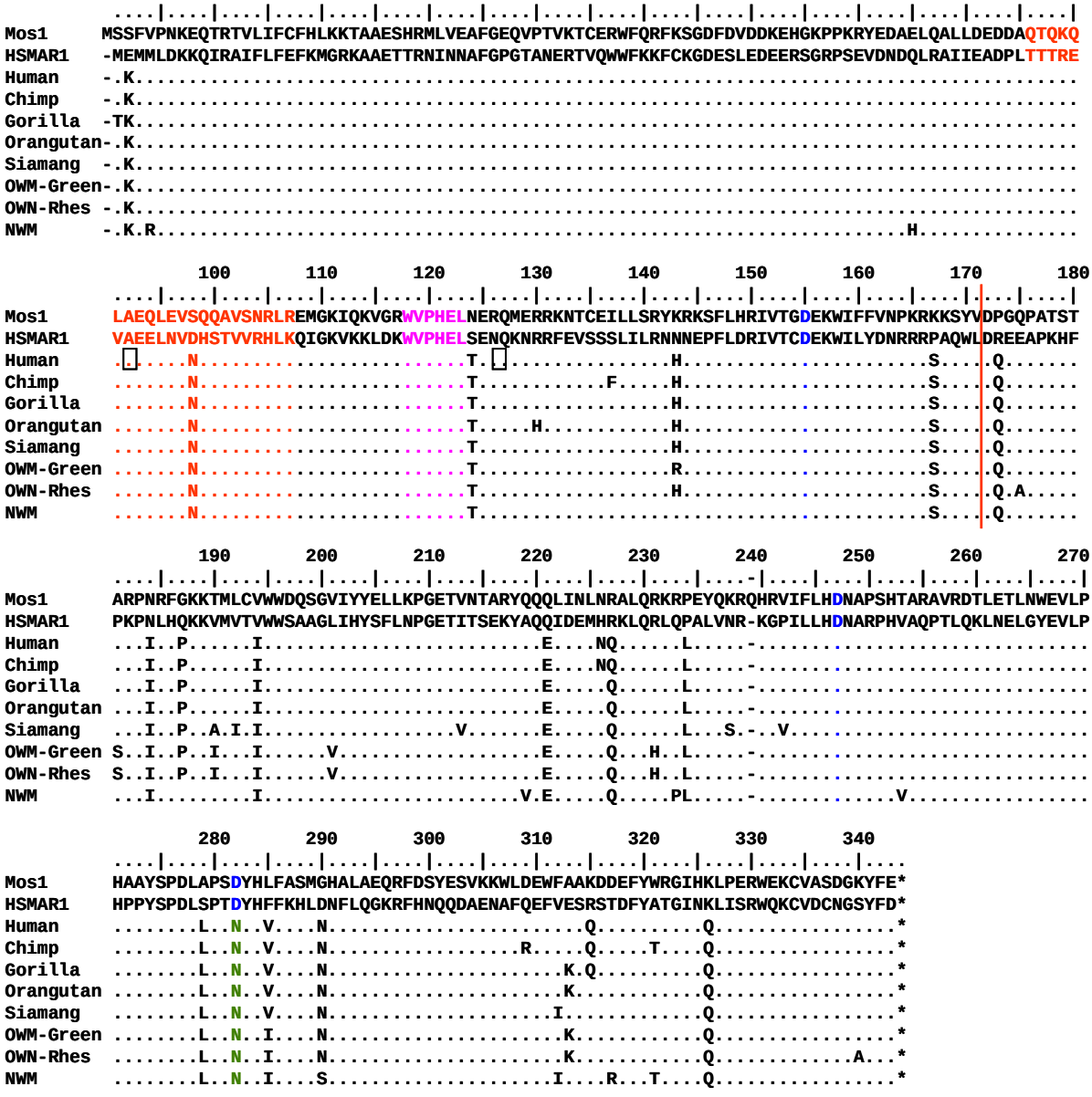
10 20 30 40 50 60 70 80 90
Mos1 MSSFVPNKEQTRTVLIFCFHLKKTAAESHRMLVEAFGEQVPTVKTCERWFQRFKSGDFDVDDKEHGKPPKRYEDAELQALLDEDDAQTQKQ
HSMAR1 -MEMMLDKKQIRAIFLFEFKMGRKAAETTRNINNAFGPGTANERTVQWWFKKFCKGDESLEDEERSGRPSEVDNDQLRAIIEADPLTTTRE
Human -.K
Chimp -.K
Gorilla -TK
Orangutan-.K
Siamang -.K
OWM-Green-.K
OWN-Rhes -.K
NWM -.K.R H
100 110 120 130 140 150 160 170 180
Mos1 LAEQLEVSQQAVSNRLREMGKIQKVGRWVPHELNERQMERRKNTCEILLSRYKRKSFLHRIVTGDEKWIFFVNPKRKKSYVDPGQPATST
HSMAR1 VAEELNVDHSTVVRHLKQIGKVKKLDKWVPHELSENQKNRRFEVSSSLILRNNNEPFLDRIVTCDEKWILYDNRRRPAQWLDREEAPKHF
Human . N T. H S Q
Chimp N T F H S Q
Gorilla N T H S Q
Orangutan N T H H S Q
Siamang N T H S Q
OWM-Green N T R S Q
OWN-Rhes N T H S Q.A
NWM N T S Q
190 200 210 220 230 240 250 260 270
Mos1 ARPNRFGKKTMLCVWWDQSGVIYYELLKPGETVNTARYQQQLINLNRALQRKRPEYQKRQHRVIFLHDNAPSHTARAVRDTLETLNWEVLP
HSMAR1 PKPNLHQKKVMVTVWWSAAGLIHYSFLNPGETITSEKYAQQIDEMHRKLQRLQPALVNR-KGPILLHDNARPHVAQPTLQKLNELGYEVLP
Human ...I..P.....I E....NQ.....L.....-
Chimp ...I..P.....I E....NQ.....L.....-
Gorilla ...I..P.....I E.....Q.....L.....-
Orangutan ...I..P.....I E.....Q.....L.....-
Siamang ...I..P..A.I.I V.....E.....Q.....L...S.-..V
OWM-Green S..I..P..I...I.....V E.....Q...H..L.....-
OWN-Rhes S..I..P..I...I.....V E.....Q...H..L.....-
NWM ...I.....I V.E.....Q.....PL.....-.....V
280 290 300 310 320 330 340
Mos1 HAAYSPDLAPSDYHLFASMGHALAEQRFDSYESVKKWLDEWFAAKDDEFYWRGIHKLPERWEKCVASDGKYFE*
HSMAR1 HPPYSPDLSPTDYHFFKHLDNFLQGKRFHNQQDAENAFQEFVESRSTDFYATGINKLISRWQKCVDCNGSYFD*
Human .....L..N..V....N Q..... Q.....*
Chimp .....L..N..V....N R..... Q.....T....Q.....*
Gorilla .....L..N..V....N K.Q..... Q.....*
Orangutan .....L..N..V....N K..... Q.....*
Siamang .....L..N..V....N I..... Q.....*
OWM-Green .....L..N..I....N K..... Q.....*
OWN-Rhes .....L..N..I....N K..... Q.....A...*
NWM .....L..N..I....S I....R...T....Q.....*

Fig. 7. Protein sequence alignment of the active *mos1* transposase from *Drosophila mauritiana* (GenBank accession no. X78906), *Hsmar1* consensus transposase (AAC52010) and MAR region from eight primate species. See Fig. 2 legend for species names and abbreviations. The catalytic DD34D triad is shown in blue, whereas the N residue replacing the last D in MAR is in green. The predicted helix–turn–helix (HTH) motif is shown in red. The motif was predicted with 100% probability in all sequences using the *npsa* prediction server (http://npsa-pbil.ibcp.fr/cgi-bin/npsa_automat.pl?page = /NPSA/npsa_hth.html). Note that the mutation D98N in MAR sequences does not seem to alter the potential of this region to form a HTH structure. In fact, the motif is predicted with a higher score of 6.40 (vs. 5.63 in the *Hsmar1* consensus). The boxed residues in the human MAR sequence mark the last residue of the deletion peptides MAR-N92 and MAR-N126, respectively (see Fig. 3). The WVPHEL motif, highly conserved in *mariner* transposases and involved in the ability of the *Mos*I transposase to assemble organized complexes of DNA with transposase tetramers (1) is shown in purple. Note that the motif is conserved in MAR and included within the MAR-N126 peptide, in agreement with the formation of at least two protein–DNA complexes with different electrophoretic mobility in EMSA experiments (Fig. 3*c*). The vertical red line represents the separation between the two halves of the proteins for which K_A/K_S analyses were conducted independently (see *Functional Contribution of the MAR Transposase*).

1. Auge-Gouillou, C., Brillet, B., Germon, S., Hamelin, M. H. & Bigot, Y. (2005) *J. Mol. Biol.* **351,** 117–130.