Supplementary Material

Table S1. Spearman's rank correlation coefficient between the rh*TPH2* genotype/haplotype and phenotypic data

Haplotype or Locus	Cortisol		ACTH		CORTRES		PERDEX		Self-biting rate	
	AM	PM	AM	PM	15 min	30 min	Night	Day	1999	2000
M2	**-0.3901**$^{\#}$	0.1672	-0.1124	0.1573	-0.0741	0.0519	**0.5043***	0.3729	0.0119	0.2234
M3	-0.1308	-0.0077	-0.0667	-0.0501	**0.5564****	0.2120	0.0935	0.1870	0.0000	0.0133
M4	0.1994	0.1246	-0.1072	-0.1072	-0.0910	-0.0820	**-0.5296***	-0.3841	-0.2921	-0.2104
M5	0.3309	0.0432	-0.0630	-0.1732	-0.0423	0.0181	**-0.5705***	-0.3483	-0.0388	-0.0243
M5'	-0.2415	-0.4087	0.1602	0.1602	-0.0637	-0.2641	0.3027	0.2596	0.0000	-0.1098
M9	0.3539	**0.4665***	-0.0696	-0.0870	-0.2851	-0.1322	0.3116	0.0104	0.1041	0.0699
-1605T>C	-0.3539	**-0.4665***	0.0696	0.0870	0.2851	0.1322	-0.3116	-0.0104	-0.1041	-0.0699
-1491Tn	-0.3539	**-0.4665***	0.0696	0.0870	0.2502	-0.0036	-0.3116	-0.0104	-0.1041	-0.1624
-1485(AT)n	-0.0062	-0.3009	0.0015	0.0573	0.2489	-0.0663	**-0.6047****	-0.2039	-0.3287	-0.1491
(AT)6	-0.0219	**0.5319***	-0.0972	-0.0486	-0.2357	-0.0302	**0.5608***	0.1645	0.1842	**0.3764**$^{\#}$
(AT)7	-0.1983	-0.2192	0.0225	0.0450	**0.5007***	0.0911	**-0.4105**$^{\#}$	-0.1457	-0.2612	-0.1372
(AT)8	0.1489	-0.2830	0.0667	-0.0501	-0.0855	-0.1588	**-0.4400**$^{\#}$	-0.2348	-0.0401	-0.0982
-1454A>G	0.2415	**0.4087**$^{\#}$	-0.1602	-0.1602	0.0637	0.2641	-0.3027	-0.2596	0.0000	0.1098
-1325In>Del	-0.1014	0.2946	-0.0972	-0.0134	0.1616	0.1951	**0.5548***	0.3364	0.0683	0.1321
-363T>G	-0.0562	0.1366	-0.0904	0.0000	0.2887	0.2037	-0.0948	-0.2933	0.1244	0.2425
2051A>C	**0.6538****	0.0385	-0.1501	-0.3503	**0.3824**$^{\#}$	**0.4729***	-0.0877	-0.3839	**-0.4068**$^{\#}$	**-0.3842**$^{\#}$
2128S>L	-0.2727	-0.2258	0.0797	0.2347	-0.1068	**-0.4552***	**-0.5012***	-0.3009	0.2339	0.1877

$^{*}p<0.05$, $^{**}p<0.01$, $^{\#}0.05\leq p<0.10$; CORTRES: cortisol response to ACH challenge; PERDEX: DEX suppression of cortisol excretion (%). For each haplotype or allele, the carrier and non-carrier were designated as "1" and "2", respectively, while for each locus the genotype was designated as "1", "2" and "3" for the wild-type homozygote, wild-mutant heterozygote and mutant-mutant homozygote, respectively. The 2051A>C genotypes were designated as "1" for AA&AC and "2" for CC.

Supplementary Material

Table S2. Distribution of the rh*TPH2* 5'-FR and 3'-UTR haplotypes in the cohort of 32 monkeys

Group	n	5'-FR haplotype											3'-UTR haplotype		
		M2	M3	M4	M4'	M5	M5'	M7	M9	N1	N2	N3	ACS	AAS	GAL
Overall	64	6 0.09	20 0.31	4 0.06	2 0.03	14 0.22	6 0.09	1 0.02	8 0.13	1 0.02	1 0.02	1 0.02	30 0.47	18 0.28	16 0.25
SW (1)	40	1	10	3	2	10	5	1	6	1	1	-	18	12	10
HFB (1a)	20	1	8	2	-	4	2	-	2	1	-	-	9	5	6
LFB (1b)	10	-	1	1	1	4	1	-	2	-	-	-	5	4	1
NW (2)	22	**5***	10	-	-	3	1	-	2	-	-	1	11	5	6
HFB (2a)	4	1	1	-	-	1	-	-	1	-	-	-	-	1	3
LFB (2b)	14	3	7	-	-	2	-	-	1	-	-	1	**9**$^{\#}$	3	2
HFB (a)	24	2	9	2	-	5	2	-	3	1	-	-	9	6	**9**$^{\#}$
LFB (b)	24	3	8	1	1	6	1	-	3	-	-	1	14	7	3
Chi-Square test (R×C)		**5':** 1, 2: p=**0.0326**; a, b: p=1.0000; 1a, 1b: p=0.1804; 2a, 2b: p=0.7397; 1a, 2a: p=0.8749; **1b**, **2b: p=0.0375** **3':** 1, 2: p=0.6248; a, b: p=0.1658; 1a, 1b: p=0.2218; 2a, 2b: p=0.1647; 1a, 2a: p=0.3029; 1b, 2b: p=0.3862													

SW: self-wounder; NW: non-wounder; HFB: high-frequency biter; LFB: low-frequency biter. $^{*}p<0.05$ for SW *vs* NW, $^{\#}p<0.05$ for HFB *vs* LFB assessed for the individual haplotype (2×2 table). The incidence of each haplotype was given for the overall group. *P* values were given for the comparisons of haplotype distribution between SIB groups (R×C table). The Fisher's exact test and Mantel-Haenszel *Chi*-Square test were used for 2×2 and R×C tables, respectively.

Table S3. The effect of the rh*TPH*2 5' (-1485(AT)$_n$) and 3' (2015A>C) genotype and their interaction on the physiology and self-biting behavior in mother- and peer-reared monkeys

Variable	Genotype	Mother-Reared				Peer-Reared			
		Mean1$_{(n)}$	Mean2$_{(n)}$	*F*	*p*	Mean1$_{(n)}$	Mean2$_{(n)}$	*F*	*p*
HIAA	5'	**33.7$_{(5)}$**	**49.5$_{(5)}$**	**4.82**	**0.070**	43.4$_{(2)}$	45.6$_{(6)}$	0.03	0.867
	3'	**49.9$_{(3)}$**	**33.3$_{(7)}$**	**5.31**	**0.061**	46.0$_{(4)}$	42.4$_{(4)}$	0.11	0.755
	5'x3'	-	-	**4.25**	**0.085**	-	-	**5.35**	**0.082**
CORT-AM	5'	29.8$_{(6)}$	24.1$_{(5)}$	0.19	0.677	32.4$_{(2)}$	33.3$_{(6)}$	0.01	0.918
	3'	**32.7$_{(3)}$**	**21.2$_{(8)}$**	**4.61**	**0.069**	**42.7$_{(4)}$**	**23.4$_{(4)}$**	**4.67**	**0.097**
	5'x3'	-	-	0.94	0.364	-	-	0.02	0.895
CORT-PM	5'	**12.7$_{(6)}$**	**21.3$_{(5)}$**	**7.79**	**0.027**	14.2$_{(2)}$	18.5$_{(6)}$	0.89	0.400
	3'	20.2$_{(3)}$	13.7$_{(8)}$	2.86	0.134	14.6$_{(4)}$	18.0$_{(4)}$	0.54	0.502
	5'x3'	-	-	2.10	0.191	-	-	1.28	0.321
ACTH-AM	5'	71.2$_{(5)}$	66.7$_{(5)}$	0.07	0.805	68.8$_{(2)}$	60.6$_{(6)}$	0.38	0.571
	3'	69.6$_{(3)}$	68.3$_{(7)}$	0.0	0.948	55.6$_{(4)}$	73.9$_{(4)}$	1.88	0.243
	5'x3'	-	-	2.01	0.206	-	-	0.40	0.563
ACTH-PM	5'	65.9$_{(5)}$	63.8$_{(5)}$	0.15	0.711	64.2$_{(2)}$	49.6$_{(6)}$	1.40	0.303
	3'	63.8$_{(3)}$	65.9$_{(7)}$	0.04	0.842	**43.6$_{(4)}$**	**70.2$_{(4)}$**	**4.64**	**0.098**
	5'x3'	-	-	**3.74**	**0.101**	-	-	0.37	0.578
CORTRES15	5'	17.4$_{(7)}$	17.9$_{(6)}$	0	0.964	17.0$_{(3)}$	14.0$_{(5)}$	1.67	0.265
	3'	**20.3$_{(3)}$**	**15.3$_{(10)}$**	**3.32**	**0.102**	**17.9$_{(3)}$**	**13.2$_{(5)}$**	**4.06**	**0.114**
	5'x3'	-	-	0.28	0.607	-	-	1.66	0.268
CORTRES30	5'	14.1$_{(7)}$	12.5$_{(6)}$	0.32	0.583	12.4$_{(3)}$	11.9$_{(5)}$	0.04	0.852
	3'	15.3$_{(3)}$	11.3$_{(10)}$	2.24	0.169	14.2$_{(3)}$	10.2$_{(5)}$	2.16	0.215
	5'x3'			0.31	0.593	-	-	0.52	0.510
DEX-N	5'	**56.4$_{(7)}$**	**93.8$_{(4)}$**	**25.2**	**0.001**	30.0$_{(2)}$	64.5$_{(4)}$	1.60	0.333
	3'	**46.0$_{(2)}$**	**75.3$_{(9)}$**	**3.14**	**0.114**	46.8$_{(3)}$	47.8$_{(3)}$	0	0.974
	5'x3'	-	-	-	-	-	-	2.71	0.241
DEX-D	5'	62.9$_{(7)}$	80.3$_{(4)}$	0.16	0.703	24.0$_{(2)}$	41.0$_{(4)}$	0.91	0.442
	3'	**35.2$_{(2)}$**	**76.8$_{(9)}$**	**3.92**	**0.083**	23.5$_{(3)}$	41.5$_{(3)}$	1.02	0.420
	5'x3'	-	-	-	-	-	-	1.81	0.311
SB-1999	5'	0.050$_{(6)}$	0.094$_{(5)}$	0.22	0.652	0.060$_{(2)}$	0.088$_{(4)}$	0.22	0.683
	3'	0.020$_{(2)}$	0.081$_{(9)}$	0.72	0.422	0.023$_{(3)}$	0.125$_{(3)}$	3.10	0.221
	5'x3'	-	-	-	-	-	-	0.09	0.792
SB-2000	5'	0.068$_{(7)}$	0.105$_{(6)}$	0.11	0.746	0.018$_{(3)}$	0.125$_{(5)}$	1.53	0.284
	3'	0.025$_{(3)}$	0.148$_{(10)}$	1.23	0.296	0.030$_{(3)}$	0.113$_{(5)}$	0.89	0.398
	5'x3'	-	-	0.06	0.813	-	-	0.29	0.618

*Statistics were performed by ANOVA2. Mean1 represents the Tukey-Kramer least-squares mean for -1845(AT)6 carrier (5') or 2051CC (3') genotype, while Mean2 represents the Tukey-Kramer least-squares mean for -1845(AT)6 non-carrier (5') or 2051AA&AC (3'). The sample size (n) for each group was shown in parenthesis.