Supplementary Table 1. Statistics of the aligned data

Samples	P1	P2	P3	P4	P5
Target Region (bp)	60,456,963	60,456,963	60,456,963	60,268,283	60,456,963
Clean Reads	78,452,810	99,872,934	98,765,276	90,160,472	89,595,150
Clean Bases	11,767,921,500	14,980,940,100	14,814,791,400	13,524,070,800	13,439,272,500
Mapped Reads	78,360,413	99,723,778	98,636,434	90,081,624	89,502,164
Mapped Bases	11,691,108,203	14,860,087,969	14,710,808,676	13,416,855,088	13,358,411,510
Mapping Rate (%)	99.88	99.85	99.87	99.91	99.9
Reads Mapped to Target Region	59,939,846	55,721,591	70,047,464	69,578,484	69,619,694
Capture Specificity (%)	76.49	55.88	71.02	77.24	77.79
Duplication Rate (%)	14.49	13.38	14.27	27.13	15.52
Uniq Rate(%)	96.1	96.29	96.1	96.86	96.03
Bases Mapped to Target Region	7,099,121,411	6,570,010,751	8,284,498,769	8,338,800,550	8,262,434,526
Mean Depth of Target Region	117.42	108.67	137.03	138.36	136.67
Coverage of Target Region (%)	99.46	99.42	99.46	99.8	99.34
Fraction of Target Covered >=4X	99.13	99.04	99.16	99.66	99.01
Fraction of Target Covered >=10X	98.47	98.3	98.61	99.34	98.4
Fraction of Target Covered >=20X	97.16	96.81	97.57	98.55	97.32
Fraction of Target Covered >=30X	95.33	94.76	96.23	97.21	95.93
Fraction of Target Covered >=50X	88.6	87.18	91.84	91.6	91.33
Bases Mapped to Flanking Region	2,892,695,743	2,724,856,654	3,394,629,606	3,208,131,250	3,340,277,212
Mean Depth of Flanking Region	61.59	58.01	72.27	68.55	71.12
Coverage of Flanking Region (%)	95.72	95.7	95.75	96.16	95.58
Fraction of Flanking Covered >=4X	94.97	94.93	95.13	95.57	94.9

Supplementary Table 2. Outline of filtering the polymorphisms

Samples	P1	P2	P3	P4	P5
Exon Enrichment kit	SureSelect Human All Exon V6				
Platform	Hiseq PE150 150 bp				
Total variation					
Single nucleotide variants	97,838	97,501	98,196	81,003	97,999
Indels	14,967	14,973	15,350	10,428	15,229
Missense, nonsense, frameshift and splice site variants					
Single nucleotide variants	11,233	10,917	11,179	9,364	11,034
Indels	636	629	647	578	642
Public databases MAF < 1%					
Single nucleotide variants	613	585	621	476	563
Indels	96	75	80	71	77
Variants were further filtered by checking our inhouse databases					
Single nucleotide variants	419	431	449	297	398
Indels	36	35	38	17	31

MAF, minor allele frequency.

Supplementary Table 3. Sequence variants identified that is associated with preeclampsia.

Patient ID	Gene	Nucleotide change	Amino acid change	Polyphen2 prediction	SIFT prediction
P2	*FKTN*	c.A1027C	p.K343Q	Probably damaging	Damaging
P2	*MYH7*	c.G3803A	p.R1268H	Probably damaging	Damaging
P2	*TTN*	c.C49544T	p.T16515M	Probably damaging	Damaging
P2	*TTN*	c.C53359T	p.R17787C	Probably damaging	Damaging
P3	*COL18A1*	c.C1108G	p.R370G	Probably damaging	Damaging
P3	*SYNE1*	c.T10616G	p.L3539W	Probably damaging	Damaging
P4	*CTLA4*	c.C505G	p.P169A	Possibly damaging	Damaging
P4	*TTN*	c.C28730T	p.P9577L	Probably damaging	Damaging