

In order to investigate whether treatmentx have any effect on the intestinal microbial abundance and function, the bray distances are first calculated, then group is subjected to a PERMANOVA test based on the bray distance.

Samples

Total 120 chicken, 61 control, 59 treatmentx

30 different pen, 16 control and 16 treatmentx only 3 or 4 chicken for one pan, one pan only has 2 chicken

Phenotype

sample label	pan	cohort Additive	weight
F1513-197	96	Control	1423
F1513-198	96	Control	1446
F1513-199	96	Control	1258
F1513-200	96	Control	1348
F1513-221	106	Control	1189
F1513-222	106	Control	1480
F1513-223	106	Control	1256
F1513-224	106	Control	1456
F1513-001	3	TreatmentX	1197
F1513-002	3	TreatmentX	1391
F1513-003	3	TreatmentX	1177
F1513-004	3	TreatmentX	1139
F1513-005	12	TreatmentX	1204
F1513-006	12	TreatmentX	1346
F1513-008	12	TreatmentX	1367
F1513-009	15	TreatmentX	1136
F1513-010	15	TreatmentX	1244
F1513-011	15	TreatmentX	1355
F1513-012	15	TreatmentX	1448
F1513-013	23	TreatmentX	1215

PERMANOVA result

phenotype	SampleNumber	Df	SumsOfSquares	MeanSquares	F.Model	R2	Pr(>F)
pen	120	31	14.805762	0.477605226	1.781930337	0.385645783	1.00E-04
treatmentx	120	1	1.946633921	1.946633921	6.3026394	0.050703987	1.00E-04

purpose

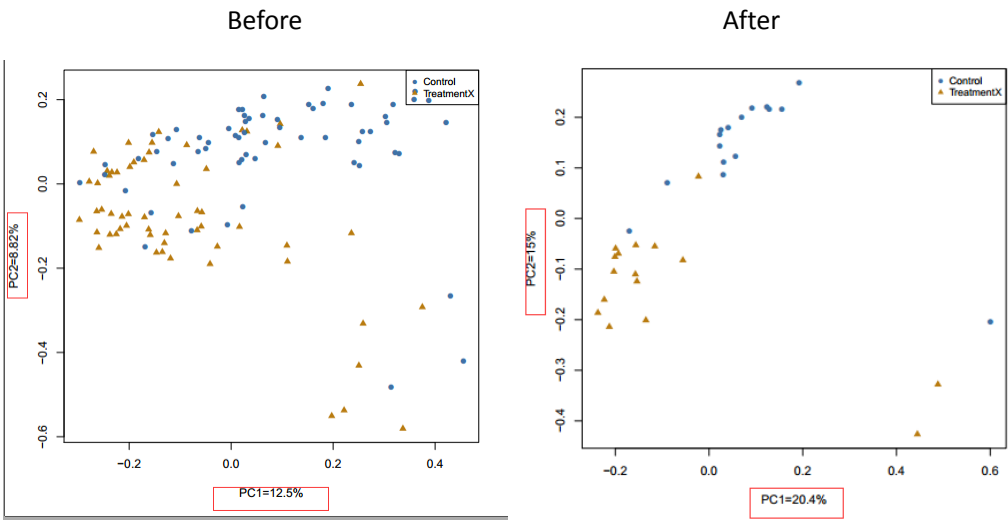
To correct the effects of the pan then find out which bacteria the treatmentx affects.

Method

I thought of a simple method to average the gene abundance of chickens in each cage as the gene abundance of the cages.

phenotype	SampleN um	Df	SumsOfSqs	Mean Sqs	F.Mod el	R2	Pr(>F)
treatmentx.before	120	1	1.946633921	1.946 634	6.302 639	0.050 704	1.00E- 04
treatmentx.after	32	1	0.852877769	0.852 878	4.371 737	0.127 19	1.00E- 04

R²: 0.050704 to 0.12719



Pc1: 12.5% to20.4%

Pc2: 8.82% to 15%