Supplementary Table 2. Description of *CD209* polymorphisms

Polymorphism		NCBI	Position on	Nucleotide	Position on cDNA [b]	Amino acid	Allele Frequency			LD group [c]	LD to DCSIGN1-336
Code	Name	rs number	NT_077812.2	change [a]	(NM_021155)	change (NP_066978)	Rare allele (DF+DHF)	DF+DHF (N=48)	controls (N=32)		Δ (P-value)
1	DCSIGN1-939	rs735240	417332	G/A	5' (repeat)		A	0.33	0.17	B	.21 (.07)
2	DCSIGN1-871	rs735239	417264	A/G	5' (repeat)		G	0.24	0.17	B	.17 (.26)
3	DCSIGN1-564		416953	A/G	5' (repeat)		G	0.01	0.00	-	-
4	**DCSIGN1-336**	**rs4804803**	**416729**	**A(2)/G(1)**	**promoter**		**G**	**0.08**	**0.08**	**A**	**-**
5	**DCSIGN1-139**	**rs2287886**	**416532**	**A(2)/G(1)**	**promoter**		**G**	**0.39**	**0.25**	**B**	**.41 ($6x10^{-5}$)**
6	DCSIGN1-116		416509	G/T	promoter		T	0.01	0.02	-	-
7	**DCSIGN1.in2+11**	**rs7252229**	**416177**	**G(2)/C(1)**	**intron 2**		**C**	**0.06**	**0.06**	**A**	**.91 ($<10^{-5}$)**
8	DCSIGN1.in2+24		416164	C/T	intron 2 (repeat)		T	0.01	0.00	-	-
9	DCSIGN1.in2 +246		415942	C/A	intron 2		A	0.01	0.00	-	-
10	DCSIGN1.in2-353		415766	A/G	intron 2		G	0.02	0.00	-	-
11	DCSIGN1.in2-173		415586	C/A	intron 2		A	0.01	0.00	-	-
12	**DCSIGN1.ex4SF**		**414519**	**G(1)/A(2)**	**exon 4**	**S210F [d]**	**A**	**0.00**	**0.00**	**-**	**-**
13	**DCSIGN1.ex4RPT**		**414401-919**	**7.5(1)/others(2)**	**exon 4**	**(23aa) repeat [e]**	**non 7.5**	**0.01**	**0.00**	**-**	**-**
14	DCSIGN1.in4-28	rs11465384	414002	G/A	intron 4		A	0.01	0.00	-	-
15	**DCSIGN1.in5-178**	**rs8105483**	**413279**	**C(2)/G(1)**	**intron 5**		**G**	**0.06**	**0.03**	**A**	**.86 ($<10^{-5}$)**
16	**DCSIGN1.ex6TI**		**413061**	**G(2)/A(1)**	**exon 6**	**T314I**	**A**	**0.01**	**0.00**	**-**	**-**
17	**DCSIGN1.in6-37**	**rs11465391**	**412159**	**G(2)/C(1)**	**intron 6**		**C**	**0.04**	**0.07**	**A**	**.69 ($<10^{-5}$)**
18	DCSIGN1.1539	rs4804802	411606	A/G	3'UTR		A	0.43	0.62	D	.33 (.01)
19	DCSIGN1.1599	rs10403018	411546	G/A	3'UTR		A	0.02	0.02	-	-
20	DCSIGN1.1667	rs4804801	411478	T/A	3'UTR		A	0.50	0.35	D	.08 (.50)
21	DCSIGN1.1899		411246	G/A	3'UTR (repeat)		A	0.00	0.02	-	-
22	DCSIGN1.1946	rs6603119	411199	T/C	3'UTR (repeat)		C	0.34	0.24	B	.39 (.004)
23	DCSIGN1.1978	rs7248772	411167	A/G	3'UTR (repeat)		G	0.36	0.27	B	.36 (.009)
24	DCSIGN1.2034	rs11465401	411111	G/A	3'UTR (repeat)		A	0.02	0.02	-	-
25	DCSIGN1.2122	rs7248637	411023	A/G	3'UTR		A	0.37	0.58	D	.30 (.02)
26	**DCSIGN1.2281**	**rs1544767**	**410864**	**T(2)/A(1)**	**3'UTR**		**T**	**0.41**	**0.50**	**D**	**.25 (.23)**
27	DCSIGN1.2426	rs1544766	410719	G/A	3'UTR		G	0.40	0.53	D	.25 (.16)

28	DCSIGN1.2893	rs12460694	410251	G/A	3'UTR (repeat)	A	0.32	0.62	D	.14 (.31)
29	DCSIGN1.2916		410226	CCC/CC	3'UTR (repeat)	CC	0.42	0.59	D	.18 (.14)
30	DCSIGN1.2929	rs11260028	410215	AG	3'UTR (repeat)	G	0.33	0.55	D	.14 (.19)
31	DCSIGN1.2994		410150	GA	3'UTR (repeat)	A	0.21	0.06	C	.36 (.06)
32	DCSIGN1.3062	rs11465409	410082	GA	3'UTR (repeat)	A	0.18	0.03	C	.15 (.35)
33	DCSIGN1.3069	rs11465410	410075	TC	3'UTR (repeat)	C	0.18	0.03	C	.15 (.35)
34	DCSIGN1.3071	rs11465411	410073	AG	3'UTR (repeat)	G	0.18	0.03	C	.15 (.35)
35	DCSIGN1.3078	rs11465412	410066	G/A	3'UTR	A	0.18	0.03	C	.15 (.35)
36	**DCSIGN1.3197**	**rs11465413**	**409947**	**A(2)/T(1)**	**3'UTR**	**T**	**0.14**	**0.14**	**C**	**.34 (.008)**
37	**DCSIGN1.3852**	**rs11465421**	**409292**	**G(1)/T(2)**	**3'UTR**	**T**	**0.25**	**0.24**	**E**	**.24 (.14)**
38	DCSIGN1.4020	rs4804800	409124	G/A	3'UTR (repeat)	G	0.43	0.54	D	.14 (.39)
39	DCSIGN1.43041	rs11260027	408812	G/A	3' to transcript	A	0.22	0.25	E	.19 (.24)
40	DCSIGN1.42955	rs11670387	408726	T/C	3' to transcript	C	0.25	0.25	E	.18 (.27)

Notes:

Polymorphisms that were selected for genotyping are shown in bold.

a. The first allele corresponds to the reference allele on NT_077812.2. Allele code (1, 2) is shown for polymorphisms that have been genotyped.

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

c. LD groups were defined as groups of polymorphisms in LD, with Δ value >0.75 with at least one member of the group, with rare allele frequency >0.02.

d. DCSIGN1.ex4SF polymorphism was identified by additional sequencing in a complementary panel of 32 dengue patients.

e. DCSIGN1.ex4RPT polymorphism consisted of a variable number of repeats of a 69-bp unit (23 amino-acids). The frequent variant has 7.5 repeats, other alleles of 8.5, 6.5, 5.5 and 4.5 repeats were identified in the Thai population.

DF, dengue fever; DHF, dengue hemorrhagic fever.