

Supplemental materials

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Figure S8. The proportion of full-length transcripts annotated in the metabolic pathways of the neural-related system.

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Figure S10. Several published genes were compared with full-length transcripts. The figure shows the comparative results for the *SK2* gene.

Figure S11. The number of overlapped transcripts among the top five immune pathways with the largest number of genes in the KEGG annotation.

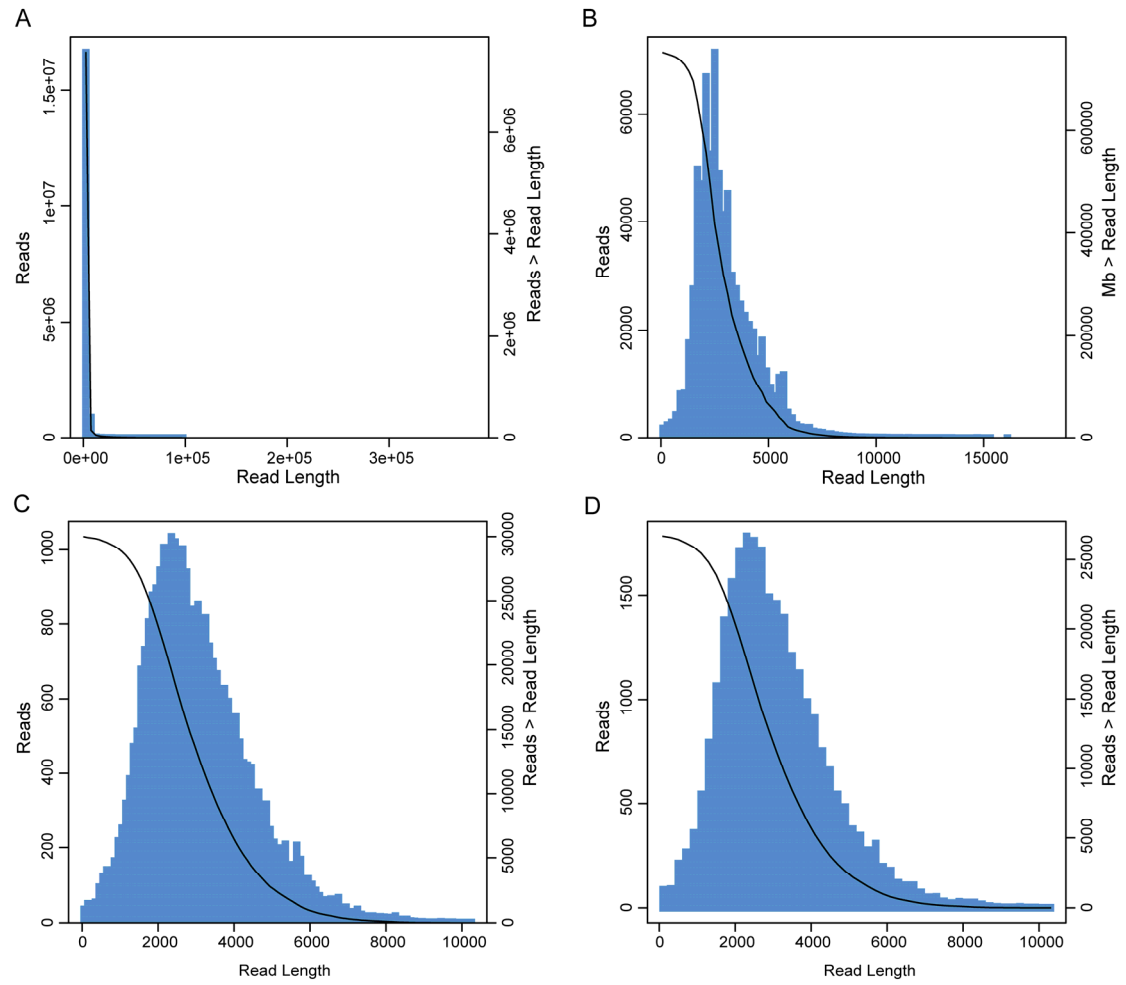


Figure S1 Tissue sample PacBio sequencing results. (A)Length distribution of subreads **(B)**Length distribution of CCS **(C)**Length distribution of Unpolished Consensus Isoforms **(D)** Length distribution of Isoform

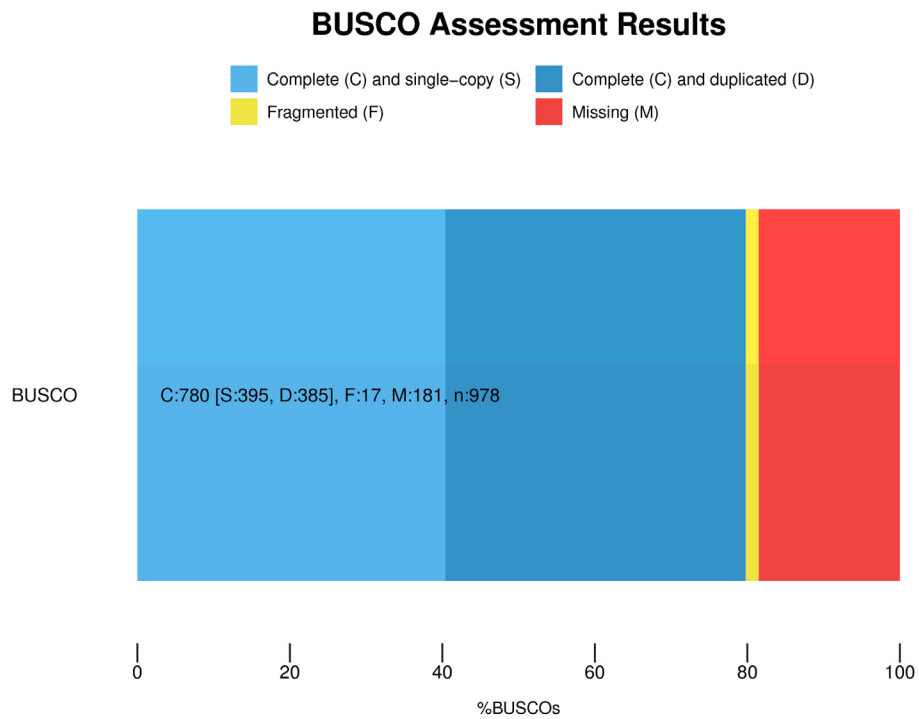


Figure S2. Benchmarking universal single-copy orthologs (BUSCO) assessment results of transcriptome generated.

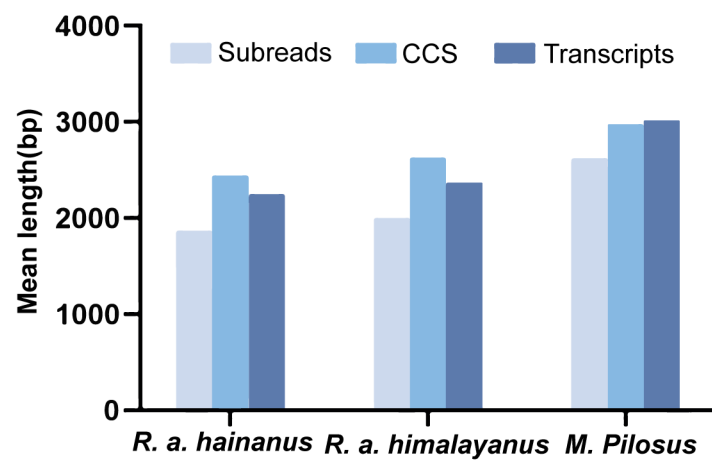


Figure S3. The mean length of the subreads, CCS and transcripts in *R. a. hainanus*, *R. a. himalayanus* and *M. Pilosus*, respectively.

Isoform0022110	TTTGCCATAATGAACCGTCCAGCCCCTGTGGAGATCTCCT	40
PRL-2ATGAACCGTCCAGCCCCTGTGGAGATCTCCT	31
Consensus	atgaaccgtccagcccctgtggagatctcct	
Isoform0022110	ATGAGAACATGCGTTTTCTGATTACTCACAACCCTACCAA	80
PRL-2	ATGAGAACATGCGTTTTCTGATTACTCACAACCCTACCAA	71
Consensus	atgagaacatgcgttttctgattactcacaaccctaccaa	
Isoform0022110	TGCTACCCTCAACAAGTTCACAGAGGAACTTAAGAAGTAT	120
PRL-2	TGCTACCCTCAACAAGTTCACAGAGGAACTTAAGAAGTAT	111
Consensus	tgctaccctcaacaagttcacagaggaacttaagaagtat	
Isoform0022110	GGAGTGACAACCTTTGGTTCGAGTTTGTGATGCTACATACG	160
PRL-2	GGAGTGACAACCTTTGGTTCGAGTTTGTGATGCTACATACG	151
Consensus	ggagtgacaactttggttcgagtttgtgatgctacatacg	
Isoform0022110	ATAAAGCTCCAGTTGAAAAAGAAGGAATCCATGTTCTAGA	200
PRL-2	ATAAAGCTCCAGTTGAAAAAGAAGGAATCCATGTTCTAGA	191
Consensus	ataaagctccagttgaaaaagaaggaatccatgttctaga	
Isoform0022110	TTGGCCATTTGATGATGGTGCGCCACCCCCTAATCAGATA	240
PRL-2	TTGGCCATTTGATGATGGTGCGCCACCCCCTAATCAGATA	231
Consensus	ttggccatttgatgatgggtgcgccaccccctaatacagata	
Isoform0022110	GTGGACGATTGGCTAAACCTATTAAAAACCAAATTTTCGTG	280
PRL-2	GTGGACGATTGGCTAAACCTATTAAAAACCAAATTTTCGTG	271
Consensus	gtggacgattggctaaacctattaaaaaccaaatttcgtg	
Isoform0022110	AAGAACCAGGTTGCTGTGTTGCAGTGCATTGTGTTGCGGG	320
PRL-2	AAGAACCAGGTTGCTGTGTTGCAGTGCATTGTGTTGCGGG	311
Consensus	aagaaccaggttgctgtgttgagtcagtcattgtgttgcggg	
Isoform0022110	ATTGGGAAGGGCACCTGTGCTGGTTGCACTTGCTTTGATT	360
PRL-2	ATTGGGAAGGGCACCTGTGCTGGTTGCACTTGCTTTGATT	351
Consensus	attgggaagggcacctgtgctggttgcaattgctttgatt	
Isoform0022110	GAATGTGGAATGAAGTATGAAGATGCAGTTCAGTTTATAA	400
PRL-2	GAATGTGGAATGAAGTATGAAGATGCAGTTCAGTTTATAA	391
Consensus	gaatgtggaatgaagtatgaagatgcagttcagtttataa	
Isoform0022110	GACAAAAAAGAAGGGGAGCATTCAATTCCAAACAGCTGCT	440
PRL-2	GACAAAAAAGAAGGGGAGCATTCAATTCCAAACAGCTGCT	431
Consensus	gacaaaaaagaaggggagcattcaattccaaacagctgct	
Isoform0022110	TTACCTGGAGAAATACCGACCTAAGATGCGATTACGCTTC	480
PRL-2	TTACCTGGAGAAATACCGACCTAAGATGCGATTACGCTTC	471
Consensus	ttacctggagaaataccgacctaagatgcgattacgcttc	
Isoform0022110	AGAGATACCAATGGGCATTGCTGTGTTTCAG..	510
PRL-2	AGAGATACCAATGGGCATTGCTGTGTTTCAGTA	503
Consensus	agagataccaatgggcattgctgtgttcag	

prl-2	...MNRPAPVEISYENMRFLITHNPTNATLNKFTEELKKY	37
Isoform0022110	FAIMNRPAPVEISYENMRFLITHNPTNATLNKFTEELKKY	40
Consensus	mnrpapveisyenmrflithnptnatlnkfteelkky	
prl-2	GVTTLVRVCDATYDKAPVEKEGIHVLDWPFDDGAPPPNQI	77
Isoform0022110	GVTTLVRVCDATYDKAPVEKEGIHVLDWPFDDGAPPPNQI	80
Consensus	gvttlvrvcdatydkapvekegihvldwpfddgappnqi	
prl-2	VDDWLNLLKTKFREEPGCCVAVHCVAGLGRAPVLVALALI	117
Isoform0022110	VDDWLNLLKTKFREEPGCCVAVHCVAGLGRAPVLVALALI	120
Consensus	vddwlnllktkfreepgccvavhcvaglgrapvlvalali	
prl-2	ECGMKYEDAVQFIRQKRRGAFNSKQLLYLEKYRPKMRLRF	157
Isoform0022110	ECGMKYEDAVQFIRQKRRGAFNSKQLLYLEKYRPKMRLRF	160
Consensus	ecgmkyedavqfirqkrrgafnsqllylekyrpkmrlrf	
prl-2	RDTNGHCCV	166
Isoform0022110	RDTNGHCCV	169
Consensus	rdtnghccv	

Figure S4

Several published genes were compared with full-length transcripts, the comparative result of the *PRL-2* gene.

Isaform001047	ATGAAAGCAATGAAAGTCTCTGAACTCTGAA	40
DPA	ATGAAAGCAATGAAAGTCTCTGAACTCTGAA	40
Consensus	atgaaagcaatgaaagtggtgtgtggaggtgtggggg	
Isaform001047	CTGAGCTCTGACACATGACCTGAGCTGAGT	80
DPA	CTGAGCTCTGACACATGACCTGAGCTGAGT	80
Consensus	ctgagctctgacacatcagctgtgtgggtgtgt	
Isaform001047	CTGAGCAAGATGATGATGATGATGATGATGAG	120
DPA	CTGAGCAAGATGATGATGATGATGATGATGAG	120
Consensus	gtgtgtgaaagtgtgtgtatgtgtgtgtgtgtgt	
Isaform001047	TGACTTATGATGATGATGATGATGATGATGAT	160
DPA	TGACTTATGATGATGATGATGATGATGATGAT	160
Consensus	tcaactctagtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	GGACTCACTTCTGATGATGATGATGATGATGAT	200
DPA	GGACTCACTTCTGATGATGATGATGATGATGAT	200
Consensus	ggactcaactctgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	TGACACAGAAATGATGATGATGATGATGATGAT	240
DPA	TGACACAGAAATGATGATGATGATGATGATGAT	240
Consensus	ctcaacagaaatgactgtgtgtgtgtgtgtgtgtgt	
Isaform001047	CTGAGCACTCTGATGATGATGATGATGATGAT	280
DPA	CTGAGCACTCTGATGATGATGATGATGATGAT	280
Consensus	ctgaaagcaactctgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	ATGATTTGACATGATGATGATGATGATGATGAT	320
DPA	ATGATTTGACATGATGATGATGATGATGATGAT	320
Consensus	atgatttggactctctagtgtgtgtgtgtgtgtgtgt	
Isaform001047	TGATGACTTCTCTCTGATGATGATGATGATGAT	360
DPA	TGATGACTTCTCTCTGATGATGATGATGATGAT	360
Consensus	tgtgtagaggtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	AAATGAGCTCTCTGACGCTCTCTGATGATGAT	400
DPA	AAATGAGCTCTCTGACGCTCTCTGATGATGAT	400
Consensus	aaatggagctctcagcgtctctgtgtgtgtgtgtgt	
Isaform001047	ACTTAACAAAGTACTGTACAGCAAGCAAGATTT	440
DPA	ACTTAACAAAGTACTGTACAGCAAGCAAGATTT	440
Consensus	acttaacaaagtactgtacagcaagcaagattct	
Isaform001047	AAATGACACTGATGATGATGATGATGATGATGAT	480
DPA	AAATGACACTGATGATGATGATGATGATGATGAT	480
Consensus	aaatgacaaagtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	AACTGTGATGATGATGATGATGATGATGATGAT	520
DPA	AACTGTGATGATGATGATGATGATGATGATGAT	520
Consensus	aaactgtgattgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	ATGATCTATGATGATGATGATGATGATGATGAT	560
DPA	ATGATCTATGATGATGATGATGATGATGATGAT	560
Consensus	atgattctatgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	AAAGAGCTGATGATGATGATGATGATGATGAT	600
DPA	AAAGAGCTGATGATGATGATGATGATGATGAT	600
Consensus	aaagagcgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	TGAGAGCAAGATCTCTGATGATGATGATGATGAT	640
DPA	TGAGAGCAAGATCTCTGATGATGATGATGATGAT	640
Consensus	tatgaaagcaaatctcagtactcgtcgtcgtcgtgt	
Isaform001047	GGTCTAAAGTGGCTTTTATGATGATGATGATGAT	680
DPA	GGTCTAAAGTGGCTTTTATGATGATGATGATGAT	680
Consensus	ggtctaaaggcacttttagactcgtcgtcgtgtgt	
Isaform001047	GGACAGCTGATGATGATGATGATGATGATGAT	720
DPA	GGACAGCTGATGATGATGATGATGATGATGAT	720
Consensus	ggacagcagctcagcagtgactcgtcgtcgtcgtgt	
Isaform001047	GGATGATGATGATGATGATGATGATGATGAT	760
DPA	GGATGATGATGATGATGATGATGATGATGAT	760
Consensus	ggatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	ACCAAGCTGATGATGATGATGATGATGATGAT	800
DPA	ACCAAGCTGATGATGATGATGATGATGATGAT	800
Consensus	accaagcagcagctgaaagtcaactgtgaaggtcta	
Isaform001047	GGTGAATGATGATGATGATGATGATGATGAT	840
DPA	GGTGAATGATGATGATGATGATGATGATGAT	840
Consensus	ggtgtgaattgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	GAATGATGATGATGATGATGATGATGATGAT	880
DPA	GAATGATGATGATGATGATGATGATGATGAT	880
Consensus	gaattgtgtcgtcgtcgtcgtcgtcgtcgtcgtcgt	
Isaform001047	ACTGTGATGATGATGATGATGATGATGATGAT	920
DPA	ACTGTGATGATGATGATGATGATGATGATGAT	920
Consensus	acttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	TTTGATGATGATGATGATGATGATGATGATGAT	960
DPA	TTTGATGATGATGATGATGATGATGATGATGAT	960
Consensus	tttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	GGATTTGATGATGATGATGATGATGATGATGAT	1000
DPA	GGATTTGATGATGATGATGATGATGATGATGAT	1000
Consensus	gattttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	GTGATGATGATGATGATGATGATGATGATGAT	1040
DPA	GTGATGATGATGATGATGATGATGATGATGAT	1040
Consensus	gtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	TGATGATGATGATGATGATGATGATGATGAT	1080
DPA	TGATGATGATGATGATGATGATGATGATGAT	1080
Consensus	tgattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	CTGATGATGATGATGATGATGATGATGATGAT	1120
DPA	CTGATGATGATGATGATGATGATGATGATGAT	1120
Consensus	ctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	AGGTGATGATGATGATGATGATGATGATGAT	1160
DPA	AGGTGATGATGATGATGATGATGATGATGAT	1160
Consensus	aggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	AAATGATGATGATGATGATGATGATGATGAT	1200
DPA	AAATGATGATGATGATGATGATGATGATGAT	1200
Consensus	aaattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	GGATGATGATGATGATGATGATGATGATGAT	1240
DPA	GGATGATGATGATGATGATGATGATGATGAT	1240
Consensus	ggatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	GTGATGATGATGATGATGATGATGATGATGAT	1280
DPA	GTGATGATGATGATGATGATGATGATGATGAT	1280
Consensus	gtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	TGATGATGATGATGATGATGATGATGATGAT	1320
DPA	TGATGATGATGATGATGATGATGATGATGAT	1320
Consensus	tgaattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	ATGTGATGATGATGATGATGATGATGATGAT	1360
DPA	ATGTGATGATGATGATGATGATGATGATGAT	1360
Consensus	agtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	GTGATGATGATGATGATGATGATGATGATGAT	1400
DPA	GTGATGATGATGATGATGATGATGATGATGAT	1400
Consensus	gtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	TTGATGATGATGATGATGATGATGATGATGAT	1440
DPA	TTGATGATGATGATGATGATGATGATGATGAT	1440
Consensus	tttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	AGTATGATGATGATGATGATGATGATGATGAT	1480
DPA	AGTATGATGATGATGATGATGATGATGATGAT	1480
Consensus	agtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	TTTGTGATGATGATGATGATGATGATGATGAT	1520
DPA	TTTGTGATGATGATGATGATGATGATGATGAT	1520
Consensus	cttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	AACTGATGATGATGATGATGATGATGATGAT	1560
DPA	AACTGATGATGATGATGATGATGATGATGAT	1560
Consensus	aaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	TGATGATGATGATGATGATGATGATGATGAT	1600
DPA	TGATGATGATGATGATGATGATGATGATGAT	1600
Consensus	tattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	AAATGATGATGATGATGATGATGATGATGAT	1640
DPA	AAATGATGATGATGATGATGATGATGATGAT	1640
Consensus	aaattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	CTGATGATGATGATGATGATGATGATGATGAT	1680
DPA	CTGATGATGATGATGATGATGATGATGATGAT	1680
Consensus	ctgaaagcagctgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	TGATGATGATGATGATGATGATGATGATGAT	1720
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Isaform001047	ATGTGATGATGATGATGATGATGATGATGAT	1760
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Isaform001047	GGATGATGATGATGATGATGATGATGATGAT	1800
DPA	GGATGATGATGATGATGATGATGATGATGAT	1800
Consensus	gtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	GAATGATGATGATGATGATGATGATGATGAT	1840
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Isaform001047	AGGTGATGATGATGATGATGATGATGATGAT	1920
DPA	AGGTGATGATGATGATGATGATGATGATGAT	1920
Consensus	aggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	GTGATGATGATGATGATGATGATGATGATGAT	1960
DPA	GTGATGATGATGATGATGATGATGATGATGAT	1960
Consensus	gtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	GGATGATGATGATGATGATGATGATGATGAT	2000
DPA	GGATGATGATGATGATGATGATGATGATGAT	2000
Consensus	ggatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	TTGATGATGATGATGATGATGATGATGATGAT	2040
DPA	TTGATGATGATGATGATGATGATGATGATGAT	2040
Consensus	tttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	TGATGATGATGATGATGATGATGATGATGAT	2080
DPA	TGATGATGATGATGATGATGATGATGATGAT	2080
Consensus	tgaagcgtctgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	AGTATGATGATGATGATGATGATGATGATGAT	2120
DPA	AGTATGATGATGATGATGATGATGATGATGAT	2120
Consensus	agtactcgtactcgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	TTTGTGATGATGATGATGATGATGATGATGAT	2160
DPA	TTTGTGATGATGATGATGATGATGATGATGAT	2160
Consensus	tttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	GTGATGATGATGATGATGATGATGATGATGAT	2200
DPA	GTGATGATGATGATGATGATGATGATGATGAT	2200
Consensus	gtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	AGTATGATGATGATGATGATGATGATGATGAT	2240
DPA	AGTATGATGATGATGATGATGATGATGATGAT	2240
Consensus	agtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	GGATGATGATGATGATGATGATGATGATGAT	2280
DPA	GGATGATGATGATGATGATGATGATGATGAT	2280
Consensus	ggatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	CTGATGATGATGATGATGATGATGATGATGAT	2320
DPA	CTGATGATGATGATGATGATGATGATGATGAT	2320
Consensus	ctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	
Isaform001047	CTG	2380
DPA	CTG	2380
Consensus	ctg	

Isoform0010147	MKTQWKVLLGLLGA ^A ALVTIITVPAVLLSKDDVIVDDRRT	40
DPP4	MKTQWKVLLGLLGAV ^A ALVTIITVPAVLLSKDDVIVDDRRT	40
Consensus	mktqwkvlglgla alvtiitvpavllskdddivddrtr	
Isoform0010147	YTLADYLKSTIRMRNYNLRWISDHEYLYKQENNVLLFNAD	80
DPP4	YTLADYLKSTIRMRNYNLRWISDHEYLYKQENNVLLFNAD	80
Consensus	ytladylkstirmrnynlrwisdheylykqennvllfnad	
Isoform0010147	HGNSSTFLENSTFDQFGHSISDYSVSPDRQFVLFYNYVK	120
DPP4	HGNSSTFLENSTFDQFGHSISDYSVSPDRQFVLFYNYVK	120
Consensus	hgnsstflenstfdqfghsisdysvspdrqfvlfeynyvk	
Isoform0010147	KWRHSYTASYDIYDLNKRQLITEERIPNDTQLIRWSPEGH	160
DPP4	KWRHSYTASYDIYDLNKRQLITEERIPNDTQLIRWSPEGH	160
Consensus	kwrhsytasydiydlnkrqliteeripndtqlirwspeg	
Isoform0010147	KLAYVWNNDIYVKNDPYSPSRVTRDGREDAISNGITDWV	200
DPP4	KLAYVWNNDIYVKNDPYSPSRVTRDGREDAISNGITDWV	200
Consensus	klayvwnndiyvknpyspsrvtredgremaisngitdwv	
Isoform0010147	YEEEIFSTHSALWWSPNGTFLAYAQFNDTDVPRIEYSVYL	240
DPP4	YEEEIFSTHSALWWSPNGTFLAYAQFNDTDVPRIEYSVYL	240
Consensus	yeeiefsthsalwvspngtflayaqfndtdvprieysvyl	
Isoform0010147	DESLQYPKTIHIPYPKAGAKNPTVKLYVVNTDNLTDLEPV	280
DPP4	DESLQYPKTIHIPYPKAGAKNPTVKLYVVNTDNLTDLEPV	280
Consensus	deslqypktihipypkagaknptvklyvvntdnltdlepv	
Isoform0010147	QIVAPASVLIGDHLYLCDVTWATKERISLQWLRRIQNYSII	320
DPP4	QIVAPASVLIGDHLYLCDVTWATKERISLQWLRRIQNYSII	320
Consensus	qivapasvligdhylcdvtwatkerislqwlrriqnysii	
Isoform0010147	DICDYNESTPKWNCLVSRQHIETSATGWVGRFKPAEPHFT	360
DPP4	DICDYNESTPKWNCLVSRQHIETSATGWVGRFKPAEPHFT	360
Consensus	dicdynestpkwnclvsrqhietsatgwvgrfkpaephft	
Isoform0010147	SDGNSFYKIMSNTEGYKHICLFQIDKPNCTFITKGAWEVI	400
DPP4	SDGNSFYKIMSNTEGYKHICLFQIDKPNCTFITKGAWEVI	400
Consensus	sdgnsfykimsntegykhiclfqidkpnctfitkgawe	
Isoform0010147	GIEALTNDYLYYISNEYKGMPPGRNLYKIQRNNYANVTCL	440
DPP4	GIEALTNDYLYYISNEYKGMPPGRNLYKIQRNNYANVTCL	440
Consensus	giealtndylyyisneykgmpgrnlykiqrnnyanvtcl	
Isoform0010147	SCELDPERCQYYSASFSGAKYYQLRCSGPQIPRYSLHSS	480
DPP4	SCELDPERCQYYSASFSGAKYYQLRCSGPQIPRYSLHSS	480
Consensus	sceldpercqyysasfsgakyyqlrcsgqpipryslhss	
Isoform0010147	SNDKELRLLENNTALYETLQNIQMPRKTLDFIHLNGTKFW	520
DPP4	SNDKELRLLENNTALYETLQNIQMPRKTLDFIHLNGTKFW	520
Consensus	sndkelrllenntalyetlqniqmprktldfihlngtkfw	
Isoform0010147	YQMILPPHFDKSKKYPLLIDVYAGPCSQKADATFKLSWAT	560
DPP4	YQMILPPHFDKSKKYPLLIDVYAGPCSQKADATFKLSWAT	560
Consensus	yqmilpphfdkskkypllidyagpcsqkadatfklswat	
Isoform0010147	YLASTENIIIVASFDRGSGYQGD ^K IMHAINRRLGTFEVED	600
DPP4	YLASTENIIIVASFDRGSGYQGD ^K IMHAINRRLGTFEVED	600
Consensus	ylasteniivasfdrgsgyqgd ^k imhainrrlgtfeved	
Isoform0010147	QIEAAKQFSKMGFVDDKRIAIWGSYGGYVTSMLVLAGSR	640
DPP4	QIEAAKQFSKMGFVDDKRIAIWGSYGGYVTSMLVLAGSR	640
Consensus	qieaakqfsmgfvddkriaiwgsygyvtsmvlagagr	
Isoform0010147	VFKCGIAPVSAWEFYDSVYTERYMGLPTPEDNLDHYKN	680
DPP4	VFKCGIAPVSAWEFYDSVYTERYMGLPTPEDNLDHYKN	680
Consensus	vfkcgiaapvsawefydsvyterymglptpednldhykn	
Isoform0010147	STVMSRAENFKLVEYLLIHGTADDNVHFQQSAQITRALVD	720
DPP4	STVMSRAENFKLVEYLLIHGTADDNVHFQQSAQITRALVD	720
Consensus	stvmsraenfkiveyllihgtaddnvhfqqsaqitralvd	
Isoform0010147	AGVDFQAMWYTDEDHGIATSTAHQHIYTHMTHFIKQCFSL	760
DPP4	AGVDFQAMWYTDEDHGIATSTAHQHIYTHMTHFIKQCFSL	760
Consensus	agvdfqamwytdedhgiatstahqhiythmthfikqcfsl	

Figure S5. Several published genes were compared with full-length transcripts, the comparative result of the *DPP4* gene.

Isoform0020210	SCAACTTCCACC	ATG	CCACCTCAGCGAGTCCCACTTGA	40
Glul	ATG	CCACCTCAGCGAGTCCCACTTGA	28
Consensus		atg	ccacctcagcgagttcccacttga	
Isoform0020210	ACAAAGGCATCAAGCAGATGTACATCTGCCCTGCTCAGGG			80
Glul	ACAAAGGCATCAAGCAGATGTACATCTGCCCTGCTCAGGG			68
Consensus			acaaaggcatcaagcagatgtacatgtccctgctcaggg	
Isoform0020210	TGATAAAGTCCAAGCTATGTACATCTGGATTGACGGTACT			120
Glul	TGATAAAGTCCAAGCTATGTACATCTGGATTGACGGTACT			108
Consensus			tgataaagtccaagctatgtacatctggattgacggctact	
Isoform0020210	GGAGAAAGGATCGCATGCAAGACCCGGACCTGGACAGTG			160
Glul	GGAGAAAGGATCGCATGCAAGACCCGGACCTGGACAGTG			148
Consensus			ggagaaggactcgatgcaagacccggacctggacagtg	
Isoform0020210	AGCCCAAGAGTATAGAAAGTTGCCCGAGTGGAAATTTTGA			200
Glul	AGCCCAAGAGTATAGAAAGTTGCCCGAGTGGAAATTTTGA			188
Consensus			agcccaagagtatagaagagttgcccgagtggaaattttga	
Isoform0020210	TGGCTCTAGTACTATGCAGTCTGAAGGCTCCACAGTGAC			240
Glul	TGGCTCTAGTACTATGCAGTCTGAAGGCTCCACAGTGAC			228
Consensus			tggctctagtactatgcagtctgaaggctccaacagtac	
Isoform0020210	ATGTATCTTGTCTCTGCTACCATGTTTCGGGACCTTTCC			280
Glul	ATGTATCTTGTCTCTGCTACCATGTTTCGGGACCTTTCC			268
Consensus			atgtatcttgtctctgctaccatgtttcgggacctttcc	
Isoform0020210	GCAAGGACCCCAACAGCTGGTGTCTGTGAAGTCTTAAA			320
Glul	GCAAGGACCCCAACAGCTGGTGTCTGTGAAGTCTTAAA			308
Consensus			gcaaggaccccaacagctgggtgtctgtgaagtctttaa	
Isoform0020210	ATACAAACCGCAACCTGCAGAGACCAATTAAAGATATAAC			360
Glul	ATACAAACCGCAACCTGCAGAGACCAATTAAAGATATAAC			348
Consensus			atacaaccgcaaacctgcagagaccaatttaagataatacc	
Isoform0020210	TGCAAAACGGATAATGGACATGGTGAGCAATCAGCATCCCT			400
Glul	TGCAAAACGGATAATGGACATGGTGAGCAATCAGCATCCCT			388
Consensus			tgcaaacggataatggacatgggtgagcaatcagcatccct	
Isoform0020210	GGTTTGGAAATGGAGCAGGAATATACCTCTCATGGGACAGAG			440
Glul	GGTTTGGAAATGGAGCAGGAATATACCTCTCATGGGACAGAG			428
Consensus			ggtttgaatggagcaggaataatactctcatgggacagag	
Isoform0020210	TGGGCAACCTTTTGGCTGGCTTCCAAATGGCTTCCCTGGG			480
Glul	TGGGCAACCTTTTGGCTGGCTTCCAAATGGCTTCCCTGGG			468
Consensus			tgggcacccttttggctggccttccaatggcttccctggg	
Isoform0020210	CCCCAAGGTCATCTACTGCGGTGTGGGAGCAGACAGAG			520
Glul	CCCCAAGGTCATCTACTGCGGTGTGGGAGCAGACAGAG			508
Consensus			ccccaaaggctccatactactgcggtgtgggagcagacagag	
Isoform0020210	CCTACGGCAGGGATATTGTGGAGGCTCACTACCGGGCTG			560
Glul	CCTACGGCAGGGATATTGTGGAGGCTCACTACCGGGCTG			548
Consensus			cctacggcagggatattgtggaggctcactacggggcctg	
Isoform0020210	CTTGTAAGCTGCGCATCAAGATCGCAGGGCAAAATGCCGAG			600
Glul	CTTGTAAGCTGCGCATCAAGATCGCAGGGCAAAATGCCGAG			588
Consensus			cttgtaagctgcgcatcaagatcgagggacaaatgccgag	
Isoform0020210	GTCAATGCCCGCCAGTGGGAATTCCAAATAGGACCTGTG			640
Glul	GTCAATGCCCGCCAGTGGGAATTCCAAATAGGACCTGTG			628
Consensus			gtcatgcccgccagtggaatttccaaataggacctgtg	
Isoform0020210	AAGGCATCGACATGGGAGATCATCTCGGTGGCCCGTTT			680
Glul	AAGGCATCGACATGGGAGATCATCTCGGTGGCCCGTTT			668
Consensus			aaggcatcgacatgggagatcatctcgggtggcccgttt	
Isoform0020210	CATCTTGACCGAGTGTGTGAAGACTTCGAGTGTATCGCT			720
Glul	CATCTTGACCGAGTGTGTGAAGACTTCGAGTGTATCGCT			708
Consensus			catcttgaccgagtggtgaagacttcggagtgtatcgct	
Isoform0020210	ACCTTTGATCCCAAGCCCATCCCTGGCAACTGGAATGGTG			760
Glul	ACCTTTGATCCCAAGCCCATCCCTGGCAACTGGAATGGTG			748
Consensus			acctttgatcccaagcccatccctggcaactggaatggtg	
Isoform0020210	CAGGCTGCCACACCAACTTCAGCACCAAGCCATGCGAGA			800
Glul	CAGGCTGCCACACCAACTTCAGCACCAAGCCATGCGAGA			788
Consensus			caggctgccacaccaacttcagcaccaaggccatgcgaga	
Isoform0020210	GGAGAAACGCTCTGAAGTACATCGAGGAGTCCATTGAGAGG			840
Glul	GGAGAAACGCTCTGAAGTACATCGAGGAGTCCATTGAGAGG			828
Consensus			ggagaacggtctgaagtacatcgaggagtccattgagagg	
Isoform0020210	CTGAGCAAGCGGCACCAAGTACCAATCCGAGCCTACGACC			880
Glul	CTGAGCAAGCGGCACCAAGTACCAATCCGAGCCTACGACC			868
Consensus			ctgagcaagcggcaccagtaaccatccgagcctacgacc	
Isoform0020210	CCAAAGGGGGCCGGGACAAATGCCCGGCGCTCACCGGATT			920
Glul	CCAAAGGGGGCCGGGACAAATGCCCGGCGCTCACCGGATT			908
Consensus			ccaaagggggccgggacaatgcccgcgctcacoggatt	
Isoform0020210	TAACGAAACCTCCAACATCAACGACTTCTCGCGCGCGTG			960
Glul	TAACGAAACCTCCAACATCAACGACTTCTCGCGCGCGTG			948
Consensus			taacgaaacctccaacatcaacgacttctcgcgcgcggtg	
Isoform0020210	GCCAACCGTAGCGCCAGCATCCGATTCCCCGGTCTGTGG			1000
Glul	GCCAACCGTAGCGCCAGCATCCGATTCCCCGGTCTGTGG			988
Consensus			gccaacctgtagcggccagcatccgattccccggctgtgg	
Isoform0020210	GCCAGGAGAAAGAGGGGTACTTTGAAGACCGGCGCCCTC			1040
Glul	GCCAGGAGAAAGAGGGGTACTTTGAAGACCGGCGCCCTC			1028
Consensus			gccaggagaagaaggggtactttgaagacccggcgccctc	
Isoform0020210	TGCCAACTGCGACCCCTTCGCAGTGACAGAAGCCCTCATC			1080
Glul	TGCCAACTGCGACCCCTTCGCAGTGACAGAAGCCCTCATC			1068
Consensus			tgccaaactgcgaccccttcgcagtgacagaagccctcatc	
Isoform0020210	CGCACGTGTCTTCTCAATGAAACTGGCGATGAGCCCTTCC			1120
Glul	CGCACGTGTCTTCTCAATGAAACTGGCGATGAGCCCTTCC			1108
Consensus			cgcacgtgtcttctcaatgaaactggcgatgagcccttcc	
Isoform0020210	AGTACAAAAAC			1131
Glul	AGTACAAAAAC			1121
Consensus			agtacaaaaac	

Isoform0020210	ATSTMTSASSHLNKGIKQMYMSLPQGDQVQAMYIWIDGT	40
GlulMATSSASSHLNKGIKQMYMSLPQGDQVQAMYIWIDGT	36
Consensus	m tsasshlnkgikqmymslpqgdqkvqamyiwidgt	
Isoform0020210	GEGLRCKTRTLDSEPKSIEELPEWNFDGSSTMQSEGSNSD	80
Glul	GEGLRCKTRTLDSEPKSIEELPEWNFDGSSTMQSEGSNSD	76
Consensus	geglrcktrtldsepk sieelpewnfdgsstmqsegsnsd	
Isoform0020210	MYLVPATMFRDPFRKDPNKLVFCEVLKYNRKPAETNLRYT	120
Glul	MYLVPATMFRDPFRKDPNKLVFCEVLKYNRKPAETNLRYT	116
Consensus	mylvpatmfrdpfrkdpnklvfcevlkynrkpaetnlryt	
Isoform0020210	CKRIMDMVSNQHPWFGMEQEYTLMGTDGHPFGWPSNGFPG	160
Glul	CKRIMDMVSNQHPWFGMEQEYTLMGTDGHPFGWPSNGFPG	156
Consensus	ckrimdmvsnqhpwfgmeqeytlmgtdghpfgwpsngfpg	
Isoform0020210	PQGPYYCGVGADRAYGRDIVEAHYRACLYAGIKIAGTNAE	200
Glul	PQGPYYCGVGADRAYGRDIVEAHYRACLYAGIKIAGTNAE	196
Consensus	pqgpYYcgvgadraygrdiveahyraclyagikiagt nae	
Isoform0020210	VMPAQWEFQIGPCEGIDMGDHLWVARFILHRVCEDFGVIA	240
Glul	VMPAQWEFQIGPCEGIDMGDHLWVARFILHRVCEDFGVIA	236
Consensus	vmpaqwefqigpcegidmgdhlwvarfilhrvcedfgvia	
Isoform0020210	TFDPKPIPGNWNAGAGCHTNFSTKAMREENGLKYIEESIER	280
Glul	TFDPKPIPGNWNAGAGCHTNFSTKAMREENGLKYIEESIER	276
Consensus	tfdpkpipgnwnagagchtnfstkamreen glkyieesier	
Isoform0020210	LSKRHQYHIRAYDPKGGRDNARRLTGFNETSNINDFSAGV	320
Glul	LSKRHQYHIRAYDPKGGRDNARRLTGFNETSNINDFSAGV	316
Consensus	lskrhqyhiraydpkggrdnarrltgfnetsnindfsagv	
Isoform0020210	ANRSASIRIPRSVGQEKKGYFEDRRPSANCDPFAVTEALI	360
Glul	ANRSASIRIPRSVGQEKKGYFEDRRPSANCDPFAVTEALI	356
Consensus	anrsasiriprsvgqe kkyfedrrpsan cdpfavteali	
Isoform0020210	RTCLLNETGDEPFQYK	376
Glul	RTCLLNETGDEPFQYK	372
Consensus	rtcllnetgdepfqyk	

Figure S6. Several published genes were compared with full-length transcripts, the comparative result of the *Glul* gene.

Isoform0025243	ATGTATTTTCATTAATCTACTAACAAATAATCGTTCCCATCC	40
ND1	ATGTATTTTCATTAATCTACTAACAAATAATCGTTCCCATCC	40
Consensus	atgtattttcattaatctactaacaataatcgttcccatcc	
Isoform0025243	TACTAGCCGTAGCATTTTAAACCTGCTAGAACGAAAAGT	80
ND1	TACTAGCCGTAGCATTTTAAACCTGCTAGAACGAAAAGT	80
Consensus	tactagccgtagcatttttaaccctgctagaaacgaaaagt	
Isoform0025243	ACTAGGTTATATACAACCTTCGAAAAGGACCAACATTGTT	120
ND1	ACTAGGTTATATACAACCTTCGAAAAGGACCAACATTGTT	120
Consensus	actaggttatatacaacttcgaaaaggaccaaacattggtt	
Isoform0025243	GGTCCTTACGGTTTACTGCAGCCAATCGCTGACGCAGTCA	160
ND1	GGTCCTTACGGTTTACTGCAGCCAATCGCTGACGCAGTCA	160
Consensus	ggtccttacggtttactgcagccaatcgctgacgcagtca	
Isoform0025243	AATTATTTACTAAAGAACCTATACAACCACTAACATCATC	200
ND1	AATTATTTACTAAAGAACCTATACAACCACTAACATCATC	200
Consensus	aattattttactaaagaacctatacaaccactaacatcatc	
Isoform0025243	TCTTACCTTATTCTATTGCTCCTACTTTAGCCCTGACT	240
ND1	TCTTACCTTATTCTATTGCTCCTACTTTAGCCCTGACT	240
Consensus	tcttaccttattctatttgctcctactttagccctgact	
Isoform0025243	TTAGCCCTAATAATATGAATCCATTACCCATACCACATC	280
ND1	TTAGCCCTAATAATATGAATCCATTACCCATACCACATC	280
Consensus	ttagccctaataatataatgaatccattaccataaccacatc	
Isoform0025243	CCCTAATTAAACATAAACCTAAGCATACTATTATACCTAGC	320
ND1	CCCTAATTAAACATAAACCTAAGCATACTATTATACCTAGC	320
Consensus	ccctaattaacataaacctaagcatactattatactagc	
Isoform0025243	TCTATCAAGTCTGGCGTCTACGCTATTCTATGATCAGGC	360
ND1	TCTATCAAGTCTGGCGTCTACGCTATTCTATGATCAGGC	360
Consensus	tctatcaagtctggcgtctacgctattctatgatcaggc	
Isoform0025243	TGAGCTTCAAATTCAAATAACGCATTAAATTGGAGCCTTAC	400
ND1	TGAGCTTCAAATTCAAATAACGCATTAAATTGGAGCCTTAC	400
Consensus	tgagcttcaaattcaaaatacgcattaattggagccttac	
Isoform0025243	GAGCAGTAGCCCAACAACTCTCTATGAAGTAACCCCTAGC	440
ND1	GAGCAGTAGCCCAACAACTCTCTATGAAGTAACCCCTAGC	440
Consensus	gagcagtagcccaacaactctctatgaagtaaccctagc	
Isoform0025243	CATTATTATTCTATCCATCCTGCTTATAAATGGCTCATTC	480
ND1	CATTATTATTCTATCCATCCTGCTTATAAATGGCTCATTC	480
Consensus	cattattattctatccatcctgcttataaatggctcattc	
Isoform0025243	ACATTAACCACTACTAATTACACACAGAATATATCTGAT	520
ND1	ACATTAACCACTACTAATTACACACAGAATATATCTGAT	520
Consensus	acattaacca actaattacaacacagaatatatctgat	
Isoform0025243	TAATTATTCCCTCATGACCTCTGGCTATAATATGATTAT	560
ND1	TAATTATTCCCTCATGACCTCTGGCTATAATATGATTAT	560
Consensus	taattat ccctcatgacctctggc ataatatgattttat	
Isoform0025243	CTCAACTTTAGCAGAACTAACCGAGCCCTTTGACTTA	600
ND1	CTCAACTTTAGCAGAACTAACCGAGCCCTTTGACTTA	600
Consensus	ctcaactttagcagaaactaaccgagccctttgactta	
Isoform0025243	ACTGAGGGAGAAATCAGAATTAGTATCTGGTTTCAACGTAG	640
ND1	ACTGAGGGAGAAATCAGAATTAGTATCTGGTTTCAACGTAG	640
Consensus	actgagggagaatcagaattagtatctggtttcaacgtag	
Isoform0025243	AATATGCAGGAGGACCCCTCGCTCTCTTCTTTCTAGCAGA	680
ND1	AATATGCAGGAGGACCCCTCGCTCTCTTCTTTCTAGCAGA	680
Consensus	aatatgcaggaggacccttcgctctcttctttctagcaga	
Isoform0025243	ATATGCTAATATTATCATAATAAATGCCCTCACAAATTATC	720
ND1	ATATGCTAATATTATCATAATAAATGCCCTCACAAATTATC	720
Consensus	atatgctaataattatcataataaatgccctcacaaattatc	
Isoform0025243	CTATTCTTAGGCGCATATAATAATCCTATATTCTCAGAAC	760
ND1	CTATTCTTAGGCGCATATAATAATCCTATATTCTCAGAAC	760
Consensus	ctattcttaggcgcataataaatcctatattctcagaac	
Isoform0025243	TTTACACCACCAACTTCACCACTAAAACCTCTTTATTCAC	800
ND1	TTTACACCACCAACTTCACCACTAAAACCTCTTTATTCAC	800
Consensus	tttacaccaccaacttcaccactaaaactctcttatttcac	
Isoform0025243	AATAATATTTTATGAATTCGAGCATCTTACCCTCGATTTC	840
ND1	AATAATATTTTATGAATTCGAGCATCTTACCCTCGATTTC	840
Consensus	aataatattttatgaattcgagcatcttaccctcgatttc	
Isoform0025243	CGATATGACCAACTAATACACCTACTATGAAAAAATTTTC	880
ND1	CGATATGACCAACTAATACACCTACTATGAAAAAATTTTC	880
Consensus	cgatatgaccaactaatacacctactatgaaaaaactttc	
Isoform0025243	TACCCCTTACTTTAGTAATATGTATATGACATGTAACCTT	920
ND1	TACCCCTTACTTTAGTAATATGTATATGACATGTAACCTT	920
Consensus	tacccttactttagtaatatgtatatgacatgtaac tt	
Isoform0025243	ACCAATTATTCTAGCAAGTATCCCAACCCATAACA...	954
ND1	ACCAATTATTCTAGCAAGTATCCCAACCCATAACA...	956
Consensus	accaattattctagcaagtatcccacccataaca	

Isoform0025243	MYFINLLTIIVPILLAVAFLTLLERKVLGYIQLRKGPNIIV	40
ND1	MYFINLLTIIVPILLAVAFLTLLERKVLGYIQLRKGPNIIV	40
Consensus	myfinllttiivpillavaflltllerkvlgylrkgpniv	
Isoform0025243	GPYGLLQPIADAVKLF ^T KEPIQPLTSSSLTLFIIAPTLALT	80
ND1	GPYGLLQPIADAVKLF ^T KEPIQPLTSSSLTLFIIAPTLALT	80
Consensus	gpygllqpiadavklftkepiqpltsssltlfiiaptlalt	
Isoform0025243	LALIIIPLPIPHPLININLSILFILALSSLAVYAILSGAS	120
ND1	LALIIIPLPIPHPLININLSILFILALSSLAVYAILSGAS	120
Consensus	laliipiplpiphplininlsilfilalsslavyails gas	
Isoform0025243	NSKYALIGALRAVAQTISYEVTLAI ^I IILSILLINGSFTLT	160
ND1	NSKYALIGALRAVAQTISYEVTLAI ^I IILSILLINGSFTLT	160
Consensus	nskyaligalravaqtisyevtlaiiilsillingsftlt	
Isoform0025243	^T LITTQEYILIIPSPLAIIFISTLAETNRAPFDL ^T EGESE	200
ND1	TLITTQEYILIIPSPLAIIFISTLAETNRAPFDL ^T EGESE	200
Consensus	littqeyiliipsplaiifistlaetnrapfdltegese	
Isoform0025243	LVSGFNVEYAGGPFALFFLAEYANII ^I IINALTIILFLGAY	240
ND1	LVSGFNVEYAGGPFALFFLAEYANII ^I IINALTIILFLGAY	240
Consensus	lvsgfnveyaggpfalfflaeyaniiiinaltiilflgay	
Isoform0025243	NNPIFSELYTTNFTTKTLLFTIIIFLIRASYPRFRYDQLIH	280
ND1	NNPIFSELYTTNFTTKTLLFTIIIFLIRASYPRFRYDQLIH	280
Consensus	nnpifselyttnfttktl lftiiflirasyprfrydqlih	
Isoform0025243	LLKNFLPLTLVICIHVTLPIILASIPPI	308
ND1	LLKNFLPLTLVICIHVTLPIILASIPPI	308
Consensus	llknflpltlvicihv tlp iilasippi	

Figure S7. Several published genes were compared with full-length transcripts, the comparative result of the *ND1* gene.

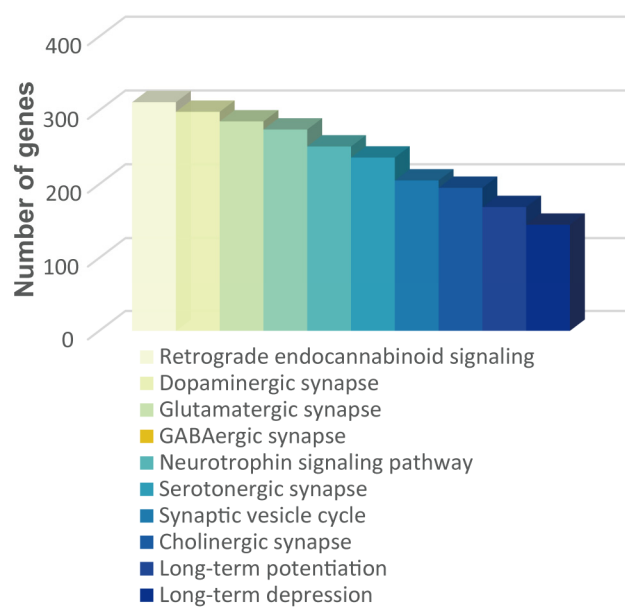


Figure S8. The proportion of full-length transcripts annotated in the metabolic pathways of the neural-related system.

Isoform0022807	ATGGATTGGGGTACCCTGCACACTTTTCATCGGGGGTGTGA	40
GJB6	ATGGATTGGGGTACCCTGCACACTTTTCATCGGGGGTGTGA	40
Consensus	atggattggggtaccctgcacactttcatcgggggtgtga	
Isoform0022807	ACAAACACTCCACCAGCATCGGGAAGGTGTGGATCACCGT	80
GJB6	ACAAACACTCCACCAGCATCGGGAAGGTGTGGATCACCGT	80
Consensus	acaaactccaccagcatcgggaaggtgtggatcacctgt	
Isoform0022807	CATCTTCATCTTCCGTGTCATGATCCTCGTGGTGGCCGCT	120
GJB6	CATCTTCATCTTCCGTGTCATGATCCTCGTGGTGGCCGCT	120
Consensus	catcttcattctccgtgtcatgatcctcgtgggtggccgct	
Isoform0022807	CAGGAAGTGTGGGGAGATGAACAGGAAGACTTTGTGTGCA	160
GJB6	CAGGAAGTGTGGGGAGATGAACAGGAAGACTTTGTGTGCA	160
Consensus	caggaaagtgtggggagatgaacaggaagactttgtgtgca	
Isoform0022807	ACACTCTGCAGCCAGGATGCAGAAACGTGTGCTATGACCA	200
GJB6	ACACTCTGCAGCCAGGATGCAGAAACGTGTGCTATGACCA	200
Consensus	acactctgcagccaggatgcagaaactgtgctatgacca	
Isoform0022807	CTTCTTCCCCGTGTCCACATCCGGCTGTGGGCCCTGCAG	240
GJB6	CTTCTTCCCCGTGTCCACATCCGGCTGTGGGCCCTGCAG	240
Consensus	cttcttccccgtgtccacatccggctgtgggccctgcag	
Isoform0022807	CTCATCTTCTGCTCTCCACCCCTGCCCTGCTTGTGGCCATGC	280
GJB6	CTCATCTTCTGCTCTCCACCCCTGCCCTGCTTGTGGCCATGC	280
Consensus	ctcatcttctgctctccaccctgccctgcttgtggccatgc	
Isoform0022807	ACGTTGCCTACTACCGGCAGGAGGCCGCCGCAAATTCAG	320
GJB6	ACGTTGCCTACTACCGGCAGGAGGCCGCCGCAAATTCAG	320
Consensus	acgttgcctactaccggcaggaggccgccgcaaattcag	
Isoform0022807	ACGAGGAGAGAAGAGAAATGAATTCAAAGACTTGAAGAC	360
GJB6	ACGAGGAGAGAAGAGAAATGAATTCAAAGACTTGAAGAC	360
Consensus	acgaggagagaagagaaatgaattcaaagacttgaagac	
Isoform0022807	ATTAAAAAGCAGAAGGTTTCGGATCGAGGGAGCCCTGTGGT	400
GJB6	ATTAAAAAGCAGAAGGTTTCGGATCGAGGGAGCCCTGTGGT	400
Consensus	attaaaaagcagaaggtttcggatcgaggagccctgtggt	
Isoform0022807	GGACGTACACCAGCAGCATATTTTCCGAATCATCTTCGA	440
GJB6	GGACGTACACCAGCAGCATATTTTCCGAATCATCTTCGA	440
Consensus	ggacgtacaccagcagcatattttccgaatcatcttcga	
Isoform0022807	AGCCTCCTTCATGTATGTGTTTTACTTCCTATACAATGGG	480
GJB6	AGCCTCCTTCATGTATGTGTTTTACTTCCTATACAATGGG	480
Consensus	agcctccttcattgtatgtgttttacttccataacaatggg	
Isoform0022807	TACCACCTGCCCTGGGTGCTGAAATGTGGGGTTGATCCTT	520
GJB6	TACCACCTGCCCTGGGTGCTGAAATGTGGGGTTGATCCTT	520
Consensus	taccacctgccctgggtgctgaaatgtggggttgatcctt	
Isoform0022807	GCCCCAATCTTGTGACTGCTTCATCTCCAGACCTACGGA	560
GJB6	GCCCCAATCTTGTGACTGCTTCATCTCCAGACCTACGGA	560
Consensus	gccccaatcttgttgactgcttcattctccagacctacgga	
Isoform0022807	GAAAACCGTGTTACCATTTTTATGATCTCTGCCTCGGTG	600
GJB6	GAAAACCGTGTTACCATTTTTATGATCTCTGCCTCGGTG	600
Consensus	gaaaaccgtgttcaccatttttatgatctctgcctcgggtg	
Isoform0022807	ATTTGCATGCTACTCAATGTGGCCGAGTTGTGCTACCTGC	640
GJB6	ATTTGCATGCTACTCAATGTGGCCGAGTTGTGCTACCTGC	640
Consensus	atttgcattgctactcaatgtggccgagttgtgctacctgc	
Isoform0022807	TGCTGAAAGTGTGTTTCAGGAAATCAAAAAGAGCCAGAC	680
GJB6	TGCTGAAAGTGTGTTTCAGGAAATCAAAAAGAGCCAGAC	680
Consensus	tgctgaaagtgtgtttcaggaaatcaaaaa agccagac	
Isoform0022807	ACAAAGAAACCACCCAGTCATGCCCTAAAGGAGAGTAAG	720
GJB6	ACAAAGAAACCACCCAGTCATGCCCTAAAGGAGAGTAAG	720
Consensus	acaaagaaaccacccagtcattgccctaaaggagagtaag	
Isoform0022807	CAAAATGAAATGAATGAGCTGATTCAGATAGTGGTCAAA	760
GJB6	CAAAATGAAATGAATGAGCTGATTCAGATAGTGGTCAAA	760
Consensus	caaatgaaatgaatgagctgatttcagatagtgggtcaaa	
Isoform0022807	ATGCAACCACTGGTTTTCCAAGT..	783
GJB6	ATGCAACCACTGGTTTTCCAAGT..TA	785
Consensus	atgcaaccactggttttccaagt	

Isoform0022807	MDWGTLLHTFIGGVNKHSTSIGKVWITVIFIFRVMILVVAA	40
GJB6	MDWGTLLHTFIGGVNKHSTSIGKVWITVIFIFRVMILVVAA	40
Consensus	mdwgtllhtfiggvnkhstsigkvwitvififrvmilvvaa	
Isoform0022807	QEVWGDEQEDFVCNTLQPGCRNVCYDHFFPVSHIRLWALQ	80
GJB6	QEVWGDEQEDFVCNTLQPGCRNVCYDHFFPVSHIRLWALQ	80
Consensus	qevwgdeqedfvcntlqpgcrnvcydhffpvshirlwalq	
Isoform0022807	LIFVSTPALLVAMHVAYYRQEAARKFRRGEKRNEFKDLED	120
GJB6	LIFVSTPALLVAMHVAYYRQEAARKFRRGEKRNEFKDLED	120
Consensus	lifvstpallvamhvayyrqeaarkfrrgekrnefkdued	
Isoform0022807	IKKQKVRIEGALWWTYTSSIFFRIIFEASFMYVFYFLYNG	160
GJB6	IKKQKVRIEGALWWTYTSSIFFRIIFEASFMYVFYFLYNG	160
Consensus	ikkqkvriegalwwtytssiffriifeasfmyvfyflyng	
Isoform0022807	YHLPWVLKCGVDPCPNLVDCFISRPTTEKTVFTIFMISASV	200
GJB6	YHLPWVLKCGVDPCPNLVDCFISRPTTEKTVFTIFMISASV	200
Consensus	yhlpwvlkcgvdpcpnlvdcfistrpttektvftifmisasv	
Isoform0022807	ICMLLNVAELCYLLLKVCFRKSKRAQTQRNHPHALKESK	240
GJB6	ICMLLNVAELCYLLLKVCFRKSKRAQTQRNHPHALKESK	240
Consensus	icmllnvaelcylllkvcfrksk aqtqrnhpshalkesk	
Isoform0022807	QNEMNELISDSGQNATTGFP	260
GJB6	QNEMNELISDSGQNATTGFP	260
Consensus	qnemnelisdsgqnattgfp	

Figure S9. Several published genes were compared with full-length transcripts, the comparative result of the *GJB6* gene.

1

Isoform0013754	ITHCAGCTTAWSPCSFNSPDMETPLQFQRGFFSE	40
SK2	ITHCAGCTTAWSPCSFNSPDMETPLQFQRGFFSE...PR	36
Consensus	ithcagcttawspcsfnspdmetylqfqrgrffse pr	
Isoform0013754	SSHLHCQQQQQSQDKPCPPFASLPHAHHPHLAHQQPGSG	80
SK2	SSHLHCQQQQQSQDKPCPPFASLPHAHHPHLAHQQPGSG	75
Consensus	sshlhcqqqq sqdkpcppfaslphahhhphlahqqpgsg	
Isoform0013754	GSSPCLRCNSCASSGAPGAGAGDNLSELLRTSSPGAF	120
SK2	GSSPCLRCNSCASSGAP...AGAGDNLSELLRTSSPGG.F	111
Consensus	gsspclrcnscassgap agagdnlslllrtsspgg f	
Isoform0013754	RTRTSSPLSGSSCCCCSRRGSQNLVSELTPSSHASALRQ	160
SK2	RTRTSSPLSGSSCCCCS.RRGSQLNVSELTPSSHASALRQ	150
Consensus	rtrtssplsgsscccc rrgsqlnvseltpsshasalrq	
Isoform0013754	QYAAQPPASASLYHQCHSLQPAASPTGSLGSLGSGPPLSHH	200
SK2	QYAAQ.PASASLYHQCHSLQPAASPTGSLGSLGSGPPLSHH	189
Consensus	qyaqq asaslyhqchslqpaasptgslgslgsgpplshh	
Isoform0013754	LAHHQHQSQARRESNPFTIAMSSCRYNGGVMRP	240
SK2	LAHHQHQSQARRESNPFTIAMSSCRYNGGVMRP	225
Consensus	h lahhqhqsqarresnpfteiamsscrynggvmrp	
Isoform0013754	LSNLSASRRNLHEMDSEAQLQPPASVGGGGCASSP	280
SK2	LSNLSASRRNLHEMDSEAQLQPPASVGGGGCASSP....	260
Consensus	lsnlsasrrnlhemdseaqlppasvgggg assp	
Isoform0013754	AAASSAPEIVVSKPEHNNSNNLALYGTGGCGSTGGGGS	320
SK2	.SASSAPEIVVSKPEHNNSNNLALYGTGGG.....GGG	293
Consensus	assapeivvskpehnnsnnlalytggg gg	
Isoform0013754	GSGHGSSSGTKSSKKKNQNIQYKLGHRRALFEKRRLSDY	360
SK2	GSGHGSSSGTKSSKKKNQNIQYKLGHRRALFEKRRLSDY	333
Consensus	gsghgsssgtksskkknqniqyklghrralfekrkrlsdy	
Isoform0013754	ALIFGMFGIVVMVETELSWGAYDKASLYSLALKCLISLS	400
SK2	ALIFGMFGIVVMVETELSWGAYDKASLYSLALKCLISLS	373
Consensus	alifgmfgivvmvietelswgaydkaslyslalkclisls	
Isoform0013754	TIILLGLIIVYHAREIQLFMVDNGADDWRIAMTYERIFFI	440
SK2	TIILLGLIIVYHAREIQLFMVDNGADDWRIAMTYERIFFI	413
Consensus	tiillgliivyhareiqlfmvdngaddwriamtyeriffi	
Isoform0013754	CLEILVCAIHPIPGNYTFTWTARLAFSYAPSTTTADVDII	480
SK2	CLEILVCAIHPIPGNYTFTWTARLAFSYAPSTTTADVDII	453
Consensus	cleilvcaihpipgnytftwtarlafsyapstttadvdii	
Isoform0013754	LSIPMFLRLYLIARVMLLHLSKLFDAASSRSIGALNKINFN	520
SK2	LSIPMFLRLYLIARVMLLHLSKLFDAASSRSIGALNKINFN	493
Consensus	lsipmflrlyliarvmlhlsklftdassrsigalnkinfn	
Isoform0013754	TRFVMKTLMTICPGTVLLVFSISLWIIAAWTVRACERYHD	560
SK2	TRFVMKTLMTICPGTVLLVFSISLWIIAAWTVRACERYHD	533
Consensus	trfvmktlmticpgtvllvfsislwiiawtvraceryhd	
Isoform0013754	QQDVTSNFLGAMWLISITFLSIGYGMVPNTYCGKGVCLL	600
SK2	QQDVTSNFLGAMWLISITFLSIGYGMVPNTYCGKGVCLL	573
Consensus	qqdvtsnflgamwlisitflsigygmvpntyckgkvcll	
Isoform0013754	TGIMGAGCTALVVAVVARKLELTKAEKHVHNFMMDTQLTK	640
SK2	TGIMGAGCTALVVAVVARKLELTKAEKHVHNFMMDTQLTK	613
Consensus	tgimgagctalvvavvarkleltkaekhvhnfmmdtqltk	
Isoform0013754	RVKNAAANVLRETWLIYKNTKLKIDHAKVRKHQRKFLQ	680
SK2	RVKNAAANVLRETWLIYKNTKLKIDHAKVRKHQRKFLQ	653
Consensus	rvknaaanvlretwliykntklkiddhakvrkhqrkflq	
Isoform0013754	AIHQLRSVKMEQRKLNQANTLVDLAKTQNIYDMISDLN	720
SK2	AIHQLRSVKMEQRKLNQANTLVDLAKTQNIYDMISDLN	693
Consensus	aihqlrsvkmeqrklndqantlvdaktqniymisdln	
Isoform0013754	ERSEDFEKRIVTLETKETLIGSIHALPGLISQTIROQQR	760
SK2	ERSEDFEKRIVTLETKETLIGSIHALPGLISQTIROQQR	733
Consensus	ersedfekrivtletketligsihalpglisqtirqqqr	
Isoform0013754	DFIEAQMENYDKHVAYNAERSR	782
SK2	DFIEAQMENYDKHVAYNAERSR	755
Consensus	dfieaqmenydkhvaynaersr	

Figure S10. Several published genes were compared with full-length transcripts, the comparative result of the *SK2* gene.

