```
CCDS10431.1     MLNLLLLALPVLASRAYAAPAPGQALQRVGIVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAHCVGPDV 80
Pan [[multiz]] MLSLLLLALPILASPAYAAPAPGQALQRAGIVGGQEAPRSKWPWQVSLRVRDRYWMHFCGGSLIHPQWVLTAAHCVGPDF 80
Pon [[inpara]] MLSLLLLALPVLASPAYAAPAPGQALQRVGIVGGQEAPRSKWPWQVSLRVHGQYWMHFCGGSLIHPQWVLTAAHCVGPDV 80
Mac [[multiz]] MLNLLLLALPVLVSPAHAAPAPGQALQRVGIVGGQEAPRSKWPWQVSLRLHGQYWMHFCGGSLIHPQWVLTAAHCVGPDV 80
Cal [[OMA]]    MLSLLLLVLPVLVSLAHSAPAPGQALPRAGIVGGQEAPGSRWPWQVSLRFHSQFWMHFCGGSLIHPQWVLTAAHCLGPDV 80
Oto [[inpara]] MLSLLVLALPILGSRVHAAPAPGQASERAGIVGGQEAPESKWPWQVSLRQHTHFWMHICGGSLIHPQWVLTAAHCVGPEV 80
Bos [[multiz]] MLHL--LALALLLSLVSAAPAPGQALQRAGIVGGQEAPGSRWPWQVSLRVSHQYWRHHCGGSLIHPQWVLTAAHCVGPEV 78
Equ [[inpara]] MPNLLVLALALLVNLGHAAPAPGQALEREGIVGGQEASGSKWPWQVSLRKNTEYWKHFCGGSLIHPQWVLTAAHCVGPDI 80

CCDS10431.1     KDLAALRVQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVNVSSHVHTVTLPPASETFPPGMPCWVTGW 160
Pan [[multiz]] KDLATLRVQLQEQHLYYQDQLLPVSRIIVHPQFYIIQTGADIALLELEEPVNVSSRVHTVTLPPASETFPPGMPCWVTGW 160
Pon [[inpara]] KDLAALRVQLREQHLYYQDQLLPVGRIIVHPQFYTAQTGADIALLELEEPVNISSHVHTVTLPPASETFPPGMPCWVTGW 160
Mac [[multiz]] KDLADLRVQLREQHLYYQDQLLPVSRIIVHPQFYAVQIGADIALLELEEPVNVSSHVHTVTLPPASETFPPGTPCWVTGW 160
Cal [[OMA]]    MDLANLRVQLREQHLYYKDRLLPVSRLIVHPQFYIVQTGADIALLELEEPVNVSSHVRTVTLPPASETFPAGTPCWVTGW 160
Oto [[inpara]] QDLADFRVQLREQHLYYHDKLLPVSRIIPHPGFYMATTGADIALLELEEPVNISHSVHTITLPPASETFPPGTPCWVTGW 160
Bos [[multiz]] HGPSYFRVQLREQHLYYQDQLLPISRIIPHPNYYSVENGADIALLELDEPVSISCHVQPVTLPPESETFPPGTQCWVTGW 158
Equ [[inpara]] EDFRDIRVQLREQHLYYRDQLLPVSRILPHPYYYTVENGADIALLELQDPVNISSHVQVVTLPPASETFPPGTPCWVTGW 160

CCDS10431.1     GDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAG 240
Pan [[multiz]] GDVDNDEPLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIIRDDMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAG 240
Pon [[inpara]] GDVDNDEHLPPPFPLKQVKVPIMENHICDAKYHLGLYTGDDVRIVRDDMLCAGNSRRDSCQGDSGGPLVCKVNGTWLQAG 240
Mac [[multiz]] GDVDNDVPLPPPFPLKQVKVPIMENHICDAKYHSGLYTGDDVRIIRDDMLCAGNSRRDTCQGDSGGPLVCKVNGTWLQAG 240
Cal [[OMA]]    GDVNTGEPLPPPFPLKQVKVPIVENQVCDMKYHAGLYTGDAVHIVRDDMLCAGNSRRDSCQGDSGGPLVCKVNDTWLQAG 240
Oto [[inpara]] GDVDNDVGLPPPFPLKQVKVPIVENHICDAKYHMGLYTGDNVHIVGDNMLCAGNTRKDSCQGDSGGPLVCKVNGTWLQAG 240
Bos [[multiz]] GNVDNGRRLPPPFPLKQVKVPVVENSVCDRKYHSGLSTGDNVPIVQEDNLCAGDSGRDSCQGDSGGPLVCKVNGTWLQAG 238
Equ [[inpara]] GDVDNGVSLPPPFPLKEVKVPIVENSVCDRKYHTGVSTGDNIRIVQADMLCAGNRRHDSCQGDSGGPLVCKVKGTWLQAG 240

CCDS10431.1     VVSWGEGCAQPNRPGIYTRVTYYLDWIHHYVPKKP- 275
Pan [[multiz]] VVSWDEGCAQPNRPGIYTRVTYYLDWIHHYVPKKHX 276
Pon [[inpara]] VVSWGEGCAQPNRPGIYTRVTYYLDWIHRYVPKKP- 275
Mac [[multiz]] VVSWDEGCAQPYRPGIYTRITYYLDWIHRYVPEKPX 276
Cal [[OMA]]    VVSWGEGCALPNRPGIYTRVTYYLDWIHQYVPKKP- 275
Oto [[inpara]] VVSWGDGCAQPNRPGIYTRVTHYLDWIHHYVPKEP- 275
Bos [[multiz]] VVSWGDGCAKPNRPGIYTRVTSYLDWIHQYVPQGPX 274
Equ [[inpara]] VVSWANSCAQPNRPGIYTRVTYYLDWIYQYVPKDS- 275
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Figure S9. The MOSAIC alignment of TPSAB1. *The MOSAIC-specific positively selected site is illustrated with the red arrow, while the site detected by several methods, including MOSAIC, is indicated in gold.*