

Column Assignments for published chicken sweeps.

This is a tab-separated file with the following columns:

1. chr - chromosome
2. start - first chromosome position
3. end - last chromosome position
4. line - The line combination in which the heterozygosity Z-score (ZH_P) < -4
5. nWin - Number of consecutive ZH_P < -4 windows that were merged.
6. nSNP - Number of SNPs that were identified in region (for merged windows, the number is that of all windows).
7. N - Sums of major (nMAJ) and minor alleles (nMIN) observed at all SNPs in the region for the line combination in column 4.
8. low - The lowest ZH_P observed for a 40 kb window in the region for the line combination in column 4.
9. AD - The lowest pooled heterozygosity (H_P) observed for a 40 kb window in the region for AD.
10. CB - The lowest pooled heterozygosity (H_P) observed for a 40 kb window in the region for CB.
11. LR - The lowest pooled heterozygosity (H_P) observed for a 40 kb window in the region for LR.
12. genes - Genes overlapping putative sweep region:
 - [1] = Gene contained within region.
 - [2] = Region contained within gene(s).
 - [3] = Region overlaps 5'-end of gene(s).
 - [4] = Region overlaps 3'-end of gene(s).
 - [5] = The 5'-end of gene(s) is within 20 kb of region.
 - [6] = The 3'-end of gene(s) is within 20 kb of region.The ENSEMBL ID of the chicken gene is, if applicable, followed by the chicken gene name and/or gene name of human ortholog(s). *Name of human one2one ortholog.

Methods

This table describes regions of the chicken genome predicted to be under positive selection in domestic chickens, as given in Supplementary Table 3 from [1].

Genomic regions identified as candidate selective sweeps in: all domestic lines (AD), two commercial broiler lines (CB) and three layer lines (LR). Consecutive 40 kb sliding windows with heterozygosity Zscores (ZH_P) < -4 were merged.

References

- [1] Rubin CJ, Zody MC, Eriksson J, Meadows JR, Sherwood E, Webster MT, Jiang L, Ingman M, Sharpe T, Ka S, Hallbook F, Besnier F, Carlborg O, Bed'hom B, Tixier-Boichard M, Jensen P, Siegel P, Lindblad-Toh K, Andersson L. (2010) Whole-genome resequencing reveals loci under selection during chicken domestication, *Nature* 464:587-591. PMID: 20220755