

**TABLE S1. Primers characteristics used to amplify target genes and one reference gene, GAPDH**

HUGOname	forward primer (5'-3')	Afterward primer (5'-3')	GB.accession	Annealing temperature	Product length (bp)
ADM	GAAGAATCCGAGTGTGTTGCC	TTTTCTCTTTAGGTTTGG	NM_001124	60°C	183bp
LEP	ATAGCCCAGGTCCTCTGATA	TTTACCTCTGCATCTCCAC	NM_000230	60°C	192bp
LPL	AAAAGATTCATAAAGCAGCAC	TAGCCACAATGACCTTTCCA	NM_000237	60°C	163bp
PCOLCE	CTCCTCCGAAGGGAATGAAC	GCAGCTTGACTTTAGGCTCAG	NM_002593	65°C	158bp
SOD1	TCAGGAGACCATGTCATCAT	TAAGGGGCCTCAGACTACAT	NM_000454	65°C	176bp
XLKD1	CTGTCTGAGGCTAGGTGGGT	CCATTCTTTTGTCTTACCG	NM_006691	60°C	154bp
VEGF	TGCCTGGAAGATTCAGGAGC	GAGCAGGAAGAGGATGAGGG	AF022375	60°C	169bp
PLAU	TAAGAGCTGGTGTCTGATTG	TAAAAGGAAGGGATAACTGG	NM_002658	60°C	233bp
HLA-DRA	TCTGTAAGGCACATGGAGGT	AAGGCAATAGACAGGGAAGC	NM_019111	60°C	220bp
LDHA	GATTCTAGGTGGAGTTGTG	TAATACCATCCAGCATCAGG	NM_005566	60°C	157bp
MIF	TCAACTATTACGACATGAACGC	AACCGTTTATTCTCCCCAC	NM_002415	60°C	167bp
MAL2	TTGCCTCCTCCAATGTTCTC	CAGTTAGCATCAATTTGAGCCAC	NM_052886	60°C	133bp
XRCC2	CATAGGGCTGAGTCTGGGAC	GCCACCTTCTGATTTGGGAAGT	NM_005431	60°C	204bp
B4GALT4	CCACCGGAACAGAGAGAAACA	TCGTGGAATATAAAGCAGTCCCA	NM_003778	60°C	195bp
DAB2	TTTCCCTACTGAACCCTACC	CCCCAAACAACCTCTGAACAAT	AK024965	60°C	151bp
PRG1	GGACTACTCTGGATCAGGCTT	CCTGTCAAGAGACCTAAGGTTGT	NM_002727	60°C	142bp
FTH1	CAGCAGAGCTAGGACTTCCG	GGTAAACTGGCCACCACAGA	AK054816	60°C	157bp
RAD21	GAGCACCAGCAATCTGAATGA	AGGCCACCCATTGATACATTAT	NM_006265	60°C	235bp
TRAF2	ACGAGGTAAAGATGCCTGCG	CCCCAGTGAGAGGAACGTG	NM_021138	60°C	111bp
ARHE	GCCAGCCAGAAATTATCCAGC	CTTGCGAAGACATGGAGC	BC012513	60°C	120bp
GAPDH	TGTTGCCATCAATGACCCCTT	CTCCACGACGTAICTCAGCG	NM_002046	60°C -65°C	202bp

**TABLE S2. Consistently differentially expressed genes in at least four samples (all above 1.5-fold)**

GB.accession	HUGOname	ratio1	ratio2	ratio3	ratio4	ratio5	Description
<i>Apoptosis</i>							
NM_003031	SIAH1	0.569	0.604	0.782	0.593	0.567	Seven in absentia homolog 1 (Drosophila)
<i>Cell adhesion</i>							
NM_002291	LAMB1	0.710	0.588	0.307	0.505	0.654	Laminin, beta 1
NM_007361	NID2	1.579	0.471	0.257	0.609	0.453	Nidogen 2
<i>Cell growth and/or maintenance</i>							
AJ420467	PAPPA	0.228	0.180	0.414	2.002	0.621	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1695532
NM_000179	MSH6	0.743	0.629	0.554	0.539	0.500	MutS homolog 6 (E. coli)
NM_001124	ADM	0.907	0.570	0.415	0.354	0.636	Adrenomedullin
NM_002050	GATA2	0.864	0.568	0.300	0.608	0.304	GATA binding protein 2
NM_002575	SERPINB2	0.599	0.399	0.934	0.598	0.500	Serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2
NM_002632	PGF	0.729	0.449	0.443	0.637	0.588	Placental growth factor, vascular endothelial growth factor-related protein
NM_002658	PLAU	0.624	1.044	0.613	0.502	0.608	Plasminogen activator, urokinase
NM_005652	TERF2	0.946	0.578	0.527	0.628	0.496	Telomeric repeat binding factor 2
<i>Cell surface receptor linked signal transduction</i>							
NM_001463	FRZB	0.408	0.449	0.333	0.540	1.419	Frizzled-related protein
NM_003177	SYK	1.726	1.869	1.789	0.991	1.725	Spleen tyrosine kinase
NM_013251	TAC3	0.437	0.162	0.075	0.554	2.203	Tachykinin 3 (neuromedin K, neurokinin beta)
<i>Cytoskeleton organization and biogenesis</i>							
AB020671	RHOIP3	1.172	1.663	1.528	1.766	2.315	KIAA0864 protein
NM_000445	PLEC1	1.853	1.274	1.537	2.129	1.762	Plectin 1, intermediate filament binding protein, 500kD
NM_001615	ACTG2	2.999	2.111	1.526	1.613	1.111	Actin, gamma 2, smooth muscle, enteric
NM_001788	CDC10	0.597	0.664	0.508	0.576	NA	CDC10 cell division cycle 10 homolog (S. cerevisiae)
NM_005717	ARPC5	0.479	0.581	0.604	0.498	0.410	Actin related protein 2/3 complex, subunit 5 (16 kD)
<i>Immune response</i>							
AK055976	TMSB4X	1.143	2.430	1.840	1.945	1.865	Thymosin, beta 4, X chromosome
AK057792	C1QG	1.748	1.722	1.750	1.375	1.794	Homo sapiens, Similar to complement component 1, q subcomponent, c polypeptide, clone MGC:17279 IMAG
NM_000416	IFNGR1	0.850	0.578	0.454	0.623	0.442	Interferon gamma receptor 1
NM_001710	BF	0.474	0.503	0.494	0.989	0.550	B-factor, properdin
NM_002415	MIF	1.664	0.727	2.583	1.788	2.593	Macrophage migration inhibitory factor (glycosylation-inhibiting factor)
NM_004106	FCER1G	2.047	1.306	2.905	1.535	2.372	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide
NM_005101	G1P2	1.127	1.950	2.323	1.560	2.011	Interferon-stimulated protein, 15 kDa
NM_019111	HLA-DRA	1.706	1.615	2.450	NA	2.321	Major histocompatibility complex, class II, DR alpha
X59405	MCP	0.503	0.628	0.627	1.510	0.526	Membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)
<i>Metabolism</i>							
NM_000237	LPL	0.210	0.191	0.078	0.296	0.467	Lipoprotein lipase

NM_000391	CLN2	1.514	1.538	1.180	1.777	1.525	Ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease)
NM_000700	ANXA1	0.559	0.687	0.505	0.374	0.547	Annexin A1
NM_001724	BPGM	0.613	0.568	0.842	0.427	0.575	2,3-bisphosphoglycerate mutase
NM_002526	NT5E	0.554	0.654	0.578	0.798	0.614	5' nucleotidase (CD73)
NM_002951	RPN2	0.531	0.503	0.414	1.762	0.632	Ribophorin II
NM_004652	USP9X	0.488	0.750	0.493	0.659	0.627	Ubiquitin specific protease 9, X chromosome (fat facets-like Drosophila)
NM_004776	B4GALT5	0.560	0.559	1.153	0.332	0.558	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5
NM_005566	LDHA	1.801	1.673	1.267	1.737	1.657	Lactate dehydrogenase A
NM_006278	SIAT4C	0.562	0.494	0.787	0.659	0.592	Sialyltransferase 4C (beta-galactosidase alpha-2,3-sialyltransferase)
NM_007066	PKIG	0.665	1.582	2.013	1.997	1.874	Protein kinase (cAMP-dependent, catalytic) inhibitor gamma
NM_012469	C20ORF14	0.564	0.618	0.372	1.831	0.361	Chromosome 20 open reading frame 14
NM_016306	DNAJB11	0.589	0.510	0.698	0.627	0.412	DnaJ (Hsp40) homolog, subfamily B, member 11
NM_030752	TCP1	0.931	0.571	0.397	0.655	0.647	T-complex 1
<i>Nucleic acid and nucleotide binding</i>							
AK056446	HSPCA	0.999	0.651	0.571	0.641	0.603	Heat shock 90kD protein 1, alpha
NM_000979	RPL18	0.628	0.374	0.533	0.566	0.708	Ribosomal protein L18
NM_001029	RPS26	1.845	2.143	3.086	1.727	1.261	Ribosomal protein S26
NM_001357	DHX9	0.548	0.605	0.650	0.900	0.637	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase II; leukophysin
NM_002155	HSPA6	0.655	1.745	0.288	0.469	0.584	Heat shock 70kD protein 6 (HSP70B')
NM_003685	KHSRP	1.985	1.776	2.206	0.933	1.700	KH-type splicing regulatory protein (FUSE binding protein 2)
NM_004396	DDX5	0.645	0.877	0.405	0.455	0.605	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kD)
NM_006666	RUVBL2	1.157	1.644	1.597	1.794	1.932	RuvB-like 2 (E. coli)
NM_015507	EGFL6	1.854	0.441	0.161	0.373	0.255	EGF-like-domain, multiple 6
<i>Regulation of transcription</i>							
M190356	BTF3L3	0.650	0.592	0.626	0.626	0.532	Basic transcription factor 3, like 3
NM_005944	MOX2	0.643	0.455	0.507	0.825	0.460	Antigen identified by monoclonal antibody MRC OX-2
<i>Response to stress</i>							
NM_000454	SOD1	0.579	0.569	0.585	0.626	0.640	Superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))
NM_003336	UBE2A	0.659	0.499	0.278	0.886	0.626	Ubiquitin-conjugating enzyme E2A (RAD6 homolog)
NM_004582	RABGGTB	0.612	0.586	0.639	0.724	0.532	Rab geranylgeranyltransferase, beta subunit
<i>Pathogenesis</i>							
NM_005770	SERF2	1.084	1.837	1.951	1.958	1.638	Small EDRK-rich factor 2
<i>Transport</i>							
BF541376	FTL	1.562	1.252	1.621	2.097	2.098	ESTs, Weakly similar to FRHUL ferritin light chain [H.sapiens]
D86550	DYRK1A	0.940	0.611	0.306	0.615	0.464	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A
NM_001660	ARF4	0.704	0.534	0.458	0.541	0.502	ADP-ribosylation factor 4
NM_003375	VDAC2	0.624	0.561	0.492	0.517	0.419	Voltage-dependent anion channel 2
NM_004800	TM9SF2	0.890	0.371	0.417	0.615	0.442	Transmembrane 9 superfamily member 2
NM_005313	GRP58	0.779	0.527	0.317	0.419	0.571	Glucose regulated protein, 58kD

NM_005415	SLC20A1	0.773	0.420	0.507	0.458	0.356	Solute carrier family 20 (phosphate transporter), member 1
NM_006356	ATP5H	0.948	0.479	0.452	0.303	0.435	ATP synthase, H+ transporting, mitochondrial F <sub>0</sub> complex, subunit d
NM_007285	GABARAPL2	1.056	0.520	0.499	0.482	0.330	GABA(A) receptor-associated protein-like 2
<i>Function Unknown</i>							
AB033059	KIAA1233	0.589	0.560	0.481	0.349	0.298	KIAA1233 protein
AB051505	KIAA1718	1.118	0.589	0.544	0.610	0.238	KIAA1718 protein
AK001840		0.621	0.622	0.365	0.505	0.453	Homo sapiens cDNA FLJ10978 fis, clone PLACE1001484
AK002107		0.942	0.596	0.539	0.635	0.541	Homo sapiens cDNA FLJ11245 fis, clone PLACE1008629
AK023644		0.511	1.304	0.610	0.401	0.607	Homo sapiens cDNA FLJ13582 fis, clone PLACE1009048
AK024330		0.722	0.472	0.258	0.621	0.565	Homo sapiens cDNA FLJ14268 fis, clone PLACE1003383
AK025198		2.620	0.005	0.520	0.052	0.105	Homo sapiens cDNA: FLJ21545 fis, clone COL06195
AK026818		0.603	0.415	0.332	1.040	0.553	Homo sapiens cDNA: FLJ23165 fis, clone LNG09846
AK027539	LOC201725	1.506	1.022	2.610	1.593	1.963	6.2 kd protein
AK027809	FLJ90650	0.599	0.154	0.357	0.534	1.620	Homo sapiens cDNA FLJ14903 fis, clone PLACE1005554
AK054697	MGC10120	1.541	1.554	2.279	0.719	1.959	Homo sapiens cDNA FLJ30135 fis, clone BRACE2000061
AK056682		1.020	0.396	0.442	0.510	0.507	Homo sapiens cDNA FLJ32120 fis, clone PEBLM1000068, highly similar to ACTIN, CYTOPLASMIC TYPE 5
AK056887		0.605	0.604	0.486	0.497	0.434	Homo sapiens cDNA FLJ32325 fis, clone PROST2003922
AK057367		0.848	1.635	1.741	1.631	1.735	Homo sapiens cDNA FLJ32805 fis, clone TESTI2002690
BC004532	H19	0.560	0.509	0.647	0.965	0.542	H19, imprinted maternally expressed untranslated mRNA
BC009447		1.101	0.579	0.615	0.591	0.657	Homo sapiens, clone MGC:15887 IMAGE:3530481, mRNA, complete cds
BC010904	XTP1	0.564	0.530	0.517	NA	0.261	Hypothetical protein FLJ11252
BC012864		2.093	0.664	3.105	1.831	2.302	Homo sapiens, clone IMAGE:3882589, mRNA
NM_002287	LAIR1	NA	1.511	1.985	1.501	1.625	Leukocyte-associated Ig-like receptor 1
NM_004261	37879	0.585	1.144	0.537	0.494	0.524	15 kDa selenoprotein
NM_005088	DXYS155E	0.925	0.583	0.524	0.615	0.546	DNA segment on chromosome X and Y (unique) 155 expressed sequence
NM_006765	N33	0.459	0.248	0.547	1.204	0.359	Putative prostate cancer tumor suppressor
NM_016038	SBDS	0.612	0.602	0.570	0.684	0.520	CGI-97 protein
NM_016068	TTC11	1.612	0.642	2.076	1.511	1.796	CGI-135 protein
NM_016542	MST4	0.807	0.411	0.409	0.550	0.441	Serine/threonine protein kinase MASK
NM_017748	FLJ20291	1.324	0.412	0.628	0.624	0.590	Hypothetical protein FLJ20291
NM_024527	FLJ11743	1.624	0.941	1.537	1.635	1.641	Hypothetical protein FLJ11743
NM_032303	MGC10940	1.529	1.615	3.468	1.455	1.689	Hypothetical protein MGC10940
NM_032839	DIRC2	0.839	0.250	0.307	0.629	0.521	Hypothetical protein FLJ14784
NM_033546	MRLC2	0.513	0.630	0.592	0.619	0.639	Myosin regulatory light chain

**NA: failed to be detected in this microarray experiment.**

**TABLE S3. The result of real-time RT-PCR for analyzing the reliability of microarray data on the No.3 Preeclamptic Sample vs. Control Experiment**

<b>HUGOname</b>	<b>Ratio_microarray</b>	<b>Ratio_real-time PCR</b>	<b>Validation(yes/no)</b>
ADM	0.415	0.270	Y
ARHE	2.890	0.973	N
B4GALT4	0.463	0.285	Y
DAB2	0.507	0.160	Y
FTH1	0.638	0.266	Y
HLA-DRA	2.450	3.345	Y
LDHA	1.337	1.803	N
LEP	8.264	9.087	Y
LPL	0.078	0.118	Y
MAL2	0.320	1.352	N
MIF	1.876	3.285	Y
PCOLCE	1.570	1.560	Y
PLAU	0.613	0.189	Y
PRG1	0.559	0.707	N
RAD21	0.657	0.986	N
SOD1	0.590	0.760	N
TRAF2	1.690	2.990	Y
VEGF	5.565	18.001	Y
XLKD1	1.269	0.860	N
XRCC2	0.412	1.803	N

\* The relative expression ratios of real-time PCR of LPL gene in the table were means of three completely identical experiments.