

Table S3. Degree of conservation of amino acid positions contiguous to non-conserved polymorphic variants.

Nucleotide position ^{a,b}	Amino acid position (protein)	Interval (-10/+10)	Local conservation (%)	Global conservation (%)	Nearest invariant position (-/+)
4216	304 (ND1)	294/314	67	77	-6/+11
5074	202 (ND2)	192/212	48	62	-12/+6
<u>7299</u>	<u>466 (COI)</u>	<u>456/476</u>	<u>90</u>	<u>95</u>	<u>-2/+2</u>
8393	10 (ATP8)	1/21	75	65	-1/+40
<u>8701</u>	<u>59 (ATP6)</u>	<u>49/69</u>	<u>73</u>	<u>77</u>	<u>-3/+2</u>
9053	176 (ATP6)	166/186	77	77	-1/+22
9091	189 (ATP6)	179/199	57	77	-14/+10
13708	458 (ND5)	448/468	68	68	-1/+7
<u>13759</u>	<u>475 (ND5)</u>	<u>465/485</u>	<u>48</u>	<u>68</u>	<u>-1/+6</u>
<u>13934</u>	<u>533 (ND5)</u>	<u>523/543</u>	<u>43</u>	<u>68</u>	<u>-6/+2</u>
13966	544 (ND5)	534/554	48	68	-9/+10
14325	117 (ND6)	107/127	14	52	-35/+24
14766	7 (CYTB)	1/21	76	83	-6/+48
15221	159 (CYTB)	149/169	95	83	-15/+4
15452	236 (CYTB)	226/246	57	83	-72/+48

^a Nucleotide changes affecting amino acid residues with a local conservation equal or higher than the global conservation are in bold.

^b Nucleotide changes affecting amino acid residues close to invariant amino acids (+4/-4 aa) are underlined.