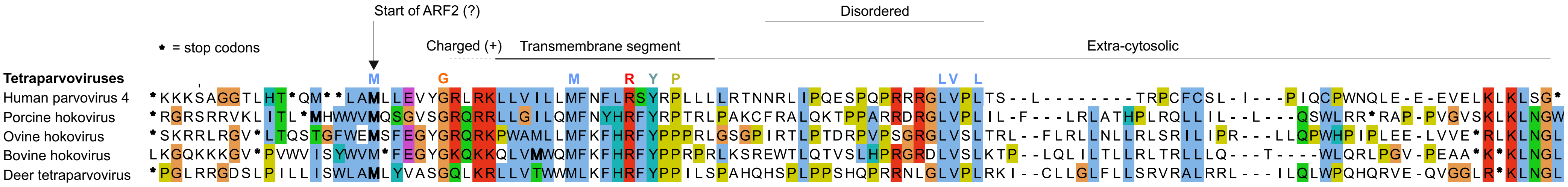

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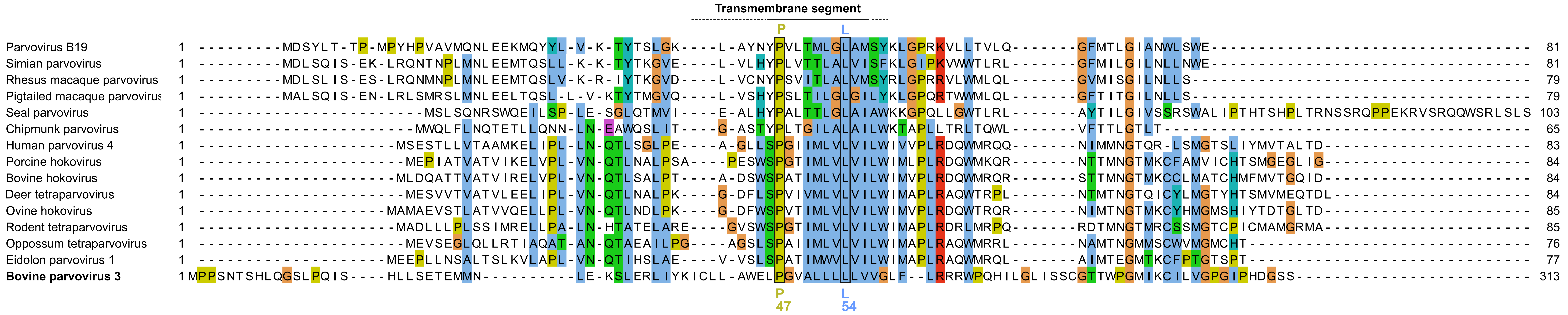
Porcine hokovirus	*RGRSRRVKLITL* **M**HWWV**M**QSGVSGRQRRLLGILQMFNYHRFYRPTRLPAKCFRALQKTPPARRDRGLVPLIL-F---LRLATHPLRQLLIL--L---QSWLRR*RAP-PVGVSKLKLNGW
Ovine hokovirus	*SKRRLRGV*LTQSTGFWE**M**SFEGYGRQRKPWAMLLMFKFHRFYPPPRLGSGPIRTLPTDRPVPSGRGLVSLTRL--FLRLLNLLRLSRILIPR---LLQPWHPIPLEE-LVVE*RLKLNGL
Bovine hokovirus	LKGQKKKGV*PVWVISYWVM*FEGYGKQKKQLV**M**WQMFKFHRFYPPRPRLKSREWTLQTVSLHPRGRDLVSLKTP--LQLILTLLRLTRLLLQ---T----WLQRLPGV-PEAA*K*KLNGL
Deer tetraparvovirus	*PGLRRGDSLPILLISWLA**M**LYVASGQLKRLLVTWWMLKFHRFYPPILSPAHQHSPLPPSHQPRRNLGLVPLRKI--CLLGLFLLSRVRALRRL---ILQLWPQHQRVE-QVGGLR*KLNGL



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Rhesus macaque parvovirus    1 ----------MDLSLIS-ES-LRQNMNPLMNLEEMTQSLV-K-R-IYTKGVD----L-VCNYPSVITLALVMSYRLGPRRVLWMLQL-------GVMISGILNLLS------------------------------------  79
Pigtailed macaque parvovirus 1 ----------MALSQIS-EN-LRLSMRSLMNLEELTQSL-L-V-KTYTMGVQ----L-VSHYPSLTILGLGILYKLGPQRTWWMLQL-------GFTITGILNLLS------------------------------------  79
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Chipmunk parvovirus          1 ------------------------MWQLFLNQTETLLQNN-LN-EAWQSLIT----G-ASTYPLTGILALAILWKTAPLLTRLTQWL-------VFTTLGTLT---------------------------------------  65
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Porcine hokovirus            1 -----------------------MEPIATVATVIKELVPL-VN-QTLNALPSA----PESWSPGTIMLVLVILWIMLPLRDQWMKQR-------NTTMNGTMKCFAMVICHTSMGEGLIG----------------------  84
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Oppossum tetraparvovirus     1 -----------------------MEVSEGLQLLRTIAQAT-AN-QTAEAILPG----AGSLSPAIIMLVLVILWIMAPLRAQWMRRL-------NAMTNGMMSCWVMGMCHT------------------------------  76
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Bovine parvovirus 3          1 MPPSNTSHLQGSLPQIS----HLLSETEMMN----------LE-KSLERLIYKICLL-AWELPGVALLLLLVVGLF--LRRRWPQHILGLISSCGTTWPGMIKCILVGPGIPHDGSS------------------------- 313
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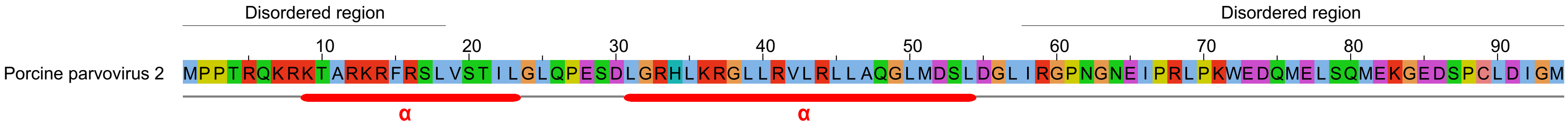
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S1 Alignment. Codon alignment of all B19V VP1 coding sequences

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S4 Alignment. Codon alignment of all pPARV2 VP1 coding sequences

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TAA---------------
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S5 Alignment. Alignment of the X-like protein of bovine parvovirus 3 with the reference alignment of the X proteins of erythroparvoviruses and tetraparvoviruses, in text format.

We used MAFFT-add to align the X-like protein of bovine parvovirus 3 with the reference alignment of the X protein of erythro- and tetraparvoviruses, which is derived from the alignment of the PLA2 domain and presented in Figure 6 (see main text).

```
>ParvovirusB19/1-81
----------MDSYLT-TP-MPYHPVAVMQNLEEKMQYYL-V-K-TYTSLGK----L-AYNYPVLTMLGLAM
SYKLGPRKVLLTVLQ-------GFMTLGIANWLSWE----------------------------------
>SimianParvo/1-81
----------MDLSQIS-EK-LRQNTNPLMNLEEMTQSLL-K-K-TYTKGVE----L-VLHYPLVTTLALVI
SFKLGIPKVWWTLRL-------GFMILGILNLLNWE----------------------------------
>RhesusMacaque/1-79
----------MDLSLIS-ES-LRQNMNPLMNLEEMTQSLV-K-R-IYTKGVD----L-VCNYPSVITLALVM
SYRLGPRRVLWMLQL-------GVMISGILNLLS------------------------------------
>PigtailedMacaque/1-79
----------MALSQIS-EN-LRLSMRSLMNLEELTQSL-L-V-KTYTMGVQ----L-VSHYPSLTILGLGI
LYKLGPQRTWWMLQL-------GFTITGILNLLS------------------------------------
>SealParvo/1-103
-------------------------MSLSQNRSWQEILSP-LE-SGLQTMVI----E-ALHYPALTTLGLAI
AWKKGPQLLGWTLRL-------AYTILGIVSSRSWALIPTHTSHPLTRNSSRQPPEKRVSRQQWSRLSLS
>ChipmunkParvo/1-65
------------------------MWQLFLNQTETLLQNN-LN-EAWQSLIT----G-ASTYPLTGILALAI
LWKTAPLLTRLTQWL-------VFTTLGTLT---------------------------------------
>Human_parvovirus_4/1-83
----------------------MSESTLLVTAAMKELIPL-LN-QTLSGLPE----A-GLLSPGIIMLVLVI
LWIVVPLRDQWMRQQ-------NIMMNGTQR-LSMGTSLIYMVTALTD----------------------
>PorcineHokoHK7/1-84
-----------------------MEPIATVATVIKELVPL-VN-QTLNALPSA----PESWSPGTIMLVLVI
LWIMLPLRDQWMKQR-------NTTMNGTMKCFAMVICHTSMGEGLIG----------------------
>YakHoko/1-84
----------------------MLDQATTVATVIRELVPL-VN-QTLSALPT----A-DSWSPATIMLVLVI
LWIMVPLRDQWMRQR-------STTMNGTMKCCLMATCHMFMVTGQID----------------------
>DeerTetraparvo|NC_031670_1_cds_YP_009315887_1_2/1-/1-84
-----------------------MESVVTVATVLEELIPL-VN-QTLNALPK----G-DFLSPVIVMLVLVI
LWIMAPLRAQWTRPL-------NTMTNGTQICYLMGTYHTSMVMEQTDL---------------------
>OvineHoko1/1-85
---------------------MAMAEVSTLATVVQELLPL-VN-QTLNDLPK----G-DFWSPVTIMLVLVI
LWIMVPLRDQWTRQR-------NIMTNGTMKCYHMGMSHIYTDTGLTD----------------------
>RodentTetraparvo/1-85
----------------------MADLLLPLSSIMRELLPA-LN-HTATELARE----GVSWSPGTIMLVLVI
LWIMAPLRDRLMRPQ-------RDTMNGTMRCSSMGTCPICMAMGRMA----------------------
>OppossumTetraparvo/1-76
-----------------------MEVSEGLQLLRTIAQAT-AN-QTAEAILPG----AGSLSPAIIMLVLVI
LWIMAPLRAQWMRRL-------NAMTNGMMSCWVMGMCHT------------------------------
>EidolonParvo1/1-77
---------------------MEEPLLNSALTSLKVLAPL-VN-QTIHSLAE----V-VSLSPATIMWVLVI
LWIMAPLRAQWMRQL-------AIMTEGMTKCFPTGTSPT------------------------------
>BovineParvovirus3/1-99
MPPSNTSHLQGSLPQIS----HLLSETEMMN----------LE-KSLERLIYKICLL-AWELPGVALLLLLV
VGLF--LRRRWPQHILGLISSCGTTWPGMIKCILVGPGIPHDGSS-------------------------
```

S6 Alignment. The X ORF has a potential AUG start codon in all erythro- and tetraparvoviruses

Codon-based nucleotide alignment of the X ORFs of erythro- and tetraparvoviruses, derived from the reference alignment of the VP1 protein by using TranslatorX, as in Fig 5 of the main text. Numbering corresponds to the VP1 CDS.

Putative AUG start codons of the X ORF are highlighted in yellow. For each species, the putative AUG start codon is conserved in all isolates (not shown in this alignment). Note how the AUGs tend to be in a similar location within erythroparvoviruses (except in chipmunk parvovirus and seal parvovirus), and within tetraparvoviruses.

UAG or **UGA**: stop codon

AUG: putative start codon of the X ORF

```
Erythroparvoviruses
Parvovirus B19        185 UAGUUGCUCGCAUUAAAAAUAACCUUAAAAAUUCUCCAGACUUAUAUAGUCAUCAUUUUCAAAGUCAUGGACAGUUAUCUGACCACCCCCAU---------GCCUUAUCAUCCAGUAGCAGUCAUG 301
Simian parvovirus     293 ACCUUAAA---CAACAUUUACAAGACUAUAUAGACAAUCCAGAUAAGUACACUUUAGACUUGUCUCAUGGACCUCUCCCAGAUUUCAGAGAA---------ACUGAGGCAGAACACAAAUCCUUUA 406
Rhesus macaque        299 AUCUACAA---AAACAAAUUGAAAACUAUAAAAAUAAUCCAAACAAAUAUACAUUACAGUUGUCUCAUGGACCUCUCCCUGAUUUCAGAGAG---------UCUGAGGCAAAACAUGAAUCCUCUA 412
Pigtailed macaque     194 UGGUUAAU---CGCAUUAAAAAAAAUUUAAAAGACAAUCCUGAUAUUUACACUGACUCCUUAAGUCAUGGCGCUCUCCCAGAUUUCCGAGAA---------UCUAAGGCUGAGCAUGAGAAGUCUA 307
Chipmunk parvovirus   311 CCGUAGCU---AACACAGCCAAGCGGUUAAAAACUGACGAGGAUCCCUUA------UCCUUUGGGGCCCCCCCACUAACAGAAAACGCCCCGGUUCCCGUUGCGGAGCCAGAUGUGGCAAUUGUUU 427
Seal parvovirus       338 GGAGGCACUAUGGAUCCUCAAAGGAGCAGGGCGCAGCACCCCCCGCUGAUCCCAGACAUAUAGCAGGCCCUCCUCUCACAUCACAGGGCCCG---------GUGUUGGGGGAGCAUGUCCCUAUCA 454

Tetraparvoviruses
Human parvovirus 4    467 UUUUUGAA---GACUCGCUAACGAACUUUGCCAAAGAAGACUUAGACACCUGGCAACAACUCCACGAGCAGUUUAUCAAACUCUUUCACCCU---------CCAGAUGUCGGAGUCCACCUUGUUA 580
Porcine hokovirus     464 UCUUUGAG---GAGAGUGUAUCUCCUUGGUCUGAGGAAGACAAAAAAAUUUUGAAACAGAUUGAAGGGCAGUUCCAGGAAAUAUUCCAUCCACCCACAGAUACGGAGGAUGGAGCCGAUAGCUACG 586
Yak hokovirus         491 UUUUUCAG---GGCAUGUUAUCUCCCAUCAAACCUGAAGAUAGACCUAUAUUAGACACCAUACAGAAGCAGUUUGAGGAGUUUUUUUAUCCUCCUAUAGUGGAACAUGCUGGACCAGGCGACUACA 613
Deer tetraparvovirus  491 ACUUUGAU---GGCAUGUUGUCACCUAUUCCAGUGGAACAACAUCCAAUUGUAGAGCAGAUAAAGGCUCAGUUUUUAAAUAUUUUUCAUCCGCCACCUAUAGCUGGAGAUGGAGUCGGUGGUGACG 613
Ovine hokovirus       491 UUUUCAAU---GGUAUGUUGACGCCGUUUGAUUCCGACCAGCGACCGGUGGUCGAGCAGAUUCACCAGCAGUUCUUAGACAUCUUUCACCCCCCACCAGUGCAUGGCCAUGGCGGAGGUGUCGACA 613
Rodent tetraparvo     467 ACUUUGAC---CAGUUCAUCACCCCGGUGGACCCCGGGGAGCCCGAGAUUCUAAAGCAGGCCUUCCAGCGCAUGGUAGAAUAUUACCACCCCGCCCCU---CAGGAUGGCGGACCUGCUCCUCCCC 586
Eidolon parvovirus    458 UUUUUGAU---GAGUCUGUGCUGGGCAGCGUUAGCGGAGACCCCGAAAACUUUGCUUUUGUGAAGCAGGCAGUAGUUAGUGCUUUUCAUCCUGCA------GAUGGAGGAGCCGCUACUGAACAGC 574
Oppossum tetraparvo   440 UUUUUACU---GACUCUAUUAGUGCGGGUGUAGCUGGAACA---CCACUCUGGGGAGAUACUGCAGAAGCUCUCAUGUCGGCCCUU---------------GCAGGGAAUGGAAGUAUCAGAGGGU 544
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