



**Supplementary Fig. 1.** The pathway “Development FGF-family signaling imagemap” illustrated schematically using MetaCore software. Genes showing DNA hypermethylation in 10 samples of late-onset endometrioid endometrial cancer tissue (LE) with somatic mutations of the *FGFR2* gene (FGFR2-M) relative to 30 LE samples without such mutations (FGFR2-W) (Welch’s t test  $P < 0.01$  and  $\Delta\beta_{\text{FGFR2-M-FGFR2-W}}$  value of more than 0.15) are indicated by red circles. Genes showing DNA hypomethylation in FGFR2-M samples relative to FGFR2-W samples (Welch’s t test  $P < 0.01$  and  $\Delta\beta_{\text{FGFR2-M-FGFR2-W}}$  value of less than -0.15) are indicated by dotted red circles. The *FGFR2* gene is indicated by a blue circle.