

Table S8 | Gene ontology analysis for red junglefowl and domestic chicken populations using DAVID version 6.8¹.

A. Red Junglefowl population

GO term	Description	P value	Genes
GO:0050789	Regulation of biological process	0.009225514	<i>ADCY1, AL158801.1, EBF2, KCNA5, PPP2R2A, CCND2, NAB1, NEFM, FURIN, BMP10, GNRH1, ARHGAP25, MYCL, NPY2R, RHOBTB2, PDIA3, ZNF302, BCAR3, NKX2-6, ADAM9, ZFHX4, KCNMA1, RCAN3, PAFAH1B1</i>
GO:0051246	Regulation of protein metabolic process	0.015403594	<i>AL158801.1, CCND2, ADAM9, FURIN, BMP10</i>
GO:0006810	Transport	0.020966967	<i>SCN2A, ATP6V1B2, KCNA5, GRIK2, MFSD2A, SLC25A37, NEFM, KCNA1, FURIN, KCTD9, SLC16A5, KCNMA1, SLC26A8, PAFAH1B1</i>
GO:0015672	Monovalent inorganic cation transport	0.022221846	<i>ATP6V1B2, KCNA5, KCNA1, KCTD9, KCNMA1</i>
GO:0022836	Gated channel activity	0.024342944	<i>KCNA5, GRIK2, KCNA1, KCTD9, KCNMA1</i>
GO:0008088	Axon cargo transport	0.039408326	<i>NEFM, PAFAH1B1</i>
GO:0051592	Response to calcium ion	0.045827198	<i>ADAM9, KCNMA1</i>

Note: Genes in bold overlap with other genes selected in domestic chicken populations

B. Ethiopian domestic chicken population

GO term	Description	P value	Genes
GO:0019229	Regulation of vasoconstriction	0.01063	<i>HRH1, AGTR1</i>

¹ <https://david.ncifcrf.gov/>

C. Saudi Arabian domestic chicken population

GO term	Description	P value	Genes
GO:0008015	Blood circulation	0.004766	<i>PRKG1, PDE5A, SEMA3A, PDE3A, HDAC4, CTNNA3, CACNA1G, GCLC</i>
GO:0008016	Regulation of heart contraction	0.007859	<i>PDE5A, SEMA3A, HDAC4, CTNNA3, CACNA1G</i>
GO:0090257	Regulation of muscle system process	0.009369	<i>PRKG1, PDE5A, MTPN, HDAC4, CTNNA3</i>
GO:0051094	Positive regulation of developmental process	0.010359	<i>TSHR, PDE5A, RHOB, SIRT1, PROX1, FLRT2, SEMA3A, RIMS1, PDE3A, IMPACT, MAP2K1, TMEM30A, HIF1AN</i>
GO:0006886	Intracellular protein transport	0.011917	<i>RHOB, SEC24C, RABGAP1L, MYO6, RIMS1</i>
GO:0060284	Regulation of cell development	0.016126	<i>PDE5A, PROX1, FLRT2, SEMA3A, RIMS1, PDE3A, HDAC4, IMPACT, MYCL, MAP2K1, TMEM30A</i>
GO:0070301	Cellular response to hydrogen peroxide	0.017447	<i>RHOB, SIRT1, IMPACT</i>
GO:0008206	Bile acid metabolic process	0.018957	<i>AKR1D1, SIRT1, PROX1</i>
GO:0045892	Negative regulation of transcription, DNA-templated	0.019806	<i>SIRT1, TFDP2, PHF14, FRK, PROX1, DACH1, HDAC4, IMPACT, AICDA, HIF1AN, GCLC</i>
GO:1902679	Negative regulation of RNA biosynthetic process	0.022875	<i>SIRT1, TFDP2, PHF14, FRK, PROX1, DACH1, HDAC4, IMPACT, AICDA, HIF1AN, GCLC</i>
GO:0043502	Regulation of muscle adaptation	0.02443	<i>PDE5A, MTPN, HDAC4</i>
GO:0005912	Adherens junction	0.025717	<i>RHOB, TNS3, ARHGAP22, TLN2, FLRT2, RSU1, CTNNA3, RPL4</i>
GO:0042391	Regulation of membrane potential	0.026217	<i>RIMS1, NETO1, KCNMA1, CTNNA3, CACNA1G, GCLC</i>
GO:2000243	Positive regulation of reproductive process	0.028393	<i>PDE5A, SEMA3A, PDE3A</i>
GO:0045595	Regulation of cell differentiation	0.030314	<i>SIRT1, GLG1, PROX1, SEMA3A, RIMS1, MYCL, MAP2K1, TMEM30A, HIF1AN, PDE5A, FLRT2, HDAC4, PDE3A, IMPACT, COL5A2</i>
GO:0055117	Regulation of cardiac muscle contraction	0.030465	<i>PDE5A, HDAC4, CTNNA3</i>
GO:0044712	Single-organism catabolic process	0.030569	<i>RP11-240B13.2, PDE5A, GK5, AKR1D1, ABHD5, LPIN1, PDE3A, HDAC4, USP13</i>
GO:0009117	Nucleotide metabolic process	0.039809	<i>TSHR, PDE5A, PRPS2, RP11-411B6.6, GRM8, MDH1B, PDE3A, HDAC4</i>
GO:0019934	Cgmp-mediated signaling	0.040082	<i>PRKG1, PDE3A</i>
GO:0034983	Peptidyl-lysine deacetylation	0.040082	<i>SIRT1, HDAC4</i>
GO:0019693	Ribose phosphate metabolic process	0.040998	<i>TSHR, PDE5A, PRPS2, RP11-411B6.6, GRM8, PDE3A, HDAC4</i>
GO:0005875	Microtubule associated complex	0.045734	<i>DYNCL11, SNX4, KIF26B, BORCS5</i>

GO:0044281	Small molecule metabolic process	0.045786	<i>GK5, PRPS2, SIRT1, LARS2, PROX1, GRM8, LPIN1, ASNSD1, MDH1B, GCLC, PDE5A, TSHR, AKR1D1, RP11-411B6.6, HDAC4, PDE3A</i>
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D. Sri Lankan domestic chicken population

GO term	Description	P value	Genes
GO:0016500	protein-hormone receptor activity	0.04484	<i>TSHR, MCHR1</i>