Comprehensive –omics of the developing turkey: databases for the future

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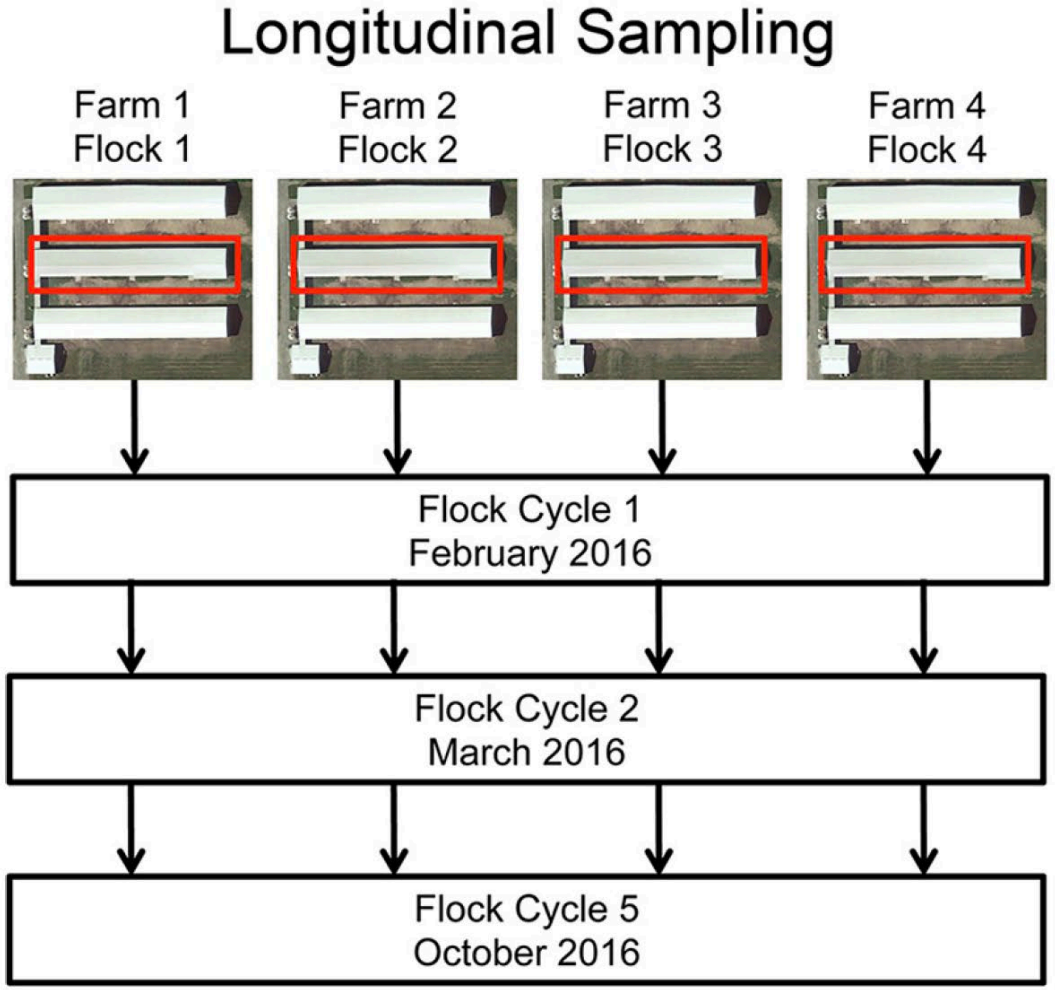
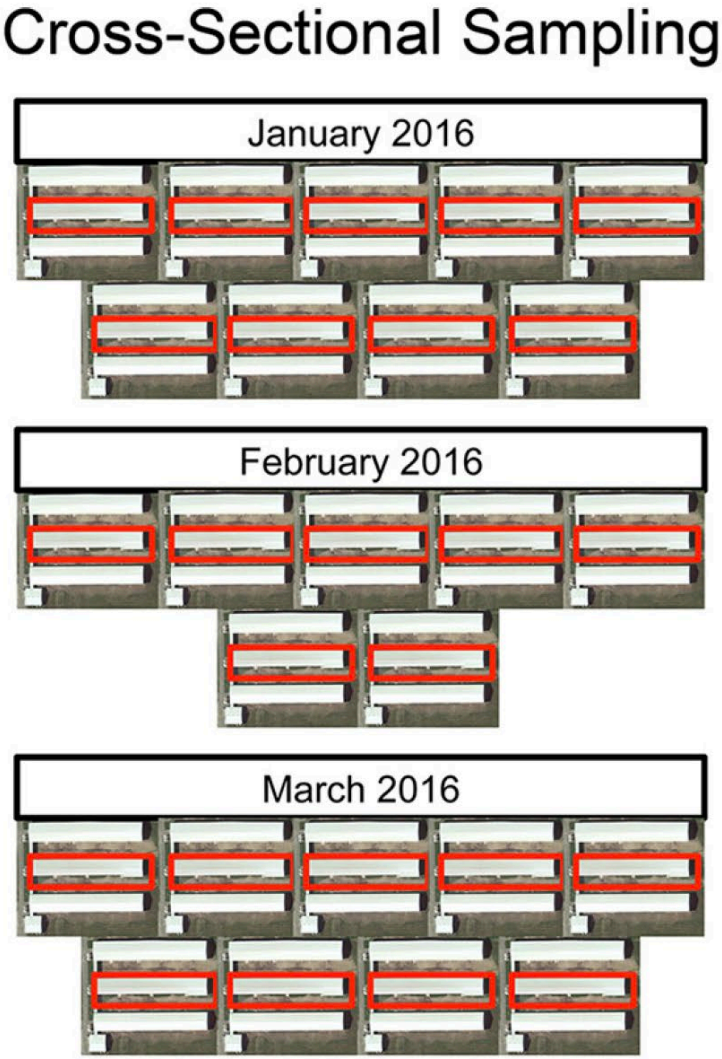
NewScientist

DAILY NEWS 6 September 2018

Probiotics are mostly useless and can actually hurt you





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FOOD MICROBIOLOGY

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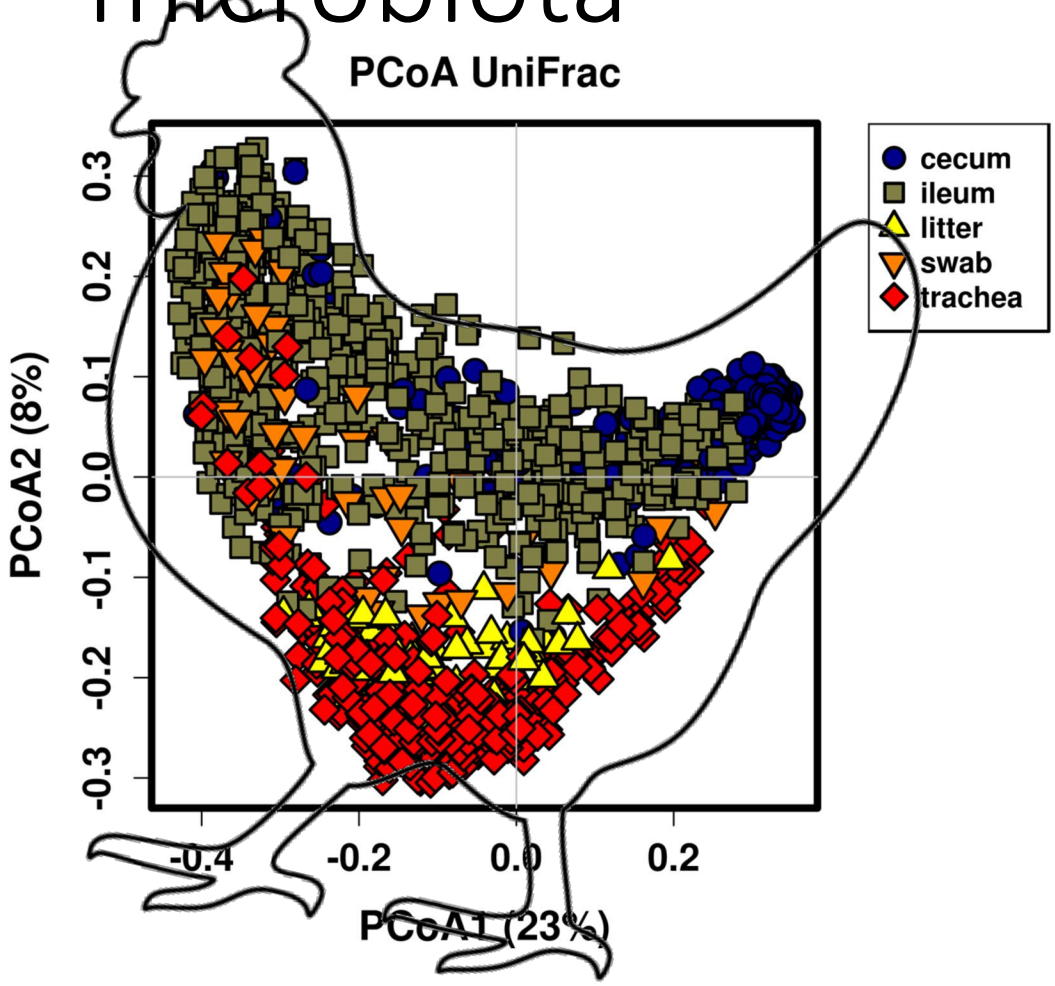
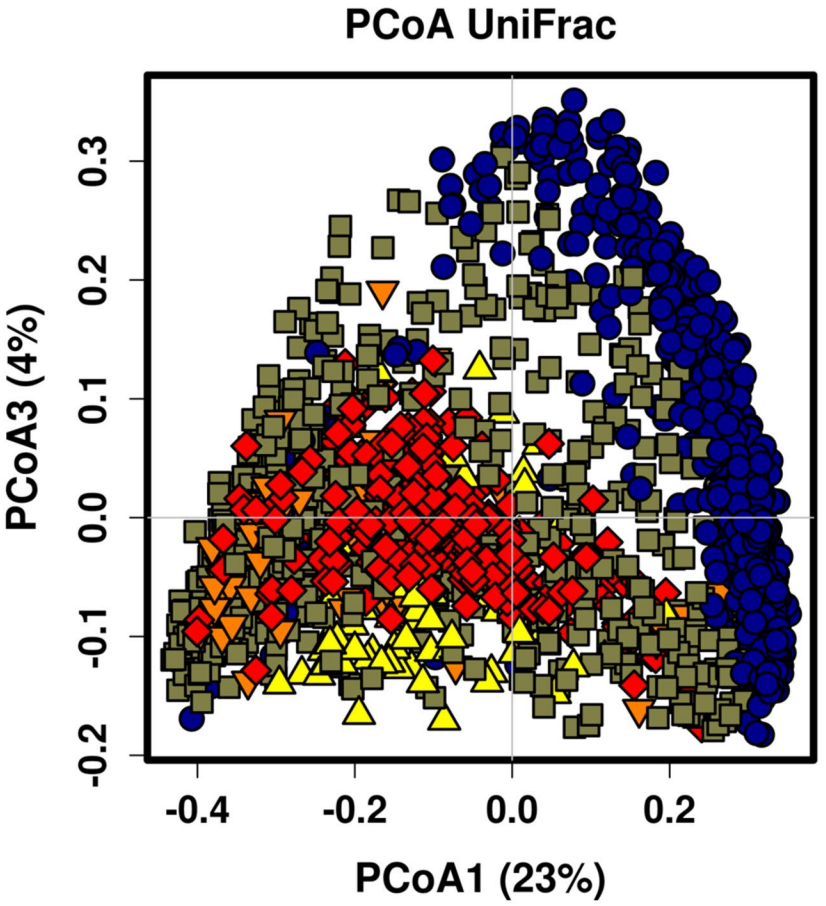
A Consistent and Predictable Commercial Broiler Chicken Bacterial Microbiota in Antibiotic-Free Production Displays Strong Correlations with Performance

Timothy J. Johnson,[a,b] Bonnie P. Youmans,[a] Sally Noll,[c] Carol Cardona,[a,b] Nicholas P. Evans,[d] T. Peter Karnezos,[d] John M. Ngunjiri,[e] Michael C. Abundo,[e,f] Chang-Won Lee[e,f]

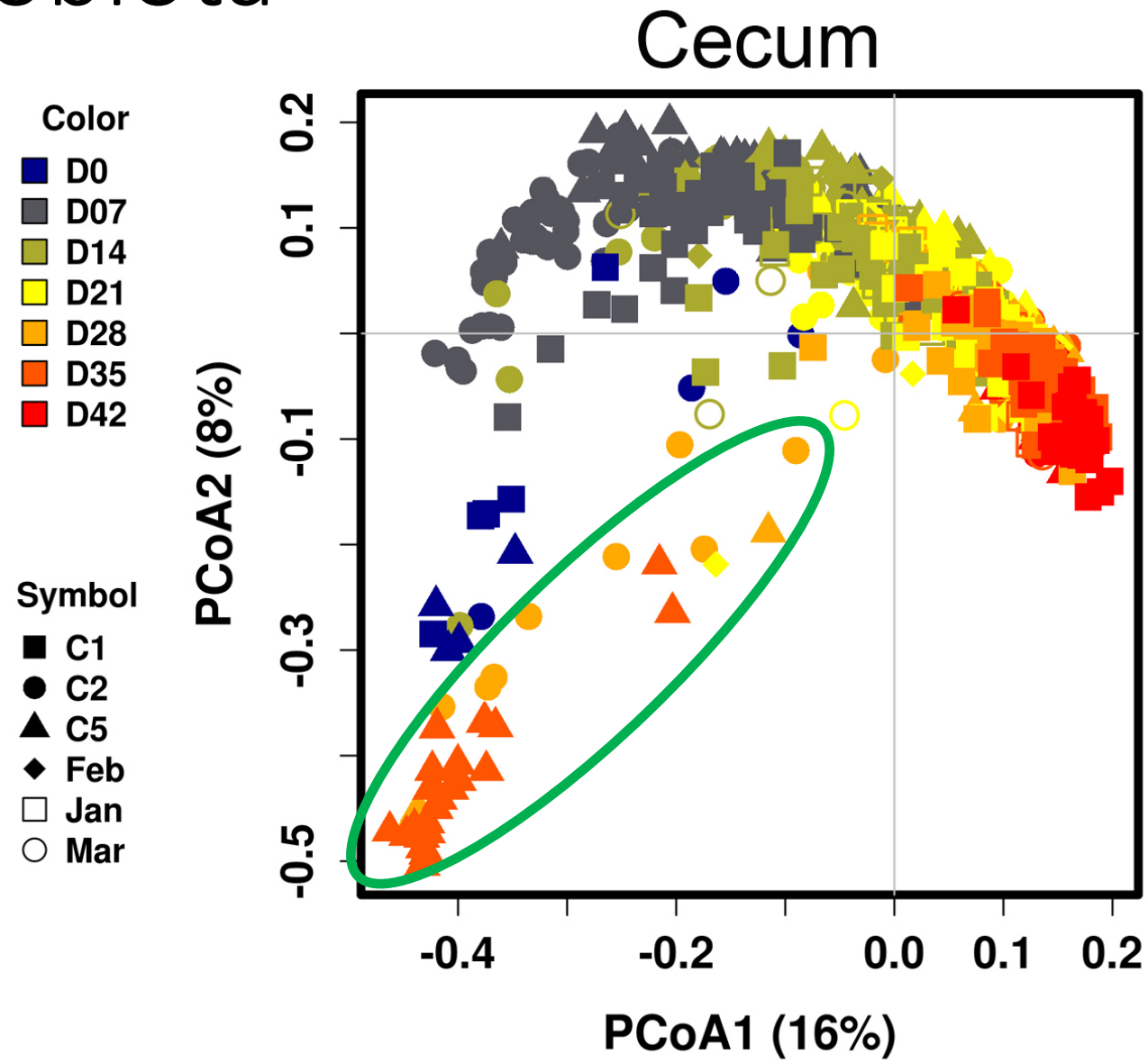
Anatomical location impacts microbiota





Johnson et al., 2018 AEM

Age is a major driver of the microbiota



Johnson et al., 2018 AEM

Tissue > Season > Age >> Flock effects

Flock (location)

Flock	Cecum		Ileum		Trachea	
Age:	P	R	P	R	P	R
Day 07	<0.001	0.053	0.02	0.037	0.002	0.105
Day 14	<0.001	0.066	0.175	0.013	<0.001	0.265
Day 21	<0.001	0.134	0.19	0.011	<0.001	0.108
Day 28	<0.001	0.095	0.05	0.027	<0.001	0.12
Day 35	0.004	0.078	0.004	0.094	<0.001	0.124
Day 42	<0.001	0.298	<0.001	0.118	0.004	0.057

Season

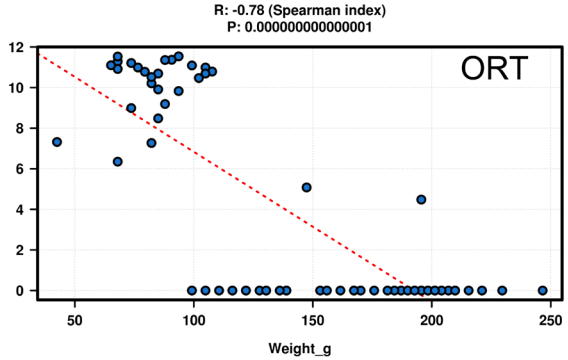
Cycle	Cecum		Ileum		Trachea	
Age:	P	R	P	R	P	R
Day 07	<0.001	0.493	<0.001	0.582	<0.001	0.625
Day 14	<0.001	0.373	<0.001	0.635	<0.001	0.447
Day 21	<0.001	0.39	<0.001	0.567	<0.001	0.431
Day 28	<0.001	0.279	<0.001	0.443	<0.001	0.202
Day 35	<0.001	0.446	<0.001	0.522	<0.001	0.299
Day 42	<0.001	0.254	<0.001	0.429	<0.001	0.24

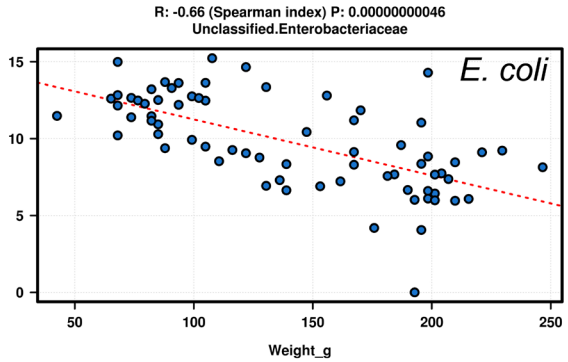
Age

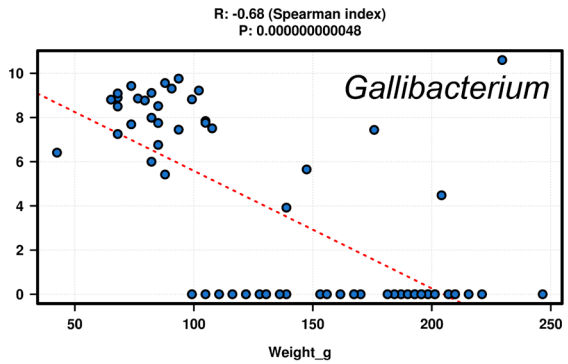
Tissue

	Cecum		Ileum		Trachea		Litter	
Across:	P	R	P	R	P	R	P	R
Age	<0.001	0.307	<0.001	0.086	<0.001	0.252	<0.001	0.488
Across:								
Sample Type	<0.001	0.636						

Adapted from Johnson et al., 2018 AEM

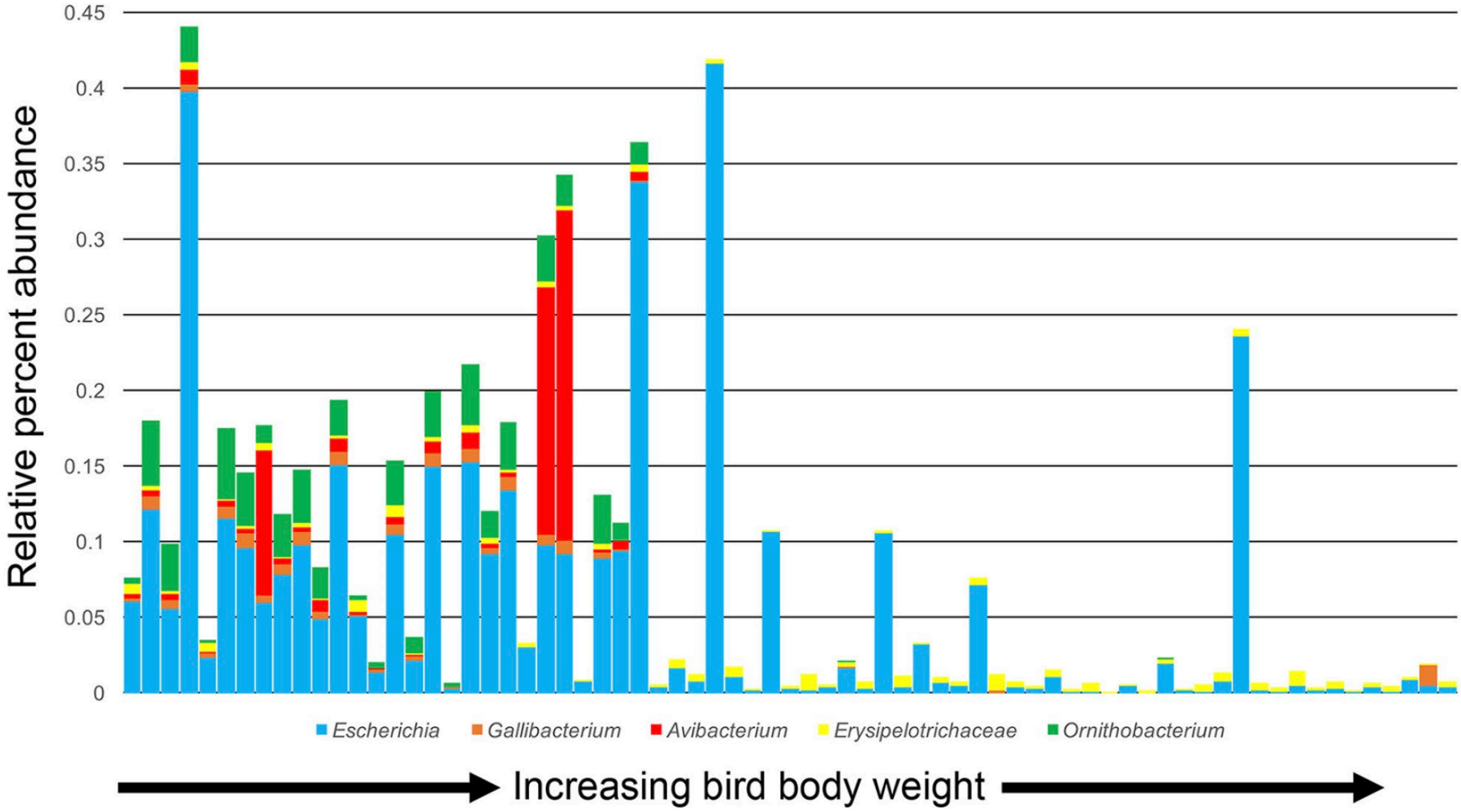






	Trachea					
	D07	D14	D21	D28	D35	D42
Achromobacter	-0.74		-0.31	-0.49	-0.37	
Acidocella	-0.32					
Acinetobacter		0.24				0.24
Aerococcus		0.37	0.32	-0.33		
Aeromicrobium	0.43	0.33				
AF12					-0.33	
Alloiococcus			0.37			
Anaerococcus	0.3	0.51	0.54			
Anaerotruncus					-0.34	-0.31
Arthrobacter	0.24					
Avibacterium	-0.76	-0.23	-0.3			
Bacillus	-0.7					
Bacteroides			0.33	-0.28	-0.37	
Bifidobacterium	0.76	0.48	-0.28			
Bilophila					-0.38	
Blautia	0.62	0.3				-0.26
Brachybacterium		0.26	0.53	-0.28	0.33	
Brevibacillus	-0.77	-0.55	-0.55	-0.33		
Brevibacterium		0.23	0.45		0.38	
Butyricimonas					-0.35	
Candidatus Arthromitus	0.51		-0.49			
Candidatus Portiera			0.25			
Comamonas			-0.32			
Carnobacterium		-0.39				
Clostridium		0.36		-0.32	-0.27	
Comamonas	-0.29					
Coprobacillus	-0.42				-0.33	
Corynebacterium	0.6	0.59			0.36	
Delftia	-0.54		-0.55			
Dehalobacterium					-0.27	-0.29
Devosia		0.42	0.24			
Dietzia	0.47	0.56	0.4	0.53	0.33	
Dorea	0.65	0.24	-0.24			-0.26
Eggerthella	0.7	0.24				-0.26
Enterococcus	0.31	0.48				0.3
Erysipelothrix	-0.65	0.27		-0.43		
Facklamia	0.42	0.53	0.39		0.27	
Faecalibacterium	0.38		0.28		-0.48	-0.27
Gallibacterium	-0.68					
Gallicola	0.44	0.48	0.28			
Gordonia		0.64		0.45		
GW34		0.32				
Helcococcus		0.51		-0.34		
Helicobacter			0.43		-0.29	
Jeotgalicoccus			0.42		0.37	
Leucobacter	0.68	0.38	0.25		0.24	
Leuconostoc	0.28	0.34				
Moraxella	-0.66					
Microbacterium		0.41				
Oligella		0.42				
Ornithobacterium	-0.78	-0.32	-0.46	-0.29		
Oscillospira	-0.36				-0.41	-0.3

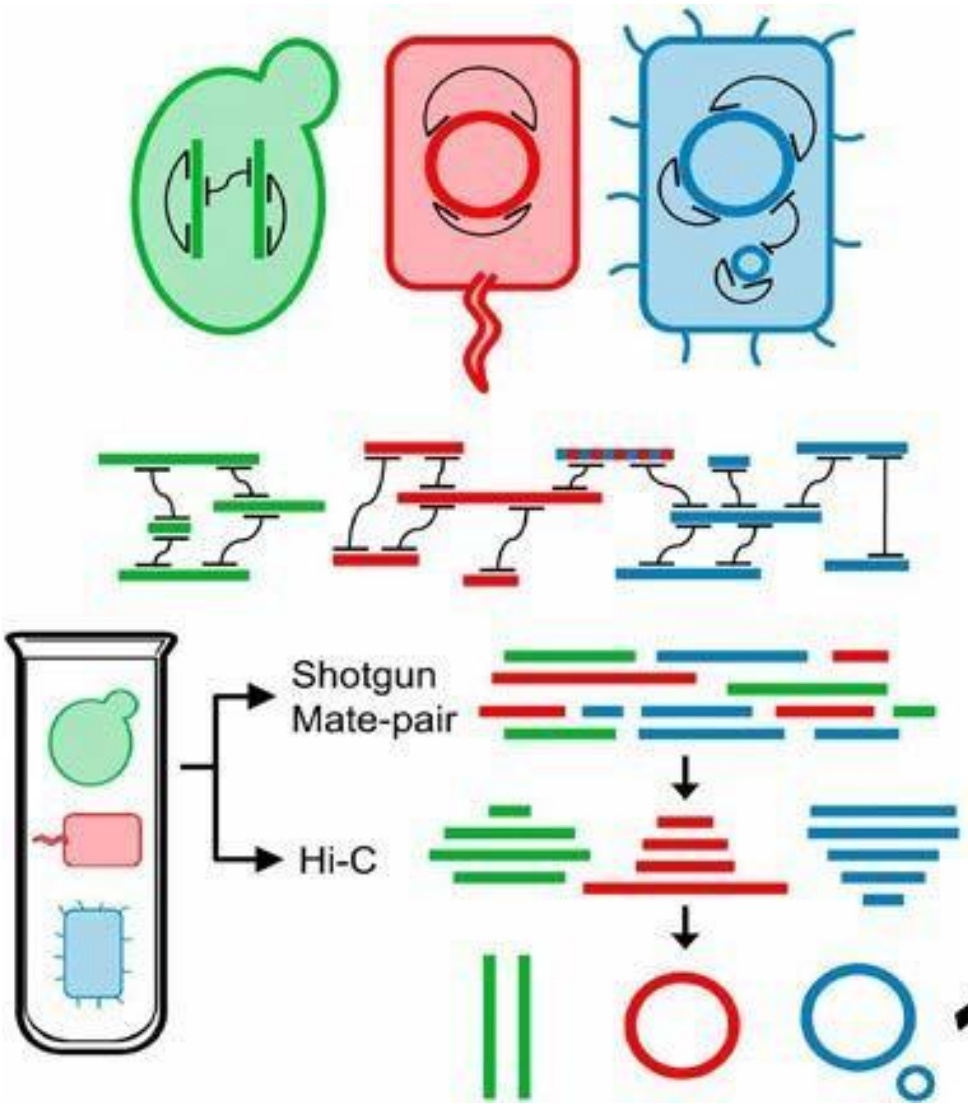
	Trachea					
	D07	D14	D21	D28	D35	D42
Paenibacillus	-0.7					
Parabacteroides					-0.3	
Paracoccus	0.38	0.41				
Pediococcus		0.47	-0.29			
Peptoniphilus	0.48	0.63	0.51	-0.28		
Peptostreptococcus		0.46	0.39	-0.45		
Phascolarctobacterium		0.28			-0.4	
Propionibacterium	0.36				0.36	
Proteus	-0.43			-0.29		
Pseudoclavibacter	0.27					
Psychrobacter	0.42	-0.47				0.29
Ralstonia	-0.57	-0.45	-0.53			
Rhodococcus	0.53	0.36				
Roseateles		-0.37	-0.48			
Rummeliibacillus				-0.49		
Sediminibacterium	-0.65	-0.63	-0.7			
Salinococcus			0.51		0.48	
Serratia	-0.53					
Sphingomonas		-0.25	-0.61			
Sporosarcina		0.45	0.39	-0.37		0.26
Staphylococcus	0.71	0.51				
Streptococcus	-0.61		-0.57	0.33		
Tissierella Soehngenia		0.4		-0.49		
Vagococcus	0.37	0.31				
Weissella	0.7	0.32	-0.6	-0.26		
Yaniella			0.44		0.33	
Unclassified 03196G20	-0.65	-0.71	-0.74			
Unclassified *Aerococcaceae*			0.4		0.44	0.24
Unclassified *Alcaligenaceae*			0.24			
Unclassified *Bacillaceae*	-0.25	0.25	0.27			
Unclassified *Barnesiellaceae*			0.25		-0.28	
Unclassified *Bifidobacteriaceae*		0.56				
Unclassified *Bradyrhizobiaceae*	-0.52	-0.49	-0.64			
Unclassified *Caulobacteraceae*	-0.52		-0.39		0.25	
Unclassified *Clostridiales*	0.3				-0.35	
Unclassified *Comamonadaceae*	-0.48		-0.64			
Unclassified *Coriobacteriaceae*	0.35					-0.38
Unclassified *Elusimicrobiales*	-0.67	-0.49	-0.69			
Unclassified *Enterobacteriaceae*	-0.66			0.26		0.28
Unclassified *Lactobacillales*		0.41				
Unclassified *Leuconostocaceae*	0.54		-0.37	-0.32		
Unclassified *Micrococcaceae*		0.4				
Unclassified *Mogibacteriaceae*	0.32	0.25				
Unclassified *Moraxellaceae*	0.37	-0.48	-0.3			0.34
Unclassified *Planococcaceae*	0.5	0.51				
Unclassified *Porphyromonadaceae*		0.3				
Unclassified *Pseudomonadaceae*		0.32	0.39	-0.39		
Unclassified *RF32*					-0.43	
Unclassified *RF39*	0.7		-0.25		-0.31	-0.32
Unclassified *Ruminococcaceae*	0.49				-0.29	-0.24
Unclassified *TM73*	0.57	0.36				
Unclassified *Xanthomonadaceae*	-0.56		-0.37			0.28

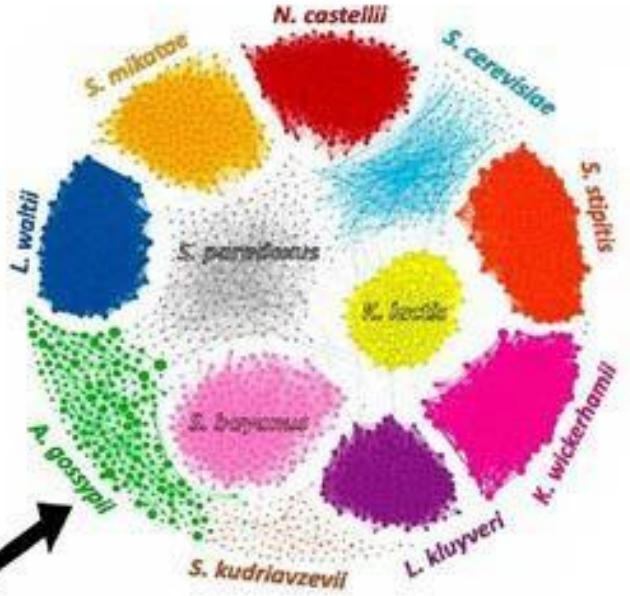

0.45
0.4
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
Relative percent abundance
Escherichia
Gallibacterium
Avibacterium
Erysipelotrichaceae
Ornithobacterium
Increasing bird body weight


Sample-palooza

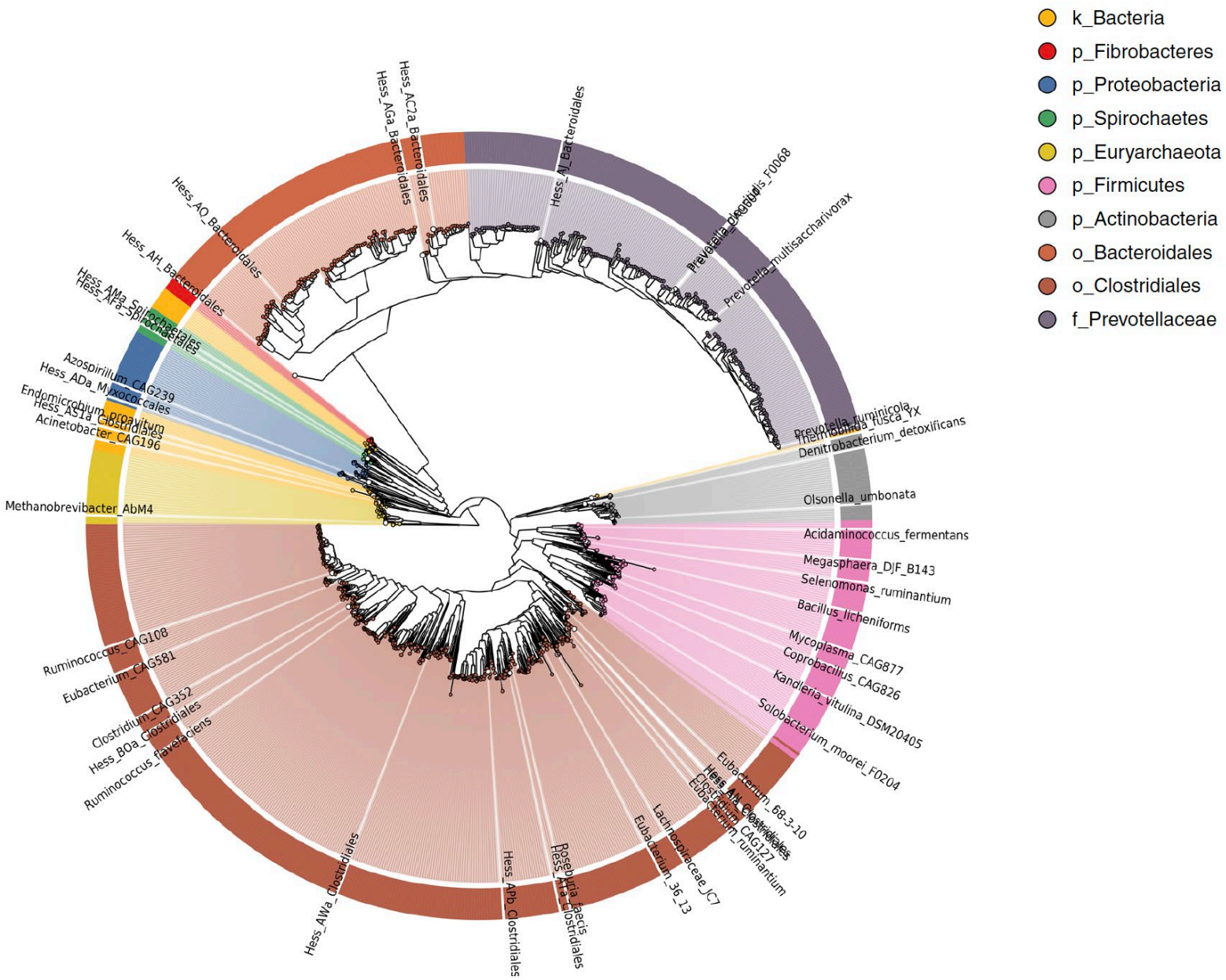
“That’s interesting, but what is going on at the gene expression / functional level?”

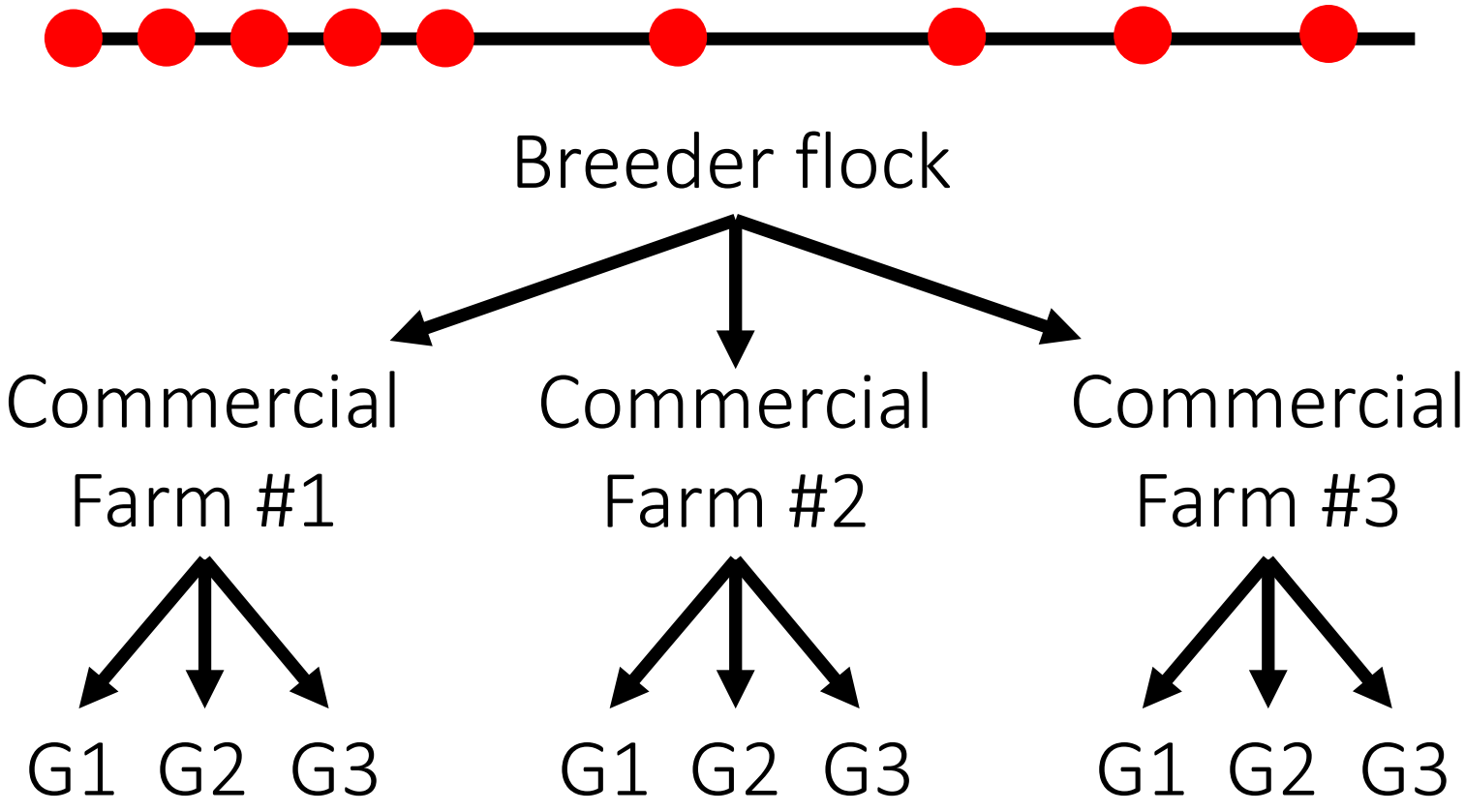
Hi-C Proximeta: creating a database of scaffolded poultry microbial genomes





Rumen metagenome: 913 scaffolded genomes





- Samples
  - Gut (comm.)
  - Trachea (comm.)
  - Sinus wash (comm.)
  - Choanal swab (comm.+breeder)
  - Cloacal swab (comm.+breeder)
- Analyses
  - 16S rRNA
  - Shotgun DNA
  - Build Hi-C database
  - RNA-Seq (host plus microbes)
  - *E. coli* vertical transmission

USDA

NIFA

PRD-CAP

Poultry Respiratory Disease Coordinated Agricultural Project