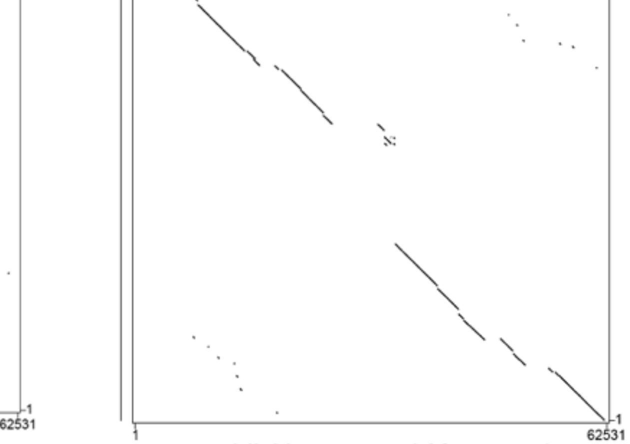

(d) Human and Marmoset

Methods

and *BHMT-2* genes from 37 species in and vertebrates), were obtained an sequences as queries.

ipmaker.bx.psu.edu/cgi-bin/ o identify the genic and intergenic and *BHMT-2* genes within and erate dot plots

m (http://www.geneious.com/) as used to align sequences and

ring the evolution of *BHMT* and d by single likelihood ancestor ffects likelihood (REL), fixed

amphibians, reptiles and birds exa that the *BHMT* gene had been dupl of mammals from other living verte divergence of extant mammalian su

- The evolutionary rate of change for *BHMT-2* relative to the rate for especially between the time that a in the appearance of *BHMT-2* in th the time of the appearance of crow mammals.
- Based on the ratio of non-synony mutation rates, the highest degree selection occurred following gene d the mammalian lineage (Figure 4).
- Seven amino acids (139, 142, 14 in the alignment) showed evidence (Table 1). Two amino acids (149 an two methods as having undergone