



**Supplementary Figure S2 (A)** Trend curves for significantly expressed genes between expression subgroups of SC cohort (i) P-EnSC-hi and P-EnSC-lo and (ii) EndoSC-hi and EndoSC-lo. Samples values for above subgroups were represented as mean  $\pm$  standard deviation, including pooled values from cancer cell lines (Ishikawa (endometrial), SKOV3 and A2780 (ovarian), were colour coded in red) and each subgroup were normalized against H-EnSC (baseline). **(B-C)** Protein validation were performed using automated simple western for samples from two cohorts; **(B)** *in vitro* expanded multipotent stem/stromal cell and **(C)** tissue cohort for (i) ER- $\alpha$  (MW: 70 kDa), (ii) ER- $\beta$  (MW: 55 kDa), (iii) E-cadherin (MW: 120 kDa and 98 kDa) along with housekeeping gene  $\beta$ -actin (MW: 47 kDa). Representative blots show the protein levels from SC<sup>+</sup> populations (H-EnSC (#17), paired-P-EnSC-lo and -EndoSC-lo (#12), paired-P-EnSC-hi and -EndoSC-hi samples (#36; #24)) and tissue cohort H-En (#H-En-2), paired low-expression variability samples (E47.1 and E47.7) and paired high-expression variability patients (#E238 and #E159), validated using a positive control (Ishikawa or MCF7 cell line).