**S6 Alignment. Alignment of the X protein of erythroparvoviruses and tetraparvoviruses, including reported endogenous erythroparvoviruses.**

The alignment, in FASTA format, includes two sequences reported to come from endogenous viruses: that of Indri indri endogenous parvovirus and Hyaena hyaena endogenous parvovirus [1].

>ParvovirusB19/1-81

------------------------------------MDSYLTT-PMPYHPVAVMQNLEEKMQYYLVKTYTSL

GKLAYNYPVLTMLGLAMSYKLGPRKVLLTVLQGFMTLGIANWLSWE--------------------------

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>SimianParvo/1-81

------------------------------------MDLSQIS-EKLRQNTNPLMNLEEMTQSLLKKTYTKG

VELVLHYPLVTTLALVISFKLGIPKVWWTLRLGFMILGILNLLNWE--------------------------

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>RhesusMacaque/1-79

------------------------------------MDLSLIS-ESLRQNMNPLMNLEEMTQSLVKRIYTKG

VDLVCNYPSVITLALVMSYRLGPRRVLWMLQLGVMISGILNLLS----------------------------

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>PigtailedMacaque/1-79

------------------------------------MALSQIS-ENLRLSMRSLMNLEELTQSLLVKTYTMG

VQLVSHYPSLTILGLGILYKLGPQRTWWMLQLGFTITGILNLLS----------------------------

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>IndriEndogenousParvovirus|RJWJ010000280/247-327

------------------------------------MNLTLVN-HLLNELNLTPPLLEQFLRDSGKTLLTYL

TEVVYTYPATATLVLATLWKTGLPLIWWTRPPGSTTSGTQKSKQKA--------------------------

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>HyaenaParvovirus-like|PITC01058066.1\_X protein Hyaena hyaena, whole genome shotgun sequence 2000-3406/223->1405

MRGVIISQFQSTLLNQSLLLISAPPRSQRLGLRWRLMSLAPPS-TWRET----ILCLENSLQRAISE-----

---VSHFPAVTTLGLAILWIQGPRLLSWTQRLAYTILGIHNYKAWGWILTPTLLRPTKSCCQPRLEKRDFRP

PW------

>SealParvo/1-103

------------------------------------MSLSQNR-SWQEI----LSPLESGLQTMVIE-----

---ALHYPALTTLGLAIAWKKGPQLLGWTLRLAYTILGIVSSRSWALIPTHTSHPLTRNSSRQPPEKRVSRQ

QWSRLSLS

>ChipmunkParvo/1-65

--------------------------------MW-QLFLNQTE-TLLQN------NLNEAWQSLITGAST--

------YPLTGILALAILWKTAPLLTRLTQWLVFTTLGTLT-------------------------------

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>Human\_parvovirus\_4/1-83

----------------------------------MSESTLLVT-AAMKE---LIPLLNQTLSG-LPEA----

---GLLSPGIIMLVLVILWIVVPLRDQWMRQQNIMMNGTQR-LSMGTSLIYMVTALTD--------------

--------

>PorcineHokoHK7/1-84

-----------------------------------MEPIATVA-TVIKE---LVPLVNQTLNA-LPSAP---

---ESWSPGTIMLVLVILWIMLPLRDQWMKQRNTTMNGTMKCFAMVICHTSMGEGLIG--------------

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>YakHoko/1-84

----------------------------------MLDQATTVA-TVIRE---LVPLVNQTLSA-LPTA----

---DSWSPATIMLVLVILWIMVPLRDQWMRQRSTTMNGTMKCCLMATCHMFMVTGQID--------------

--------

>OvineHoko1/1-85

---------------------------------MAMAEVSTLA-TVVQE---LLPLVNQTLND-LPKG----

---DFWSPVTIMLVLVILWIMVPLRDQWTRQRNIMTNGTMKCYHMGMSHIYTDTGLTD--------------

--------

>DeerTetraparvo|NC\_031670\_1\_cds\_YP\_009315887\_1\_2/1-/1-84

-----------------------------------MESVVTVA-TVLEE---LIPLVNQTLNA-LPKG----

---DFLSPVIVMLVLVILWIMAPLRAQWTRPLNTMTNGTQICYLMGTYHTSMVMEQTDL-------------

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>RodentTetraparvo/1-85

----------------------------------MADLLLPLS-SIMRE---LLPALNHTATE-LAREG---

---VSWSPGTIMLVLVILWIMAPLRDRLMRPQRDTMNGTMRCSSMGTCPICMAMGRMA--------------

--------

>EidolonParvo1/1-77

----------------------------------MEEPLLNSALTSLKV---LAPLVNQTIHS-LAEV----

---VSLSPATIMWVLVILWIMAPLRAQWMRQLAIMTEGMTKCFPTGTSPT----------------------

--------

>OppossumTetraparvo/1-76

--------------------------------MEVSEGLQLLR-TIAQ------ATANQTAEAILPGA----

---GSLSPAIIMLVLVILWIMAPLRAQWMRRLNAMTNGMMSCWVMGMCHT----------------------

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# References

1. Campbell MA, Loncar S, Kotin RM, Gifford RJ. Comparative analysis reveals the long-term coevolutionary history of parvoviruses and vertebrates. Quental TB, editor. PLOS Biol. 2022;20: e3001867. doi:10.1371/journal.pbio.3001867