

S1 Table. Variable sites in 20 Japanese and 10 rhesus macaque *TAS2R38* alleles and their frequencies.

Nucleotide Change		T2C	T9G	C10G	G19A	G164T,C	G191A	C243T	T349C	G368A	G607A	G704A	C736T	T812C	G886A	C930G	A959C	C969T	C972T	C992T	N	Freq.(%)	
Amino Acid Change		M1T	T3T	L4V	V7I	C55F,S	R64Q	F81F	Y117H	R123H	V203I	R235H	L246F	I271T	V296I	T310T	K320T	A323A	D324D	T331I			
Japanese macaques	Paha	T	T	C	A	G	G	C	T	A	G	G	C	T	G	C	A	C	C	C	519	43.47	
	<i>Mf-A</i>	T	T	C	G	G	G	C	T	G	A	G	C	T	G	C	A	C	C	C	519	43.47	
	<i>Mf-B</i>	C	373	31.24
	<i>Mf-C</i>	G	.	.	.	A	77	6.45
	<i>Mf-D</i>	.	.	G	19	1.59
	<i>Mf-E</i>	.	.	G	G	A	25	2.09
	<i>Mf-F</i>	.	.	G	A	G	A	29	2.43
	<i>Mf-G</i>	T	.	G	A	10	0.84
	<i>Mf-H</i>	.	.	G	C	.	G	A	.	.	A	15	1.26
	<i>Mf-I</i>	T	.	21	1.76
	<i>Mf-J</i>	A	8	0.67
	<i>Mf-K</i>	C	C	23	1.93
	<i>Mf-L</i>	.	.	G	A	17	1.42
	<i>Mf-M</i>	T	10	0.84
	<i>Mf-N</i>	.	G	C	4	0.34
	<i>Mf-O</i>	C	.	.	C	.	.	.	33	2.76
	<i>Mf-P</i>	.	.	G	A	C	2	0.17
	<i>Mf-Q</i>	A	3	0.25
	<i>Mf-R</i>	.	G	G	.	.	.	A	4	0.34
<i>Mf-S</i>	.	.	.	A	G	.	.	.	A	1	0.08	
<i>Mf-T</i>	.	.	G	C	.	G	.	.	.	A	1	0.08	
rhesus macaques ^a	<i>Mm-a</i>	G	13	12.04	
	<i>Mm-b</i>	G	T	T	39	36.11	
	<i>Mm-d</i>	.	.	.	A	G	11	10.19	
	<i>Mm-f</i>	G	.	T	T	T	4	3.70	
	<i>Mm-g</i>	.	.	.	A	C	G	9	8.33	
	<i>Mm-i</i>	.	.	.	A	T	T	18	16.67
	<i>Mm-j</i>	.	.	.	A	C	G	G	6	5.56	
	<i>Mm-k</i>	.	.	.	A	G	G	4	3.70	
	<i>Mm-l</i>	G	G	3	2.78	
	<i>Mm-m</i>	G	G	1	0.93	

^aThree rhesus macaque alleles, *Mm-c*, *-e*, and *-h*, defined in our previous study (Suzuki et al. 2010) were excluded, as the haplotype phase was inferred by other methods.