

**Table S2A. HVR-1 analyses: including/excluding partial sequences**

			Including partial sequences												Excluding partial sequences											
Nodes	Monophyly	Equus subgenera	Unrooted Analyses						Rooted Analyses						Unrooted Analyses						Rooted Analyses					
			ACGT?			YR?			ACGT?			YR?			ACGT, No?			YR, No?			ACGT, No?			YR, No?		
			Boot strap	aL	PP	Boot strap	aL	PP	Boot strap	aL	PP	Boot strap	aL	PP	Boots trap	aL	PP	Boots trap	aL	PP	Boots trap	aL	PP	Boots trap	aL	PP
A	Caballines, Hippidions, NWSL		67,5	85	1,00	48,4	81	0,81	-	-	-	-	-	-	70,7	86	1,00	46,6	78	0,81	-	-	-	-	-	
B	Hippidions, NWSL		41	37	0,58	-	-	-	-	-	-	-	-	-	39,5	23	-	-	-	-	-	-	-	-	-	
C2	Hippidions	<i>Hippidion</i>	98,5	97	1,00	74,4	91	1,00	94,5	98	1,00	64,9	93	0,98	99,0	96	1,00	70,5	91	1	96,0	97	1,00	77,6	-	1,00
D	<i>Hippidion saldiasi / principale</i>	<i>Hippidion</i>	92,6	92	1,00	79,4	87	0,98	90	-	1,00	75,7	87	0,99	90,6	92	1,00	75,2	85	0,98	89,7	93	1,00	76,7	-	0,98
E	<i>Hippidion devillei</i>	<i>Hippidion</i>	100	97	1,00	75,2	80	0,99	86,9	-	0,88	61,3	77	0,91	100,0	98	1,00	79,6	84	0,99	85,1	75	0,86	66,3	-	0,92
F	NWSL		98,7	97	1,00	87,1	95	-	-	-	0,7	-	-	-	98,8	97	1,00	83,9	95	-	-	-	0,75	-	-	-
G	Caballines	<i>Equus</i>	99,4	97	1,00	86	95	1,00	26,2	75	0,56	-	-	-	99,7	98	1,00	83,3	94	1,00	28,3	78	0,64	-	-	-
H	Non-caballine horses		67,5	85	1,00	48,4	81	0,81	5,7	-	-	-	-	-	70,7	86	1,00	46,6	78	0,81	2,0	66	-	-	-	-
I	Sussemionas		99,4	99	1,00	-	-	-	88,5	98	1,00	-	-	-	99,0	99	1,00	-	-	-	90,4	99	1,00	-	-	-
C1	<i>E. quagga / E. capensis</i>	<i>Quagga</i>	98,6	99	1,00	-	-	-	-	-	-	-	-	-	98,0	99	1,00	-	-	-	-	-	-	-	-	-
J	<i>E. quagga / E. capensis</i> subclade	<i>Quagga</i>	80	88	1,00	76,1	94	1,00	80,5	94	1,00	64	86	0,93	78,7	88	0,95	79,8	95	1,00	79,0	96	1,00	65,3	-	0,94
K	<i>E. quagga boehmi</i>	<i>Quagga</i>	86,7	80	0,96	-	-	-	-	-	0,68	-	-	-	87,8	75	1,00	-	-	-	-	-	-	-	-	-
L	<i>E. hartmannae</i>	<i>Hippotigris</i>	100	100	1,00	96,5	99	1,00	89,9	98	1,00	83,7	96	1,00	100,0	100	1,00	91,0	98	1,00	91,1	99	1,00	90,5	96	1,00
M	<i>E. grevyi</i>	<i>Dolichohippus</i>	63,1	39	0,78	-	-	-	99,3	-	-	-	-	-	58,6	3	0,69	-	-	-	-	-	-	-	-	-
N	<i>E. grevyi, E. hemionus, E. hydruntinus, E. kiang</i>		23,9	79	0,55	-	-	-	3,8	87	-	-	-	-	24,8	64	0,60	-	-	-	39,0	78	-	-	-	-
O	<i>E. kiang</i>	<i>Hemionus</i>	88	94	1,00	-	-	-	94	93	0,92	-	-	-	85,3	92	0,99	-	-	-	80,0	93	0,91	-	-	-
P	<i>E. asinus, E. hartmannae</i>	<i>Asinus and Hippotigris</i>	98,7	77	0,58	-	-	-	29,7	94	-	-	-	-	36,5	77	0,61	-	-	-	-	-	-	-	-	-
Q	<i>E. asinus</i> (excluding CH1069), <i>E. hartmannae</i>	<i>Asinus and Hippotigris</i>	41,7	78	0,58	-	-	-	-	-	0,67	-	-	-	40,6	79	0,59	-	-	-	30,4	94	0,82	-	-	-

Most of the HVR-1 sequences were complete, but for a few samples samples (ACAD3615, ACAD3629, CH561, TZ9 and *E. hydruntinus* sequence under Accession Nb. DQ464012) only partial sequences could have been recovered. **Left part:** these sequences were included or in the analyses and missing fragments were accordingly coded as missing data (?). **Right part:** These sequences were removed from the datasets. Bootstrap and approximate Likelihood Ratio Test (aLRT) supports and posterior probabilities (PP) for major phylogenetic nodes are reported based on ACGT coded datasets or YR-coded datasets.

**Table S2B. HVR-1, HVR-2 and cyt b merged analyses**

	Length (pb)	Data coded	Topology ( <i>E. asinus, E. caballus, H. saldiasi</i> )			Topology ( <i>E. caballus, H. saldiasi</i> )		
			Bootstrap	aLRT	Post. Probs	Bootstrap	aLRT	Post. Probs
HVR-1*, Cytb, HVR-2	755	ACGT	100,0	100,0	1,00	98,1	93,0	1,00
HVR-1*, Cytb, HVR-2	755	YR	100,0	100,0	1,00	66,7	72,0	0,76
HVR-1, Cytb, HVR-2	814	ACGT	100,0	100,0	1,00	94,6	92,0	0,99
HVR-1, Cytb, HVR-2	814	YR	100,0	100,0	1,00	50,0	-	-

The analyses were rooted with rhinos (*Rhinoceros unicornis* and *Ceratotherium simum*) and the phylogenetic relationships within equids were assessed thanks to bootstrap, approximate Likelihood Ratio Test (aLRT) supports and posterior probabilities (PP) of nodes (note that this topology is described as topology T in suppl fig S3, topology T). Accession Nb. *Equus caballus*: X79547 (complete genome). *Equus asinus*: X97337 (complete genome). *Hippidion saldiasi*: DQ007562, DQ007615, AY152859 (HVR-1, HVR-2 and cyt b, respectively). *Rhinoceros unicornis*: X97336 (complete genome). *Ceratotherium simum*: Y07726 (complete genome). \*: removing the first 60 nucleotides (positions 15518-15577 according to the complete horse mitochondrial genome; Accession Nb. X79547) to avoid alignment ambiguities.