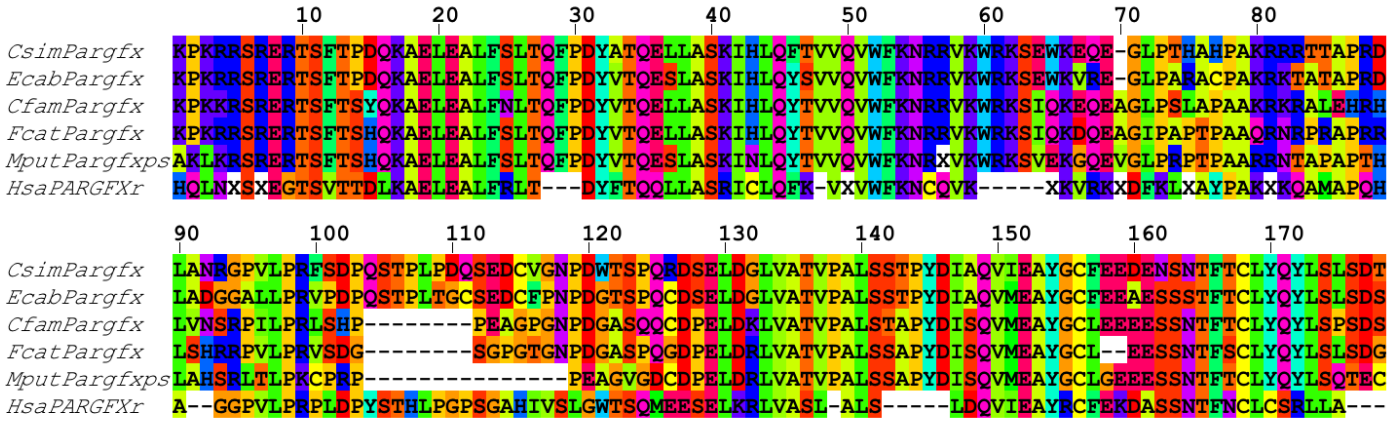
A



B

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HsapOTX2     GGQNKVRPAKKK--TSPAREVSSES-------GTSGQ-FTPPSSTSV--------PTIASSS----------APVSIWSPASISPLSDPLS
MdomCrx      GGTSKARPAKKK--CVSPPRGGAEPGPE--PPG-------PYSPAPA--------PSATPPS----------ASVSIWSP-GLSPLSDP--
BtauCrx      GAQAKARPAKRK--AGTSPRSSTDVCPD--PLGISDS-YSPPLPGPS--------GSPTTAV----------ATVSIWSPASESPLPEA--
LafrCrx      GGSSKARPAKRK--AGTSPRASTDTCPD--PLGISDS-YSPPLPGPS--------ASPTTAV----------ATVSIWSPASESPLPEA--
HsapCRX      GGQAKARPAKRK--AGTSPRPSTDVCPD--PLGISDS-YSPPLPGPS--------GSPTTAV----------ATVSIWSPASESPLPEA--
CfamPargfx   GLPSLAPAAKRK--RALEHRHLVNSRPI--LPRLSHP-PEAGPG----------NPDGASQQCDP--
FcatPargfx   GIPAPTPAAQRN--RPRAPRRLSHRRPV--LPRVSDG-SGPGTG----------NPDGASPQGDP--
EcabPargfx   GLPARACPAKRK--TATAPRDLADGGAL--LPRVPDPQSTPLTGC----------SEDCFPNPDGTSPQCDS--
BtauArgfx    KPPSQVLPA-KD--V---PTVSTSPHSF--LLAISDS-YNSLSPQPL--------DTFPWAG----------DSMIMEIPTSDVQTQDP--
SscrArgfx    KPPNQTLLA-KK--T---PTASTSPHSF--FPEVSDS-SIFLSTRPL--------GPFQCAG----------NSTITESPTSDVQMQDP--
EcabArgfx    KQQNQILPA-KT--VPNSPTASSSPCSFV-XPAVSDF-CSSFXTSAL--------RPFPWAW----------DSIITESPTRDVQMQDL--
SaraArgfx    KMSKKKLLN-NK--LPNLPQQPTNAHTS--YPAVSDF-CSSSHTHPL--------GPSNCTQ----------DSIMTLSLPSDIQMPDT--
HsapARGFX    KQRNQILPSKKN--VPTSPRTSPSPYAF--SPVISDF-YSSLPSQPL--------DPSNWAW----------NSTFTESSTSDFQMQDT--
HsapLEUTX    GPANQTTSVKKE--ETPSAITTANIRPV--SPGISDA-NDHDLREPS--------GIKNPGG----------ASASARVSSWDSQSYDI--
FcatLeutx    KSPNQTISIKEE--QPPLPVTSANTHPG--SPSILDA-CDHELPQSP--------DSVQSAG----------AGPSKWNSSWDSPPYDL--
EcabLeutx    GGPNQTTSAKEE--EAPLPVTSAATHLT--SPAVSDD-CGHEPPKPS--------GIEQPGG----------AGASVWN-SWDPQLQNL--
LafrLeutxA   EEPNHVAPVKKE--EMPLPITDANPGPV--SARSLDA-SEPDPPEPP--------GAGQPGG----------AGACVWNSSWDSHTHDA--
PcapLeutx1   EDLGQVVPVEEEEKETPLLTTDANALP---VGTRSYA-CKPCPPQQH--------ESGKPAG----------AGACVWNSSRDSETHDV--
ChofLeutx    EAPNQTVSVEKE--ETPLATTASRSSL---SPGISDA-RGPVPSEYP--------GTEQLNG----------AGASACISSWDSQPYDR--
DnovLeutx    EAPTKTVSVKEE--ETPLAITDAQSPP---SPGISDP-RNPETPEGS--------GSEHPKG----------AGASAENSSWNSRPCDL--

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HsapOTX1     VSVPEPLAAPSNTSCMQRS--VAAGAATAAASYPMSYGQG----GSYGQGYP------TP-SSSYFGGV-DCSSYLAPM
HsapOTX2     ----------TSSSCMQR-------------SYPMTYTQA----SGYSQGYA------G--STSYFGGM-DCGSYLTPM
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BtauCrx      ----------------QRAGLVASGPSLTSAPYAMTYAPA-SAFCSSPSAYG------S--PSSYFSGL---DPYLSPM
LafrCrx      ----------------QRAGLVASGPALTSAPYAMTYAPA-SAFCSSPSAYG------S--PSSYFSGL---DPYLSPM
HsapCRX      ----------------QRAGLVASGPSLTSAPYAMTYAPA-SAFCSSPSAYG------S--PSSYFSGL---DPYLSPM
CfamPargfx   ----------------ELDKLVATVPALSTAPYDISQVME--AYGCLEEEE----------SSNTFTCL---YQYLSPS
FcatPargfx   ----------------ELDRLVATVPALSSAPYDISQVME--AYGCLEE-----------SSNTFSCL---YQYLSLS
EcabPargfx   ----------------ELDGLVATVPALSSTPYDIAQVME--AYGCFEEAE----------SSSTFTCL---YQYLSLS
BtauArgfx    ----------------QLERLVASVPALYSDAFDITQIME--LYSVPDEDD---------ITNSSFYSL---YQYLSPT
SscrArgfx    ----------------QLERLVASVPALYSDAYDIDQIMK--LYSFPDDNE---------LDSSSFHSL---YQYLSPI
EcabArgfx    ----------------QLERLVASVPALYSDAYDIAQIMK--LYSFPDEDE---------ISSSSFQYL---YWYLSPT
SaraArgfx    ----------------QLESLEATVPALFPDSYDITQIME--LYSFPDE-E---------LTSSSFECL---YQYLSPQ
HsapARGFX    ----------------QWERLVASVPALYSDAYDIFQIIE--LYNLPDENE---------ISSSSFHCL---YQYLSPT
HsapLEUTX    ----------------EQICLGASNPPWASTLFEIDEFVK--IYDLPGEDD----------TSS----L---NQYLFPV
FcatLeutx    ----------------QQICLGDPDPPWASIPYDIDQLIQ--LYALPGDDD----------------L---DQYLSPV
EcabLeutx    ----------------QQICLGVSDPPWASVPTDMDEFIQ--LYALPGDDD----------PSS----L---DEYLFPK
LafrLeutxA   ----------------QEINLDILDPPWATIPCDIDEFVE--LYALPGDDD----------PSS----L---DQYLLPR
PcapLeutx1   ----------------LEINLDVLSPPWAAAPCDIEEFVE--LYALPGDDD----------PSS----L---DQYLSPK
ChofLeutx    ----------------QEIFLGSSYPPWASILCDIDQFVE--LYALPGEDD----------PSN----F---DQYLFPK
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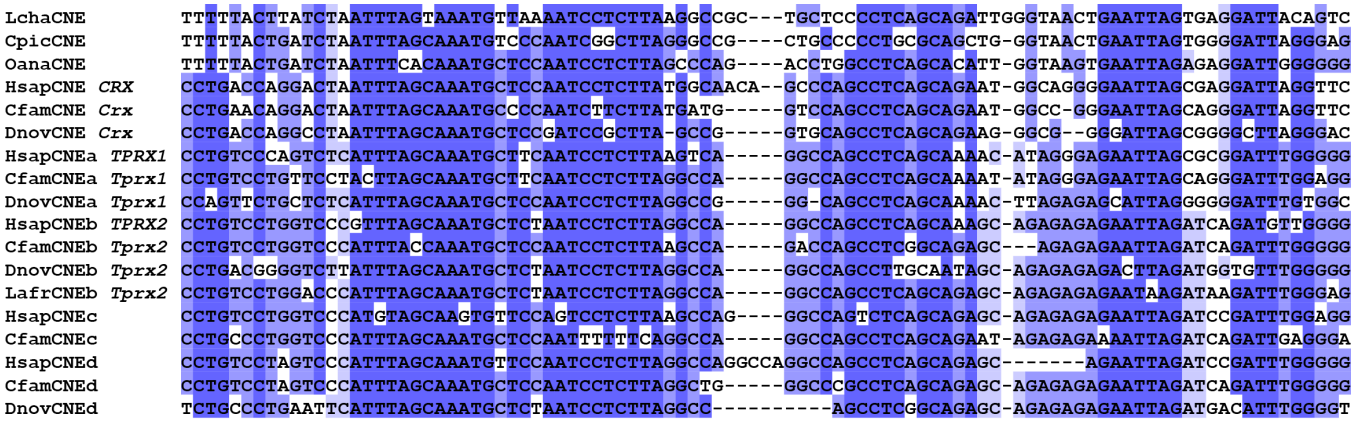
C



D

Human ARGFX coding sequence

Exon 1 (excluding 5’ untranslated region)
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GGATCCAGCTAGTCCCA

Exon 2 (lower case is part of Alu element)
gtttcactctgttatccaagctggagtgcagtggcacggtctcggcttactgcagcctcaacctcccaggttcaactgatcctccc
acctcagcctcccgagtagctgcgactacag

Exon 3
CAATACGGAGAAGGCATAAAGAACGTACTTCTTTCACCCACCAACAGTATGAGGAGCTAGAAGCTCTGTTTAGCCAGACCATGTTC
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Exon 4 (excluding 3’ untranslated region)
GTTTGGTTCAGGAACCGGCGATTCAAATTGAAGAAGCAGCAGCAGCAGCAATCAGCAAAGCAACGAAACCAGATCCTTCCATCCAA
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Human DPRX coding sequence

Exon 1 (excluding 5’ untranslated region)
ATGCCAGGCTCAGAGGATCTTCGTAAAG

Exon 2
GCAAGGACCAGATGCATTCACACAGGAAACGAACCATGTTCACTAAGAAGCAACTGGAAGATCTGAACATCTTGTTCAATGAGAAC
CCATACCCAAACCCCAGCCTTCAGAAAGAAATGGCCTCGAAAATAGACATACACCCAACAGTACTGCAG

Exon 3 (excluding 3’ untranslated region)

GTCTGGTTCAAGAATCACAGAGCAAAACTCAAGAAAGCGAAATGCAAGCATATTCATCAAAAACAAGAAACTCCACAACCGCCAAT
ACCAGAGGGTGGGGTCTCCACCAGTGTCGGCCTGAGAAATGCAGACACACTACCCAGATTGCCCAACGCTGCTCACCCGATCGGCC
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CCATTCTGGCTCTCCTGCCTGTTCATCTAACCAAAGTCGAGAGAGATGA

Human LEUTX coding sequence

Exon 1 (excluding 5′ untranslated region)
ATGTTTG

Exon 2
AAGGGCCAAGGCGTTATCGTCGGCCACGCACAAGATTTCTCTCCAAACAACTCACAGCATTGAGAGAATTGCTTGAAAAGACCATG
CACCCAAGTTTGGCTACAATGGGGAAACTGGCTTCAAAGCTACAACTTGATCTATCCGTAGTAAAG

Exon 3 (excluding 3′ untranslated region)
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GACAACTTCAGTGAAGAAGGAGGAGACTCCCTCAGCCATAACTACTGCAAACATTCGTCCAGTAAGTCCTGGAATCTCTGATGCAA
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CAGTGTAA

Human TPRX1 coding sequence

Exon 1 (excluding 5′ untranslated region)
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Exon 2
GCCCTCCCCTGGCCCTGGACCCTCCAAGGAGACAGCGGCAGGAGCGCACGGTCTACACTGAAAGCCAGCAGAAAGTGCTAGAATTT
TACTTTCAGAAGGACCAGTACCCGAACTACGACCAGCGACTGAATCTGGCGGAGATGCTCAGCCTCAGGGAGCAACAGCTGCAG

Exon 3 (excluding 3′ untranslated region)
GTGTGGTTCAAGAATCGCCGCGCCAAACTAGCTCGGGAGCGGCGGCTCCAGCAGCAGCCCCAGCGCGTCCCTGGGCAGAGAGGCCG
AGGAGCCCGCGCTGCGCCCCTAGTCCCTGCAGCCTCTGCCTCCGCACCTCAGCGGGGCCCCTCGGGAATCCTTCCAGCGGCGGAAC
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CAAAAAACACTCAGGGTCTCAGCCCCAAGAGGAGGGTGGCTCTGTGAATGAAAATCACTCAGGCCCCAGGTTATTACTGGATTTAT
AG

Human TPRX2 coding sequence

Exon 1 (excluding 5′ untranslated region)
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Exon 2
GCCCTCCCCTGGCCCTGGACCCTCCAAGGAGACAGCGGCAGGAGCGCACGGTCTACACTGAAAGCCAGCAGAAAGTGCTAGAATTT
TACTTTCAGAAGGACCAGTACCCGAACTACGACCAGCGACTGAATCTGGCGGAGATGCTCAGCCTCAGGGAGCAACAGCTGCAG

Exon 3 (excluding 3’ untranslated region)
GTGTGGTTCAAGAATCGCCGCGCCAAACTAGCTCGGGAGCGGCGGCTCCAGCAGCAGCCCCAGCGCGTCCCTGGGCAGAGAGGCCG
AGGAGCCCGCGCTGCGCCCCTAGTCCCTGTAGCCGCTGCCTCCTTCCCTGGGGGTCCTGAGTTCCCGCAGGGCAGGGGTTCCTGGA
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