

ERRATA

In the original article “Association analysis of nine mis-sense polymorphisms in the coagulation factor V gene with severe preeclampsia in pregnant Japanese women,” by H. Watanabe et al. [J Hum Genet (2002) 47:131–135], there were errors in Tables 3 and 4. The correct tables are shown below.

Table 3. Genotypic and allelic distributions of *F5* gene polymorphisms

Polymorphism	Population	Genotype count			<i>P</i> *	Allele count		<i>P</i> *
M385T	Patients	MM	MT	TT	0.13	M	T	0.05
	Controls	123	10	0		256	10	
R485K ^a	Patients	KK	RK	RR	0.03	K	R	0.02
	Controls	192	30	2		414	34	
N789T	Patients	NN	NT	TT	0.48	N	T	0.30
	Controls	102	98	24		302	146	
K830R	Patients	KK	KR	RR	0.77	K	R	0.78
	Controls	82	42	9		206	60	
H837R	Patients	TT	TC	CC	0.97	T	C	0.86
	Controls	139	74	11		352	96	
E897K	Patients	LL	LI	II	0.84	L	I	0.64
	Controls	114	90	20		318	130	
S1240S (3894C/T)	Patients	HH	HR	RR	0.35	H	R	0.19
	Controls	70	51	12		251	15	
L1257I	Patients	MM	VM	VV	0.93	M	V	1.00
	Controls	117	16	0		411	37	
H1299R	Patients	DD	DG	GG	0.29	D	G	0.18
	Controls	189	33	2		411	37	

* *P* calculated by Fisher's exact test

^a Previously reported by Watanabe et al. 2001

Table 4. Analysis of linkage disequilibrium for all possible two-way comparisons among nine polymorphisms ($n = 357$)

SNPs	M385T	R485K (2.7kb) ^a	N789T (10.0kb) ^a	K830R (10.1kb) ^a	S1240S (11.3kb) ^a	L1257I (11.4kb) ^a	H1299R (11.5kb) ^a	V1736M (22.9kb) ^a	D2194G (38.3kb) ^a
M385T (0.06) ^b		$D' = 0.835$ $r = 0.327$ $P < 0.001$	$D' = 0.875$ $r = 0.799$ $P < 0.001$	$D' = 0.574$ $r = 0.077$ $P = 0.040$	$D' = 0.967$ $r = 0.386$ $P < 0.001$	$D' = 0.654$ $r = 0.045$ $P = 0.235$	$D' = 0.875$ $r = 0.790$ $P < 0.001$	$D' = 0.966$ $r = 0.362$ $P < 0.001$	$D' = 0.875$ $r = 0.799$ $P < 0.001$
R485K (0.29) ^b			$D' = 0.611$ $r = 0.263$ $P < 0.001$	$D' = 0.637$ $r = 0.522$ $P < 0.001$	$D' = 0.648$ $r = 0.636$ $P < 0.001$	$D' = 0.764$ $r = 0.318$ $P < 0.001$	$D' = 0.645$ $r = 0.279$ $P < 0.001$	$D' = 0.605$ $r = 0.577$ $P < 0.001$	$D' = 0.639$ $r = 0.274$ $P < 0.001$
N789T (0.07) ^b				$D' = 1.000$ $r = 0.148$ $P < 0.001$	$D' = 0.973$ $r = 0.425$ $P < 0.001$	$D' = 0.417$ $r = 0.032$ $P = 0.407$	$D' = 0.959$ $r = 0.959$ $P < 0.001$	$D' = 0.971$ $r = 0.399$ $P < 0.001$	$D' = 0.937$ $r = 0.936$ $P < 0.001$
K830R (0.22) ^b					$D' = 0.973$ $r = 0.811$ $P < 0.001$	$D' = 0.905$ $r = 0.126$ $P < 0.001$	$D' = 0.912$ $r = 0.135$ $P < 0.001$	$D' = 0.860$ $r = 0.672$ $P < 0.001$	$D' = 0.910$ $r = 0.134$ $P < 0.001$
S1240S (0.29) ^b						$D' = 0.855$ $r = 0.145$ $P < 0.001$	$D' = 1.000$ $r = 0.440$ $P < 0.001$	$D' = 0.915$ $r = 0.858$ $P < 0.001$	$D' = 0.945$ $r = 0.414$ $P < 0.001$
L1257I (0.07) ^b							$D' = 0.159$ $r = 0.012$ $P = 0.746$	$D' = 0.734$ $r = 0.134$ $P < 0.001$	$D' = 0.125$ $r = 0.009$ $P = 0.804$
H1299R (0.07) ^b								$D' = 1.000$ $r = 0.415$ $P < 0.001$	$D' = 0.938$ $r < 0.938$ $P < 0.001$
V1736M (0.31) ^b									$D' = 0.971$ $r = 0.399$ $P < 0.001$
D2194G (0.07) ^b									

The H837R and E897K polymorphisms were excluded because of complete linkage disequilibrium with the K830R polymorphism

^aDistance from M385T polymorphism

^bFrequency of minor allele