Supplementary Table 1 Primer sequences using quantitative real time polymerase chain reaction.

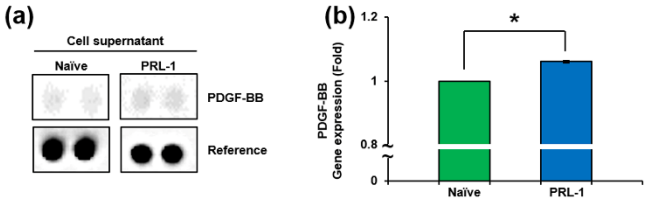
Gene	Primer	Annealing Temperature (℃)	NM number
hAlu	F: 5’-GGA GGC TGA GGC AGG AGA A-3’	60	NM_002715
	R: 5’-CGG AGT CTC GCT CTG TCG CCC A-3’		
hPRL-1	F: 5’-TAC TGC TCC ACC AAG AAG CC-3’	64.3	NM_001385254.1
	R: 5’-AGG TTT ACC CCA TCC AGG TC-3’		
PDGFBB	F: 5'-CTCAGAGAGATGGAGGTGCTCTC-3'	60	NM_031524.1
	R: 5'-GCCCAGAGGAGTTCATGTCTTAT-3'		
PDGFRα	F: 5'-GAGGACGATTCTGCCATCAT-3'	58	NM_012802.1
	R: 5'-CAGTTCTGACGTGGCTTTCA-3'		
PDGFRβ	F: 5'-TGTTCGTGCTATTGCTCCTG-3'	58	NM_031524.1
	R: 5'-TGTCAGCACACTGGAGAAGG-3'		
VEGF	F: 5'-ACTGGACCCTGGCTTTACTG-3'	59	NM_001110333.2
	R: 5'-ACGCACTCCAGGGCTTCATC-3'		
VEGFR2	F: 5'-AAGCAAATGCTCAGCAGGAT-3'	58	NM_013062.2
	R: 5'-TAGGCAGGGAGAGTCCAGAA-3'		
HIF1α	F: 5'-TCGGCGAAGTAAAGAATCTGAA-3'	56	NM_024359.1
	R: 5'-CAAATCACCAGCATCCAGAAG-3'		
Endoglin	F: 5'-AAGGTGTGACTGTACACAAG-3'	56	NM_001010968.3
	R: 5'-CCAGATCTGCATATTGTGGT-3'		
PKCδ	F: 5'-AAGCATTCAACGCCAGGTTC-3'	60	NM_198780.3
	R: 5'-GGGCGAGTCTGTCAGCTCAAT-3'		
Erg-3	F: 5’-CAT GCT AGA AAC ACA GAT TTA CCT T-3’	60	NM_133397.2
	R: 5’- ACC TGG ATT AGC AAG GCG AC-3’		
Nobox	F : 5’- AGC CAG TGC AGA TCT GCA CCG-3’	60	NM_001192013.1
	R : 5’- TGT CAC TGC CAG GAA CAT CCC TC-3’		
Lhx8	F : 5’- GTA TCA CTT GGC TTG CTT-3’	56	NM_001012219.2
	R : 5’- ATT ACC GTT CTC CAC TTC-3’		
GAPDH	F: 5'-TCC CTC AAG ATT GTC AGC AA-3'	55	NM_017008.4
	R: 5'-AGA TCC ACA ACG GAT ACA TT-3'		

Supplementary Table 2 Comparison of follicle counts after transplantation *in vivo*.

		Primordial (%)	Primary (%)	Secondary (%)	Antral (%)	Atresia (%)
Normal		39.92±2.42	17.72±0.60	14.88±0.70	10.02±0.77	17.45±0.99
NTx	1w	27.48±3.44	11.65±0.10*	21.54±5.43	21.20±1.94*	18.13±6.26
	3w	18.08±2.45*	10.35±1.90*	17.73±2.52	27.28±4.86*	26.57±1.35*
	5w	26.96±3.50*	9.88±1.39*	16.81±6.89	22.35±2.38*	24.00±5.17
Naïve	1w	33.92±2.60**	8.83±2.30	19.74±2.22	19.02±1.68	18.49±3.46
	3w	16.70±5.63	6.04±0.53**	17.53±3.68	38.56±9.11	21.17±2.78**
	5w	26.20±7.61	8.04±1.28	17.20±3.19	29.84±7.26	18.72±4.35
PRL-1	1w	38.30±2.16**	10.61±1.20	12.71±2.11**	22.20±2.49	16.18±4.70
	3w	30.59±4.16**, #	6.32±1.22**	18.91±4.01	29.36±2.52	14.82±0.60**, #
	5w	35.03±3.69**	5.73±0.79**	15.02±2.67	26.46±1.15	17.76±0.60**

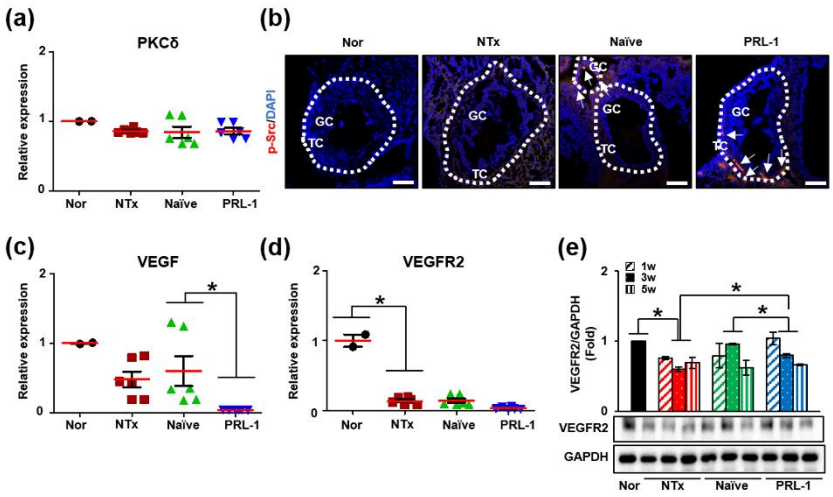
*, NTx vs. Nor (p<0.05). **, Tx vs. NTx (p<0.05). #, Naïve vs. PRL-1.

Supplementary Figure. 1



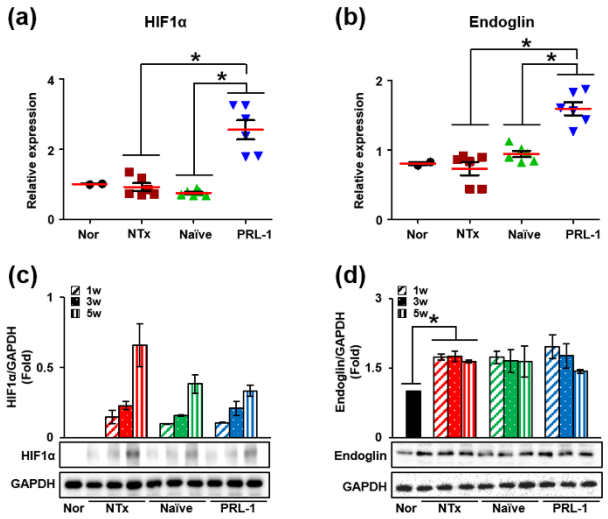
Supplementary Fig.1 The level of PDGF in PRL-1 compared to Naïve.(a-b) The intensity of PDGF-BB was expressed dot blot by cytokine array and Image J program. The data were representative of three independent experiments and expressed as means ± S.D. Significant indicates * $p<0.05$, Naïve vs. PRL-1

Supplementary Figure. 2



Supplementary Fig.2 Effect of PRL-1 on PDGF downstream in ovary of OVX rats. (a) The mRNA expression of PKCδ in ovary was analyzed by qRT-PCR. (b) The gene expression and localization of p-Src in ovary were analyzed by IF staining. (c) The mRNA expression of VEGF and (d) VEGFR2 in ovary were analyzed by qRT-PCR. (e) The gene expression of VEGFR in ovary was analyzed by western blot. The data were representative of three independent experiments and expressed as means ± S.D. Significant indicates * p<0.05, Normal vs. NTx, NTx vs. Tx (Naive and PRL-1), Naive vs. PRL-1 in each time point.

Supplementary Figure. 3



Supplementary Fig.3 Effect of PRL-1 on angiogenesis in ovary of OVX rats.(a) The mRNA expression of HIF1α and (b) Endoglin in ovary were analyzed by qRT-PCR. (c) The gene expression of HIF1α and (d) Endoglin in ovary were analyzed by western blot. The data were representative of three independent experiments and expressed as means ± S.D. Significant indicates * p<0.05, Normal vs. NTx, NTx vs. Tx (Naive and PRL-1), Naive vs. PRL-1 in each time point.