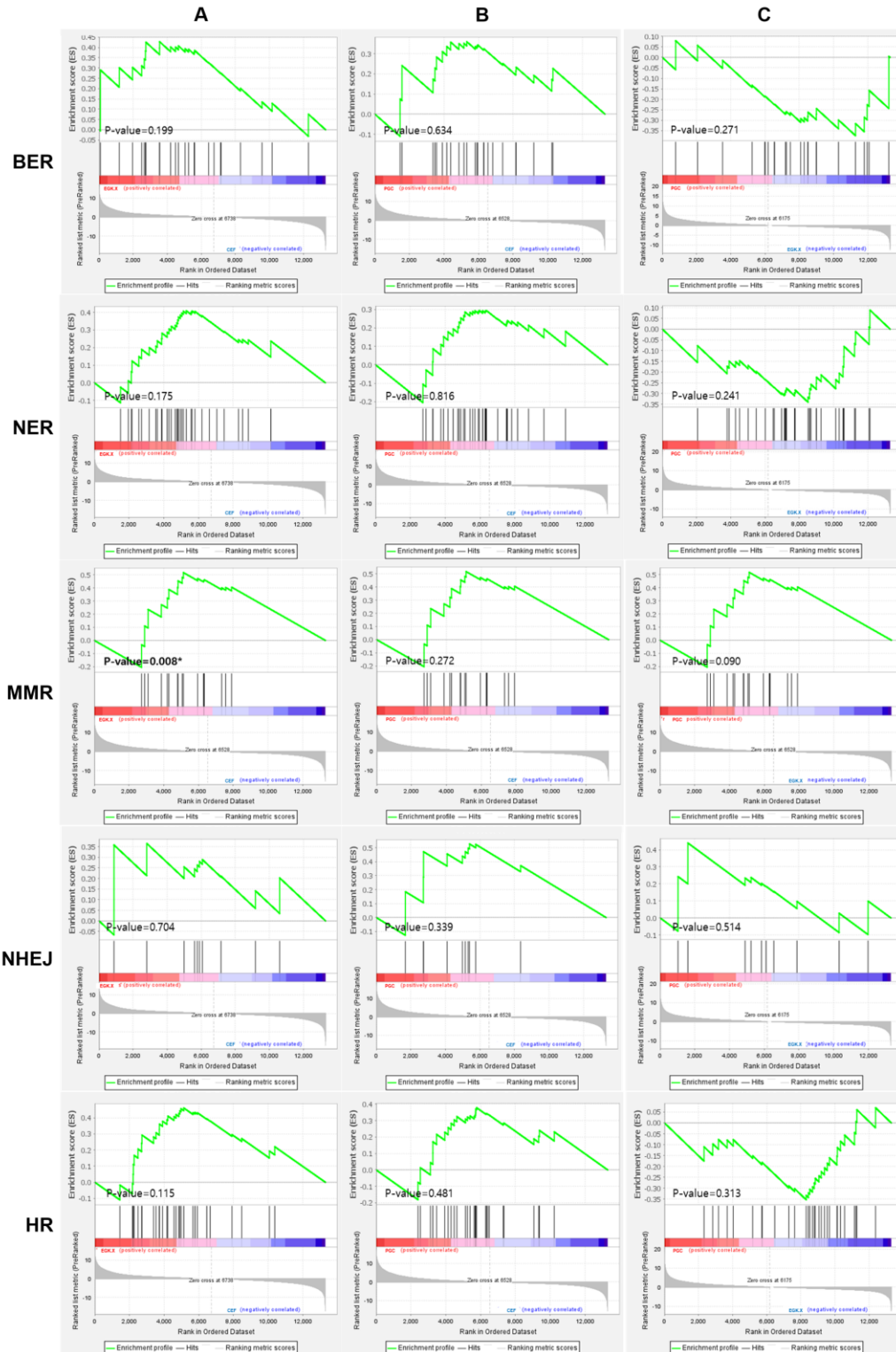
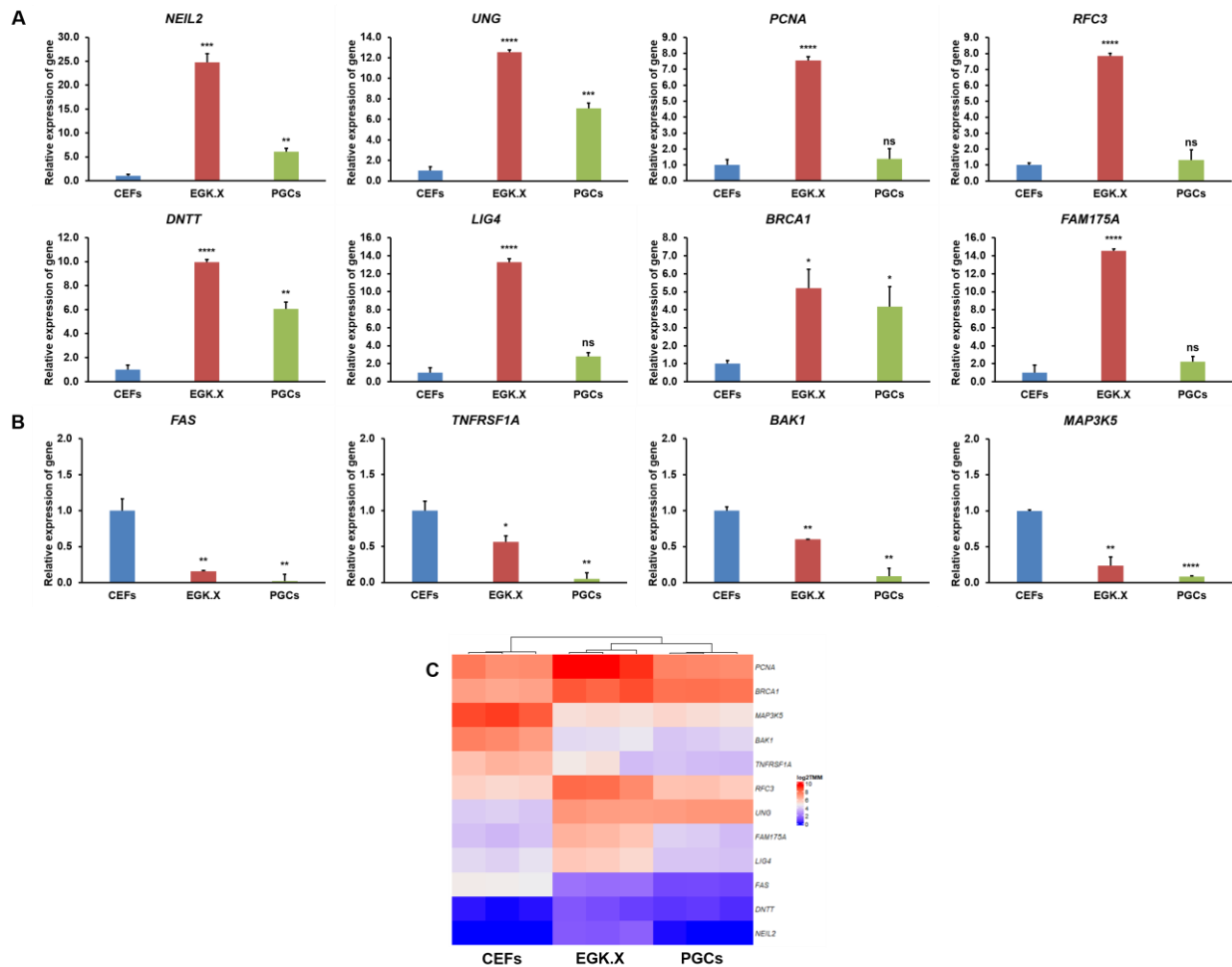


Supplementary Figure S1. Involvement of BER, NER, MMR, NHEJ, HR, and apoptosis pathway genes in other pathways.



Supplementary Figure S2. GSEA of DNA repair (BER, NER, MMR, NHEJ, and HR) pathway at CEFs versus EGK.X blastoderms (A), CEFs versus PGCs (B), and EGK.X blastoderms versus PGCs (C) conditions.



Supplementary Figure S3. RT-qPCR validation of DNA repair and apoptosis pathway genes. **A**, candidate genes from the BER pathway (*NEIL2* and *UNG*), NER/MMR pathway (*PCNA* and *RFC3*), NHEJ pathway (*DNTT* and *LIG4*), and HR pathway (*BRCA1* and *FAM175A*). **B**, candidate genes from the extrinsic (*FAS* and *TNFRSF1A*), intrinsic (*BAK1*), and FAS-JNK (*MAP3K5*) mediated apoptosis pathway. Genes were amplified with their specific qPCR primers. The relative expression of genes was normalized with the chicken *GAPDH* and a reference sample (CEFs), and analyzed by the $2^{-\Delta\Delta C_t}$ method. Significant differences between the CEFs and other test samples were determined by Student's *t*-test. Statistical significance was ranked as * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, or **** $P < 0.0001$. ns: non-significant. **C**, Heatmaps using \log_2 TMM values of the normalized read counts of genes shown in **A** and **B** were prepared separately for better visualization.