

Supplementary Table S1 Enriched KEGG pathways (FDR < 0.05) from over-representation analysis of 3541 genes in the hypernetwork connected to EEC-interacting polar TE genes.

Gene set	Description	Size	Ratio	FDR
hsa04740	Olfactory transduction	448	5.753	<1.00E–16
hsa04060	Cytokine–cytokine receptor interaction	294	2.700	<1.00E–16
hsa04080	Neuroactive ligand-receptor interaction	277	2.476	2.00E–11
hsa05320	Autoimmune thyroid disease	53	3.513	3.97E–05
hsa04650	Natural killer cell-mediated cytotoxicity	131	2.394	1.17E–04
hsa00040	Pentose and glucuronate interconversions	34	4.035	1.27E–04
hsa04620	Toll-like receptor signalling pathway	104	2.544	1.56E–04
hsa00140	Steroid hormone biosynthesis	60	3.103	1.71E–04
hsa00053	Ascorbate and aldarate metabolism	27	4.355	1.73E–04
hsa04630	JAK-STAT signalling pathway	162	2.117	3.85E–04
hsa04622	RIG-I-like receptor signalling pathway	70	2.660	1.44E–03
hsa04623	Cytosolic DNA-sensing pathway	63	2.644	3.53E–03
hsa04742	Taste transduction	83	2.361	4.74E–03
hsa04657	IL-17 signalling pathway	93	2.213	8.06E–03
hsa00860	Porphyrin and chlorophyll metabolism	42	2.800	1.56E–02
hsa05150	<i>Staphylococcus aureus</i> infection	56	2.450	2.35E–02
hsa04062	Chemokine signalling pathway	189	1.711	2.62E–02
hsa00830	Retinol metabolism	67	2.194	4.65E–02

FDR, false discovery rate; EEC, endometrial epithelial cell; TE, trophectoderm.