Supplementary Table 4. Description of *CLEC4G* (*LSECtin*) and *CLEC4M* (*CD209L)* polymorphisms

Polymorphism		NCBI	Position on	Nucleotide	Position on cDNA [b]	Amino acid	Allele Frequency		LD to *DCSIGN1-336*
Code	Name	rs number	NT_077812.2	change [a]		change	Rare allele	Thai (N=80)	Δ (P-value)
CLEC4G (*LSECtin*, cDNA: NM_198492, protein: NP_940894)									
1	LSECtin-217		401200	G/A	promoter		A	0.02	.04 (.49)
2	LSECtin.ex2+2		400652	C/T	exon2	G19G	T	0.05	.10 (.43)
3	LSECtin.in2+50	rs11260026	400493	C/G	intron2		C	0.70	.09 (.38)
4	LSECtin.in2-30	rs12978097	400231	C/T	intron2		T	0.40	.27 (.06)
5	LSECtin.in7-30		398848	G/A	intron7		A	0.01	-
6	LSECtin.ex9+325		398062	A/G	3'UTR		G	0.02	.04 (.47)
7	LSECtin.ex9+397		397990	G/A	3'UTR		A	0.01	-
CLEC4M (*CD209L*, cDNA: NM_014257, protein:NP_055072)									
1	DCSIGN2-593		431556	C/T	5' (repeat)		T	0.02	.14 (.28)
2	DCSIGN2-577	rs11260029	431572	T/C	5' (repeat)		C	0.17	.13 (.12)
3	DCSIGN2-553		431596	A/T	promoter		T	0.005	-
4	DCSIGN2-343		431806	C/A	promoter		A	0.005	-
5	DCSIGN2-323	rs571497	431826	G/A	promoter		A	0.005	-
6	DCSIGN2-198	rs2287887	431951	C/A	promoter		A	0.44	.07 (.58)
7	DCSIGN2.in2-180		433887	G/A	intron2 (repeat)		A	0.30	.03 (.82)
8	DCSIGN2.in2-125	rs594793	433942	G/T	intron2		T	0.14	.13 (.30)
9	DCSIGN2.ex4RPT		434570/435089	7.5/others	exon4	(23aa) repeat	non 7.5	0.31	.15 (.19)
10	DCSIGN2.in4+93	rs868875	435162	A/G	intron4 (repeat)		G	0.22	.13 (.26)
11	DCSIGN2.in4+133	rs868876	435222	A/T	intron4 (repeat)		T	0.28	.15 (.16)
12	DCSIGN2.in4+336	rs475896	435425	C/G	intron4		G	0.21	.07 (.70)
13	DCSIGN2.ex5DN	rs2277998	435624	G/A	exon5	D291N	A	0.15	.12 (.31)
14	DCSIGN2.ex5+92		435629	C/T	exon5	S292S	T	0.005	.03 (.69)
15	DCSIGN2.in5+7	rs562607	435696	G/C	intron5		C	0.44	0 (.93)
16	DCSIGN2.in5+260	rs560634	435949	G/T	intron5		T	0.005	-
17	DCSIGN2.in5+309	rs874492	435997	A/T	intron5 (repeat)		T	0.14	.13 (.24)
18	DCSIGN2.in5-219	rs558705	436179	A/G	intron5		A	0.42	.08 (.49)
19	DCSIGN2.in5-116	rs557094	436282	C/G	intron5		G	0.005	-
20	DCSIGN2.in6+150	rs2161525	436660	T/C	intron6		C	0.39	.16 (.26)
21	DCSIGN2.in6+445	rs8113469	436955	C/T	intron6 (repeat)		T	0.50	.07 (.62)
22	DCSIGN2.in6-653	rs12610506	437067	G/A	intron6 (repeat)		A	0.13	0 (.94)
23	DCSIGN2.in6-511	rs8105492	437209	G/T	intron6 (repeat)		T	0.40	0 (.97)

24	DCSIGN2.in6-316	rs657855	437404	C/T	intron6		T	0.05	.08 (.27)
25	DCSIGN2.in6-268	rs9329374	437452	T/C	intron6 (repeat)		C	0.48	0 (.89)
26	DCSIGN2.in6-256		437464	A/G	intron6		G	0.01	-
27	DCSIGN2.in6-34	rs3745376	437686	G/T	intron6		T	0.10	.10 (.09)
28	DCSIGN2.ex7+127		437846	C/T	exon7	P392P	T	0.005	-
29	DCSIGN2.ex7+153		437872	T/A	3'UTR		A	0.005	-
30	DCSIGN2.ex7+217		437936	G/A	3'UTR		A	0.08	.09 (.25)
31	DCSIGN2.ex7+259	rs1045997	437978	C/T	3'UTR		T	0.07	.09 (.25)
32	DCSIGN2.ex7+551	rs15282	438270	C/T	3'UTR		T	0.25	.14 (.40)
33	DCSIGN2.72839		438610	A/T	3' to transcript		T	0.07	.04 (.64)
34	DCSIGN2.72945	rs684388	438716	T/C	3' to transcript		C	0.44	.12 (.41)
35	DCSIGN2.73428		439199/439210	(CAA)4/(CAA)3	3' to transcript		(CAA)3	0.13	.09 (.51)
36	DCSIGN2.73510		439281	T/C	3' to transcript		C	0.005	-

Notes:

[a] The first allele corresponds to the reference allele on NT_077812.2.

[b] Polymorphisms located in repeated regions (LINE, SINE, LTR) are indicated.