

Figure S1. Nucleotide and predicted amino acid sequences of Tibetan porcine STING. The numbers on the left refer to positions of the nucleotides or amino acid residues. The stop codon is indicated by *.

1	ATGCCCTACTCCAGCCTGCATCCATCCATCCCACAGCCCAGGGGCTCAGGGCTCAGGAG
1	M P Y S S L H P S I P Q P R G L R A Q E
61	GCAGCCCTGGTCCTTCTAGGTGCCTGCCTGGTGGCCCTTTGGGGGCTGGGGGAGCTGCCA
21	A A L V L L G A C L V A L W G L G E L P
121	GAATACACGCTCCGGTGGCTGGTGTCCACCTGGCCTCCCAGCAGATAGGACTGCTGGTG
41	E Y T L R W L V L H L A S Q Q I G L L V
181	AAGGGGCTTGCAGTCTGGCGGAGGAGCTGTGCCACGTCCACTCCAGGTACCAGAGCAGC
61	K G L C S L A E E L C H V H S R Y Q S S
241	TACTGGAGGGCTGCGTGGGCTGCCTGGGCTGCCCCATCCGCTGTGGAGCCCTGCTGCTG
81	Y W R A A W A C L G C P I R C G A L L L
301	CTGTCTGCTACTTCTACTTCTCCATCCGAGACAAGGCTGGCCTGCCCTCCCTCCCTGGATG
101	L S C Y F Y F S I R D K A G L P L P W M
361	CTGGCCCTCCTGGGCTCTCGCAGGCCCTAAACATCCTCCTGGGCTCCAGCACCTGGCC
121	L A L L G L S Q A L N I L L G L Q H L A
421	CCAGCTGAAGTCTCTGCAATCTGTGAAAAAAGGAACCTCAACGTGGCTCATGGACTGGCC
141	P A E V S A I C E K R N F N V A H G L A
481	TGGTCTTATTACATCGGGTACCTGCGGCTGATCCTCCAGGGCTCCGGGCCCGGATCCAA
161	W S Y Y I G Y L R L I L P G L R A R I Q
541	GCTTATAATCAGCGCCACAAGAACGTACTCGGGGCATAGGGAACCAACGGCTGCACATC
181	A Y N Q R H K N V L G G I G N H R L H I
601	CTCTTTCCGTTGACTGTGGGGCGCCGACGACCTGAGCGTGGCTGACCCCAACATTCCG
201	L F P L D C G A P D D L S V A D P N I R
661	TTCCTGCACAAGCTGCCCCAGCAAAAGTCCGACCGTGTGGCATCAAGGGCCGGGTGTAC
221	F L H K L P Q Q S A D R A G I K G R V Y
721	ACCAACAGCATCTATGAGCTTCTGGAGAACGGGCAGCCGGCAGGCGTCTGTGTCTCTGGAG
241	T N S I Y E L L E N G Q P A G V C V L E
781	TACGCCACTCCCTTGCAGACCTTGTTGCGCATGTACAGGATGGCCGCGCTGGCTTCAGC
261	Y A T P L Q T L F A M S Q D G R A G F S
841	CGGGAGGATCGGCTCGAGCAGGCCAAACTCTTCTGCCGGACCCCTCGAAGACATCCTGGCA
281	R E D R L E Q A K L F C R T L E D I L A
901	GATGCCCCGTAGGGCTCAGAACAACTGCCGCCTCATCGTCTACCAGGAACCCACAGAGGGA
301	D A P E A Q N N C R L I V Y Q E P T E G
961	GGCAGCTTCTCCCTGTGCGCAGGAGATTCTCCGGCACCTTCGGCAGGAGGAAAGGGAGGTT
321	G S F S L S Q E I L R H L R Q E E R E V
1021	ACCATGGGCAGTGGGAGACCTCAGTGGTGGCCACTTCTCCACGCTGTCCCAAGAGCCT
341	T M G S A E T S V V P T S S T L S Q E P
1081	GAGCTCCTCATCAGTGGCATGGAAACAGCCTCTTCCACTCCGCTCAGATATCTTCTGA
361	E L L I S G M E Q P L P L R S D I F *