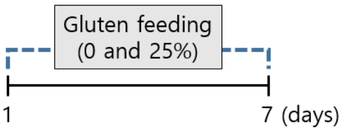
Supplemental_Files

[1st Experiment during 7 days]

- Animals: total 60 birds (30 birds per group,10 birds/cage and 3 cages/group)

- Birds and feed were weighed per cage at 1 and 7 day-old (7 days).

- Samples: randomly sacrificed at 7 day-old (n=3/group) for RNA-sequencing



[2nd Experiment during 28 days]

- Animals: total 60 birds (30 birds per group, 10 birds/cage, and 3 cages/group)

- Birds and feed were weighed per cage at 21 and 28 day-old (7 days).

- Samples: randomly sacrificed at 28-day-old (n=3/group) for RNA-sequencing

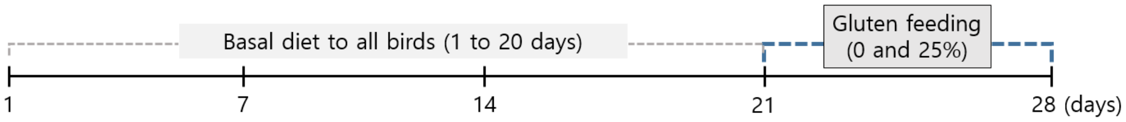


Fig. S1. Experimental design and animal used.

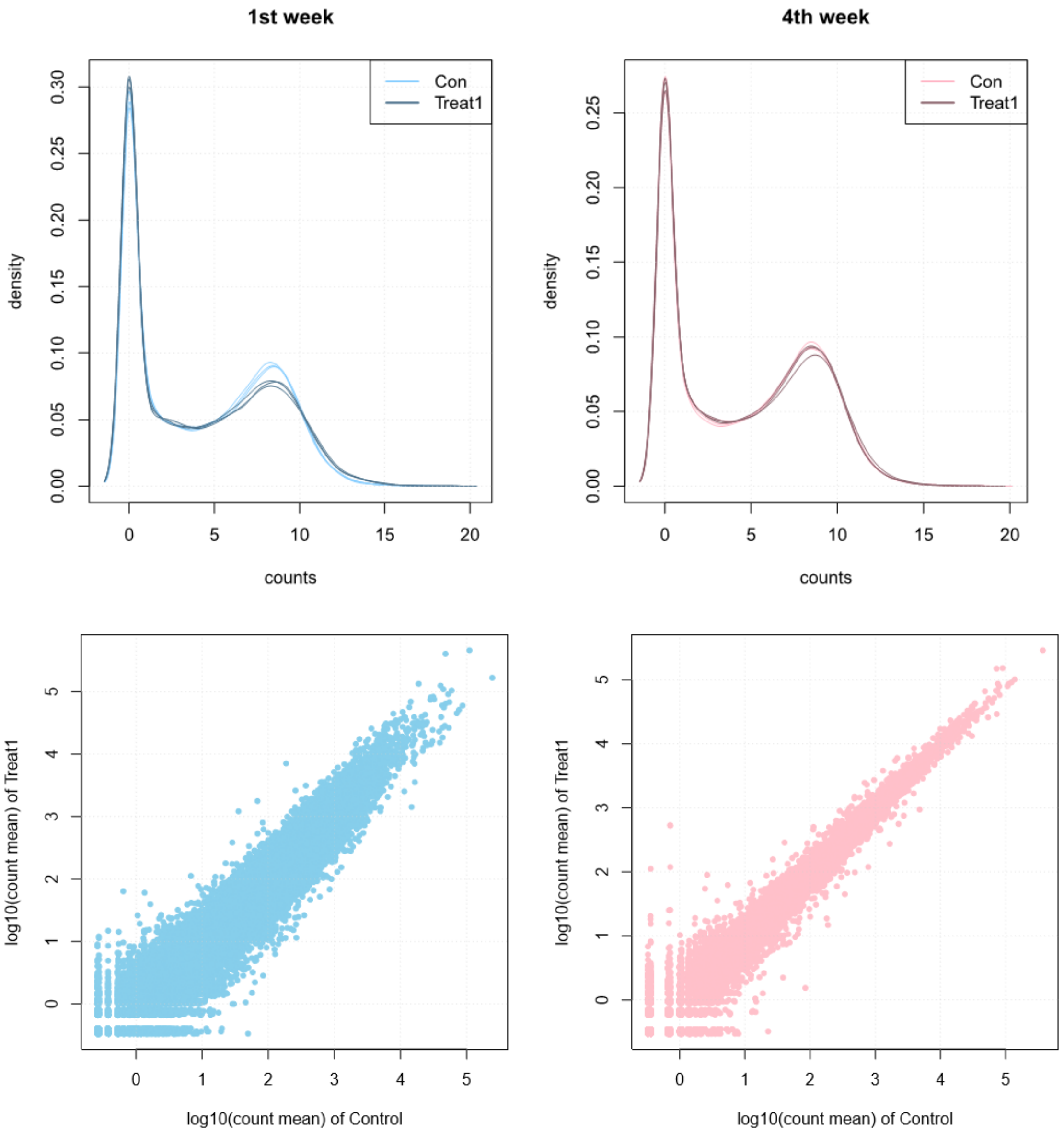


Fig. S2. Density plot and correlation plot to evaluate and cluster the quality of RNA-seq data. Left; Plots for broiler groups at 1week of age. Right; plots for the broiler groups at 4 weeks of age. 'Control' meant non-gluten fed individuals and 'Treat' meant 25%-gluten-fed individuals.

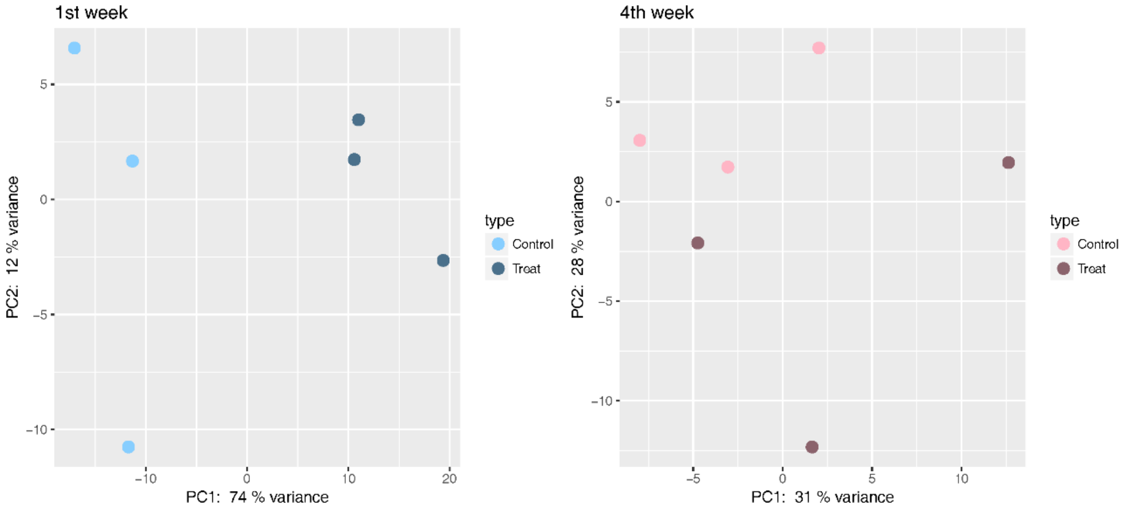


Fig. S3. Principal Component Analysis (PCA) plots for whole genome RNA-seq data to explore the relationships between small intestine samples from different chicken groups. Left; PCA plot for the broiler groups at 1 week of age. Right; PCA plot for the broiler groups at 4 weeks of age. ‘Control’ meant non-gluten fed individuals and ‘Treat’ meant 25%-gluten-fed individuals.

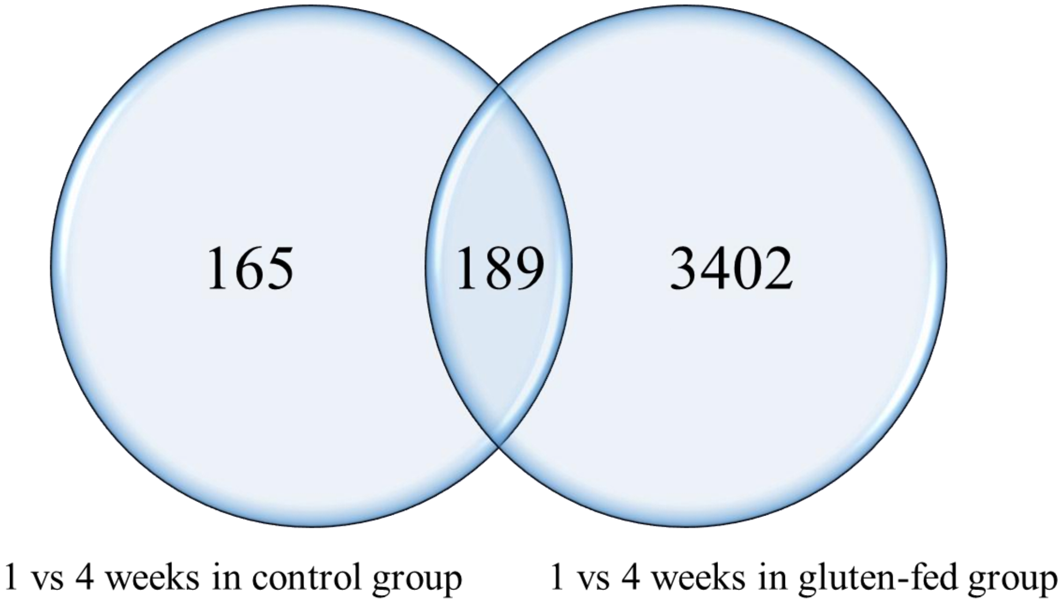


Fig. S4. Venn diagrams of DEGs from 1 week and 4 weeks comparison in control and gluten-fed groups.

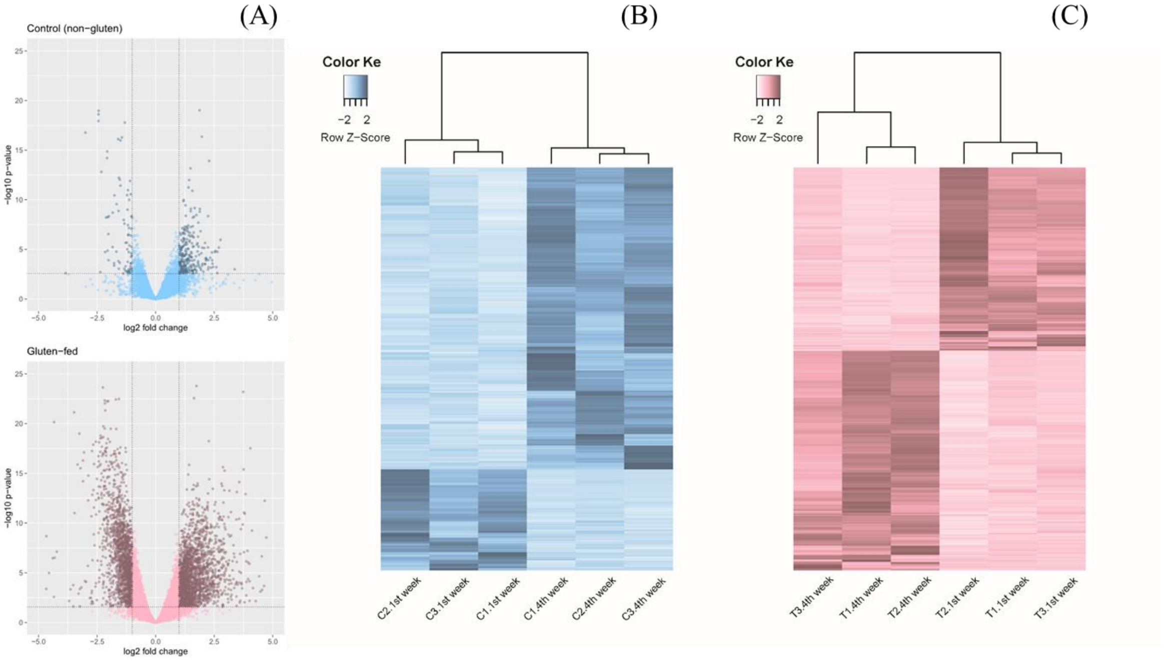


Fig. S5. A comparison of the gene expression pattern between 1 week and 4 week of ange in the control and gluten-fed groups, respectively. (A); A volcano plot of the control (A, upper) and the gluten-fed (A, lower) chicken groups. We extracted DEGs that showed |log2 (fold change) | > 1 and FDR (adjusted P-value) < 0.05. Each dot line in x-axis (log2 fold change) and y-axis (adjusted P-value) indicated significant level in this analysis. (B, C); A heatmap of DEGs comparing gene expression between 1st week and 4th week in control (blue) and gluten-fed (pink) groups. C1.1st week, C2.1st week, C3.1st week and C1.4th week, C2.4th week, C3.4th week were in the control group, and T1.1st week, T2.1st week, T3.1st week and T1.4th week, T2.4th week, T3.4th week belonged to the gluten-fed group.

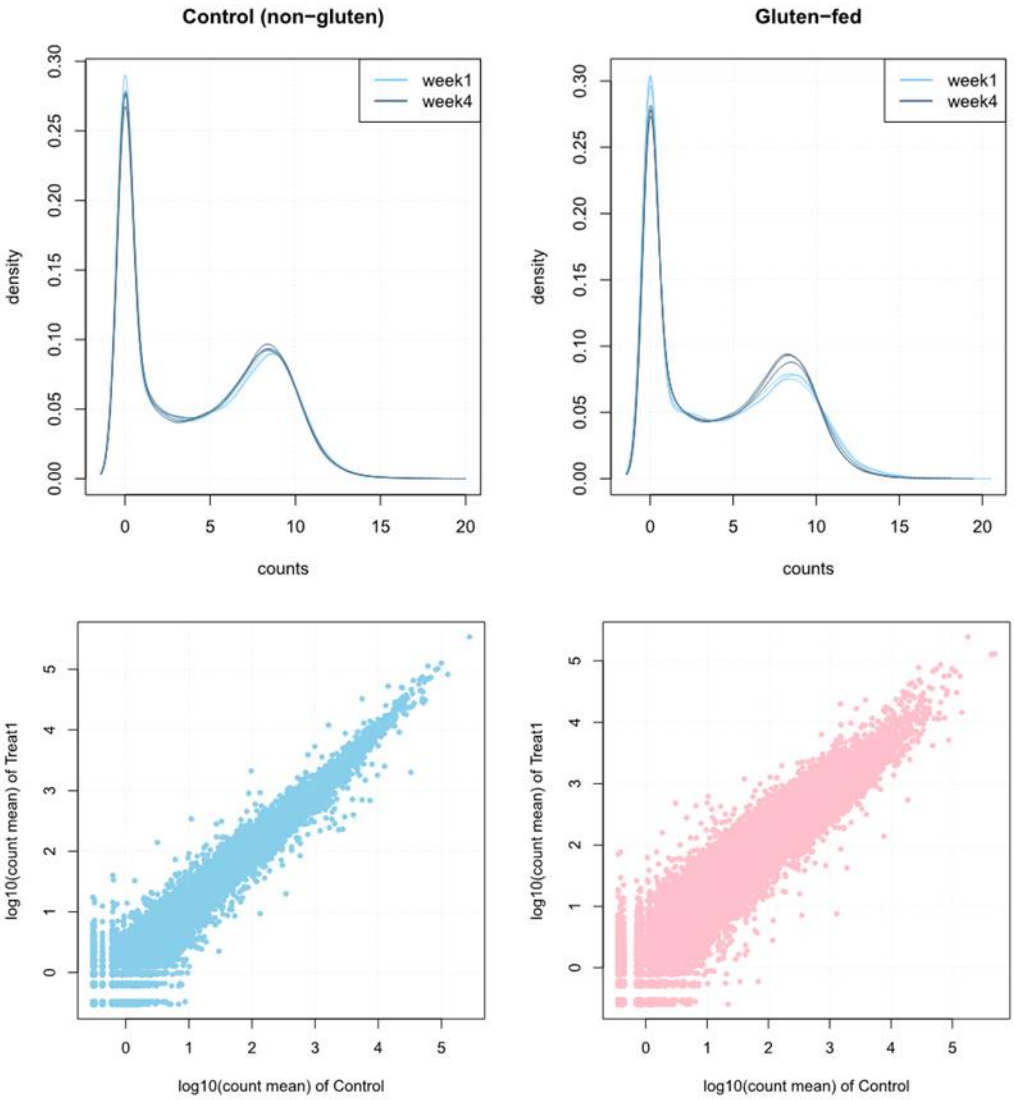


Fig. S6. Density plot and correlation plot to evaluate and cluster the quality of RNA-seq data. Left; Plots for broiler control groups Right; plots for the broiler gluten-fed groups. ‘Control’ meant non-gluten fed individuals and ‘Treat’ meant 25%-gluten-fed individuals.

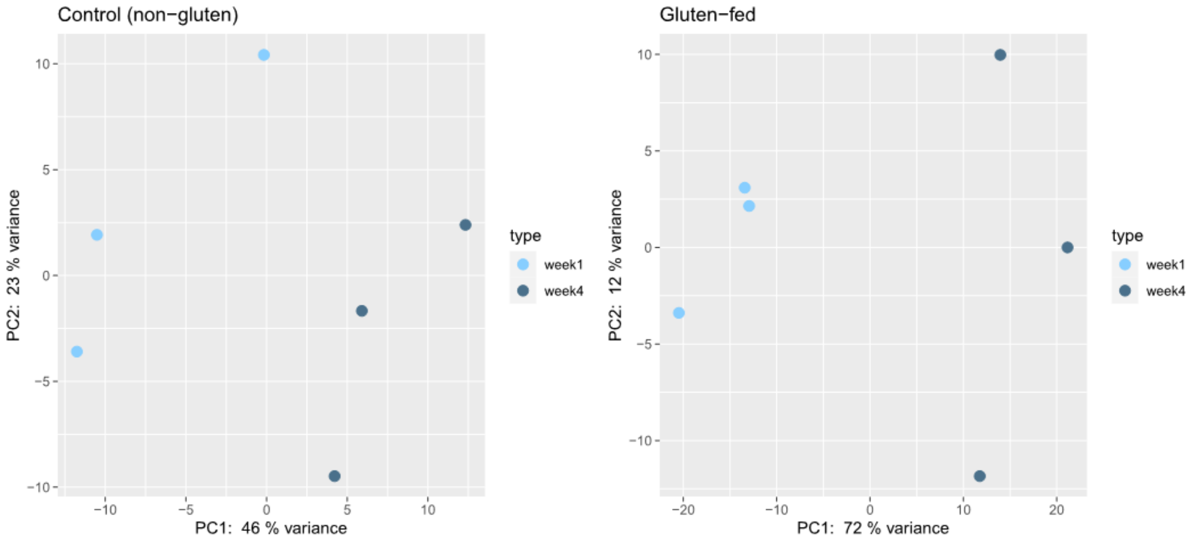


Fig. S7. Principal Component Analysis (PCA) plots for whole genome RNA-seq data to explore the relationships between small intestine samples from different chicken groups. Left; PCA plot for the broiler control groups. Right; PCA plot for the broiler gluten-fed groups. ‘Control’ meant non-gluten fed individuals and ‘Treat’ meant 25%-gluten-fed individuals.

Table S1. RNA-seq reads and mapping rate of intestine samples from twelve chickens fed diets containing different gluten concentrations.

Sampe ID	Read Order	Yield (bases)	# Reads	GC%	Passed Trimmomatic	aligned concordantly exactly 1 time	Overall alignment rate
C1_1005	1	1,095,420,680	14,413,430	47	12,420,582 (86.17%)	85.80%	93.94%
C1_1005	2	1,095,420,680	14,413,430	50	12,420,582 (86.17%)		
C2_1005	1	1,234,030,924	17,150,252	48	16,461,345 (95.98%)	88.10%	95.20%
C2_1005	2	1,234,030,924	17,150,252	49	16,461,345 (95.98%)		
C3_1005	1	1,303,419,152	16,648,983	48	16,109,220 (96.75%)	88.52%	95.40%
C4_1005	2	1,303,419,152	16,648,983	48	16,109,220 (96.75%)		
T1_1005	1	1,213,243,024	18,731,135	46	18,148,388 (96.88%)	88.70%	95.99%
T1_1005	2	1,213,243,024	18,731,135	47	18,148,388 (96.88%)		
T2_1005	1	1,265,322,708	16,769,454	47	15,980,521 (95.29%)	88.97%	95.93%
T2_1005	2	1,265,322,708	16,769,454	48	15,980,521 (95.29%)		
T3_1005	1	1,394,384,920	16,701,298	47	16,186,465 (96.91%)	89.10%	95.96%
T4_1005	2	1,394,384,920	16,701,298	48	16,186,465 (96.91%)		
C1_1026	1	1,285,965,904	16,237,249	50	15,319,675 (94.34%)	86.26%	93.68%
C1_1026	2	1,285,965,904	16,237,249	50	15,319,675 (94.34%)		
C2_1026	1	1,269,298,648	15,963,724	49	15,353,491 (96.17%)	87.89%	94.70%
C2_1026	2	1,269,298,648	15,963,724	49	15,353,491 (96.17%)		
C3_1026	1	1,339,684,756	18,347,170	49	17,576,913 (95.80%)	87.53%	94.41%
C4_1026	2	1,339,684,756	18,347,170	50	17,576,913 (95.80%)		
T1_1026	1	1,398,186,668	18,611,793	48	17,985,512 (96.63%)	87.71%	94.64%
T1_1026	2	1,398,186,668	18,611,793	48	17,985,512 (96.63%)		
T2_1026	1	1,340,234,084	16,920,604	48	16,348,937 (96.62%)	88.26%	95.05%
T2_1026	2	1,340,234,084	16,920,604	48	16,348,937 (96.62%)		
T2_1026	1	1,298,578,940	17,627,431	47	17,044,490 (96.69%)	88.38%	95.62%
T2_1026	2	1,298,578,940	17,627,431	48	17,044,490 (96.69%)		

Table S2. List of primers of the DEG's selected for verification of sequencing analysis data using real-time qPCR

Gene	Primer forward (5`> 3`)	Primer reverse (5`> 3`)
FABP6	CAGGGCAACATGGCATTCAC	TCCTGGGAAATGCTGAGTCC
SCD	TCTTCTCCCACATTGGCTGG	TACCAGGGCACTAGAGTGGG
PRDX1	GGTTTCTGACACAAAGCGTG	AGCCTGAGGGTCTCATCAAC
IRAK1BP1	AGCCCACCTCATTTCTACCAC	CCTCCCCATTCCTTTGTTTCTTC
ß-actin	CAACACAGTGCTGTCTGGTGGTA	ATCGTACTCCTGCTTGCTGATCC

Table S3. Effects of dietary amount of gluten on the growth performance of chickens during the 1 to 7 day post-hatch period (means ± S.E.).

Items	Dietary Gluten concentration		p-value
	0% Glu	25% Glu	
1-day body weight (g/bird)	40.04 ± 1.19	38.76 ± 1.56	0.5483
7-day body weight (g/bird)	113.43 ± 5.17	88.49 ± 6.37	0.0384
Body weight gain (g/1-7 days/bird)	73.38 ± 4.01	49.73 ± 4.82	0.0196
Feed intake (g/bird/1-7 days)	96.67 ± 3.33	66.67 ± 6.01	0.012
Feed conversion ratio (1-7 days)	1.32 ± 0.03	1.34 ± 0.01	0.5243

60 birds were fed 0% or 25% wheat gluten diet during the 1 to 7 day post-hatch period.

n=3 (30 birds/group, 10 birds/cage, and 3 cages/group,).

Table S4. Effects of dietary amount of gluten on the growth performance of chickens during the 21 to 28 day post-hatch period (means ± S.E.).

Items	Dietary Gluten concentration		p-value
	0% Glu	25% Glu	
21-day body weight (g/bird)	313.97 ± 10.27	325.04 ± 8.74	0.4577
28-day body weight (g/bird)	554.73 ± 10.25	510.38 ± 9.3	0.0327
Body weight gain (g/21-28 days/bird)	240.76 ± 8.27	185.34 ± 0.66	0.0026
Feed intake (g/bird/21-28 days)	400 ± 2.89	330 ± 12.58	0.0056
Feed conversion ratio (21-28 days)	1.66 ± 0.05	1.78 ± 0.07	0.224

60 birds were fed 0% or 25% wheat gluten diet during the 21 to 28 day post-hatch period.

n=3 (30 birds/group, 10 birds/cage, and 3 cages/group,).

Table S5. Differentially expressed genes (DEGs) between non-gluten and gluten-fed groups of 1-week-old chicken (adjusted P-value 0.05, |log2FC|: 2)

EnsembleID	gene_name	gene_full_name	gene_biotype	CHR	STA	STO	baseMean	log2FoldChange	pvalue
ENSGALG00000040369	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	protein_coding	1	3,543,236	3,579,756	628.31	-2.15	2.08.E-15
ENSGALG00000034992	FRMD4A	FERM domain containing 4A	protein_coding	1	6,872,404	6,904,583	12.89	-2.18	2.05.E-04
ENSGALG00000008060	PRKAR2B	protein kinase cAMP-dependent type II regulatory subunit beta	protein_coding	1	14,466,581	14,547,811	45.3	-2.05	1.13.E-05
ENSGALG00000008554	IL17REL	interleukin 17 receptor E like	protein_coding	1	20,036,081	20,070,713	13.25	2.14	1.79.E-04
ENSGALG00000008635	-	-	protein_coding	1	20,345,887	20,349,591	22.38	2.22	1.71.E-05
ENSGALG00000009895	GRIP1	glutamate receptor interacting protein 1	protein_coding	1	34,431,194	34,578,266	26.2	-2.04	5.23.E-05
ENSGALG00000040855	PTPRR	protein tyrosine phosphatase, receptor type R	protein_coding	1	35,908,165	35,944,608	1193.96	2.03	2.45.E-15
ENSGALG00000032272	-	-	protein_coding	1	48,099,163	48,099,621	130.2	2.03	5.01.E-07
ENSGALG00000011856	FMC1	formation of mitochondrial complex V assembly factor 1 homolog	protein_coding	1	49,141,973	49,142,442	223.91	2.1	5.13.E-12
ENSGALG00000011992	EP300	E1A binding protein p300	protein_coding	1	49,814,540	49,870,572	604.63	-2.22	6.87.E-11
ENSGALG00000012796	KIAA1549	KIAA1549	protein_coding	1	56,292,882	56,362,827	98.28	-2.01	4.32.E-08
ENSGALG00000012834	AKR1D1	aldo-keto reductase family 1 member D1	protein_coding	1	56,606,803	56,640,860	172.52	2.07	8.08.E-10
ENSGALG00000036355	C7orf73	chromosome 7 open reading frame 73	protein_coding	1	58,456,261	58,462,431	2065.9	2.41	5.22.E-17
ENSGALG00000013022	-	-	protein_coding	1	61,471,636	61,671,542	52.85	-2.28	3.67.E-08
ENSGALG00000014412	CSTA	cystatin A	protein_coding	1	76,773,166	76,778,171	591.91	2.19	4.70.E-10

EnsembleID	gene_name	gene_full_name	gene_biotype	CHR	STA	STO	baseMean	log2FoldChange	pvalue
ENSGALG00000014413	CCDC58	coiled-coil domain containing 58	protein_coding	1	76,787,499	76,796,808	716.61	2.33	1.23.E-18
ENSGALG00000014554	ATN1	Atrophin 10	protein_coding	1	77,317,847	77,325,309	60.75	-2.01	1.18.E-06
ENSGALG00000031560	USF3	upstream transcription factor family member 3	protein_coding	1	79,232,533	79,256,355	102.36	-2.21	6.70.E-13
ENSGALG00000014981	COX17	COX17, cytochrome c oxidase copper chaperone	protein_coding	1	80,152,053	80,153,980	1795.65	2.08	9.06.E-23
ENSGALG00000015077	ARHGAP31	Rho GTPase Activating Protein 31	protein_coding	1	80,711,561	80,764,144	52.81	-2.05	4.36.E-06
ENSGALG00000015307	ABI3BP	ABI Family Member 3 Binding Protein	protein_coding	1	84,985,337	85,117,095	105.91	-2.27	2.48.E-06
ENSGALG00000015730	TMPRSS15	transmembrane protease, serine 15	protein_coding	1	99,575,737	99,632,199	10.18	2.08	1.83.E-03
ENSGALG00000015751	ATP5J	ATP synthase, H+ transporting, mitochondrial Fo complex subunit F6	protein_coding	1	102,543,808	102,548,326	6537.69	2.15	5.41.E-18
ENSGALG00000015835	GRIK1	glutamate ionotropic receptor kainate type subunit 1	protein_coding	1	104,161,063	104,236,516	60.9	-2.26	1.88.E-06
ENSGALG00000022813	NDUFV3	NADH:ubiquinone oxidoreductase subunit V3	protein_coding	1	109,599,316	109,606,438	1841.56	2.09	2.09.E-16
ENSGALG00000016202	HSF2BP	heat shock transcription factor 2 binding protein	protein_coding	1	109,998,577	110,032,898	145.3	2.02	1.98.E-08
ENSGALG00000016287	NR0B1	nuclear receptor subfamily 0 group B member 1	protein_coding	1	115,909,469	115,911,505	63.57	2.14	4.77.E-07
ENSGALG00000016511	ADGRG2	adhesion G protein-coupled receptor G2	protein_coding	1	120,395,079	120,415,594	82.92	-2.07	7.71.E-06
ENSGALG00000016843	COL4A2	collagen type IV alpha 2 chain	protein_coding	1	138,904,303	139,053,712	1368.33	-2.38	4.16.E-13
ENSGALG00000036258	PCDH8	protocadherin 8	protein_coding	1	165,685,515	165,689,031	19.01	-2.34	5.89.E-05
ENSGALG00000017040	-	-	protein_coding	1	171,268,903	171,314,194	96.76	-2.14	1.49.E-06

EnsembleID	gene_name	gene_full_name	gene_biotype	CHR	STA	STO	baseMean	log2FoldChange	pvalue
ENSGALG00000017046	POSTN	periostin	protein_coding	1	171,990,657	172,022,731	322.52	-2.22	2.60.E-08
ENSGALG00000017229	FAT3	FAT atypical cadherin 3	protein_coding	1	186,427,685	186,783,045	23.68	-2.1	6.84.E-06
ENSGALG00000017334	DCHS1	dachsous cadherin-related 1	protein_coding	1	194,348,213	194,364,645	23.34	-2.66	3.08.E-07
ENSGALG00000042836	KCNH2	potassium voltage-gated channel subfamily H member 2	protein_coding	2	322,430	330,338	21.07	-2.12	1.04.E-04
ENSGALG00000040783	-	-	protein_coding	2	597,338	671,104	105.22	-2.29	9.99.E-11
ENSGALG00000032561	MAP4	Microtubule Associated Protein 4	protein_coding	2	681,365	708,854	141.98	-2.14	1.01.E-09
ENSGALG00000027765	MRC1L-D	macrophage mannose receptor 1-like	protein_coding	2	19,491,773	19,522,296	12.99	-2.12	1.82.E-04
ENSGALG00000028304	MRC1	Mannose Receptor C-Type 1	protein_coding	2	19,570,298	19,596,231	17.55	-2.44	8.72.E-06
ENSGALG00000010259	COL28A1	collagen type XXVIII alpha 1 chain	protein_coding	2	24,735,576	24,796,883	104.49	-3.11	2.58.E-12
ENSGALG00000010997	DFNA5	DFNA5, deafness associated tumor suppressor	protein_coding	2	31,663,719	31,688,494	1743.89	2.9	5.08.E-19
ENSGALG00000028983	-	-	protein_coding	2	32,700,853	32,703,521	45.19	-2.16	1.18.E-08
ENSGALG00000041491	ACKR4	atypical chemokine receptor 4	protein_coding	2	42,466,371	42,467,444	25.72	-2.6	3.99.E-07
ENSGALG00000041625	LSM5	LSM5 homolog, U6 small nuclear RNA and mRNA degradation associated	protein_coding	2	48,282,152	48,286,922	1148.3	2.05	2.61.E-15
ENSGALG00000037258	MRPL32	mitochondrial ribosomal protein L32	protein_coding	2	51,330,705	51,332,926	695.87	2.11	4.30.E-15
ENSGALG00000037863	SEC61G	Sec61 translocon gamma subunit	protein_coding	2	52,289,895	52,293,714	3070.2	2.28	2.76.E-14
ENSGALG00000042534	NFATC1	nuclear factor of activated T-cells 1	protein_coding	2	56,746,642	56,868,269	24.06	-2.1	2.46.E-05
ENSGALG00000012715	CAP2	cyclase associated actin cytoskeleton regulatory protein 2	protein_coding	2	62,171,926	62,225,717	153.31	-2.02	4.62.E-08

EnsembleID	gene_name	gene_full_name	gene_biotype	CHR	STA	STO	baseMean	log2FoldChange	pvalue
ENSGALG00000013124	FHOD3	formin homology 2 domain containing 3	protein_coding	2	83,340,744	83,708,432	63.63	-2.15	1.93.E-09
ENSGALG00000014935	GREB1L	GREB1 like retinoic acid receptor coactivator	protein_coding	2	102,634,399	102,704,531	20.66	-2.09	9.37.E-05
ENSGALG00000036749	MRPS28	mitochondrial ribosomal protein S28	protein_coding	2	121,346,830	121,347,204	564.82	2.02	8.05.E-15
ENSGALG00000037867	MRPL53	mitochondrial ribosomal protein L53	protein_coding	2	121,886,469	121,890,988	973.02	2.12	4.39.E-21
ENSGALG00000032282	CALB1	calbindin 1	protein_coding	2	124,959,171	124,977,043	41530.51	2.11	4.56.E-09
ENSGALG00000045196	LAPTM4B	lysosomal protein transmembrane 4 beta	protein_coding	2	127,896,686	127,957,080	49.37	-2.47	1.06.E-09
ENSGALG00000036618	ENY2	ENY2 Transcription And Export Complex 2 Subunit	protein_coding	2	132,606,889	132,612,643	795.87	2.14	3.34.E-16
ENSGALG00000037618	ASAP1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	protein_coding	2	140,681,764	140,794,785	26.85	-2.12	5.95.E-06
ENSGALG00000030878	RPLP1	ribosomal protein lateral stalk subunit P1	protein_coding	2	145,812,305	145,813,467	16169.24	2.02	4.41.E-19
ENSGALG00000032790	SCRIB	Scribble Planar Cell Polarity Protein	protein_coding	2	149,349,274	149,417,049	188.27	-2.09	2.25.E-10
ENSGALG00000008931	COMMD1	copper metabolism domain containing 1	protein_coding	3	8,983,259	9,052,594	1174.22	2.36	1.90.E-29
ENSGALG00000008815	LRRN4	leucine rich repeat neuronal 4	protein_coding	3	15,330,848	15,337,331	30.48	-2.28	2.16.E-04
ENSGALG00000028520	-	-	protein_coding	3	15,591,701	15,594,391	10237.95	2.36	2.12.E-29
ENSGALG00000030269	-	-	protein_coding	3	17,576,337	17,583,720	1566.42	2	6.01.E-24
ENSGALG00000009890	MRPS10	mitochondrial ribosomal protein S10	protein_coding	3	22,900,173	22,906,415	1091.85	2.47	4.54.E-25
ENSGALG00000010664	KIF26B	kinesin family member 26B	protein_coding	3	34,440,793	34,727,673	23.78	-2.84	1.21.E-07
ENSGALG00000010812	-	-	protein_coding	3	37,306,402	37,666,241	90.55	-2.01	7.19.E-07
ENSGALG00000011013	PCNX2	pecanex homolog 2 (Drosophila)	protein_coding	3	38,978,661	39,103,295	16.6	-2.1	1.82.E-04

EnsembleID	gene_name	gene_full_name	gene_biotype	CHR	STA	STO	baseMean	log2FoldChange	pvalue
ENSGALG00000011086	-	-	protein_coding	3	40,139,164	40,141,584	227.95	-2.29	3.96.E-11
ENSGALG00000036240	AKAP12	A-kinase anchoring protein 12	protein_coding	3	48,974,017	48,992,482	114.1	-2.54	6.15.E-08
ENSGALG00000014950	-	-	protein_coding	3	63,962,962	63,969,961	7052.51	2.23	4.14.E-33
ENSGALG00000015066	WASF1	WAS protein family member 1	protein_coding	3	66,877,458	66,903,951	37.07	-2.31	5.94.E-06
ENSGALG00000015733	MDN1	midasin AAA ATPase 1	protein_coding	3	75,720,534	75,772,576	54.56	-2.25	3.52.E-08
ENSGALG00000031219	MDN1	Midasin AAA ATPase 1	protein_coding	3	75,794,168	75,800,647	70.41	-2.15	1.75.E-10
ENSGALG00000015812	SMIM8	small integral membrane protein 8	protein_coding	3	76,778,797	76,781,338	209.11	2.01	8.28.E-13
ENSGALG00000015892	IRAK1BP1	interleukin 1 receptor associated kinase 1 binding protein 1	protein_coding	3	79,909,975	79,920,267	40.89	2.26	1.59.E-09
ENSGALG00000015910	CD109	CD109 molecule	protein_coding	3	81,650,139	81,729,852	17.08	-2.03	2.10.E-04
ENSGALG00000016392	RPS7	ribosomal protein S7	protein_coding	3	94,094,085	94,102,761	18511.83	2.3	3.11.E-22
ENSGALG00000016502	TP53I3	tumor protein p53 inducible protein 3	protein_coding	3	104,675,725	104,680,874	323.83	2.33	1.06.E-14
ENSGALG00000029837	OST4	oligosaccharyltransferase complex subunit 4, non-catalytic	protein_coding	3	104,940,625	104,941,375	2103.48	2.37	2.15.E-15
ENSGALG00000005553	NLGN3	neuroligin 3	protein_coding	4	2,335,565	2,353,557	14.03	-2.01	3.58.E-04
ENSGALG00000006822	PCDH19	protocadherin 19	protein_coding	4	5,247,920	5,296,040	11.77	-2.21	5.40.E-04
ENSGALG00000007646	-	-	protein_coding	4	11,976,831	12,094,695	150.4	-2.25	2.20.E-09
ENSGALG00000009985	LSM6	LSM6 homolog, U6 small nuclear RNA and mRNA degradation associated	protein_coding	4	31,621,811	31,626,778	679.92	2.11	2.77.E-13
ENSGALG00000039411	COL25A1	collagen type XXV alpha 1 chain	protein_coding	4	37,840,437	37,922,607	11.35	-2.03	9.54.E-04
ENSGALG00000011319	ADGRL3	adhesion G protein-coupled receptor L3	protein_coding	4	48,307,262	48,698,041	11.48	-2.29	1.63.E-04

EnsembleID	gene_name	gene_full_name	gene_biotype	CHR	STA	STO	baseMean	log2FoldChange	pvalue
ENSGALG00000011986	FABP2	fatty acid binding protein 2	protein_coding	4	55,073,379	55,075,812	76097.44	2.59	6.37.E-12
ENSGALG00000013771	KIAA1211	capping protein inhibiting regulator of actin dynamics	protein_coding	4	65,222,692	65,243,920	1240.63	-2.14	1.21.E-20
ENSGALG00000022950	MRPL35	mitochondrial ribosomal protein L35	protein_coding	4	86,078,408	86,079,963	1458.56	2.17	1.67.E-15
ENSGALG00000016017	SLC4A11	solute carrier family 4 member 11	protein_coding	4	89,436,576	89,527,283	8.37	-2.09	1.13.E-03
ENSGALG00000016105	DYSF	dysferlin	protein_coding	4	91,217,010	91,267,485	99.34	-2.81	8.35.E-15
ENSGALG00000041253	MYRF	chromosome 5 open reading frame, human C11orf9	protein_coding	5	183,511	218,679	551.59	-2.15	2.28.E-11
ENSGALG00000037020	SCT	secretin	protein_coding	5	533,877	538,465	1432.86	3.14	1.20.E-21
ENSGALG00000045362	-	-	protein_coding	5	1,570,918	1,572,157	38.82	2.31	5.78.E-06
ENSGALG00000003748	ANO5	anoctamin 5	protein_coding	5	2,699,425	2,749,644	1547.22	2.03	1.61.E-12
ENSGALG00000005948	RPL27A	ribosomal protein L27a	protein_coding	5	9,732,157	9,735,693	14894.23	2.04	3.19.E-13
ENSGALG00000007178	-	-	protein_coding	5	16,777,263	16,794,363	86.86	-2.09	1.81.E-08
ENSGALG00000009282	ELMSAN1	ELM2 and Myb/SANT domain containing 1	protein_coding	5	26,124,345	26,142,266	93.23	-2.04	7.49.E-10
ENSGALG00000009415	SMOC1	SPARC related modular calcium binding 1	protein_coding	5	27,718,429	27,835,276	19.22	-2.26	2.32.E-05
ENSGALG00000009844	ACTC1	actin alpha cardiac muscle 1	protein_coding	5	32,283,463	32,288,278	117.35	-3.25	2.77.E-12
ENSGALG00000028537	NDUFB1	NADH:ubiquinone oxidoreductase subunit B1	protein_coding	5	44,628,424	44,630,940	6224.79	2.01	2.69.E-16
ENSGALG00000011581	KIF26A	kinesin family member 26A	protein_coding	5	50,787,246	50,883,770	60.24	-2.01	5.97.E-08
ENSGALG00000012361	NIN	ninein	protein_coding	5	58,040,392	58,064,238	20.47	-2.03	1.86.E-05
ENSGALG00000012425	FERMT2	fermitin family member 2	protein_coding	5	58,397,292	58,433,351	233.73	-2.08	1.05.E-07

EnsembleID	gene_name	gene_full_name	gene_biotype	CHR	STA	STO	baseMean	log2FoldChange	pvalue
ENSGALG00000002314	CDHR1	cadherin related family member 1	protein_coding	6	3,035,224	3,068,706	12.08	-2.12	5.37.E-04
ENSGALG00000045809	-	-	protein_coding	6	9,405,270	9,406,436	16922.96	2.24	9.79.E-20
ENSGALG00000004167	SRGN	serglycin	protein_coding	6	10,819,703	10,821,527	703.97	2.14	1.65.E-15
ENSGALG00000004446	NPFFR1	neuropeptide FF receptor 1	protein_coding	6	11,517,725	11,521,258	14.75	-2.98	1.90.E-06
ENSGALG00000004871	RPS24	ribosomal protein S24	protein_coding	6	13,151,895	13,157,847	18939.1	2.09	7.27.E-23
ENSGALG00000005739	SCD	stearoyl-CoA desaturase	protein_coding	6	17,493,789	17,509,405	137.32	-3.95	3.50.E-19
ENSGALG00000039528	PLCE1	phospholipase C epsilon 1	protein_coding	6	20,124,539	20,190,565	10.93	-2	1.20.E-03
ENSGALG00000042871	SLIT1	slit guidance ligand 1	protein_coding	6	22,380,435	22,411,706	28.65	-2.29	9.36.E-06
ENSGALG00000034645	USMG5	up-regulated during skeletal muscle growth 5 homolog	protein_coding	6	23,607,715	23,611,523	4144.38	2.25	2.78.E-29
ENSGALG00000008409	-	-	protein_coding	6	24,242,948	24,251,760	6152.38	2.04	1.63.E-29
ENSGALG00000003578	FN1	fibronectin 1	protein_coding	7	4,390,375	4,439,659	1110.04	-2.32	2.78.E-10
ENSGALG00000038311	COL18A1	collagen, type XVIII, alpha 1	protein_coding	7	6,633,230	6,662,722	205.61	-2.06	1.04.E-07
ENSGALG00000036145	-	-	protein_coding	7	6,803,175	6,803,883	193.74	-2.24	3.59.E-09
ENSGALG00000009070	HSPE1	heat shock protein family E (Hsp10) member 1	protein_coding	7	10,247,822	10,254,145	6974.3	2.18	1.27.E-20
ENSGALG00000020836	FAM237A	family with sequence similarity 237 member A	protein_coding	7	12,480,858	12,488,246	11.41	3.68	9.54.E-09
ENSGALG00000035605	UBR3	Ubiquitin Protein Ligase E3 Component N-Recognin 3	protein_coding	7	18,632,759	18,667,992	64.16	-2.22	2.83.E-11
ENSGALG00000043198	SPEG	SPEG complex locus	protein_coding	7	22,259,564	22,269,563	53.32	-2.03	9.14.E-07
ENSGALG00000041013	TNS1	tensin 1	protein_coding	7	22,734,389	22,773,379	706.28	-2.8	2.46.E-15
ENSGALG00000011813	HEG1	heart development protein with EGF like domains 1	protein_coding	7	28,102,696	28,133,209	47.21	-2.42	3.68.E-06

EnsembleID	gene_name	gene_full_name	gene_biotype	CHR	STA	STO	baseMean	log2FoldChange	pvalue
ENSGALG00000002667	OLFML2B	olfactomedin like 2B	protein_coding	8	3,792,799	3,798,695	153.8	-2.02	4.61.E-08
ENSGALG00000002931	REG4	regenerating family member 4	protein_coding	8	4,258,298	4,259,712	205.83	2.55	3.99.E-05
ENSGALG00000002988	PHGDH	phosphoglycerate dehydrogenase	protein_coding	8	4,264,703	4,268,005	13.52	2.53	1.12.E-04
ENSGALG00000010243	PRDX1	peroxiredoxin 1	protein_coding	8	21,219,080	21,225,390	28905.36	2.07	2.09.E-17
ENSGALG00000017380	-	-	protein_coding	8	21,669,092	21,670,565	8211.87	2.05	8.75.E-17
ENSGALG00000041436	DOCK7	Dedicator Of Cytokinesis 7	protein_coding	8	27,623,103	27,657,436	75.3	-2.07	5.50.E-09
ENSGALG00000002193	ARHGEF4	Rho guanine nucleotide exchange factor 4	protein_coding	9	2,275,486	2,312,749	8.26	-2.08	1.12.E-03
ENSGALG00000005327	RBP2	retinol binding protein 2	protein_coding	9	5,912,771	5,923,652	9856.79	2.64	3.08.E-13
ENSGALG00000046152	-	-	protein_coding	9	13,227,054	13,232,017	24.66	-4.21	2.21.E-12
ENSGALG00000007611	RPL35A	ribosomal protein L35a	protein_coding	9	15,170,655	15,173,497	100.6	2.76	1.67.E-14
ENSGALG00000009312	RPL22L1	ribosomal protein L22 like 1	protein_coding	9	19,805,323	19,807,348	3605.04	2.36	5.47.E-21
ENSGALG00000001325	-	-	protein_coding	10	2,375,742	2,379,385	8.31	2.21	4.09.E-04
ENSGALG00000002759	PEAK1	pseudopodium enriched atypical kinase 1	protein_coding	10	2,987,920	3,016,419	227.35	-2.22	2.20.E-10
ENSGALG00000031853	-	-	protein_coding	10	7,968,924	7,969,340	702.16	2.05	1.89.E-14
ENSGALG00000027704	NET1	Neuroepithelial Cell Transforming 1	protein_coding	10	13,862,869	14,132,878	129.04	-2.1	4.10.E-10
ENSGALG00000007349	RASL12	RAS like family 12	protein_coding	10	17,793,895	17,798,756	192.89	2.61	1.44.E-23
ENSGALG00000044618	-	-	protein_coding	10	17,798,993	17,805,421	5710.79	2.07	4.53.E-17
ENSGALG00000007358	CILP	cartilage intermediate layer protein	protein_coding	10	17,819,516	17,827,876	21.29	-2.04	3.22.E-04
ENSGALG00000035587	MAP1A	Microtubule Associated Protein 1A	protein_coding	10	20,228,740	20,232,267	13.23	-2.15	1.76.E-04
ENSGALG00000043662	NDRG4	NDRG family member 4	protein_coding	11	398,197	412,942	38.17	-2.03	1.82.E-06

EnsembleID	gene_name	gene_full_name	gene_biotype	CHR	STA	STO	baseMean	log2FoldChange	pvalue
ENSGALG00000002467	MTSS1L	MTSS1L, I-BAR domain containing	protein_coding	11	1,761,866	1,771,769	44.13	-2.48	1.45.E-06
ENSGALG00000003767	NKD1	naked cuticle homolog 1	protein_coding	11	6,364,520	6,468,658	9.52	-2.25	3.76.E-04
ENSGALG00000032626	C19orf12	Chromosome 19 Open Reading Frame 12	protein_coding	11	8,516,741	8,520,318	832.28	2.3	6.49.E-11
ENSGALG00000033720	CA7	carbonic anhydrase 7	protein_coding	11	11,454,156	11,462,000	260.5	2.02	1.16.E-19
ENSGALG00000032679	GCSH	glycine cleavage system protein H	protein_coding	11	15,629,428	15,636,795	2446.96	2.27	4.61.E-26
ENSGALG00000005408	BCO1	Gallus gallus beta-carotene oxygenase 1 (BCO1), mRNA	protein_coding	11	15,677,760	15,691,537	1723.53	2.05	5.99.E-09
ENSGALG00000006250	TRAPPC2L	trafficking protein particle complex 2 like	protein_coding	11	18,758,510	18,761,077	932.09	2.04	9.27.E-19
ENSGALG00000006222	ANKRD11	Ankyrin Repeat Domain 11	protein_coding	11	18,867,563	18,881,659	94.32	-2.19	2.45.E-10
ENSGALG00000026978	RPL29	ribosomal protein L29	protein_coding	12	578,802	582,447	14589.19	2.69	1.62.E-20
ENSGALG00000038242	CACNA2D2	calcium voltage-gated channel auxiliary subunit alpha2delta 2	protein_coding	12	1,481,230	1,608,215	12.99	-2.09	3.59.E-04
ENSGALG00000001849	BSN	bassoon presynaptic cytomatrix protein	protein_coding	12	2,472,587	2,517,710	51.26	-2.64	1.20.E-09
ENSGALG00000005120	-	-	protein_coding	12	5,812,606	5,860,849	77.73	-3.11	2.80.E-10
ENSGALG00000036763	CELSR3	cadherin EGF LAG seven-pass G-type receptor 3	protein_coding	12	9,026,357	9,037,049	12.51	-2.64	1.93.E-05
ENSGALG00000041750	ADAMTS9	ADAM metallopeptidase with thrombospondin type 1 motif 9	protein_coding	12	13,758,522	13,821,336	72.61	-2.12	9.21.E-08
ENSGALG00000044387	SLC4A9	solute carrier family 4 member 9	protein_coding	13	1,526,801	1,543,148	11.1	-2.24	4.07.E-04
ENSGALG00000028565	PCDHGC3	Gallus gallus protocadherin gamma subfamily A, 2 (PCDHGA2), mRNA	protein_coding	13	1,828,640	1,876,670	183.95	-2.21	8.14.E-08

EnsembleID	gene_name	gene_full_name	gene_biotype	CHR	STA	STO	baseMean	log2FoldChange	pvalue
ENSGALG00000001916	SLIT3	slit guidance ligand 3	protein_coding	13	4,204,850	4,675,881	88.84	-2.31	9.27.E-09
ENSGALG00000001445	FABP6	fatty acid binding protein 6	protein_coding	13	7,872,426	7,910,143	225350.81	3	8.66.E-42
ENSGALG00000036723	SPINK9	Serine Peptidase Inhibitor Kazal Type 9	protein_coding	13	8,164,300	8,168,967	353.16	2.61	4.94.E-11
ENSGALG00000030613	PDGFRB	platelet derived growth factor receptor beta	protein_coding	13	13,256,919	13,269,462	35.43	-2.71	1.60.E-06
ENSGALG00000032974	ADAMTS2	ADAM metallopeptidase with thrombospondin type 1 motif 2	protein_coding	13	13,664,069	13,829,628	91.85	-2.23	1.29.E-07
ENSGALG00000005714	PKD1	polycystin 1, transient receptor potential channel interacting	protein_coding	14	6,339,857	6,422,473	161.84	-2.46	4.53.E-11
ENSGALG00000006520	MYH11	myosin, heavy chain 11, smooth muscle	protein_coding	14	7,610,019	7,666,669	9937.16	-2.05	1.20.E-09
ENSGALG00000030546	CLEC19A	C-type lectin domain family 19 member A	protein_coding	14	8,455,910	8,461,828	20.47	3.25	2.38.E-08
ENSGALG00000002201	PPL	periplakin	protein_coding	14	13,315,606	13,335,789	127	-2.11	5.68.E-07
ENSGALG00000041298	-	-	protein_coding	14	15,017,286	15,034,742	164.87	-2.13	9.87.E-11
ENSGALG00000044654	C22orf39	chromosome 22 open reading frame 39	protein_coding	15	664,843	665,327	203.45	2.06	2.77.E-11
ENSGALG00000005676	TTC28	tetratricopeptide repeat domain 28	protein_coding	15	7,602,100	7,718,375	58	-2.65	2.63.E-08
ENSGALG00000020999	DYNLL1	dynein light chain 1, cytoplasmic-like	protein_coding	15	9,332,406	9,334,064	61.98	2.41	1.86.E-07
ENSGALG00000008066	UQCR10	ubiquinol-cytochrome c reductase, complex III subunit X	protein_coding	15	11,093,312	11,094,737	6899.65	2.39	1.00.E-20
ENSGALG00000032221	-	-	protein_coding	16	316,102	318,484	299.45	2.81	7.16.E-22
ENSGALG00000008456	CACNA1B	calcium voltage-gated channel subunit alpha1 B	protein_coding	17	2,601,746	2,859,437	60.72	-2.06	2.15.E-08
ENSGALG00000030256	PRRC2B	Proline Rich Coiled-Coil 2B	protein_coding	17	6,650,694	6,657,396	41.94	-2.48	2.11.E-08
ENSGALG00000002546	COL5A1	collagen type V alpha 1	protein_coding	17	7,910,288	8,039,020	388.16	-2.28	7.49.E-10

EnsembleID	gene_name	gene_full_name	gene_biotype	CHR	STA	STO	baseMean	log2FoldChange	pvalue
		chain							
ENSGALG00000004418	SSTR2	somatostatin receptor 2	protein_coding	18	9,063,416	9,065,697	68.22	-2.13	3.73.E-05
ENSGALG00000001465	RPL38	ribosomal protein L38	protein_coding	18	9,191,872	9,194,395	9365.48	2.26	4.46.E-13
ENSGALG00000040308	BAHCC1	BAH domain and coiled-coil containing 1	protein_coding	18	9,287,316	9,295,387	153.37	-2	8.79.E-10
ENSGALG00000039269	RNF213	ring finger protein 213	protein_coding	18	9,594,760	9,619,312	1014.5	-2.5	1.44.E-16
ENSGALG00000007623	CACNA1G	calcium voltage-gated channel subunit alpha1 G	protein_coding	18	10,279,329	10,388,753	37.31	-2.31	1.07.E-07
ENSGALG00000007926	ATP5H	ATP synthase, H+ transporting, mitochondrial Fo complex subunit D	protein_coding	18	10,720,628	10,723,334	7296.54	2.08	9.26.E-21
ENSGALG00000034960	MLXIPL	MLX interacting protein like	protein_coding	19	169,275	184,322	1627.18	-2.16	1.01.E-10
ENSGALG00000001028	RNF43	ring finger protein 43	protein_coding	19	527,581	580,075	68.62	-2.27	3.82.E-12
ENSGALG00000043703	ELN	Elastin	protein_coding	19	763,219	769,060	158.01	-2.52	2.28.E-08
ENSGALG00000030450	CLIP2	CAP-GLY domain containing linker protein 2	protein_coding	19	2,751,696	2,795,240	64.98	-2.21	1.49.E-06
ENSGALG00000021572	SSH2	slingshot protein phosphatase 2	protein_coding	19	6,084,890	6,123,770	123.33	-2.22	1.63.E-12
ENSGALG00000003409	SOGA1	suppressor of glucose, autophagy associated 1	protein_coding	20	2,806,856	2,819,565	68.72	-2.52	1.21.E-11
ENSGALG00000005338	RPS21	ribosomal protein S21	protein_coding	20	8,125,418	8,130,006	8305.23	2.64	1.45.E-17
ENSGALG00000036838	PXDNL	peroxidasin like	protein_coding	20	9,238,310	9,277,145	7.35	-2.58	1.20.E-04
ENSGALG00000006138	HELZ2	helicase with zinc finger 2	protein_coding	20	9,941,292	9,949,052	428.24	-2.52	2.15.E-13
ENSGALG00000002232	RERE	arginine-glutamic acid dipeptide repeats	protein_coding	21	3,032,375	3,042,010	329.05	-2.04	1.02.E-10
ENSGALG00000030881	-	-	protein_coding	21	3,147,679	3,148,119	15.09	-2.8	4.47.E-07
ENSGALG00000036932	SPEN	spen family	protein_coding	21	4,241,963	4,297,458	922.28	-2.26	8.55.E-11

EnsembleID	gene_name	gene_full_name	gene_biotype	CHR	STA	STO	baseMean	log2FoldChange	pvalue
		transcriptional repressor							
ENSGALG00000035362	-	-	protein_coding	21	4,396,357	4,404,128	12.18	-2.74	4.44.E-06
ENSGALG00000030603	ANTXR1	anthrax toxin receptor 1	protein_coding	22	156,208	246,299	16.23	-2.08	7.07.E-04
ENSGALG00000028409	SNRPG	small nuclear ribonucleoprotein polypeptide G pseudogene 15	protein_coding	22	3,583,762	3,585,400	490.98	2.1	2.60.E-09
ENSGALG00000024024	TGFA	transforming growth factor alpha	protein_coding	22	3,594,207	3,607,707	9.43	-2.17	4.93.E-04
ENSGALG00000033061	CAMK2B	calcium/calmodulin dependent protein kinase II beta	protein_coding	22	4,681,046	4,697,103	17.77	-2.06	2.68.E-05
ENSGALG00000035184	SDC3	syndecan 3	protein_coding	23	439,987	458,290	25.38	-2.07	1.48.E-05
ENSGALG00000002298	COL8A2	collagen type VIII alpha 2 chain	protein_coding	23	4,146,476	4,152,419	14.53	-2.01	1.46.E-04
ENSGALG00000029197	KIRREL3	kin of IRRE like 3 (Drosophila)	protein_coding	24	454,235	690,429	450.79	-2.67	3.14.E-13
ENSGALG00000037065	SC5D	sterol-C5-desaturase	protein_coding	24	3,531,094	3,534,293	172.62	-2.03	1.00.E-12
ENSGALG00000006751	THY1	Thy-1 cell surface antigen	protein_coding	24	4,170,622	4,174,870	92.85	-2.27	6.97.E-07
ENSGALG00000030027	MCAM	melanoma cell adhesion molecule	protein_coding	24	4,208,870	4,217,491	236.35	-2.97	1.69.E-17
ENSGALG00000006818	KMT2A	lysine methyltransferase 2A	protein_coding	24	4,346,754	4,388,918	201.98	-2.29	1.73.E-13
ENSGALG00000007685	BCL9L	B-cell CLL/lymphoma 9-like	protein_coding	24	5,578,946	5,589,603	181	-2.07	3.65.E-12
ENSGALG00000024094	-	-	protein_coding	25	2,126,269	2,147,947	338.76	-2.01	1.48.E-08
ENSGALG00000014638	ASH1L	ASH1 like histone lysine methyltransferase	protein_coding	25	2,206,557	2,239,618	818.98	-2.03	7.00.E-12
ENSGALG00000045486	-	-	protein_coding	25	2,805,162	2,806,394	115.26	-2.28	1.20.E-08
ENSGALG00000000584	-	-	protein_coding	26	375,289	387,140	17.58	-2.22	4.86.E-05

EnsembleID	gene_name	gene_full_name	gene_biotype	CHR	STA	STO	baseMean	log2FoldChange	pvalue
ENSGALG00000037370	NAV1	neuron navigator 1	protein_coding	26	621,402	647,088	7.42	-2.11	1.58.E-03
ENSGALG00000000362	NAV1	Neuron Navigator 1	protein_coding	26	649,777	660,363	36.58	-2.25	1.01.E-05
ENSGALG00000028721	LMOD1	leiomodin 1	protein_coding	26	1,113,766	1,123,749	360.5	-2.1	1.82.E-08
ENSGALG00000038399	PLEKHA6	pleckstrin homology domain containing A6	protein_coding	26	1,727,670	1,742,914	262.59	-2.12	2.12.E-19
ENSGALG00000031776	NFASC	neurofascin	protein_coding	26	1,889,290	1,965,785	43.82	-2.53	3.99.E-07
ENSGALG00000042137	ELK4	ELK4, ETS transcription factor	protein_coding	26	2,200,895	2,205,209	17.86	-2.06	3.72.E-05
ENSGALG00000001378	C1orf74	Chromosome 1 Open Reading Frame 74	protein_coding	26	3,165,104	3,165,577	220.36	2.03	8.33.E-12
ENSGALG00000034456	PRELP	proline and arginine rich end leucine rich repeat protein	protein_coding	26	5,170,534	5,172,975	50.56	-2.78	3.04.E-07
ENSGALG00000045669	-	-	protein_coding	27	1,645,180	1,646,391	21.93	-2.49	2.77.E-05
ENSGALG00000032628	SRCIN1	SRC kinase signaling inhibitor 1	protein_coding	27	4,277,584	4,332,557	86.06	-2	2.09.E-07
ENSGALG00000000474	RPL36	ribosomal protein L36	protein_coding	28	662,317	665,141	6193.32	2.14	4.05.E-16
ENSGALG00000024398	RPS28	Ribosomal Protein S28	protein_coding	28	874,867	875,414	7307.27	2.19	2.10.E-13
ENSGALG00000041643	cNFI-C	nuclear factor I C	protein_coding	28	1,096,192	1,134,022	99.2	-2.52	5.60.E-11
ENSGALG00000001084	ATP8B3	ATPase phospholipid transporting 8B3	protein_coding	28	2,286,962	2,297,493	11.58	-2.32	1.05.E-04
ENSGALG00000015195	RPS15	ribosomal protein S15	protein_coding	28	3,225,919	3,227,645	12627.14	2.27	5.00.E-17
ENSGALG00000015192	GZMM	Granzyme M	protein_coding	28	3,241,767	3,243,886	7.38	2.05	2.31.E-03
ENSGALG00000003499	MAST3	microtubule associated serine/threonine kinase 3	protein_coding	28	4,037,999	4,047,856	19.02	-2.07	8.91.E-05
ENSGALG00000003742	CPAMD8	C3 and PZP like, alpha-2-macroglobulin domain containing 8	protein_coding	28	4,229,272	4,253,848	41.91	-2.55	2.14.E-06
ENSGALG00000029330	MED29	mediator complex subunit 29	protein_coding	32	50,270	51,540	1587.47	2.13	1.37.E-14

EnsembleID	gene_name	gene_full_name	gene_biotype	CHR	STA	STO	baseMean	log2FoldChange	pvalue
ENSGALG00000031702	KMT2D	lysine methyltransferase 2D	protein_coding	33	542,155	562,006	272.09	-2.56	4.98.E-10
ENSGALG00000041592	SMARCC2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin subfamily c member 2	protein_coding	33	693,527	702,193	306.59	-2.31	1.28.E-12
ENSGALG00000031973	ANKRD52	ankyrin repeat domain 52	protein_coding	33	728,697	744,086	112.52	-2.17	5.02.E-14
ENSGALG00000038757	RBMS2	RNA binding motif single stranded interacting protein 2	protein_coding	33	789,750	795,759	117.12	-2.17	1.48.E-09
ENSGALG00000040960	-	-	protein_coding	33	1,612,235	1,619,106	24.19	-2.35	5.51.E-06
ENSGALG00000029588	BAZ2A	Bromodomain Adjacent To Zinc Finger Domain 2A	protein_coding	33	1,634,536	1,648,011	348.79	-2.16	2.93.E-12
ENSGALG00000002371	RUSC2	RUN and SH3 domain containing 2	protein_coding	Z	8,966,840	8,999,279	56.19	-2.11	8.71.E-09
ENSGALG00000017405	NPR3	natriuretic peptide receptor 3	protein_coding	Z	10,035,886	10,086,792	99.4	-2.04	1.73.E-06
ENSGALG00000014833	RPL37	ribosomal protein L37	protein_coding	Z	12,918,346	12,920,975	12617.03	2.03	1.06.E-14
ENSGALG00000014891	ITGA1	integrin subunit alpha 1	protein_coding	Z	15,771,740	15,844,439	317.87	-2.32	4.27.E-09
ENSGALG00000014933	HEXB	hexosaminidase subunit beta	protein_coding	Z	24,225,312	24,240,840	7292.12	2.19	2.02.E-41
ENSGALG00000038817	CKS2	CDC28 protein kinase regulatory subunit 2	protein_coding	Z	43,552,761	43,555,632	104	2.23	2.58.E-10
ENSGALG00000000428	HINT1	Histidine Triad Nucleotide Binding Protein 1	protein_coding	Z	44,899,734	44,903,752	6095.04	2.4	6.65.E-28
ENSGALG00000015425	LPL	lipoprotein lipase	protein_coding	Z	54,528,388	54,543,657	246.14	-2.24	6.81.E-12
ENSGALG00000027483	GLRX	glutaredoxin	protein_coding	Z	57,343,843	57,352,236	7566.86	2.11	1.14.E-20
ENSGALG00000015616	ACOT12	acyl-CoA thioesterase 12	protein_coding	Z	63,702,151	63,732,906	100.88	2.36	7.60.E-09
ENSGALG00000015721	SVEP1	complement C3b/C4b	protein_coding	Z	66,544,053	66,667,293	72.28	-2.48	2.35.E-06

EnsembleID	gene_name	gene_full_name	gene_biotype	CHR	STA	STO	baseMean	log2FoldChange	pvalue
		receptor 1 (Knops blood group)							
ENSGALG00000028063	LOX	lysyl oxidase	protein_coding	Z	80,979,473	80,988,177	66.89	-2.38	3.78.E-06
ENSGALG00000038200	GATAD2B	GATA Zinc Finger Domain Containing 2B	protein_coding	AADN04000896.1	9,517	40,496	146.64	-2.69	2.79.E-13
ENSGALG00000034566	-	-	protein_coding	AADN04001110.1	723	11,866	41.74	2.02	3.68.E-04
ENSGALG00000044619	-	-	protein_coding	AADN04001162.1	4,420	13,082	65.93	-3.34	1.37.E-09
ENSGALG00000041630	NFIX	nuclear factor I X	protein_coding	AADN04001212.1	1,096	9,881	69.46	-2.59	1.48.E-07
ENSGALG00000035760	LENG8	leukocyte receptor cluster member 8	protein_coding	AADN04001595.1	21	4,578	189.35	-2.52	4.48.E-19
ENSGALG00000033643	PFAS	Phosphoribosylformylglycinamidine Synthase	protein_coding	AADN04001659.1	7,382	24,051	14.21	-2.63	6.02.E-06
ENSGALG00000039574	-	-	protein_coding	AADN04001796.1	2,908	14,644	88.15	-2.84	8.34.E-10
ENSGALG00000041300	AHNAK	AHNAK Nucleoprotein	protein_coding	AADN04001796.1	10,836	20,427	498.39	-2.82	1.20.E-11
ENSGALG00000030075	FCGBP	IgGFc-binding protein-like	protein_coding	AADN04001799.1	21	21,602	40.31	-2.28	2.74.E-05
ENSGALG00000030044	-	-	protein_coding	AADN04001829.1	2,364	6,963	454.09	-3.27	9.99.E-17
ENSGALG00000033116	CLEC2B	C-Type Lectin Domain Family 2 Member B	protein_coding	AADN04002035.1	8,168	14,005	93.03	-2.63	1.36.E-13
ENSGALG00000044239	-	-	protein_coding	AADN04002522.1	1,058	2,100	7993.64	-3.12	1.04.E-19
ENSGALG00000032162	-	-	protein_coding	AADN04004787.1	9,152	14,421	104.17	-2.25	7.10.E-08
ENSGALG00000046284	-	-	protein_coding	AADN04005402.1	5,309	6,819	21.24	-2.55	7.01.E-07
ENSGALG00000029841	-	-	protein_coding	AADN04005808.1	558	9,890	18.69	-2.18	9.53.E-05
ENSGALG00000041009	-	-	protein_coding	AADN04006541.1	9,106	11,559	78.69	-2.25	2.27.E-08
ENSGALG00000042461	-	-	protein_coding	AADN0400	2,045	11,913	387.19	-2.48	1.46.E-12

EnsembleID	gene_name	gene_full_name	gene_biotype	CHR	STA	STO	baseMean	log2FoldChange	pvalue
				6627.1					
ENSGALG00000030910	-	-	protein_coding	AADN04007056.1	21	2,869	77.92	-2.02	3.07.E-11
ENSGALG00000037845	-	-	protein_coding	AADN04007297.1	7,839	10,812	53.19	-2.42	2.77.E-07
ENSGALG00000041925	-	-	protein_coding	AADN04008956.1	1,779	5,324	10.54	-2.49	5.24.E-05
ENSGALG00000041562	CIC	Capicua Transcriptional Repressor	protein_coding	AADN04009324.1	21	5,532	127.67	-2.07	2.78.E-14
ENSGALG00000038714	NDUFB7	NADH:ubiquinone oxidoreductase subunit B7	protein_coding	AADN04011608.1	794	4,566	2144.75	2.26	1.29.E-17
ENSGALG00000041777	-	-	protein_coding	AADN04011972.1	1,028	7,457	55.15	-2.77	1.80.E-09
ENSGALG00000042828	-	-	protein_coding	AADN04012514.1	21	6,123	138	-3.1	2.45.E-17
ENSGALG00000036191	CHD8	Chromodomain Helicase DNA Binding Protein 8	protein_coding	AADN04014142.1	878	2,080	103.33	-2.31	1.07.E-08
ENSGALG00000045002	MAT2A	Methionine Adenosyltransferase 2A	protein_coding	AADN04014543.1	1,127	5,735	116.4	-2	3.68.E-13
ENSGALG00000041603	-	-	protein_coding	AADN04016065.1	21	2,167	14.58	-2.57	4.61.E-06
ENSGALG00000042066	SALL2	Spalt Like Transcription Factor 2	protein_coding	AADN04016442.1	2,341	4,966	23.1	-3.76	6.53.E-11
ENSGALG00000033623	-	-	protein_coding	AADN04016568.1	147	4,886	30.42	-3.43	2.83.E-12
ENSGALG00000033409	-	-	protein_coding	AADN04019134.1	21	3,567	26.07	-2.32	1.15.E-04
ENSGALG00000035265	-	-	protein_coding	AADN04019134.1	21	3,567	35.23	-3.01	4.07.E-09
ENSGALG00000045640	SIGLEC1	Sialic Acid Binding Ig Like Lectin 1	protein_coding	AADN04024605.1	911	5,580	9.15	-2.35	3.97.E-04
ENSGALG00000032698	-	-	protein_coding	KQ759409.1	13,609	18,212	45.77	-2.52	1.14.E-08
ENSGALG00000039573	WIZ	RAS protein activator like 3	protein_coding	KQ759480.1	21,194	69,218	284.7	-2.03	1.92.E-13

EnsembleID	gene_name	gene_full_name	gene_biotype	CHR	STA	STO	baseMean	log2FoldChange	pvalue
ENSGALG00000043736	-	-	protein_coding	KQ759484.1	111,140	121,198	51.73	-2.21	2.36.E-09
ENSGALG00000030904	LRP1	LDL receptor related protein 1	protein_coding	KQ759536.1	654	69,248	1051.74	-2.13	6.46.E-11
ENSGALG00000041471	-	-	protein_coding	KQ759552.1	18,701	20,662	1428.36	-2.14	1.55.E-13
ENSGALG00000041685	CAPN1	calpain 1	protein_coding	KQ759558.1	168	14,763	362.38	-2.02	1.99.E-11
ENSGALG00000029524	-	-	protein_coding	KQ759610.1	8,191	14,355	153.76	-3.04	2.35.E-11
ENSGALG00000041283	SRRM2	Serine/Arginine Repetitive Matrix 2	protein_coding	KQ759647.1	6,531	10,871	17.56	-2.71	5.92.E-07
ENSGALG00000035354	-	-	protein_coding	KQ759661.1	21	10,191	15.2	-2.22	6.01.E-05
ENSGALG00000044788	-	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	protein_coding	LGE64	793,673	797,335	130.35	-2.03	2.31.E-08

Table S6. Differentially expressed genes (DEGs) between non-gluten and gluten-fed groups of 4-week-old chicken (adjusted P-value : 0.05, |log2FC|: 1)

EnsembleID	gene_name	gene_full_name	gene_biotype	CHR	STA	STO	baseMean	log2Fold Change	pvalue
ENSGALG00000016142	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	protein_coding	1	110,239,567	110,260,524	745.98	1.08	1.07E-08
ENSGALG00000009479	SAMD9L	sterile alpha motif domain containing 9 like	protein_coding	2	22,911,382	22,916,121	54.20	1.07	1.46E-05
ENSGALG00000009700	PDK4	pyruvate dehydrogenase kinase 4	protein_coding	2	23,905,072	23,914,501	3714.07	1.10	1.43E-07
ENSGALG00000010997	DFNA5	DFNA5, deafness associated tumor suppressor	protein_coding	2	31,606,777	31,631,552	282.84	1.30	4.31E-08
ENSGALG00000013575	IFI6	interferon alpha inducible protein 6	protein_coding	2	89,717,661	89,722,211	4072.64	1.14	3.33E-08
ENSGALG00000045085	IFIT5	interferon induced protein with tetratricopeptide repeats 5	protein_coding	6	20,187,816	20,191,669	1520.74	1.14	5.00E-07
ENSGALG00000010752	CDCP2	CUB domain containing protein 2	protein_coding	8	25,496,702	25,500,343	39.60	-1.07	1.46E-05
ENSGALG00000000162	DMB1	major histocompatibility complex, class II, DM beta 1	protein_coding	16	2,586,004	2,588,894	2765.32	-1.01	2.05E-08
ENSGALG00000034960	MLXIPL	MLX interacting protein like	protein_coding	19	365,079	380,126	1734.86	-1.44	2.15E-12
ENSGALG00000034566	-	-	protein_coding	-	-	-	38.31	-1.06	1.26E-05
ENSGALG00000036145	-	-	protein_coding	-	-	-	447.31	-1.77	4.81E-14
ENSGALG00000039991	-	-	protein_coding	-	-	-	20.19	-1.48	1.82E-09
ENSGALG00000040998	-	-	protein_coding	-	-	-	42.60	-2.12	1.18E-17
ENSGALG00000031341	MGAM	maltase-glucoamylase (alpha-glucosidase)	protein_coding	KZ626839.1	681,601	721,084	50804.07	-1.11	5.56E-10
ENSGALG00000023738	IRX6	interferon alpha inducible protein 6	protein_coding	KZ626839.1	681,601	721,084	190.22	-1.13	2.80E-06