Raw data files

Table 1 Main composition of cow milk and goat milk (%)

Main components	Goat milk			Cow milk		
	1	2	3	1	2	3
Protein	3.11	3.39	3.25	3.74	3.17	3.53
Carbohydrate	3.98	3.22	5.16	4.48	6.15	5.03
Total fat	4.19	3.55	3.84	4.77	3.02	2.68
Ash	6.31	6.68	6.54	5.33	6.04	6.42
Hydrolysis amino acids						
Asp	0.22	0.31	0.34	0.18	0.30	0.15
Glu	0.68	0.77	0.98	0.64	0.75	0.77
Ser	0.08	0.14	0.14	0.16	0.13	0.13
His	0.1	0.17	0.06	0.06	0.12	0.06
Gly	0.05	0.07	0.03	0.05	0.09	0.04
Thr	0.11	0.21	0.19	0.28	0.15	0.14
Arg	0.07	0.12	0.08	0.12	0.11	0.10
Ala	0.14	0.08	0.08	0.14	0.22	0.03
Tyr	0.16	0.2	0.21	0.24	0.15	0.27
Cys-s	0.05	0.06	0.07	0.04	0.06	0.02
Val	0.11	0.14	0.14	0.24	0.21	0.12
Met	0.04	0.08	0.06	0.15	0.07	0.05
Phe	0.2	0.11	0.08	0.16	0.12	0.05
Ile	0.12	0.19	0.14	0.18	0.20	0.04
Leu	0.3	0.21	0.15	0.33	0.18	0.27
Lys	0.17	0.13	0.24	0.27	0.24	0.15
Pro	0.24	0.37	0.23	0.24	0.18	0.45
Trp	0.07	0.11	0.09	0.04	0.10	0.04
TAA	2.91	3.47	3.31	3.52	3.57	2.69
AAAs	0.36	0.31	0.29	0.4	0.27	0.32
BCAAs	0.53	0.54	0.43	0.75	0.59	0.43
HAAs	1.27	1.36	1.00	1.53	1.37	1.09
PCAAs	0.34	0.42	0.38	0.45	0.66	0.12
NCAAs	0.9	1.08	1.32	0.82	1.05	0.92
EAAs	1.22	1.35	1.15	1.71	1.39	0.92

TAA: Total amino acids.

Aromatic amino acids (AAAs): Phe, Tyr.

Branch chain amino acids (BCAAs): Leu, Ile, Val.

Hydrophobic amino acids (HAAs): Ala, Val, Ile, Leu, Phe, Pro, Met, Gly, Trp

Positively charged amino acids (PCAAs）: Arg, His, Lys.

Negatively charged amino acids (NCAAs): Glu, Asp

Essential amino acids (EAAs): Thr, Cys,Val, Met, Ile, Leu, Phe, Lys, His.

Table 2 Free amino acides of cow milk and goat milk (mg/100g)

Main components	Goat milk			Cow milk		
	1	2	3	1	2	3
Asp	0.048	0.054	0.055	0.068	0.057	0.066
Glu	0.241	0.183	0.101	0.249	0.285	0.329
Ser	0.032	0.027	0.005	0.044	0.030	0.031
His	0.064	0.056	0.034	0.078	0.086	0.084
Gly	0.058	0.061	0.083	0.273	0.189	0.138
Thr	0.149	0.237	0.177	0.199	0.245	0.156
Arg	0.056	0.048	0.039	0.106	0.107	0.098
Ala	0.037	0.027	0.041	0.089	0.099	0.086
Tyr	0.032	0.018	0.040	0.079	0.064	0.060
Cys-s	0.015	0.017	0.017	0.023	0.020	0.022
Val	0.192	0.123	0.248	0.155	0.142	0.116
Met	0.019	0.011	0.022	0.031	0.027	0.017
Phe	0.032	0.041	0.024	0.038	0.028	0.039
Ile	0.032	0.023	0.032	0.047	0.037	0.021
Leu	0.027	0.017	0.031	0.039	0.042	0.035
Lys	0.048	0.054	0.067	0.077	0.061	0.046
Pro	0.008	0.005	0.006	0.126	0.133	0.154
Trp	0.028	0.029	0.036	0.090	0.100	0.085
TAA	1.350	0.934	0.922	2.760	1.430	0.951
AAAs	0.088	0.129	0.064	0.287	0.186	0.108
BCAAs	0.182	0.283	0.259	0.358	0.172	0.104
HAAs	0.529	0.516	0.249	0.688	0.784	0.902
PCAAs	0.188	0.149	0.128	0.377	0.205	0.161
NCAAs	0.233	0.284	0.166	0.457	0.301	0.296
EAAs	0.549	0.632	0.672	0.788	0.714	0.617

TAA: Total amino acids.

Aromatic amino acids (AAAs): Phe, Tyr.

Branch chain amino acids (BCAAs): Leu, Ile, Val.

Hydrophobic amino acids (HAAs): Ala, Val, Ile, Leu, Phe, Pro, Met, Gly, Trp

Positively charged amino acids (PCAAs）: Arg, His, Lys.

Negatively charged amino acids (NCAAs): Glu, Asp

Essential amino acids (EAAs): Thr, Cys,Val, Met, Ile, Leu, Phe, Lys, His.

Table 3 Sleep latency with sodium pentobarbital (min)

	CT	Model	DZP	GM	CM
1	6.01	9.28	3.84	6.38	7.28
2	4.98	8.22	4.38	4.58	8.22
3	6.78	7.66	2.88	5.88	6.48
4	5.67	8.24	4.3	6.28	7.99
5	5.03	9.27	3.26	7.25	6.82
6	6.02	7.41	4.02	4.88	7.92
7	6.41	8.03	3.69	6.72	9.77
8	6.48	6.99	4.26	6.82	6.38
9	5.67	9.35	3.25	7.37	8.26
10	5.83	7.42	3.71	5.37	7.93

Table 4 Sleep time with sodium pentobarbital (min)

	CT	Model	DZP	GM	CM
1	36.82	14.28	43.27	33.29	19.20
2	34.91	18.93	42.28	28.25	30.55
3	26.37	22.55	42.08	27.39	26.39
4	27.34	24.37	33.28	33.39	29.38
5	28.36	17.47	45.82	34.28	25.93
6	27.91	18.43	32.57	26.21	18.42
7	32.56	24.72	33.62	26.93	26.28
8	26.71	22.78	42.81	30.15	26.84
9	32.44	19.04	36.29	27.48	22.39
10	35.71	20.19	47.37	27.48	30.28

Table 5 Sleep time in 12 hours (min)

	CT	Model	DZP	GM	CM
1	236.9	79.3	210.7	183.2	120.4
2	249.3	77.3	243.9	169.4	118.2
3	277.1	63.2	205.3	143.9	139.8
4	261.7	104.2	237.5	143.4	163.5
5	222.7	84.3	218.5	153.0	143.2
6	256.3	77.9	208.3	179.3	123.8
7	217.6	84.6	229.3	194.3	118.8
8	262.8	63.9	248.9	127.9	163.4
9	246.3	96.1	205.6	115.3	132.5
10	210.5	87.3	217.8	184.2	124.4

Table 6 The levels of 5-HT in hypothalamus （ng/mL）

CT	Model	DZP	GM	CM
127.93	89.29	139.28	120.39	94.28
134.28	94.38	126.27	94.38	106.38
120.83	74.23	115.35	105.28	117.39
113.92	83.55	120.35	98.28	84.28
116.93	73.09	128.38	118.28	92.38
124.73	75.28	148.38	115.27	102.38
125.38	82.12	118.38	104.29	84.37
114.38	94.62	118.29	94.28	88.51
127.38	98.35	134.28	93.22	103.28
130.29	74.38	122.39	108.29	118.28

Table 7 the levels of GABA in hypothalamus (μmol/mL)

CT	Model	DZP	GM	CM
7.48	2.73	6.01	4.39	3.48
7.04	2.11	5.82	5.22	5.23
6.26	3.72	6.28	4.38	4.88
4.77	3.02	7.22	6.02	5.38
5.82	2.83	5.41	5.34	4.72
6.92	3.51	6.24	4.88	5.00
5.02	2.88	7.03	6.38	4.28
5.33	3.61	5.73	5.03	5.2
4.61	2.91	7.92	4.33	4.22
5.92	4.16	6.82	4.19	5.62

Table 8 the levels of NE in hypothalamus (ng/mL)

CT	Model	DZP	GM	CM
6.02	8.99	4.38	4.28	5.39
6.62	7.28	4.89	6.37	7.38
5.38	9.04	3.35	7.37	6.99
5.82	8.29	5.02	5.38	7.83
4.72	8.26	4.27	5.38	8.43
6.88	8.48	5.39	6.33	5.36
5.68	7.52	5.24	6.37	6.39
6.03	9.36	4.07	5.29	7.23
6.03	7.66	6.22	4.05	6.49
5.17	5.83	4.63	5.37	5.38

Table 9 the levels of DA in hypothalamus (pg/mL)

CT	Model	DZP	GM	CM
128.39	137.48	113.28	128.93	135.88
125.29	142.99	117.37	124.38	145.77
110.76	139.47	120.29	103.27	120.47
132.98	152.47	103.77	137.28	103.88
115.53	155.23	121.53	136.2	117.82
118.77	142.66	114.37	105.37	135.28
130.29	136.34	125.34	110.32	135.29
124.39	132.16	103.24	105.27	118.25
122.05	143.68	107.44	126.28	142.44
104.35	155.06	116.78	139.22	126.82

Table 10 Relative abundance at the phylum level

Taxonomy	CT	Model	DZP	GM	CM
Firmicutes	0.696495	0.370618	0.644471	0.590556	0.481523
Bacteroidota	0.127103	0.368732	0.170402	0.154478	0.253057
Proteobacteria	0.036689	0.031412	0.112684	0.046052	0.058235
Desulfobacterota	0.020778	0.034313	0.029526	0.126681	0.065087
Verrucomicrobiota	0.002649	0.174749	0.025143	0.034273	0.104696
Actinobacteriota	0.063615	0.003476	0.005869	0.009915	0.008784
Patescibacteria	0.018843	0.001648	0.002214	0.003184	0.011254
Campilobacterota	0.000835	0.005824	0.001846	0.01203	0.005178
Chloroflexi	0.007908	0.001271	0.001581	0.004338	0.002196
Acidobacteriota	0.006525	0.00128	0.001410	0.003718	0.002326
Others	0.018560	0.006678	0.004854	0.014774	0.007678

Table 11 Relative abundance at the genus level

Taxonomy	CT	Model	DZP	GM	CM
Lactobacillus	0.304542	0.093769	0.490585	0.291219	0.138536
Acinetobacter	0.005236	0.007630	0.100694	0.004616	0.009156
Dubosiella	0.174713	0.098336	0.028686	0.038965	0.017634
Akkermansia	0.002623	0.174749	0.025143	0.034201	0.104664
Muribaculaceae	0.088111	0.183977	0.109213	0.081891	0.152889
Escherichia-Shigella	0.009206	0.103527	0.032669	0.035288	0.033154
Staphylococcus	0.037254	0.000494	0.000835	0.001307	0.045625
Turicibacter	0.062263	0.013454	0.011523	0.013463	0.009821
Bacteroides	0.000651	0.001226	0.000965	0.007733	0.026297
Faecalibaculum	0.041381	0.015847	0.036765	0.070342	0.034912
Others	0.274019	0.30699	0.162925	0.420976	0.427317

Table 12 Relative abundance at the family level

Taxonomy	CT	Model	DZP	GM	CM
Lactobacillaceae	0.304565	0.093769	0.490585	0.291223	0.138536
Erysipelotrichaceae	0.279651	0.128693	0.078124	0.146885	0.077315
Moraxellaceae	0.005250	0.007630	0.100694	0.004616	0.009183
Desulfovibrionaceae	0.020361	0.034151	0.029360	0.126645	0.065025
Akkermansiaceae	0.002623	0.174749	0.025143	0.034201	0.104664
Muribaculaceae	0.088111	0.183977	0.109213	0.081891	0.152889
Bacteroidaceae	0.009206	0.103527	0.032669	0.035288	0.033154
Lachnospiraceae	0.015659	0.058118	0.015430	0.045535	0.092427
Staphylococcaceae	0.037254	0.000494	0.000835	0.001307	0.045625
Enterobacteriaceae	0.000651	0.001226	0.000965	0.007773	0.026454
Others	0.236670	0.213665	0.116981	0.224636	0.254728

Table 13 Heatmap analysis of the different genera among the five groups

Taxon	CT	Model	DZP	GM	CM
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	0.0937 67	0.13 8571	0.29 1164	0.49 0576	0.30 4536
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter	0.0076 11	0.00 917	0.00 4629	0.10 0694	0.00 5237
k__Bacteria;p__Firmicutes;c__Bacilli;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Dubosiella	0.0983 33	0.01 764	0.03 8982	0.02 8684	0.17 4722
k__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Akkermansiaceae;g__Akkermansia	0.1747 46	0.10 4669	0.03 419	0.02 5119	0.00 262
k__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Muribaculaceae	0.1839 77	0.15 3016	0.08 1857	0.10 9185	0.08 8236
k__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	0.1035 24	0.03 3168	0.03 5334	0.03 2726	0.00 9192
k__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	0.0005 04	0.04 5632	0.00 1294	0.00 082	0.03 7245
k__Bacteria;p__Firmicutes;c__Bacilli;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Turicibacter	0.0134 64	0.00 9812	0.01 347	0.01 1528	0.06 2243
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	0.0012 22	0.02 6292	0.00 773	0.00 0963	0.00 0636
k__Bacteria;p__Firmicutes;c__Bacilli;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Faecalibaculum	0.0158 53	0.03 4913	0.07 0314	0.03 6753	0.04 1391
k__Bacteria;p__Firmicutes;c__Bacilli;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Allobaculum	0.0004 12	0.01 0763	0.02 1946	0.00 0729	0.00 1021
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Listeriaceae;g__Listeria	0.0000 29	0.00 0024	0.01 8809	0.00 014	0.00 0358
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Sutterellaceae;g__Parasutterella	0.0133 39	0.00 2359	0.01 9923	0.00 3095	0.00 1893
k__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	0.0003 98	0.00 1342	0.00 374	0.00 1717	0.05 0864

k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridia_UCG-014;f__Clostridia_UCG-014;g__Clostridia_UCG-014	0.009791	0.027862	0.005933	0.005035	0.006927
k__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Eubacterium_coprostanoligenes_group;g__Eubacterium_coprostanoligenes_group	0.003644	0.025067	0.005684	0.003585	0.000895
k__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcaceae;g__Romboutsia	0.013266	0.009863	0.000791	0.004904	0.005355
k__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;g__Rikenella	0.007823	0.018231	0.003448	0.005119	0.004692
k__Bacteria;p__Desulfobacterota;c__Desulfovibrionia;o__Desulfovibrionales;f__Desulfovibrionaceae;g__Desulfovibrio	0.001521	0.010517	0.003386	0.002503	0.004638
k__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Alloprevotella	0.016511	0.009699	0.000633	0.002459	0.001178
k__Bacteria;p__Patescibacteria;c__Saccharimonadia;o__Saccharimonadales;f__Saccharimonadaceae;g__Candidatus_Saccharimonas	0.001368	0.010992	0.002435	0.000199	0.007733
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Morganellaceae;g__Proteus	0.000857	0.009958	0.001593	0.000369	0.001312
k__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Blautia	0.007307	0.005645	0.000206	0.001122	0.001435
k__Bacteria;p__Campilobacterota;c__Campylobacteria;o__Campylobacterales;f__Helicobacteraceae;g__Helicobacter	0.005809	0.005172	0.002049	0.001843	0.000851
k__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Tannerellaceae;g__Parabacteroides	0.029959	0.003306	0.008241	0.003357	0.005598
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridia_vadinBB60_group;f__Clostridia_vadinBB60_group;g__Clostridia_vadinBB60_group	0.011486	0.002136	0.001518	0.001015	0.000903
k__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Lachnospiraceae_NK4A136_group	0.007005	0.003559	0.002111	0.001442	0.000723
k__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;g__Alistipes	0.008805	0.005889	0.007037	0.001684	0.001017
k__Bacteria;p__Deferribacterota;c__Deferribacteres;o__Deferribacterales;f__Deferribacteraceae;g__Mucispirillum	0.002786	0.003265	0.008399	0.001352	0.005361
k__Bacteria;p__Bacteroidota;c__SJA-28;o__SJA-28;f__SJA-28;g__SJA-28	0.000511	0.001012	0.000026	0.000738	0.004414
k__Bacteria;p__Nitrospirota;c__Nitrospiria;o__Nitrospirales;f__Nitrospiraceae;g__Nitrospira	0.001154	0.001555	0.002815	0.001329	0.004796
k__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Marinifilaceae;g__Butyricimonas	0.006587	0.002522	0.001635	0.000011	0.000034
k__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Oscillospiraceae;g__Colidextribacter	0.003091	0.000446	0.000395	0.001234	0.000583
k__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Lachnospiraceae_UCG-006	0.001123	0.003634	0.001429	0.000575	0.000242
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	0.000807	0.001174	0.003375	0.000426	0.000308
k__All	0.151611	0.222458	0.240269	0.100409	0.130505

Table 14 The mRNA expression of $GABA_AR$ in hypothalamus

Name	Ct value of β-actin	Ct value of $GABA_AR$	$2^{(-\Delta\Delta Ct)}$
CT1	15.52	25.14	0.94
CT2	15.66	25.57	0.77
CT3	16.95	26.52	0.97
CT4	16.41	26.16	0.86
CT5	17.33	26.85	1.01
CT6	18.17	27.59	1.08
CT7	19.82	28.73	1.54
Model1	17.27	27.84	0.50
Model2	17.33	27.54	0.64
Model3	17.21	28.08	0.40
Model4	17.66	27.95	0.61
Model5	16.98	27.54	0.50
Model6	16.84	27.68	0.41
Model7	16.82	27.21	0.56
DZP1	16.57	26.26	0.92
DZP2	16.46	26.49	0.72
DZP3	16.04	26.01	0.76
DZP4	16.13	26.14	0.73
DZP5	16.26	26.38	0.68
DZP6	17.75	27.83	0.70
DZP7	17.04	26.58	1.02
GM1	16.57	26.49	0.78
GM2	16.84	26.37	1.03
GM3	16.36	25.94	0.99
GM4	16.95	26.84	0.80
GM5	16.84	26.73	0.80
GM6	17.05	26.73	0.92
GM7	16.82	27.16	0.58
CM1	17.04	27.27	0.63
CM2	16.48	26.64	0.66
CM3	16.84	26.73	0.80
CM4	16.82	27.17	0.58
CM5	17.46	27.37	0.79
CM6	16.81	26.48	0.93
CM7	17.49	27.46	0.76

Table 15 The mRNA expression of CREB in hypothalamus

Name	Ct value of β-actin	Ct value of CREB	$2^{(-\Delta\Delta Ct)}$
CT1	16.93	26.49	0.87
CT2	16.94	26.11	1.14
CT3	16.84	26.42	0.86
CT4	17.03	26.34	1.04
CT5	17.53	26.48	1.33
CT6	16.94	26.43	0.91
CT7	17.45	27.11	0.81
Model1	17.45	27.73	0.53
Model2	16.74	27.34	0.42
Model3	17.37	27.64	0.53
Model4	16.59	27.48	0.35
Model5	17.27	28.17	0.34
Model6	16.88	27.15	0.53
Model7	17.84	28.17	0.51
DZP1	18.22	27.93	0.78
DZP2	18.36	28.02	0.81
DZP3	18.53	28.62	0.60
DZP4	18.03	27.84	0.73
DZP5	17.83	27.37	0.88
DZP6	18.43	27.94	0.90
DZP7	17.93	28.03	0.60
GM1	18.68	28.30	0.84
GM2	18.78	28.38	0.84
GM3	18.87	28.11	1.09
GM4	18.96	29.03	0.61
GM5	19.06	28.64	0.86
GM6	19.15	28.94	0.74
GM7	19.25	28.94	0.79
CM1	18.47	28.27	0.74
CM2	18.48	28.44	0.66
CM3	17.93	27.73	0.74
CM4	18.38	27.88	0.91
CM5	18.22	28.38	0.57
CM6	17.46	27.13	0.81
CM7	18.36	27.84	0.92

Table 16 The mRNA expression of BDNF in hypothalamus

Name	Ct value of β-actin	Ct value of BDNF	$2^{(-\Delta\Delta Ct)}$
CT1	17.77	25.47	1.20
CT2	18.03	25.74	1.19
CT3	17.48	25.38	1.04
CT4	17.54	25.48	1.01
CT5	18.37	26.52	0.87
CT6	17.73	26.02	0.79
CT7	18.03	26.04	0.96
Model1	17.49	26.93	0.36
Model2	18.33	27.37	0.47
Model3	17.38	26.93	0.33
Model4	18.39	27.27	0.53
Model5	18.47	27.04	0.65
Model6	17.85	26.83	0.49
Model7	17.58	26.73	0.44
DZP1	17.38	26.03	0.62
DZP2	18.12	26.83	0.59
DZP3	17.88	26.22	0.77
DZP4	18.48	26.34	1.07
DZP5	18.32	26.83	0.68
DZP6	17.33	25.75	0.73
DZP7	18.02	26.03	0.96
GM1	18.38	26.46	0.92
GM2	18.47	26.41	1.01
GM3	18.03	26.53	0.69
GM4	17.83	26.19	0.76
GM5	18.49	26.77	0.80
GM6	18.47	26.65	0.86
GM7	17.39	25.78	0.74
CM1	19.27	27.38	0.90
CM2	18.99	27.63	0.62
CM3	19.38	27.46	0.92
CM4	19.85	27.97	0.89
CM5	18.79	27.35	0.66
CM6	19.26	28.13	0.53
CM7	18.55	26.82	0.81

Table 17 The mRNA expression of TrkB in hypothalamus

Name	Ct value of β-actin	Ct value of TrkB	$2^{(-\Delta\Delta Ct)}$
CT1	18.37	25.08	1.28
CT2	17.39	24.63	0.89
CT3	18.49	25.33	1.17
CT4	17.46	25.17	0.64
CT5	18.03	25.35	0.84
CT6	18.46	25.41	1.09
CT7	18.51	25.22	1.28
Model1	17.54	25.39	0.58
Model2	17.66	25.38	0.64
Model3	17.84	25.48	0.67
Model4	18.29	26.87	0.35
Model5	18.31	26.58	0.43
Model6	17.33	25.85	0.37
Model7	18.03	26.49	0.38
DZP1	17.11	24.31	0.91
DZP2	17.48	25.17	0.65
DZP3	18.47	25.79	0.84
DZP4	17.49	25.35	0.58
DZP5	18.03	25.47	0.77
DZP6	18.53	25.92	0.80
DZP7	18.42	25.77	0.82
GM1	18.56	26.11	0.72
GM2	18.11	25.46	0.82
GM3	18.04	25.51	0.76
GM4	18.45	25.67	0.90
GM5	17.64	24.85	0.91
GM6	17.77	25.14	0.81
GM7	18.02	25.10	0.99
CM1	19.55	26.93	0.81
CM2	18.63	26.15	0.73
CM3	19.04	26.47	0.78
CM4	18.76	26.33	0.71
CM5	18.69	25.89	0.91
CM6	19.33	26.94	0.69
CM7	19.02	26.52	0.74

Table 18 Peptide content of *in vitro* gastric digestion of milk and goat milk (%)

Time	Cow milk			Goat milk		
(min)	1	2	3	1	2	3
15	0.021	0.017	0.025	0.028	0.022	0.028
30	0.045	0.046	0.044	0.045	0.044	0.046
60	0.081	0.089	0.092	0.078	0.099	0.095
90	0.154	0.101	0.117	0.132	0.124	0.127

Table 19 Peptide content of *in vitro* intestinal digestion of milk and goat milk (%)

Time	Cow milk			Goat milk		
(min)	1	2	3	1	2	3
15	0.125	0.133	0.135	0.137	0.126	0.126
30	0.158	0.164	0.168	0.178	0.165	0.162
60	0.237	0.337	0.278	0.385	0.385	0.391
90	0.573	0.594	0.548	0.644	0.732	0.781
120	0.927	0.968	0.991	1.104	1.168	1.320
180	1.375	1.473	1.669	1.823	1.658	1.732

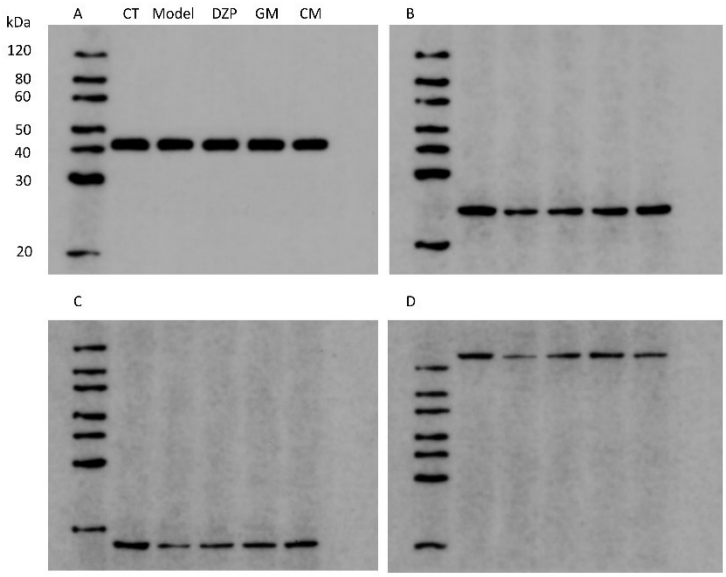

Figure S2 The image of the full gel and blot, uncropped and unprocessed in the hypothalamus, A-D were β-actin, CREB, BDNF and TrkB, respectively