

Large-scale genome-wide SNP analysis reveals the rugged (and ragged) landscape of global ancestry, phylogeny, and demographic history in chicken breeds

Natalia V. DEMENTIEVA¹, Yuri S. SHCHERBAKOV¹, Olga I. STANISHEVSKAYA¹,
Anatoly B. VAKHRAMEEV¹, Tatiana A. LARKINA¹, Artem P. DYSIN¹, Olga A. NIKOLAEVA¹,
Anna E. RYABOVA¹, Anastasiia I. AZOVTSEVA¹, Olga V. MITROFANOVA¹, Grigoriy K. PEGLIVANYAN¹,
Natalia R. REINBACH¹, Darren K. GRIFFIN², Michael N. ROMANOV^{2,3}

¹Russian Research Institute of Farm Animal Genetics and Breeding – Branch of the L. K. Ernst Federal Research Centre for Animal Husbandry, Pushkin, St. Petersburg, 196601, Russia

²School of Biosciences, University of Kent, Canterbury, CT2 7NJ, UK

³L. K. Ernst Federal Research Center for Animal Husbandry, Dubrovitsy, Podolsk, Moscow Oblast, 142132, Russia

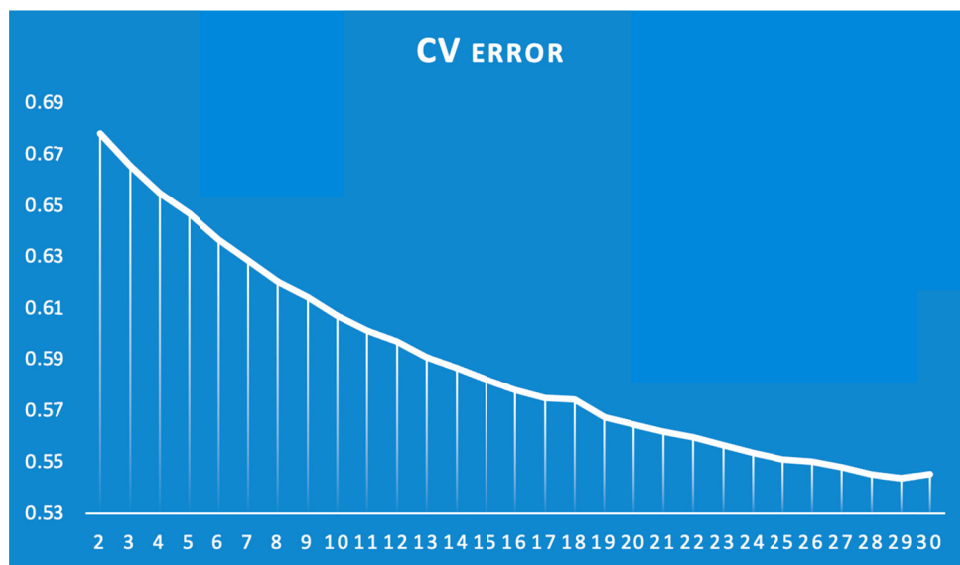


Fig. S1 CV error plot of the ADMIXTURE analysis, with the optimal number of ancestral populations being $K=29$.