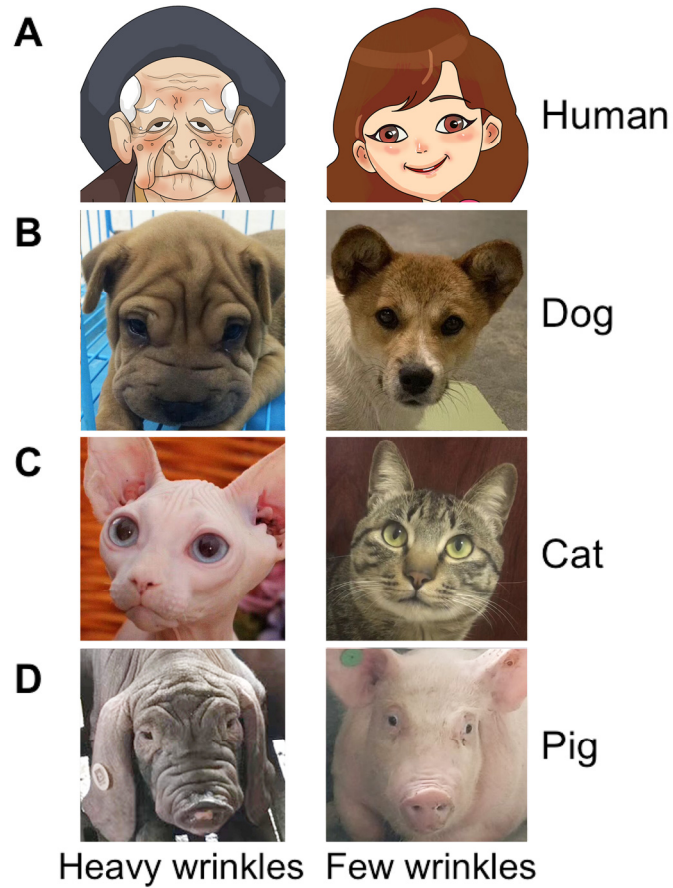**Figure S1. Comparison of heavy and few facial wrinkles in different species.** (**A**) human. The screenshot of male head was captured from a cartoon grandpa with a hat; the screenshot of female head was captured from a cartoon lady with brown hair. (**B**) dog. Left head was from a Chinese Shar-pei dog; right head was from a Chinese Tianyuan dog. (**C**) cat. Left head was from a Canadian Sphynx cat; right head was from a Chinese Lihua cat. And (**D**) Pig. Left head was from a Chinese Erhualian pig; right head was from a Large White pig.
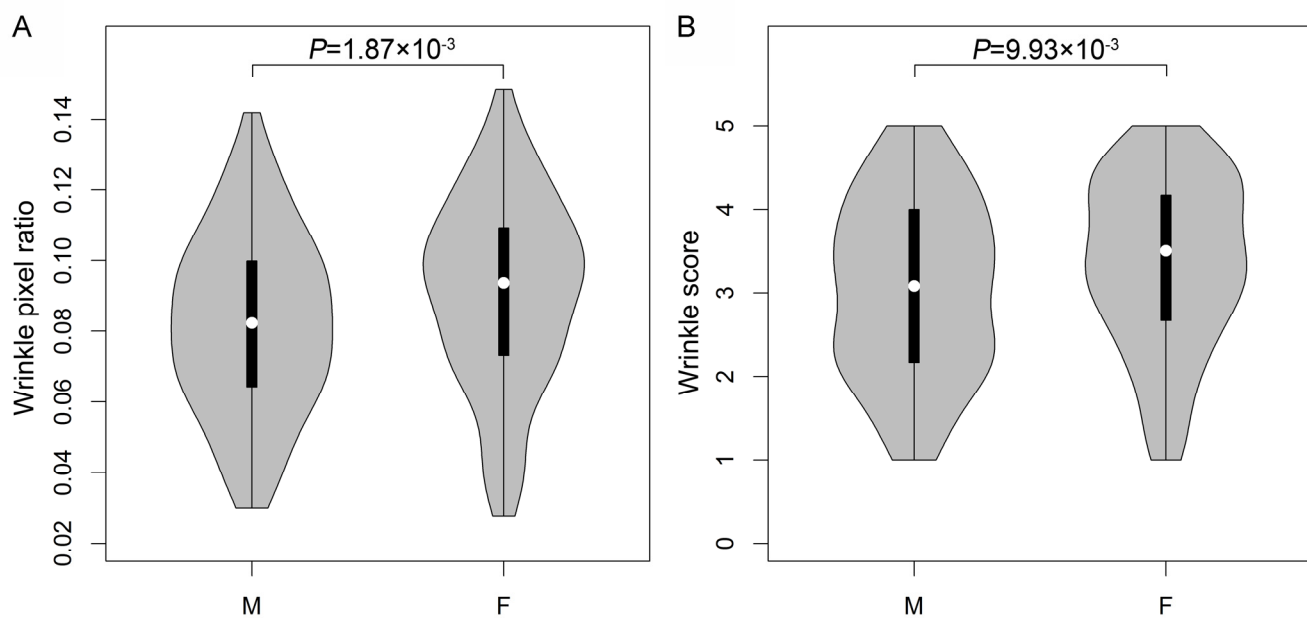
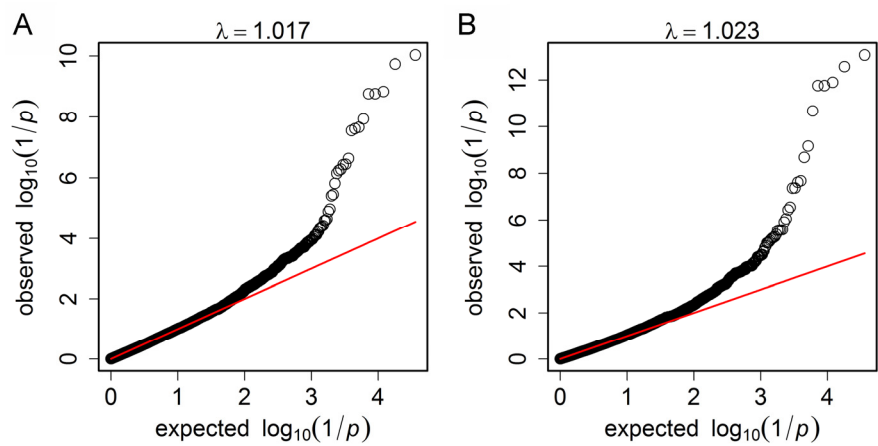**Figure S2. The difference of facial wrinkles between females and males.**
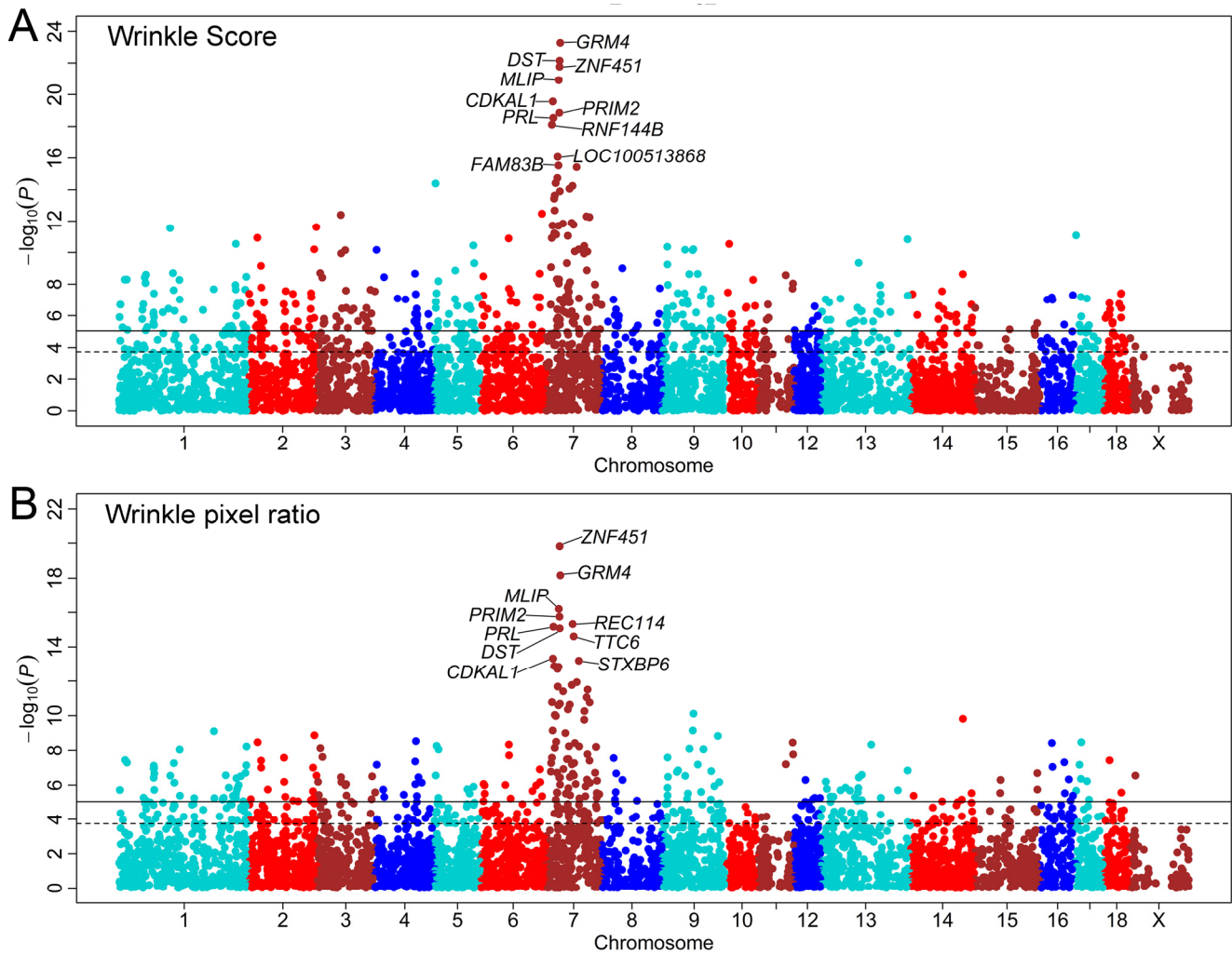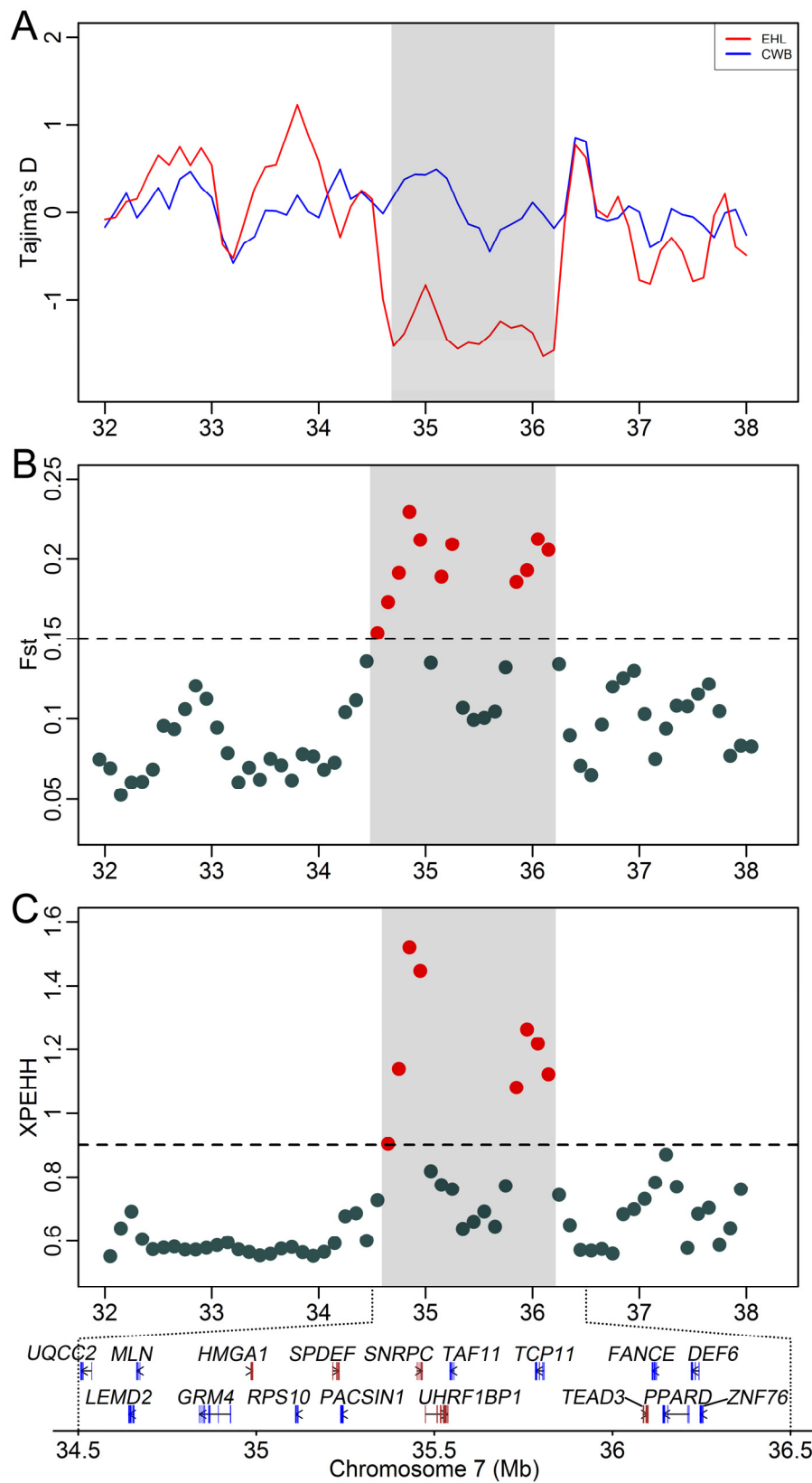

Figure S3. QQ plots for the GWAS of facial wrinkles. (A) wrinkle pixel ratio. (B) Winkle score.

Figure S4. Genome-wide gene association analysis for facial wrinkles. (**A**) wrinkle pixel ratio. (**B**) Winkle score. The dashed line delineates the suggestive significance threshold; the solid line delineates the genome-wide significant threshold.

Figure S5. Evolutionary and selection analyses on the candidate region affecting swine facial wrinkles using the whole-genome sequencing data. (**A**) Tajima's D tests. (**B**) Population differentiation analysis between Erhualian pigs and Chinese wild boars. (**C**) XPEHH score estimation.
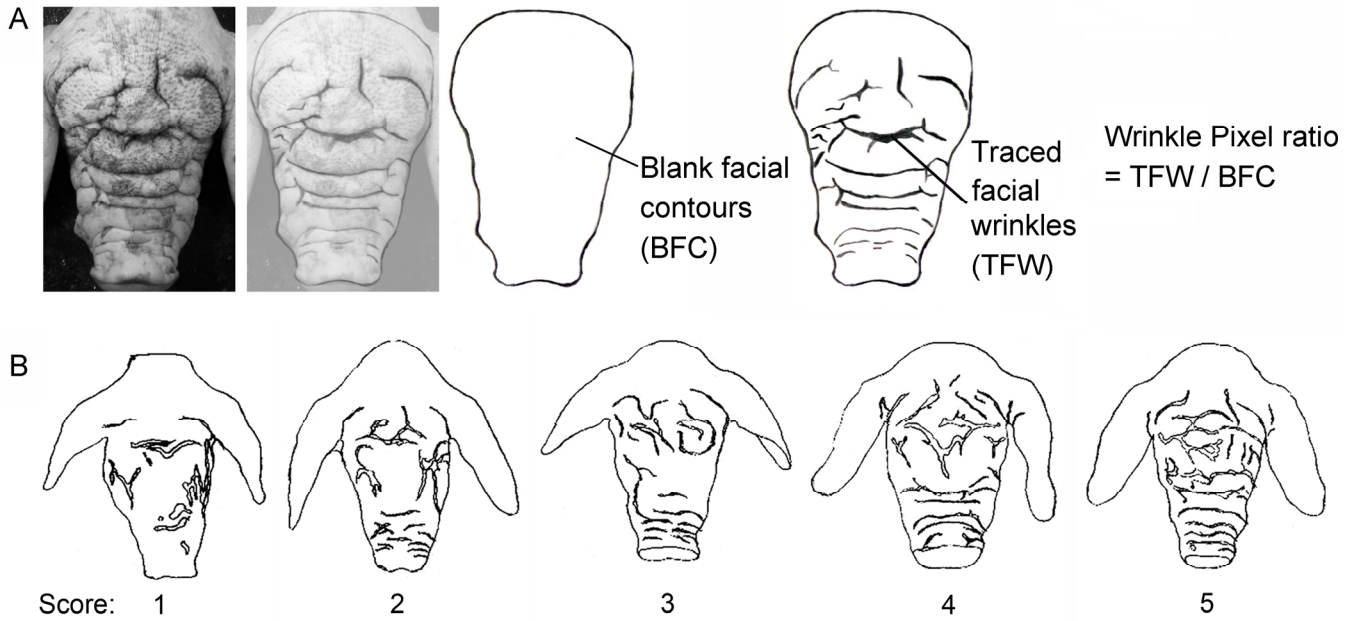
Figure S6. Two traits of swine facial wrinkles. (A) Estimation of wrinkle pixel ratio. (B) The criterion panel of facial wrinkle score.