Highly abundant ASVs (>1.0% in at least one input group) shared between T1 and T2 birds across all samples

T1 bird ASV abundances				T2 bird ASV abundances		
Conv_Abund	Egg_Abund	Env_Abund	ASV and Taxonomy	Conv_Abund	Egg_Abund	Env_Abund
8.929	**36.467**	**7.759**	ASV_1_Enterococcaceae_Enterococcus	**16.175**	**38.578**	**8.062**
5.656	0.607	**16.78**	ASV_2_Peptostreptococcaceae_Romboutsia	**1.154**	**4.757**	**22.177**
33.583	**2.781**	**3.156**	ASV_3_Lachnospiraceae_NA	**17.431**	0.555	**2.506**
12.287	**14.322**	**2.235**	ASV_4_Lachnospiraceae_NA	**12.351**	**1.056**	0.812
0.015	0.024	**9.046**	ASV_5_Clostridiaceae_1_Clostridium_sensu_stricto_1	**3.426**	**7.934**	**1.965**
2.351	0.284	**2.232**	ASV_6_Enterobacteriaceae_Escherichia/Shigella	**9.603**	**9.132**	**2.716**
7.925	0.089	0.906	ASV_7_Lachnospiraceae_NA	**5.558**	0.193	0.061
1.38	**2.543**	**1.315**	ASV_8_Lachnospiraceae_NA	0.587	**3.566**	**1.427**
1.443	0.004	0.048	ASV_9_Enterococcaceae_Enterococcus	0.912	**4.636**	0.068
0.947	**4.21**	**1.106**	ASV_10_Enterobacteriaceae_Klebsiella	0.528	0.031	**4.774**
1.164	0.503	**2.322**	ASV_11_Clostridiaceae_1_Clostridium_sensu_stricto_1	0.303	0.105	**5.946**
0.647	**2.103**	0.154	ASV_12_Enterococcaceae_Enterococcus	**3.507**	0.587	0.612
0.107	0.002	**5.544**	ASV_13_Erysipelotrichaceae_Turicibacter	0.002	0.002	**1.686**
0.495	**4.461**	0.318	ASV_14_Lachnospiraceae_NA	0.233	**1.166**	0.212
1.985	0.217	0.373	ASV_16_Ruminococcaceae_Flavonifractor	**2.366**	0.066	0.905
0.013	0.803	**1.889**	ASV_19_Lachnospiraceae_NA	0.074	0.184	**2.605**
1.093	0.15	**1.064**	ASV_21_Lachnospiraceae_NA	**1.266**	0.091	0.062
0.684	0.005	**1.683**	ASV_26_Peptostreptococcaceae_Terrisporobacter	0.004	0.001	**2.435**
2.196	0.018	0.205	ASV_30_Lachnospiraceae_NA	**1.505**	0.027	0.016

Highly abundant ASVs (>1.0% in at least one input group) exclusive to either T1 or T2 birds across all samples

			ASVs exclusive to T1 birds and abundances
0.661	**4.575**	0.253	ASV_17_Lachnospiraceae_Fusicatenibacter
0.71	0.055	**1.2**	ASV_23_Peptostreptococcaceae_Romboutsia
0.082	**1.9**	0.425	ASV_25_Ruminococcaceae_Ruminiclostridium_9
0	**NA**	**3.298**	ASV_31_Ruminococcaceae_Subdoligranulum
0	0.001	**1.72**	ASV_34_Ruminococcaceae_Ruminiclostridium_5
0.076	**2.987**	0.001	ASV_35_Enterococcaceae_Enterococcus
2.423	0.046	0.001	ASV_41_Lachnospiraceae_Sellimonas
0.03	**2.547**	0	ASV_42_Enterococcaceae_Enterococcus
0.456	0.033	**1.36**	ASV_44_Peptostreptococcaceae_Romboutsia
0.199	**1.334**	0.001	ASV_52_Lachnospiraceae_NA
0.285	**1.335**	0.003	ASV_55_Lachnospiraceae_NA

ASVs exclusive to T2 birds and abundances			
ASV_15_Lachnospiraceae_NA	0.283	**1.598**	**3.559**
ASV_20_Lachnospiraceae_Eisenbergiella	0.495	**1.544**	0.647
ASV_22_Lachnospiraceae_Lachnoclostridium	**1.582**	0.058	0.544
ASV_24_Bacillaceae_NA	0.092	**1.007**	0.42
ASV_27_Lachnospiraceae_Blautia	**1.202**	0.064	0.473
ASV_28_Lachnospiraceae_NA	0.421	**1.472**	0.677
ASV_29_Lachnospiraceae_NA	0.085	0.377	**3.052**
ASV_36_Lachnospiraceae_NA	0.148	**1.039**	0.602
ASV_38_Lachnospiraceae_Sellimonas	0.04	0.028	**2.844**
ASV_39_Lachnospiraceae_NA	**1.895**	0.118	0.025
ASV_40_Lachnospiraceae_Sellimonas	0.027	0.006	**1.216**
ASV_45_Peptostreptococcaceae_Romboutsia	0.02	0.219	**1.128**
ASV_70_Clostridiaceae_1_Clostridium_sensu_stricto_1	0.038	0.043	**1.136**