

```

Oran : MSPKRRQLTFEKSITIDVEVKNPDLRKGELARRFNIPSTLSTILKNKRALLASE RKYGVASTCRKTNKLS YDKLEGLLMAWFQOIRANGLPVNGIILKEKALRIABELGMDFETASN : 120
Vour : MSPKRRQLTFEKSITIDVEVKNPDLRKGELARRFNIPSTLSTILKNKRALLASE RKYGVASTCRKTNKLS YDKLEGLLIAWFQOIRANGLPVNGIILKEKALRIABELGMDFETASN : 120
Hosa : MSPKRRQLTFEKSITIDVEVKNPDLRKGELARRFNIPSTLSTILKNKRALLASE RKYGVASTCRKTNKLS YDKLEGLLIAWFQOIRANGLPVNGIILKEKALRIABELGMDFETASN : 120
Mupa : MSPKRRQLTFEKSITIDVEVKNPDLRKGELARRFNIPSTLSTILKNKRALLASE RKYGVASTCRKTNKLS YDKLEGLLIAWFQOIRANGLPVNGIILKEKALRIABELGMDFETASN : 120
Ptal : MSPKRRQLTFEKSITIDVEVKNPDLRKGELARRFNIPSTLSTILKNKRALLASE RKYGVASTCRKTNKLS YDKLEGLLIAWFQOIRANGLPVNGIILKEKALRIABELGMDFETASN : 120
Feca : MSPKRRQLTFEKSITIDVEVKNPDLRKGELARRFNIPSTLSTILKNKRALLASE RKYGVASTCRKTNKLS YDKLEGLLIAWFQOIRANGLPVNGIILKEKALRIABELGMDFETASN : 120

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CENP-B N-terminal DNA-binding domain **Tc5 transposase DNA-binding domain**

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Oran : GWLDRFRRRNGVVRRIAVRRAWSRAPE-----GSRWVEEDPLRVAEGYASQDVFNARETGLWYNELDQAPAPHGRARPGGEPCTERLVLLCA : 210
Vour : GWLDRFRRRNGVVRRIAVRRAQPSIPAQPIPLRAIASAIAADGGGGGGGSGGGGSRWVEEDPLRVAEGYASQDVFNARETGLWYNELDQAPAPHGRARPGGEPCTERLVLLCA : 240
Hosa : GWLDRFRRRNGVVRRIAVRRAQPSIPAQPIPLRAIASAIAADGGGGGGGSGGGGSRWVEEDPLRVAEGYASQDVFNARETGLWYNELDQAPAPHGRARPGGEPCTERLVLLCA : 231
Mupa : GWLDRFRRRNGVVRRIAVRRAQPSIPAQPIPLRAIASAIAADGGGGGGGSGGGGSRWVEEDPLRVAEGYASQDVFNARETGLWYNELDQAPAPHGRARPGGEPCTERLVLLCA : 231
Ptal : GWLDRFRRRNGVVRRIAVRRAQPSIPAQPIPLRAIASAIAADGGGGGGGSGGGGSRWVEEDPLRVAEGYASQDVFNARETGLWYNELDQAPAPHGRARPGGEPCTERLVLLCA : 231
Feca : GWLDRFRRRNGVVRRIAVRRAQPSIPAQPIPLRAIASAIAADGGGGGGGSGGGGSRWVEEDPLRVAEGYASQDVFNARETGLWYNELDQAPAPHGRARPGGEPCTERLVLLCA : 231

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Oran : NADSEKLEPLVLEKSKSINIRTLPCDYTANRKGCVTGLAKYLKALDRMAESRKRILLVNRPEFLDLSLRHQVAFPPAGCGHICPLERGVVQVQKGHYRQAMLLKAMA : 330
Vour : NADSEKLEPLVLEKSKSINIRTLPCDYTANRKGCVTGLAKYLKALDRMAESRKRILLVNRPEFLDLSLRHQVAFPPAGCGHICPLERGVVQVQKGHYRQAMLLKAMA : 356
Hosa : NADSEKLEPLVLEKSKSINIRTLPCDYTANRKGCVTGLAKYLKALDRMAESRKRILLVNRPEFLDLSLRHQVAFPPAGCGHICPLERGVVQVQKGHYRQAMLLKAMA : 347
Mupa : NADSEKLEPLVLEKSKSINIRTLPCDYTANRKGCVTGLAKYLKALDRMAESRKRILLVNRPEFLDLSLRHQVAFPPAGCGHICPLERGVVQVQKGHYRQAMLLKAMA : 347
Ptal : NADSEKLEPLVLEKSKSINIRTLPCDYTANRKGCVTGLAKYLKALDRMAESRKRILLVNRPEFLDLSLRHQVAFPPAGCGHICPLERGVVQVQKGHYRQAMLLKAMA : 347
Feca : NADSEKLEPLVLEKSKSINIRTLPCDYTANRKGCVTGLAKYLKALDRMAESRKRILLVNRPEFLDLSLRHQVAFPPAGCGHICPLERGVVQVQKGHYRQAMLLKAMA : 347

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DDE superfamily endonuclease

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Oran : ALEEDRRCLOLGLNEALFVAAWQAVDRAIDIAQFTEAGFGGALFELAAKSPFDLDDLEEDDDI--DDEE-----DDEE----- : 410
Vour : ALEEDRRCLOLGLNEALFVAAWQAVDRAIDIAQFTEAGFGGALFELAAKSPFDLDDLEEDDDI--DDEE-----DDEE----- : 450
Hosa : ALEEDRRCLOLGLNEALFVAAWQAVDRAIDIAQFTEAGFGGALFELAAKSPFDLDDLEEDDDI--DDEE-----DDEE----- : 453
Mupa : ALEEDRRCLOLGLNEALFVAAWQAVDRAIDIAQFTEAGFGGALFELAAKSPFDLDDLEEDDDI--DDEE-----DDEE----- : 456
Ptal : ALEEDRRCLOLGLNEALFVAAWQAVDRAIDIAQFTEAGFGGALFELAAKSPFDLDDLEEDDDI--DDEE-----DDEE----- : 465
Feca : ALEEDRRCLOLGLNEALFVAAWQAVDRAIDIAQFTEAGFGGALFELAAKSPFDLDDLEEDDDI--DDEE-----DDEE----- : 459

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Oran : -----SSGLESDWVYAGVVAIACGIVC DRG--ATCLIEPDSSESESESEEDDIDDEDIDDEEEDDDDDDDIDDEEVVPSFGEMAYFAMVKRYLT : 515
Vour : -EVEGDEEEESSGLESDWVYAGVVAIACGIVC DRG--ATCLIEPDSSESESESEEDDIDDEDIDDEEEDDDDDDDIDDEEVVPSFGEMAYFAMVKRYLT : 555
Hosa : VDSDDEEEDSSGLESDWVYAGVVAIACGIVC DRG--ATCLIEPDSSESESESEEDDIDDEDIDDEEEDDDDDDDIDDEEVVPSFGEMAYFAMVKRYLT : 559
Mupa : DDSDDEEEDSSGLESDWVYAGVVAIACGIVC DRG--ATCLIEPDSSESESESEEDDIDDEDIDDEEEDDDDDDDIDDEEVVPSFGEMAYFAMVKRYLT : 560
Ptal : DDSDDEEEDSSGLESDWVYAGVVAIACGIVC DRG--ATCLIEPDSSESESESEEDDIDDEDIDDEEEDDDDDDDIDDEEVVPSFGEMAYFAMVKRYLT : 569
Feca : DDSDDEEEDSSGLESDWVYAGVVAIACGIVC DRG--ATCLIEPDSSESESESEEDDIDDEDIDDEEEDDDDDDDIDDEEVVPSFGEMAYFAMVKRYLT : 566

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Centromere protein B dimerisation domain

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Oran : SFPIDRVQSHILHLEHDLVHVTRKHARQAVRSTGHC-- : 555
Vour : SFPIDRVQSHILHLEHDLVHVTRKHARQAVRSTGHC-- : 597
Hosa : SFPIDRVQSHILHLEHDLVHVTRKHARQAVRSTGHC-- : 599
Mupa : SFPIDRVQSHILHLEHDLVHVTRKHARQAVRSTGHC-- : 600
Ptal : SFPIDRVQSHILHLEHDLVHVTRKHARQAVRSTGHC-- : 609
Feca : SFPIDRVQSHILHLEHDLVHVTRKHARQAVRSTGHC-- : 606

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Figure S6A. Alignment of CENPB proteins. The Latin abbreviation of the species. Oran: Ornithorhynchus anatinus; Vour: Vombatus ursinus; Hosa: Homo sapiens; Mupa: Mus pahari; Ptal: Pteropus alecto; Feca: Felis catus.

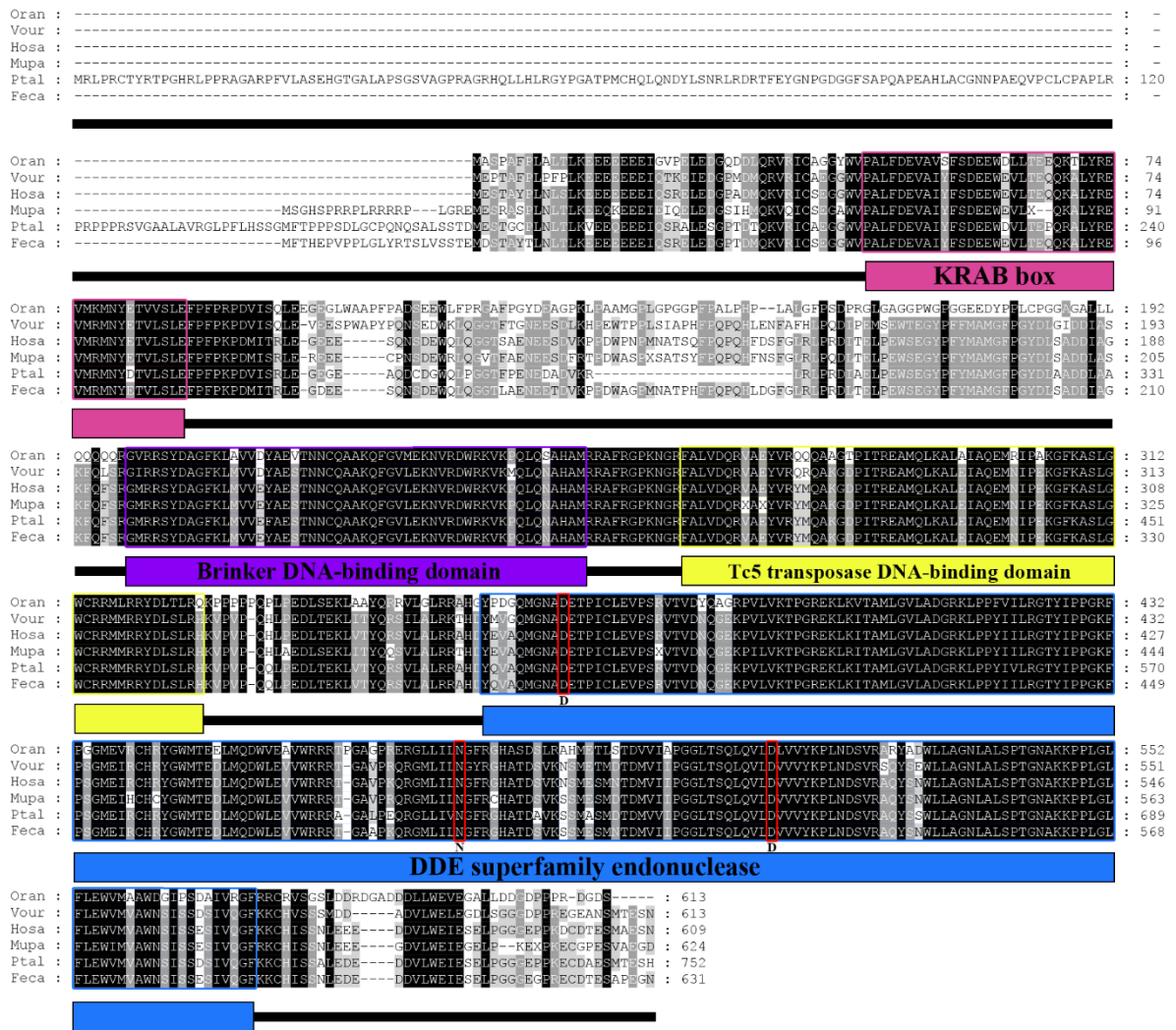


Figure S6B. Alignment of POGK proteins. The Latin abbreviation of the species. Oran: *Ornithorhynchus anatinus*; Vour: *Vombatus ursinus*; Hosa: *Homo sapiens*; Mupa: *Mus pahari*; Ptal: *Pteropus alecto*; Feca: *Felis catus*.

Lach : -----MPTDLFMECEEELEPWKIDLVIEAIEVYVANDNHFATSSLSQSSSASAPP---PVTPISSAGIQNIPKTKVVFIFANN----- : 90
Xela : -----XMTDLFMECEEELEPWKIDLVIEAIEVYVANDNHFATSSLSQSSSASAPP---PVTPISSAGIQNIPKTKVVFIFANN----- : 94
Povi : -----MPTDLFMECEEELEPWKIDLVIEAIEVYVANDNHFATSSLSQSSSASAPP---PVTPISSAGIQNIPKTKVVFIFANN----- : 94
Egga : -----MPTDLFMECEEELEPWKIDLVIEAIEVYVANDNHFATSSLSQSSSASAPP---PVTPISSAGIQNIPKTKVVFIFANN----- : 94
Oran : -----MPTDLFMECEEELEPWKIDLVIEAIEVYVANDNHFATSSLSQSSSASAPP---PVTPISSAGIQNIPKTKVVFIFANN----- : 85
Saha : -----MPTDLFMECEEELEPWKIDLVIEAIEVYVANDNHFATSSLSQSSSASAPP---PVTPISSAGIQNIPKTKVVFIFANN----- : 119
Hosa : -----MRGGWGRMPTDLFMECEEELEPWKIDLVIEAIEVYVANDNHFATSSLSQSSSASAPP---PVTPISSAGIQNIPKTKVVFIFANN----- : 101

Lach : -----SGVIVVQGRHSLELQSISGPPVGVVMTPOMLRPMHMONANHFITAVLQIPIFIQGFVVRNVR---VQNNVNOVGIVLNVQOGQVTRFI : 184
Xela : -----QSPFMSSQPLLLQNTST---GLEVYSVQMLRPMHMONANHFSSSMTIPIFIQGFVVRNVR---VQNNVNOVGIVLNVQOGQVTRFI : 188
Povi : -----MPTDLFMECEEELEPWKIDLVIEAIEVYVANDNHFATSSLSQSSSASAPP---PVTPISSAGIQNIPKTKVVFIFANN----- : 106
Egga : -----MPTDLFMECEEELEPWKIDLVIEAIEVYVANDNHFATSSLSQSSSASAPP---PVTPISSAGIQNIPKTKVVFIFANN----- : 106
Oran : -----MPTDLFMECEEELEPWKIDLVIEAIEVYVANDNHFATSSLSQSSSASAPP---PVTPISSAGIQNIPKTKVVFIFANN----- : 177
Saha : -----MPTDLFMECEEELEPWKIDLVIEAIEVYVANDNHFATSSLSQSSSASAPP---PVTPISSAGIQNIPKTKVVFIFANN----- : 234
Hosa : -----MPTDLFMECEEELEPWKIDLVIEAIEVYVANDNHFATSSLSQSSSASAPP---PVTPISSAGIQNIPKTKVVFIFANN----- : 193

Lach : -----LVAPAGTQVVKPIVGVPOVFSMAQVVRGGVLRVPAINTFTTVIPATLITIRSTPQSAQC---TKSTPSIS---AAGPPLAPPPP---PPPPAPPANPKI : 295
Xela : -----LVAPAGTQVVKPIVGVPOVFSMAQVVRGGVLRVPAINTFTTVIPATLITIRSTPQSAQC---TKSTPSIS---AAGPPLAPPPP---PPPPAPPANPKI : 294
Povi : -----LVAPAGTQVVKPIVGVPOVFSMAQVVRGGVLRVPAINTFTTVIPATLITIRSTPQSAQC---TKSTPSIS---AAGPPLAPPPP---PPPPAPPANPKI : 289
Egga : -----LVAPAGTQVVKPIVGVPOVFSMAQVVRGGVLRVPAINTFTTVIPATLITIRSTPQSAQC---TKSTPSIS---AAGPPLAPPPP---PPPPAPPANPKI : 289
Oran : -----LVAPAGTQVVKPIVGVPOVFSMAQVVRGGVLRVPAINTFTTVIPATLITIRSTPQSAQC---TKSTPSIS---AAGPPLAPPPP---PPPPAPPANPKI : 273
Saha : -----LVAPAGTQVVKPIVGVPOVFSMAQVVRGGVLRVPAINTFTTVIPATLITIRSTPQSAQC---TKSTPSIS---AAGPPLAPPPP---PPPPAPPANPKI : 345
Hosa : -----LVAPAGTQVVKPIVGVPOVFSMAQVVRGGVLRVPAINTFTTVIPATLITIRSTPQSAQC---TKSTPSIS---AAGPPLAPPPP---PPPPAPPANPKI : 304

Lach : -----LVNVVTVKRS-----LTGEAKDQTLISFNITIPD---PAIIVSSASTSQAITPAARORP-----VTTFHESVNYCPKGNHYRITDALSDFHMCYCPDFEETL : 397
Xela : -----LVNVVTVKRS-----LVAVSGNINVNSIIVIPSTNNSN---NNNSVTVILPPPSGKIVASISSTVSSSE---RIFCPORRTFRVVALRHMCCYCPDFD : 408
Povi : -----LVNVVTVKRS-----LVGENSNVAKLNTNIVPILCOVPGVLVLSNPAHASAGASDSSSQVSSPFAHLDQGGCVYCRONA FRVVALRHMCCYCPDFE : 401
Egga : -----LVNVVTVKRS-----LVGENSNVAKLNTNIVPILCOVPGVLVLSNPAHASAGASDSSSQVSSPFAHLDQGGCVYCRONA FRVVALRHMCCYCPDFE : 399
Oran : -----LVNVVTVKRS-----LVGENSNVAKLNTNIVPILCOVPGVLVLSNPAHASAGASDSSSQVSSPFAHLDQGGCVYCRONA FRVVALRHMCCYCPDFE : 380
Saha : -----LVNVVTVKRS-----LVGENSNVAKLNTNIVPILCOVPGVLVLSNPAHASAGASDSSSQVSSPFAHLDQGGCVYCRONA FRVVALRHMCCYCPDFE : 456
Hosa : -----LVNVVTVKRS-----LVGENSNVAKLNTNIVPILCOVPGVLVLSNPAHASAGASDSSSQVSSPFAHLDQGGCVYCRONA FRVVALRHMCCYCPDFE : 414

ZNF

Lach : -----KPEETQIKKIPTLPTSAITTTSSAIVFAPSKSYIVTVPVATVAPAKPAALVPAIQAPESSOPEQADGNISSGKLMVLVDDFYGKDKLAEVYVNBKTEVSPFC : 517
Xela : -----LPSFTQQA---TSTDT---VSNATPSSITSTALPACGQSS---QEETCQKLMVLVDDFYGKDKLAEVYVNBKTEVSPFC : 497
Povi : -----KPEEL-----SENIQTP-KPSPBPKI---AAVASPPSSEPLFALSFAAPFSS---DGLGAGASKLMVLVDDFYGKDKLAEVYVNBKTEVSPFC : 494
Egga : -----KPEEL-----SENIQSA-KPSPBPKI---TAVASPPSSEPLFALSFAAPFSS---ENVVSSGKLMVLVDDFYGKDKLAEVYVNBKTEVSPFC : 492
Oran : -----KPEEL-----PEAGPPPARABPKI---APVSPAASSEPLFALSFAAPFSS---EAGGAGASKLMVLVDDFYGKDKLAEVYVNBKTEVSPFC : 475
Saha : -----KPEEL-----SENIHSAIKPSPBPKI---APHFSTPSEPLFALSFAAPFSS---ENSGVTSKLMVLVDDFYGKDKLAEVYVNBKTEVSPFC : 549
Hosa : -----KPEEL-----SENIQSA-KPSPBPKI---APVSPAASSEPLFALSFAAPFSS---ENVGAVGKLMVLVDDFYGKDKLAEVYVNBKTEVSPFC : 508

Lach : -----RLKNNIRFMNHMKHVEIDQONGEVVHTTCQHCYRQFSTPPLQCHLEIVHSYESTTKKICEWAPSEPLFLQHMKDTHKPGEMPTVQVCCYRSSLVSEVDFHFRM : 637
Xela : -----RLKNNIRFMNHMKHVEIDQONGEVVHTTCQHCYRQFSTPPLQCHLEIVHSYESTTKKICEWAPSEPLFLQHMKDTHKPGEMPTVQVCCYRSSLVSEVDFHFRM : 617
Povi : -----RLKNNIRFMNHMKHVEIDQONGEVVHTTCQHCYRQFSTPPLQCHLEIVHSYESTTKKICEWAPSEPLFLQHMKDTHKPGEMPTVQVCCYRSSLVSEVDFHFRM : 614
Egga : -----RLKNNIRFMNHMKHVEIDQONGEVVHTTCQHCYRQFSTPPLQCHLEIVHSYESTTKKICEWAPSEPLFLQHMKDTHKPGEMPTVQVCCYRSSLVSEVDFHFRM : 612
Oran : -----RLKNNIRFMNHMKHVEIDQONGEVVHTTCQHCYRQFSTPPLQCHLEIVHSYESTTKKICEWAPSEPLFLQHMKDTHKPGEMPTVQVCCYRSSLVSEVDFHFRM : 595
Saha : -----RLKNNIRFMNHMKHVEIDQONGEVVHTTCQHCYRQFSTPPLQCHLEIVHSYESTTKKICEWAPSEPLFLQHMKDTHKPGEMPTVQVCCYRSSLVSEVDFHFRM : 669
Hosa : -----RLKNNIRFMNHMKHVEIDQONGEVVHTTCQHCYRQFSTPPLQCHLEIVHSYESTTKKICEWAPSEPLFLQHMKDTHKPGEMPTVQVCCYRSSLVSEVDFHFRM : 628

ZNF

ZNF

ZNF

ZNF

Lach : -----LYCLKVFNKNAYQVHFVHRHOKSVYHCNKCRQLQFLFAKDKIEHKLQHHKTRFKPKOLEGLKPGTKVTVIRASGDRVPLVAVPAQDAALQQHQQOQQOQQOQQH : 757
Xela : -----LYCLKVFNKNAYQVHFVHRHOKSVYHCNKCRQLQFLFAKDKIEHKLQHHKTRFKPKOLEGLKPGTKVTVIRASGDRVPLVAVPAQDAALQQHQQOQQOQQOQQH : 711
Povi : -----LYCLKVFNKNAYQVHFVHRHOKSVYHCNKCRQLQFLFAKDKIEHKLQHHKTRFKPKOLEGLKPGTKVTVIRASGDRVPLVAVPAQDAALQQHQQOQQOQQOQQH : 710
Egga : -----LYCLKVFNKNAYQVHFVHRHOKSVYHCNKCRQLQFLFAKDKIEHKLQHHKTRFKPKOLEGLKPGTKVTVIRASGDRVPLVAVPAQDAALQQHQQOQQOQQOQQH : 708
Oran : -----LYCLKVFNKNAYQVHFVHRHOKSVYHCNKCRQLQFLFAKDKIEHKLQHHKTRFKPKOLEGLKPGTKVTVIRASGDRVPLVAVPAQDAALQQHQQOQQOQQOQQH : 691
Saha : -----LYCLKVFNKNAYQVHFVHRHOKSVYHCNKCRQLQFLFAKDKIEHKLQHHKTRFKPKOLEGLKPGTKVTVIRASGDRVPLVAVPAQDAALQQHQQOQQOQQOQQH : 765
Hosa : -----LYCLKVFNKNAYQVHFVHRHOKSVYHCNKCRQLQFLFAKDKIEHKLQHHKTRFKPKOLEGLKPGTKVTVIRASGDRVPLVAVPAQDAALQQHQQOQQOQQOQQH : 724

ZNF

Lach : -----LSQPAPSEIASFNIAIRNAANITVYKSDLLSNFOAKRTHGKRCLECSIDLEFNHFPTVYVCSLCRYSTCCSRAYANHMHNHVPKSPKYLALFKITASEVM : 871
Xela : -----TDSLALSYLSMOKRTVYKMSLSNHNRP-----HGRQCLECSIDLEFNHFPTVYVCSLCRYSTCCSRAYANHMHNHVPKSPKYLALFKITASEVM : 823
Povi : -----LSQAPSEIASFNIAIRNAANITVYKSDLLSNFOAKRTHGKRCLECSIDLEFNHFPTVYVCSLCRYSTCCSRAYANHMHNHVPKSPKYLALFKITASEVM : 813
Egga : -----LSQAPSEIASFNIAIRNAANITVYKSDLLSNFOAKRTHGKRCLECSIDLEFNHFPTVYVCSLCRYSTCCSRAYANHMHNHVPKSPKYLALFKITASEVM : 811
Oran : -----LSQAPSEIASFNIAIRNAANITVYKSDLLSNFOAKRTHGKRCLECSIDLEFNHFPTVYVCSLCRYSTCCSRAYANHMHNHVPKSPKYLALFKITASEVM : 794
Saha : -----LSQAPSEIASFNIAIRNAANITVYKSDLLSNFOAKRTHGKRCLECSIDLEFNHFPTVYVCSLCRYSTCCSRAYANHMHNHVPKSPKYLALFKITASEVM : 868
Hosa : -----LSQAPSEIASFNIAIRNAANITVYKSDLLSNFOAKRTHGKRCLECSIDLEFNHFPTVYVCSLCRYSTCCSRAYANHMHNHVPKSPKYLALFKITASEVM : 826

ZNF

Lach : -----CDFVTVLGDAMAKHLVFNPSHSSTSTPEKHNRYQSR---ERSQKVRSLNGSSKQMLDTVGVTAEE-----APESVKGLEKLSLY : 958
Xela : -----CDFVTVLGDAMAKHLVFNPSHSSTSTPEKHNRYQSR---ERSQKVRSLNGSSKQMLDTVGVTAEE-----APESVKGLEKLSLY : 902
Povi : -----CDFVTVLGDAMAKHLVFNPSHSSTSTPEKHNRYQSR---ERSQKVRSLNGSSKQMLDTVGVTAEE-----APESVKGLEKLSLY : 909
Egga : -----CDFVTVLGDAMAKHLVFNPSHSSTSTPEKHNRYQSR---ERSQKVRSLNGSSKQMLDTVGVTAEE-----APESVKGLEKLSLY : 903
Oran : -----CDFVTVLGDAMAKHLVFNPSHSSTSTPEKHNRYQSR---ERSQKVRSLNGSSKQMLDTVGVTAEE-----APESVKGLEKLSLY : 880
Saha : -----CDFVTVLGDAMAKHLVFNPSHSSTSTPEKHNRYQSR---ERSQKVRSLNGSSKQMLDTVGVTAEE-----APESVKGLEKLSLY : 978
Hosa : -----CDFVTVLGDAMAKHLVFNPSHSSTSTPEKHNRYQSR---ERSQKVRSLNGSSKQMLDTVGVTAEE-----APESVKGLEKLSLY : 944

ZNF

Lach : -----EENSFTGLDQTSSEQKGESETP-----VNNKQLSIRKLRVLFALCCVQAAEHFNQIRIRRWLRKCCSSDMEEESSSLKDGSRQAEAMMVEVNLQREQQPVNEETH : 1070
Xela : -----HTINVDELEKREBEVEVQEVKN-----KQQLSVKKLRVLFALCCVQAAEHFNQIRIRRWLRKCCSSDMEEESSSLKDGSRQAEAMMVEVNLQREQQPVNEETH : 1011
Povi : -----ECLNVDDQDEGPPAKVPPAG-----KQQLSVKKLRVLFALCCVQAAEHFNQIRIRRWLRKCCSSDMEEESSSLKDGSRQAEAMMVEVNLQREQQPVNEETH : 1017
Egga : -----ECLNVDDQDEGPPAKVPPAG-----KQQLSVKKLRVLFALCCVQAAEHFNQIRIRRWLRKCCSSDMEEESSSLKDGSRQAEAMMVEVNLQREQQPVNEETH : 1010
Oran : -----ECLNVDDQDEGPPAKVPPAG-----KQQLSVKKLRVLFALCCVQAAEHFNQIRIRRWLRKCCSSDMEEESSSLKDGSRQAEAMMVEVNLQREQQPVNEETH : 988
Saha : -----ECLNVDDQDEGPPAKVPPAG-----KQQLSVKKLRVLFALCCVQAAEHFNQIRIRRWLRKCCSSDMEEESSSLKDGSRQAEAMMVEVNLQREQQPVNEETH : 1090
Hosa : -----ECLNVDDQDEGPPAKVPPAG-----KQQLSVKKLRVLFALCCVQAAEHFNQIRIRRWLRKCCSSDMEEESSSLKDGSRQAEAMMVEVNLQREQQPVNEETH : 1057

Figure continued

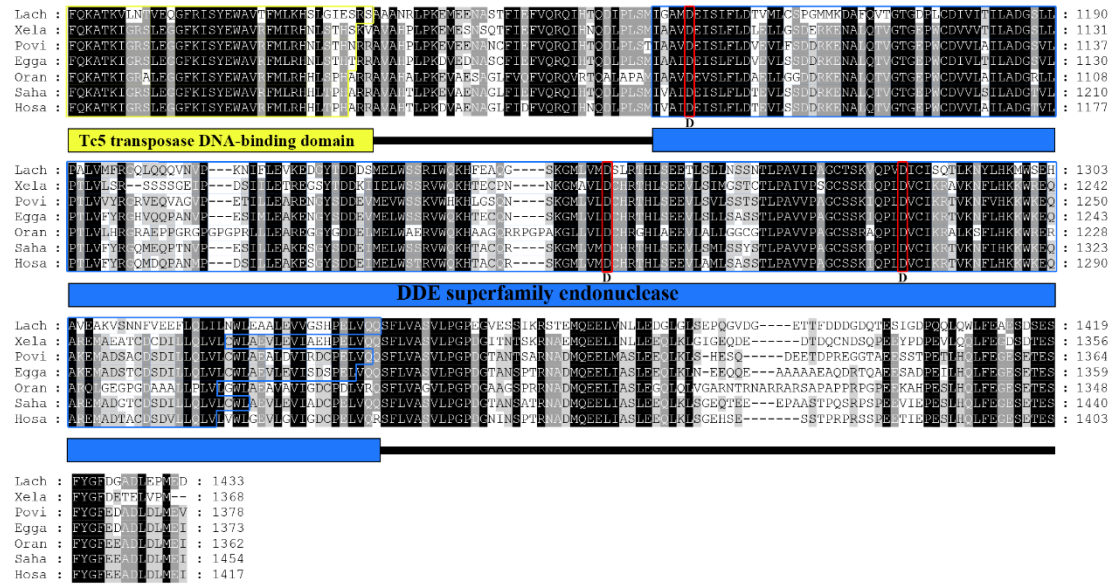


Figure S6C. Alignment of POGZ proteins. The Latin abbreviation of the species. Lach: Latimeria chalumnae; Xela: Xenopus laevis; Povi: Pogona vitticeps; Egga: Egretta garzetta; Oran: Ornithorhynchus anatinus; Saha: Sarcophilus harrisii; Hosa: Homo sapiens.

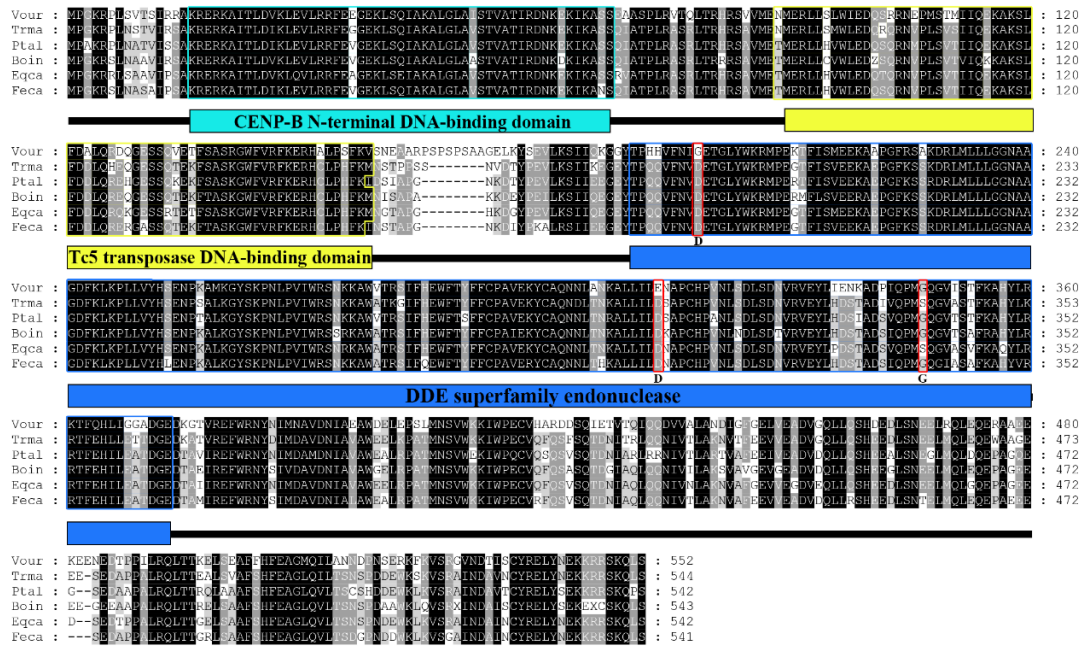


Figure S6D. Alignment of CENPBD1 proteins. The Latin abbreviation of the species. Your: *Vombatus ursinus*; Trma: *Trichechus manatus latirostris*; Ptal: *Pteropus alecto*; Boin: *Bos indicus*; Eqca: *Equus caballus*; Feca: *Felis catus*.

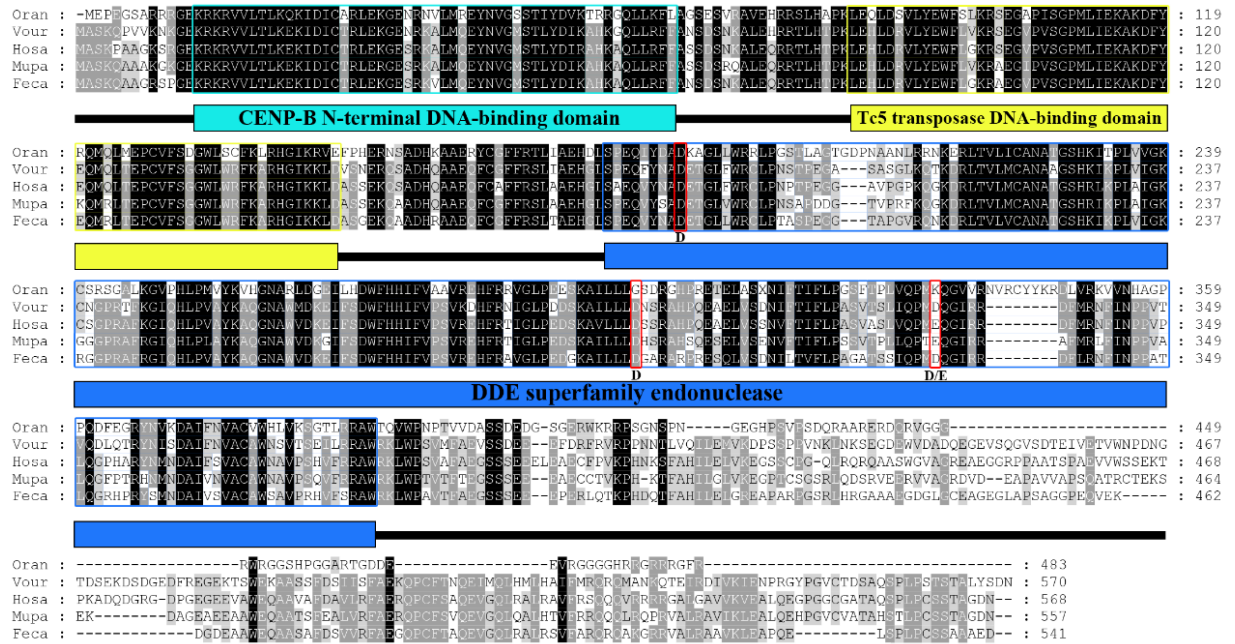


Figure S6E. Alignment of JRK proteins. The Latin abbreviation of the species. Oran: *Ornithorhynchus anatinus*; Vour: *Vombatus ursinus*; Hosa: *Homo sapiens*; Mupa: *Mus pahari*; Feca: *Felis catus*.

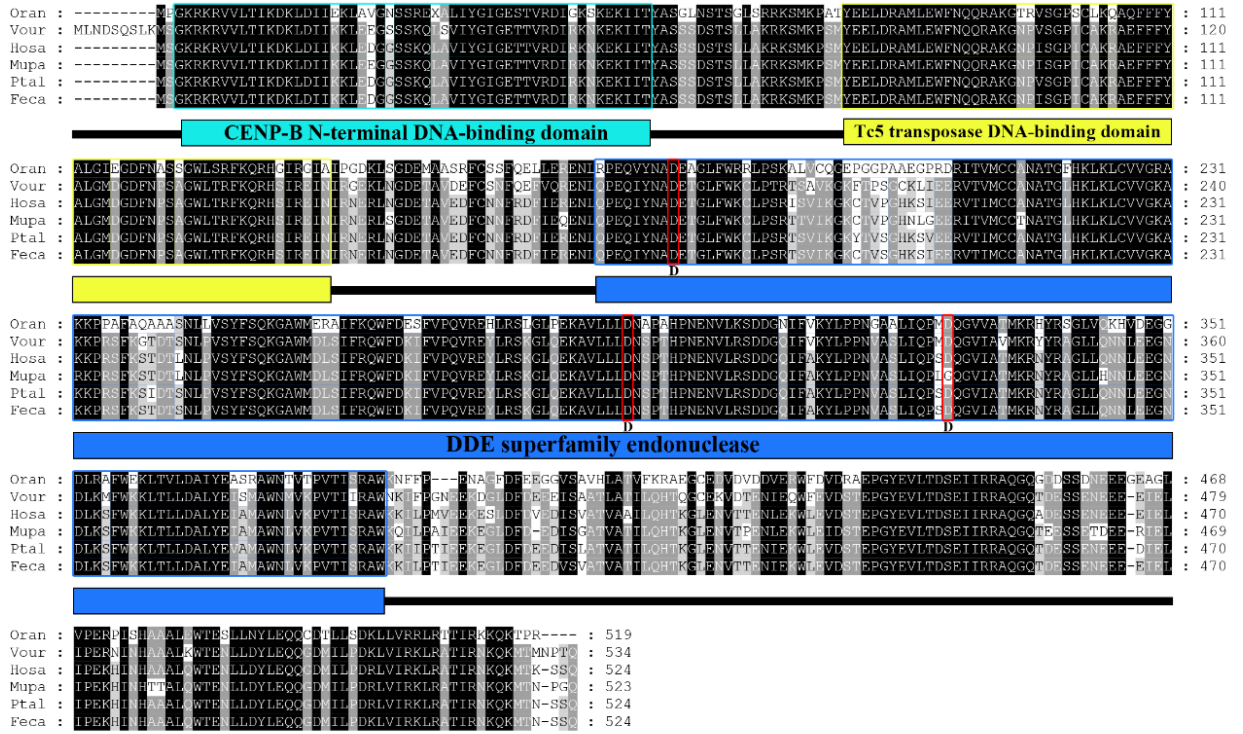


Figure S6F. Alignment of JRKL proteins. The Latin abbreviation of the species. Oran: *Ornithorhynchus anatinus*; Vour: *Vombatus ursinus*; Hosa: *Homo sapiens*; Mupa: *Mus pahari*; Ptal: *Pteropus alecto*; Feca: *Felis catus*.

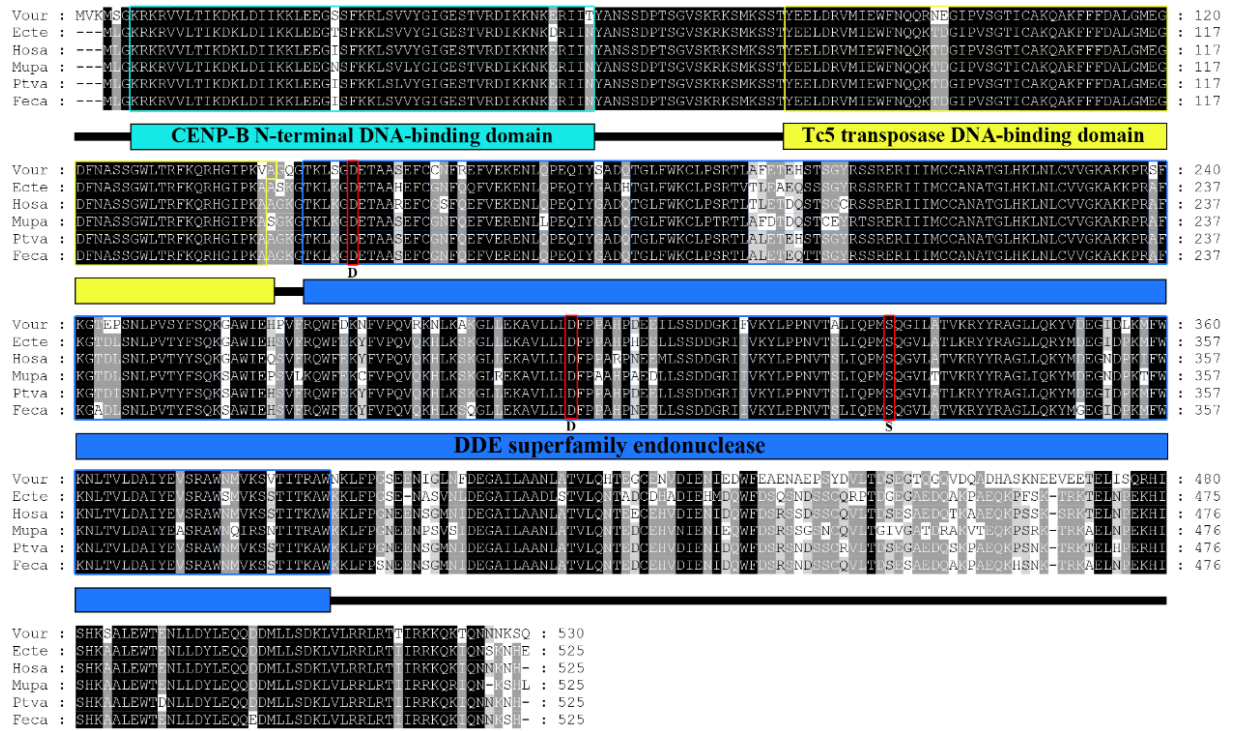


Figure S6G. Alignment of TIGD2 proteins. The Latin abbreviation of the species. Your: Vombatus ursinus; Ecte: Echinops telfairi; Hosa: Homo sapiens; Mupa: Mus pahari; Ptva :Pteropus vampyrus; Feca: Felis catus.

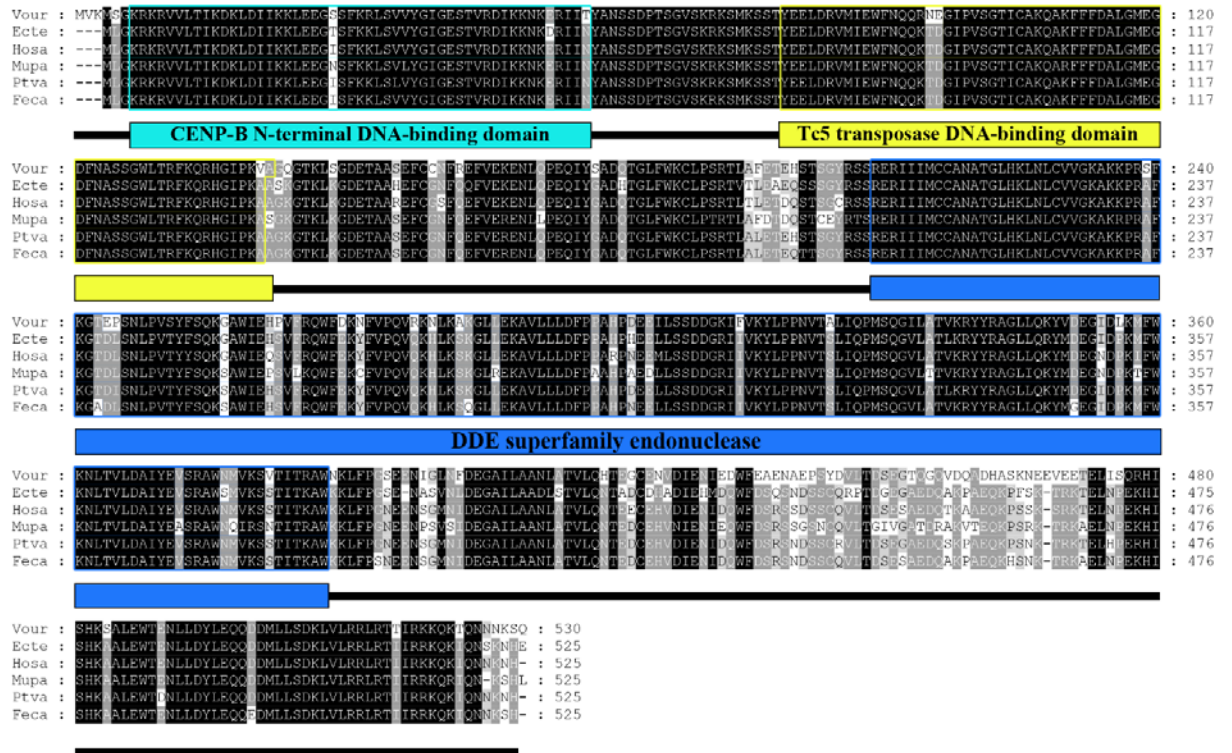


Figure S6H. Alignment of TIGD3 proteins. The Latin abbreviation of the species. Vour: Vombatus ursinus; Ecte: Echinops telfairi ; Hosa: Homo sapiens; Mupa: Mus pahari; Ptva Pteropus vampyrus; Feca: Felis catus.

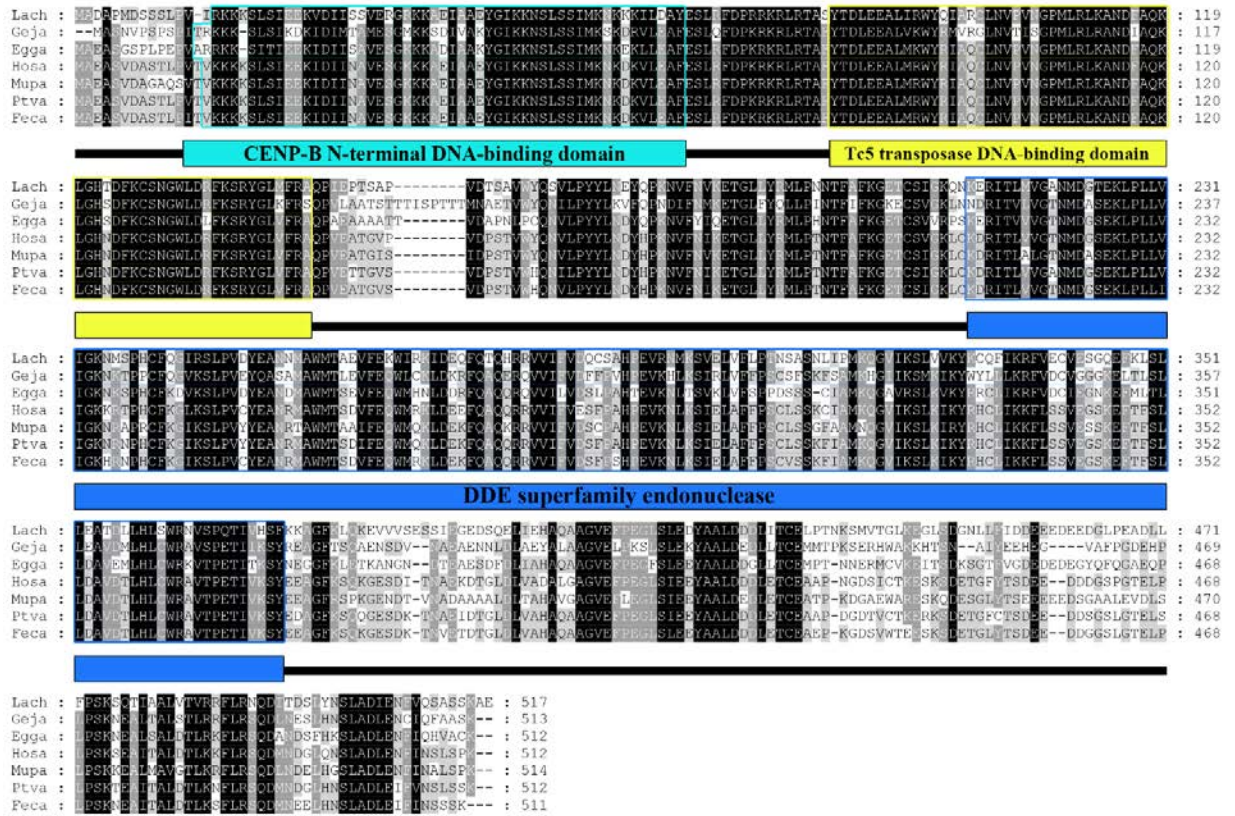


Figure S6I. Alignment of TIGD4 proteins. The Latin abbreviation of the species. Lach: Latimeria chalumnae; Geja: Gekko japonicus; Egga: Egretta garzetta ; Hosa: Homo sapiens; Mupa: Mus pahari; Ptva: Pteropus vampyrus; Feca: Felis catus.

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Xela : -----MVRMAFRRKAYSIKDKLRAIERVKNQEROATVSRDFGVPGGTLR : 43
Geja : -----MAERRAYSIKDKLRAIQRVKSERQASVSRDFGVPGGTLR : 40
Oran : MHPAASSPSSCRPLLQPPPILEGPEEEEEERSSMGAERTRPPSALPG-PAGVGASGVTTTPGSLSPSGLPPSGSTPCMAARMAERRAYSIKDKLRAIERVKGGERQASVSRDFGVPGGTLR : 119
Vour : -----MAERRAYSIKDKLRAIERVKGGERQASVSRDFGVPGGTLR : 40
Hosa : MYPAG-----PPAGVPRRRGRRLPG-----PPAPAPVPAARPPP-PAGPRPRVAVRMAERRAYSIKDKLRAIERVKGGERQASVSRDFGVPGGTLR : 89
Feca : MYPAG-----PPTGPAPRRGRHPLGRPAQLRLPAFTPAPAVRPPP-PAGPRPRVAVRMAERRAYSIKDKLRAIERVKGGERQASVSRDFGVPGGTLR : 94

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CENP-B N-terminal DNA-binding domain

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Xela : GWLKDEPKLWFLQLGSDGTHHKMLANEEIDRAVSWFLTRQOOSIPLSGPIIQAEAFARQIYGRCTFKASHGWRRWOKRHGISSGRYYEAEPLAAGPAPGPPVWKEPAL : 160
Geja : GWLKDEPKLWFLQLGSDGTHSNKYCLANEEIDRAVSWFLTRRHGIIPLSGPIIQAEAFARQIYGRCTFKASHGWRRWOKRHGISSGRYYRETGDGCVGTVGNSEALKKATES : 160
Oran : GWLKDEPKLWFLQLGSDGTHHKMLANEEIDRAVSWFLTRRHGIIPLSGPIIQAEAFARQIYGRCTFKASHGWRRWOKRHGISSGRYYEAEPLAAGPAPGPPVWKEPAL : 236
Vour : GWLKDEPKLWFLQLGSDGTHHKMLANEEIDRAVSWFLTRRHGIIPLSGPIIQAEAFARQIYGRCTFKASHGWRRWOKRHGISSGRYYEAEPLAAGPAPGPPVWKEPAL : 160
Hosa : GWLKDEPKLWFLQLGSDGTHHKMLANEEIDRAVSWFLTRRHGIIPLSGPIIQAEAFARQIYGRCTFKASHGWRRWOKRHGISSGRYYEAEPLAAGPAPGPPVWKEPAL : 209
Feca : GWLKDEPKLWFLQLGSDGTHHKMLANEEIDRAVSWFLTRRHGIIPLSGPIIQAEAFARQIYGRCTFKASHGWRRWOKRHGISSGRYYEAEPLAAGPAPGPPVWKEPAL : 214

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Tc5 transposase DNA-binding domain

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Xela : AK-----TVVADSGYGEQIYENITLYWKLLDTRDMILAKQPD-----YTHKDRVIVLLAANLTGSHKLPVLVVGKIDPPSLRHNQKIPASYYPDAHLAR : 261
Geja : VLISSAFSDLPSPDPTN-----SDRSGYHVEQIYTSIHLIYWKLLDQVRAIRTCIRSQPP-AHSQPRVKDRVVLLAANLTGSHKLPVLVVGEEARWHRHREKIPVGYGACAHLESP : 279
Oran : AG-----PEPAAAGYGEQIYENITLYWKLLDQVRAIRTCIRSQPP-AHSQPRVKDRVVLLAANLTGSHKLPVLVVGKIDPPSLRHNQKIPASYYPDAHLAR : 343
Vour : PDLVIGDHPSPM-PPPTTDCYGEQIYENITLYWKLLDQVRAIRTCIRSQPP-AHSQPRVKDRVVLLAANLTGSHKLPVLVVGKIDPPSLRHNQKIPASYYPDAHLAR : 275
Hosa : PSG--AGPLDRAPAPPDAEAGYGEQIYENITLYWKLLDQVRAIRTCIRSQPP-AHSQPRVKDRVVLLAANLTGSHKLPVLVVGKIDPPSLRHNQKIPASYYPDAHLAR : 325
Feca : PPGSSSGPLERAPAPPDAEAGYGEQIYENITLYWKLLDQVRAIRTCIRSQPP-AHSQPRVKDRVVLLAANLTGSHKLPVLVVGKIDPPSLRHNQKIPASYYPDAHLAR : 332

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Xela : ELLRQWFEFEVPEVVRVYLRSSLQQKAVLLVNHHPGPRP-----DLDLTPDQENIRLFLSES-----TNKTHSMDQGVTSFFKQ : 338
Geja : ALLCWLFEFEVPEVVRVYLRSSLQQKAVLLVNHHPGPRP-----GSGDLPLATDSDIRALFLSKMARDSPGGGGHSAIHLWQGMVSEFKQ : 368
Oran : ALLRQWFEFEVPEVVRVYLRSSLQQKAVLLVNHHPGPRP-PRPSPGAEGRRAARRRPGPRVVGAGPGEFGTCTPPELRITDCAVRLVFLSGSG-----TGGGLPAIILQGVVSEFKQ : 457
Vour : TLLRQWFEFEVPEVVRVYLRSSLQQKAVLLVNHHPGPRPDPDRPSP-ECEGEAGKRO---RTAGGLGPGPAVCHPSELATDCAVRLVFLSKSS-----AGKIPAILQGVVSEFKQ : 386
Hosa : PLLRQWFEFEVPEVVRVYLRSSLQQKAVLLVNHHPGPRP-ASMPALD-SEDEVRCR-----PEP-LGPPSELATDCAVRLVFLSKGS-----SAHLPAILQGVVSEFKQ : 427
Feca : PLLRQWFEFEVPEVVRVYLRSSLQQKAVLLVNHHPGPRP-ARTPALEENEALRRCR-----PEP-LSSPELATDCAVRLVFLSKGS-----SAHLPAILQGVVSEFKQ : 435

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DDE superfamily endonuclease

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Xela : LYKRELLKMYSDS-LSLSEVYTSRUKDMYLAQCSNHWIQGSIKRWLYLRLAEFTNASAE-----TDEEYYSKFADELSVAAYKQLLEEDIERVHLDDSIP- : 442
Geja : VYKRELLRLALALAEERNSEES-----LQCLTST-----RLDFSHNE-----KDMNLEFESDILPACTEKCSLAYG---- : 434
Oran : LYKRELLRLAVSAGSSPLDQVRSMLKDMYLAQCSNHWIQGSIKRWLYLRLAEFTNASAE-----PREPDE-RKPRAHPGAPGEDEARHGEVGGDLRRLAATERLAPDVEVHLHDDGAGG : 576
Vour : LYKRELLRLAVSAGSSPLDQVRSMLKDMYLAQCSNHWIQGSIKRWLYLRLAEFTNASAE-----PREPDEERLVQPHPGASGEDEAEHHSKVSDDLHRLAAYKRLAPDVEVHLHDDGAGG : 506
Hosa : LYKRELLRLAVSAGSSPLDQVRSMLKDMYLAQCSNHWIQGSIKRWLYLRLAEFTNASAE-----SAGQPA-QAEAAHRSRVSDDLHRLAAYKRLAPDVEVHLHDDGAGG : 537
Feca : LYKRELLRLAVSAGSSPLDQVRSMLKDMYLAQCSNHWIQGSIKRWLYLRLAEFTNASAE-----CVGQPAGQAEAAHRSRVSDDLHRLAAYKRLAPDVEVHLHDDGAGG : 546

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Xela : VIDITDG-----SVCTFLVPGDSSGDIIVSVDKGG-----PVPSSAFAHLEKRLALWDEAQDIQKSLILVQLRSLITLQFQAQLQSKPTDCTGSP : 534
Geja : -----QPPSLAERRKN----- : 446
Oran : LGEPLGEGEERPERPKHGM--AAATLPPVGPAGREFAAGMRIPVPTAGEARLEALWDEAQDIQKSLILVQLRSLITLQFQAQLQSKPTDCTGSP : 674
Vour : LGEPLGEGEEDDEDG---GGREQP---SCGGFPLAGPPQGEAGTGGSPVPTAGEARLEALWDEAQDIQKSLILVQLRSLITLQFQAQLQSKPTDCTGSP : 601
Hosa : DGGPPEGCREEVG---PALPPAAPASLPSAMGGGEDEATDYGCTSPVPTAGEARLEALWDEAQDIQKSLILVQLRSLITLQFQAQLQSKPTDCTGSP : 642
Feca : DGGPPEGCREEVG---PALPPAAPASLPSAMGGGEDEA-----AVPTAGEARLEALWDEAQDIQKSLILVQLRSLITLQFQAQLQSKPTDCTGSP : 649

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Figure S6J. Alignment of TIGD5 proteins. The Latin abbreviation of the species. Xela: *Xenopus laevis*; Geja: *Gekko japonicus*; Oran: *Ornithorhynchus anatinus*; Vour: *Vombatus ursinus*; Hosa: *Homo sapiens*; Feca: *Felis catus*.

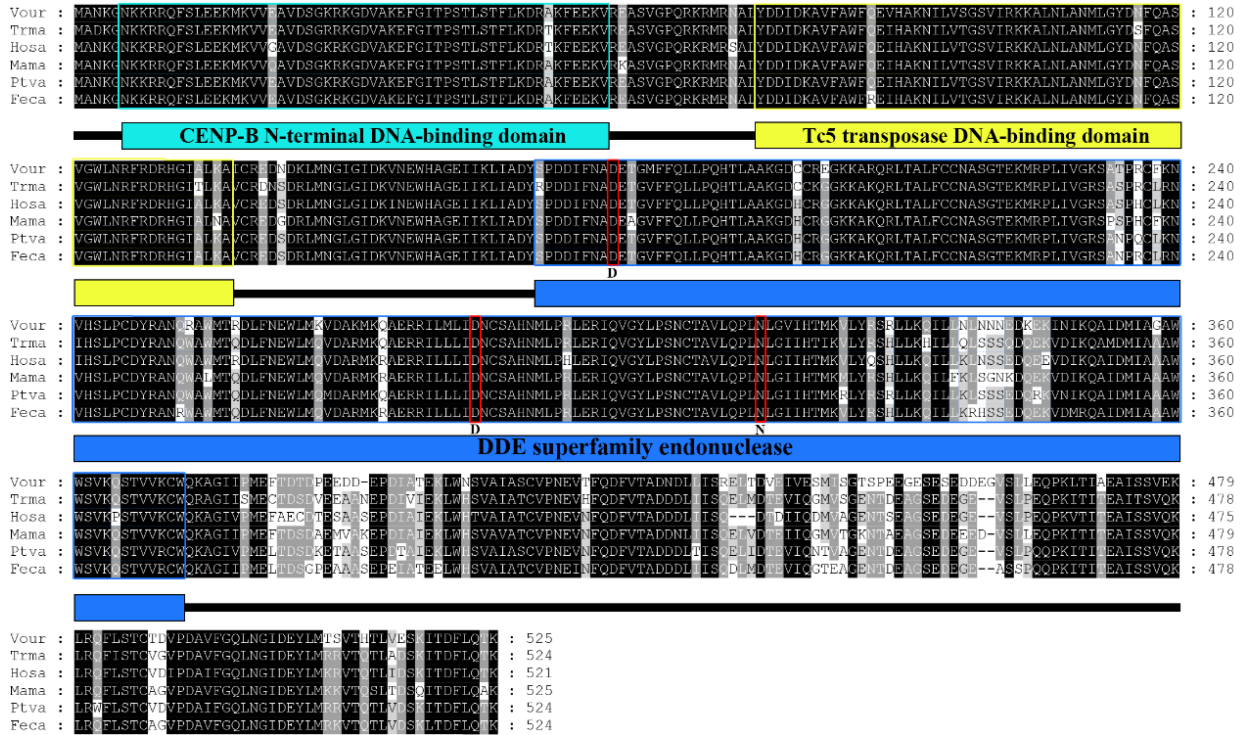


Figure S6K. Alignment of TIGD6 proteins. The Latin abbreviation of the species. Vour: Vombatus ursinus; Trma: Trichechus manatus latirostris; Hosa: Homo sapiens; Mama: Marmota marmota marmota; Ptva: Pteropus vampyrus; Feca: Felis catus.

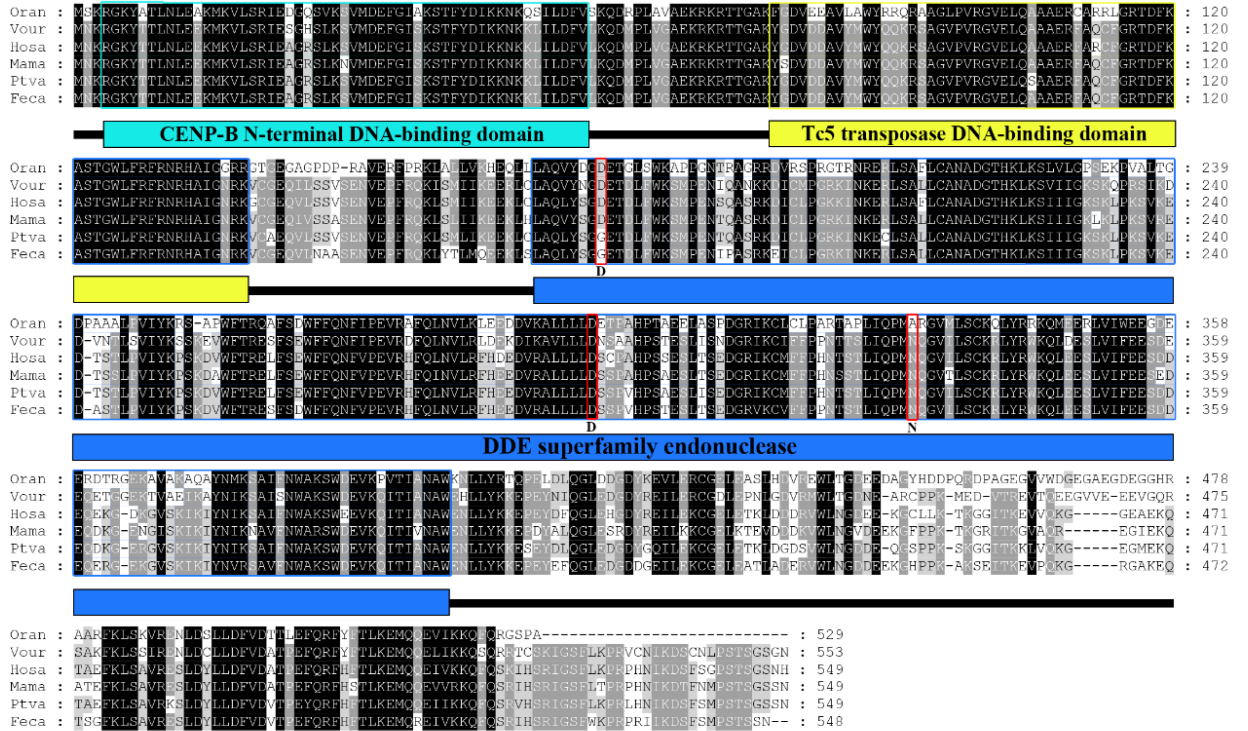


Figure S6L. Alignment of TIGD7 proteins. The Latin abbreviation of the species. Oran: Ornithorhynchus anatinus; Vour: Vombatus ursinus; Hosa: Homo sapiens; Mama: Marmota marmota marmota; Ptva: Pteropus vampyrus; Feca: Felis catus.