Supplemental Information Supplemental Tables 1 and 2

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Supplemental Table 1. Maternal and infant characteristics

	PE (<i>n</i> = 5)	nPTL (<i>n</i> = 5)	P value
Maternal age, yr	29.0 (5.9)*	25.6 (6.3)	0.40
BMI, kg/m ²	27.4 (4.2)	26.0 (5.0)	0.68
Systolic blood pressure, mmHg	148 (11)	112 (7)	< 0.001
Diastolic blood pressure, mmHg	88 (5)	65 (13)	< 0.01
Proteinuria, designation	+1 to +3	0	NA
Gestational age at delivery, week	31.2 (2.5)	29.5 (3.7)	0.45
Birth weight, g	1365 (528)	1572 (694)	0.61

*mean ± SD, 2-tailed Student's t-test.

Supplemental Table 2. Reagents, sources and concentrations

Reagent	Source	Concentration
Polyclonal anti-SEMA3B	Novus Biologicals	Diluted 1:1000
Polyclonal anti-NRP-1 (C-19) and	Santa Cruz Biotechnology Inc. (Santa	2 μg/ml (IB)
NRP-2 (C-9)	Cruz, CA)	
Monoclonal anti-VEGF R2	Dr. K. Chwalisz (Scherring AG, Berlin,	1:500
	Germany)	
Polyclonal anti-PI3K p85	Upstate USA Inc (Charlottesville, VA)	1:100
Polyclonal anti-PI3K p100 α	Epitomics (Burlingame, CA), Becton	1:2000
	Dickinson (San Jose, CA)	250 ng/ml
Polyclonal anti-Akt, anti-p-Akt	Cell Signaling Technology (Danvers, MA)	1:1000
(Ser473) and anti-p-GSK3 α/β		1:1000
(Ser21/Ser9)		1:1000
Monoclonal anti-GSK3 (4G-IE)	Upstate Cell Signaling Solutions (Billerica,	1 μg/ml
	MA)	
Monoclonal anti-V5	Invitrogen Corp (Carlsbad, CA)	160 ng/ml
Monoclonal anti- α -actin (AC-40)	Sigma-Aldrich Corp (Saint Louis, MO)	1:500
(rat) monoclonal anti-cytokeratin	Generated in collaboration with Dr. C.	1:200
(7D3)	Damsky (Damsky <i>et al.</i> , 1992)	
NRP1-Fc, NRP2-Fc and CD6-Fc	R&D Systems (Minneapolis, MN)	400 ng/ml
fusion proteins		
Monoclonal anti-VEGF (A4.6.1)	Dr. Napoleone Ferrara (Genentech,	400 ng/ml
	South San Francisco, CA)	
Wortmannin	Calbiochem Signal Transduction (San	2 μM
	Diego, CA)	
Complete EDTA-free Protease	Roche Applied Science (Indianapolis, IN)	_
inhibitor cocktail		
LiCL	Sigma-Alrich Corp	20 mM
SEMA3B	Produced in house	50-100 ng/ml
		(COS-1 cells),
		2 μg/ml (<i>E. coli</i>)
VEGF ₁₆₅	R&D Systems	40 ng/ml
		medium;
		60 pg/filter



Supplemental Figure 1. Diagram of the cellular organization of the human maternalfetal interface in normal pregnancy and in preeclampsia. (A) Villous cytotrophoblasts (vCTBs) progenitors, the specialized (fetal) epithelial cells of the placenta, differentiate and invade the uterine wall (interstitial invasion; iCTBs), where they also breach maternal blood vessels (endovascular invasion). The basic structural units of the placenta are the chorionic villi, composed of a stromal villous core (VC) with fetal blood vessels, surrounded by a basement membrane and overlain by vCTBs. During differentiation, these cells detach from the basement membrane and adopt one of two fates. They either fuse to form the multinuclear syncytiotrophoblasts (STBs) that cover floating villi or join a column of cytotrophoblasts (cCTBs) at the tips of anchoring villi (AV). The syncytial covering of floating villi mediates the nutrient, gas and waste exchange between fetal and maternal blood. The anchoring villi, through the attachment of cCTBs, establish physical connections between the fetus and the mother. iCTBs penetrate the uterine wall through the first third of the myometrium. A subset of these cells home to uterine spiral arterioles and remodel these vessels by replacing the endothelial lining and intercalating within the muscular walls. To a lesser extent, they also remodel uterine veins. (B) In PE, the interstitial and the endovascular components of CTB invasion are restricted. As a result, interstitial invasion is shallow and many uterine arterioles retain their original structures.



Supplemental Figure 2. Confirmation of the expression patterns of selected genes that were misexpressed in sPE. Taqman qRT-PCR was performed using cDNA samples prepared from CTBs that were isolated from the placentas of women whose pregnancies were complicated by preterm labor with no sign of infection (nPTL) or severe preeclampsia (sPE). The analyses were done on cells immediately after isolation (0 h) and after 12, 24, or 48 h of culture. The reactions were done in triplicate. The relative gene expression levels of each transcript were plotted on the y-axis. Data points are the mean ± standard deviation. Fold change differences between the sPE and nPTL samples at each time point were assessed using a Student's t-test. The values shown are the mean ± SD. p values are displayed at bottom of each panel.

nPTL	sPE	
0 12 24 48	0 12 24 48	Symbol Title
		TNFSF10 tumor necrosis factor (ligand) superfamily, member 10
		NFKBIA nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
		CYCS cytochrome c, somatic
		MCL1 myeloid cell leukemia sequence 1 (BCL2-related)
		TFG TRK-fused gene
		JUN jun oncogene
		BIRC2 baculoviral IAP repeat-containing 2
		BCL2A1 BCL2-related protein A1
		NR3C1 nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)
		TNFRSF1A tumor necrosis factor receptor superfamily, member 1A
		BNIP3L BCL2/adenovirus E1B 19kDa interacting protein 3-like
		TNFRSF1B tumor necrosis factor receptor superfamily, member 1B
		IRF1 interferon regulatory factor 1
		SFRS2IP splicing factor, arginine/serine-rich 2, interacting protein
		XIAP X-linked inhibitor of apoptosis
		LASP4 caspase 4, apoptosis-related cysteine peptidase
		IKE/ Interferon regulatory factor /
		KELA v-rei reticuloendotnellosis viral oncogene homolog A (avian)
		CASP1 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)
		INFROFIUE LUTIOF RECFOSIS factor receptor superfamily, member 10b
		INFRSF21 tumor necrosis factor receptor superfamily, member 21
		BLIZIII BLIZ-IKE II (apoptosis iatintator)
		CASP2 cospose 2 apoptosis related systeme poptidase
		CASPS Caspase 5, apoptosis related cystellie peptidase
		IRF2 interferon regulatory factor 2
		FADD Fas (TNERSE6)-associated via death domain
		BID BH3 interacting domain death agonist
		MDM2 Mdm2 p53 binding protein homolog (mouse)
		BIRC3 baculoviral IAP repeat-containing 3
		MAP3K1 mitogen-activated protein kinase kinase kinase 1
		CASP2 caspase 2, apoptosis-related cysteine peptidase
		BCL2L2 BCL2-like 2
		NFKB1 nuclear factor of kappa light polypeptide gene enhancer in B-cells 1
		TRADD TNFRSF1A-associated via death domain
		IRF3 interferon regulatory factor 3
		CHUK conserved helix-loop-helix ubiquitous kinase
		IRF6 interferon regulatory factor 6
		BCL2L1 BCL2-like 1
		TRAF3 TNF receptor-associated factor 3
		NFKBIE nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon
		NEKBIG nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta
		VIAP2K4 mitogen-activated protein Kinase Kinase 4
		LANDIO Caspase recruitment domain family, member 16
		DAU DULZ-dssouldieu dgomisi on uen uedin CASD2 casaasa 2 aaaatad cyctaina pantidasa
		LASTO LASPASE O, APUPLUSISTICIALED LYSICITE PEPLUASE IKRKE inhihitar of kanna light nolynentide gene enhancer in R-celle kinase ensilon
		G7MB granzyme B (granzyme 2) cytotoxic T-lymphocyte-associated sering estarces 1)
		TP53 tumor protein p53
		TNF tumor necrosis factor
		TRAF1 TNF receptor-associated factor 1
		FAS Fas (TNF receptor superfamily, member 6)
		CD40 CD40 molecule, TNF receptor superfamily member 5
		IKBKG inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma
		PARP1 poly (ADP-ribose) polymerase 1
		IKBKB inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta
		DFFA DNA fragmentation factor, 45kDa, alpha polypeptide
		IRF5 interferon regulatory factor 5



Supplemental Figure 3. CTBs isolated from the placentas of nPTL and sPE patients did not upregulate genes that are associated with apoptosis over 48 h of culture.



Supplemental Figure 4. Hypoxia upregulated SEMA3B expression after 48 h in culture. Transfected COS-1 cells (A) and chorionic villus explants established from normal (18 and 20 wk) second trimester placentas (B) were cultured for 48 h in standard conditions (20% O_2) or in a hypoxia chamber (2% O_2). Vertical lines denote noncontiguous lanes from the same gel. The entire experiment was done a total of three times. SEMA3B expression was quantified by immunoblot analysis.