

A	ZkorHBA_NCB1	ATGGTGGTGTCTCCGGCTCACAAGGCGAAGGTCAAGGCCCTGGCCAAAGCTCGGGGGCCAGGTGGGGAACCTTGGGGC	80
	ZkorHBA_Transcriptome	ATGGTGGTGTCTCCGGACACAAGGCTAAACATCAAGGCTCCCTGGCAAGATTGGGGCCATTGGTGGGGAACCTTGGGGC	80
	ZkorHBA_NCB1	CGAGCCCTAGACAGGATGTTCAACCACTTCCCCACCACCAAGACCTACTTCCCTCACTTCGATGTAAGCCACGGCTCCG	160
	ZkorHBA_Transcriptome	CGAGCCCTAGACAGGATGTTCAACCACTTCCCCACCACCAAGACCTACTTCCCTCACTTCGATGTAAGCCACGGCTCCG	160
	ZkorHBA_NCB1	CCAGGTCAAGGCCACGGCAAGAGGTGCGCATGCGCTGACCAACCCCGGAAGCCACCTCGATGACCTGCCAGTCCG	240
	ZkorHBA_Transcriptome	CCAGGTCAAGGCCACGGCAAGAGGTGCGCATGCGCTGACCAACCCCGGAAGCCACCTCGATGACCTGCCAGTCCG	240
	ZkorHBA_NCB1	CTGTCTCTCTGACCCACCTGCACCCCAACAAGCTGCGTGTGACCCCGTTAACTTCAAGTCTCTGACCCACTGCCTGCT	320
	ZkorHBA_Transcriptome	CTGTCTCTCTGACCCACCTGCACCCCAACAAGCTGCGTGTGACCCCGTTAACTTCAAGTCTCTGACCCACTGCCTGCT	320
	ZkorHBA_NCB1	GCTGACCTGCCAACCACACCCCAATGAATTCAGTCCCTCCCTGGACAAATTCTCGCCAAAGCTGA	400
	ZkorHBA_Transcriptome	GCTGACCTGCCAACCACACCCCAATGAATTCAGTCCCTCCCTGGACAAATTCTCGCCAAAGCTGA	400
ZkorHBA_NCB1	GCACCGTGGTACCTCCAAATACCGTTA	428	
ZkorHBA_Transcriptome	GCACCGTGGTACCTCCAAATACCGTTA	428	
ZkorHBA_NCB1	MVLSPADKAVKAAVCKVGGHCGELGAEALERMFTSFPPTTKTYFPHFDVSHGSAQVKAHGKKVADALITNAANHLLDLP	80	
ZkorHBA_Transcriptome	MVLSPADKAVKAAVCKVGGHCGELGAEALERMFTSFPPTTKTYFPHFDVSHGSAQVKAHGKKVADALITNAANHLLDLP	80	
ZkorHBA_NCB1	LISALSDLHAHKL RVDPVNFKLLISHCLLVTLANHPNEFTPAVHASL DKFLIASVSTVLTISKY	141	
ZkorHBA_Transcriptome	LISALSDLHAHKL RVDPVNFKLLISHCLLVTLANHPNEFTPAVHASL DKFLIASVSTVLTISKY	141	
B	ZkorHBB_NCB1	ATGGTGCACCTTTCCGCTGAGCAAAAGCTGCACTCATCTCCCTGTGGGCAAGGTGAATGTGATCAAGTCTGCTGCTGA	80
	ZkorHBB_Transcriptome	ATGGTGCACCTGACTGATGCTGCAAGGCTGCTGTCATCCCTGTGGGCAAGGTGAATGTGATCAAGTCTGCTGCTGA	80
	ZkorHBB_NCB1	GACCTTGGCAGGCTGCTGCTGTCTACCOATGACCCACAGGTTCTTTCACTCCTTTGGGACCTGTCTTCCCTTTG	160
	ZkorHBB_Transcriptome	AGCCCTTGGCAGGCTGCTGCTGTCTACCOATGACCCACAGGTTCTTTCACTCCTTTGGGACCTGTCTTCCCTTTG	160
	ZkorHBB_NCB1	CCATTATGGCCAAACCCAAAGTGAAGTCTCATGGCAAGGCTGCTGAACTCCTTCACTGATGCGCTGAAACATCTGCAG	240
	ZkorHBB_Transcriptome	CCATTATGGCCAAACCCAAAGTGAAGTCTCATGGCAAGGCTGCTGAACTCCTTCACTGATGCGCTGAAACATCTGCAG	240
	ZkorHBB_NCB1	AACTCAAGGGCACCTTTTCCATCTGAGTGACCTGCACTGTGACAACTGCACCTGCATCCCGACAACCTCAAGCTCCT	320
	ZkorHBB_Transcriptome	AACTCAAGGGCACCTTTTCCATCTGAGTGACCTGCACTGTGACAACTGCACCTGCATCCCGACAACCTCAAGCTCCT	320
	ZkorHBB_NCB1	GGCAATGTGATGCTGATTGTTCTGGCCACCACCTGGGCAAGGATTTACCCCGGGGCTCAGGCTGCTTCCAGAGG	400
	ZkorHBB_Transcriptome	GGCAATGTGATGCTGATTGTTCTGGCCACCACCTGGGCAAGGATTTACCCCGGGGCTCAGGCTGCTTCCAGAGG	400
ZkorHBB_NCB1	TGGTGGCTGCTGTGGCTACTGCCCTGCCTCACAAGTACCACTA	443	
ZkorHBB_Transcriptome	TGGTGGCTGCTGTGGCTACTGCCCTGCCTCACAAGTACCACTA	443	
ZkorHBB_NCB1	MVHLSCGEKAAVLSLVGKVNVDVCGEITLGRLLVVYPWTCRFFFSFGDLSFAHAIMGNPKVSAHGKVKVLSNFSFDGLKHLID	80	
ZkorHBB_Transcriptome	MVHLTDAEKAVNQLVGVKVNVDLGGELGRLLVVYPWTCRFFFSFGDLSASAIMGNPKVSAHGKVKVLSNFSFDGLKHLID	80	
ZkorHBB_NCB1	NLKGTFSHLISELHCDKLVDPENFKLLIGNVIVLVAHLLGKDFTPAACAAFGKVVAGVATALAHKY	146	
ZkorHBB_Transcriptome	NLKGTFSHLISELHCDKLVDPENFKLLIGNVIVLVAHLLGKDFTPAACAAFGKVVAGVATALAHKY	146	

C	PikaHBA_NCBI	ATCGTCTGTCTCCCGCTCACAAGGCCAACGTCAAGGCCCGCTGGCGCAAGGTGGGGGCGACGGCCGCGATATGGCG	80
	PikaHBA_Transcriptome	ATCGTCTGTCTCCCGCTCACAAGGCCAACGTCAAGGCCCGCTGGCGCAAGGTGGGGGCGACGGCCGCGATATGGCG	80
	PikaHBA_NCBI	CGAGCCCTGGACAGGATGTTCTGACCTTCCCACCACCAAGACCTACTTCCCACCTTCGACCTGACCCACGGCTCCG	160
	PikaHBA_Transcriptome	CGAGCCCTGGACAGGATGTTCTGACCTTCCCACCACCAAGACCTACTTCCCACCTTCGACCTGACCCACGGCTCCG	160
	PikaHBA_NCBI	CCACGTCAGGCGCCACGGCAAGAGCTGCCGATGCCCTACCCAGCTCGTGGACACTTGGACGACCTCCCGCGCGC	240
	PikaHBA_Transcriptome	CCACGTCAGGCGCCACGGCAAGAGCTGCCGATGCCCTACCCAGCTCGTGGACACTTGGACGACCTCCCGCGCGC	240
	PikaHBA_NCBI	CTGTCCCGCTCAGCGACTGCACGCCCAAAAGCTGGCGGTGCACCCTGTTAACTTCAAGCTCCTGCTCACTGCCTGCT	320
	PikaHBA_Transcriptome	CTGTCCCGCTCAGCGACTGCACGCCCAAAAGCTGGCGGTGCACCCTGTTAACTTCAAGCTCCTGCTCACTGCCTGCT	320
	PikaHBA_NCBI	GCTGACCTGCCCAACCACCAOCCCAATGAATTCACCTCCTGGCGTGCACGCTCCTGCACAAGTTCTGCCAACGCTGA	400
	PikaHBA_Transcriptome	GCTGACCTGCCCAACCACCAOCCCAATGAATTCACCTCCTGGCGTGCACGCTCCTGCACAAGTTCTGCCAACGCTGA	400
	PikaHBA_NCBI	GCACGCTGCTCACCTCCAAGTATCGTTA	428
	PikaHBA_Transcriptome	GCACGCTGCTCACCTCCAAGTATCGTTA	428
	PikaHBA_NCBI	IWLSPADKANVKAAVGKVGCHAGEYGAELERVFLSFPPTTKTYFPHFDVTHGSAGVKAHGKKVADALTQVVDHLDDLPGA	80
	PikaHBA_Transcriptome	IWLSPADKANVKAAVGKVGCHAGEYGAELERVFLSFPPTTKTYFPHFDVTHGSAGVKAHGKKVADALTQVVDHLDDLPGA	80
	PikaHBA_NCBI	LSALLSDLHACKLRVDPVNFKLLAHCLLVTLANHHIPNEFTPAVHASLIDKFLIANVSTVLTISKY	141
	PikaHBA_Transcriptome	LSALLSDLHACKLRVDPVNFKLLAHCLLVTLANHHIPNEFTPAVHASLIDKFLIANVSTVLTISKY	141
D	PikaHBB_NCBI	ATCGTGCACCTTTCCGTCAGCACAAGCTGCACCTCCTTCCCTGTGGGCAAGCTGAATGTGATGAAGTTGCTGCTGA	80
	PikaHBB_Transcriptome	ATCGTGCACCTTTCCGTCAGCACAAGCTGCACCTCCTTCCCTGTGGGCAAGCTGAATGTGATGAAGTTGCTGCTGA	80
	PikaHBB_NCBI	GACCTGGCCAGGCTCCTGTTGTCTTCCCATGCACCCAGACGTTCTTTGATTCCTTTGTCACCTGTCTCTCCCGATG	160
	PikaHBB_Transcriptome	GACCTGGCCAGGCTCCTGTTGTCTTCCCATGCACCCAGACGTTCTTTGATTCCTTTGTCACCTGTCTCTCCCGATG	160
	PikaHBB_NCBI	CTGTTATGGCAATTTCTAAGGTGAAGCCTCATGCACAAGAGTGAATGATGATGATGATGATGATGATGATGATGATGAT	240
	PikaHBB_Transcriptome	CTGTTATGGCAATTTCTAAGGTGAAGCCTCATGCACAAGAGTGAATGATGATGATGATGATGATGATGATGATGATGAT	240
	PikaHBB_NCBI	AGCCTCAAGGCCACCTTTGCCAAGCTCAGTGCCTGCATGTGACAAGCTGCATGTGACCCCGAGAATTTCAAGCTCCT	320
	PikaHBB_Transcriptome	AGCCTCAAGGCCACCTTTGCCAAGCTCAGTGCCTGCATGTGACAAGCTGCATGTGACCCCGAGAATTTCAAGCTCCT	320
	PikaHBB_NCBI	GGCAACGTCCTGTTGTTGTGCTGTCCACCACTTGGCGCTGAATCACTCCCGAGATGCAGGCTGCCTGCCAGAACGG	400
	PikaHBB_Transcriptome	GGCAACGTCCTGTTGTTGTGCTGTCCACCACTTGGCGCTGAATCACTCCCGAGATGCAGGCTGCCTGCCAGAACGG	400
	PikaHBB_NCBI	TGCTGTCTGCTGTGCCAATGCCCTGCTCACAAGTACCACTA	443
	PikaHBB_Transcriptome	TGCTGTCTGCTGTGCCAATGCCCTGCTCACAAGTACCACTA	443
	PikaHBB_NCBI	IWHLSGEEKSAVLSLWGVNVDVGGETLGRLLVFPVTCRFFDSFGDLSSPDAVMNSKVKAHGKKVMNAFSEGLHLLD	80
	PikaHBB_Transcriptome	IWHLSGEEKSAVLSLWGVNVDVGGETLGRLLVFPVTCRFFDSFGDLSSPDAVMNSKVKAHGKKVMNAFSEGLHLLD	80
	PikaHBB_NCBI	SLIKGTFAKLSSELHCDKLVDPENFKLLGNVLVWVLSHHFGAEFTPGMCAAVGKVVSGVANLAAHKY	146
	PikaHBB_Transcriptome	SLIKGTFAKLSSELHCDKLVDPENFKLLGNVLVWVLSHHFGAEFTPGMCAAVGKVVSGVANLAAHKY	146

附图 1. 高原麝鼠和高原鼠兔从测序结果中筛选的和从 NCBI 下载的 *Hb-α* 和 *Hb-β* 编码序列比对结果

Supplemental Fig. 1. The alignment results between the coding sequences of *Hb-α* and *Hb-β* screened from the results of Iso-Seq and downloaded from NCBI of plateau zokor and plateau pika. *A*: The alignment results of *Hb-α* and its deduced amino acids sequences of plateau zokor. *B*: The alignment results of *Hb-β* and its deduced amino acids sequences of plateau zokor. *C*: The alignment results of *Hb-α* and its deduced amino acids sequences of plateau pika. *D*: The alignment results of *Hb-β* and its deduced amino acids sequences of plateau pika.