia</i>	0	0.0592161,			4.3548	0.0369	0		4.3548
		0.0004237	0						
<i>Ferruginibacter</i>	0	0.4441208,			4.3548	0.0369	0		4.3548
		0.003178	0						
<i>Dokdonella</i>	0.011919,	3.3161017,			3.8571	0.0495	4.3548	0.0369	4.3548
	0.000145	0.0237288	0						
<i>Oceanobacillus</i>	0	1.6876589,			4.3548	0.0369	0		4.3548
		0.012076	0						
<i>BDI-7_clade</i>	0	0.1776483,			4.3548	0.0369	0		4.3548
		0.00127	0						
<i>Pseudaminobacter</i>	0.005959,	1.3027542,	0.00199,		3.8571	0.0495	3.8571	0.0495	3.8571
	0.000073	0.0093	0.00003						
<i>Lactobacillus</i>	0	0.9474576,	0.00398,		4.3548	0.0369	4.3548	0.0369	3.8571
		0.0067797	0.00006						
<i>Stenotrophomonas</i>	0.011919,	0.6809852,	0.00398,		3.8571	0.0495	3.8571	0.0495	3.8571
	0.000145	0.00487	0.00006						
<i>Ochrobactrum</i>	7.276508,	4.7076801,	2.08,		3.8571	0.0495	3.8571	0.0495	3.8571
	0.088379	0.033686	0.03						
<i>Candidatus_Accum<ulibacter< i=""></ulibacter<></i>	0	1.2139301,			4.3548	0.0369	0		4.3548
		0.008686	0						
<i>Bacillus</i>	0.005959,	2.8127648,	0.00398,		3.8571	0.0495	3.8571	0.0495	3.8571
	0.000073	0.020127	0.00006						
<i>Pseudomonas</i>	22.07386,	5.240625,	2.42,		3.8571	0.0495	3.8571	0.0495	3.8571
	0.268	0.0375	0.04						
<i>Staphylococcus</i>	0	0.3552966,			4.3548	0.0369	0		4.3548
		0.0025424	0						

^aData represent median and interquartile range (IQR) values from pooled populations (i.e from each sheep) of eggs/larvae/adults (male and female) come from three different sheep (natural infection).

Supplementary Table S7: An average composition of significantly different microbial taxa associated with *H. contortus* eggs, larvae and adults using 16S rRNA gene (V5-V7 region). *P*-values were calculated using Kruskal-Wallis test. The level of significance was determined at *P* < 0.05.

Phylum									
V5-V7 region	Eggs	Larvae	Adults	Eggs vs adults		Eggs vs larvae		Larvae vs adults	
	Median, IQR ^a	Median, IQR ^a	Median, IQR ^a	Chi-square	<i>p</i> -value	Chi-square	<i>p</i> -value	Chi-square	<i>p</i> -value
Bacteroidetes	0.003944, 0.000023	0.72159937, 0.0091729	0.003616, 0.00005	3.8571	0.0495	3.8571	0.0495	3.8571	0.0495
Proteobacteria	33.8843, 0.19932	45.448425, 0.5777345	35.9174, 0.49747	3.8571	0.0495	3.8571	0.0495	3.8571	0.0495
Gemmatimonadetes	0.006574, 0.000038	0.21586306, 0.002744	0.005424, 0.000075	3.8571	0.0495	3.8571	0.0495	3.8571	0.0495
Actinobacteria	0.010518, 0.00006	0.203528, 0.002587	0.012655, 0.000175	3.8571	0.0495	3.8571	0.0495	3.8571	0.0495
Firmicutes	0.084145, 0.000495	0.0801777, 0.0010192	0.047005, 0.000651	3.8571	0.0495	3.8571	0.0495	3.8571	0.0495

Class									
V5-V7	Eggs	Larvae	Adults	Eggs vs adults		Eggs vs larvae		Larvae vs adults	
	Median, IQR ^a	Median, IQR ^a	Median, IQR ^a	Chi-square	<i>p</i> -value	Chi-square	<i>p</i> -value	Chi-square	<i>p</i> -value
Actinobacteria	0.009203, 0.000054	0.203528, 0.002587	0.003616, 0.00005	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Gammaproteobacteria	32.58268, 0.19167	7.333177, 0.093219	34.90498, 0.48345	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Betaproteobacteria	0.649497, 0.00382	32.83586, 0.4174	0.305534, 0.004232	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Coriobacteriia	0.001315, 0.000008	0 0.000425	0.009039, 0.000126	4.3548	0.0369	3.8571	0.0495	4.3548	0.0369
Clostridia	0.009203, 0.000054	0 0.000425	0.030734, 0.000425	4.3548	0.0369	3.8571	0.0495	4.3548	0.0369
Bacilli	0.074942, 0.00044	0.080178, 0.00102	0.016271, 0.000225	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Gemmatimonadetes	0.006574, 0.000038	0.215863, 0.002744	0.005424, 0.000075	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Alphaproteobacteria	0.652127, 0.003836	5.279394, 0.06711	0.706886, 0.00979	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Sphingobacteriia	0.003944, 0.000023	0.721599, 0.009173	0.003616, 0.00005	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463

Order									
V5-V7 region	Eggs	Larvae	Adults	Eggs vs adults		Eggs vs larvae		Larvae vs adults	
	Median, IQR ^a	Median, IQR ^a	Median, IQR ^a	Chi- square	p- value	Chi- square	p- value	Chi- square	p- value
Rhodospirillales	0.003944, 0.000023	0.117183, 0.00149	0	3.9706	0.0463	4.3548	0.0369	4.5	0.0339
Enterobacteriales	0.678422, 0.00399	0.567411, 0.007212	31.52242, 0.4366	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Coriobacteriales	0.001315, 0.000008	0 0.000126	0.009039, 0.000025	4.3548	0.0369	3.8571	0.0495	4.3548	0.0369
Xanthomonadales	0.040758, 0.00024	1.332183, 0.016934	0.001808, 0.000025	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Micrococcales	0.009203, 0.000054	0.17269, 0.002195	0.001808, 0.000025	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Sphingobacteriales	0.003944, 0.000023	0.721599, 0.00917	0.003616, 0.000005	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Sphingomonadales	0.005259, 0.00003	0.166523, 0.002117	0	3.9706	0.0463	4.3548	0.0369	4.5	0.0339
Caulobacteriales	0.007889, 0.000047	0.604417, 0.007684	0.010847, 0.00015	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Clostridiales	0.009203, 0.000054	0 0.000425	0.030734, 0.000425	4.3548	0.0369	3.8571	0.0495	4.3548	0.0369
Bacillales	0.074942, 0.00044	0.080178, 0.00102	0.016271, 0.000225	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Corynebacteriales	0	0.030838,	0.001808,	4.5	0.0339	4.3548	0.0369	3.9706	0.0463
Burkholderiales	0.649497, 0.00382	32.83586, 0.4174	0.305534, 0.004232	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Rhizobiales	0.635035, 0.003736	4.391271, 0.05582	0.696039, 0.009641	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Gemmatimonadales	0.006574, 0.000038	0.215863, 0.002744	0.005424, 0.000075	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Pseudomonadales	31.8635, 0.18743	5.433582, 0.069071	3.359065, 0.046524	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463

Family									
V5-V7 region	Eggs	Larvae	Adults	Eggs vs adults		Eggs vs larvae		Larvae vs adults	
	Median, IQR ^a	Median, IQR ^a	Median, IQR ^a	Chi-square	p-value	Chi-square	p-value	Chi-square	p-value
Mycobacteriaceae	0	0.030838, 0.000392	0.001810, 0.000002	4.5	0.0339	4.5	0.0339	4.0909	0.0431
Gemmamimonadaceae	0.006574, 0.000038	0.215863, 0.002744	0.005420, 0.000008	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Bradyrhizobiaceae	0.002630, 0.000015	0.468731, 0.005958	0.001810, 0.000002	3.9706	0.0463	3.9706	0.0463	4.0909	0.0431
Pseudomonadaceae	31.863496, 0.187432	5.433582, 0.069071	3.360000, 0.05	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Enterobacteriaceae	0.678422, 0.00399	0.567412, 0.007213	31.5, 0.4	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Coriobacteriaceae	0.001315, 0.000008	0	0.00904, 0.00012	4.3548	0.0369	3.8571	0.0495	4.3548	0.0369
Caulobacteraceae	0.007889, 0.000047	0.604417, 0.007684	0.0108, 0.0002	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Hyphomicrobiaceae	0.00263, 0.000015	0.203528, 0.002587	0	3.9706	0.0463	4.3548	0.0369	4.5	0.0339
Chitinophagaceae	0.00263, 0.000015	0.672259, 0.008545	0.00362, 0.00005	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Rhodospirillaceae	0.003944, 0.000023	0.117183, 0.00149	0	3.9706	0.0463	4.3548	0.0369	4.5	0.0339
Staphylococcaceae	0.003944, 0.000023	0.018503, 0.000236	0.00542, 0.00008	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Comamonadaceae	0.011833, 0.000007	0.339213, 0.004312	0.00181, 0.00002	3.9706	0.0463	3.9706	0.0463	4.0909	0.0431
Burkholderiaceae	0.011833, 0.000007	0.450229, 0.005724	0.00542, 0.00008	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Sphingomonadaceae	0.005259, 0.000003	0.166523, 0.002117	0	3.9706	0.0463	4.3548	0.0369	4.5	0.0339
Microbacteriaceae	0.009203, 0.000055	0.172690, 0.002195	0.00181, 0.00002	3.9706	0.0463	3.9706	0.0463	4.0909	0.0431
Xanthomonadaceae	0.040758, 0.000024	1.332184, 0.016935	0.0235, 0.0004	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Ruminococcaceae	0.009203, 0.000055	0	0.0307, 0.0004	4.3548	0.0369	3.8571	0.0495	4.3548	0.0369
Phyllobacteriaceae	0.015777, 0.000093	1.005305, 0.012779	0.0145, 0.0002	3.9706	0.0463	3.9706	0.0463	4.0909	0.0431
Rhizobiaceae	0.005259, 0.000003	0.02467, 0.000313	0.00362, 0.00005	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Sphingobacteriaceae	0.001315, 0.000008	0.04934, 0.000627	0	3.9706	0.0463	4.3548	0.0369	4.5	0.0339
Brucellaceae	0.60348, 0.00355	2.430001, 0.0309	0.674, 0.009	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Alcaligenaceae	0.625831, 0.003681	32.046413, 0.407369	0.298, 0.004	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Paenibacillaceae	0.070998, 0.000418	0.061675, 0.000784	0.0108, 0.0002	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
Rhodobiaceae	0.001315, 0.000008	0.203528, 0.002587	0	3.9706	0.0463	4.3548	0.0369	4.5	0.0339

Genus									
V5-V7	Eggs	Larvae	Adults	Eggs vs adults		Eggs vs larvae		Larvae vs adults	
	Median, IQR ^a	Median, IQR ^a	Median, IQR ^a	Chi-square	p-value	Chi-square	p-value	Chi-square	p-value
<i>Sphingobacterium</i>	0.00131, 0.00009	0.0493400, 0.000627	0	4.0909	0.0431	1	0.3173	4.5	0.0339
<i>Ruminococcus</i>	0.00394, 0.000026	0 0.000126	0.0090390, 0.000126	1	0.3173	3.9706	0.0463	4.3548	0.0369
<i>Pseudomonas</i>	31.9, 0.157212	5.433582, 0.069071	3.3590650, 0.046524	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
<i>Ralstonia</i>	0.0118, 0.000068	0.450229, 0.005724	0.005424, 0.000075	4.0909	0.0431	3.9706	0.0463	3.9706	0.0463
<i>Atopobium</i>	0.00131, 0.00009	0 0.0001256	0.009039, 0.0001256	1	0.3173	3.9706	0.0463	4.3548	0.0369
<i>Azospirillum</i>	0.00394, 0.000026	0.117183, 0.00149	0	4.0909	0.0431	1	0.3173	4.5	0.0339
<i>Gemmimonas</i>	0.00657, 0.000043	0.215863, 0.00274	0.005424, 0.000075	4.0909	0.0431	3.9706	0.0463	3.9706	0.0463
<i>Sphingopyxis</i>	0.00526, 0.000035	0.154188, 0.00196	0	4.0909	0.0431	4.5	0.0339	4.5	0.0339
<i>Parvibaculum</i>	0.00131, 0.00009	0.203528, 0.002587	0	4.0909	0.0431	1	0.3173	4.5	0.0339
<i>GKS98_freshwater_group</i>	0.626, 0.003672	32.046413, 0.407369	0.298302, 0.004132	3.9706	0.0463	3.8571	0.0495	3.9706	0.0463
<i>Paenibacillus</i>	0.071, 0.000406	0.061675, 0.000784	0.010847, 0.000015	4.0909	0.0431	3.9706	0.0463	3.9706	0.0463
<i>Devasia</i>	0.00263, 0.000017	0.178858, 0.002274	0	4.0909	0.0431	1	0.3173	4.5	0.0339
<i>Staphylococcus</i>	0.00394, 0.000026	0.018503, 0.000236	0.005424, 0.000075	4.0909	0.0431	3.9706	0.0463	3.9706	0.0463
<i>Microbacterium</i>	0.0092, 0.00005	0.160355, 0.002038	0.001808, 0.000025	4.0909	0.0431	3.9706	0.0463	3.9706	0.0463
<i>Bosea</i>	0.00131, 0.00009	0.037005, 0.00047	0	4.0909	0.0431	1	0.3173	4.5	0.0339
<i>Brevundimonas</i>	0.00789, 0.000042	0.604417, 0.007684	0.010847, 0.00015	4.0909	0.0431	3.9706	0.0463	3.9706	0.0463
<i>Aquamicrobium</i>	0	0.086345, 0.001097	0.001808, 0.000025	4.5	0.0339	4.3548	0.0369	3.9706	0.0463
<i>Rhizobium</i>	0.00526, 0.000035	0.02467, 0.000314	0.003616, 0.00005	4.0909	0.0431	3.9706	0.0463	3.9706	0.0463
<i>Afipia</i>	0	0.12335, 0.001568	0	4.5	0.0339	0	0	4.5	0.0339
<i>Mycobacterium</i>	0	0.030838, 0.000392	0.001808, 0.000025	4.5	0.0339	4.3548	0.0369	3.9706	0.0463
<i>Escherichia-Shigella</i>	0.678, .004418	0.567411, 0.007212	31.522416, 0.436599	4.0909	0.0431	3.9706	0.0463	3.9706	0.0463
<i>Lysinimonas</i>	0	0.012335, 0.000157	0	4.5	0.0339	0	0	4.5	0.0339
<i>Rhodopseudomonas</i>	0.00131, 0.00009	0.308376, 0.00392	0.001808, 0.000025	4.0909	0.0431	3.9706	0.0463	3.9706	0.0463
<i>Dokdonella</i>	0.0197, 0.00008	0.647589, 0.008232	0.005424, 0.000075	4.0909	0.0431	3.9706	0.0463	3.9706	0.0463
<i>Sphingomonas</i>	0	0.012335, 0.000157	0	4.5	0.0339	0	0	4.5	0.0339
<i>Hyphomicrobium</i>	0	0.02467, 0.000314	0	4.5	0.0339	0	0	4.5	0.0339
<i>Pseudaminobacter</i>	0.0158, 0.000124	0.91896, 0.011682	0.012655, 0.000175	4.0909	0.0431	3.9706	0.0463	3.9706	0.0463

^aData represent median and interquartile range (IQR) values from pooled populations (i.e. from each sheep) of eggs/larvae/adults (male and female) come from three different sheep (natural infection).

Supplementary Table S8: Microbial community composition associated with the different life-cycle stages of *H. contortus* (V3-V4 region)

Genus	<i>H. contortus</i> eggs ^a	<i>H. contortus</i> larvae ^a	<i>H. contortus</i> adults ^a
<i>Brevundimonas</i>	0.0000368552±0.005951424	0.8008475±0.003116797	1.990000e-003±0.0000156179
<i>Trichococcus</i>	0	0.1483051±0.000577185	0
<i>Turneriella</i>	0	0.2966102±0.001154369	0
<i>Aeriscardovia</i>	0.000442262±0.07141708	0	0.0298±0.000234269
<i>Acinetobacter</i>	0	0.4449153±0.001731554	0
<i>Lentibacillus</i>	0.000147421±0.02380569	9.461864±0.03682439	0.00796±0.0000624716
<i>Ruminococcus</i>	0.001068801±0.1725913	0	0.0378±0.00029674
<i>Ralstonia</i>	0.000368552±0.05951424	0.6525424±0.002539613	0
<i>Sphingopyxis</i>	0.0000368552±0.005951424	0.1186441±0.000461748	0
<i>Dechloromonas</i>	0	1.038136±0.004040293	0
<i>Kroppenstedtia</i>	0.000147421±0.02380569	4.597457±0.01789273	0.0219±0.000171797
<i>Atopobium</i>	0.000294842±0.04761139	0	0.00597±0.0000468537
<i>Flavobacterium</i>	0	0.4449153±0.001731554	0
<i>Leuconostoc</i>	0.0000368552±0.005951424	0.2076271±0.000808059	3.980000e-003±0.0000312358
<i>Sorangium</i>	0	0.08898305±0.000346311	0
<i>Atopostipes</i>	0.000810814±0.1309313	0	0
<i>Piscinibacter</i>	0	0.1483051±0.000577185	0
<i>Flavonifractor</i>	0.0000368552±0.005951424	0	0.00597±0.0000468537
<i>Zoogloea</i>	0	0.7415254±0.002885924	0
<i>Weissella</i>	0.0000368552±0.005951424	0.3855932±0.00150068	0
<i>Herbaspirillum</i>	0	0.1186441±0.000461748	0
<i>Rhizobium</i>	0	0.2966102±0.001154369	0.00597±0.0000468537
<i>Pediococcus</i>	0	0.1186441±0.000461748	0
<i>Luteibacter</i>	0.0000737104±0.01190285	0.05932203±0.000230874	3.980000e-003±0.0000312358
<i>Achromobacter</i>	0.000552828±0.08927135	29.868640±0.116245	0.0378±0.00029674
<i>Thermomonas</i>	0	0.2966102±0.001154369	0
<i>Azotobacter</i>	0.01418925±2.291298	1.305085±0.005079225	0.175±0.001374376
<i>Intestinimonas</i>	0.0000368552±0.005951424	0	1.990000e-003±0.0000156179
<i>Thauera</i>	0	0.6525424±0.002539613	0
<i>Escherichia-Shigella</i>	0.02620405±4.231462	1.097458±0.004271167	35.90±0.2815597
<i>Delftia</i>		2.283898±0.008888645	0.00597±0.0000468537
<i>Prevotella</i>	0.000515973±0.08331993	0	0
<i>Mycoplasma</i>	0	0	0.0537±0.000421684
<i>Azospirillum</i>	0	0.2669491±0.001038932	0
<i>Lautropia</i>	0	0.05932203±0.000230874	0
<i>Ferruginibacter</i>	0	0.4449153±0.001731554	0
<i>Dokdonella</i>	0.0000737104±0.01190285	3.322034±0.01292894	0
<i>Oceanobacillus</i>	0	1.690678±0.006579906	0
<i>BDI-7_clade</i>	0	0.1779661±0.000692622	0
<i>Pseudaminobacter</i>	0.0000368552±0.005951424	1.305085±0.005079225	1.990000e-003±0.0000156179
<i>Lactobacillus</i>	0	0.9491525±0.003693982	3.980000e-003±0.0000312358
<i>Stenotrophomonas</i>	0.0000737104±0.01190285	0.6822034±0.00265505	3.980000e-003±0.0000312358

<i>Ochrobactrum</i>	0.0450002±7.266688	4.716102±0.01835447	2.07±0.01627386
<i>Candidatus_Accumulibacter</i>	0	1.216102±0.004732915	0
<i>Bacillus</i>	0.0000368552±0.005951424	2.817797±0.01096651	3.980000e-003±0.0000312358
<i>Pseudomonas</i>	0.1365117±22.044070	5.250000±0.02043234	2.42±0.019007
<i>Staphylococcus</i>	0	0.3559322±0.001385243	0

^aData represent median and interquartile range (IQR) values from pooled populations (i.e from each sheep) of eggs/larvae/adults (male and female) come from three different sheep ± standard deviation (SD).

Supplementary Table S9: Microbial community composition associated with the different life-cycle stages of *H. contortus* (V5-V7 region) isolated from ovine hosts at the genus

Genus	<i>H. contortus</i> Eggs ^a	<i>H. contortus</i> Larvae ^a	<i>H. contortus</i> Adults ^a
<i>Sphingobacterium</i>	1.310000e-003±3.866980e-006	0.04913106±0.000362117	0
<i>Ruminococcus</i>	3.940000e-003±0.0000116009	0	0.009014423±0.0000662498
<i>Pseudomonas</i>	31.90±0.09371617	5.410558±0.03987813	3.349760±0.02461842
<i>Ralstonia</i>	0.0118±0.0000348028	0.4483209±0.003304317	0.005408654±0.0000397499
<i>Atopobium</i>	1.310000e-003±0.00000386698	0	0.009014423±0.0000662498
<i>Azospirillum</i>	3.940000e-003±0.0000116009	0.1166863±0.000860028	0
<i>Gemmimonas</i>	0.00657±0.0000193349	0.2149484±0.001584262	0.005408654±0.0000397499
<i>Sphingopyxis</i>	0.00526±0.0000154679	0.1535346±0.001131616	0
<i>Parvibaculum</i>	1.310000e-003±0.00000386698	0.2026656±0.001493733	0
<i>GKS98_freshwater_group</i>	0.626±0.001840681	31.910620±0.235195	0.297476±0.002186243
<i>Paenibacillus</i>	0.071±0.000208817	0.06141382±0.000452646	0.01081731±0.0000794997
<i>Devosia</i>	2.630000e-003±0.00000773395	0.1781001±0.001312674	
<i>Staphylococcus</i>	3.940000e-003±0.0000116009	0.01842415±0.000135794	0.005408654±0.0000397499
<i>Microbacterium</i>	0.0092±0.0000270688	0.1596759±0.00117688	0.001802885±0.00001325
<i>Bosea</i>	1.310000e-003±0.00000386698	0.0368483±0.000271588	0
<i>Brevundimonas</i>	0.00789±0.0000232019	0.6018555±0.004435933	0.01081731±0.0000794997
<i>Aquamicrobium</i>	0	0.08597936±0.000633705	0.001802885±0.00001325
<i>Rhizobium</i>	0.00526±0.0000154679	0.02456553±0.000181058	0.003605769±0.0000264999
<i>Afipia</i>	0	0.1228276±0.000905292	0
<i>Mycobacterium</i>	0	0.03070691±0.000226323	0.001802885±0.00001325
<i>Escherichia-Shigella</i>	0.678±0.00199536	0.5650072±0.004164345	31.435100±0.2310262
<i>Lysinimonas</i>	0	0.01228276±0.0000905292	0
<i>Rhodopseudomonas</i>	1.310000e-003±0.00000386698	0.3070691±0.002263231	0.001802885±0.00001325
<i>Dokdonella</i>	0.0197±0.0000580046	0.6448452±0.004752785	0.005408654±0.0000397499
<i>Sphingomonas</i>	0	0.01228276±0.0000905292	0
<i>Hyphomicrobium</i>	0	0.02456553±0.000181058	0
<i>Pseudaminobacter</i>	0.0158±0.0000464037	0.915066±0.006744429	0.01262019±0.0000927497

^aData represent average values from pooled populations (i.e from each sheep) of eggs/larvae/adults (male and female) come from three different sheep± standard deviation (SD).

Supplementary Table S10: Microbial community composition associated with the adult stage of *H. contortus* at population (clusters of male and female worms) and individual (single adult female worm) levels (V3-V4 region) isolated from ovine hosts at the genus level.

Genus	<i>H. contortus</i> adults (population level)(Average, \pm SD) ^a	<i>H. contortus</i> adults (Individual female worm level)(Average, \pm SD) ^b
<i>Brevundimonas</i>	1.990000e-003 \pm 0.0000156179	0.00163131 \pm 0.00015272
<i>Trichococcus</i>	0	0
<i>Turneriella</i>	0	0
<i>Aeriscardovia</i>	0.0298 \pm 0.000234269	0.02447166 \pm 0.00228877
<i>Lentibacillus</i>	0.00796 \pm 0.0000624716	0.004894266 \pm 0.000458
<i>Ruminococcus</i>	0.0378 \pm 0.00029674	0.19414332 \pm 0.01815669
<i>Ralstonia</i>	0	0
<i>Sphingopyxis</i>	0	0
<i>Dechloromonas</i>	0	0
<i>Kroppenstedtia</i>	0.0219 \pm 0.000171797	0.00815722 \pm 0.00076303
<i>Atopobium</i>	0.00597 \pm 0.0000468537	0.004894266 \pm 0.0004577
<i>Flavobacterium</i>	0	0
<i>Sorangium</i>	0	0
<i>Atopostipes</i>	0	0
<i>Piscinibacter</i>	0	0
<i>Flavonifractor</i>	0.00597 \pm 0.0000468537	0.004894266 \pm 0.0004577
<i>Zoogloea</i>	0	0
<i>Weissella</i>	0	0
<i>Herbaspirillum</i>	0	0
<i>Rhizobium</i>	0.00597 \pm 0.0000468537	0.00163131 \pm 0.00015272
<i>Pediococcus</i>	0	0
<i>Luteibacter</i>	3.980000e-003 \pm 0.0000312358	0.003262955 \pm 0.000305
<i>Achromobacter</i>	0.0378 \pm 0.00029674	0.02773495 \pm .002593656
<i>Thermomonas</i>	0	0
<i>Intestinimonas</i>	1.990000e-003 \pm 0.0000156179	0.00163131 \pm 0.00015272
<i>Thauera</i>	0	0
<i>Escherichia-Shigella</i>	35.90 \pm 0.2815597	29.4119116 \pm 2.75065773
<i>Delftia</i>	0.00597 \pm 0.0000468537	0.003262955 \pm 0.000305
<i>Prevotella</i>	0	
<i>Mycoplasma</i>	0.0537 \pm 0.000421684	0.044049058 \pm 0.0041198
<i>Azospirillum</i>	0	0
<i>Lautropia</i>	0	0
<i>Ferruginibacter</i>	0	0
<i>Dokdonella</i>	0	0
<i>Oceanobacillus</i>	0	0
<i>BD1-7_clade</i>	0	0
<i>Pseudaminobacter</i>	1.990000e-003 \pm 0.0000156179	0.00163131 \pm 0.00015272
<i>Lactobacillus</i>	3.980000e-003 \pm 0.0000312358	0.00163131 \pm 0.00015272

<i>Stenotrophomonas</i>	3.980000e-003±0.0000312358	0.004894266 ± 0.0004577
<i>Ochrobactrum</i>	2.07±0.01627386	1.699978513 ± 0.1589851
<i>Candidatus_Accumulibacter</i>	0	0
<i>Bacillus</i>	3.980000e-003±0.0000312358	0.00163131 ± 0.00015272
<i>Pseudomonas</i>	2.42±0.019007	1.16812319 ± 0.10924532
<i>Leuconostoc</i>	3.980000e-003±0.0000312358	0
<i>Azotobacter</i>	0.175±0.001374376	0
<i>Acinetobacter</i>	0	0.004894266 ± 0.0004577
<i>Staphylococcus</i>	0	0.00652591 ± 0.00061032
<i>Sphingomonas</i>	0	0.00163131 ± 0.00015272
<i>Aquamicrobiium</i>	0	0.00163131 ± 0.00015272
<i>RC9_gut_group</i>	0	0.003262955 ± 0.000305
<i>Shinella</i>	0	0.003262955 ± 0.000305

^aData represent average values from pooled populations (i.e from each sheep) of adults (clusters of male and female) come from three different sheep± standard deviation (SD).

^bData represent average values from individual single female worms (i.e from each sheep) come from three different sheep± standard deviation (SD).