

Figure S1. All sample pearson of *A. cerana*.

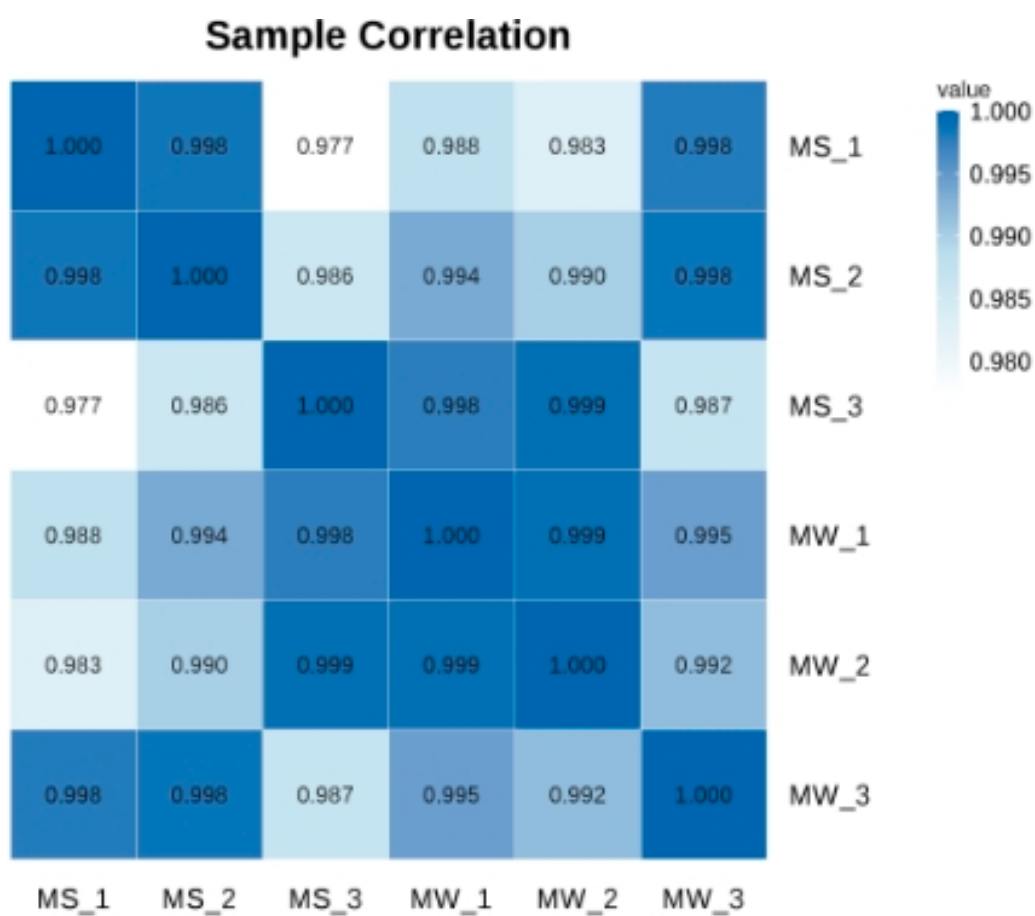


Figure S2. All sample pearson of *A. mellifera*.

Table S1. Primer sequences of 11 genes used in qPCR.

mRNA name	Gene ID	Primer Sequences (5'to 3')
<i>β-Actin</i>	NM_001185146.1	Forward: CCTAGCACCATCCACCATGAA Reverse: GAAGCAAGAATTGACCCACCAA
<i>CYP9E2</i>	LOC108004123	Forward: AAACATGGGCTCGTTGGTC Reverse: GGCGTGGTGAAGTCGTAAA
<i>CAMTA1</i>	LOC107995465	Forward: ATCTACGGCTGTTATGTGC Reverse: GTTTAGGTAGTGAACGAGGAC
<i>OtopLc</i>	LOC108002750	Forward: GAATCTGTCTGGTCTGGTTGA Reverse: CGTGGTGGTAGTGGTTGTG
<i>SLC17A8</i>	LOC107994928	Forward: GGTATGTGCGGGTTGATTT Reverse: GCCATTTGGGTTTGTCTT
<i>His2A</i>	LOC108003508	Forward: GGCTGCTGCAGTGTTGGAAT Reverse: GCAAGTTGAAGATGACGAGGTA
<i>At1g62600</i>	LOC726418	Forward: CGGCGGAAGTTGGATATACAC Reverse: CTGTGATGAACGAACGACGAT
<i>SETMAR</i>	LOC113218652	Forward: CACACGCATCTTTGGTCACT Reverse: AGGTCAGGACTATATGGTGGAT
<i>TpnC47D</i>	LOC494501	Forward: TGCCTGCCACTTCCAGAG Reverse: TCAGCGATCATTCCGTCCAT
<i>SLC26A10</i>	LOC100576446	Forward: GGTAGCAACTTACAGCACTCAA Reverse: ACCGCAGTAGCAACTTCCA
<i>CCKAR</i>	LOC410654	Forward: CCAACGAGGAGCAACAAGATT Reverse: CCAGCACGATCACGAACAG

Table S2. Different ages analysis of self-grooming behavior.

Groups	<i>Apis cerana</i> (n=360)		<i>Apis mellifera</i> (n=360)		Z-values	P-values
ages	WG	SG	WG	SG		
5	50 (83.33%)	10 (16.67%)	51 (85%)	9 (15%)	-0.249	0.803
7	40 (66.67%)	20 (33.33%)	53 (88.33%)	7 (11.67%)	-2.83	0.005**
9	17 (28.33%)	43 (71.67%)	46 (76.67%)	14 (23.33%)	-5.279	<0.0001****
11	29 (48.33%)	31 (51.67%)	43 (71.67%)	17 (28.33%)	-2.598	0.009**
13	32 (53.33%)	28 (46.67%)	47 (78.33%)	13 (21.37%)	-2.875	0.004**
15	35 (58.33%)	25 (41.67%)	44 (73.33%)	16 (26.67%)	-1.725	0.085
H-values	41.283		7.718			
p-values	<0.0001****		0.173			

p<0.05*, p<0.01**, p<0.001***.WG: weak grooming; SG: strong grooming.

Table S3. RNA-seq data summary and mapped information of *A. cerana* and *A. mellifera*.

sample	Raw Reads	Clean Reads	GC (%)	Q20 (%)	Q30 (%)	Unique Mapped (%)	Multiple Mapped (%)	Total Mapped (%)	Exon (%)	Intron (%)	Intergenic (%)
CS_1	44334054	44133054	41.26	97.81	93.68	80.43	3.89	84.31	79.06	12.17	8.77
CS_2	37922452	37780584	40.48	98.11	94.41	86.46	3.17	89.63	81.18	12.98	5.85
CS_3	39014690	38845838	40	97.89	93.80	82.89	3.09	85.98	81.86	10.13	8.01
CW_1	43972952	43773054	41.78	98.05	94.21	82.32	3.47	85.79	79.53	13.51	6.96
CW_2	38452026	38294230	41.08	98.17	94.49	83.25	3.81	87.06	81.33	11.81	6.86
CW_3	46726902	46537632	40.34	97.89	93.74	81.72	3.75	85.47	81.45	11.15	7.40
MS_1	40809116	40637580	40.65	98.26	94.65	67.89	3.81	71.70	87.84	10.37	1.79
MS_2	46779512	46580218	40.55	98.02	93.98	72.01	4.26	76.27	86.90	11.03	2.07
MS_3	39892396	39714684	40.18	98.19	94.44	75.93	5.34	81.27	90.85	7.57	1.58
MW_1	36709590	36553108	40.05	98.14	94.36	71.13	3.91	75.04	88.74	8.50	2.76
MW_2	37008178	36848772	39.76	98.26	94.65	74.58	3.66	78.24	88.77	8.79	2.43
MW_3	46690506	46484600	40.17	97.99	93.91	74.80	5.45	80.25	87.96	9.87	2.16

CW: weak grooming of *A. cerana*; CS: strong grooming of *A. cerana*; MW: weak grooming of *A. mellifera*; MS: strong grooming of *A. mellifera*. GC: GC ratio of filtered sequence bases; Q20: the percentage of bases with mass value of more than 20 in the total number of bases in Clean Data; Q30: The percentage of bases with a mass value of more than 30 in the total number of bases in Clean Data..

Table S4. *A. cerana* and *A. mellifera* gene HTR2A and gene SLC17A8 homologous.

<i>Apis_cerana</i> id	<i>Apis_mellifera</i> id	identity (%)	alignment length	mismatches	bit score
XM_028664372.1	XM_026443084.1	99.045	733	5	1485
XM_028664372.1	XM_026443085.1	98.609	575	6	1150
XM_017052091.2	XM_016914051.2	99.437	533	3	1108