The Genetics of Cranial Sensory Ganglia Development and Evolution

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Hillary 2020

Supplementary Appendix

S1) Sequences identified or used in this study

S1.1) Transcripts mapping to new identified lamprey loci

Transcripts retrieved from different lamprey transcriptomes as detailed in chapter 2 and corresponding to lamprey loci in the japanese lamprey (*Lethenteron camtschaticum*) genome assembly (Mehta et al., 2013) presented in chapter 3.

DRGX

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HMXB

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S1.2) Gene fragments / In situ probes

S1.2a) Lamprey Sequences

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S1.4) NCBI Derived Sequence IDs

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	ERR_Branchiostoma	AAU88062
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PITX1_Homo_sapiens	NP_002644.4
PITX1_Xenopus_tropicalis	NP_001007500.1
PRRX1_Gallus_gallus	NP_001264653.1
PRRX1_Homo_sapiens	NP_008833.1
PRRX1_Xenopus_tropicalis	XP_004913839.1
PRRX1a_Danio_rerio	NP_999899.1
PRRX1b_Danio_rerio	XP_005160700.1
SHOX1_Anolis_carolinensis	XP_016847844.1
SHOX1_Callorhinchus_milii	XP_007889486.1
SHOX1_Danio_rerio	NP_001119883.1
SHOX1_Gallus_gallus	NP_001073192.1
SHOX1_Homo_sapiens	NP_000442.1
SHOX1_Xenopus_tropicalis	XP_002937019.2
SHOX2_Anolis_carolinensis	XP_008104403.1
SHOX2_Callorhinchus_milii	XP_007886592.1
SHOX2_Danio_rerio	XP_021337040.1
SHOX2_Gallus_gallus	XP_015147272.2
SHOX2_Homo_sapiens	NP_006874.1
SHOX2_Xenopus_laevis	XP_018119245.1
UNCX_Danio_rerio	XP_005164261.1
UNCX_Gallus_gallus	XP_015149815.1

	UNCX_Homo_sapiens	NP_001073930.1
	UNCX_Xenopus_tropicalis	NP_001305673.1
HMX	HMX3_Gallus_gallus	NP_001007986.1
	HMX3_Mus_musculus	NP_032283.3
	HMX3_Thamnophis_sirtalis	XP_013918275.1
	HMX3_Xenopus_tropicalis	NP_001072829.1
	HMX3_Homo_sapiens	NP_001099044.1
	HMX3_Danio_rerio	NP_571709.2
	HMX2_Anolis_carolinensis	XP_003218649.1
	HMX2_Danio_rerio	NP_001108570.3
	HMX2_Homo_sapiens	NP_005510.1
	HMX2_Mus_musculus	NP_001355289.1
	HMX2_Xenopus_tropicalis	XP_002937849.1
	HMX2_like_Callorhinchus_milii	XP_007889664.1
	HMX1_Callorhinchus_milii	XP_007889718.1
	HMX1_Danio_rerio	NP_001106998.1
	HMX1_Gallus_gallus	NP_990864.2
	HMX1_Homo_sapiens	NP_061815.2
	HMX1_Mus_musculus	NP_034575.1
	HMX1_Thamnophis_sirtalis	XP_013926293.1
	HMX3_A_like_Callorhinchus_milii	XP_007902123.1
	SOHO_Danio_rerio	NP_001038836.2
	SOHO_Gallus_gallus	NP_990717.1
	SOHO_Xenopus_tropicalis	XP_002940265.1
	HMX2_Gallus_gallus	XP_025007794.1
	HMX1_Xenopus_tropicalis	XP_002940264.3
CSAD	csad_Anolis_carolinensis	XP_003216712.1
	csad_Callorhinchus_milii	XP_007908691.1
	csad_Chrysemys_picta_bellii	XP_008167751.1
	csad_Danio_rerio	XP_009295318.1
	csad_Gallus_gallus	XP_025001258.1
	csad_Homo_sapiens	NP_057073.4
	csad_Mus_musculus	NP_001346055.1
	csad_Xenopus_tropicalis	XP_017947211.1
GAD	GAD1_Anolis_carolinensis	XP_016852168.1
	GAD1_Callorhinchus_milii	XP_007888154.1
	GAD1_Chrysemys_picta_bellii	XP_005290495.1
	GAD1_Danio_rerio	NP_919400.1
	GAD1_Gallus_gallus	NP_990244.1
	GAD1_Homo_sapiens	NP_000808.2

	GAD1_Mus_musculus	NP_032103.2
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	GAD2_Callorhinchus_milii	XP_007899367.1
	GAD2_Chrysemys_picta_bellii	XP_008161255.2
	GAD2_Danio_rerio	NP_001017708.2
	GAD2_Gallus_gallus	XP_015137540.1
	GAD2_Homo_sapiens	NP_000809.1
	GAD2_Mus_musculus	NP_032104.2
HDC	hdc_Anolis_carolinensis	XP_003228927.2
	hdc_Chrysemys_picta_bellii	XP_005307312.1
	hdc_Danio_rerio	NP_001096063.1
	hdc_Gallus_gallus	NP_001280217.1
	hdc_Homo_sapiens	NP_002103.2
	hdc_Mus_musculus	NP_032256.3
	hdc_Xenopus_tropicalis	XP_017947930.2
PRDM	PRDM1_Anolis_carolinensis	XP_008118908.1
	PRDM1_Callorhinchus_milii	XP_007897304.1
	PRDM1_Chrysemys_picta_bellii	XP_005287756.1
	PRDM1_Danio_rerio	NP_955809.2
	PRDM1_Gallus_gallus	XP_004940410.1
	PRDM1_Homo_sapiens	XP_011534365.1
	PRDM1_Mus_musculus	XP_006512566.1
	PRDM1_Xenopus_tropicalis	XP_002937203.1
	PRDM12_Chrysemys_picta_bellii	XP_005293390.1
	PRDM12_Danio_rerio	XP_005171781.2
	PRDM12_Gallus_gallus	XP_005055625.1
	PRDM12_Homo_sapiens	NP_067632.2
	PRDM12_Mus_musculus	NP_001116834.1
	PRDM12_Xenopus_tropicalis	NP_001072898.1
	PRDM13_Anolis_carolinensis	XP_008117566.1
	PRDM13_Callorhinchus_milii	XP_007891148.1
	PRDM13_Chrysemys_picta_bellii	XP_023958257.1
	PRDM13_Danio_rerio	NP_001313383.1
	PRDM13_Gallus_gallus	XP_025004996.1
	PRDM13_Homo_sapiens	NP_067633.2
	PRDM13_Mus_musculus	NP_001074240.1
	PRDM13_Xenopus_tropicalis	XP_002932206.1
	PRDM14_Anolis_carolinensis	XP_008106773.1
	PRDM14_Chrysemys_picta_bellii	XP_005309855.1
	PRDM14_Danio_rerio	NP_001157303.1

PRDM14_Homo_sapiens	NP_078780.1
PRDM14_Mus_musculus	NP_001074678.2
PRDM14_Xenopus_tropicalis	XP_002937124.2
PRDM4_Anolis_carolinensis	XP_003220940.1
PRDM4_Callorhinchus_milii	XP_007903292.1
PRDM4_Chrysemys_picta_bellii	XP_008177579.1
PRDM4_Danio_rerio	NP_001116215.1
PRDM4_Gallus_gallus	XP_416301.4
PRDM4_Homo_sapiens	NP_036538.3
PRDM4_Mus_musculus	NP_001289815.1
PRDM4_Xenopus_tropicalis	NP_001072257.1
PRDM5_Anolis_carolinensis	XP_016849600.1
PRDM5_Callorhinchus_milii	XP_007889679.1
PRDM5_Chrysemys_picta_bellii	XP_005290344.1
PRDM5_Danio_rerio	NP_001002301.2
PRDM5_Gallus_gallus	XP_420628.3
PRDM5_Homo_sapiens	XP_024784442.1
PRDM5_Mus_musculus	NP_081823.2
PRDM5_Xenopus_tropicalis	XP_002940365.2

Table S1. NCBI Accession IDs of NCBI derived sequences used in phylogenetic reconstructions

S2) ALIGNMENTS USED FOR PHYLOGENETIC RECONSTRUCTION

S2.1) PROX (CHAPTER 3)

```
>Amphioxus|Prox|Prox|PROS/1-63 63 bp
SPPHPGSLTPTHLKKAKLMFFYTRYPSSSTLKQHFPDVKFNRCITSQLIKWFSNFREFYYIQM
>Lamprey_ProxA/1-63 63 bp
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>Lamprey_ProxB/1-63 63 bp
HHHLQEGLTPSHLKKAKLMFFYSRYPSSNMLKIYFSDVKFNRCITSQLIKWFSNFREFYYIQV
>Lamprey_ProxC/1-63 63 bp
GPHGQEGLTPGHLKKAKLMFYYSRYPSSTMLKIYFPDVKFNRCITSQLIKWFSNFREFYYIQM
>Human|PROX2|Prox|PROS/1-63 63 bp
LVHIQEGLNPGHLKKAKLMFFFTRYPSSNLLKVYFPDVQFNRCITSQMIKWFSNFREFYYIQM
>Mouse|Prox2|Prox|PROS/1-63 63 bp
SIHIQEGLSPGHLKKAKLMFFFTRYPSSSLLKAYFPDVQFNRCITSQMIKWFSNFREFYYIQM
>Chicken|Prox2|Prox|PROS/1-61 63 bp
--HIQEGLSPGHLKKAKLMFFFTRYPSSSLLKAYFPDVQFNRCITSQMIKWFSNFREFYYIQM
>Zebrafish|prox1b|Prox|PROS/1-59 63 bp
----QEGLSPCHLKKAKLMFFYTRYPSSSTLKTYFPDVKFNRCVTSQLIKWFSNFREFFYIQM
>Lamprey_ProxD/1-63 63 bp
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>Zebrafish|prox2|Prox|PROS/1-60 63 bp
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>Human|PROX1|Prox|PROS/1-63 63 bp
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>Mouse|Prox1|Prox|PROS/1-63 63 bp
GSAMQEGLSPNHLKKAKLMFFYTRYPSSNMLKTYFSDVKFNRCITSQLIKWFSNFREFYYIQM
>Chicken|PROX1|Prox|PROS/1-63 63 bp
GSAMQEGLSPNHLKKAKLMFFYTRYPSSNMLKTYFSDVKFNRCITSQLIKWFSNFREFYYIQM
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>Zebrafish|prox1|Prox|PROS/1-63 63 bp
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>Frog|prox1|Prox|PROS/1-63 63 bp
QLYMQEGLSPNHLKKAKLMFFYTRYPSSNMLKTFFSDVKFNRCITSQLIKWFSNFREFYYIQM
>Nematode|ceh-26|Prox|PROS/1-63 63 bp
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>Honeybee|Pros|Prox|PROS/1-63 63 bp
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>Fruitfly|pros|Prox|PROS/1-63 63 bp
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>Beetle|Pros|Prox|PROS/1-63 63 bp
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```

S2.2) ERR (CHAPTER 3)

```
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RDTKDCLIDKRQRNRCQYCRYQKCLAMGMKREAVQEERQRSREKSDTE---AESTSSTS-----------EE
MPVERILEAELAVEP-KIEAFGDAGLPNSTNDPVTNICHAADKQLFTLVEWAKRIPHFSDLPLEDQVILLRA
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TFLMEMLETPHQIS
>RXRG_Homo/1-417 446 bp
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VAPPSSQLNV-----NSVSSSEDIKPLPGLPVKHICAICGDRSSGKHYGVYSCEGCKGFFKRTIRKDLIYTC
RDNKDCLIDKRQRNRCQYCRYQKCLVMGMKREAVQEERQRSRERAES-EAECATSGH-------------ED
MPVERILEAELAVEPKESYGDMNMEN--STNDPVTNICHAADKQLFTLVEWAKRIPHFSDLTLEDQVILLRA
GWNELLIASFSHRSVSVQDGILLATGLHVHRSSAHSAGVGSIFDVLTELVSKMKDMQMDKSELGCLRAIVLF
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TFLMEMLETPLQIT
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RDNKDCLIDKRQRNRCQYCRYQKCLAMGMKREAVQEERQGSRE----RENEAESTSGGS-----------ED
MPVERILEAELAVEPKEAYSDVNTES--STNDPVTNICHAADKQLFTLVEWAKRIPHFSDLTLEDQVILLRA
GWNELLIASFSHRSVSVQDGILLATGLHVHRSSAHSAGVGSIFDVLTELVSKMKDMQMDKSELGCLRAIVLF
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TFLMEMLETPLQVT
>RXRA_Xenopus/1-445 446 bp
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>ER2a_Danio/1-433 446 bp
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>ER2_Homo/1-433 446 bp
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>ER2_Anolis/1-434 446 bp
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DLLLEMLNAHTLRG
>ERc_lamprey/1-346 446 bp
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DILLDILTDQVSEG
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KLFLEMLEAKM---
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VWLEVLVLGVAYRSLGCEDEVVFAEDFVLDEEMSRVAGLTELNAAISQLARRFRALQLDREEFVMLKAIALT
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KLFLEMLEAKV---
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S2.3) NK HOMEOBOX (CHAPTER 3)

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>Mouse|Nkx6-2|Nk6|ANTP 60 bp
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>Chicken|NKX6-2|Nk6|ANTP 60 bp
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>Frog|nkx6-2|Nk6|ANTP 60 bp
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>Zebrafish|nkx6.2|Nk6|ANTP 60 bp
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>Amphioxus|Nkx6|Nk6|ANTP 60 bp
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>Human|NKX6-1|Nk6|ANTP 60 bp
RKHTRPTFSGQQIFALEKTFEQTKYLAGPERARLAYSLGMTESQVKVWFQNRRTKWRKKH
>Mouse|Nkx6-1|Nk6|ANTP 60 bp
RKHTRPTFSGQQIFALEKTFEQTKYLAGPERARLAYSLGMTESQVKVWFQNRRTKWRKKH
>Frog|nkx6-1|Nk6|ANTP 60 bp
RKHTRPTFSGQQIFALEKTFEQTKYLAGPERARLAYSLGMTESQVKVWFQNRRTKWRKKH
>Zebrafish|nkx6.1|Nk6|ANTP 60 bp
RKHTRPTFSGQQIFALEKTFEQTKYLAGPERARLAYSLGMTESQVKVWFQNRRTKWRKRH
>Frog|nkx6-3|Nk6|ANTP 60 bp
KKHTRPTFTGHQIFALEKTFEQTKYLAGPERARLAFSLGMSESQVKVWFQNRRTKWRKKS
>Human|NKX6-3|Nk6|ANTP 60 bp
KKHTRPTFTGHQIFALEKTFEQTKYLAGPERARLAYSLGMTESQVKVWFQNRRTKWRKKS
>Mouse|Nkx6-3|Nk6|ANTP 60 bp
KKHTRPTFTGHQIFALEKTFEQTKYLAGPERARLAYSLGMTESQVKVWFQNRRTKWRKKS
>Chicken|NKX6-3|Nk6|ANTP 60 bp
KKHTRPTFTGHQIFALEKTFEQTKYLAGPERARLAYSLGMTESQVKVWFQNRRTKWRKKS
>Zebrafish|nkx6.3|Nk6|ANTP 60 bp
KKHTRPTFSGHQIFALEKTFEQTKYLAGPERARLAYSLGMTESQVKVWFQNRRTKWRKKS
>Frog|nkx1-2la|Nk1|ANTP 60 bp
PRRARTAFTYEQLVALESRFRSSRYLSVCERLSLALTLHLTETQVKIWFQNRRTKWKKQQ
>Frog|nkx1-2lb|Nk1|ANTP 60 bp
PRRARTAFTYEQLVALESRFRSSRYLSVCERLSLALTLHLTETQVKIWFQNRRTKWKKQQ
>Chicken|NKX1-1|Nk1|ANTP 60 bp
PRRARTAFTYEQLVALENKFKSTRYLSVCERLNLALSLSLTETQVKIWFQNRRTKWKKQN
>Frog|nkx1-2|Nk1|ANTP 60 bp
PRRARTAFTYEQLVALENKFKSTRYLSVCERLNLALSLSLTETQVKIWFQNRRTKWKKQN
>Zebrafish|nkx1.2lb|Nk1|ANTP 60 bp
PRRARTAFTYEQLVALENKFKSTRYLSVCERLNLALSLSLTETQVKIWFQNRRTKWKKQN
>Human|NKX1-1|Nk1|ANTP 60 bp
PRRARTAFTYEQLVALENKFKATRYLSVCERLNLALSLSLTETQVKIWFQNRRTKWKKQN
>Mouse|Nkx1-1|Nk1|ANTP 60 bp
PRRARTAFTYEQLVALENKFKATRYLSVCERLNLALSLSLTETQVKIWFQNRRTKWKKQN
>Amphioxus|Nkx1a|Nk1|ANTP 60 bp
PRRARTAFTYEQLVALENKFKQTRYLSVCERLNLALSLSLTETQVKIWFQNRRTKWKKQN
>Amphioxus|Nkx1b|Nk1|ANTP 60 bp
PRRVRTAFTYEQLVALENKFKQTRYLSVCERLNLALSLSLTETQVKIWFQNRRTKWKKQN
>Chicken|NKX1-2|Nk1|ANTP 60 bp
PRRARTAFTYEQLVALENKFRATRYLSVCERLNLALSLSLTETQVKIWFQNRRTKWKKQH
>Zebrafish|nkx1.2la|Nk1|ANTP 60 bp
PRRARTAFTYEQLVALENKLRATRYLSVCERLNLALSLSLTETQVKIWFQNRRTKWKKQN
>Human|NKX1-2|Nk1|ANTP 60 bp
PRRARTAFTYEQLVALENKFRATRYLSVCERLNLALSLSLTETQVKIWFQNRRTKWKKQN
>Mouse|Nkx1-2|Nk1|ANTP 60 bp
PRRARTAFTYEQLVALENKFRATRYLSVCERLNLALSLSLTETQVKIWFQNRRTKWKKQN
>Zebrafish|hmx4|Nk5/Hmx|ANTP 60 bp
KKKTRTIFSKRQIFQLESTFDMKRYLSSAERACLANSLQLTETQVKIWFQNRRNKLKRQL
>Frog|hmx4|Nk5/Hmx|ANTP 60 bp
KKKTRTIFSKSQIFQLESTFDMKRYLSSAERACLANSLQLTETQVKIWFQNRRNKLKRQM
>Frog|hmx4b|Nk5/Hmx|ANTP 60 bp
KKKTRTIFSKSQIFQLESTFDMKRYLSSAERACLANSLQLTETQVKIWFQNRRNKLKRQM
>Chicken|SOHO-1|Nk5/Hmx|ANTP 60 bp
KKKTRTIFSKSQVFQLESTFDVKRYLSSAERAGLAAALHLTETQVKIWFQNRRNKLKRQL
>Human|HMX2|Nk5/Hmx|ANTP 60 bp
KKKTRTVFSRSQVYQLESTFDMKRYLSSSERACLASSLQLTETQVKTWFQNRRNKWKRQL
>Mouse|Hmx2|Nk5/Hmx|ANTP 60 bp
KKKTRTVFSRSQVYQLESTFDMKRYLSSSERACLASSLQLTETQVKTWFQNRRNKWKRQL
```

```
>Chicken|HMX2|Nk5/Hmx|ANTP 60 bp
KKKTRTVFSRSQVYQLESTFDMKRYLSSSERACLASSLQLTETQVKTWFQNRRNKWKRQL
>Zebrafish|hmx2|Nk5/Hmx|ANTP 60 bp
KKKTRTVFSRSQVYQLESTFDMKRYLSSSERACLASSLQLTETQVKTWFQNRRNKWKRQL
>Frog|hmx2|Nk5/Hmx|ANTP 60 bp
KKKTRTVFSRSQVYQLESTFDMKRYLSSSERACLASSLQLTETQVKTWFQNRRNKWKRQL
>Chicken|HMX2-like|Nk5/Hmx|ANTP 60 bp
KKKTRTVFSRSQVYQLESTFDMKRYLSSSERACLASSLQLTETQVKTWFQNRRNKWKRQL
>Human|HMX1|Nk5/Hmx|ANTP 60 bp
KKKTRTVFSRSQVFQLESTFDLKRYLSTAERAGLAASLQLTETQVKIWFQNRRNKWKRHV
>Zebrafish|LOC100333298|Nk5/Hmx|ANTP 60 bp
KKKTRTVFSRAQVFQLESTFDLKRYLSSSERAGLAASLHLTETQVKIWFQNRRNKWKRQI
>Mouse|Hmx1|Nk5/Hmx|ANTP 60 bp
RKKTRTVFSRSQVFQLESTFDLKRYLSSAERAGLAASLQLTETQVKIWFQNRRNKWKRQL
>Chicken|HMX1|Nk5/Hmx|ANTP 60 bp
KKKTRTVFSRSQVFQLESTFDVKRYLSSSERAGLAASLHLTETQVKIWFQNRRNKWKRQL
>HMXA_lampetra 60 bp
KKKTRTVFSRSQVFQLESTFDMKRYLSSAERAGLAASLHLTETQVKIWFQNRRNKWKRQL
>HMXB_lampetra 60 bp
KKKTRTVFSRSQVFQLESTFDMKRYLSSAERAGLAASLHLTETQVKIWFQNRRNKWKRQL
>HMXC_lampetra 60 bp
KKKTRTVFSRSQVFQLESTFDMKRYLSSAERAGLAASLHLTETQVKIWFQNRRNKWKRQL
>Amphioxus|Hmx|Nk5/Hmx|ANTP 60 bp
KKKTRTVFSRQQVFQLESTFDMKRYLSSSERAGLAASLHLTETQVKIWFQNRRNKWKRQL
>Zebrafish|hmx1|Nk5/Hmx|ANTP 60 bp
KKKTRTVFSRSQVFQLESTFDMKRYLSSSERAGLAASLHLTETQVKIWFQNRRNKWKRQL
>Frog|hmx1|Nk5/Hmx|ANTP 60 bp
KKKTRTVFSRSQVFQLESTFDMKRYLSSSERAGLAASLHLTETQVKIWFQNRRNKWKRQL
>Human|HMX3|Nk5/Hmx|ANTP 60 bp
KKKTRTVFSRSQVFQLESTFDMKRYLSSSERAGLAASLHLTETQVKIWFQNRRNKWKRQL
>Mouse|Hmx3|Nk5/Hmx|ANTP 60 bp
KKKTRTVFSRSQVFQLESTFDMKRYLSSSERAGLAASLHLTETQVKIWFQNRRNKWKRQL
>Chicken|HMX3|Nk5/Hmx|ANTP 60 bp
KKKTRTVFSRSQVFQLESTFDMKRYLSSSERAGLAASLHLTETQVKIWFQNRRNKWKRQL
>Zebrafish|hmx3|Nk5/Hmx|ANTP 60 bp
KKKTRTVFSRSQVFQLESTFDMKRYLSSSERAGLAASLHLTETQVKIWFQNRRNKWKRQL
>Frog|hmx3|Nk5/Hmx|ANTP 60 bp
KKKTRTVFSRSQVFQLESTFDMKRYLSSSERAGLAASLHLTETQVKIWFQNRRNKWKRQL
>Frog|nkx2-8|Nk2.2|ANTP 60 bp
KKKRRVLFSKAQTLELERRFRQQRYLSAPERDQLAHILHLTPTQVKIWFQNHRYKMKRVK
>Zebrafish|nkx2.2b|Nk2.2|ANTP 60 bp
KRKRRILFSKTQTFELERRFRQQRYLSAPEREHLAKLLHLTPTQVKIWFQNHRYKVKRAR
>Human|NKX2-2|Nk2.2|ANTP 60 bp
KRKRRVLFSKAQTYELERRFRQQRYLSAPEREHLASLIRLTPTQVKIWFQNHRYKMKRAR
>Mouse|Nkx2-2|Nk2.2|ANTP 60 bp
KRKRRVLFSKAQTYELERRFRQQRYLSAPEREHLASLIRLTPTQVKIWFQNHRYKMKRAR
>Frog|nkx2-2|Nk2.2|ANTP 60 bp
KRKRRVLFSKAQTYELERRFRQQRYLSAPEREHLASLIRLTPTQVKIWFQNHRYKMKRAR
>Zebrafish|nkx2.2a|Nk2.2|ANTP 60 bp
KRKRRVLFSKAQTYELERRFRQQRYLSAPEREHLASLIRLTPTQVKIWFQNHRYKMKRAR
>Amphioxus|Nkx2-2|Nk2.2|ANTP 60 bp
KRKRRVLFSKAQTYELERRFRQQRYLSAPEREHLARLIRLTPTQVKIWFQNHRYKCKRAQ
>Mouse|Nkx2-9|Nk2.2|ANTP 60 bp
RRKRRVLFSKAQTLELERRFRQQRYLSAPEREQLARLLRLTPTQVKIWFQNHRYKLKRGR
>Chicken|Nkx2-9|Nk2.2|ANTP 60 bp
-RKRRVLFSKAQTLELERRFRQQRYLSAPEREQLARLLRLTPTQVKIWFQNHRYKLKRGR
>Zebrafish|nkx2.9|Nk2.2|ANTP 60 bp
RKKRRVLFSKAQTYELERRFRQQRYLSAPEREQLAHLLRLTPTQVKIWFQNHRYKMKRAR
>Human|NKX2-8|Nk2.2|ANTP 60 bp
RKKRRVLFSKAQTLELERRFRQQRYLSAPEREQLASLLRLTPTQVKIWFQNHRYKLKRAR
>Mouse|Nkx2-6|Nk4|ANTP 60 bp
QRKSRVLFSQAQVLALERRFKQQRYLTAPEREHLASALQLTSTQVKIWFQNRRYKSKSQR
>Chicken|NKX2-6|Nk4|ANTP 60 bp
RRKPRVLFSQTQVLELERRFKQQKYLSALEREHLANVLQLTSTQVKIWFQNRRYKCKRQR
>Frog|nkx2-6|Nk4|ANTP 60 bp
RRKPRVLFSQMQVFELERRFKQQRYLSAPEREQLALALKLTSTQVKIWFQNRRYKCKRQK
>Zebrafish|nkx2.7|Nk4|ANTP 60 bp
RRKPRVLFSQTQVFELERRFKQQRYLSAPERDHLALALKLTSTQVKIWFQNRRYKCKRQR
>Chicken|NKX2-5|Nk4|ANTP 60 bp
RRKPRVLFSQAQVYELERRFKQQKYLSAPERDHLANVLKLTSTQVKIWFQNRRYKCKRQR
>Frog|nkx2-5|Nk4|ANTP 60 bp
RRKPRVLFSQAQVYELERRFKQQKYLSAPERDHLANVLKLTSTQVKIWFQNRRYKCKRQR
>Zebrafish|nkx2.5|Nk4|ANTP 60 bp
RRKPRVLFSQAQVYELERRFKQQKYLSAPERDHLANVLKLTSTQVKIWFQNRRYKCKRQR
>Human|NKX2-5|Nk4|ANTP 60 bp
```

RRKPRVLFSQAQVYELERRFKQQRYLSAPERDQLASVLKLTSTQVKIWFQNRRYKCKRQR
>Mouse|Nkx2-5|Nk4|ANTP 60 bp
RRKPRVLFSQAQVYELERRFKQQRYLSAPERDQLASVLKLTSTQVKIWFQNRRYKCKRQR
>Human|NKX2-6|Nk4|ANTP 60 bp
RRKPRVLFSQAQVLALERRFKQQRYLSAPEREHLASALQLTSTQVKIWFQNRRYKCKRQR
>Frog|nkx2-3|Nk4|ANTP 60 bp
RRKPRVLFSQAQVFELERRFKQQRYLSAPEREHLANSLKLTSTQVKIWFQNRRYKCKRQR
>Human|NKX2-3|Nk4|ANTP 60 bp
RRKPRVLFSQAQVFELERRFKQQRYLSAPEREHLASSLKLTSTQVKIWFQNRRYKCKRQR
>Mouse|Nkx2-3|Nk4|ANTP 60 bp
RRKPRVLFSQAQVFELERRFKQQRYLSAPEREHLASSLKLTSTQVKIWFQNRRYKCKRQR
>Zebrafish|nkx2.3|Nk4|ANTP 60 bp
RRKPRVLFSQAQVFELERRFKQQRYLSAPEREHLASTLKLTSTQVKIWFQNRRYKCKRQR
>Amphioxus|Csx|Nk4|ANTP 60 bp
RRKPRVLFSQAQVFELERRFKQQRYLSAPEREQLAQMLKLTSTQVKIWFQNRRYKCKRQR
>Frog|nkx2-1lb|Nk2.1|ANTP 60 bp
KRKRRVLFSQAQVYELEKRFEHQKYLTAPEREQLAKHIHLTPNQVKIWFQNHRYKMKRQA
>Zebrafish|nkx2.1c|Nk2.1|ANTP 60 bp
RRKRRVLFSQAQVCELERRFKQQKYLSAPEREHLASMIHLTPTQVKIWFQNHRYKMKRQA
>Human|NKX2-1|Nk2.1|ANTP 60 bp
RRKRRVLFSQAQVYELERRFKQQKYLSAPEREHLASMIHLTPTQVKIWFQNHRYKMKRQA
>Mouse|Nkx2-1|Nk2.1|ANTP 60 bp
RRKRRVLFSQAQVYELERRFKQQKYLSAPEREHLASMIHLTPTQVKIWFQNHRYKMKRQA
>Chicken|NKX2-1|Nk2.1|ANTP 60 bp
RRKRRVLFSQAQVYELERRFKQQKYLSAPEREHLASMIHLTPTQVKIWFQNHRYKMKRQA
>Frog|nkx2-1|Nk2.1|ANTP 60 bp
RRKRRVLFSQAQVYELERRFKQQKYLSAPEREHLASMIHLTPTQVKIWFQNHRYKMKRQA
>Frog|nkx2-1a|Nk2.1|ANTP 60 bp
RRKRRVLFSQAQVYELERRFKQQKYLSAPEREHLASMIHLTPTQVKIWFQNHRYKMKRQA
>Human|NKX2-4|Nk2.1|ANTP 60 bp
RRKRRVLFSQAQVYELERRFKQQKYLSAPEREHLASMIHLTPTQVKIWFQNHRYKMKRQA
>Mouse|Nkx2-4|Nk2.1|ANTP 60 bp
RRKRRVLFSQAQVYELERRFKQQKYLSAPEREHLASMIHLTPTQVKIWFQNHRYKMKRQA
>Zebrafish|nkx2.1a|Nk2.1|ANTP 60 bp
RRKRRVLFSQAQVYELERRFKQQKYLSAPEREHLASMIHLTPTQVKIWFQNHRYKMKRQA
>Zebrafish|nkx2.1b|Nk2.1|ANTP 60 bp
RRKRRVLFSQAQVYELERRFKQQKYLSAPEREHLASMIHLTPTQVKIWFQNHRYKMKRQA
>Amphioxus|Nkx2-1|Nk2.1|ANTP 60 bp
RRKRRVLFSQAQVYELERRFKQQKYLSAPEREHLAQLINLTPTQVKIWFQNHRYKCKRQD
>Frog|nkx2-4|Nk2.1|ANTP 60 bp
RRKRRVLFSQAQVYELERRFKQQKYLSAPXREHLVQ------------------------
>Zebrafish|nkx3-1|Nk3|ANTP 60 bp
KKRSRAAFTHLQVLELEKKFSRQRYLSAPERTHLASALHLTETQVKIWFQNRRYKTKRRQ
>Human|NKX3-1|Nk3|ANTP 60 bp
QKRSRAAFSHTQVIELERKFSHQKYLSAPERAHLAKNLKLTETQVKIWFQNRRYKTKRKQ
>Mouse|Nkx3-1|Nk3|ANTP 60 bp
QKRSRAAFSHTQVIELERKFSHQKYLSAPERAHLAKNLKLTETQVKIWFQNRRYKTKRKQ
>Frog|nkx3-1|Nk3|ANTP 60 bp
QKRSRAAFSHSQVIELERKFSSQKYLSAPERAQLAKSLKLTETQVKIWFQNRRYKTKRKQ
>Frog|nkx3-2l|Nk3|ANTP 60 bp
KKRSRAAFSHAQVYELERRFSLQRYLSGPERADLAAALKLTETQVKIWFQNRRYKTKRKL
>Amphioxus|Nkx3|Nk3|ANTP 60 bp
KKRSRAAFSHAQVFELERRFSHQRYLSGPERADLAAALKLTETQVKIWFQNRRYKTKRRQ
>Human|NKX3-2|Nk3|ANTP 60 bp
KKRSRAAFSHAQVFELERRFNHQRYLSGPERADLAASLKLTETQVKIWFQNRRYKTKRRQ
>Mouse|Nkx3-2|Nk3|ANTP 60 bp
KKRSRAAFSHAQVFELERRFNHQRYLSGPERADLAASLKLTETQVKIWFQNRRYKTKRRQ
>Frog|nkx3-2|Nk3|ANTP 60 bp
KKRSRAAFSHAQVFELERRFNHQRYLSGPERADLAASLKLTETQVKIWFQNRRYKTKRRQ
>Zebrafish|nkx3.2|Nk3|ANTP 60 bp
KKRSRAAFSHAQVFELERRFNHQRYLSGPERADLAASLKLTETQVKIWFQNRRYKTKRRQ
>Zebrafish|nkx3.3|Nk3|ANTP 60 bp
KKRSRAAFSHAQVYELARRFNLQRYLSGPERADLAGALKLTETQVKIWFQNRRYKTKRRQ

S2.4) PRD HOMEOBOX (CHAPTER 3)

>UNCX_Homo_sapiens/1-304 311 bp
----MMDGRLLEHPHAQFGGSLGGVVGFPYPLGHH-HVYELAGHQLQSAAAAASVLLGGSCAAPLLPAACGV
GGDGQPFKLSDSGDPDKESP--GCKRRRTRTNFTGWQLEELEKAFNESHYPDVFMREALALRLDLVESRVQV
WFQNRRAKWRKKENTKKGPGRPAHNSHPTTCSGEPMDPEEIARKELEKMELLKSQGRHLHSPGGLSLHSGLS
PEPPEPAGTAPAPPGEPPAPGTCDPAFYPSQRQPLGFLVPQAALKGAPAVPPAPPAQASFGAFSGPGGASPD
AVASGAPAPAPAPFRDLASAAAT
>UNCX_Gallus_gallus/1-299 311 bp
----MMDSRILEHPHAQFGGM----VGFPYPLGHHHVYELAGHQLQSAAASVPFSLLSGSCAAPLIPSGCGV

```
SADTQPFKLADSGDPDKESP--GCKRRRTRTNFTGWQLEELEKAFNESHYPDVFMREALALRLDLVESRVQV
WFQNRRAKWRKKENTKKGPGRPAHNSHPTTCSGEPMDPEEIARKELEKMELLKSQSRHLHSPSGLSLHSTPS
SDSDSGPEAKPRGQPPPPPPAAAASSEPPPSSQPLGFIVPQTALKANPGPEAGQPPRDSPLPAANPGPP--A
FSAEAPAGAQPGPSSTDTAAGPA
>UNCX_Danio_rerio/1-304 311 bp
----MMDSRILDPPHAQFGGSLGGMVSFPYHLSHH-HVYELAGHQLQSTAAVPFSLLNGSCTAPLLSSGCGM
NGDNQQYKLTDSGDPDKDSP--GCKRRRTRTNFTGWQLEELEKAFNESHYPDVFMREALALRLDLIESRVQV
WFQNRRAKWRKKENTKKGPGRPAHNSHPTTCSGEPMDPEEIARRELERLELLKSQNKLLPGDLFHTPGSDSE
QSLHCDPRRKPPMDFPVPTPRPLIGKGHFLLYQPLGFIVPQTALKSGPATDITFAGNPGHRNAKENNSVARA
IKGQSQSGNISCSTQSSSPQTTI
>UNCX_Xenopus_tropicalis/1-304 311 bp
----MMDSRILEHPHAQFGGSMSGMVGFPYPLGHH-HVYELASHQLQSAAAAVPFLLNGSCTAPLLPSGCGL
NGDSQQYKLSDSIDPD--KESPGCKRRRTRTNFTGWQLEELEKAFNESHYPDVFMREALALRLDLVESRVQV
WFQNRRAKWRKKENTKKGPGRPAHNSHPTTCSGEPMDPEEIARKELEKMEMLRNQNRLQHSPGDMSLHTGLS
QNLDSSVEANHNSGLCPNGRGAAFQKLNPFSVQPLGFIVPQASIKSNSAQELPSPGIKDSLHNSNSGQPAQN
LYPNHTNSTQSTTLTVCKTENGD
>PITX1_Danio_rerio/1-269 311 bp
---------------------------------MNVDMASSFHLPRSASSTR---ETLENTSS-ESSDTEAA
EKERSVEQRSDDGNAD-DPK--KKKQRRQRTHFTSQQLQELEATFQRNRYPDMSTREEIAVWTNLTEARVRV
WFKNRRAKWRKRERNQQMDLCKNSYLPQFSGLMQPYDDVY-PTYTYNNWTLSTKNFTFFNSMSPLTSQSMFS
APSSISSMSMASGMGHSAVPGMPTTGLNNIGNNGIGGSTINPAMS-SSTCPYGPPVSPYSVYRDTCNSSLAT
LRLKSKQHPSFGYSGLQSPGSSL
>PITX1_Homo_sapiens/1-292 311 bp
-------------MDAFKGGMSLEREGLRPPPPPPHDMGPAFHLARPADPREPLESSDTELPE-KERGGEPK
GPEDSGAGGTGCGGADDPAK--KKKQRRQRTHFTSQQLQELEATFQRNRYPDMSMREEIAVWTNLTEPRVRV
WFKNRRAKWRKRERNQQLDLCKGGYVPQFSGLVQPYEDVYAAGYSYNNWALSTKSFTFFNSMSPLSSQSMFS
APSSISSMTMPSSMGPGAVPGMPNSGLNNI--NNLTGSSLNSAMS-PGACPYGTPASPYSVYRDTCNSSLAS
LRLKSKQHSSFGYGGLQGPASGL
>PITX1_Xenopus_tropicalis/1-289 311 bp
-------------MDSFKGAMNLERLPESLRPQPSHDMATSFHLQRSSEAR----DPMDNSAS-ESSDTEIA
EKERSGEPKGEDGNGDDPTK--KKKQRRQRTHFTSQQLQELEATFQRNRYPDMSMREEIAVWTNLTEARVRV
WFKNRRAKWRKRERNQQMDLCKNGYVPQFSGLMQPYDEMY-AGYPYNNWALSTKSFTFFNSMSPLSSQSMFS
GPSSISSMSMPSSMGHSAVPGMPNSSLNNINNNNISSSSLNSAMS-STACPYGPPGSPYTVYRDTCNSSLAS
LRLKSKQHSTFGYSSLQSPASSL
>PITX1_Gallus_gallus/1-287 311 bp
-------------MDSFKGGMNLERLPESLRPQPSHDMASSFHLQRSSEPR----DPIENSAS-ESSDTEVP
EKERSGEQKNEDGAADDPAK--KKKQRRQRTHFTSQQLQELEATFQRNRYPDMSMREEIAVWTNLTEPRVRV
WFKNRRAKWRKRERNQQMDLCKNGYVPQFSGLMQPYDDMY-AGYPYNKWALSTKSFTFFNSMSPLSSQSMFS
APSSISSMNMPSGMGHSAVPGMANSGLNNI--NNISGSSLNSAMS-SPACPYGPPGSPYSVYRDTCNSSLAS
LRLKSKQHSSFGYSSLQSPGSSL
>ALX1_Danio_rerio/1-282 311 bp
----EYLSDKFSLKSPAIKGSDYYMDQVMDTLDNVQYYNKASPKCVQAFPMQSNDSSVTYCAPLHAMENCCS
LRVSPATSGPDKTDLDLGEKCDSSKKRRHRTTFTSAQLEELEKVFQKTHYPDVYVREQLAMRTELTEARVQV
WFQNRRAKWRKRERYGQIQQAKSHFAATYDISMLPRTDSY-SQISNNLWTPSAGSSVVSSCMIPRGSPPVTS
PYPHSPAAEHGYVGFPNHQFGVNHVSLNNFFA--------------SANSHAAFETKPEFERRSSS---IAV
LRMKAKEHTANISWAM-------
>ALX1_Xenopus_tropicalis/1-286 311 bp
YMGAGTLEHVMDSMDTDSFYNKSPAGKCVQAFSAIQRAEHHVRMERASPCQDTNAAKVEGQAVGRPMETCCS
LAVSPGKAMADKVDLDLGDKCDSSKKRRHRTTFTSLQLEELEKVFQKTHYPDVYVREQLALRTELTEARVQV
WFQNRRAKWRKRERYGQIQQAKSHFAATYDISVLPRADSY-PQIQNNLWANPSGGSVVTSCMLPREPSACMT
PYSHSTRTDSPYTSFTNHQNQFSHVPLNNFFT--------------GSANGHSFEAKPEFERRSSS---IAV
LRMKAKEHTANISWAM-------
>ALX1_Homo_sapiens/1-286 311 bp
YMGAGPLEHVMETLDNESFYSKASAGKCVQAFGPLPRAEHHVRLERTSPCQDSSVTKVEGQPLNRAMDNCNS
LRMSPVKGMQEKGELDLGDKCDSSKKRRHRTTFTSLQLEELEKVFQKTHYPDVYVREQLALRTELTEARVQV
WFQNRRAKWRKRERYGQIQQAKSHFAATYDISVLPRTDSY-PQIQNNLWANASGGSVVTSCMLPRDTSSCMT
PYSHSPRTDSSYTGFSNHQNQFSHVPLNNFFT--------------GATNGHAFETKPEFERRSSS---IAV
LRMKAKEHTANISWAM-------
>ALX1_Gallus_gallus/1-286 311 bp
YMGAGTLEHVMETLDNESFYSKTSGSKCVQAFNPLQRAEHHVRLDRTSPCQDNNVTKVEGQPLNRPLDNCNN
LRMSPVKGMQEKGELDLGDKCDSSKKRRHRTTFTSLQLEELEKVFQKTHYPDVYVREQLALRTELTEARVQV
WFQNRRAKWRKRERYGQIQQAKSHFAATYDISVLPRTDSY-PQIQNNLWANTASGSVVTSCMIPRDTSSCMT
PYSHSPRTDSGYTGFSNHQNQFSHVPLNNFFT--------------GATNGHAFETKPEFERRSSS---IAV
LRMKAKEHAANISWAM-------
>PAX6b_Danio_rerio/1-294 311 bp
YKRECPSIFAWEIRDRLLSEGVCTNDNIPSVSSIN-RVLRNLASEKQQMGADGMYNGQSGTWGQPNQDGCQQ
QDNGGENTNSISSNGEDSDETQKRKLQRNRTSFTQEQIEALEKEFERTHYPDVFARERLAAKIDLPEARIQV
WFSNRRAKWRREEKLRNQRRQASNSSSHIPISSSFNTSVY-QAIPQPTTPFTTGSMLGRPDTALTNTYTGLP
PMP-------SFTMANNLPMQPSQTS------SYSCMLPSSPSVNGRSFDTYTPPHMQAHMNSQTMATSGTA
STGLSPGVS--VPVQVPGTEPDM
>PAX6a_Danio_rerio/1-294 311 bp
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SDGGGENTNSISSNGEDSDETQKRKLQRNRTSFTQEQIEALEKEFERTHYPDVFARERLAAKIDLPEARIQV
WFSNRRAKWRREEKLRNQRRQASNSSSHIPISSSFSTSVY-QPIPQPTTPFTSGSMLGRSDTALTNTYSALP
PMP-------SFTMANNLPMQPSQTS------SYSCMLPTSPSVNGRSYDTYTPPHMQAHMNSQSMAASGTT
```

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STGLSPGVS--VPVQVPGSEPDM
>PAX6_Xenopus_tropicalis/1-297 311 bp
YKRECPSIFAWEIRDRLLSEGVCTNDNIPSVSSIN-RVLRNLASEKQQMGADGMYNGQTGTWGQPAQDGCQP
QEGGGGGENTNSISSNDSDEAQKRKLQRNRTSFTQEQIEALEKEFERTHYPDVFARERLAAKIDLPEARIQV
WFSNRRAKWRREEKLRNQRRQASNTPSHIPISSSFSTSVY-QPIPQPTTPFTSGSMLGRTDTALTNSYSALP
PMP-------SFTMGNNLPMQPPVPSQTS---SYSCMLPTSPSVNGRSYDTYTPPHMQTHMNSQPMGTSGTA
STGLSPGVS--VPVQVPGSEPDM
>PAX6_Gallus_gallus/1-297 311 bp
YKRECPSIFAWEIRDRLLSEGVCTNDNIPSVSSIN-RVLRNLASEKQQMGADGMYNGQTGTWGQPAQDGCPQ
QEGGGENTNSISSNGEDSDEMRKRKLQRNRTSFTQEQIEALEKEFERTHYPDVFARERLAAKIDLPEARIQV
WFSNRRAKWRREEKLRNQRRQASNTPSHIPISSSFSTSVY-QPIPQPTTPFTSGSMLGRTDTALTNTYSALP
PMPSFT-MANNLPMQPPVPSQTS---------SYSCMLPTSPSVNGRSYDTYTPPHMQTHMNSQPMGTSGTT
STGLSPGVS--VPVQVPGSEPDM
>PAX6_Homo_sapiens/1-297 311 bp
YKRECPSIFAWEIRDRLLSEGVCTNDNIPSVSSIN-RVLRNLASEKQQMGADGMYNGQTGSWGQPTQDGCQQ
QEGGGENTNSISSNGEDSDEAQKRKLQRNRTSFTQEQIEALEKEFERTHYPDVFARERLAAKIDLPEARIQV
WFSNRRAKWRREEKLRNQRRQASNTPSHIPISSSFSTSVY-QPIPQPTTPFTSGSMLGRTDTALTNTYSALP
PMP-------SFTMANNLPMQPPVPSQTS---SYSCMLPTSPSVNGRSYDTYTPPHMQTHMNSQPMGTSGTT
STGLSPGVS--VPVQVPGSEPDM
>PAX5_Danio_rerio/1-258 311 bp
YKRQNPTMFAWEIRDRLLAERVCDNDSVPSVSSIN-RIIRTKVQQPPGQSGAVSAVAVTQVSAVTSDAAGSS
YSISGILGISSPADAS------KRKR--------DDPLQDSPLANGHSHSGRDFLRKQM-------------
----RGELFTPQQLETTDSAMASLAGGLE---------------------EMKNSLANQTGAELGSTVAGPQ
SYPLVSGRDLASTTLPGYPPHVPPTGQGSYSTPSLTGMVPGGDFSGSPYSHPQYSTYNESWRFANPSLLYGS
LLGSERAASSGLFPGQTPQPTGS
>PAX5_Xenopus_tropicalis/1-293 311 bp
YKRQNPTMFAWEIRDRLLAERVCDNDTVPSVSSIN-RIIRTKVQQPTNQQVPPSNGSVTQVSSVSTDSAGSS
YSISGILGITSSNAETIQESPVLRKQMRG-DLFTQQQLDVLDRVFERQHYTDIFTKPEQQVRW-LPRLDQVE
FSGGSAAQWRDFRLALHHPHSRTSTEYSAMASLTGGLD------------EMKSSLTSPSSADIGGSVPGPQ
SYPLVTGRDLASTTLPGYPPHVPPAGQGSYSAPTLTGMVPGSDFSGSPYSHPQYSSYNDSWRFPNPGLLGSP
YYYSARGGAPPATAAAYDRH---
>PAX5_Homo_sapiens/1-230 311 bp
YKRQNPTMFAWEIRDRLLAERVCDNDTVPSVSSIN-RIIRTKVQQPPNQPVPASSGSVTQVSSVSTDSAGSS
YSISGILGITSPSADTIQESPVLRKQMRG-DLFTQQQLEVLDRVFERQHYSDIFT---------TTEPI---
----------KPEQTTEYSAMASLAGGLD---------------------DMKANLASPTPADIGSSVPGPQ
SYPIVT-----GSEFSG-----------------------------SPYSHPQYSSYNDSWRFPNPGLLGSP
YYYSAARGAAPPAAATAYDRH--
>PAX5_Gallus_gallus/1-265 311 bp
YKRQNPTMFAWEIRDRLLAERVCDNDTVPSVSSINRIIRTKVQQPPNQQVPVSSHGSVTQVSSVSTDSAGSS
YSISGILGIASPGTESIQEPPVLRKQMRG-DLFTQQQLEVLDRVFERQHYSDIFT---------TTEPI---
----------KPEQATEYSAMASLAGGLD---------------------DMKANITSPTSADLGASVPGPQ
SYPIVTGRELASTTLPGYPPHVPPAGQGSYSAPALTGMVPGSEFSGSPYSHPQYSTYNDSWRFPNPGLLGSP
YYYSAARGAAPPAAAAAYDRH--
>PAX8_Danio_rerio/1-301 311 bp
YKRQNPTMFAWEIRDRLLAEGVCDGDTVPSVSSINRIIRTKVQQPFNLPLDTKGLPGHTLIPSPQSDSLGST
YSINGLLGITQTTADGDSDQCRARKQLRT-EHFPSA---ALDCGFERHYSSDSFSQSKAEQQLNLDEGKISR
NLAAHQGYAVVTEALQPLPLCLKQEVSPEVNSLSPSPHIISGSAFLDLSAASSCGSAHLSHGFSSFSHHAPV
HGQFSSGREVASSMLPGYPPHIPTAQTGFSS-STIAGMVSAPEYTGQSYSHPAYSSYSEAWRFTNSSILGSP
YYYSATRPPPPAAAYDHL-----
>PAX8_Homo_sapiens/1-304 311 bp
YKRQNPTMFAWEIRDRLLAEGVCDNDTVPSVSSIN-RIIRTKVQQPFNLPMDSCVPGHTLIPSPQSDSLGST
YSINGLLGIAQPGSDKDQDSCRGPRKHLRTDAFSQHHLEPLECPFERQHYPEAYASPSHTKGEQYPLPLLNS
TLDDGKATLTPSNT----PLGRNLSTHQTYPVVADPHSPFAIKQETPEVSSSLSSSAFLDLQQVGSGVPPFN
AFPHAAGREMVGPTLPGYPPHIPTSGQGSYASSAIAGMVAGSEYSGNAYGHTPYSSYSEAWRFPNSSLLSSP
YYYSTSRPS--APPTTATAFDHL
>PAX8_Xenopus_tropicalis/1-308 311 bp
YKRQNPTMFAWEIRDRLLAEGVCDNDTVPSVSSIN-RIIRTKVQQLFNLPMESCVPGQTLIPSPHSDSLGST
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AMDDGKSSLTSTNTTIGRNLSTHQGYSALSELSAFTIKQEASDSSSASSTLCSPTFLDLQPISSGCSAPSFS
AFSHPAGRDVVGSTLPGYPPHIPSGQGNYASSAIAGMVAAGGDYSGNAYSHGAYAAYGESWRFPSSSLLGSP
YYYSATRTA--PPPTTAGAYDLL
>OTX1_Danio_rerio/1-250 311 bp
--------------------------------------MMSYLKQPPYAM-----NGLGLSGA---------
AMDLLHPSVGYPAT--------PRKQRRERTTFTRSQLDILEALFAKTRYPDIFMREEVALKINLPESRVQV
WFKNRRAKCRQQQQSGSSTKTRPAKKKSSPTRESTGSESSGQFTPPAVSSSTNNTGICSTSTSISTVSSIWS
PAISPG-SAPPSVSLPEPVAPSNTSCMQRSVSGTASSTYPMPYNQTTGYSQGYPTPSGSYFSGVDCGSYLAP
MHSHHPHQLSPMTASSMPTHPHH
>OTX1_Xenopus_tropicalis/1-249 311 bp
--------------------------------------MMSYLKQPPYGM-----NGLGLTGP---------
AMDLLHPSVGYPAT--------PRKQRRERTTFTRSQLDVLEALFAKTRYPDIFMREEVALKINLPESRVQV
WFKNRRAKCRQQQQQQQSSSGAGVKSRPAKKKCSPARESSGSESSGQFTPSSSSSSSSNSSGNPGLATAPLN
GSTSTASIWSPASISPGTGPGSGPDPLGTGSASSSAASYPMSYSQAAGYTQGYPAPSSSYFSGVDCSSYLAP
MH--SHHHPHQLSPMAPSSMSGH
>OTX1_Homo_sapiens/1-249 311 bp
--------------------------------------MMSYLKQPPYGMN----GLGLAGPA---------
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-MDLLHPSVGYPAT--------PRKQRRERTTFTRSQLDVLEALFAKTRYPDIFMREEVALKINLPESRVQV
WFKNRRAKCRQQQQSGSGTKSRPAKKKSSPVRESSGSESSGQFTPPAVSSSSSSSASSSSANPAAAAAAGLG
GNPVAAASISPGSAPASVSVPEPLAAPSNTSCATAAASYPMSYGQGGSYGQGYPTPSSSYFGGVDCSSYLAP
MH--SHHHPHQLSPMAPSSMAGH
>OTX1_Gallus_gallus/1-249 311 bp
--------------------------------------MMSYLKQPPYG------MNGLGLPG--------P
AMDLLHPSVGYPAT--------PRKQRRERTTFTRSQLDVLEALFAKTRYPDIFMREEVALKINLPESRVQV
WFKNRRAKCRQQQQSGGGAKSRPAKKKSSPARESSGSESSGQFTPPAAASSSASSGAAAAAAGATPASLGTT
ASSIWSGAAPAGVTVPEPLPPAGASCMQRAGPAASASYPVSYGQGGGYGQGYPAPPSSSYFGGVDCSSYLAP
MH--SHHHPHQLSPMGPSSVPGH
>PRRX1b_Danio_rerio/1-228 311 bp
----MTSSYAHVMDRQATISSRL--ESPITANLENLQAKKNFSVSHLLDLE----EAREMVGSQVDESVGET
GRTMLESPGLTSGSDTNSEEKKKRKQRRNRTTFNSSQLQALERVFERTHYPDAFVREDLARRVNLTEARVQV
WFQNRRAKFRRNERAMLASKNASLLK------------------------SYSGDVTAVEQPIVPRPAPRPN
DYLSWG-SAAPYSWYPRPPMRVPQKMLPTETP--------------QPTHPLVPTPLPPRE-----------
-----------------------
>PRRX1_Homo_sapiens/1-209 311 bp
----MTSSYGHVLERQPALGGRLDS---PGNLDTL-QAKKNFSVSHLLDLE----EAGDMVAAQADENVGEA
GRSLLESPGLTSGSDTNSEEKKKRKQRRNRTTFNSSQLQALERVFERTHYPDAFVREDLARRVNLTEARVQV
WFQNRRAKFRRNERAMLANKNASLLK------------------------SYSGDVTAVEQPIVPRPAPRPT
DYLSWG---TASPYRSSSLPRCCLHE--------------------GLHNGF--------------------
-----------------------
>PRRX1a_Danio_rerio/1-235 311 bp
TSSYHVMDRQATLPNRL--------ETAITANQDHLQAKKNFSVSHLLDLE----EAREMVGAQAEESAGEA
GRSMLESPGLTSGSDTNAEEKKKRKQRRNRTTFNSSQLQALERVFERTHYPDAFVREDLARRVNLTEARVQV
WFQNRRAKFRRNERAMLASKNASLLK------------------------SFSGEVTAVEQPIVPRPAPRPN
DYLSWG-SSPSYSAMATYSPSCANN---------------------TTAQGMNMANS------------IAN
LRLKAKEYSLNQVPTVN------
>PRRX1_Xenopus_tropicalis/1-240 311 bp
----MTSSYNHHVLDRQGPLGSRLESPITASLDNL-QAKKNFSVSHLLDLE----EAGEMVGAQAEDGSGEA
GRSLLESPGLTSGSDTNAEQKKKRKQRRNRTTFNSSQLQALERVFERTHYPDAFVREDLARRVNLTEARVQV
WFQNRRAKFRRNERAMLANKNASLLK------------------------SYAGDVTAVEQPIVPRPAPRPN
EYLSWG-TASPYSAMATYSSTCANT---------------------NPAQGMNMANS------------IAN
LRLKAKEYSLQRNQVPTVN----
>PRRX1_Gallus_gallus/1-237 311 bp
----MASSYAHAMERQALLPARLDG---PAGLDNL-QAKKNFSVSHLLDLE----EAGDMVAAQGDEGGGEP
GRSLLESPGLTSGSDTNSEEKKKRKQRRNRTTFNSSQLQALERVFERTHYPDAFVREDLARRVNLTEARVQV
WFQNRRAKFRRNERAMLASKNASLLK------------------------SYSGDVTAVEQPIVPRPAPRPT
DYLSWG-TASPYSAMATYSTTCTNA---------------------SPAQGMNMANS------------IAN
LRLKAKEYSLQRNQVPTVN----
>ARX_Oryzias_latipes/1-304 311 bp
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EENCGDAGALSPKDEEDGEDCLKRKQRRYRTTFTSYQLEELERAFQKTHYPDVFTREELAMRLDLTEARVQV
WFQNRRAKWRKREKAGVQ-AHPPGLPFPGPLSAGHPLSHYLEGGPFPPHPAAAAAAAAFPSLAPPPHN-GSA
PPLATPAAMFRHPAFIGPTFGRLFSSMGPLTSTAAALLRQPAPPVENPSHAGSVLPDPSSSSSSTSAAAIAA
LRLKAKEHS--AQLTQLNILPAG
>ARX_Xenopus_tropicalis/1-308 311 bp
DARSVPRSEKTDRILLLGGAGENTWVSISRSKSYRENSAPLLREEHSPEGLLQQSSATTACTSDEDDDDEED
EDEEEEEEEEDEANKQDGEDCLKRKQRRYRTTFTSYQLEELERAFQKTHYPDVFTREELAMRLDLTEARVQV
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>ARX_Homo_sapiens/1-308 311 bp
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WFQNRRAKWRKREKAGAQ-THPPGLPFPGPLSATHPLSPYLDASPFPPHHPALDSAWTAAAAAAAAAFPSLP
PPPGSAAAVFRHPAFISPAFGRLFSTMAPLTSSTAAALLRQPTPAVEGAVASGALADPATAAADRRASSIAA
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>ARX_Gallus_gallus/1-290 311 bp
GGGRLPSGPRGERPEGRPEGGAGAGDTLKISHAPQVSISRSKSYRENAPFAPPPPRPGPAAPAEEDEEEEEL
EEDDEEELLGEDGGGLDGEECLKRKQRRYRTTFTSYQLEELERAFQKTHYPDVFTREELAMRLDLTEARVQV
WFQNRRAKWRKREKAGAQTHPPALDSAWTAA-------------------AAAAAAAAFPGLPPPPPGSAAL
PPAGTPAAVFRHPAFISPAFGRLFSTVAPLGSPGAAALLRQPAPAAAEGAVGAGLGEPGSAAADRRASSIAA
LRLKAKEHA--AQLTQLNVLPGG
>SHOX_SHOX_KE994509.1/1-85 311 bp
------------------------------------------------------------------------
-----------DGDSE-----------REDSDF------------------------------GVSKGRCQV
WFQNRRAKCRKQENQMHKGVLIGTTSHLEACRVAPYVNMGALRMPF-------QQVTLHTRNTCTHTHT---
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------EHV--------------
>SHOX_KE996193.1/1-70 311 bp
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WFQNRRAKCRKQENQLHRGVFFSASSHLDACHVAPYLSINSLRLPFQQVQ-------------------GIS
PHA---------------------------------------------------------------------
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>SHOX_SHOX_KE993821.1/1-139 311 bp
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---------------------------------------------------------------------LQV
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SRPCSG-SARASAACKAPPLESPEASLQT-----------------RNSSTPPLSSAGAQVSSVSKHSSLAD
LRMKARRHA--ASLGL-------
>SHOX2_Xenopus_laevis/1-277 311 bp
MEELAFVSKSFDHKIKEKKEMITYREVLESGPARGKESGCGEGAREDGLAGTRCIGGGGGGGGLELDLSVER
IRETGSPKLTEVSPEMRKEELKKIKQRRSRTNFTLEQLNELERLFDETHYPDAFMREELSQRLGLSEARVQV
WFQNRRAKCRKQENQLHKGVLIGAGSQFEACRVAPYVNVGALRMPF----QQVQAQLQLDS-AVAHAHHHLH
PHLTAH---APYMMFPAPPFGLPLATLAA-----------------ETATAASVVAAAAAAKTSSKNSSIAD
LRLKAKKHA--AALGL-------
>SHOX2_Callorhinchus_milii/1-275 311 bp
MEELAFVSKSFDQKVKEKKEGITYREVLESGPVRAREPCMGEGNRDEVNGAQ---RGSSRCPSTEPETGPER
PGDSGTPKLADPGNGDRKEDAKKIKQRRSRTNFTLEQLNELERLFDETHYPDAFMREELSQRLGLSEARVQV
WFQNRRAKCRKQENQLHKGVLIGAANQFEACRVAPYVNVGTLRMPFQQDVLSFQVQAQLQLDSVAHAHHHLH
PHLAAH---APYMMFPPPHFGLPLA---------------------TLAESATVVAAAAAAKTTSKNSSIAD
LRLKAKKHA--AALGL-------
>SHOX2_Danio_rerio/1-275 311 bp
MEELAFVSKSFDQKVKEKKEVITYREVLETGSVRNRESLSADPNREEISSITR--SGVRSSPVEADMLASER
SRDSSSPKLTDGNTDMRKEDCKKIKQRRSRTNFTLEQLNELERLFDETHYPDAFMREELSQRLGLSEARVQV
WFQNRRAKCRKQENQLHKGVLIGAASQFEACRVAPYVNVGALRMPF----QQVQAQLQLDS-AVAHAHHHLH
SHLAAH---APYMMFPAPPFGLPLATLAA-----------------ESASAASVVAAAAAAKTTNKNSSIAD
LRLKAKKHA--AALGL-------
>SHOX2_Gallus_gallus/1-275 311 bp
MEELAFVSKSFDPKAKEKKELITYREVLESGPLRGAREPGGAAAEPGRDETGSPAAGGGRSPPEPDAAAADR
AADAATPKLSDVSPELRKEDAKKIKQRRSRTNFTLEQLNELERLFDETHYPDAFMREELSQRLGLSEARVQV
WFQNRRAKCRKQENQLHKGVLIGAASQFEACRVAPYVNVGALRMPF----QQVQAQLQLDS-AVAHAHHHLH
PHLAHA----PYMMFPAPPFGLPLATLA------------------ESASAASVVAAAAAAKTTSKNSSIAD
LRLKAKKHA--AALGL-------
>SHOX2_Anolis_carolinensis/1-192 311 bp
-------------------------MLSREVLEFLARVRNQFKKLPEALRTD---DGTEYFSP------ELK
ERKEEAKGMEDEGQA-------KIKQRRSRTNFTLEQLNELERLFDETHYPDAFMREELSQRLGLSEARVQV
WFQNRRAKCRKQENQLHKGVLIGAASQFEACRVAPYVNVGALRMPFQQDSFQVQAQLQLDSAVAAHAHHHLH
PHLAAH---APYMMFPAPPF----------------------------------------------------
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>SHOX1_Callorhinchus_milii/1-139 311 bp
----------------------------------------------------------MACGD---------
---------------------------------------------------------------------LCV
WFQNRRAKCRKQENQMHKGVILGSGSHMDACRVAPYVNMGALRMPFQ------QVQAQLQLDGVAHAHPHPA
PSPGRP---RPYLMFPXPPFGLPIASIA------------------ESASAAAAAAAAAAVKTSSKNSSIAD
LRLKARKHA--EALGL-------
>SHOX1_Danio_rerio/1-264 311 bp
MEELAFVSKSFDQKTK---------ESSKESITYREVLESGLARARELGNSETNLTNNNHCPVEHVELEKEK
LKEFSVTRASD-GIYDKKEDVKKLKQRRSRTNFTLEQLNELERLFDETHYPDAFMREELSQRLGLSEARVQV
WFQNRRAKCRKQENQMHKGVILGTASHLDACRVAPYVNMGALRMPF----QQVQAQLQLEGVG-THSHPHLH
PHLAAH---APYLMFPPPPFGLPIASLA------------------DSASAAAAVVAAAKSNSKNSS--IAD
LRLKARKHAEALGL---------
>SHOX1_Xenopus_tropicalis/1-269 311 bp
MEELAFVSKSFDQKSKESNGGGSSK---KETITYREVLETGLARVRELGNSETNLDTSNHCPLHGADSDKDK
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WFQNRRAKCRKQENQMHKGVILGTGSHLETCRVAPYVNMGALRMPFQ------QVQAQLQLEGVAHAHPHLH
PHLAAH---APYLMFPPPPFGLPIASLA------------------DTASAAAVVAAAAKSNSKNSS--IAD
LRLKARKHAEALGL---------
>SHOX1_Anolis_carolinensis/1-273 311 bp
MEELAFVSKSFDQKSKEGAGGGGGGGHKKESITYREVLEGGLARSRELGPAEAGSGGGGGCPVEGDKDSSSK
LKDFGHAARGAEGIYEKREEVKKLKQRRSRTNFTLEQLNELERLFDETHYPDAFMREELSQRLGLSEARVQV
WFQNRRAKCRKQENQMHKGVILGTASHLDACRVAPYVNMGALRMPFQ------QVQAQLQLEGVTHAHPHLH
PHLAAH---APYLMFPPPPFGLPIASLA------------------DSASAAAVVAAAAKSNSKNSS--IAD
LRLKARKHA--EALGL-------
>SHOX1_Gallus_gallus/1-271 311 bp
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WFQNRRAKCRKQENQMHKGVILGTASHLDACRVAPYVNMGALRMPFQ------QVQAQLQLEGVAHAHPHLH
PHLAAH---APYLMFPPPPFGLPIASLA------------------ESASAAAVVAAAAKSNSKNSS--IAD
LRLKARKHA--EALGL-------
>SHOX1_Homo_sapiens/1-272 311 bp
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WFQNRRAKCRKQENQMHKGVILGTANHLDACRVAPYVNMGALRMPFQ------QVQAQLQLEGVAHAHPHLH
PHLAAH---APYLMFPPPPFGLPIASLA------------------ESASAAAVVAAAAKSNSKNSS--IAD
LRLKARKHA--EALGL-------
>SHOX2_Homo_sapiens/1-205 311 bp
MEELAFVSKSFDQKSKDGNGGGGGGGGKKDSITYREVLESGLARSRELGTSDSSLEGGGHCPVDHVDNDKEK
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>PAX7_Xenopus_tropicalis/1-298 311 bp
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WFSNRRARWRKQAGANQLAAFNHLLPGGFPPTGMPALPPYQLPESSYSAALGQDGGSTVHRPQPLPPSSMHQ
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>PAX7_Oryzias_latipes/1-303 311 bp
YKRENPGMFSWEIRDKLLKDGVCDRSTVPSGEASSVSSISRVLRARFGKK-----DDEDDCDK-KDEDGEKK
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>PAX7_Homo_sapiens/1-300 311 bp
YKRENPGMFSWEIRDRLLKDGHCDRSTVPSGLVSSISRVLRIKFGKK--------EEEDEADK-KEDDGEKK
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WFSNRRARWRKQAGANQLAAFNHLLPGGFPPTGMPTLPPYQLPDSTYPTTISQDGGSTVHRPQPLPPSTMHQ
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>PAX7_Gallus_gallus/1-298 311 bp
YKRENPGMFSWEIRDRLLKDGHCDRSTVPSVSSISRVLRIKFGKK----------EEEEDCDK-KEEDGEKK
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WFSNRRARWRKQAGANQLAAFNHLLPGGFPPTGMPTLPPYQLPDSTYPTTISQDGGSTVHRPQPLPPSTMHQ
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QRSDSIKSVDSLPTSQSYCPPTY
>PHOX2Ba_Danio_rerio/1-154 311 bp
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TDPDST------------QPSLPLIGDQKQ----------------DSRDRPPPEELPLLLG-------LTS
LEAQQRGHQIPCVDSVCLC----
>PHOX2Bb_Danio_rerio/1-268 311 bp
----MYKMEYSYLNSSAYESCMAGMDTSSLASAYADFSSCSQASGFQYNPIRTTFGATSGCPSTLRDHQSSP
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VLSSQRQNGAKATLVKTSMF---
>PHOX2B_Xenopus_tropicalis/1-279 311 bp
----MYKMEYSYLNSSAYESCMAGMDTSSLASAYADFSSCSQASGFQYNPIRTTFGATSGCPSTLRDHQSSP
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S2.5) GAD (CHAPTER 3)

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S2.6) PRDM FAMILY (CHAPTER 3)

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SPSSVKSSSALSSPVKDNFS----------------------------------------
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FTVLYGYSKKQGQNAGHAIS----------GLSFPPSTGKLVNTSEIKTYDDNTL--MWE
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VLYGAGAGAVDAQPPLL---------------------------------------DRAA
LQLPEGLTVLQRVTPEGPQLGVFCTQTLPKGLRFGPFQGKIVNTSEIKTYDDNSL--MWE
IF-EDGRLSHFIDG-KGASGNWMALVNCARFPEEQNLVAVQCQSKIYYESCKTIPPGQEL
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VLYGYTCGSDSRRSQQT---------------VTHALSGLRIPTACST-GLDSHILDRDS
LQLPEGLTVLDTSYGTLPKAGVFCKNLIPKGAKFGPFQGKVVHPSEIKTYGDNSL--MWE
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LVWYGNSHNTFLGIPGVPGLEEDQKKN----------------------------KHEDF
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LVWYGNSHNTFLGIPGVPGLEEEQKKN----------------------------KHEDF
HPADSATGTAGRMR------------------CVICHRGFNSRSNLRSHMRIHTLDKPFV
CRFCNRRFSQSSTLRNHVRLHTGERPYKCQVCQSAYSQLAGLRAHQKSARHRPPSTALQA
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LVWYGNFPNTFLGIPGVPGMEEEQKKS----------------------------KHEEF
GSVDVVPTMTGRMR------------------CVICHRGFNSRSNLRSHMRIHTLDKPFV
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HSPTLPVPH------------------PATLAHHIPTMVL--------------------
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GLKPQGLSLAEV-ITSDIL------HSFLYGRWRNVLGEQLFEEKSS-------------
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LVLPSEVIIAQSSIPGEGL-GIFSKTWIKAGTEMGPFTGRVISPEHVDLCKNNNL--MWE
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-------------------------HSNPKTAFTA---EVLAQSFS--------------
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LVWYGNSHNTFLGIPGVPGLEEEQKKN----------------------------KHEDF
HTVETGASTAGRMR------------------CVICHRGFNSRSNLRSHMRIHTLDKPFV
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HSPALPGPH------------------PASLAHHIPTMVL--------------------
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S2.7) ERR EXPANDED (CHAPTER 4)

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>RXR_Ciona 457 bp
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KCITMGMKKEAVQEER---QKN--REQDECHGDGG--------HDDMP-VDKILQAELAS
DPEELINMQEPID--------TSVCKAADHQLFTLVEWAKRVPMFGTLPLDDQVTLLRAG
WNELLIASFSHRSIEIPDGIILASGLRVYRQSAHSAGVGAIFDVLTELIAKMRDMSMDRT
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LCSICGDRASGKHYGVYSCEGCKGFFKRTVRKDLSYACREEKSCIIDKRQRNRCQYCRYQ
KCLAMGMKREAVQEERQR-TKE--RDQSEVESTSS-------LHSDMP-----IERILEA
E-KRVECMEQQGNYENAV---SHICNATNKQLFQLVAWAKHIPHFTSLPLEDQVLLLRAG
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EPGPYVDT-----PRDPV---TNICQAADKQLFTLVEWAKRIPHFTELPLDDQVTLLRAG
WNELLIAAFSHRSIQVKDGILLATGLHVHRNSAHSAGVGTIFDVLTELVAKMREMKMDKT
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>RXR_Mizuhopecten 457 bp
PITDSLDSSVSSASGCISSGSGGMMSSNLSMNSSVNSPPDIKPDLSQ-----NMASPPGS
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WNELLIAAFSHRSIVVKDGILLATGLHVHRSSAHQAGVGTIFDVLTELVAKMREMKMDKT
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>RXR_Crassostrea 457 bp
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>RXRG_Homo 457 bp
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>RXRG_Gallus 457 bp
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>ER_Capitella 457 bp
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>ER_Saccoglossus 457 bp
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KCLLMGMLKEGVRLDRVRGGRQKYRRNPV--SNSYTMQLLYQSNTTSLCDVKILEVLNSY
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>ERRGr_Oryzias 457 bp
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>ERR_Capitella 457 bp
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KCLRMGMLKEGVRLDRVRGGRQKYKRNSDVSNPTFSVSQSFSPQAKMPDDNKMLAALLSI
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KCLRMGMLKEGVRLDRVRGGRQKYKRNPD----SYSFSVSHIPAARKSPDNKILTSLINI
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>ERR_Mizuhopecten 457 bp
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WLEILCLNLVFRSCPYIGYIRFAEDLQMTADCKKCQCSPELDNLTRKLAKKFTNMGVTKE
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WLEVLCLNLVYRSCPYSGYLCFAEDLKVGSDVKTYNVPPEFDNLTRKLCKKFTLLGVSKE
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WLEVLCLNLVFRSCPYSGYLCFAEDLKVSNDVKTYNVPPEFDNLTRKLCKKFTLLGVSKE
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>ERR_Saccoglossus 457 bp
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>ERRG2_Oryzias 457 bp
-----------MSVRGLDPACH------PSIKLEPSSPPSSQGDVSPPQPSPGSSSSDTN
SSYGPLKNLAHSNGLDSPGLQGHSNGGSNRR----------CGEEEGQVKCEFILGSVKR
LCLVCGDVASGYHYGVASCEACKAFFKRTIQGNIEYSCPASNECEITKRRRKSCQACRFV
KCLAVGMLREGVRLDRVRGGRQKYKRRIDAENSLYHSQN--PLPQKKTVENKVVSLLLVA
EPEAIFAMPDPMVAESDIKALTTLCDLADRELVVNIGWAKHIPGFASLSLADQMSLLQSG
WMEILILRVVFRSLAFE-DLVYADDYIMDEEQSKLAGLLDLNNAILQLVKKYKSIGLEKE
EFVVLKAIALANSDSMQIEDTEAVQRLQDELHGALQDYEFTHHPEDPRRTGKVIMTLPLL
RQTAARAVQHFCSIKQDGRVPMHKLFLELLEAKA---
>ERRA_Chrysemys 457 bp
WGNTDTWTDLETCREATPAMSSRDHRAEFFIKTEPASP----DSLAQRSPSGSSDASGP-
-------------PHDPE-----PGALTRRRH--------DNNPDEVLPRGKYVLSSLKR
LCLVCGDVASGYHYGVASCEACKAFFKRTIQGSIEYSCPASNECEITKRRRKACQACRFT
KCLRVGMLKEGVRLDRVRGGRQKYKRRPEVDGAPFTPQIATATSKKPAPINPMVSHLLVA
EPEKLYAMPDPALPDGPLRATSALCDLADREIVVIIGWAKNIPGFPALSLADQMSVLQSA
WLEVLVLGVAWRSLPCEDEVVFAEDFALDEEGARAAGLWELSAALLQLVRKYRALRLERE
EYVLLKALALANSDSVHIEDMAAVQRLRDVLHEALLEYEGSRRPEEPRRAGKLLLTLPLL
RQTAARALHHFYGIKLGGKVPMHKLFLEMLEAMMD--
>ERRA_Anolis 457 bp
---------MSSRERRAE----------FFIKTEPASP----DSLVQHSPSGSSDTSAG-
---------GAPQELEAP------GAQPAGTGASRRRH--DEDPDEPPGRGKYMLSSMKR
LCLVCGDVASGYHYGVASCEACKAFFKRTIQGSIEYSCPATNECEITKRRRKACQACRFT
KCLRVGMLKEGVRLDRVRGGRQKYKRRPEVEGATYTPQIATVTPKKPAPMNTMVSHLLVA
EPEKLYAMPDPALPDGPPKAASTLCDLADREIVVIIGWAKNIPGFPALSLADQMSVLQSV
WLEVLLLGVAWRSLPCEDEIVFAEDFALDEEAARTAGLLELSGVVLQLVRKYRALRLERE
EYVLLKALALANSDSVHIEDMAAVQRLRDVLHEALLEYEASRRPEEPRRAGRLLLTLPLL
RQTATRVLHHFYSLKLEGKVPMHKLFLEMLEAMMD--
>ERRB_lamprey 457 bp
--------------------------------MGPGGP----------------------
--------NGRKRYDDSP------------------------PGADVQTKCEYMLNAMKR
LCLVCGDVASGYHYGVASCEACKAFFKRTIQGNIEYSCPASNECEITKRRRKACQACRFM
KCLKVGMLRE---------GRHRPPGDSLGRTTRSTAPATRVCCARMLVVNKIVSHLIVA
EPDKIYAMPDPTVPDSDIKALTTLCDLADRELVVIIGWAKHVPGFSALSLGDQMSLLQSA
WMEVLLLGVAFRSLPYEDELVYAEDFVMDEELSRLAGLLDLNSAVLQLVRKYKALKLERE
EFVALKAIALVNSDSMHIEDVEGVQKLQDVLHEALQELQGSQHAEDPRRAGKLLMTLPLL
```

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RQTATRAVQHFYSVKLEGKVPMHKLFLEMLEAKVPDL
>ERRC_lamprey 457 bp
-------------------ASGADGPLSAYIKTEPSSPGSLGDAASQPSPGELSDASSGS
YTRHGSGSPTPAHLLQAPPPAPPTPATPGLRKPARYEPGGAAADEGQPSKCEYMLSTLKR
LCLVCGDVASGYHYGVASCEACKAFFKRTIQGNIEYSCPASNECEITKRRRKSCQACRFM
KCLTVGMLKEGVRLDRVRGGRQKYKRRIDAENSPFGPQL--DQPAKKP-LNKIISHLLVA
EPEKMFAMPDPAVPEGEVKALTTLCDLADRELVVIIGWAKHVPGFSVLSLGDQMSLLQSA
WMEVLLLGVVFRSLPCDDELVWADDYVMDEESSRVAGLLDLNSTILQLVRKYKSLALDRE
EFVTLKAIALANSDMHIEDGGAVQRLQDGLHEALQEHGASQHADEPRRAGKLLMTLPLL
R------------------------------------
>ERRD_lamprey_partial 457 bp
------------------------------------------------------------
-----------------P----------------------------------------KK
LCLVCGDVASGYHYGVASCEACKAFFKRTIQ-NIEYSCPAASECEITKRRRKSCQACRFT
KCLRVGMLKE---------GEC--------------------------------------
----------------DVTALTTLCDLADRELVLIIGWAKHVPS----------------
------------------------------------------------------------
-------------DSTHIEDGDGVQRLRDALHEALWEHAGSARRDDPRRAGKLLMTLPLL
RQTAARAVQHFHALKLEGRVPMHKLFLEMLEAKI---
>ERRB2_Oryzias 457 bp
---------MPSDDRHLSSSCG------SYVKTEPSSPSSLVDTGSHHSPSGNSDASGG-
-------YIGRSHALDSPPMFNPGMLGGGSSCLRRYEECPSSMADDSPIKCEYMLNAIKR
LCLVCGDIASGYHYGVASCEACKAFFKRTIQGNIEYSCPATNECEITKRRRKSCQACRFM
KCLKVGMLKEGVRLDRVRGGRQKYKRRLDSENGAYTLSI--PPPAKKP-LTKIVSHLLVV
EPEKIYAMPDPTMPDGDVKALTTLCDLADRELVVIIGWAKHIPGFATLSLADQMSLLQSA
WMEILVLSIVFRSLPCDDEIVYAEDYVVDEEQARISGLLDLHVAIVPLVRRYKKLRMEKE
EFVMLKAIALANSDSMHIENIEAVQKLQDSLHEALQDFEASQHPEDPRRVGKLLMTLPLL
RQTATKAVQHFYSIKMQGKVPMHKLFLEMLEAKA---
>ERR_locA_Eptatretus 457 bp
---------MLPTLQLSPSMAGSNRSFNPYIKTEPSSP----DPLGRHSPSGSSDSSGA-
------QHSPPPLTLLPPIGYGPGPGVPAVAGVGQR----CCADDDVEPKCEYMLNAIKR
LCLVCGDVASGYHYGVASCEACKAFFKRTIQGNIEYSCPATNECEITKRRRKACQACRFM
KCLKVGMLREGVRLDRVRGGRQKYKRRIDAENSPYNPQL--SQPIKKPLVNKIISHLIVA
EPDKIYAMPDPTVPESDVKALTTLCDLADRQLVVIIGWAKHVPGFSTLSLGDQMSLLQSA
WMEILLLGVVFRSLPYEDELVFAEDFVMDEELSRLAGLLDLNSAVLQLVKKYKALKLEKE
EFVTLKAIALVNSDSMHIEDAPGVQKLQDVLHEALQEYEACQHGEDGRRAGKLLMTLPLL
RQTATKAVQHFYAVKLEGKVPMHKLFLEMLEAKV---
>ERRG_Homo 457 bp
HYEEELLCRMSNKDRHIDSSCS------SFIKTEPSSPASLTDSVNHHSPGGSSDASGS-
---YSSTMNGHQNGLDSPPLYPSGGSGPVRK---LYDDCSSTIVEDPQTKCEYMLNSMKR
LCLVCGDIASGYHYGVASCEACKAFFKRTIQGNIEYSCPATNECEITKRRRKSCQACRFM
KCLKVGMLKEGVRLDRVRGGRQKYKRRIDAENSPYNPQL--VQPAKKP-YNKIVSHLLVA
EPEKIYAMPDPTVPDSDIKALTTLCDLADRELVVIIGWAKHIPGFSTLSLADQMSLLQSA
WMEILILGVVYRSLSFEDELVYADDYIMDEDQSKLAGLLDLNNAILQLVKKYKSMKLEKE
EFVTLKAIALANSDSMHIEDVEAVQKLQDVLHEALQDYEAGQHMEDPRRAGKMLMTLPLL
RQTSTKAVQHFYNIKLEGKVPMHKLFLEMLEAKV---
>ERRG_Xenopus 457 bp
---------MSSKDRHIDSSCS------SYIKTEPSSPASLTDSINHHSPGGSSDASGS-
---YSSTMNGHQNGLDSPPLYPSGGNGPVRK---RYDDCSSTIAEESQTKCEYMLNAMKR
LCLVCGDIASGYHYGVASCEACKAFFKRTIQGNIEYSCPATNECEITKRRRKSCQACRFM
KCLKVGMLKEGVRLDRVRGGRQKYKRRIDAENSPYNPQL--VQPAKKP-YNKIVSHLLVA
EPEKIYAMPDPTVPDSDIKALTTLCDLADRELVVIIGWAKHIPGFSTLSLADQMSLLQSA
WMEILILGIVNRSLSFEDELVYAEDYIMDEDQSKLAGLLELNNAILQLVKKYKTMKLEKE
EFVTLKAIALANSDSMHIEDIEAVQKLQDVLHEALQDYEAGQHIEDPRRAGKLLMTLPLL
RQTSTKAVQHFYNIKLEGKVPMHKLFLEMLEAKV---
>ERRG_Chrysemys 457 bp
HYEEELLCRMSSKDRHIDSSCS------SYIKTEPSSPASLTDSINHHSPGGSSDASGSY
----SSTMNGHQNGLDSPPLYPSAGLGGNGPVRKRYDDCSSTIAEDSQTKCEYMLNSMKR
LCLVCGDIASGYHYGVASCEACKAFFKRTIQGNIEYSCPATNECEITKRRRKSCQACRFM
KCLKVGMLKEGVRLDRVRGGRQKYKRRIDAENSPYNPQL--VQPAKKP-YNKIVSHLLVA
EPEKIYAMPDPTVPDSDIKALTTLCDLADRELVVIIGWAKHIPGFSTLSLADQMSLLQSA
WMEILILGVVYRSLSFEDELVYAEDYIMDEDQSKLAGLLDLNNAILQLVKKYKSMKLEKE
EFVTLKAIALANSDSMHIEDVEAVQKLQDVLHEALQDYEAGQHMEDPRRAGKMLMTLPLL
RQTSTKAVQHFYNIKLEGKVPMHKLFLEMLEAKV---
>ERRG_Anolis 457 bp
GTMWKLLCRMSSKDRHIDSSCS------SYIKTEPSSPASLTDSINHHSPGGSSDASGS-
---YSSTMNGHQNGLDSPPLYPSGGNGPVRK---RYDDCSSTIAEDSQTKCEYMLNSMKR
LCLVCGDIASGYHYGVASCEACKAFFKRTIQGNIEYSCPATNECEITKRRRKSCQACRFM
KCLKVGMLKEGVRLDRVRGGRQKYKRRIDAENSPYNPQL--VQPAKKP-YNKIVSHLLVA
EPEKIYAMPDPTVPDSDIKALTTLCDLADRELVVIIGWAKHIPGFSTLSLADQMSLLQSA
WMEILILGVVYRSLSFE-DLVYAEDYIMDEDQSKLAGLLDLNNAILQLVKKYKSMKLEKE
EFVTLKAIALANSDSMHIEDVEAVQKLQDVLHEALQDYEAGQHMEDPRRAGKMLMTLPLL
RQTSTKAVQHFYNIKLEGKVPMHKLFLEMLEAKV---
>ERRG_Gallus 457 bp
---------MSSKDRHIDSSCS------SYIKTEPSSPASLTDSINHHSPGGSSDASGS-
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---YSSTMNGHQNGLDSPPLYPSGGNGPVRK---RYDDCSSTIAEDSQTKCEYMLNSMKR
LCLVCGDIASGYHYGVASCEACKAFFKRTIQGNIEYSCPATNECEITKRRRKSCQACRFM
KCLKVGMLKEGVRLDRVRGGRQKYKRRIDAENSPYNPQL--VQPAKKP-YNKIVSHLLVA
EPEKIYAMPDPTVPDSDIKALTTLCDLADRELVVIIGWAKHIPGFSTLSLADQMSLLQSA
WMEILILGVVYRSLSFE-DLVYAEDYIMDEDQSKLAGLLDLNNAILQLVKKYKSMKLEKE
EFVTLKAIALANSDSMHIEDVEAVQKLQDVLHEALQDYEAGQHMEDPRRAGKMLMTLPLL
RQTSTKAVQHFYNIKLEGKVPMHKLFLEMLEAKV---
>ERRG1_Oryzias 457 bp
---------MSSKERHLESSCP-----SSYIKTEPSSPASLTDSLNHHSPGGSSDASGS-
---YSSTMNGHPNGLDSPSLYGSPAGGPGSK---RYEDCSSTIGEDSQIKCEYMLNSMKR
LCLVCGDIASGYHYGVASCEACKAFFKRTIQGNIEYSCPATNECEITKRRRKSCQACRFM
KCLTVGMLREGVRLDRVRGGRQKYKRRIDADNSPYNPQL--ALPPKKPADNKIVSHLLVA
EPEKIYAMPDPTVPDSDIKALTTLCDLADRELVVNIGWAKHIPGFSTLSLADQMSLLQSA
WMEILILRVVYRSLSFEDKLVYAEDYIMDEDQSKLAGLLDLNNAILQLVKKYKSMKLEKE
EFVTLKAIALANSDSMHIEDVDAVQKLQDVLHEALQDYEASQHQEDPRRGGKLLMTLPLL
RQTSTKAVQHFYSIKQDGKVPMHKLFLELLEAKV---
>ERRG_Lepisosteus 457 bp
HSEEELLCRMSSKDRHIDSSCP------SYIKTEPSSPASLTDSINHHSPGGSSDASGS-
---YSSTMNGHQNGLDSPTLYGPGGLGPNSAASKRYEDCSSTITEDSQIKCEYMLNSMKR
LCLVCGDIASGYHYGVASCEACKAFFKRTIQGNIEYSCPATNECEITKRRRKSCQACRFM
KCLTVGMMREGVRLDRVRGGRQKYKRRIDAENSPYNPQL--ALPAKKPADNKIVSHLLVA
EPEKIYAMPDPTVPDSDIKALTTLCDLADRELVVNIGWAKHIPGFSTLSLADQMSLLQSA
WMEILILRVVYRSLSFEDKLVYAEDYIMDEDQSKLAGLLDLNNAILQLVKKYKSMKLEKE
EFVTLKAIALANSDSMHIEDVEAVQKLQDVLHEALQDYEAGQHAEDPRRAGKLLMTLPLL
RQTSTKAVQHFYSIKQDGKVPMHKLFLELLEAKV---
>ERRGa_Danio 457 bp
---------MSNKDRHIESSCP------SYIKTEPSSPASLTDSVNHHSPGGSSDASGS-
---YSSTMNGHQNGLDSPTLYGPGALGPSGTGAKRYEDCSSTITEDSQIKCEYMLNSMKR
LCLVCGDIASGYHYGVASCEACKAFFKRTIQGNIEYSCPATNECEITKRRRKSCQACRFM
KCLTVGMMREGVRLDRVRGGRQKYKRRIDAENSPYNPQL--ALPPKKP-YNKIVSHLLVA
EPEKIYAMPDPTVPDSDIKALTTLCDLADRELVVNIGWAKHIPGFSTLSLADQMSLLQSA
WMEILILRVVYRSLSFE-DLVYAEDYIMDEDQSKLAGLLDLNNAILQLVKKYKSMKLEKE
EFVTLKAIALANSDSMHIEDVEAVQKLQDVLHEALQDYEAGQHVEDPRRAGKLLMTLPLL
RQTSTKAVQHFYSIKQDGKVPMHKLFLELLEAKV---
>ERRA_lamprey 457 bp
-----------------------------------------------HHH--HHNHH---
-------------GLDSP-PVGFHGMPNAAVPRRRYEDCSPQLTDDPTAKCEYMLNAMKR
LCLVCGDVASGYHYGVASCEACKAFFKRTIQGSIEYSCPATNECEITKRRRKSCQACRFM
KCLKVGMLKEGVRLDRVRGGRQKYKRRIDAENSPYNPQL--AQTVKKPLVNKVISHLLVA
EPEKIYAMPDPTVPEGDIKALTTLCDLADRELVVIIGWAKHIPGFSTLSLGDQMSLLQSA
WMEILLLGVVFRSLPYEDELVWAEDYVMDEELSKVAGLLDLNSAILQLVRKYKALKLDKE
EFVALKAIALANSDSMHIEDGEAVQKLQDVLHEALQDFEGSMHGEDARRVGKLLMTLPLL
RQTATRAVQHFYSVKLEGKVPMHKLFLEMLEAKV---
>ERR_locC_Eptatretus 457 bp
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-------------------------------------------------KCEYMLNAMKR
LCLVCGDVASGYHYGVASCEACKAFFKRTIQGSIEYSCPATNECEITKRRRKSCQACRFM
KCLKVGMMKEGVRLDRVRGGRQKYKRRIDAENSPFNPQL--PQPMKKPLVNKIVSHLLVA
EPEKIYAMPDPSIPDSDIKALTTLCDLADRELVVIIGWAKHIPGFSTLSLGDQMSLLQSA
WMEILLLGVVFRSLHFDDELVFAEDYVMDEELSRLAGLLDLNSAILQLVRKYKSLKLDKE
EFVTLKAIALANSDSMHIEDSEAVQKLQDVLHEALQDYEGNQHSEDVRRAGKLLMTLPLL
RQTATKAVQHFYSIKLEGKVPMHKLFLEMLEAKV---
>ERRB_Homo 457 bp
---------MSSDDRHLGSSCG------SFIKTEPSSPSSGIDALSHHSPSGSSDASGGF
----GLALGTHANGLDSPPMFAGLGGTPCRK---SYEDCASGIMEDSAIKCEYMLNAIKR
LCLVCGDIASGYHYGVASCEACKAFFKRTIQGNIEYSCPATNECEITKRRRKSCQACRFM
KCLKVGMLKEGVRLDRVRGGRQKYKRRLDSESSPYSLQI--SPPAKKP-LTKIVSYLLVA
EPDKLYAMPPPGMPEGDIKALTTLCDLADRELVVIIGWAKHIPGFSSLSLGDQMSLLQSA
WMEILILGIVYRSLPYDDKLVYAEDYIMDEEHSRLAGLLELYRAILQLVRRYKKLKVEKE
EFVTLKALALANSDSMYIEDLEAVQKLQDLLHEALQDYELSQRHEEPWRTGKLLLTLPLL
RQTAAKAVQHFYSVKLQGKVPMHKLFLEMLEAKVGQE
>ERRB_Anolis 457 bp
ILHCRLLGRMSTDERHLTSSCG------SFIKTEPSSPSSGIDAISHHSPSGSSDASGG-
---YGLTMGGHPNGLDSPPMFNSIGGGPCRK---RYEDCASAIMEDSPTKCEYMLNAIKR
LCLVCGDIASGYHYGVASCEACKAFFKRTIQGNIEYSCPATNECEITKRRRKSCQACRFM
KCLKVGMLKEGVRLDRVRGGRQKYKRRLDSENSTYSLQI--PPPAKKP-LTKIVSHLLVA
EPEKIYAMPDPTMPESDIKALTTLCDLADRELVVIIGWAKHIPGFSNLSLGDQMSLLQSA
WMEILILGIVYRSLPYEDKLVYAEDYIMDEEHSRLTGLLELYLAILQLVRRYKKLKVEKE
EFVTLKALALANSDSMHIEDMEAVQKLQDLLHEALQDYELSQRHEEPRRAGKLLLTLPLL
RQTAAKAVQHFYSIKLQGKVPMHKLFLEMLEAKV---
>ERRB_Gallus 457 bp
GYHNQLLGRMATEERHLSSSCG------SFIKTEPSSPSSGIDAISHHSPSGSSDASGG-
---YGIAMGGHPNGLDSPPMFNGIGGGSCRK---RYDDCASAIMEDSPTKCEYMLNAIKR
LCLVCGDIASGYHYGVASCEACKAFFKRTIQGNIEYSCPATNECEITKRRRKSCQACRFM
KCLKVGMLKEGVRLDRVRGGRQKYKRRLDSESSTYSLQI--PPPAKKP-LTKIVSHLLVA
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EPEKIYAMPDPTMPESDIKALTTLCDLADRELVVIIGWAKHIPGFSNLSLGDQMSLLQSA
WMEILILGIVYRSLPYE-DLVYAEDYIMDEEHSRLTGLLELYLAILQLVRRYKKLKVEKE
EFVTLKALALANSDSMHIEDMDAVQKLQDLLHEALQDYELSQRNEEPRRAGKLLLTLPLL
RQTAAKAVQHFYSIKLQGKVPMHKLFLEMLEAKV---
>ERRB_Chrysemys 457 bp
---------MSTEERHLTSSCG------SFIKTEPSSPSSGIDAISHHSPSGSSDASGG-
---YGIAMGGHPNGLDSPPMFNGIGGGSCRK---RYDDCASAIMEDSPTKCEYMLNAIKR
LCLVCGDIASGYHYGVASCEACKAFFKRTIQGNIEYSCPATNECEITKRRRKSCQACRFM
KCLKVGMLKEGVRLDRVRGGRQKYKRRLDSESSTYSLQI--PPPAKKP-LTKIVSHLLVA
EPEKIYAMPDPTMPESDIKALTTLCDLADRELVVIIGWAKHIPGFSNLSLGDQMSLLQSA
WMEILILGIVYRSLPYE-DLVYAEDYIMDEEHSRLTGLLELYLAILQLVRRYKKLKVEKE
EFVTLKALALANSDSMHIEDMEAVQKLQDLLHEALQDYELSQRHEEPRRAGKLLLTLPLL
RQTAAKAVQHFYSIKLQGKVPMHKLFLEMLEAKV---
>ERRB_Danio 457 bp
---------MAAEERHMTSSCG------SYIKTEPSSPSSLVDSASHPSPGAHSDASGG-
---YASAINSHSTGLDSPPMFTAPGASSCRK---RFEDCSTLLDDPAAIKCEYMLNSIKR
LCLVCGDIASGYHYGVASCEACKAFFKRTIQGNIEYSCPATNECEITKRRRKSCQACRFM
KCLKVGMLKEGVRLDRVRGGRQKYKRRMDAENTAYGLTL--PPPAKKP--TKIVSHLLVA
EPEKIYAMPDPTMPESDIKALTTLCDLADRELVVIIGWAKHIPGFSSLSLGDQMSLLQSA
WMEILILSIVFRSLPYE-DLVYAEDYVMDEEHSRLTGLLDLYLSILQLVRKYKKLKVEKE
EFVTLKAIALANSDSMHIEDVESVQKLQDALHEALQDYESCQHAEDPRRAGKLLMTLPLL
RQTATKAIQHFYSIKMQGKVPMHKLFLEMLEAKV---
>ERRB_Lepisosteus 457 bp
NYHNQLLNRMAADDRHLTSSCG------SYIKTEPSSPSSVIDTVSHHSPSGNSDASGG-
---YVSTMNGHSNGLDSPPMFPGLGGGACRK---RYDDCSSTIMEDSPIKCEYMLNSIKR
LCLVCGDIASGYHYGVASCEACKAFFKRTIQGNIEYSCPATNECEITKRRRKSCQACRFM
KCLKVGMLKEGVRLDRVRGGRQKYKRRMDSESSAYGLTL--PPPAKKP-LTKIVSHLLVA
EPEKIYAMPDPTMPESDIKALTTLCDLADRELVVIIGWAKHIPGFSNLSLGDQMSLLQSA
WMEILILSIVFRSLPYEDELVYAEDYIMDEEHSRLTGLLDLYVSILQLVRKYKKLKVEKE
EFVTLKAIALANSDSMHIEDVEAVQKLQDALHEALQDYEASQHQEDPRRAGKLLMSLPLL
RQTATKAVQHFYSIKLQGKVPMHKLFLEMLEAKV---
>ERRB1_Oryzias 457 bp
---------MAADERHLPSSCG------SYIKTEPSSPSSVIDTVSHHSPSGNSDASGG-
---YVSTMNSHSNGLDSPPMFTPLGAGTCRK---RYDDCSSTIMEDSSIKCEYMLNSLKR
LCLVCGDIASGYHYGVASCEACKAFFKRTIQGNIEYSCPATNECEITKRRRKSCQACRFM
KCLKVGMLKEGVRLDRVRGGRQKYKRRLDSENNPYGLTL--PPPTKKP-LTKIVSHLLVA
EPEKIYAMPDPTMPESDIKALTTLCDLADRELVVIIGWAKHIPGFSTLSLGDQMSLLQSA
WMEILILSIVFRSLPYEDELVYAEDYIMDEEHSRLTGLLDLYVSILQLVRKYKKLKVEKE
EFVTLKAIALANSDSMHIEDMEAVQKLQDALHEALQDFECSQHQEDPRRAGKLLMTLPLL
RQTATKAVQHFYSIKVQGKVPMHKLFLEMLEAKV---

S2.8) HMX (CHAPTER 5)

>HMX2_Xenopus_tropicalis 348 bp
MSTKEEP----TKSAP----ATLSSFTIQSILQGTTSDRGR--------TAARVYTREAI
SCPSTSSDEDEQDESWRGHGCNCPDPGDKDSKGQAPHPCGAHRC----------------
----PNRTQMPSPSQQDYTEEKDSHYPQSLGDR---------------------------
--------HKDGGDK------MGNSKKKTRTVFSRSQVYQLESTFDMKRYLSSSERACLA
SSLQLTETQVKTWFQNRRNKWKRQLSAELEAANMAH-ASAQTLVGMPLVFRDNSILR---
--------VPVPRS------IAFPAPLYY-PSSNVSLPLYNLYNKMEY
>HMX2_Danio_rerio 348 bp
MNNSEDS----GSKCSP---APISSFTIQSILGTSNDGVRSA-------GKDSPKSQPRK
RTLSVSSEDDCSAGE-DSGDCYCSEPGVPESC----NPHQPLNFCLGATKGLLPVQDGID
RRPHLTPSILPDY-KEEQGRACSQMSPVSEDR----------------------------
--------QRDGPDK-----QNNSAKKKTRTVFSRSQVYQLESTFDMKRYLSSSERACLA
SSLQLTETQVKTWFQNRRNKWKRQLSAELEAANMAH-ASAQTLVGMPLVFRENSLLR---
--------VPVPRS------IAFPTPLYYPGSNLPALPLYNLYNKD--
>HMX2_Anolis_carolinensis 348 bp
MSNKEEPSKGCPAAAATTTTAPISSFTIQSILGNSKSVGPTSEGGA---PAAVSSWPGRK
RSLSVSSEEEEPDEGWKPPACFCGPKEAPHKR----QPLAAFTCLGTAAKGVGAPL----
----LSSERGPSFLSSAPPPPLPPPDLKEEKERPFAPASSPASPALL-------------
--------GVERGPR-----EASSAKKKTRTVFSRSQVYQLESTFDLKRYLSSSERACLA
SSLQLTETQVKTWFQNRRNKWKRQLSAELEAANMAH-ASAQTLVGMPLVFRDNALLR---
--------VPVPRS------LAFPAPLYYPSSSLSALPLYNLYNKIDY
>HMX2_Gallus_gallus 348 bp
MSSKEEQ----SKCCPPA--APGSTFTIQSILGSGSADGPREP------GPKAAPWPPRG
RNLSLSSDEEEPNESWKHRACFCPEAHGPAEPCRK-QQPLGFARLGSTKGSGTAAGGAER
PP--FLSA-SPQDFKEDKEKPLGPPSPSYGDR----------------------------
--------QRDSGDR-----QAGAAKKKTRTVFSRSQVYQLESTFDMKRYLSSSERACLA
SSLQLTETQVKTWFQNRRNKWKRQLSAELEAANMAH-ASAQTLVGMPLVFRDNSLLR---
--------VPVPRS------IAFPAPLYYPGSNLSALPLYNLYNKIEY
>HMX2_Homo_sapiens 348 bp
MGSKEDA----GKGCPAA--GGVSSFTIQSILGGGPSEAPREP----------VGWPARK

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RSLSVSSEEEEPDDGWKAPACFCPDQHGPKEQGPKHHPPIPFPCLGTPKGSGGSGPGGL-
ERTPLSPS-HSDF-KEEKERLLPAGSPSPGSERP--------------------------
--------RDGGAER-----QAGAAKKKTRTVFSRSQVYQLESTFDMKRYLSSSERACLA
SSLQLTETQVKTWFQNRRNKWKRQLSAELEAANMAH-ASAQTLVSMPLVFRDSSLLR---
--------VPVPRS------LAFPAPLYYPGSNLSALPLYNLYNKLDY
>HMX2_Mus_musculus 348 bp
MGSKEDV----GKGCPAA--GGVSSFTIQSILGGGPSEAPREP----------AGWPARK
RSLSVSSEEEEPEEGWKAPACFCPDPHGPKEPSPKHHTPIPFPCLGTPKGSGGAGPAASE
RTPFLSPS-HPDF-KEEKERLLPAGSPSPGPERP--------------------------
--------RDGGAER-----QTGAAKKKTRTVFSRSQVYQLESTFDMKRYLSSSERACLA
SSLQLTETQVKTWFQNRRNKWKRQLSAELEAANMAH-ASAQTLVGMPLVFRDSSLLR---
--------VPVPRS------LAFPAPLYYPSSNLSALPLYNLYNKLDY
>SOHO_Xenopus_tropicalis 348 bp
-MSKSQN----ECK------PLSINFTIDSILKLSSSRAGRLRP-----QEGLAERPPAG
SRELLVQGGAEGEGDAPREERRVRFPGHGNGHCLVTAQALAY------------------
----CVDQ-QPKH-RELPCRAESPDSLLDEPSP---------------------------
--------TPEKPNK----KNKLLAKKKTRTIFSKSQIFQLESTFDMKRYLSSAERACLA
NSLQLTETQVKIWFQNRRNKLKRQMSAELDGPPVEQTEDANHGVALPVFYKENSFLN---
-----RCVLPMTFPMIY---PGSTFPYLCFPTPSKYYSLTQGDG----
>HMX2_like_Callorhinchus_milii 348 bp
MDKEETI----QCQ------PLSLKFTIDSILKPSPS------------CKELKSDNAKQ
PAIAISERMADSNPRNESTKMDIRHVKDYRKMS---QESMNTAYLTTPS-----------
----LQFTIDAKH-TVKNTEPFGSLDSPDNSDDTA-------------------------
--------RVKLSKK-----TKILAKKKTRTIFSKSQIFQLESTFDMKRYLSSAERACLA
NSLQLTETQVKIWFQNRRNKLKRQLSAELEVTNTTE--PVPKIVQMPTMYKESSFLR---
-----RCLLPVSFPVLY---PGNSTPYLCFPDASKYLHILDGDL----
>SOHO_Gallus_gallus 348 bp
MVQLGGG----RGAPPPLL-APPSAFSIDSILQPGPRCQARE---------------QGR
ARCALPEDEEEEEEEEEEGPAEEHPTKGSTDSGSER------------------------
----LLAE-GPRRADAEAEGAVSPLSTERFRGCRQPSLR---------------------
--------DTGGCGRESGRCSAAGGKKKTRTIFSKSQVFQLESTFDVKRYLSSAERAGLA
AALHLTETQVKIWFQNRRNKLKRQLSAEPEGPGQAEPPGEPPPPPAPSLYKDSALFS---
-----RCLLPLPFPLFY---PGSAIPYLCLPGPVKHFSLLDGDV----
>SOHO_Danio_rerio 348 bp
MSKEDA-----SCR------PASLKFTIDNILNSKTSSRN-------------FDSCHSR
ASLVVCRDGCLHHPGESEDPCKEG------------SDARLHGIDK--------------
----LNRE------GDATVDALKAVDMRSESADSCDDAQ---------------------
--------QKNNGKK-----NKLMTKKKTRTIFSKRQIFQLESTFDMKRYLSSAERACLA
NSLQLTETQVKIWFQNRRNKLKRQLSTELEGPNSEF-GDIGKTVPLPALYKENNLLG---
-----RCMLPMPLPVVY---PGGSAPYFYFSNASKYFSLFDGDI----
>HMX1_Danio_rerio 348 bp
MHEKSQQ----QHTSTT---SRGSSFFIENLLGSCRTEKPVCPI---------KDNDGTE
RANALKRYPNAYRKEMCVQAS---SAGFKTEI----SPLEWKGRETSRSPREESRN----
---------SSEYSRSDRDTPLASEPLDGVVDRKMSGCAVDEGDDARQLFDERS------
--------GPDTSEP------GSARKKKTRTVFSRSQVFQLESTFDMKRYLSSSERAGLA
ASLHLTETQVKIWFQNRRNKWKRQLAADLEAVNFNH--NSQRIVRVPILYHDKATPM---
--STLSFNVSQVSPPLMGFSNSVNYPLSSFAHS---VNLMTSQMTGLV
>HMX3_A_like_Callorhinchus_milii 348 bp
MPETAQE----SPTP-----PKESPFSIKNLLNCDRKPSKPKTF-----LSAVKGAVEG-
AAFALPHCRESGFPRFEIPAQRFALPAHYLER----SPAWWYPCTLS-SGIHLPRTEVV-
EKTNVRDSDSP-----DRDSPEPGLRLQSDAKERDDSKSPDELVLEESSDAEDAKREDHG
GGGGGGGGGGEWKKRTESPDKKPCRKKKTRTVFSRSQVFQLESTFDMKRYLSSSERAGLA
ASLHLTETQVKIWFQNRRNKWKRQLAAELEAANLSH--AAQRIVRVPILYHENSVTD---
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>HMX3_Xenopus_tropicalis 348 bp
MPETGQE----SSNPP----AKESPFSIKSLLTCEPSRAVRPHKAL---FTPIKGALDG-
AAFALSPLTDLTFPRLEIPAQRFALPAHYLER----SPAWWYSYTLA-HGGHTPRTEVPD
KSLLLGPT-SPVS-GGERDSPEPIHPLKAELEAKDSESKSPEEIILEESEPEEGKKDDSG
EDWKK---REESPDK------KPCRKKKTRTVFSRSQVFQLESTFDMKRYLSSSERAGLA
ASLHLTETQVKIWFQNRRNKWKRQLAAELEAANLSH-AAAQRIVRVPILYHENSSSA---
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>HMX3_Danio_rerio 348 bp
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QK--ARDS-SPTT-GTDRDSPELVLKSDPDAKDDEDDNKSGDEIVLEESDTEDGKKEGGI
DDWK----KSDDGAD-----KKPCRKKKTRTVFSRSQVFQLESTFDMKRYLSSSERAGLA
ASLHLTETQVKIWFQNRRNKWKRQLAAELEAANLSH-AAAQRIVRVPILYHENSASE---
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>HMX3_Gallus_gallus 348 bp
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KS--LLRDSSPAS-GTDRDSP-EPLLQGGDAEQKERDPKSPAEIVLEESDSEEGKKEGG-
--------AEDWKKREESPEKKPCRKKKTRTVFSRSQVFQLESTFDMKRYLSSSERAGLA
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-SSAAGGGGPGPQPL-----LTFPHPVYYSHPSVTSVPLLRPV-----
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>HMX3_Thamnophis_sirtalis 348 bp
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AGFALSQMGDLAFPRFEIPAQRFALPAHYLER----SPAWWYPYSLT--GGHLPRPEASV
EKC-LLRDSSPASGGTDRDSPEEPLLK----AEKALDTKSPDEIILEESDSEEAKKEESG
AEDWPKREEAGSPEK-----KPPCRKKKTRTVFSRSQVFQLESTFDLKRYLSSSERAGLA
ASLHLTETQVKIWFQNRRNKWKRQLAAELEAANLSH-AAAQRIVRVPILYHESAGADAGA
SGAAGATSAPVSQPL-----LTFPHPVYYSHPVVTSVPLLRPV-----
>HMX3_Mus_musculus 348 bp
MPEPGPDASGTPPPQPPPQPPKESPFSIRNLLNGDHHRPPPKPQPPPRTAAAAKGALEGA
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KA--LLRDSSPAS-GTDRDSPEP--LLKADPDHKELDSKSPDEIILEESDSEEGKKEGEA
VPGAAGTTGAESPEK-----KPACRKKKTRTVFSRSQVFQLESTFDMKRYLSSSERAGLA
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AAAAAGAPVPVSQPL-----LTFPHPVYYSHPVVSSVPLLRPV-----
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KA--LLRDSSPAS-GTDRDSPEP--LLKADPDHKELDSKSPDEIILEESDSEESKKEGEA
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>HMX1_Xenopus_tropicalis 348 bp
MPDDSTE----PQSTSTA--ARVSSFFMENLLGAESKEEKKR---------------KGA
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----IGCT-SPDT--SDRDSPEIAEAGEGPGRGLRKHSESPGERREDYACKEEEEEE---
--------KAEQDSD-----QRSSRKKKTRTVFSRSQVFQLESTFDMKRYLSSSERAGLA
ASLHLTETQVKIWFQNRRNKWKRQLAADLEAANISH--TSQRIVRVPILYHENSAAT---
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>HMX1_Callorhinchus_milii 348 bp
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----PKRG-SASS-EEEQCFSLTASDRDSPQGSDKGDRHEEVCSKEGGELQEEKRAELE-
--------SNEAAKDQTDPNQKTGRKKKTRTVFSRSQVFQLESTFDMKRYLSSSERAGLA
ASLHLTETQVKIWFQNRRNKWKRQLAADLEAVNLSH--SSQRIVRVPILYHENSPSG---
---ALGFSLPQVSPPLVSFSSSINYPLATFPSS---MPFLRSQMSGLV
>HMX1_Gallus_gallus 348 bp
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GGRGAPRCGPHSPLRLGASGCPLRD-----------AAVGWYRRAF--------------
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--------EAGEAEQ-----RAAGRKKKTRTVFSRSQVFQLESTFDVKRYLSSSERAGLA
ASLHLTETQVKIWFQNRRNKWKRQLAADLEAANLSH--AAQRIVRVPILYHENSPAS---
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>HMXB_hafish 348 bp
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RG--ISPD-TSLSPLSERDSPSTREVRREESVNVQRISVCPAINTGNVANISKEEANHNL
--------EPEKCEETVDGEKKSGRKKKTRTVFSRSQVFQLESTFDMKRYLSSAERAGLA
ASLHLTETQVKIWFQNRRNKWKRQLAAELEAANLSQ--NAQRLVRVPILYHESPATQ---
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>HMX1_Homo_sapiens 348 bp
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>HMX1_Mus_musculus 348 bp
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--------AAAATGE-----ARGGRRKKTRTVFSRSQVFQLESTFDLKRYLSSAERAGLA
ASLQLTETQVKIWFQNRRNKWKRQLAAELEAASLSP-PGAQRLVRVPVLYHESPPAAGPA
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>HMXB_lampetra 348 bp
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SAHVHGGASHLTRPLL----QGFAHPLPYMHQAIGSPMPVMRSMTGLV
>HMX1_Thamnophis_sirtalis 348 bp
MPDQASG----TVQAAS---ARVSSFFIANLLAAQTKRRRRGDEEEEEEEAAEEESGPRQ
AREETPAPRAQPGRPCPLACCQAPGPRLELSSPLRESALEWYRRARKAFRSCASPET---
----SDRD-SPEI-AEGATQPKASRQPRGTADPNAVEEKSTEPGRGRPGSGGGVADGKQR
PE------EPEASEA-----RAGGRKKKTRTVFSRSQVFQLESTFDVKRYLSSSERAGLA
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>HMXA_hagfish 348 bp
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AACRAGDRACESPPQ--HGSPRAPPKKKTRTVFSRSQVFQLESTFDMKRYLSSAERAGLA
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------------------------------------------------------------
------------------------------------------------------------
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S2.9) HMX CNE (CHAPTER 5)

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ACC---TTTTC-----------CATTATGGTGG--------AATATTATTTGTACGGAATCCATTAAATTCA
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CAATCCAG--CCCTAATGGT-AGGCTGTAGCGTTTCCAGAAGA---------------AAATTTTTGAAAGG
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CAATCCAG--CCCTAATGGT-AGGCTGTAGCGTTTCCAGAAGA---------------AAATTTTTGAAAGG
T----GGTTTGC---------AGAAAGCGAAGCTGTTATGACACTAGAA--ATTGCTTTATTGATAGCCTCG
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>uHMXcne_mouse/466-1570
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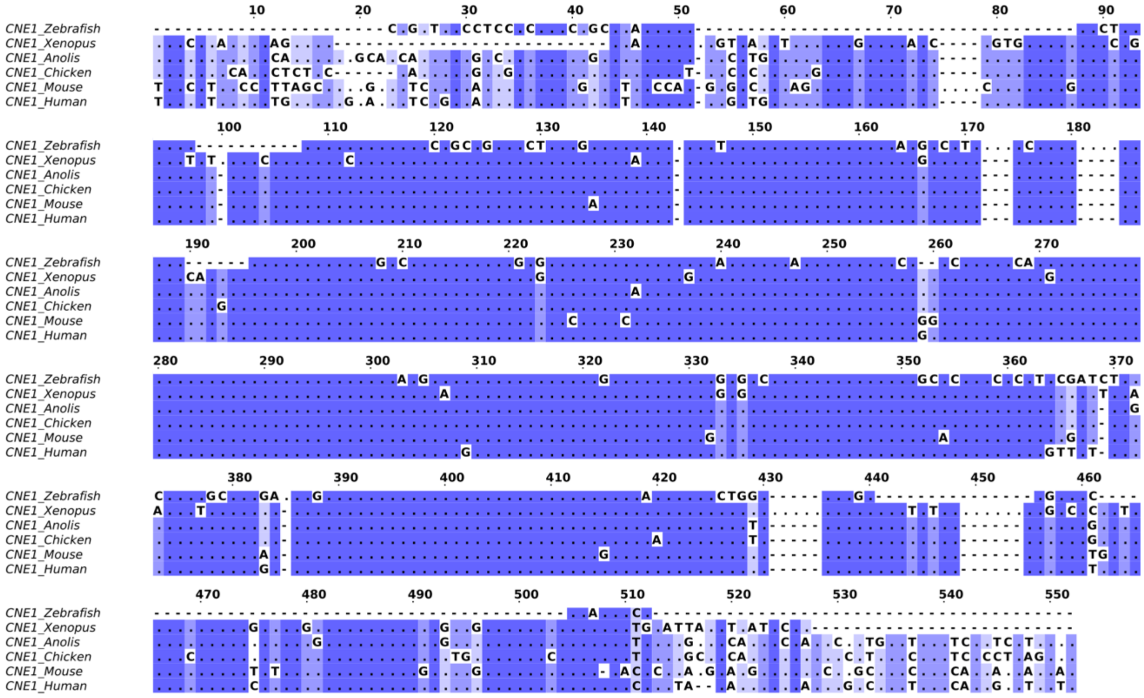
S3) CNE SEQUENCES AND ALIGNMENTS

S3.1) ERR CNE and alignments

CNE sequences as portrayed in Figure 3.5A, B. Alignment image files are followed by sequences in FASTA format.



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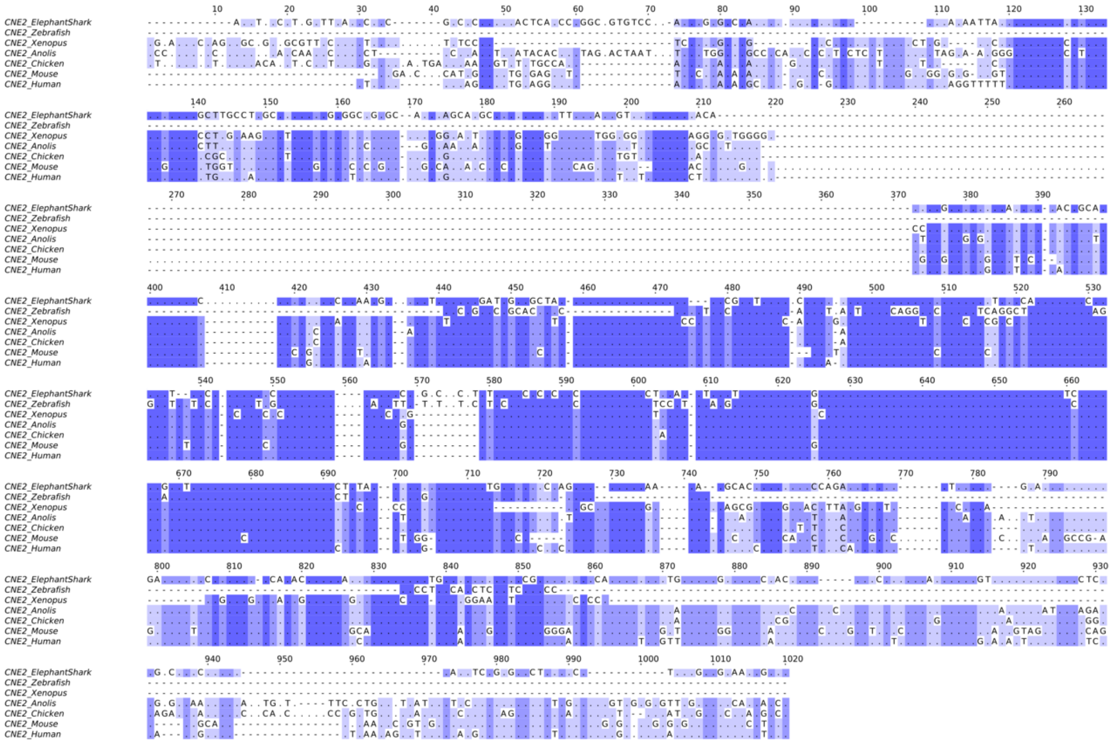

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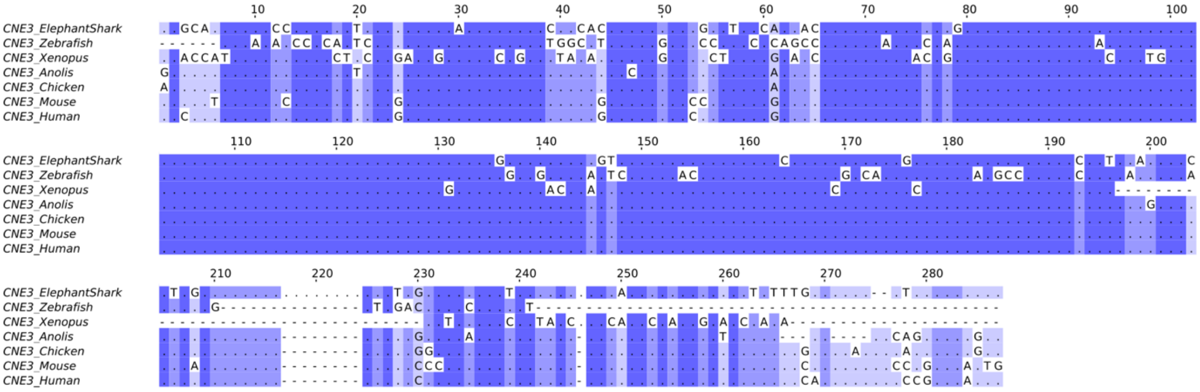

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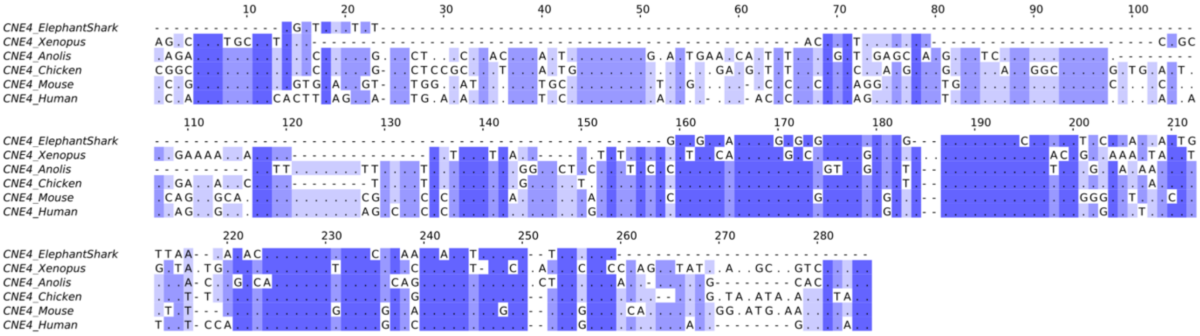

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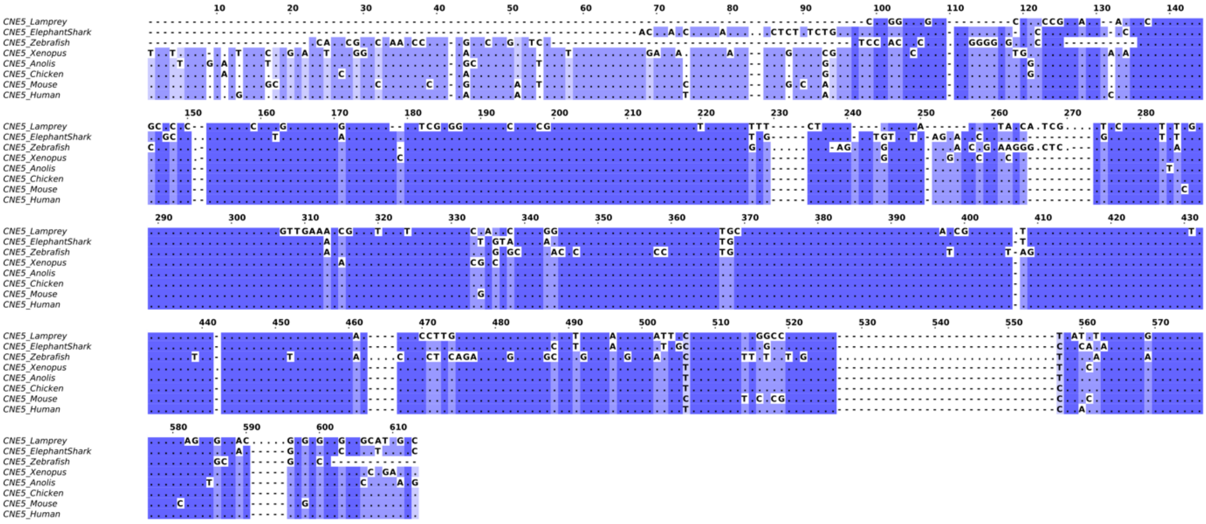
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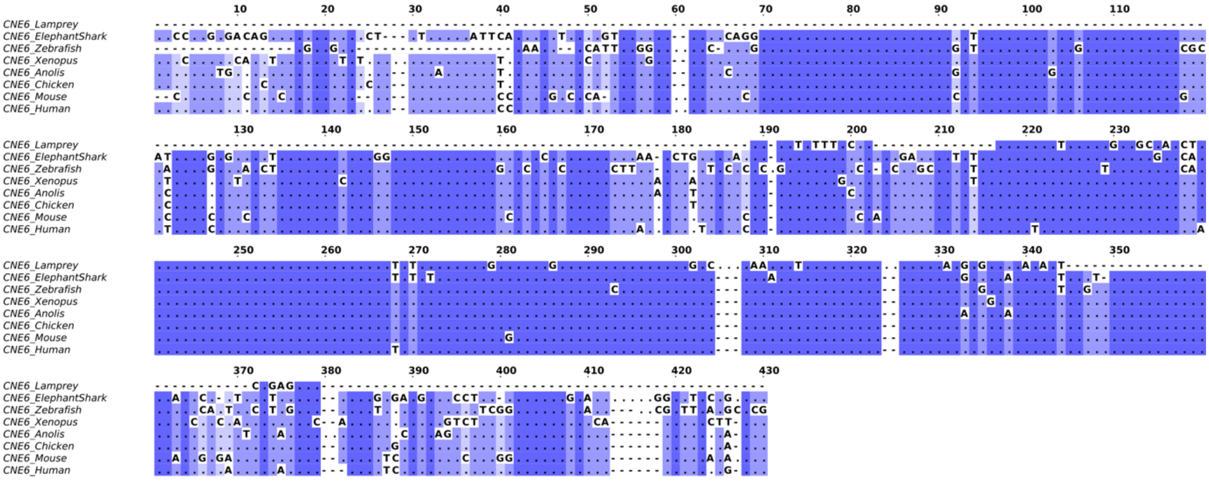
CNE5_Chicken
CNE5_Mouse
CNE5_Human

CNE5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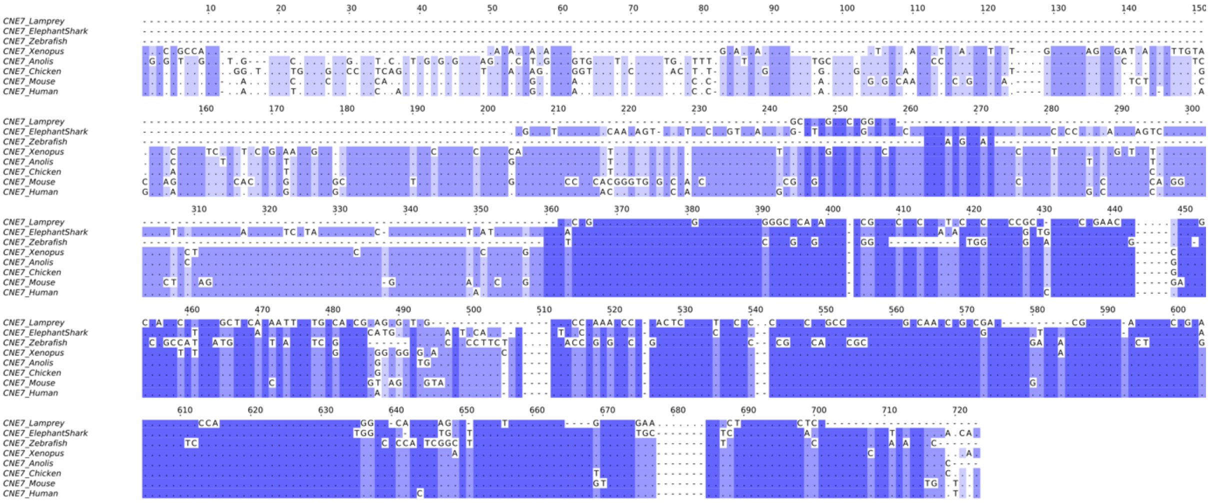
CNE6_Anolis
CNE6_Chicken
CNE6_Mouse
CNE6_Human

CNE6



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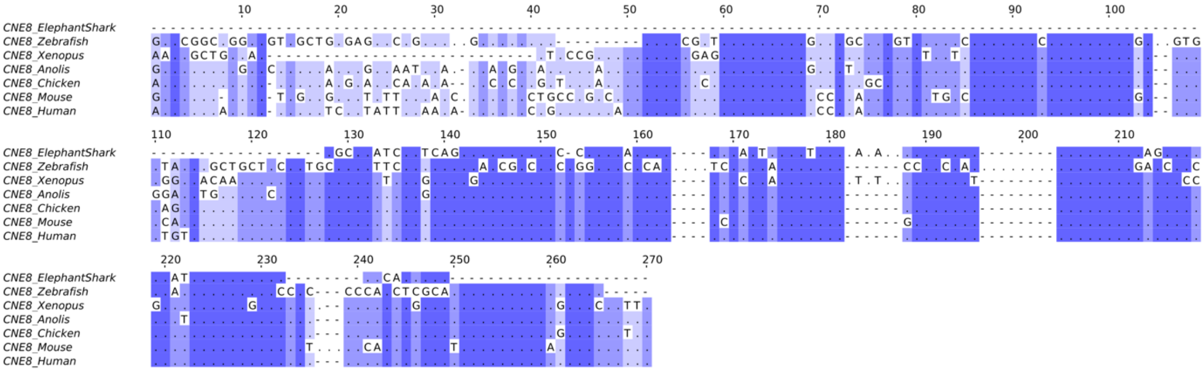

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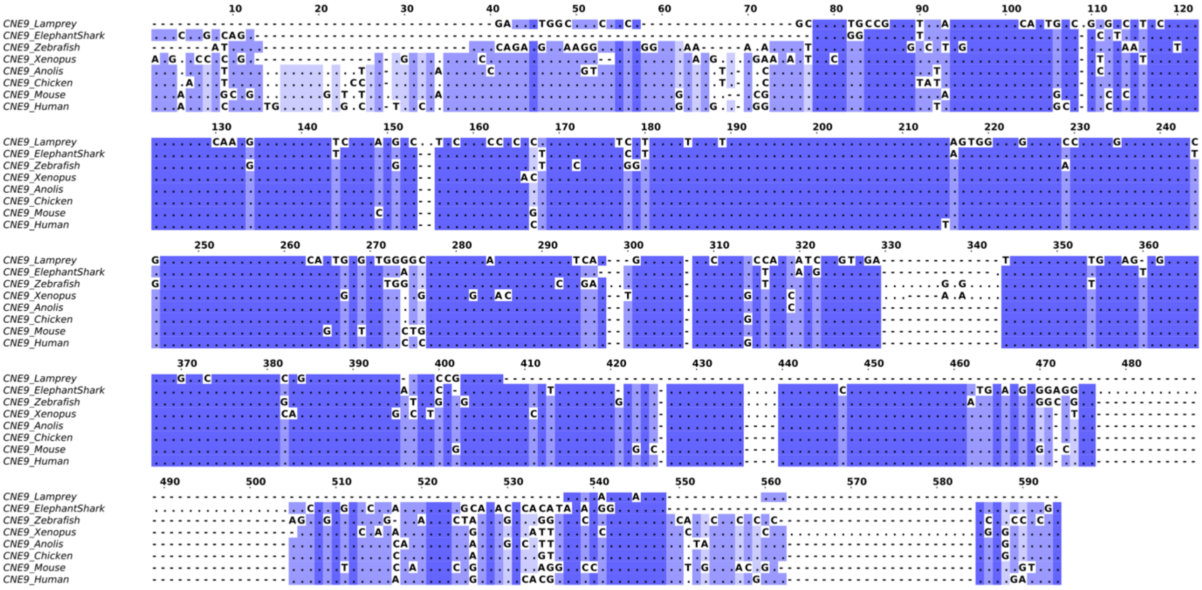

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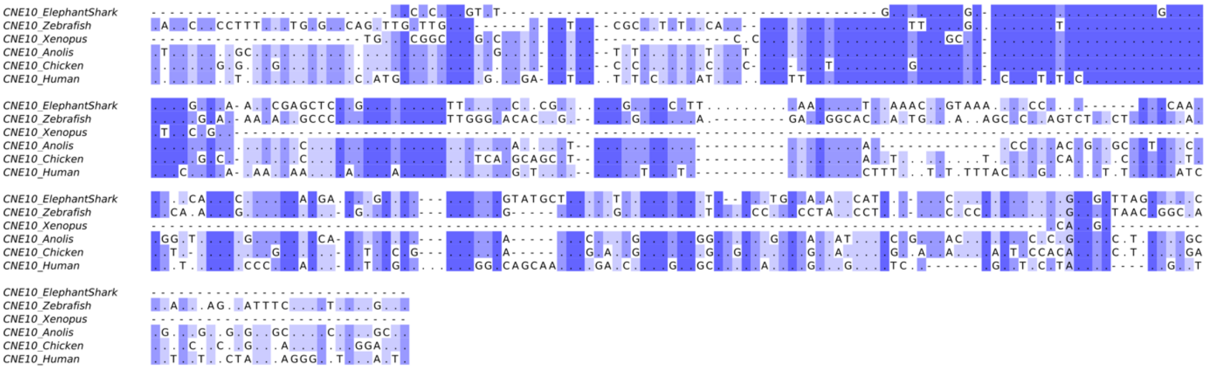

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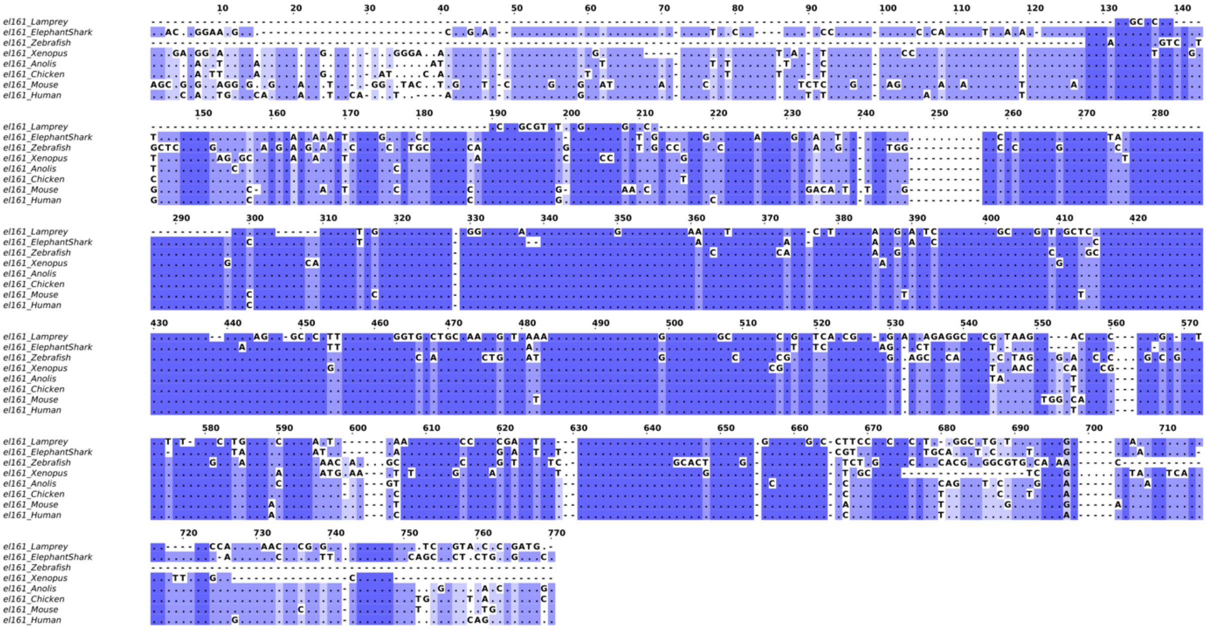

EL161

ERRγ CNE SEQUENCES

CNE1

> CNE1_Anolis
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CNE2

> CNE2_Anolis
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CNE3

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CNE4

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CNE5

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CNE6

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CNE7

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Hmx uCNE cloned piece

> uHMXcne_cloned
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S4) *P. marinus* Additional Hmx Scaffold

BLASTN alignment of the *P. marinus* Hmx homeobox containing gene model (PMZ_0038761-RA, Query) on scaffold_00813 with the *P. marinus* Hmx locus (Sbjct) of scaffold_00015. See Materials and Methods for more details.

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Identity=  2448/2455 (99.71%) ,  Positive=  2448/2455 (99.71%)
Query Matches 1 to 2448 Hit Matches = 7402804 to 7400350

Query:             1 ATGACGGACAAGCAGTCCCCGCCGTGTAGCGCGGCGCCCAAGTTCAGCATCCAGCGCATC 60
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:       7402804 ATGACGGACAAGCAGTCCCCGCCGTGTAGCGCGGCGCCCAAGTTCAGCATCCAGCGCATC 7402745

Query:            61 CTGGGCACGGACCTGGCCGACTCGTGCAGGAGACCGAGCCAAGGCGCCATCAAGGGCGAC 120
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:       7402744 CTGGGCACGGACCTGGCCGACTCGTGCAGGAGACCGAGCCAAGGCGCCATCAAGGGCGAC 7402685

Query:           121 GCGTGGAGAGGCTTCCCGCTGTCCGCGGCCGGCGTCGACCTGTCCCTGTTCTCGTCGAGC 180
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:       7402684 GCGTGGAGAGGCTTCCCGCTGTCCGCGGCCGGCGTCGACCTGTCCCTGTTCTCGTCGAGC 7402625

Query:           181 AACGGCCCCCACTACGCGGCGGGCGCGAGGGAGGCGCTCTGCGGGTGTAAGAAGAAGAAG 240
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:       7402624 AACGGCCCCCACTACGCGGCGGGCGCGAGGGAGGCGCTCTGCGGGTGTAAGAAGAAGAAG 7402565

Query:           241 CGGCTCCAGGGAGCGACAGCCCCCGGACGGTGCCGCCCCGGGCAGGCGGCGGACATCGAG 300
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Sbjct:       7402564 CGGCTCCAGGGAGCGACAGCCCCCGGACGGTGCCGCCCCGGGCAGGCGGCGGACATCGAG 7402505

Query:           301 GCGCTCGTGTCGCCCGCGTCAAGCGTCTCGTCTGACGGTAAGGTGGGGGGGGG-CAGAGC 360
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Query:           361 AGAGCGCCAGGCTGGTTTGTTGTGATGCTGCTGCTGCTGCTGTCGATGTCGGCTACAACA 420
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Query:           421 ATAGTAACGGTAGCAGCGGCTGCGTTGAGCAAAGCTGAAGGATCCAGCAATGACCACCAA 480
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Query:           481 CAGCCACCACCACCACCAATGCGAATAAGACCCCCCCCC-TACCCACCACTCTTAACAAT 540
                     ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct:       7402324 CAGCCACCACCACCACCAATGCGAATAAGACCCCCCCCCCTACCCACCACTCTTAACAAT 7402265

Query:           541 AGCTATCAGCAACACTAACTACCGGCATTGACATTATCAACACCACCACTAGCGCCACCA 600
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:       7402264 AGCTATCAGCAACACTAACTACCGGCATTGACATTATCAACACCACCACTAGCGCCACCA 7402205

Query:           601 CCAACGGCCAACCAAAACACCACCAACAACTACAACAAAACACCAATACTGTAACAAGAA 660
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Query:           661 CCATCATCACCATTAAATAAACAATAGCCACCGCCACCAACAACTAATATCAAAAACCAC 720
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Sbjct:       7402144 CCATCATCACCATTAAATAAACAATAGCCACCGCCACCAACAACTAATATCAAAAACCAC 7402085

Query:           721 CAACAGCCATCAACAACAATAACCAGCAGCAGTAGCAACACCACTACAACCATCACCACC 780
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Sbjct:       7402084 CAACAGCCATCAACAACAATAACCAGCAGCAGTAGCAACACCACTACAACCATCACCACC 7402025

Query:           781 AAGGCTCTCGGGATCGCCCGGTTGTAGTAACAGCAGTAGCGGACCCGTGTCAAGTAGATT 840
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Sbjct:       7402024 AAGGCTCTCGGGATCGCCCGGTTGTAGTAACAGCAGTAGCGGACCCGTGTCAAGTAGATT 7401965

Query:           841 GACCATTGCTCCACACCCAAGTCTAGTTTATGGTCAGTATAATTGCATTGCCCACGTGGA 900
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Sbjct:       7401964 GACCATTGCTCCACACCCAAGTCTAGTTTATGGTCAGTATAATTGCATTGCCCACGTGGA 7401905

Query:           901 TAACTCGATGTAGCCACTCGCAGTGCTGATTTGACAGGTGTGCCAATAATTAACCAACAC 960
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Query:      961 GGTCGGCCAGTTAAGCGTCTGCCGGTTAAGAGTGAACAGGTTTATGGAGCAAATAGATAG 1020
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Query:     1021 AAGTGATGTTATAAACGAGTGAATAAACACAATGTCATGGGTGTACTTTTTGTAGTTAAG 1080
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Query:     1081 TATTGCCACATACATGTGTGTGTGT--ATTACAGTTGCTTTGATATAGATTTGCGTTGTT 1140
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Sbjct:  7401724 TATTGCCACATACATGTGTGTGTGTGTATTACAGTTGCTTTGATATAGATTTGCGTTGTT 7401665

Query:     1141 GGAGTATGCCCGTATATTTGGGTTGTTTATTCGCAACAACATGAATATATTCGCTTGTTA 1200
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Sbjct:  7401664 GGAGTATGCCCGTATATTTGGGTTGTTTATTCGCAACAACATGAATATATTCGCTTGTTA 7401605

Query:     1201 CCGAACGAAATATATTTAACGGCGACCTTTCCCCCGTAAATATTTAATTGTCTAGATCGA 1260
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Sbjct:  7401604 CCGAACGAAATATATTTAACGGCGACCTTTCCCCCGTAAATATTTAATTGTCTAGATCGA 7401545

Query:     1261 AGTAATTAATAATTTGTGTTGTTTTAAAAATACATTGTCAGGCTTATAAGCTTATCGGAG 1320
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Query:     1321 AGGACGTAAAATATGCCTCGGGAAAGTTTGAATTGAATAATTTTCTGCCACTTTCAGTGC 1380
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Sbjct:  7401484 AGGACGTAAAATATGCCTCGGGAAAGTTTGAATTGAATAATTTTCTGCCACTTTCAGTGC 7401425

Query:     1381 TAACGTACTCGTTTGTTTAATCAGAGATCTACGTCCGAACACGTTCCGTAACAAGATGAC 1440
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Sbjct:  7401424 TAACGTACTCGTTTGTTTAATCAGAGATCTACGTCCGAACACGTTCCGTAACAAGATGAC 7401365

Query:     1441 GAAGATAATTCTGACGCGTGAAACACAACACGGTTATTAGTGTTTCGGGGGGAAGGAGAC 1500
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Sbjct:  7401364 GAAGATAATTCTGACGCGTGAAACACAACACGGTTATTAGTGTTTCGGGGGGAAGGAGAC 7401305

Query:     1501 AACGCGAAAAACATATTGTATGCGCGCTTCGCTATGAACGAGACGGCCGAAGTTCGATTC 1560
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Query:     1561 CCGACCACGGCTAACATCGGTAGCGAGTGGTGTCTGATCCGCGGTCCTGTGTGCGACTAC 1620
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Sbjct:  7401244 CCGACCACGGCTAACATCGGTAGCGAGTGGTGTCTGATCCGCGGTCCTGTGTGCGACTAC 7401185

Query:     1621 GACTAACAACTCTAAATCATGGACGATATTAATGTCGCACTGTCCGAAAGTTTAACGTGA 1680
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Query:     1681 CAGAGGTGTAAATGCGATTCACCAATATATATAACGGCGAGAATTGGTGAATTGCATATA 1740
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Query:     1741 AAGATATAATCGAATAACTCGTCAATAACTTACAATCTCGAATAGTTGCTTCATATATGC 1800
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Query:     1981 GCACCGCAGCCACCAAAGAGACGTCCTTAGATTTATCAAACCCGGACGACGTCGCCGAAA 2040
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  7400824 GCACCGCAGCCACCAAAGAGACGTCCTTAGATTTATCAAACCCGGACGACGTCGCCGAAA 7400765

Query:     2041 GGGTCTCGCCGGACTTCAAGGCCCCGCCGCAGAAGCGCTCGGCGAGTCGGGTCACGGCGG 2100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query:     2101 ACGACAGAGACTCCCAGACGGAGGAGAGGGACGCGGAGAGCGCCGCGTGTCGGGCCGGGG 2160
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Query:         2161 ACAGGGCCTGCGAGAGCCCCCCTCAGCACGGCAGCCCGCGTGCGCCCCCCAAGAAGAAGA 2220
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Query:         2221 CGCGGACCGTGTTCTCACGGAGC-AAGTGTTCCAGCTGGAGTCGACGTTCGACATGAAGC 2280
                    ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
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Query:         2281 GCTACCTGAGCAGCGCGGAGCGCGCGGGGCTCGCCGCGTCGCTGCACCTCACCGAGACGC 2340
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Query:         2341 AGGTGAAGATCTGGTTCCAGAACCGGCGCAACAAGTGGAAGCGCCAGCTCGCCGCCGAGC 2400
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Query:         2401 TCGAGGCCGCAAAC-TGGCGCA-GTGTCGGCGGCGCACAGACTCGTGCGTGTGCC 2448
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S5) *L. camtschaticum Hmx* gene sequence alignment

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CGCAATGCCGCCCT-TTCGCCTCGTCGAGAAGTCCATTGCCCCGTGGCAC--CCCTACCTCCCGTT---CGG
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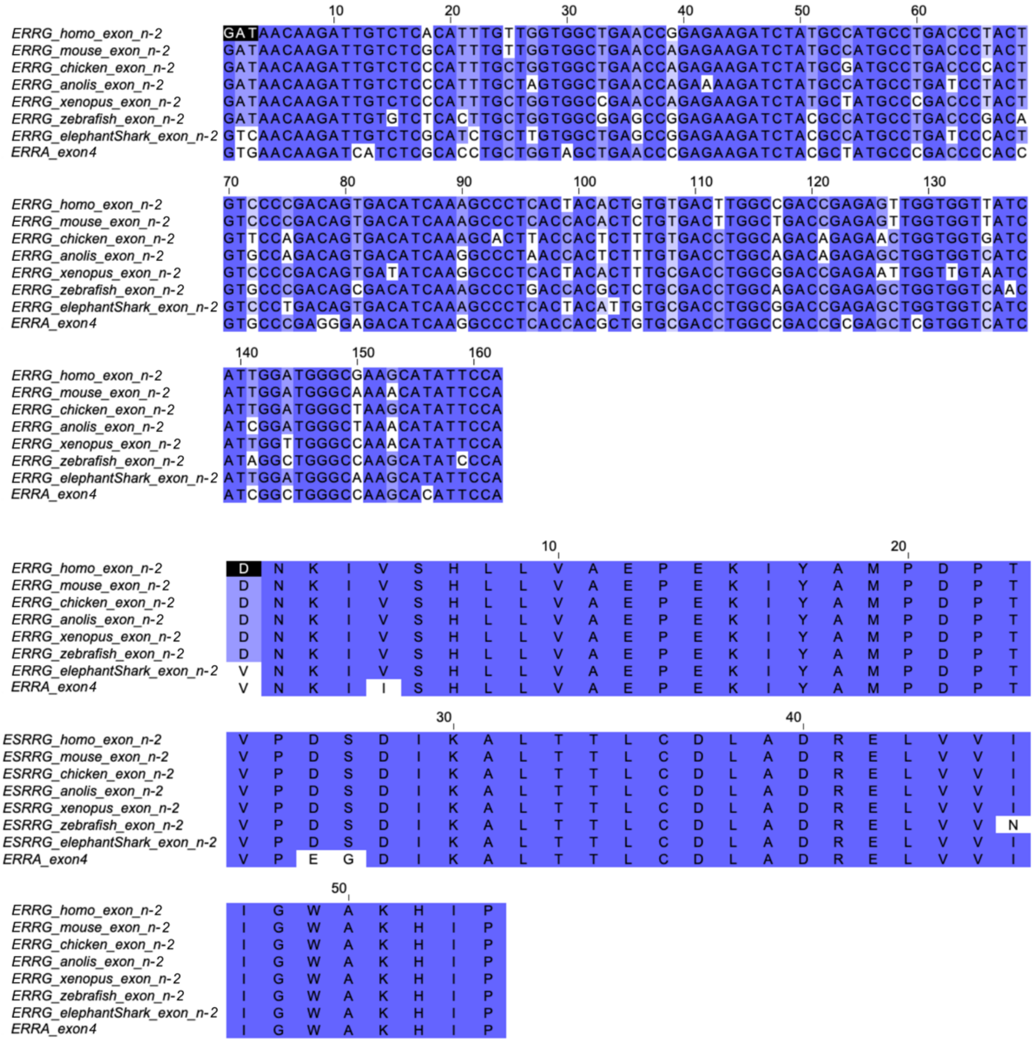
S6) Vertebrate *ERRγ/ERRA* last exon alignments



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ERRG_homo_exon_n-2            GATAACAAGATTGTCTCACATTTGTTGGTGGCTGAACCGGAGAAGATCTATGCCATGCCTGACCCTACT
ERRG_mouse_exon_n-2           GATAACAAGATTGTCTCGCATTTGTTGGTGGCTGAACCAGAGAAGATCTATGCCATGCCTGACCCTACT
ERRG_chicken_exon_n-2         GATAACAAGATTGTCTCCCATTTGCTGGTGGCTGAACCAGAGAAGATCTATGCGATGCCTGACCCCACT
ERRG_anolis_exon_n-2          GATAACAAGATTGTCTCCCATTTGCTAGTGGCTGAACCAGAAAAGATCTATGCCATGCCTGATCCTACT
ERRG_xenopus_exon_n-2         GATAACAAGATTGTCTCCCATTTGCTGGTGGCCGAACCAGAGAAGATCTATGCTATGCCCGACCCTACT
ERRG_zebrafish_exon_n-2       GATAACAAGATTGTGTCTCACTTGCTGGTGGCGGAGCCGGAGAAGATCTACGCCATGCCTGACCCGACA
ERRG_elephantShark_exon_n-2   GTCAACAAGATTGTCTCGCATCTGCTTGTGGCTGAGCCGGAGAAGATCTACGCCATGCCTGATCCCACT
ERRA_exon4                    GTGAACAAGATCATCTCGCACCTGCTGGTAGCTGAACCCGAGAAGATCTACGCTATGCCCGACCCCACC

ERRG_homo_exon_n-2            GTCCCCGACAGTGACATCAAAGCCCTCACTACACTGTGTGACTTGGCCGACCGAGAGTTGGTGGTTATC
ERRG_mouse_exon_n-2           GTCCCCGACAGTGACATCAAAGCCCTCACCACACTCTGTGACTTGGCTGACCGAGAGTTGGTGGTTATC
ERRG_chicken_exon_n-2         GTTCCAGACAGTGACATCAAAGCACTTACCACTCTTTGTGACCTGGCAGACAGAGAACTGGTGGTGATC
ERRG_anolis_exon_n-2          GTGCCAGACAGTGACATCAAGGCCCTAACCACTCTTTGTGACCTGGCAGACAGAGAGCTGGTGGTCATC
ERRG_xenopus_exon_n-2         GTCCCCGACAGTGATATCAAGGCCCTCACTACACTTTGCGACCTGGCGGACCGAGAATTGGTTGTAATC
ERRG_zebrafish_exon_n-2       GTGCCCGACAGCGACATCAAAGCCCTGACCACGCTCTGCGACCTGGCAGACCGAGAGCTGGTGGTCAAC
ERRG_elephantShark_exon_n-2   GTCCCTGACAGTGACATCAAAGCCCTCACTACATTGTGCGACCTGGCGGACCGAGAGCTGGTGGTCATC
ERRA_exon4                    GTGCCCGAGGGAGACATCAAGGCCCTCACCACGCTGTGCGACCTGGCCGACCGCGAGCTCGTGGTCATC

ERRG_homo_exon_n-2            ATTGGATGGGCGAAGCATATTCCA
ERRG_mouse_exon_n-2           ATTGGATGGGCAAAACATATTCCA
ERRG_chicken_exon_n-2         ATTGGATGGGCTAAGCATATTCCA
ERRG_anolis_exon_n-2          ATCGGATGGGCTAAACATATTCCA
ERRG_xenopus_exon_n-2         ATTGGTTGGGCCAAACATATTCCA
ERRG_zebrafish_exon_n-2       ATAGGCTGGGCCAAGCATATCCCA
ERRG_elephantShark_exon_n-2   ATTGGATGGGCAAAGCATATTCCA
ERRA_exon4                    ATCGGCTGGGCCAAGCACATTCCA
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ERRG_homo_exon_n-2            D N K I V S H L L V A E P E K I Y A M P D P T
ERRG_mouse_exon_n-2           D N K I V S H L L V A E P E K I Y A M P D P T
ERRG_chicken_exon_n-2         D N K I V S H L L V A E P E K I Y A M P D P T
ERRG_anolis_exon_n-2          D N K I V S H L L V A E P E K I Y A M P D P T
ERRG_xenopus_exon_n-2         D N K I V S H L L V A E P E K I Y A M P D P T
ERRG_zebrafish_exon_n-2       D N K I V S H L L V A E P E K I Y A M P D P T
ERRG_elephantShark_exon_n-2   V N K I V S H L L V A E P E K I Y A M P D P T
ERRA_exon4                    V N K I I S H L L V A E P E K I Y A M P D P T

ESRRG_homo_exon_n-2           V P D S D I K A L T T L C D L A D R E L V V I
ESRRG_mouse_exon_n-2          V P D S D I K A L T T L C D L A D R E L V V I
ESRRG_chicken_exon_n-2        V P D S D I K A L T T L C D L A D R E L V V I
ESRRG_anolis_exon_n-2         V P D S D I K A L T T L C D L A D R E L V V I
ESRRG_xenopus_exon_n-2        V P D S D I K A L T T L C D L A D R E L V V I
ESRRG_zebrafish_exon_n-2      V P D S D I K A L T T L C D L A D R E L V V N
ESRRG_elephantShark_exon_n-2  V P D S D I K A L T T L C D L A D R E L V V I
ERRA_exon4                    V P E G D I K A L T T L C D L A D R E L V V I

ERRG_homo_exon_n-2            I G W A K H I P
ERRG_mouse_exon_n-2           I G W A K H I P
ERRG_chicken_exon_n-2         I G W A K H I P
ERRG_anolis_exon_n-2          I G W A K H I P
ERRG_xenopus_exon_n-2         I G W A K H I P
ERRG_zebrafish_exon_n-2       I G W A K H I P
ERRG_elephantShark_exon_n-2   I G W A K H I P
ERRA_exon4                    I G W A K H I P
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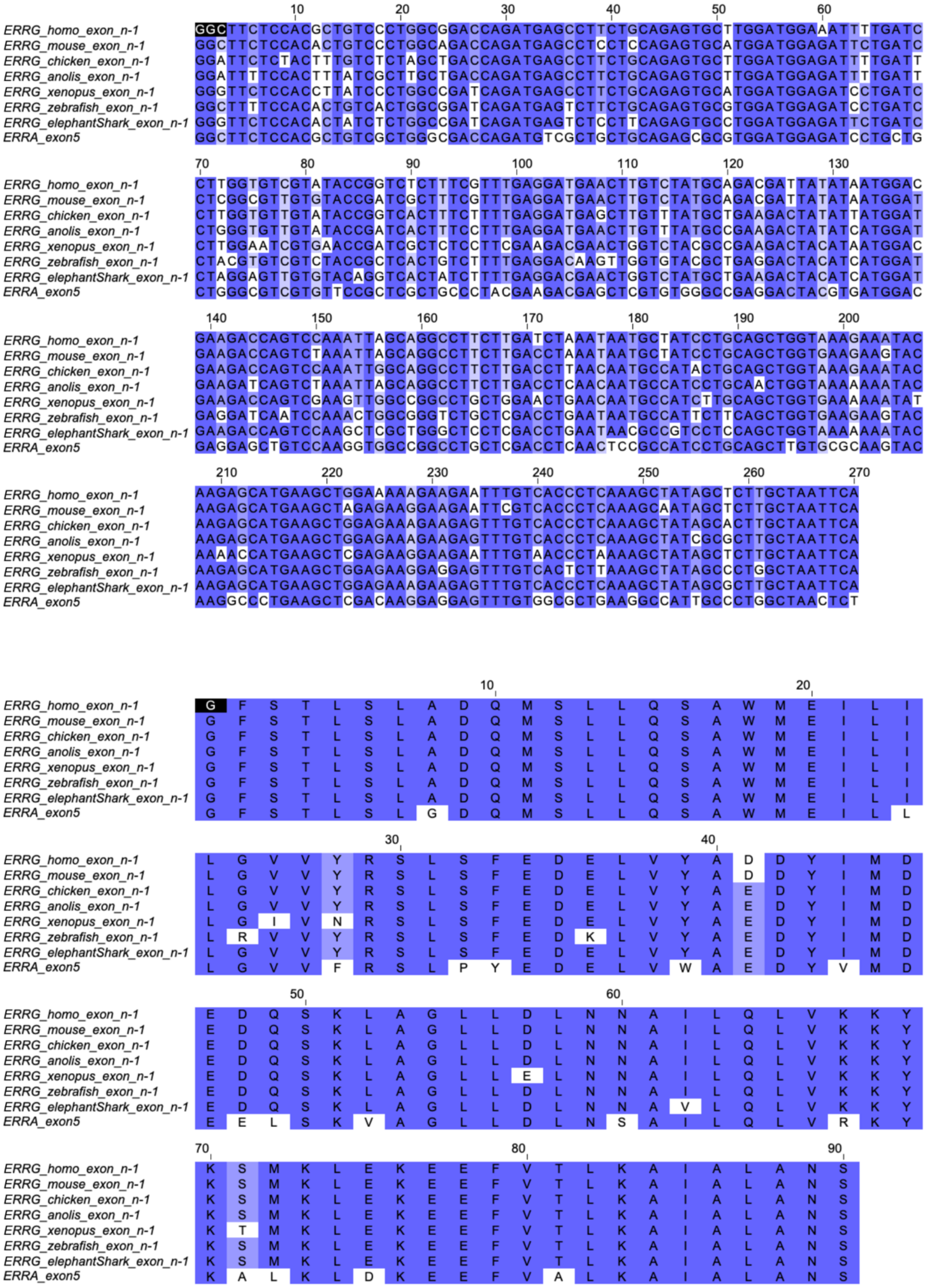
ERRγ exon n-2 (n=last exon) from different jawed vertebrates and *ERRa* DNA alignment above. Translated aminoacid sequence alignment below corresponding to DNA alignment. The encoded aminoacid sequence corresponds to the first part of the ligand binding domain (see full protein alignment below).



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ERRG_chicken_exon_n-1          GGATTCTCTACTTTGTCTCTAGCTGACCAGATGAGCCTTCTGCAGAGTGCTTGGATGGAGATTTTGATT
ERRG_anolis_exon_n-1           GGATTTTCCACTTTATCGCTTGCTGACCAGATGAGCCTTCTGCAGAGTGCTTGGATGGAGATTTTGATT
ERRG_xenopus_exon_n-1          GGGTTCTCCACCTTATCCCTGGCCGATCAGATGAGCCTTCTGCAGAGTGCATGGATGGAGATCCTGATC
ERRG_zebrafish_exon_n-1        GGCTTTTCCACACTGTCACTGGCGGATCAGATGAGTCTTCTGCAGAGTGCGTGGATGGAGATCCTGATC
ERRG_elephantShark_exon_n-1    GGGTTCTCCACACTATCTCTGGCCGATCAGATGAGTCTCCTTCAGAGTGCCTGGATGGAGATTCTGATC
ERRA_exon5                     GGCTTCTCCACGCTGTCGCTGGGCGACCAGATGTCGCTGCTGCAGAGCGCGTGGATGGAGATCCTGCTG

ERRG_homo_exon_n-1             CTTGGTGTCGTATACCGGTCTCTTTCGTTTGAGGATGAACTTGTCTATGCAGACGATTATATAATGGAC
ERRG_mouse_exon_n-1            CTCGGCGTTGTGTACCGATCGCTTTCGTTTGAGGATGAACTTGTCTATGCAGACGATTATATAATGGAT
ERRG_chicken_exon_n-1          CTTGGTGTTGTATACCGGTCACTTTCTTTTGAGGATGAGCTTGTTTATGCTGAAGACTATATTATGGAT
ERRG_anolis_exon_n-1           CTGGGTGTTGTATACCGATCACTTTCCTTTGAGGATGAACTTGTTTATGCCGAAGACTATATCATGGAT
ERRG_xenopus_exon_n-1          CTTGGAATCGTGAACCGATCGCTCTCCTTCGAAGACGAACTGGTCTACGCCGAAGACTACATAATGGAC
ERRG_zebrafish_exon_n-1        CTACGTGTCGTCTACCGCTCACTGTCTTTTGAGGACAAGTTGGTGTACGCTGAGGACTACATCATGGAT
ERRG_elephantShark_exon_n-1    CTAGGAGTTGTGTACAGGTCACTATCTTTTGAGGACGAACTGGTCTATGCTGAAGACTACATCATGGAT
ERRA_exon5                     CTGGGCGTCGTGTTCCGCTCGCTGCCCTACGAAGACGAGCTCGTGTGGGCCGAGGACTACGTGATGGAC

ERRG_homo_exon_n-1             GAAGACCAGTCCAAATTAGCAGGCCTTCTTGATCTAAATAATGCTATCCTGCAGCTGGTAAAGAAATAC
ERRG_mouse_exon_n-1            GAAGACCAGTCTAAATTAGCAGGCCTTCTTGACCTAAATAATGCTATCCTGCAGCTGGTGAAGAAGTAC
ERRG_chicken_exon_n-1          GAAGACCAGTCCAAATTGGCAGGCCTTCTTGACCTTAACAATGCCATACTGCAGCTGGTAAAGAAATAC
ERRG_anolis_exon_n-1           GAAGATCAGTCTAAATTAGCAGGCCTTCTTGACCTCAACAATGCCATCCTGCAACTGGTAAAAAAATAC
ERRG_xenopus_exon_n-1          GAAGACCAGTCGAAGTTGGCCGGCCTGCTGGAACTGAACAATGCCATCTTGCAGCTGGTGAAAAAATAT
ERRG_zebrafish_exon_n-1        GAGGATCAATCCAAACTGGCGGGTCTGCTCGACCTGAATAATGCCATTCTTCAGCTGGTGAAGAAGTAC
ERRG_elephantShark_exon_n-1    GAAGACCAGTCCAAGCTCGCTGGGCTCCTCGACCTGAATAACGCCGTCCTCCAGCTGGTAAAAAAATAC
ERRA_exon5                     GAGGAGCTGTCCAAGGTGGCCGGCCTGCTCGACCTCAACTCCGCCATCCTGCAGCTTGTGCGCAAGTAC

ERRG_homo_exon_n-1             AAGAGCATGAAGCTGGAAAAAGAAGAATTTGTCACCCTCAAAGCTATAGCTCTTGCTAATTCA
ERRG_mouse_exon_n-1            AAGAGCATGAAGCTAGAGAAGGAAGAATTCGTCACCCTCAAAGCAATAGCTCTTGCTAATTCA
ERRG_chicken_exon_n-1          AAGAGCATGAAGCTGGAGAAAGAAGAGTTTGTCACCCTCAAAGCTATAGCACTTGCTAATTCA
ERRG_anolis_exon_n-1           AAGAGCATGAAGCTGGAGAAAGAAGAGTTTGTCACCCTCAAAGCTATCGCGCTTGCTAATTCA
ERRG_xenopus_exon_n-1          AAAACCATGAAGCTCGAGAAGGAAGAATTTGTAACCCTAAAAGCTATAGCTCTTGCTAATTCA
ERRG_zebrafish_exon_n-1        AAGAGCATGAAGCTGGAGAAGGAGGAGTTTGTCACTCTTAAAGCTATAGCCCTGGCTAATTCA
ERRG_elephantShark_exon_n-1    AAGAGCATGAAGCTGGAGAAAGAAGAGTTTGTCACCCTCAAAGCTATAGCGCTTGCTAATTCA
ERRA_exon5                     AAGGCCCTGAAGCTCGACAAGGAGGAGTTTGTGGCGCTGAAGGCCATTGCCCTGGCTAACTCT
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ERRG_mouse_exon_n-1            G F S T L S L A D Q M S L L Q S A W M E I L I
ERRG_chicken_exon_n-1          G F S T L S L A D Q M S L L Q S A W M E I L I
ERRG_anolis_exon_n-1           G F S T L S L A D Q M S L L Q S A W M E I L I
ERRG_xenopus_exon_n-1          G F S T L S L A D Q M S L L Q S A W M E I L I
ERRG_zebrafish_exon_n-1        G F S T L S L A D Q M S L L Q S A W M E I L I
ERRG_elephantShark_exon_n-1    G F S T L S L A D Q M S L L Q S A W M E I L I
ERRA_exon5                     G F S T L S L G D Q M S L L Q S A W M E I L L

ERRG_homo_exon_n-1             L G V V Y R S L S F E D E L V Y A D D Y I M D
ERRG_mouse_exon_n-1            L G V V Y R S L S F E D E L V Y A D D Y I M D
ERRG_chicken_exon_n-1          L G V V Y R S L S F E D E L V Y A E D Y I M D
ERRG_anolis_exon_n-1           L G V V Y R S L S F E D E L V Y A E D Y I M D
ERRG_xenopus_exon_n-1          L G I V N R S L S F E D E L V Y A E D Y I M D
ERRG_zebrafish_exon_n-1        L R V V Y R S L S F E D K L V Y A E D Y I M D
ERRG_elephantShark_exon_n-1    L G V V Y R S L S F E D E L V Y A E D Y I M D
ERRA_exon5                     L G V V F R S L P Y E D E L V W A E D Y V M D

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ERRG_mouse_exon_n-1            E D Q S K L A G L L D L N N A I L Q L V K K Y
ERRG_chicken_exon_n-1          E D Q S K L A G L L D L N N A I L Q L V K K Y
ERRG_anolis_exon_n-1           E D Q S K L A G L L D L N N A I L Q L V K K Y
ERRG_xenopus_exon_n-1          E D Q S K L A G L L E L N N A I L Q L V K K Y
ERRG_zebrafish_exon_n-1        E D Q S K L A G L L D L N N A I L Q L V K K Y
ERRG_elephantShark_exon_n-1    E D Q S K L A G L L D L N N A V L Q L V K K Y
ERRA_exon5                     E E L S K V A G L L D L N S A I L Q L V R K Y

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ERRG_mouse_exon_n-1            K S M K L E K E E F V T L K A I A L A N S
ERRG_chicken_exon_n-1          K S M K L E K E E F V T L K A I A L A N S
ERRG_anolis_exon_n-1           K S M K L E K E E F V T L K A I A L A N S
ERRG_xenopus_exon_n-1          K T M K L E K E E F V T L K A I A L A N S
ERRG_zebrafish_exon_n-1        K S M K L E K E E F V T L K A I A L A N S
ERRG_elephantShark_exon_n-1    K S M K L E K E E F V T L K A I A L A N S
ERRA_exon5                     K A L K L D K E E F V A L K A I A L A N S
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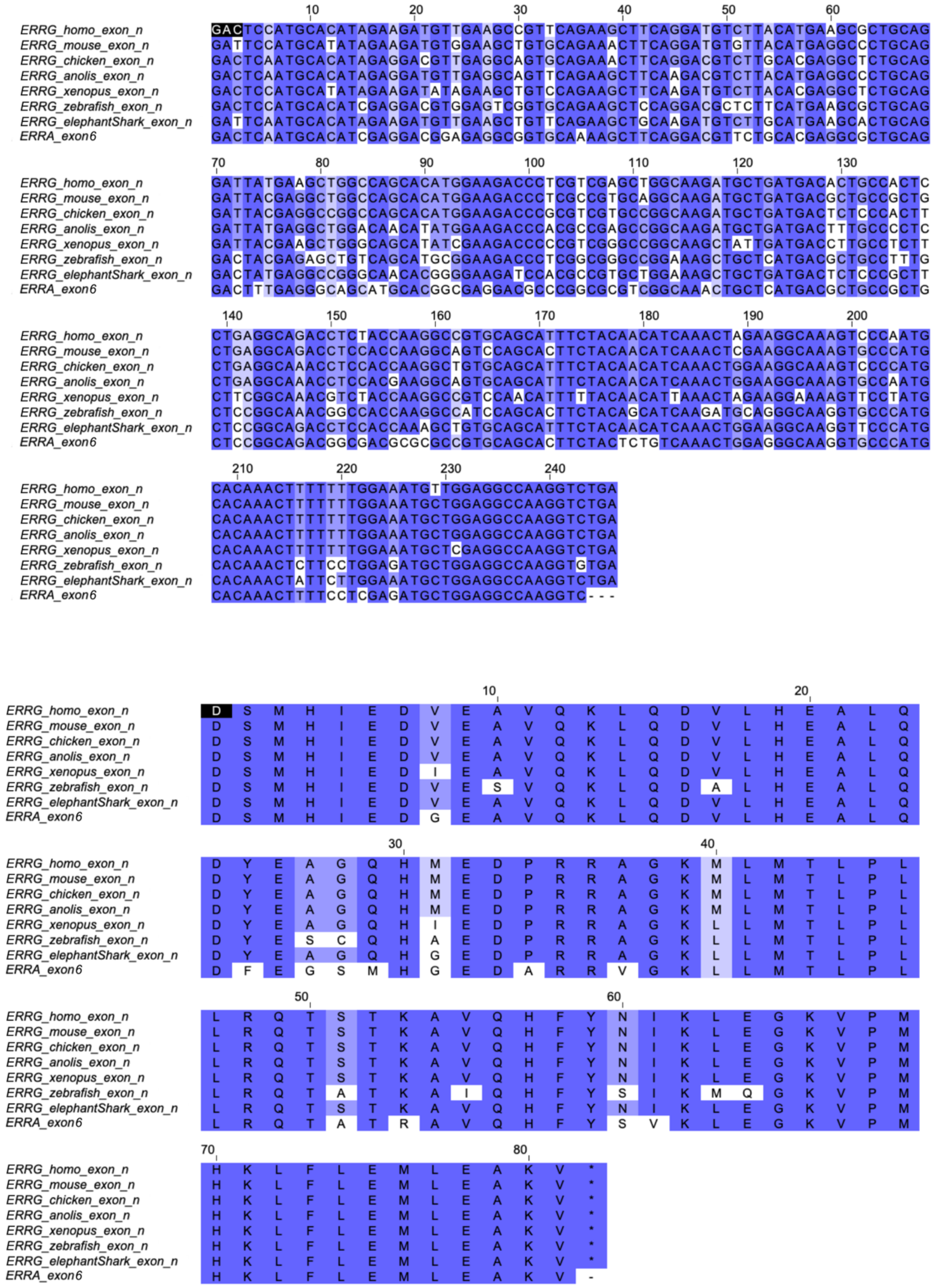
ERRγ exon n-1 (n=last exon) from different jawed vertebrates and *ERRa* DNA alignment above. Translated aminoacid sequence alignment below corresponding to DNA alignment. The encoded aminoacid sequence corresponds to the second part of the ligand binding domain(see full protein alignment below).



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ERRG_mouse_exon_n          GATTCCATGCATATAGAAGATGTGGAAGCTGTGCAGAAACTTCAGGATGTGTTACATGAGGCCCTGCAG
ERRG_chicken_exon_n        GACTCAATGCACATAGAGGACGTTGAGGCAGTGCAGAAACTTCAGGACGTCTTGCACGAGGCTCTGCAG
ERRG_anolis_exon_n         GACTCAATGCACATAGAGGATGTTGAGGCAGTTCAGAAGCTTCAAGACGTCTTACATGAGGCCCTGCAG
ERRG_xenopus_exon_n        GACTCCATGCATATAGAAGATATAGAAGCTGTCCAGAAGCTTCAAGATGTCTTACACGAGGCTCTGCAG
ERRG_zebrafish_exon_n      GACTCCATGCACATCGAGGACGTGGAGTCGGTGCAGAAGCTCCAGGACGCTCTTCATGAAGCGCTGCAG
ERRG_elephantShark_exon_n  GATTCAATGCACATAGAAGATGTTGAAGCTGTTCAGAAGCTGCAAGATGTCTTGCATGAAGCACTGCAG
ERRA_exon6                 GACTCAATGCACATCGAGGACGGAGAGGCGGTGCAAAAGCTTCAGGACGTTCTGCACGAGGCGCTGCAG

                           70        80        90        100       110       120       130
ERRG_homo_exon_n           GATTATGAAGCTGGCCAGCACATGGAAGACCCTCGTCGAGCTGGCAAGATGCTGATGACACTGCCACTC
ERRG_mouse_exon_n          GATTACGAGGCTGGCCAGCACATGGAAGACCCTCGCCGTGCAGGCAAGATGCTGATGACGCTGCCGCTG
ERRG_chicken_exon_n        GATTACGAGGCCGGCCAGCACATGGAAGACCCGCGTCGTGCCGGCAAGATGCTGATGACTCTCCCACTT
ERRG_anolis_exon_n         GATTATGAGGCTGGACAACATATGGAAGACCCACGCCGAGCCGGCAAGATGCTGATGACTTTGCCCCTC
ERRG_xenopus_exon_n        GATTACGAAGCTGGGCAGCATATCGAAGACCCCCGTCGGGCCGGCAAGCTATTGATGACCTTGCCTCTT
ERRG_zebrafish_exon_n      GACTACGAGAGCTGTCAGCATGCGGAAGACCCTCGGCGGGCCGGAAAGCTGCTCATGACGCTGCCTTTG
ERRG_elephantShark_exon_n  GACTATGAGGCCGGGCAACACGGGGAAGATCCACGCCGTGCTGGAAAGCTGCTGATGACTCTCCCGCTT
ERRA_exon6                 GACTTTGAGGGCAGCATGCACGGCGAGGACGCCCGGCGCGTCGGCAAACTGCTCATGACGCTGCCGCTG

                             140       150       160       170       180       190       200
ERRG_homo_exon_n           CTGAGGCAGACCTCTACCAAGGCCGTGCAGCATTTCTACAACATCAAACTAGAAGGCAAAGTCCCAATG
ERRG_mouse_exon_n          CTGAGGCAGACCTCCACCAAGGCAGTCCAGCACTTCTACAACATCAAACTCGAAGGCAAAGTGCCCATG
ERRG_chicken_exon_n        CTGAGGCAAACCTCCACCAAGGCTGTGCAGCATTTCTACAACATCAAACTGGAAGGCAAAGTCCCCATG
ERRG_anolis_exon_n         CTGAGGCAAACCTCCACGAAGGCAGTGCAGCATTTCTACAACATCAAACTGGAAGGCAAAGTGCCAATG
ERRG_xenopus_exon_n        CTTCGGCAAACGTCTACCAAGGCCGTCCAACATTTTTACAACATTAAACTAGAAGGAAAAGTTCCTATG
ERRG_zebrafish_exon_n      CTCCGGCAAACGGCCACCAAGGCCATCCAGCACTTCTACAGCATCAAGATGCAGGGCAAGGTGCCCATG
ERRG_elephantShark_exon_n  CTCCGGCAGACCTCCACCAAAGCTGTGCAGCATTTCTACAACATCAAACTGGAAGGCAAGGTTCCCATG
ERRA_exon6                 CTCCGGCAGACGGCGACGCGCGCCGTGCAGCACTTCTACTCTGTCAAACTGGAGGGCAAGGTGCCCATG

                             210       220       230       240
ERRG_homo_exon_n           CACAAACTTTTTTTGGAAATGTTGGAGGCCAAGGTCTGA
ERRG_mouse_exon_n          CACAAACTTTTTTTGGAAATGCTGGAGGCCAAGGTCTGA
ERRG_chicken_exon_n        CACAAACTTTTTTTGGAAATGCTGGAGGCCAAGGTCTGA
ERRG_anolis_exon_n         CACAAACTTTTTTTGGAAATGCTGGAGGCCAAGGTCTGA
ERRG_xenopus_exon_n        CACAAACTTTTTTTGGAAATGCTCGAGGCCAAGGTCTGA
ERRG_zebrafish_exon_n      CACAAACTCTTCCTGGAGATGCTGGAGGCCAAGGTGTGA
ERRG_elephantShark_exon_n  CACAAACTATTCTTGGAAATGCTGGAGGCCAAGGTCTGA
ERRA_exon6                 CACAAACTTTTCCTCGAGATGCTGGAGGCCAAGGTC---
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                                                     10                      20
ERRG_homo_exon_n           D S M H I E D V E A V Q K L Q D V L H E A L Q
ERRG_mouse_exon_n          D S M H I E D V E A V Q K L Q D V L H E A L Q
ERRG_chicken_exon_n        D S M H I E D V E A V Q K L Q D V L H E A L Q
ERRG_anolis_exon_n         D S M H I E D V E A V Q K L Q D V L H E A L Q
ERRG_xenopus_exon_n        D S M H I E D I E A V Q K L Q D V L H E A L Q
ERRG_zebrafish_exon_n      D S M H I E D V E S V Q K L Q D A L H E A L Q
ERRG_elephantShark_exon_n  D S M H I E D V E A V Q K L Q D V L H E A L Q
ERRA_exon6                 D S M H I E D G E A V Q K L Q D V L H E A L Q

                                           30                  40
ERRG_homo_exon_n           D Y E A G Q H M E D P R R A G K M L M T L P L
ERRG_mouse_exon_n          D Y E A G Q H M E D P R R A G K M L M T L P L
ERRG_chicken_exon_n        D Y E A G Q H M E D P R R A G K M L M T L P L
ERRG_anolis_exon_n         D Y E A G Q H M E D P R R A G K M L M T L P L
ERRG_xenopus_exon_n        D Y E A G Q H I E D P R R A G K L L M T L P L
ERRG_zebrafish_exon_n      D Y E S C Q H A E D P R R A G K L L M T L P L
ERRG_elephantShark_exon_n  D Y E A G Q H G E D P R R A G K L L M T L P L
ERRA_exon6                 D F E G S M H G E D A R R V G K L L M T L P L

                                   50                  60
ERRG_homo_exon_n           L R Q T S T K A V Q H F Y N I K L E G K V P M
ERRG_mouse_exon_n          L R Q T S T K A V Q H F Y N I K L E G K V P M
ERRG_chicken_exon_n        L R Q T S T K A V Q H F Y N I K L E G K V P M
ERRG_anolis_exon_n         L R Q T S T K A V Q H F Y N I K L E G K V P M
ERRG_xenopus_exon_n        L R Q T S T K A V Q H F Y N I K L E G K V P M
ERRG_zebrafish_exon_n      L R Q T A T K A I Q H F Y S I K M Q G K V P M
ERRG_elephantShark_exon_n  L R Q T S T K A V Q H F Y N I K L E G K V P M
ERRA_exon6                 L R Q T A T R A V Q H F Y S V K L E G K V P M

                           70                  80
ERRG_homo_exon_n           H K L F L E M L E A K V *
ERRG_mouse_exon_n          H K L F L E M L E A K V *
ERRG_chicken_exon_n        H K L F L E M L E A K V *
ERRG_anolis_exon_n         H K L F L E M L E A K V *
ERRG_xenopus_exon_n        H K L F L E M L E A K V *
ERRG_zebrafish_exon_n      H K L F L E M L E A K V *
ERRG_elephantShark_exon_n  H K L F L E M L E A K V *
ERRA_exon6                 H K L F L E M L E A K V -
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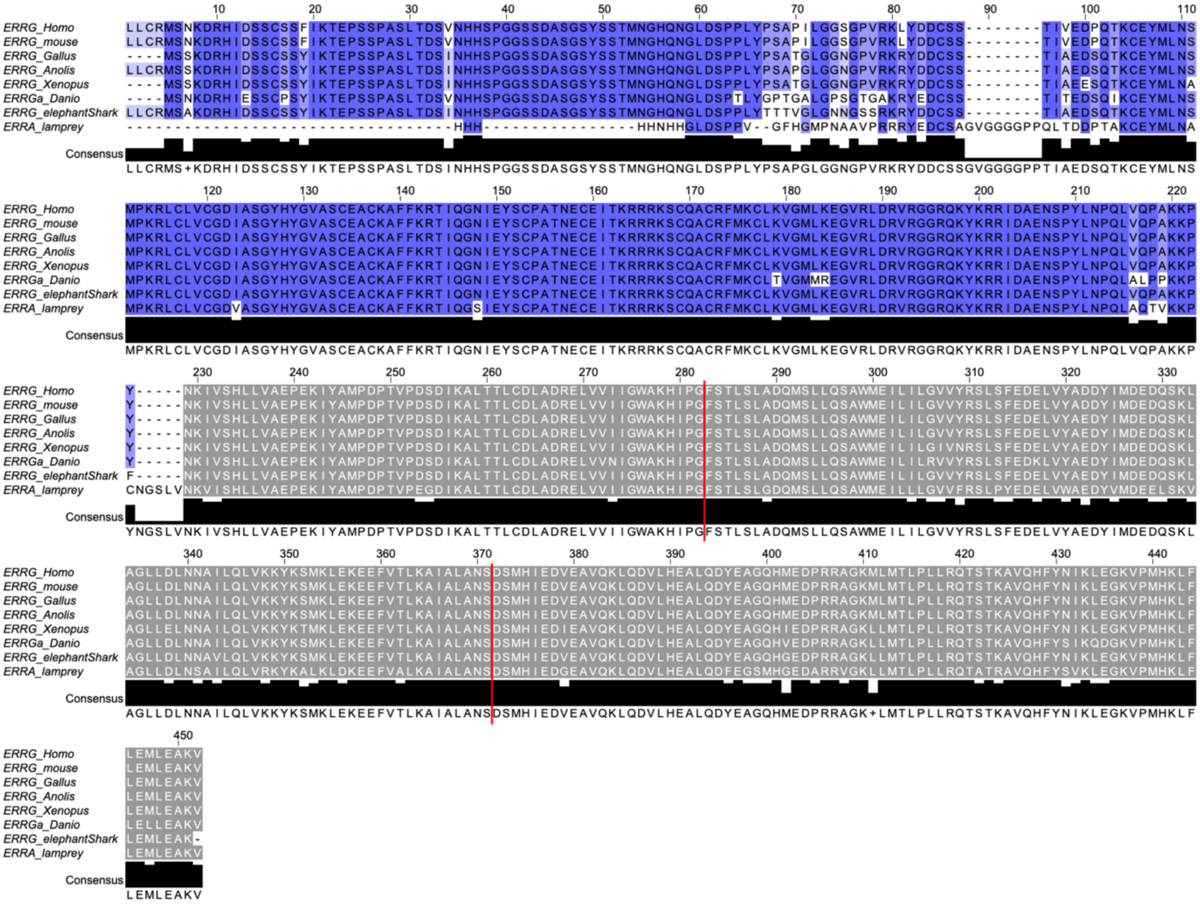
ERRγ exon n (n=last exon) from different jawed vertebrates and *ERRa* DNA alignment above. Translated aminoacid sequence alignment below corresponding to DNA alignment. The encoded aminoacid sequence corresponds to the third part of the ligand binding domain (see full protein alignment below).



ERRγ and ERRa protein alignment above. Ligand binding domain sequence is annotated with grey colour. Red lines indicate exon boundaries. The ligand binding domain is split in three parts, encoded by the last three exons (see above).

S7) Differentially regulated genes after *ciHMX* overexpression

Gene model	log2FoldChange	padj	EXPRESSION	Gene name
KH.C12.452	3.943945434	1.91E-46		
KH.L141.43	3.345641248	7.55E-74	BTN	S35G2
KH.C7.773	3.091644457	1.03E-15		ZNT10_ZNT5_ZNT7
KH.C1.1157	2.681981421	1.08E-79		KCND2_KCND3_KCND1
KH.L24.10	2.672948063	8.62E-80	BTN	COE3_COE1_COE2
KH.C10.175	2.341633022	8.55E-12	EPI	
KH.C4.649	2.279563102	2.08E-10	BTN	
KH.L112.16	2.27821521	2.27E-32		
KH.C4.115	2.273959241	3.10E-67	BTN	
KH.C6.129	2.271803413	1.02E-07	BTN	NGN1_NGN3_NGN2
KH.C14.402	2.221462456	0.086122873		
KH.S575.2	2.180612194	7.23E-10		
KH.C12.154	2.173151814	3.69E-08		
KH.C3.499	2.070711555	1.63E-10		
KH.C2.42	2.052100592	1.52E-50	BTN	PO4F3_PO4F2_PO4F1
KH.L128.2	2.050192817	6.39E-53	BTN	NEC2_FURIN_NEC1
KH.C6.145	1.989508716	1.20E-136		CHRD
KH.C12.182	1.856966054	2.09E-12		
KH.L139.24	1.802582911	1.04E-15		
KH.C7.92	1.752459533	0.088974627		
KH.C3.474	1.722752126	3.27E-09	BTN	MDGA1_PGBM_MDGA2
KH.S346.10	1.722258948	3.64E-15		KCNQ5_KCNQ1_KCNQ3
KH.C1.396	1.632075912	1.44E-62	BTN	SOGA3_MTCL1_SOGA1
KH.C2.503	1.628253539	1.55E-26		LOXL3_LOXL4_LOXL2
KH.C10.545	1.588513197	8.94E-07		
KH.C5.490	1.558107236	9.15E-11		
KH.S1075.1	1.528720891	1.06E-35	BTN	CECR5
KH.S663.4	1.526991912	1.69E-29		TX264
KH.C7.700	1.501655652	0.008601732		
KH.C2.1128	1.479425327	2.43E-20		BGLR_BGP11
KH.C2.14	1.46511129	1.23E-21	BTN	
KH.C7.140	1.464032136	9.99E-17		
KH.C6.185	1.463122069	5.69E-42	BTN	ONEC2_HNF6_ONEC3
KH.C3.318	1.422997776	0.00099123		
KH.C12.301	1.422451884	2.42E-10	BTN	FSTL5_FSTL4
KH.C7.131	1.422099739	5.40E-07	BTN	ADA2A_ADA2B_ADA2C
KH.C11.589	1.401248765	0.000709293		
KH.L172.15	1.35458692	1.65E-20	BTN	
KH.C3.591	1.351395688	5.71E-10	BTN	
KH.C12.521	1.337194137	0.062053784		CALM_TNNC2_CALL6
KH.C2.402	1.334927376	2.08E-09	BTN	MB211_MB212_MB213
KH.C7.550	1.328342687	0.014930653		
KH.C3.328	1.319450987	9.06E-05		
KH.C1.118	1.290871678	9.33E-06	BTN	
KH.C1.502	1.279996807	3.58E-16		CSMD3_CSMD1_CSMD2_LYAM3
KH.C1.90	1.279462653	4.54E-17		S2536_S2533_ODC
KH.S583.2	1.275430456	0.000585906		
KH.C9.65	1.244859682	0.000508827	BTN	DPP4_DPP10_DPP6
KH.L6.1	1.24241483	0.004334484	BTN	RFNG_LFNG_MFNG
KH.C1.1221	1.238118557	0.005578012		
KH.C4.358	1.180492135	1.06E-14		TSP2_TSP1_TSP4
KH.C3.462	1.163210488	0.018051995	EPI	
KH.C4.378	1.1564813	4.88E-07		INSM2_INSM1
KH.C5.451	1.145774831	0.013502688		
KH.S698.1	1.143024431	1.46E-05		
KH.C2.785	1.14043133	1.60E-12		VASN_FLRT1_LRRC4
KH.C3.843	1.113443396	3.53E-07		
KH.C9.352	1.104673867	0.000487532		AN33B_ANR33
KH.S1148.2	1.097062153	0.05167602	BTN	KCNJ3_KCNJ5_KCNJ6
KH.C12.135	1.093643799	9.84E-08		LIGO1
KH.C11.160	1.081912209	2.41E-12		CXG1_CXG2_CXD3
KH.S765.1	1.059003011	3.72E-28		
KH.S2128.1	1.04768674	0.00327893		
KH.C6.128	1.0474983	1.30E-39		CELF3_CELF5_CELF6
KH.C5.630	1.033522173	3.57E-09		
KH.C4.761	1.027123951	0.000364		ADH1A_ADH1B_ADH1G
KH.L172.21	1.010661485	0.000321667		AS3MT
KH.C1.659	1.009207729	0.025578558		
KH.L19.15	0.992223819	3.48E-12		
KH.C2.614	0.983190437	0.000198612		ADA

KH.C4.777	0.968668038	7.64E-07		SVEP1_CFAH_FHR5
KH.C9.462	0.966339458	1.26E-16	BTN	SCN2A_SCN1A_SCN3A
KH.C1.274	0.965516325	4.77E-17		MYT1L_MYT1_ST18
KH.C9.872	0.958032118	3.58E-16		ATOH8
KH.L154.42	0.927125861	0.00552532		SOX9_SOX10_SOX8
KH.C9.496	0.924624563	1.38E-18	EPI	
KH.L92.3	0.903212779	0.097684318		ASM3B_ASM3A_ASM
KH.C8.890	0.9030028	0.028998296		FOXD4_FOXD1_FOXD3
KH.L50.6	0.902634945	1.49E-08		DLL1_DLK2_DLK1
KH.L118.4	0.889144561	5.24E-09		CTRB2_CTRB1_CTRL
KH.C2.56	0.887857413	0.000141456		PCYOX_PCYXL
KH.C4.394	0.885474704	5.16E-18	BTN	TRAF4_TRAF2_TRAF6
KH.C10.40	0.829577915	0.08025203	EPI	SERC
KH.C6.205	0.828221026	1.03E-05		
KH.C1.1067	0.828139151	0.083284044	BTN	NCS1_NCALD_HPCA
KH.C10.464	0.824895287	0.001089833	BTN	
KH.L9.43	0.815635538	1.23E-06		FZD7_FZD3_FZD6
KH.C8.396	0.809093653	0.037587566		FOXD4_FOXD1_FOXD3
KH.L119.20	0.809003501	0.001784585	BTN	
KH.S1313.1	0.808256887	7.58E-07	BTN	
KH.C2.805	0.806635772	1.68E-06		
KH.L18.43	0.797819822	4.82E-06		KCP_VWF_OTOGL
KH.L96.61	0.796639923	0.047953427		
KH.S761.6	0.795169599	6.76E-06		CSAD_DCE1_DCE2
KH.C3.178	0.778514962	0.009362151	BTN	SEGN_CALB2_CALB1
KH.C9.770	0.774468917	5.54E-05		
KH.C1.481	0.760821765	5.90E-07	EPI	HPGDS_GSTA3_GSTA2
KH.C7.4	0.75701097	3.29E-16		MOT14_MOT5_MOT1
KH.C7.173	0.753354327	1.65E-05		CTR2_CTR1_S7A14
KH.C9.162	0.744793522	5.46E-05		RGS4_RGS8_RGS21
KH.C2.924	0.744586006	0.07458612		S22A5_S22A4_S22AF_S22AO_S22A9_S22AA
KH.C1.340	0.743848746	4.44E-05		MMP14_MMP24_MMP15_MMP16
KH.C2.765	0.739973383	6.79E-09		RIMS2_RIMS1_PCLO
KH.L170.66	0.736975079	2.10E-13	BTN	
KH.C1.983	0.736706414	3.40E-06		KLF10_KLF11_SP4
KH.C12.352	0.732076616	0.008208232		MUC5A_MUC2_VWF
KH.S1526.1	0.723302956	8.00E-07		RIMS2_RIMS1_RIMS3
KH.C1.314	0.705098558	3.27E-06		RGS19_RGS17_RGS20
KH.C11.220	0.702945288	1.21E-08		BMI1_PCGF3_PCGF2
KH.L167.5	0.702861227	6.90E-10		S6A11_S6A13_S6A12
KH.L9.36	0.700242094	5.01E-05		KCNK9_KCNK3_KCNKF
KH.C3.67	0.69128245	0.017607758		IRX6_IRX4_IRX2
KH.C3.273	0.686781976	0.000335033		NRX1A_NRX2A_NRX3A
KH.C2.245	0.684331386	0.009557468		B3GN2_B3GN7_B3GN6
KH.C9.102	0.682264064	5.04E-10		FA78B_FA78A
KH.C8.263	0.679673025	1.87E-08		ZSWM6_ZSWM5_ZSWM4
KH.C9.672	0.679463322	0.000245899		RGS4_RGS8_RGS21
KH.L22.28	0.678766467	0.024092381		GABR1_GABR2
KH.C9.587	0.673116765	0.000125532		CI171
KH.C4.102	0.669219454	3.65E-06		ATS6_ATS7_ATS12
KH.L154.30	0.660981587	0.009557468		BACH2_ZBT46_ZBT44_BCL6_BCL6B
KH.S1346.2	0.65980493	0.019794563		KIF1A_KIF1C_KIF28
KH.C2.674	0.655922962	0.001887583		GCYB1_GCYB2_GCYA2
KH.C11.185	0.649484166	0.000645008		KI26B_KI26A_KIF9
KH.C11.8	0.64637951	5.29E-07		S39A1_S39A3_S39A2
KH.C2.731	0.63822025	0.093131578		TECTA
KH.L81.2	0.637245099	8.92E-05		RGL1_GNDS_RGL3
KH.C7.465	0.635511906	0.007028038		ST1C2_ST6B1_ST1C4
KH.C3.157	0.613740296	0.04155289		KIF1A_KIF1C_KIF28
KH.C9.237	0.609076424	1.51E-07		DYH7_DYH3_DYH1
KH.C7.122	0.608048897	0.020908569		ST1C2_ST6B1_ST1C4
KH.C4.760	0.604005906	9.18E-08	BTN	CD5R1_CD5R2
KH.L18.74	0.596555544	0.001050799		EFHC1_EFHC2
KH.L23.9	0.595702389	0.007580986		TAB1
KH.C3.285	0.595665556	0.04512507		TEKT4_TEKT1_TEKT3
KH.C4.628	0.593611975	0.007064123	PALPS	PTN13_FRPD2
KH.C7.157	0.590548836	0.008882908		
KH.C14.20	0.583965588	0.024772167		
KH.C2.433	0.583914424	0.062053784		GLP1R_PTH1R_GLP2R_GLR
KH.L9.14	0.583737889	0.030824843		JIP1_JIP2
KH.C2.336	0.582902121	0.000350108		BMP6_BMP5_BMP7
KH.L157.6	0.581600645	5.89E-08		SIK3_SIK2_SIK1
KH.C3.640	0.580469906	6.35E-08		S38A4_S38A3_S38A2

KH.C7.692	0.577766143	0.008853928		
KH.C10.125	0.562623989	0.001151871		
KH.C7.334	0.562505962	0.000910568		GLI2_GLI3_GLI1
KH.L18.65	0.562109064	0.000491192	BTN	PDE6C_PDE6B_PDE6A_PDE11
KH.C1.744	0.559777779	0.035978816		
KH.C10.406	0.55868389	0.010788185		
KH.L71.1	0.550425954	0.006727196		RBPMS_RBPS2
KH.C11.495	0.543271918	0.023107566	BTN	SSR2_RL3R1_SSR5
KH.C3.354	0.541454869	1.02E-05		
KH.C9.192	0.539303811	0.000702787		RUND1
KH.C10.25	0.535201226	0.040283242		RSPH1_MORN1_ALS2
KH.C1.432	0.531700785	0.000232659		CHKA_CHKB_EKI1_EKI2
KH.C9.32	0.525673037	2.84E-05		PCD18_PCD19_PCDA6
KH.C8.223	0.523122418	0.000432245	PALPS	HTD2
KH.L152.2	0.514957216	0.000357402	BTN	ISL1_ISL2_LHX9
KH.C10.250	0.509223451	7.09E-08		RFOX3_RFOX2_RFOX1
KH.S1159.1	0.5023677	0.001101716		FLI1
KH.C8.585	0.494019791	0.004953359	BTN	ANO4_ANO5_ANO7
KH.C12.8	0.492111533	3.34E-06		
KH.C7.207	0.492047448	0.006626831		FOXP4_FOXP1_FOXP2
KH.C10.488	0.491687132	0.016852055		RSH4A_RSH6A
KH.C10.493	0.47869781	0.024747551		
KH.L96.50	0.477974984	0.000224135		TLE4_TLE1_TLE3
KH.C10.566	0.469481895	0.010495547		
KH.C9.78	0.468720133	0.008588384		FUT6_FUT5_FUT3
KH.C14.435	0.468157008	0.003247267	PALPS	ANR10_ASB2_ANR37
KH.C7.770	0.460364809	0.040992484		DLX1_DLX6_DLX5
KH.C3.312	0.456076723	0.000124507		HES1_HES4_HES6_HES2
KH.L4.36	0.455717712	1.88E-05		HMGB3_HMGB1_HMGB4
KH.S1462.1	0.45502436	0.039038435		KCP_BMPER_VWF
KH.C3.699	0.438087697	0.000343276		ABCG2_ABCG4_ABCG1
KH.S618.2	0.433890978	0.090592935		MCF2L_MCF2_MF2L2
KH.S1090.3	0.432949916	0.093148967	BTN	
KH.C8.892	0.427456476	1.44E-05		TBA1C_TBA1A_TBA3C
KH.S980.1	0.41906413	5.46E-05		BPTF
KH.C1.822	0.417466025	0.000636868		
KH.L40.4	0.414810772	0.034876462		4EBP2_4EBP1_4EBP3
KH.C5.112	0.409291897	0.012492498		DPYD
KH.L173.8	0.405679405	0.054745457		PTHB1
KH.C1.1079	0.396946962	0.086662908	EPI	DUS1_DUS4_DUS2
KH.C7.523	0.394584861	0.0055762		SOX4_SOX11_SOX12
KH.C2.506	0.394207702	0.000251303	BTN	LBR_DHCR7_ERG24
KH.C7.717	0.393266102	0.00920775		
KH.C4.539	0.390037226	0.00353646		FLI1_ERG_FEV
KH.S583.1	0.38969261	0.063391173		IQCD
KH.L116.85	0.389489602	0.000203437		TBB4B_TBB2B_TBB5_TBB2A_TBB3
KH.C13.66	0.388582712	0.000429903		CAC1S_CAC1C_CAC1F
KH.C12.380	0.384881564	0.00282307		PLCD_PLCC_PLCE_LCLT1
KH.L18.112	0.380987849	0.051656139		BPTF
KH.C7.594	0.378703135	0.010905179		ABCG2_ABCG4_ABCG1
KH.C4.719	0.374155155	0.003645126	BTN	SEM6A_SEM6D_SEM6B
KH.S982.4	0.364953596	0.048119507		
KH.L65.10	0.360870385	0.061714754		DYRK4_DYRK2_DYRK3
KH.C6.65	0.358100968	0.001114652	BTN	CAC1G_CAC1I_CAC1H
KH.C14.166	0.357776026	0.009165625		ZNT10_ZNT5_ZNT1
KH.C5.654	0.357490698	0.042618208		
KH.C13.96	0.355104816	0.075395536		THEM6
KH.C11.108	0.350573676	0.028388773		MED14
KH.C7.21	0.34824942	0.000433962		TITIN_PALLD_MYPN_MYOTI
KH.C1.329	0.344406526	0.000555563		RAB7A_RAB10_RAN
KH.C10.459	0.343719203	0.001034585		
KH.C9.371	0.343261463	0.06362278		MUSK_DDR2_DDR1
KH.C8.159	0.342133114	0.041264801		NAC1_NAC3_NAC2
KH.L9.16	0.340038358	0.00721804		CCND3_CCND2_CCND1
KH.C14.448	0.338576408	0.0462673		TFAP4
KH.C3.596	0.338244201	0.018640958		
KH.C1.916	0.336057115	0.013679087		PPBT_PPBI_PPBN
KH.C10.403	0.335607168	0.042921561		
KH.C1.964	0.335601568	0.061713842		LRIQ1
KH.L18.39	0.3315942	0.02617062		MIB1_MIB2
KH.L162.6	0.329452058	0.042657696		CACB2_CACB4_CACB1
KH.L118.3	0.329040729	0.097684318		SHAN2_SHAN3
KH.C2.36	0.328762821	1.41E-05		FRIH_FTMT_FHL17
KH.L46.15	0.323422382	0.085107582		S18B1

KH.L10.5	0.319675118	0.015635363		KCRB_KCRS_KCRM
KH.C1.777	0.319241804	0.025094995		ZEB1_ZEB2_ZN232
KH.C1.478	0.315691809	0.018320988		MINT
KH.L96.41	0.314630361	0.018450211		AMPD2_AMPD3_AMPD1
KH.L154.10	0.313945919	0.005243183		SMTN_SMTL2_SMTL1
KH.C1.448	0.311693709	0.083593129		RPGP1_RPGP2_SI1L2_SI1L3
KH.L68.2	0.308190293	0.031692999		STMN2
KH.L87.11	0.306944604	0.044961828		KCC4_PHKG2_PHKG1
KH.C1.677	0.305999937	0.000552731		KDM5A_KDM5C_KDM5D
KH.C12.263	0.302676021	0.002688155		SESN1_SESN3_SESN2
KH.C4.739	0.30210907	0.005102615		CIC_BBX
KH.C1.571	0.30198168	0.001794522		PLOD3_PLOD1_PLOD2
KH.C8.372	0.29941707	0.097684318		ASAH2
KH.C2.69	0.293319318	0.013102248		AQP4_AQP1_MIP
KH.S403.5	0.290787158	0.006674179		PPGB_CPVL
KH.C1.94	0.286500526	0.012104144		MIB1_ANK3_MIB2
KH.S1172.1	0.28633983	0.08787409	PALPS	
KH.C11.235	0.286319334	0.040833597		ELOV4_ELOV1_ELOV5
KH.L96.13	0.284965572	0.018883907		BIG3
KH.C4.441	0.282486946	0.057442011		
KH.C7.448	0.282448783	0.001592084		RPC1_RPA1_RPB1
KH.C2.780	0.282370763	0.031590025		SRSF4_SRSF6_SRSF5
KH.C12.608	0.28124609	0.097684318		TET1_TET2_TET3
KH.C1.535	0.277339952	0.024772167		GWL_MAST2_MAST1_MAST3
KH.C1.264	0.276582239	0.00598449		YBOX1_YBOX3_YBOX2
KH.S1482.2	0.27624296	0.01136005		ABCD2_ABCD1_ABCD3
KH.C2.441	0.266321767	0.060450523		RIR1
KH.L131.10	0.265940398	0.04801649		MFSD6
KH.C8.400	0.265637679	0.015248563		RAB3C_RAB3A_RAB3B
KH.C5.558	0.265569543	0.097072021		RIMB1_RIMB2_RIM3A
KH.L6.5	0.261665783	0.024998629		SMCA2_SMCA4
KH.C2.466	0.261222388	0.055955974		
KH.C9.571	0.252751322	0.068071975		ANR50_ANKH1_ANR17
KH.C3.389	0.249061282	0.038304425		RAB2A_RAB14_RAB2B
KH.C14.103	0.24339654	0.009398627		TM131_T131L
KH.C1.116	0.240379783	0.005879466		HCFC1_HCFC2_KLDC3
KH.C9.64	0.239957538	0.06740945		NH2L1_NHP2
KH.C3.329	0.23518887	0.031584931		SAHH3_SAHH2_SAHH
KH.C12.317	0.231196116	0.047708753		ROAA_HNRDL_HNRPD
KH.C14.534	0.230911354	0.031945791		ADCY9_ADCY8_ADCY3
KH.L107.1	0.230340868	0.090305267		SMRC2_SMRC1
KH.C12.278	0.229314839	0.040396279		CHD9_CHD8_CHD7
KH.C8.314	0.229287155	0.082543836		ARI5B_ARI5A
KH.C2.57	0.224250101	0.058419148		YTHD2_YTHD1_YTHD3
KH.C8.248	0.220583963	0.020628153		COOA1_CO4A6_CO9A1_COMA1_COJA1_COLA1
KH.C9.589	0.218934216	0.02100212		BRD4_BRDT_BRD3
KH.C4.623	0.216709503	0.039839545		PSMD2
KH.S638.5	0.215887163	0.081423556		MTMRD_MTMR5_MADD
KH.C10.81	0.213157354	0.07458612		2A5A_2A5D_2A5G
KH.L58.2	0.212091465	0.027565982		HNRL1_HNRPU_HNRL2
KH.C10.61	0.211415028	0.093876898		DYR1A_DYRK4_DYR1B
KH.C12.116	0.209648199	0.089303505		PAX8_PAX5_PAX2
KH.C1.931	0.188974369	0.07914117		GRB1L_GREB1
KH.L57.1	0.18509673	0.090933668		NOMO1_NOMO2_NOMO3
KH.C9.38	0.184754491	0.07147826		FUBP3_FUBP2_FUBP1
KH.C5.114	-0.181693301	0.046679653		S61A2_S61A1
KH.C3.676	-0.19098569	0.074857596		
KH.C1.262	-0.19575947	0.05207987		KTAP2
KH.L141.10	-0.197362354	0.085336196		
KH.C2.1086	-0.198754674	0.064823044		RPN2
KH.C9.16	-0.200778149	0.052593965	PALPS	S4A4_S4A10_S4A8
KH.C1.835	-0.203141631	0.029060659		ERGI1_ERGI3
KH.L122.10	-0.205931883	0.0462673		L2HDH
KH.C1.1299	-0.206105373	0.013517667		VIGLN
KH.C9.559	-0.21029273	0.086122873		UAP1_UAP1L
KH.C14.391	-0.221863783	0.08025203		SEM6A_SEM6D_SEM6B
KH.C4.253	-0.236253438	0.08842486		SRC8_HCLS1_DBNL
KH.C3.502	-0.24436911	0.003977762		SYNE2_SYNE1_SYNE3
KH.C4.90	-0.250121789	0.046025597	PALPS	S35F6
KH.C9.203	-0.251591833	0.063208445	EPI	CGL
KH.C7.425	-0.257468553	0.039637129		S35E3
KH.S655.2	-0.262236054	0.011240461	EPI	CO4A1_CO4A6_CO4A3_CO4A2
KH.C2.421	-0.265657292	0.0552781		BMP3_BMP2_GDF6_CDKL2_CDKL1_CDKL5

KH.C2.10	-0.267311024	0.002497765		HXK1_HXK2_HKDC1
KH.C3.672	-0.268926378	0.033462165		S38A7_S38A8_S38A1
KH.C8.476	-0.26979224	0.06229849	EPI	LOXL3_LOXL4_LOXL2
KH.C14.520	-0.271304264	0.00142898		
KH.C2.403	-0.273428127	0.070366808		DYH9_DYH11_DYH17
KH.S115.2	-0.28350369	0.046679653		EVA1C
KH.C5.147	-0.28399621	0.036248559		MYO10_MYO7A_MYO7B
KH.C2.447	-0.285109201	0.050122766		HPDL
KH.C2.473	-0.287230313	0.021309724		UXS1_TGDS
KH.C7.61	-0.293727518	0.001904106		
KH.C9.157	-0.295425596	0.028215515	EPI	
KH.C1.182	-0.296964317	0.049503689		
KH.L116.70	-0.302378269	0.013679087		ARGI2_ARGI1
KH.C3.72	-0.303324297	0.084793804		NOTC1_NOTC2_NOTC3
KH.C12.20	-0.304398116	0.001901603		CLIC6_CLIC1_CLIC4_CLIC5_CLIC2
KH.C11.389	-0.305636687	0.004152964		HMCN1_HMCN2_NPHN
KH.L154.34	-0.314192773	2.71E-05		ACTC_ACTB_ACTG_ACTA
KH.S494.4	-0.315313847	0.032430429		S26A5_S26A4_S26A6
KH.C2.187	-0.316496055	0.000952194	EPI	PAPS1_PAPS2
KH.C4.467	-0.318727002	0.062170691	PALPS	YLAT2_BAT1_XCT
KH.C9.132	-0.319802415	0.0552781	PALPS	NOE2_NOE3_NOE1
KH.C5.398	-0.321527201	0.072678808	EPI	
KH.S651.3	-0.324482823	0.001151871		MDR1_MDR3_ABCB5
KH.C1.33	-0.33163201	0.078116376		
KH.L71.9	-0.334080119	0.029938022		SOCS2_CISH_SOCS3
KH.C1.244	-0.335819997	4.41E-06		CO4A1_CO4A6_CO4A2
KH.C12.118	-0.342361757	0.003287953		FXL20_FBXL2_FBXL4
KH.L164.5	-0.3456463	0.001151016		NEO1_PRTG_DCC
KH.C1.837	-0.346871594	0.027839321		
KH.C10.190	-0.3503102	0.012492498		HMCN1_PRS33_KLKB1
KH.L20.58	-0.351638244	0.021621306		EDIL3_DCBD2_DCBD1
KH.L116.14	-0.353224157	0.044424695		G3ST1_G3ST3_G3ST2
KH.C4.191	-0.354443996	0.004514729		SO1C1_SO1B1_SO2B1_SO1B3_SO3A1
KH.C3.684	-0.355043822	0.093533121		
KH.C3.264	-0.356949299	0.001518033		
KH.C12.280	-0.357604247	0.006654528		
KH.C12.32	-0.358710009	0.012679267		TSN9_CD63_CD151
KH.C10.172	-0.360375497	0.093889092		KIRR2_KIRR1_KIRR3
KH.C5.596	-0.361019858	0.03659767	EPI	
KH.C7.288	-0.362666017	0.006067737		
KH.L71.2	-0.372266049	0.000122123		FSCN1_FSCN2_FSCN3
KH.C9.650	-0.372522132	0.046679653		ST1C2_ST1C3_ST1B1
KH.S1180.1	-0.373260152	2.52E-05		GMPPB_GMPPA
KH.C8.24	-0.375220999	0.005204375	EPI	
KH.C4.260	-0.37526185	0.001185496		
KH.L37.43	-0.376215815	0.078227829		SRR
KH.L147.1	-0.378177131	0.000101701		NOTC1_NOTC2_NOTC3
KH.C10.220	-0.379351355	0.087474988	PALPS	
KH.C8.101	-0.388567259	0.017749608		ROR2_ROR1_MUSK
KH.C13.105	-0.388825013	0.062053784		PLCH1_PLCH2_PLCD3
KH.L48.1	-0.389117919	5.46E-05		
KH.C4.254	-0.391597976	0.000501103		AT8B2_AT8B4_AT8B1
KH.S546.3	-0.391973998	5.07E-05		
KH.C1.1258	-0.392541026	0.066183463	EPI	B3GT1_B3GT5_B3GT2
KH.C9.637	-0.393100889	0.026030904		
KH.C1.23	-0.394346351	0.004246024		GRHL1_GRHL2_GRHL3
KH.C4.339	-0.39600383	0.000328872		MRP5_MRP9_ABCCB
KH.C7.230	-0.396910713	0.001572248		
KH.C2.676	-0.403057222	0.005733223		JIP4_JIP3_ARHGH_ARHGA_ARGAL
KH.C12.191	-0.405782561	0.062053784		S23A2_S23A1_S23A3
KH.C3.191	-0.409843993	0.084326992		WBS27
KH.C5.154	-0.410629365	0.095000441		KLF2_KLF4_KLF1
KH.C9.859	-0.411398211	0.086122873	EPI	RAC1_RAC2_RAC3
KH.C7.501	-0.414864516	9.37E-05		
KH.C1.1083	-0.415524129	0.000190817		EPHA4_EPHA7_EPHB2
KH.C1.819	-0.41666239	0.000111854	EPI	
KH.C12.561	-0.421300186	0.020777197		
KH.C10.551	-0.421799693	1.55E-05		
KH.S403.4	-0.422925597	8.70E-06		HEM1_KBL_HEM0_SPTC2
KH.S651.1	-0.426928677	0.009097691		
KH.C2.922	-0.42772101	0.000106638	EPI	
KH.L73.2	-0.431347704	0.00440345	EPI	UROM_GP2_TECTA

KH.C8.611	-0.433082411	0.082221021		
KH.L10.9	-0.441183866	0.00685969		
KH.C1.599	-0.443975665	0.000227527		
KH.C8.741	-0.452341554	0.072678808	PALPS	
KH.C2.133	-0.459740413	0.001721135		HMCN1
KH.C9.62	-0.461394947	0.006155167		ABRAL
KH.C13.17	-0.462675894	0.071930863		
KH.S1042.1	-0.465839768	0.017918379		
KH.C10.251	-0.467287083	0.024998629		
KH.C13.36	-0.46835728	0.006004468		RLBP1_TTPAL_CLVS1
KH.C12.49	-0.469205392	2.29E-05		CO4A6_COLA1_CO9A2_COOA1_CO4A2
KH.C7.581	-0.473057983	0.000234871	EPI	B4GT1_B4GT2_B4GT4
KH.C13.87	-0.473787423	1.33E-05		LRIG2_TPBG_LRIG1
KH.C9.251	-0.475582893	5.29E-09	PALPS	
KH.C4.224	-0.475939706	3.34E-07	PALPS	CD166_BCAM_MUC18
KH.C5.326	-0.476628538	0.000126656		FUT8
KH.C12.511	-0.47755589	0.030454979		FZD10_FZD4_FZD9
KH.C1.1121	-0.478838316	0.082543836		ST1C2_ST1C4_ST1E1
KH.C11.428	-0.48631021	1.98E-06		LRP6_LRP4_LRP5
KH.C1.429	-0.486456131	6.11E-05		GPC5_GPC3_GPC4
KH.S655.3	-0.488513845	0.02399365		
KH.C3.897	-0.488564933	0.042921561		
KH.C5.367	-0.490636932	0.002252864		
KH.C5.13	-0.491171418	6.52E-07	EPI	
KH.L18.128	-0.494580701	1.78E-05		MDGA1
KH.C6.133	-0.499597722	1.73E-06		ADK
KH.C14.474	-0.500434366	0.001518033		
KH.C9.565	-0.504331249	0.012517204		ANXA7_ANXA4_ANXA1
KH.S2051.1	-0.505917101	0.005174908		PXDN_PERT_PERE
KH.C1.802	-0.508391999	0.000420294	EPI	COCA1_COKA1_COEA1
KH.C1.212	-0.513184036	5.19E-12	EPI	D19L1_D19L2_D19L3
KH.C2.229	-0.515497444	0.000224135		
KH.S164.12	-0.516076418	0.054465282		SOX14_SOX21_SOX2
KH.S164.28	-0.517915996	0.001199879		FUT6_FUT5_FUT7
KH.S544.3	-0.525546014	0.097684318		DMTA2_DMRTA_DMRT1
KH.C5.384	-0.527954436	1.56E-07	PALPS	TECTA_GP2
KH.C7.261	-0.532422401	9.13E-08		S6A17_S6A15_S6A19
KH.C4.425	-0.535471081	0.000547055		RHAG_RHCG_RHBG
KH.C1.825	-0.538780153	0.097072021		RXFP1_RXFP2_FSHR
KH.C11.518	-0.538861961	0.010071834		ABCG2_ABCG4_ABCG1
KH.S908.2	-0.539145002	0.006103624	PALPS	TECTA_CILP2_CILP1
KH.C4.201	-0.542124694	0.00336702	PALPS	
KH.C6.219	-0.543370237	0.000253893		FLRT1_FLRT2_FLRT3
KH.C1.1240	-0.543438392	1.28E-10	EPI	KLH20_KLHL5_KLHL3
KH.C8.863	-0.544148064	7.52E-06		TRIM2_TRIM3_LIN41
KH.C8.182	-0.544587638	1.65E-12		B4GT1_B4GT2_B4GT4
KH.C10.417	-0.545030729	7.67E-05		
KH.C5.16	-0.547916855	3.14E-16		CD109_PZP_A2MG
KH.C3.245	-0.549007971	1.37E-06		
KH.C5.580	-0.550740743	5.00E-07		FUT8
KH.L116.28	-0.551402075	1.07E-11	EPI	UGPA
KH.C11.663	-0.554255769	0.030240727		KREM1_KREM2
KH.L37.72	-0.555104408	0.001623883	PALPS	CPMD8_PZP_A2MG
KH.C1.40	-0.555289044	5.02E-05	EPI	
KH.L149.2	-0.555524254	0.041264801		
KH.C9.602	-0.555941497	0.000126885		GCYB1_GCYB2_GCYA2
KH.C8.115	-0.557033906	5.78E-09	EPI	
KH.C14.420	-0.557494946	0.016058339		
KH.C12.536	-0.558467691	0.003419312		
KH.S1524.1	-0.560116275	5.12E-07	EPI	
KH.C2.248	-0.560516619	3.32E-13	PALPS	KLH26_KLH13_KLHL9_KLH31
KH.C13.184	-0.562785302	0.019882465	PALPS	B3GT1_B3GT2_B3GN5
KH.C14.153	-0.565621959	2.09E-09		PIM3_PIM1_PIM2
KH.C9.561	-0.565677467	1.98E-07		IKZF2_IKZF1_IKZF3_IKZF4
KH.L153.79	-0.566040409	1.33E-05		PITX2_PITX3_PITX1
KH.L170.29	-0.571227377	0.004045856		
KH.L18.100	-0.57306986	0.003341215	EPI	
KH.L18.117	-0.573673474	0.000645825		PPA6
KH.C2.992	-0.574263533	0.029325638		
KH.L20.48	-0.576366431	0.015791882		SG196
KH.L106.16	-0.582425452	0.011690309		NODAL_BMP10_GDF2
KH.L171.4	-0.583170448	0.004389752		HMCN1_CORIN_PRS48
KH.C11.158	-0.584928829	0.000180472		FUT8
KH.C4.150	-0.58720533	0.001778642		

KH.C11.489	-0.594252607	5.39E-11	PALPS	BAI3_HMCN1_SEM5B
KH.C6.115	-0.597144063	8.64E-08		MCFD2
KH.C4.341	-0.600916622	0.000106638		FOXB1_FOXB2_FOXA2
KH.C10.350	-0.602612776	0.003527257	PALPS	UST_HS2ST
KH.C9.579	-0.603787949	0.001823746		WSCD2_WSCD1
KH.C10.147	-0.608801176	0.005539659		S22A5_S22A4_S22A3_S22A7_S22A8_S22AO
KH.C14.408	-0.6093453	2.78E-07	PALPS	CDX2_CDX1_CDX4
KH.C2.251	-0.609385861	9.35E-05	EPI	
KH.C9.49	-0.610579062	0.011485096		RGS4_RGS5_RGS1
KH.C8.915	-0.610933209	5.45E-11		
KH.C3.149	-0.611452444	2.46E-05		PLS1_PLS3_PLS5
KH.C1.1018	-0.613942834	0.066507538	EPI	
KH.C11.394	-0.615438942	0.013206224	EPI	
KH.C1.1100	-0.617827197	0.000229154		PCD18_PCD17_PCDGH
KH.C1.591	-0.619547357	0.002463059		S6A14_SC6A5_SC6A9
KH.C6.176	-0.621661154	0.012492498		NHRF3_NHRF4
KH.C8.747	-0.622370948	0.087767455		FOXI3_FOXI2_FOXI1
KH.C1.327	-0.623558817	1.07E-05		
KH.S779.1	-0.626377722	0.058333714		ACTA_ACTC_ACTS_ACTG_ACTB_ACTBL
KH.C1.922	-0.626715269	0.003542117		BARH1_TLX1_BARH2
KH.C7.123	-0.627191587	1.79E-06		
KH.C7.154	-0.630321931	2.43E-10	EPI	UXS1
KH.C7.136	-0.630739979	0.002209201		
KH.C7.211	-0.631555682	4.25E-24		
KH.C3.170	-0.641977265	3.29E-06	PALPS	FOXF1_FOXF2_FOXL1
KH.C9.40	-0.64259315	5.48E-13		
KH.S803.3	-0.642784707	2.21E-12	EPI	CO7A1_FINC
KH.L19.6	-0.645635509	4.04E-16		TSN33
KH.C10.74	-0.647175525	0.021082165		AA1R_AA2AR_AA2BR
KH.C10.407	-0.649286387	2.75E-06		
KH.L10.31	-0.657345202	1.57E-07	EPI	
KH.L152.12	-0.657403611	0.061738194		GAS2_GA2L3
KH.L63.13	-0.657669572	3.03E-05	EPI	MZB1
KH.C12.650	-0.659265903	0.002436131	EPI	
KH.C7.720	-0.660199133	0.06749191		PXDN_PXDNL_ISLR
KH.C8.489	-0.661344274	0.001937536	EPI	
KH.C2.867	-0.664574989	0.08025203		
KH.L116.32	-0.667070635	0.093826271		TSHR_RXFP1_LSHR
KH.C1.764	-0.667332292	8.96E-05		
KH.S164.31	-0.668629432	0.068528016		FUT6_FUT5_FUT4
KH.C5.330	-0.669071895	3.95E-05		
KH.C12.9	-0.672895277	8.92E-05		UN93A_UN93B
KH.C3.718	-0.675335057	3.74E-05	PALPS	
KH.S417.3	-0.675703427	0.01144311		G3ST1_G3ST3
KH.C14.414	-0.675738438	9.78E-11		PIM3_PIM1_PIM2
KH.L18.33	-0.676808218	5.13E-05	PALPS	ZN420_ZN135_ZN251
KH.C9.445	-0.679571248	0.000407368	EPI	ENDOU
KH.C14.446	-0.679738901	7.67E-09		
KH.C14.271	-0.690126739	0.000169891		
KH.C1.188	-0.690187756	1.15E-10	EPI	
KH.L50.21	-0.691734169	0.000913543		GXLT2_GXLT1
KH.C3.666	-0.691952058	0.001904106		PDE9A_PDE11_PDE4C
KH.S164.10	-0.696777024	0.00019483		
KH.C2.411	-0.700215135	0.037296428	EPI	
KH.C3.411	-0.700732838	3.93E-05		LFTY2_LFTY1_BMP4
KH.C7.281	-0.706238575	4.97E-22	PALPS	SC6A5_SC6A7_SC6A9
KH.L96.43	-0.707806762	0.015343623		TM11D_TMPS3_ACRO_TRYB2
KH.C11.199	-0.708863035	1.14E-10		ODC_TXTP_UCP5
KH.S761.3	-0.70995902	0.000826455		S38A4_S38A3_S38A2_S38A1
KH.C2.649	-0.711646307	0.000110015	EPI	
KH.S870.2	-0.712225557	1.57E-09		GIN1_NYNRI_RTL1
KH.C7.64	-0.713444844	1.42E-09		GCYB1_GCYB2_GCYA2_ANPRB
KH.C1.870	-0.714207934	3.28E-15	PALPS	S6A14_SC6A5_SC6A7
KH.C1.495	-0.715283729	7.57E-05		PLMN_KLKB1_CTRL
KH.C1.1093	-0.715992115	1.02E-14	EPI	
KH.C7.43	-0.716155324	6.02E-06		AP2E_AP2A_AP2B
KH.C11.711	-0.716262358	6.39E-09	EPI	
KH.C3.231	-0.719991215	0.07584265	EPI	
KH.C3.503	-0.723774424	8.77E-15	EPI	PLEC_DESP_EPIPL
KH.L63.14	-0.724370002	0.002699947		
KH.C2.201	-0.72641504	0.039081504		
KH.C1.1252	-0.727350983	2.06E-05		
KH.S1721.1	-0.727401762	0.000459593		TTC22

KH.C2.20	-0.729675629	8.54E-16		
KH.C11.308	-0.731447938	0.015396008	PALPS	
KH.C9.3	-0.732921569	2.87E-15	EPI	TECTA_UROM_GP2
KH.L8.1	-0.733689176	1.15E-11	EPI	ESRP1_ESRP2_HNRH2
KH.L37.12	-0.735889892	5.83E-09	EPI	
KH.C2.655	-0.736088505	2.79E-09		TMTC3_TMTC4_TMTC1
KH.C10.496	-0.739276608	2.36E-13		HMCN1_PRS33_PRS38
KH.S1155.2	-0.744284692	3.44E-10		
KH.C1.1109	-0.749516501	0.05121983	EPI	
KH.C14.146	-0.750054662	0.00991513		GAPR1
KH.C8.176	-0.753897482	3.29E-16	EPI	
KH.L116.41	-0.759218081	0.001523867		
KH.S2649.1	-0.764677671	0.090933668	PALPS	ANPRC
KH.L63.12	-0.76600456	1.18E-07		
KH.C8.918	-0.768816253	0.016320298		
KH.L5.10	-0.770261521	0.008991548		TM175
KH.L147.25	-0.771789918	0.000539379	EPI	CSMD1_SVEP1_CR1
KH.C2.609	-0.774500564	8.22E-06		
KH.C10.367	-0.775115831	0.072083605		SIX3_SIX6_SIX1
KH.C13.119	-0.775728992	9.48E-18	EPI	CAH14_CAH9_CAH6
KH.C7.210	-0.776303987	2.88E-13		NHRF3_PDZ1P_NHRF2
KH.C12.390	-0.777376404	1.60E-12		MRF_MRFL
KH.C14.154	-0.78211307	3.06E-17		
KH.C7.542	-0.782706885	0.000388766		RFNG_LFNG_MFNG
KH.L106.9	-0.783107841	1.04E-07		
KH.C5.346	-0.786381905	5.88E-07		DDC_DCHS_GADL1
KH.C5.27	-0.78979322	0.006174667		FUT6_FUT5_FUT3
KH.L73.8	-0.792856625	0.001307005		S39AA_S39AC_S39A4
KH.C11.722	-0.792886435	0.00421788		
KH.L59.3	-0.795517354	0.000166742	EPI	GLIP1_GPRL1_PI16_CRIS2
KH.C9.204	-0.798380896	4.76E-14	EPI	GMPPB_GMPPA
KH.C2.453	-0.803334716	4.33E-06	EPI	KGP1_KGP2_PRKX
KH.C5.519	-0.803382872	0.00037281		B4GT7
KH.C14.56	-0.807799145	2.94E-23		BAI3_HMCN1_AGRB2
KH.C12.408	-0.812250661	1.96E-08		MGT5A_MGT5B
KH.L168.1	-0.815544976	0.000651942		
KH.C5.385	-0.816105338	3.82E-09	EPI	
KH.C5.52	-0.818584073	2.90E-16	EPI	CAHM2_FA26E_FA26F
KH.C6.12	-0.818781792	1.07E-18	EPI	
KH.C3.762	-0.821836992	0.000369847		
KH.C4.71	-0.824209409	6.08E-10		HS3S1_NDST2_NDST4
KH.L36.8	-0.824593517	1.55E-26	EPI	HMCN1_SEM5B_SEM5A
KH.C1.201	-0.827059335	4.75E-05		MOT14_MOT9_MOT12
KH.C3.781	-0.829467035	3.44E-14	EPI	VIME_GFAP_NFM
KH.C12.544	-0.832226267	0.00026288		B3GT1_B3GT5_B3GT2
KH.L96.103	-0.834226991	1.90E-11		
KH.C14.535	-0.840046734	3.49E-13	EPI	
KH.C2.125	-0.843723632	5.10E-05		FGF9_FGF20_FGF16
KH.C5.240	-0.850045072	6.57E-26	EPI	LRP6_LRP4_LRP1
KH.S2590.2	-0.850785814	0.051656139		
KH.C3.304	-0.850831047	2.00E-06		RGS4_RGS8_RGS5
KH.L141.68	-0.853397281	0.01660026	EPI	
KH.C4.648	-0.855144174	2.29E-05		RHAG_RHCG_RHBG
KH.C8.475	-0.856289793	2.62E-05	PALPS	SO1B3_SO1C1_SO1B1
KH.S1391.3	-0.859944701	0.057360956		
KH.L153.109	-0.863649061	0.021169852		
KH.L119.31	-0.864344819	0.036102158		PLEC_DESP_EPIPL
KH.C2.380	-0.865298639	1.01E-11	EPI	LARP6
KH.C2.594	-0.867691372	0.03414779	EPI	
KH.S1248.1	-0.869441374	0.097684318		
KH.C3.305	-0.874020881	4.19E-19		
KH.C11.279	-0.874705052	0.046679653		CHSTB
KH.C11.299	-0.874888568	1.37E-13		FUT8
KH.C2.373	-0.880825112	1.56E-07	PALPS	
KH.C2.696	-0.881936729	0.071420742		CHSTB
KH.L108.10	-0.882448959	4.14E-21		KLH13_KLHL9_KLH36
KH.L97.7	-0.887397777	0.000402785		ACM3_ACM2_ACM5
KH.S1957.1	-0.888692214	9.96E-06		GMPPB
KH.C12.146	-0.889816967	0.000262934		
KH.C5.537	-0.891294252	0.00037281		CHST1_CHST3_CHST6
KH.S389.10	-0.891422795	0.00023371	PALPS	
KH.L40.18	-0.898090553	4.88E-07	PALPS	ZF69B_ZSA5D_ZN713
KH.C13.146	-0.899790529	2.51E-10		HMCN1_SEM5B_ATS9
KH.S423.1	-0.901607272	1.69E-09	PALPS	ANPRA_ANPRB_ANPRC
KH.S406.9	-0.906254465	2.70E-05		ARI3B_ARI3A_ARI3C

KH.C9.656	-0.907167344	2.27E-06	EPI	
KH.C8.844	-0.908359388	8.54E-16		
KH.S1641.1	-0.91141116	9.31E-07	EPI	
KH.C2.694	-0.912037512	1.29E-14	EPI	UROM_GP2
KH.L168.6	-0.913987478	4.27E-10		
KH.C8.117	-0.91543746	3.30E-13		
KH.S390.3	-0.916230169	0.000351015	EPI	KCD15_KCTD1
KH.C9.543	-0.918556346	1.59E-24	EPI	VIME_GFAP_PERI_DESM
KH.L141.32	-0.923238066	0.008056902		
KH.L132.16	-0.924474245	1.29E-30	EPI	MATN3_MATN2_MATN4
KH.S1783.2	-0.924697613	1.74E-06		
KH.C10.127	-0.926034935	6.85E-10		HMCN1_TMPS6_FA9
KH.C14.293	-0.927564796	7.51E-05	EPI	COCA1_MATN2_MATN4
KH.C2.637	-0.928906563	0.020777197	EPI	B3GT1_B3GT5_B3GN5
KH.L5.14	-0.934794527	4.04E-20		B4GT1_B4GT2_B4GT4
KH.L45.4	-0.938407972	0.035033255		
KH.S345.1	-0.940010091	0.004666161	EPI	
KH.C11.454	-0.943314591	0.012061471	EPI	
KH.C6.198	-0.944213883	3.89E-05	EPI	HMCN1_TSP1_AGRB2
KH.C8.395	-0.944291741	7.06E-10		
KH.C1.93	-0.945113085	4.54E-17		
KH.C14.163	-0.947553396	1.57E-10	EPI	
KH.C7.164	-0.952706607	2.10E-27	EPI	CSMD3_SVEP1_CR2_CSMD2
KH.C2.244	-0.95542729	1.87E-13		
KH.C3.650	-0.960193457	0.005733223		
KH.C1.747	-0.964847788	5.42E-11	EPI	S22A5_S22A4_S22AG
KH.C2.802	-0.966344922	6.76E-06	EPI	
KH.L95.5	-0.972911321	0.033145792		
KH.L131.17	-0.978878552	5.67E-09	EPI	
KH.L4.50	-0.980978726	5.59E-05		
KH.C11.512	-0.988018342	4.99E-21	EPI	LYAM3_SVEP1_LYAM2
KH.C13.16	-0.995185693	2.06E-05	EPI	HMCN1_PROP_AGRB2
KH.C1.602	-0.998962685	0.000552731		
KH.C5.531	-1.017797975	4.20E-08		S35E3
KH.C3.251	-1.018317159	7.66E-12	EPI	
KH.L171.19	-1.021430519	1.14E-09		
KH.C11.222	-1.027980545	0.002608196		
KH.C9.147	-1.029248179	1.13E-07	EPI	
KH.C14.337	-1.04355923	0.002132183		
KH.C5.235	-1.045498003	1.13E-24		
KH.L141.61	-1.051101214	6.34E-18	EPI	
KH.C4.247	-1.052942538	0.093826271	EPI	
KH.C2.377	-1.054419682	1.41E-19	EPI	TMPS9_PRSS8_KLK5
KH.C8.121	-1.054468437	1.28E-36	EPI	HMCN1_SSPO_ATS9_SPON1
KH.C13.90	-1.0566627	6.70E-06		ANPRA_ANPRB_GUC2D
KH.C8.164	-1.059449258	0.024884063	EPI	
KH.C14.356	-1.059672791	0.000513573	EPI	
KH.C5.37	-1.060122521	2.20E-16		
KH.C3.611	-1.072027945	0.000122941		
KH.L132.4	-1.072153315	6.90E-51		MEGF6_FBN1_MATN2
KH.L84.20	-1.075520834	0.000245899		S22A5_S22A4_S22A3
KH.L116.100	-1.076382468	6.87E-15	EPI	LGR5_LRIG3_LRIG2_TRIL_TLR9_PGS2
KH.L147.16	-1.076825735	3.75E-14		
KH.C11.293	-1.0774256	4.56E-47		
KH.C11.539	-1.080030985	0.001344597	EPI	S20A1_S20A2
KH.C1.1013	-1.080534236	4.04E-08		
KH.C10.506	-1.08201337	0.00062522	PALPS	
KH.L96.44	-1.082334974	3.37E-31	EPI	
KH.C3.654	-1.082412531	3.17E-06		
KH.C9.803	-1.083411271	0.00142898		
KH.C5.21	-1.08356047	6.07E-25		
KH.C14.54	-1.084554388	8.19E-08		
KH.L4.7	-1.088242231	0.000266939		
KH.C3.438	-1.093718726	5.43E-24	EPI	LYAM3_CSMD3_LYAM2
KH.C14.549	-1.098376858	0.087767455	EPI	
KH.C1.525	-1.107960142	1.34E-18	EPI	
KH.C11.184	-1.109519534	0.025094995	EPI	GALE_TGDS
KH.C2.919	-1.136206156	0.00240298		BTBDJ_BTBD3_BTBD6
KH.S351.4	-1.138203909	9.69E-21		PLEC_DESP_EPIPL
KH.C14.261	-1.139625138	6.52E-07		
KH.C7.521	-1.147136618	2.90E-09		PLMN_APOA_TPA
KH.C1.757	-1.154483879	1.09E-14		
KH.C1.434	-1.159424424	4.31E-09		B3GT5_B3GT2_YI036
KH.C2.54	-1.173472779	1.34E-08		

KH.C7.58	-1.184104434	1.82E-60		TMPS9_TMPS5_BSSP4_PRSS8
KH.C9.572	-1.190457348	0.000788785		
KH.C9.209	-1.197266478	1.28E-36		NR4A3_NR4A2_NR4A1
KH.S511.1	-1.20168528	3.44E-08	EPI	
KH.C5.208	-1.212047231	7.51E-17	EPI	
KH.C12.186	-1.216495184	0.031436754		
KH.L96.108	-1.216895962	1.82E-14		YLAT2_BAT1_YLAT1
KH.C10.215	-1.23124943	0.041335183		
KH.C10.144	-1.236149272	2.27E-08		CORIN_TMPS2_FA11
KH.C10.67	-1.23965963	1.65E-20		
KH.L142.14	-1.254211888	8.48E-08		EMX1_EMX2_VAX1
KH.L108.30	-1.269976832	0.000744094		
KH.C7.354	-1.302396604	1.97E-11	EPI	
KH.C8.603	-1.332934504	0.013182032		
KH.L170.71	-1.335403258	0.035296043		AQP8_AQP1
KH.C8.510	-1.335657523	9.85E-60		MATN1_HMCN1_CO6A5_SSPO
KH.C1.611	-1.341176401	0.005767041		FCL
KH.C8.433	-1.342316136	3.50E-71		FAT1_SNED1_DLL1
KH.C14.201	-1.348914774	0.072678808	EPI	MDGA1_ENTK_MALR1
KH.L164.4	-1.353457147	7.79E-07		
KH.C2.809	-1.358004767	0.059827682		
KH.C4.146	-1.380467186	0.019271062		CTRB2_CTRB1_CTRL
KH.L92.8	-1.401335718	2.24E-07	EPI	
KH.C3.764	-1.406288115	5.38E-07		
KH.L22.52	-1.429271289	0.006202682	PALPS	
KH.C8.877	-1.47209271	0.048828337	EPI	
KH.C1.3	-2.548728424	0.018240226		
KH.L60.8	-3.982772136	0.019004446		