Supplementary Table I - **Demographics details of the patients included in the study.** POP - Progesterone only pill, LNG-IUS - levonorgestrel-releasing intrauterine system, PM – postmenopausal.

Supplementary table II - **All potential LGR5 regulating Transcription factors.** A list of all potential transcription factors that were identified by amalgamating the following lists of genes; 1.) 116 transcription factors that are over-represented in the human *LGR5* gene promoter (5000 up and 2000 down-stream) region as compared to a background set of sequences were constructed with oPPOSUM and ranked according to the z-score as previously described (Mathew et al. 2016); 2.) all transcription factors which bind to *LGR5* gene promotor as identified with Con Tra V3 as previously (Broos et al. 2011). 3.) a list of 94 genes when perturbed (over expression/ knockout/ knockdown), would affect the expression of LGR5 that was produced using Nextbio knockout atlas application in Illumina’s BaseSpace Correlation Engine (BSCE;(Kupershmidt et al. 2010) software package was previously known as NextBio; https://www.illumina.com/informatics/research/biological-data-interpretation/nextbio.html; Illumina, San Diego, CA, USA) in May 2017.

Supplementary table III. **Potential LGR5 regulating genes that are differentially regulated in the secretory phase endometrium**. All published Microarray datasets available in Nextbio correlation engine of normal, premenopausal endometrial samples from women not on hormonal treatments without any endometrial pathology with robust assignment to a cycle stage were included in meta-analysis (which considers only the top 5,000 genes feature in these bio sets in order to decrease potential noise) to obtain the top differentially regulated genes in the progesterone dominant secretory phase of the cycle in comparison with the oestrogen dominant proliferative menstrual cycle phase (n=65) (Burney et al. 2007; Talbi et al. 2006; Nguyen et al. 2012; Sigurgeirsson et al. 2017). 133 genes that were already identified as LGR5 regulating genes out of 313 genes in Supplementary table II were amongst the top 500 differentially regulated genes identified in the secretory phase.

Supplementary table IV - **Potential *LGR5* regulating genes that are differentially expressed in the endometrial side population cells**. The only published microarray study examining the sorted healthy normal endometrial epithelial side population cells that represent the primitive endometrial epithelial stem cell population, against the unsorted, therefore more differentiated epithelial cells (Cervello et al. 2010) (n=8/group) was considered and included in the Nextbio-meta-analysis to identify the potential LGR5 regulating genes in the epithelial stem cells. Forty eight out of the 313 LGR5 regulating genes identified in the Supplementary table II were differentially expressed in the epithelial side population.