

Figure S1 Principal Component analysis (PCA) of primary endometrial epithelial cell transcriptomes from nine patients, four proliferative (non-receptive) samples (orange) and five mid-secretory phase (receptive) samples (blue). PCA calculated on DEGs (n=440, $p < 0.01$) between proliferative and mid-secretory samples. Data from Chi et al 2020.

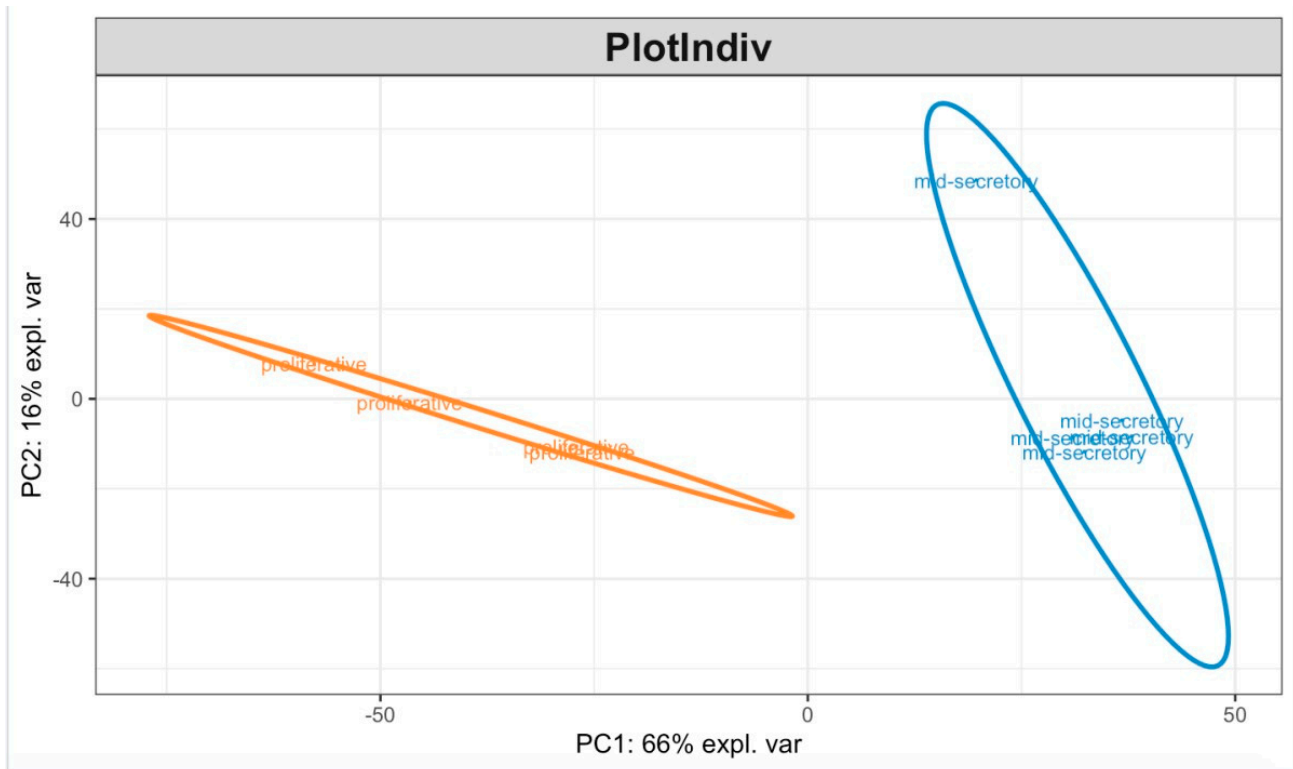


Table S1 Genes identified in the hypernetwork clusters from bulk transcriptome EEC.

EEC cluster 1	EEC cluster 2	EEC cluster 3
ADCYAP1R1	ANXA2	APOE
COL27A1	ANXA4	CLCF1
COMP	APOL1	CRYAB
CPM	C3	CTSB
CTSH	C4BPA	CTSW
DPP4	CD44	CXCL2
EMID1	CP	CXCR4
FGFR3	CXCL14	EFEMP1
IHH	DEFB1	GNLY
IL15RA	DKK1	GPX3
IL2RB	GAST	GRN
PAPLN	IL1R1	HABP2
PCSK5	IL6ST	IGFBP1
PDGFC	ITGA3	IGFBP3
PRLR	MST1R	LAMB3
S100A4	MUC16	LGALS3
SCARA5	PPFIBP2	LYPD3
SERPINA5	SCGB2A1	MMP10
SERPINE1	SFN	RBP4
TFPI	STC1	S100A13
TGM2	TRPM8	SERPING1
TIMP3	AIMP1	SLPI
VIM		THBD
WFDC2		TMPRSS13
ADAMTS5		ADM
		APOD

Table S2: Genes iden-tified in the hypernetwork clusters from single-cell LE, CE and GE transcriptomes.

LE cluster	CE cluster	GE cluster
ATP1A1	ACTG1	MTRNR2L1
CD55	ADM	EPB41L2
CNDP2	AKR7A2	IGFBP4
ACSL4	ANXA1	
ANXA4	ANXA2	
CKB	ATP5O	
CRYAB	ATPIF1	
CRISP3	BLOC1S1	
ENPP3	BTG2	
FAM213A	CALM3	
GRN	CCDC80	
HSP90B1	CD24	
IL6	CD55	
MDK	CD81	
PPIB	CKB	
PSAT1	CLDN3	
PTGS1	CRISP3	
RNASET2	CRYAB	
RPS26	CTGF	
SERPINA5	CXCL2	
SLC26A2	CXCL8	
VIM	DDX5	
WLS	DNAJA1	
	DNAJB1	
	DNPH1	
	DSP	
	DSTN	
	EDN1	
	EPHA2	
	EPPIN	
	EZR	
	FUZ	
	GAPDH	
	HNRNPA1	
	HSP90AA1	
	HSP90AB1	
	HSPA1B	
	HSPA5	
	HSPA8	
	HSPH1	
	IDH2	
	IGFBP4	
	IK	
	IL18	
	ITGB1	
	ITGB8	
	KRT18	
	KRT19	
	LGALS1	
	LGALS3	
	MAPK15	
	MDK	
	METRNL	
	NAMPT	
	NCL	
	PAEP	
	PARK7	
	PFN2	
	PPP1R7	
	PSMB5	
	QPR1	
	RHOB	
	RND3	
	RPL31	
	RPL4	
	RPS10	
	S100A11	
	S100A6	
	SCPEP1	
	SERPINA6	
	SFPQ	
	SFRP4	
	SLC26A2	
	SLPI	
	SOD2	
	SPAG9	
	SQSTM1	
	TNFAIP3	
	TPM3	
	TPT1	
	TSPAN6	
	UBC	
	VIM	
	WFDC2	
	YWHAZ	