

**Figure S1.** The linkage disequilibrium (LD) decay of the population. The x-axis and y-axis were distance between adjacent SNP and their average square of correlation coefficient (r2). 200 kb was chosen as the LD decay distance (dark red dotted line).



**Figure S2.** The GO-and-KEGG-based network analysis of candidate genes of GESS on success traits using ClueGO application in Cytoscape. Main terms and pathways with Benjamini-Hochberg-corrected P-value < 0.05 and genes who shared between terms and pathways were shown.



**Figure S3.** The GO-and-KEGG-based network analysis of candidate genes of GESS on calving traits using ClueGO application in Cytoscape. Main terms and pathways with Benjamini-Hochberg-corrected P-value < 0.05 and genes who shared between terms and pathways were shown.



**Figure S4.** The GO-and-KEGG-based network analysis of candidate genes of GED on success traits using ClueGO application in Cytoscape.Main terms and pathways with Benjamini-Hochberg-corrected P-value < 0.05 and genes who shared between terms and pathways were shown.



**Figure S5.** The GO-and-KEGG-based network analysis of candidate genes of GED on calving traits using ClueGO application in Cytoscape. Main terms and pathways with Benjamini-Hochberg-corrected P-value < 0.05 and genes who shared between terms and pathways were shown.