**Supplementary Figure**: Alignments of  $\beta$ -hexosaminidase  $\beta$ -subunit amino acids sequences from 54 mammalian species predicted from codons surrounding the deleted Leu137 codon in the affected Shiba Inu

Consensus	ARXRGIE	RVXPEF	рхронтх	S W G K G O X X		ХХХХХХСР	X N P X X N X T Y X F X X X X F X
Identity							
<ul> <li>I. Normal dog</li> <li>2. Affected dog</li> <li>3. African savanna elephant</li> <li>4. Alpaca</li> <li>5. American beaver</li> <li>6. American mink</li> <li>7. American pika</li> <li>8. Amur tiger</li> <li>9. Arabian camel</li> <li>10. Donkey</li> <li>11. Bactrian camel</li> <li>12. Big brown bat</li> <li>13. Bilack flying fox</li> <li>14. Black snub-nosed monkey</li> <li>15. Bolivian squirrel monkey</li> <li>16. Indian cattle</li> <li>17. Bottlenose dolphin</li> <li>18. Cape elephant shrew</li> <li>19. Cape golden mole</li> <li>20. European cattle</li> <li>21. Chetah</li> <li>22. Chimese tree shrew</li> <li>26. Crab-eading macaque</li> <li>27. Domestic guinea pig</li> <li>30. Drill</li> <li>31. Giant panda</li> <li>32. Goiden collared manakin</li> <li>34. Golden snub-nosed monkey</li> <li>35. Golden hamster</li> <li>36. Gray mouse lemur</li> <li>37. Gray short-tailed opossum</li> <li>38. Grean monkey</li> <li>39. House mouse</li> <li>40. Human</li> <li>41. Killer whale</li> <li>42. Large flying fox</li> <li>43. Leopard</li> <li>44. Lesser Egyptian jerboa</li> <li>45. Little forwn bat</li> <li>46. Ma's night monkey</li> <li>47. Malayan pangolin</li> <li>48. Norway rat</li> <li>49. Olive baboon</li> <li>50. Pacific walrus</li> <li>51. Pig</li> <li>20. Polar bear</li> <li>33. Rabbit</li> <li>54. Rhesus monkey</li> <li>55. Water buffalo</li> </ul>	I       I	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	、LQLQQQQLLLLUQQLUQQQLQQLLQAQLAQZLQZQQL + F + F + F + F + F + F + F + F + F + F	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	GAGOGONUEGGGGURRAGGGAURE - GRUGGRGAGRPGGRORORORGKGDR NSOUNCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	PPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	<pre>KKQKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK</pre>

Modified from a report generated with Geneious Basic version 10.1.2 commercial software.<sup>1</sup>

Kearse, M., Moir, R., Wilson, A., Stones-Havas, S., Cheung, M., Sturrock, S., Buxton, S., Cooper, A., Markowitz, S., Duran, C., Thierer, T., Ashton, B., Mentjies, P., & Drummond, A. (2012). Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics*, *28*(12), 1647-1649.