



Supplemental Figure 3. GO analysis based on biological process. We identified 703 stigma-specific genes, 1257 ovary-specific genes and 122 embryo sac-dependent genes. Based on biological process, the stigma-specific genes were enriched in 18 GO terms (A), the ovary-specific genes were enriched in 24 terms (B), and the embryo sac-dependent genes were overrepresented in 11 terms (C) ($P < 0.05$).