

SUPPLEMENTAL FIGURE LEGENDS

Supplemental Figure S1. Genomic organization of *Hox* clusters in coelacanth and shark. The annotations of *HoxA* (A), *HoxC* (B) and *HoxD* (C) clusters in coelacanth (*Latimeria menadoensis*) and/or horn shark (*Heterodontus francisci*) were generated from sequence alignments of regions orthologous with other vertebrate species. Genomic sequences were found at NCBI: coelacanth *HoxA* cluster (AC147788, from *Hoxa13* to *Hoxa9*), coelacanth *HoxC* cluster (AC151571, from *Hoxc9* to *Hoxc1*), horn shark *HoxA* cluster (AF479755 and AF224262, from *Hoxa13* to *Hoxa1*) and horn shark *HoxD* cluster (AF224263, from *Hoxd13* to *Hoxd5*). The coding sequences of individual *Hox* gene was identified using nucleotide BLAST searches at NCBI. The correct relative sizes of predicted *Hox* gene exons (black boxes) and introns (white or colored boxes), as well as for intergenic regions (thick lines) allow for direct size comparisons between species. The apparent large size of the *HoxC* cluster in coelacanth is due to the persistence *Hoxc1*. Colors indicate either a 1.5- to 3-fold increase (blue color), or more than a 3-fold increase (red color) in intronic (colored boxes) or intergenic (colored lines) regions. Gaps in the genomic sequences are indicated by dotted lines for intergenic regions and dotted boxes for genes.

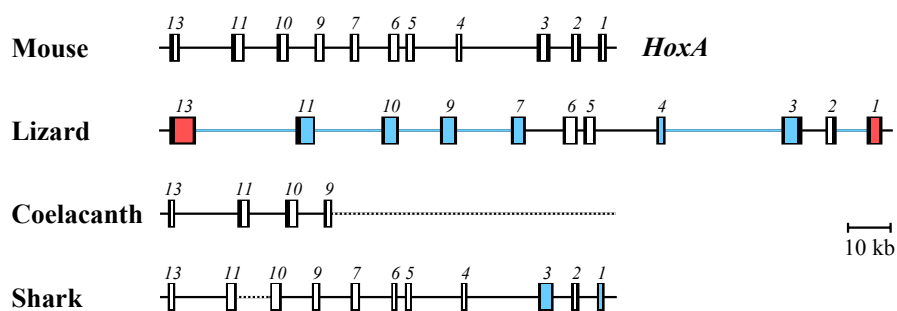
Supplemental Figure S2. Identification of repetitive sequences present in the *HoxA* (A), *HoxB* (B), *HoxC* (C) and *HoxD* (D) clusters. Dot plots were produced in mouse, chicken, lizard and *Xenopus* by comparing each vertebrate *Hox* cluster with itself, using BLASTN on the EMBOSS explorer server (<http://pro.genomics.purdue.edu/emboss/>). The position of BLASTN hits along the different *Hox* clusters are shown by black dots. Red circles indicate the presence of small regions containing conserved repetitive elements in *Xenopus*. Note that the numerous dots present in the lizard *Hox* clusters mainly correspond to repetitive transposable elements.

Supplemental Figure S3. Sequence comparisons of vertebrate *HoxA*, *HoxB* and *HoxD* clusters. Global genomic alignments of the *HoxA* (A), *HoxB* (B) and *HoxD* (C) clusters between the lizard, chicken, human, mouse, *Xenopus* and zebrafish genomes. Sequence comparisons were realized by using the lizard *Hox* cluster as a reference sequence. Nucleotidic homologies relative to the lizard sequence are given by histogram peaks. A red peak indicates significant nucleotide homology (at least 100 bp with more than 50% identity). Conserved elements are denoted by dashed boxes of different colors: blue indicates homology peaks between lizard and chicken only, whereas green indicates homology peaks common to lizard, chicken and mammals, but absent from *Xenopus* and zebrafish.

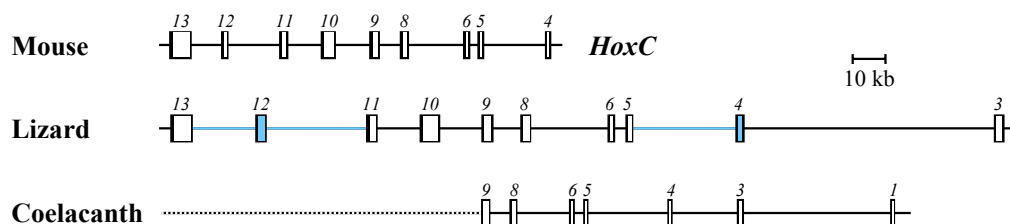
Supplemental Figure S4. Sequence comparisons between vertebrate *HoxC* clusters. Global genomic alignments of the anterior part of the *HoxC* cluster from *Hoxc9* to *Hoxc4* (A) or from *Hoxc4* to *Hoxc3* (B) between the indicated genomes. Sequence comparisons were realized by using the lizard *Hox* cluster as a reference. Nucleotidic homologies relative to the lizard sequence are given by histogram peaks. A red peak indicates strong nucleotide homology (at least 100 bp with more than 50% identity). Conserved elements between the lizard, coelacanth and *Xenopus* genomes are shown by red dashed boxes.

Supplemental Table S1. List of the sizes of those genes used as developmental-specific and non developmental-specific in mouse, lizard, chicken and *Xenopus*.

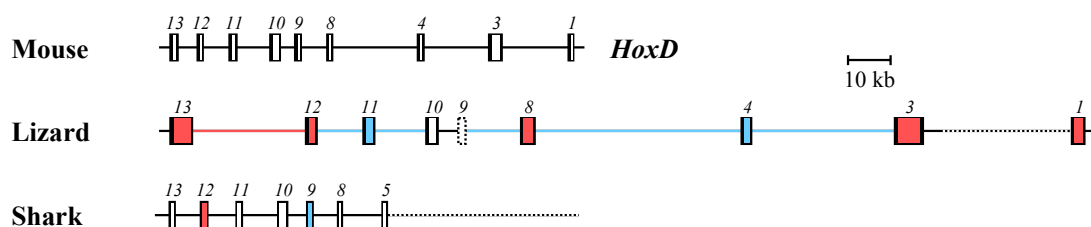
A

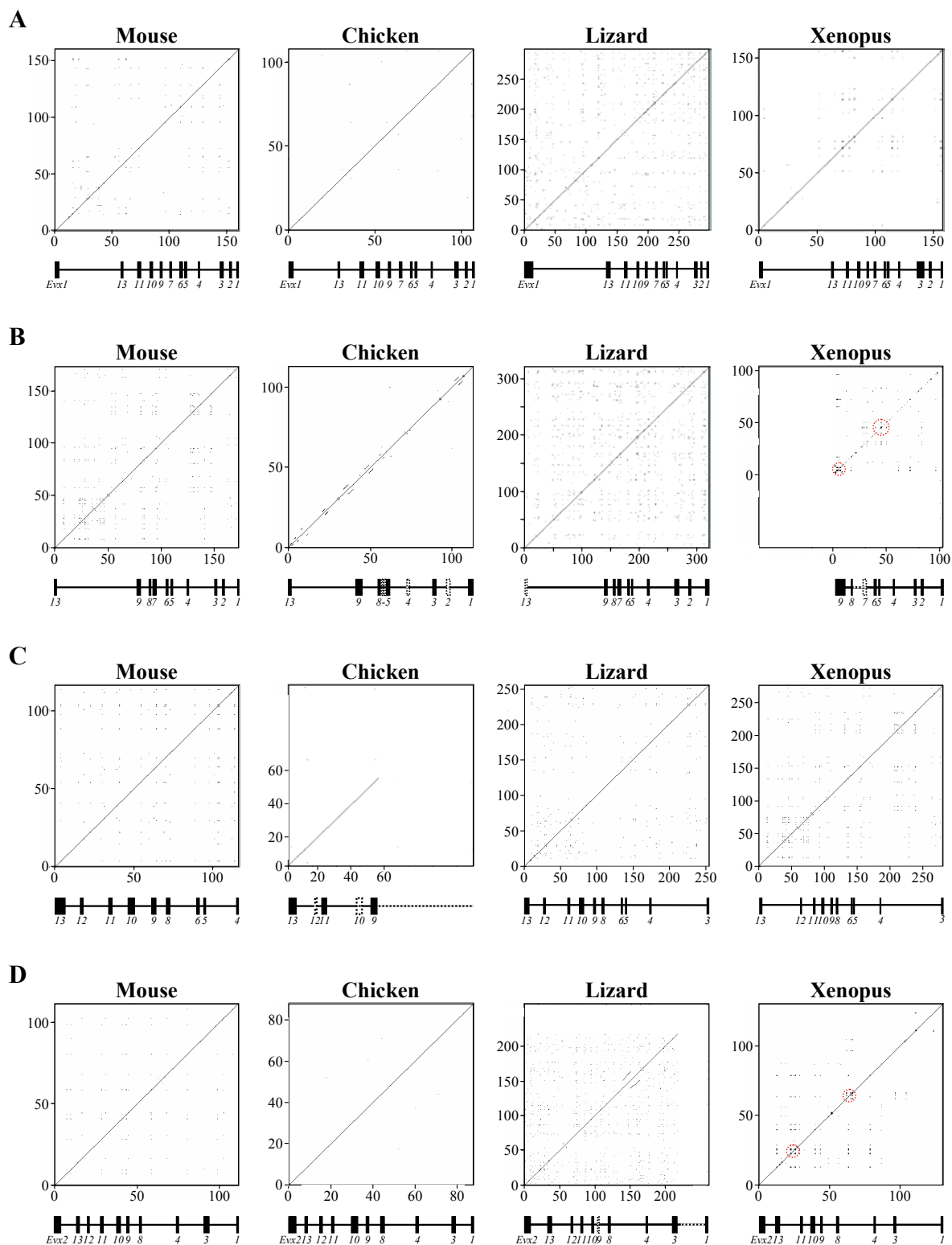


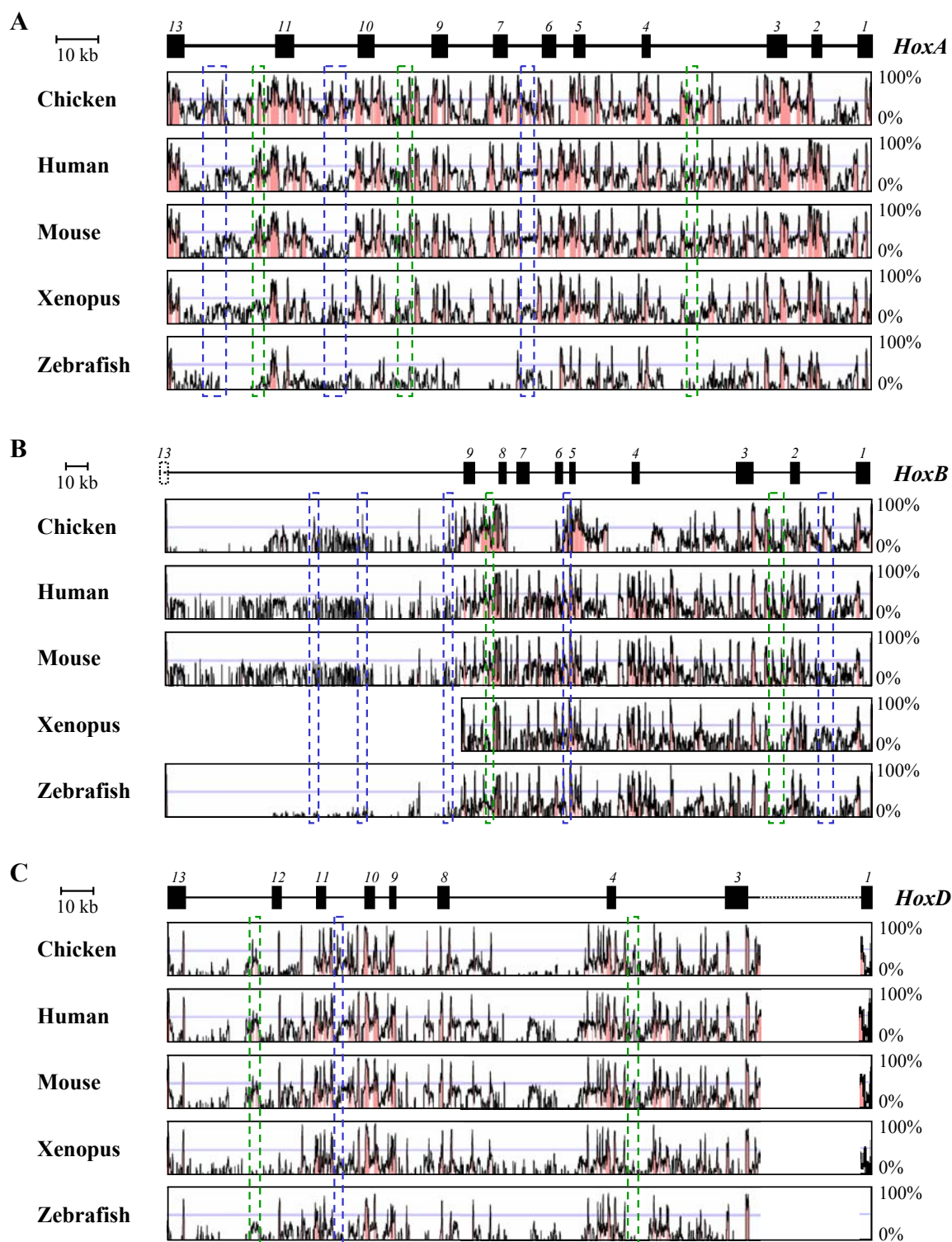
B

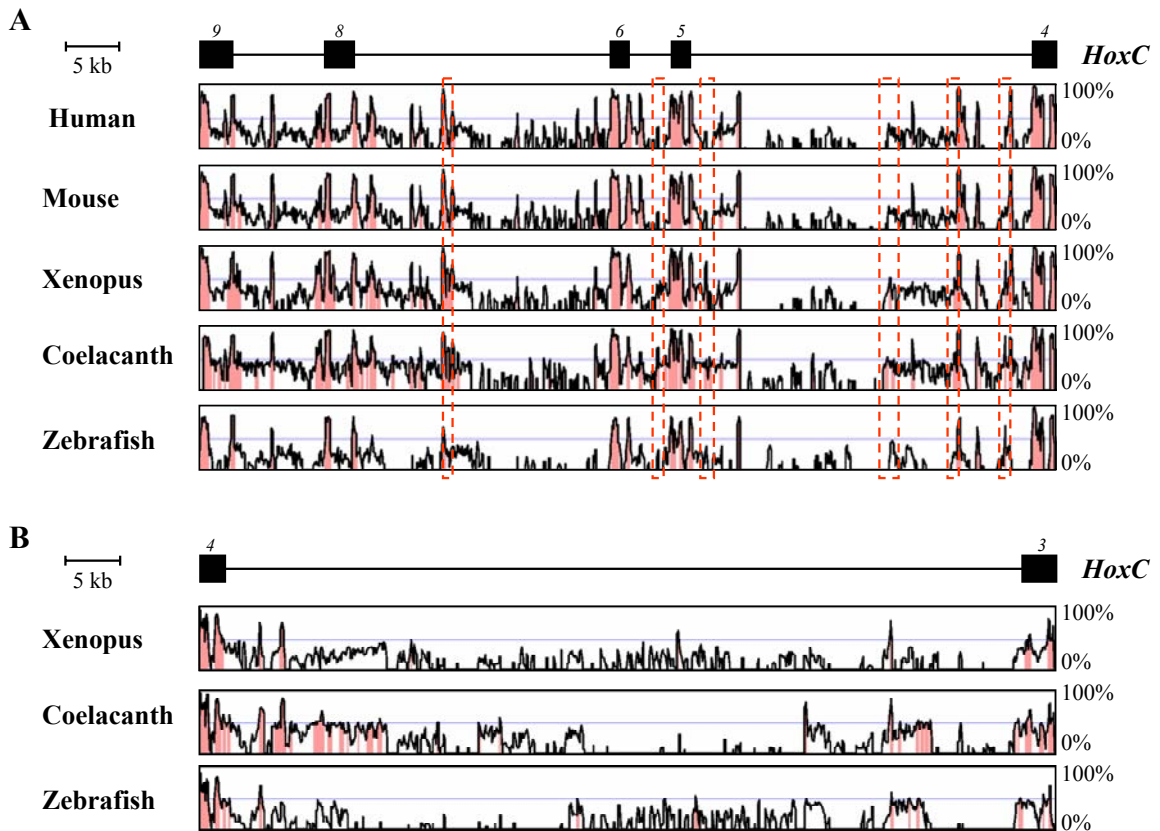


C









Supp Table S1

Developmental genes

	Mouse	Lizard	Chicken	Xenopus
Aqp1	10.5	33.5	17.4	-
Axin2	30.4	61.4	24.5	25.2
b-catenin (part)	10.0	14.0	8.2	9.5
Bcl2l11	34.0	36.7	-	30.9
Bcl9l	9.8	12.0	12.3	10.7
BMP2	8.2	12.7	4.1	8.3
BMP4 (part)	2.4	8.0	2.1	3.6
BMP7	70.2	95.4	41.6	50.3
BTG2	2.0	3.9	2.1	2.5
Brachyury	7.4	17.8	6.7	6.1
Cdx1	16.5	47.9	8.9	16.0
Cdx2 (part)	2.6	13.5	2.3	3.0
Chordin	8.3	63.9	1.8	12.4
C-myc	2.8	3.9	2.7	2.3
Dhh	4.7	29.0	9.7	22.1
Dact1	8.8	26.4	8.3	4.6
Dact2	81.5	82.4	76.1	-
Dax3	94.4	127.9	63.7	41.6
Dicer1	61.8	62.3	64.2	35.8
Dll1	7.7	13.7	8.0	7.3
Dll3	7.1	16.8	-	7.4
Dlx1	3.0	10.1	3.5	6.6
Dlx5	4.2	10.8	2.3	4.9
Dvl2 (part)	4.2	11.1	7.1	3.6
Dusp6	4.2	10.5	4.8	5.0
Egr1	3.7	4.6	3.1	3.6
Emx2	4.8	24.5	5.0	4.7
Epha1	13.6	56.6	29.8	14.8
EphA4	147.0	186.8	93.5	45.0
EYA1	140.8	103.0	99.2	66.5
FGF7	55.7	29.1	33.4	34.5
FGF8	6.1	23.0	7.2	8.2
FGFR1 (part)	41.7	86.3	16.0	-
FoxC1	4.0	9.1	3.8	3.5
Foxd1	2.1	3.6	-	1.9
Frzd1	28.9	41.2	12.2	12.5
Gata4	31.7	44.0	14.6	23.9
Gbx2	2.8	3.6	-	3.4
Gdf11	6.6	24.8	5.4	53.8
GDNF	22.0	20.0	-	-
Gfra1	197.0	238.0	135.0	-
Gli3	266.2	291.3	212.5	131.6
Goosecoid	1.6	13.4	1.1	2.5
Hand2	2.0	14.7	3.0	1.1
Has2 (part)	20.3	23.4	11.6	15.3
Hes1	1.9	2.5	-	2.0
Hes5 (part)	0.4	1.8	0.4	-
Hes7 (part)	0.93	2.4	-	-
Hesx1	1.9	4.3	2.5	3.0
Hey1	3.0	6.1	2.9	3.3
Hey2	10.4	23.6	13.7	29.3
Id1	1.1	5.5	0.7	-
lhh	5.6	31.3	9.8	36.8
Irx3	2.4	19.6	3.2	3.0
Isl1	11.4	37.0	14.0	9.1
ITGa5	7.2	46.6	15.5	-
Jag1	34.1	52.4	37.0	38.7
Jag2	20.6	101.0	61.9	49.7
Kitl	80.4	67.2	57.5	-
KLF10	5.2	7.9	3.6	5.2
Lim1 (part)	2.8	20.5	2.4	7.0
Lnfg	7.1	40.7	4.3	10.3

Meis1	138.2	171.1	93.3	108.0
Meox1	15.4	10.0	4.6	-
Mil2 (part)	9.9	27.4	12.6	12.9
Msx1	3.3	5.8	2.1	2.5
Myf5	1.8	8.5	1.2	3.0
Myf6	1.4	8.4	1.5	3.5
MyoD	2.3	9.5	3.2	4.1
Nkd1	70.8	178.2	116.2	-
Nodal (part)	1.7	11.3	1.0	3.0
Noggin	1.9	3.2	2.3	1.4
Notch1	44.1	74.0	36.0	-
NR2F1	8.8	15.0	-	8.7
NR2F2	13.0	29.8	10.7	12.1
Odd1 (part)	1.6	8.7	1.5	2.5
Pax1 (part)	2.4	8.4	2.9	3.2
Pax2	78.6	132.1	81.1	54.2
Pax6	18.4	38.0	9.9	20.4
Pax9	15.6	44.5	19.1	25.6
PDGFRA	38.7	67.6	27.4	19.4
Pdx1	4.9	30.0	3.4	22.3
Per1	7.9	16.5	17.3	16.0
Pitx1	5.4	21.2	6.1	9.2
Ptc1	47.3	86.7	54.8	59.1
Rara (part)	23.4	156.7	-	41.1
RBM22	11.2	11.4	11.5	7.1
Ret (part)	30.6	93.0	36.1	30.4
SALL1	12.0	21.4	10.6	16.3
Scleraxis	2.0	25.8	0.9	0.8
Sehl1 (part)	16.1	10.0	15.6	10.9
Shh	10.2	32.6	11.3	21.5
Six1	2.9	15.9	1.1	4.1
Six2	3.1	20.2	9.0	5.9
Six4	9.9	32.6	8.1	13.2
Slit3 (part)	216.9	268.4	233.2	153.4
Snail 1	4.6	9.5	3.1	3.0
Sox8	4.8	20.7	4.9	8.4
Sox9	5.2	9.7	4.8	4.5
Sp5	3.1	7.3	1.9	3.5
Tbx5	42.8	15.9	29.7	25.9
Tbx18	26.2	46.0	22.2	22.5
Tcf21	2.6	6.5	2.2	2.6
TGFb1	17.6	36.5	-	17.4
Tnfrsf19	80.0	59.0	27.2	55.2
TRUB2	10.9	12.8	3.3	-
Twist1	2.1	9.6	2.5	2.3
WDR40a	21.0	11.0	27.0	10.2
Wnt3a	25.8	33.8	3.9	35.7
Wnt11 (part)	6.9	21.9	15.2	26.3
WT1	47.1	66.8	33.1	40.0
Zic2	3.7	6.1		3.1
Zic5	6.5	10.7		4.1

Other non-developmental genes

	Mouse	Lizard	Chicken	Xenopus
Aatf	90.6	75.4	40.4	79.9
Abca5	56.1	59.2	21.6	57.8
Acaca	204.5	146.4	94.6	196.1
Adamts14	72.5	112.1	17.6	73.4
Aloxe3	22.3	17.6	4.2	22.3
Ankra2	7.8	6.6	5.8	4.8
Arid4A	82.3	60.5	44.9	38.3
Asah2 (part)	46.9	20.8	12.3	36.6
Atp2b1	55.1	46.0	30.2	50.8
Atxn7l4	42.1	30.3	22.1	9.8

Aurkb (part)	3.0	3.5	3.0	21.8
Bcl2l1	49.2	47.1	-	-
Bms1	35.0	30.8	20.9	18.4
Brf1	38.1	197.2	121.7	124.2
Btbd3	8.9	16.9	10.5	4.3
Btf3	6.7	6.9	6.3	5.8
Ccdc108	29.7	33.2	15.9	20.7
Chic2	38.2	31.1	22.5	18.1
Clcn1	23.8	42.1	29.0	15.3
Clmn	84.1	92.9	62.4	61.3
Cnih	12.7	13.8	6.7	6.3
CopZ1	25.9	21.7	-	-
Crl51	16.5	7.7	4.0	4.4
Cyld	42.1	19.2	18.6	34.1
Daam1	96.6	115.0	55.9	50.4
Ddhd1	62.4	42.6	68.5	28.9
Dlg4 (part)	14.3	47.0	28.1	42.3
Dnajc14	12.3	23.3	-	23.2
Eif3b	23.1	9.6	15.2	10.1
ExoC2	151.9	101.3	122.2	97.4
Fbxo8	41.0	22.9	16.7	10.1
Fbxw4	81.3	70.1	60.0	112.0
Femo2	91.6	90.0	98.2	48.8
Flt3 (part)	23.3	15.9	10.1	9.1
Fmod	6.4	10.9	3.2	7.0
Fto	336.0	313.1	257.3	169.2
Gad1	38.3	80.3	24.1	27.0
Galnact2	20.8	21.9	14.3	9.9
Gars	41.5	17.9	20.0	18.7
Ggnbp2	29.8	11.0	13.0	21.5
Glde	76.6	52.3	41.5	24.4
Gmrs	416.4	307.2	347.9	289.5
Gucy2e	12.9	26.7	33.9	13.0
H13 (part)	26.1	20.4	8.7	-
Hat1 (part)	32.5	26.9	13.2	30.0
Hdac9	157.4	100.4	94.7	102.2
Hif1an	8.4	13.7	7.7	12.9
innpp5e	10.4	14.5	7.7	7.8
Kdr	40.4	50.1	34.9	17.5
Lin7a	140.3	42.7	28.1	31.9
Lmbr1	131.1	30.1	50.0	33.4
Lrrc9	47.5	31.7	26.5	30.9
Loc76539	22.4	23.4	15.0	-
Mgea5	33.0	27.8	23.8	29.0
Mkks	11.5	15.0	5.3	5.5
Mnat1	149.3	127.3	115.3	-
Mocs2 (part)	6.1	5.7	5.1	5.2
Mrm1	4.8	6.2	5.4	-
Mrps28	34.2	5.0	18.5	7.1
Nkx2-2	7.2	10.5	6.6	7.0
Ntsc1b	14.8	11.6	5.1	8.5
Parp8 (part)	72.7	72.4	52.4	78.1
Pdk1	26.8	19.8	9.1	12.1
Pdzd8	47.0	56.3	50.0	46.8
Plcl4	27.0	63.6	15.6	54.1
Pnliprp1	11.3	19.2	10.1	6.9
Polr2h	4.1	6.7	1.6	6.5
Ppfia2 (part)	195.8	106.9	107.5	83.4
Ppr1r12A	115.2	120.5	122.9	54.1
Prepl	18.4	29.3	13.7	28.2
Prfl	4.1	2.4	-	4.6
Prr8	86.9	76.6	84.0	28.3
PsmA3	19.8	16.8	8.6	14.3
Ptpqr	202.7	94.3	100.2	115.0
Rab11fip2	39.3	33.7	31.5	28.1
Rdh5	4.9	6.5	16.1	4.2

Rdh14	4.4	6.6	4.4	3.1
Rnf32	27.0	17.8	11.7	15.6
Scrg1 (part)	3.1	1.4	1.6	9.3
Sec16a (part)	21.3	34.6	17.6	10.3
Slc2a12	29.9	11.7	19.2	6.9
Slc6a7	13.1	20.8	6.2	34.3
Slc25a21	463.0	282.4	224.3	-
Snx8 (part)	18.9	14.0	12.2	-
Snx13	66.4	39.6	44.1	39.5
Stmn2	52.1	31.3	34.5	18.9
Tacc1	46.9	58.0	15.8	
Tekt4	4.9	16.6	12.0	7.7
Timm50	5.2	39.5	-	-
Tmem107	2.0	5.4	-	-
Tmem171	6.3	5.3	5.8	7.1
Tmem183a	14.0	14.0	11.8	10.7
Top2a	29.2	35.5	14.7	17.1
Tpds2	34.5	13.5	15.5	8.1
Trmt5	4.3	4.2	2.8	3.1
Trub1	32.4	41.7	23.9	-
Ttyh3	15.5	45.7	38.5	45.4
Tuba1b	1.8	5.2	2.1	2.2
Uvrag	231.6	88.0	67.7	70.7
Vamp2	1.4	1.5	-	-
Wdr35	53.3	36.6	36.6	25.9
Wdr51b	47.6	19.6	23.1	29.1
Whsc111 (part)	40.6	12.3	9.6	32.2
Wipf (part)	9.2	6.3	-	3.6
Xrn2	53.3	52.4	41.1	36.3