Table S1. Basal diet composition of Hy-Line Brown laying hens (as-fed basis)

Item	Values
Ingredients (%)	
Corn	50.4
Soybean meal (CP 46%)	18.7
Wheat grain	10.0
Corn gluten meal	2.0
Wheat bran	5.0
Animal fat	4.4
Limestone	7.5
Dicalcium phosphate	1.4
Salt	0.3
DL-Met (50%)	0.1
Vitamin premix[1]	0.1
Trace mineral premix[2]	0.1
Calculated values	
Metabolizable energy (ME) (kcal/kg)	2,904
Crude Protein (CP) (%)	15.02
Lysine (Lys) (%)	0.78
Met + Cys (%)	0.65
Ca (%)	3.25
Total P (%)	0.61
Analyzed composition	
Met + Cys (%)	0.68
CP (%)	15.6
Lys (%)	0.85
Ca (%)	3.41
Available P	0.48

[1]Provided per kg of diet: vitamin A, 125,000 IU; vitamin D_3, 2,500 IU; vitamin E, 10 mg; vitamin K_3, 2 mg; vitamin B_1, 1 mg; vitamin B_2, 5 mg; vitamin B_6, 1 mg; vitamin B_{12}, 15 mg; folic acid, 500mg; niacin, 35,000mg; Ca-Pantothenate, 10,000mg and biotin, 50mg

[2]Provided per kg of diet: 8 mg Mn (as MnO_2); 60 mg Zn (as $ZnSO_4$); 40 mg Fe (as $FeSO_4 \cdot 7H_2O$); 5 mg Cu (as $CuSO_4 \cdot 5H_2O$); 0.3 mg Co (as $CoSO_4 \cdot 5H_2O$); 1.5 mg I (as KI); and 0.15 mg Se (as $Na_2SeO_3 \cdot 5H_2O$).

Table S2. Bacterial genera (n = 173) present in laying hens

Genus (#1~44)	Genus (#45~88)	Genus (#89~132)	Genus (#96~173)
f_[Paraprevotellaceae];g_[Prevotella]	*f_[Paraprevotellaceae];g_CF231*	*Helicobacter*	*Pontibacter*
f_Lachnospiraceae;g_[Ruminococcus]	*Chryseobacterium*	*Herbaspirillum*	*Prevotella*
f_Clostridiaceae;g_02d06	*Cloacibacterium*	*Holdemania*	*Propionibacterium*
Acinetobacter	*Clostridium*	*o_Alteromonadales;f_HTCC2188;g_HTCC*	*Proteiniclasticum*
Actinobacillus	*f_Lachnospiraceae;g_Clostridium*	*Hylemonella*	*Proteus*
Actinomyces	*Comamonas*	*Hyphomicrobium*	*Pseudoclavibacter*
Adlercreutzia	*Coprobacillus*	*Janthinobacterium*	*Pseudomonas*
Aequorivita	*Coprococcus*	*Jeotgalicoccus*	*Pseudonocardia*
Aeriscardovia	*Corynebacterium*	*Kaistobacter*	*Pseudoramibacter.Eubacterium*
Aerococcus	*Dehalobacterium*	*Kocuria*	*Pseudoxanthomonas*
Aeromonas	*Delftia*	*Lachnospira*	*Psychrobacter*
Agrobacterium	*Demequina*	*Lactobacillus*	*Roseburia*
Akkermansia	*Desemzia*	*Lactococcus*	*Rothia*
Alicyclobacillus	*Desulfovibrio*	*Leptotrichia*	*Ruminococcus*
Alistipes	*Devosia*	*Leucobacter*	*Rummeliibacillus*
Alkalibacterium	*Dialister*	*Listeria*	*Salinicoccus*
Alkaliphilus	*Dietzia*	*Luteimonas*	*Sediminibacterium*
Alloiococcus	*Dorea*	*Lysinibacillus*	*Serratia*
Amaricoccus	*Dyadobacter*	*Lysobacter*	*Slackia*
Anaerococcus	*Enhydrobacter*	*Mesorhizobium*	*f_Clostridiaceae;g_SMB53*
Anaerofustis	*Enterobacter*	*Methylobacterium*	*Sneathia*
Anaeroplasma	*Enterococcus*	*Methylophaga*	*Solibacillus*
Anaerostipes	*Epulopiscium*	*Micrococcus*	*Sphingobacterium*
Anaerotruncus	*Escherichia*	*Moraxella*	*Sphingomonas*
Arthrobacter	*Eubacterium*	*Mucispirillum*	*Spirosoma*
Bacillus	*Facklamia*	*Mycobacterium*	*Sporosarcina*
Bacteroides	*Faecalibacterium*	*Mycoplana*	*Staphylococcus*
Barnesiella	*Fimbriimonas*	*Myroides*	*Stenotrophomonas*
Bartonella	*Finegoldia*	*Myxococcus*	*Streptococcus*
Bilophila	*Flavobacterium*	*Natronobacillus*	*Succinatimonas*
Blautia	*Flexispira*	*Nevskia*	*Sutterella*
Brachybacterium	*Fusobacterium*	*Novosphingobium*	*Trichococcus*
Bradyrhizobium	*Gallibacterium*	*Ochrobactrum*	*Truepera*
Brevibacterium	*Gallicola*	*Odoribacter*	*Turicibacter*

Brevundimonas	*Geobacillus*	*Oligella*	*Vagococcus*
Butyricimonas	*Gillisia*	*Oscillospira*	*Variovorax*
Campylobacter	*Gluconacetobacter*	*Pandoraea*	*Wautersiella*
Candidatus.Arthromitus	*Gordonia*	*Parabacteroides*	*Weissella*
Candidatus.Cardinium	*Granulicatella*	*Paracoccus*	*Wohlfahrtiimonas*
Cardiobacterium	*f_[Tissierellaceae];g_GW-34*	*Paraprevotella*	*Yaniella*
Carnobacterium	*Haemophilus*	*Peptococcus*	*Zoogloea*
Caulobacter	*Halomonas*	*Phascolarctobacterium*	
f_Erysipelotrichaceae;g_cc_115	*f_Alteromonadaceae;g_HB2-32-21*	*Phenylobacterium*	
Cellulosimicrobium	*Helcococcus*	*Planomicrobium*	

Table S3. Highly abundant KEGG functions in laying hens groups

Function (#1~20)	Function (#21~40)	Function (#41~60)	Function (#61~80)
DNA repair and recombination proteins	Pentose phosphate pathway	Fatty acid biosynthesis	Sulfur metabolism
Ribosome	Glycine, serine and threonine metabolism	Valine, leucine and isoleucine degradation	Lysine degradation
Purine metabolism	Mismatch repair	Thiamine metabolism	Lipopolysaccharide biosynthesis
Two-component system	Peptidoglycan biosynthesis	Bacterial chemotaxis	Phenylalanine metabolism
Peptidases	Butanoate metabolism	Base excision repair	Geraniol degradation
Pyrimidine metabolism	Bacterial secretion system	Glycerolipid metabolism	Biosynthesis of unsaturated fatty acids
Chromosome	Nitrogen metabolism	Lipopolysaccharide biosynthesis proteins	Peroxisome
Secretion system	DNA replication	Nucleotide excision repair	RNA polymerase
Ribosome Biogenesis	Propanoate metabolism	Protein kinases	D-Glutamine and D-glutamate metabolism
Amino acid related enzymes	Galactose metabolism	Cytoskeleton proteins	Toluene degradation
Amino sugar and nucleotide sugar metabolism	Lipid biosynthesis proteins	Photosynthesis proteins	Plant-pathogen interaction
Arginine and proline metabolism	Terpenoid backbone biosynthesis	Photosynthesis	RNA transport
DNA replication proteins	Protein export	Selenocompound metabolism	Inositol phosphate metabolism
Aminoacyl-tRNA biosynthesis	Phosphotransferase system (PTS)	Tryptophan metabolism	Bisphenol degradation
Methane metabolism	Histidine metabolism	Prenyltransferases	D-Alanine metabolism
Glycolysis / Gluconeogenesis	Carbon fixation in photosynthetic organisms	Flagellar assembly	Tropane, piperidine and pyridine alkaloid biosynthesis
Bacterial motility proteins	Glyoxylate and dicarboxylate metabolism	Drug metabolism - other enzymes	Caprolactam degradation
Fructose and mannose metabolism	Glycerophospholipid metabolism	Sulfur relay system	Drug metabolism - cytochrome P450
Homologous recombination	Translation factors	Aminobenzoate degradation	Glutamatergic synapse
Starch and sucrose metabolism	Cell cycle - Caulobacter	beta-Alanine metabolism	Ascorbate and aldarate metabolism