

Gene Evidence Report

October 16, 2025

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Gene Index

Gene Name	Evidence Types Available
ADAP2	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
ADRA1B	Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence
ARL11	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
CAV3	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Orthofinder genetree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
CYYR1	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
DIP2A	Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence
DLEU7	Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence
DNM3	Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence
ELOVL3	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
FREM2	Important gene stats, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence
GPR78	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
GPR82	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Syntenic evidence, Transcriptomic evidence Pogona vitticipes

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Gene Name	Evidence Types Available
GRK4	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
HHLA2	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
HPGDS	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
HSD17B1	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
IFTAP	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
IL13RA2	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
IL26	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
IL34	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
IL5RA	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Orthofinder genetree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
INTS6	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
KDM3A	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
KREMEN1	Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Orthofinder genetree, Syntenic evidence
LAPTM5	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Syntenic evidence, Transcriptomic evidence Pogona vitticipes

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Gene Name	Evidence Types Available
LCP1	Important gene stats, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence
LRCH1	Important gene stats, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence
MAN2B2	Important gene stats, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence
MATK	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
MOB1A	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
NOTCH2	Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence
OLAH	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
PLAAT1	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Orthofinder genetree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
RBBP7	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
RIPPLY3	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
RUBCNL	Important gene stats, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence
SH2D1A	Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence
SH2D2A	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
SIAH3	Important gene stats, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence
SLC24A1	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes

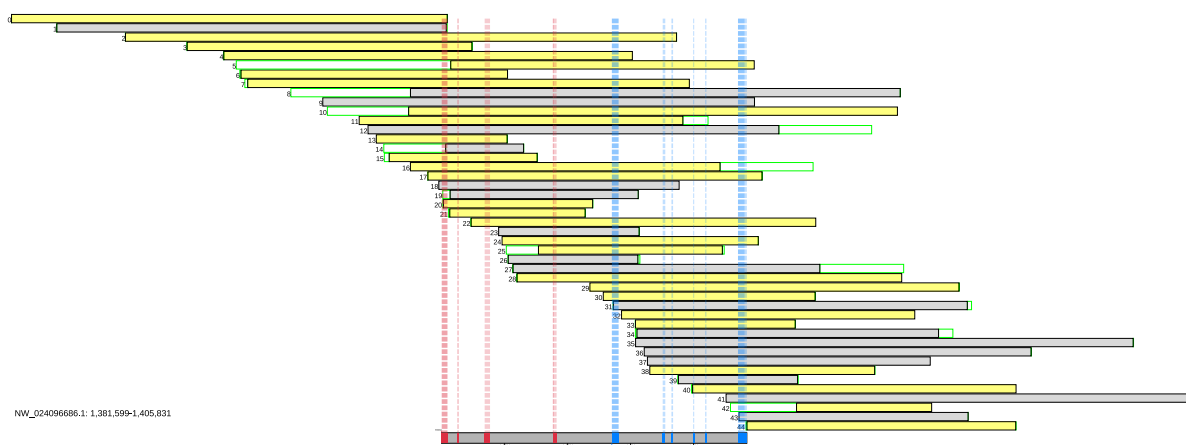
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Gene Name	Evidence Types Available
SLC9A5	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
SSTR4	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
STAP1	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
STOML3	Important gene stats, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence
SUV39H2	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
TBC1D14	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
TMEM273	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
TNIP2	Important gene stats, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence
UNKL	Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence
UTS2B	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
WNT2	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes
YBX3	Important gene stats, Lastz Alignment evidence, Lastz gene tree, Orthofinder genetree, Syntenic evidence
ZNF438	Assembly verification Evidence, Important gene stats, Intergenic distance phylogenetic signal evidence, Lastz Alignment evidence, Lastz gene tree, Syntenic evidence, Transcriptomic evidence Pogona vitticipes

1 ADAP2

Assembly verification Evidence

Crotalus_tigris-PacBio



Podarcis_muralis-PacBio

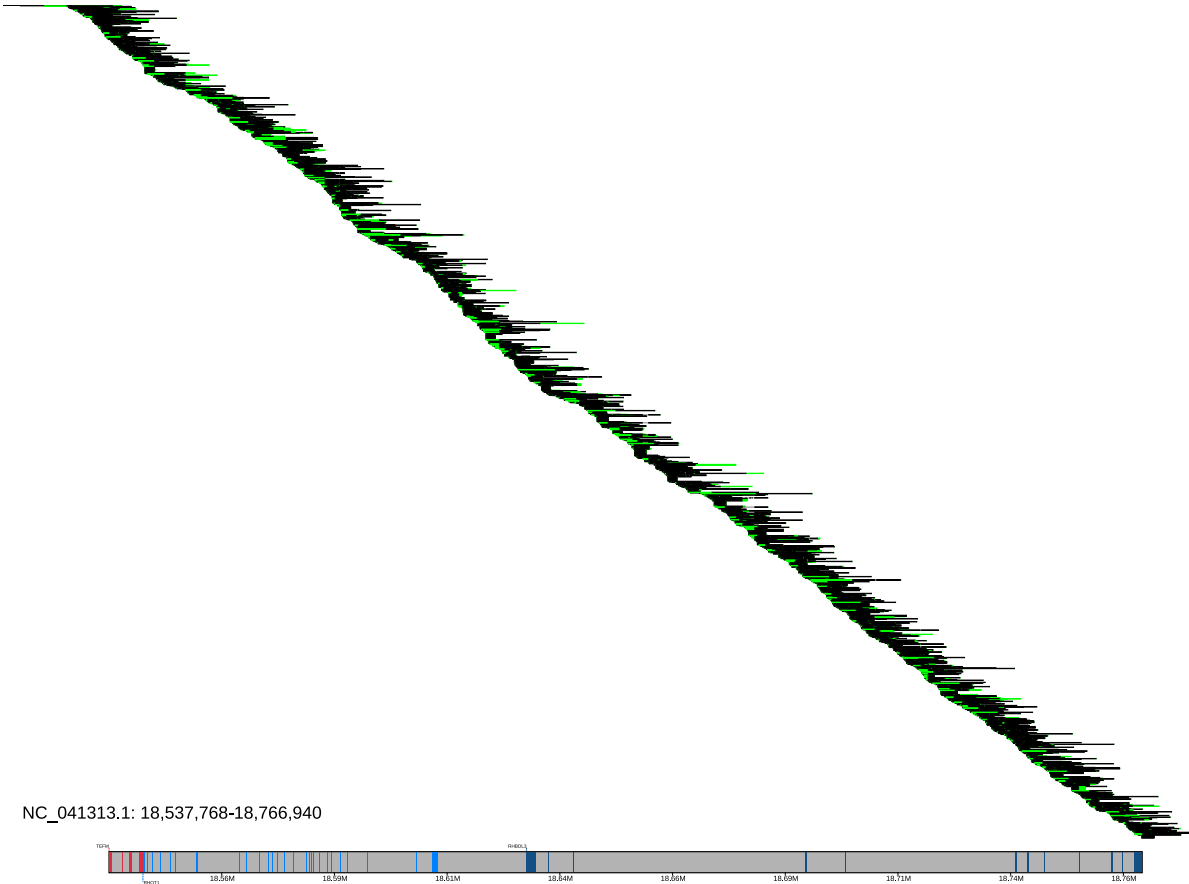


Figure 2: ADAP2:NC_041313.1:18537768-18766940.pdf

Pogona_vitticeps-Nanopore

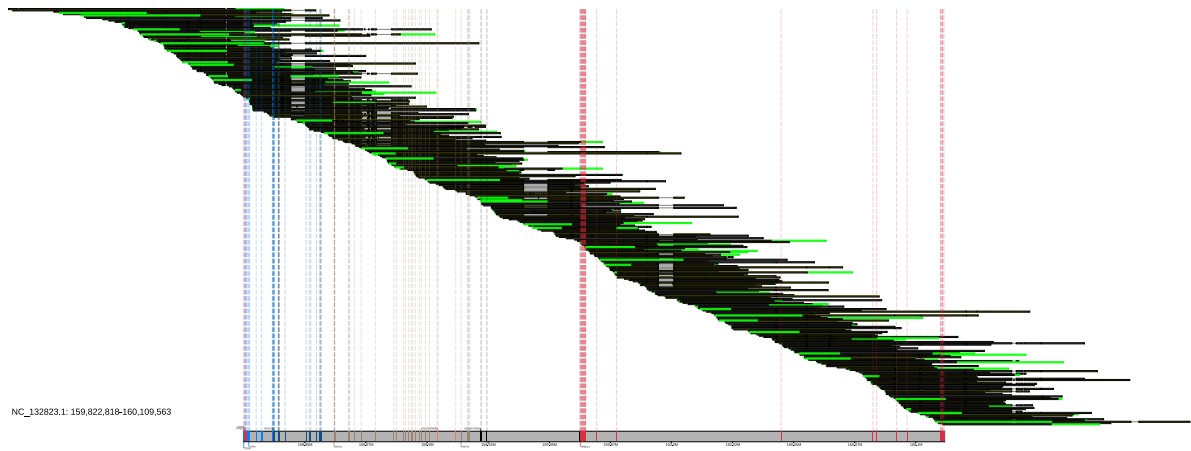


Figure 3: ADAP2:NC_132823.1:159822818-160109563.pdf

Important gene stats

ADAP2_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
ADAP2	20.31320755	52.5003 +/- 3.70015	3.99165 +/- 0.239421	74.0443 +/- 13.0076	Yes	ADAP1;LOC118090835;

Intergenic distance phylogenetic signal evidence

ADAP2_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
ADAP2	220	19	201	5	1.06469123150611e-05	0.0069811852322884

ADAP2_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
ADAP2	220	19	201	5	1.06469123150611e-05	0.0069811852322884



Figure 4: Heatmap_of_deletion_plot.png

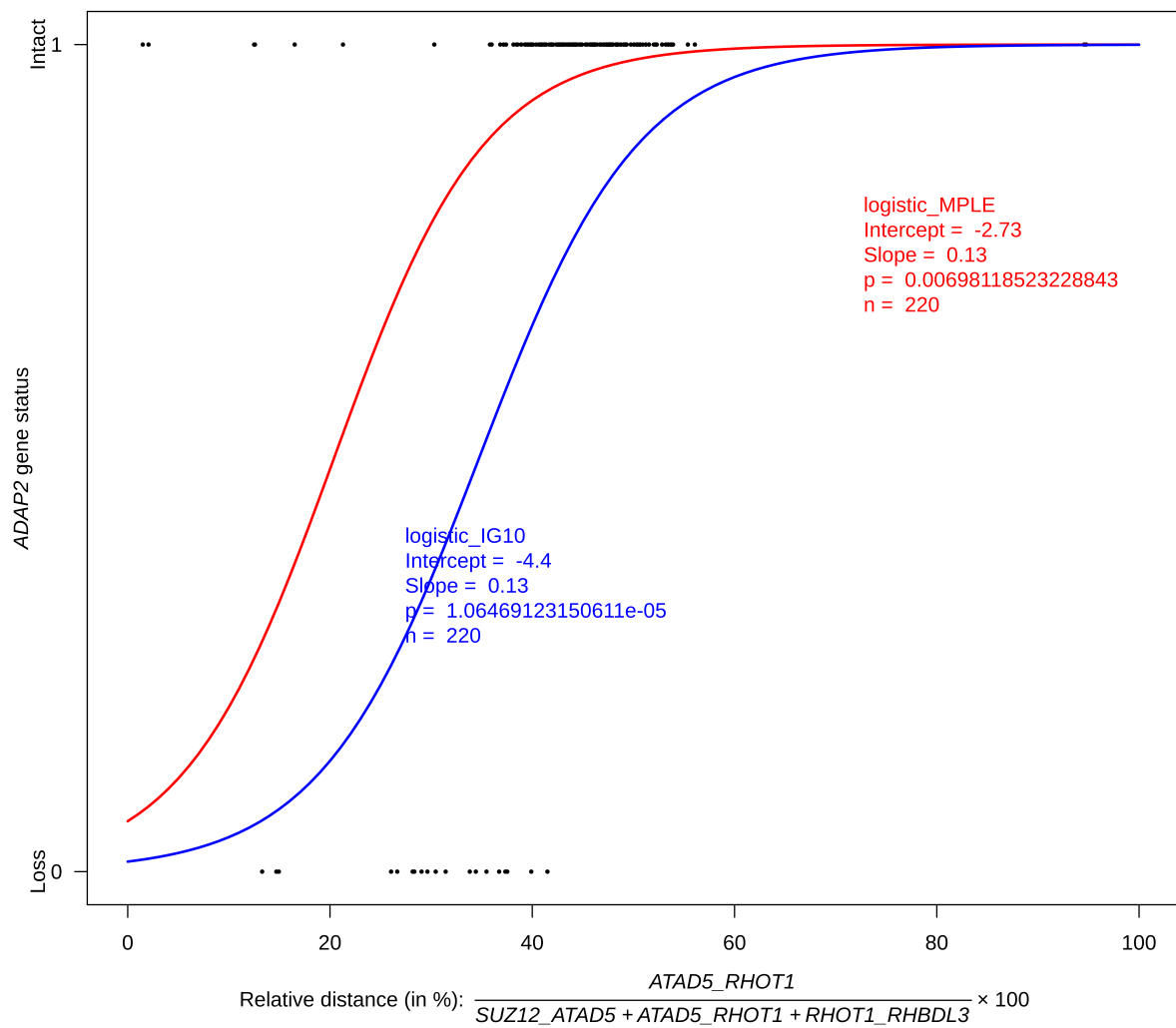


Figure 5: Phylogenetic_signal_of_deletion_plot.png



Figure 6: Heatmap_of_deletion_plot.png

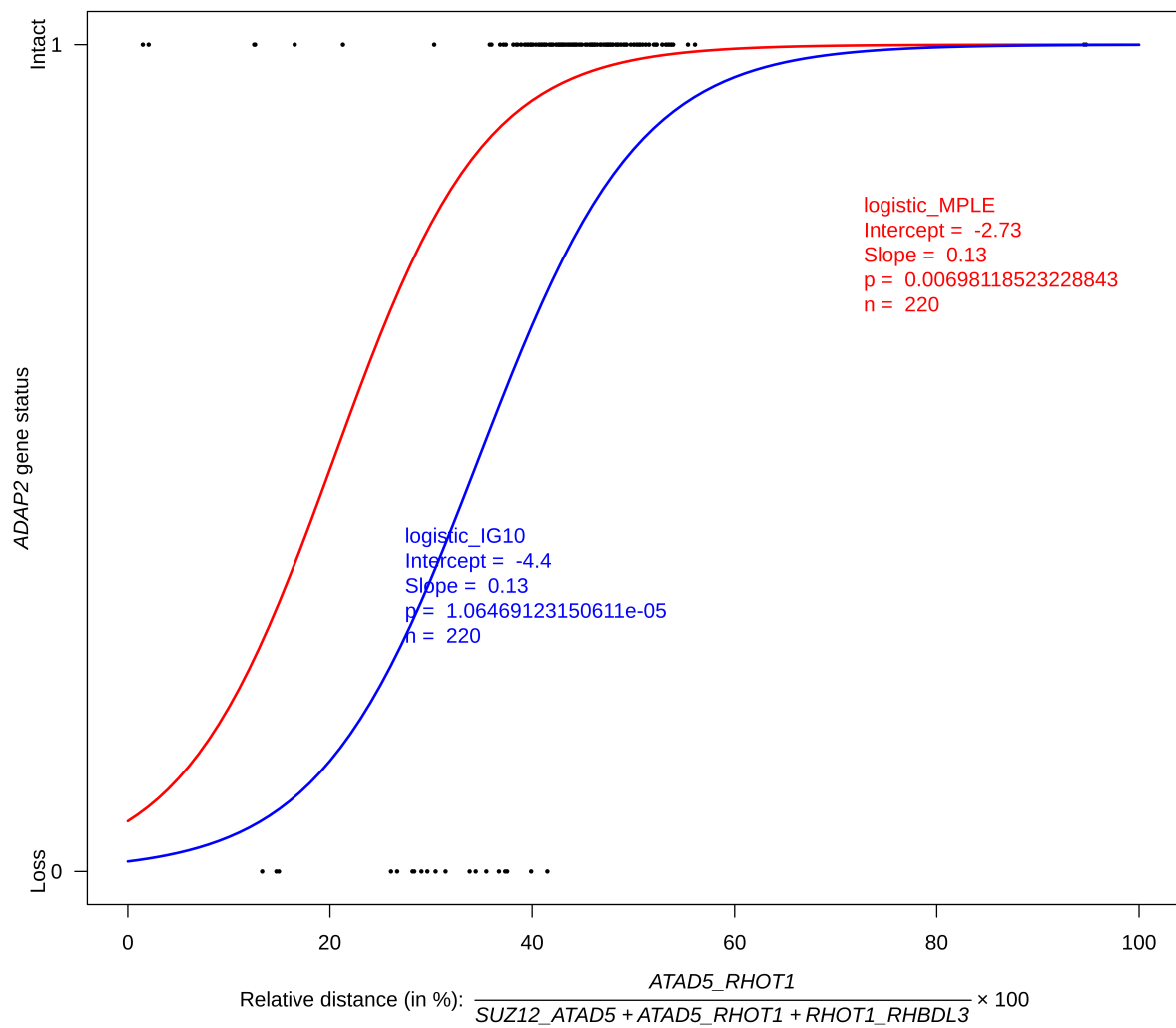


Figure 7: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence

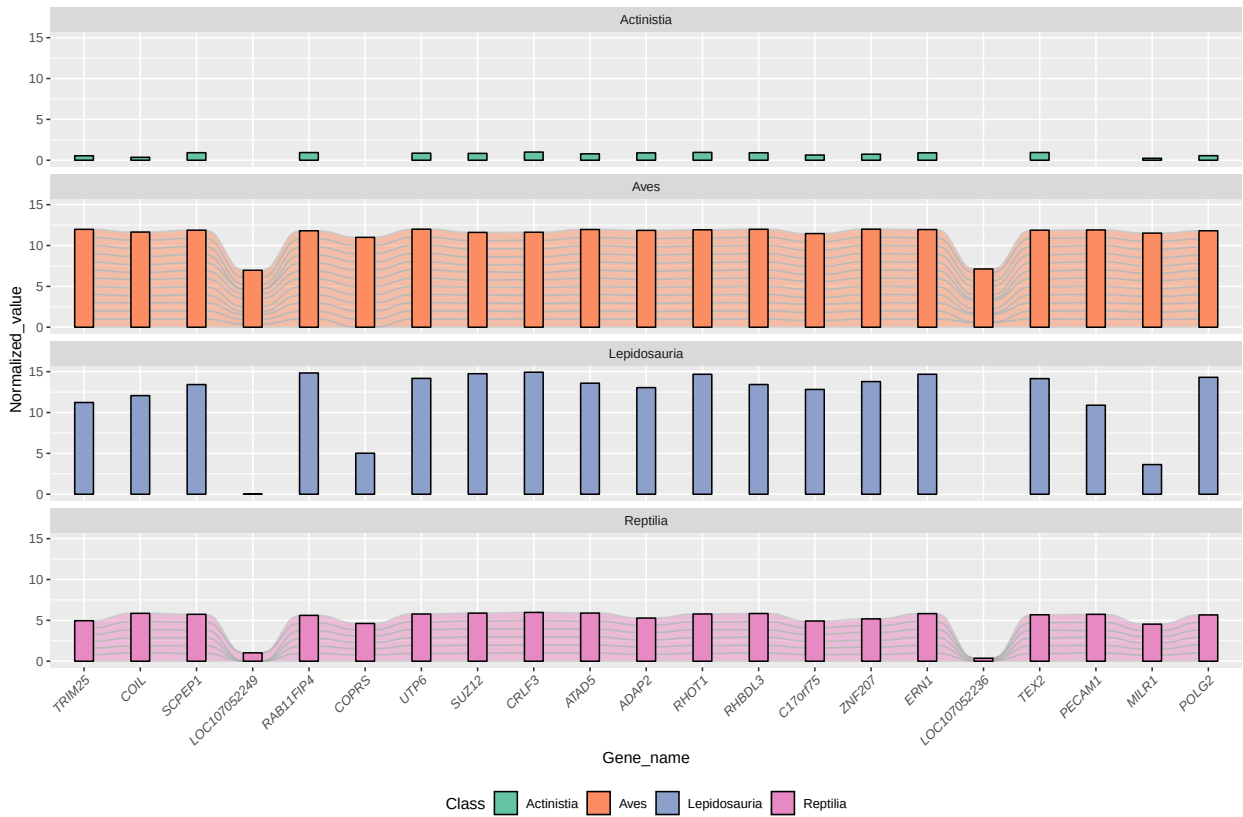


Figure 8: ADAP2.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

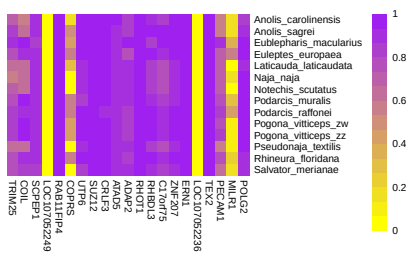


Figure 9: ADAP2.FS_Exonic.Final.Gallus_gallus.21_genes_heatmap.pdf

Lastz gene tree

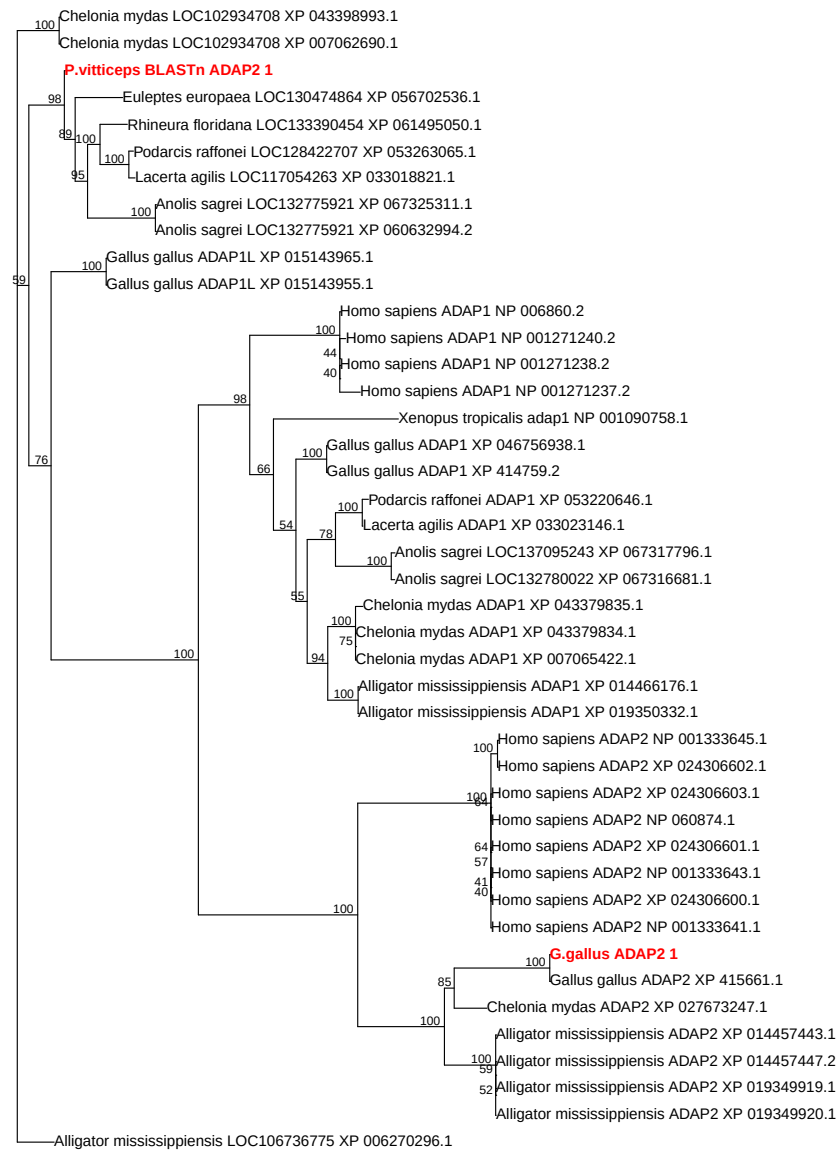


Figure 10: ADAP2.combined.mafft.aln.highlighted.pdf

Syntenic evidence

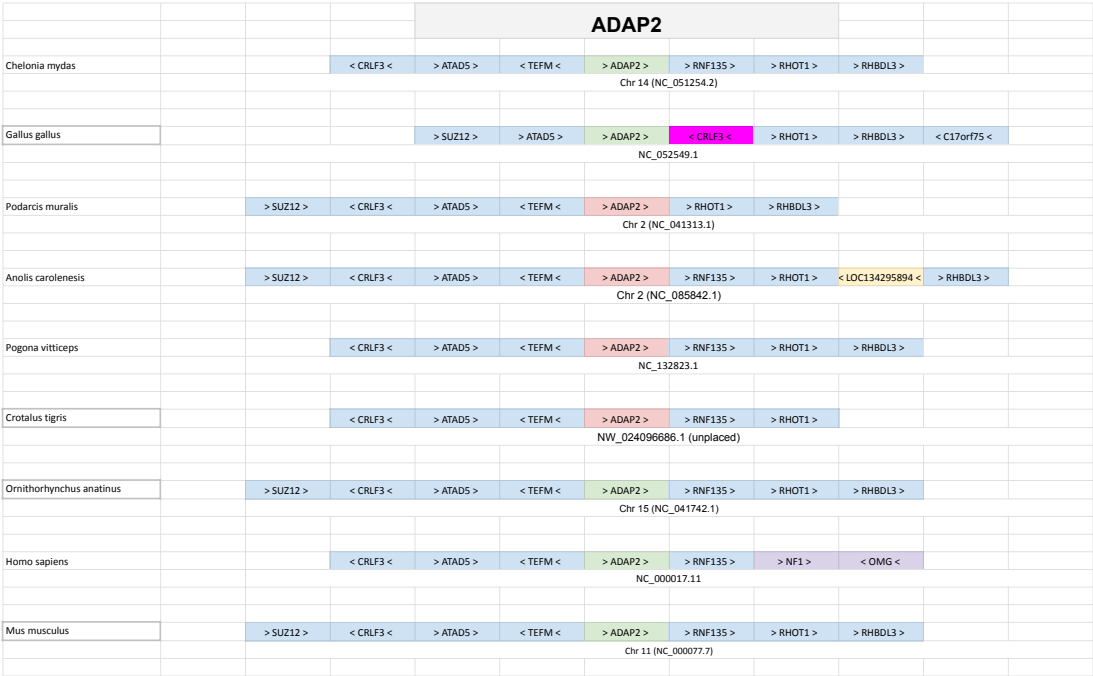


Figure 11: ADAP2.pdf

ADAP2.txt

Synteny analysis of ADAP2

We conducted a detailed syntenic analysis of ADAP2 across multiple squamate species as well as in representative outgroup lineages. The analysis demonstrated that the ADAP2 syntenic block is largely conserved across squamates. However, in Gallus gallus, the neighboring gene CRLF3 exhibited a change in both orientation and relative position compared to the squamate arrangement. In the synteny plots, red blocks indicate the absence of ADAP2, while green blocks mark its presence. Light blue blocks represent genes conserved across lineages, and light purple blocks denote instances where a different flanking gene is present.

Transcriptomic evidence *Pogona vitticeps*

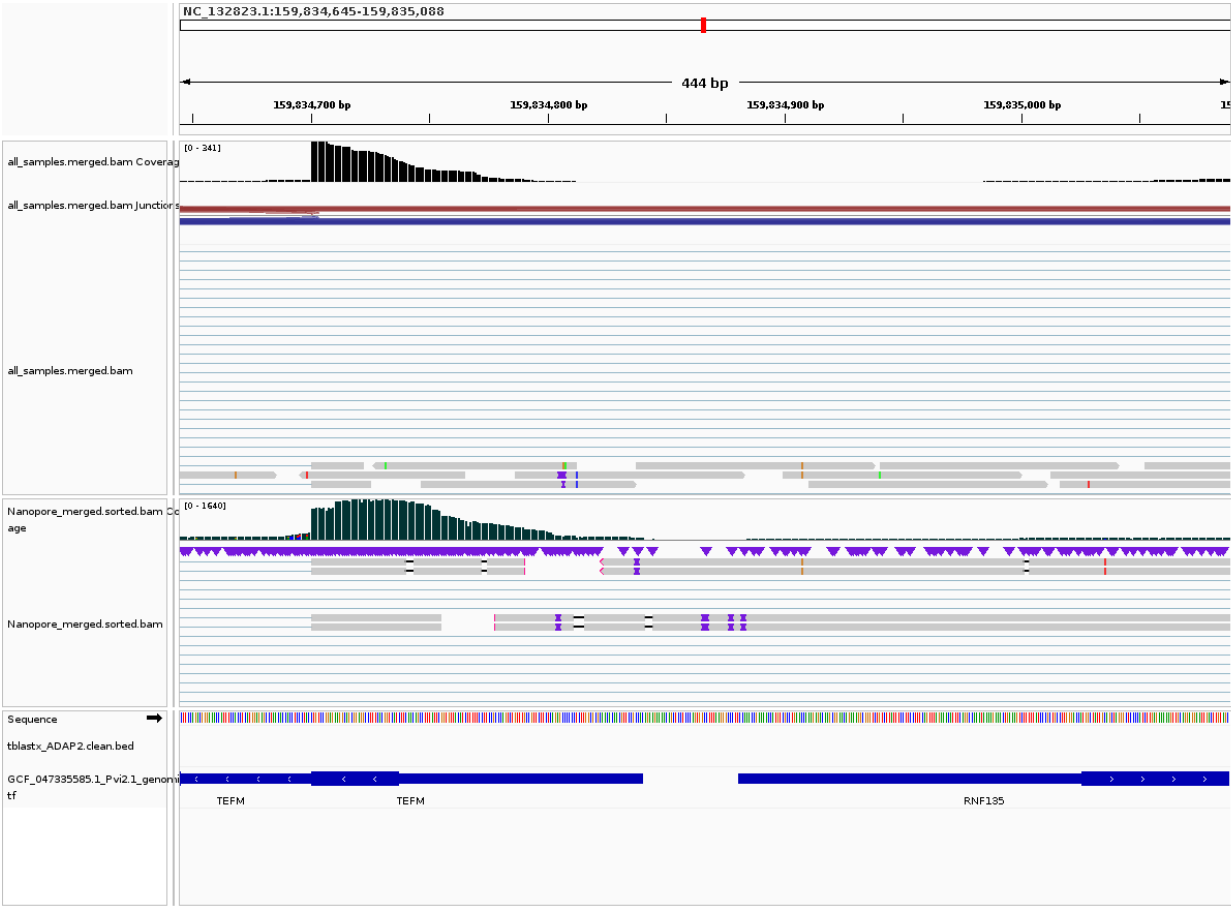


Figure 12: ADAP2.png

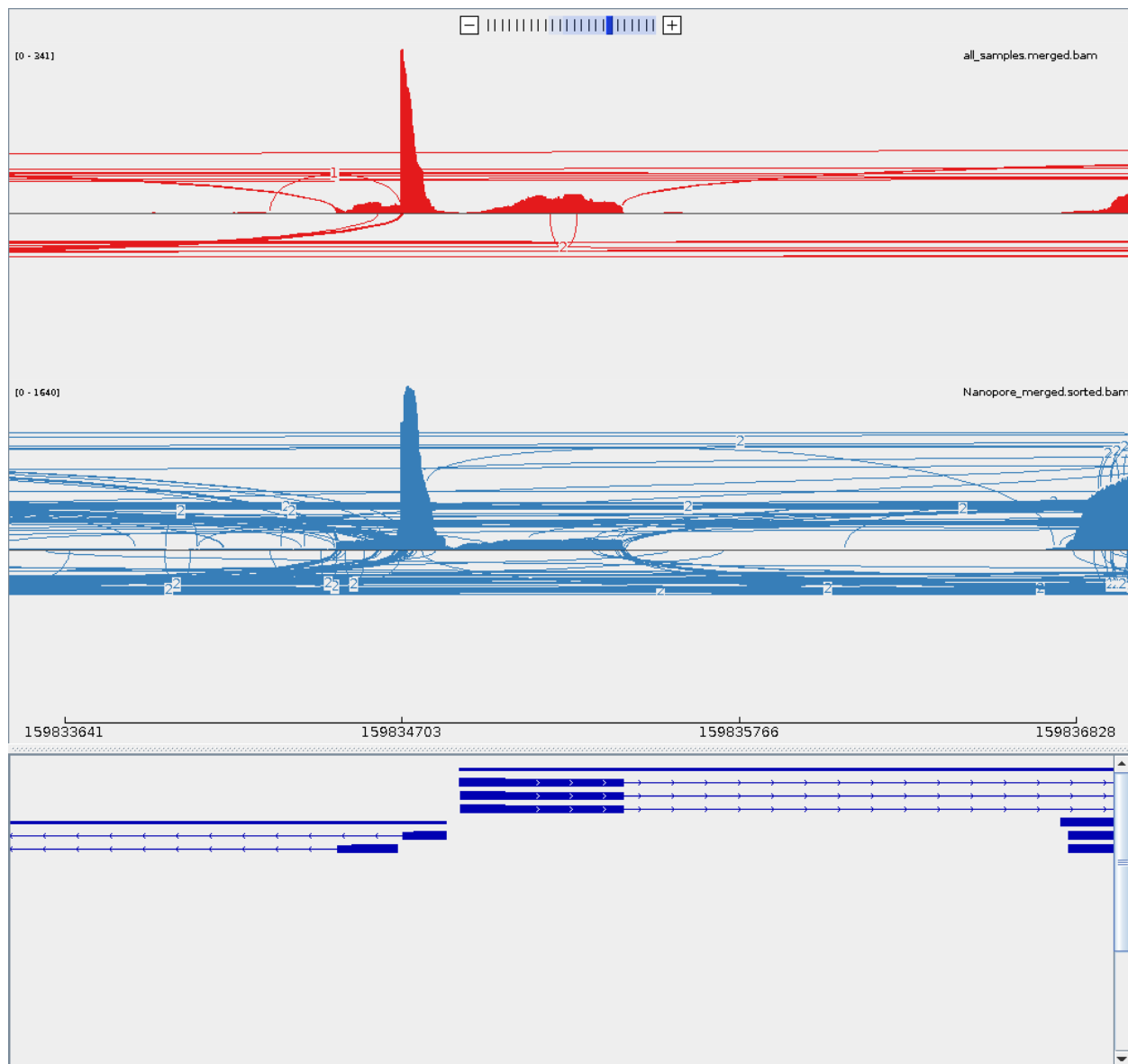


Figure 13: ADAP2_Shash.png

2 ADRA1B

Important gene stats

ADRA1B_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
ADRA1B	51.39622642	56.4815 +/- 8.36232	4.39439 +/- 0.691117	75.0088 +/- 13.6392	Yes	ADRA1A;ADRA1D;

Intergenic distance phylogenetic signal evidence

ADRA1B_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
ADRA1B	202	11	191	0	0.0104566879789757	0.999999999999998

ADRA1B_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
ADRA1B	202	11	191	0	0.0104566879789757	0.999999999999998

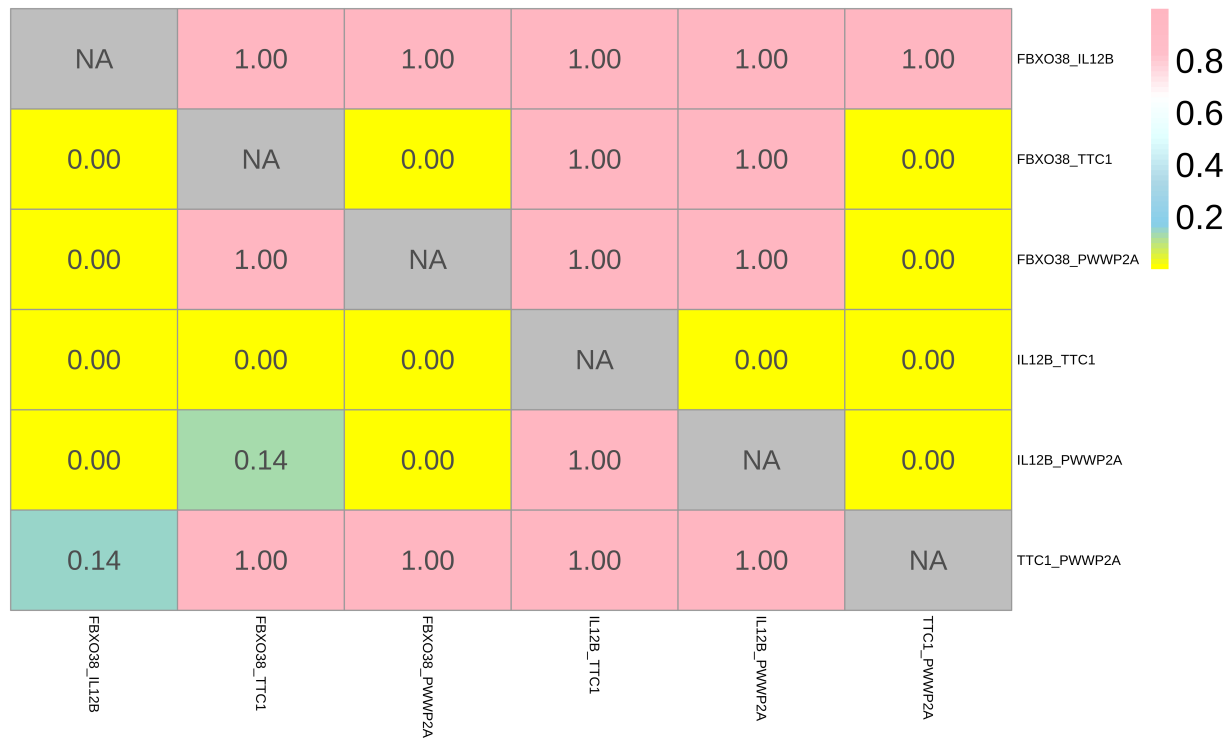


Figure 14: Heatmap_of_deletion_plot.png

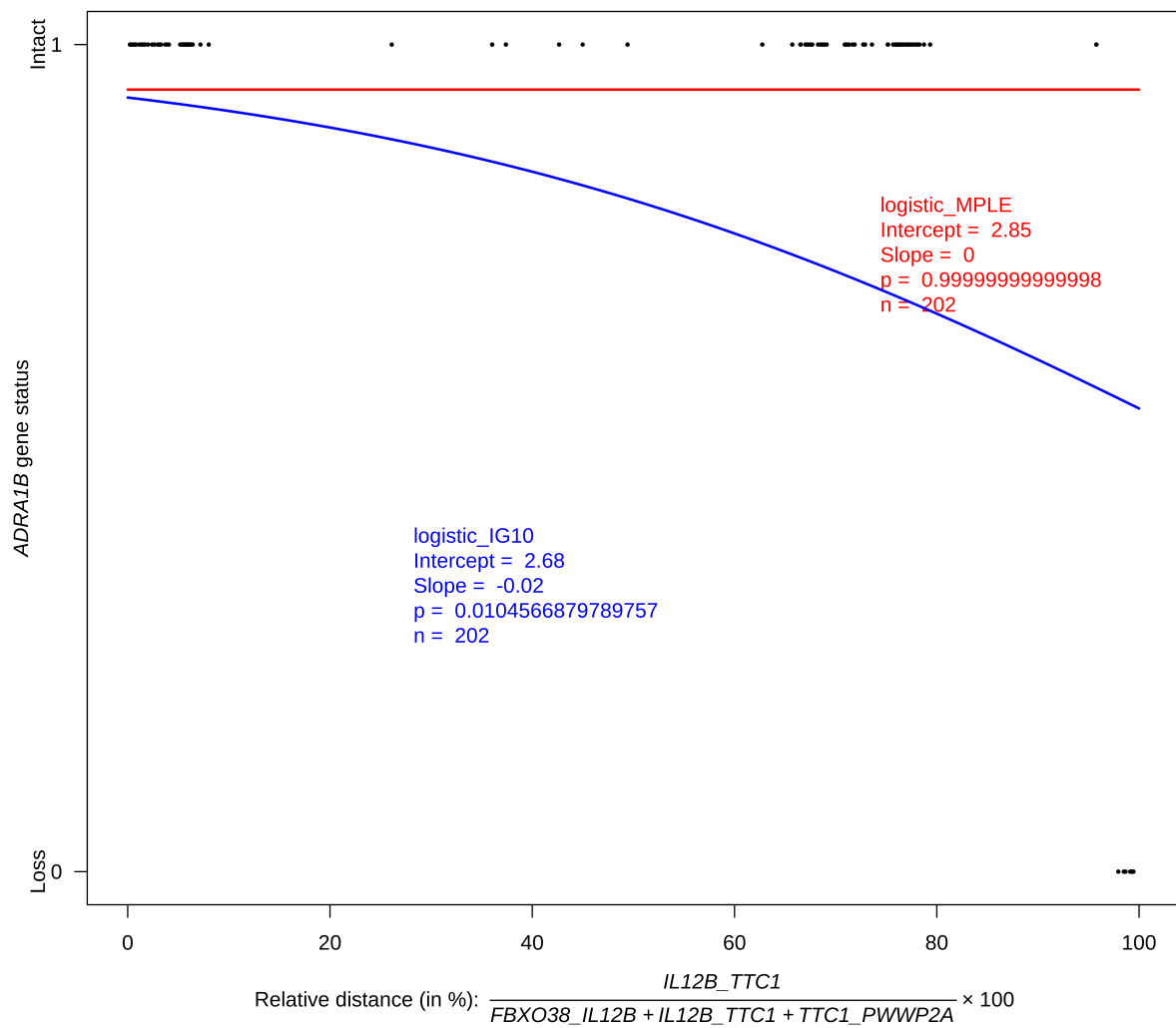


Figure 15: Phylogenetic_signal_of_deletion_plot.png

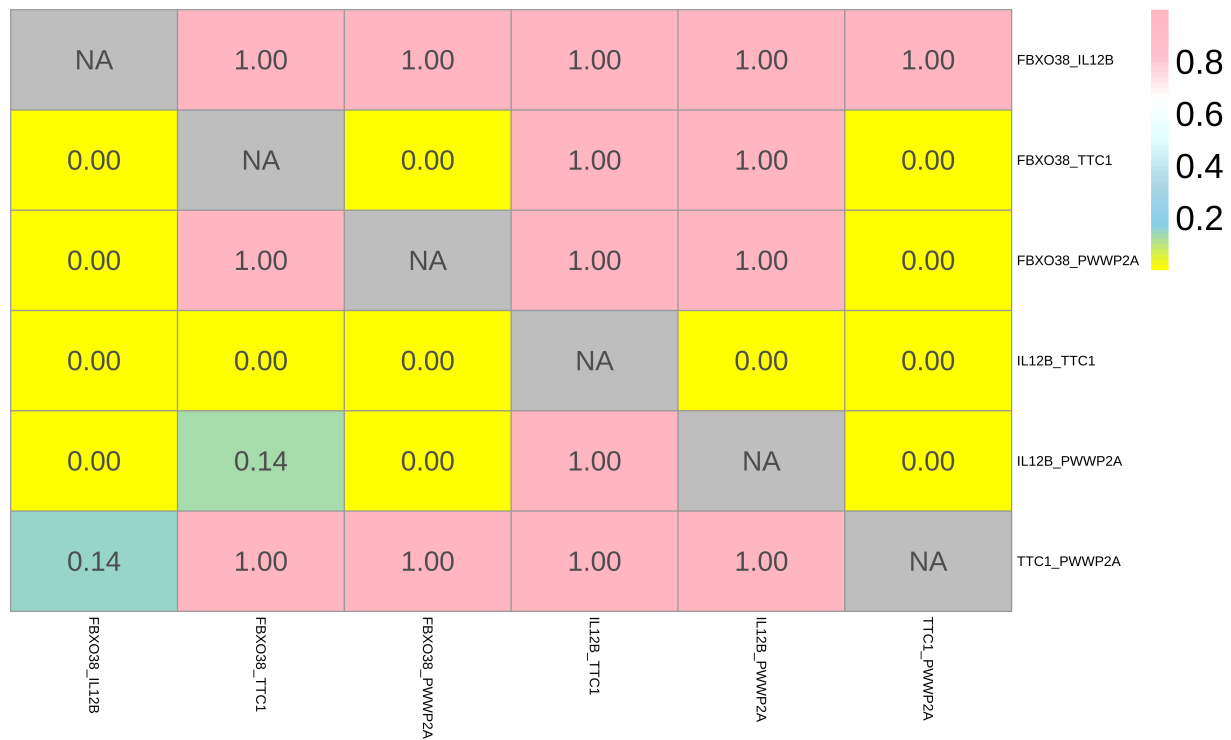


Figure 16: Heatmap_of_deletion_plot.png

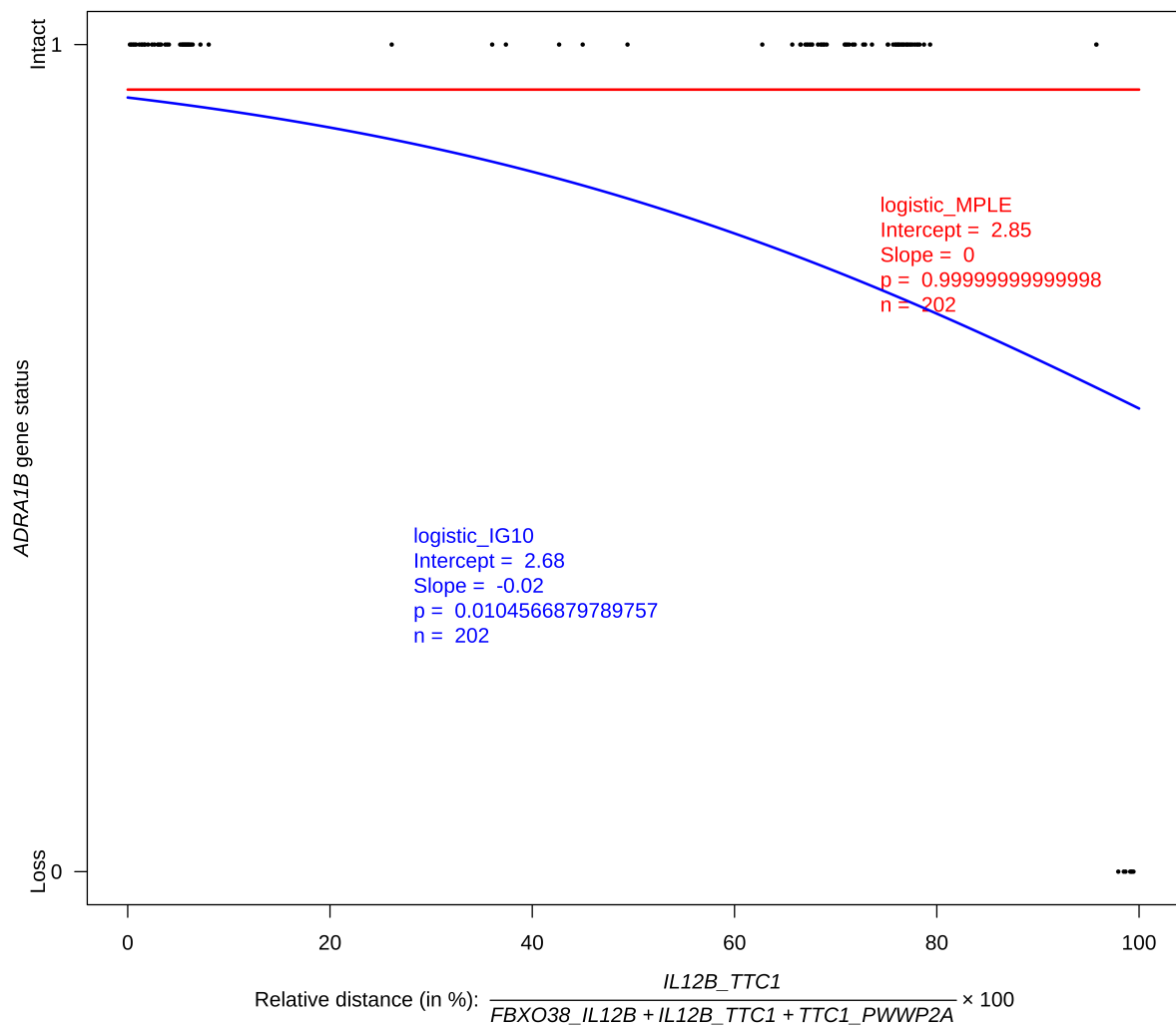


Figure 17: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence

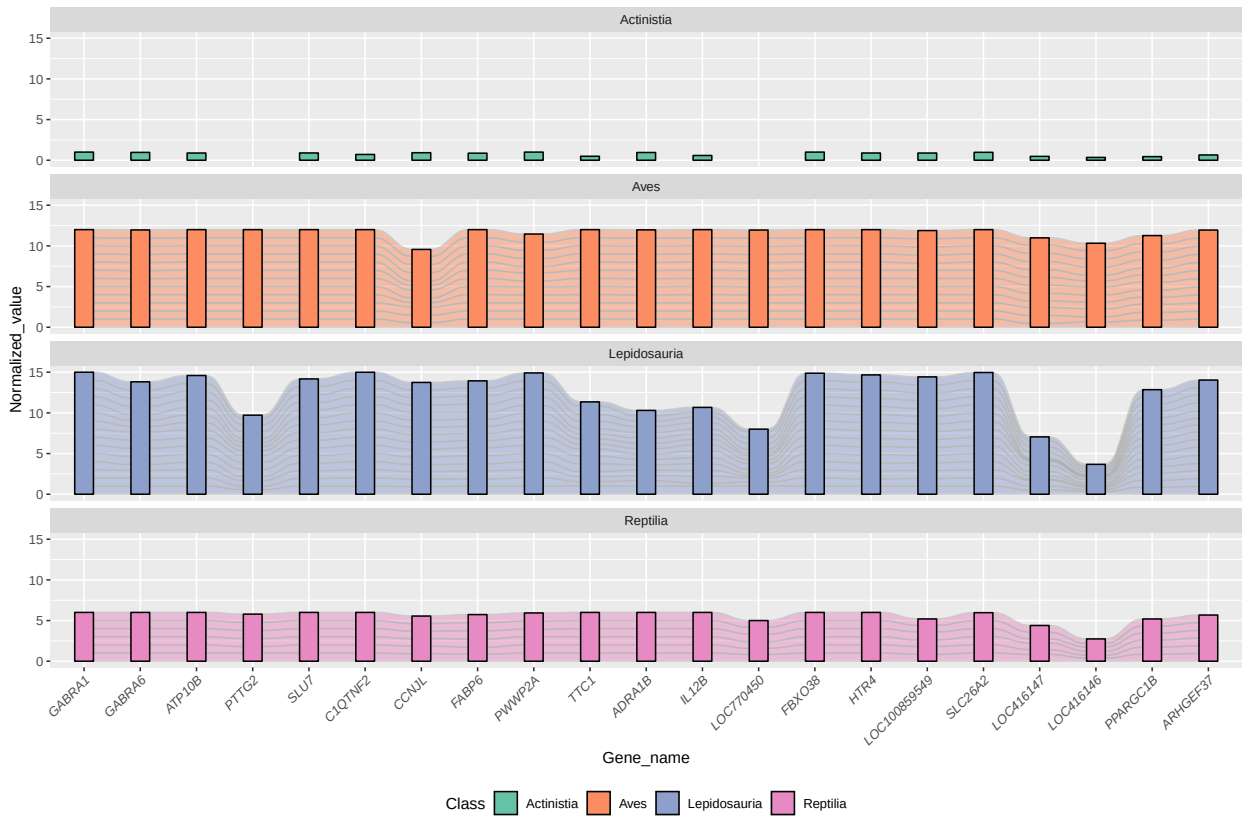


Figure 18: ADRA1B.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Lastz gene tree



Figure 20: ADRA1B.combined.mafft.aln.highlighted.pdf

[illegible]

Figure 21: ADRA1B.pdf

ADRA1B.txt

Synteny analysis of ADRA1B

The syntenic block for ADRA1B shows clear evidence of intrachromosomal

- ↪ rearrangement in squamates when compared to the conserved
- ↪ arrangement in outgroup species. In several squamate lineages, the
- ↪ syntenic genes have been repositioned to a new locus on the same
- ↪ chromosome, often after skipping a number of intervening genes.

In the synteny plots, red blocks indicate the absence of the target gene,

- while green blocks mark its presence. Light blue blocks represent
- flanking genes that are conserved across lineages, and light purple
- blocks denote instances where a different flanking gene is present.
- A bright yellow color indicates a change in the gene's orientation.

3 ARL11

Assembly verification Evidence

Crotalus_tigris-PacBio

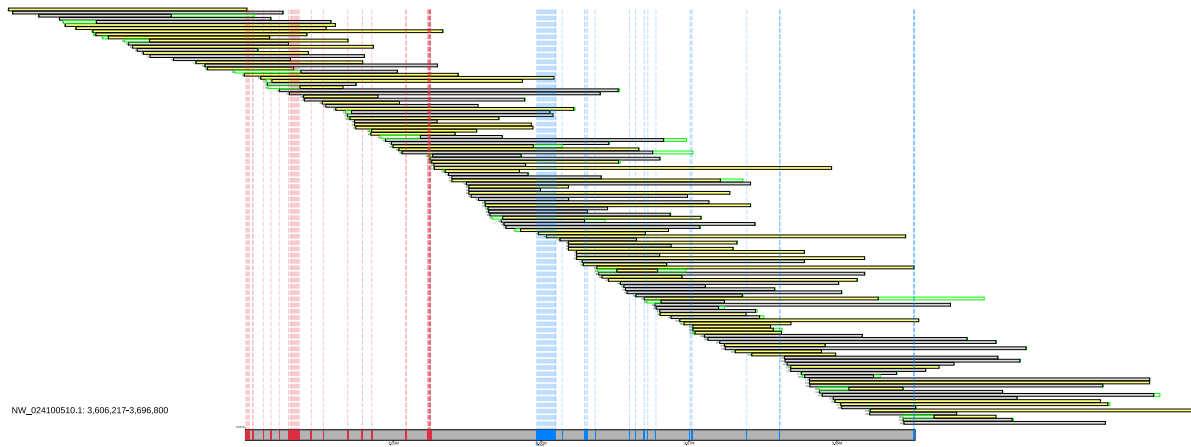


Figure 22: ARL11:NW_024100510.1:3606217-3696800.pdf

Podarcis_muralis-PacBio

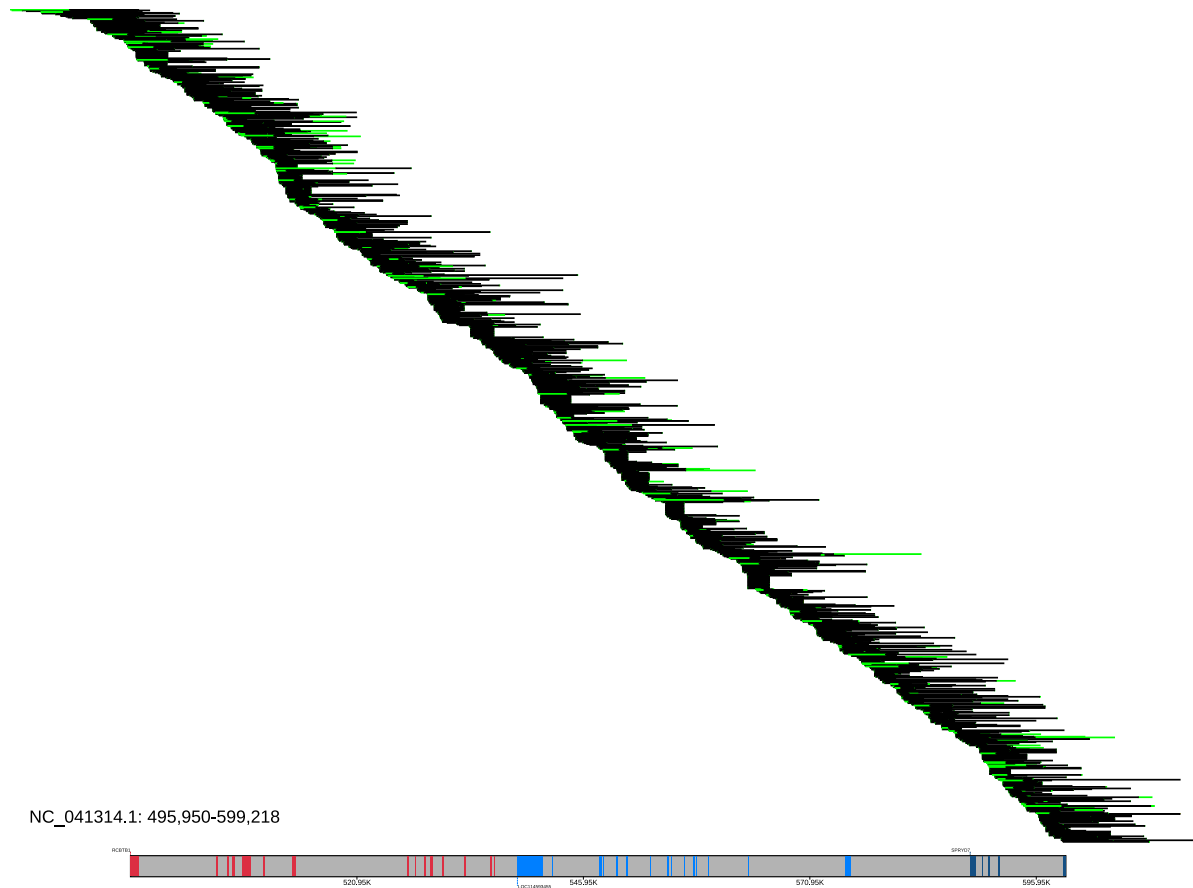


Figure 23: ARL11:NC_041314.1:495950-599218.pdf

Pogona_vitticeps-Nanopore

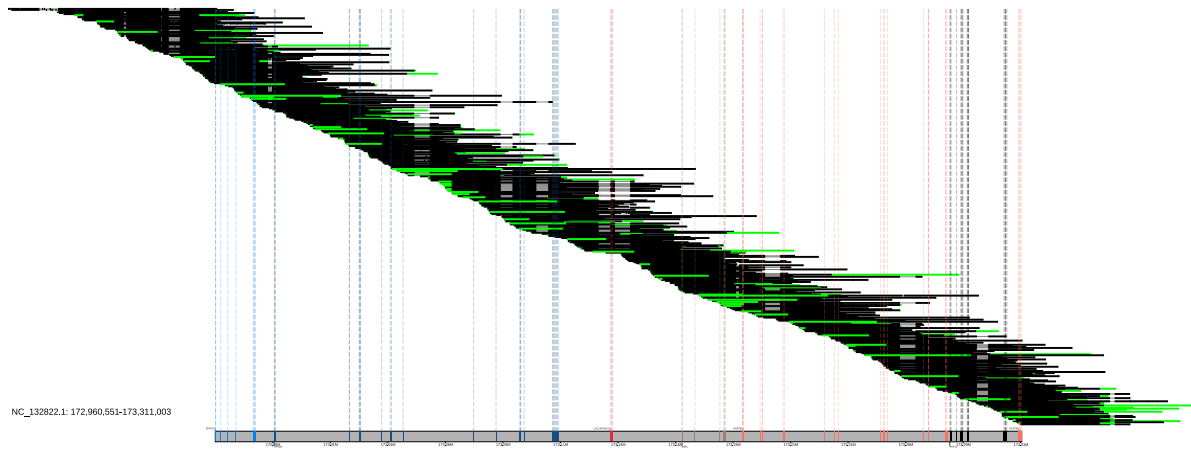


Figure 24: ARL11:NC_132822.1:172960551-173311003.pdf

Important gene stats

ARL11_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
ARL11	18.21673004	58.9158 +/- 6.00298	4.02177 +/- 0.339975	64.5555 +/- 14.0787	Yes	ARF3;

Intergenic distance phylogenetic signal evidence

ARL11_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
ARL11	148	15	133	2	0.471653974378396	0.95538545201915

ARL11_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
ARL11	148	15	133	2	0.471653974378396	0.95538545201915



Figure 25: Heatmap_of_deletion_plot.png

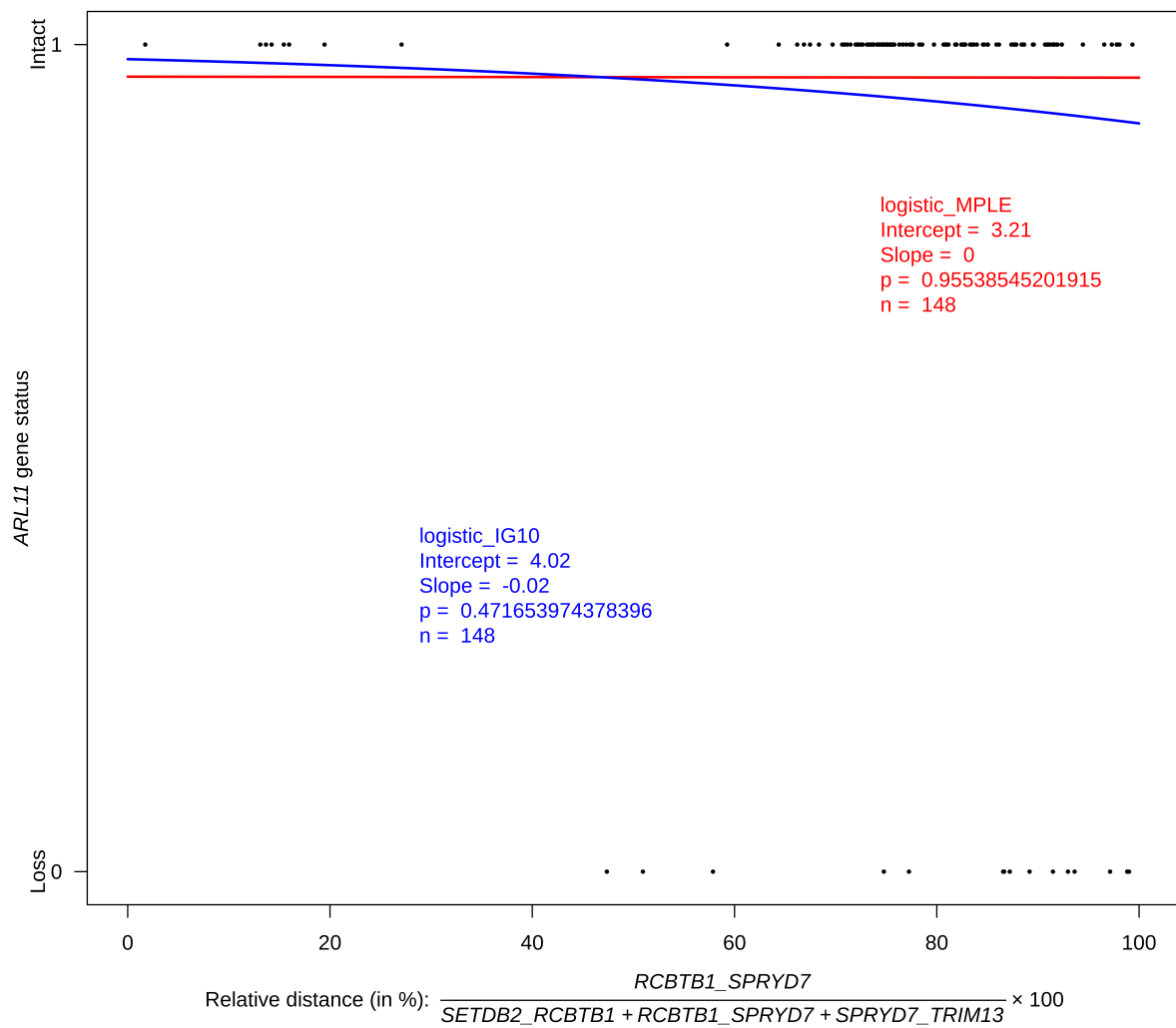


Figure 26: Phylogenetic_signal_of_deletion_plot.png

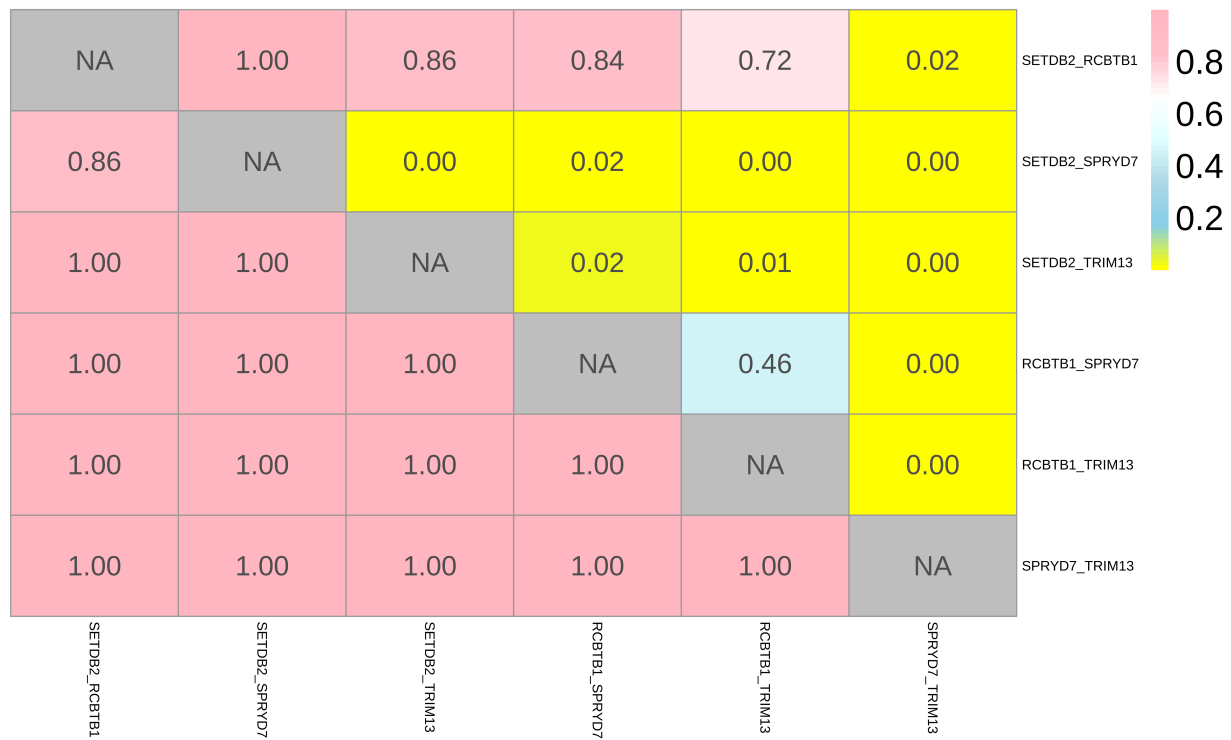


Figure 27: Heatmap_of_deletion_plot.png

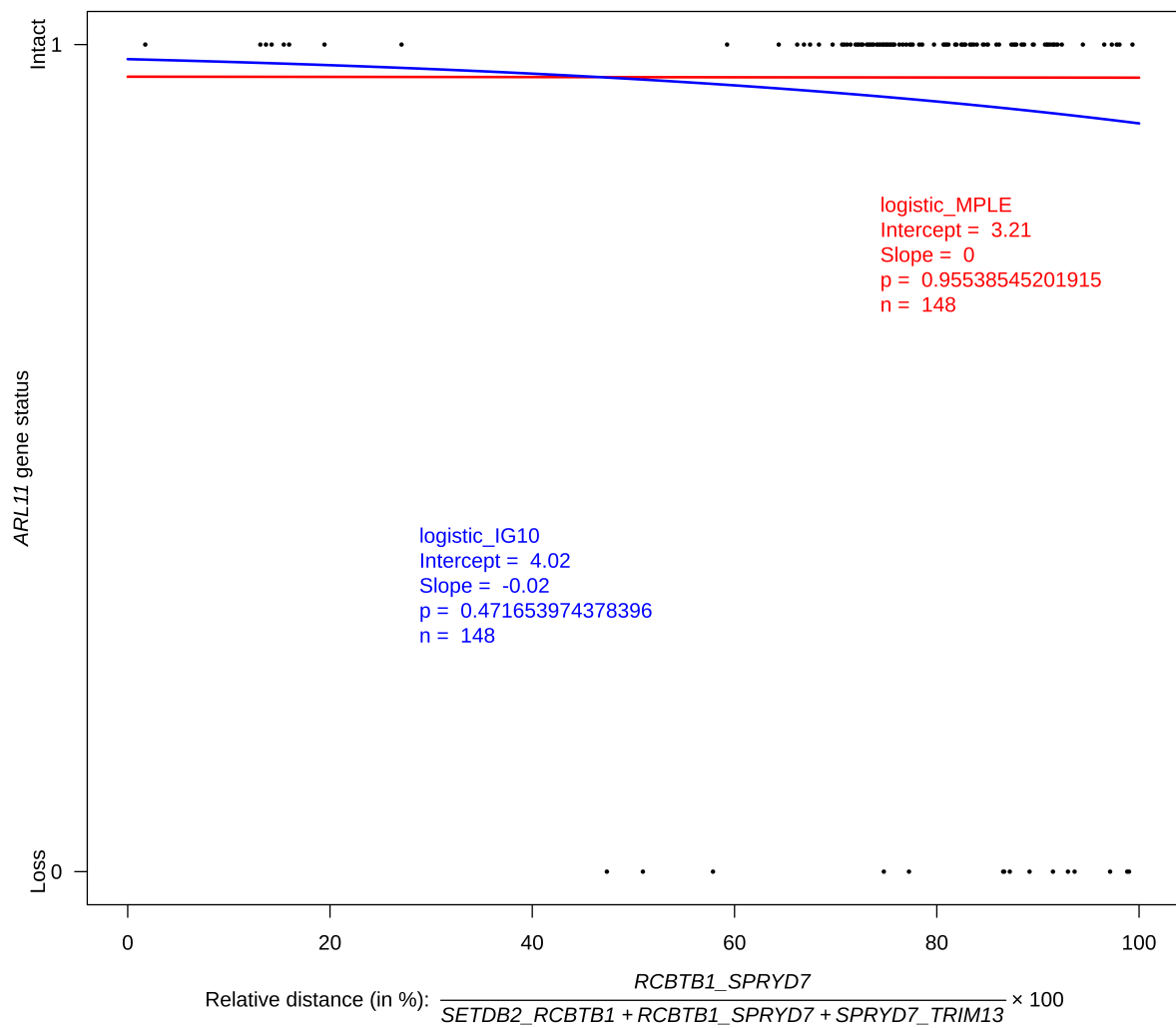


Figure 28: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence

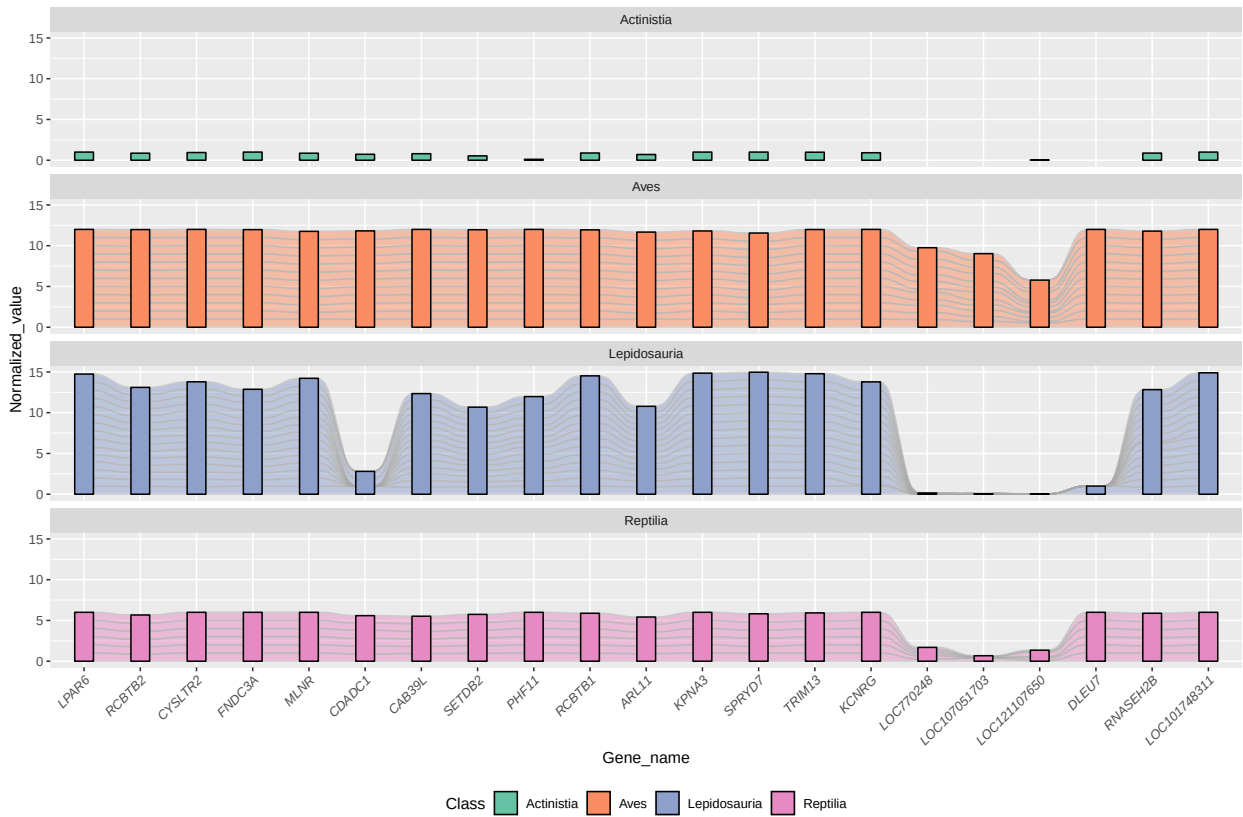


Figure 29: ARL11.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Lastz gene tree

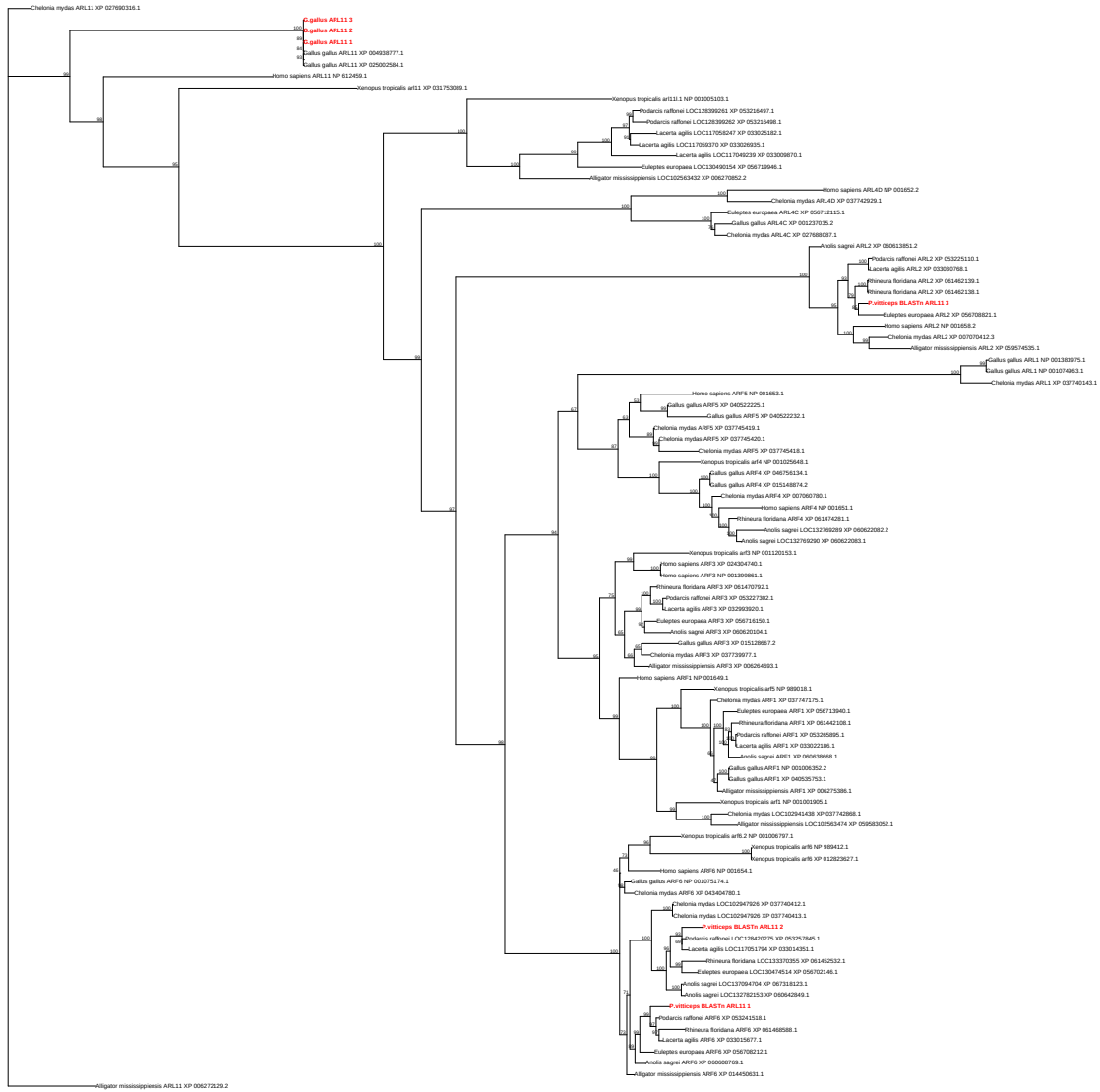


Figure 31: ARL11.combined.mafft.aln.highlighted.pdf

We conducted a syntenic analysis of ARL11 in squamates and representative

→ outgroups. In squamates, ARL11 is absent. In *Mus musculus*, the

→ flanking genes PHF11 and RCBTB1 appear after several intervening

→ blocks indicate the absence of ARL11, green blocks mark its presence

↪ light purple blocks denote different flanking genes.

Transcriptomic evidence *Pogona vitticeps*

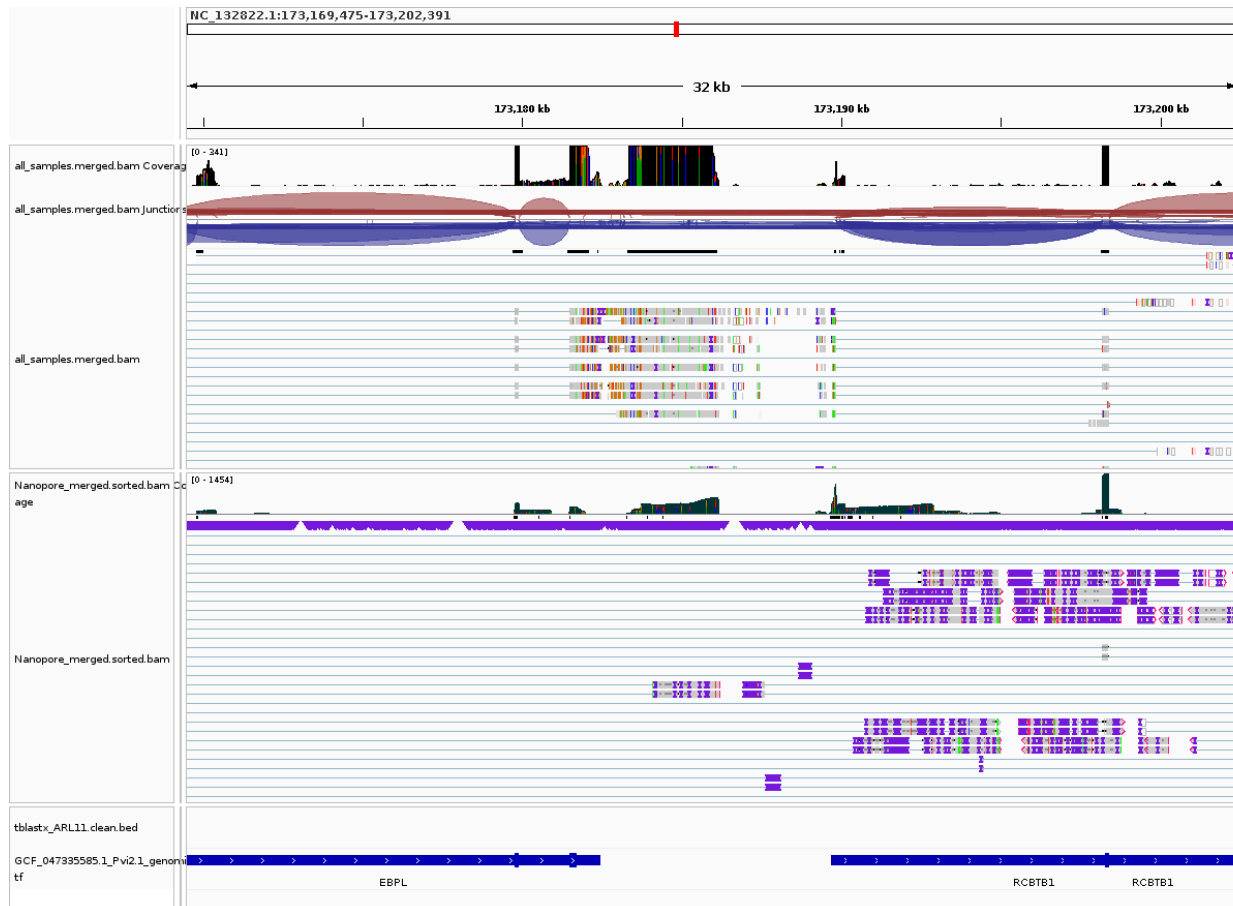


Figure 33: ARL11.png

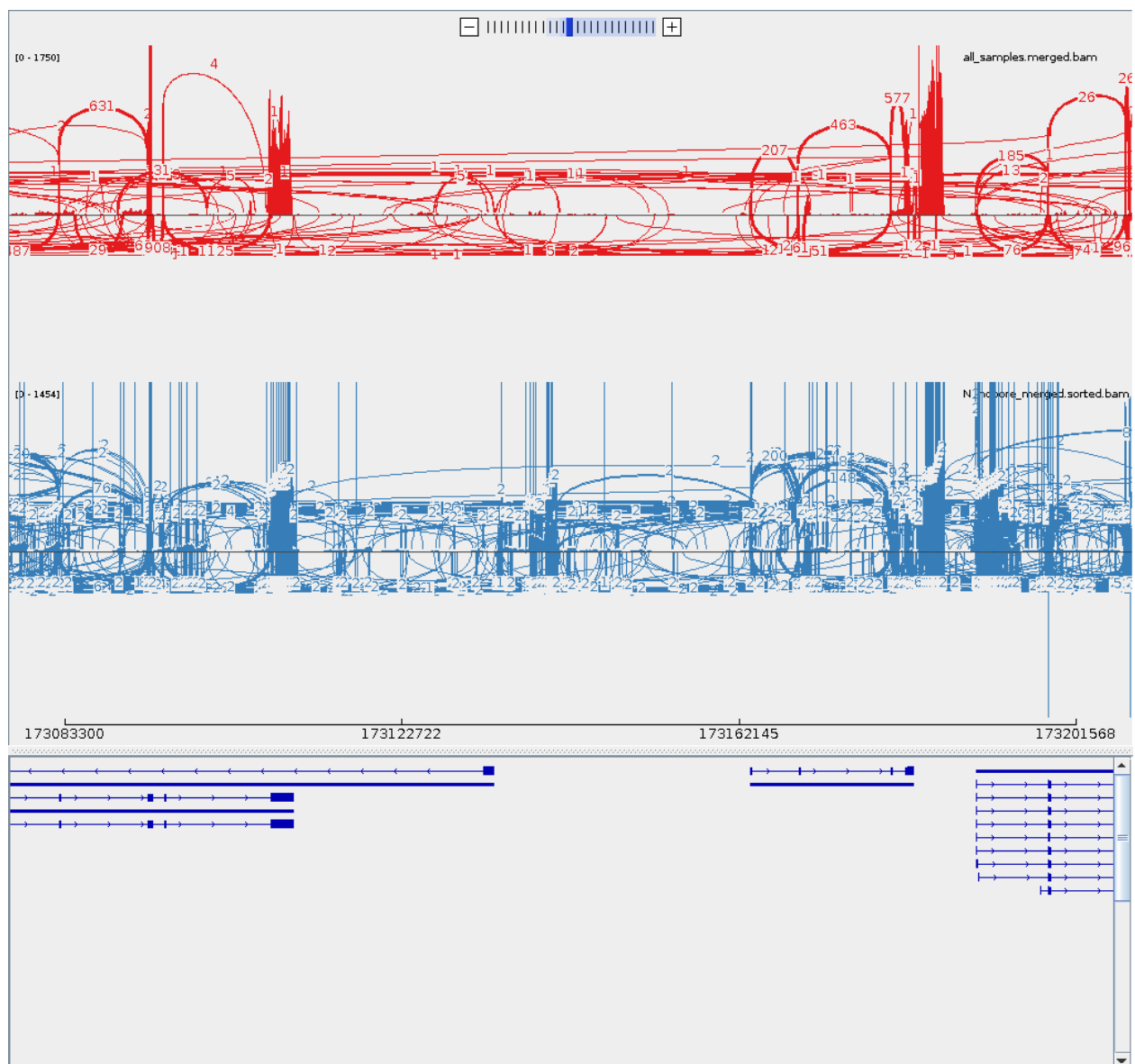


Figure 34: ARL11_Shash.png

4 CAV3

Assembly verification Evidence

Crotalus_tigris-PacBio

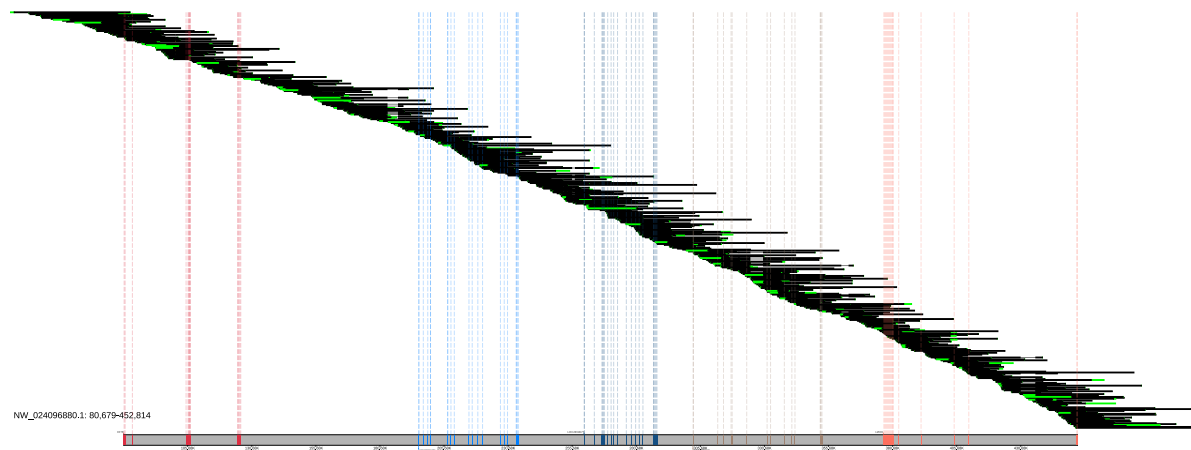


Figure 35: CAV3:NW_024096880.1:80679-452814.pdf

Podarcis_muralis-PacBio

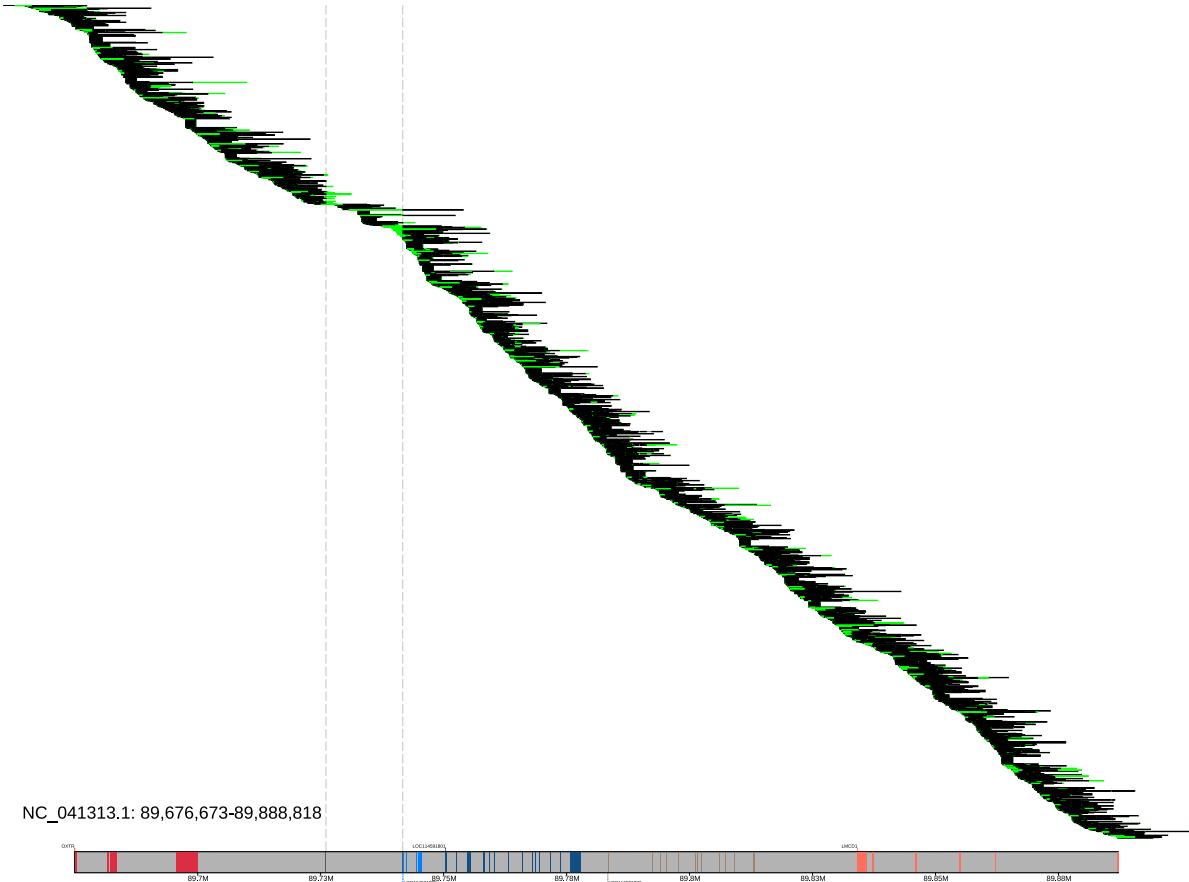


Figure 36: CAV3:NC_041313.1:89676673-89888818.pdf

Pogona_vitticeps-Nanopore

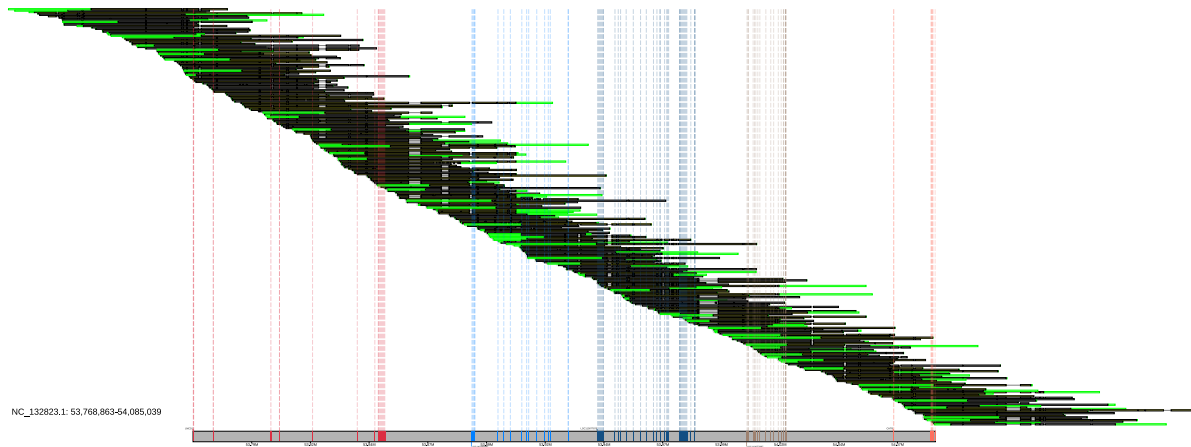


Figure 37: CAV3:NC_132823.1:53768863-54085039.pdf

Important gene stats

CAV3_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
CAV3	76.53612167	55.213 +/- 3.43846	3.94688 +/- 0.303124	81.629 +/- 9.79473	Yes	CAV1;LOC132767837;

Intergenic distance phylogenetic signal evidence

CAV3_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
CAV3	222	19	203	2	0.6524128565133	0.997474563711845

CAV3_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
CAV3	222	19	203	2	0.6524128565133	0.997474563711845

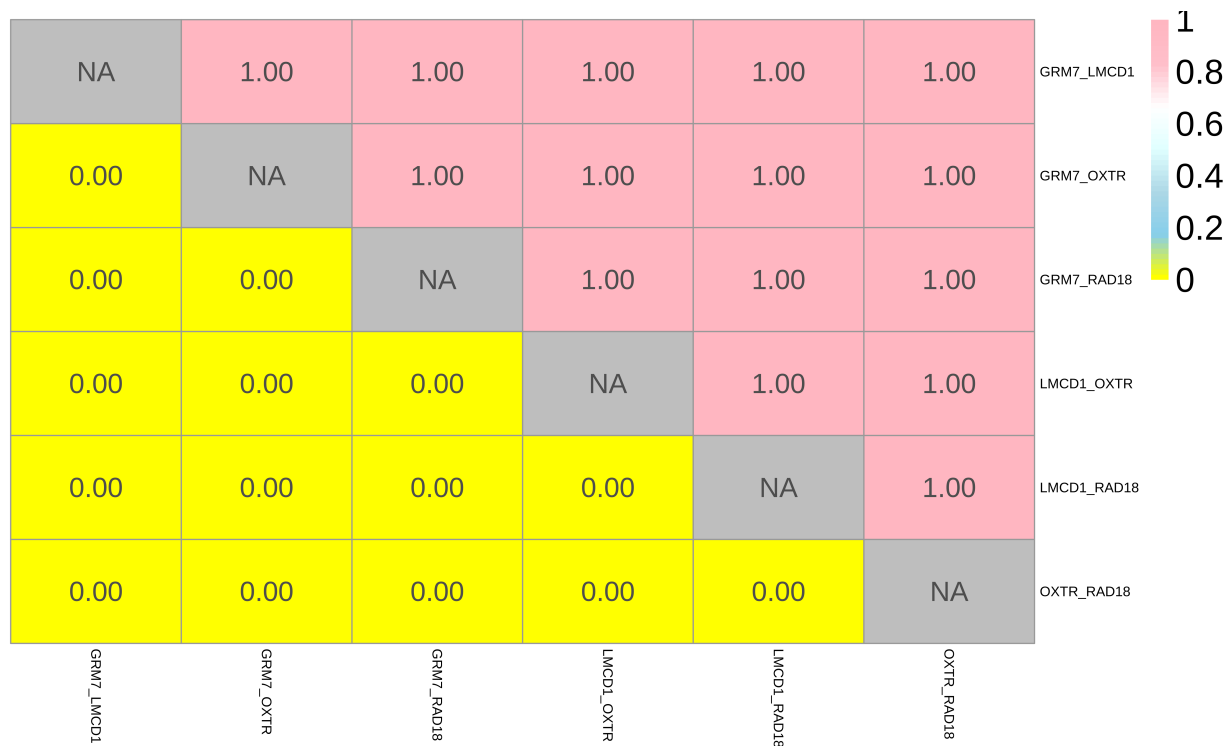


Figure 38: Heatmap_of_deletion_plot.png

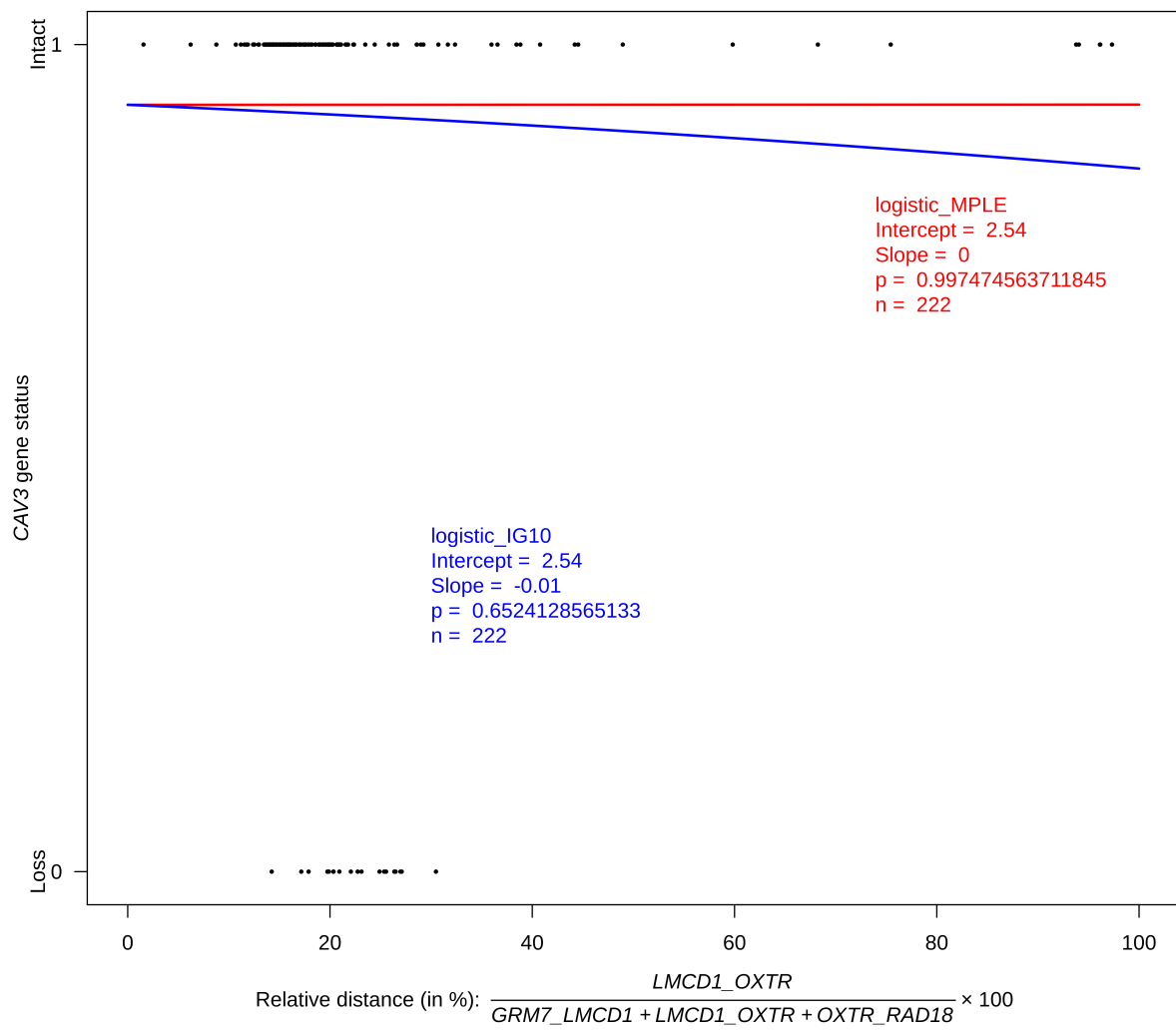


Figure 39: Phylogenetic_signal_of_deletion_plot.png

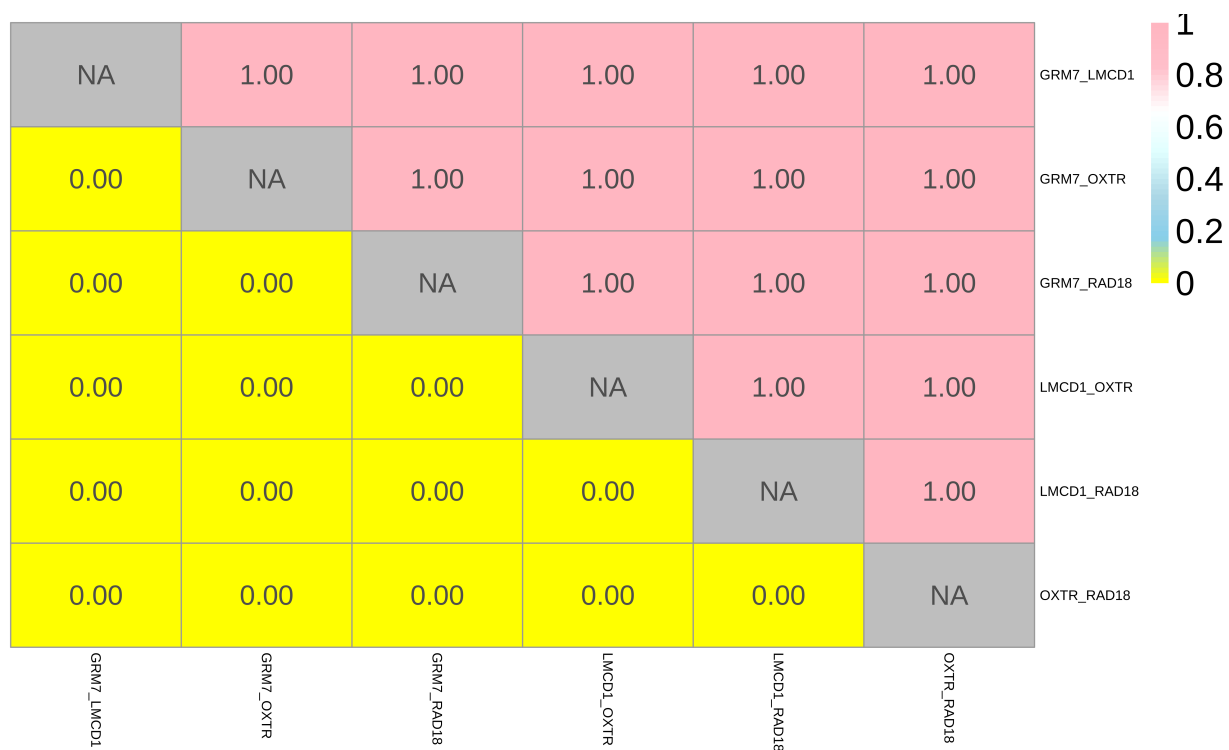


Figure 40: Heatmap_of_deletion_plot.png

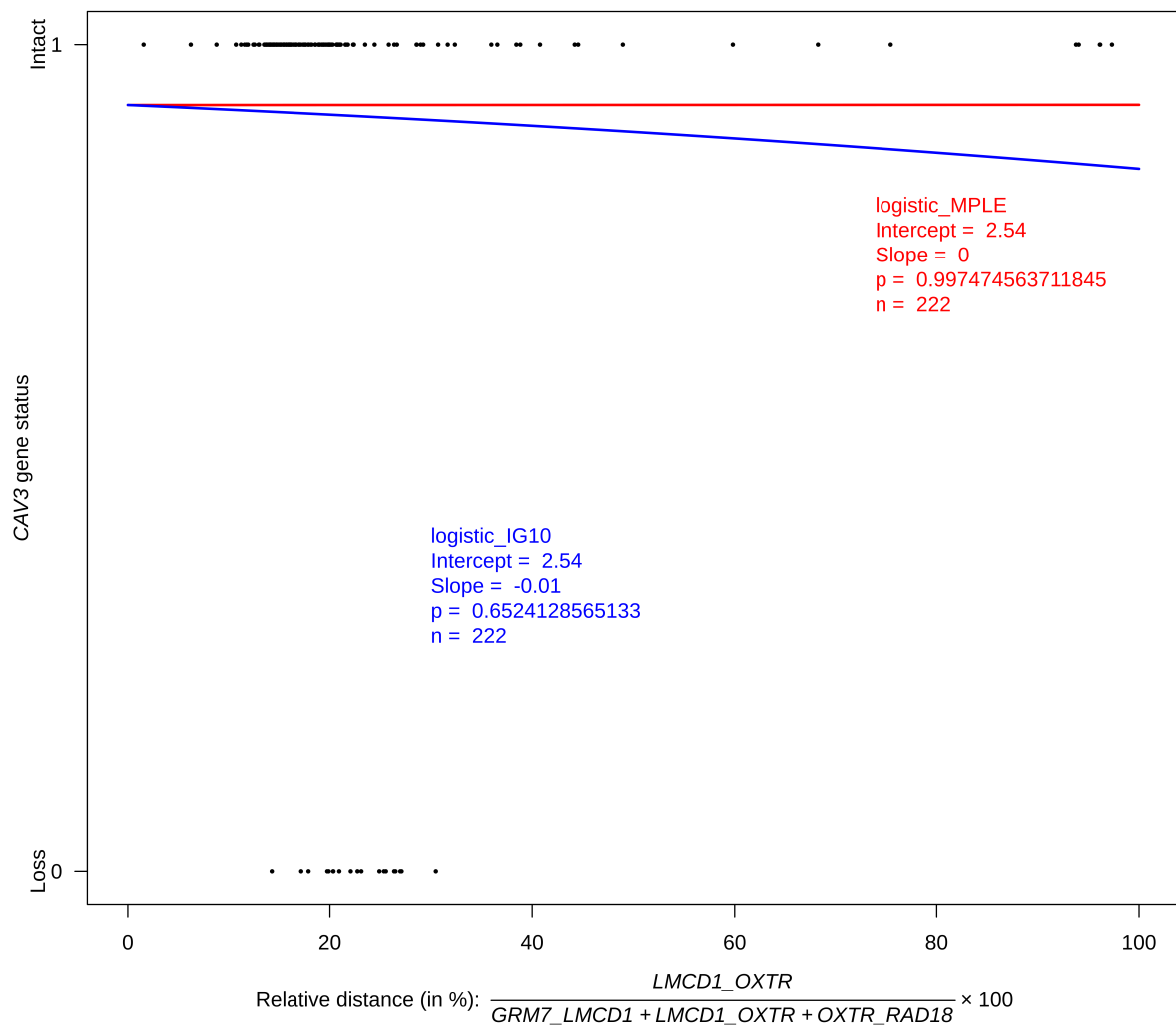


Figure 41: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence

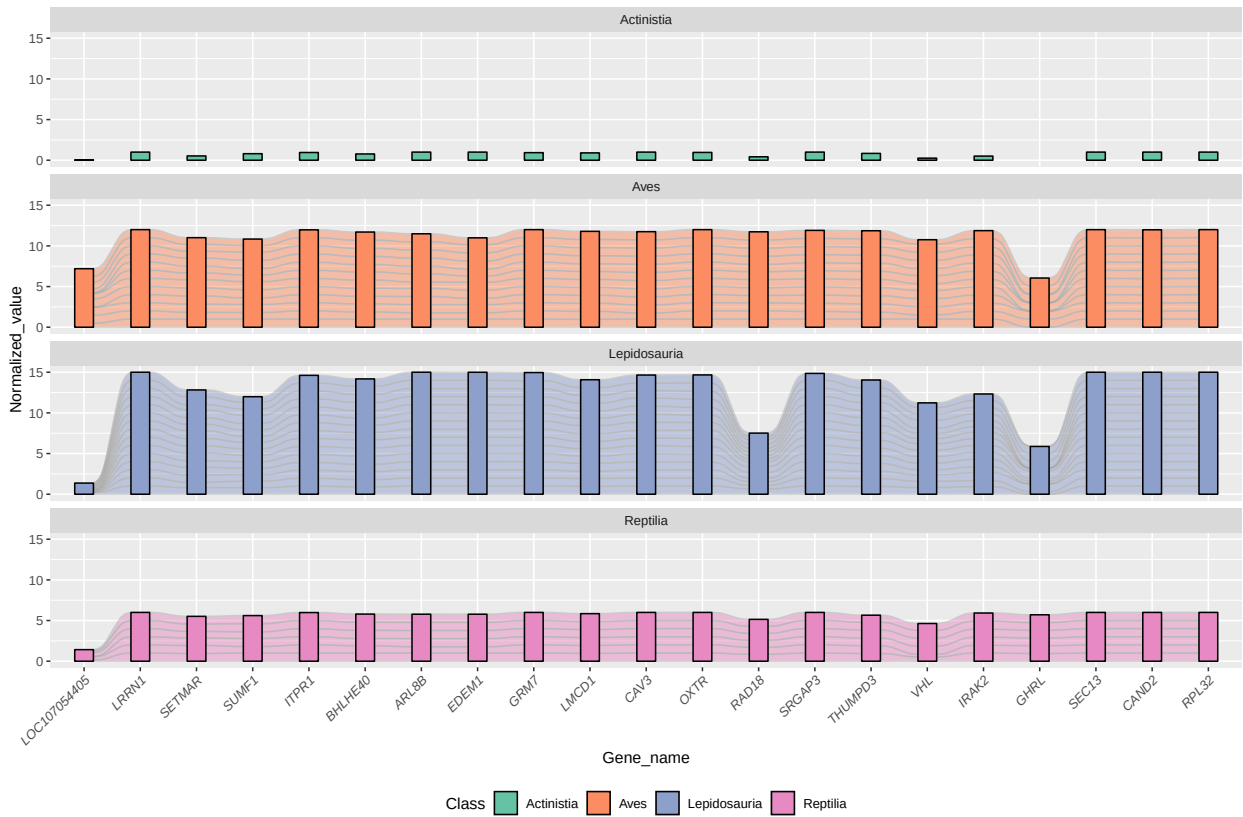


Figure 42: CAV3.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

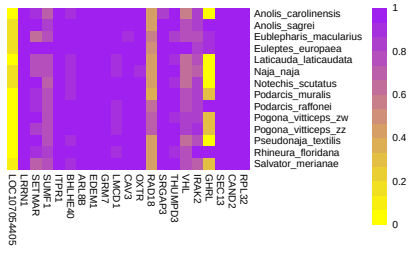


Figure 43: CAV3.FS_Exonic.Final.Gallus_gallus.21_genes_heatmap.pdf

Lastz gene tree

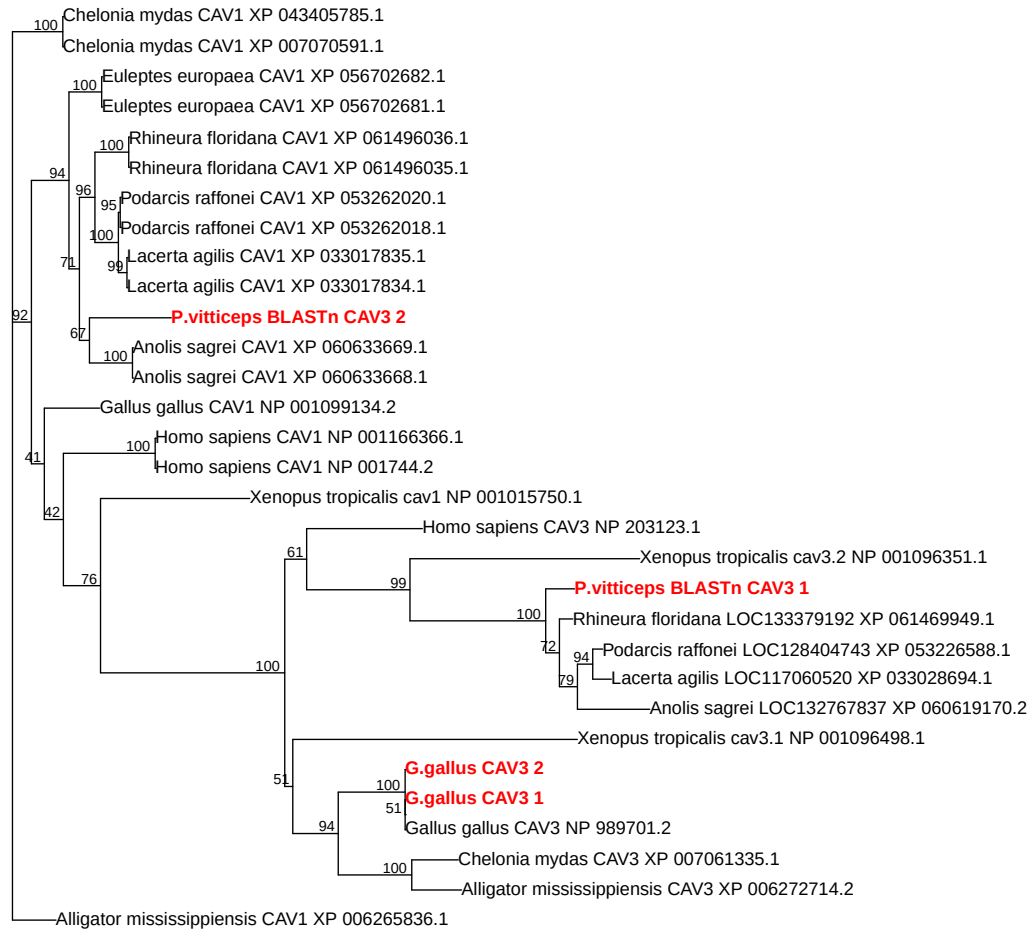


Figure 44: CAV3.combined.mafft.aln.highlighted.pdf

Orthofinder genetree

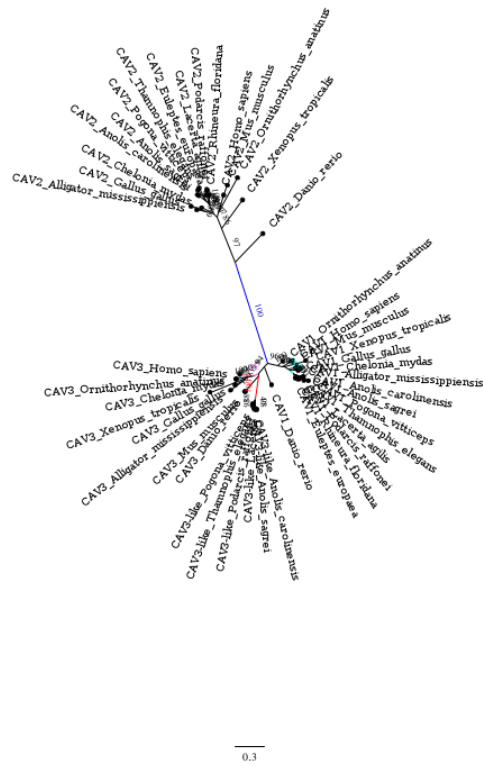


Figure 45: CAV3-2-1-3L.PRANK.aln.contree.png

Syntenic evidence

				CAV3						
Chelonia mydas				> LMCD1 >	< SSUH2 <	< ARIH1 <	> CAV3 >	< OXTR <	< RAD18 <	< SRGAP3 <
				Chr 7 (NC_057853.1)						
Gallus gallus				> EDEM1 >	> GRM7 >	> LMCD1 >	> CAV3 >	< OXTR <	< RAD18 <	< SRGAP3 <
				Chr 12 (NC_052543.1)						
Podarcis muralis						SSUH2				
				> GRM7 >	> LMCD1 >	4591802, LOC11451	> CAV3 >	< OXTR <	< RAD18 <	< SRGAP3 <
				Chr 2 (NC_041313.1)						
Anolis carolinensis				> GRM7 >	> LMCD1 >	< SSUH2 <	> CAV3 >	< OXTR <	< RAD18 <	< SRGAP3 <
				Chr 2 (NC_085842.1)						
Pogona vitticeps				> GRM7 >	> LMCD1 >	< SSUH2 <	> CAV3 >	< OXTR <	< RAD18 <	< SRGAP3 <
				Chr 2 (NC_132823.1)						
Crotalus tigris						SSUH2				
				> GRM7 >	> LMCD1 >	< LOC120310478 <	> CAV3 >	< OXTR <	< RAD18 <	< SRGAP3 <
				NW_024096880.1 (unplaced)			NW_024097896.1 (unplaced)			
Ornithorhynchus anatinus				> GRM7 >	> LMCD1 >	< SSUH2 <	> CAV3 >	< OXTR <	< RAD18 <	< SRGAP3 <
				Chr X1 (NC_041749.1)						
Homo sapiens				> GRM7 >	> LMCD1 >	< SSUH2 <	> CAV3 >	< OXTR <	< RAD18 <	< SRGAP3 <
				Chr 3 (NC_000003.12)						
Mus musculus				> GRM7 >	> LMCD1 >	< SSUH2 <	> CAV3 >	< OXTR <	< RAD18 <	> Gm26799 >
				Chr 6 (NC_000072.7)						

Figure 46: CAV3.pdf

CAV3.txt

Synteny analysis of CAV3

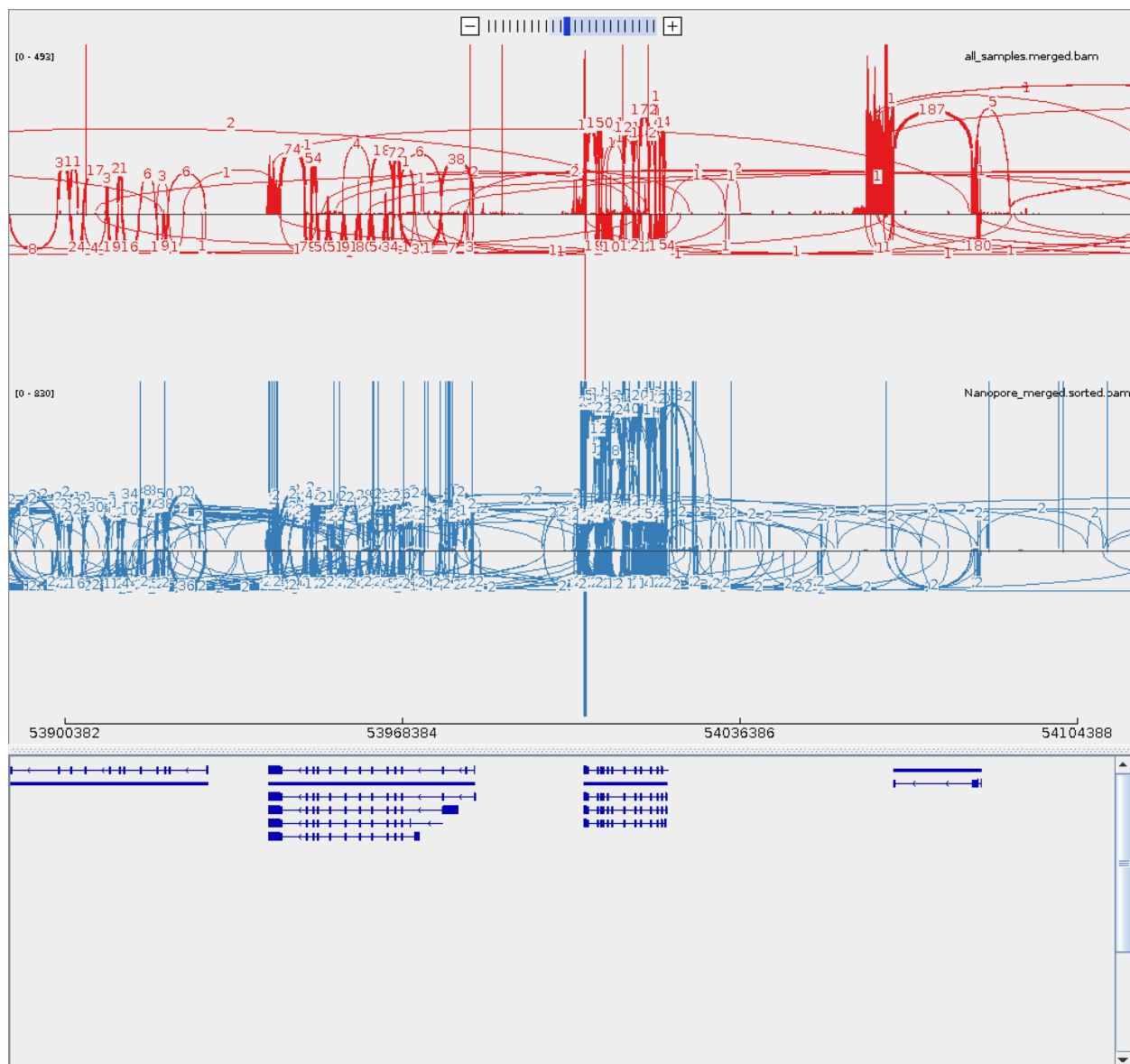
We analyzed the synteny of CAV3 in squamates and representative outgroups.

- The CAV3 syntenic block is fairly conserved. In *Anolis carolinensis*
- , CAV3 coding sequences produced hits on CAV3.2, which is located at
- a different genomic locus, but no hits were observed at the
- expected CAV3 locus. In the synteny plots, red blocks indicate the
- absence of CAV3, green blocks mark its presence, light blue blocks
- represent genes conserved across lineages, and light purple blocks
- denote different flanking genes.

Transcriptomic evidence Pogona vitticeps



Figure 47: CAV3.png



5 CYYR1

Assembly verification Evidence

Crotalus_tigris-PacBio

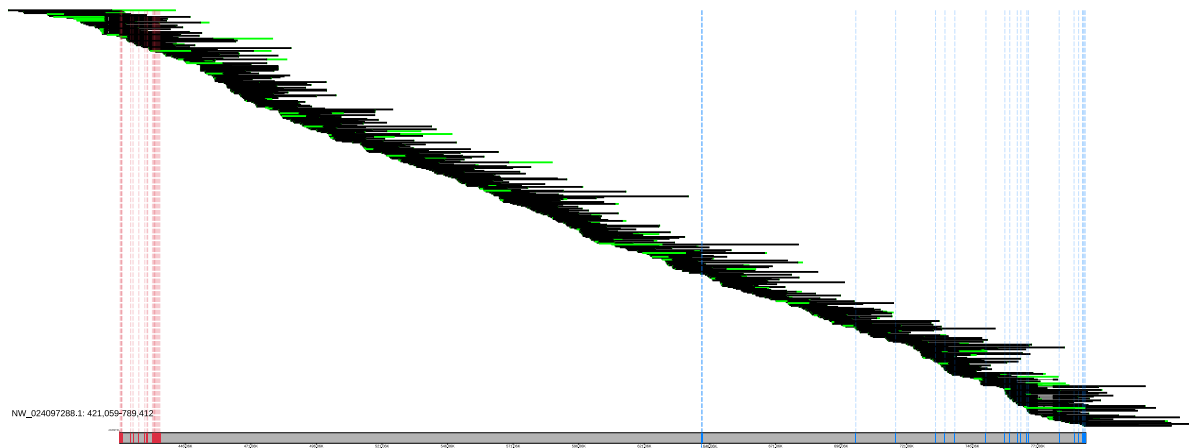


Figure 49: CYYR1:NW_024097288.1:421059-789412.pdf

Podarcis_muralis-PacBio

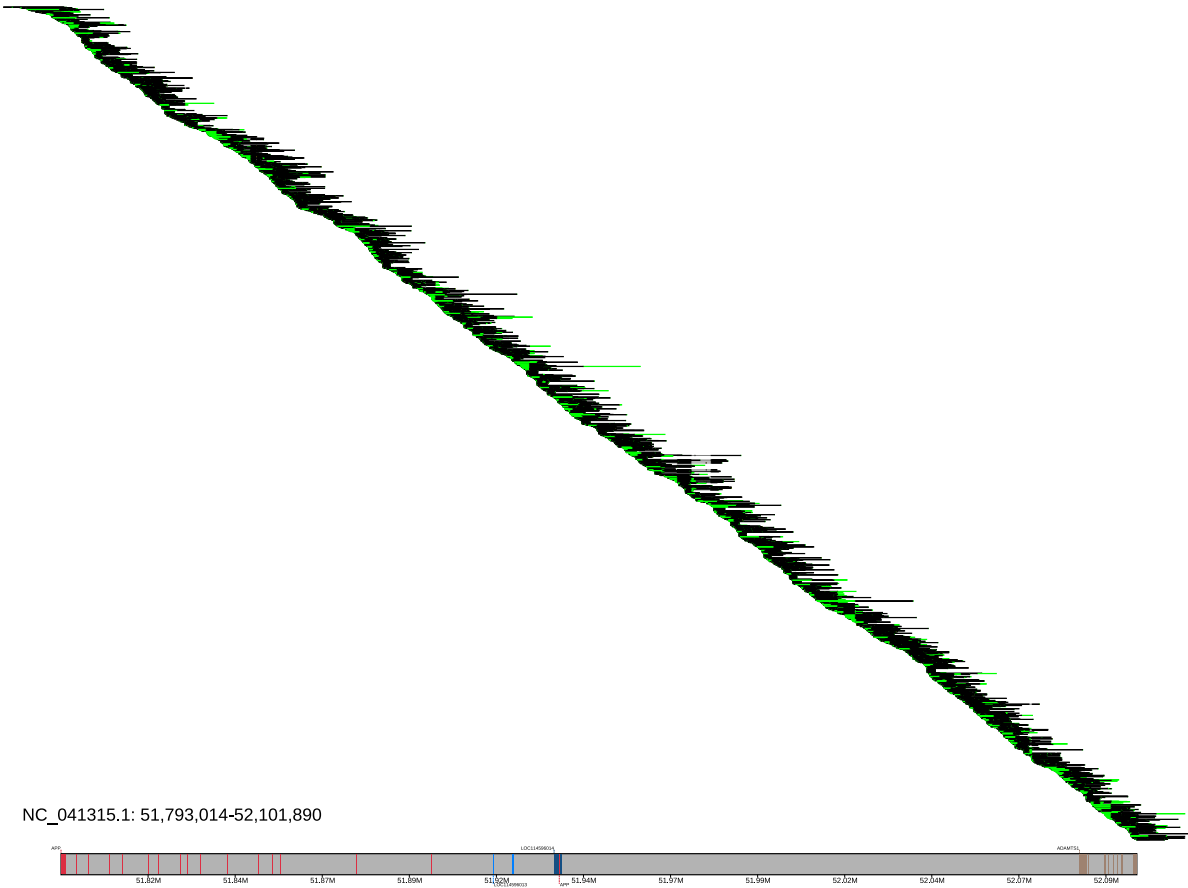


Figure 50: CYR1:NC_041315.1:51793014-52101890.pdf

Pogona_vitticeps-Nanopore

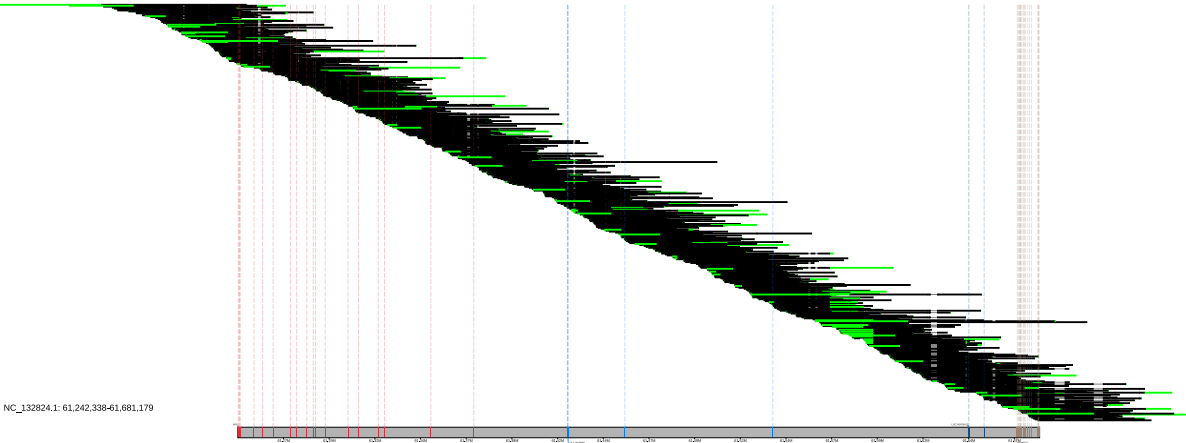


Figure 51: CYYR1:NC_132824.1:61242338-61681179.pdf

Important gene stats

CYYR1_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
CYYR1	10.59813084	55.4314 +/- 4.33048	4.19354 +/- 0.419557	39.7123 +/- 12.4778	No	Na

Intergenic distance phylogenetic signal evidence

CYYR1_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
CYYR1	232	18	214	1	0.178342543434396	0.402780509513178

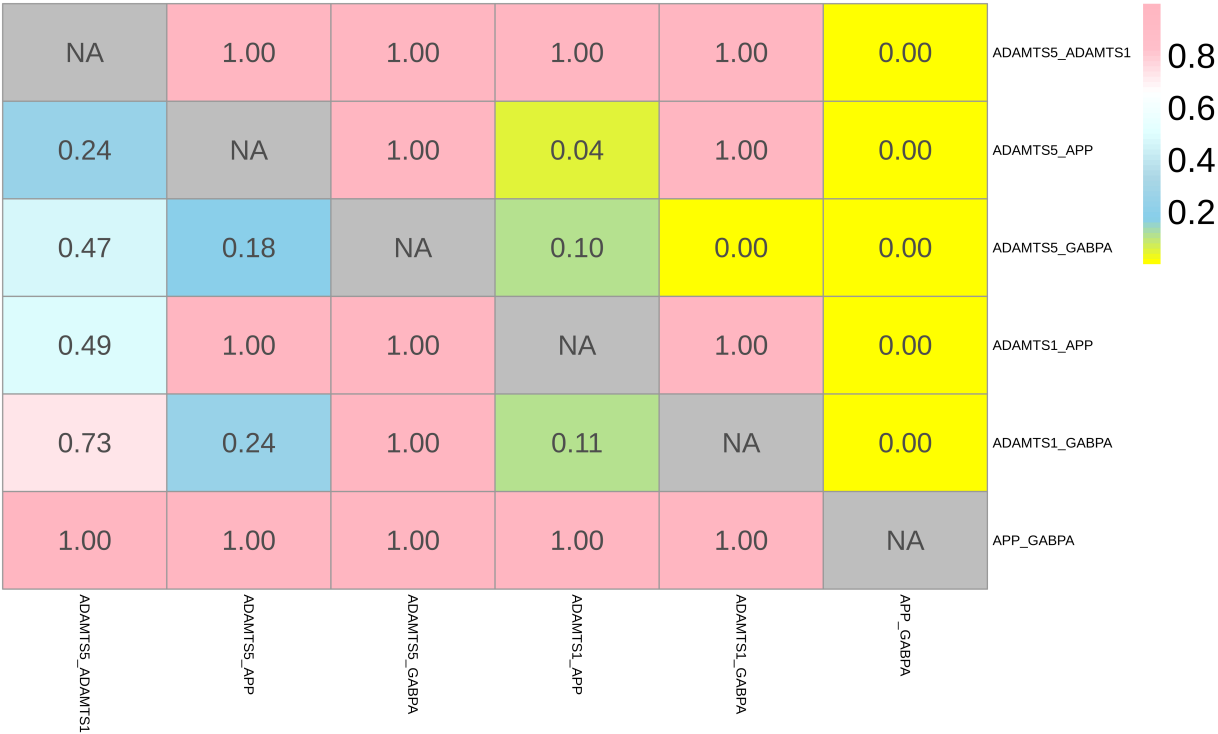


Figure 52: Heatmap_of_deletion_plot.png

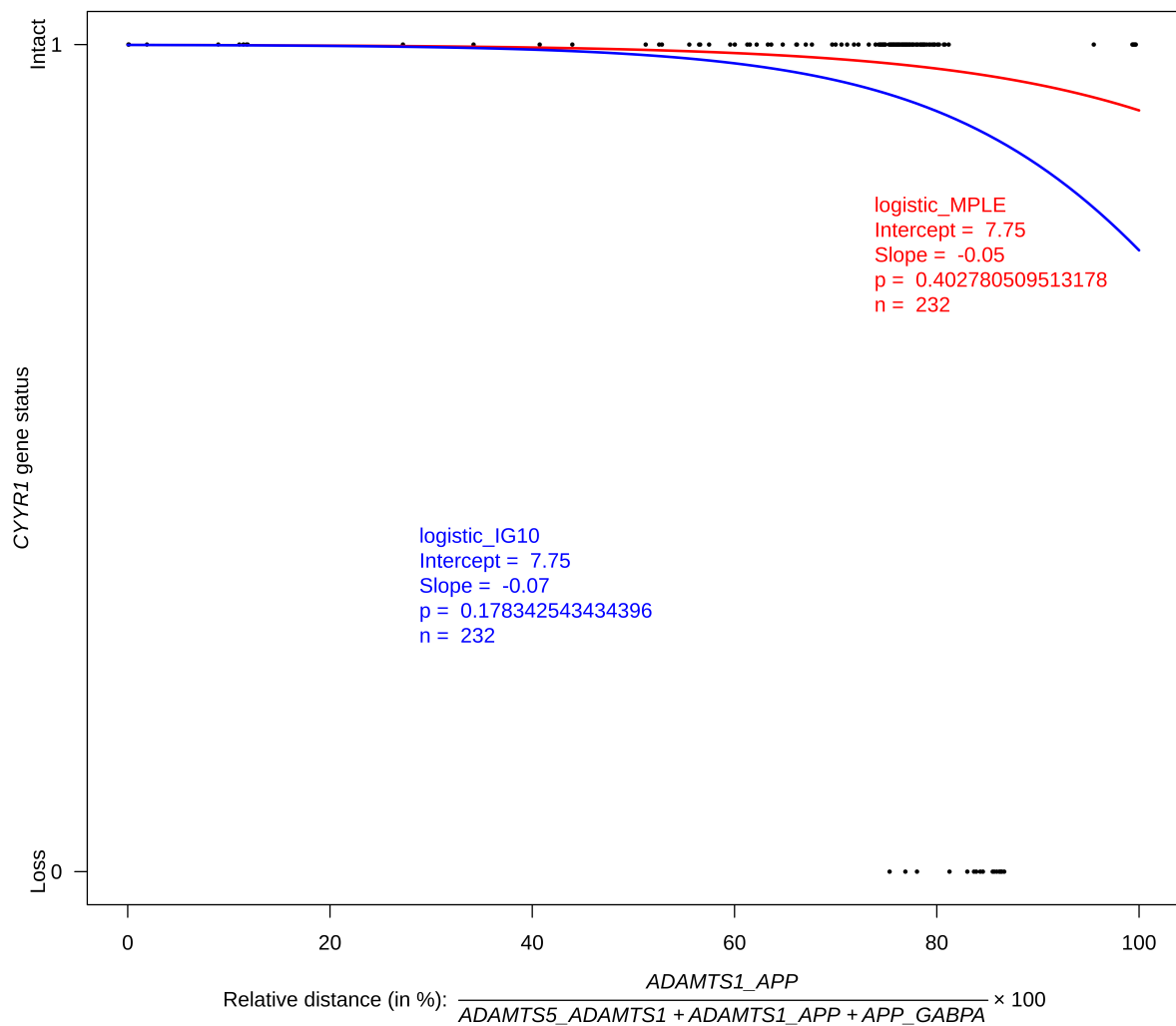


Figure 53: Phylogenetic_signal_of_deletion_plot.png

CYR1_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
CYR1	232	18	214	1	0.178342543434396	0.402780509513178

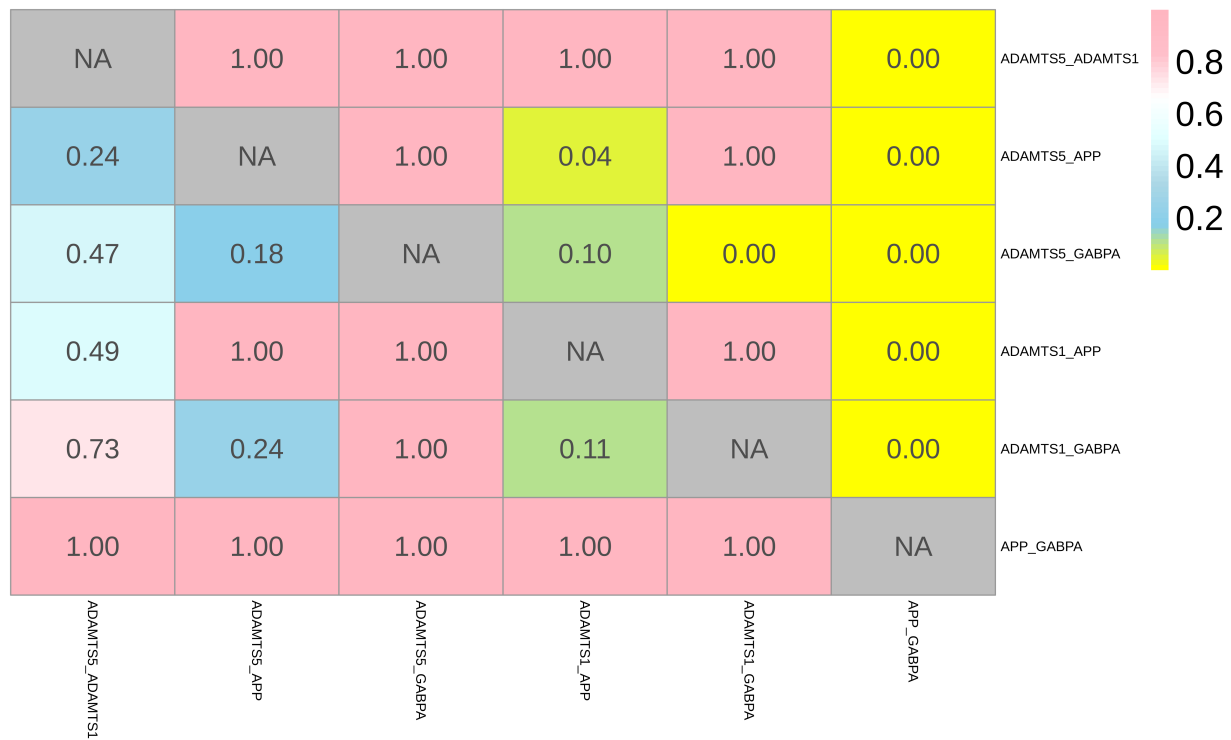


Figure 54: Heatmap_of_deletion_plot.png

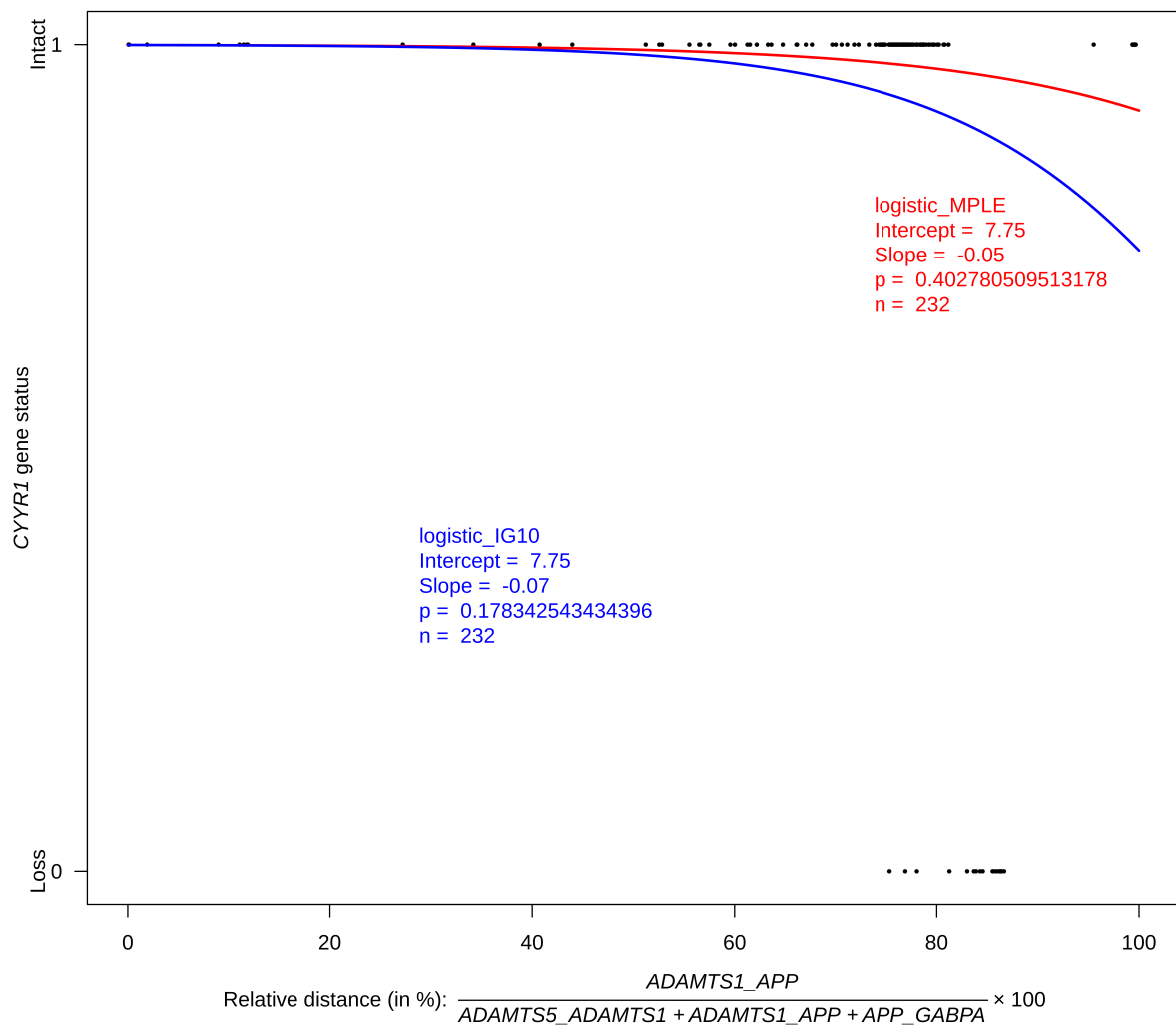


Figure 55: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence

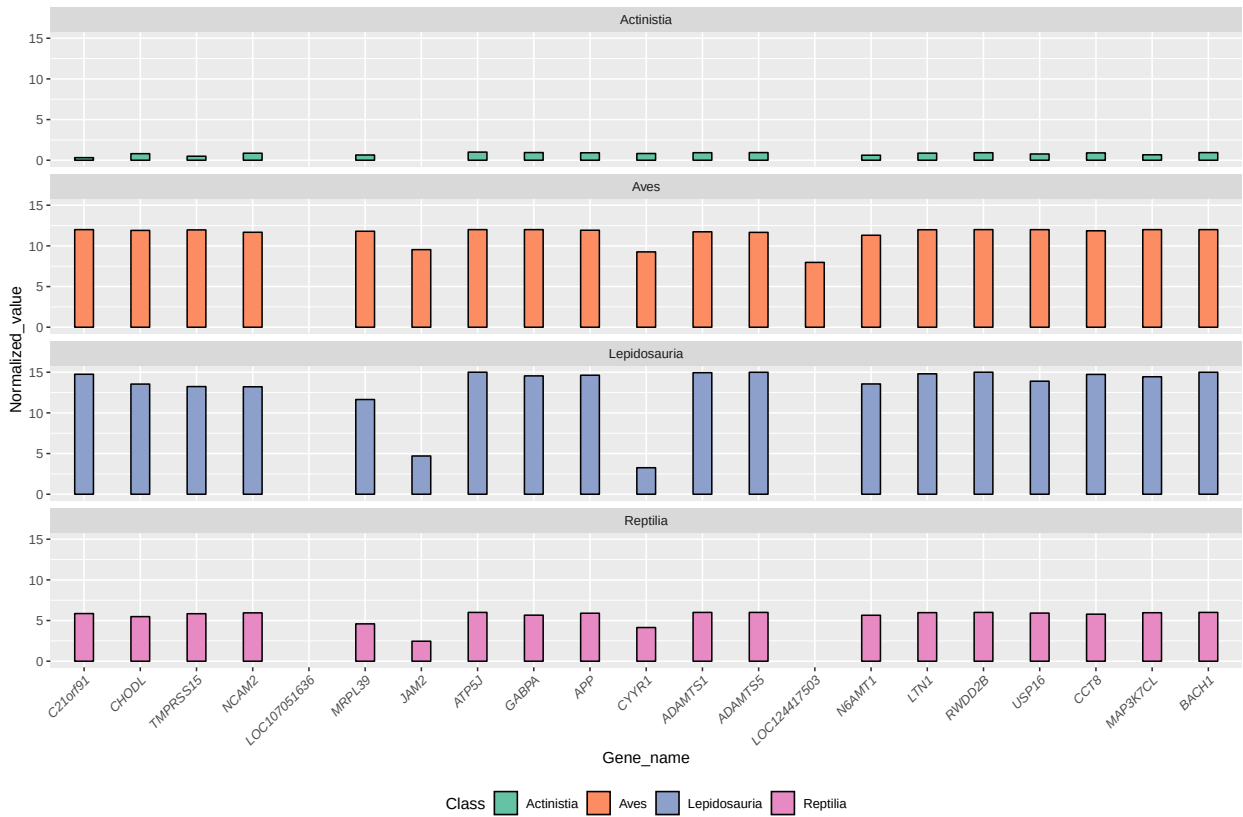
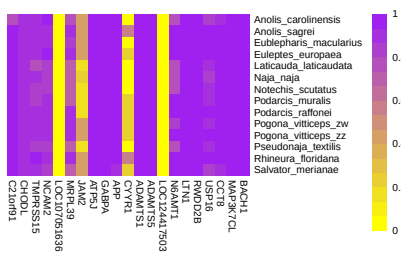


Figure 56: CYR1.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf



Lastz gene tree

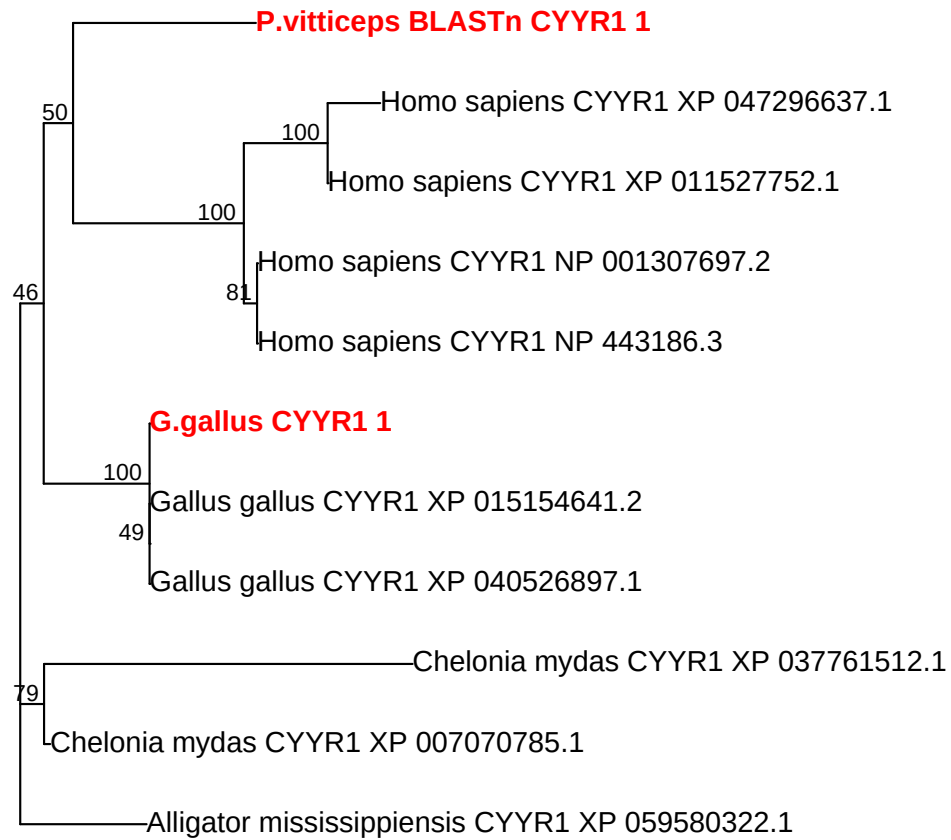


Figure 58: CYR1.combined.mafft.aln.highlighted.pdf

Syntenic evidence



Figure 59: CYR1.pdf

CYR1.txt

Synteny analysis of CYR1

We analyzed the syntenic of CYR1 in squamates and representative outgroups

→ . The CYR1 syntenic block is conserved. In Pogona vitticeps, BLASTN

→ hits were observed at the syntenic locus where CYR1 is expected,

→ indicated by a lighter orange color in the plot. In other squamate

→ species, CYR1 was absent at the corresponding locus. In the syntenic

→ plots, red blocks indicate the absence of CYR1, green blocks mark

→ its presence, light blue blocks represent genes conserved across

→ lineages, and light purple blocks denote different flanking genes.

Transcriptomic evidence Pogona vitticeps

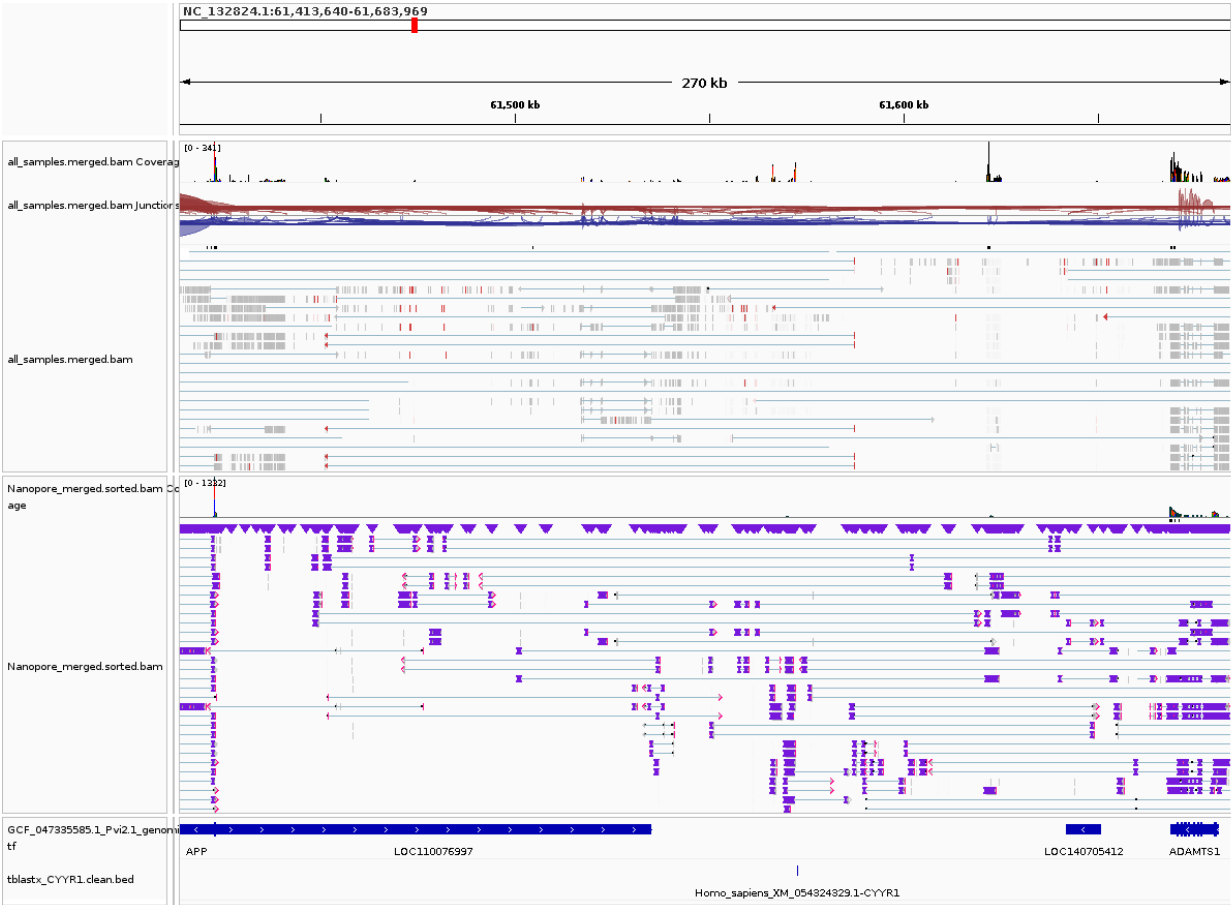


Figure 60: CYYR1.png

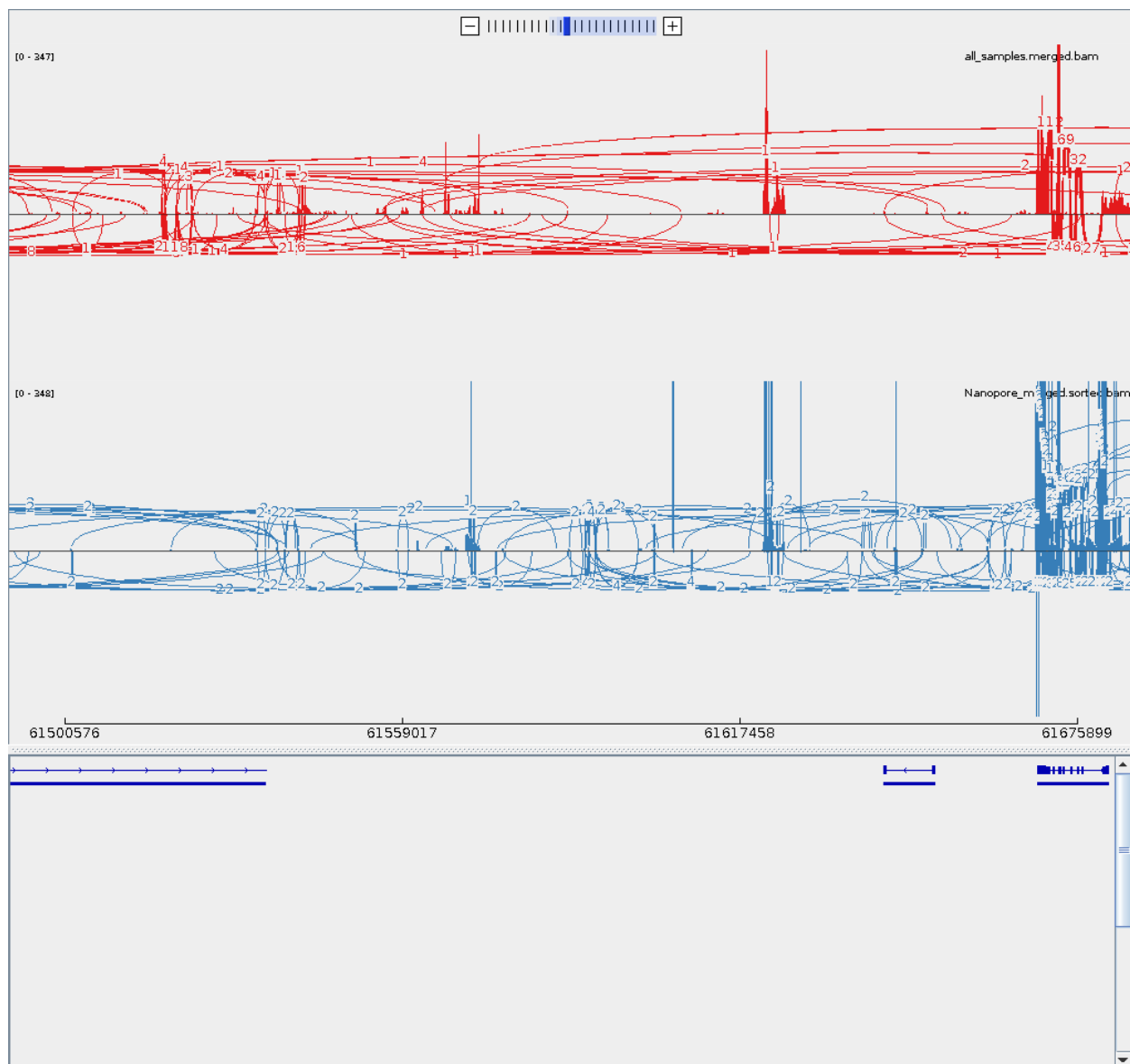


Figure 61: CYYR1_Shash.png

6 DIP2A

Important gene stats

DIP2A_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
DIP2A	36.45283019	55.4715 +/- 5.38179	3.93514 +/- 0.313701	80.5567 +/- 8.79243	Yes	DIP2C;

Intergenic distance phylogenetic signal evidence

Lastz Alignment evidence

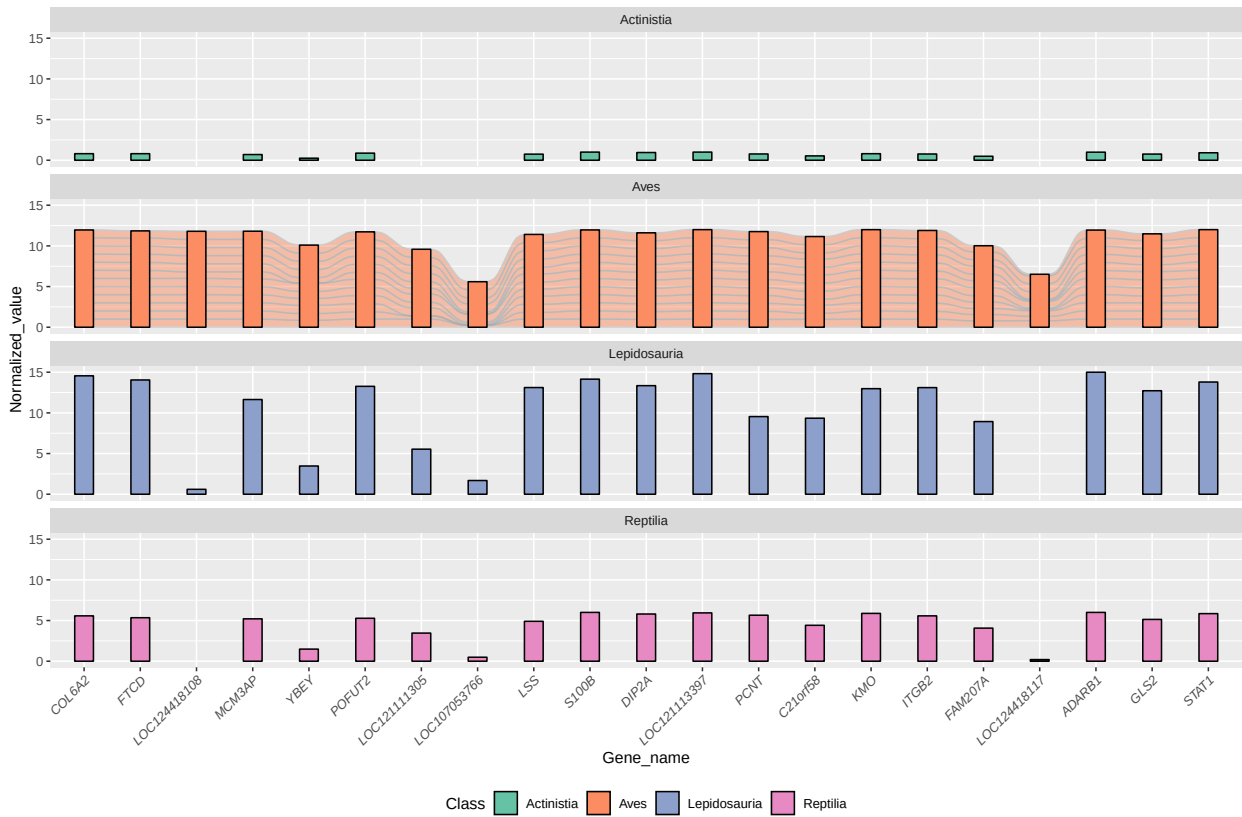


Figure 62: DIP2A.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Lastz gene tree



Figure 64: DIP2A.combined.mafft.aln.highlighted.pdf

Syntenic evidence

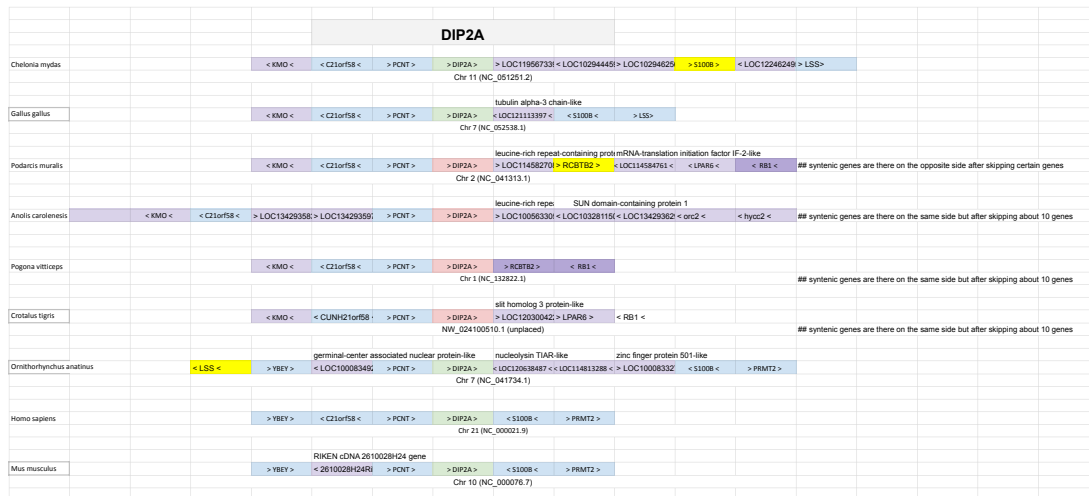


Figure 65: DIP2A.pdf

DIP2A.txt

Synteny analysis of DIP2A

The analysis of the

DIP2A syntenic block reveals that it has undergone various

- intrachromosomal rearrangements in different squamate lineages when
→ compared to the conserved arrangement in outgroup species. In
→ lizards such as

Anolis carolinensis and *Pogona vitticeps*, as well as the snake *Crotalus*

- tigris, the block has been repositioned to a new location on the
- same chromosome after skipping approximately 10 genes. The
- rearrangement is more complex in the lizard

Podarcis muralis, where the syntenic genes have moved to the opposite side
→ of the chromosome, indicating an inversion event in addition to
→ being repositioned.

In the synteny plots, red blocks indicate the absence of the target gene,
→ while green blocks mark its presence. Light blue blocks represent
→ flanking genes that are conserved across lineages, and light purple
→ blocks denote instances where a different flanking gene is present.

7 DLEU7

Important gene stats

DLEU7_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
DLEU7	6.536231884	58.6675 +/- 6.68348	4.67307 +/- 0.818282	68.5223 +/- 21.0771	No	Na

Intergenic distance phylogenetic signal evidence

DLEU7_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
DLEU7	220	14	206	1	0.556066259873286	0.958848505984217

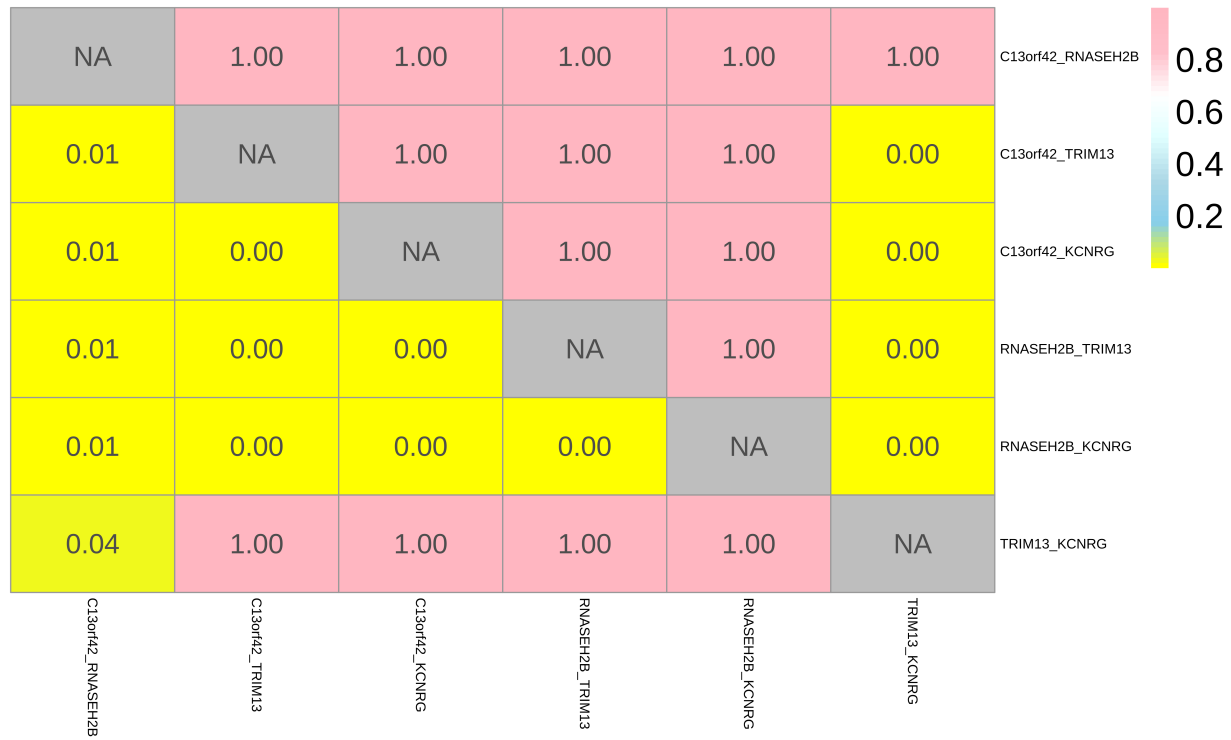


Figure 66: Heatmap_of_deletion_plot.png

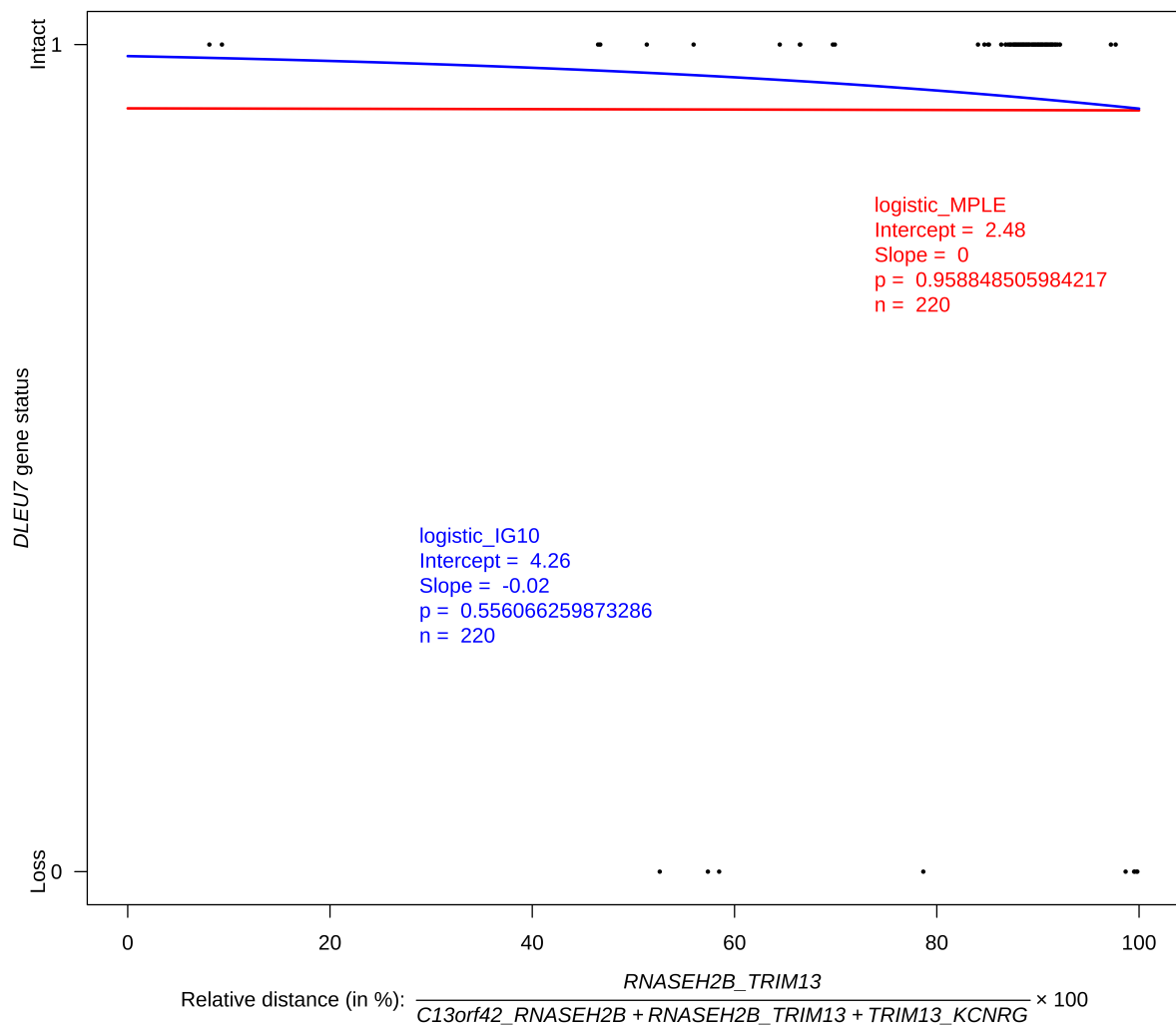


Figure 67: Phylogenetic_signal_of_deletion_plot.png

DLEU7_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
DLEU7	220	14	206	1	0.556066259873286	0.958848505984217

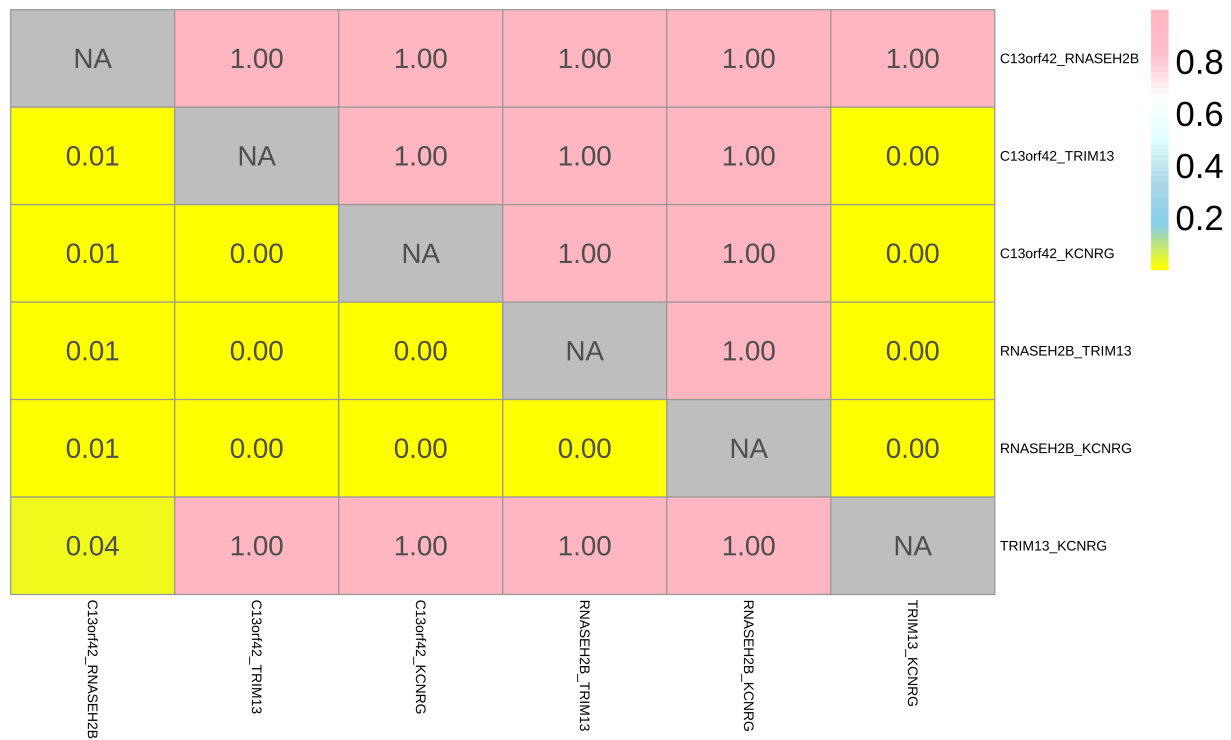


Figure 68: Heatmap_of_deletion_plot.png

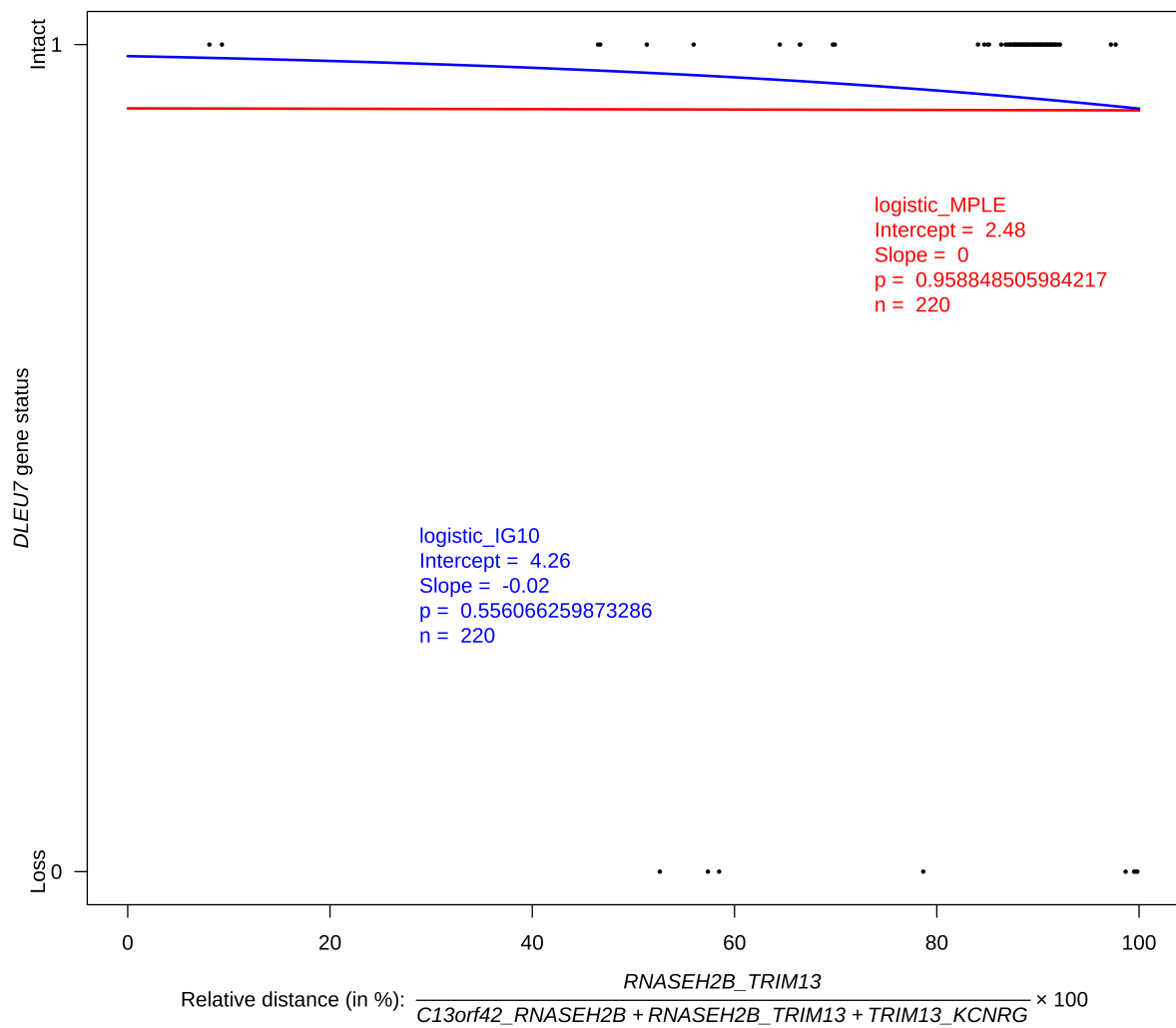


Figure 69: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence

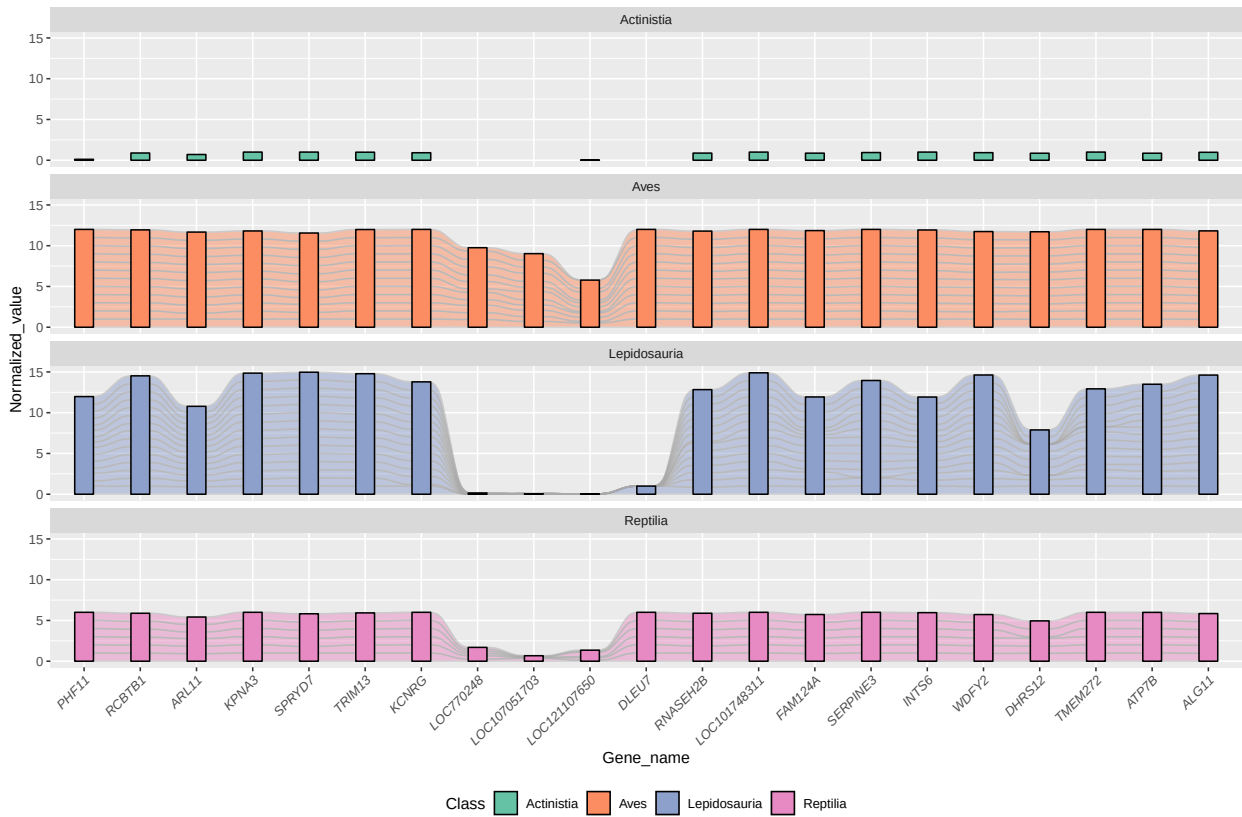


Figure 70: DLEU7.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Lastz gene tree

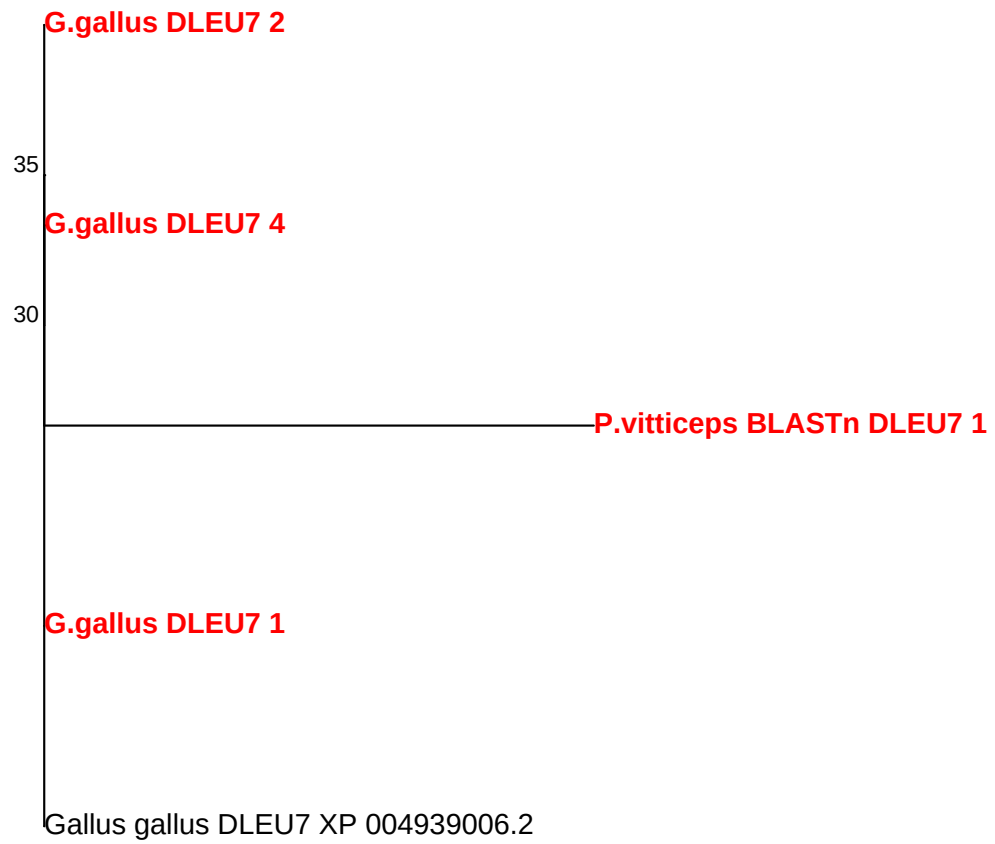


Figure 72: DLEU7.combined.mafft.aln.highlighted.pdf

Syntenic evidence

DLEU7											
	guanylate cyclase soluble subunit beta-2-like										
Chelonis mydas	< fam124a <	> c1h13orf42 >	> LOC10293142 <	< RNA5EH2B <	> DLEU7 >	< LOC12246333 >	< LOC11402249 <	< LOC11402250 <	< TRIM13 <	< KCNRG <	
	Chr 1 (NC_057849.1)										
	protein C13orf42 RNA5EH2B										
Gallus gallus	< FAM124A <	> C13orf42 >	> LOC101748111 >	> LOC101748282 >	< RNA5EH2B <	> LOC107051700 >	> DLEU7 >	< LOC101748122 <	< LOC107051703 <	< LOC121307650 <	< LOC12417627 >
	Chr 1 (NC_052532.1)										
	translation initiation factor IF-2-like isoform X1										
Podarcis muralis	> LOC11459332 >	> LOC11459372 >	> LOC11459372 >	< RNA5EH2B <	> DLEU7 >	> SF3B6 >	> WDCP >	< FKBP1B <	# syntenic genes are there on the same side but after skipping about 10 genes		
	Chr 3 (NC_041314.1)										
	guanylate cyclase soluble subunit beta-2-like										
Anolis carolinensis	< fam124a <	> c1h13orf42 >	> LOC13429310 <	< RNA5EH2B <	> DLEU7 >	> SF3B6 >	< FKBP1B <	> WDCP >	# syntenic genes are there on the opposite side after skipping certain genes		
	Chr 1 (NC_085841.1)										
	WD repeat and coiled-coil-containing protein										
Pogona vitticeps	< FAM124A <	> C13orf42 >	< RNA5EH2B <	> DLEU7 >	> SF3B6 >	> LOC11027614 <	< FKBP1B <	# syntenic genes are there on the same side but after skipping about 10 genes			
	Chr 1 (NC_132822.1)										
	guanylate cyclase soluble subunit beta-2-like										
Crotalus tigris	> CUNH13orf42 >	> LOC12029825 <	< RNA5EH2B <	> DLEU7 >	> SF3B6 >	< FKBP1B <					
	NW_024100212.1 (unplaced)				NW_024100281.1 (unplaced)						
	guanylate cyclase soluble subunit beta-2-like										
Oreothyrichus anatinus	< FAM124A <	> C20H13orf42 >	> LOC10008292 <	< RNA5EH2B <	> DLEU7 >	< LOC12063905 >	< LOC12063796 <	< LOC10317046 <	< KCNRG <	< TRIM13 <	
	Chr 20 (NC_041747.1)										
	WD repeat and coiled-coil-containing protein										
Homo sapiens	< FAM124A <	> C13orf42 >	< RNA5EH2B <	> DLEU7 >	< DLEU1 <	> DLEU2 >	< KCNRG <	< TRIM13 <			
	Chr 13 (NC_000013.11)										
	homolog C13orf42 guanylate cyclase 1, soluble, beta 2										
Mus musculus	< FAM124A <	> Gm4131 >	> Guqy1b2 >	< RNA5EH2B <	> DLEU7 >	> DLEU2 >	< KCNRG <	< TRIM13 <			
	Chr 14 (NC_000080.7)										

Figure 73: DLEU7.pdf

DLEU7.txt

Synteny analysis of DLEU7

The syntenic block containing DLEU7 has undergone various intrachromosomal
 ↳ rearrangements in squamate reptiles compared to the conserved
 ↳ arrangement seen in outgroups . In lizards such as Podarcis muralis
 ↳ and Pogona vitticeps, the syntenic genes have been transposed to a
 ↳ new location on the same chromosome after skipping approximately 10
 ↳ genes. The rearrangement in

Anolis carolinensis is more complex, involving genes are on the opposite
 ↳ side with respect to focal gene in addition to being repositioned
 ↳ to a new locus.

In the synteny plots, red blocks indicate the absence of the target gene,
 ↳ while green blocks mark its presence. Light blue blocks represent

- ↪ flanking genes that are conserved across lineages, and light purple
- ↪ blocks denote instances where a different flanking gene is present.

8 DNM3

Important gene stats

DNM3_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
DNM3	45.125	49.5403 +/- 3.10816	3.94183 +/- 0.256482	74.3804 +/- 12.3108	Yes	Naja_naja.SRR10428157.blast;Rhabdophis_nuchalis.SRR28573917.blast;

Intergenic distance phylogenetic signal evidence

DNM3_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
DNM3	355	17	338	0	1	0.999999999999809

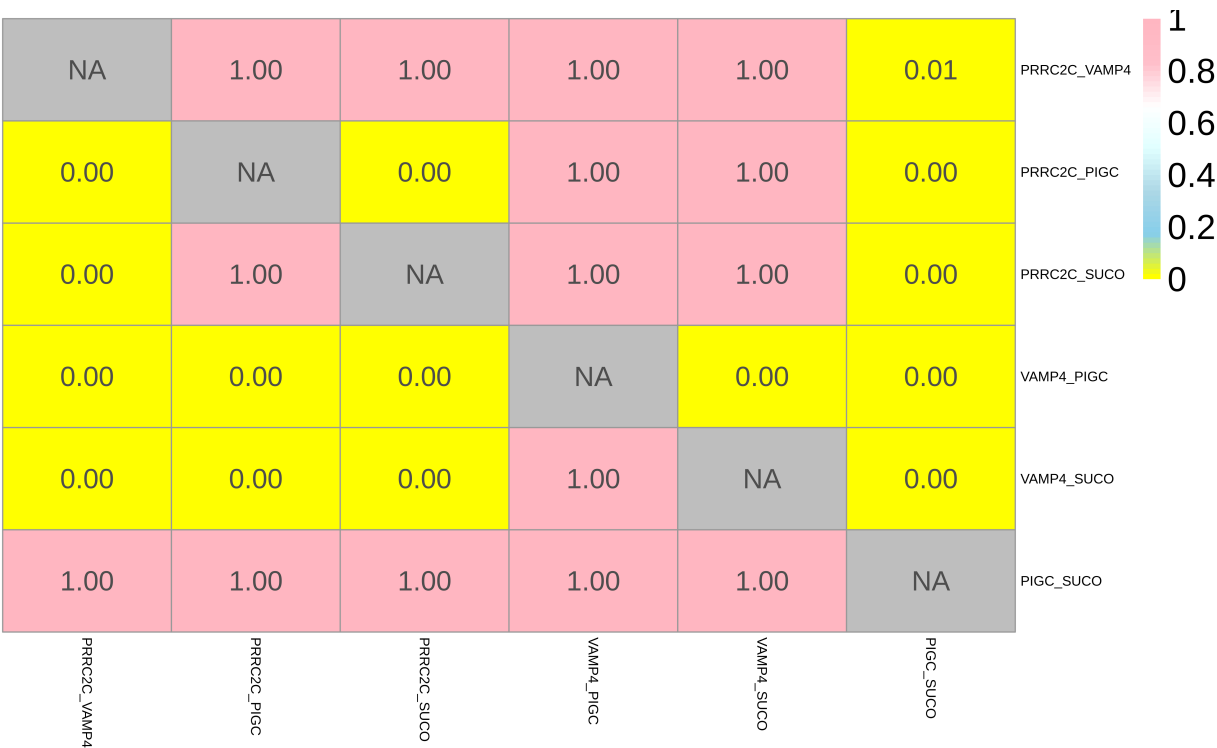


Figure 74: Heatmap_of_deletion_plot.png

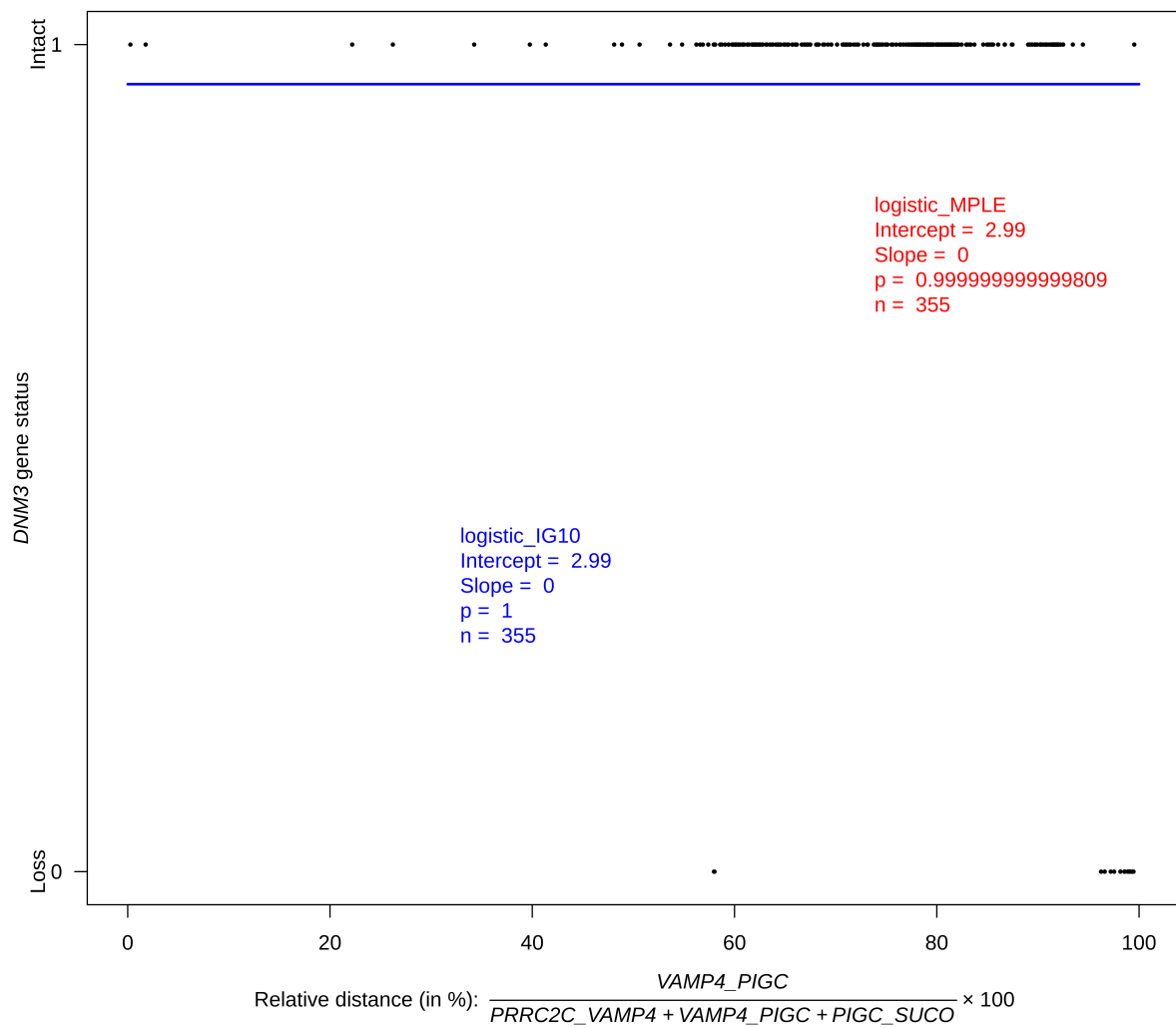


Figure 75: Phylogenetic_signal_of_deletion_plot.png

DNM3_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
DNM3	355	17	338	0	1	0.999999999999809

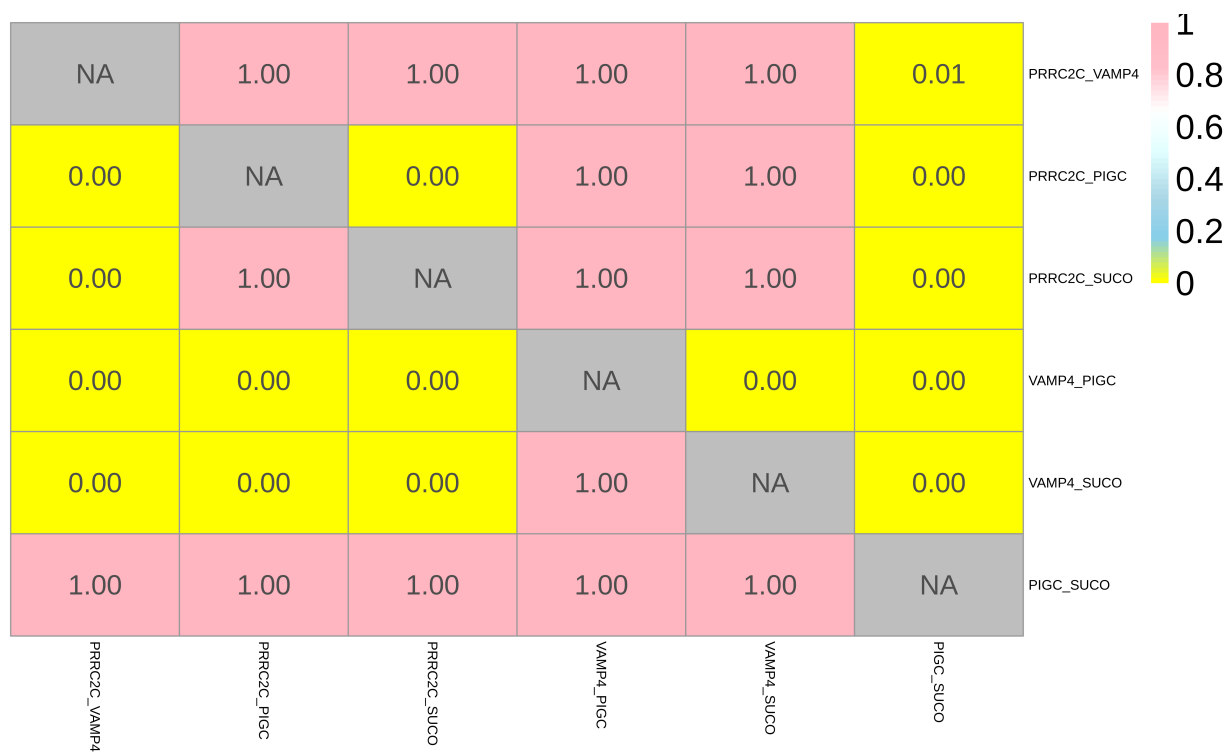


Figure 76: Heatmap_of_deletion_plot.png

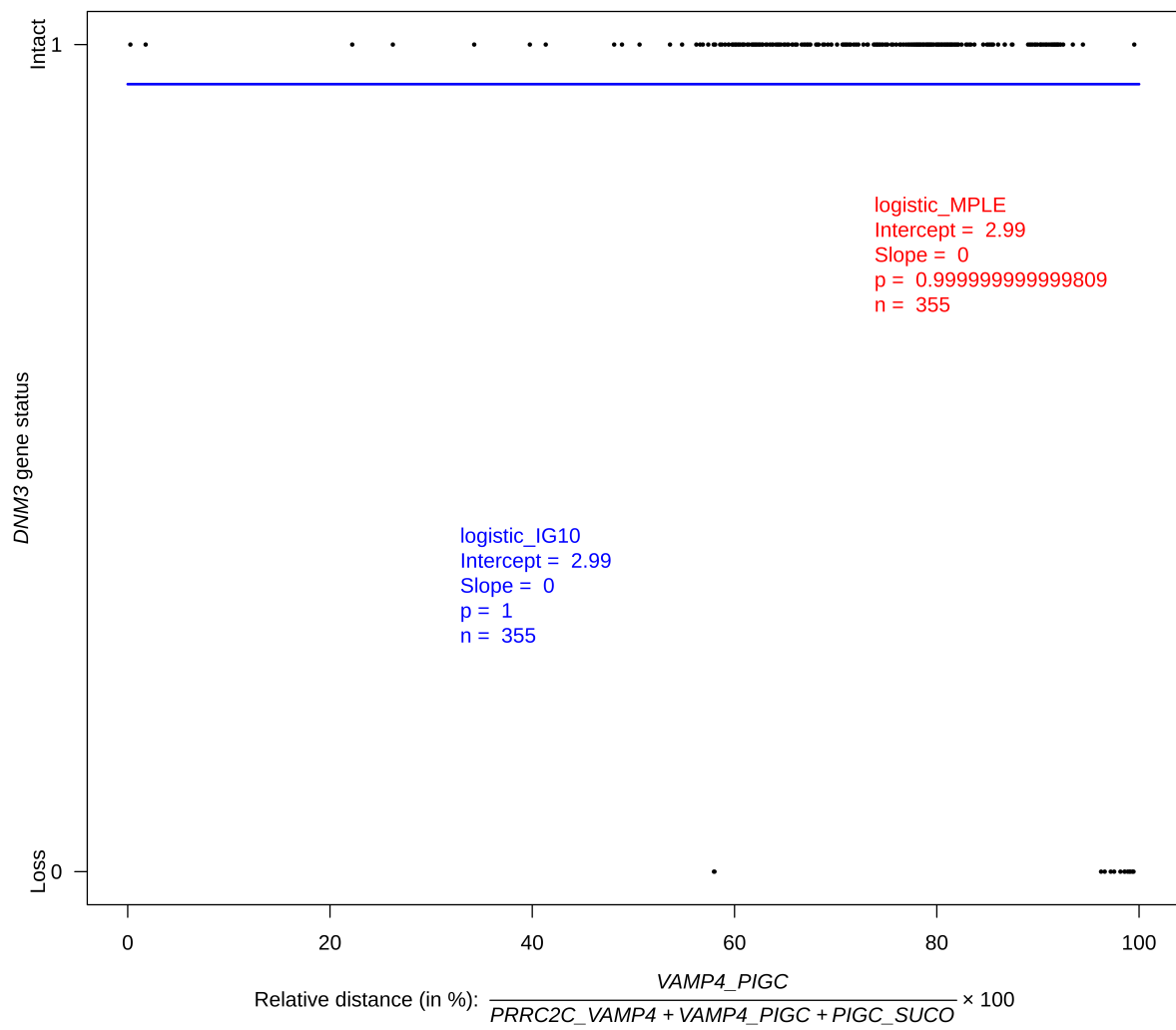


Figure 77: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence

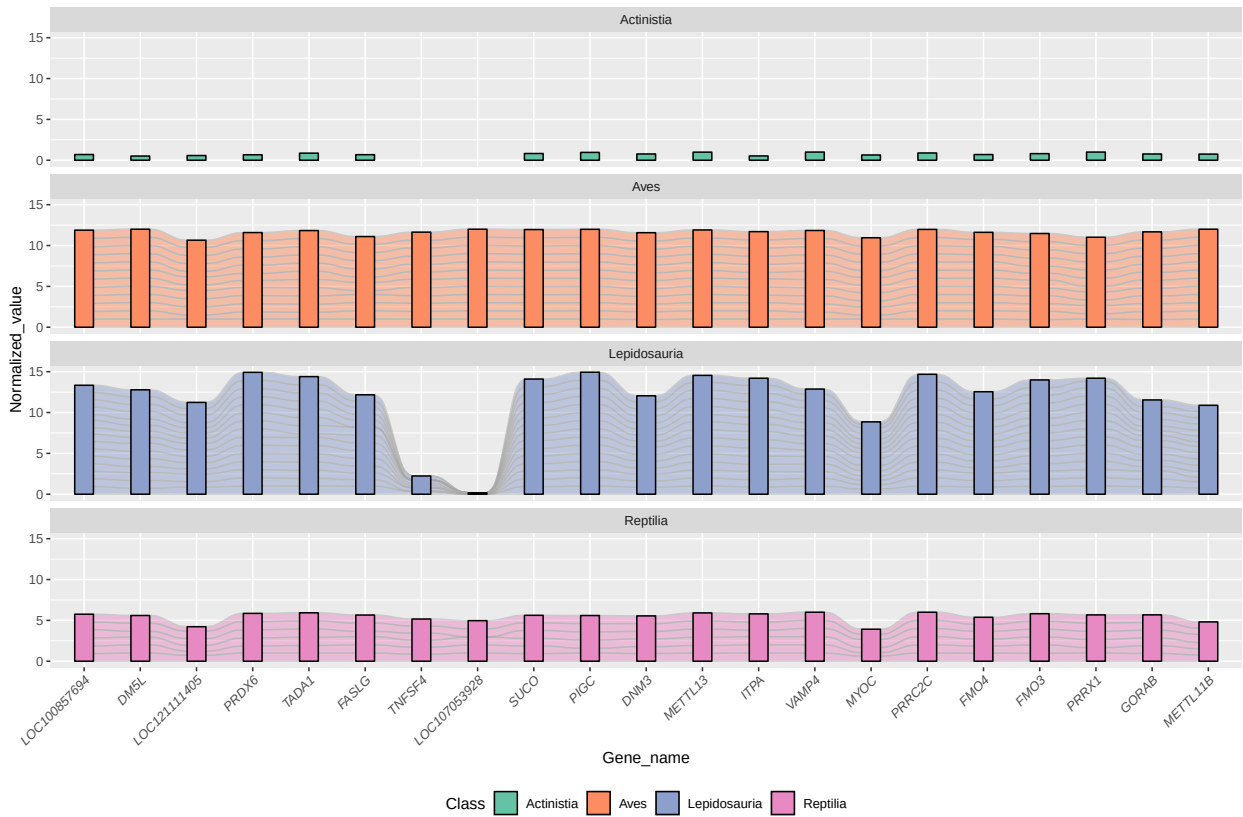


Figure 78: DNM3.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Lastz gene tree

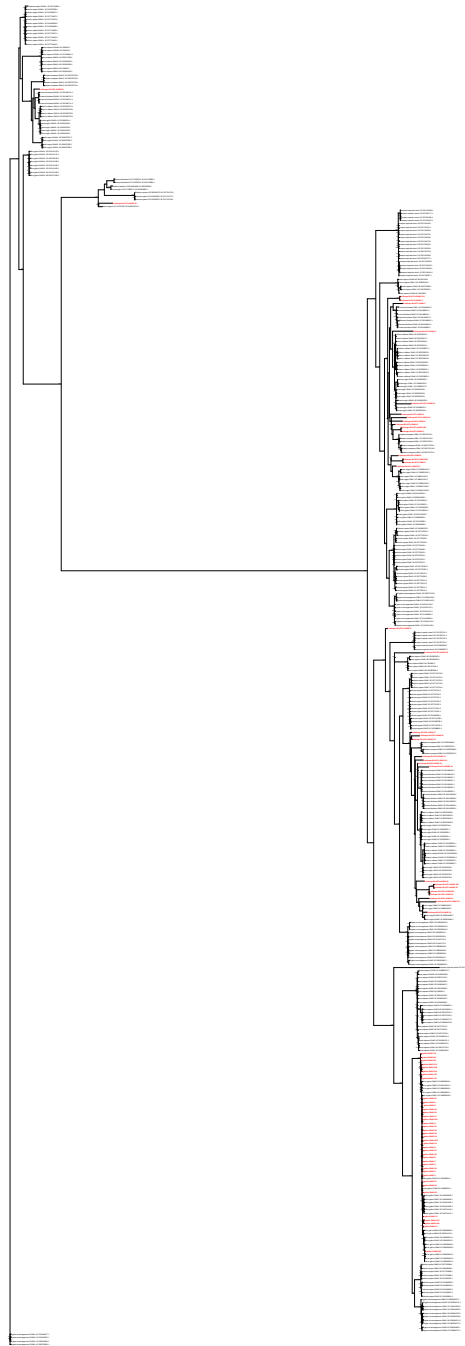


Figure 80: DNM3.combined.mafft.aln.highlighted.pdf

Syntenic evidence

	DNM3										
	dimethylarginine monooxygenase			allograft inflammatory vesicle-associated membrane protein 4			phosphatidylinositol glycan anchor biosynthesis class C				
<i>Chelonia mydas</i>	> LOC10293643 > PRRC2C >	> LOC11401978 < LOC10293664 >	> MITTL13 >	> DNM3 >	> LOC11866694 <	< PIGC <	> SUCO >				
	Chr 8 (NC_057854.1)										
<i>Gallus gallus</i>	< MYOC <	> VAMP4 >	> ITPA >	> MITTL13 >	> DNM3 >	< PIGC <	> SUCO >				
	Chr 8 (NC_052539.1)										
<i>Podarcis muralis</i>	> PRRC2C >	< MYOC <	< VAMP4 <	< ITPA <	> EE1F1AKNMT >	> DNM3 >	> UAP1 >	> DDR2 >	> HSD17B7 >	## syntenic genes are there on the opposite side after skipping certain genes	
	Chr 6 (NC_041317.1)										
<i>Anolis carolinensis</i> < fastig <	< SUCO <	> PRRC2C >	< VAMP4 <	< ITPA <	> MITTL13 >	> DNM3 >	> UAP1 >	> DDR2 >	> HSD17B7 >	## syntenic genes are scattered on the opposite flank	
	Chr 4 (NC_085844.1)										
<i>Pogona vitticeps</i>	> PRRC2C >	< MYOC <	< VAMP4 <	< ITPA <	> MITTL13 >	> DNM3 >	> UAP1 >	> DDR2 >	> HSD17B7 >	## syntenic genes are there on the opposite side after skipping certain genes	
	Chr 4 (NC_132825.1)										
<i>Crotalus tigris</i>	> PRRC2C >	< MYOC <	< VAMP4 <	< ITPA <	> EE1F1AKNMT >	> DNM3 >	> UAP1 >	> DDR2 >	> LOC1203105 > > HSD17B7 >	### SYNTENIC GENE PRESENT ON NW_024100509.1 (unplaced) SCAFFOLD	
	NW_024056887.1 (unplaced)										
	diacyclin domain receptor tyrosine kinase 2										
<i>Ornithorynchus</i> > PRRC2C >	> MYOCOS >	< MYOC <	< VAMP4 <	> ITPA >	> EE1F1AKNMT >	> DNM3 >	< PIGC <	> SUCO >			
	Chr 16 (NC_041743.1)										
	PSEUDO GENE										
<i>Homo sapiens</i>	< MYOC <	> VAMP4 >	> MITTL13 >	> RPS19P3 >	> DNM3 >	< DNM3OS <	< LOC102724528 <	> C1orf105 >	< PIGC <	> SUCO >	
	Chr 1 (NC_000001.11)										
<i>Mus musculus</i>	> PRRC2C >	> MYOCOS >	< MYOC <	> VAMP4 >	> MITTL13 >	> DNM3 >	> 4930558K2GR <	< PIGC <	> SUCO >		

Figure 81: DNM3.pdf

DNM3.txt

Synteny analysis of DNMT3

The DNMT3 syntenic block, which is conserved in outgroups like *Chelonia mydas* and *Gallus gallus*, has undergone significant rearrangements in squamates. In lizards such as *Podarcis muralis* and *Pogona vitticeps*, the syntenic genes have been inverted and moved to a new location on the same chromosome. A similar inversion and scattering of the flanking genes is observed in *Anolis carolinensis*. Similarly, in *Crotalus tigris*, where the syntenic block is fragmented across at least two different unplaced scaffolds.

In the synteny plots, red blocks indicate the absence of the target gene,
→ while green blocks mark its presence. Light blue blocks represent
→ flanking genes that are conserved across lineages, and light purple
→ blocks denote instances where a different flanking gene is present.
→ A bright yellow color indicates a change in the gene's orientation.

9 ELOVL3

Assembly verification Evidence

Crotalus_tigris-PacBio

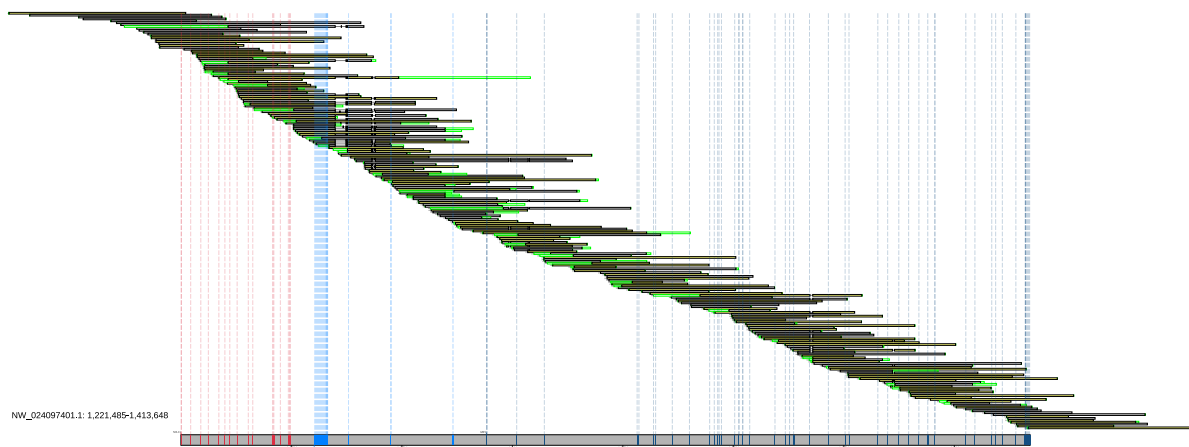


Figure 82: ELOVL3:NW_024097401.1:1221485-1413648.pdf

Podarcis_muralis-PacBio

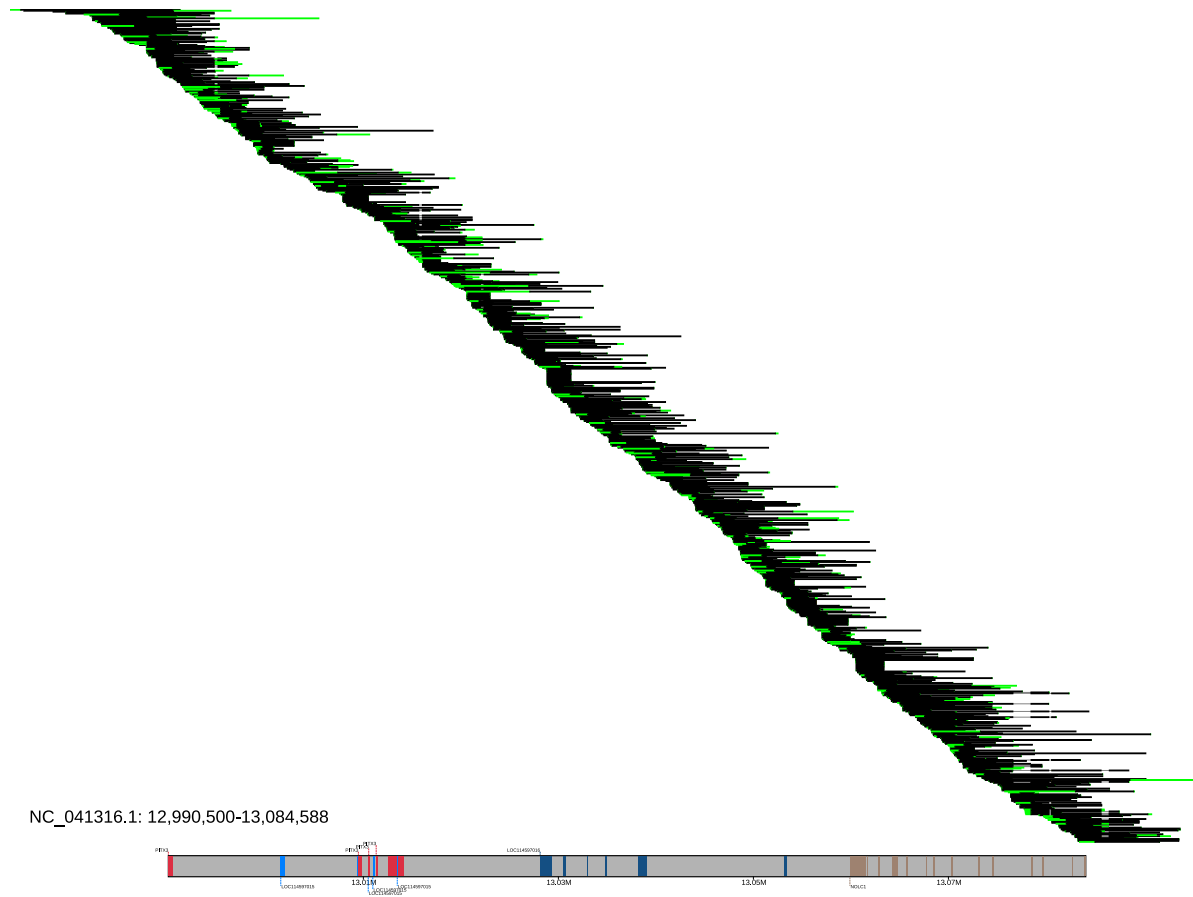


Figure 83: ELOVL3:NC_041316.1:12990500-13084588.pdf

Pogona_vitticeps-Nanopore

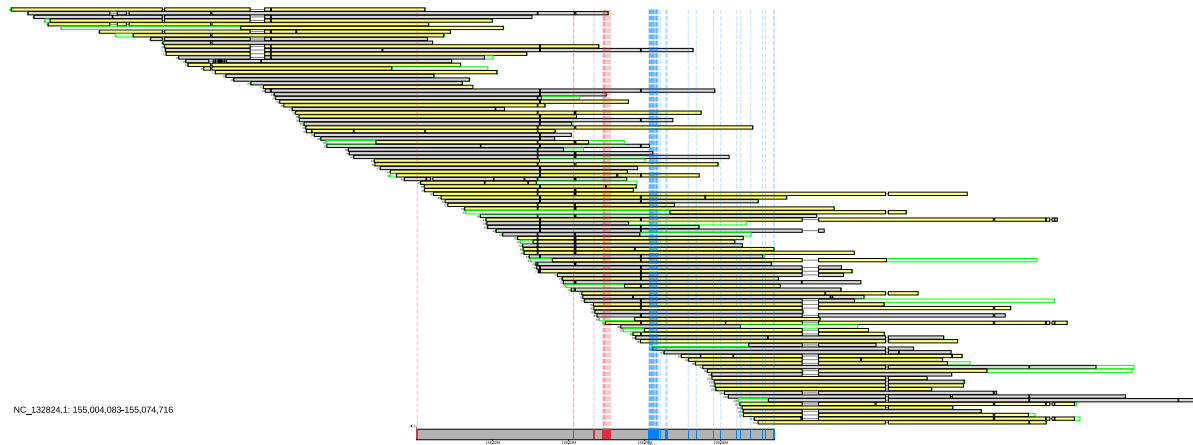


Figure 84: ELOVL3:NC_132824.1:155004083-155074716.pdf

Important gene stats

ELOVL3_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
ELOVL3	15.48175182	49.773 +/- 3.19973	3.79555 +/- 0.218244	74.2877 +/- 15.4959	Yes	ELOVL6;

Intergenic distance phylogenetic signal evidence

ELOVL3_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
ELOVL3	213	12	201	5	1	0.999999999999985



Figure 85: Heatmap_of_deletion_plot.png

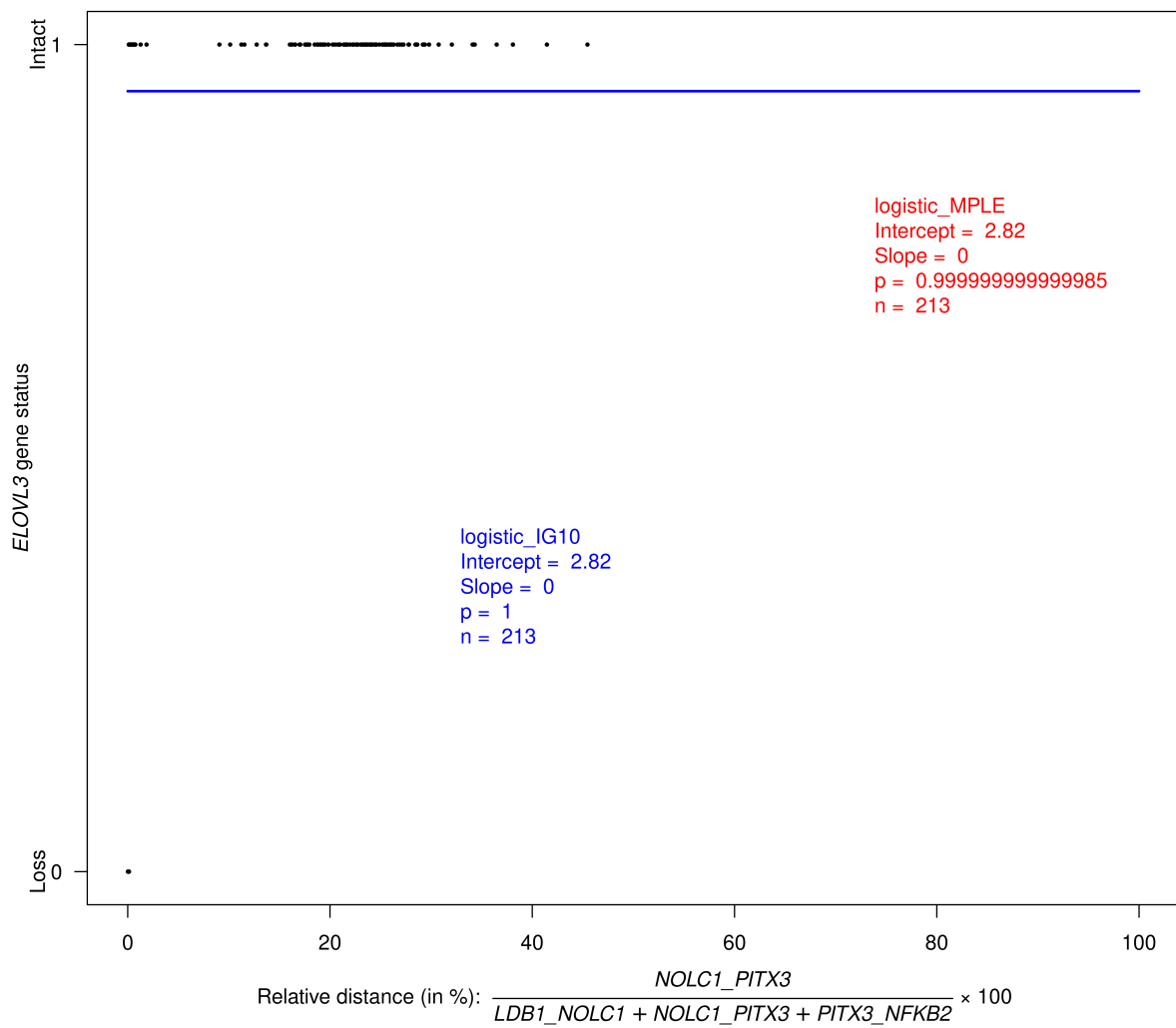


Figure 86: Phylogenetic_signal_of_deletion_plot.png

ELOVL3_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
ELOVL3	213	12	201	5	1	0.999999999999985

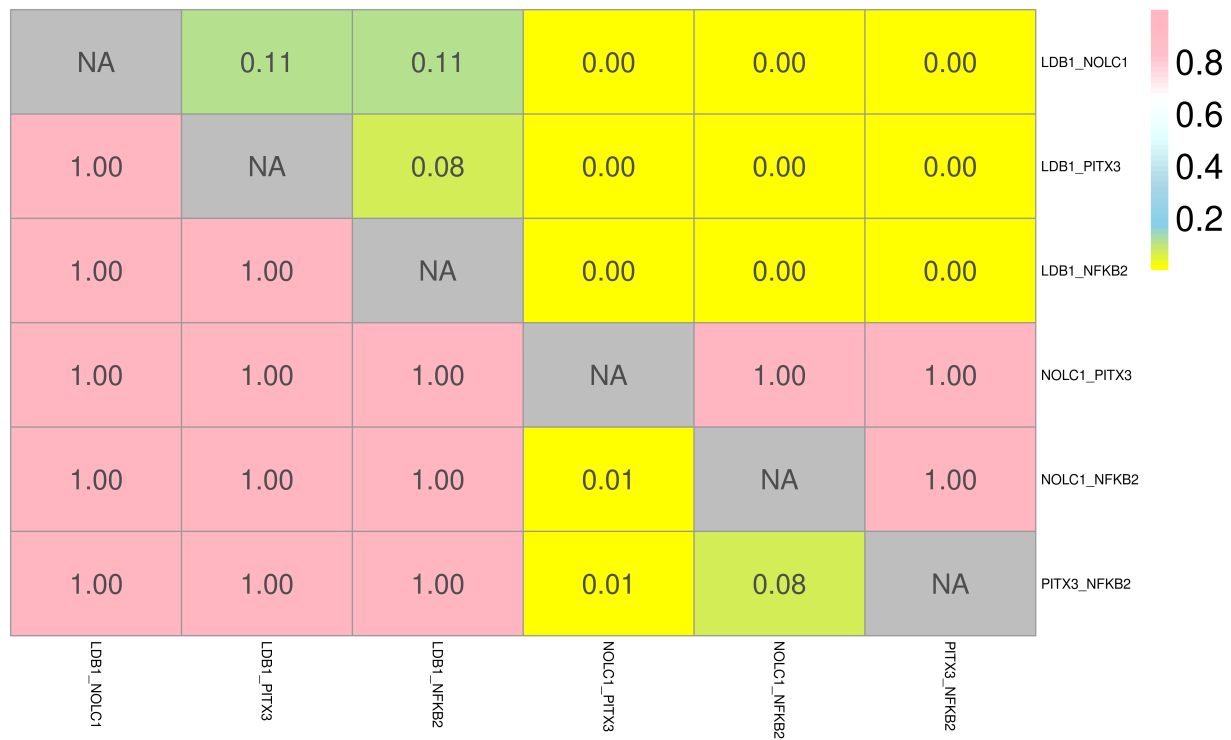


Figure 87: Heatmap_of_deletion_plot.png

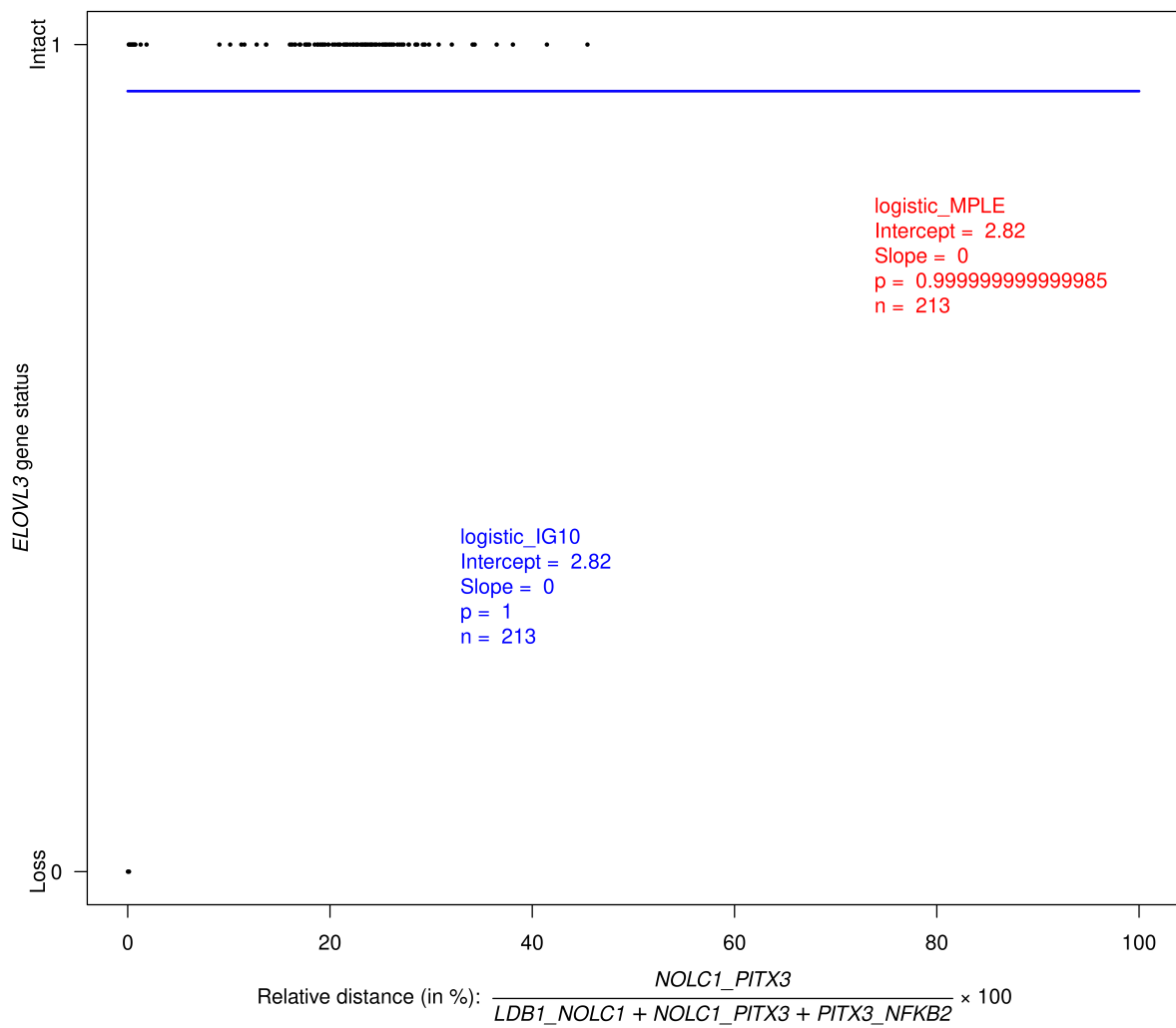


Figure 88: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence

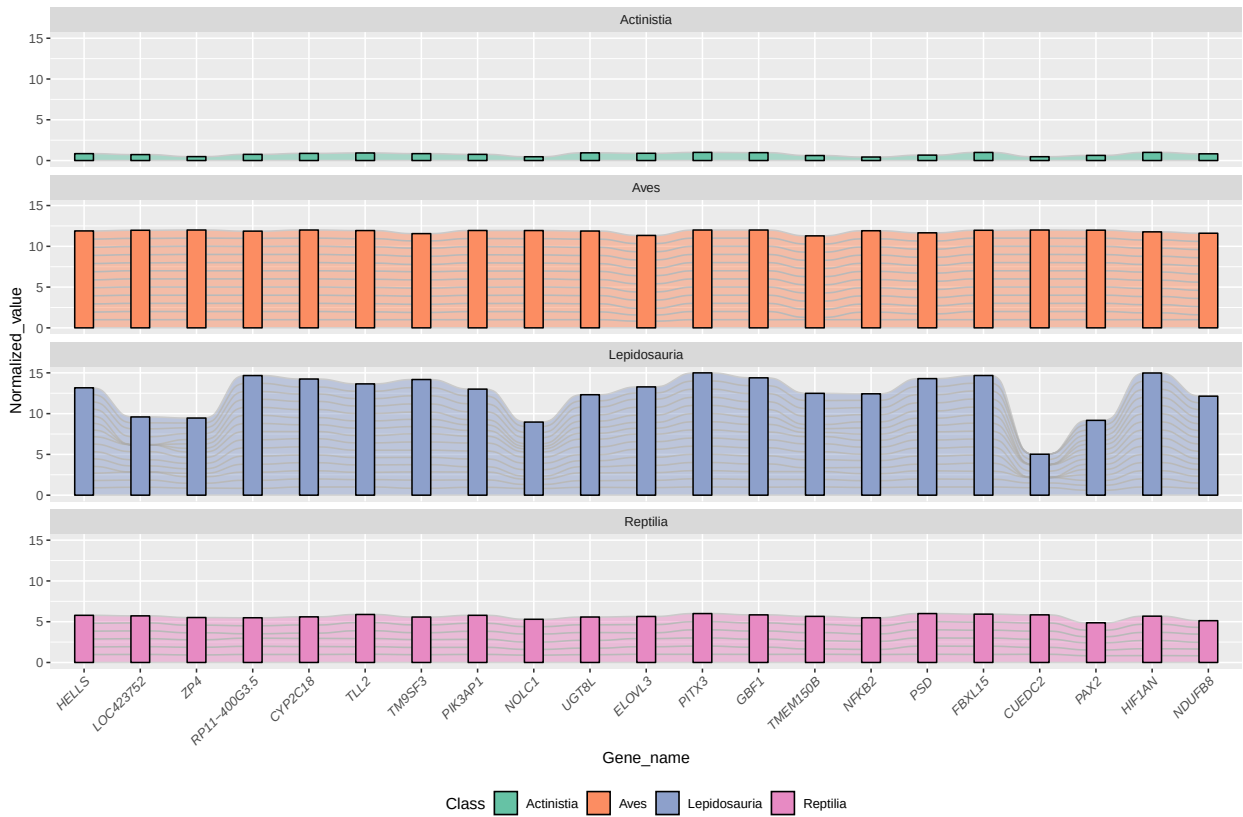


Figure 89: ELOVL3.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Lastz gene tree

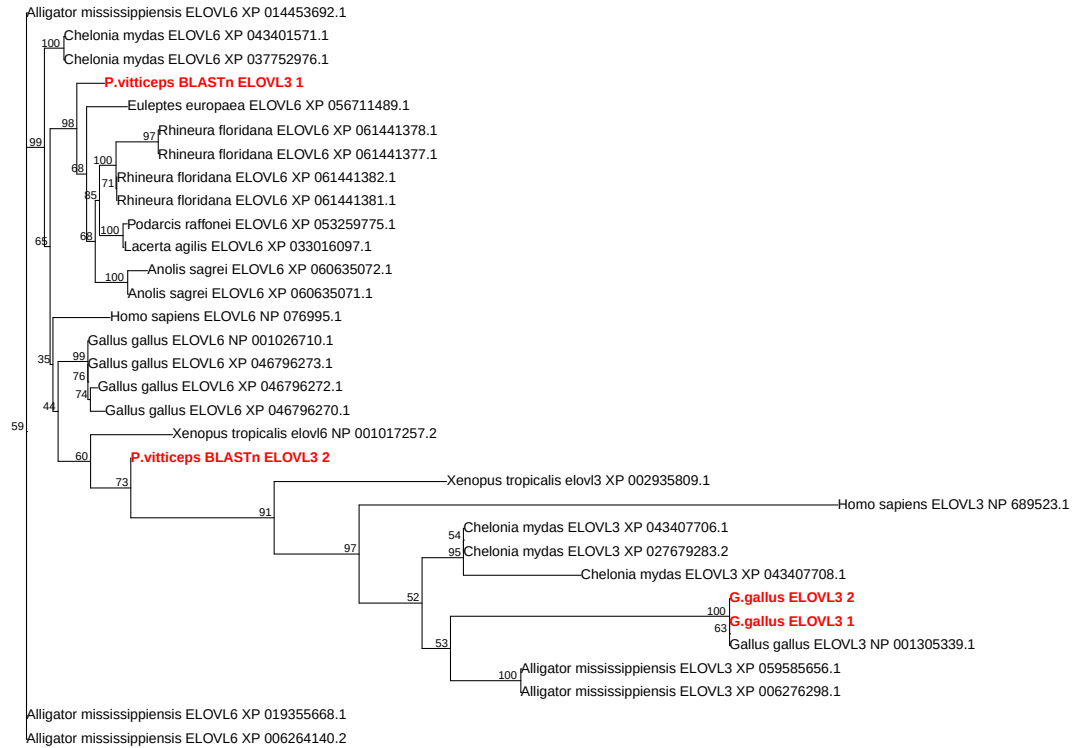


Figure 91: ELOVL3.combined.mafft.aln.highlighted.pdf

Syntenic evidence



Figure 92: ELOVL3.pdf

ELOVL3.txt

Synteny analysis of ELOVL3

We analyzed the synteny of ELOVL3 in squamates and representative outgroups. The ELOVL3 syntenic block is conserved, with few different genes in flank in some lineages. In the synteny plots, red blocks indicate the absence of ELOVL3, green blocks mark its presence, light blue blocks represent genes conserved across lineages, and light purple blocks denote different flanking genes.

Transcriptomic evidence *Pogona vitticeps*



Figure 93: ELOVL3.png

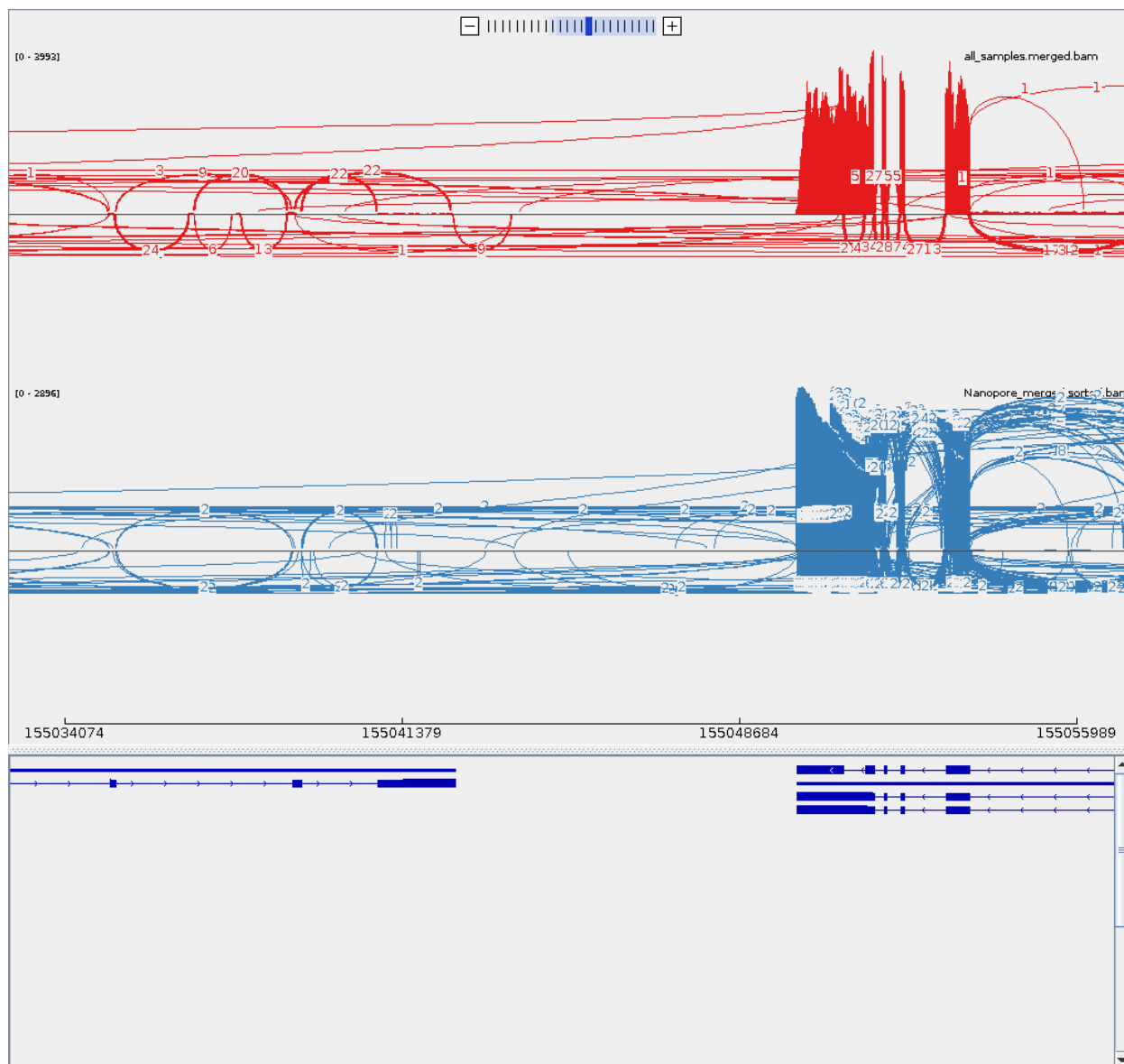


Figure 94: ELOVL3_Shash.png

10 **FREM2**

Important gene stats

FREM2_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
FREM2	57.92830189	51.3994 +/- 3.34555	3.9797 +/- 0.234791	81.0875 +/- 9.49476	Yes	FREM3;

Lastz Alignment evidence

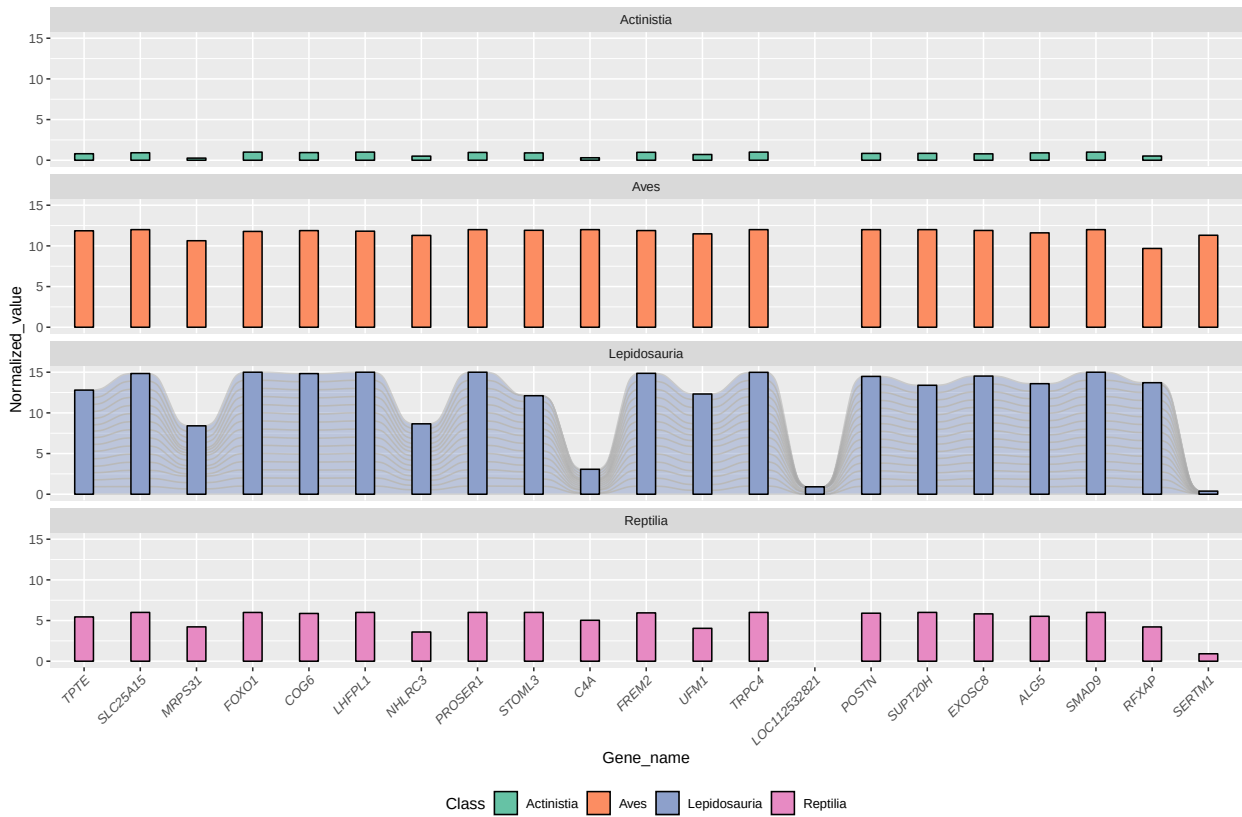


Figure 95: FREM2.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Lastz gene tree

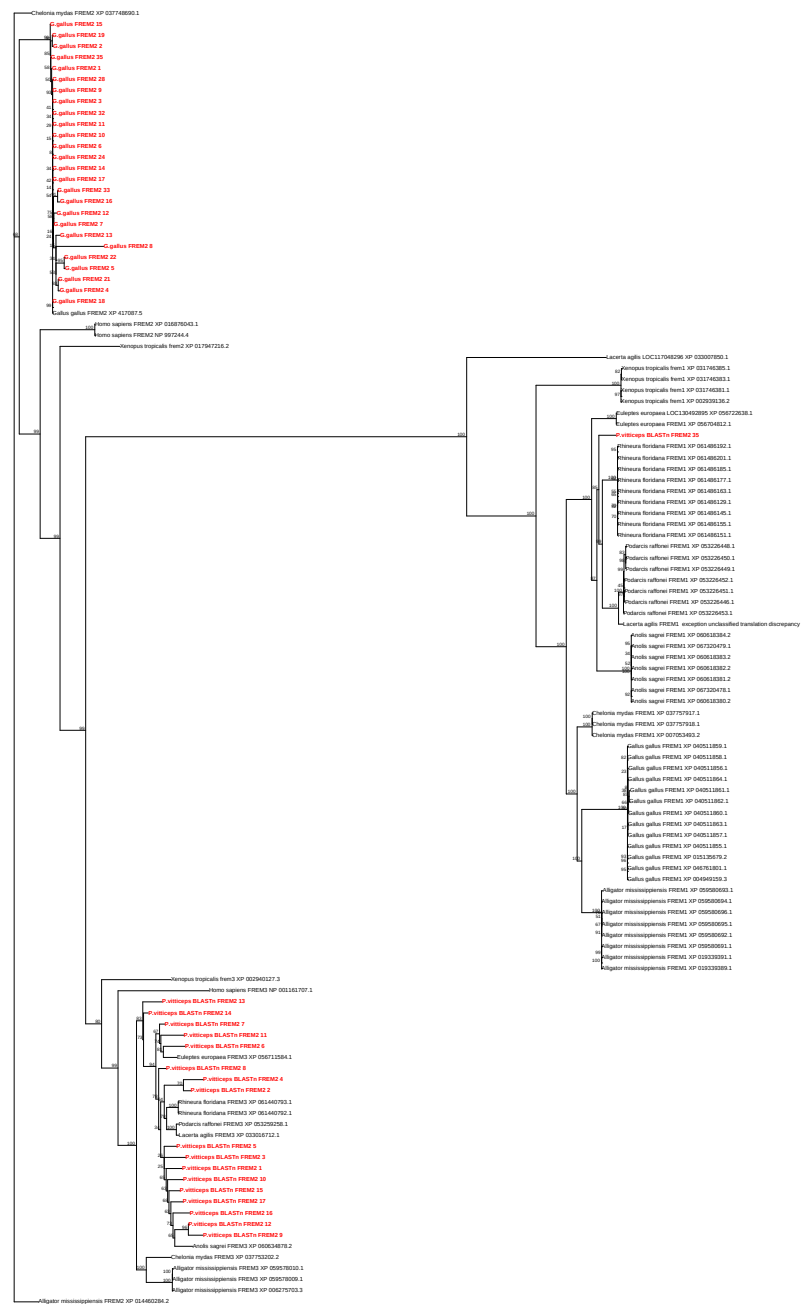


Figure 97: FREM2.combined.mafft.aln.highlighted.pdf

Syntenic evidence

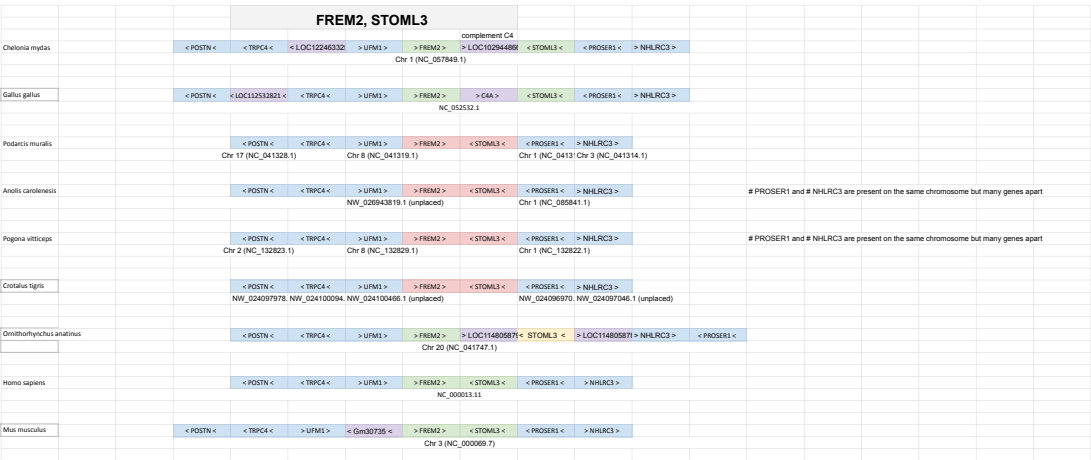


Figure 98: FREM2.pdf

FREM2.txt

Synteny analysis of FREM2

The syntenic genes for FREM2 are located on multiple chromosomes,
→ indicating an interchromosomal rearrangement. Additionally, one of
→ the flanking genes also shows evidence of an intrachromosomal
→ rearrangement.

In the synteny plots, red blocks indicate the absence of the target gene,
→ while green blocks mark its presence. Light blue blocks represent
→ flanking genes that are conserved across lineages, and light purple
→ blocks denote instances where a different flanking gene is present.

11 GPR78

Assembly verification Evidence

Crotalus_tigris-PacBio

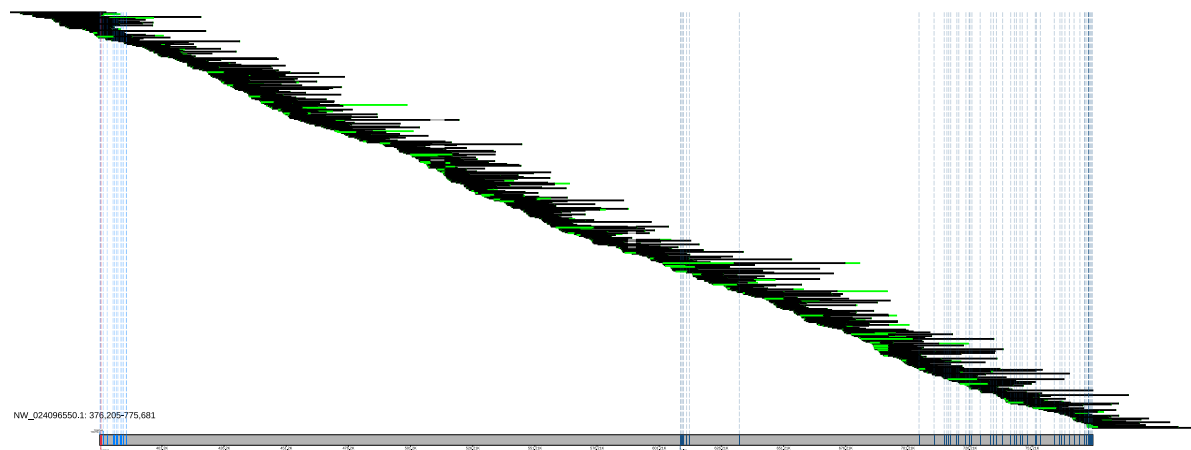


Figure 99: GPR78:NW_024096550.1:376205-775681.pdf

Podarcis_muralis-PacBio

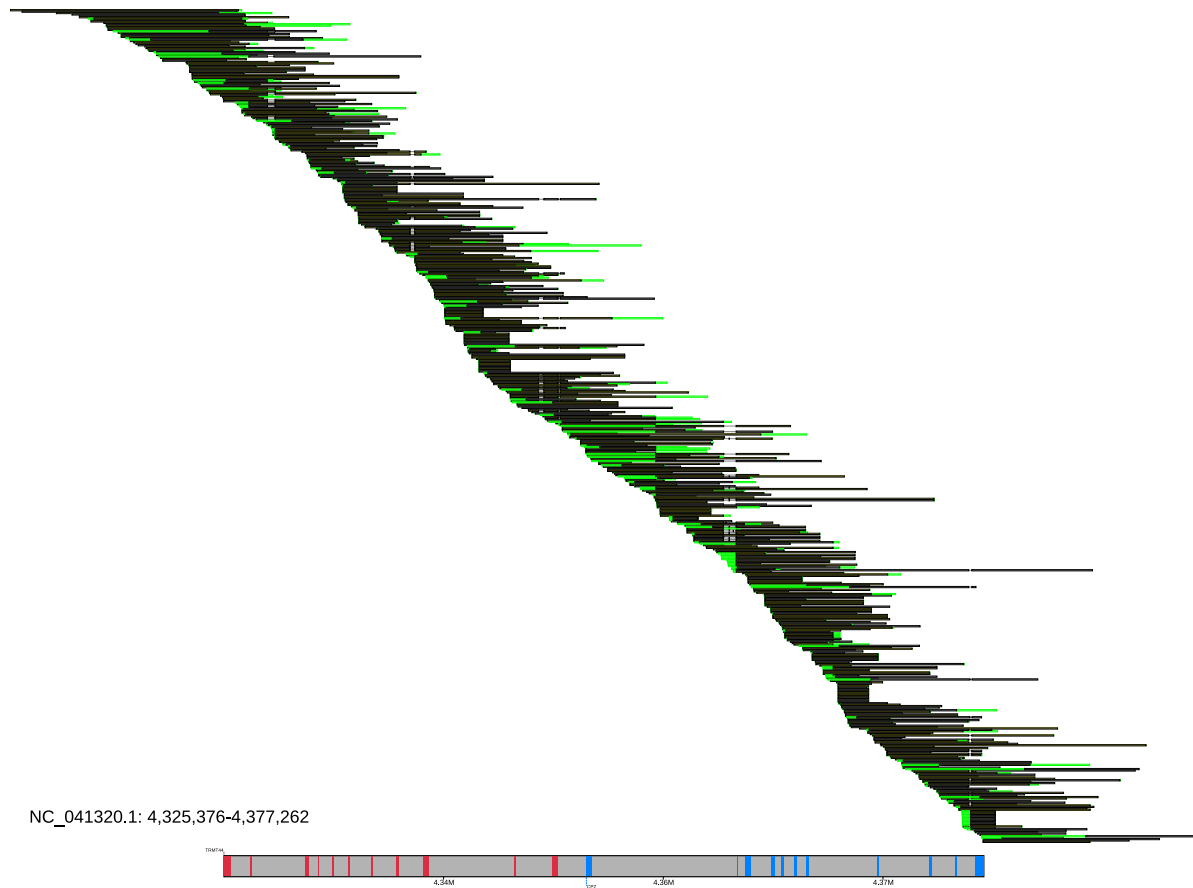


Figure 100: GPR78:NC_041320.1:4325376-4377262.pdf

Pogona_vitticeps-Nanopore

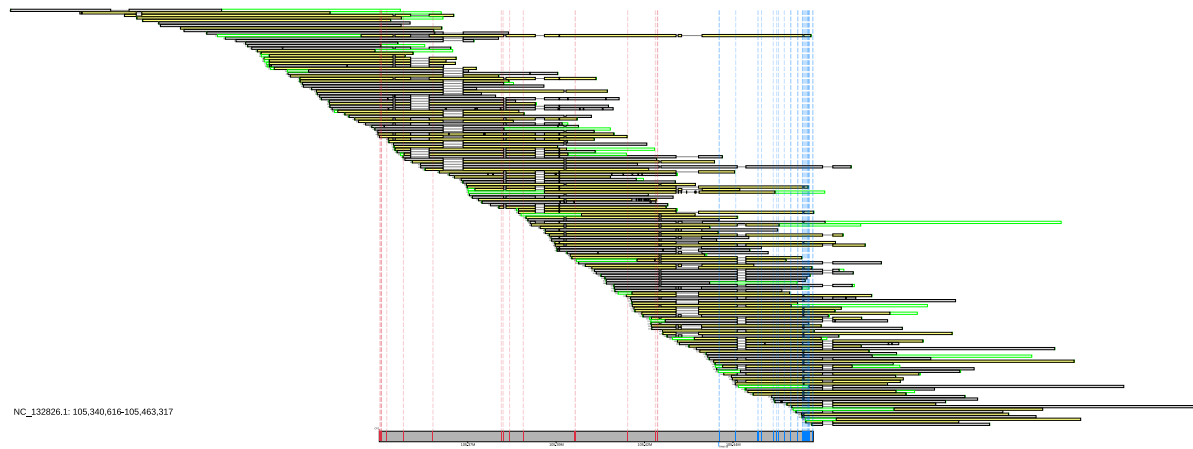


Figure 101: GPR78:NC_132826.1:105340616-105463317.pdf

Important gene stats

GPR78_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
GPR78	4.29787234	52.6397 +/- 7.43689	3.93229 +/- 0.387976	62.9799 +/- 13.5948	Yes	GPR26;

Intergenic distance phylogenetic signal evidence

GPR78_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
GPR78	163	14	149	0	0.279131481259864	0.981726340989877

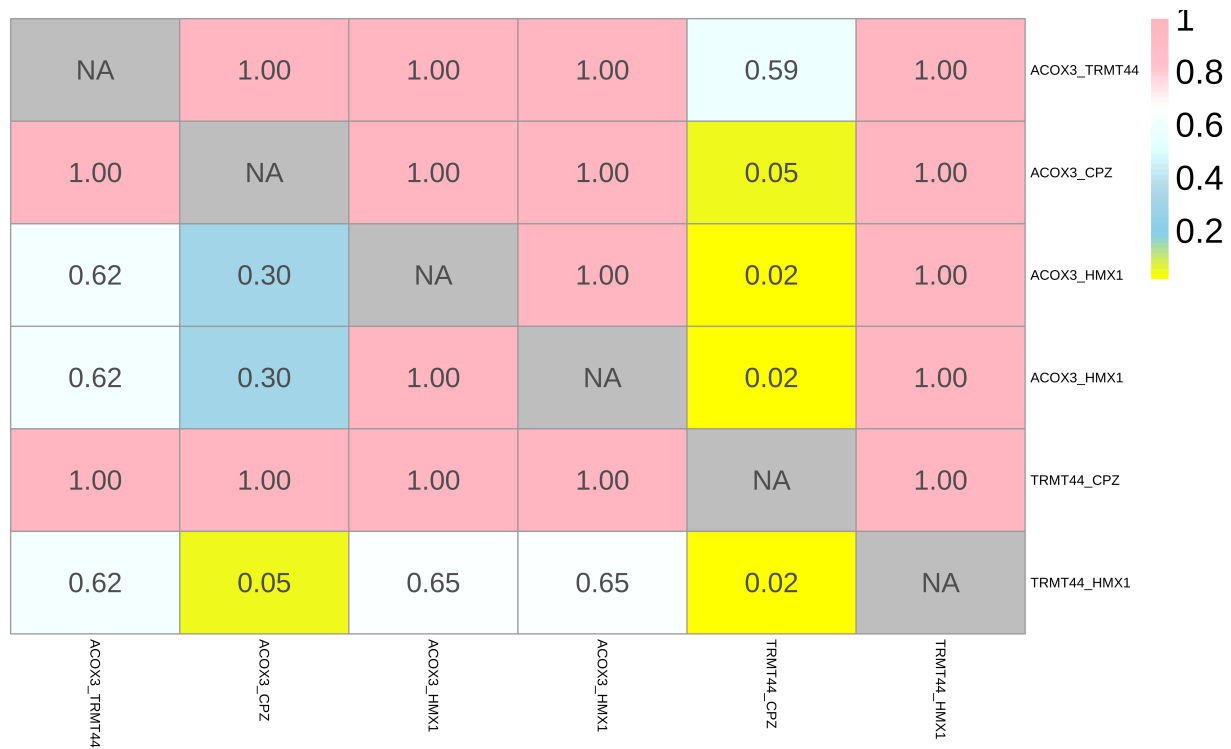


Figure 102: Heatmap_of_deletion_plot.png

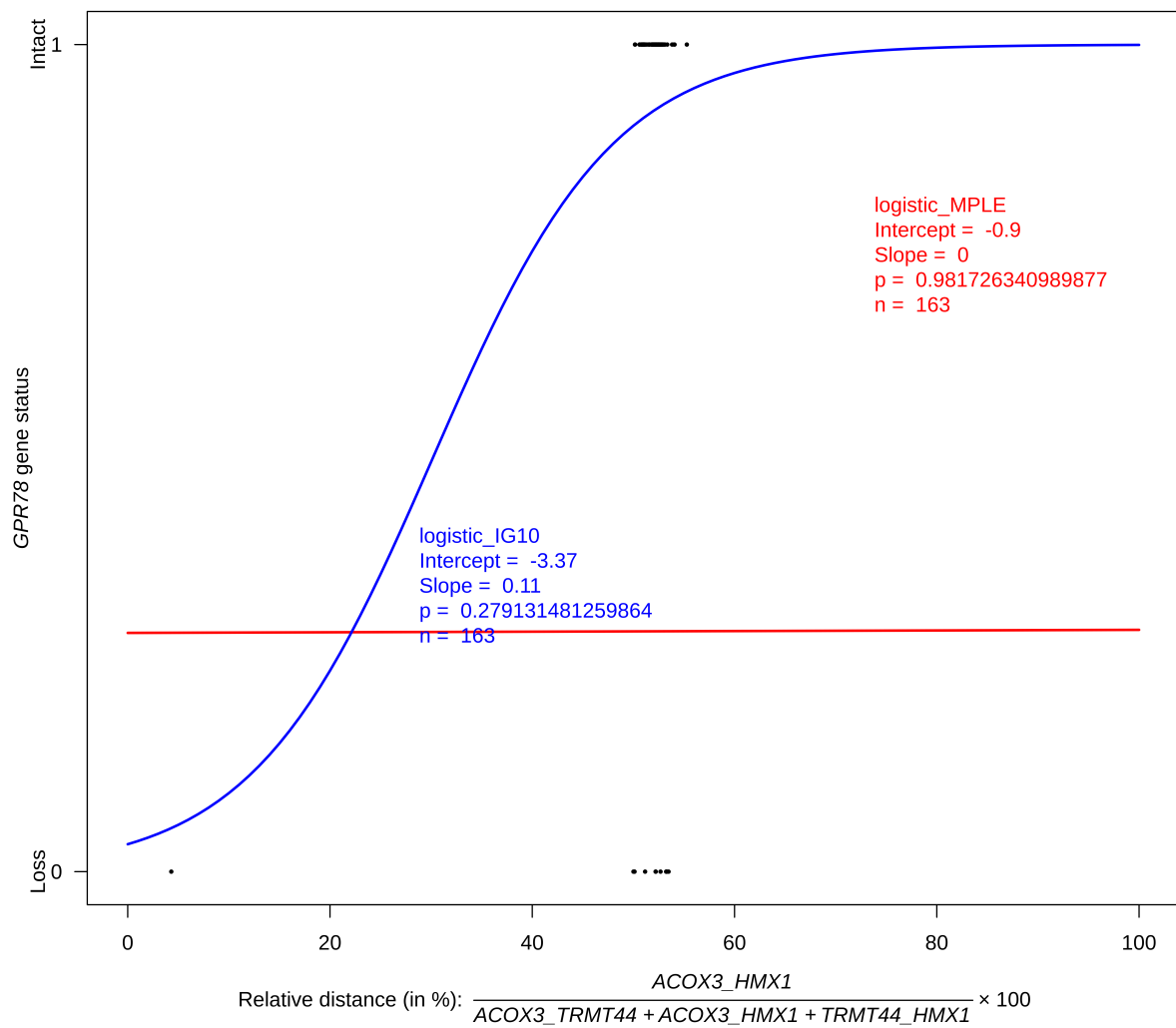


Figure 103: Phylogenetic_signal_of_deletion_plot.png

GPR78_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
GPR78	163	14	149	0	0.279131481259864	0.981726340989877

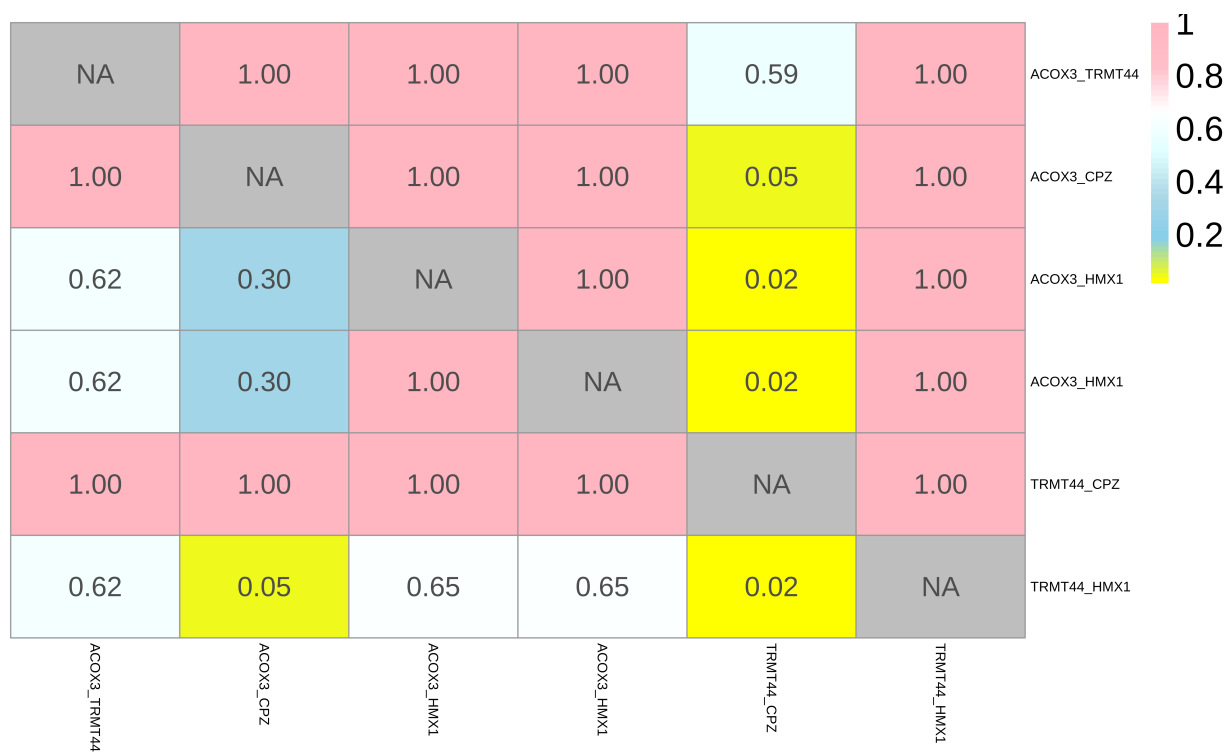


Figure 104: Heatmap_of_deletion_plot.png

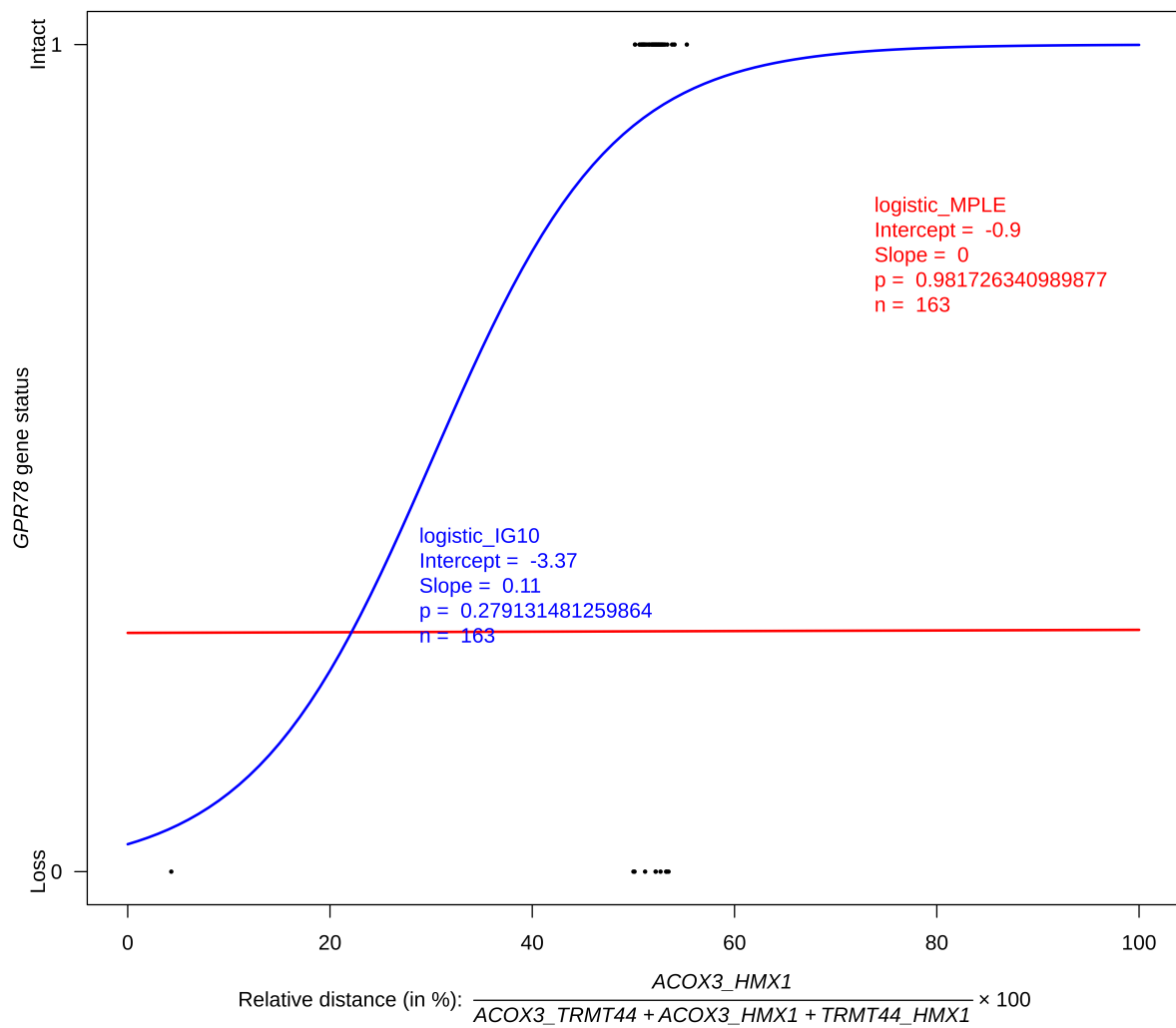


Figure 105: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence

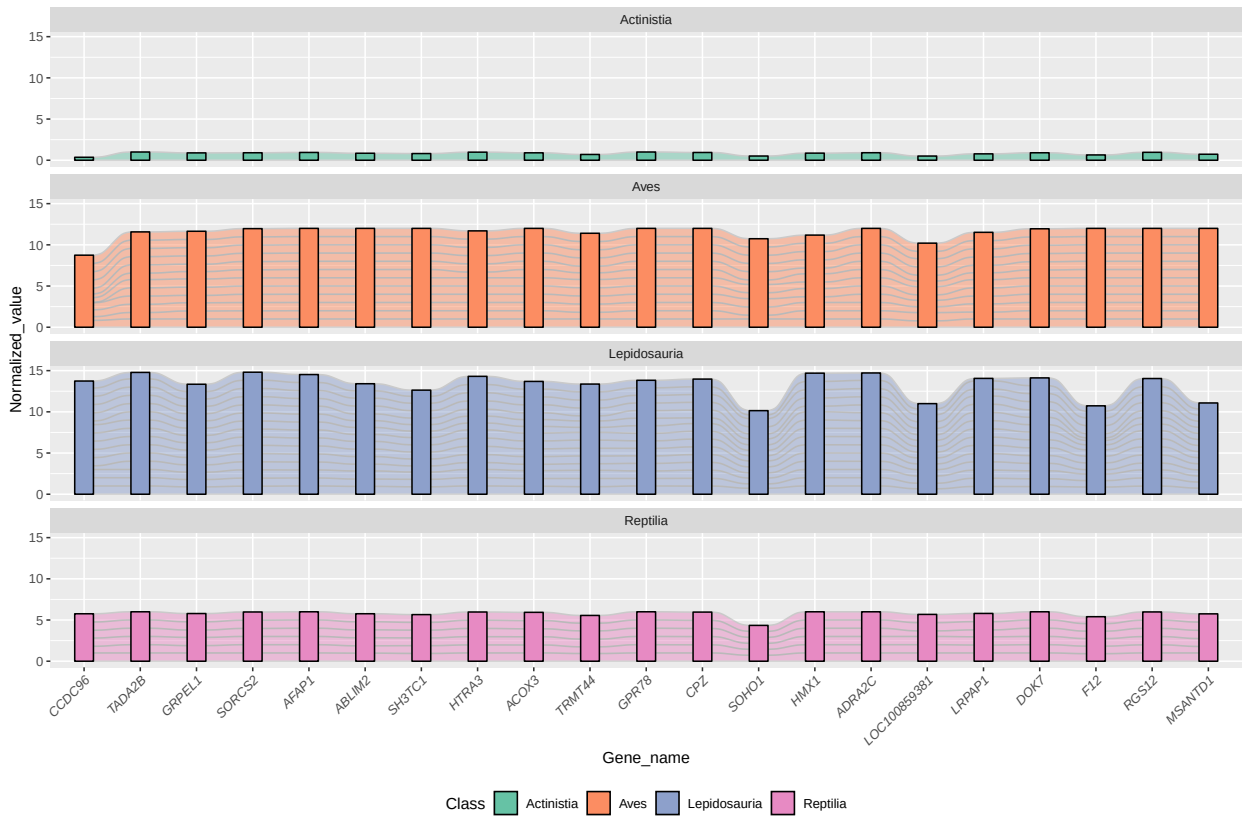


Figure 106: GPR78.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

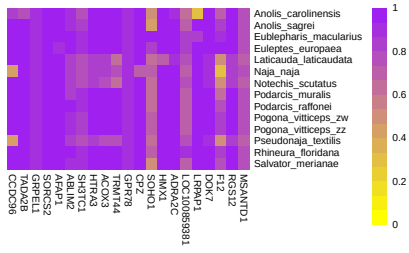


Figure 107: GPR78.FS_Exonic.Final.Gallus_gallus.21_genes_heatmap.pdf

Lastz gene tree

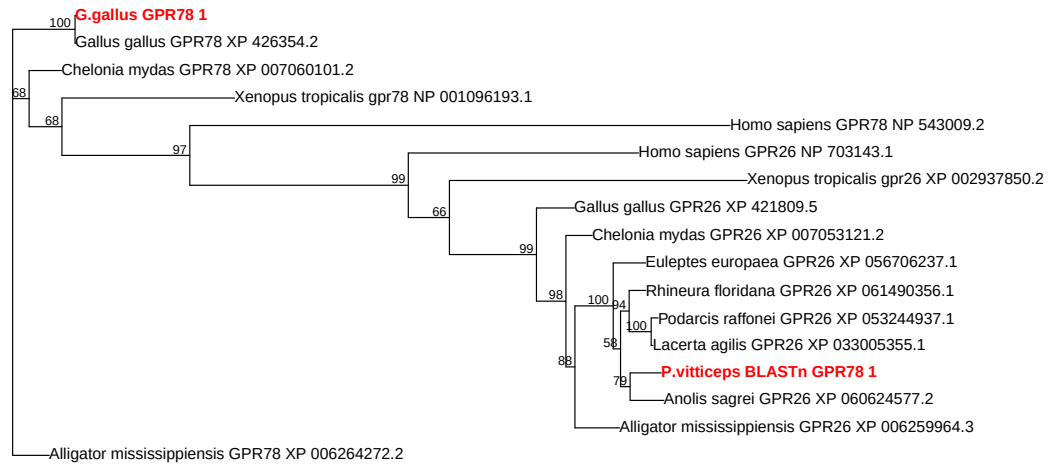


Figure 108: GPR78.combined.mafft.aln.highlighted.pdf

Syntenic evidence



Figure 109: GPR78.pdf

GPR78.txt

Synteny analysis of GPR78

We analyzed the synteny of GPR78 in squamates and representative outgroups

- . The GPR78 syntenic block is conserved, except for one flanking
- gene in *Crotalus tigris*. In the synteny plots, red blocks indicate
- the absence of GPR78, green blocks mark its presence, light blue
- blocks represent genes conserved across lineages, and light purple
- blocks denote different flanking genes.

Transcriptomic evidence *Pogona vitticeps*

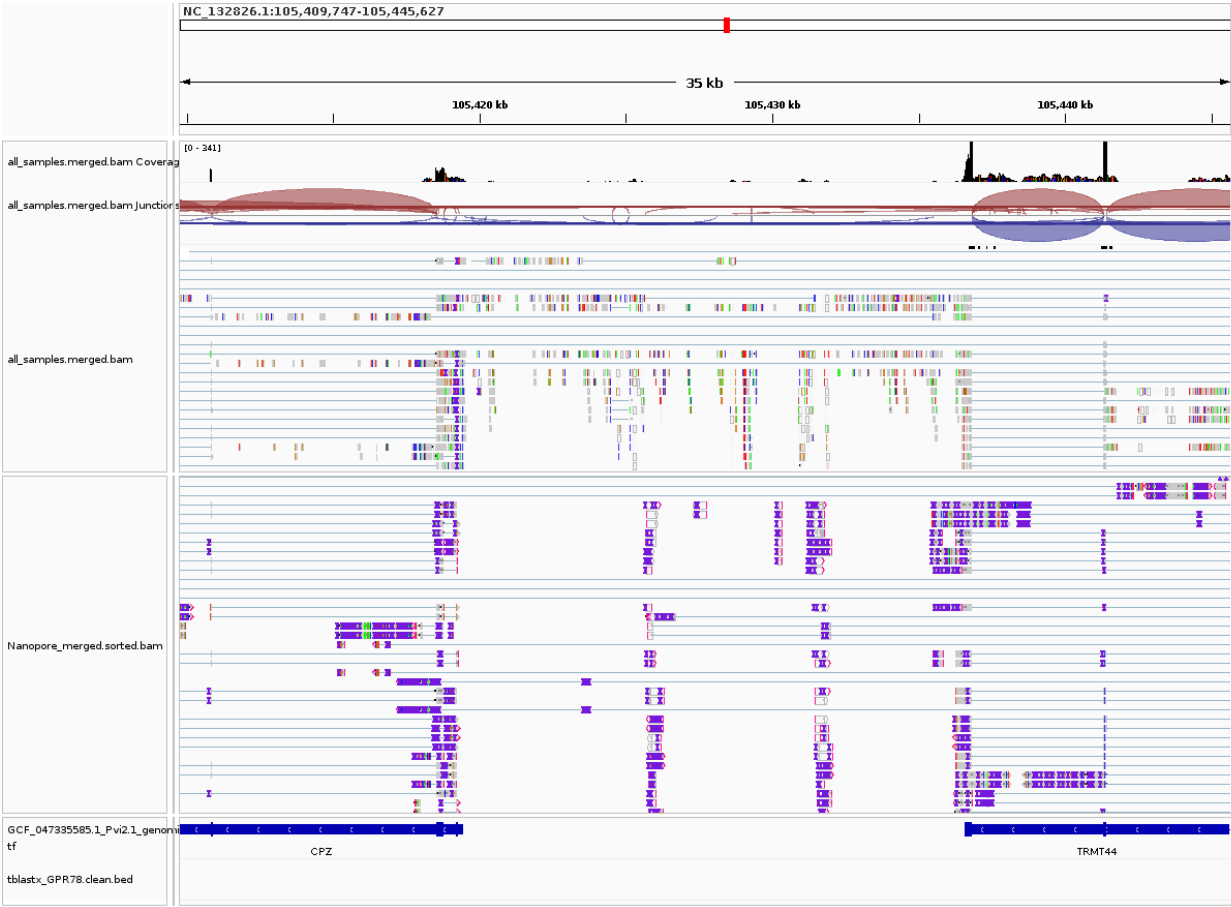


Figure 110: GPR78.png

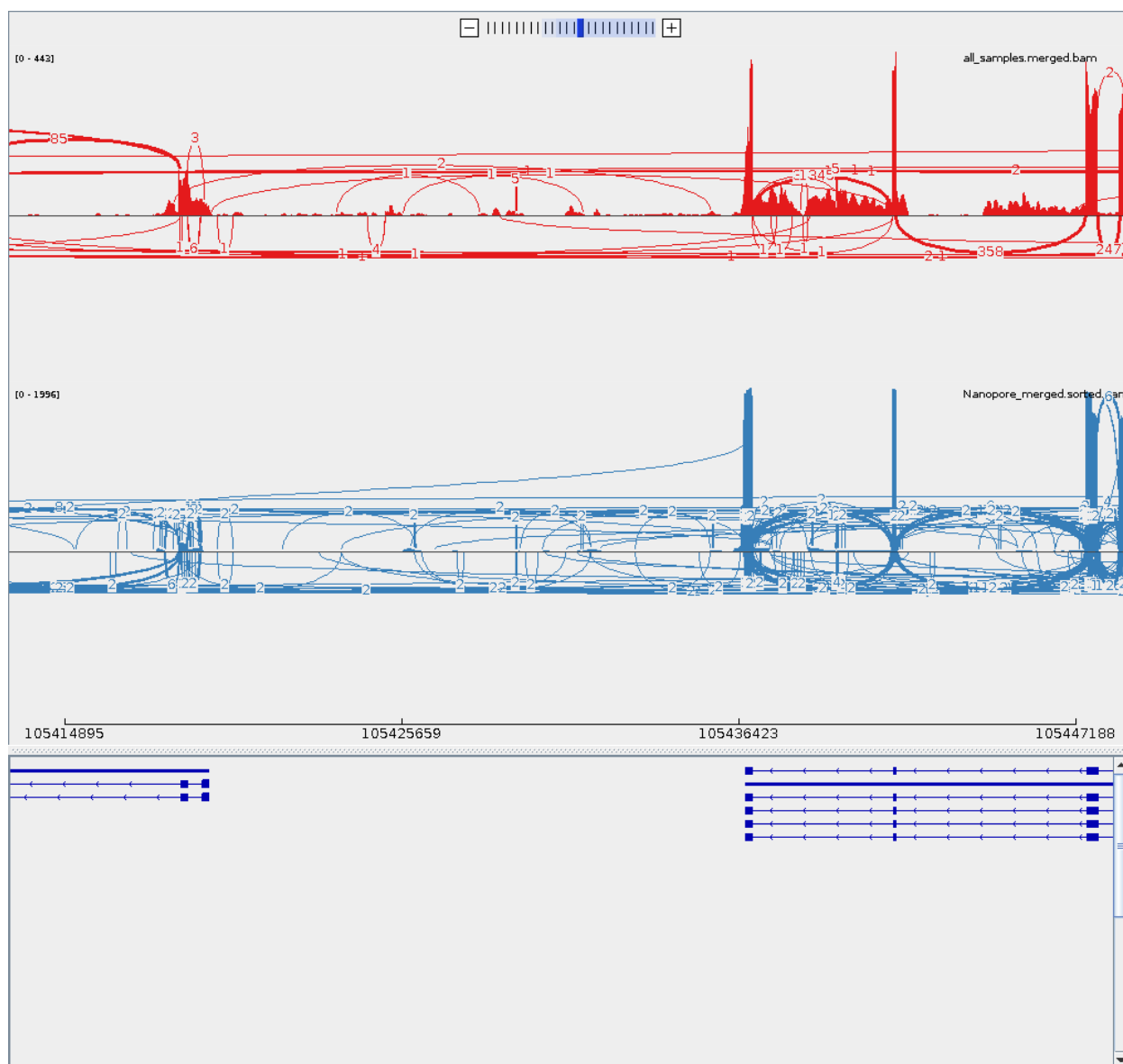


Figure 111: GPR78_Shash.png

12 GPR82

Crotalus_tigris-PacBio

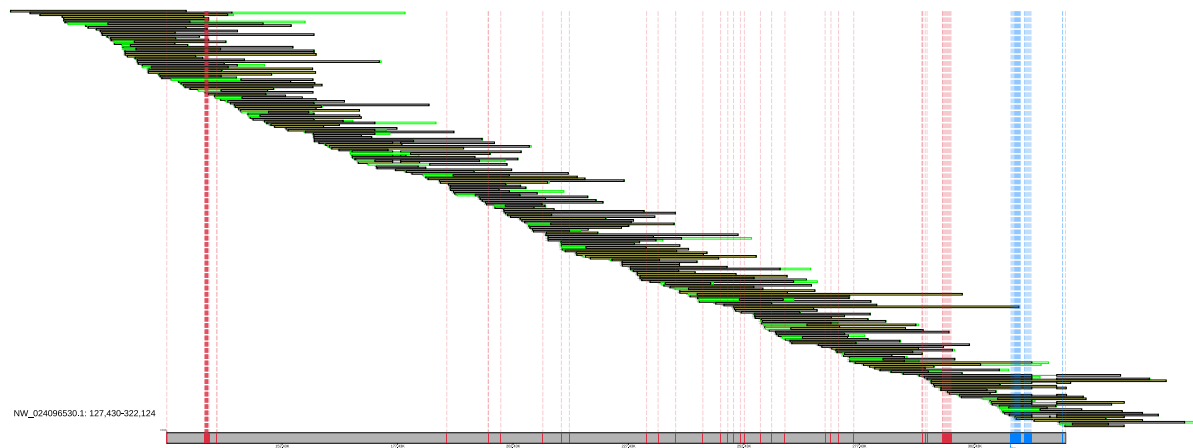


Figure 112: GPR82:NW_024096530.1:127430-322124.pdf

Podarcis_muralis-PacBio

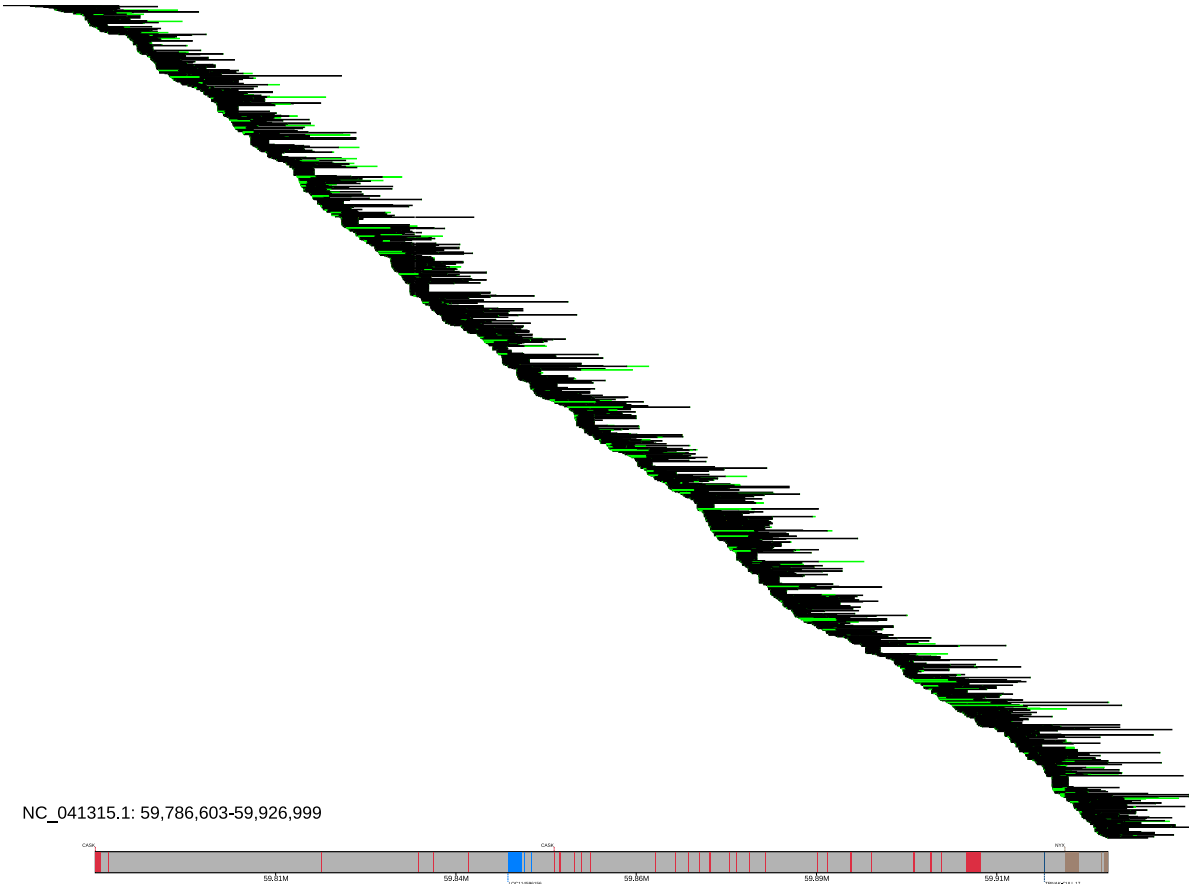


Figure 113: GPR82:NC_041315.1:59786603-59926999.pdf

Pogona_vitticeps-Nanopore

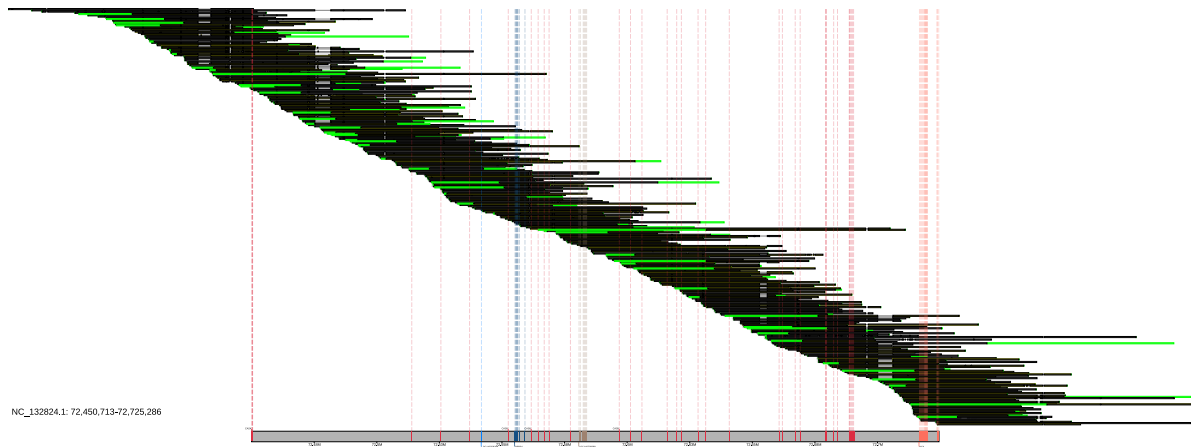


Figure 114: GPR82:NC_132824.1:72450713-72725286.pdf

Important gene stats

GPR82_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
GPR82	4.288888889	39.561 +/- 4.45795	3.45261 +/- 0.22181	72.8518 +/- 18.12	Yes	Na

Intergenic distance phylogenetic signal evidence

GPR82_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
GPR82	87	3	84	0	0.382280983326333	0.999983793641907

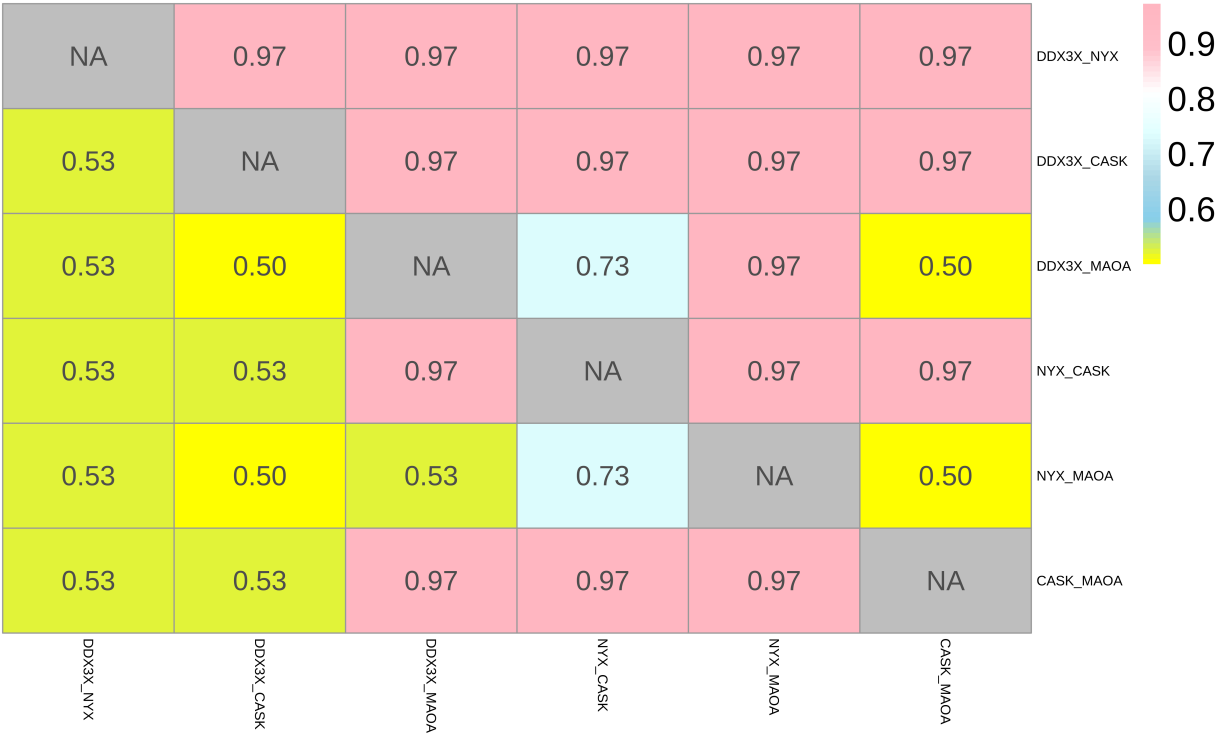


Figure 115: Heatmap_of_deletion_plot.png

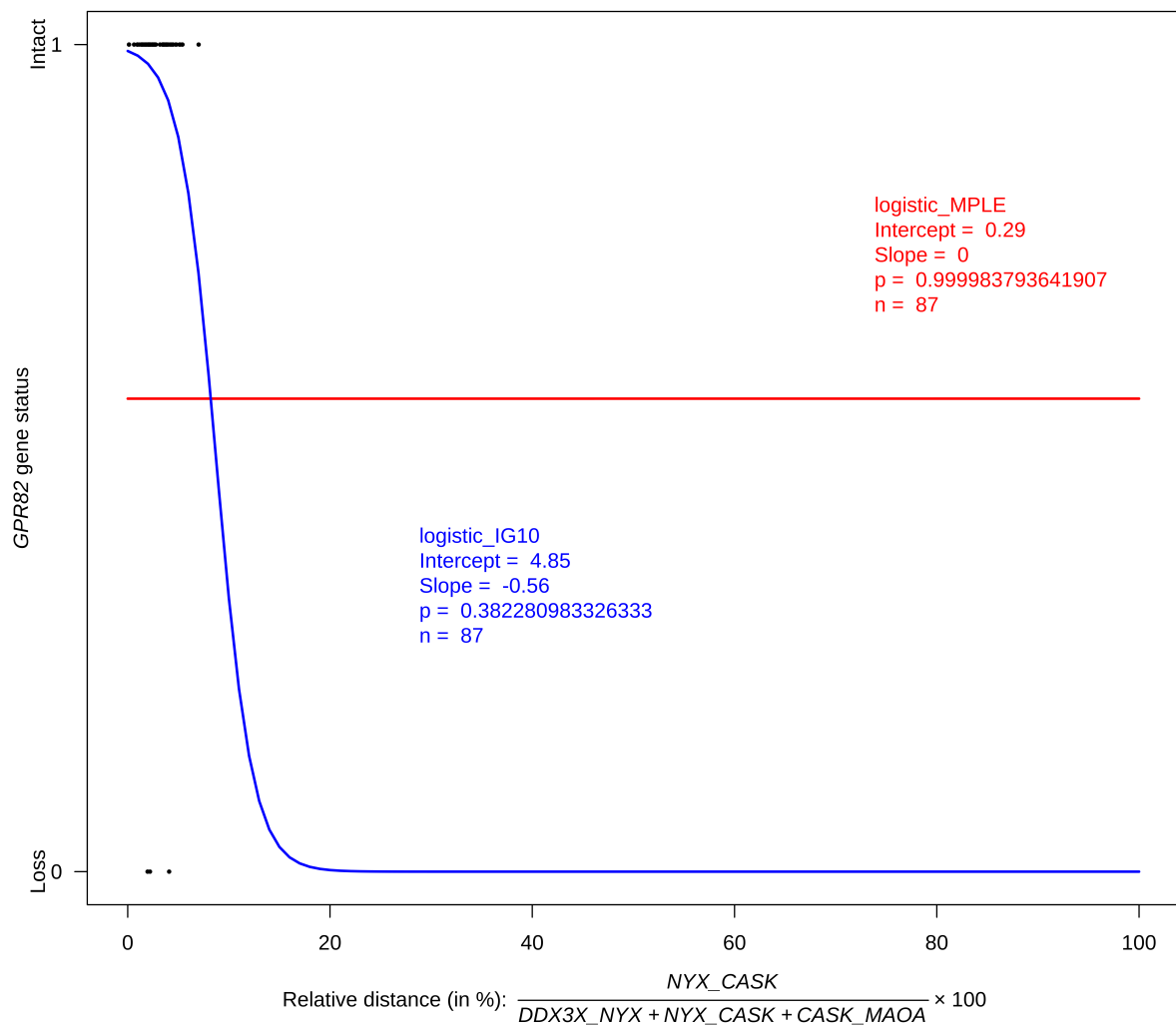


Figure 116: Phylogenetic_signal_of_deletion_plot.png

GPR82_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
GPR82	87	3	84	0	0.382280983326333	0.999983793641907

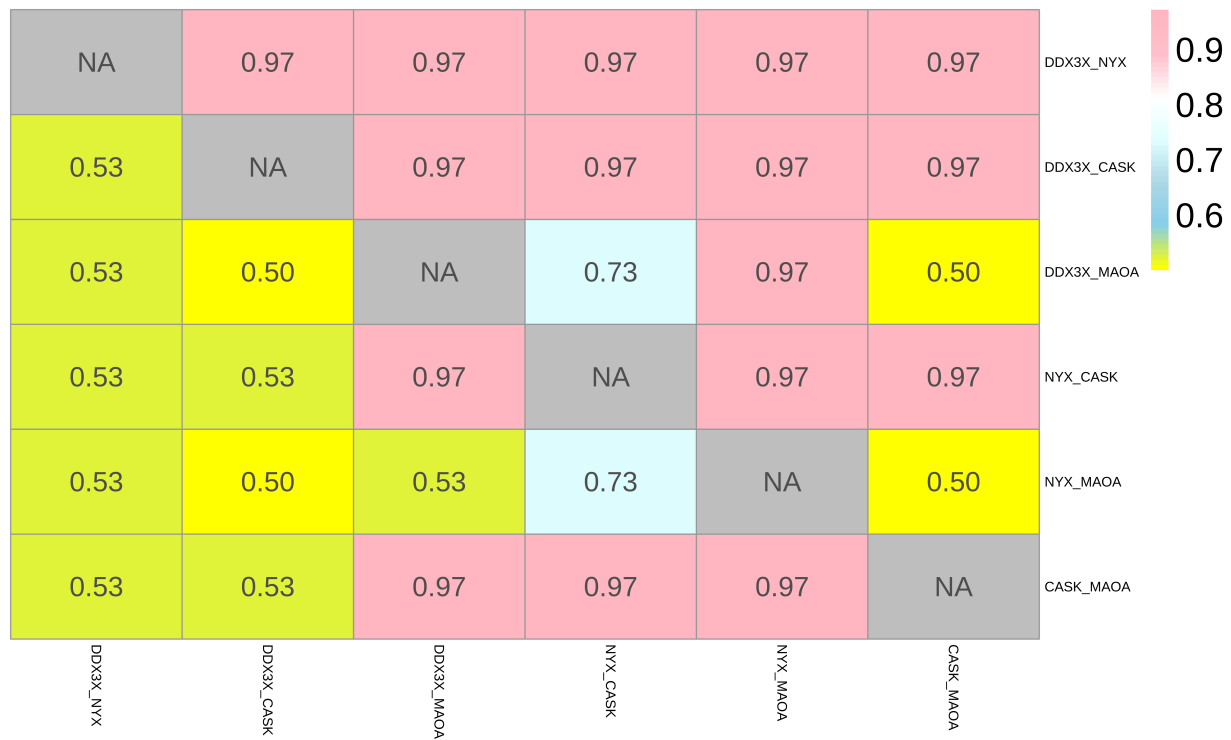


Figure 117: Heatmap_of_deletion_plot.png

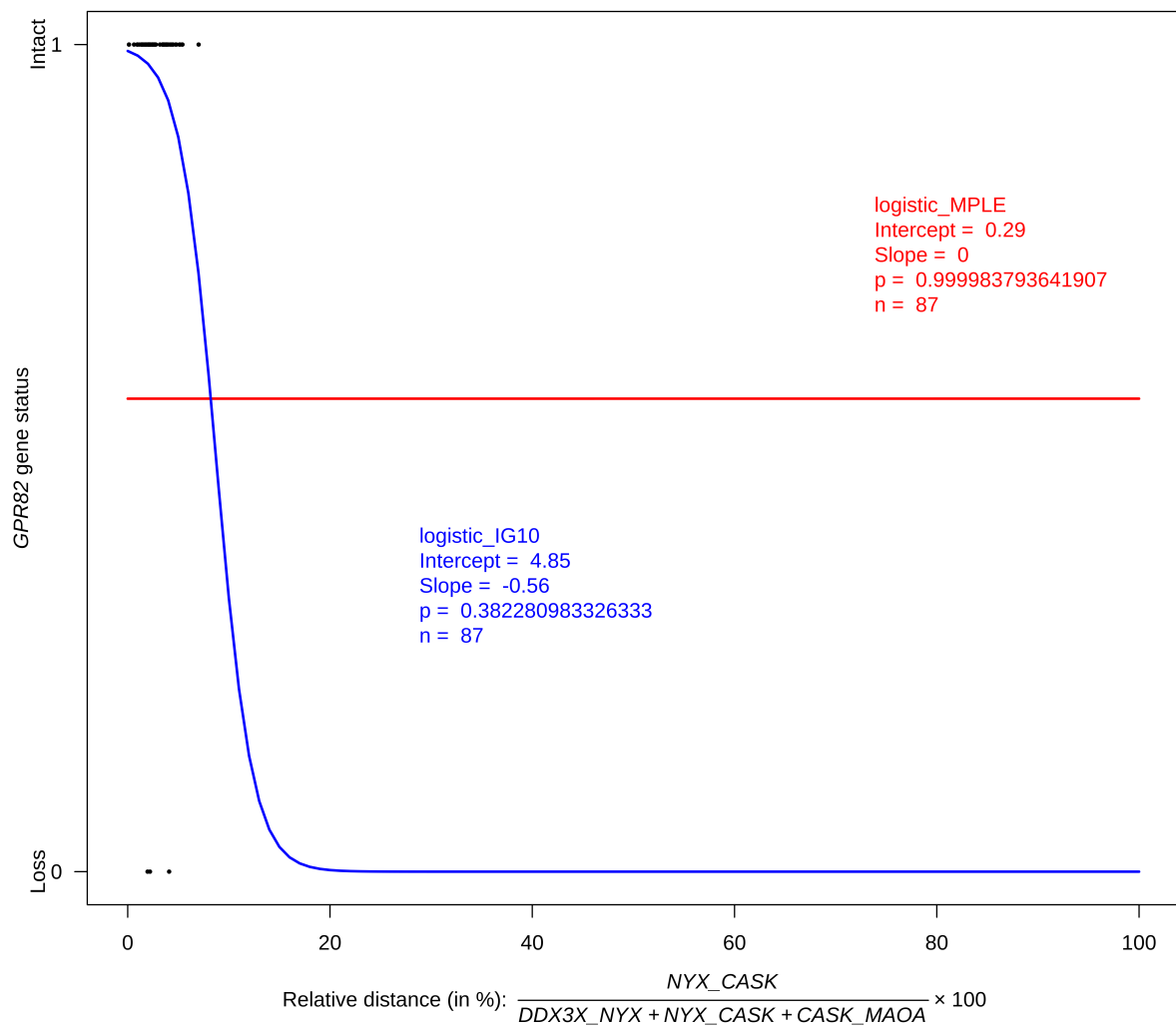


Figure 118: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence



Figure 119: GPR82.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Syntenic evidence

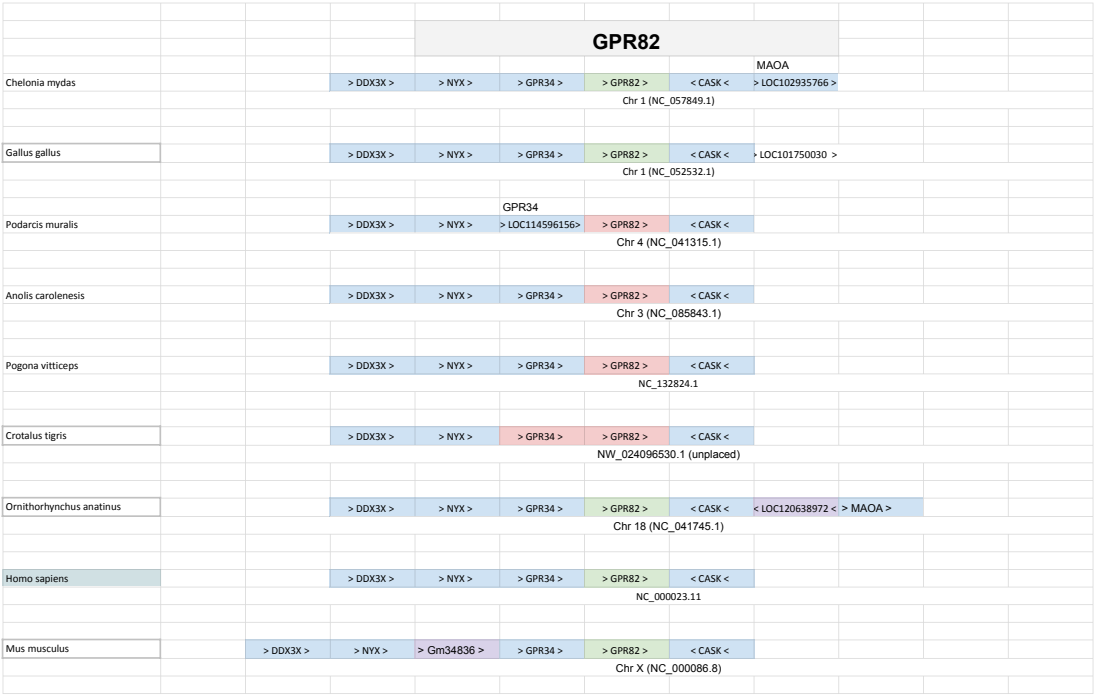


Figure 121: GPR82.pdf

GPR82.txt

Synteny analysis of GPR82

We analyzed the synteny of GPR82 in squamates and representative outgroups

→ . The GPR82 syntenic block is conserved, with no notable changes in

→ gene order or orientation. In the synteny plots, red blocks indicate

→ the absence of GPR82, green blocks mark its presence, light blue

→ blocks represent genes conserved across lineages, and light purple

→ blocks denote different flanking genes.

Transcriptomic evidence *Pogona vitticeps*



Figure 122: GPR82.png

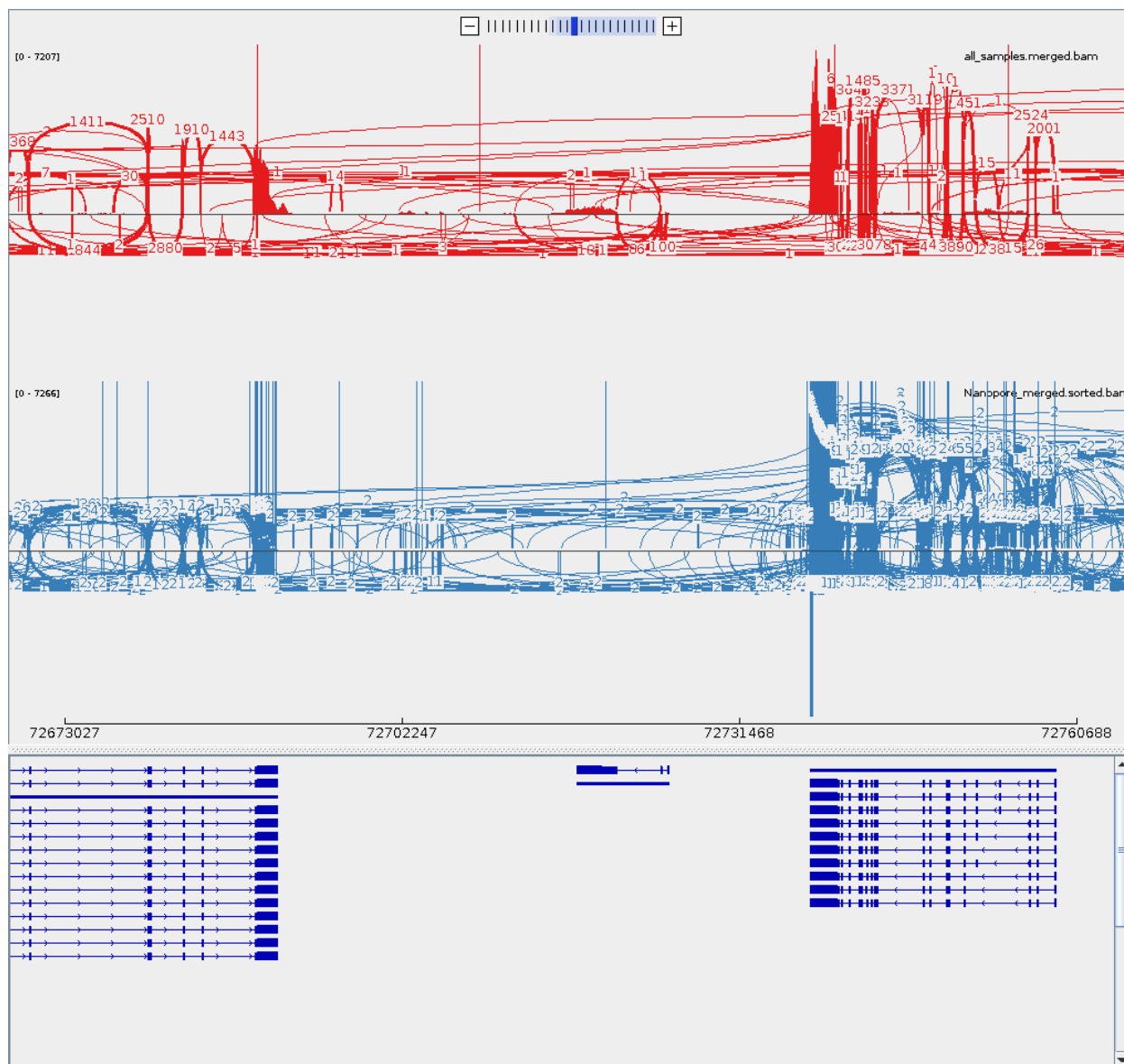


Figure 123: GPR82_Shash.png

13 GRK4

Assembly verification Evidence

Crotalus_tigris-PacBio

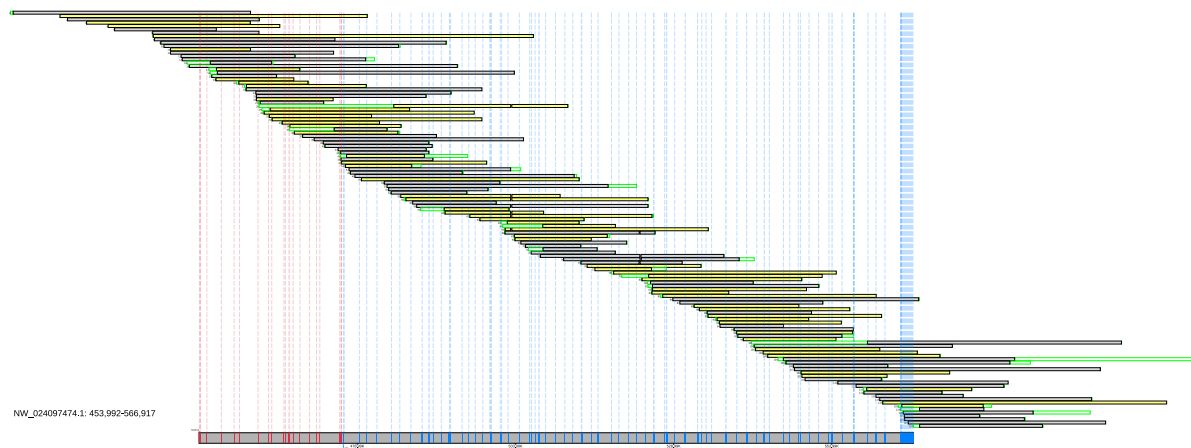


Figure 124: GRK4:NW_024097474.1:453992-566917.pdf

Podarcis_muralis-PacBio

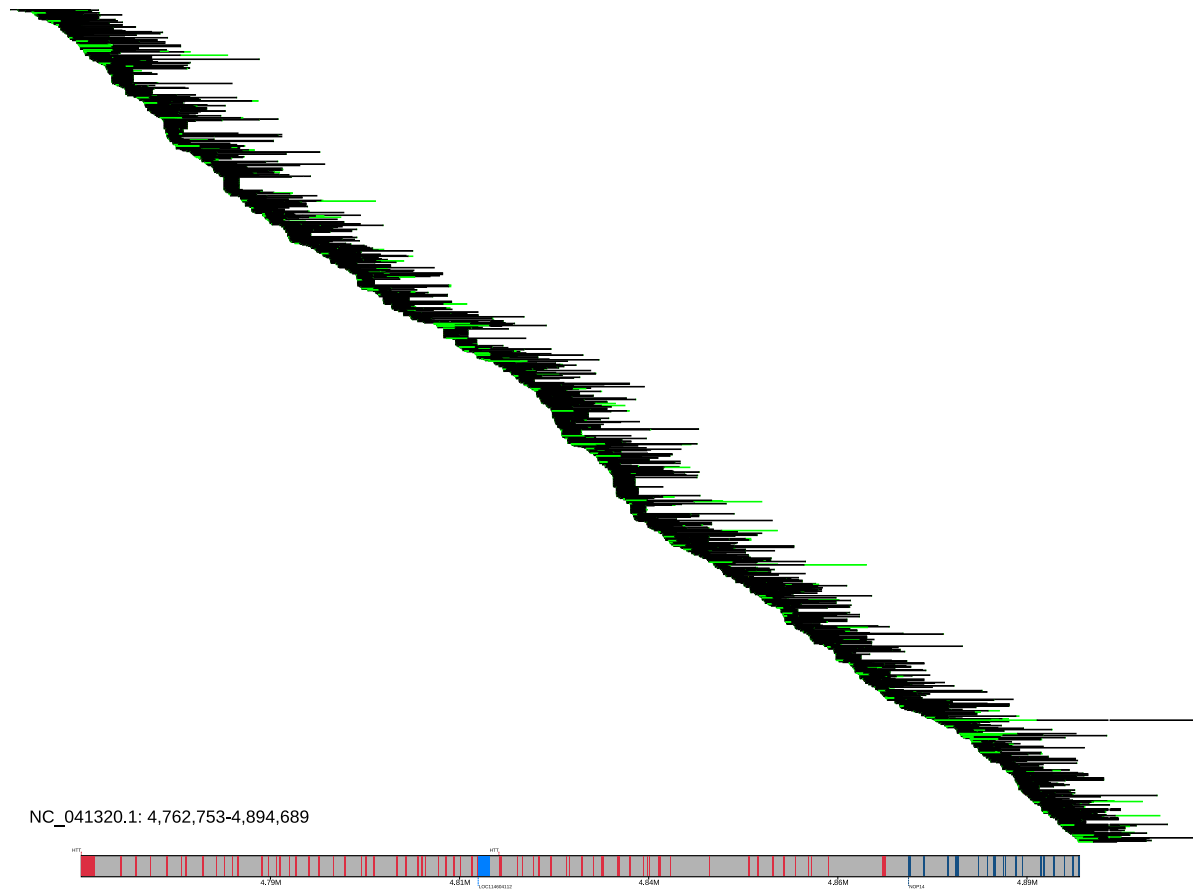


Figure 125: GRK4:NC_041320.1:4762753-4894689.pdf

Pogona_vitticeps-Nanopore

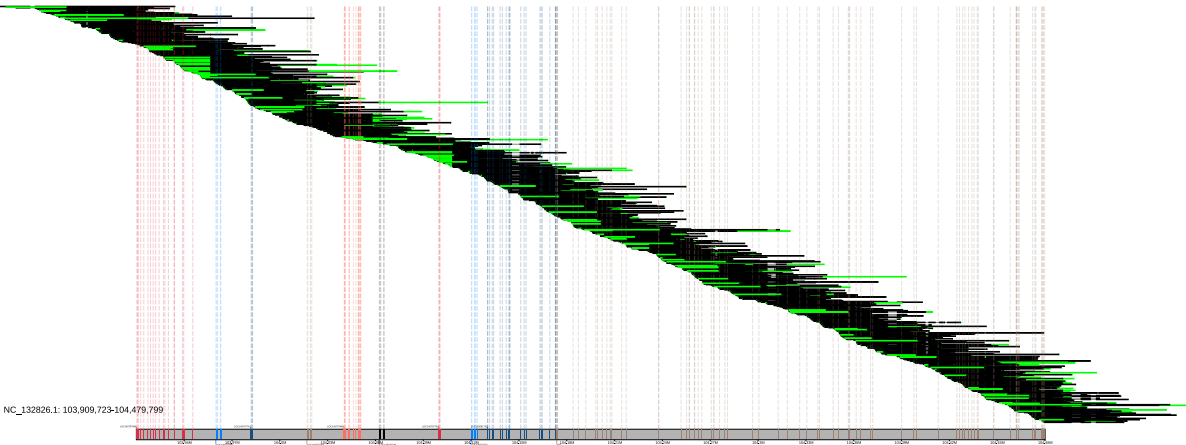


Figure 126: GRK4:NC_132826.1:103909723-104479799.pdf

Important gene stats

GRK4_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
GRK4	35.24528302	45.7815 +/- 4.83479	3.70486 +/- 0.343829	69.8844 +/- 9.00266	Yes	GRK6;LOC116517055;

Intergenic distance phylogenetic signal evidence

GRK4_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
GRK4	218	16	202	5	0.0100146231837285	0.9999999999999941

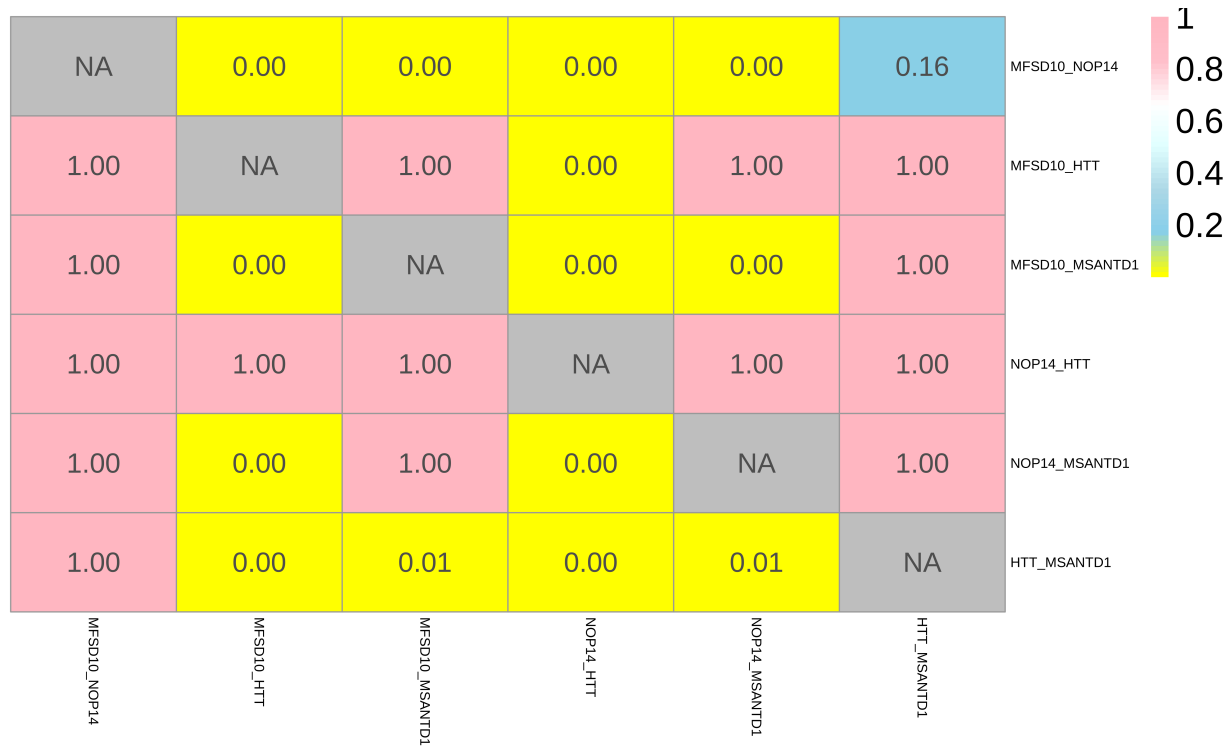


Figure 127: Heatmap_of_deletion_plot.png

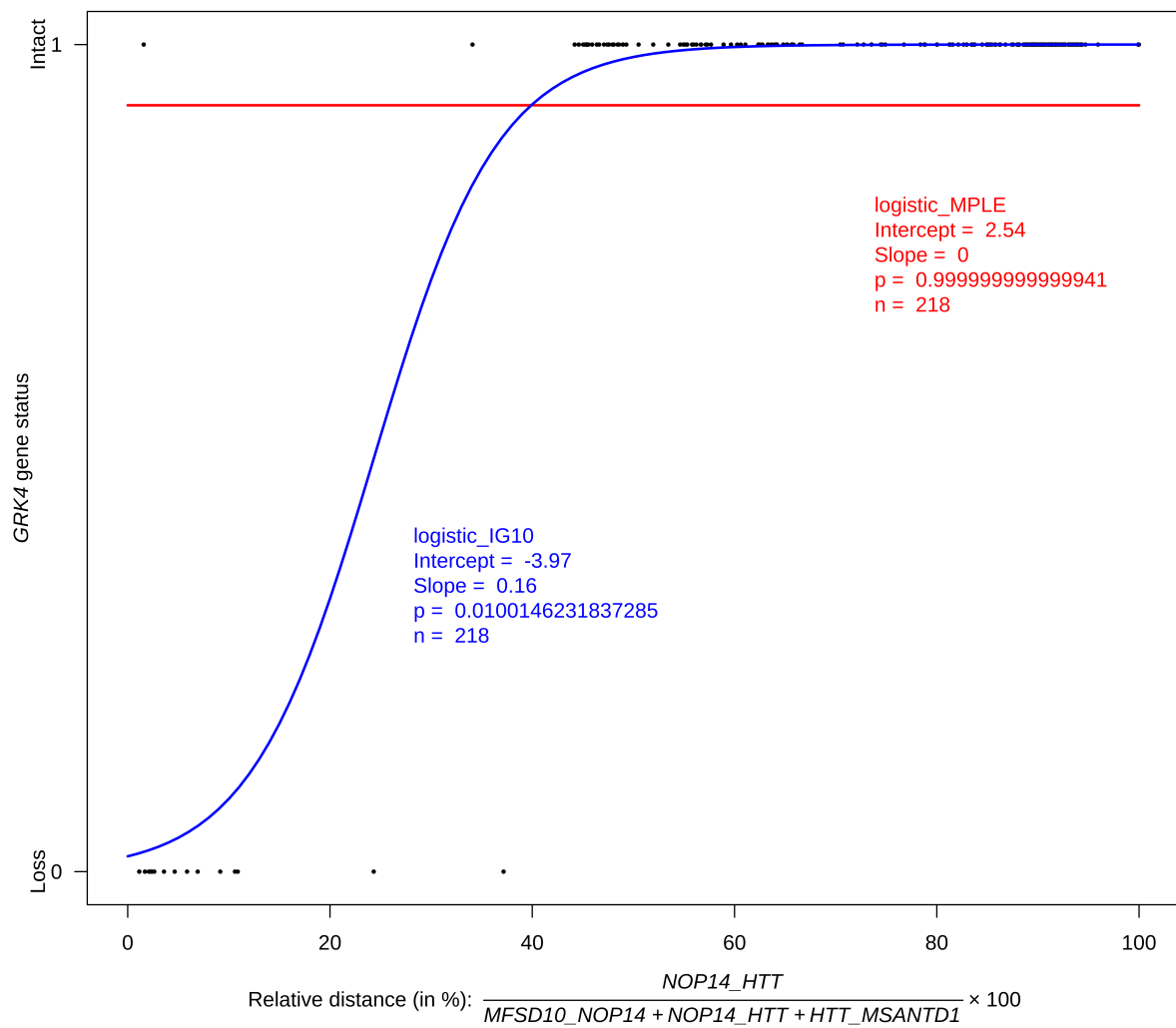


Figure 128: Phylogenetic_signal_of_deletion_plot.png

GRK4_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
GRK4	218	16	202	5	0.0100146231837285	0.999999999999941

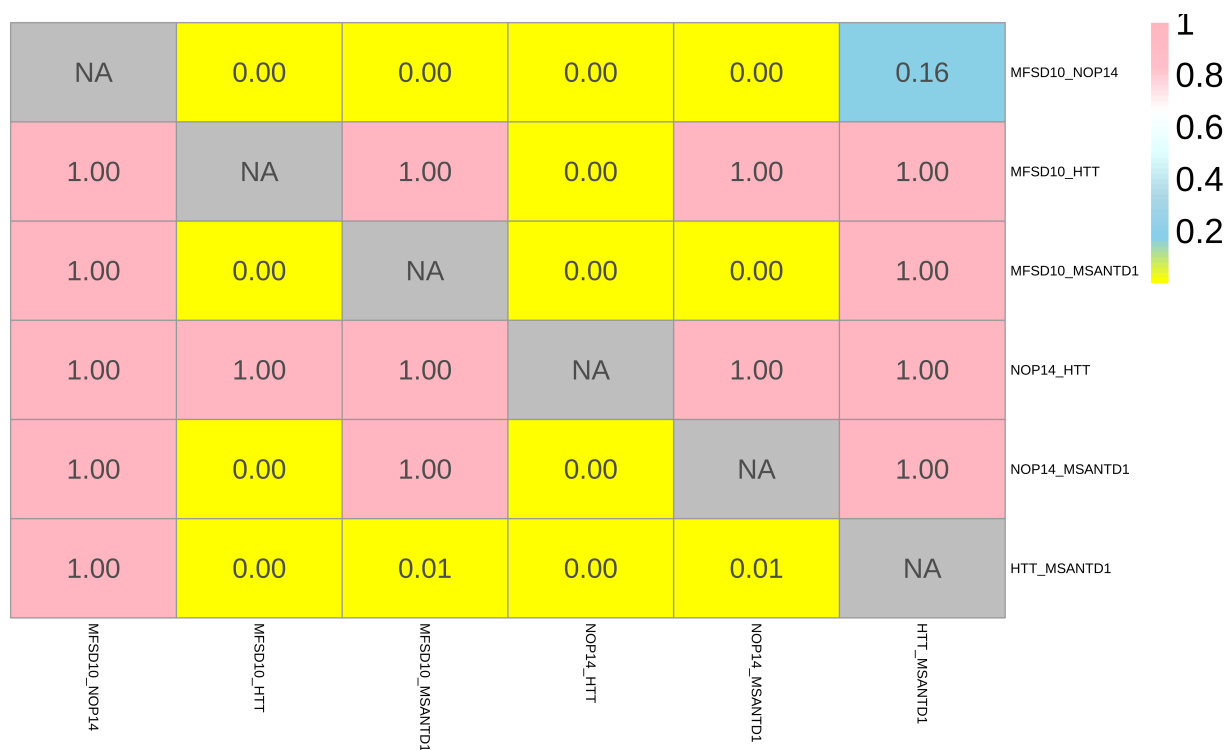


Figure 129: Heatmap_of_deletion_plot.png

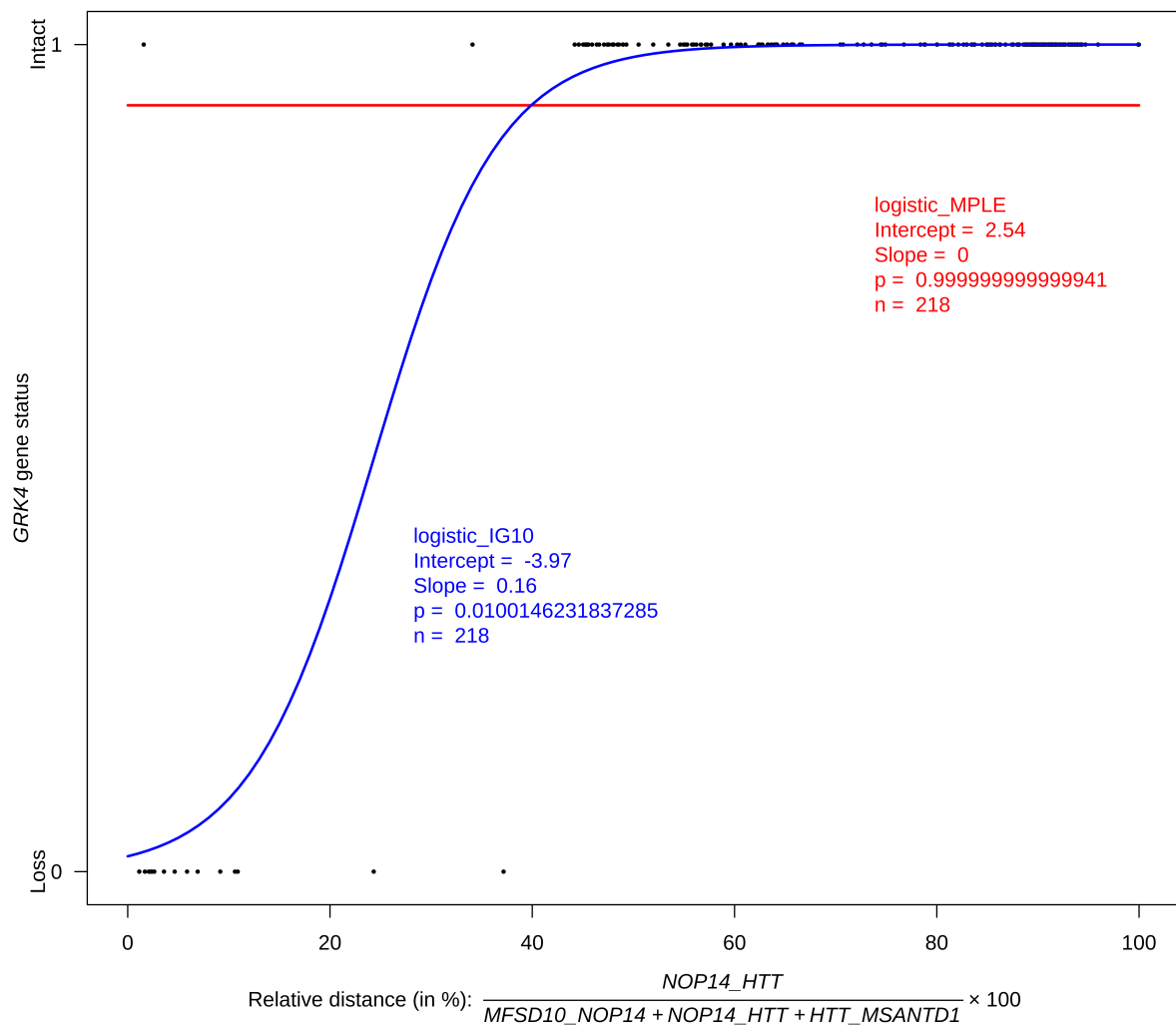


Figure 130: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence

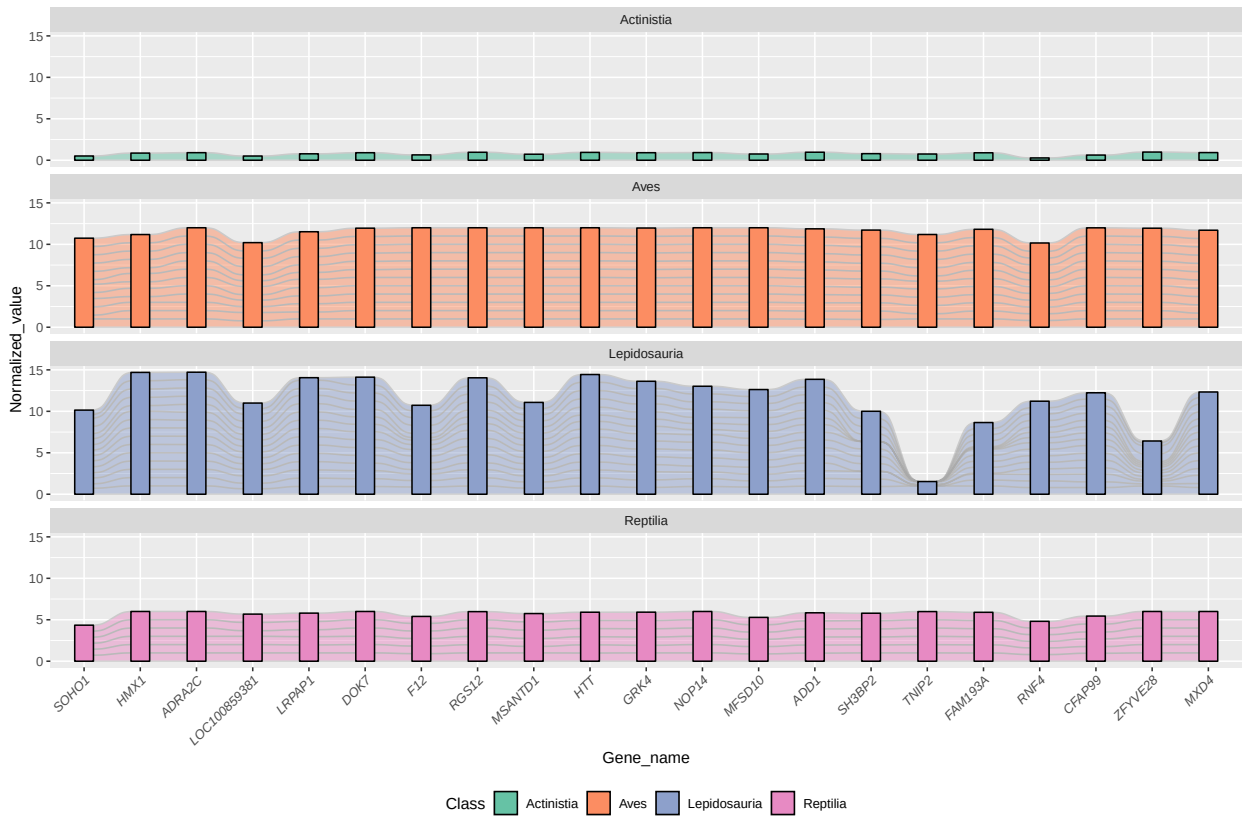


Figure 131: GRK4.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Lastz gene tree



Figure 133: GRK4.combined.mafft.aln.highlighted.pdf

Syntenic evidence



Figure 134: GRK4.pdf

GRK4.txt

Synteny analysis of GRK4

We analyzed the synteny of GRK4 in squamates and representative outgroups.

- The GRK4 syntenic block is conserved, with no notable changes in
- gene order or orientation. In the synteny plots, red blocks indicate
- the absence of GRK4, green blocks mark its presence, light blue
- blocks represent genes conserved across lineages, and light purple
- blocks denote different flanking genes.

Transcriptomic evidence *Pogona vitticeps*

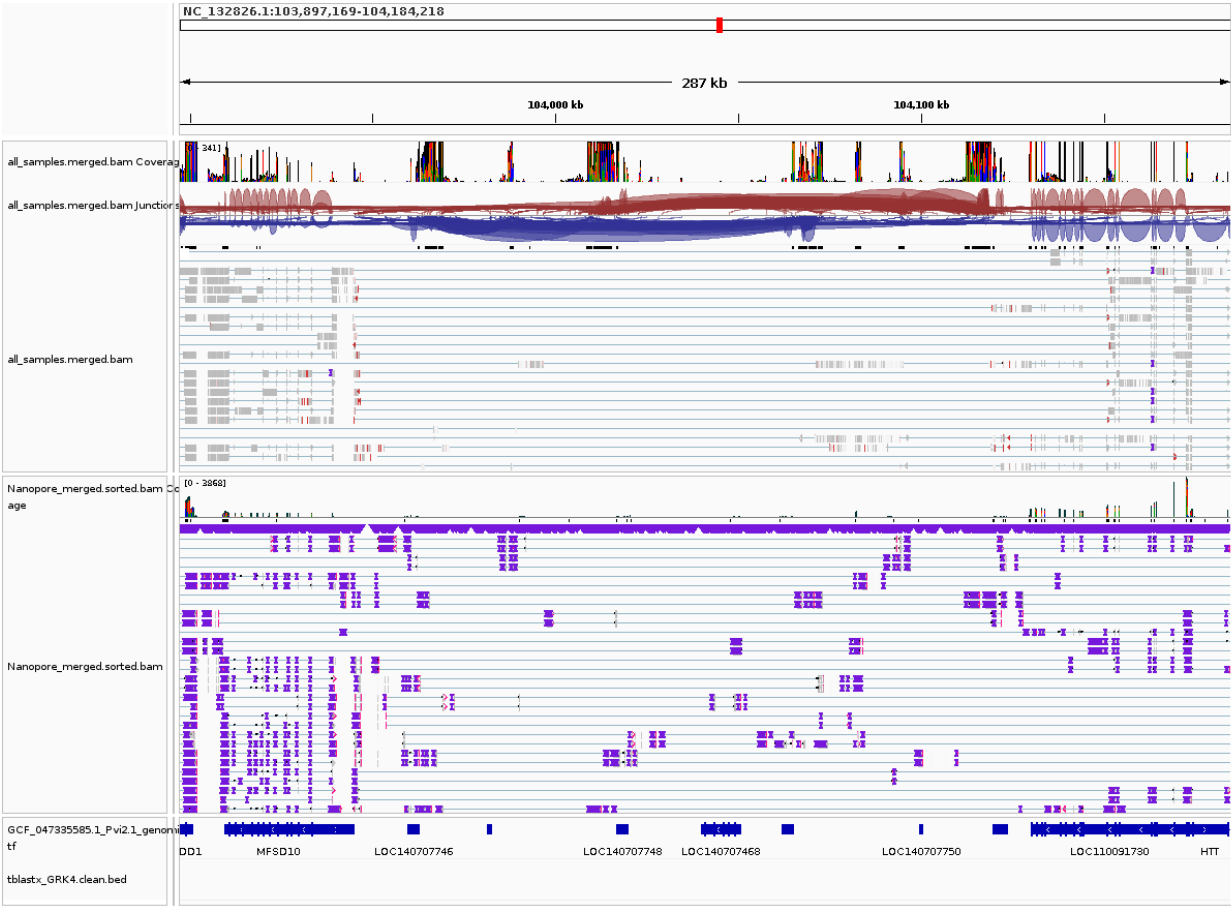


Figure 135: GRK4.png

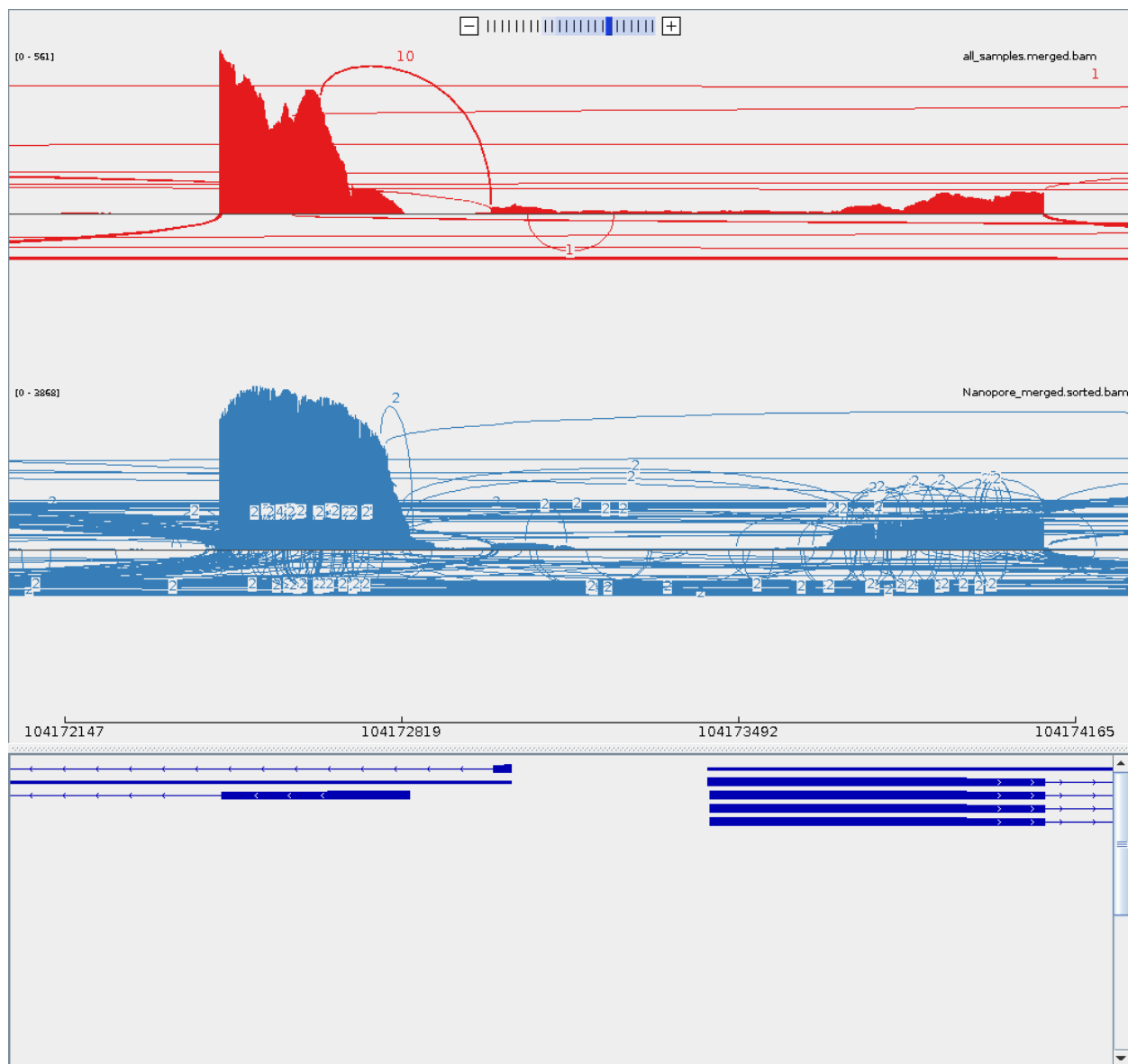


Figure 136: GRK4_Shash.png

14 HHLA2

Assembly verification Evidence

Crotalus_tigris-PacBio

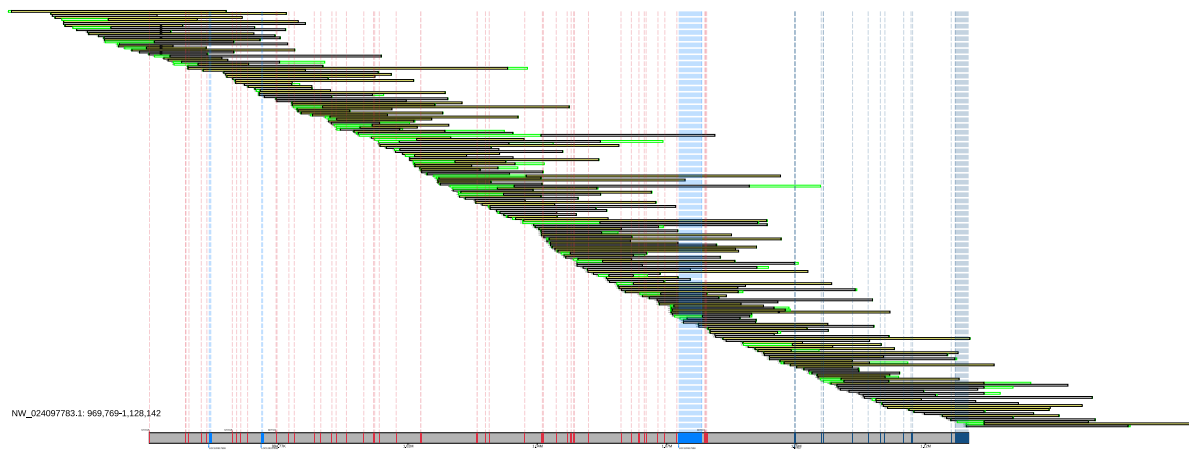


Figure 137: HHLA2:NW_024097783.1:969769-1128142.pdf

Podarcis_muralis-PacBio

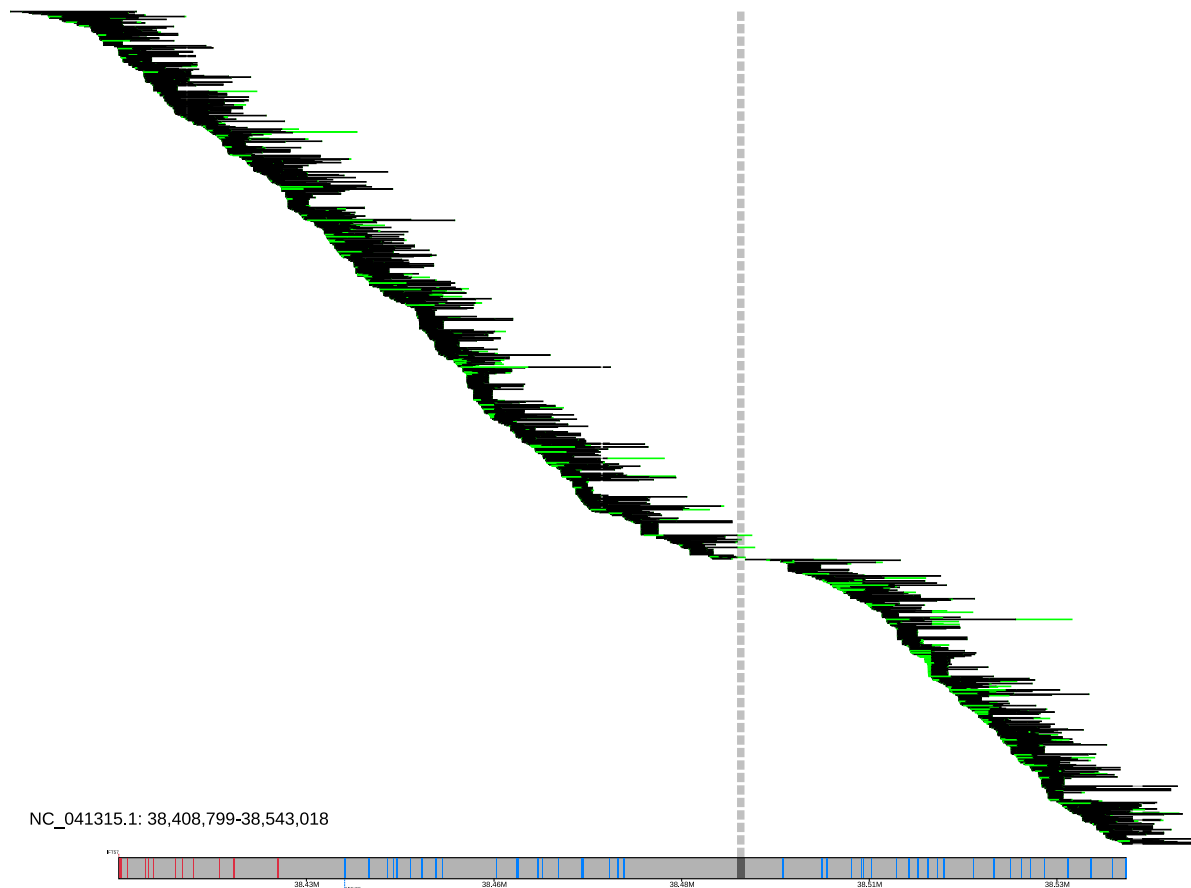


Figure 138: HHLA2:NC_041315.1:38408799-38543018.pdf

Pogona_vitticeps-Nanopore

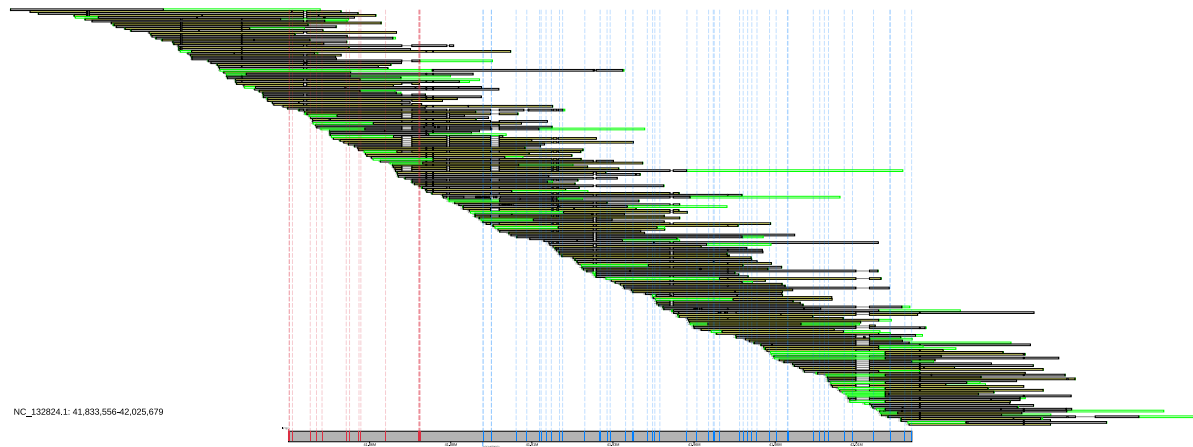


Figure 139: HHLA2:NC_132824.1:41833556-42025679.pdf

Important gene stats

HHLA2_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
HHLA2	3.107692308	41.3174 +/- 2.80653	3.4385 +/- 0.160297	57.8293 +/- 14.5582	Yes	Na

Intergenic distance phylogenetic signal evidence

HHLA2_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
HHLA2	182	17	165	5	1	0.999999999999973

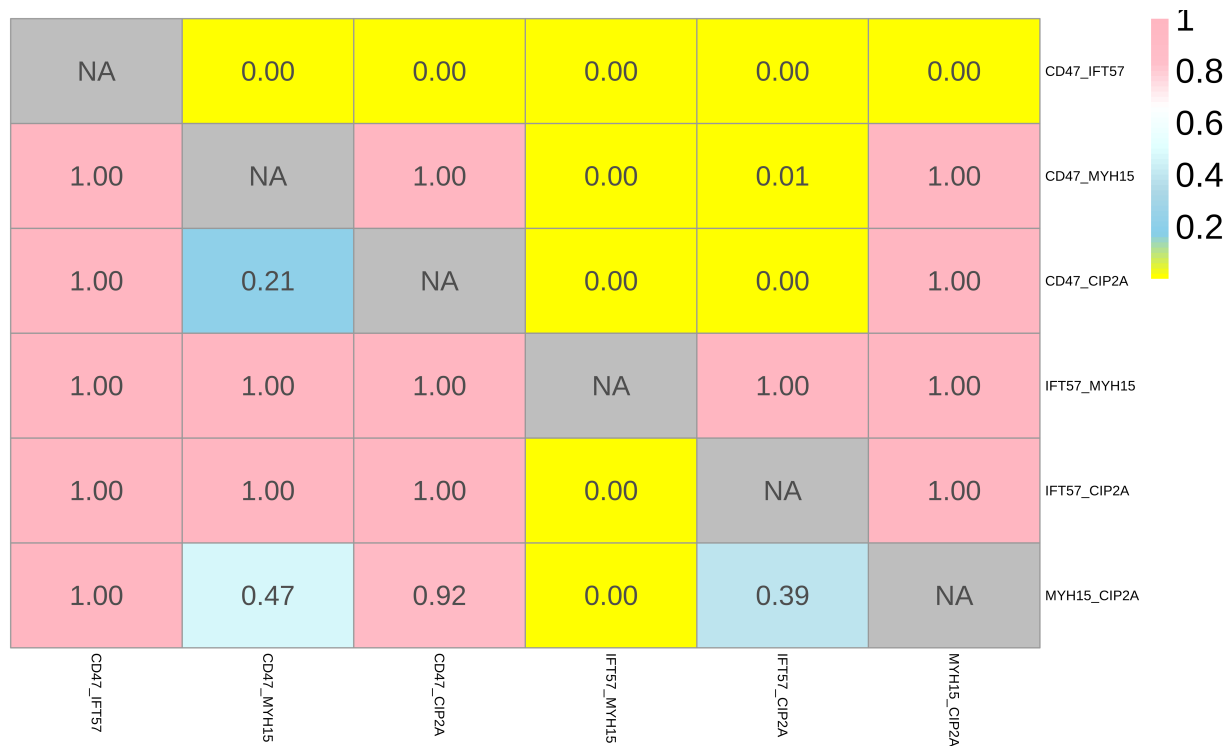


Figure 140: Heatmap_of_deletion_plot.png

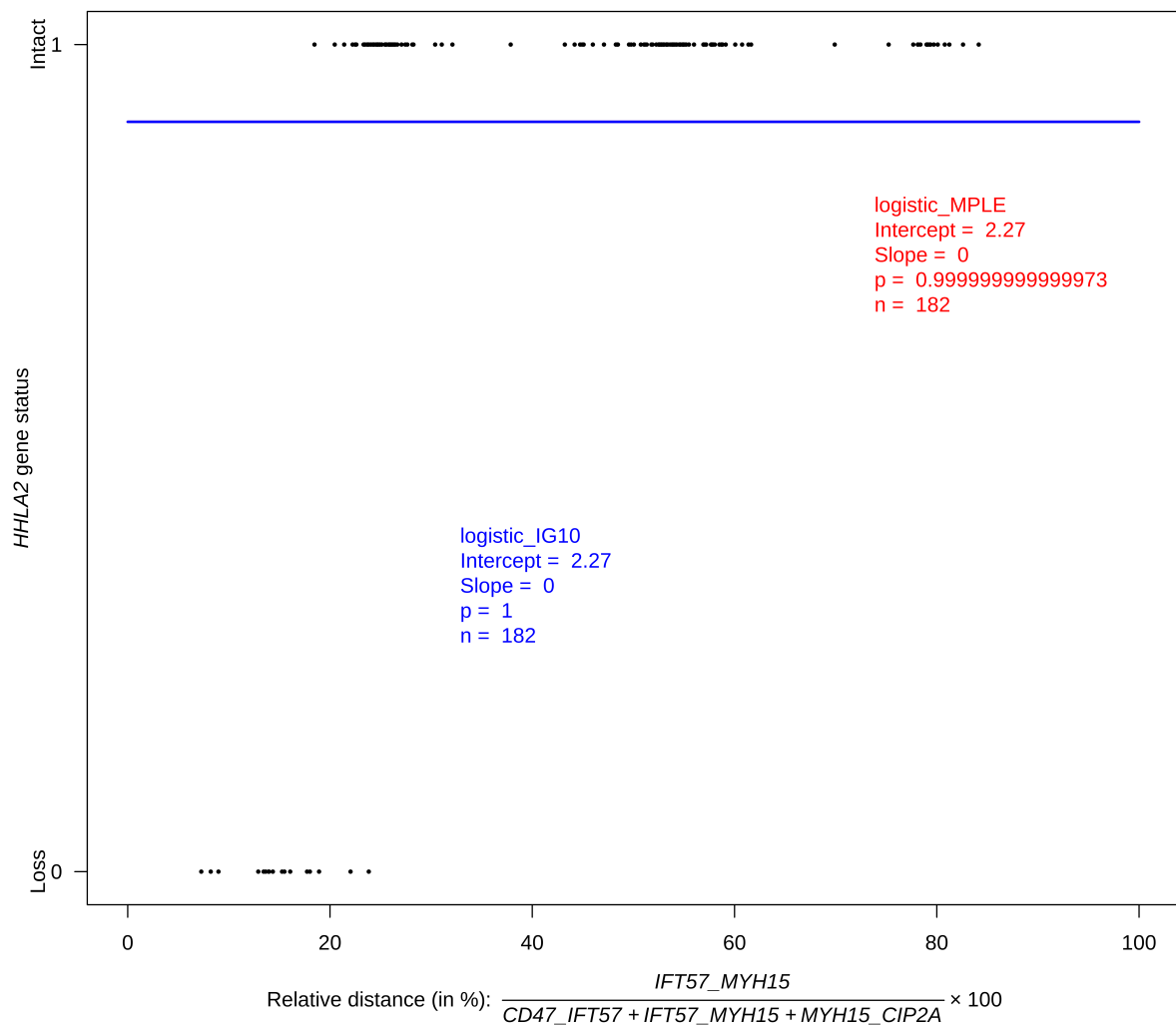


Figure 141: Phylogenetic_signal_of_deletion_plot.png

HHLA2_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
HHLA2	182	17	165	5	1	0.999999999999973

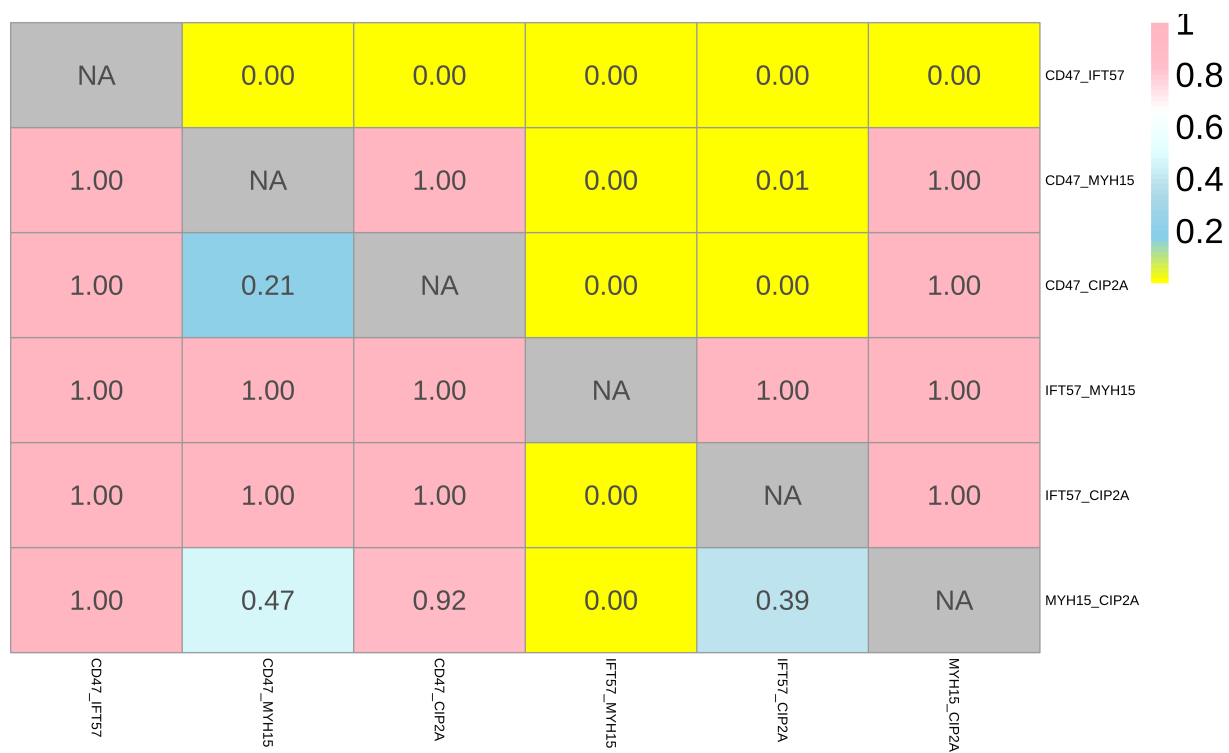


Figure 142: Heatmap_of_deletion_plot.png

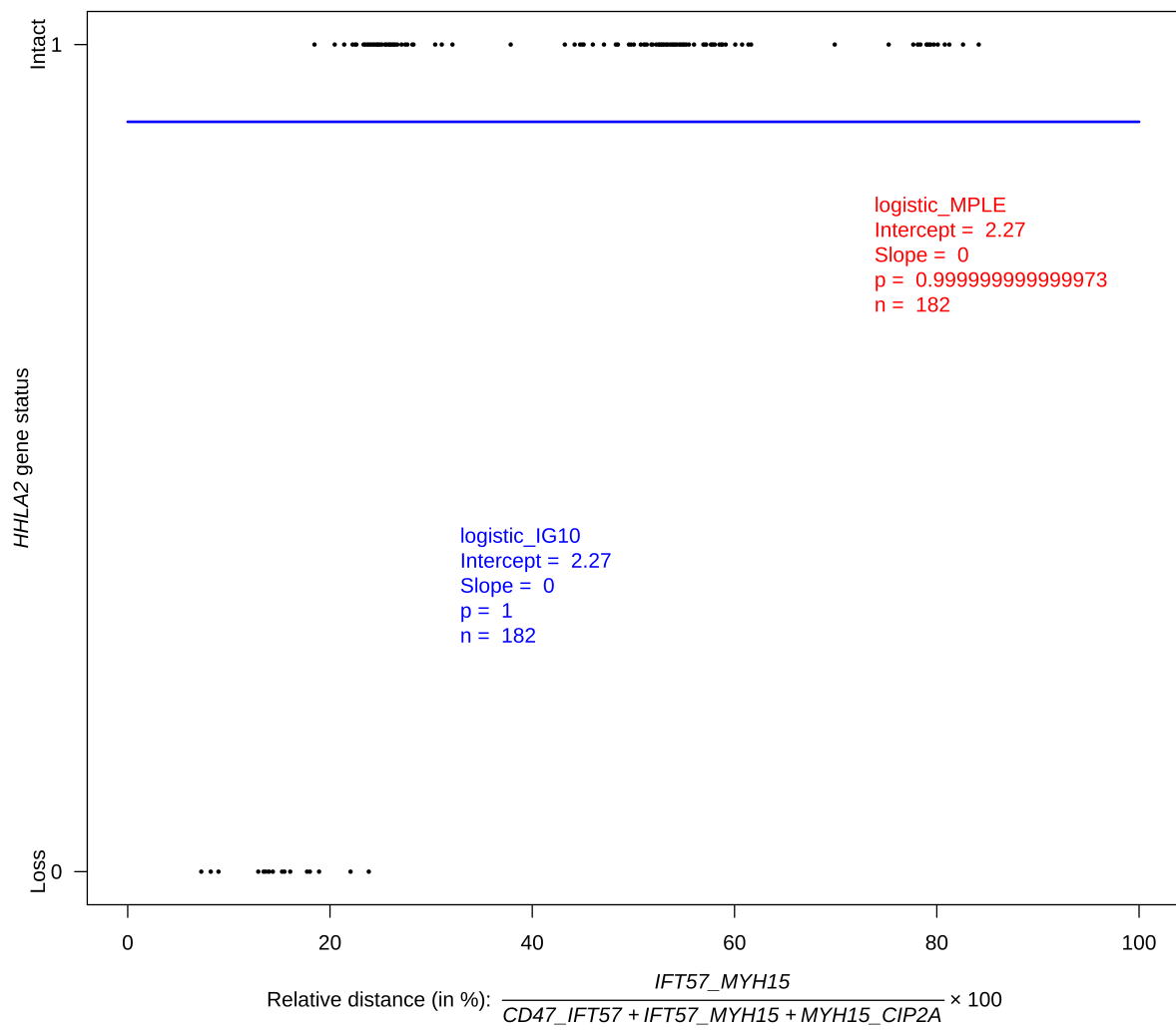


Figure 143: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence



Figure 144: HHLA2.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Lastz gene tree

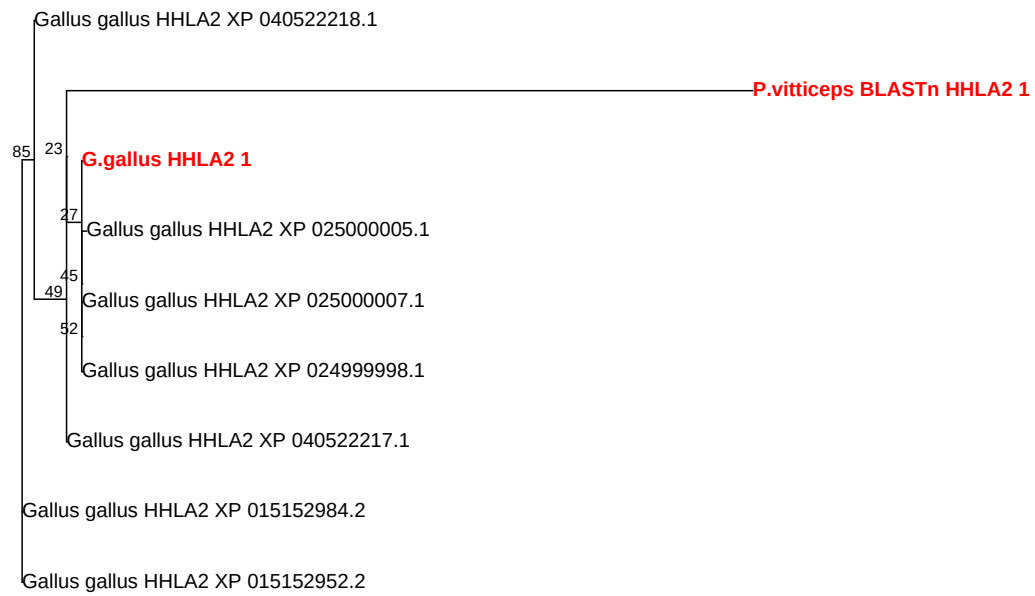


Figure 146: HHLA2.combined.mafft.aln.highlighted.pdf

Syntenic evidence

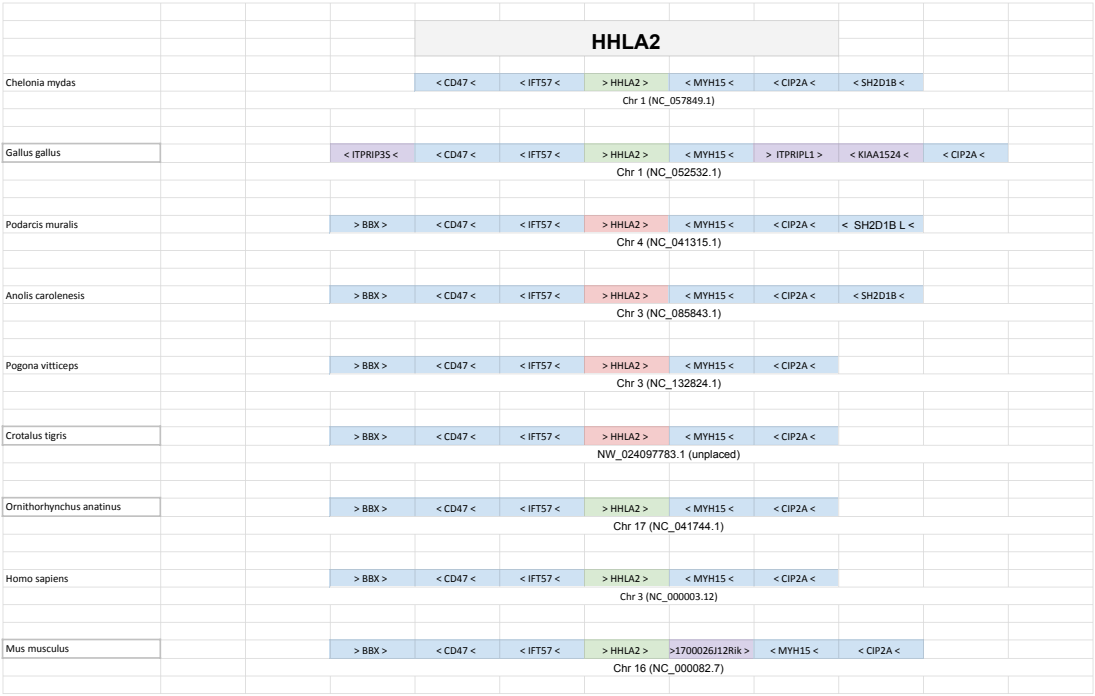


Figure 147: HHLA2.pdf

HHLA2.txt

Synteny analysis of HHLA2

We analyzed the synteny of HHLA2 in squamates and representative outgroups
→ . The HHLA2 syntenic block is conserved, with no notable changes in
→ gene order or orientation. In the synteny plots, red blocks indicate
→ the absence of HHLA2, green blocks mark its presence, light blue
→ blocks represent genes conserved across lineages, and light purple
→ blocks denote different flanking genes.

Transcriptomic evidence *Pogona vitticeps*



Figure 148: HHLA2.png

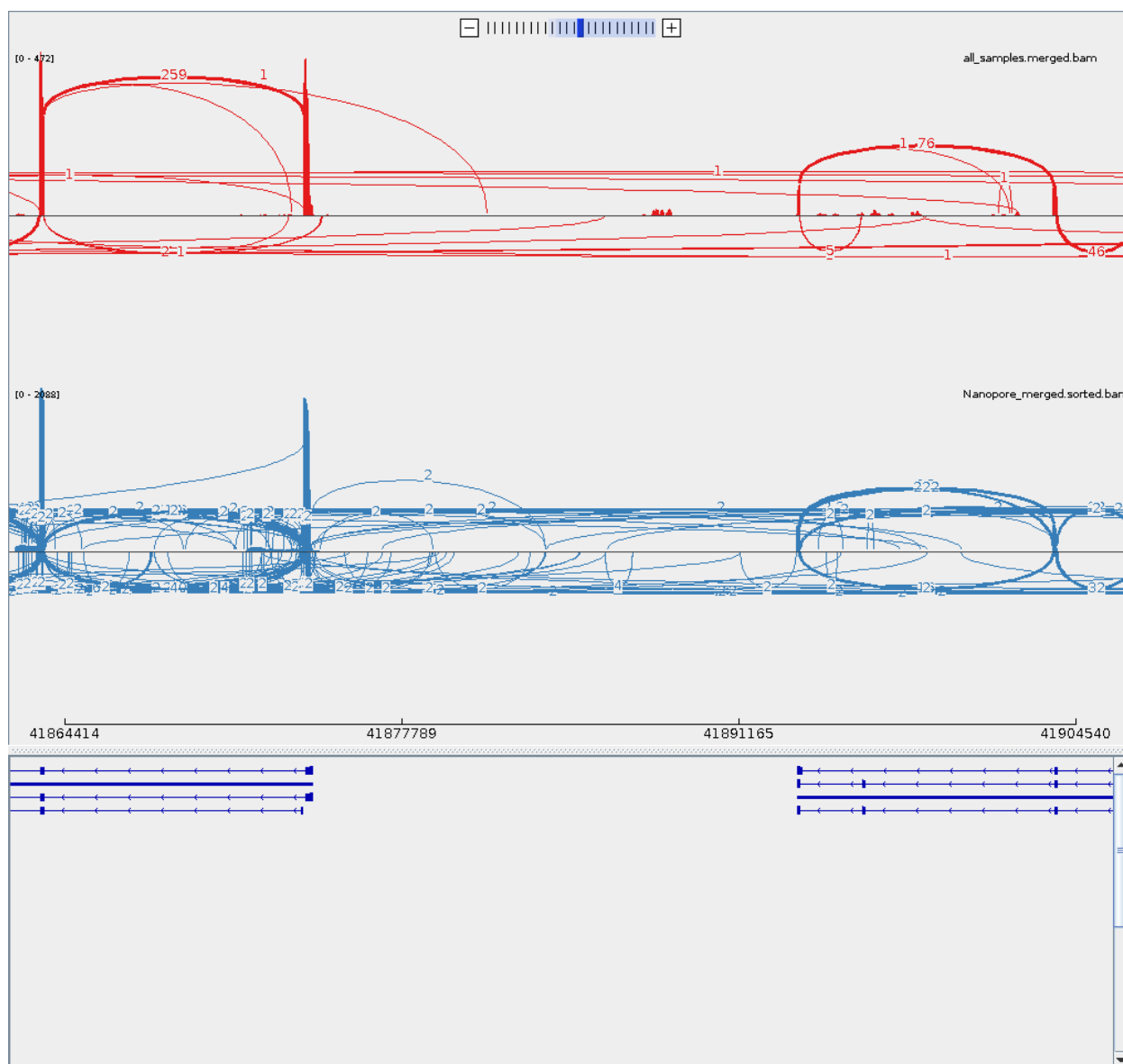


Figure 149: HHLA2_Shash.png

15 HPGDS

Assembly verification Evidence

Crotalus_tigris-PacBio

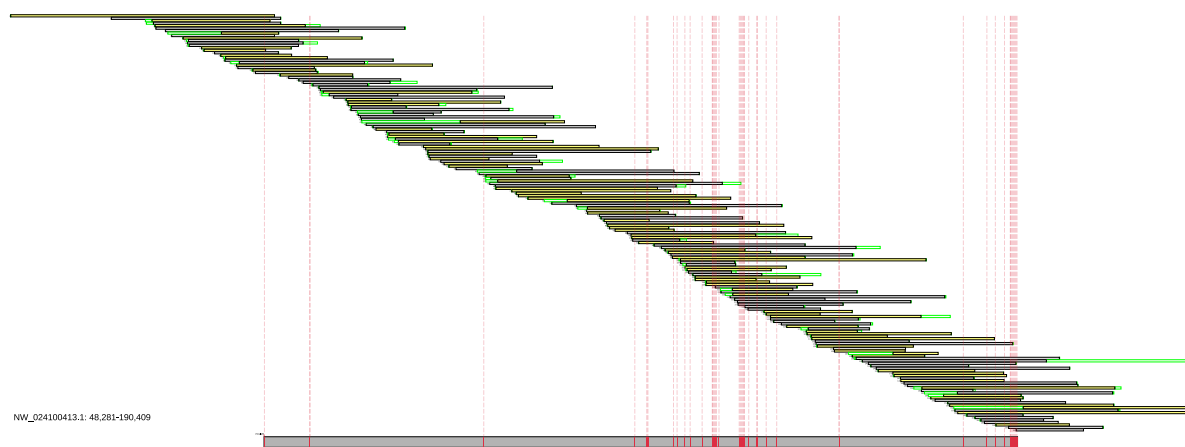


Figure 150: HPGDS:NW_024100413.1:48281-190409.pdf



Figure 151: HPGDS:NW_024100620.1:362577-418987.pdf

Podarcis_muralis-PacBio

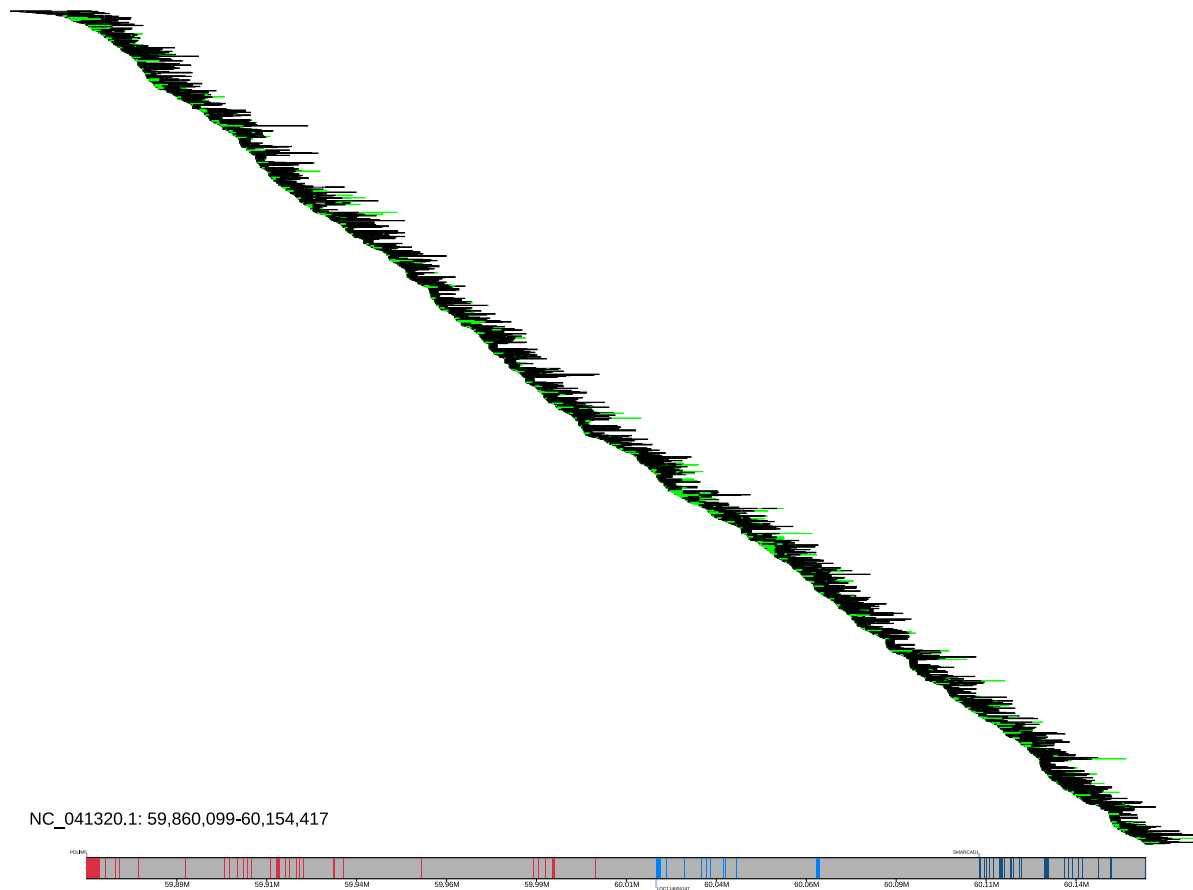


Figure 152: HPGDS:NC_041320.1:59860099-60154417.pdf

Pogona_vitticeps-Nanopore

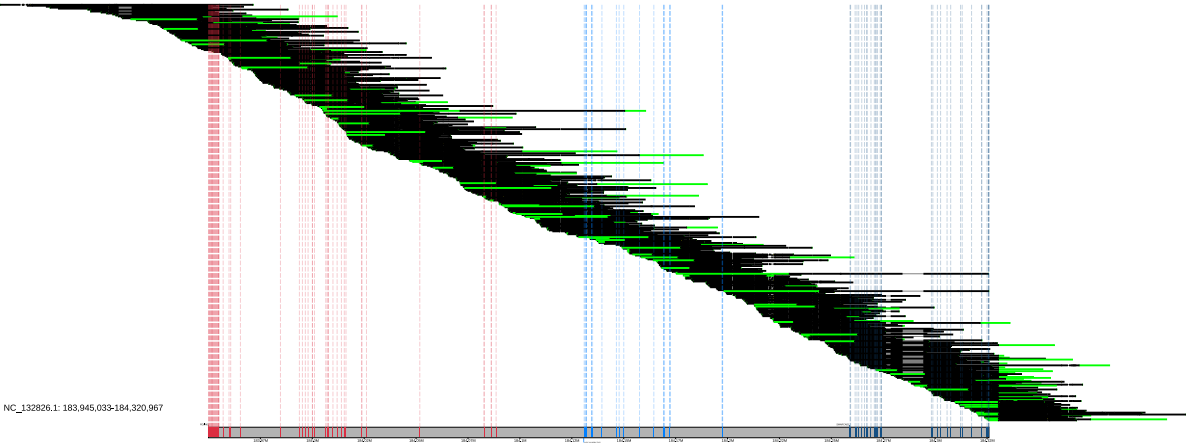


Figure 153: HPGDS:NC_132826.1:183945033-184320967.pdf

Important gene stats

HPGDS_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
HPGDS	6.769230769	44.3697 +/- 4.14415	3.54395 +/- 0.145823	78.621 +/- 11.8559	Yes	Na

Intergenic distance phylogenetic signal evidence

HPGDS_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
HPGDS	201	19	182	0	0.661856627169581	0.998183574489019



Figure 154: Heatmap_of_deletion_plot.png

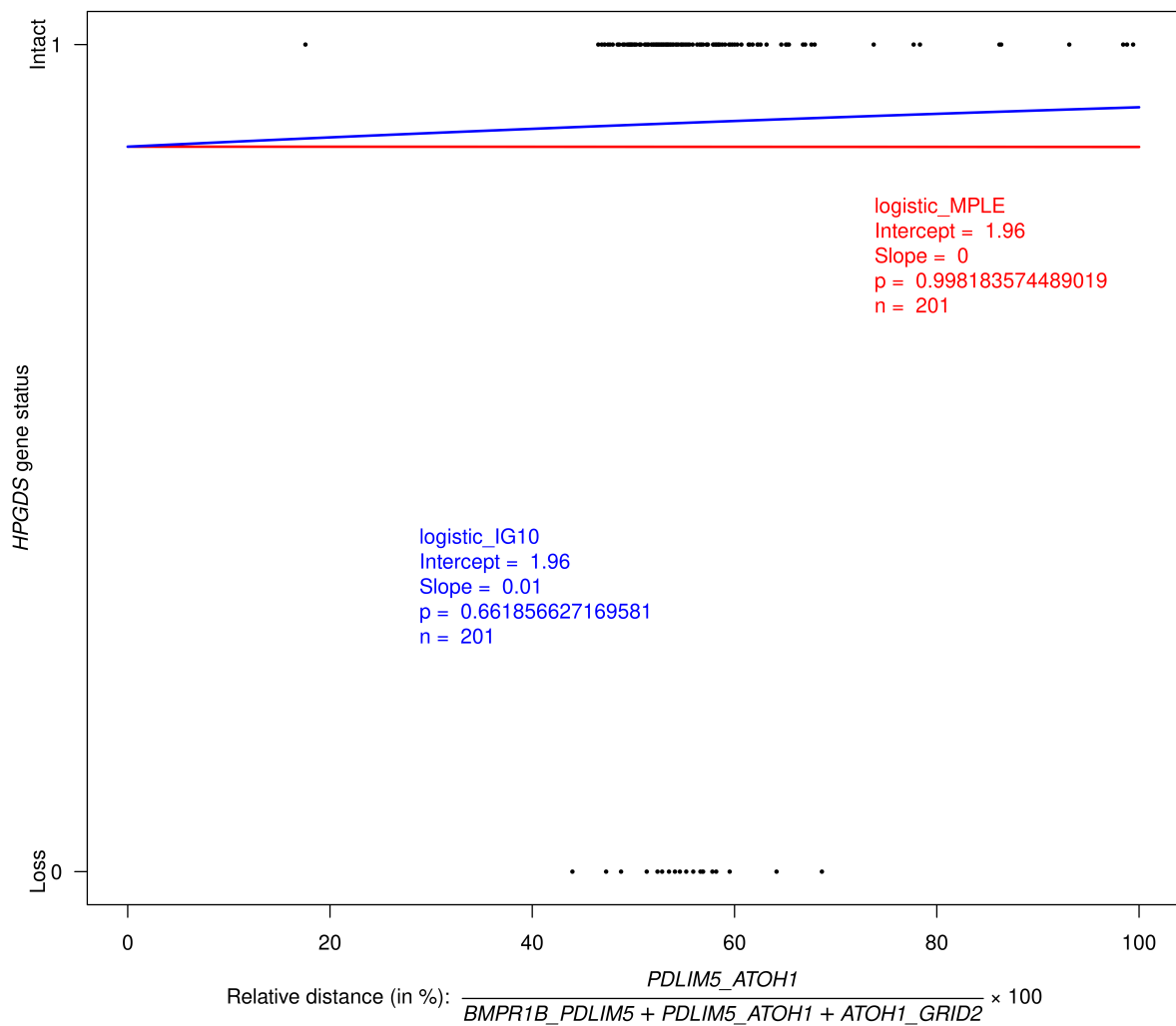


Figure 155: Phylogenetic_signal_of_deletion_plot.png

HPGDS_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
HPGDS	201	19	182	0	0.661856627169581	0.998183574489019

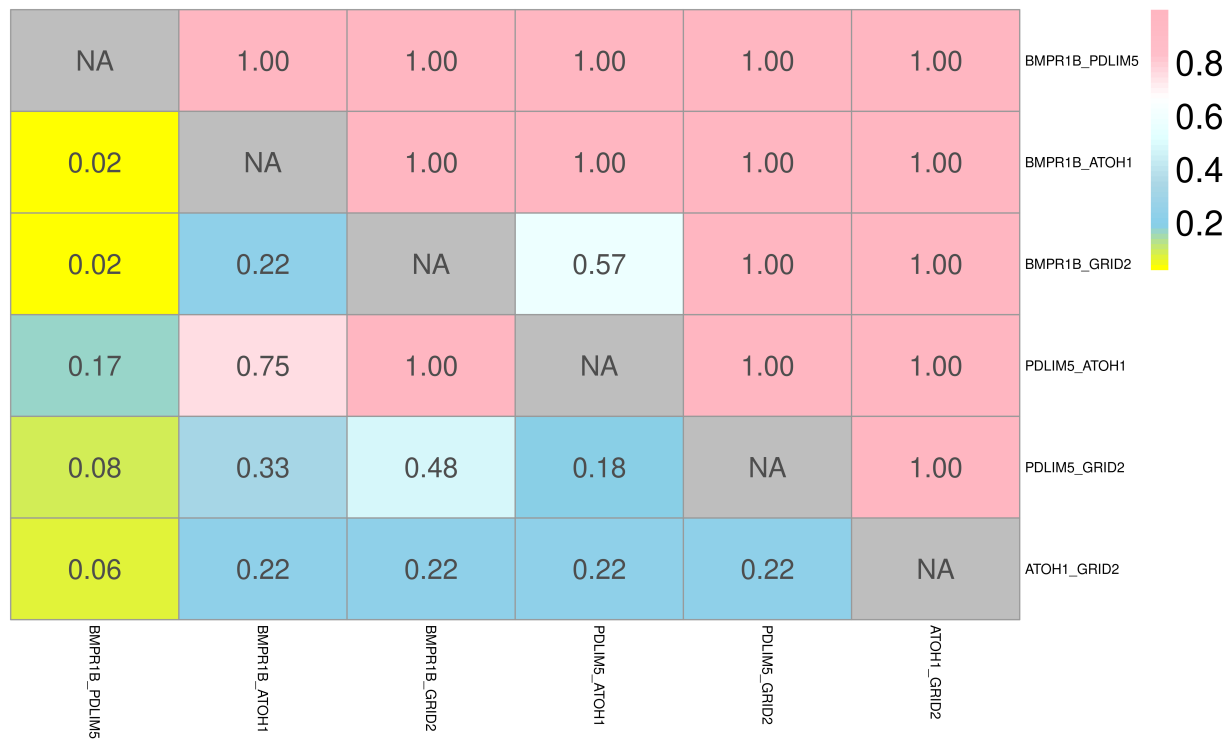


Figure 156: Heatmap_of_deletion_plot.png

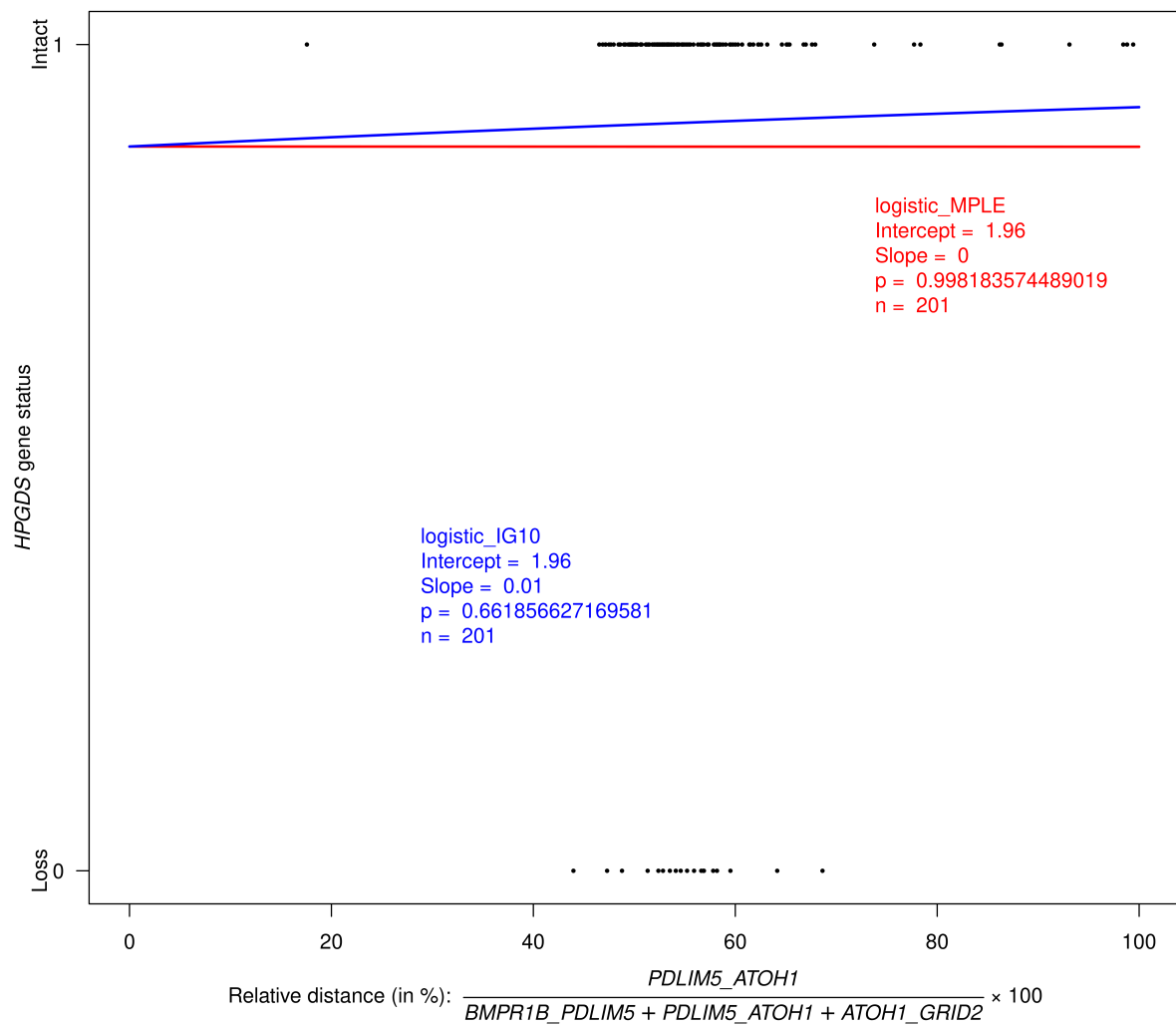


Figure 157: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence

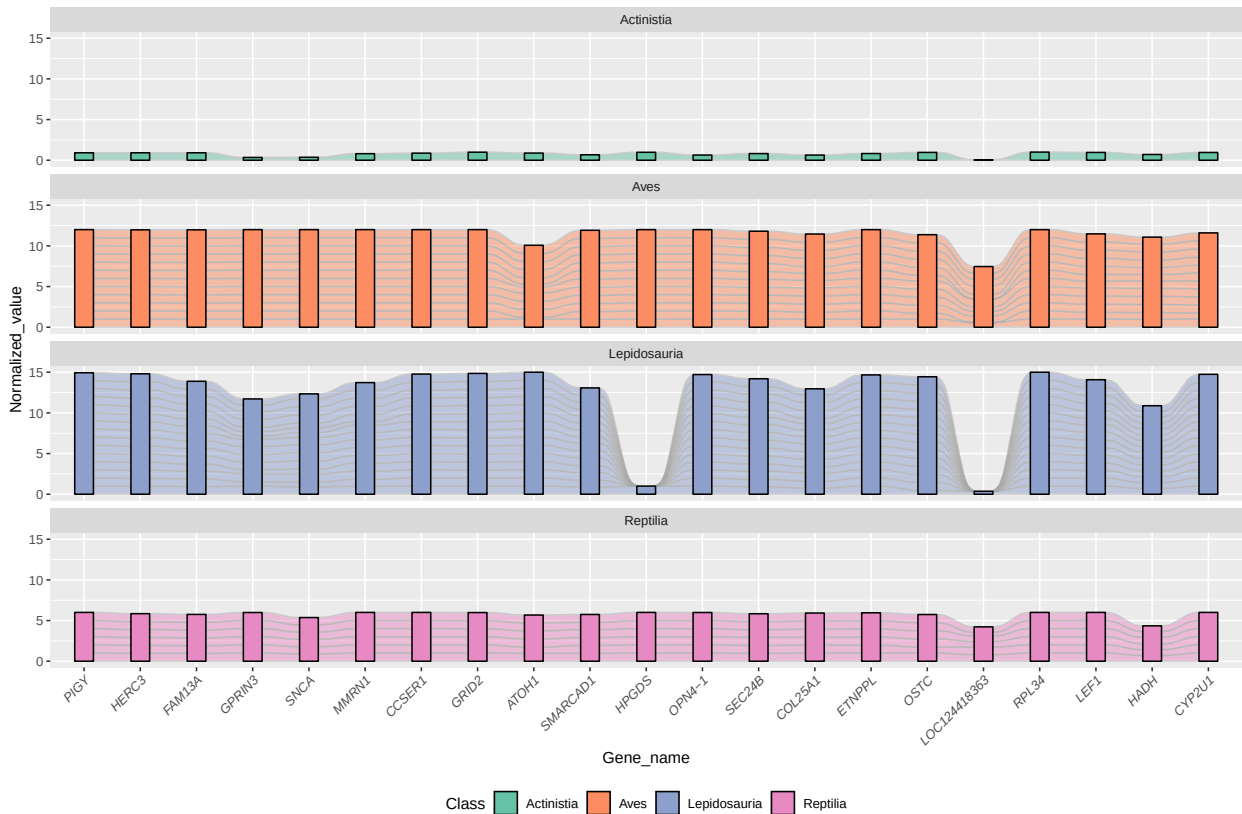


Figure 158: HPGDS.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

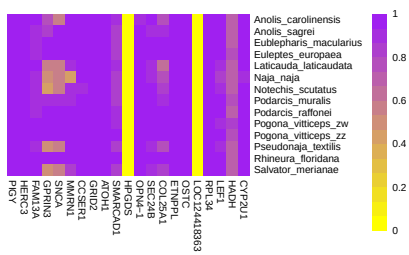


Figure 159: HPGDS.FS_Exonic.Final.Gallus_gallus.21_genes_heatmap.pdf

Syntenic evidence

HPGDS							
genbank prediction hpgds							
Chelonia mydas	> UNC5C >	< BMPR1B <	< PDLM5 <	> LOC102931316 <	< SMARCAD1 <	< ATOH1 <	< GRID2 <
Chr 4 (NC_057852.1)							
Gallus gallus		< COL25A1 <	> SEC24B >	< OPN4-1 <	> HPGDS >	< SMARCAD1 <	< ATOH1 <
Chr 4 (NC_052535.1)							
Podarcis muralis	> UNC5C >	< BMPR1B <	< PDLM5 <	> HPGDS >	< melanopsin <	< SMARCAD1 <	< ATOH1 <
Chr 9 (NC_041320.1)							
Anolis carolinesis	> UNC5C >	< BMPR1B <	< PDLM5 <	> HPGDS >	< melanopsin <	< SMARCAD1 <	
Chr 5 (NC_085845.1)							
Pogona vitticeps	> UNC5C >	< BMPR1B <	< PDLM5 <	> HPGDS >	< melanopsin like <	< SMARCAD1 <	< GRID2 <
Chr 5 (NC_132826.1)							
Crotalus tigris	> UNC5C >	< BMPR1B <	< PDLM5 <	> HPGDS >	< opn4 <	< SMARCAD1 <	< GRID2 <
NW_024100413.1 (unplaced) NW_024100620.1 (unplaced)							
Ornithorhynchus anatinus	> MGARP >	< ELF2 >	< NOCT <	> HPGDS >	< SMARCAD1 <	< ATOH1 <	< GRID2 <
Chr 12 (NC_041739.1)							
Homo sapiens	> UNC5C >	< BMPR1B <	< PDLM5 <	> HPGDS >	< SMARCAD1 <	< ATOH1 <	< GRID2 <
Chr 4 (NC_000004.12)							
Mus musculus	< Ndnf <	< Tnfr3 <	< Qrfpr1 <	> HPGDS >	< SMARCAD1 <	< ATOH1 <	< GRID2 <
Chr 6 (NC_000072.7)							

Figure 160: HPGDS.pdf

HPGDS.txt

Synteny analysis of HPGDS

We analyzed the synteny of HPGDS in squamates and representative outgroups

- ↪ . The HPGDS syntenic block is conserved, except for one flanking
 ↪ gene in *Gallus gallus*, *Ornithorhynchus anatinus*, and *Mus musculus*.
 ↪ In these species, the flank is located on the same side and in the
 ↪ same orientation, but it appears only after skipping several
 ↪ intervening genes. In the synteny plots, red blocks indicate the
 ↪ absence of HPGDS, green blocks mark its presence, light blue blocks
 ↪ represent genes conserved across lineages, and light purple blocks
 ↪ denote different flanking genes.

Transcriptomic evidence *Pogona vitticeps*

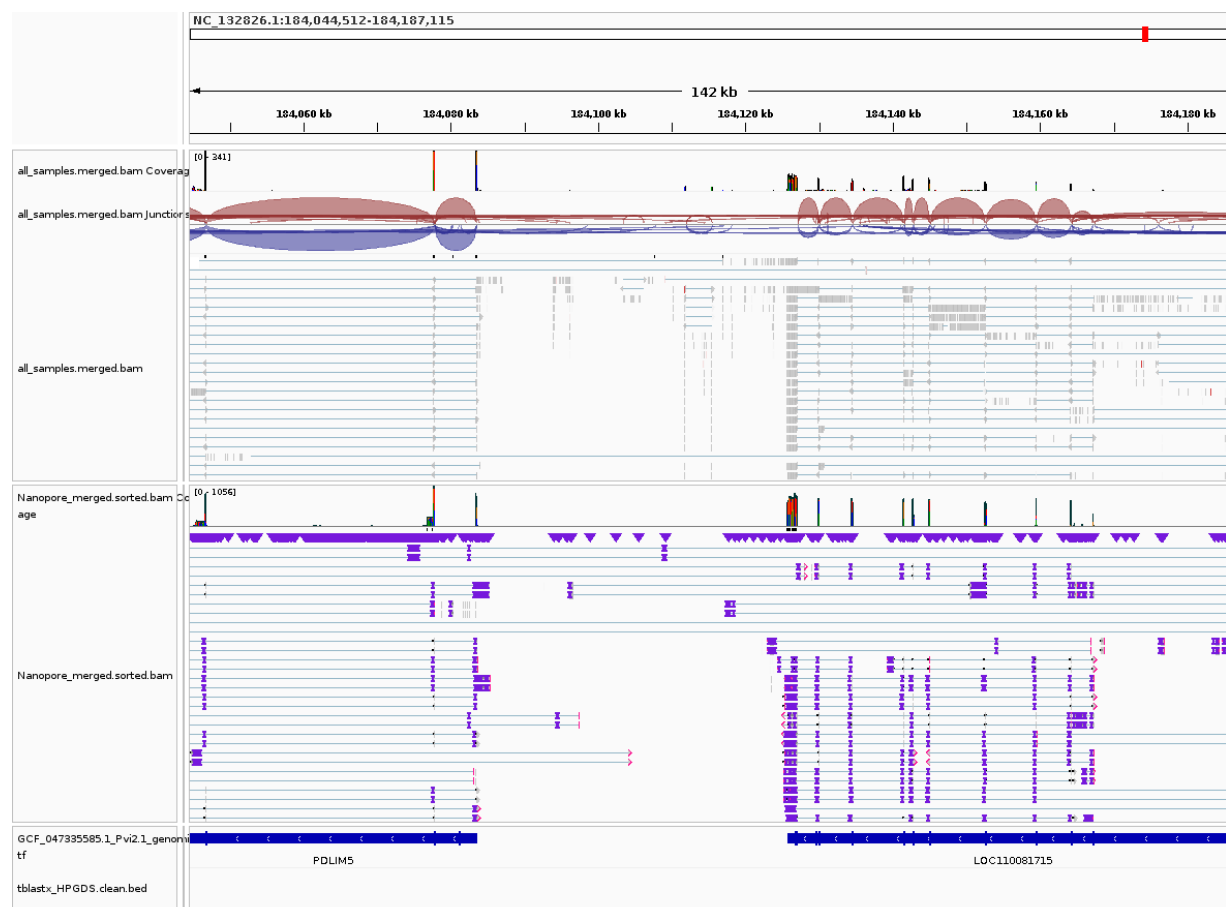


Figure 161: HPGDS.png

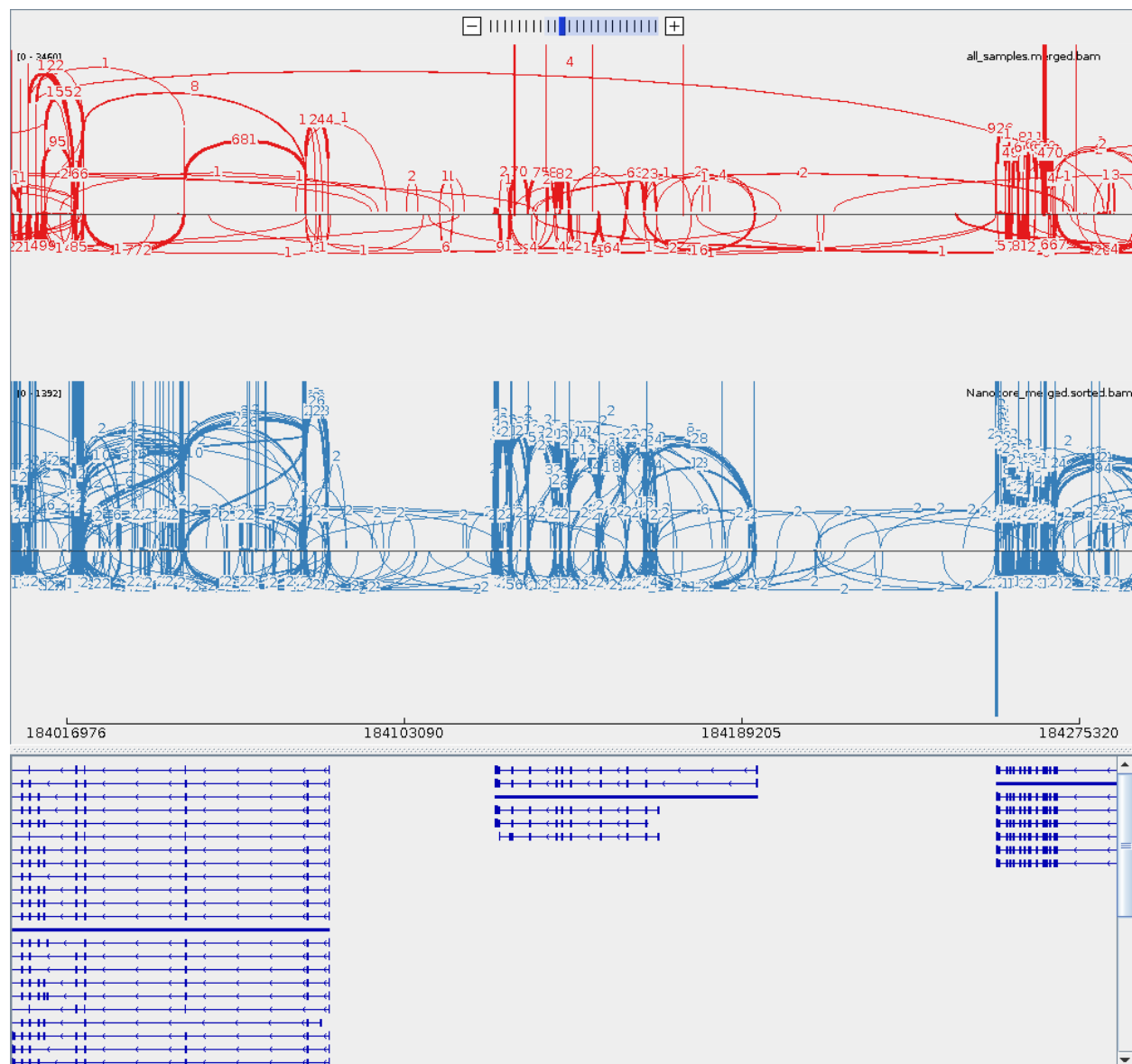


Figure 162: HPGDS_Shash.png

16 HSD17B1

Assembly verification Evidence

Crotalus_tigris-PacBio

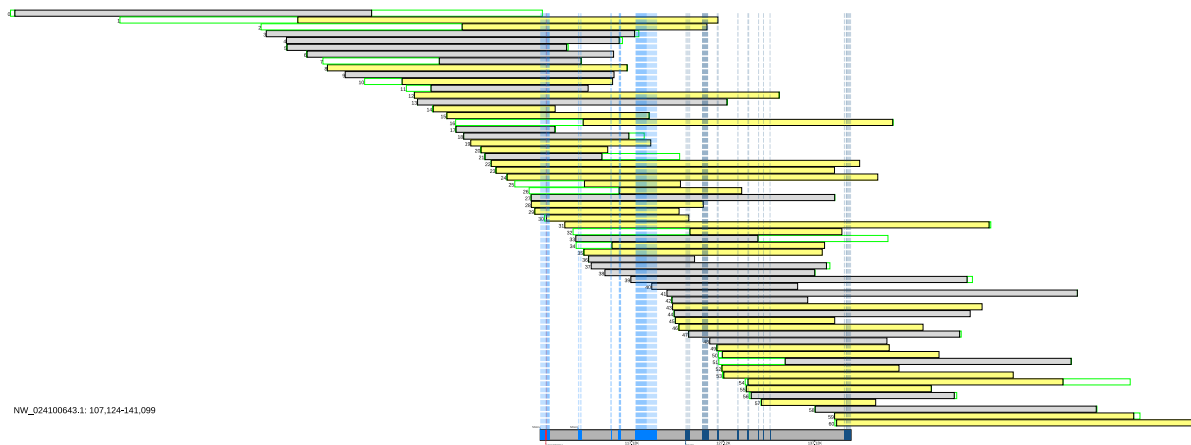


Figure 163: HSD17B1:NW_024100643.1:107124-141099.pdf

Podarcis_muralis-PacBio

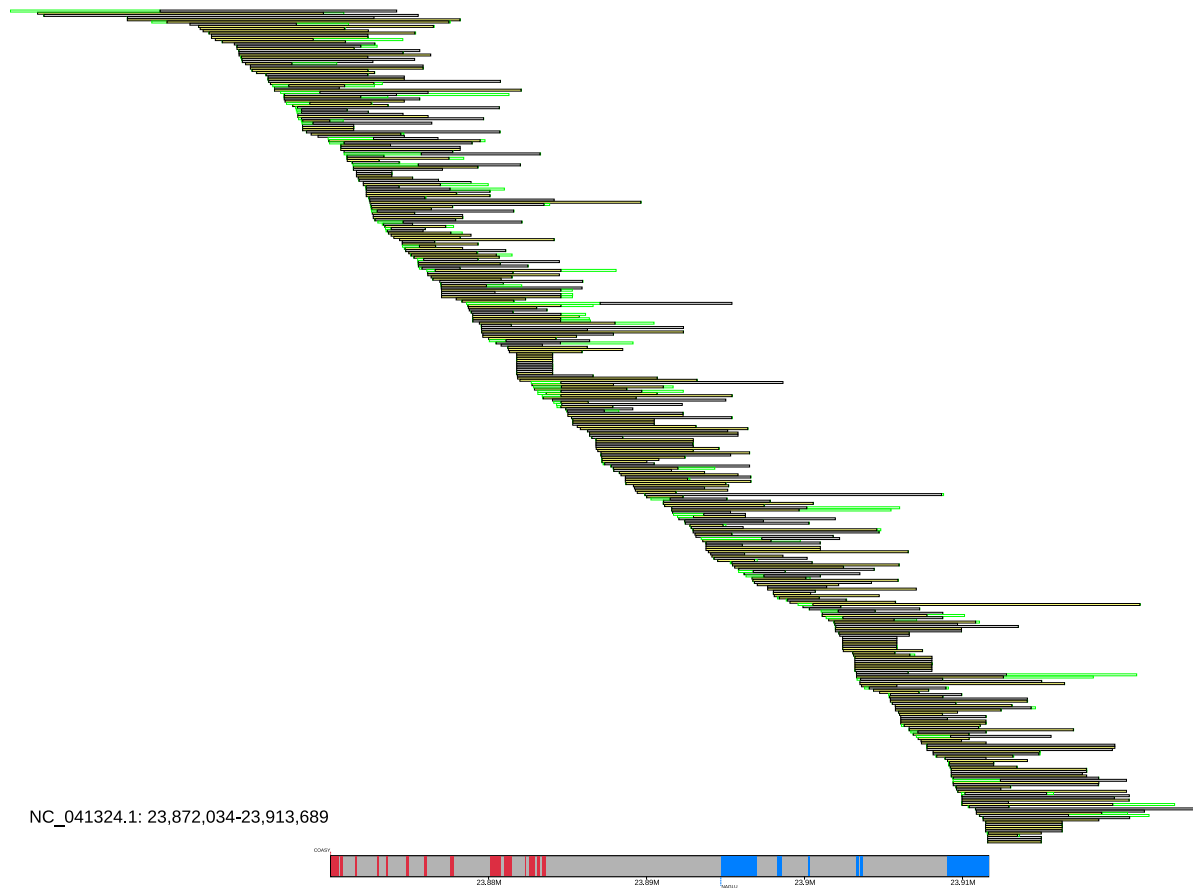


Figure 164: HSD17B1:NC_041324.1:23872034-23913689.pdf

Pogona_vitticeps-Nanopore

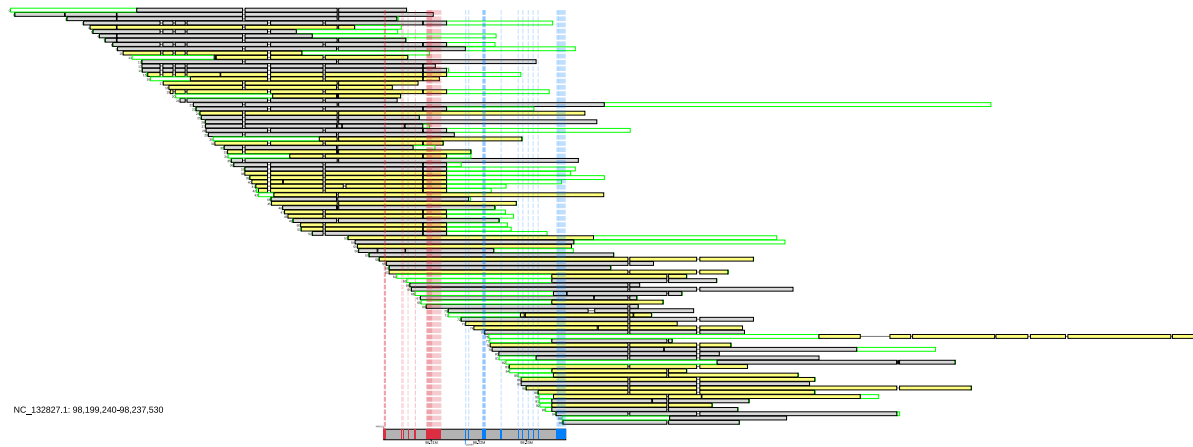


Figure 165: HSD17B1:NC_132827.1:98199240-98237530.pdf

Important gene stats

HSD17B1_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
HSD17B1	6.078125	61.3505 +/- 8.20655	4.40981 +/- 0.649158	60.3058 +/- 12.3821	Yes	FNBP1L;LOC110077992;LOC118095402;RDH8;

Intergenic distance phylogenetic signal evidence

HSD17B1_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
HSD17B1	179	17	162	3	1	0.999999999999687

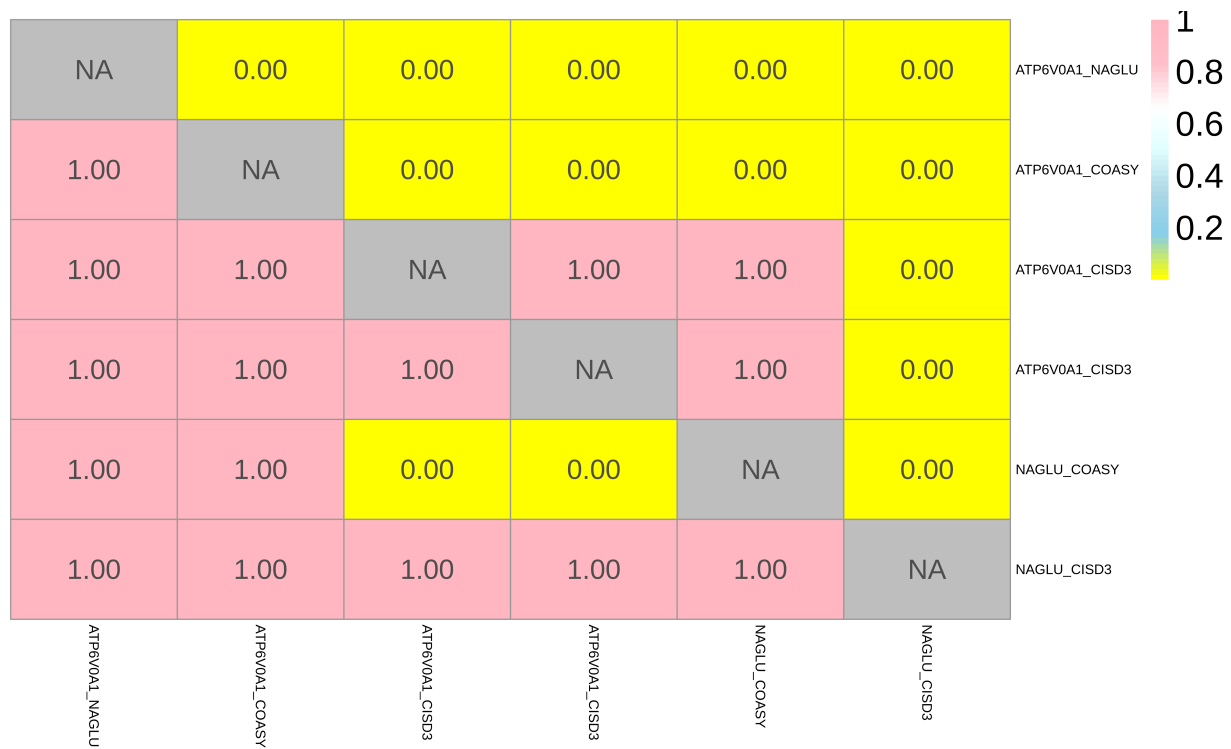


Figure 166: Heatmap_of_deletion_plot.png

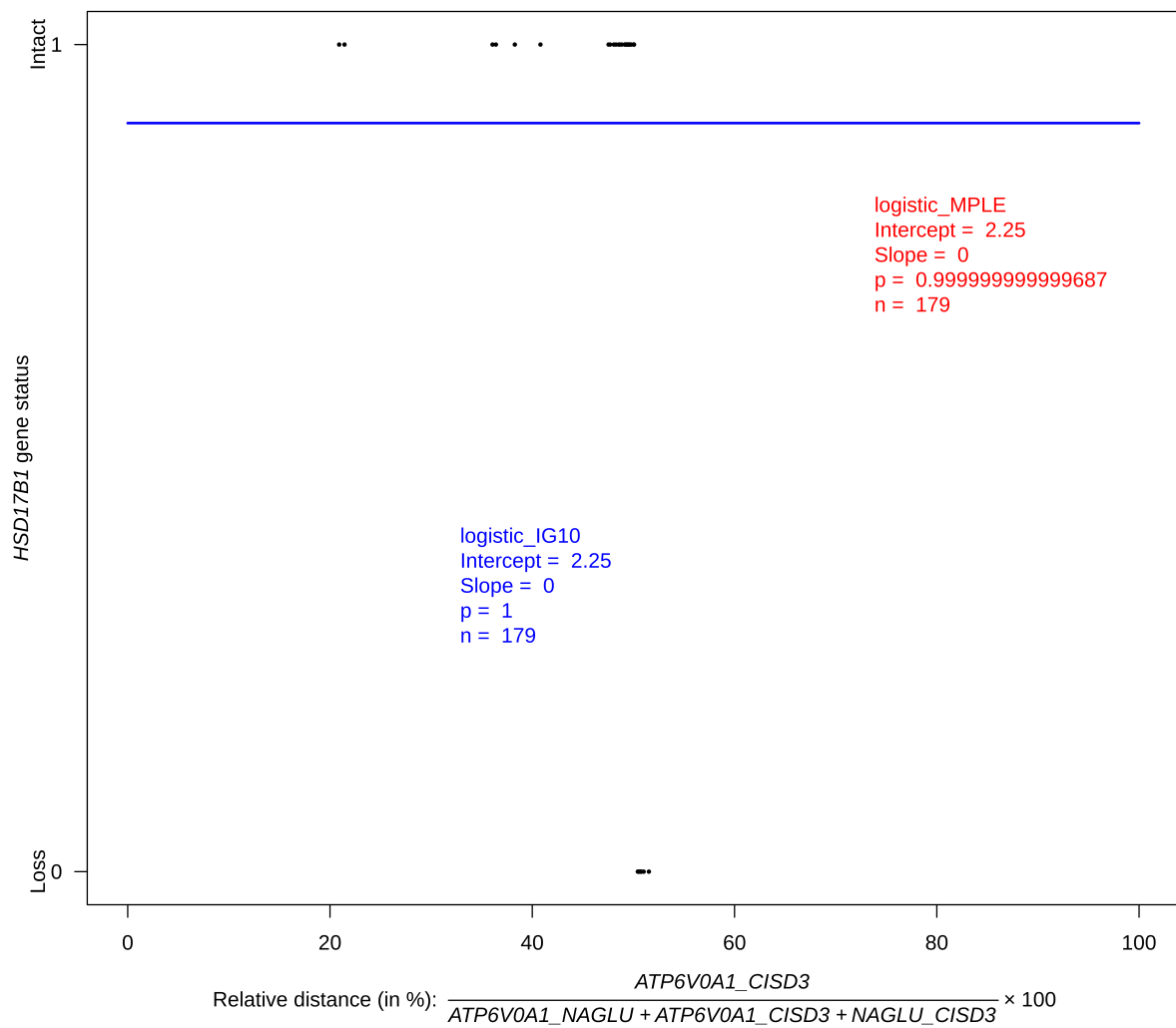


Figure 167: Phylogenetic_signal_of_deletion_plot.png

HSD17B1_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
HSD17B1	179	17	162	3	1	0.999999999999687

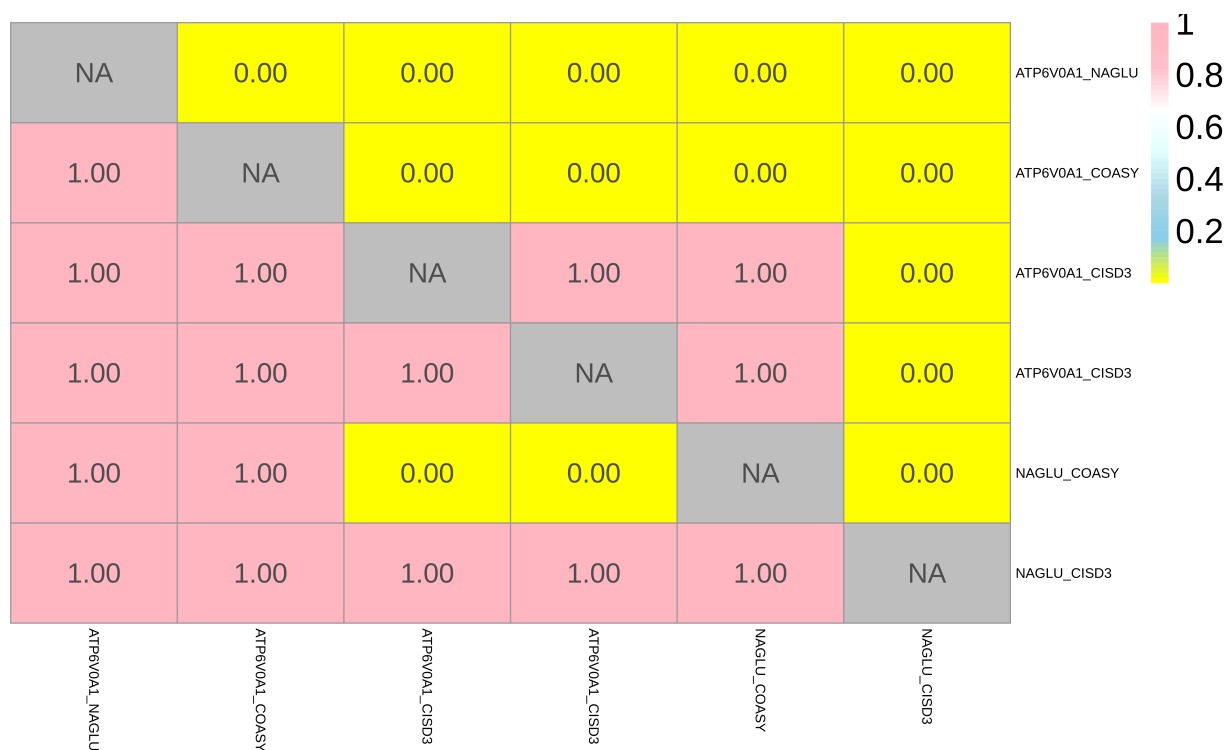


Figure 168: Heatmap_of_deletion_plot.png

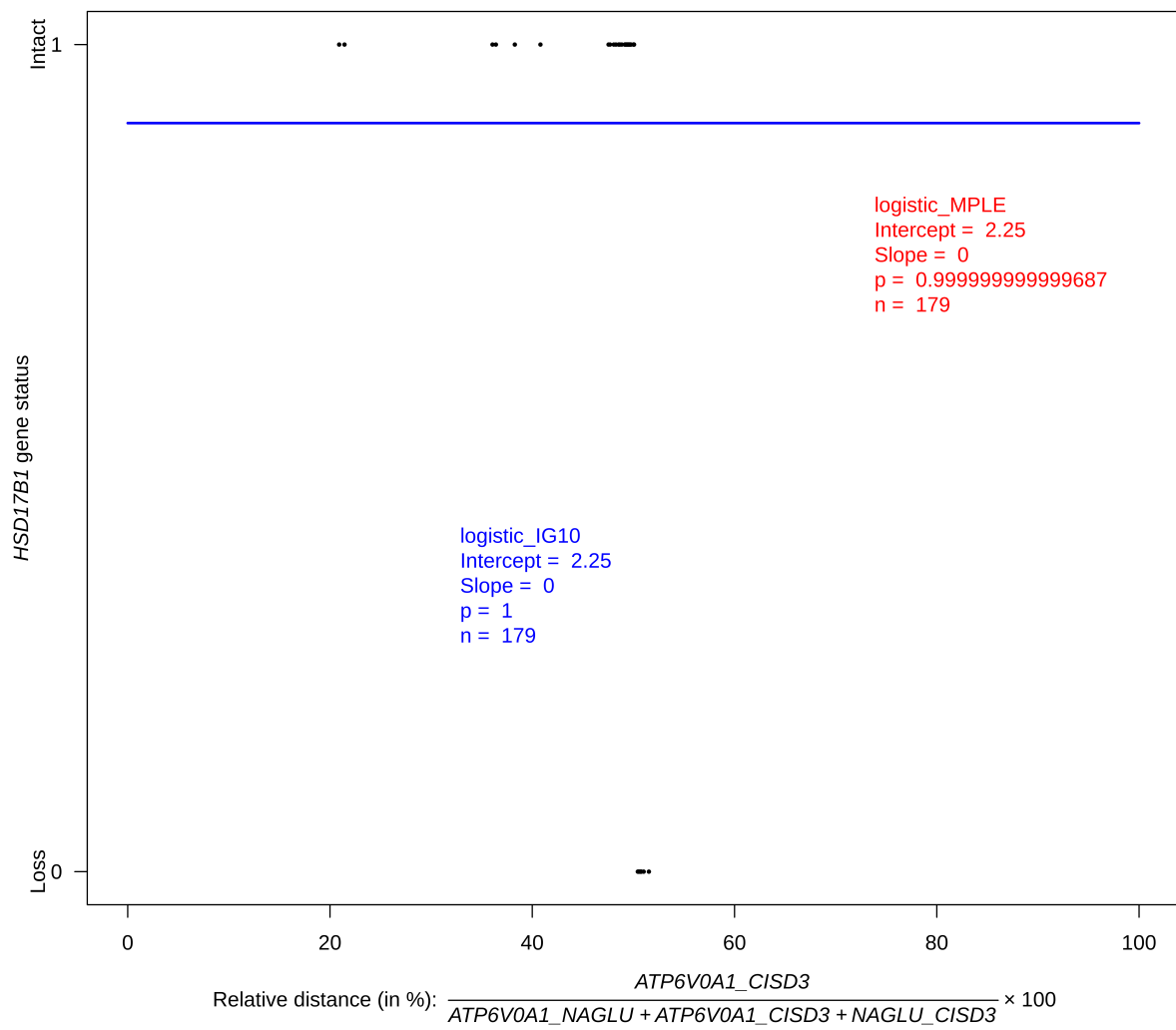


Figure 169: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence

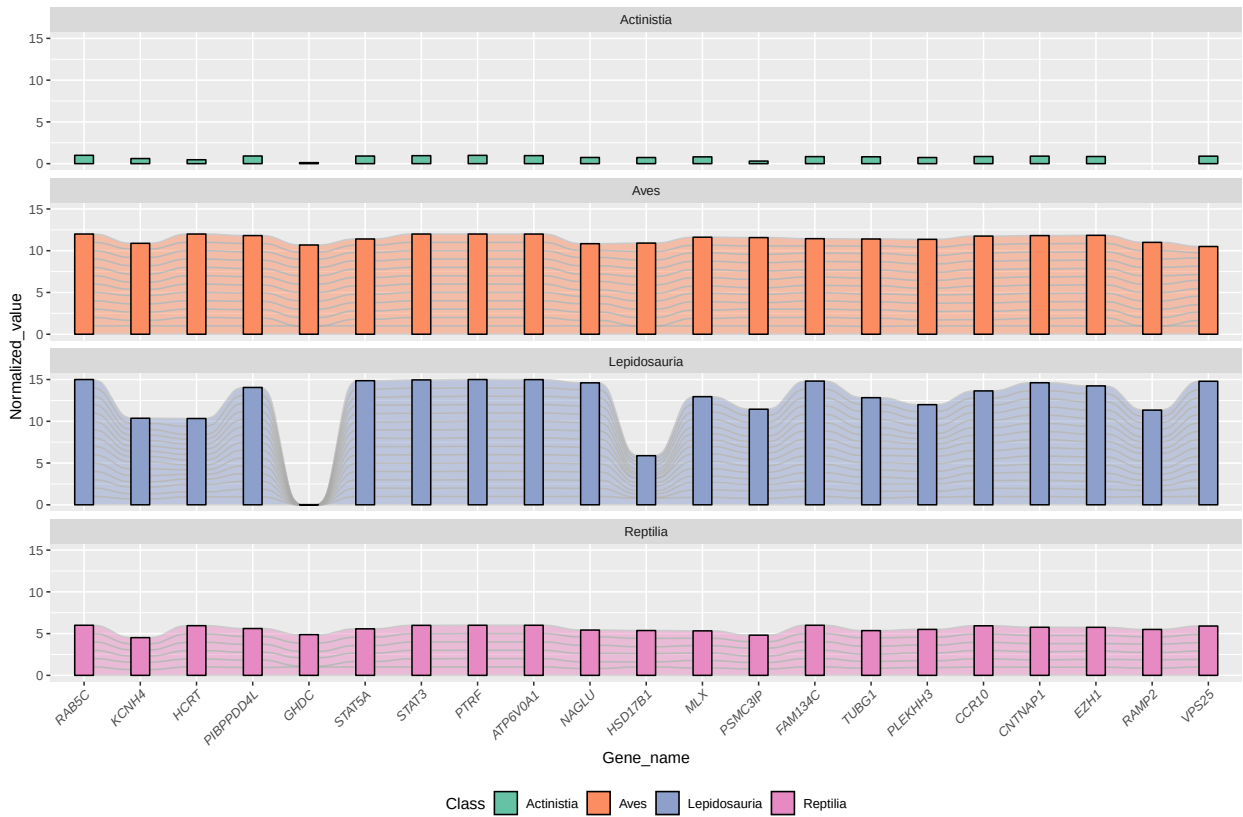


Figure 170: HSD17B1.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

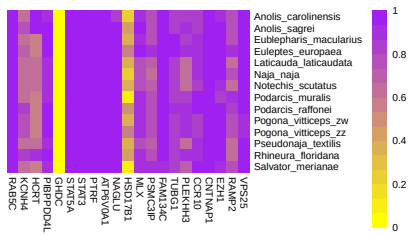


Figure 171: HSD17B1.FS_Exonic.Final.Gallus_gallus.21_genes_heatmap.pdf

Lastz gene tree

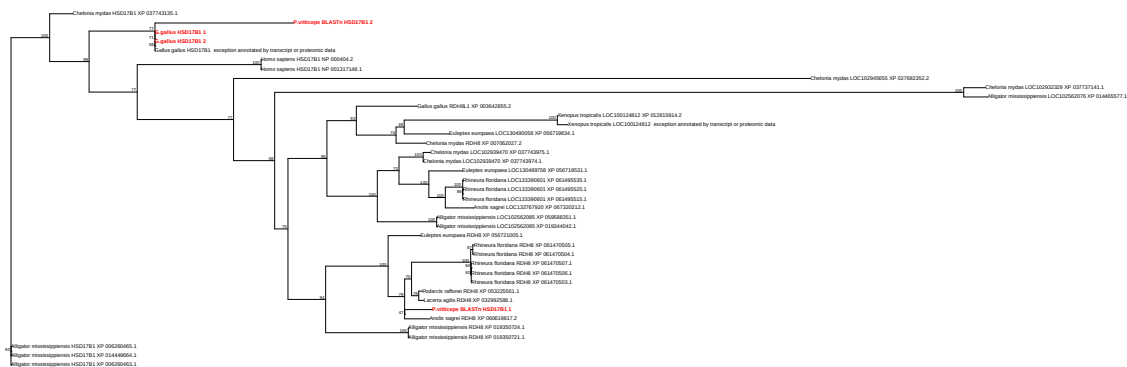


Figure 172: HSD17B1.combined.mafft.aln.highlighted.pdf

Syntenic evidence

					HSD17B1			
								coenzyme Q-binding protein COQ10 homolog B
Chelonia mydas		< CAVIN1 <	> ATP6V0A1 >	< LOC11402285 >	> HSD17B1 >	> NAGLU >	> COASY >	> LOC102942725 >
								Chr 27 (NC_057860.1)
								#BLAST
Gallus gallus		< PTRF <	> ATP6V0A1 >	> NAGLU >	> HSD17B1 >	> COASY >	> MLX >	< PSMC3IP <
								Chr 27 (NC_052558.1)
								coenzyme Q-binding protein COQ10 homolog B, mitochondrial-like
Podarcis muralis		> RAB5C >	> KAT2A >	> NAGLU >	> HSD17B1 >	> COASY >	> LOC11458270 <	< C1SD3 <
								Chr 13 (NC_041324.1)
								coenzyme Q-binding protein COQ10 homolog B, mitochondrial-like
Anolis carolinensis		> RAB5C >	> KAT2A >	> NAGLU >	> HSD17B1 >	> COASY >	> LOC10056733 <	< C1SD3 <
								Chr 6 (NC_085846.1)
								coenzyme Q-binding protein COQ10 homolog B
Pogona vitticeps			> KAT2A >	> NAGLU >	> HSD17B1 >	> COASY >	> LOC12030353 <	< C1SD3 <
								NW_024100643.1 (unplaced)
								coenzyme Q-binding protein COQ10 homolog B
Crotalus tigris		> RAB5C >	> KAT2A >	> NAGLU >	> HSD17B1 >	> COASY >	> LOC12030353 <	< C1SD3 <
								Chr 6 (NC_132827.1)
								PSMC3IP
Ornithorhynchus anatinus		< CAVIN1 <	> ATP6V0A1 >	> NAGLU >	> HSD17B1 >	> COASY >	> MLX >	< LOC100081660 <
								Chr 11 (NC_041738.1)
Homo sapiens		< CAVIN1 <	> LOC10272523 >	> ATP6V0A1 >	> NAGLU >	> HSD17B1 >	> COASY >	> MLX >
								Chr 17 (NC_000017.11)
Mus musculus		< CAVIN1 <	> ATP6V0A1 >	> NAGLU >	> HSD17B1 >	> COASY >	> MLX >	< PSMC3IP <
								Chr 11 (NC_000077.7)

Figure 173: HSD17B1.pdf

HSD17B1.txt

Synteny analysis of HSD17B1

We analyzed the synteny of HSD17B1 in squamates and representative outgroups. The innermost flanking gene is conserved, while the outer flanking genes differ in squamates. Despite this variation, the HSD17B1 syntenic block itself is conserved. In the synteny plots, red blocks indicate the absence of HSD17B1, green blocks mark its presence, light blue blocks represent genes conserved across lineages, and light purple blocks denote different flanking genes.

Transcriptomic evidence Pogona vitticeps



Figure 174: HSD17B1.png

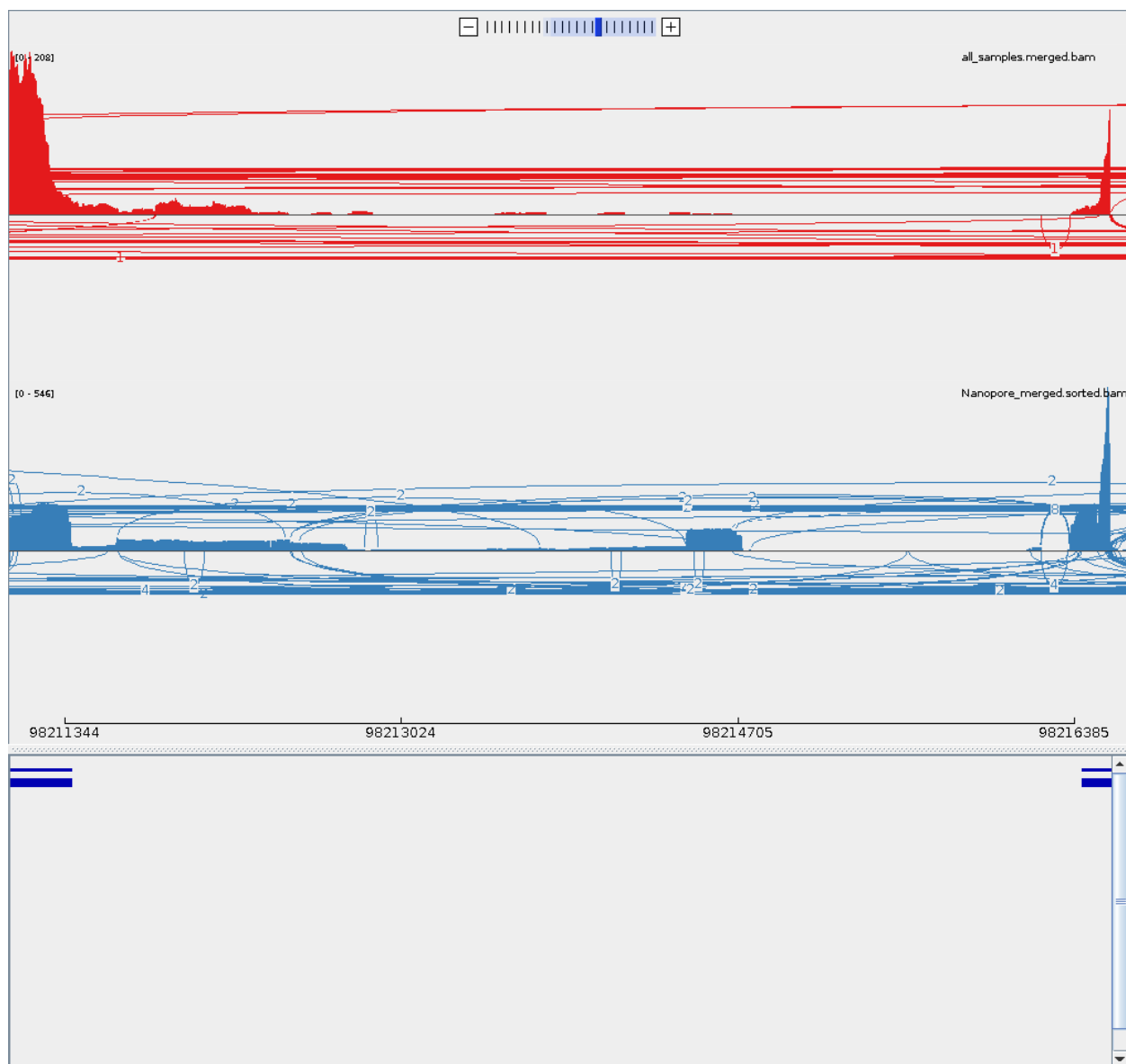


Figure 175: HSD17B1_shash.png

17 IFTAP

Assembly verification Evidence

Podarcis_muralis-PacBio

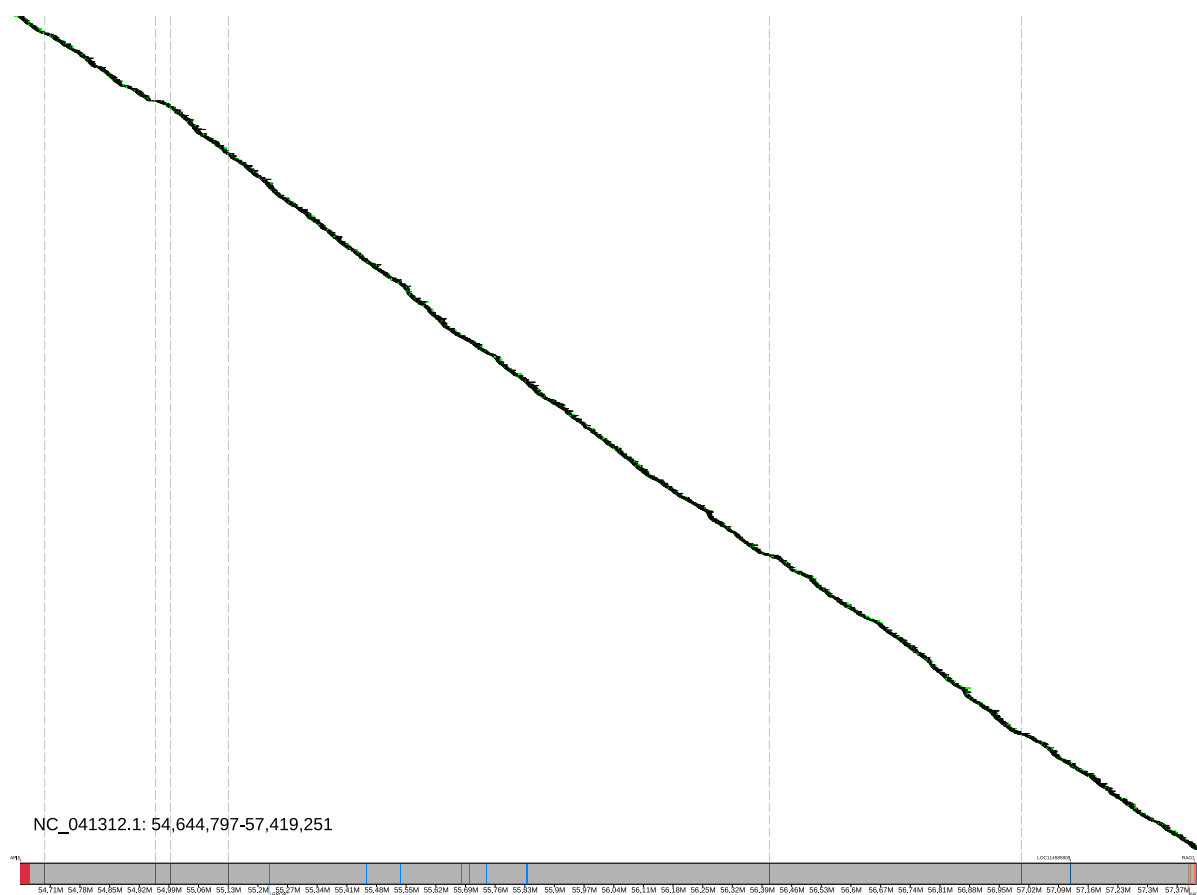


Figure 176: IFTAP:NC_041312.1:54644797-57419251.pdf

Pogona_vitticeps-Nanopore

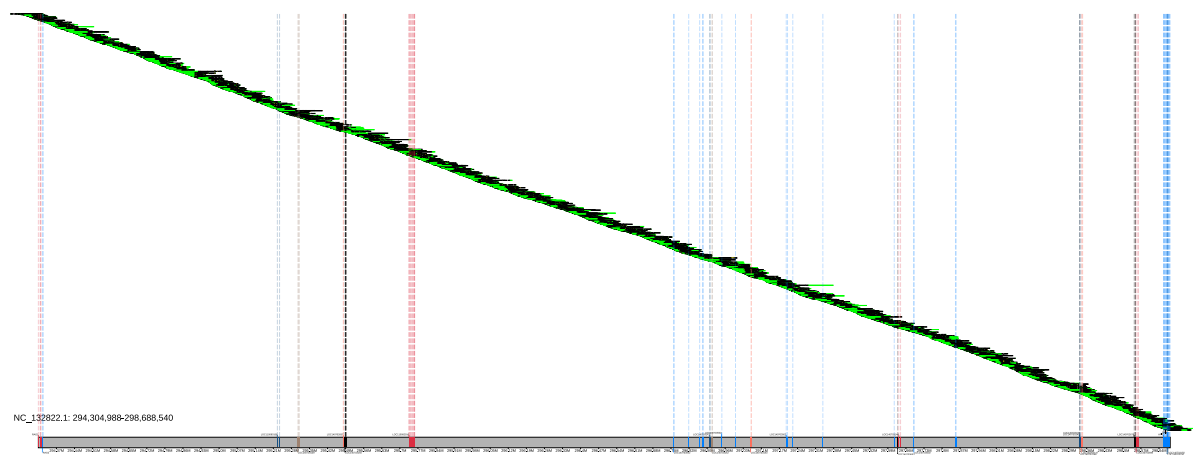


Figure 177: IFTAP:NC_132822.1:294304988-298688540.pdf

Important gene stats

IFTAP_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
IFTAP	6.123595506	45.0773 +/- 4.55662	3.68508 +/- 0.337665	58.6763 +/- 14.5696	No	Na

Intergenic distance phylogenetic signal evidence

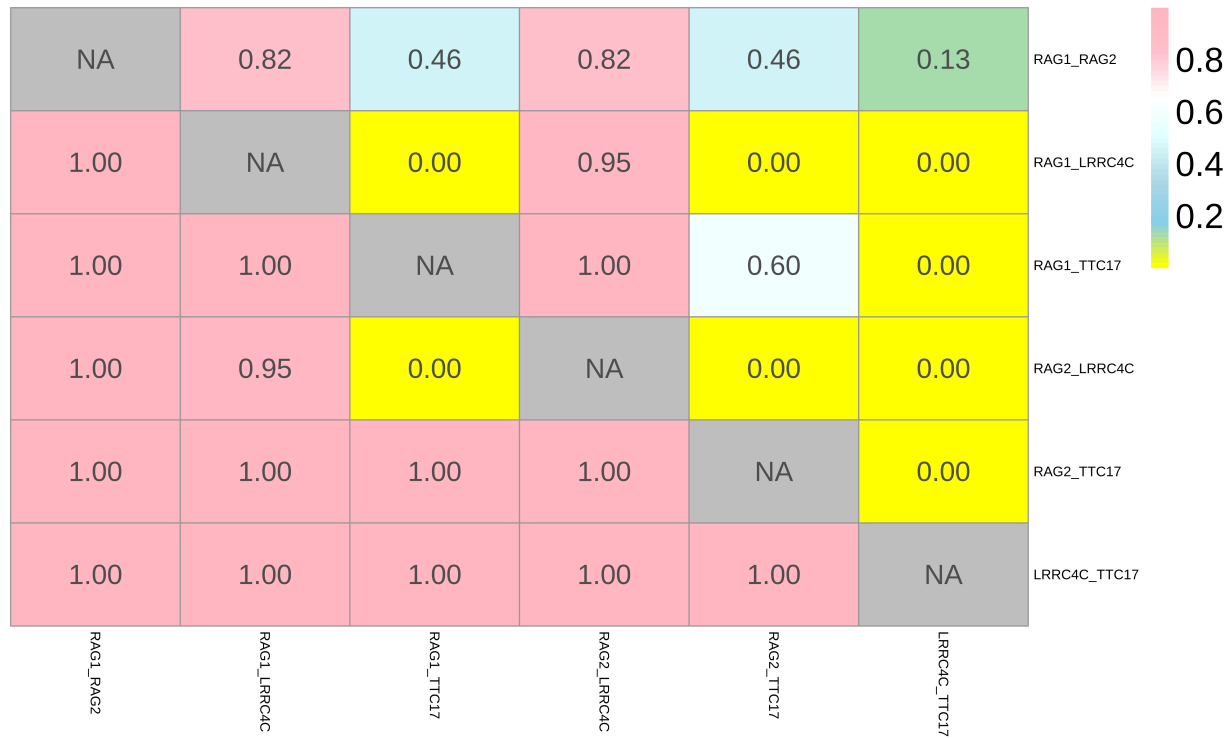


Figure 178: Heatmap_of_deletion_plot.png

IFTAP_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
IFTAP	218	19	199	0	0.110326447612994	0.294441806600901

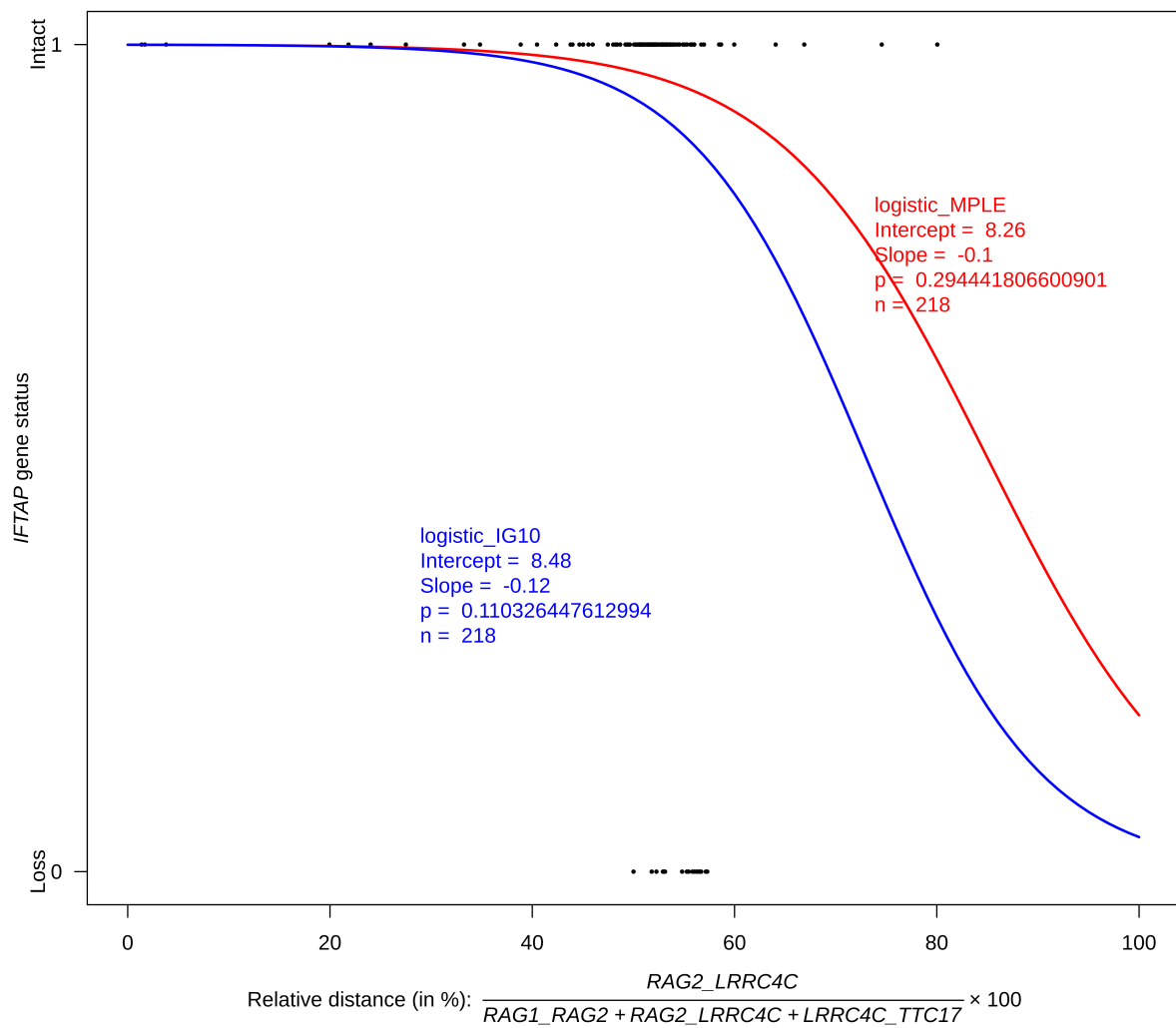


Figure 179: Phylogenetic_signal_of_deletion_plot.png

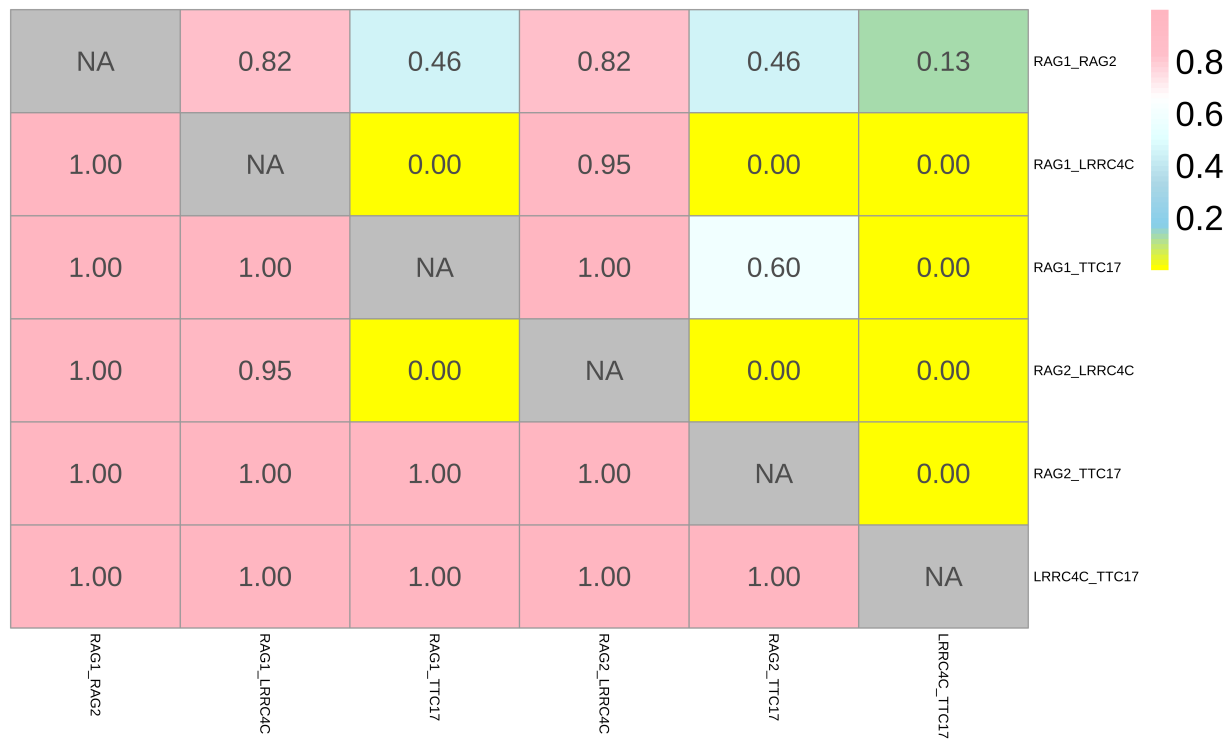


Figure 180: Heatmap_of_deletion_plot.png

IFTAP_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
IFTAP	218	19	199	0	0.110326447612994	0.294441806600901

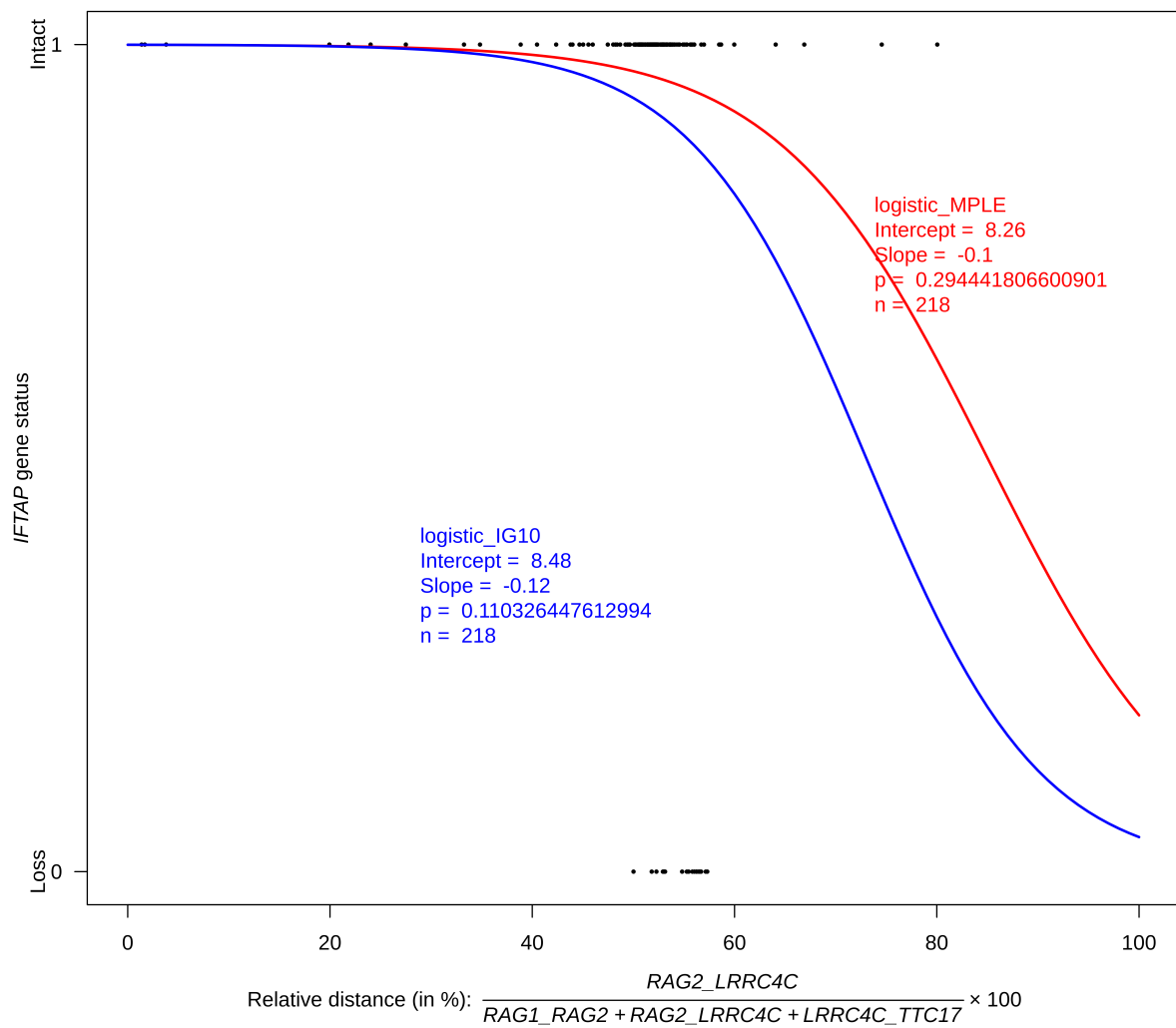


Figure 181: Phylogenetic_signal_of_deletion_plot.png

Syntenic evidence

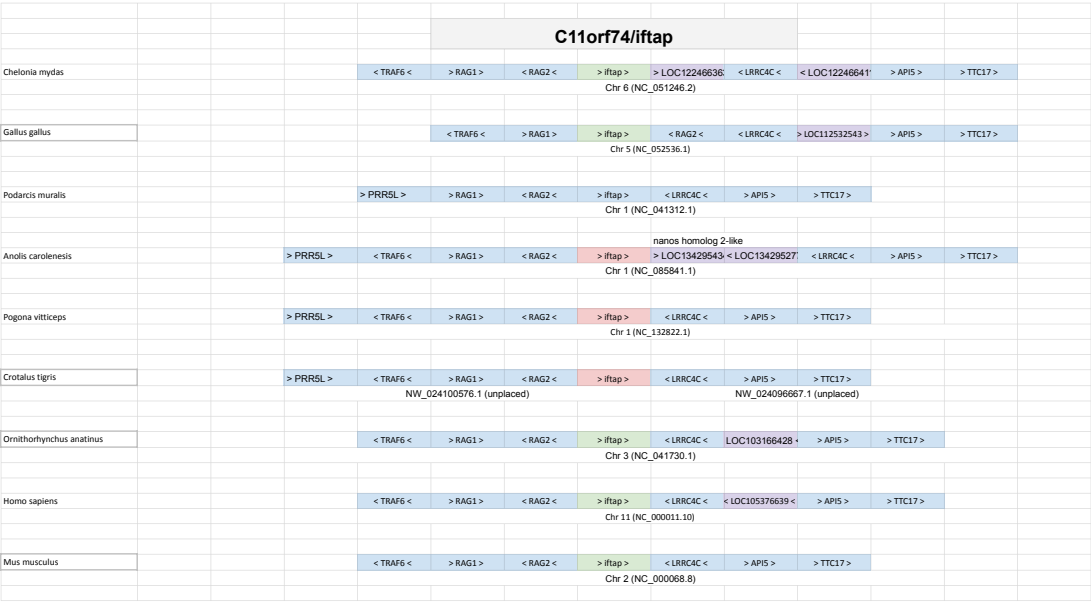


Figure 182: IFTAP.pdf

IFTAP.txt

Synteny analysis of IFTAP

We analyzed the synteny of IFTAP in squamates and representative outgroups

→ . The IFTAP syntenic block is conserved overall, with a few

→ deviations in the arrangement of neighboring genes. In the synteny

→ plots, red blocks indicate the absence of IFTAP, green blocks mark

→ its presence, light blue blocks represent genes conserved across

→ lineages, and light purple blocks denote different flanking genes

Transcriptomic evidence *Pogona vitticeps*

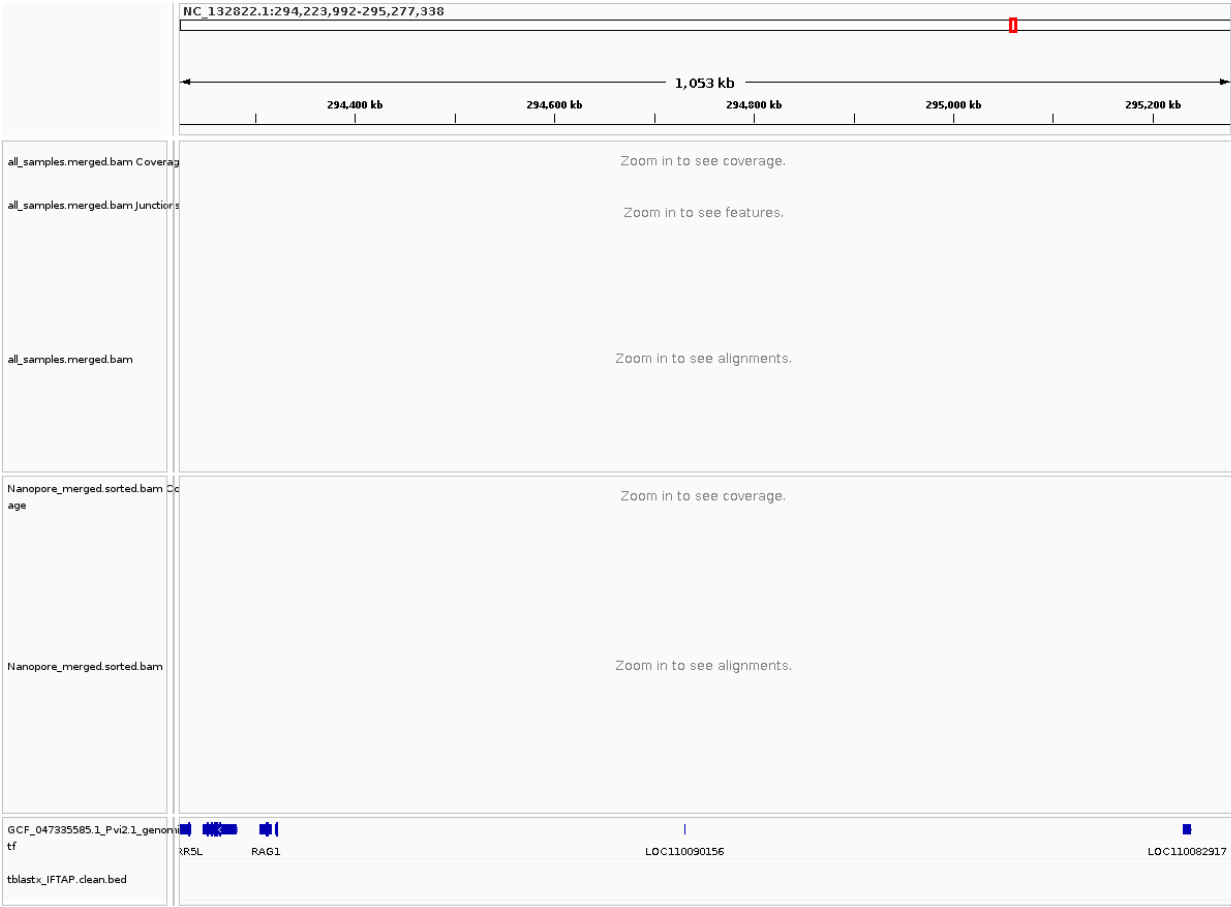


Figure 183: IFTAP.png

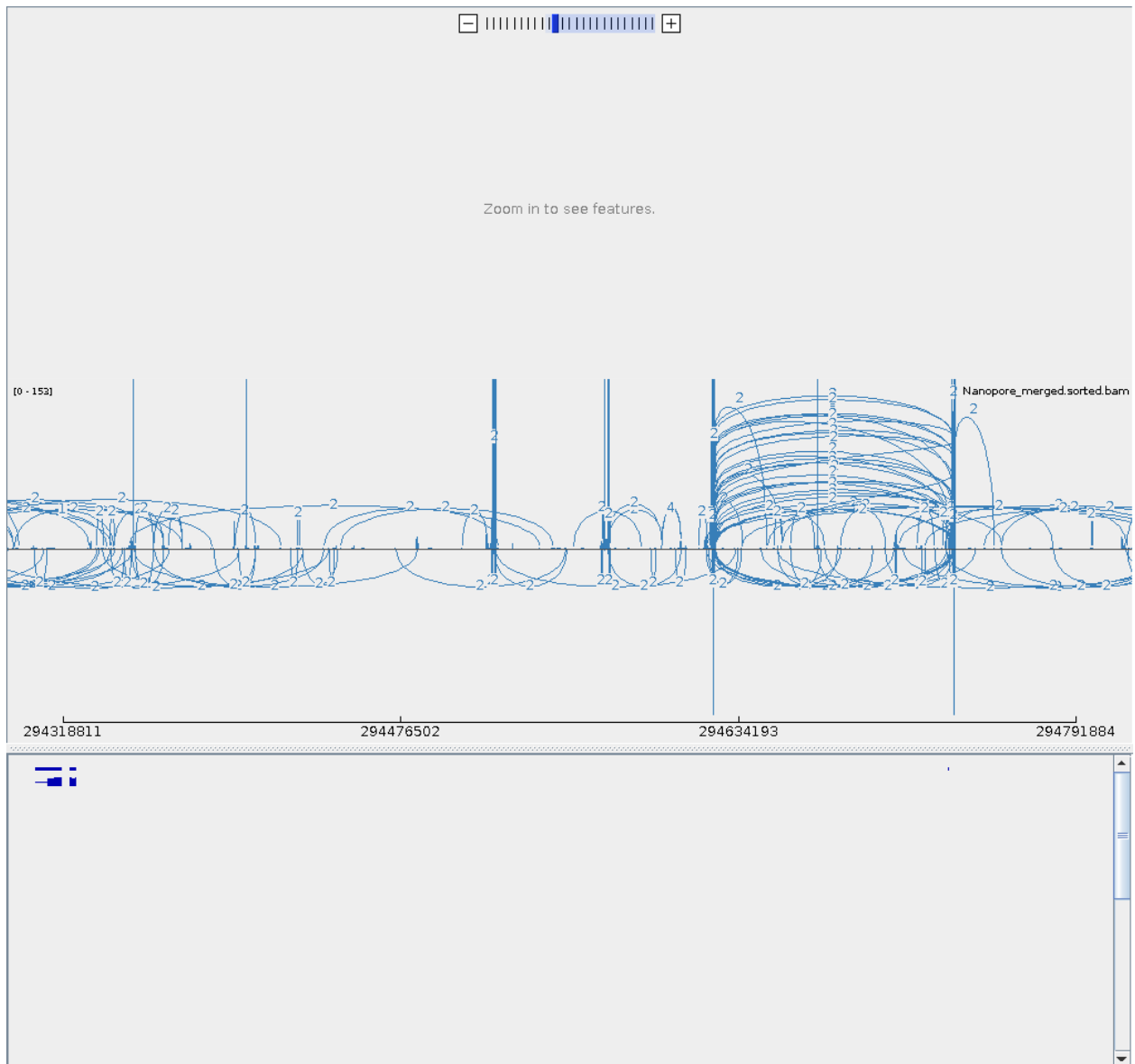


Figure 184: IFTAP_Sashimi.png

18 IL13RA2

Assembly verification Evidence

Crotalus_tigris-PacBio

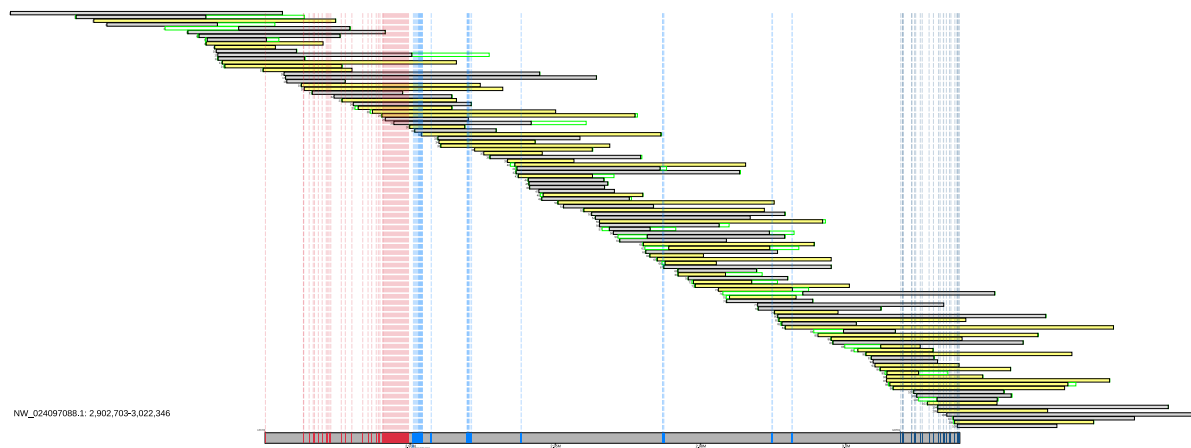


Figure 185: IL13RA2:NW_024097088.1:2902703-3022346.pdf

Podarcis_muralis-PacBio

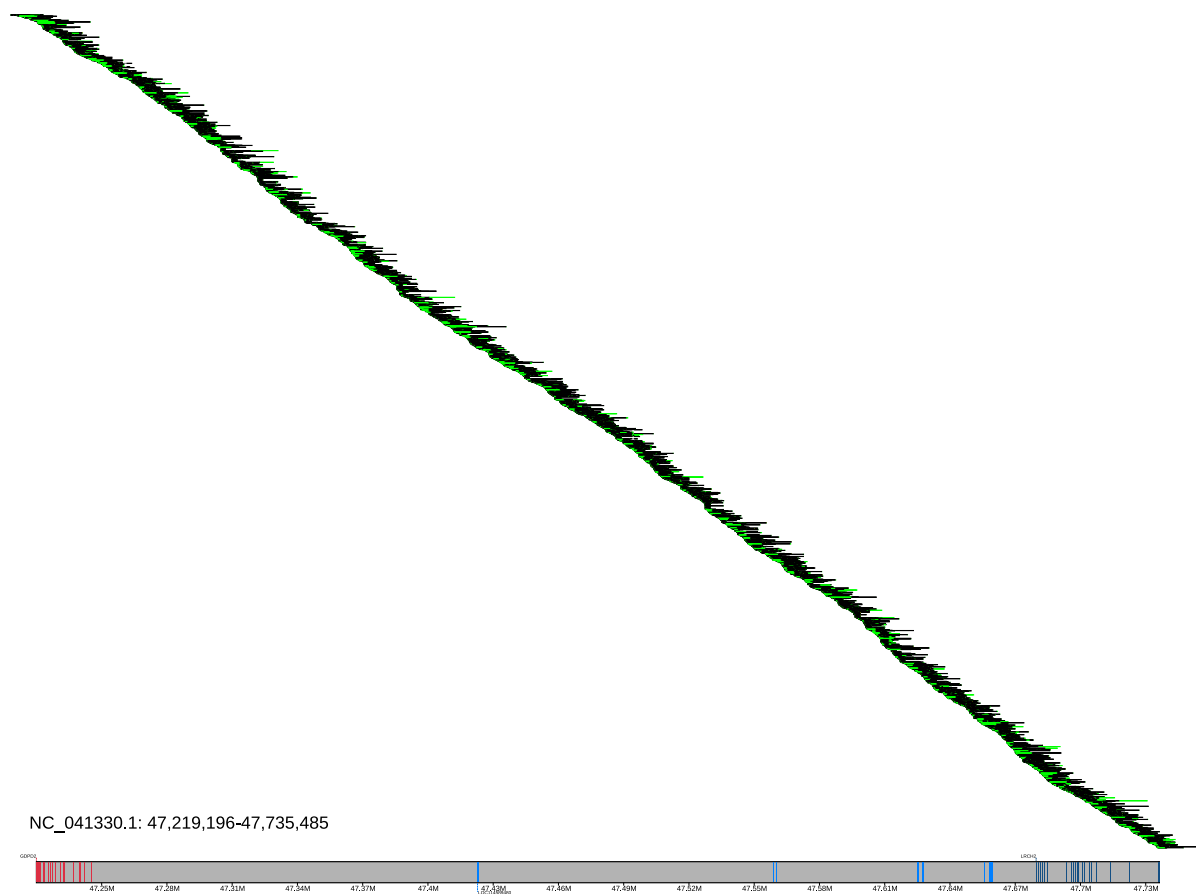


Figure 186: IL13RA2:NC_041330.1:47219196-47735485.pdf

Pogona_vitticeps-Nanopore

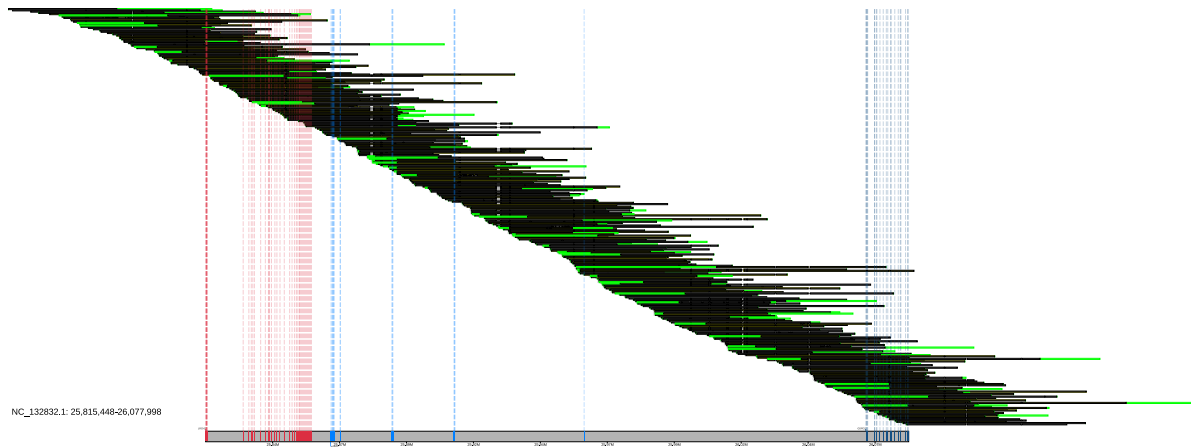


Figure 187: IL13RA2:NC_132832.1:25815448-26077998.pdf

Important gene stats

IL13RA2_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
IL13RA2	3.515625	44.8741 +/- 7.27592	3.57663 +/- 0.360549	59.4176 +/- 16.4018	Yes	Na

Intergenic distance phylogenetic signal evidence



Figure 188: Heatmap_of_deletion_plot.png

IL13RA2_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
IL13RA2	133	10	123	2	0.883005650433288	0.982688187296743

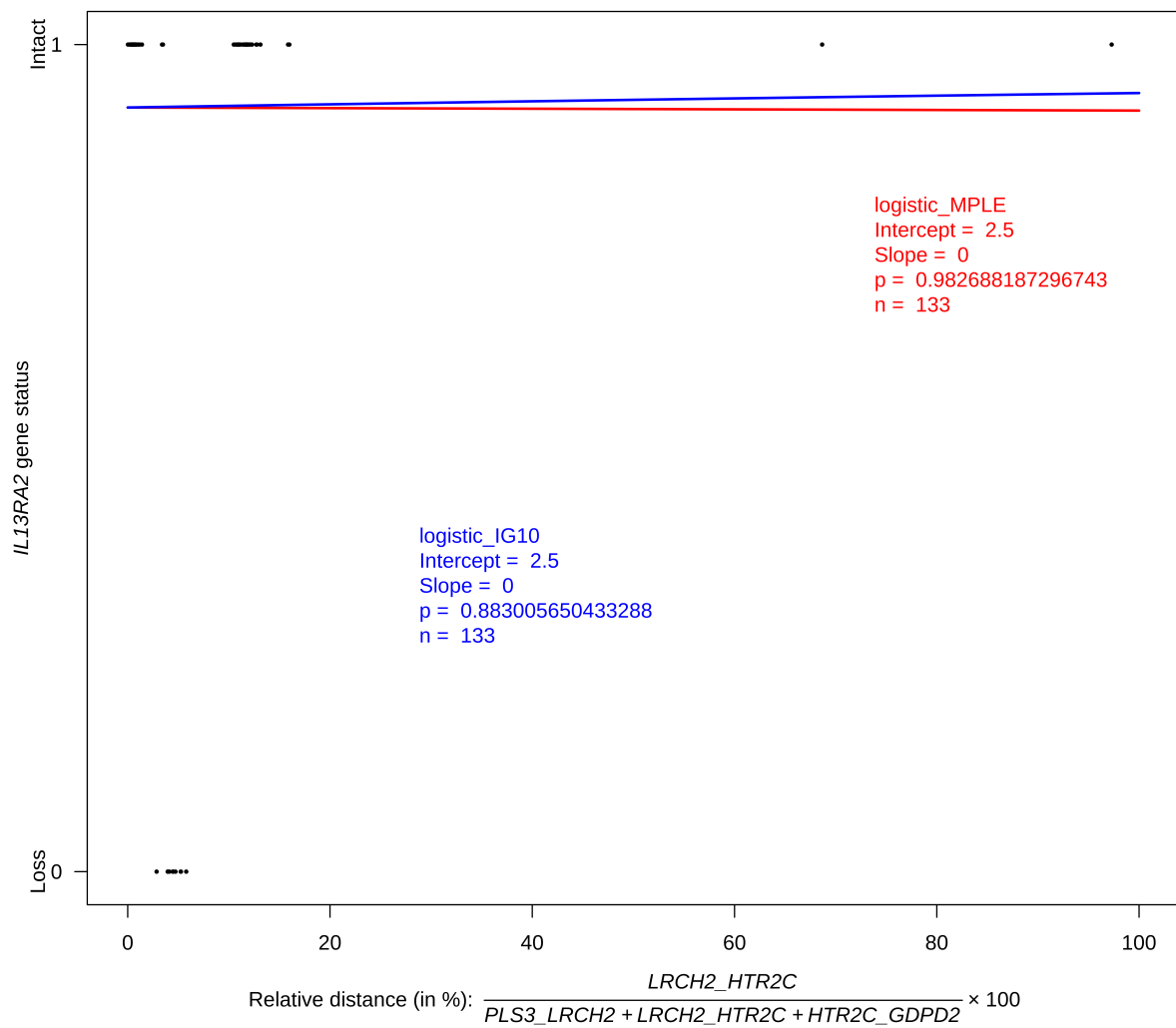


Figure 189: Phylogenetic_signal_of_deletion_plot.png



Figure 190: Heatmap_of_deletion_plot.png

IL13RA2_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
IL13RA2	133	10	123	2	0.883005650433288	0.982688187296743

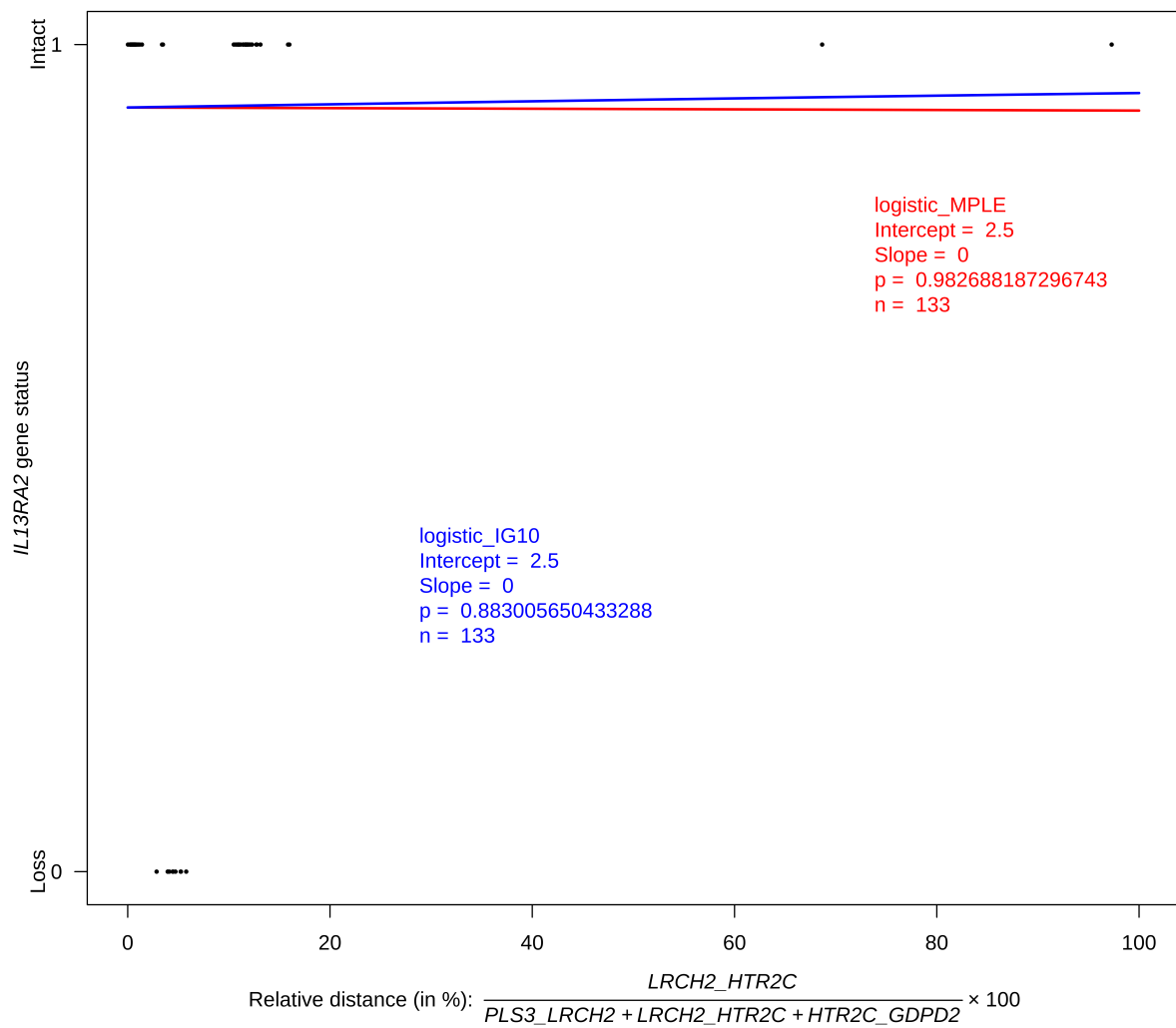


Figure 191: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence

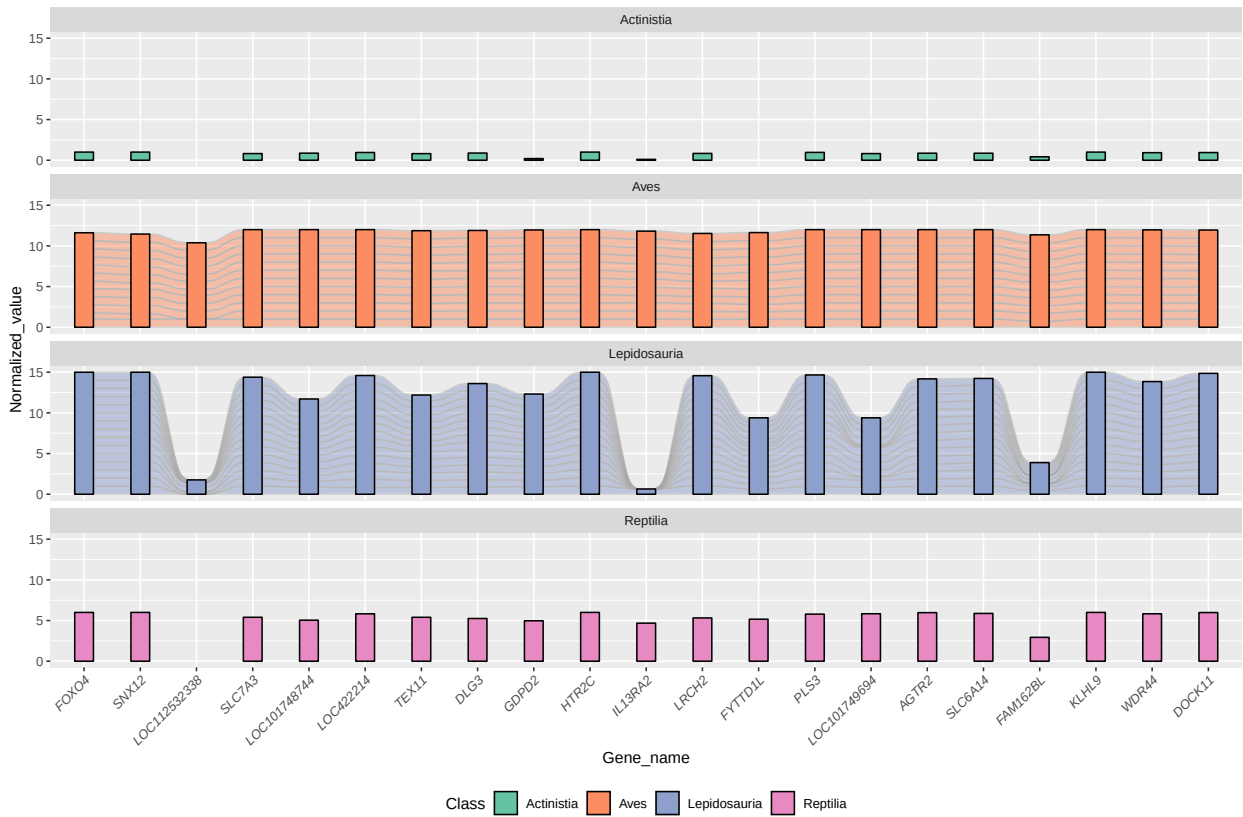


Figure 192: IL13RA2.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

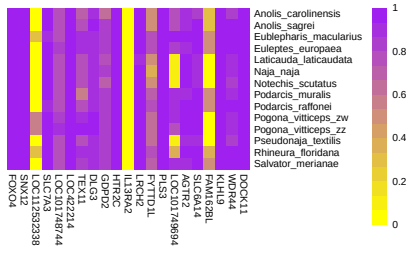


Figure 193: IL13RA2.FS_Exonic.Final.Gallus_gallus.21_genes_heatmap.pdf

Lastz gene tree

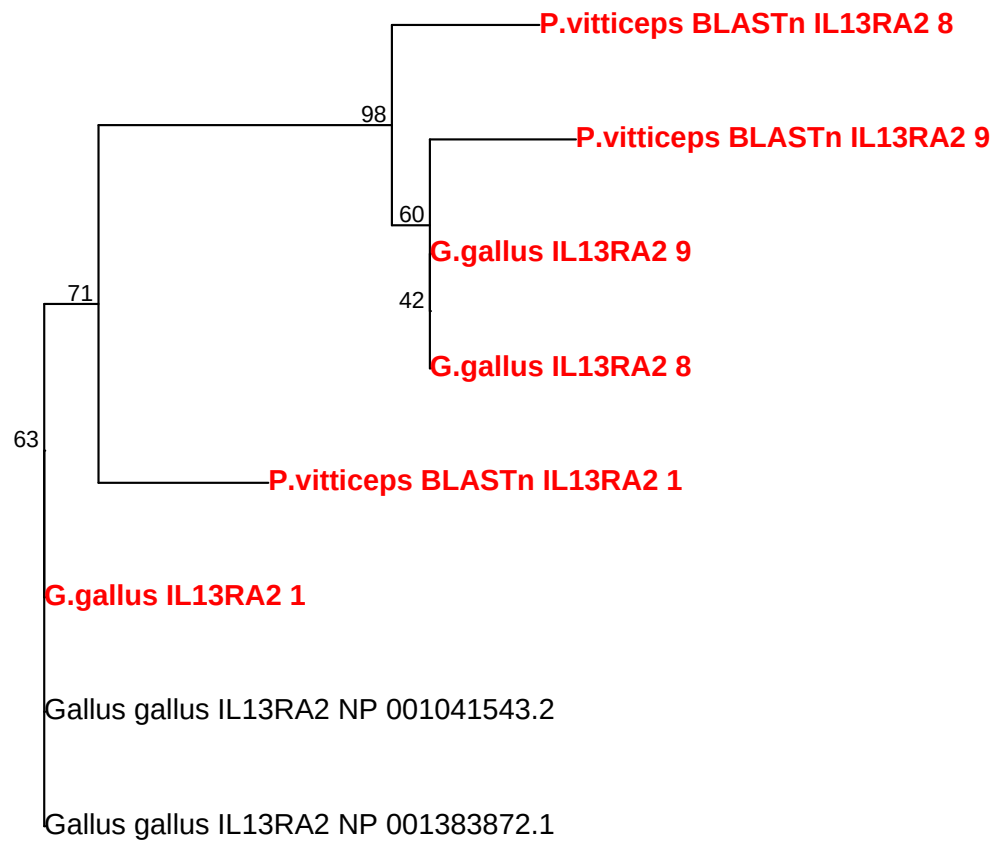


Figure 194: IL13RA2.combined.mafft.aln.highlighted.pdf

Syntenic evidence

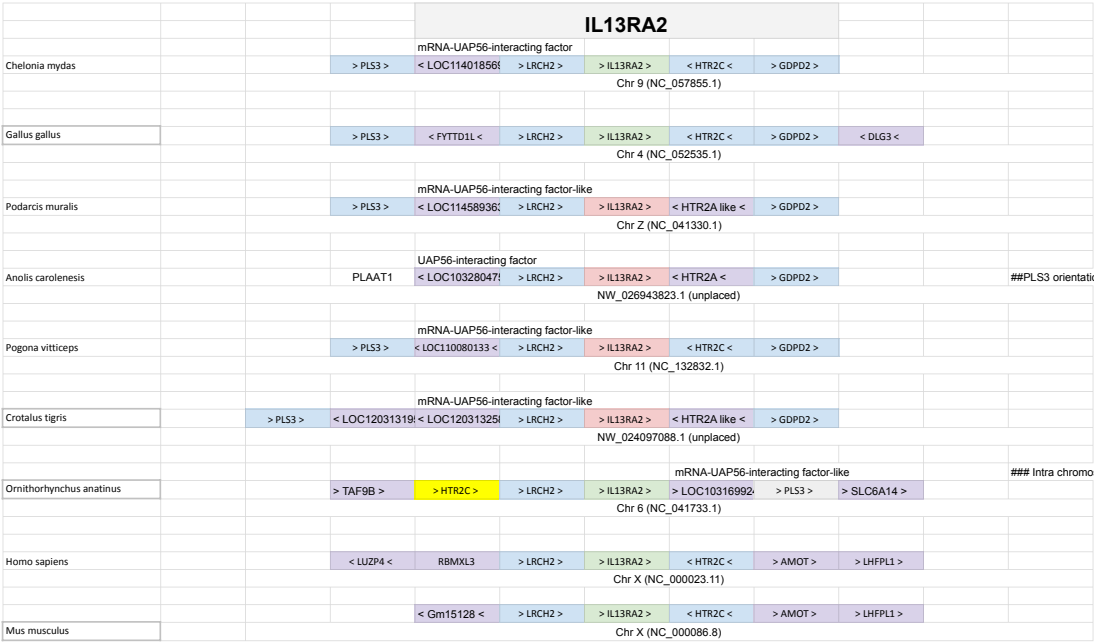


Figure 195: IL13RA2.pdf

IL13RA2.txt

Synteny analysis of IL13RA2

We analyzed the synteny of IL13RA2 in squamates and representative outgroups. The innermost flanking gene is conserved in all species, with slight variations in the relative positioning of some neighboring genes. For example, in Ornithorhynchus anatinus, the positions of HTR2C and PLS3 differ with respect to the focal gene, suggesting intrachromosomal rearrangements within the locus. Despite these shifts, the IL13RA2 locus itself remains conserved. In the synteny plots, red blocks indicate the absence of IL13RA2, green blocks mark its presence, light blue blocks represent genes conserved across lineages, and light purple blocks denote different flanking genes.

Transcriptomic evidence *Pogona vitticeps*

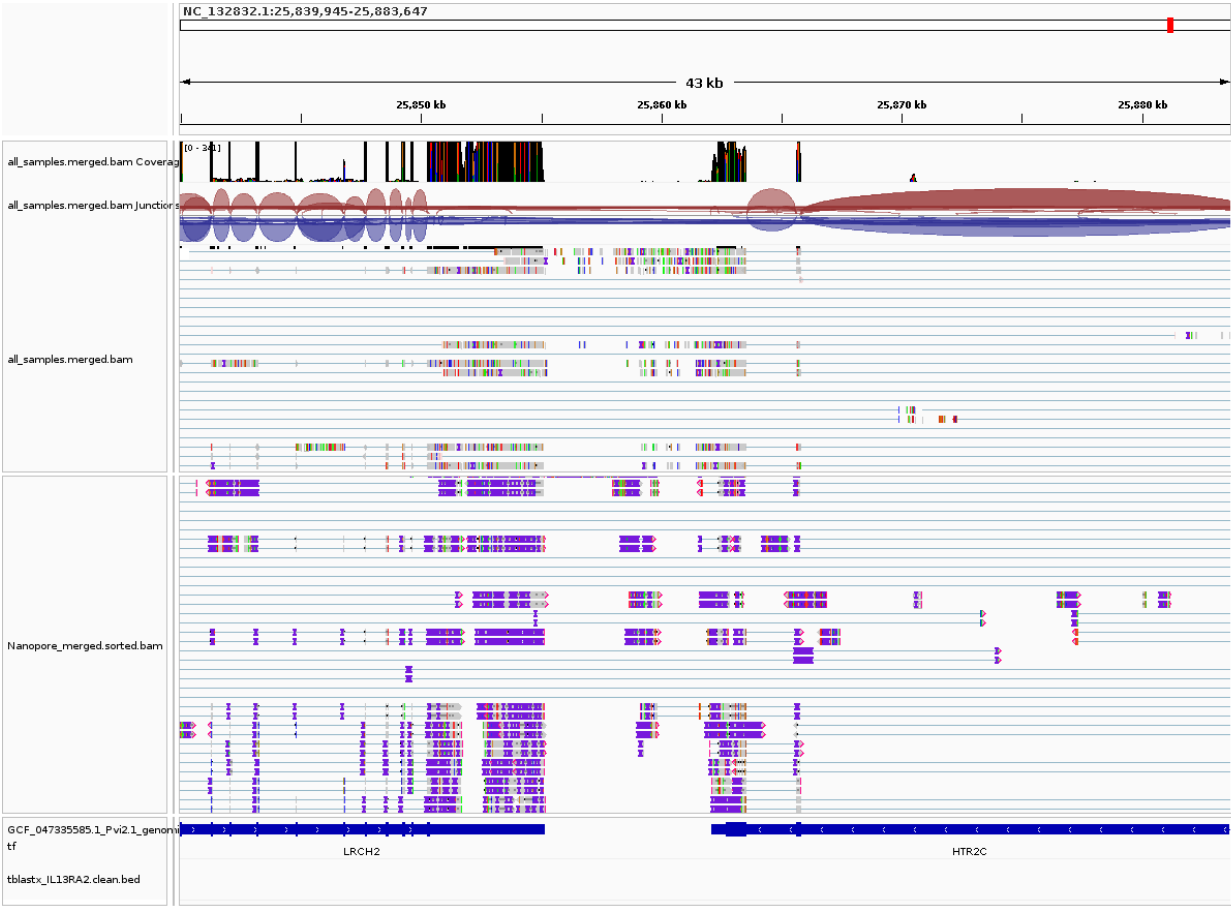


Figure 196: IL13RA2.png

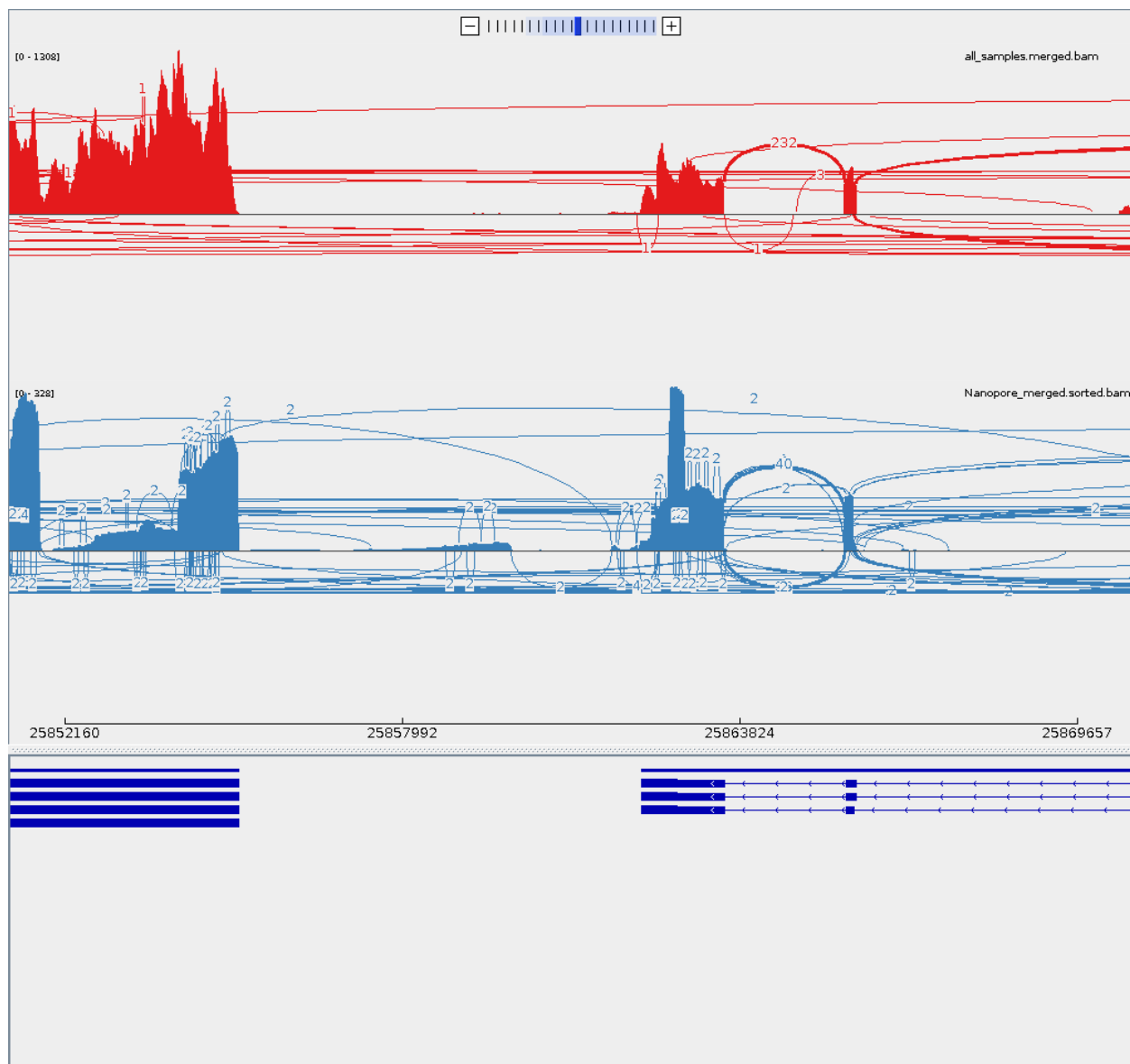


Figure 197: IL13RA2_Shash.png

19 IL26

Assembly verification Evidence

Crotalus_tigris-PacBio

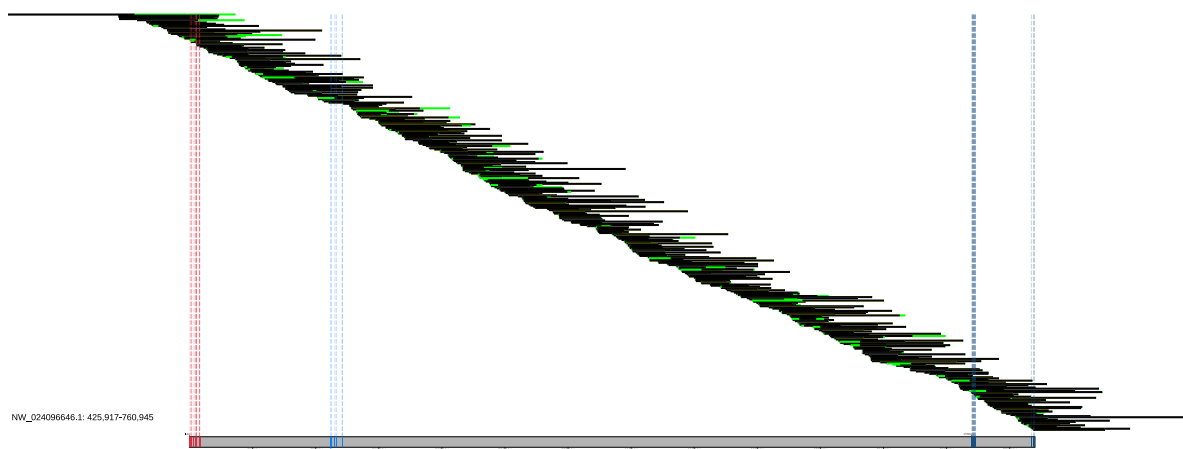


Figure 198: IL26:NW_024096646.1:425917-760945.pdf

Podarcis_muralis-PacBio

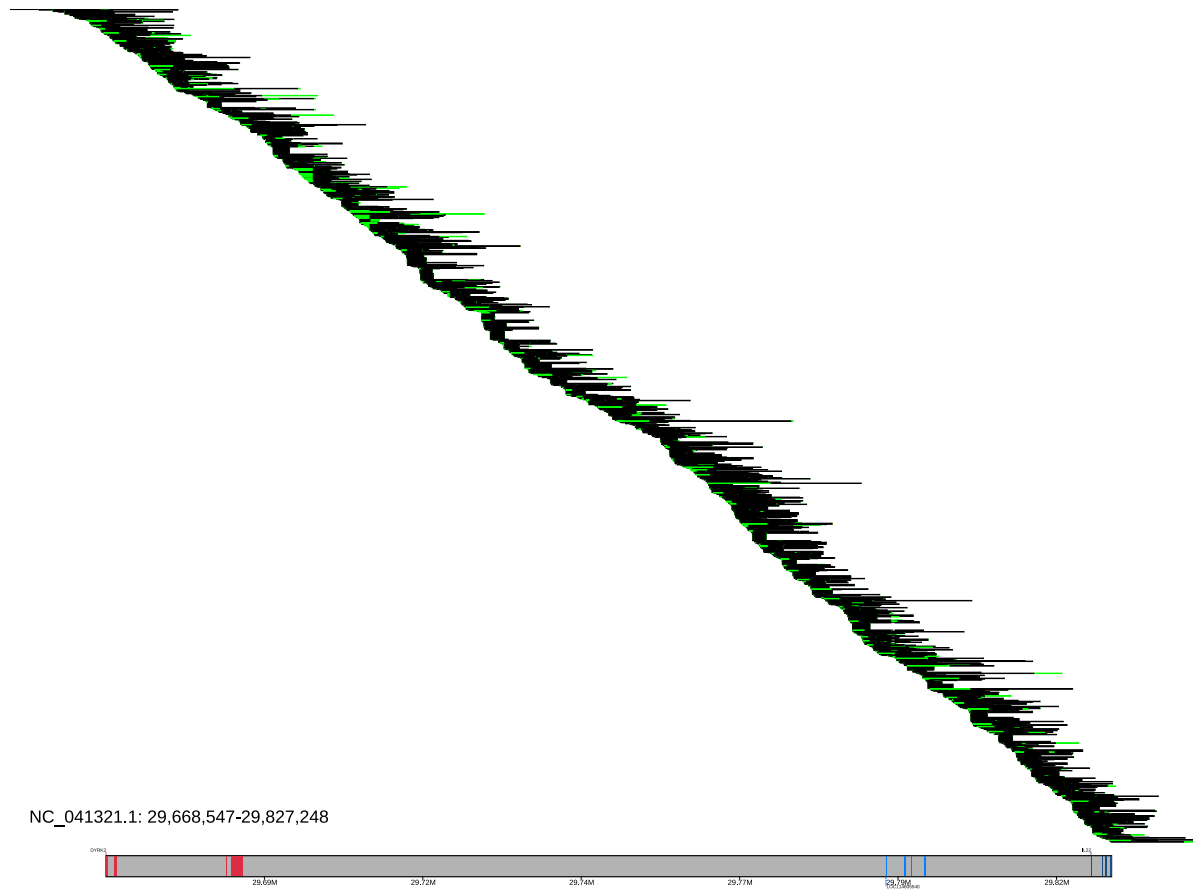


Figure 199: IL26:NC_041321.1:29668547-29827248.pdf

Pogona_vitticeps-Nanopore

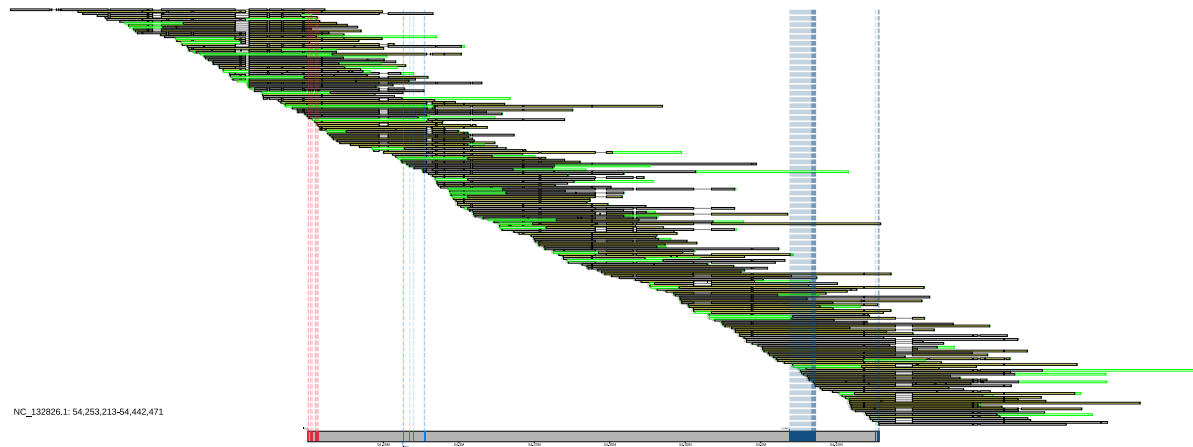


Figure 200: IL26:NC_132826.1:54253213-54442471.pdf

Important gene stats

IL26_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
IL26	7.847058824	40.7438 +/- 1.82733	3.38781 +/- 0.196974	73.3158 +/- 18.2191	No	Na

Intergenic distance phylogenetic signal evidence

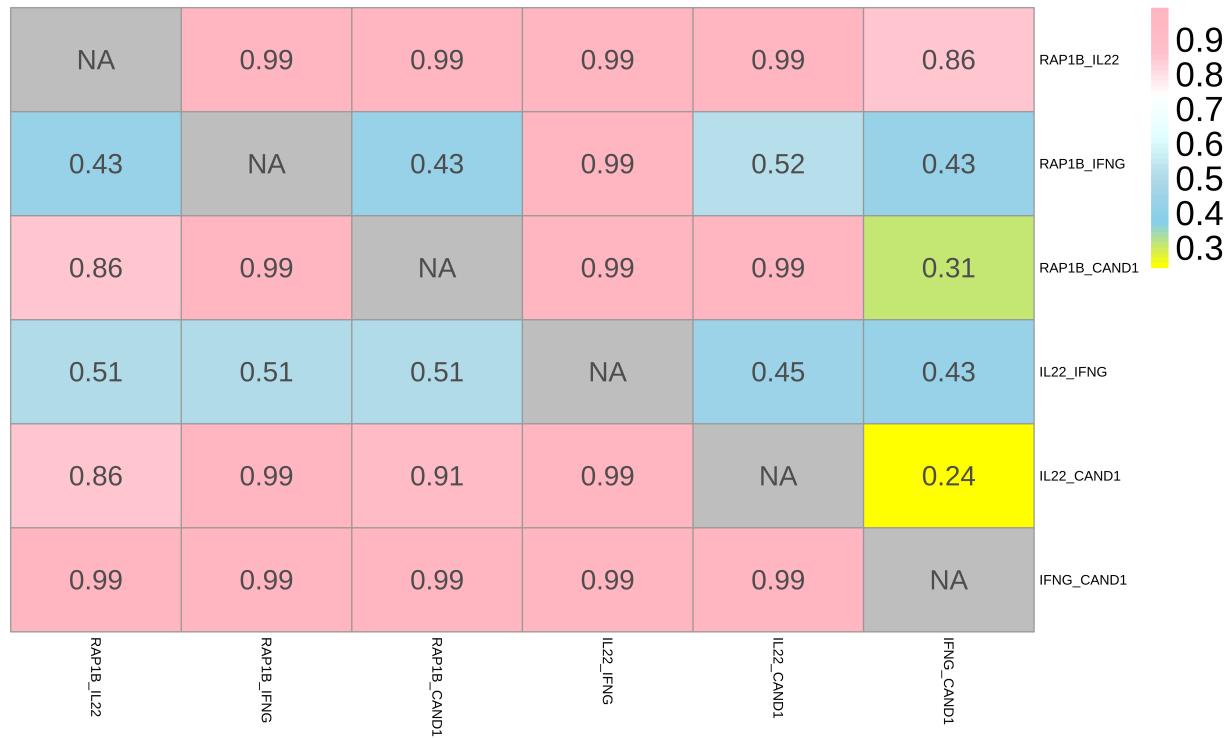


Figure 201: Heatmap_of_deletion_plot.png

IL26_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
IL26	127	6	121	0	0.373757038832395	0.998396937482384

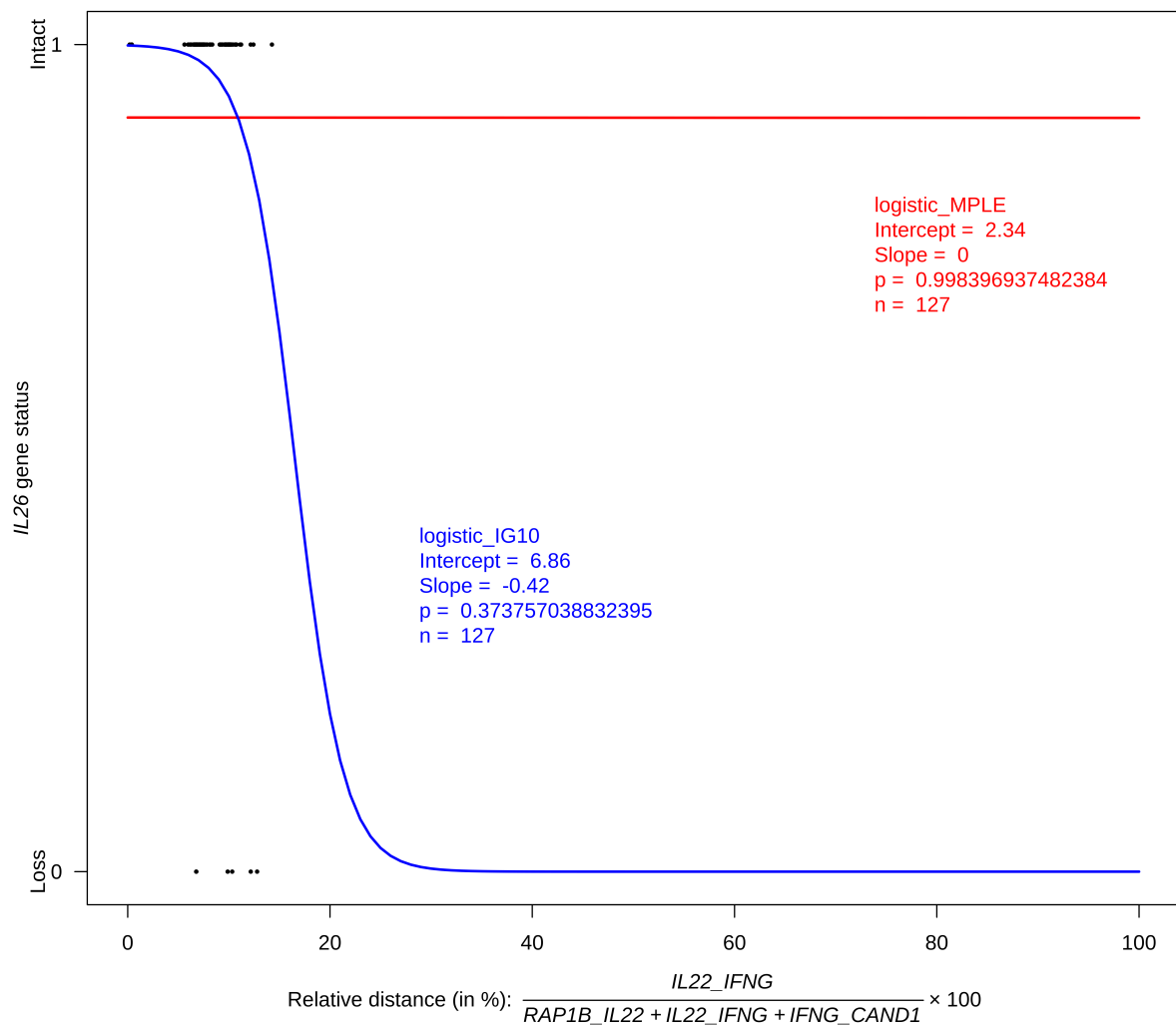


Figure 202: Phylogenetic_signal_of_deletion_plot.png

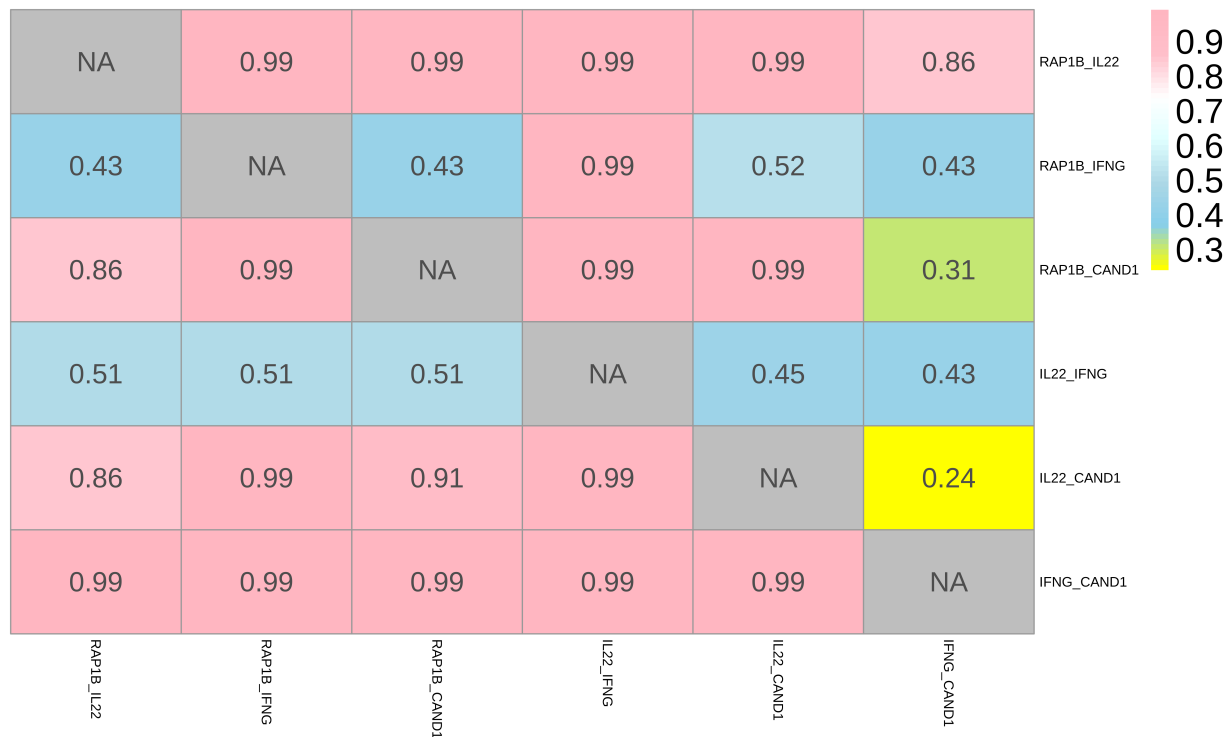


Figure 203: Heatmap_of_deletion_plot.png

IL26_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
IL26	127	6	121	0	0.373757038832395	0.998396937482384

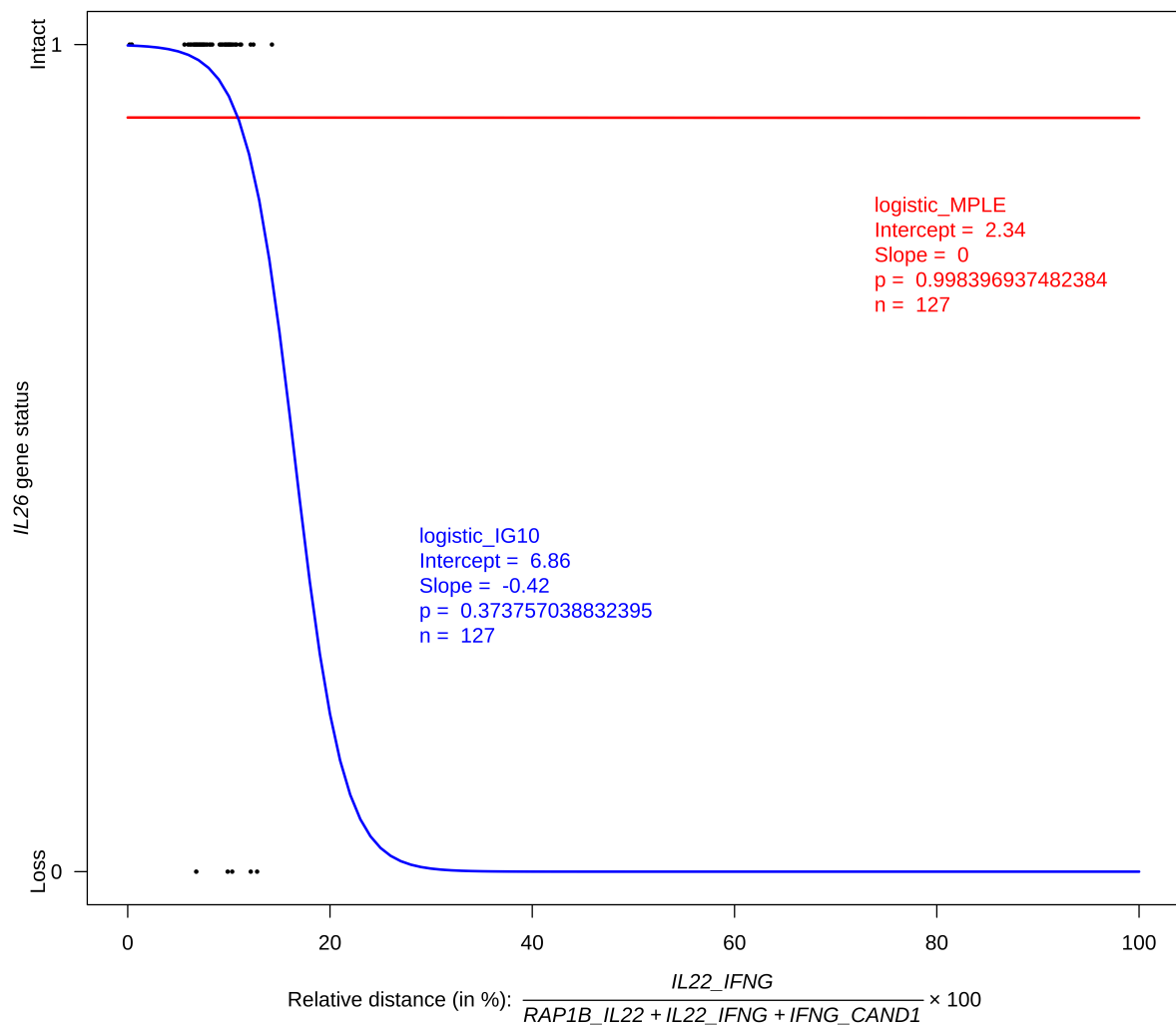


Figure 204: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence

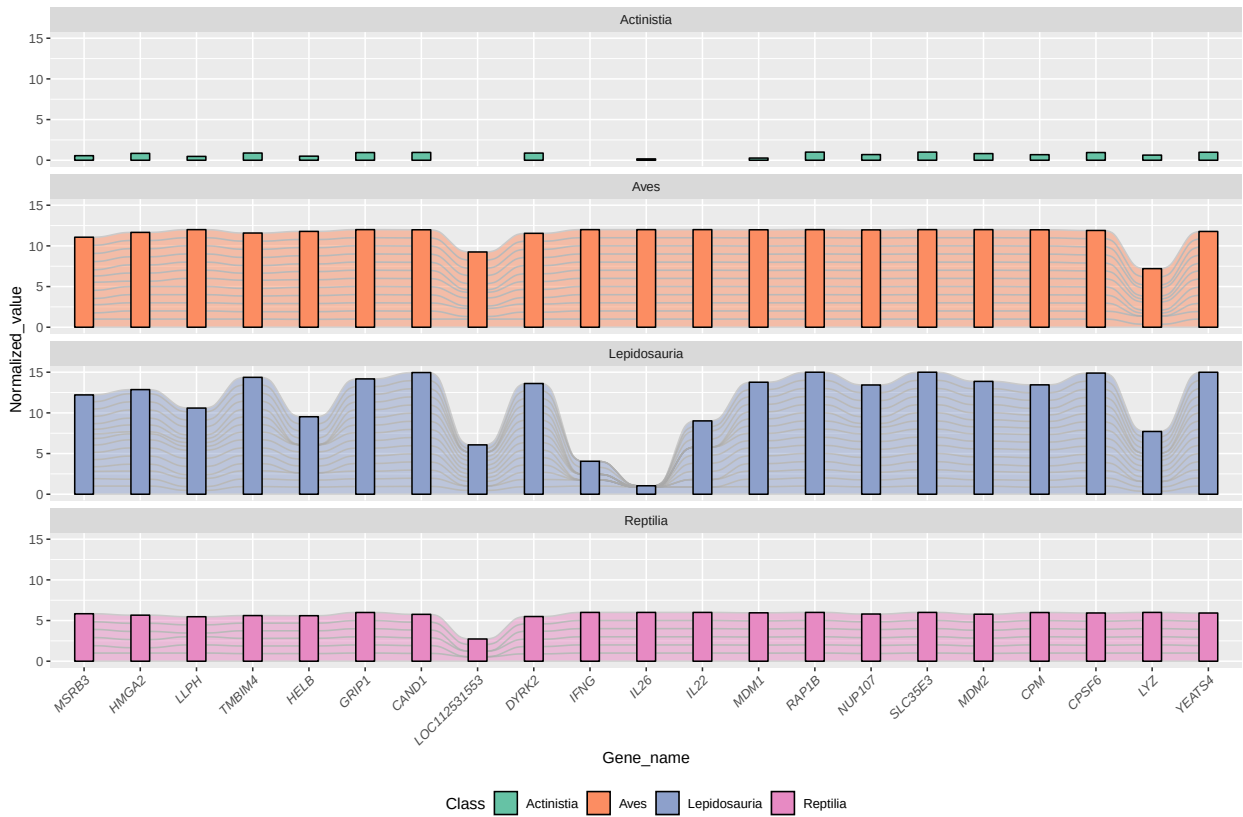


Figure 205: IL26.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

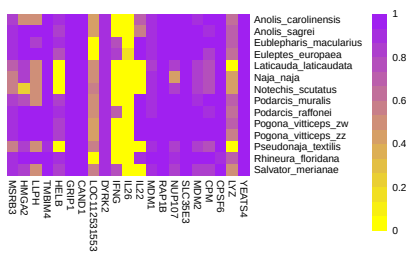


Figure 206: IL26.FS_Exonic.Final.Gallus_gallus.21_genes_heatmap.pdf

Syntenic evidence

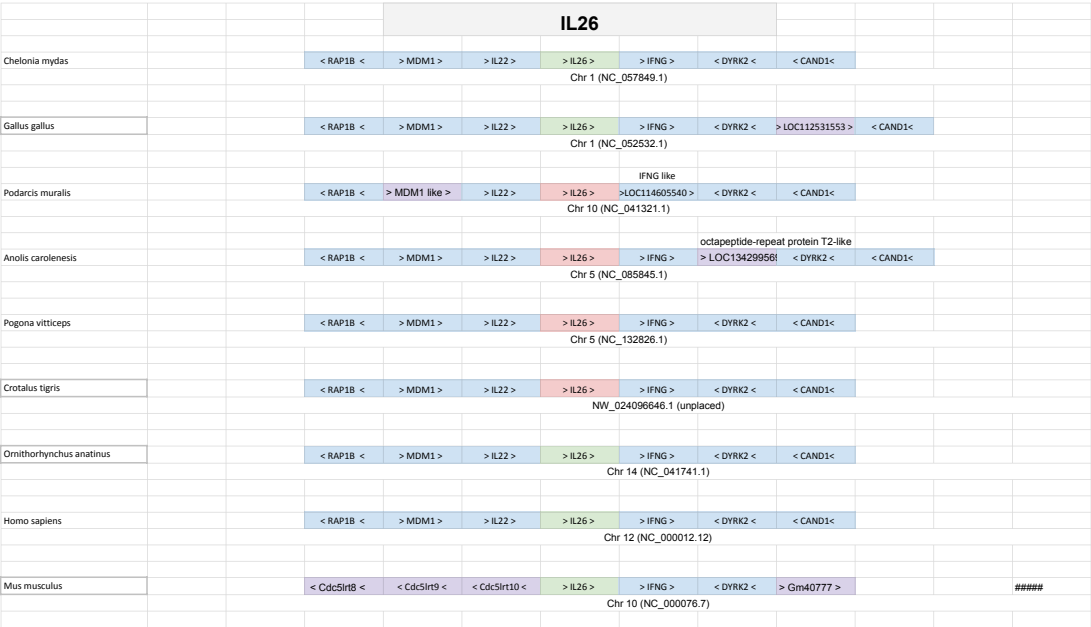


Figure 207: IL26.pdf

IL26.txt

Synteny analysis of IL26

We analyzed the synteny of IL26 in squamates and representative outgroups.

- The IL26 syntenic block is conserved, including in Mus musculus. In
- this species, the flanking genes RAP1B, MDM1, and IL22 are located
- on the same side and in the same orientation relative to IL26, but
- they appear only after multiple intervening copies of Cdc5lrt.
- Although this arrangement is not clearly represented in the synteny
- plot, the overall locus of IL26 remains conserved. In the synteny
- plots, red blocks indicate the absence of IL26, green blocks mark
- its presence, light blue blocks represent genes conserved across
- lineages, and light purple blocks denote different flanking genes.

Transcriptomic evidence Pogona vitticeps



Figure 208: IL26.png

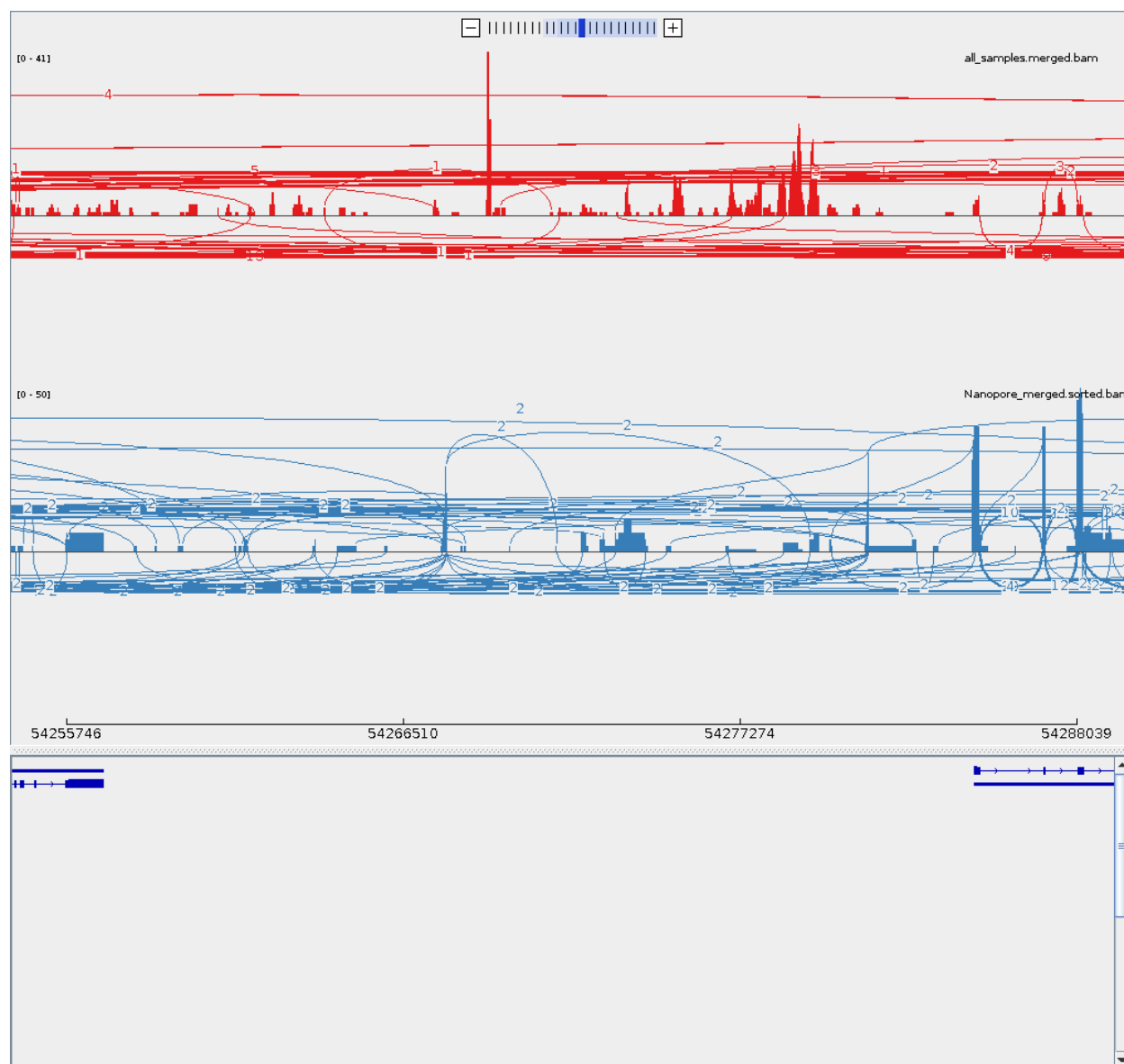


Figure 209: IL26_Shash.png

20 IL34

Assembly verification Evidence

Crotalus_tigris-PacBio

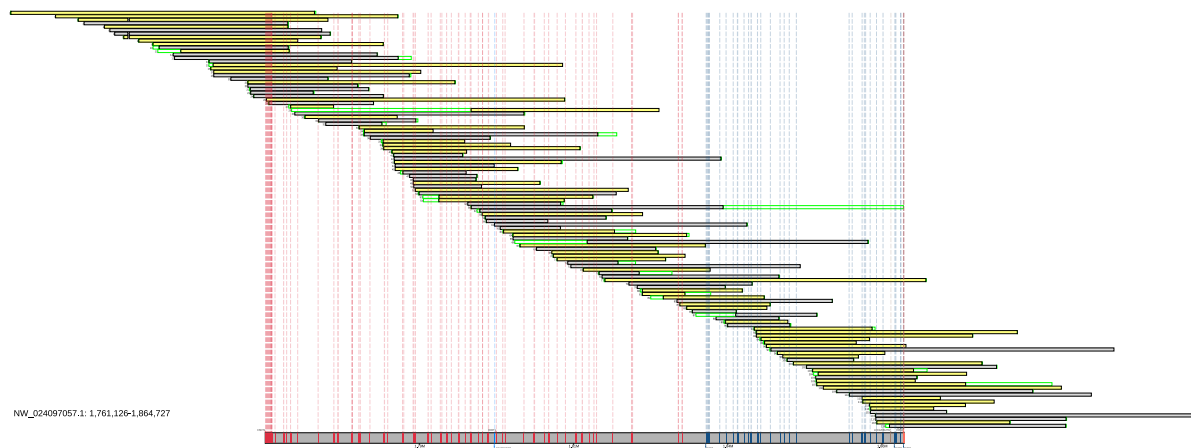


Figure 210: IL34:NW_024097057.1:1761126-1864727.pdf

Podarcis_muralis-PacBio

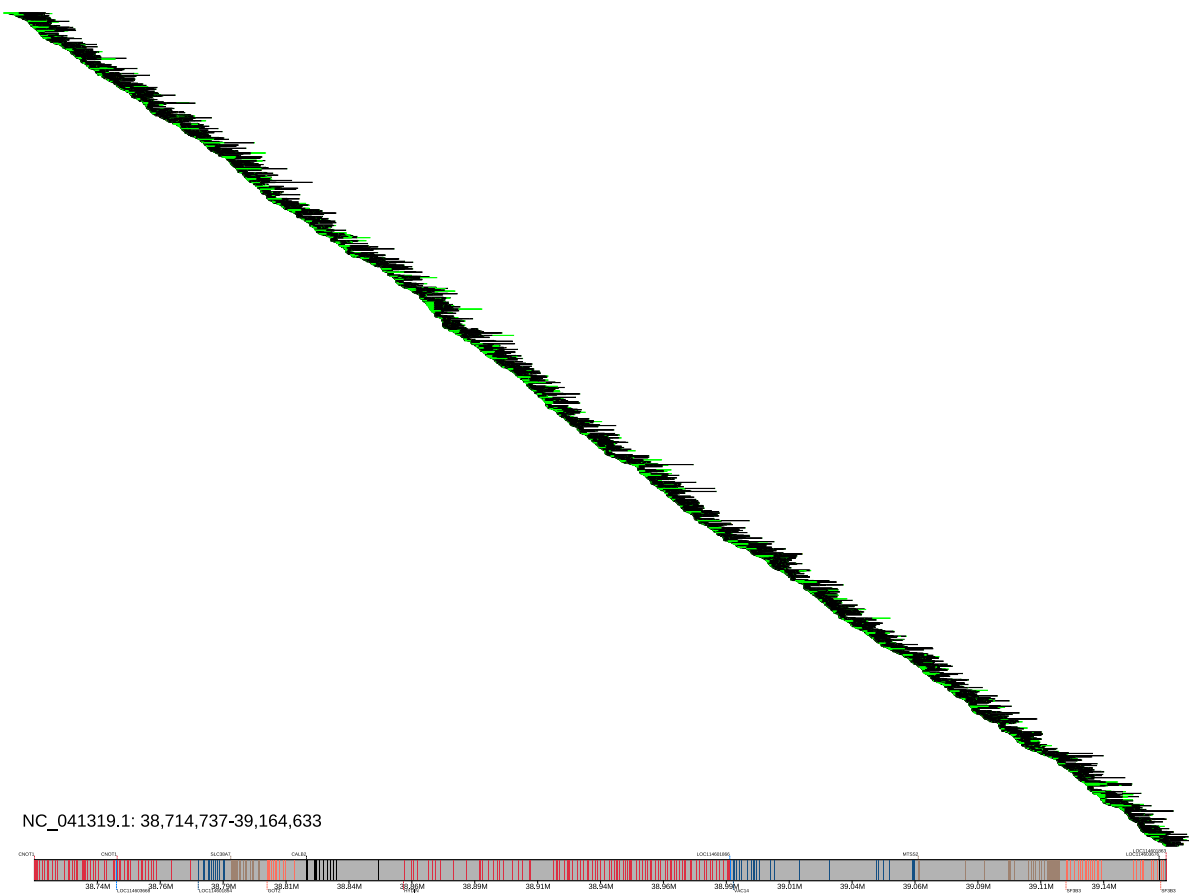


Figure 211: IL34:NC_041319.1:38714737-39164633.pdf

Pogona_vitticeps-Nanopore

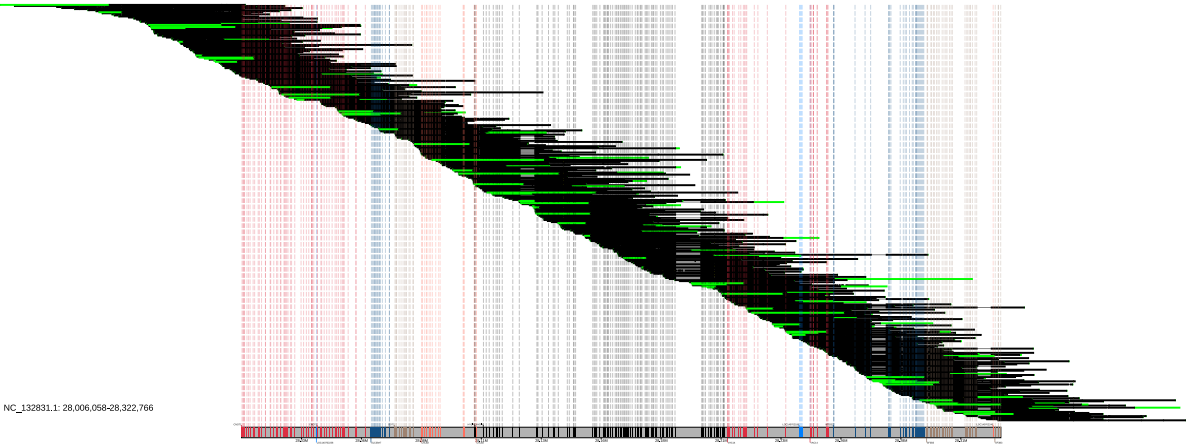


Figure 212: IL34:NC_132831.1:28006058-28322766.pdf

Important gene stats

IL34_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
IL34	5.805555556	56.7649 +/- 6.8111	4.00404 +/- 0.406849	56.9855 +/- 18.4373	No	Na

Intergenic distance phylogenetic signal evidence

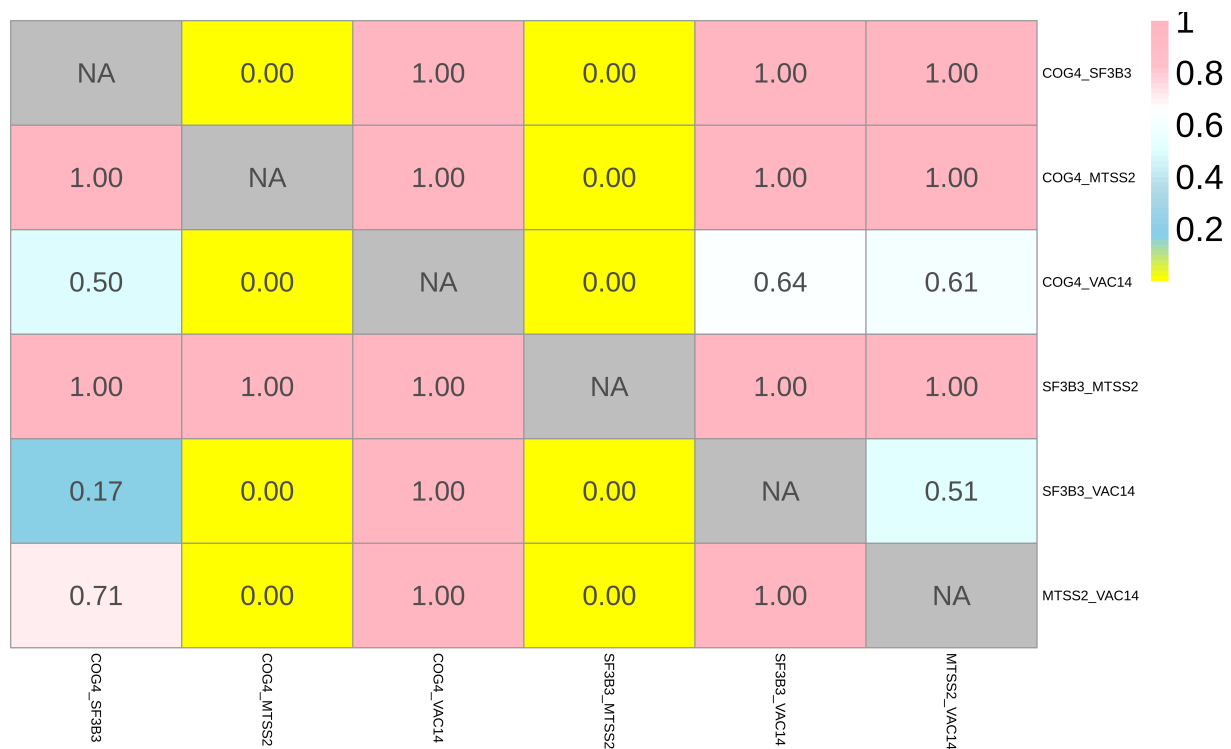


Figure 213: Heatmap_of_deletion_plot.png

IL34_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
IL34	234	16	218	5	0.0100580707205588	0.0044296593815778

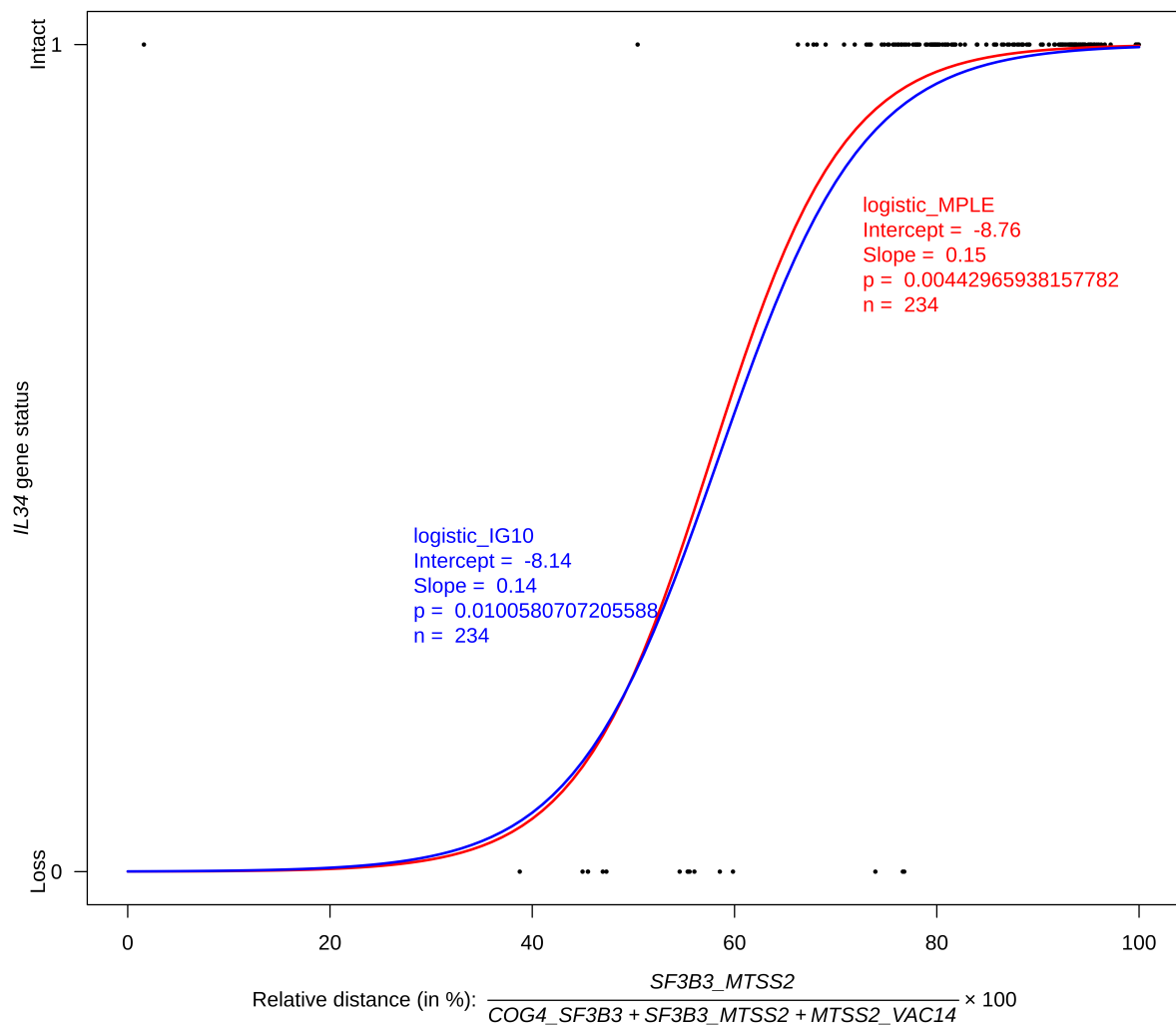


Figure 214: Phylogenetic_signal_of_deletion_plot.png

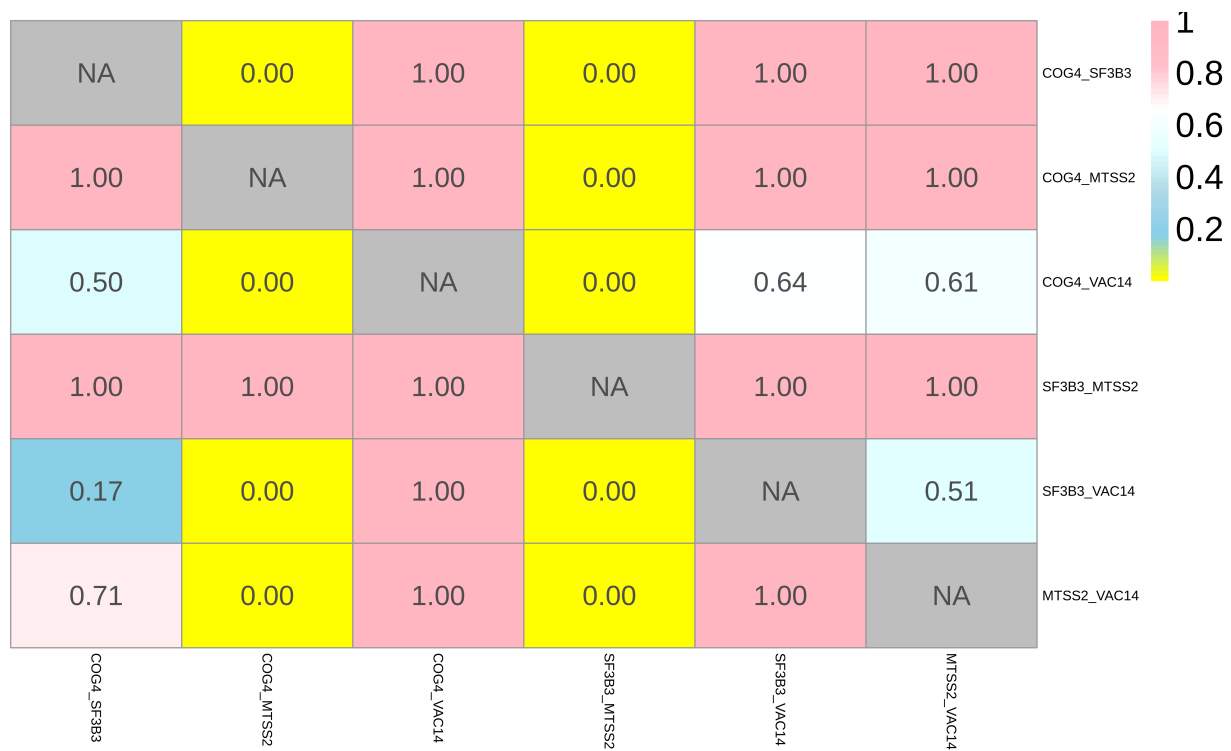


Figure 215: Heatmap_of_deletion_plot.png

IL34_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
IL34	234	16	218	5	0.0100580707205588	0.0044296593815778

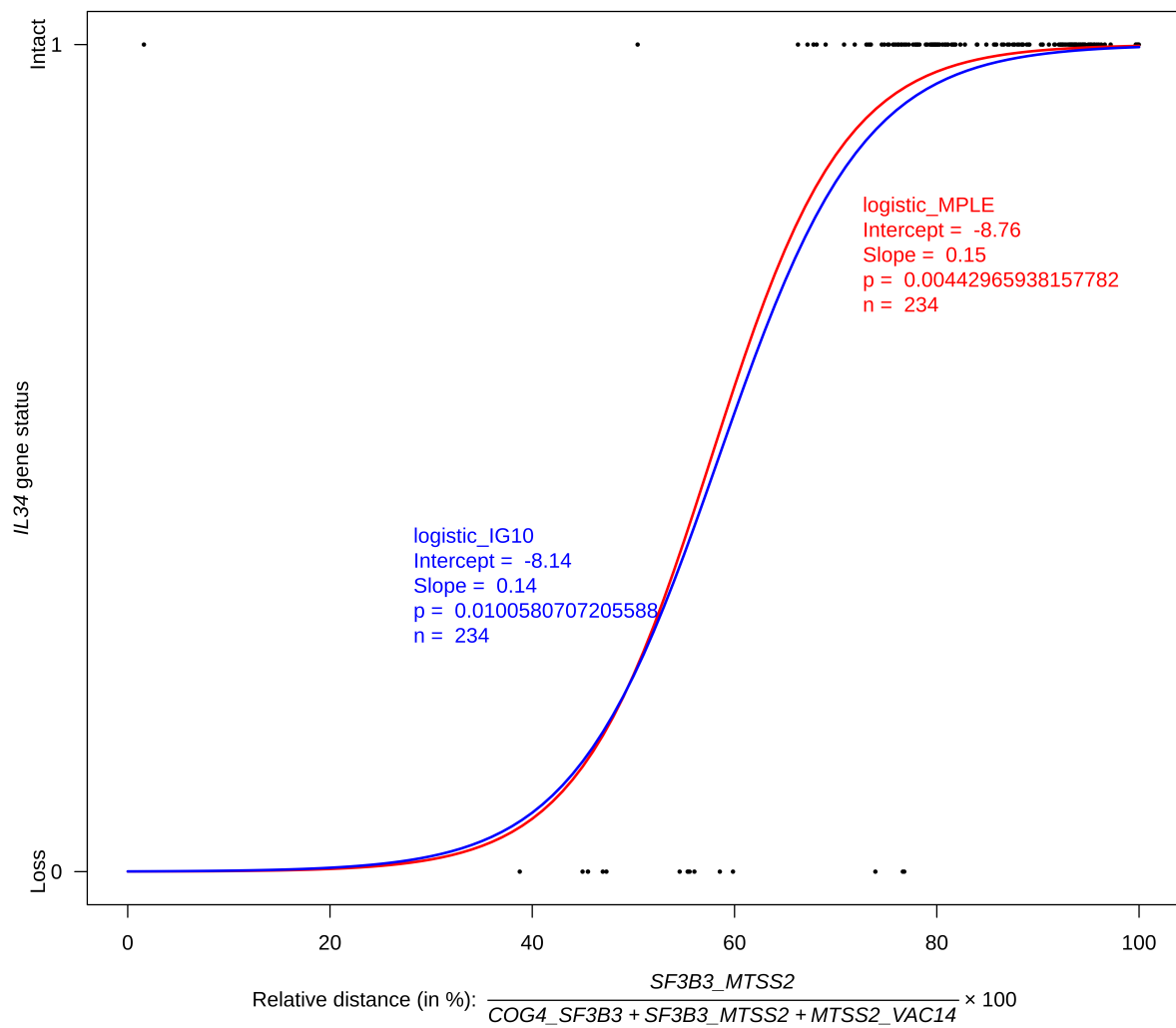


Figure 216: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence

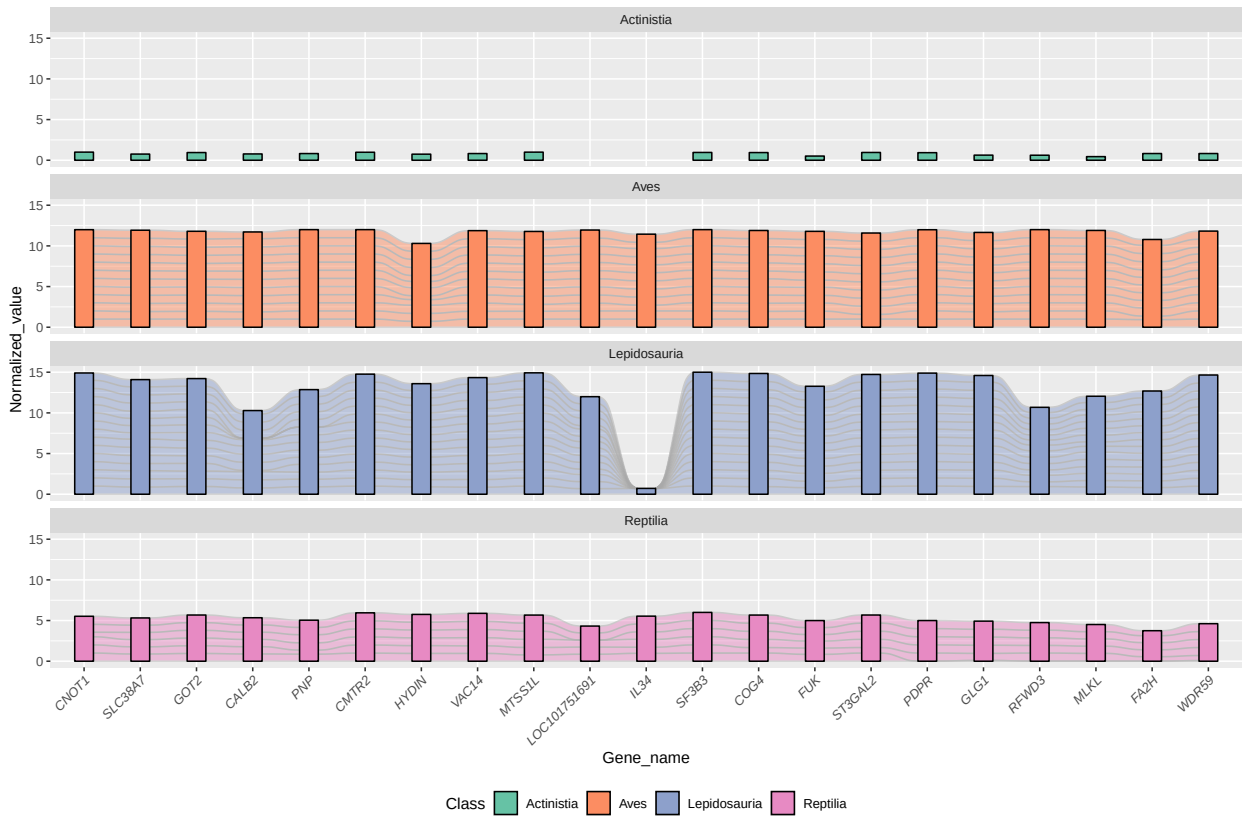


Figure 217: IL34.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

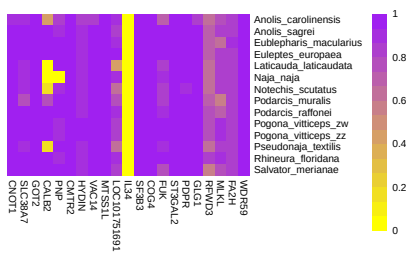


Figure 218: IL34.FS_Exonic.Final.Gallus_gallus.21_genes_heatmap.pdf

Syntenic evidence



Figure 219: IL34.pdf

IL34.txt

Synteny analysis of IL34

We analyzed the synteny of IL34 in squamates and representative outgroups.

- ↪ The IL34 syntenic block is conserved, except for one flanking side
- ↪ that shows variation in Chelonia mydas and Crotalus tigris. In the
- ↪ synteny plots, red blocks indicate the absence of IL34, green blocks
- ↪ mark its presence, light blue blocks represent genes conserved
- ↪ across lineages, and light purple blocks denote different flanking
- ↪ genes.

Transcriptomic evidence Pogona vitticeps



Figure 220: IL34.png

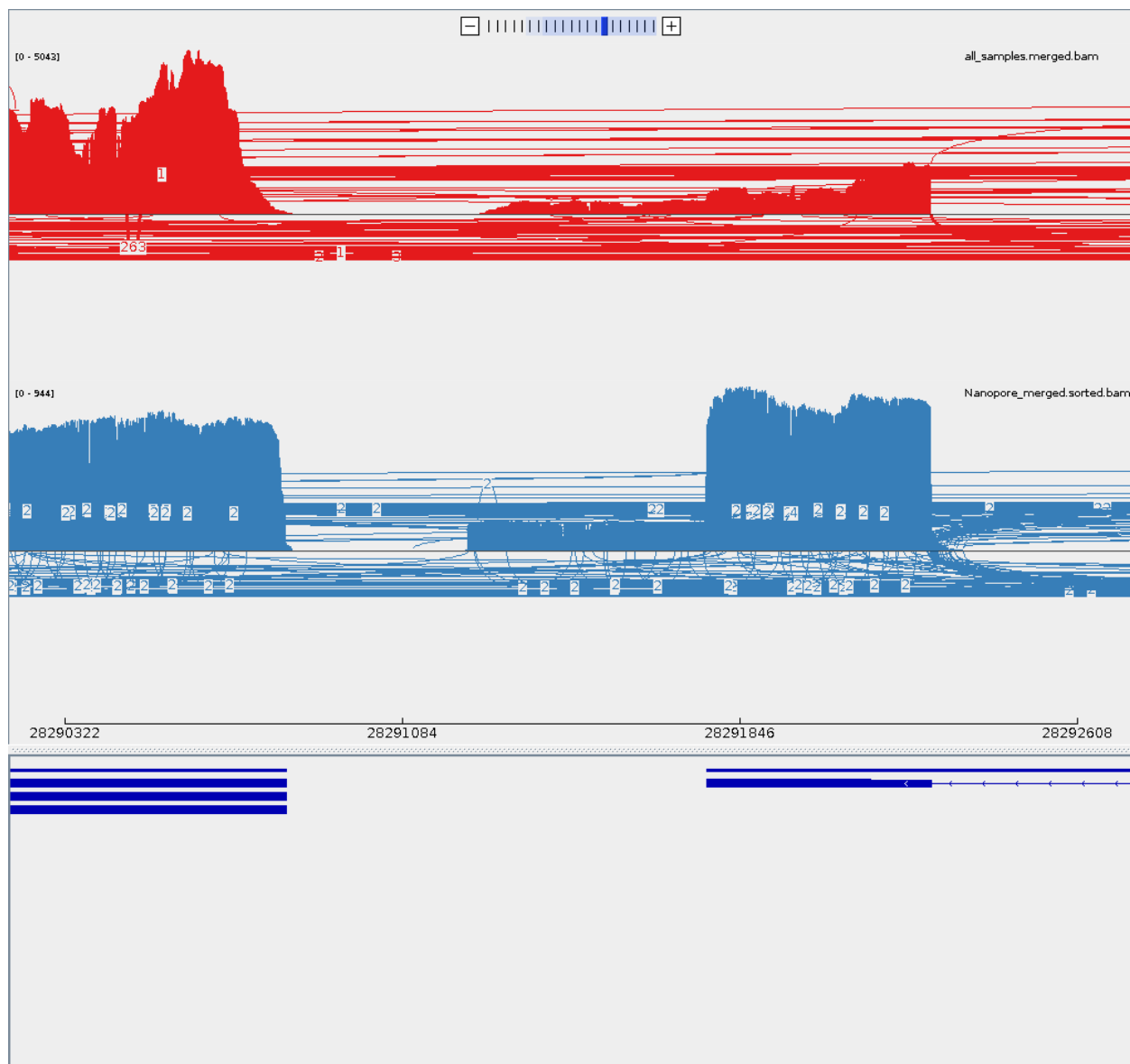


Figure 221: IL34_Shash.png

21 IL5RA

Assembly verification Evidence

Crotalus_tigris-PacBio

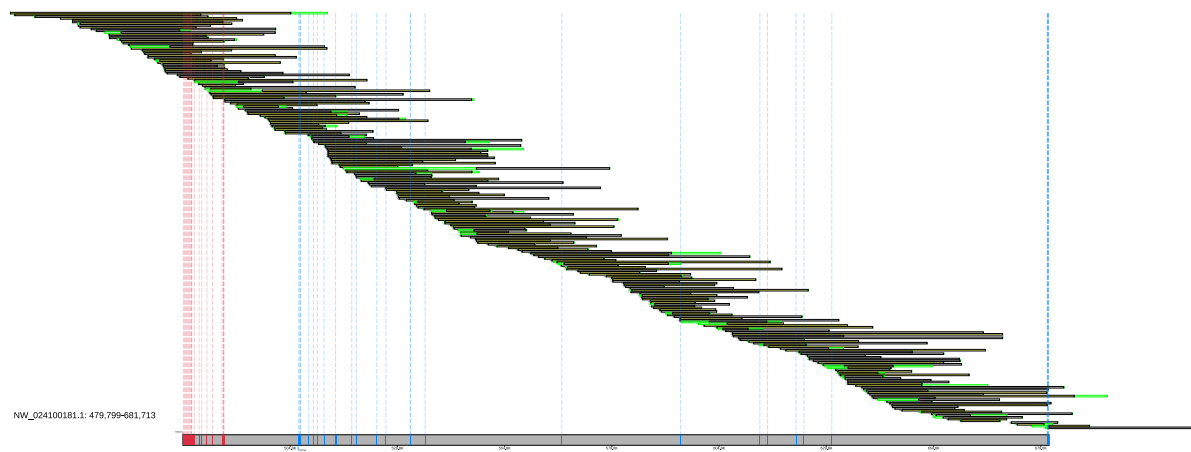


Figure 222: IL5RA:NW_024100181.1:479799-681713.pdf

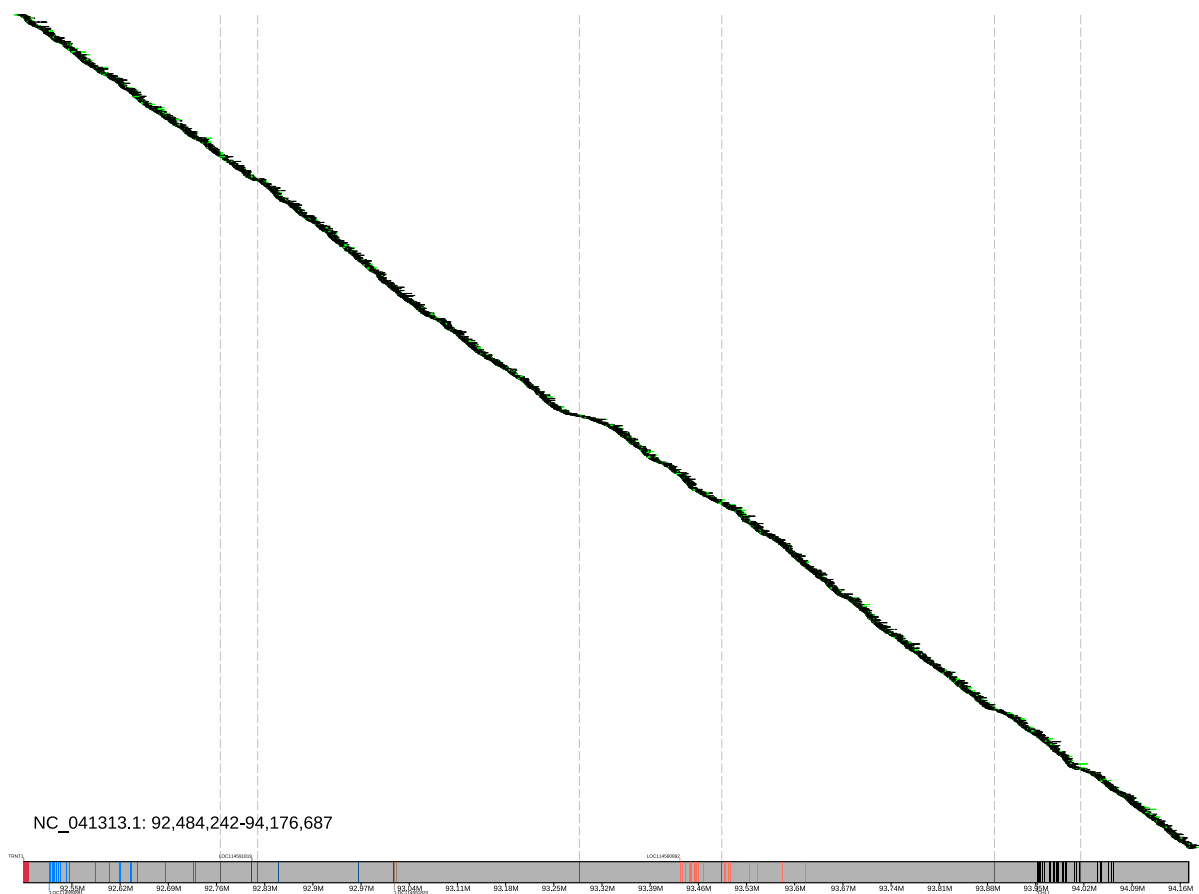


Figure 223: IL5RA:NC_041313.1:92484242-94176687.pdf

Pogona_vitticeps-Nanopore

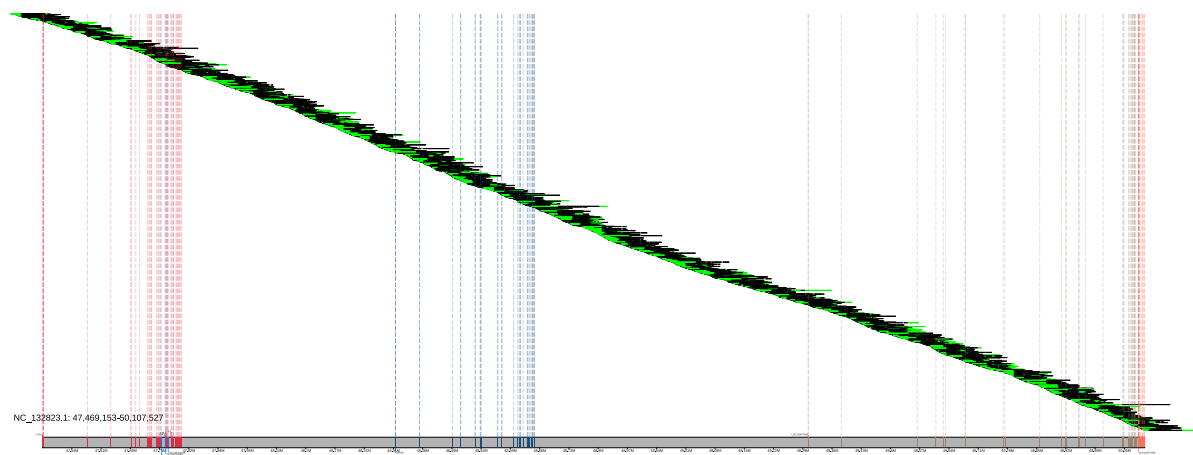


Figure 224: IL5RA:NC_132823.1:47469153-50107527.pdf

Important gene stats

IL5RA_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
IL5RA	2.84	46.4164 +/- 6.10891	3.63884 +/- 0.383528	63.9802 +/- 14.2906	Yes	Na

Intergenic distance phylogenetic signal evidence



Figure 225: Heatmap_of_deletion_plot.png

IL5RA_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
IL5RA	115	2	113	5	0.0993023435649779	0.148988027492763

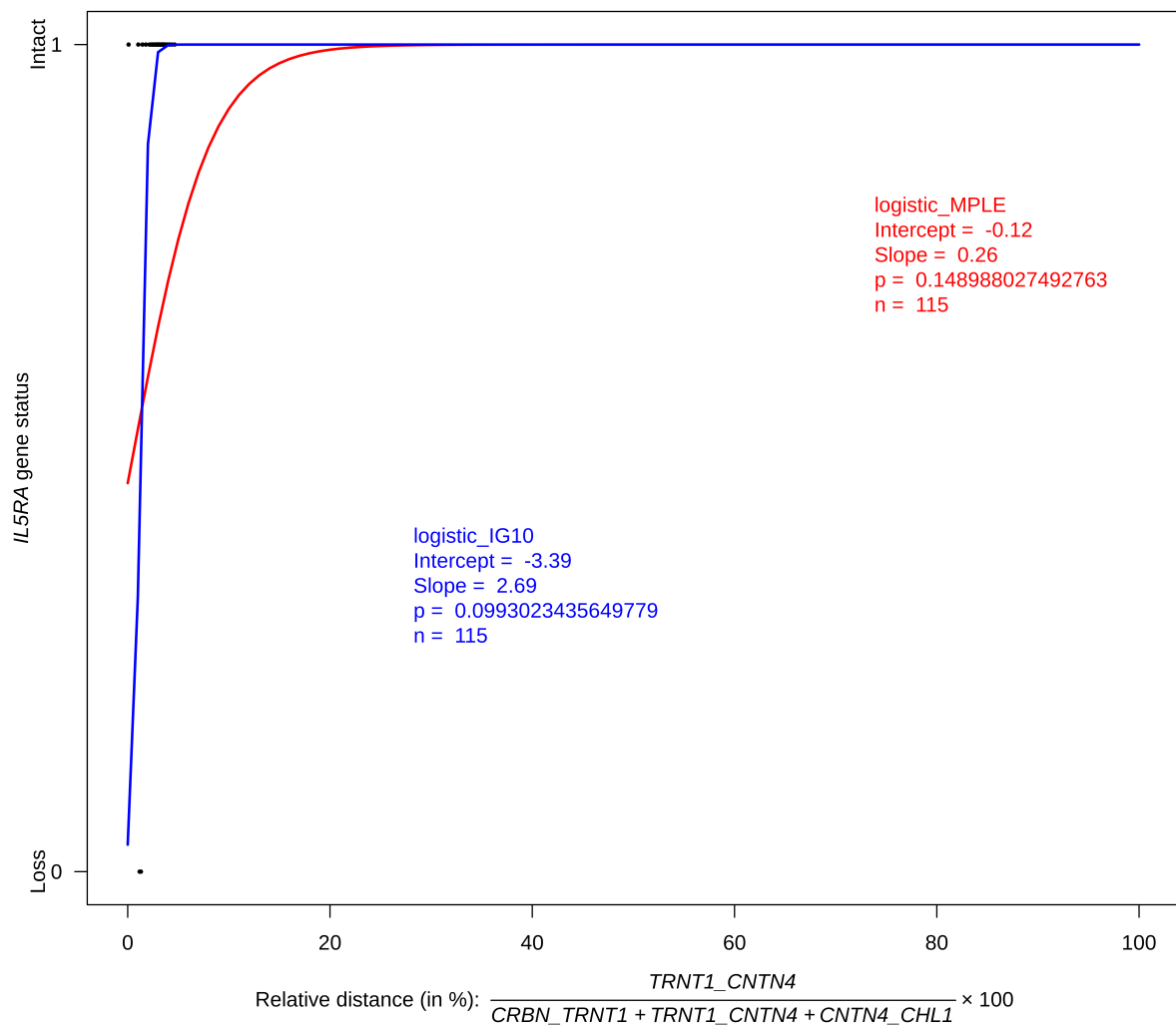


Figure 226: Phylogenetic_signal_of_deletion_plot.png



Figure 227: Heatmap_of_deletion_plot.png

IL5RA_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
IL5RA	115	2	113	5	0.0993023435649779	0.148988027492763

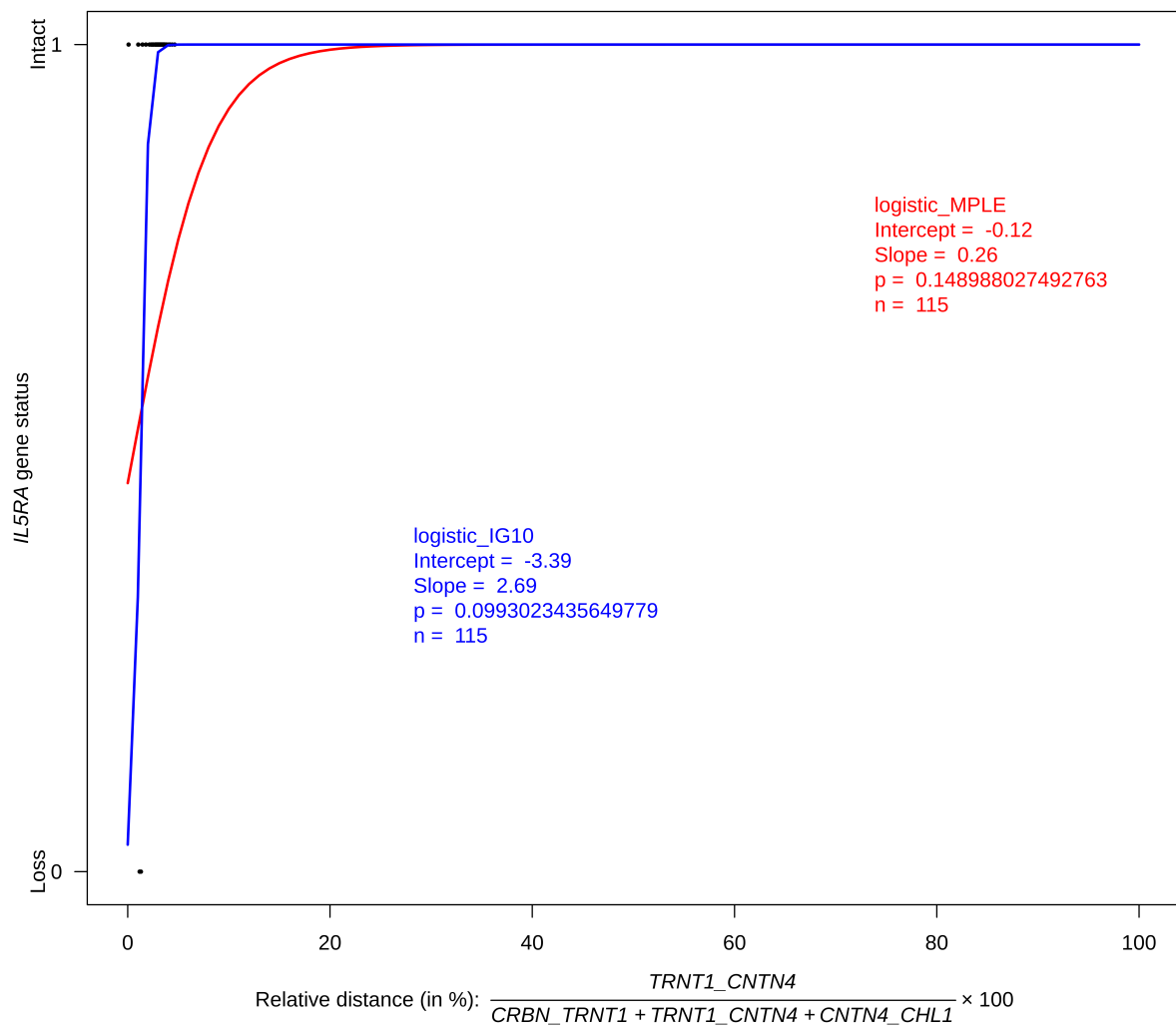


Figure 228: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence

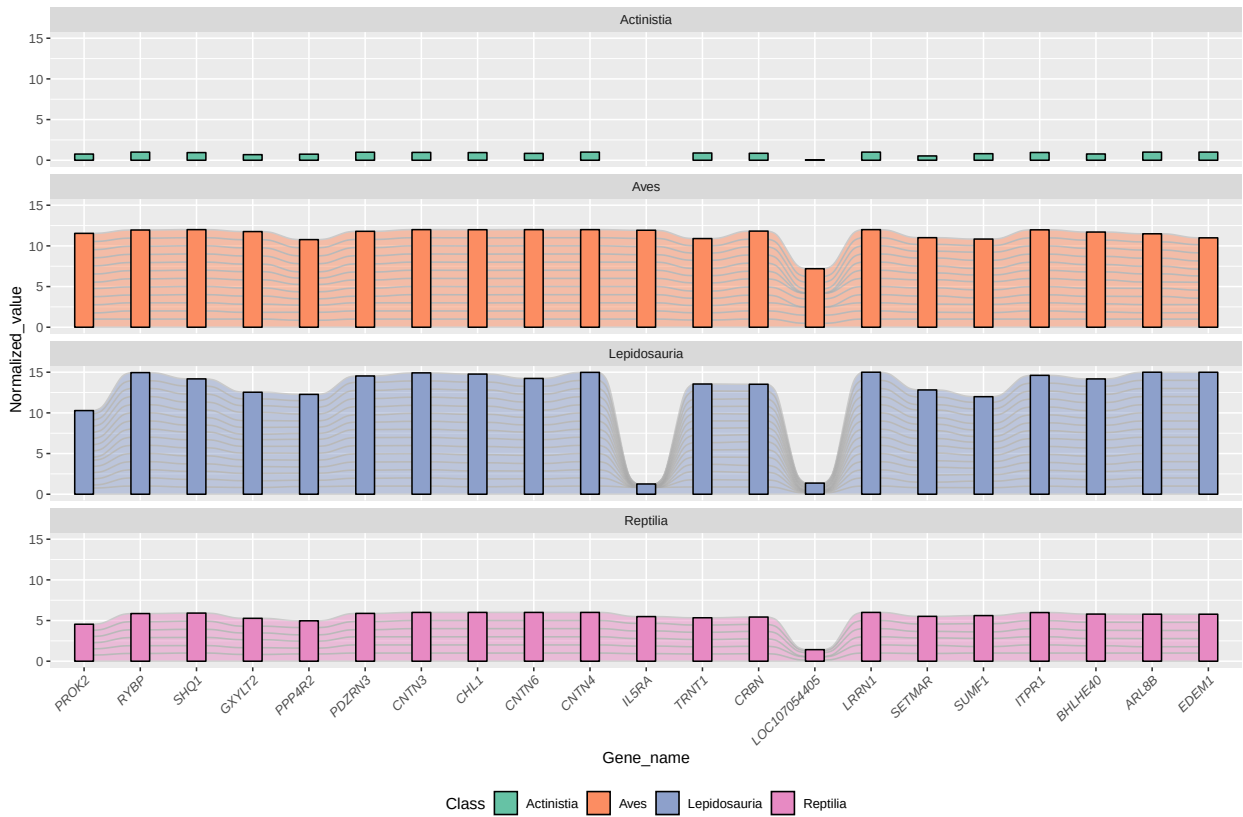


Figure 229: IL5RA.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Orthofinder genetree

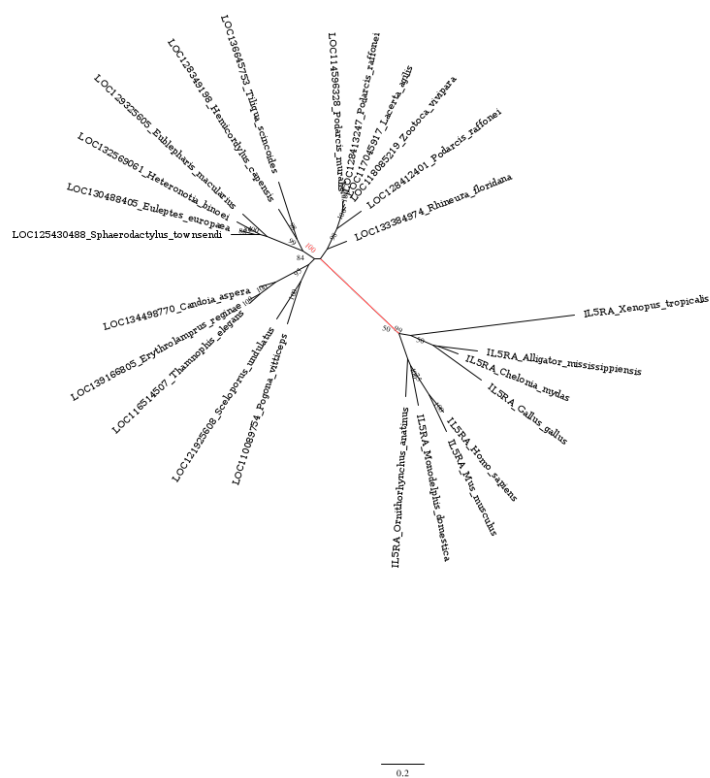


Figure 231: Il5ra-il5ralike.PRANK.aln.contree.png

Syntenic evidence

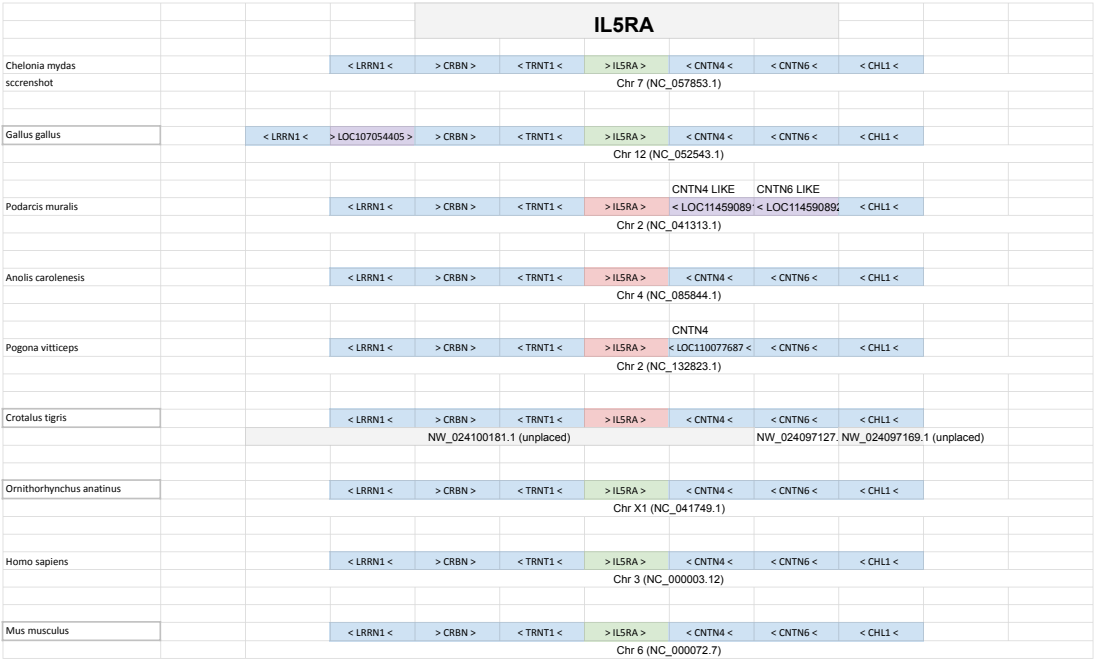


Figure 232: IL5RA.pdf

IL5RA.txt

Synteny analysis of IL5RA

We analyzed the synteny of IL5RA in squamates and representative outgroups

→ . The IL5RA syntenic block is conserved overall In the synteny plots

→ , red blocks indicate the absence of IL5RA, green blocks mark its

→ presence, light blue blocks represent genes conserved across

→ lineages, and light purple blocks denote different flanking genes.

Transcriptomic evidence Pogona vitticeps



Figure 233: IL5RA.png

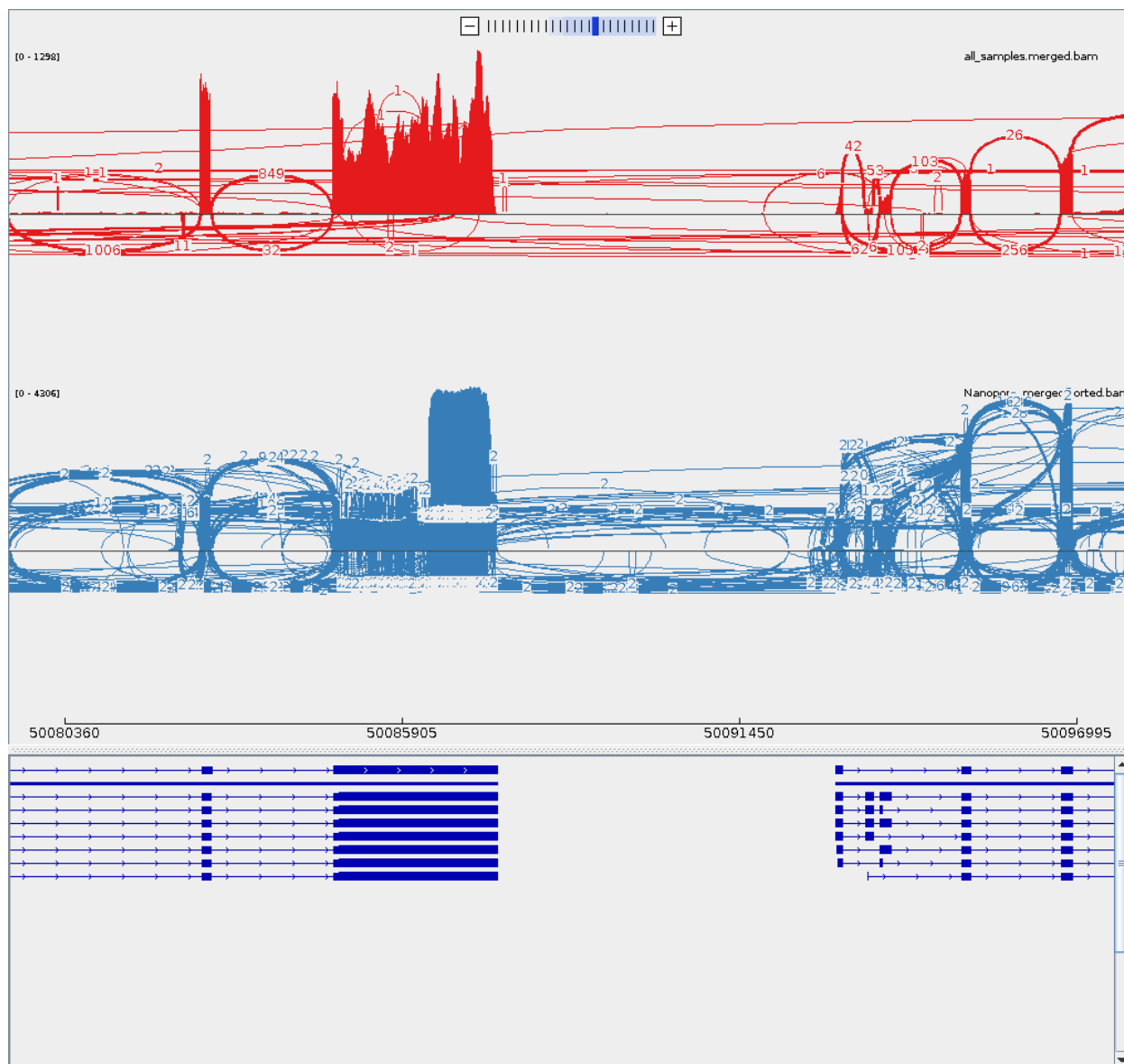


Figure 234: IL5RA_Shash.png

22 INTS6

Assembly verification Evidence

Crotalus_tigris-PacBio

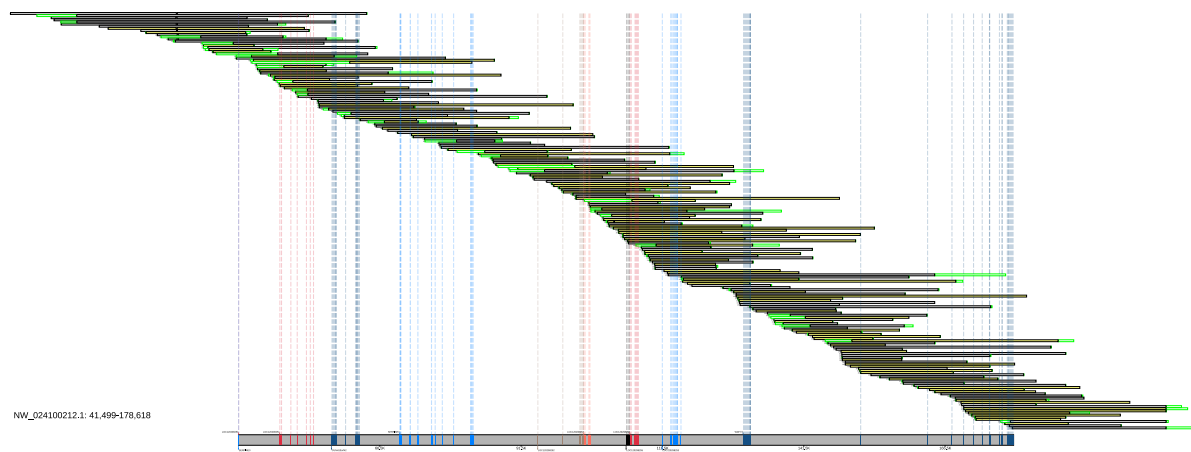


Figure 235: INTS6:NW_024100212.1:41499-178618.pdf

Podarcis_muralis-PacBio

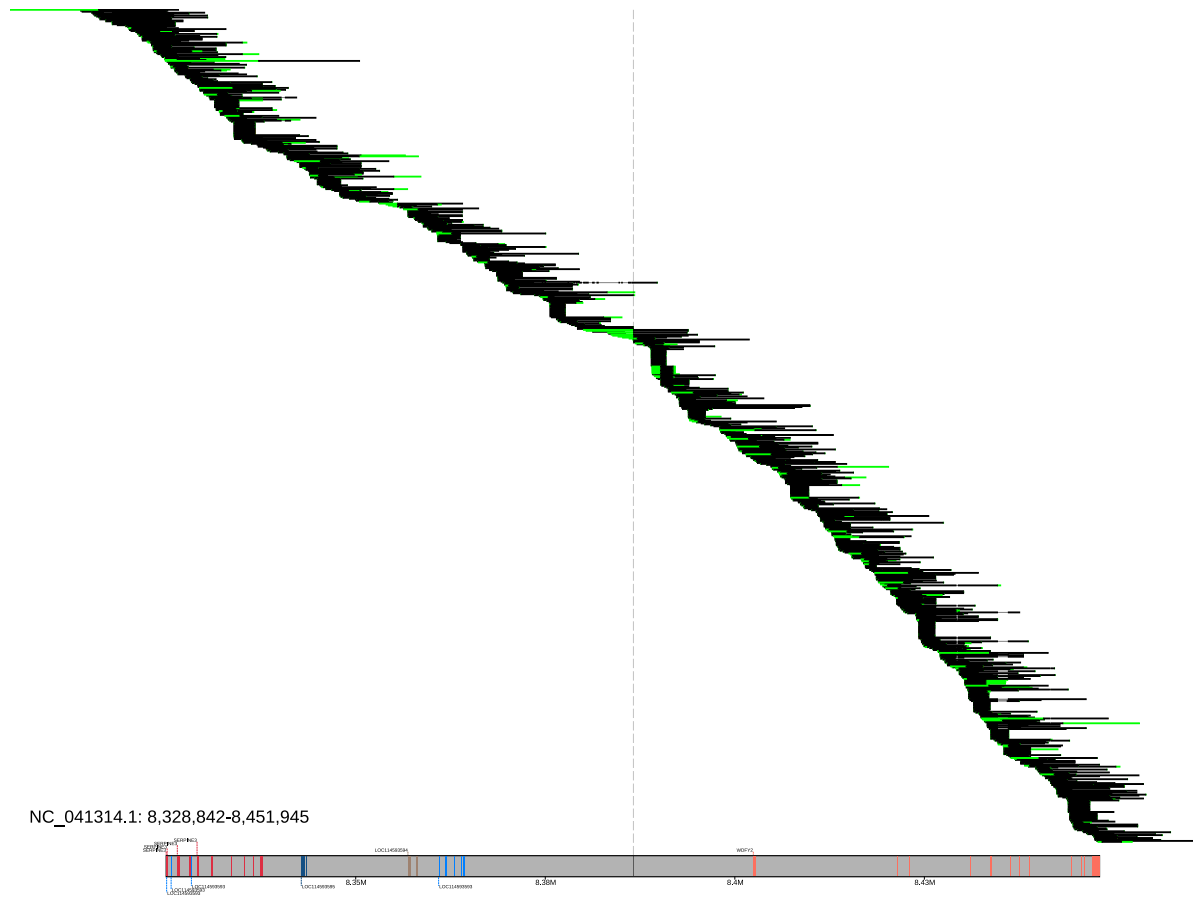


Figure 236: INTS6:NC_041314.1:8328842-8451945.pdf

Pogona_vitticeps-Nanopore

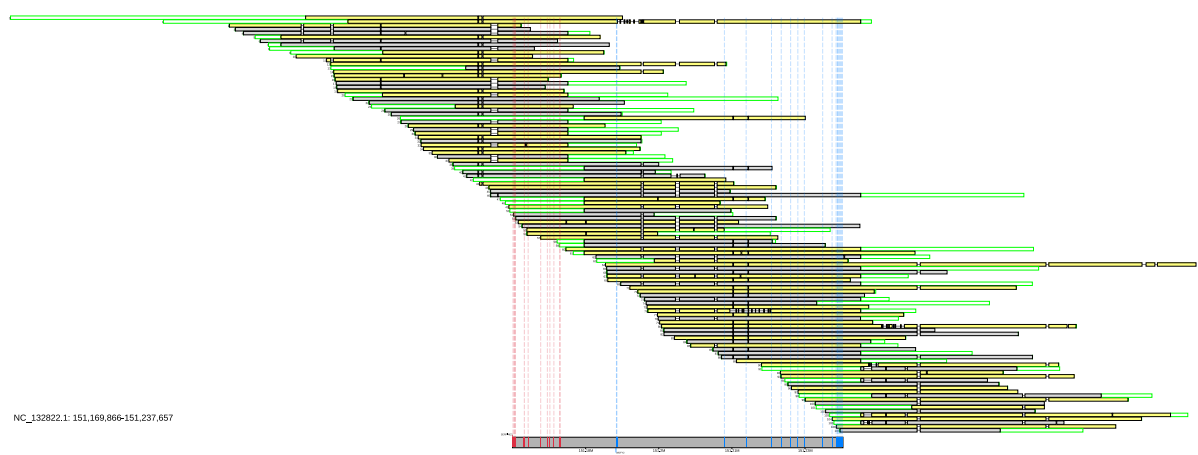


Figure 237: INTS6:NC_132822.1:151169866-151237657.pdf

Important gene stats

INTS6_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
INTS6	39.86259542	46.7108 +/- 6.36098	3.75537 +/- 0.299495	80.1962 +/- 14.1326	Yes	LOC110088158;

Intergenic distance phylogenetic signal evidence

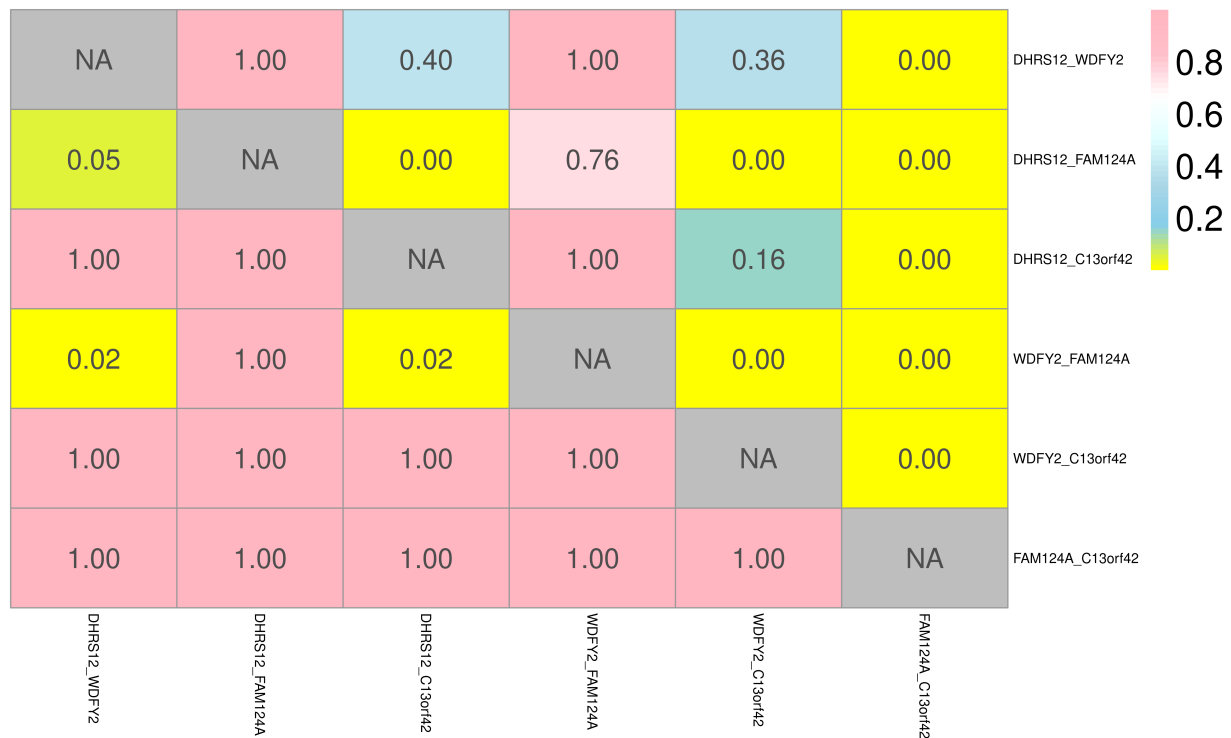


Figure 238: Heatmap_of_deletion_plot.png

INTS6_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
INTS6	273	10	263	0	1	0.9999999999999909

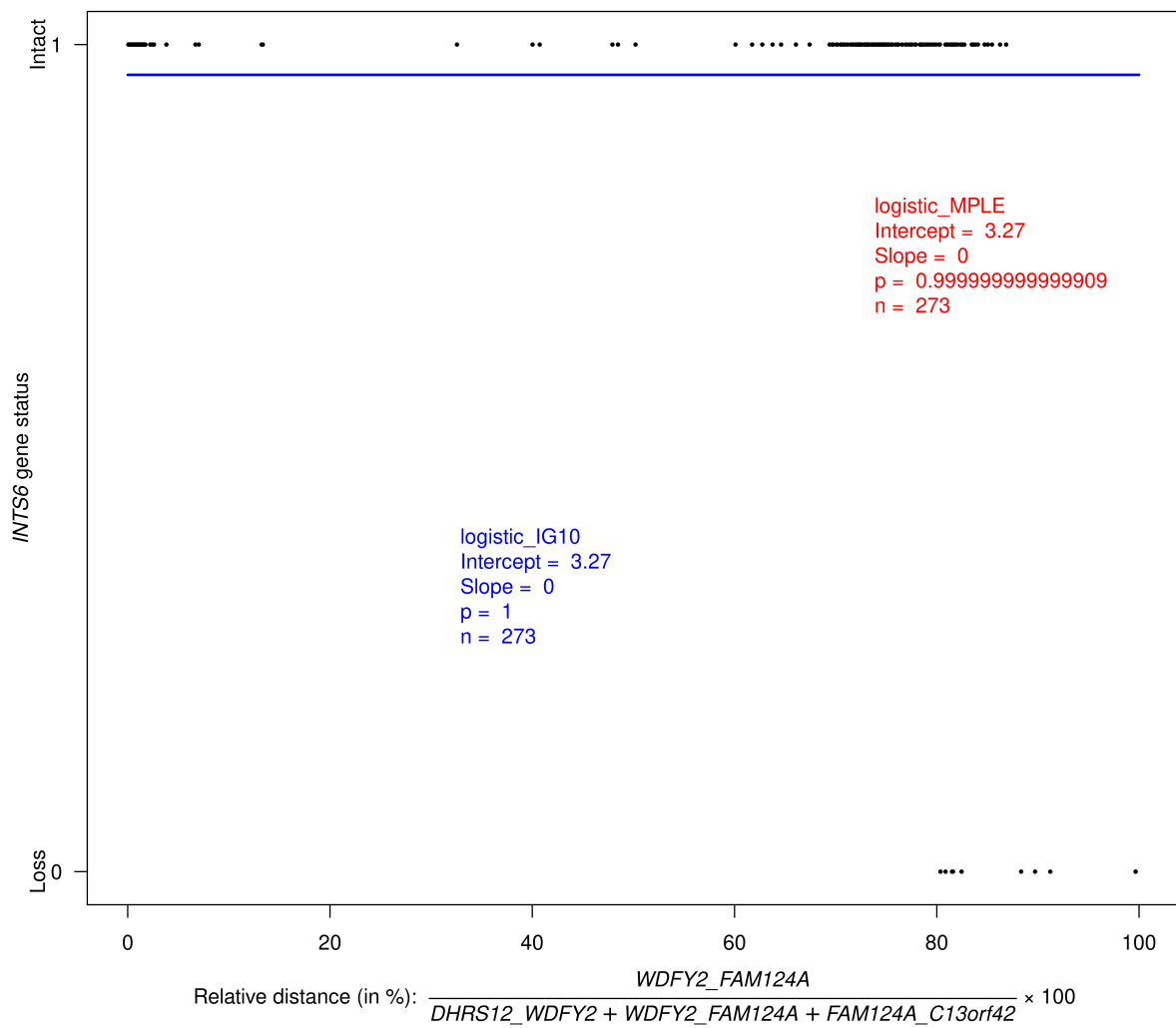


Figure 239: Phylogenetic_signal_of_deletion_plot.png



Figure 240: Heatmap_of_deletion_plot.png

INTS6_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
INTS6	273	10	263	0	1	0.9999999999999909

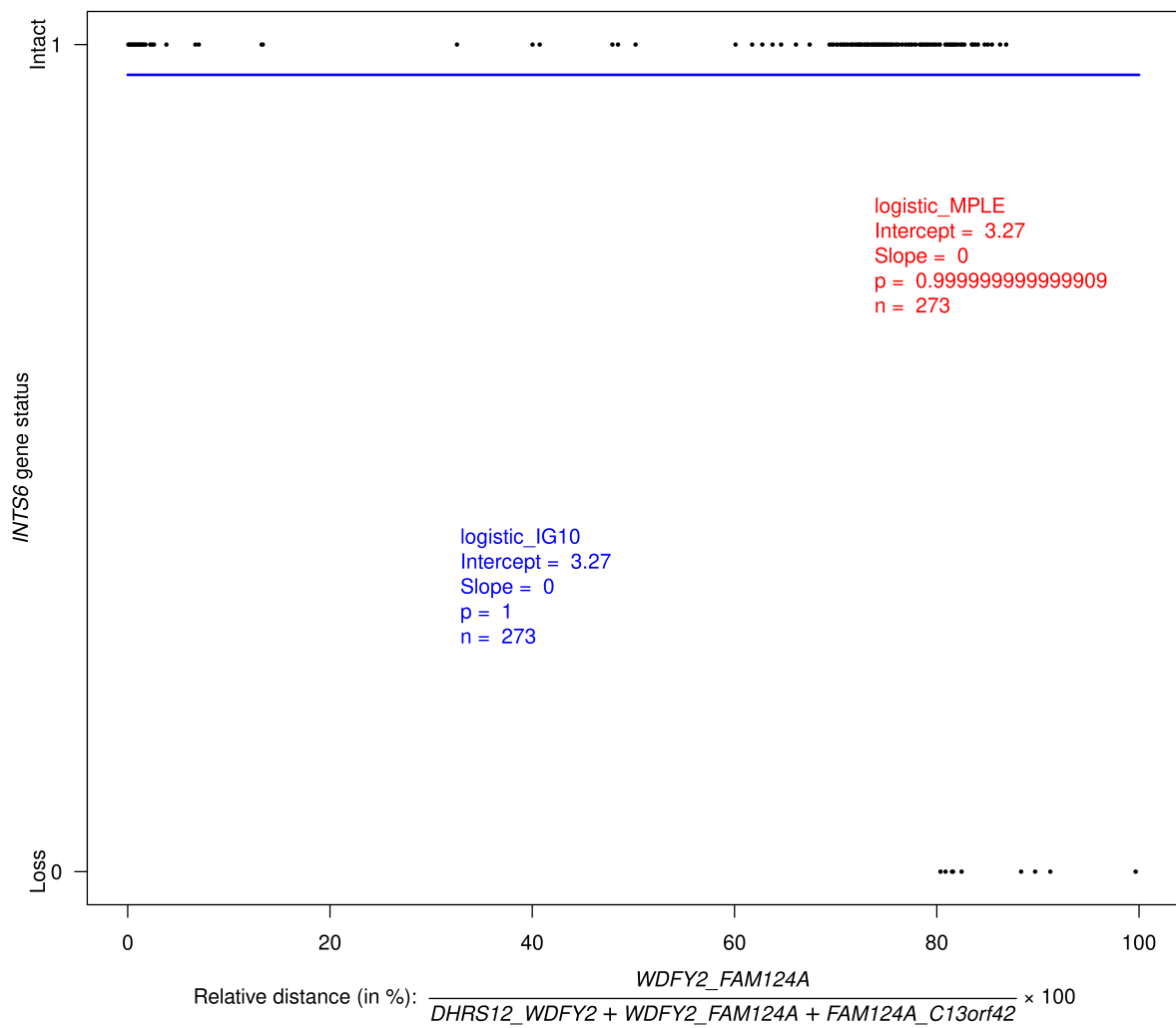


Figure 241: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence

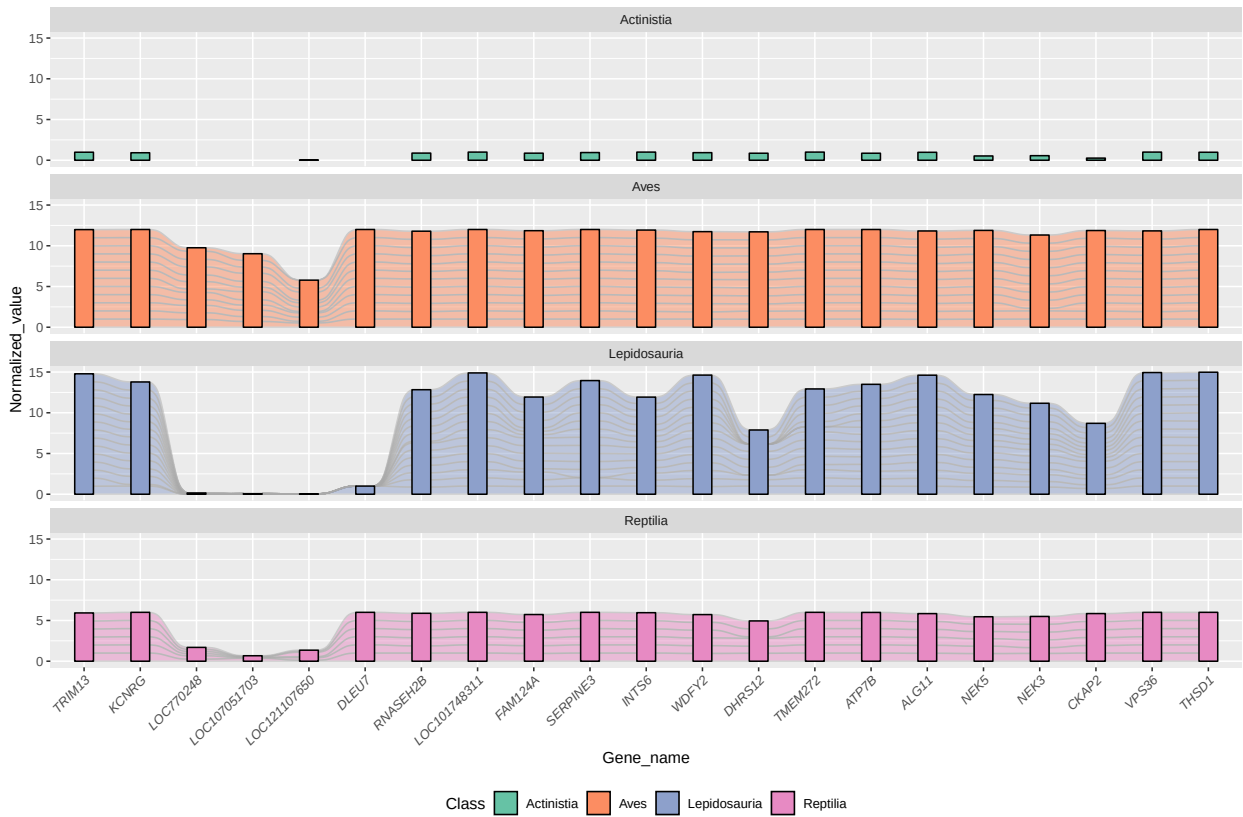


Figure 242: INTS6.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Lastz gene tree

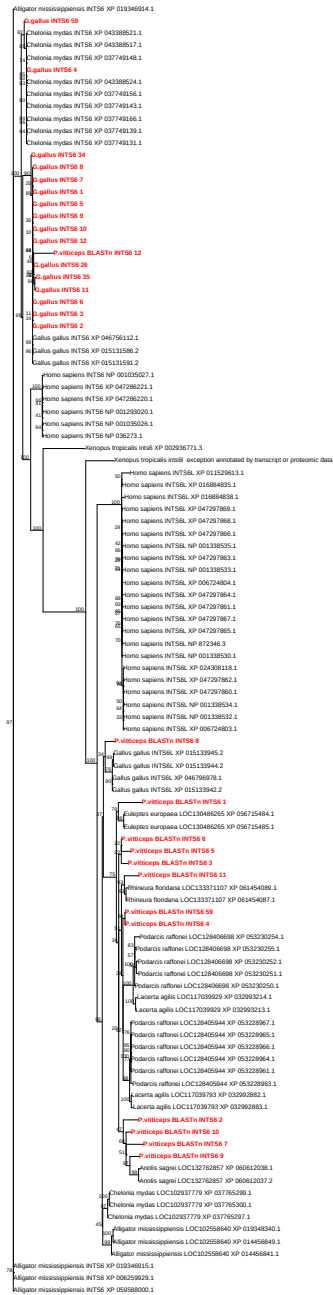


Figure 244: INTS6.combined.mafft.aln.highlighted.pdf

Syntenic evidence



Figure 245: INTS6.pdf

INTS6.txt

Synteny analysis of INTS6

We analyzed the synteny of INTS6 in squamates and representative outgroups

→ . The INTS6 syntenic block is conserved, with no notable changes in

→ gene order or orientation. In the synteny plots, red blocks indicate

→ the absence of INTS6, green blocks mark its presence, light blue

→ blocks represent genes conserved across lineages, and light purple

→ blocks denote different flanking genes.

Transcriptomic evidence *Pogona vittipes*



Figure 246: INTS6.pdf

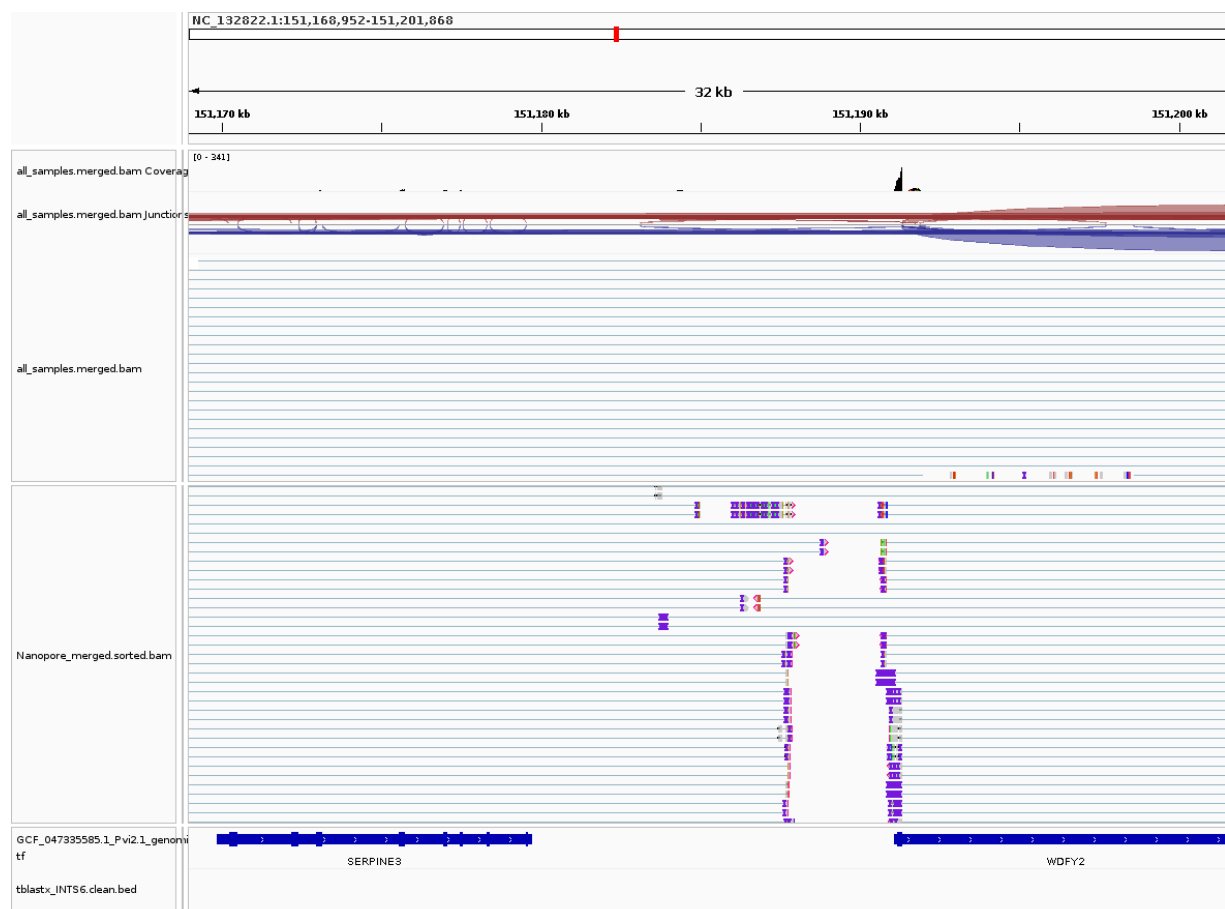


Figure 247: INTS6.png

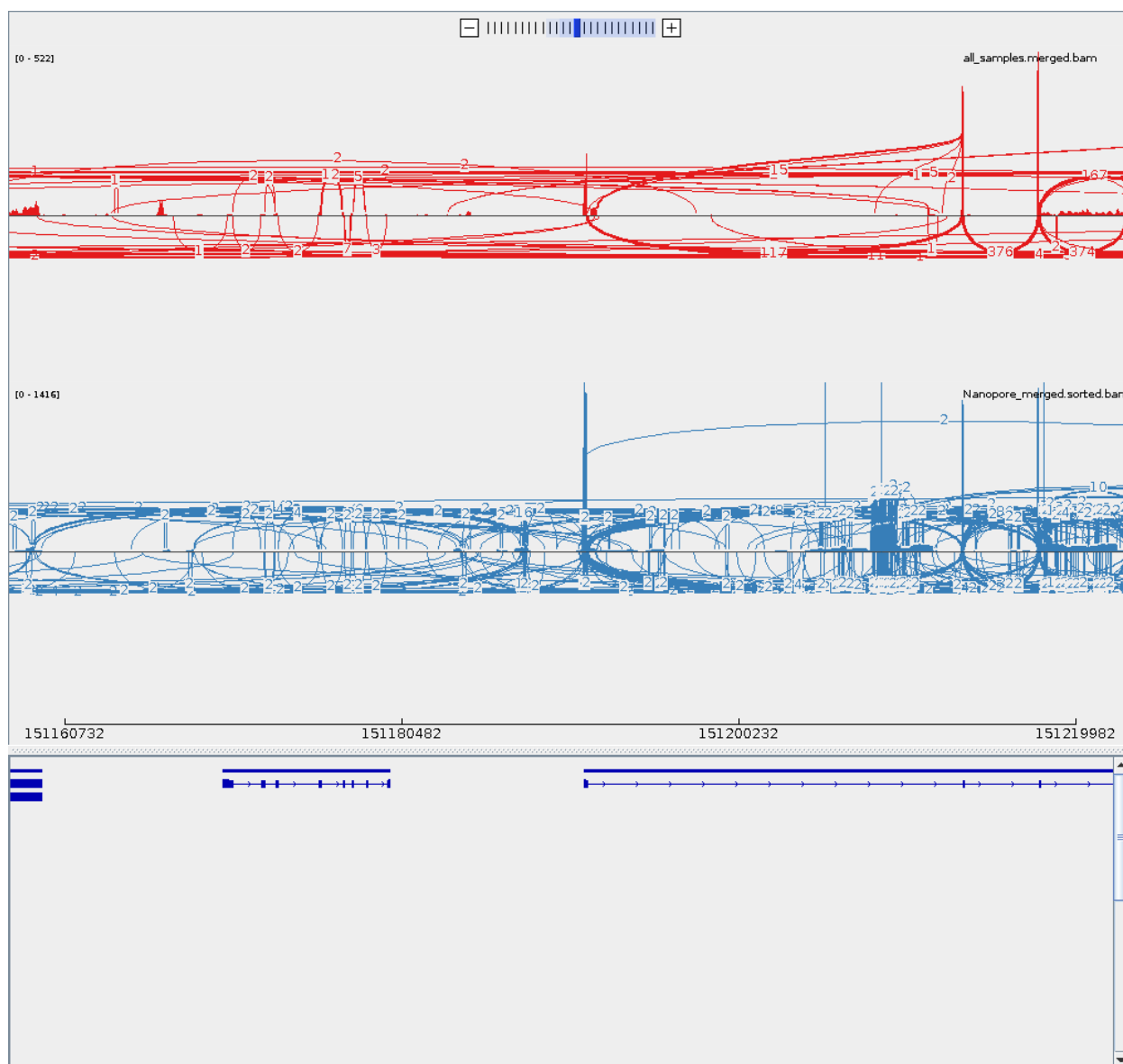


Figure 248: INTS6_Shash.png

23 KDM3A

Assembly verification Evidence

Crotalus_tigris-PacBio

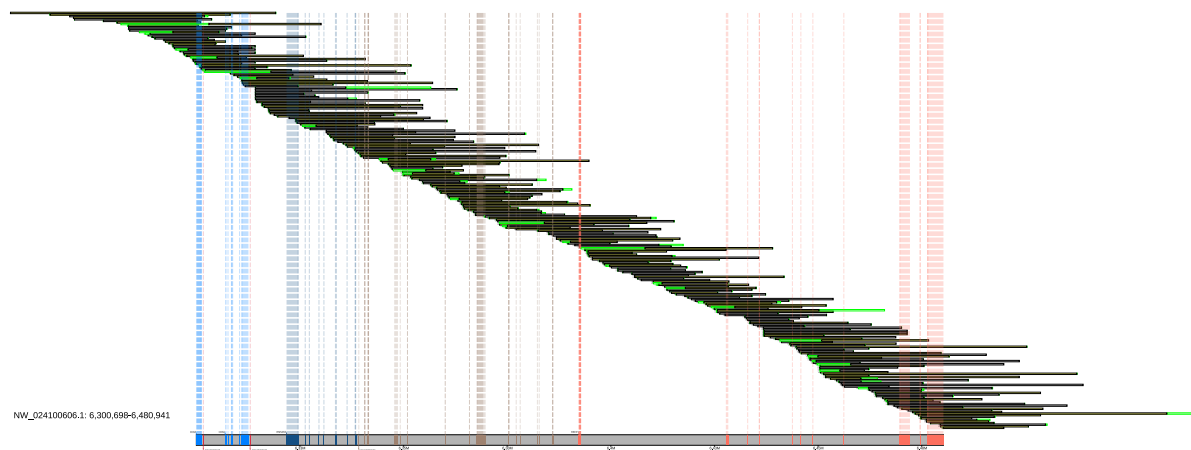


Figure 249: KDM3A:NW_024100606.1:6300698-6480941.pdf

Podarcis_muralis-PacBio

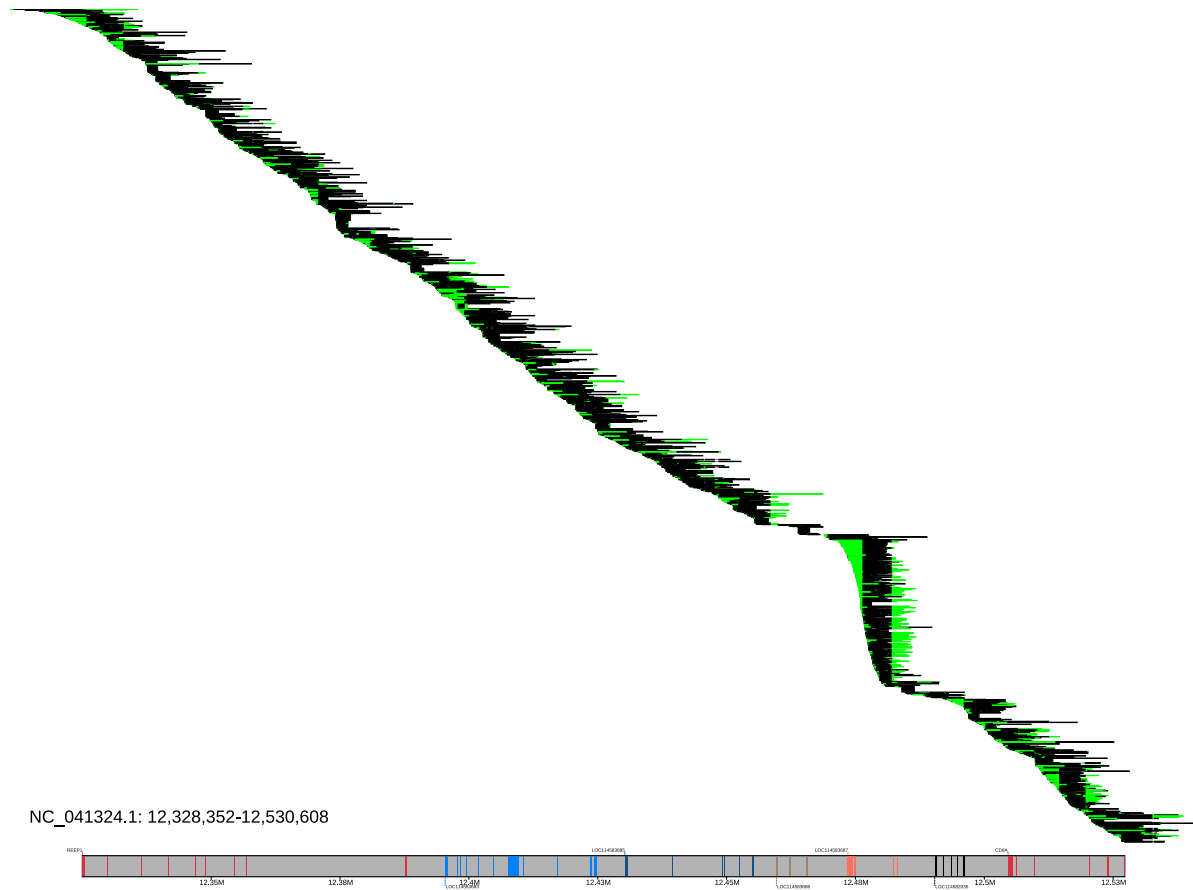


Figure 250: KDM3A:NC_041324.1:12328352-12530608.pdf

Pogona_vitticeps-Nanopore

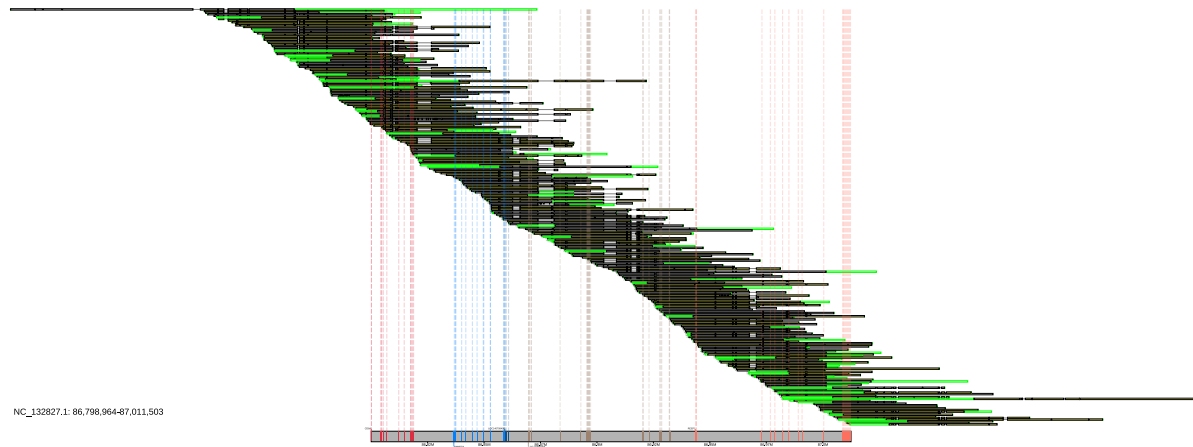


Figure 251: KDM3A:NC_132827.1:86798964-87011503.pdf

Important gene stats

KDM3A_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
KDM3A	28.625	45.3335 +/- 1.88272	3.54689 +/- 0.101889	81.2266 +/- 12.4636	Yes	KDM3B;

Intergenic distance phylogenetic signal evidence



Figure 252: Heatmap_of_deletion_plot.png

KDM3A_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
KDM3A	194	15	179	5	0.186489140470159	0.0486672521393962

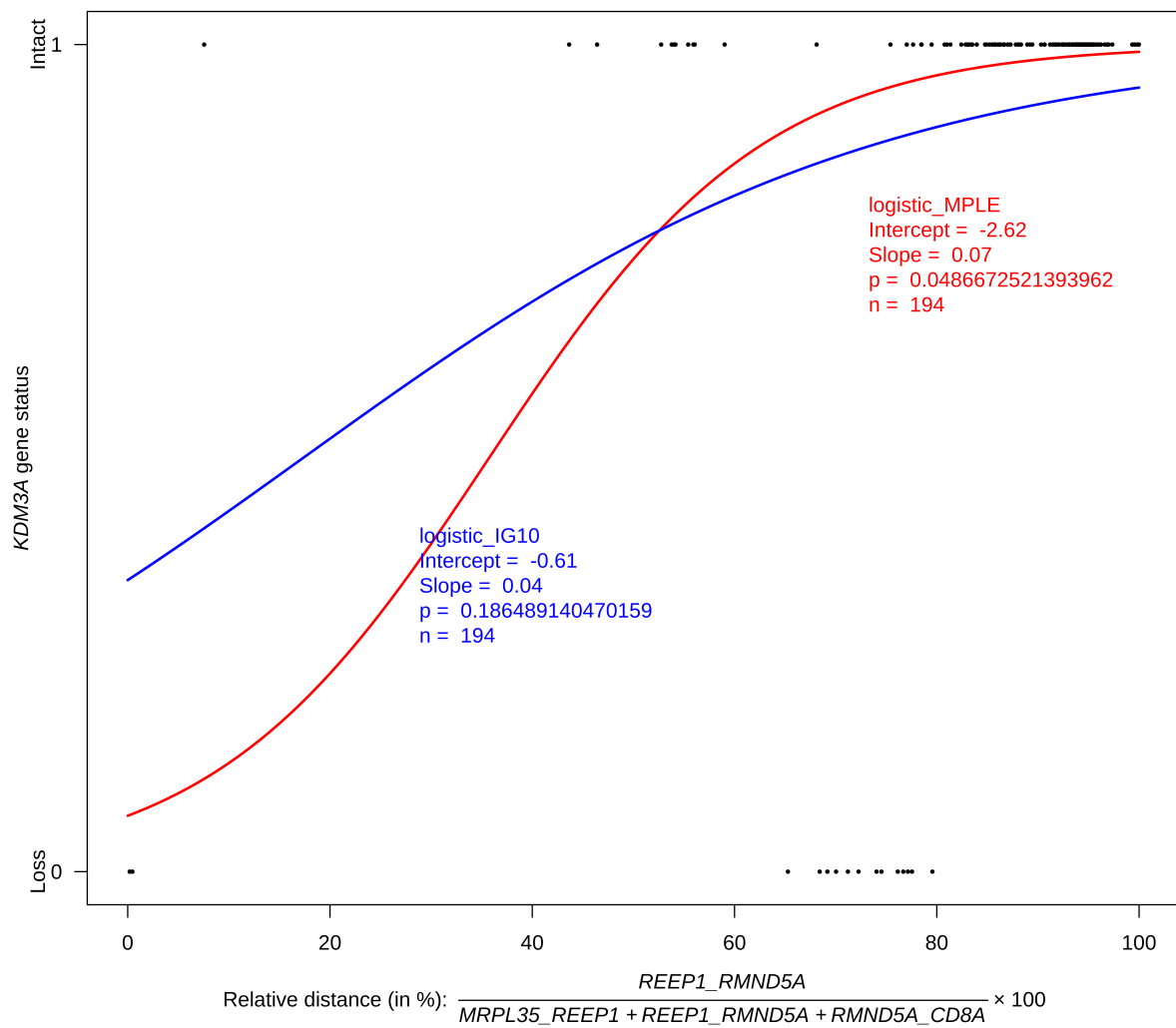


Figure 253: Phylogenetic_signal_of_deletion_plot.png

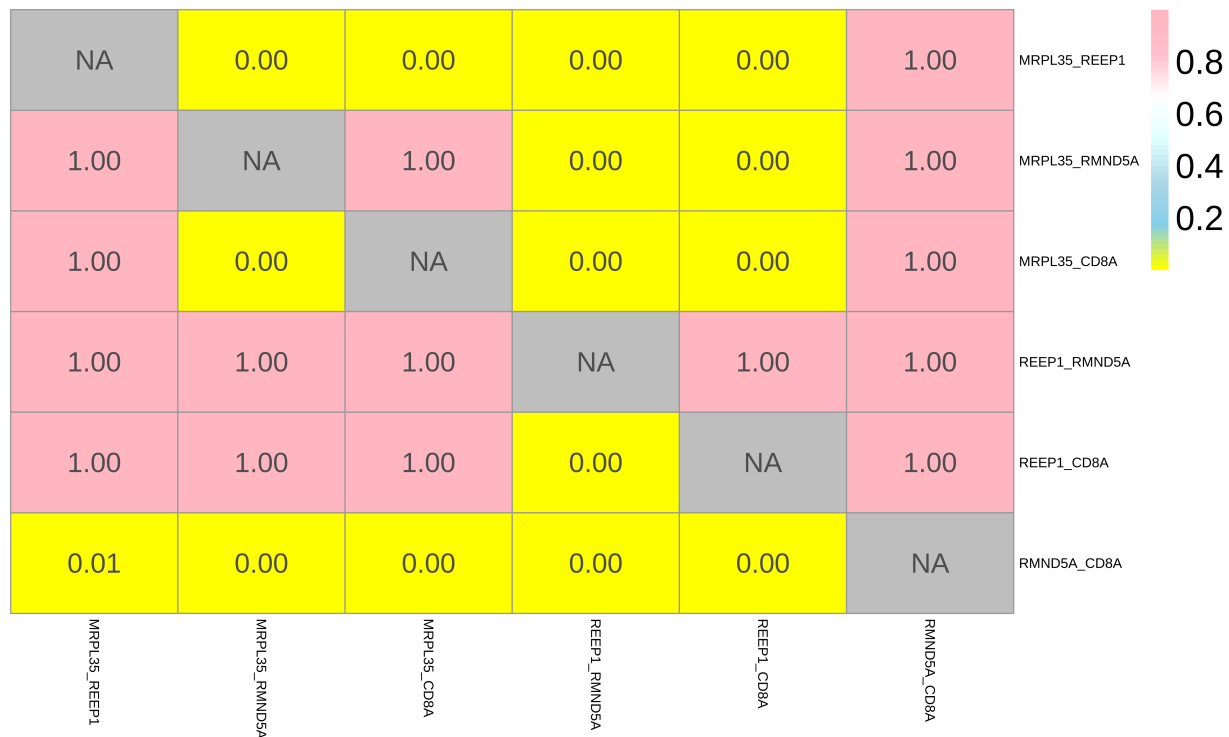


Figure 254: Heatmap_of_deletion_plot.png

KDM3A_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
KDM3A	194	15	179	5	0.186489140470159	0.0486672521393962

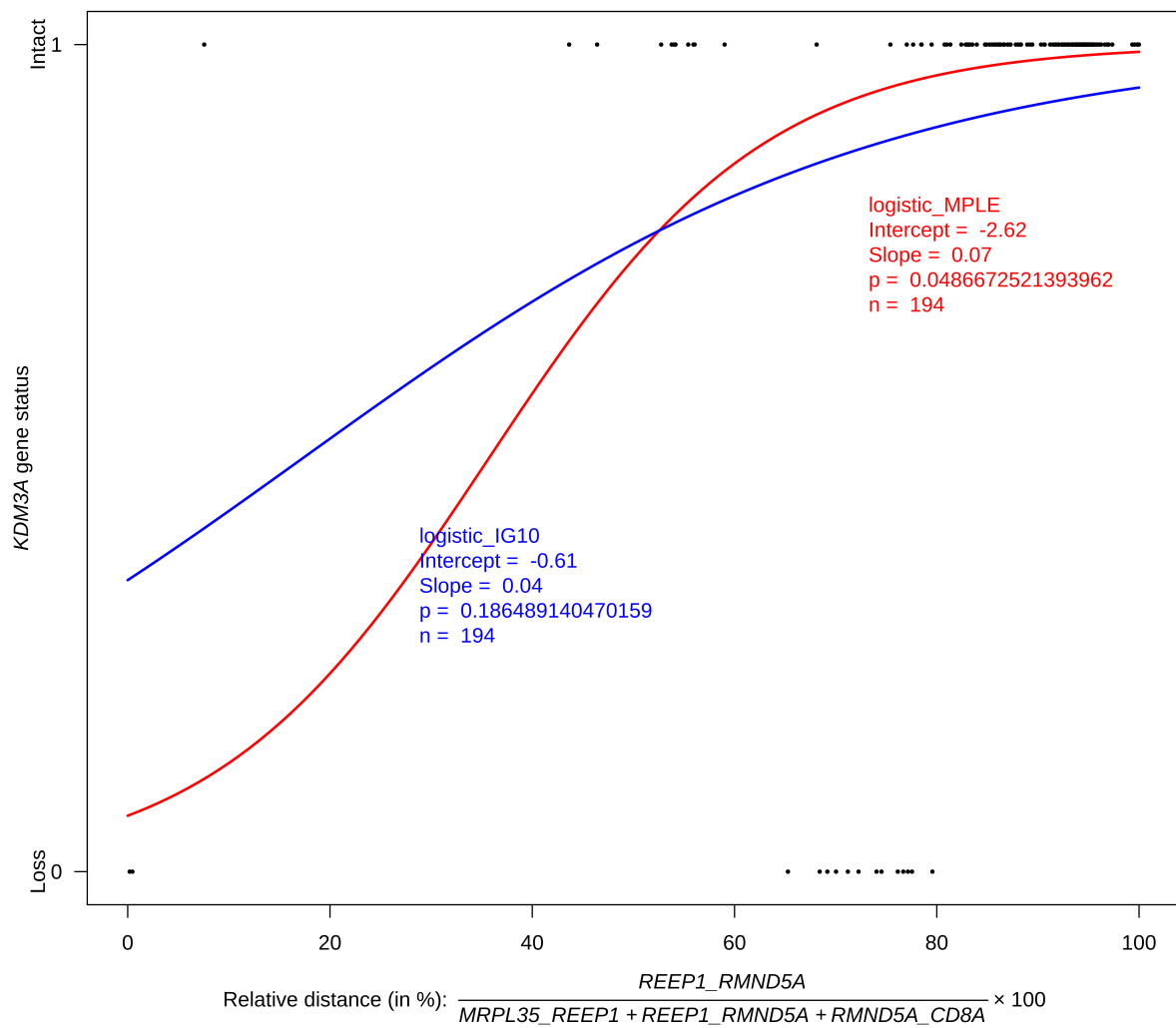


Figure 255: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence

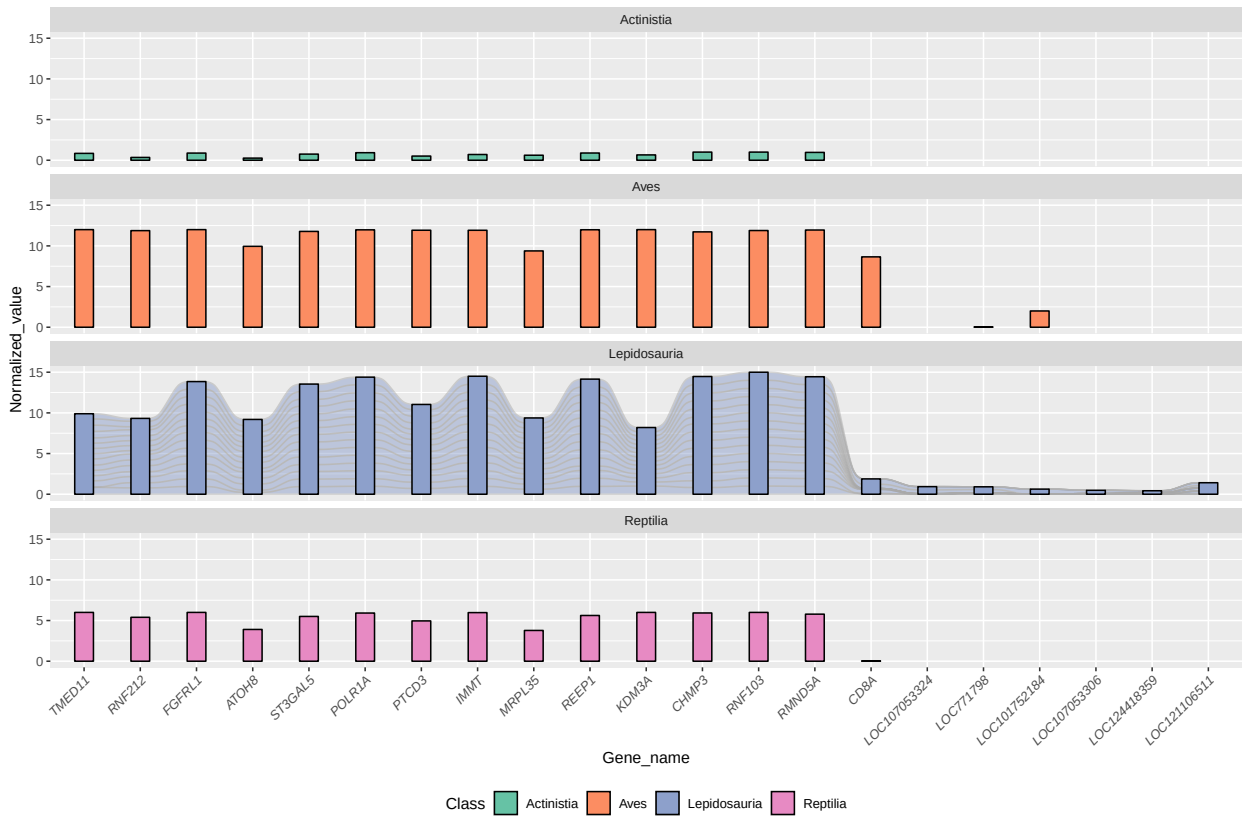


Figure 256: KDM3A.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Lastz gene tree

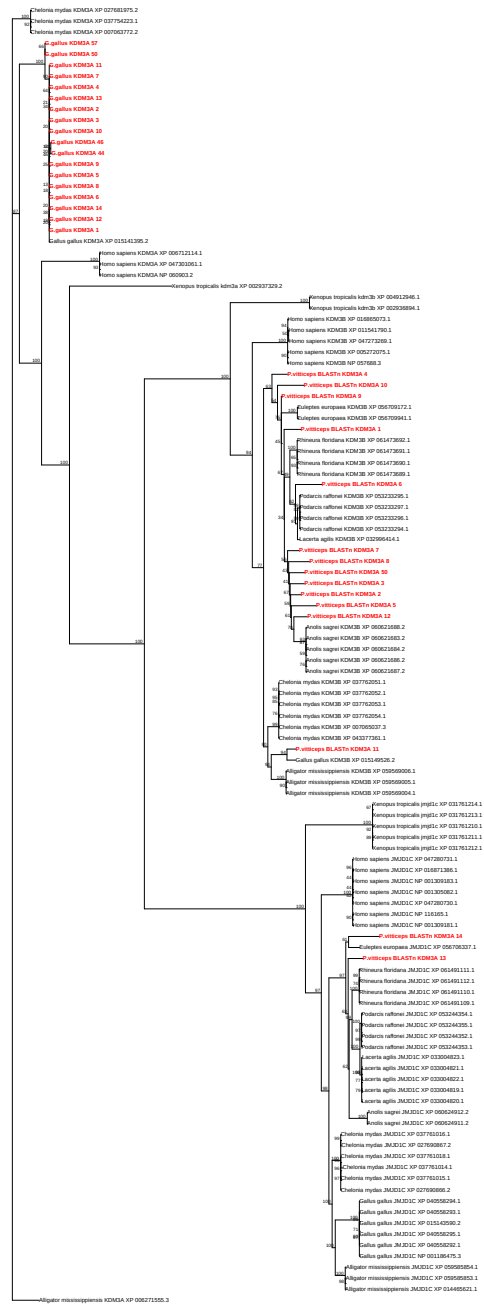


Figure 258: KDM3A.combined.mafft.aln.highlighted.pdf

Syntenic evidence

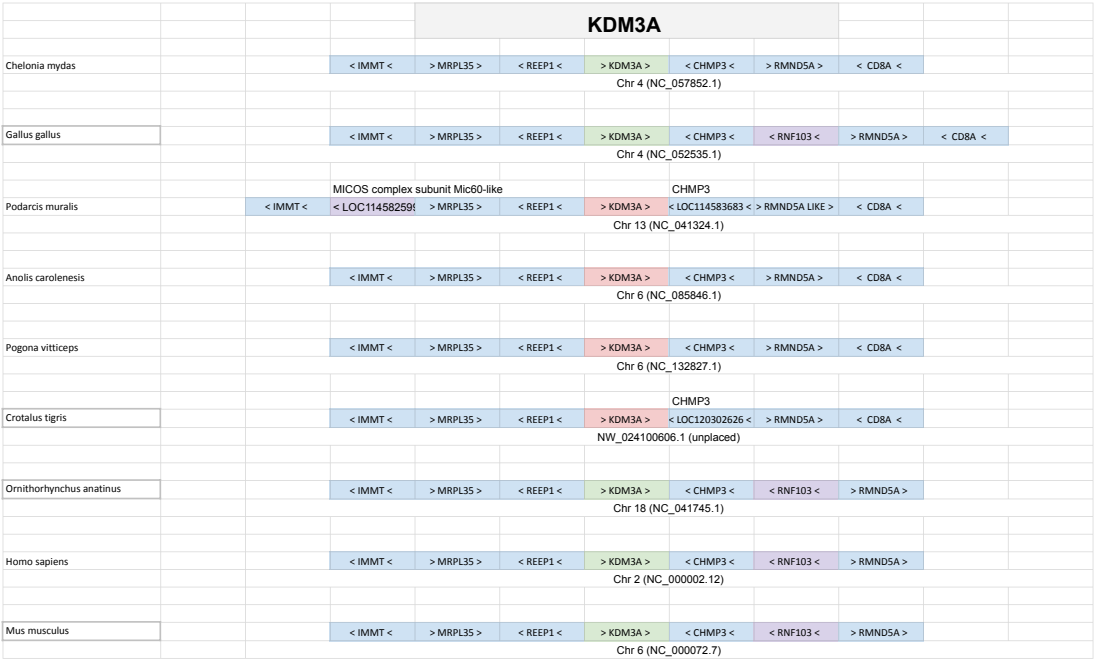


Figure 259: KDM3A.pdf

KDM3A.txt

Synteny analysis of KDM3A

We analyzed the synteny of KDM3A in squamates and representative outgroups

→ . The KDM3A syntenic block is conserved overall, with a notable

→ deviation in a few species where RNF103 is present as a flanking

→ gene instead of RMND5A. In the synteny plots, red blocks indicate

→ the absence of KDM3A, green blocks mark its presence, light blue

→ blocks represent genes conserved across lineages, and light purple

→ blocks denote different flanking genes.

Transcriptomic evidence *Pogona vitticeps*

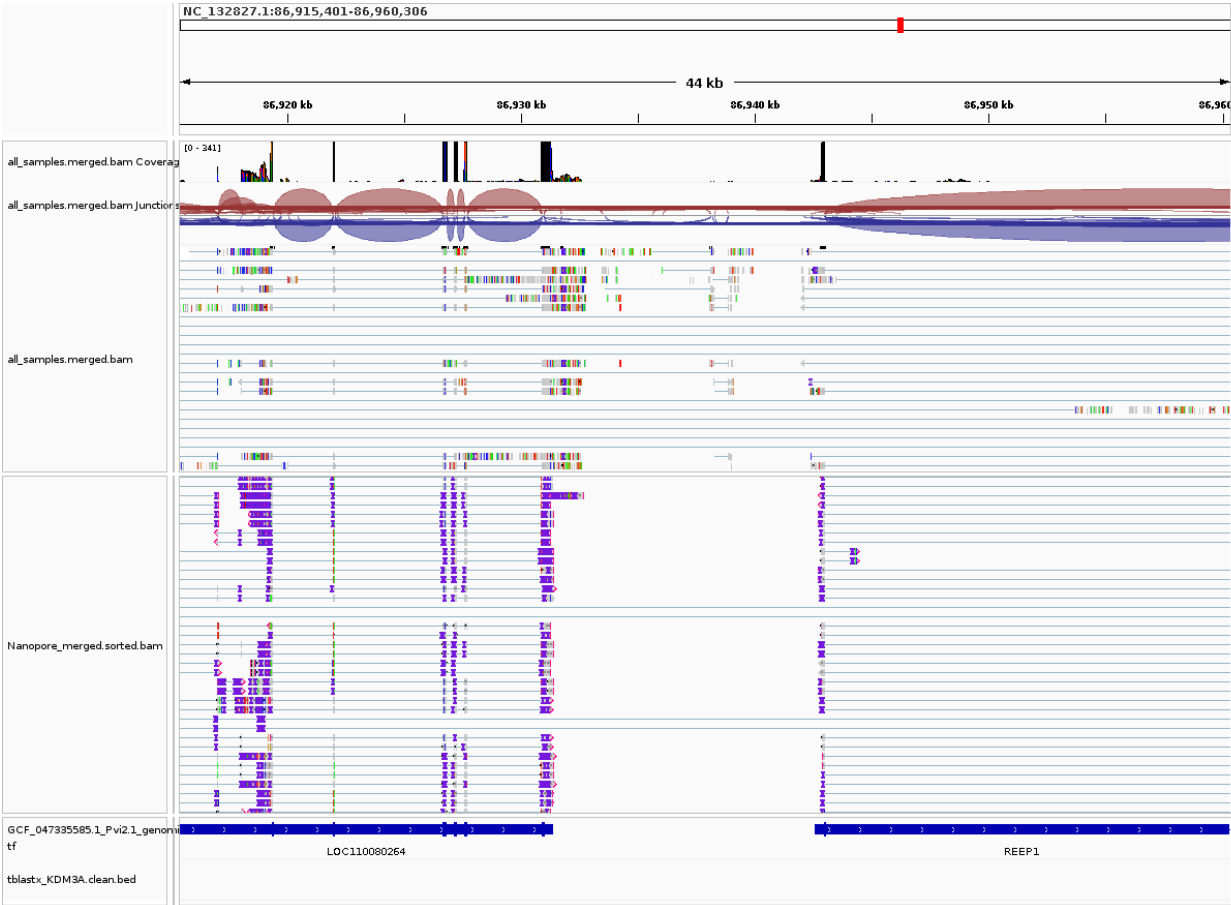


Figure 260: KDM3A.png

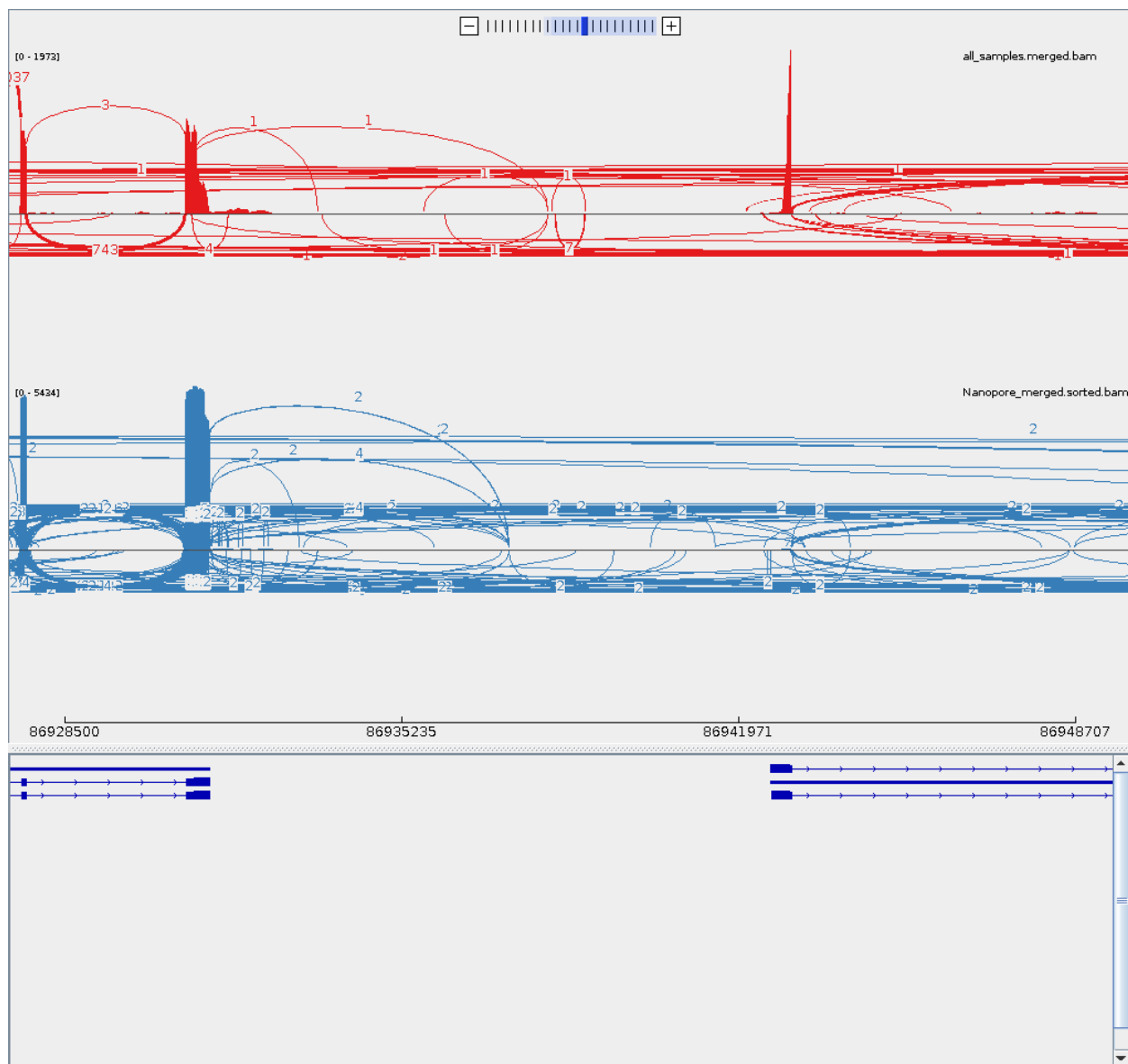


Figure 261: KDM3A_Sashimi.png

24 KREMEN1

Important gene stats

KREMEN1_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
KREMEN1	15.4765625	53.9625 +/- 4.72681	4.09823 +/- 0.358499	69.8107 +/- 13.1707	Yes	Anolis_sagrei.SRR30050337.blast;Naja_naja.SRR10428157.blast;SUSD2;

Intergenic distance phylogenetic signal evidence

Lastz Alignment evidence

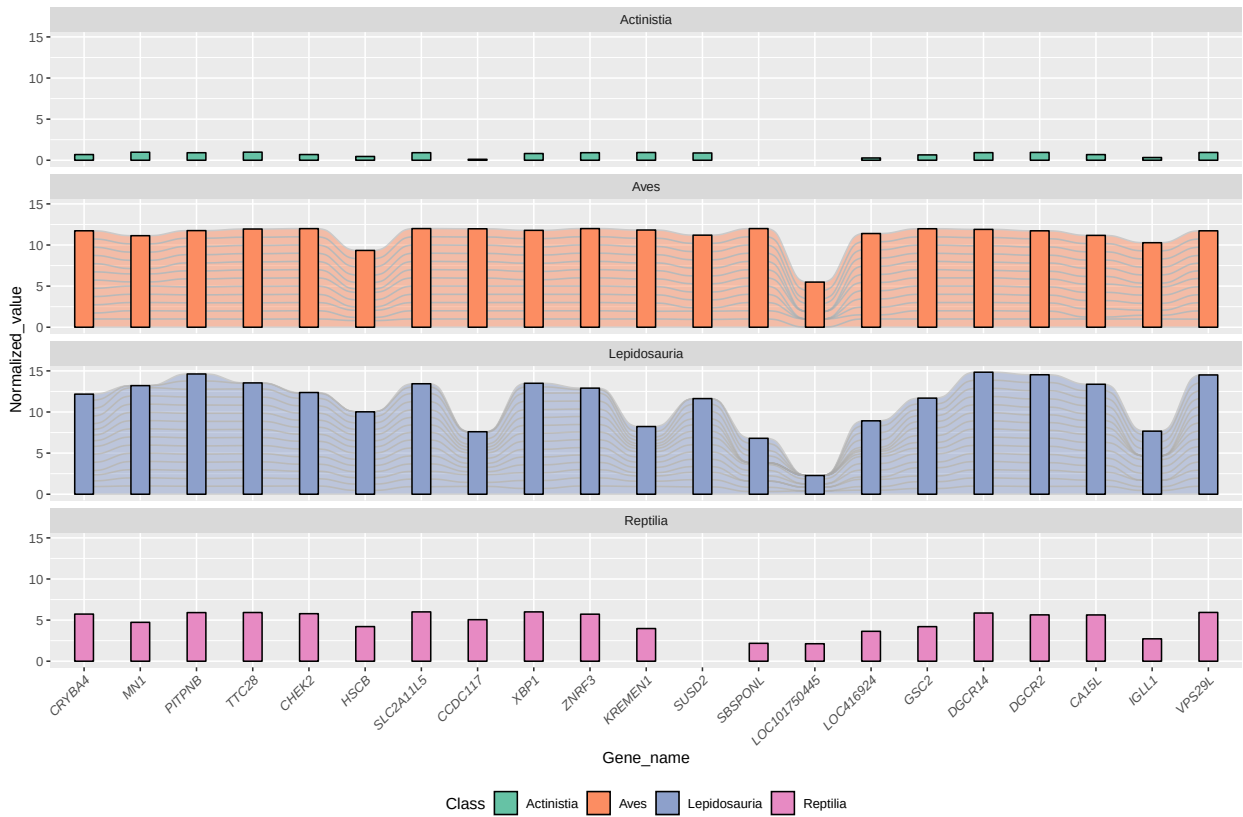


Figure 262: KREMEN1.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Lastz gene tree

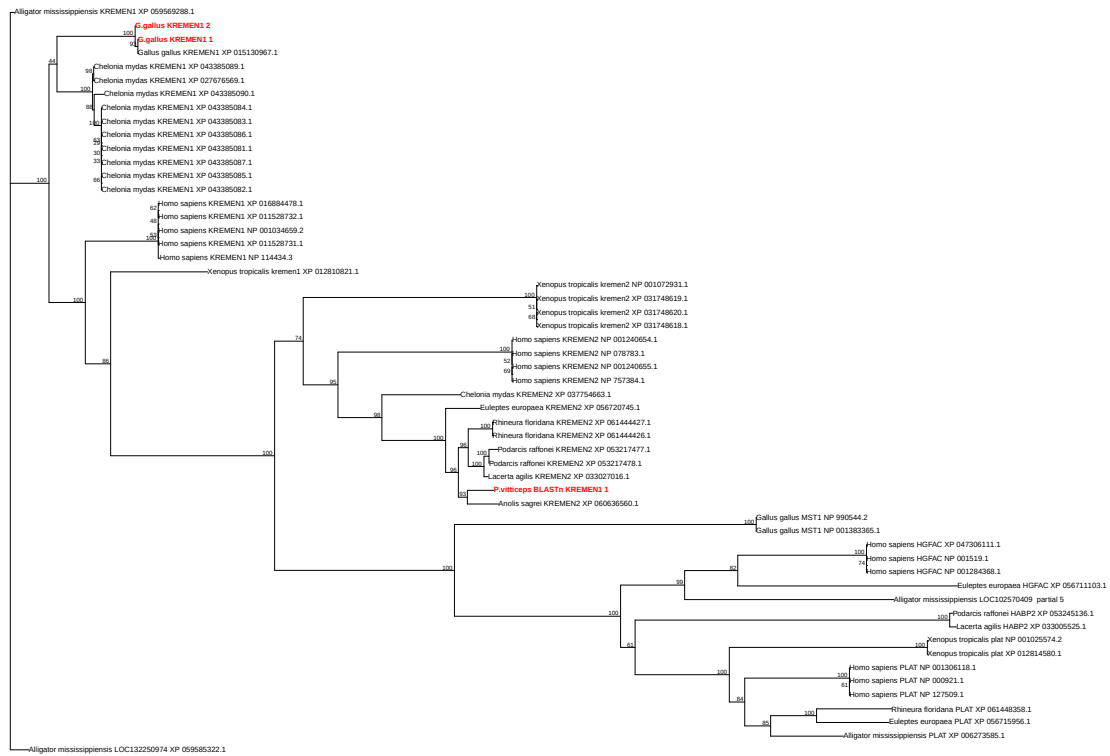


Figure 264: KREMEN1.combined.mafft.aln.highlighted.pdf

Orthofinder genetree

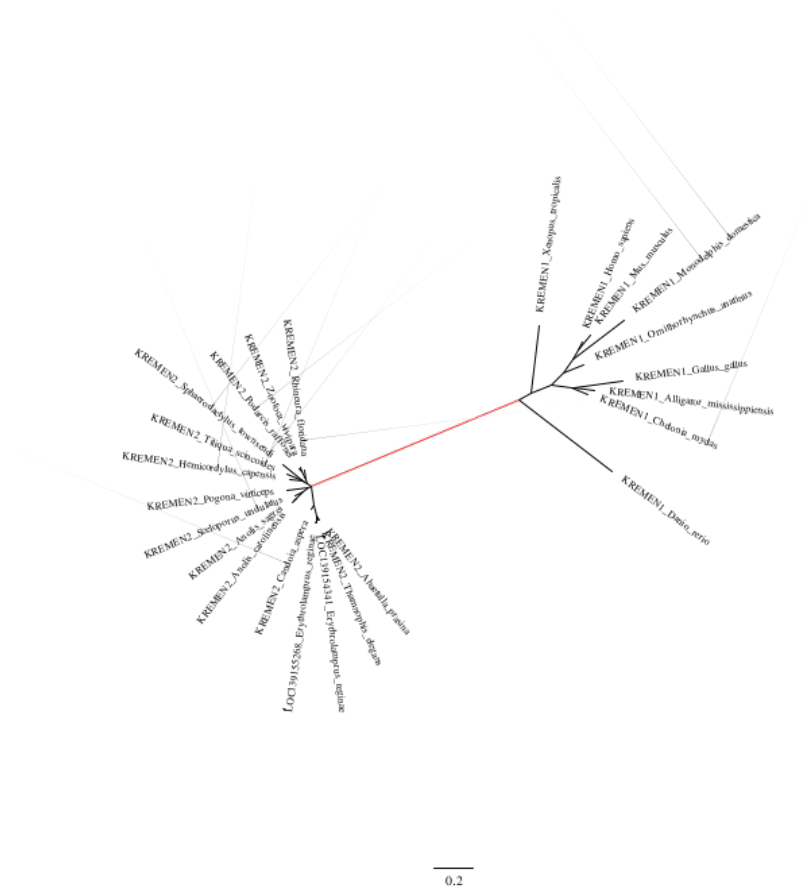


Figure 265: Kremen1_2.PRANK.aln.contree.png

Syntenic evidence

				KREMEN1									
						ZNRF3							
Chelonia mydas			# chromosome en	> KREMEN1 >	< ZNRF3 <	> LOC114019161 >	> XBP1 >	< CCDC117 <					
				Chr 15 (NC_057856.1)									
			WW domain-binding protein 11										
Gallus gallus			> LOC101750445 >	< S8SPONL <	< SUS02 <	> KREMEN1 >	< ZNRF3 <	> XBP1 >	< CCDC117 <				
				Chr 15 (NC_052546.1)									
Podarcis muralis			< EWSR1 <	> RHBDD3 >	< EMID1 <	> KREMEN1 >	< ZNRF3 <	> XBP1 >	< CCDC117 <			## same chromosome but far off	
			Chr 16 (NC_041327.1) ##				Chr 16 (NC_041327.1) ##						
Anolis carolensis			< EWSR1 <	> RHBDD3 >	> KREMEN1 >		E3 ubiquitin-prote	XBP1	coiled-coil domain-containing protein 117-like				
			Chr X (NC_085847.1)				NW_026943835.1 (unplaced)						
Pogona vitticeps			< EWSR1 <	> RHBDD3 >	< EMID1 <	> KREMEN1 >	< ZNRF3 <	> XBP1 >	< CCDC117 <			## same chromosome but far off	
			Chr 14 (NC_132835.1) ##				Chr 14 (NC_132835.1) ##						
Crotalus tigris			< EWSR1 <	> RHBDD3 >	< EMID1 <	> KREMEN1 >	< ZNRF3 <	> XBP1 >	< CCDC117 <				
			NW_024100632.1 (unplaced)				NW_024097560.1 (unplaced)						
Ornithorhynchus anatinus			> CCDC117 >	< XBP1 <	> ZNRF3 >	> KREMEN1 >	> EMID1 >	< MYO1H <	> FOXN4 >	< ACACB <	< UNG <		
			Chr 21 (NC_041748.1)										
Homo sapiens			< XBP1 <	> ZNRF3 >	< C22orf31 <	> KREMEN1 >	> EMID1 >	< RHBDD3 <	> EWSR1 >				
			NC_000022.11										

Figure 266: KREMEN1.pdf

KREMEN1.txt

Synteny analysis of KREMEN1

The KREMEN1 syntenic block, which is conserved in outgroups shows
→ evidence of significant intrachromosomal rearrangements in squamates
→ . In several lizard species, including
Podarcis muralis and Pogona vitticeps, the block has undergone an
→ intrachromosomal transposition, moving to a distant location on the
→ same chromosome.
In Anolis carolinensis, the block is fragmented, with genes located on
→ different chromosomes, while in the snake Crotalus tigris, the
→ genes are scattered across multiple unplaced scaffolds. These
→ findings indicate both intrachromosomal repositioning have

→ occurred in this syntenic region.

In the synteny plots, red blocks indicate the absence of the target gene,
→ while green blocks mark its presence. Light blue blocks represent
→ flanking genes that are conserved across lineages, and light purple
→ blocks denote instances where a different flanking gene is present.
→ A bright yellow color indicates a change in the gene's orientation.

25 LAPT M5

Assembly verification Evidence

Crotalus_tigris-PacBio

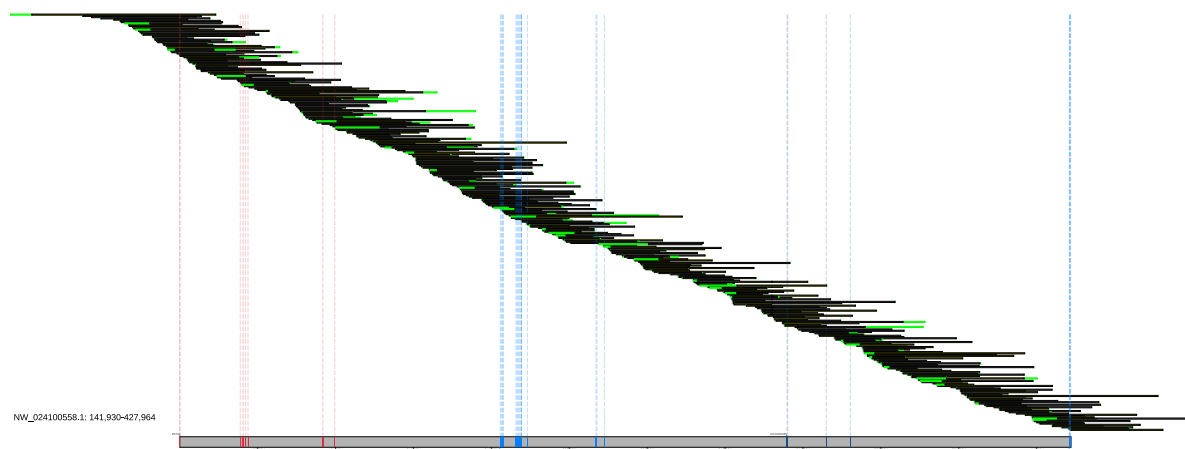


Figure 267: LPTM5:NW_024100558.1:141930-427964.pdf

Podarcis_muralis-PacBio

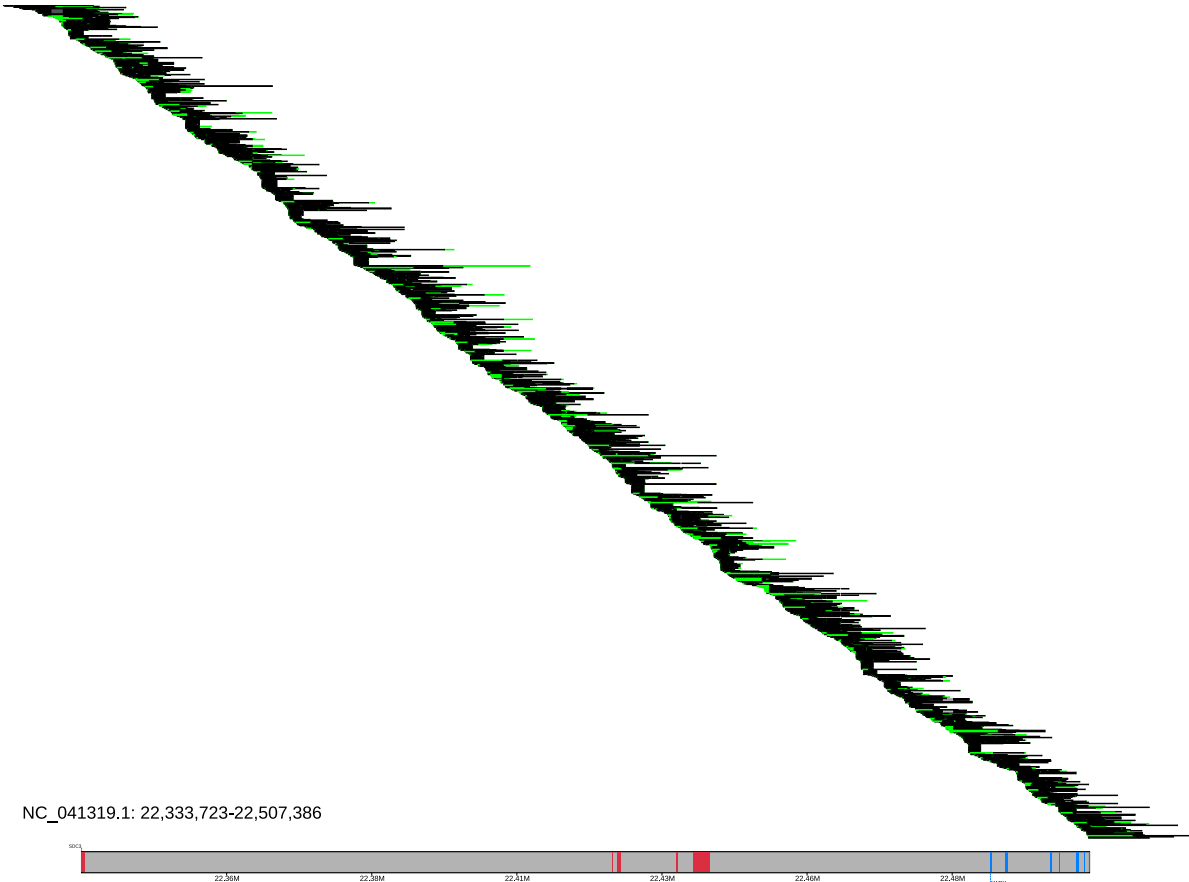


Figure 268: LPTM5:NC_041319.1:22333723-22507386.pdf

Pogona_vitticeps-Nanopore

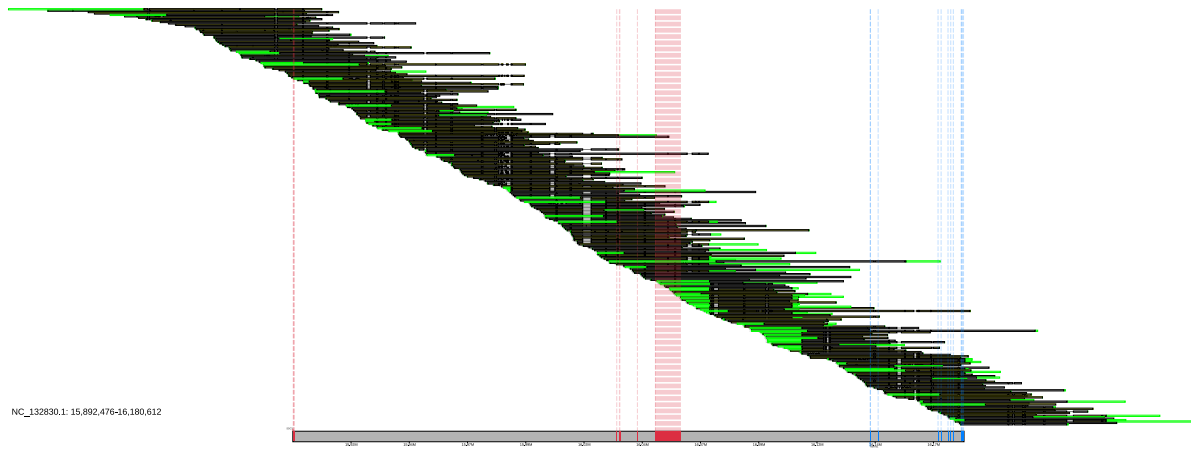


Figure 269: LAPTM5:NC_132830.1:15892476-16180612.pdf

Important gene stats

LAPTM5_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
LAPTM5	5.18487395	53.8563 +/- 4.43106	3.91501 +/- 0.379312	74.3232 +/- 15.2316	No	Na

Intergenic distance phylogenetic signal evidence

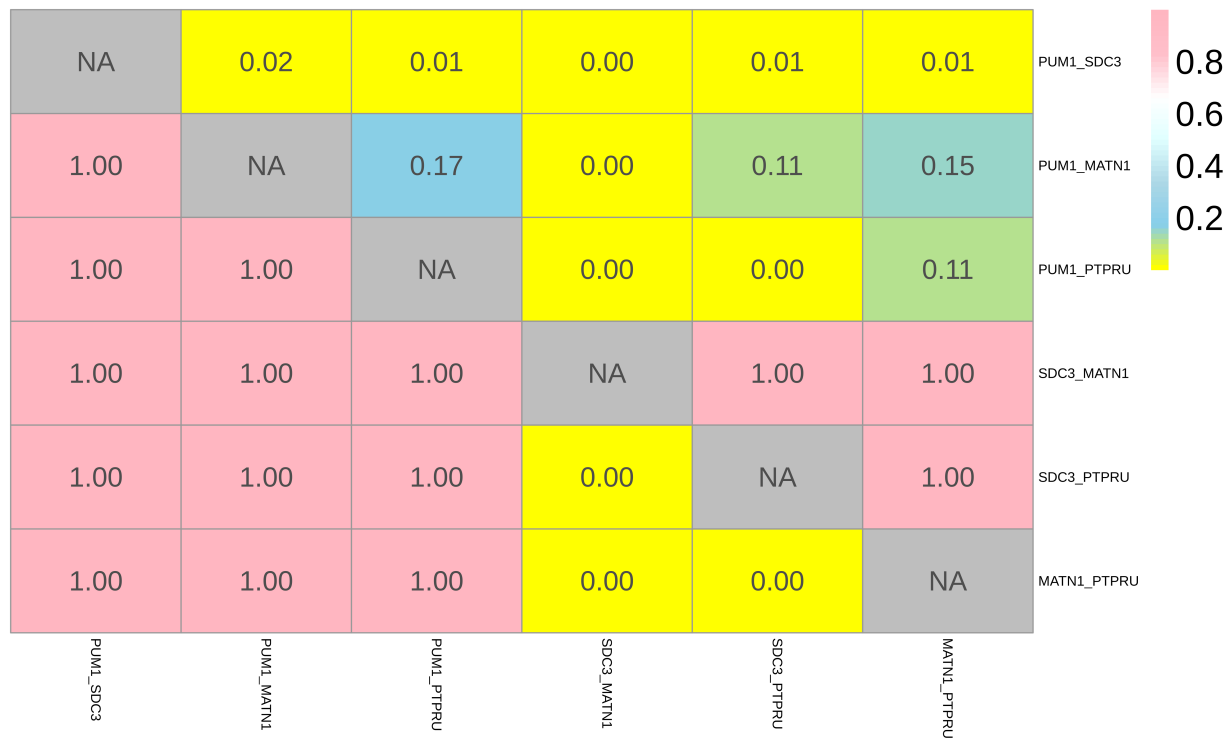


Figure 270: Heatmap_of_deletion_plot.png

LAPTM5_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
LAPTM5	208	15	193	5	0.161298401512695	1

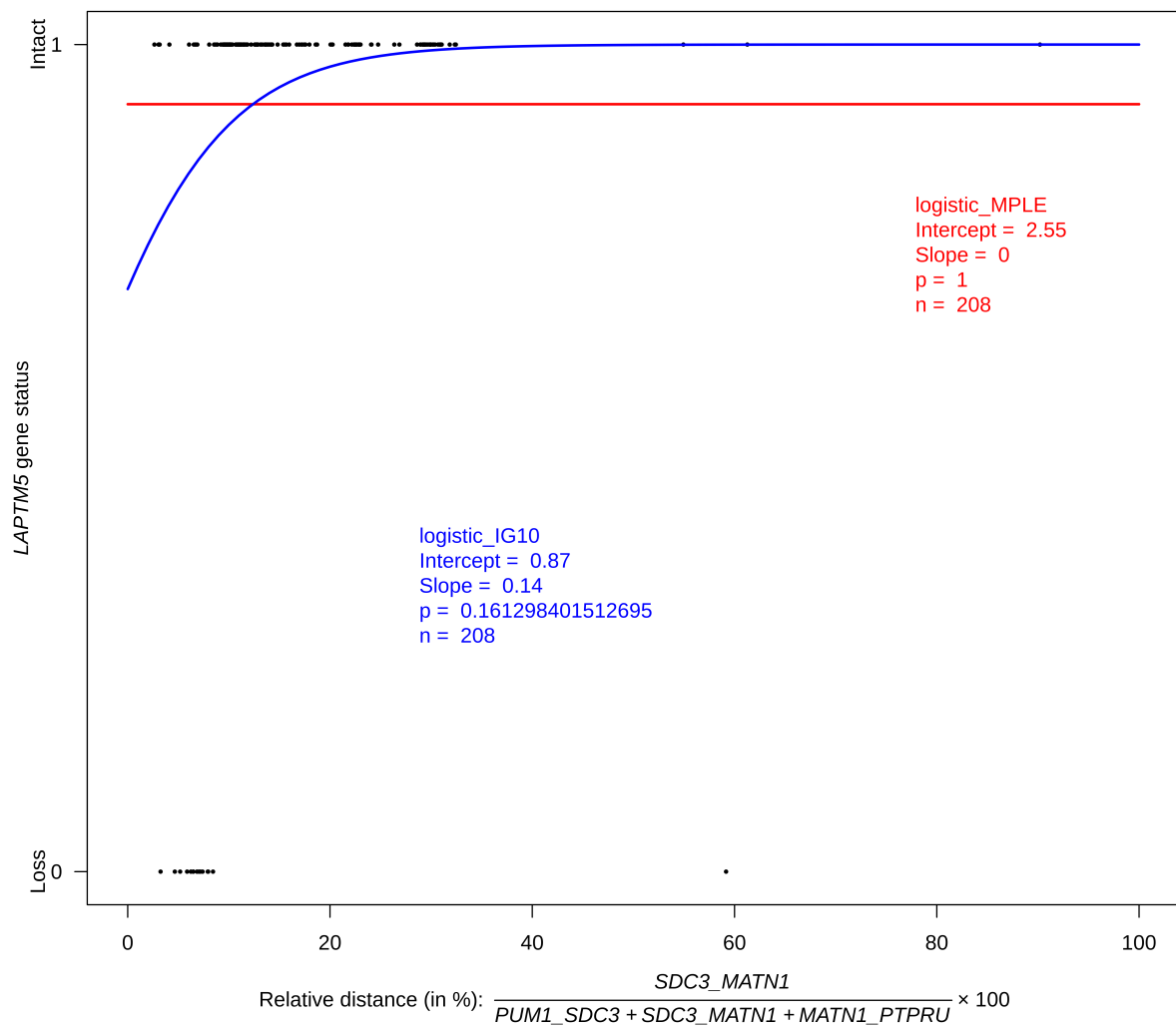


Figure 271: Phylogenetic_signal_of_deletion_plot.png

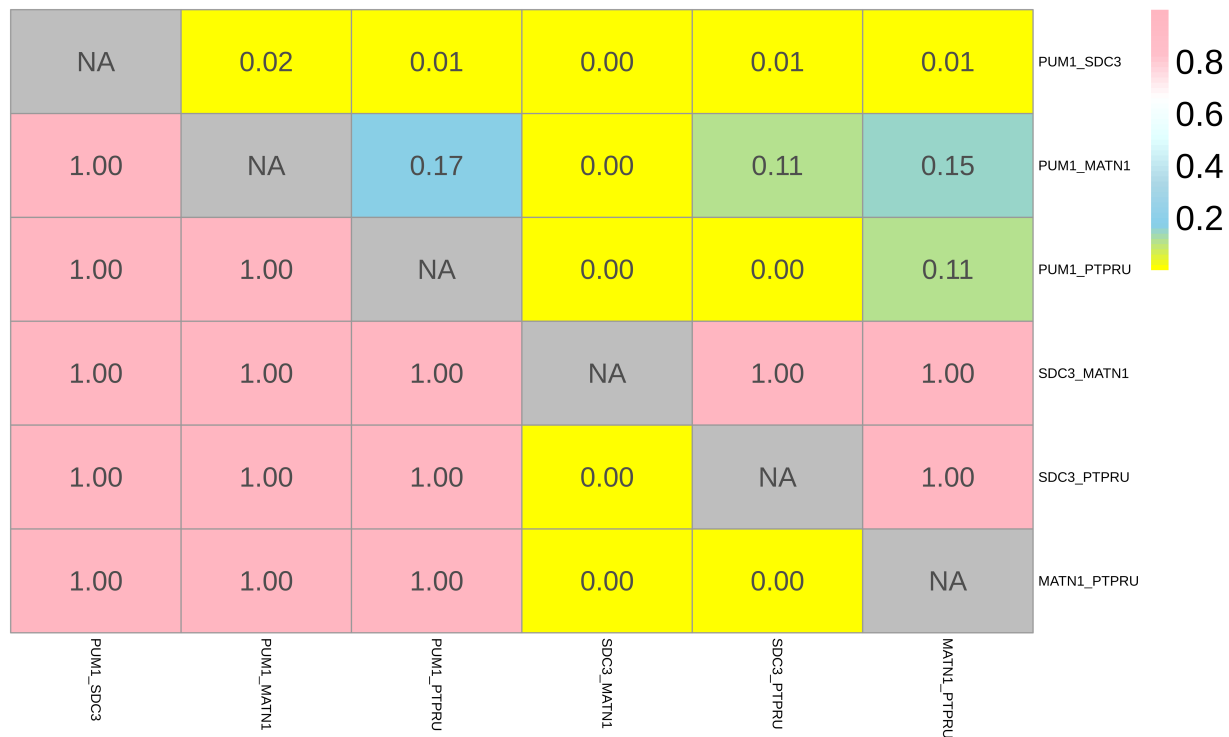


Figure 272: Heatmap_of_deletion_plot.png

LAPTM5_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
LAPTM5	208	15	193	5	0.161298401512695	1

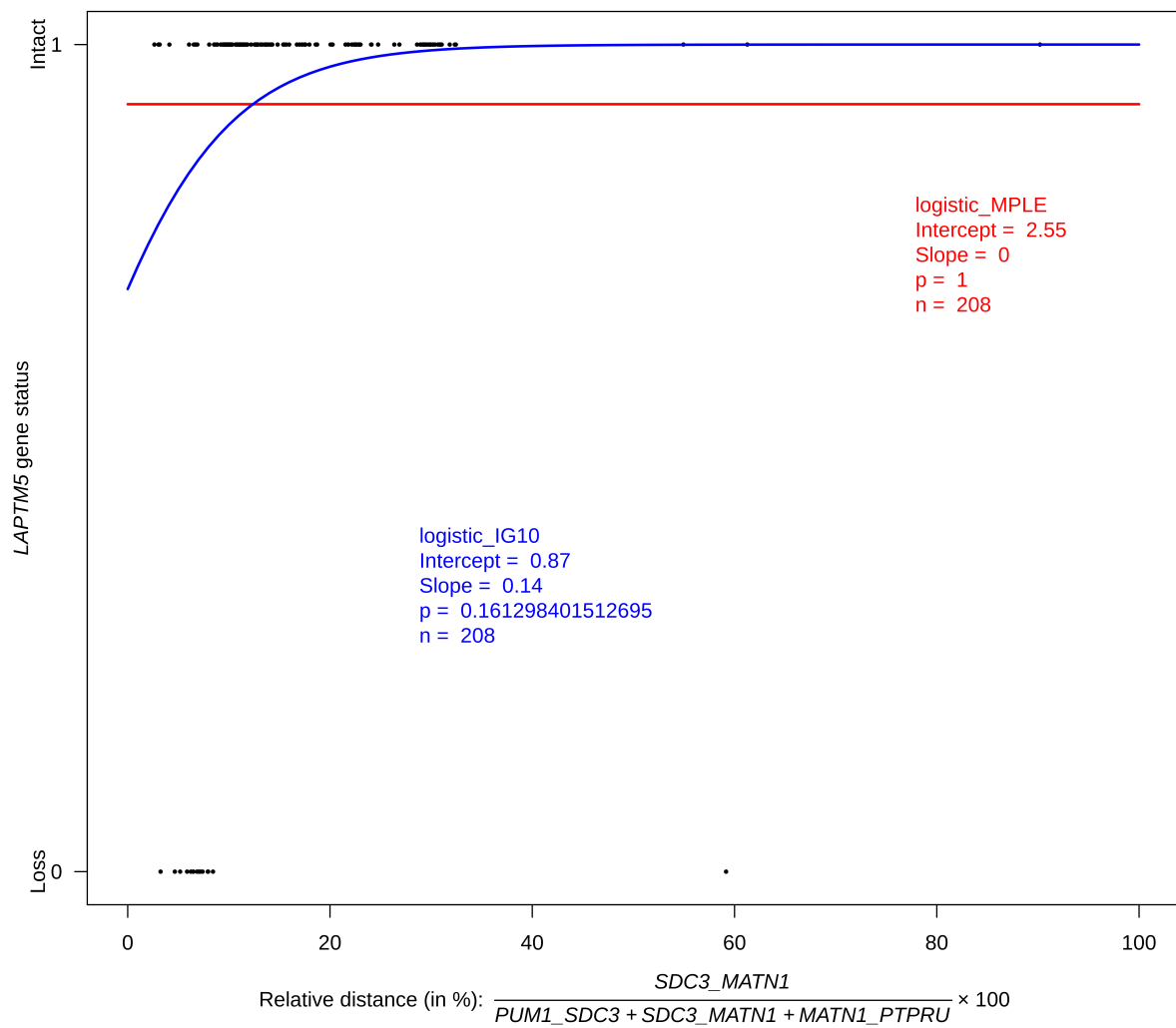


Figure 273: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence

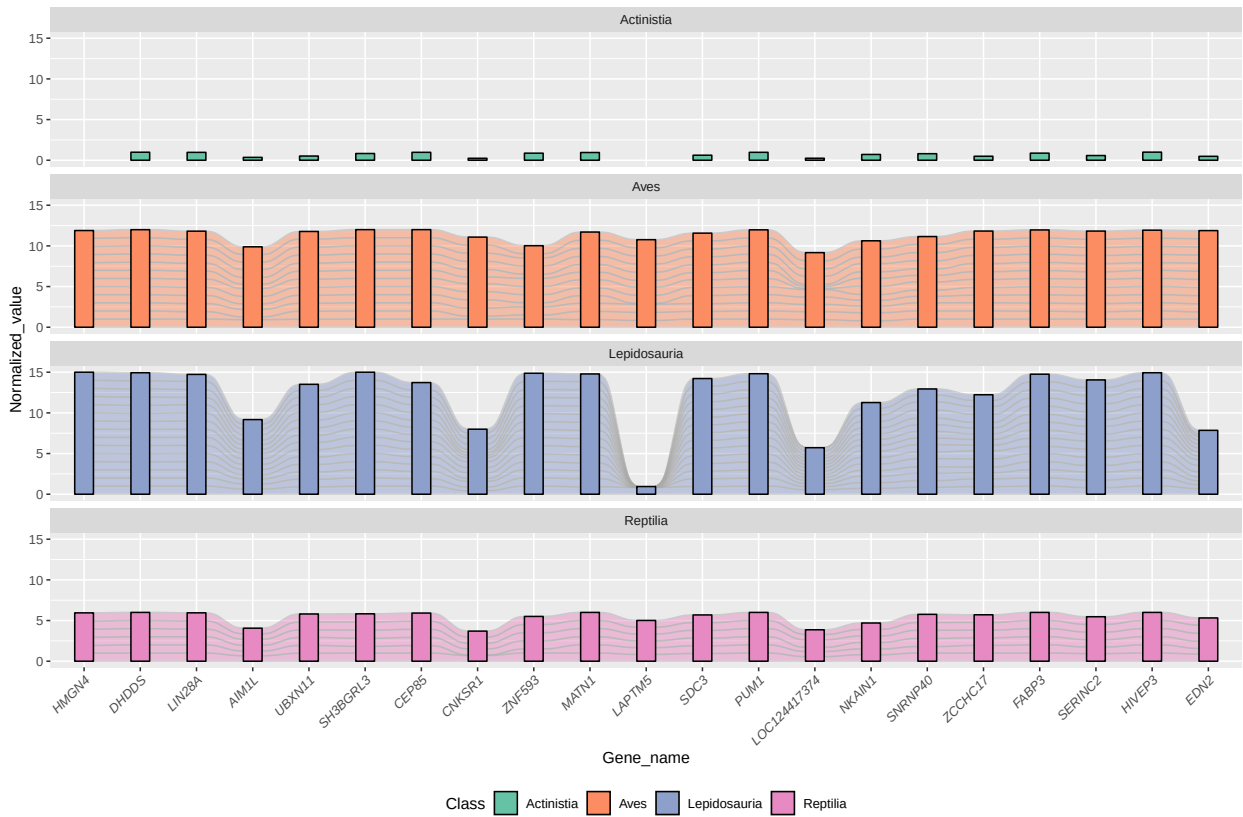


Figure 274: LAPTM5.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

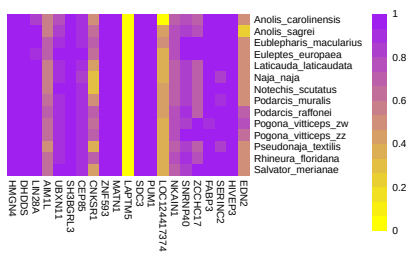


Figure 275: LAPTM5.FS_Exonic.Final.Gallus_gallus.21_genes_heatmap.pdf

Syntenic evidence

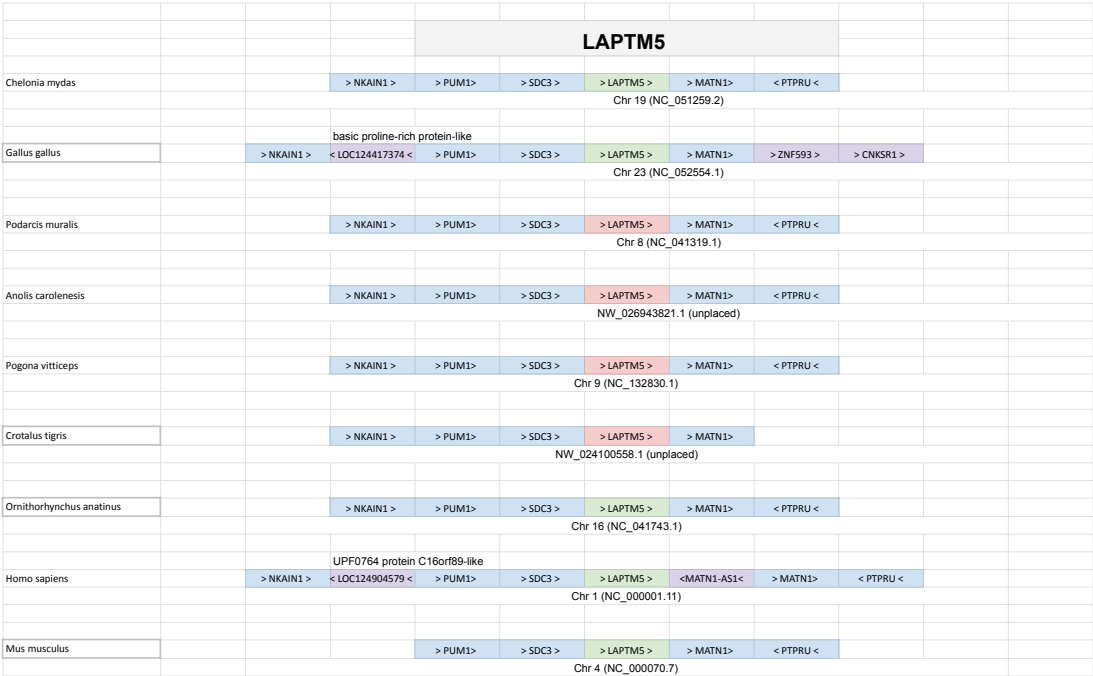


Figure 276: LAPT M5.pdf

LAPT M5.txt

Synteny analysis of LAPT M5

We analyzed the synteny of LAPT M5 in squamates and representative outgroups. The LAPT M5 syntenic block is conserved, with no notable changes in gene order or orientation. In the synteny plots, red blocks indicate the absence of LAPT M5, green blocks mark its presence, light blue blocks represent genes conserved across lineages, and light purple blocks denote different flanking genes.

Transcriptomic evidence Pogona vitticeps



Figure 277: LPTM5.png

26 LCP1

Important gene stats

LCP1_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
LCP1	54.36363636	46.7889 +/- 1.98135	3.5337 +/- 0.112685	85.7078 +/- 8.834	Yes	LOC118083762:Naja_naja_SRR10428157.blast;PLS1;Rhabdophis_nuchalis.SRR28573917.blast;

Lastz Alignment evidence

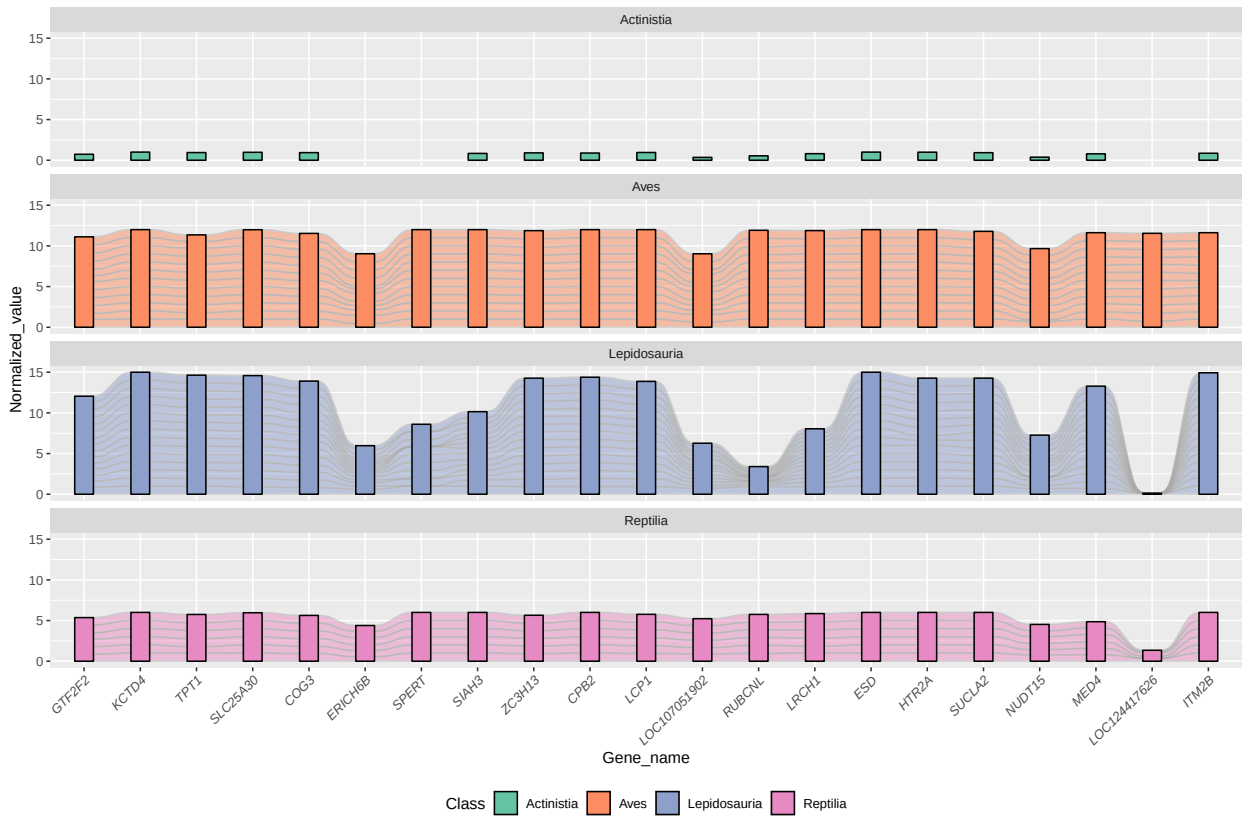


Figure 278: LCP1.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Lastz gene tree

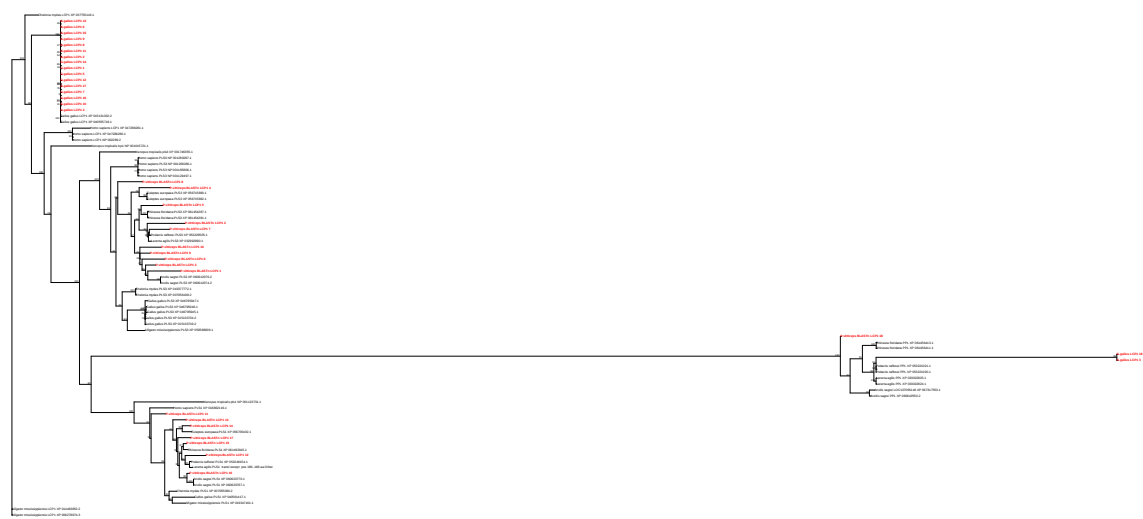


Figure 280: LCP1.combined.mafft.aln.highlighted.pdf

Syntenic evidence

	SIAH3, LCP1, LRCH1, RUBCNL																		
Chelonia mydas	> SUCIA2 >	< LOC11996202 >	> HTR2A >	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	> CPB2 >	> ZC3H13 >	> SIAH3 >	< CRY2 <	> ERICHBB >	< COG3 <					
	Chr 1 (NC_057948.1)																		
Gallus gallus	> SUCIA2 >	> HTR2A >	> ESD >	< LRCH1 <	> RUBCNL >	< LOC10053892 <	> LCP1 >	> CPB2 >	> ZC3H13 >	> SIAH3 >	< SPRT <								
	NC_029332.1																		
Podarcis muralis	> SUCIA2 >	< NPLRC3 <	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	> CPB2 >	< ZC3H13 <	> SIAH3 >	< COG3 <	< SPRT <	# same chromosome but on another side after skipping two genes						
	Chr 1 (NC_04131) Chr 3 (NC_041314.1) Chr 5 (NC_041316.1) #																		
Anolis carolinensis	> SUCIA2 >	> HTR2A >	< NPLRC3 <	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	< p98b1 <	< sp98b24 <	< drapc15 <	> z3br13 >	< CPB2 <	> SIAH3 >	< COG3 <	< drp2 <	> ERICHBB >		
	Chr 1 (NC_085841.1) Chr 1 (NC_085841.1) Chr 1 (NC_085841.1) Chr 3 (NC_085843.1)																		
Pogona vitticeps	> SUCIA2 >	> HTR2A >	< NPLRC3 <	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	< p98b1 <	< sp98b24 <	< drapc15 <	> z3br13 >	< CPB2 <	> SIAH3 >	< COG3 <	< srsb1 <	# same chromosome but after skipping genes		
	Chr 1 (NC_132822.1) Chr 1 (NC_132822.1) Chr 1 (NC_132822.1) Chr 3 (NC_132824.1)																		
Crotalus tigris	> SUCIA2 >	> HTR2A >	< NPLRC3 <	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	< p98b1 <	< sp98b24 <	< drapc15 <	> z3br13 >	< CPB2 <	> SIAH3 >	< COG3 <	> ERICHBB >			
	NW_02410010.1 (unplaced) NW_024097046.1 (unplaced) NW_024098059.1 (unplaced) NW_024098025.1 (unplaced)																		
Oreodontherapsidus sinuatus	> SUCIA2 >	< LOC103170461 >	> HTR2A >	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	> CPB2 >	> ZC3H13 >	> SIAH3 >	> ERICHBB >	< COG3 <						
	Chr 20 (NC_041747.1)																		
Homo sapiens	> SUCIA2 >	> HTR2A >	< HTR2A-AS1 <	> ESD >	< LRCH1 <	< FRAP1AF1 <	> LOC100338 >	> RUBCNL >	< LRRC63 <	> LOC107884571 >	> LCP1 >	> CPB2 >	< CPB2-AS1 <	> ZC3H13 >	< LOC103170391 <	> SIAH3 >	< CRY2 <	> ERICHBB >	< COG3 <
	Chr 13 (NC_000333.12) Chr 13 (NC_000333.12) Chr 13 (NC_000333.12) Chr 13 (NC_000333.12)																		
Monodelphis domestica	> SUCIA2 >	< GNAI210 <	> HTR2A >	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	> CPB2 >	< GNAI212 <	> ZC3H13 >	< GNAI212 <	> SIAH3 >	< CRY2 <	< GNAI219 <	> ERICHBB >	< COG3 <		

Figure 281: LCP1.pdf

LCP1.txt

Syntenic analysis of LCP1

The syntenic block for LCP1 shows evidence of both interchromosomal and

- intrachromosomal rearrangements within squamates. In species such as
- *Anolis carolinensis* and *Pogona vitticeps*, the flanking genes are
- located on two different chromosomes, indicating a break in synteny.
- Furthermore, in lizards like *Podarcis muralis*, along with
- interchromosomal the block appears to have undergone an
- intrachromosomal rearrangement, with flanking genes repositioned to
- a different location on the same chromosome after skipping several
- intervening genes. The block is highly fragmented in the snake
- *Crotalus tigris*, with genes located on multiple unplaced scaffolds.

In the synteny plots, red blocks indicate the absence of the target gene,
→ while green blocks mark its presence. Light blue blocks represent
→ flanking genes that are conserved across lineages, and light purple
→ blocks denote instances where a different flanking gene is present.

27 LRCH1

Important gene stats

LRCH1_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
LRCH1	10.03018868	50.0946 +/- 5.52148	4.08014 +/- 0.282842	70.2256 +/- 15.47	Yes	LRCH2;

Lastz Alignment evidence

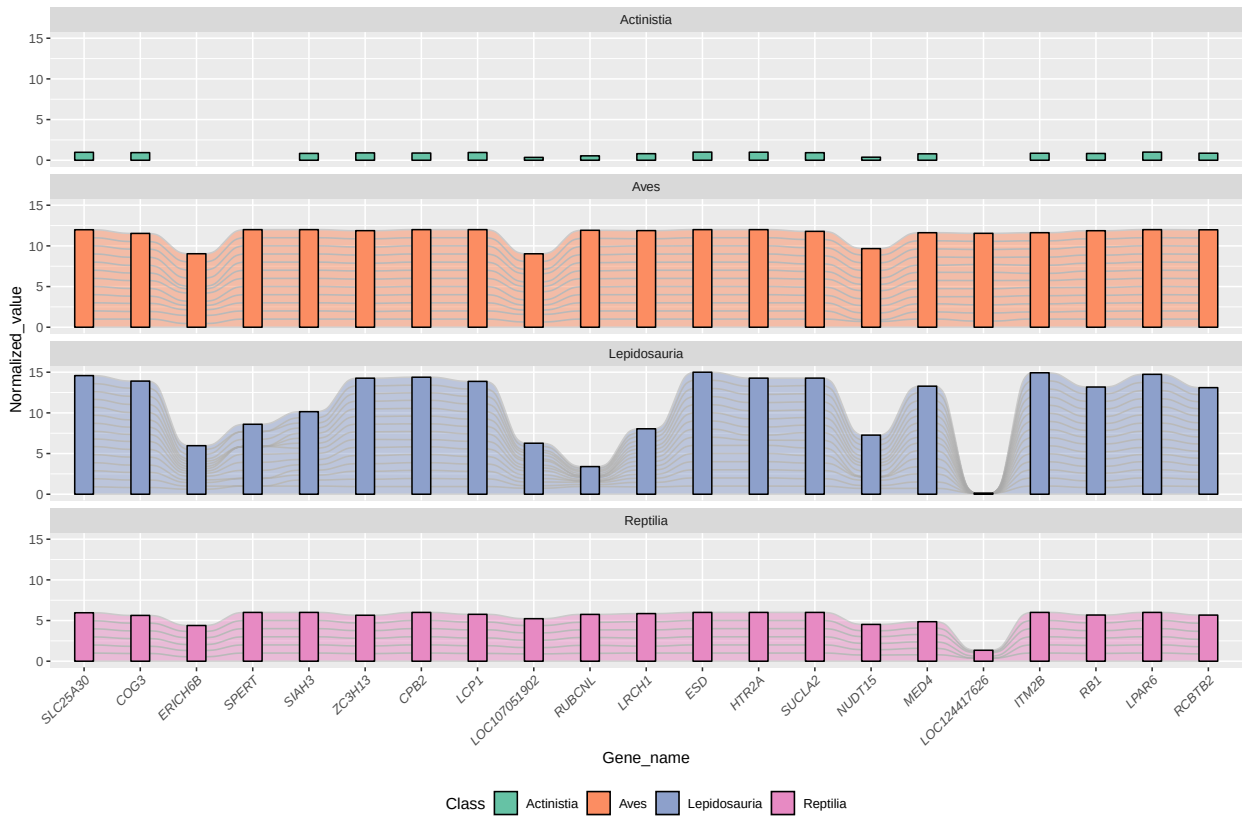


Figure 282: LRCH1.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Lastz gene tree



Figure 284: LRCH1.combined.mafft.aln.highlighted.pdf

Syntenic evidence

	SIAH3, LCP1, LRCH1, RUBCNL																		
<i>Chelonia mydas</i>	> SUCIA2 >	< LOC11596522 >	> HTR2A >	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	> CPB2 >	> ZC3H13 >	> SIAH3 >	< CBP2 <	> ERICHBB >	< COG3 <					
								Chr 1 (NC_057948.1)											
<i>Gallus gallus</i>	> SUCIA2 >	> HTR2A >	> ESD >	< LRCH1 <	> RUBCNL >	< LOC10050802 <	> LCP1 >	> CPB2 >	> ZC3H13 >	> SIAH3 >	< SIRT1 <								
						NC_023322.1													
<i>Podarcis muralis</i>	> SUCIA2 >	< NPLRC3 <	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	> CPB2 >	< ZC3H13 <	> SIAH3 >	< COG3 <	< SIRT1 <							
	Chr 1 (NC_041314.1)				Chr 3 (NC_041314.1)			Chr 5 (NC_041316.1) #	Chr 6 (NC_041316.1)						# same chromosome but on another side after skipping two genes				
<i>Anolis carolinensis</i>	> SUCIA2 >	> HTR2A >	< NPLRC3 <	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	< p981 <	< sp9824 <	< drg15 <	> z3h13 >	< CPB2 <	> SIAH3 >	< COG3 <	< drg2 <	> ERICHBB >		
								Chr 1 (NC_085841.1)								Chr 3 (NC_085841.1)			
<i>Pogona vitticeps</i>	> SUCIA2 >	> HTR2A >	< NPLRC3 <	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	< p981 <	< sp9824 <	< drg15 <	> z3h13 >	< CPB2 <	> SIAH3 >	> z3h1 >	< sirt1 <			
	Chr 1 (NC_128222.1) #							Chr 1 (NC_128222.1)							Chr 3 (NC_128224.1)		# same chromosome but after skipping genes		
<i>Crotalus tigris</i>	> SUCIA2 >	> HTR2A >	< NPLRC3 <	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	< p981 <	< sp9824 <	< drg15 <	> z3h13 >	< CPB2 <	> SIAH3 >	< COG3 <	> ERICHBB >			
	NW_024007046.1 (unplaced)					NW_024007046.1 (unplaced)				NW_024008059.1 (unplaced)						NW_024008055.1 (unplaced)			
<i>Geophis heterochilus</i>	> SUCIA2 >	< LOC103170481 >	> HTR2A >	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	> CPB2 >	> ZC3H13 >	> SIAH3 >	> ERICHBB >	< COG3 <						
								Chr 20 (NC_041747.1)											
<i>Homo sapiens</i>	> SUCIA2 >	> HTR2A >	< HTR2A-AS1 <	> ESD >	< LRCH1 <	< FRAP1AF1 <	> LOC100338 >	> RUBCNL >	< LRRC63 <	> LOC107884571 >	> LCP1 >	> CPB2 >	< CPB2-AS1 <	> ZC3H13 >	< LOC101703191 <	> SIAH3 >	< CBP2 <	> ERICHBB >	< COG3 <
							Chr 13 (NC_000333.3)												
<i>Monia monia</i>	> SUCIA2 >	< Gm41210 <	> HTR2A >	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	> CPB2 >	< Gm35679 <	> ZC3H13 >	< Gm41212 <	> SIAH3 >	< CBP2 <	< Gm36219 <	> ERICHBB >	< COG3 <		

Figure 285: LRCH1.pdf

LRCH1.txt

Synteny analysis of LRCH1

The syntenic block for

LRCH1 shows evidence of both interchromosomal and intrachromosomal
 ↳ rearrangements within squamates. In species such as

Anolis carolinensis and *Pogona vitticeps*, the flanking genes are located
 ↳ on two different chromosomes, indicating a break in synten.
 ↳ Furthermore, in lizards like

Podarcis muralis, the block appears to have also undergone an
 ↳ intrachromosomal rearrangement, with flanking genes repositioned to
 ↳ a different location on the same chromosome after skipping several

↪ intervening genes. The block is highly fragmented in the snake
Crotalus tigris, with genes located on multiple unplaced scaffolds.

In the synteny plots, red blocks indicate the absence of the target gene,
↪ while green blocks mark its presence. Light blue blocks represent
↪ flanking genes that are conserved across lineages, and light purple
↪ blocks denote instances where a different flanking gene is present.

Important gene stats

MAN2B2_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
MAN2B2	2.393442623	51.9499 +/- 7.1057	3.84645 +/- 0.35974	66.1567 +/- 11.0682	Yes	Na

Lastz Alignment evidence

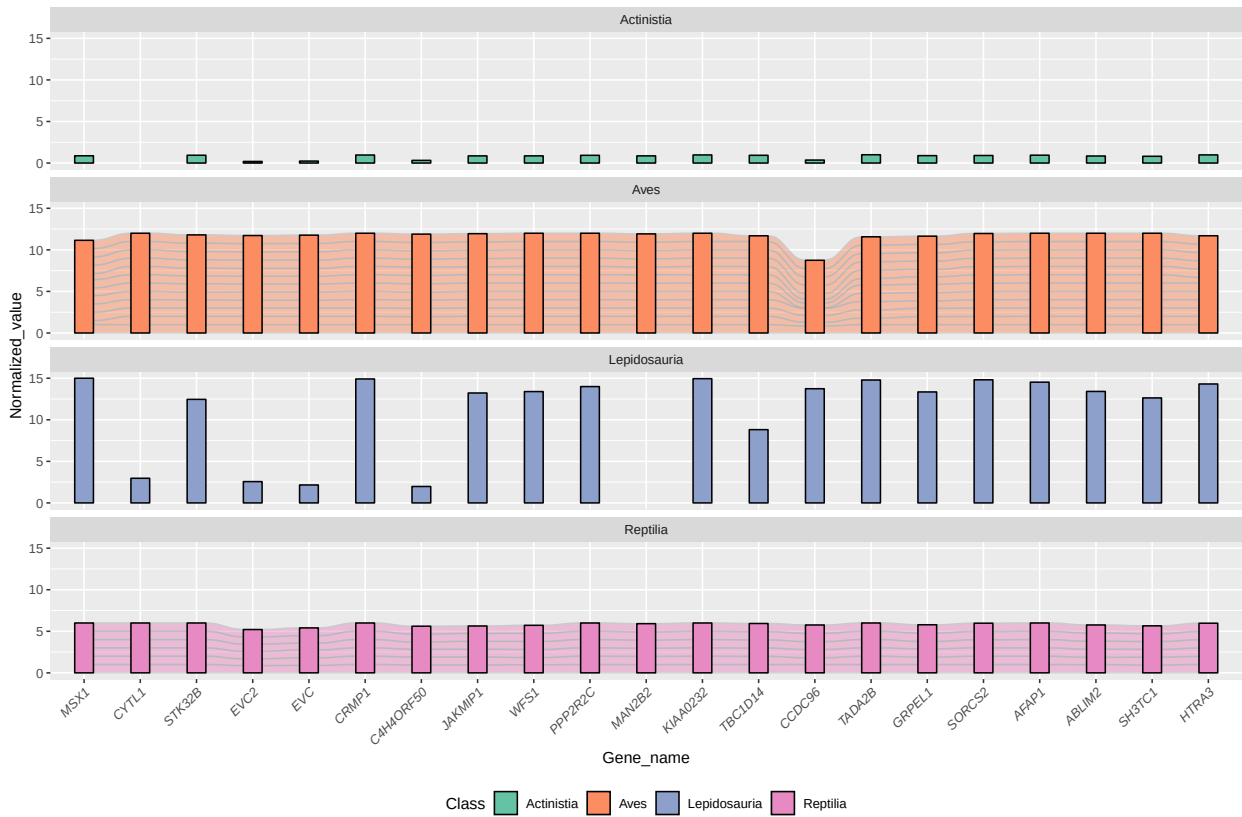


Figure 286: MAN2B2.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

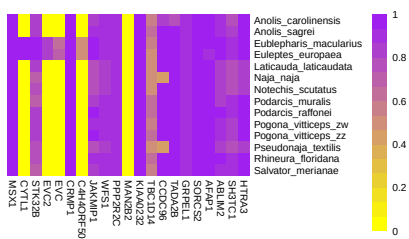


Figure 287: MAN2B2.FS_Exonic.Final.Gallus_gallus.21_genes_heatmap.pdf

Lastz gene tree

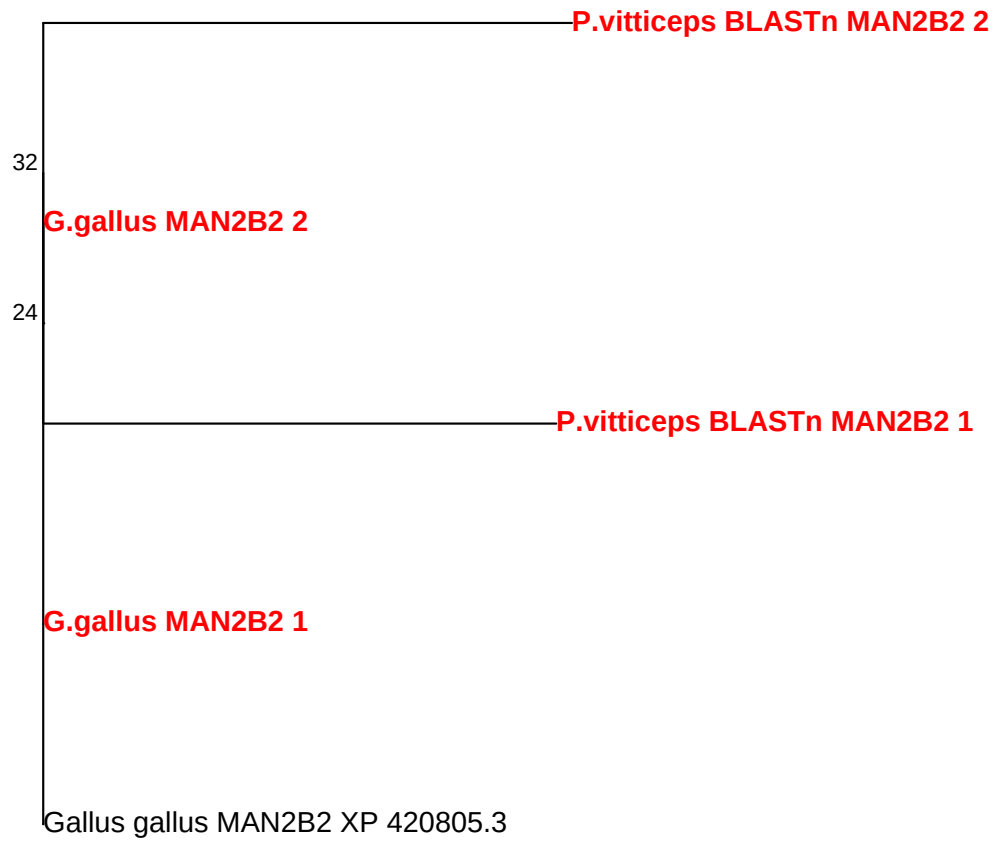


Figure 288: MAN2B2.combined.mafft.aln.highlighted.pdf

Syntenic evidence

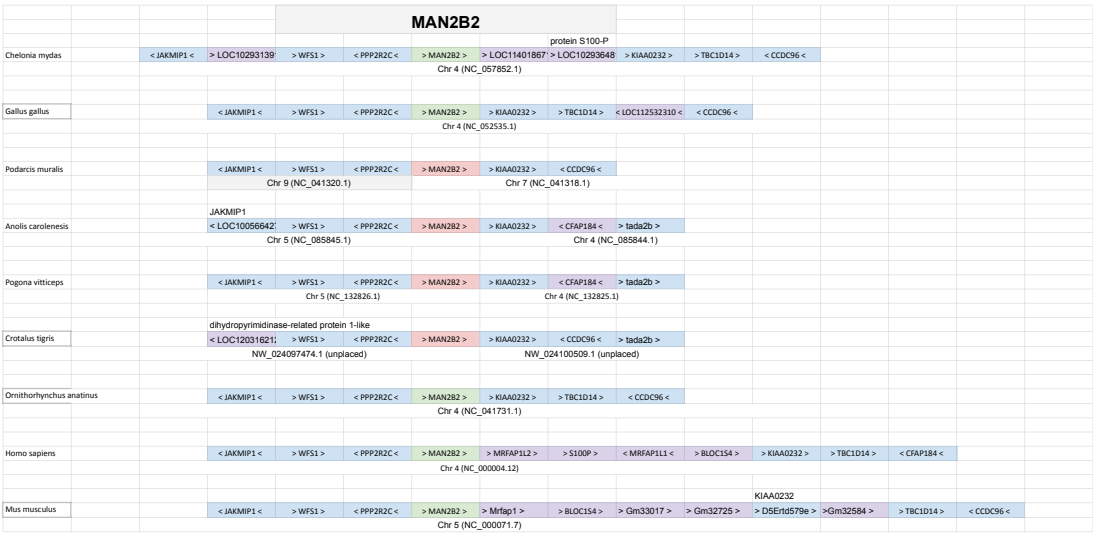


Figure 289: MAN2B2.pdf

MAN2B2.txt

Synteny analysis of MAN2B2

In squamates, the flanking genes for MAN2B2 are present on two different
→ chromosomes, presenting a case of interchromosomal rearrangement.

In the synteny plots, red blocks indicate the absence of the target gene,
→ while green blocks mark its presence. Light blue blocks represent
→ flanking genes that are conserved across lineages, and light purple
→ blocks denote instances where a different flanking gene is present.

29 **MATK**

Assembly verification Evidence

Crotalus_tigris-PacBio

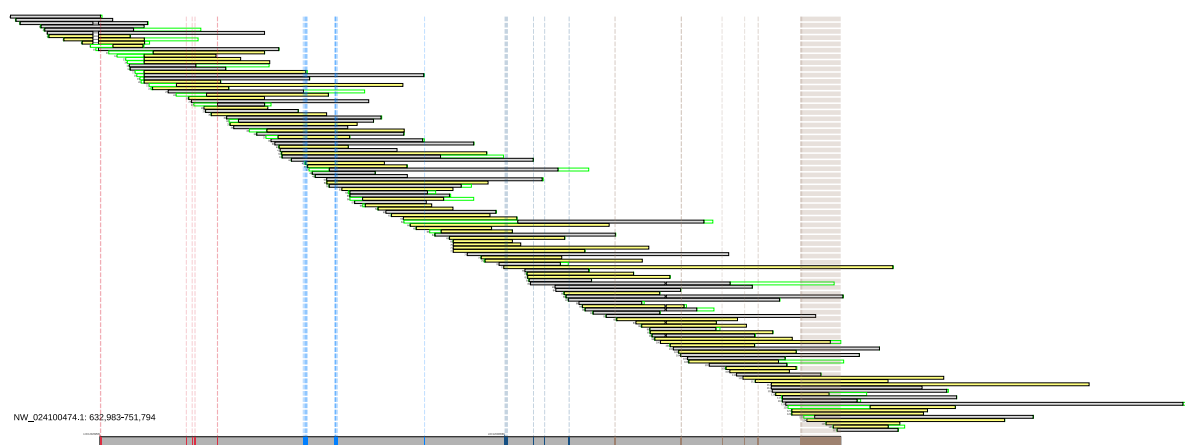


Figure 290: MATK:NW_024100474.1:632983-751794.pdf

Pogona_vitticeps-Nanopore

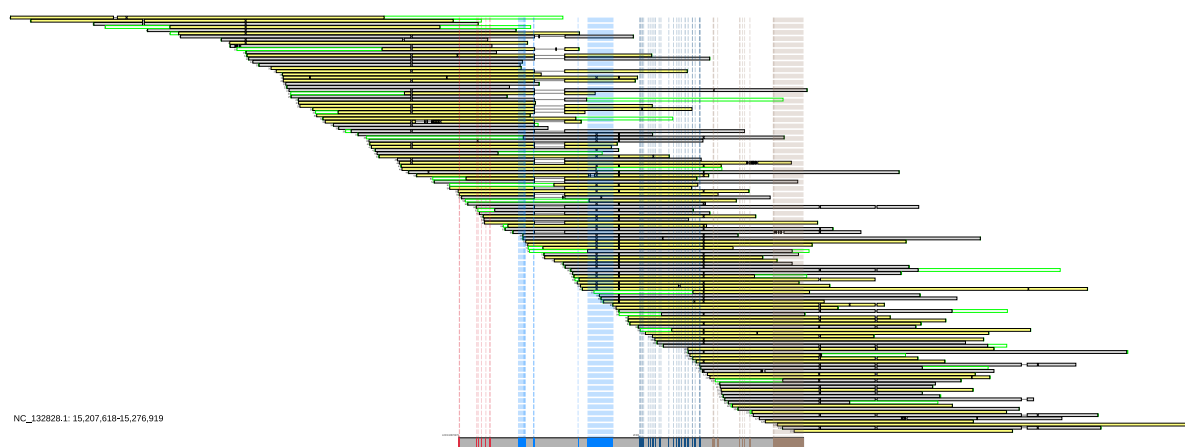


Figure 291: MATK:NC_132828.1:15207618-15276919.pdf

Important gene stats

MATK_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
MATK	13.77358491	58.2254 +/- 6.2216	4.24347 +/- 0.451004	69.4954 +/- 11.892	Yes	CSK;EPHA2;

Intergenic distance phylogenetic signal evidence

Lastz Alignment evidence

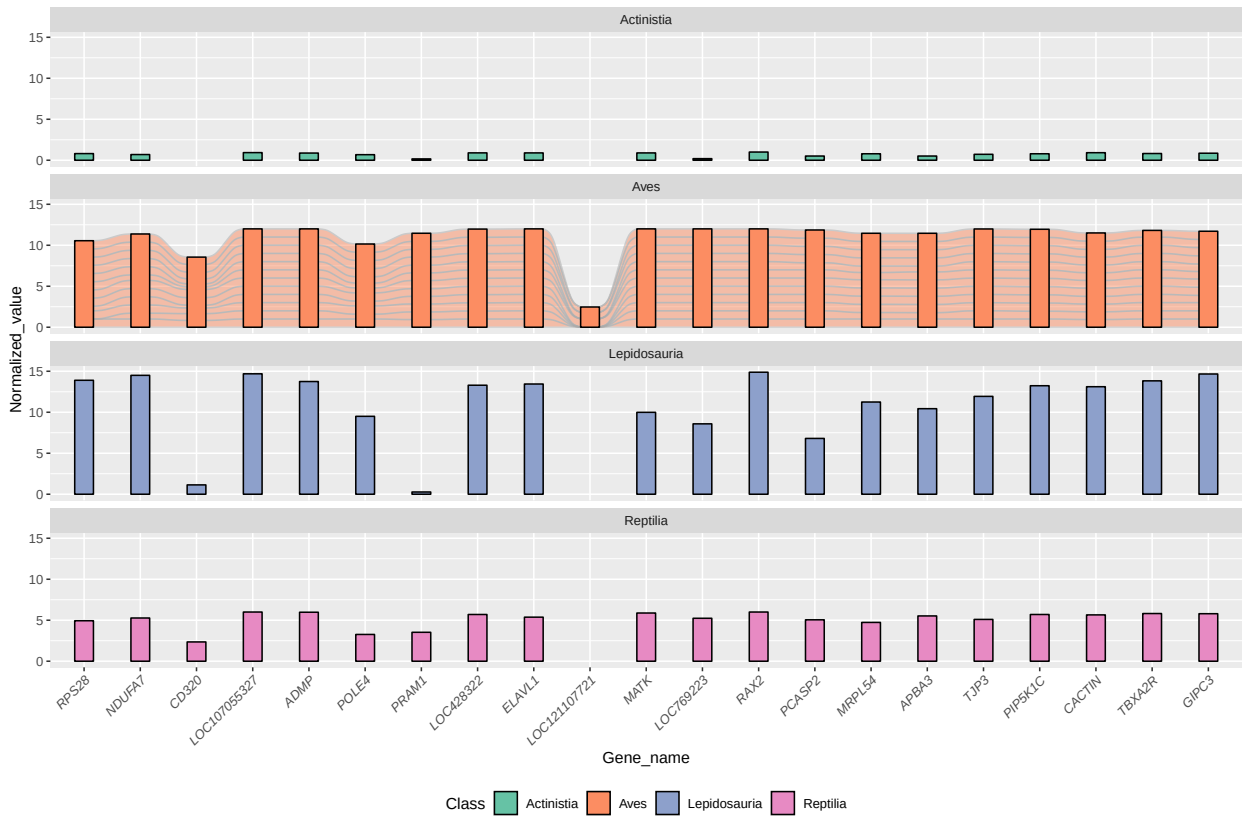


Figure 292: MATK.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

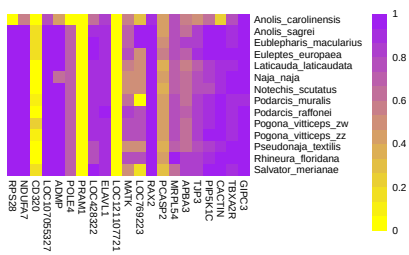


Figure 293: MATK.FS_Exonic.Final.Gallus_gallus.21_genes_heatmap.pdf

Lastz gene tree

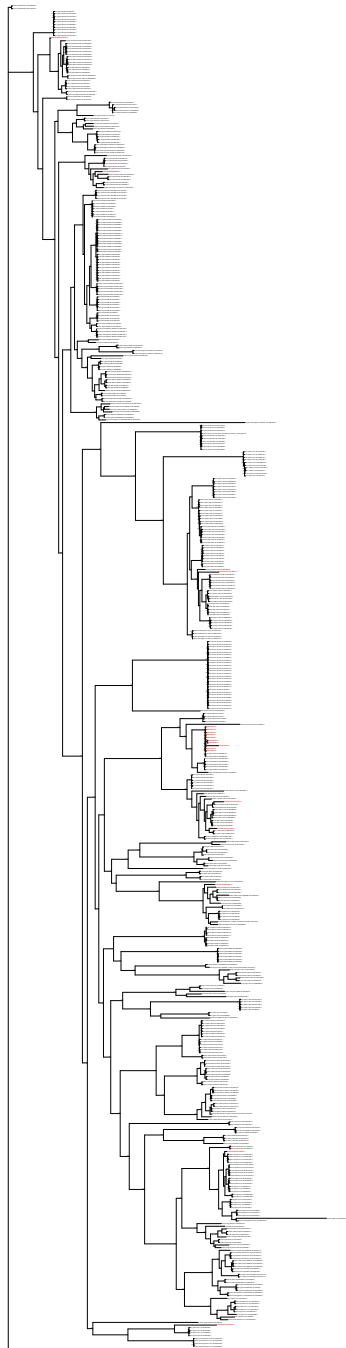


Figure 294: MATK.combined.mafft.aln.highlighted.pdf

We analyzed the synteny of MATK in representative squamate and outgroup

→ species. The MATK syntenic block is conserved, with the gene

↪ consistently retained across all examined lineages. In reptiles such as *Chelonoidis mydas*, *Emura vittata*, and *Crotalus tigris*, *MATK* is

↪ as *Chelonia mydas*, *Pogona vitticeps*, and *Crotalus tigris*, MATK is flanked by genes including *ELAVL1*, *ZEB2*, *PX1*, and *Reep6* like

→ flanked by genes including ELAVL1, ZFR2, RX1, and Reep6-like,
→ reflecting a largely conserved arrangement. In *Gallus gallus*, the

- ↪ reflecting a largely conserved arrangement. In *Gallus gallus*, the
- ↪ locus shows modest variation, with neighboring genes such as *FAAT5*-

→ locus shows modest variation, with neighboring genes such as EAA15-like, IF2-like, and LOC769223 occupying the flanking positions. In

→ like, IF2-like, and LOC769223 occupying the flanking positions. In mammals (*Homo sapiens*, *Mus musculus*, and *Ornithorhynchus anatinus*).

- mammals (*Homo sapiens*, *Mus musculus*, and *Ornithorhynchus anatinus*),
- MATK remains embedded within a conserved context involving ZFR2.

→ RAX2, MRPL54, and APBA3. Overall, the analysis supports that MATK

- has been retained in a conserved genomic neighborhood, despite minor

→ lineage-specific variations in the composition of surrounding

$\mathcal{F}_1$ $\mathcal{F}_2$ $\mathcal{F}_3$ $\mathcal{F}_4$ $\mathcal{F}_5$ $\mathcal{F}_6$ $\mathcal{F}_7$ $\mathcal{F}_8$ $\mathcal{F}_9$ $\mathcal{F}_{10}$ $\mathcal{F}_{11}$ $\mathcal{F}_{12}$ $\mathcal{F}_{13}$ $\mathcal{F}_{14}$ $\mathcal{F}_{15}$ $\mathcal{F}_{16}$ $\mathcal{F}_{17}$ $\mathcal{F}_{18}$ $\mathcal{F}_{19}$ $\mathcal{F}_{20}$ $\mathcal{F}_{21}$ $\mathcal{F}_{22}$ $\mathcal{F}_{23}$ $\mathcal{F}_{24}$ $\mathcal{F}_{25}$ $\mathcal{F}_{26}$ $\mathcal{F}_{27}$ $\mathcal{F}_{28}$ $\mathcal{F}_{29}$ $\mathcal{F}_{30}$ $\mathcal{F}_{31}$ $\mathcal{F}_{32}$ $\mathcal{F}_{33}$ $\mathcal{F}_{34}$ $\mathcal{F}_{35}$ $\mathcal{F}_{36}$ $\mathcal{F}_{37}$ $\mathcal{F}_{38}$ $\mathcal{F}_{39}$ $\mathcal{F}_{40}$ $\mathcal{F}_{41}$ $\mathcal{F}_{42}$ $\mathcal{F}_{43}$ $\mathcal{F}_{44}$ $\mathcal{F}_{45}$ $\mathcal{F}_{46}$ $\mathcal{F}_{47}$ $\mathcal{F}_{48}$ $\mathcal{F}_{49}$ $\mathcal{F}_{50}$ $\mathcal{F}_{51}$ $\mathcal{F}_{52}$ $\mathcal{F}_{53}$ $\mathcal{F}_{54}$ $\mathcal{F}_{55}$ $\mathcal{F}_{56}$ $\mathcal{F}_{57}$ $\mathcal{F}_{58}$ $\mathcal{F}_{59}$ $\mathcal{F}_{60}$ $\mathcal{F}_{61}$ $\mathcal{F}_{62}$ $\mathcal{F}_{63}$ $\mathcal{F}_{64}$ $\mathcal{F}_{65}$ $\mathcal{F}_{66}$ $\mathcal{F}_{67}$ $\mathcal{F}_{68}$ $\mathcal{F}_{69}$ $\mathcal{F}_{70}$ $\mathcal{F}_{71}$ $\mathcal{F}_{72}$ $\mathcal{F}_{73}$ $\mathcal{F}_{74}$ $\mathcal{F}_{75}$ $\mathcal{F}_{76}$ $\mathcal{F}_{77}$ $\mathcal{F}_{78}$ $\mathcal{F}_{79}$ $\mathcal{F}_{80}$ $\mathcal{F}_{81}$ $\mathcal{F}_{82}$ $\mathcal{F}_{83}$ $\mathcal{F}_{84}$ $\mathcal{F}_{85}$ $\mathcal{F}_{86}$ $\mathcal{F}_{87}$ $\mathcal{F}_{88}$ $\mathcal{F}_{89}$ $\mathcal{F}_{90}$ $\mathcal{F}_{91}$ $\mathcal{F}_{92}$ $\mathcal{F}_{93}$ $\mathcal{F}_{94}$ $\mathcal{F}_{95}$ $\mathcal{F}_{96}$ $\mathcal{F}_{97}$ $\mathcal{F}_{98}$ $\mathcal{F}_{99}$ $\mathcal{F}_{100}$

↪ flanking genes. In the synteny plots, red blocks indicate the
↪ absence of MATK, green blocks mark its presence, light blue blocks
↪ represent genes conserved across lineages, and light purple blocks
↪ denote different flanking genes.

Transcriptomic evidence Pogona vitticeps

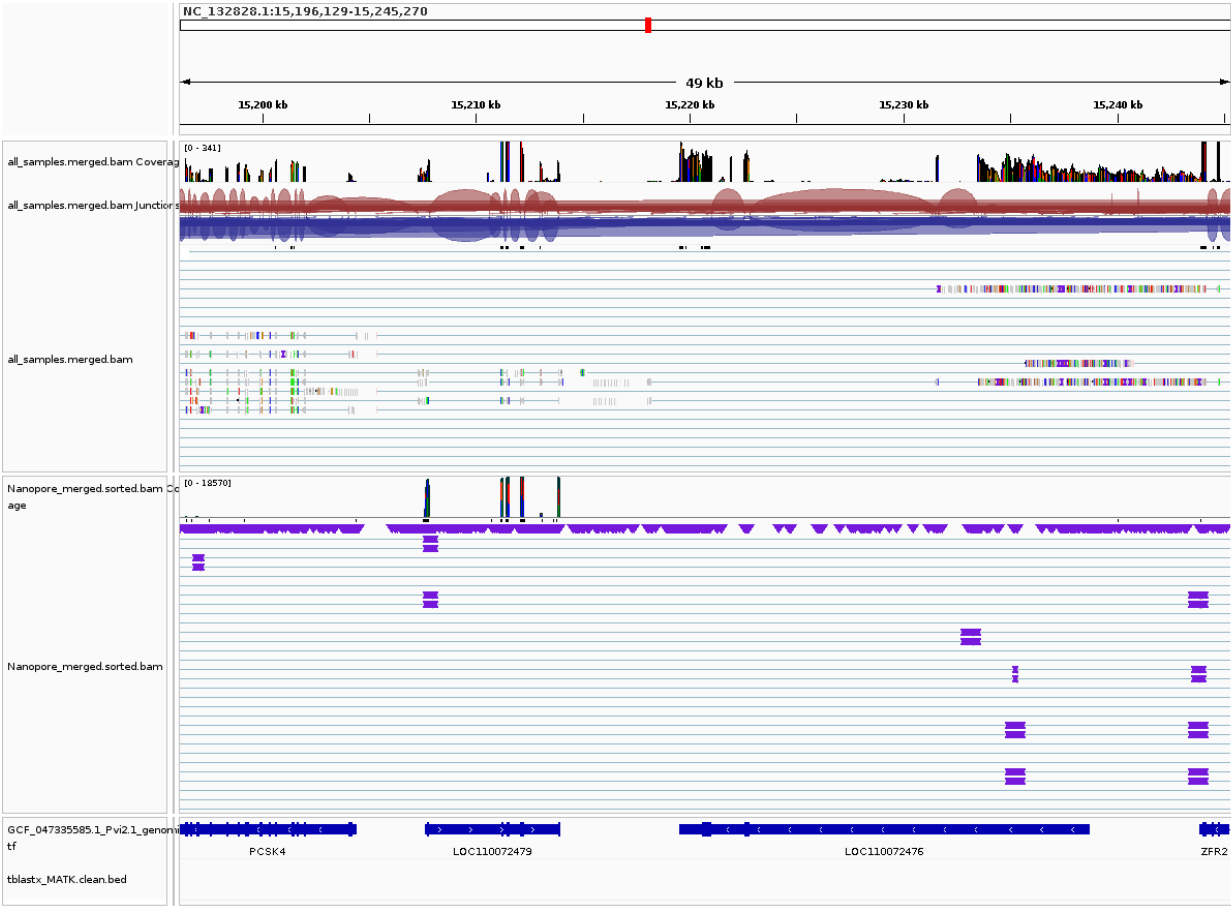


Figure 296: MATK.png

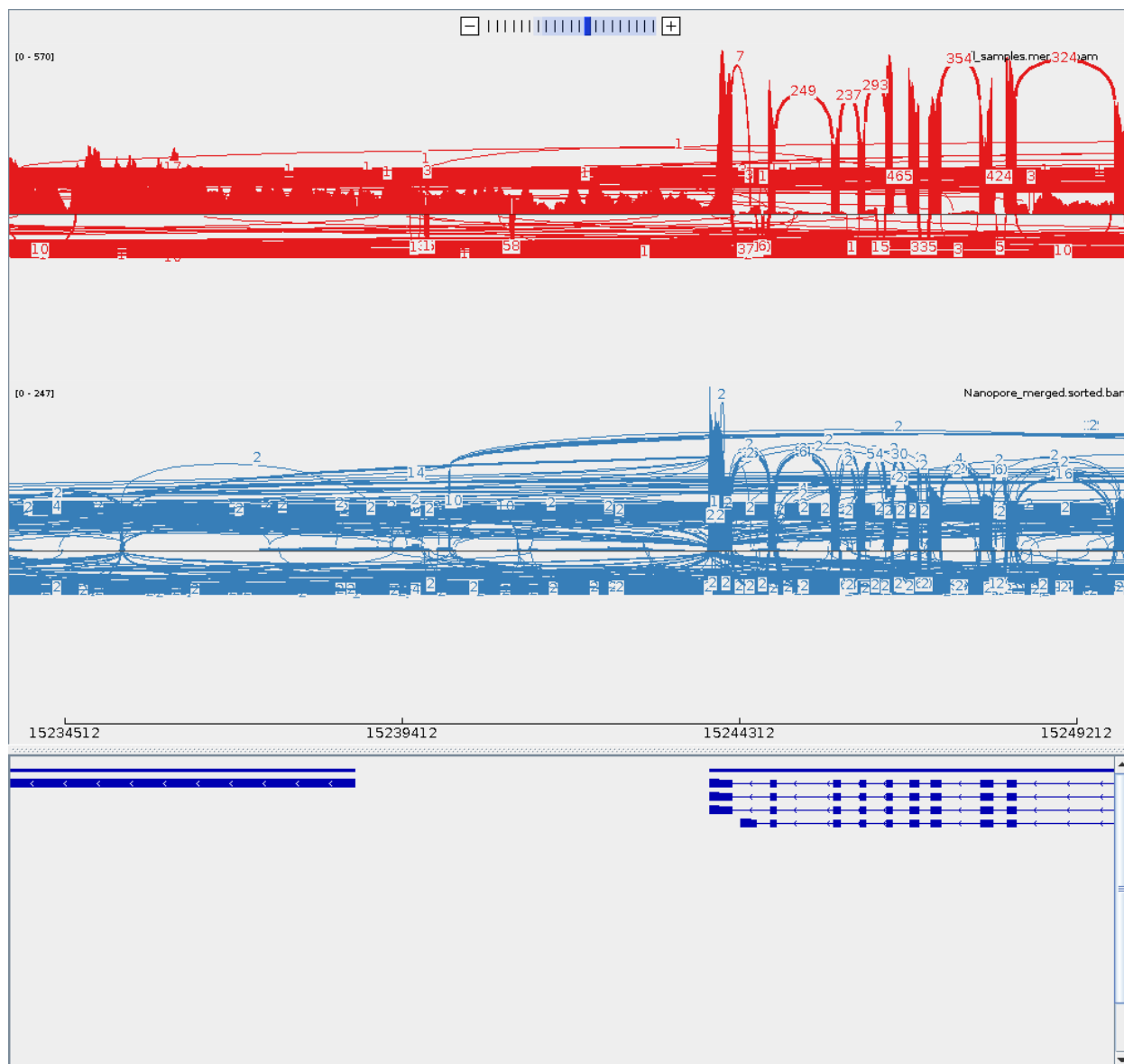


Figure 297: MATK_Sashimi.png

30 MOB1A

Assembly verification Evidence

Crotalus_tigris-PacBio

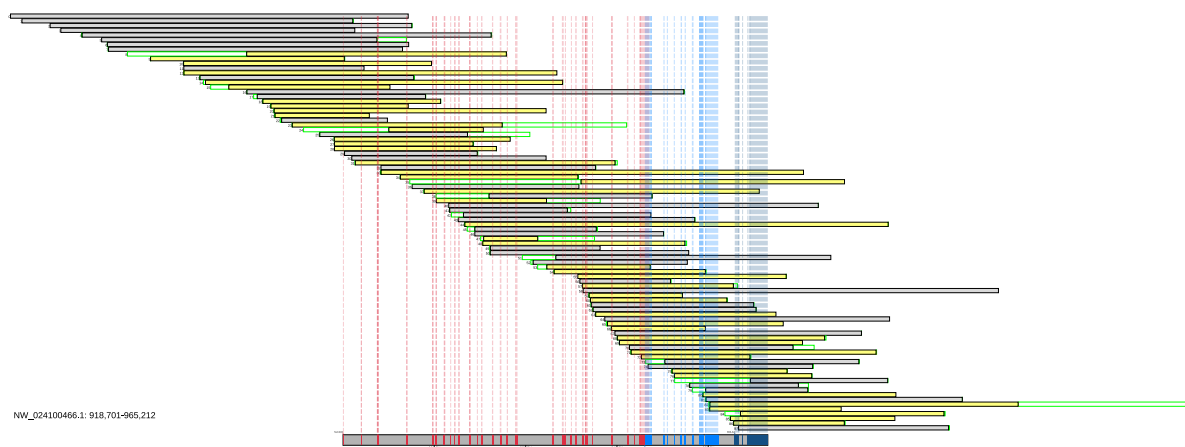


Figure 298: MOB1A:NW_024100466.1:918701-965212.pdf

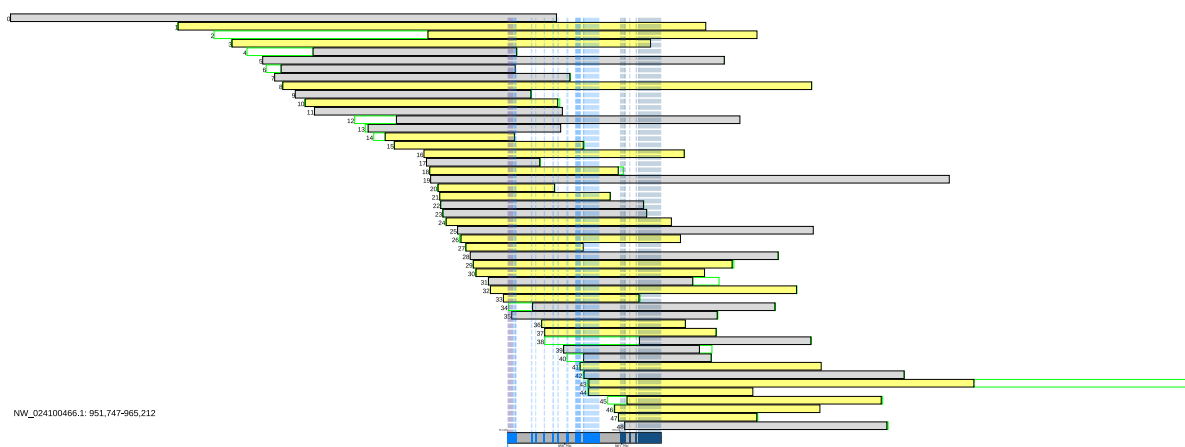


Figure 299: MOB1A:NW_024100466.1:951747-965212.pdf

Podarcis_muralis-PacBio

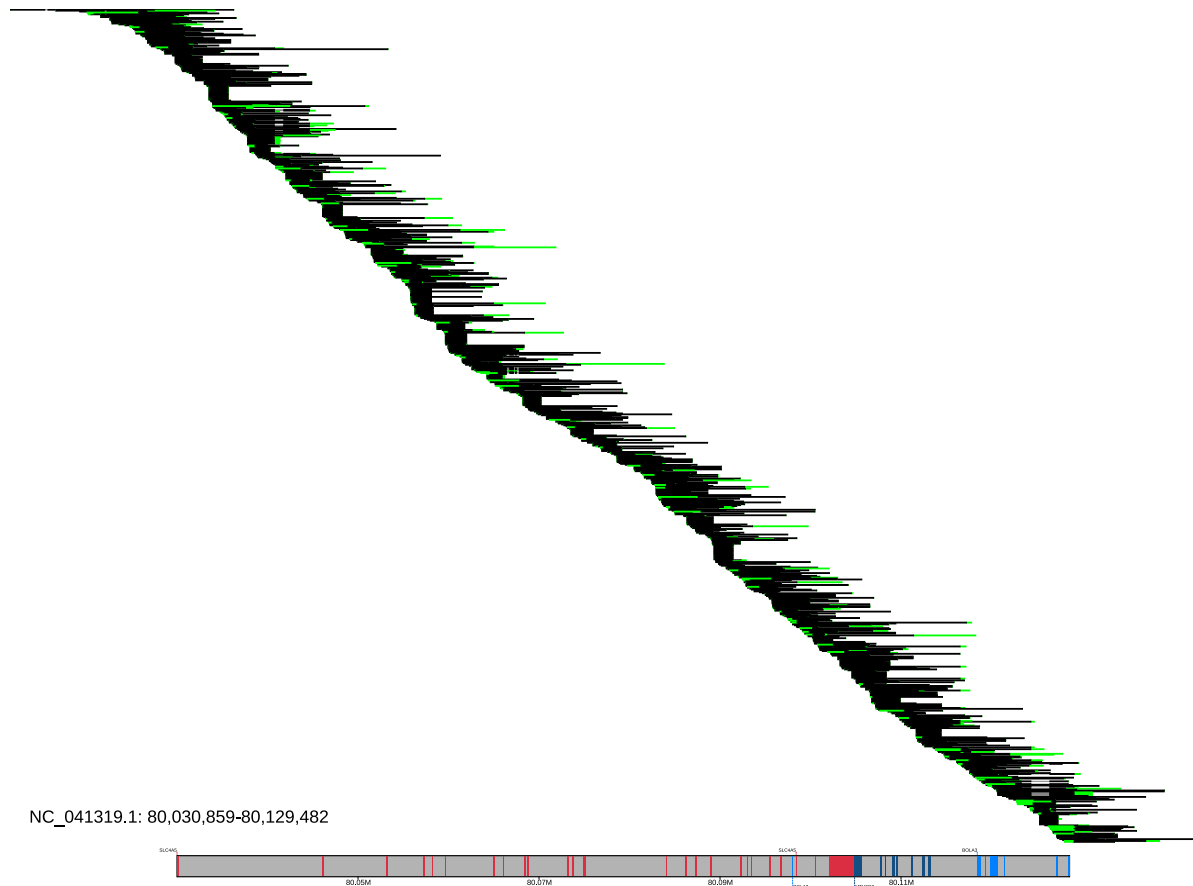


Figure 300: MOB1A:NC_041319.1:80030859-80129482.pdf

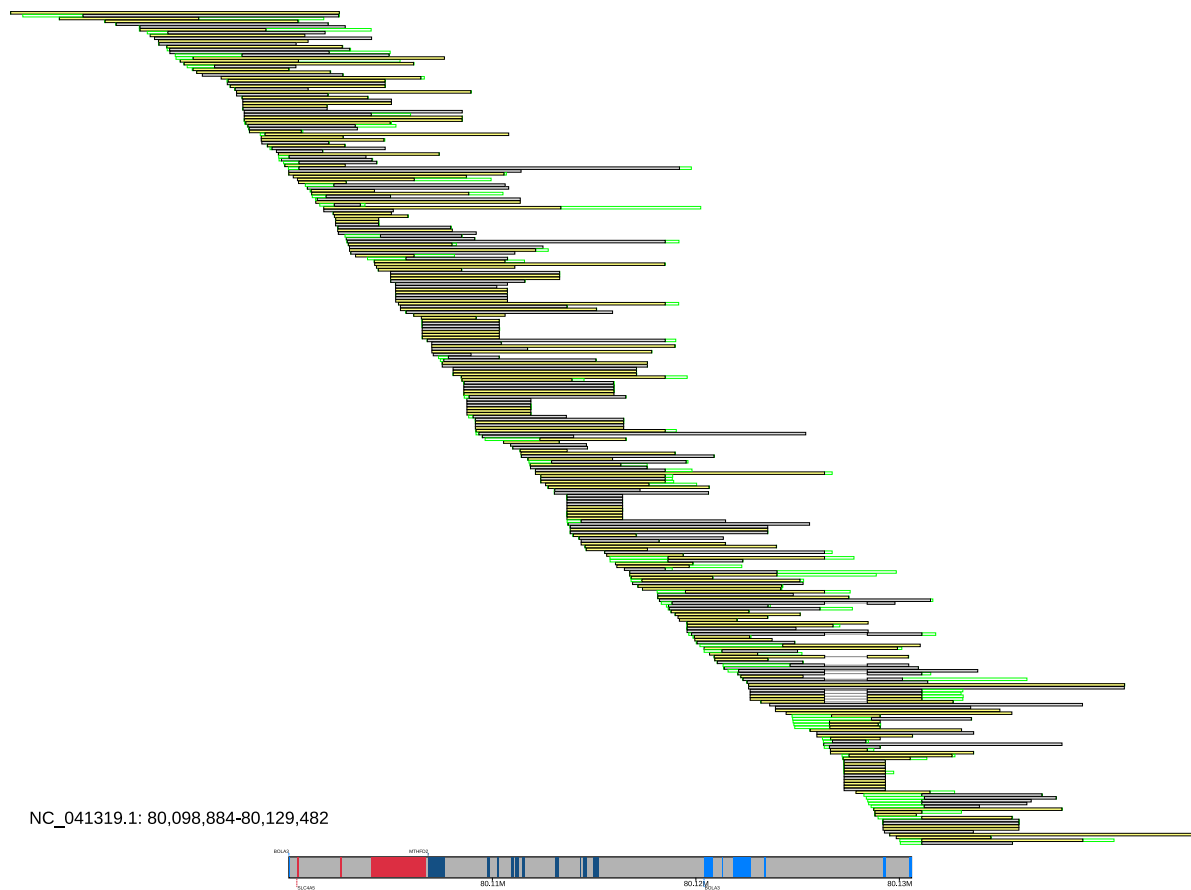


Figure 301: MOB1A:NC_041319.1:80098884-80129482.pdf

Pogona_vitticeps-Nanopore

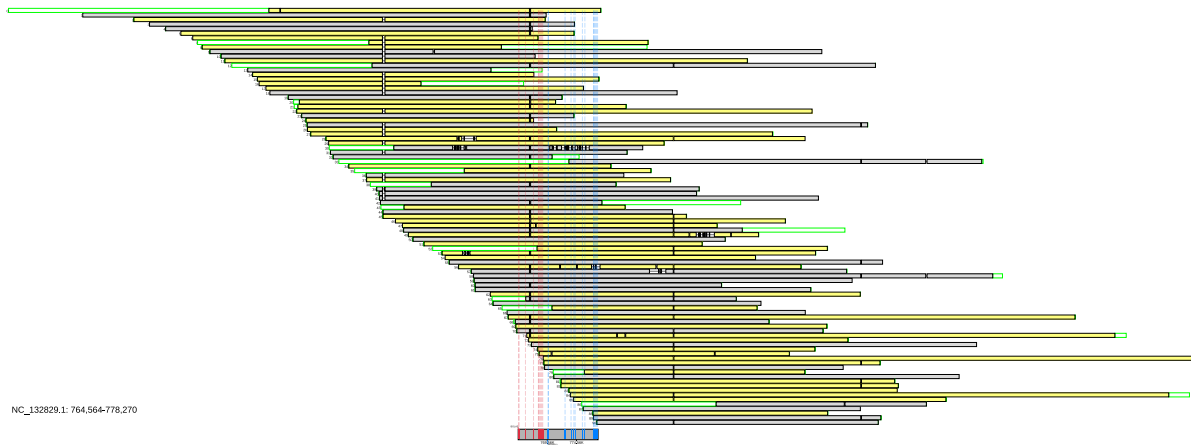


Figure 302: MOB1A:NC_132829.1:764564-778270.pdf

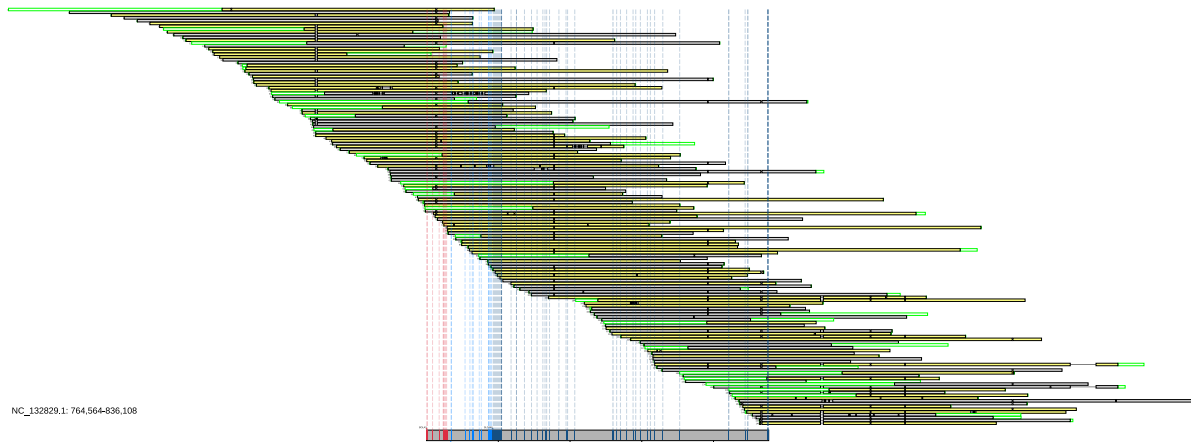


Figure 303: MOB1A:NC_132829.1:764564-836108.pdf

Important gene stats

MOB1A_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
MOB1A	53.93939394	45.399 +/- 5.77235	3.61132 +/- 0.275567	75.3051 +/- 8.77393	Yes	MOB1B;

Intergenic distance phylogenetic signal evidence



Figure 304: Heatmap_of_deletion_plot.png

MOB1A_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
MOB1A	144	14	130	5	0.138496564551302	0.93352016065076

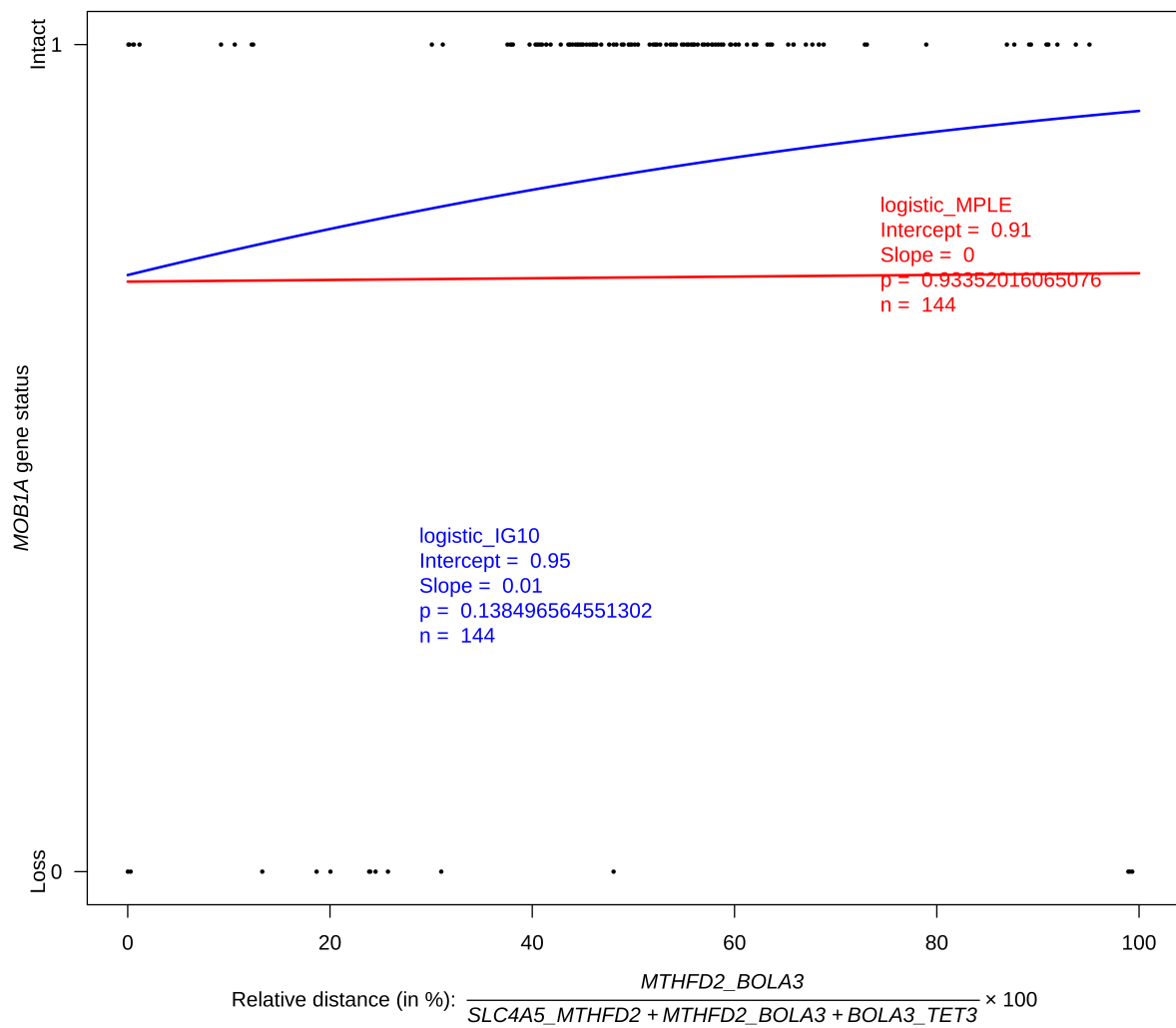


Figure 305: Phylogenetic_signal_of_deletion_plot.png

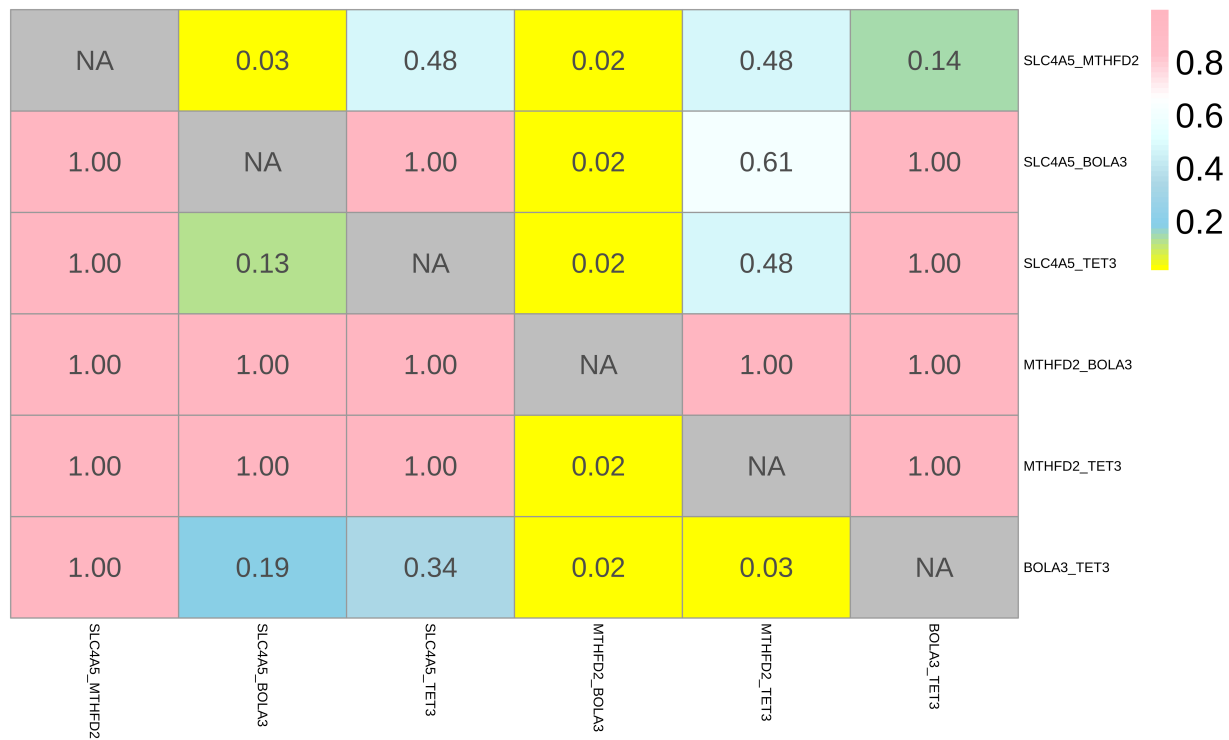


Figure 306: Heatmap_of_deletion_plot.png

MOB1A_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
MOB1A	144	14	130	5	0.138496564551302	0.93352016065076

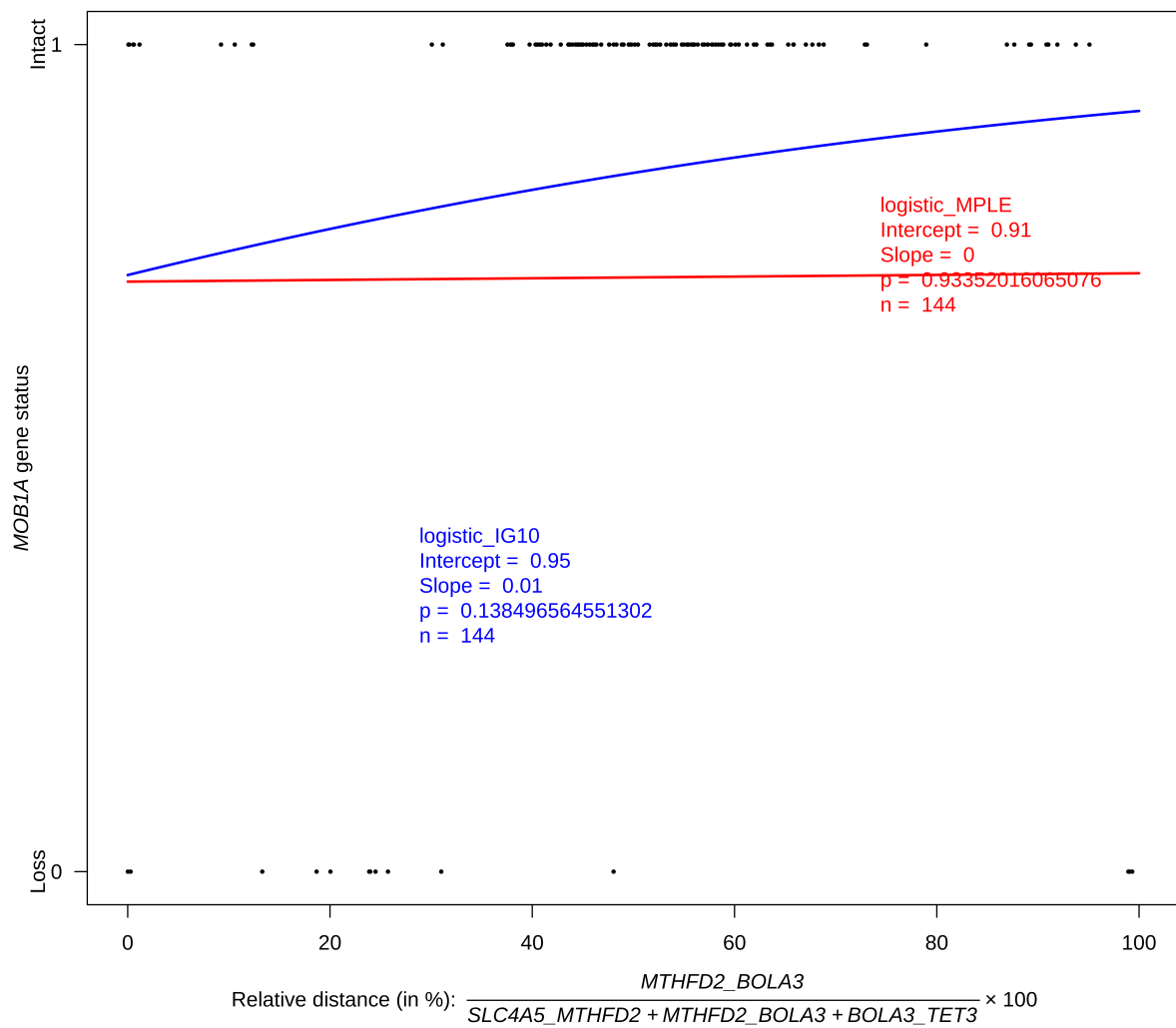


Figure 307: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence

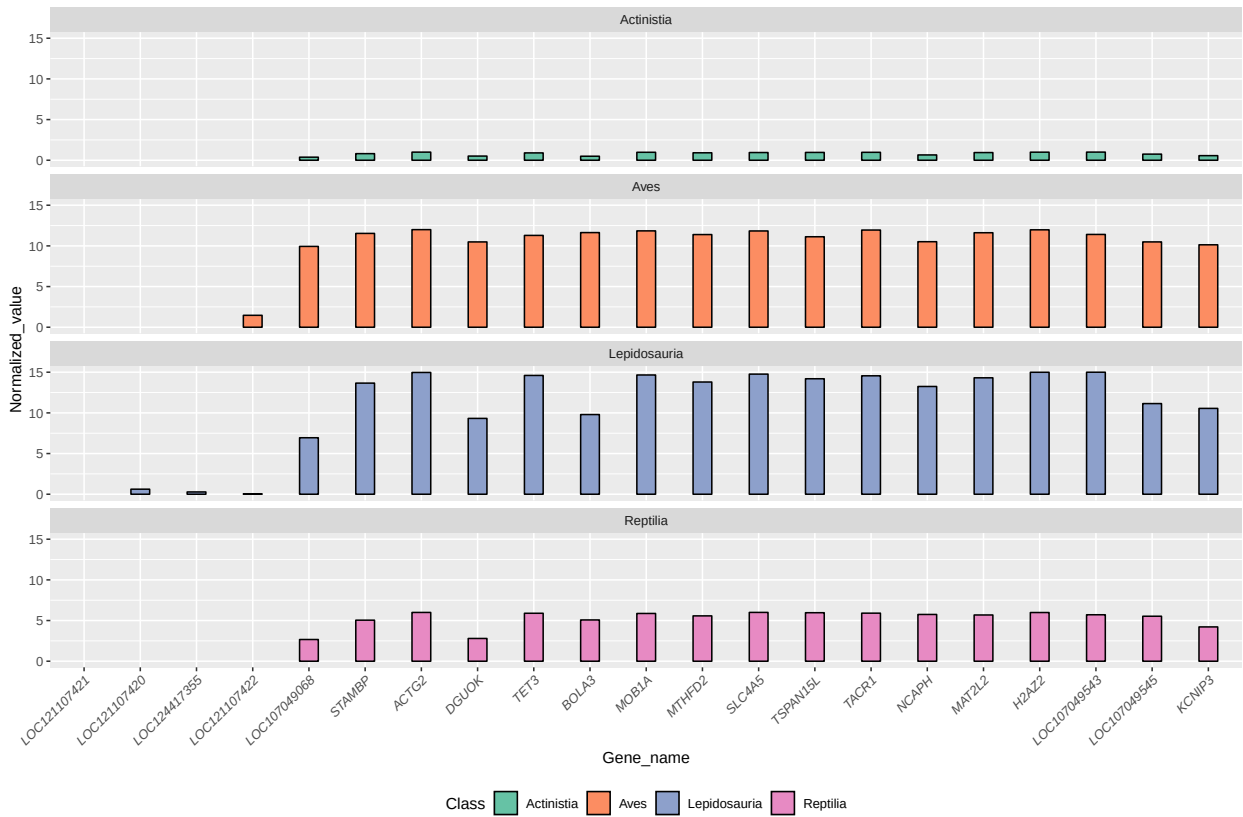


Figure 308: MOB1A.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Lastz gene tree

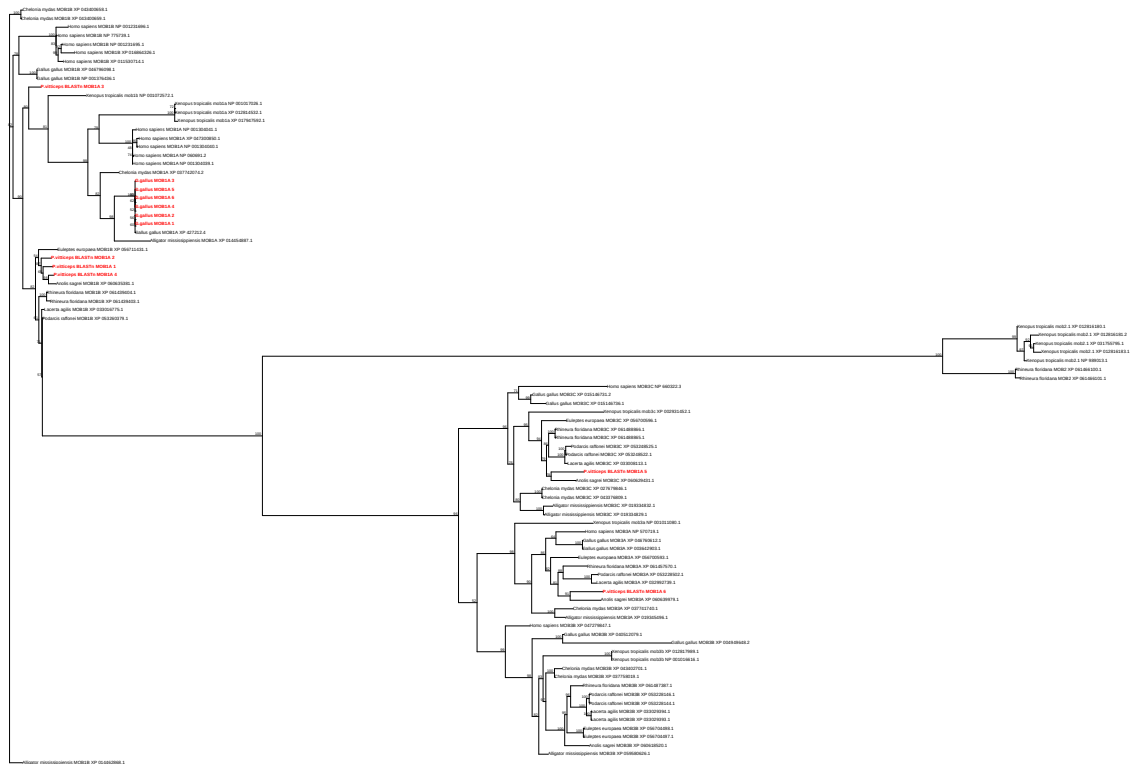


Figure 310: MOB1A.combined.mafft.aln.highlighted.pdf

Syntenic evidence

				MOB1A						
Chelonia mydas		> TSPAN15 >	> SLC4A5 >	< MTHFD2 <	> MOB1A >	> BOLA3 >	< TET3 <	< DGUOK <		
					Chr 26 (NC_057859.1)					
Gallus gallus		> TSPAN15L >	> SLC4A5 >	< MTHFD2 <	> MOB1A >	> BOLA3 >	< TET3 <	< DGUOK <		
					Chr 22 (NC_052553.1)					
Podarcis muralis		> TSPAN15L >	> SLC4A5 >	< MTHFD2 <	> MOB1A >	> BOLA3 >	< TET3 <	< DGUOK <		
					Chr 8 (NC_041319.1)					
Anolis carolensis		> TSPAN15 >	> SLC4A5 >	< MTHFD2 <	> MOB1A >	> BOLA3 >	< rassf2 <	< slc23a2 <		
					NW_026943819.1 (unplaced)					
Pogona vitticeps		> TSPAN15L >	> SLC4A5 >	< MTHFD2 <	> MOB1A >	> BOLA3 >	< TET3 <	< DGUOK <		
					Chr 8 (NC_132829.1)					
Crotalus tigris		> TSPAN15L >	> SLC4A5 >	< MTHFD2 <	> MOB1A >	> BOLA3 >	< TET3 <	< DGUOK <		
					NW_024100466.1 (unplaced)					
Ornithorhynchus anatinus		< TACR1 <	> SLC4A5 >	< MTHFD2 <	> MOB1A >	> BOLA3 >	< TET3 <	< DGUOK <		
					Chr 5 (NC_041732.1)					
Homo sapiens		> DCTN1 >	> SLC4A5 >	< MTHFD2 <	> MOB1A >	> BOLA3 >	< TET3 <	< DGUOK <		
					Chr 2 (NC_000002.12)					
Mus musculus		> DCTN1 >	> SLC4A5 >	< MTHFD2 <	> MOB1A >	> BOLA3 >	< TET3 <	< DGUOK <		

Figure 311: MOB1A.pdf

MOB1A.txt

Synteny analysis of MOB1A

We analyzed the synteny of MOB1A in squamates and representative outgroups

→ . The MOB1A syntenic block is conserved, with no notable changes in

→ gene order or orientation. In the synteny plots, red blocks indicate

→ the absence of MOB1A, green blocks mark its presence, light blue

→ blocks represent genes conserved across lineages, and light purple

→ blocks denote different flanking genes.

Transcriptomic evidence *Pogona vitticeps*

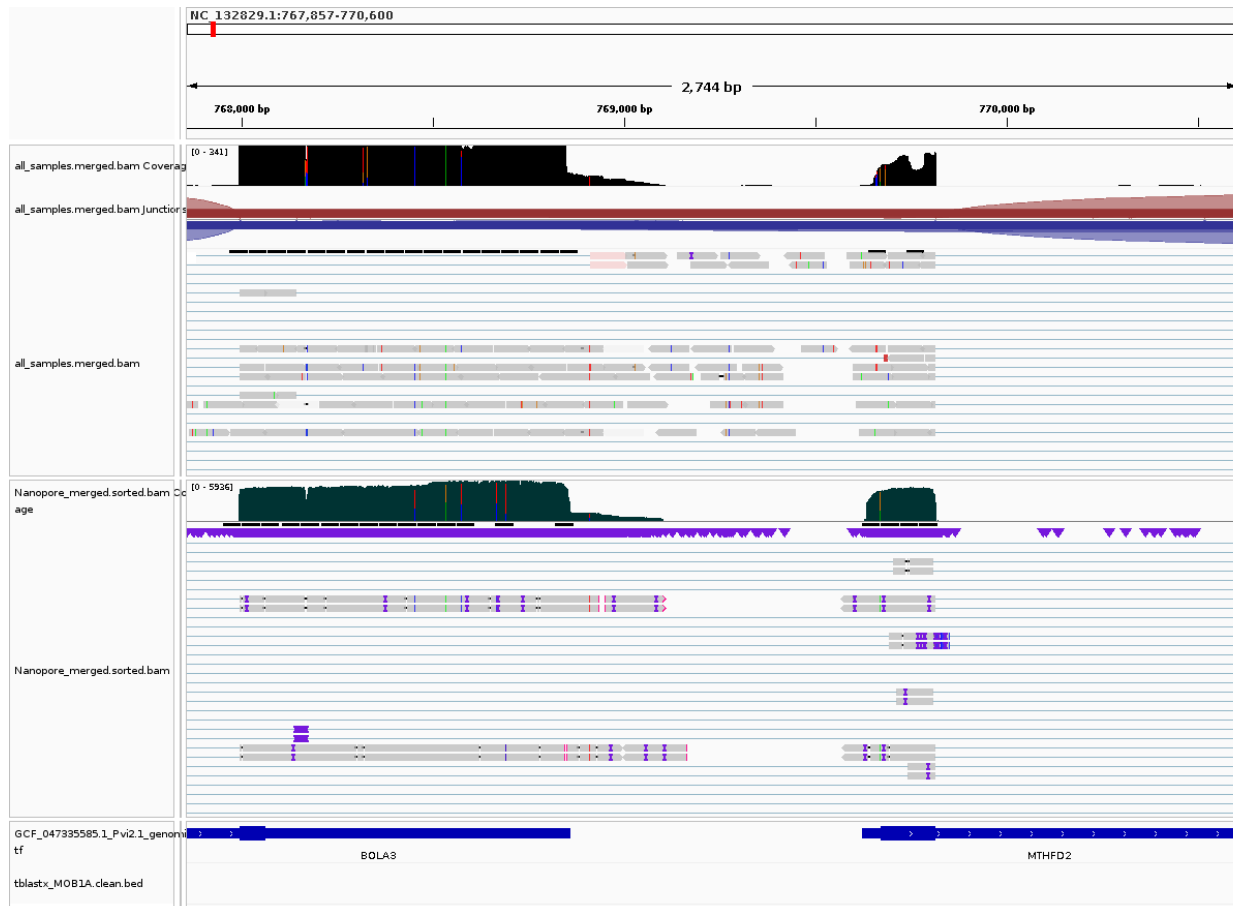


Figure 312: MOB1A.png

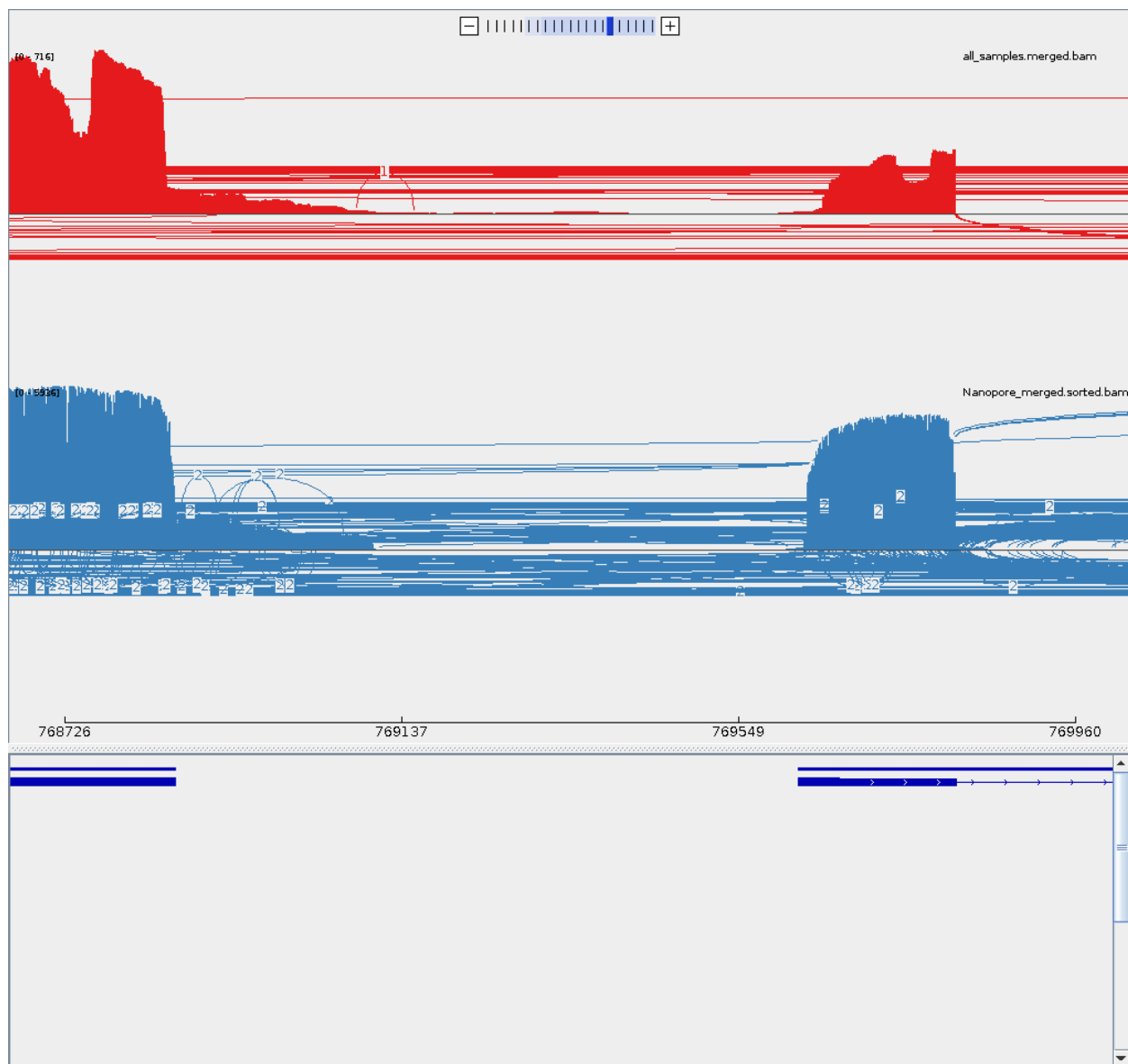


Figure 313: MOB1A_Sashimi.png

31 NOTCH2

Important gene stats

NOTCH2_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
NOTCH2	37.4469697	55.3053 +/- 3.0102	3.8579 +/- 0.196868	82.3156 +/- 11.2934	Yes	Naja_naja.SRR10428157.blast;NOTCH1;Rhabdophis_nuchalis.SRR28573917.blast;

Intergenic distance phylogenetic signal evidence

Lastz Alignment evidence

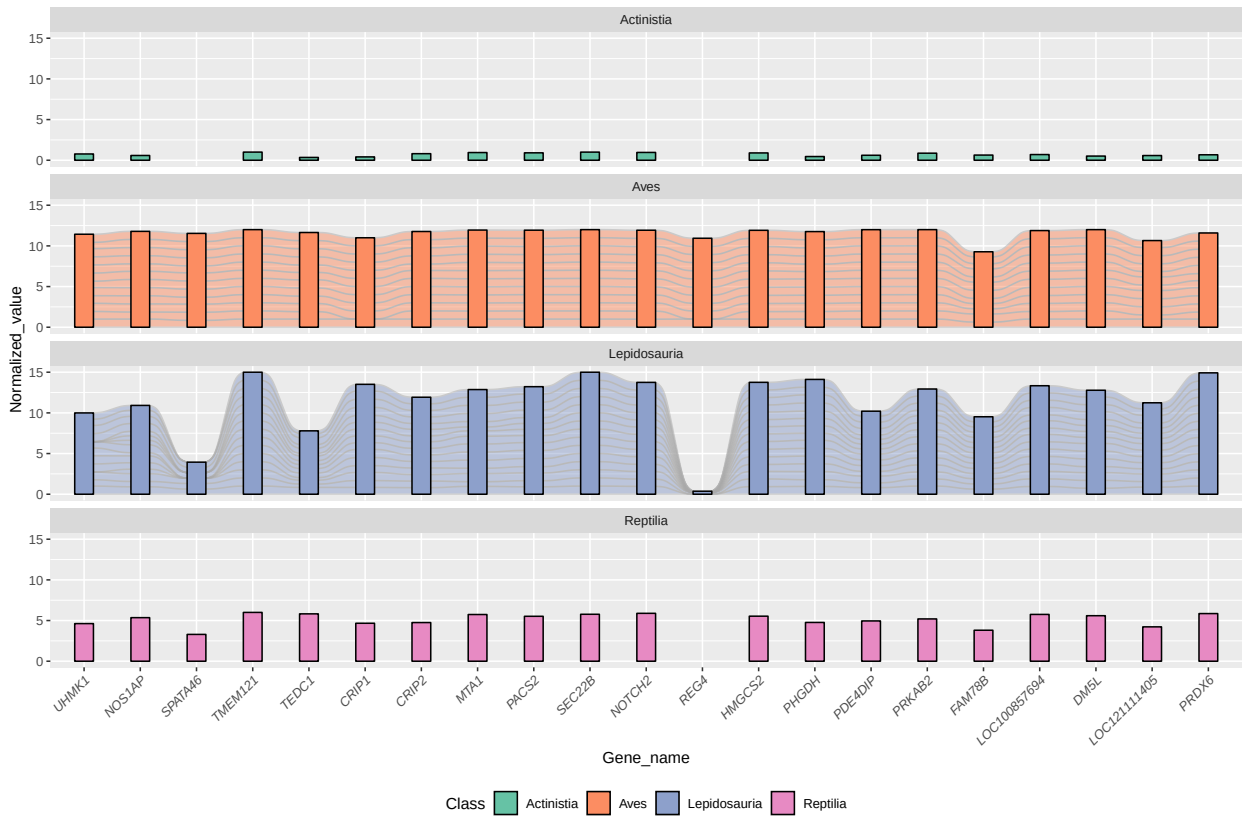


Figure 314: NOTCH2.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf



Figure 315: NOTCH2.FS_Exonic.Final.Gallus_gallus.21_genes_heatmap.pdf

Lastz gene tree

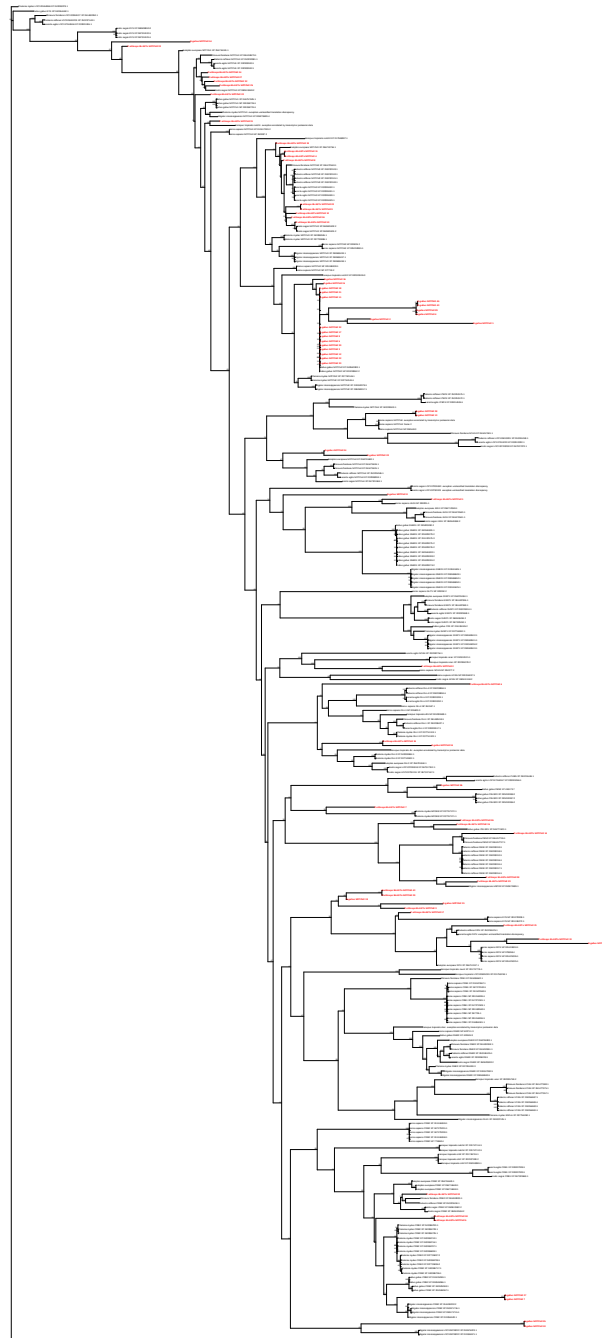


Figure 316: NOTCH2.combined.mafft.aln.highlighted.pdf

Syntenic evidence

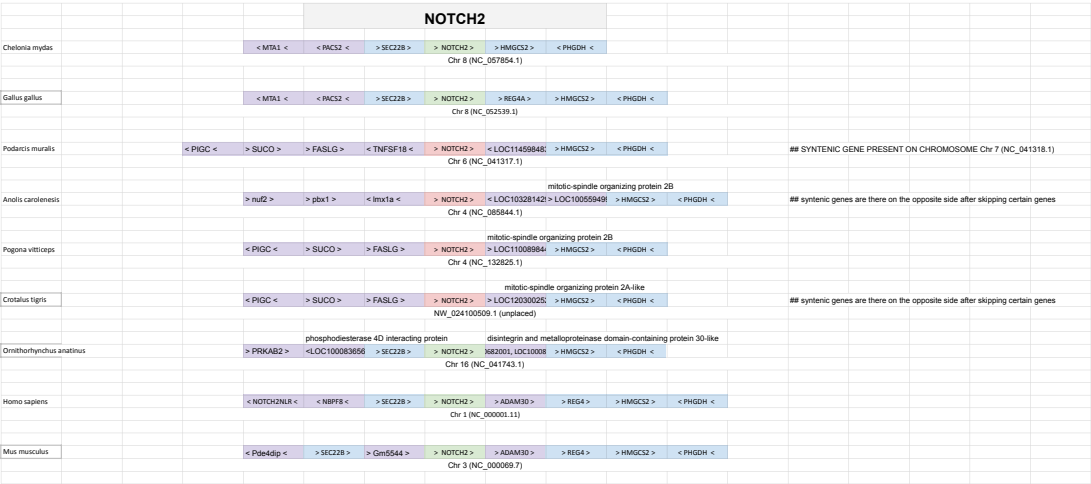


Figure 317: NOTCH2.pdf

NOTCH2.txt

Synteny analysis of NOTCH2

The analysis of the NOTCH2 syntenic block reveals its pronounced
→ instability across different squamate lineages. A significant
interchromosomal rearrangement is observed in the lizard *Podarcis muralis*,
→ where at least one of the flanking genes has moved to a different
→ chromosome (Chr 7). In addition to this break, the main gene block
→ has also undergone complex intrachromosomal rearrangements. For
→ instance, in both

Podarcis muralis and the snake *Crotalus tigris*, the syntenic genes have
→ been inverted and repositioned to a new location on their respective
→ chromosomes.

32 OLAH

Assembly verification Evidence

Crotalus_tigris-PacBio

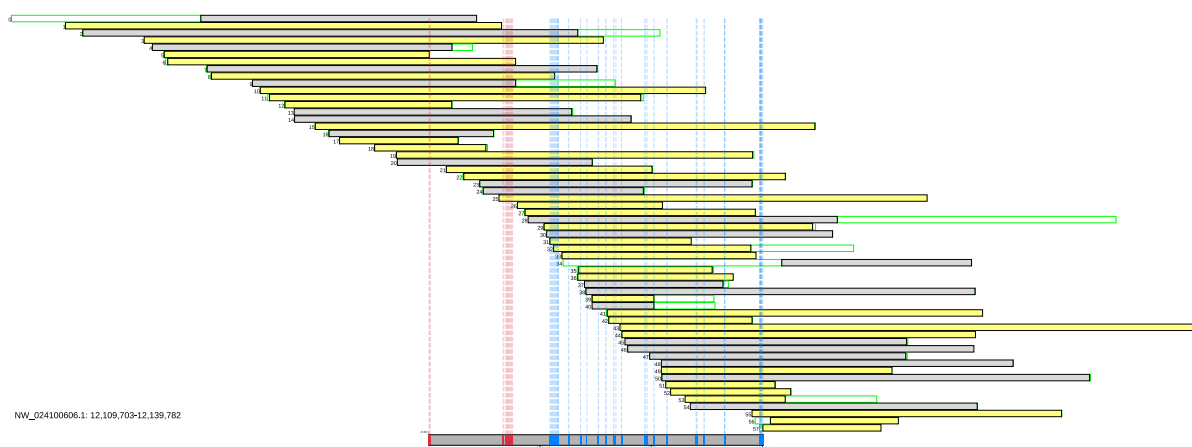


Figure 318: OLAH:NW_024100606.1:12109703-12139782.pdf

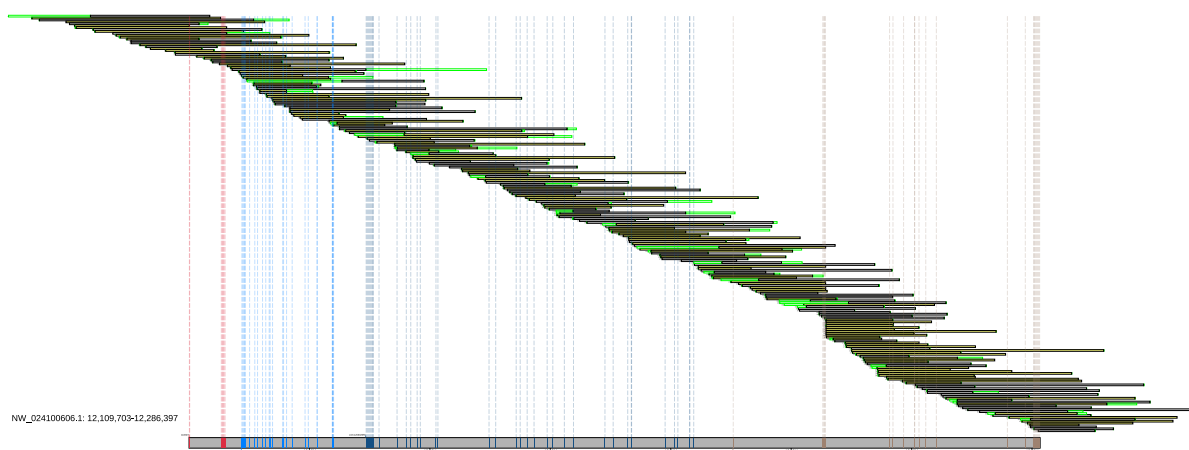


Figure 319: OLAH:NW_024100606.1:12109703-12286397.pdf

Podarcis_muralis-PacBio

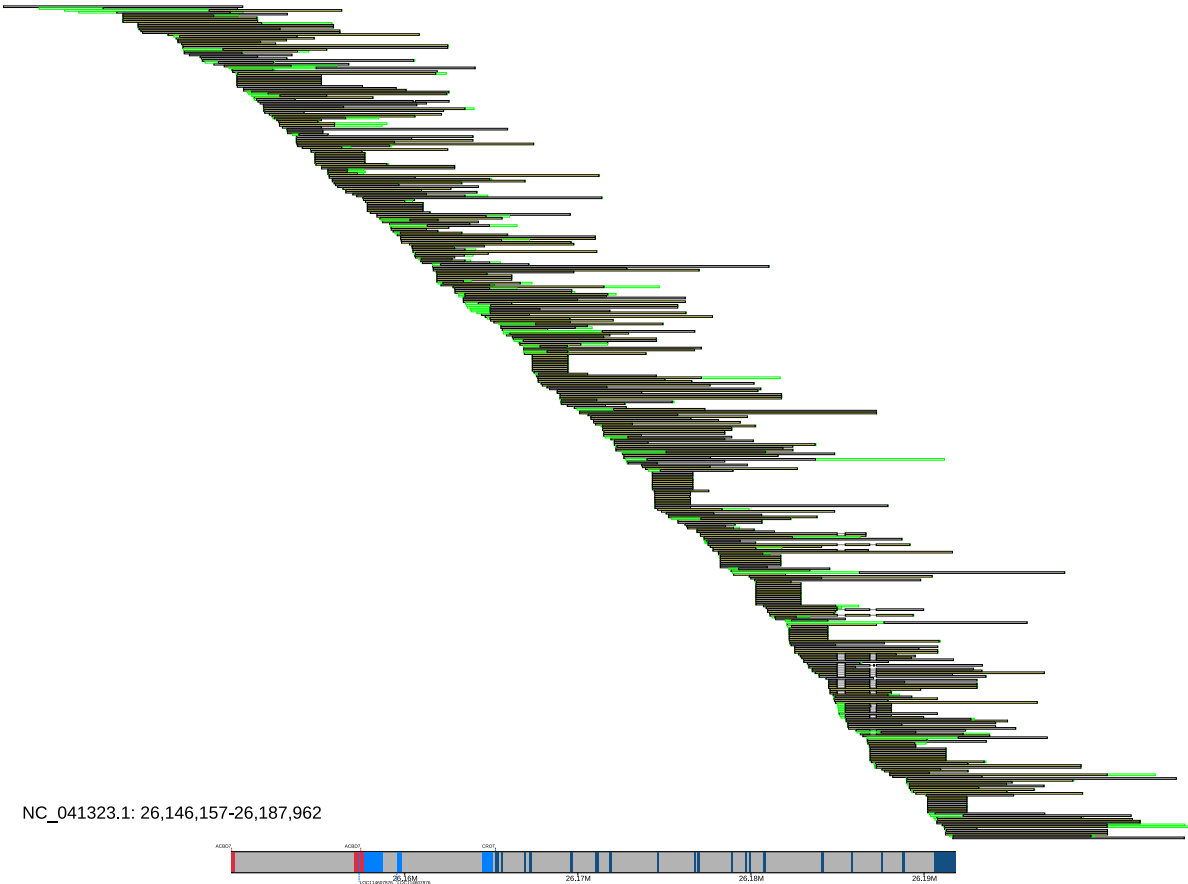


Figure 320: OLAH:NC_041323.1:26146157-26187962.pdf

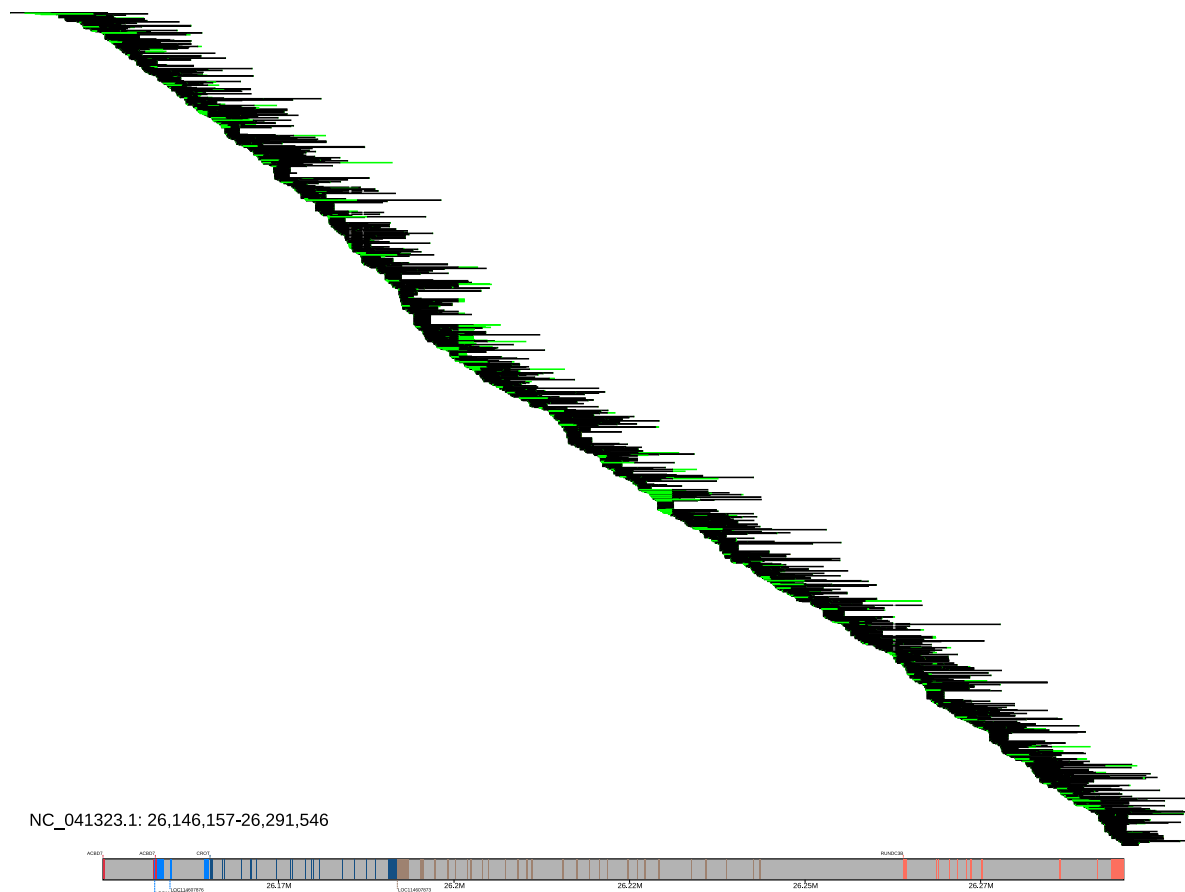


Figure 321: OLAH:NC_041323.1:26146157-26291546.pdf

Pogona_vitticeps-Nanopore

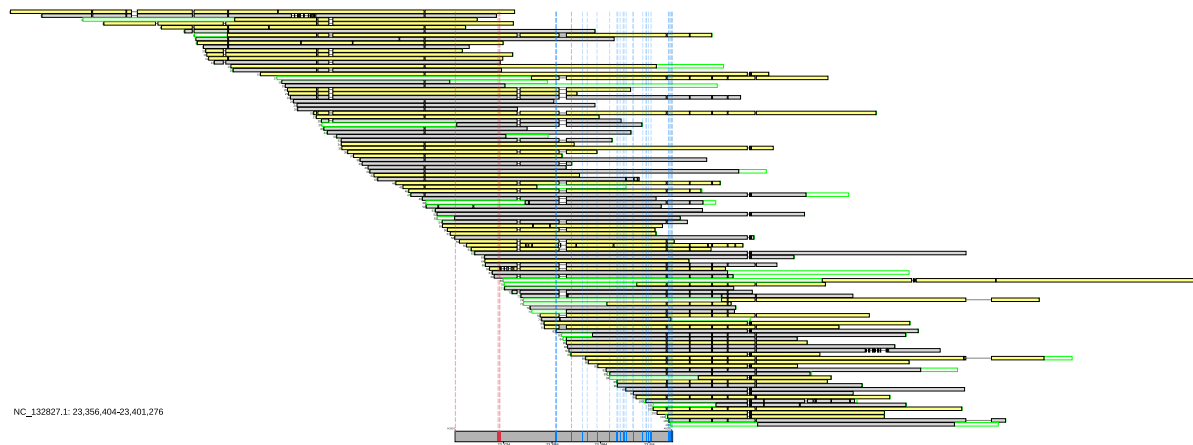


Figure 322: OLAH:NC_132827.1:23356404-23401276.pdf

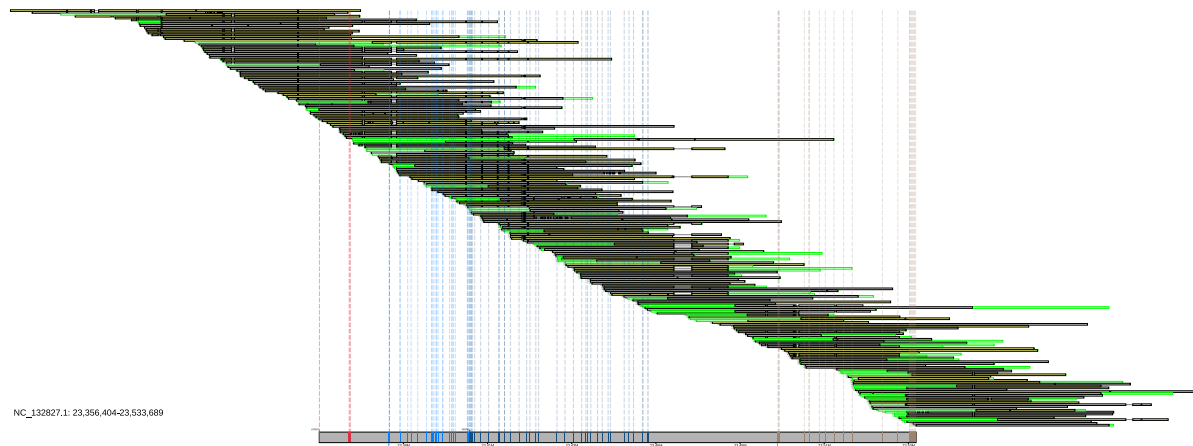


Figure 323: OLAH:NC_132827.1:23356404-23533689.pdf

Important gene stats

OLAH_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
OLAH	9.611940299	45.0695 +/- 5.21935	3.71636 +/- 0.293517	50.5596 +/- 8.14627	No	Na

Intergenic distance phylogenetic signal evidence

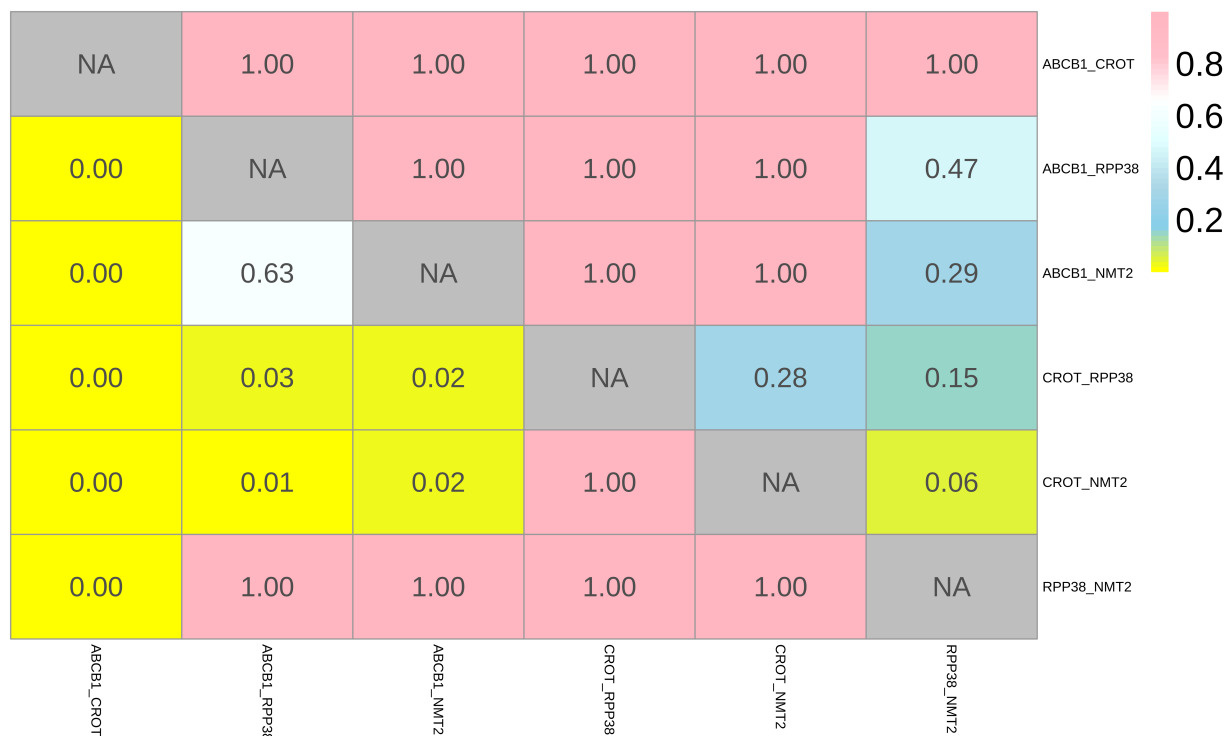


Figure 324: Heatmap_of_deletion_plot.png

OLAH_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
OLAH	80	15	65	0	0.174036103657125	0.392376938746692

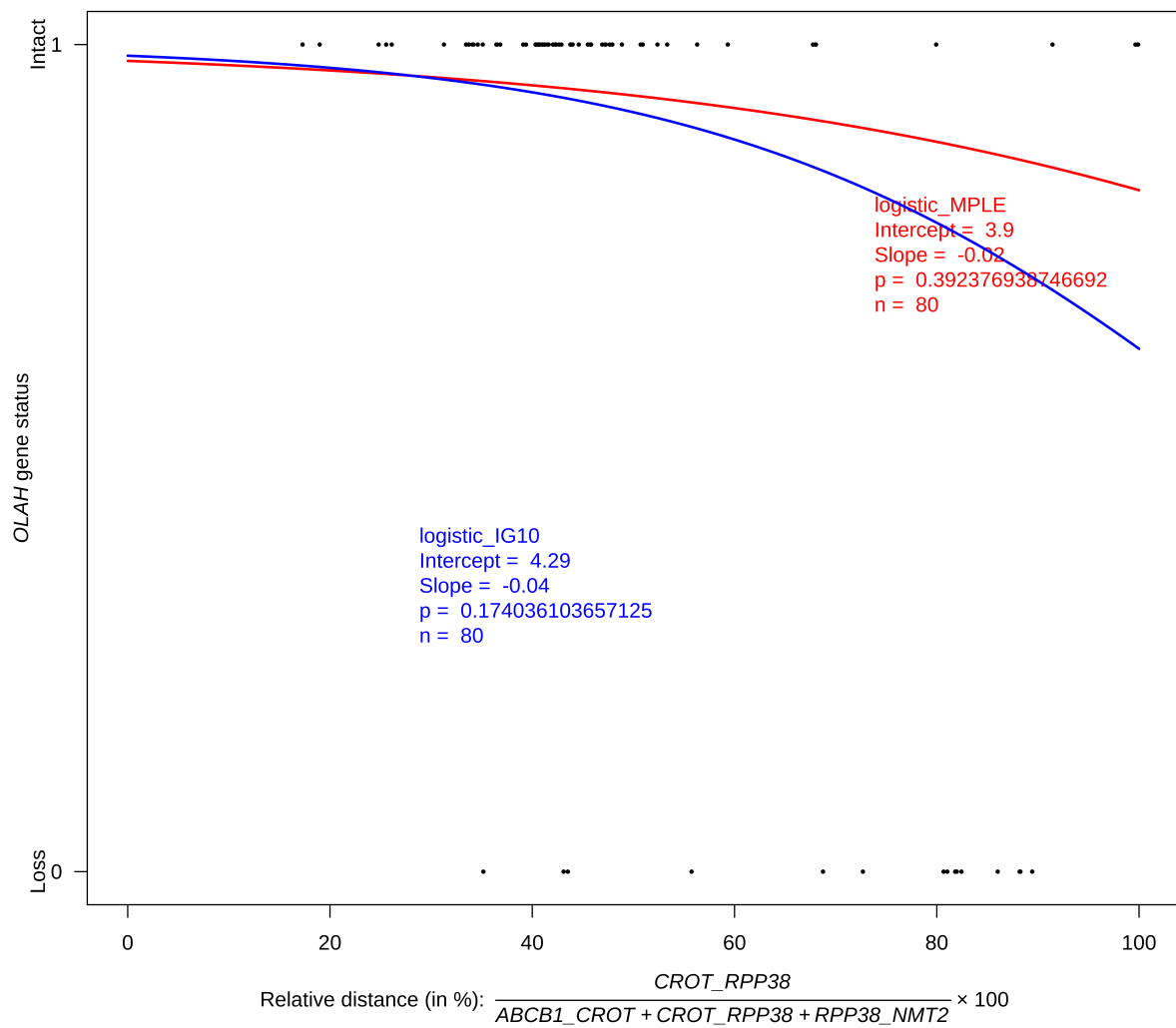


Figure 325: Phylogenetic_signal_of_deletion_plot.png

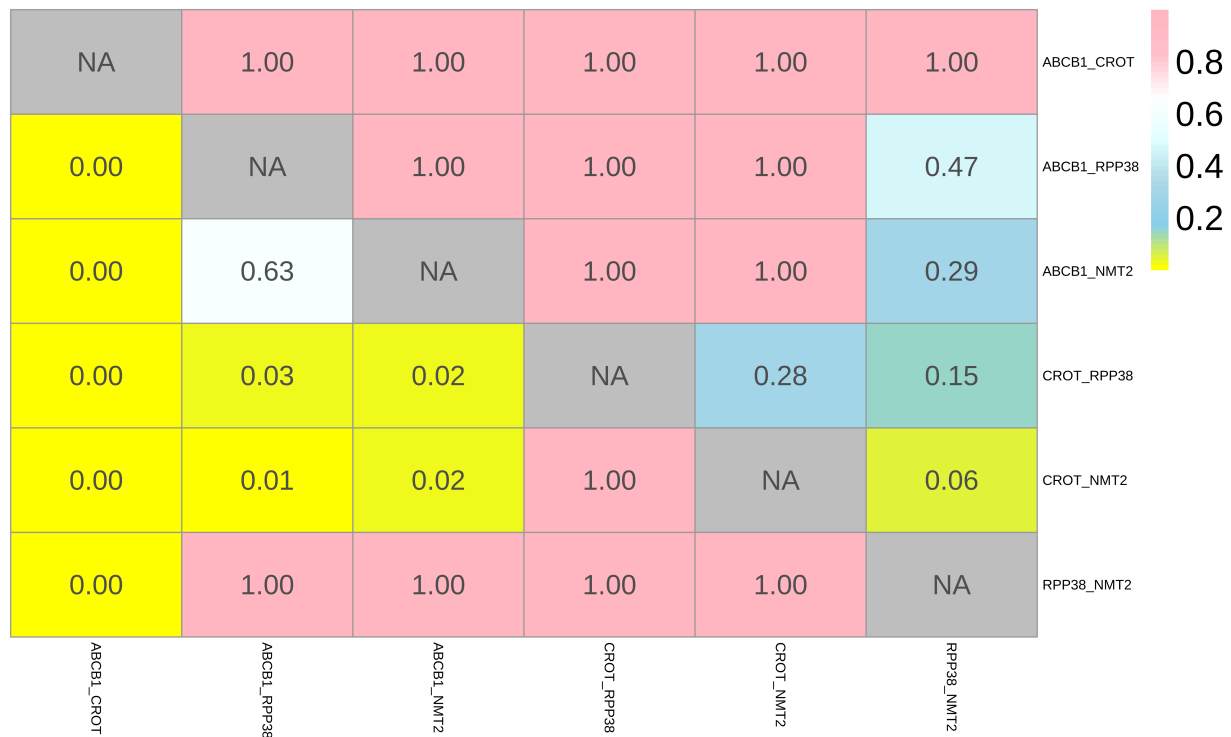


Figure 326: Heatmap_of_deletion_plot.png

OLAH_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
OLAH	80	15	65	0	0.174036103657125	0.392376938746692

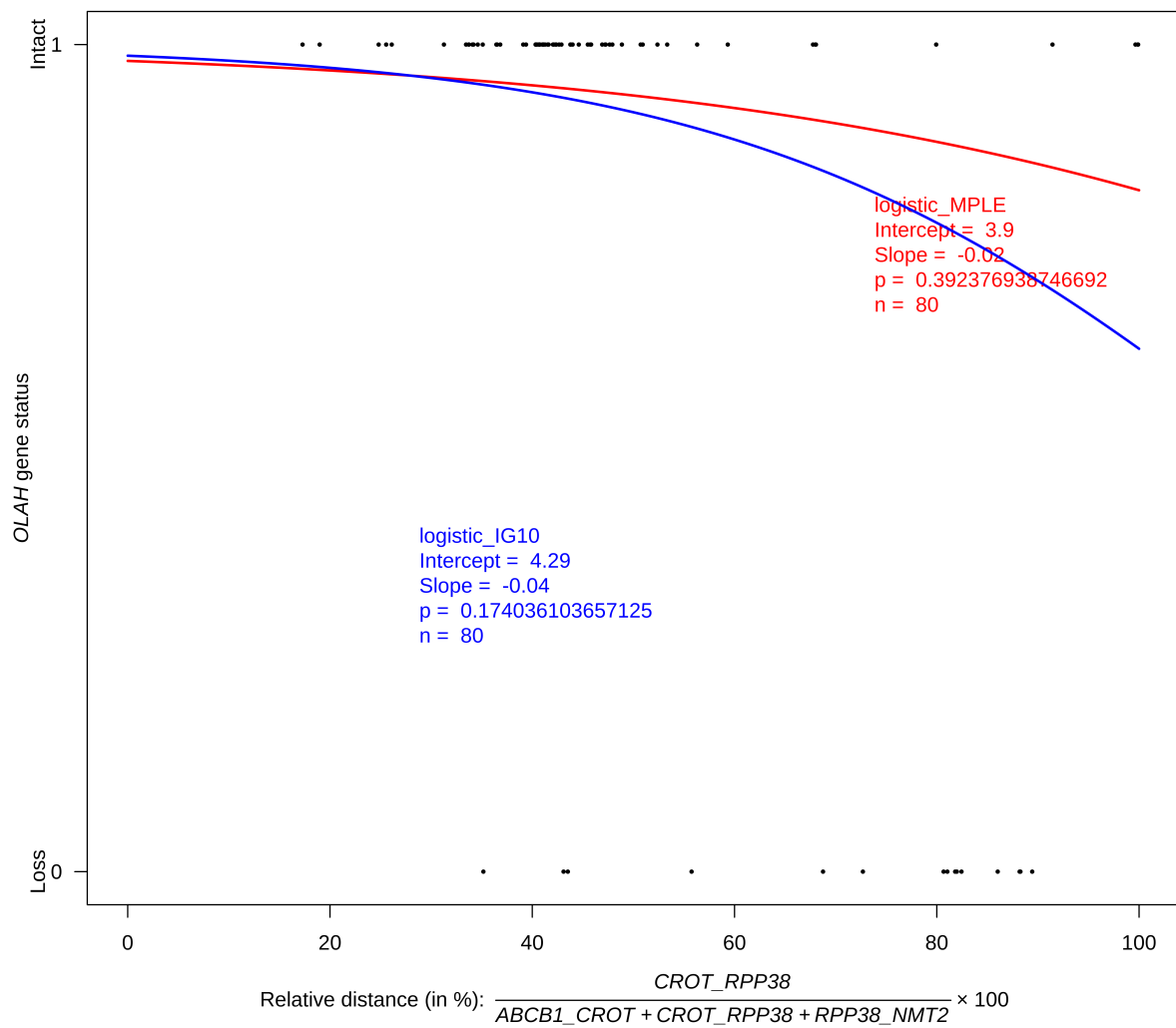


Figure 327: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence

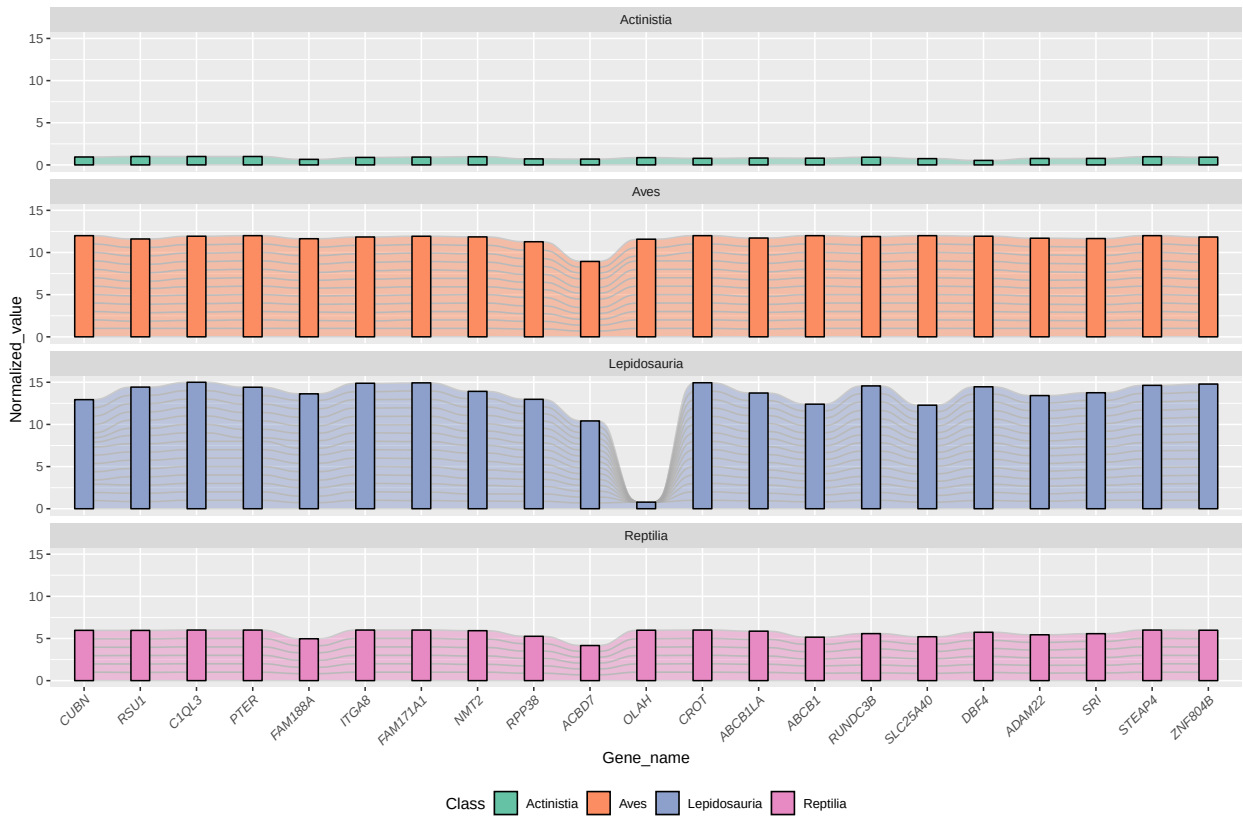


Figure 328: OLAH.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Syntenic evidence



Figure 330: OLAH.pdf

OLAH.txt

Synteny analysis of OLAH

We analyzed the synteny of OLAH in squamates and representative outgroups.

- The OLAH syntenic block is conserved overall, with notable lineage-specific changes. In Anolis carolinensis, the neighboring genes RPP38 and ACBD7 occur in a different order. In Crotalus tigris, the flanking gene CROT appears in an inverted orientation, indicated by yellow blocks in the synteny plot. In Homo sapiens and Mus musculus, one flank is not conserved; the locus is associated with RUNDC3B, ABCB1, and CROT, but located on different chromosomes. Specifically, this flank is present on chromosome 7 (NC_000007.14) in humans and chromosome 5 (NC_000071.7) in mice, representing cases of interchromosomal rearrangement. In the synteny plots, red blocks indicate the absence of OLAH, green blocks mark its presence, light blue blocks represent genes conserved across lineages, light purple

↪ blocks denote different flanking genes, and yellow blocks highlight
↪ gene inversions.

Transcriptomic evidence *Pogona vitticeps*

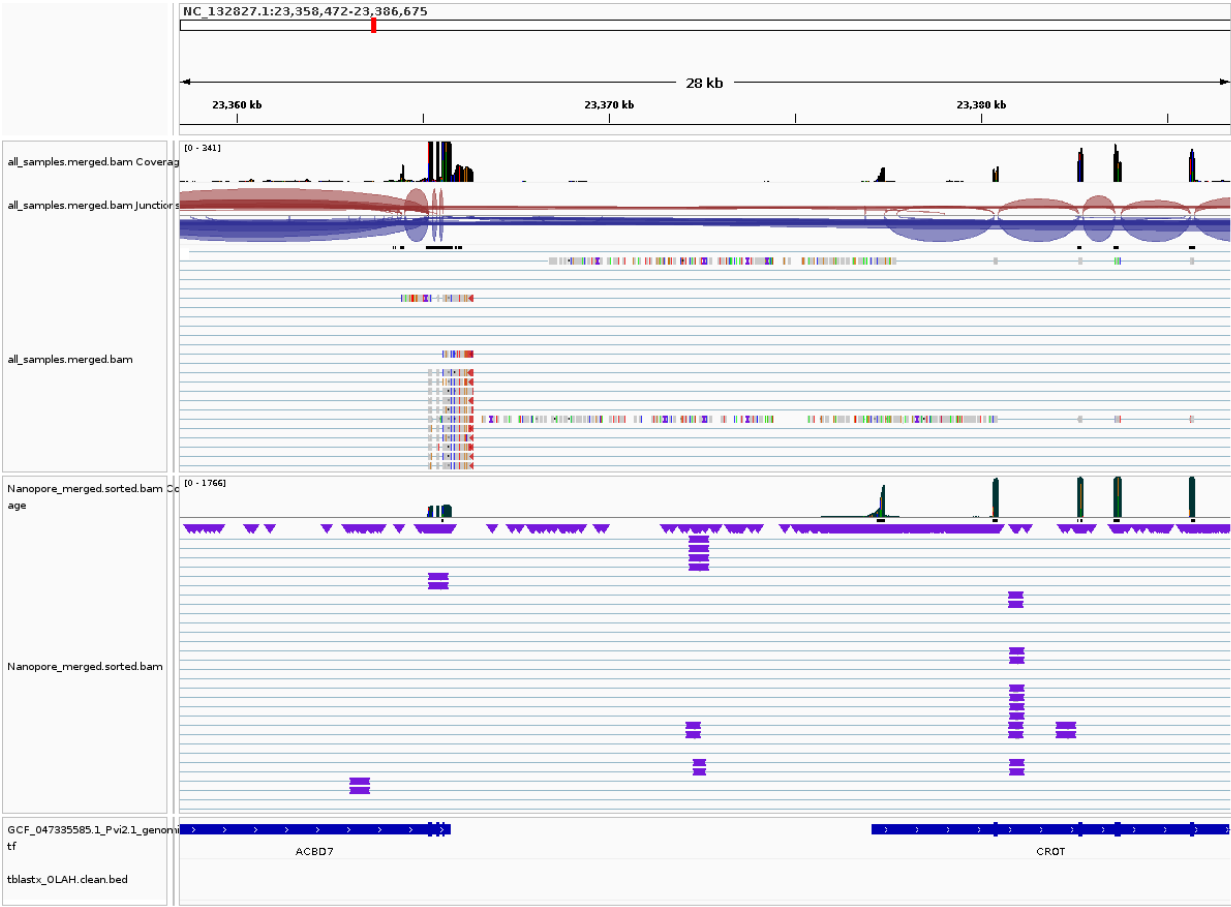


Figure 331: OLAH.png

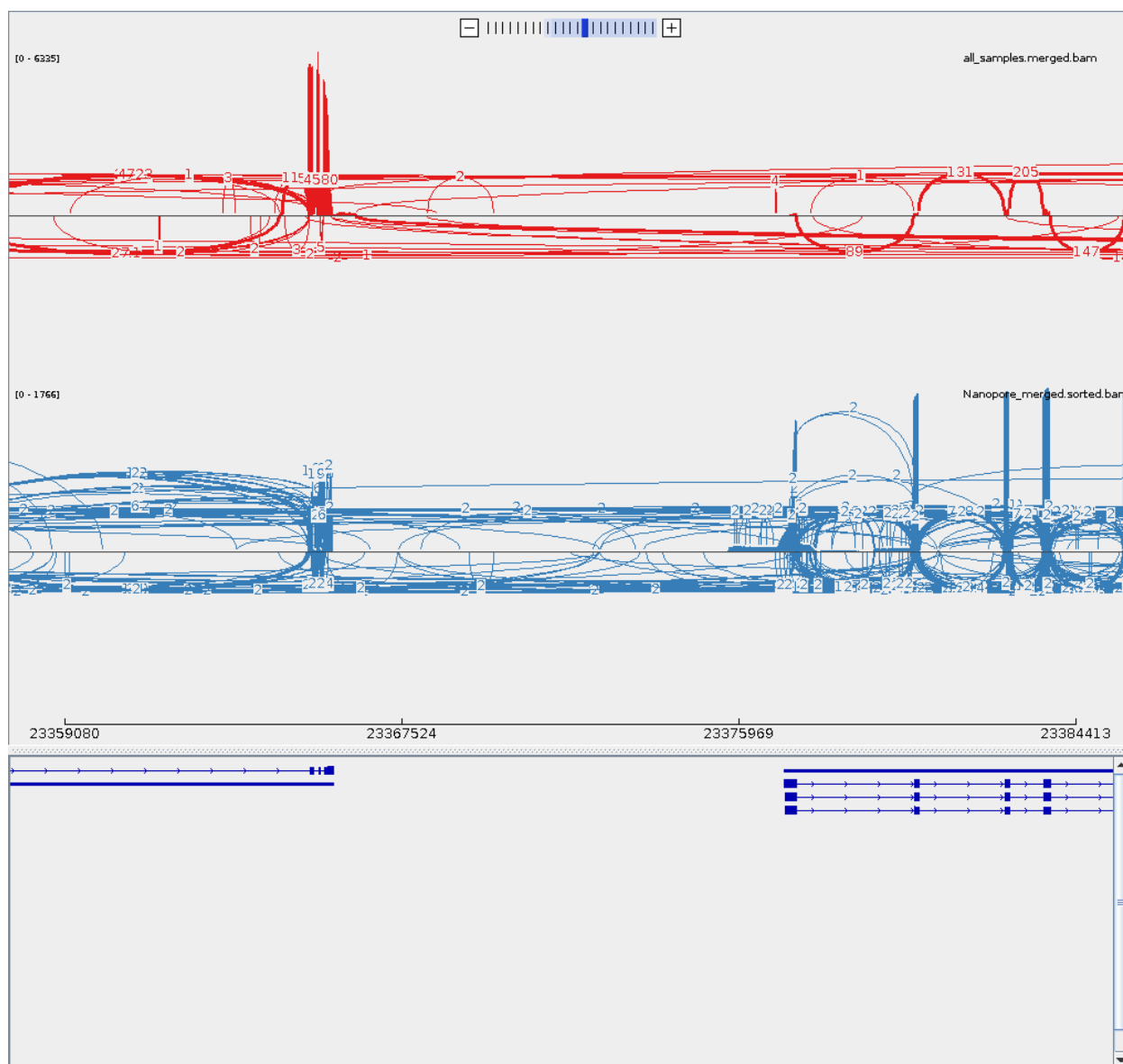


Figure 332: OLAH_Shash.png

33 PLAAT1

Crotalus_tigris-PacBio

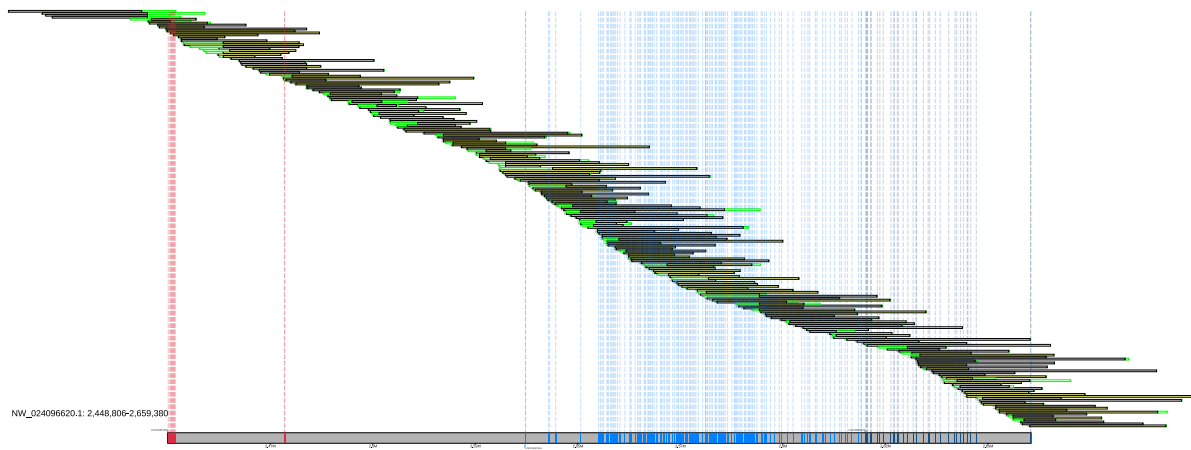


Figure 333: PLAAT1:NW_024096620.1:2448806-2659380.pdf

Podarcis_muralis-PacBio

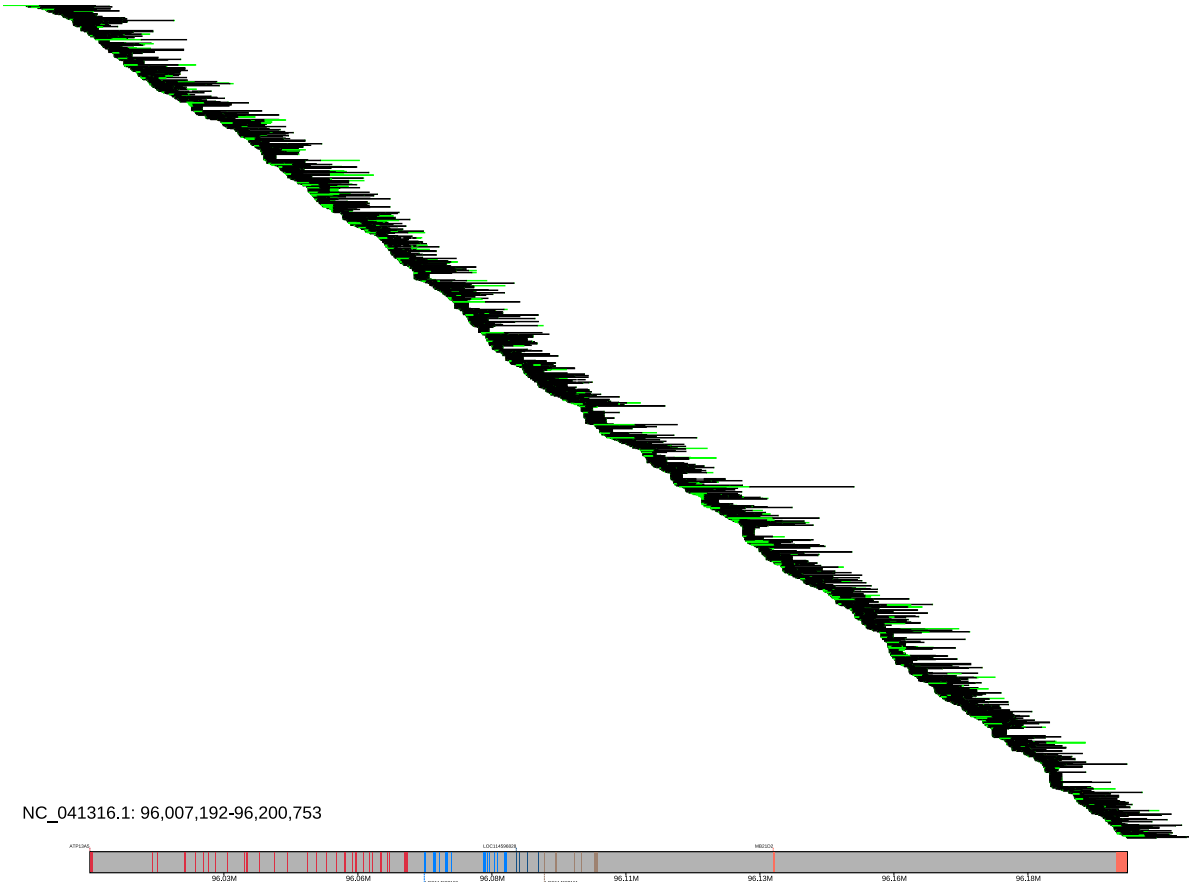


Figure 334: PLAAT1:NC_041316.1:96007192-96200753.pdf

Pogona_vitticeps-Nanopore

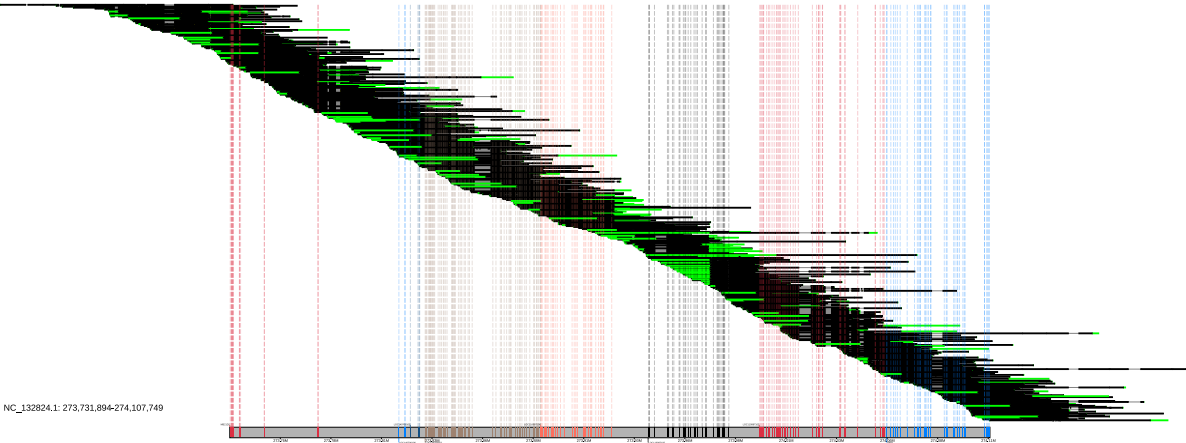


Figure 335: PLAAT1:NC_132824.1:273731894-274107749.pdf

Important gene stats

PLAAT1_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
PLAAT1	11.87916667	52.0082 +/- 5.74363	3.90504 +/- 0.357933	53.9965 +/- 9.15298	No	LOC116520146;LOC132764394;

Intergenic distance phylogenetic signal evidence

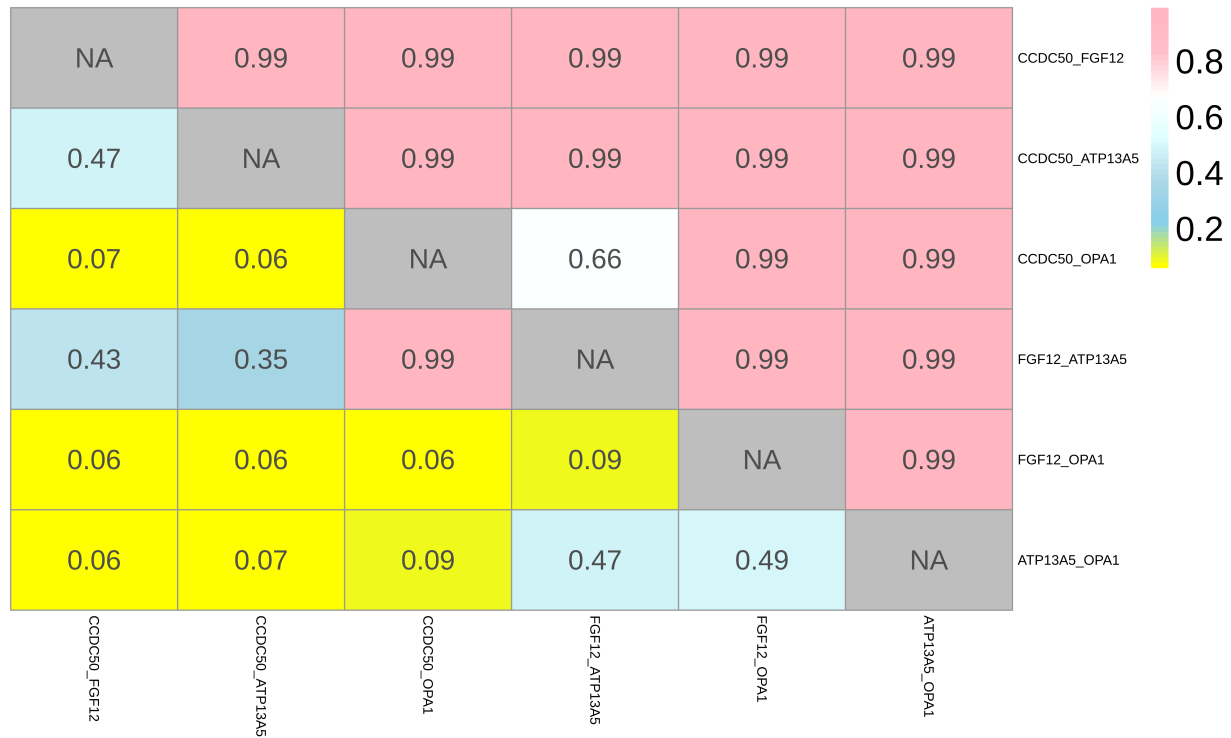


Figure 336: Heatmap_of_deletion_plot.png

PLAAT1_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
PLAAT1	81	2	79	0	0.169912327019424	0.621539305352812

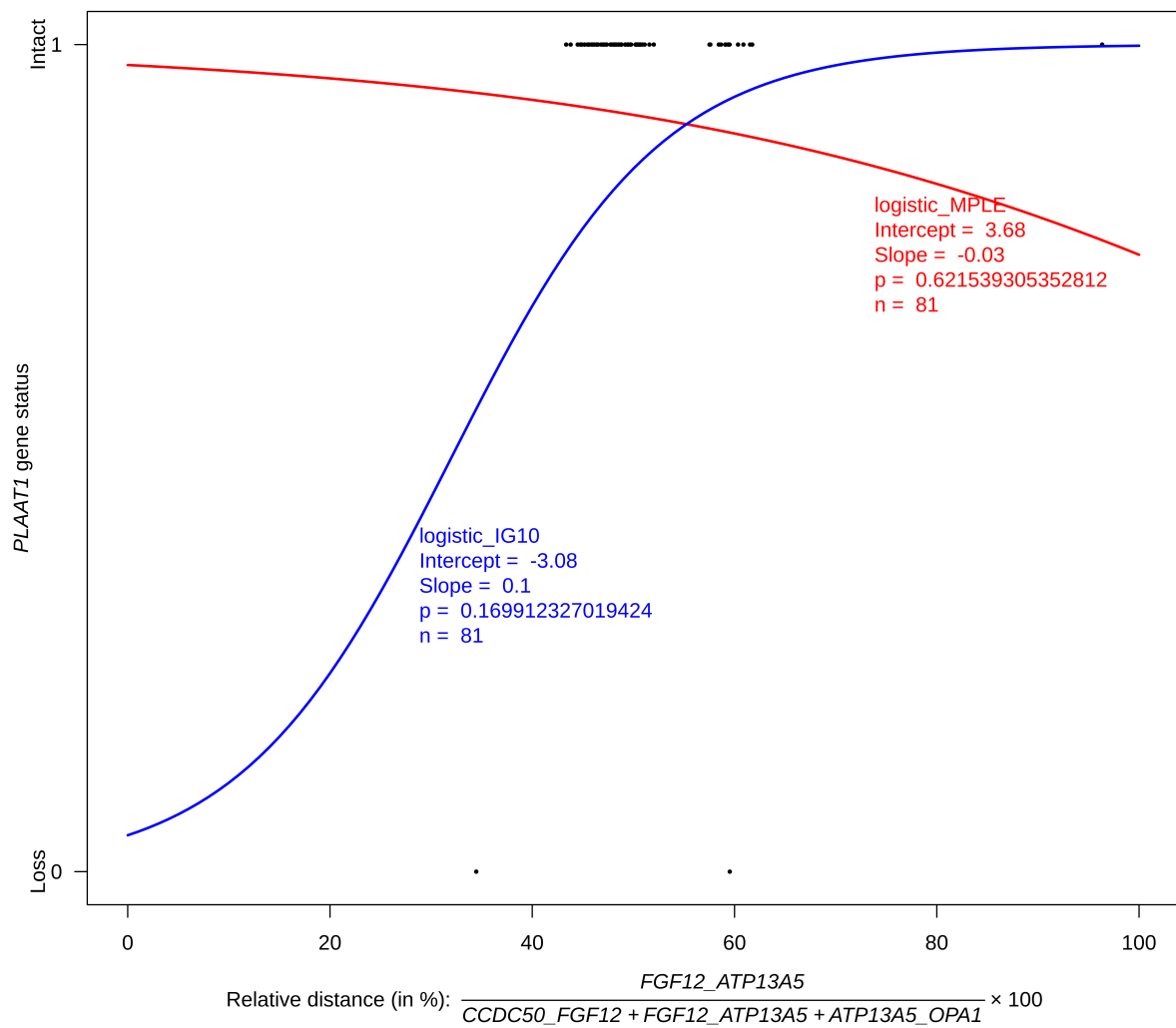


Figure 337: Phylogenetic_signal_of_deletion_plot.png

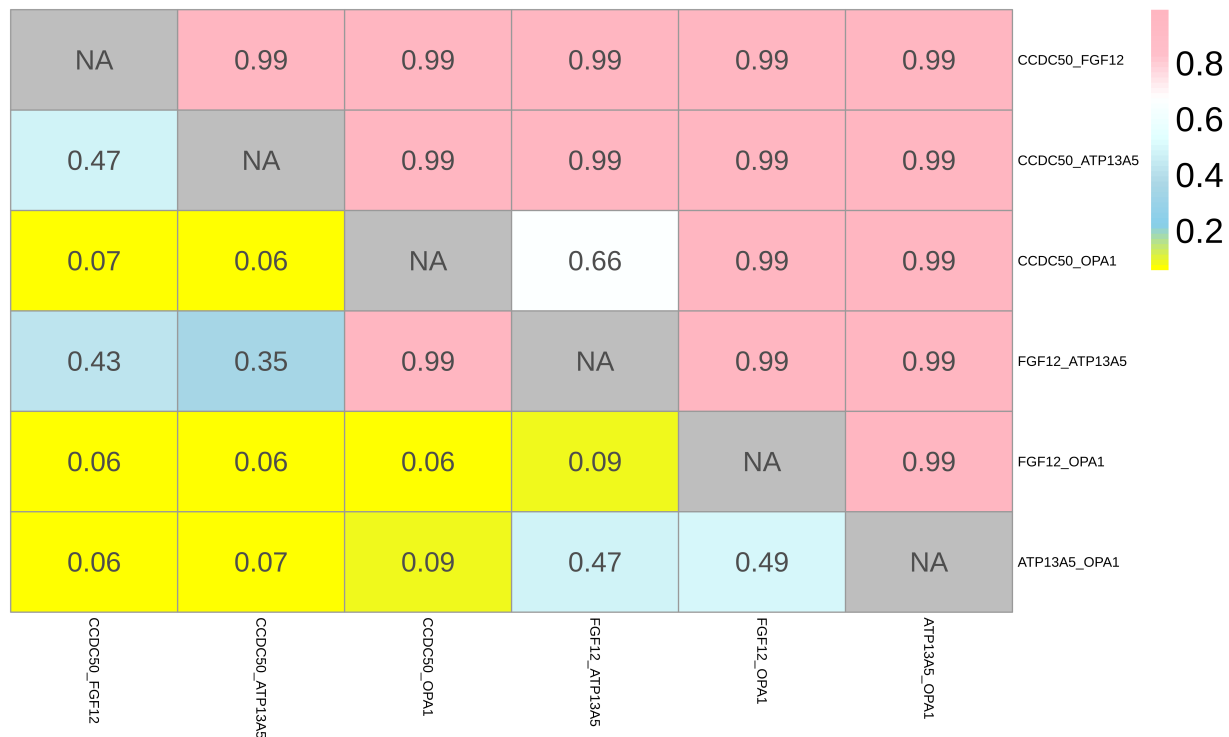


Figure 338: Heatmap_of_deletion_plot.png

PLAAT1_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
PLAAT1	81	2	79	0	0.169912327019424	0.621539305352812

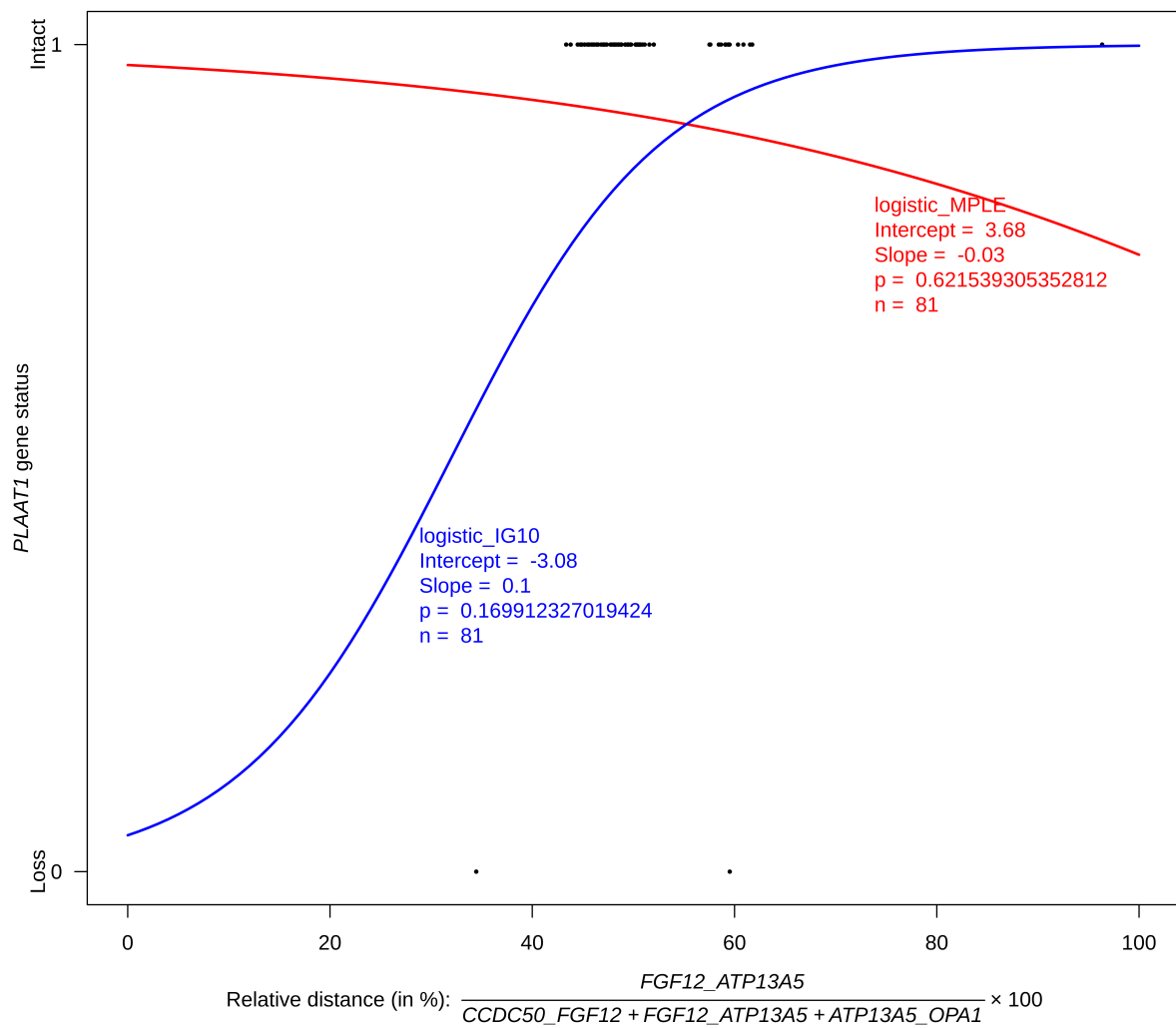


Figure 339: Phylogenetic_signal_of_deletion_plot.png

Orthofinder genetree



Figure 340: Plaat1.PRANK.aln.contree.png

Syntenic evidence

						HRASLS/PLAAT1				
Chelonia mydas		> CCDC50 >	< FGF12 <	< MB21D2 <	> zonadhesin >	> HRASLS >	< ATP13A5 <	< ATP13A4 <	> OPA1 >	
Gallus gallus		> CCDC50 >	< FGF12 <	< MB21D2 <	> FCGBP >	> HRASLS >	< ATP13A5 <	< ATP13A4 <	> OPA1 >	
Podarcis muralis		> CCDC50 >	< FGF12 <	< MB21D2 <	> HRASLS >	> LOC11459816 >	> LOC11459816 >	< ATP13A5 <	< ATP13A4 <	> OPA1 >
Anolis carolinensis		< ATP13A4 <	< ATP13A5 <	< FGF12 <	< MB21D2 <	> HRASLS >	< l1rap <	> LOC10328216 <	< cldn16 <	> cldn1 >
Intra chromosomal rearrangement										
Pogona vitticeps		> CCDC50 >	< FGF12 <	< MB21D2 <	> PLAAT1 >	ATP13A5	ATP13A4			
						2, LOC110087106, k	LOC110087103 <	> OPA1 >		
Crotalus tigris		< FGF12 <	< MB21D2 <	< LOC120307153 <	> PLAAT1 >	> LOC120307151 >	< LOC120307154 <	< LOC120307155 <	> OPA1 >	
		NW_024098285.1 (unplaced)						NW_024096620.1 (unplaced)		
Ornithorhynchus anatinus		> CCDC50 >	< FGF12 <	< MB21D2 <	> PLAAT1 >	> LOC12063851 >	> zonadhesin >	< ATP13A5 <	< ATP13A4 <	> OPA1 >
Homo sapiens		> CCDC50 >	< FGF12 <	< MB21D2 <	> PLAAT1 >	< ATP13A5 <	< ATP13A4 <	> OPA1 >		
Mus musculus		> CCDC50 >	< FGF12 <	< MB21D2 <	> PLAAT1 >	< ATP13A5 <	< ATP13A4 <	> OPA1 >		

Figure 341: PLAAT1.pdf

PLAAT1.txt

Synteny analysis of PLAAT1

We analyzed the synteny of PLAAT1 in squamates and representative outgroups. The PLAAT1 syntenic block is conserved, with the exception of one flanking side in Anolis carolinensis, where the arrangement differs from the conserved pattern. In the synteny plots, red blocks indicate the absence of PLAAT1, green blocks mark its presence, light blue blocks represent genes conserved across lineages, and light purple blocks denote different flanking genes.

Transcriptomic evidence *Pogona vitticeps*

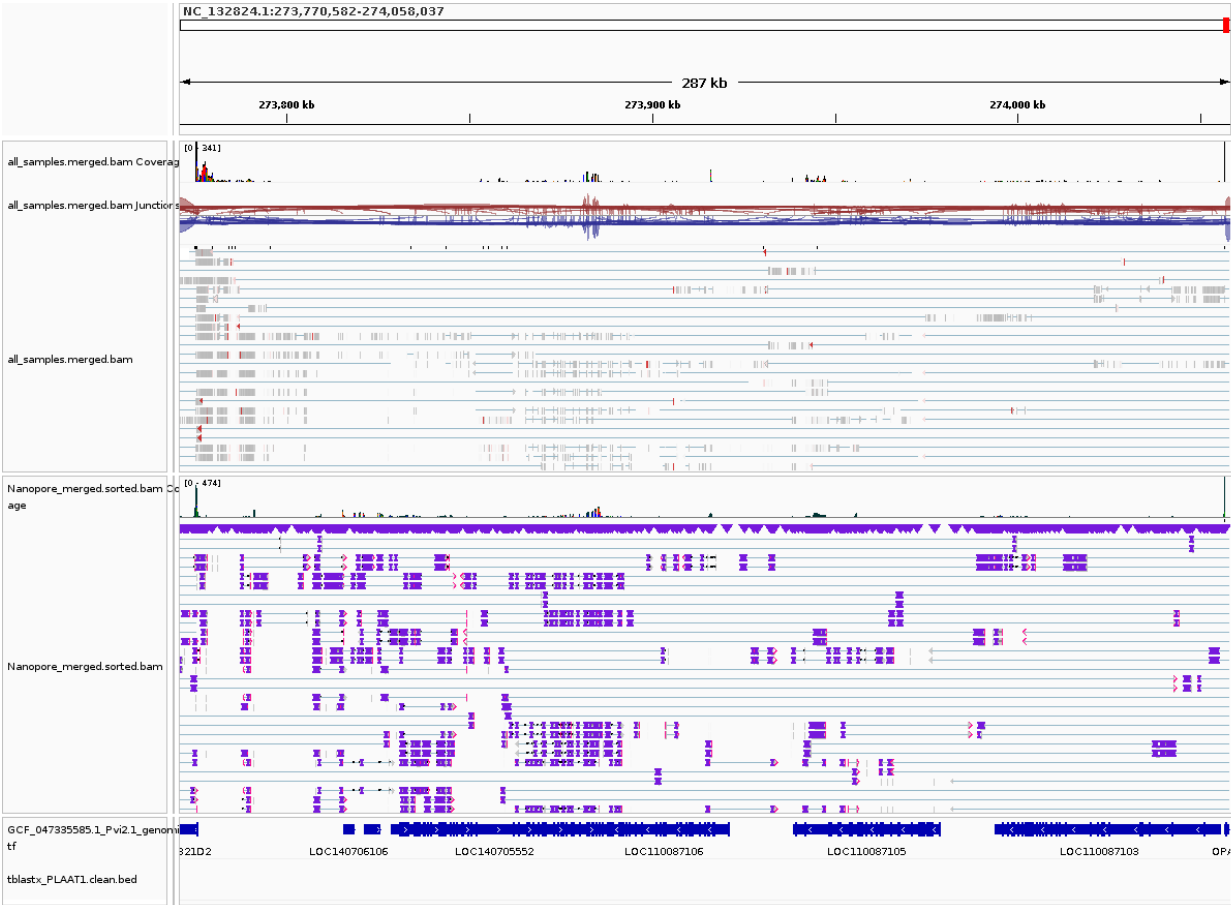


Figure 342: PLAAT1.png

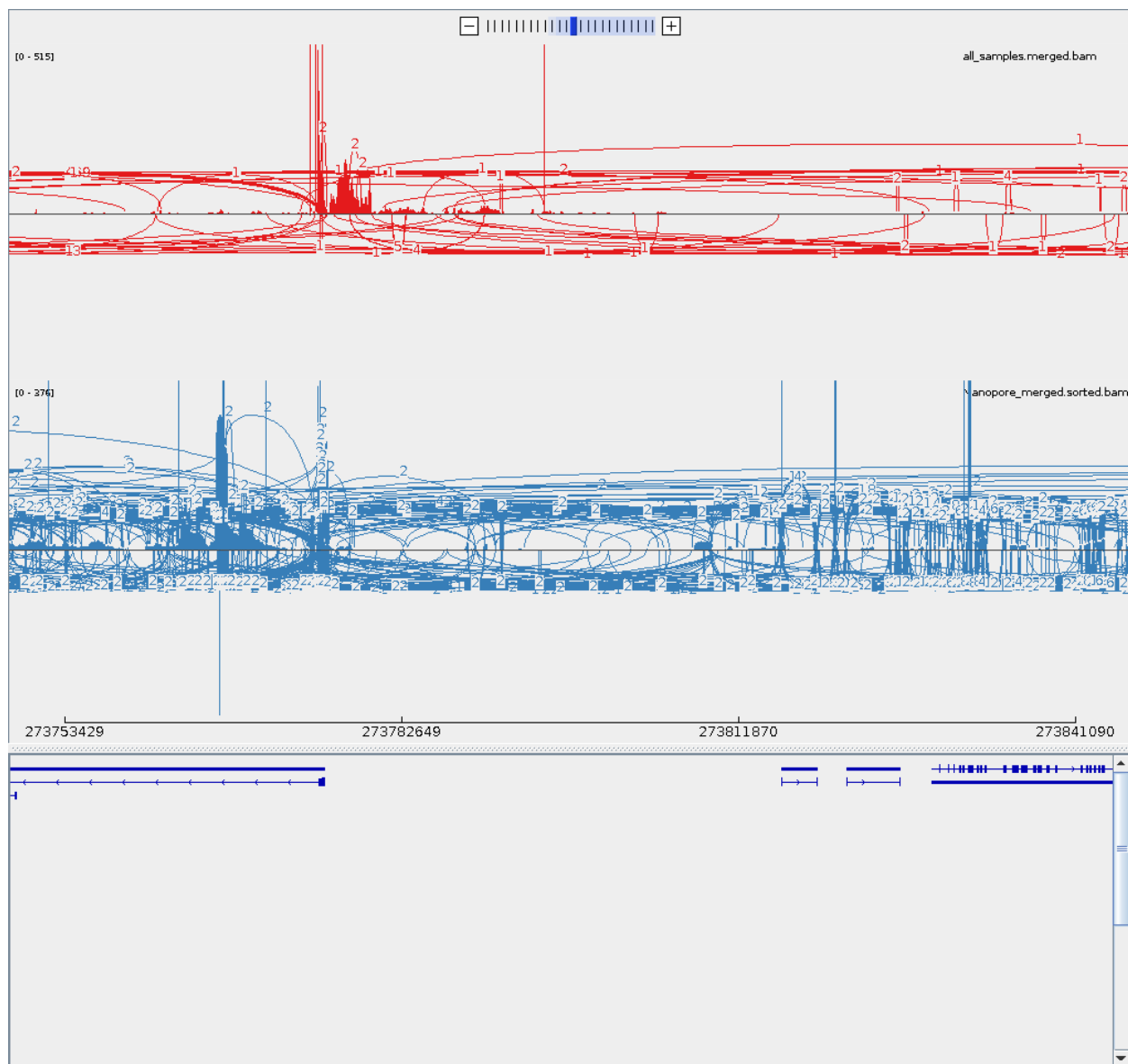


Figure 343: PLAAT1_Shash.png

34 RBBP7

Crotalus_tigris-PacBio

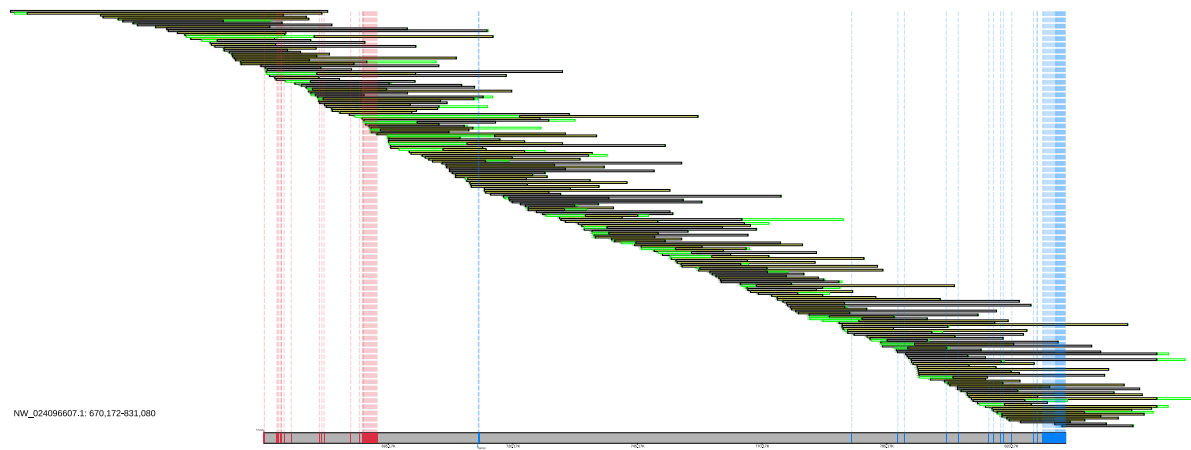


Figure 344: RBBP7:NW_024096607.1:670172-831080.pdf

Podarcis_muralis-PacBio

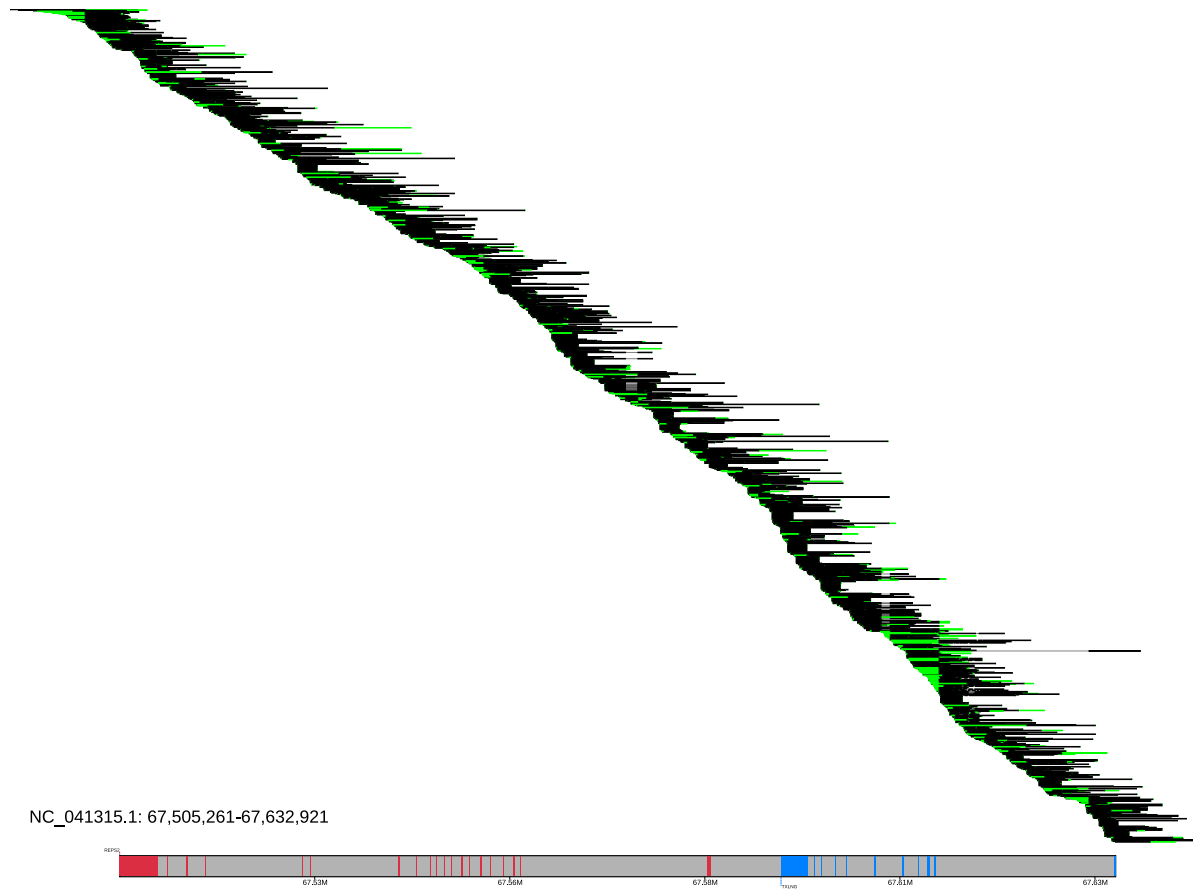


Figure 345: RBBP7:NC_041315.1:67505261-67632921.pdf

Pogona_vitticeps-Nanopore

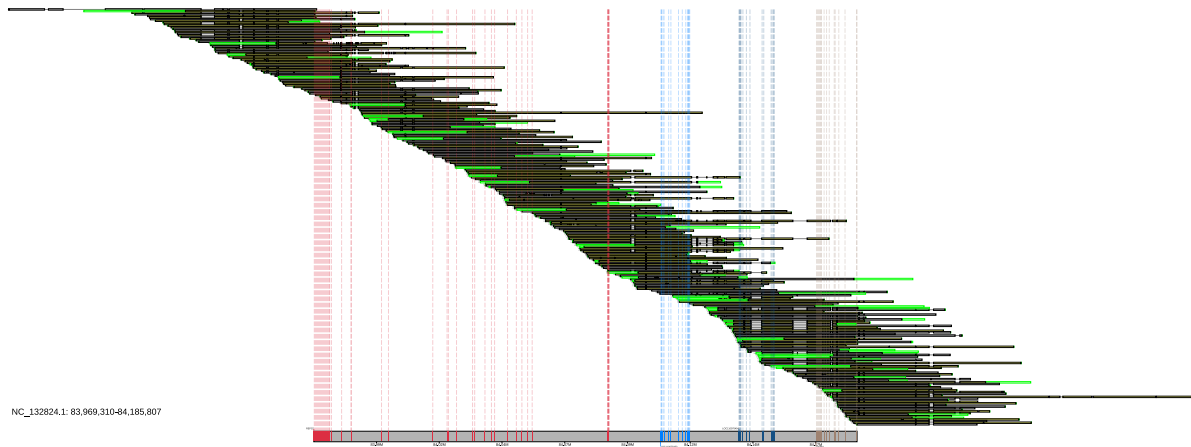


Figure 346: RBBP7:NC_132824.1:83969310-84185807.pdf

Important gene stats

RBBP7_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
RBBP7	60.34090909	45.9117 +/- 2.06375	3.51884 +/- 0.178754	74.3113 +/- 9.64778	Yes	RBBP4;

Intergenic distance phylogenetic signal evidence

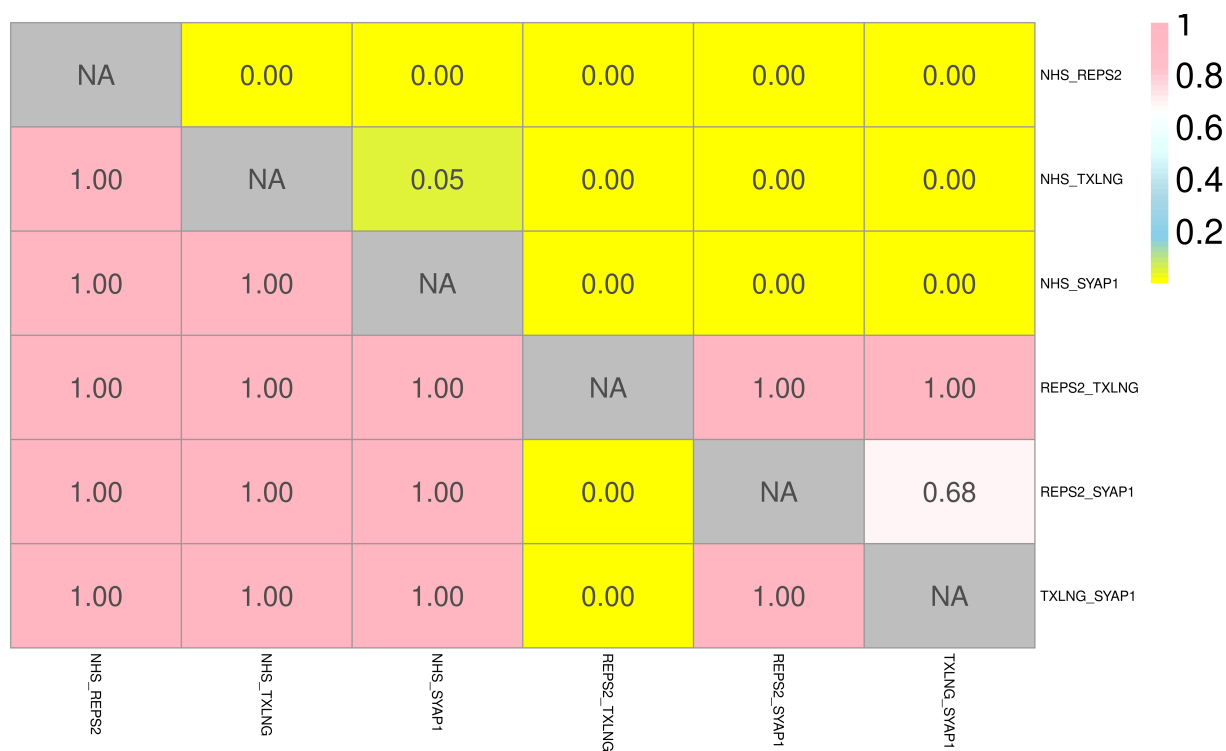


Figure 347: Heatmap_of_deletion_plot.png

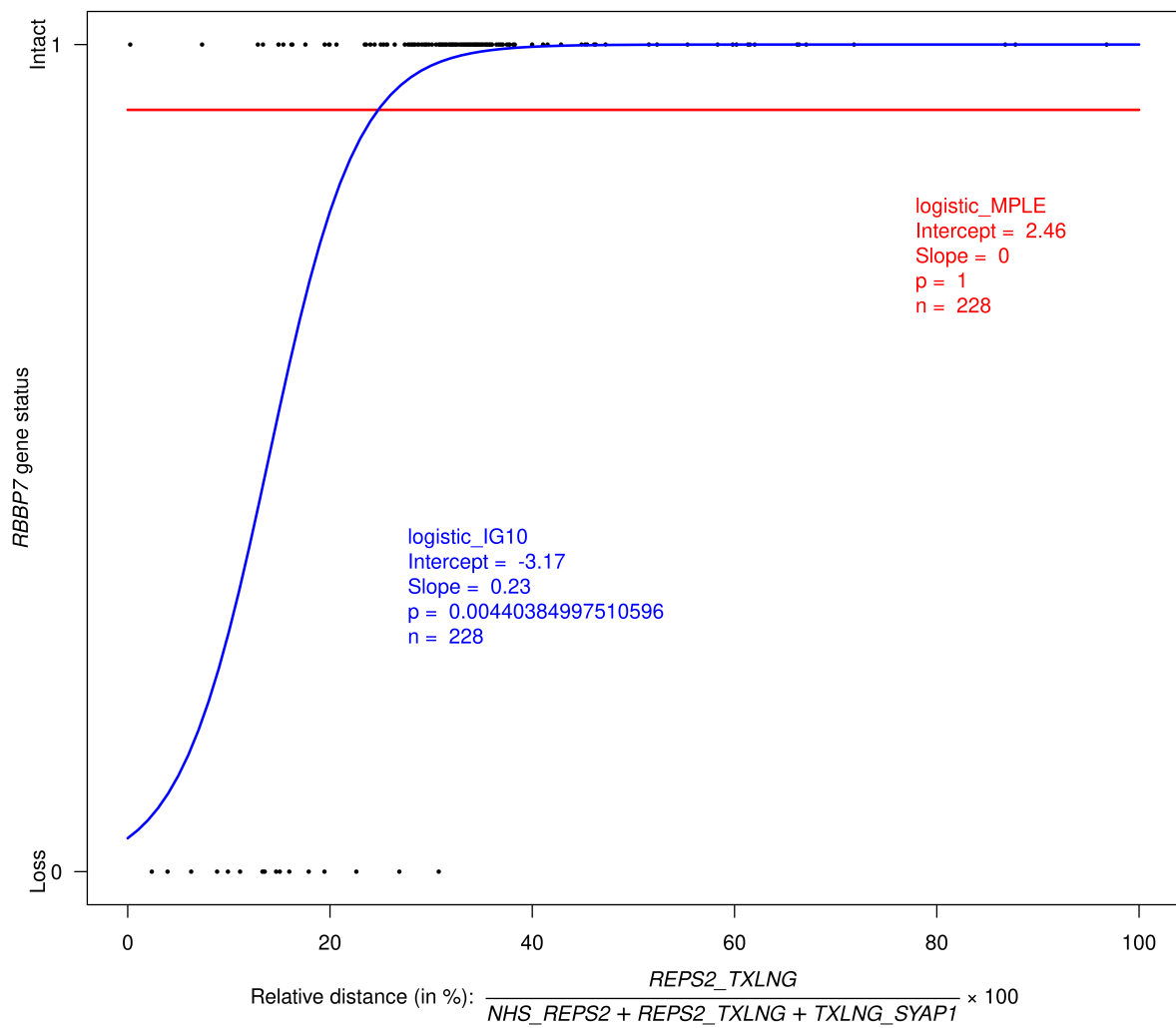


Figure 348: Phylogenetic_signal_of_deletion_plot.png

RBBP7_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
RBBP7	228	18	210	5	0.0044038499751059	1

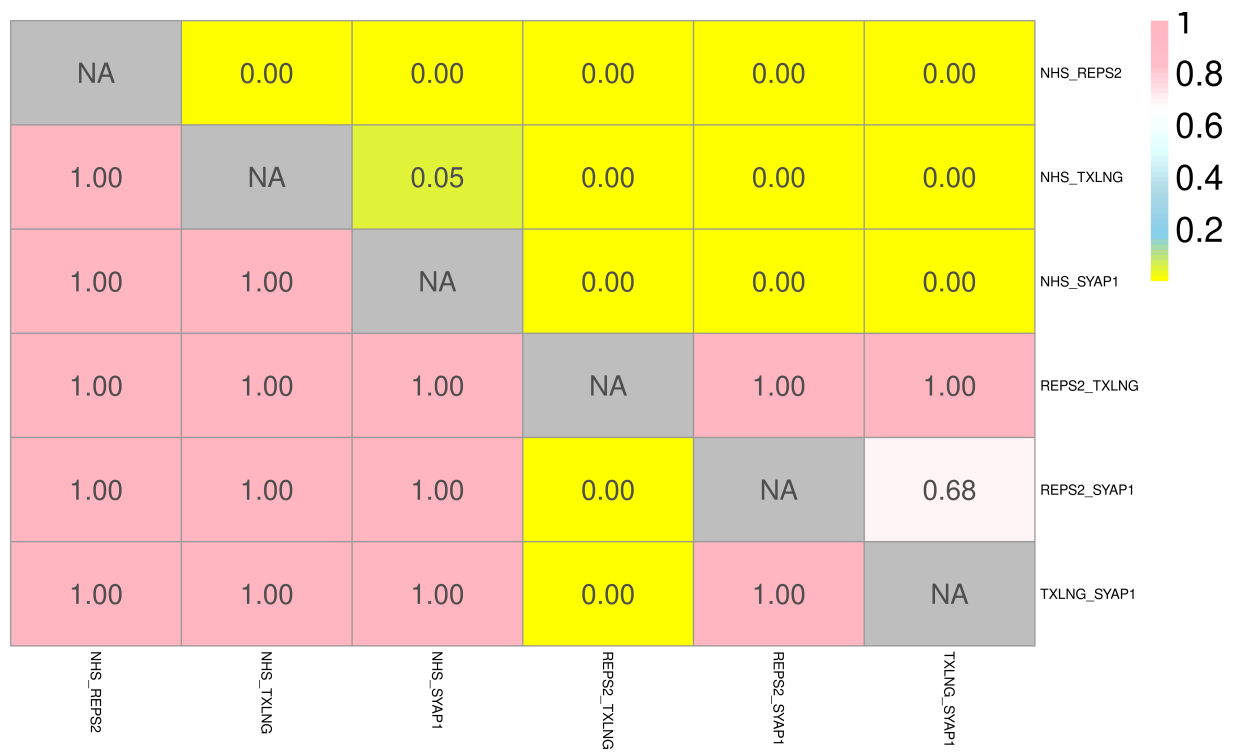


Figure 349: Heatmap_of_deletion_plot.png

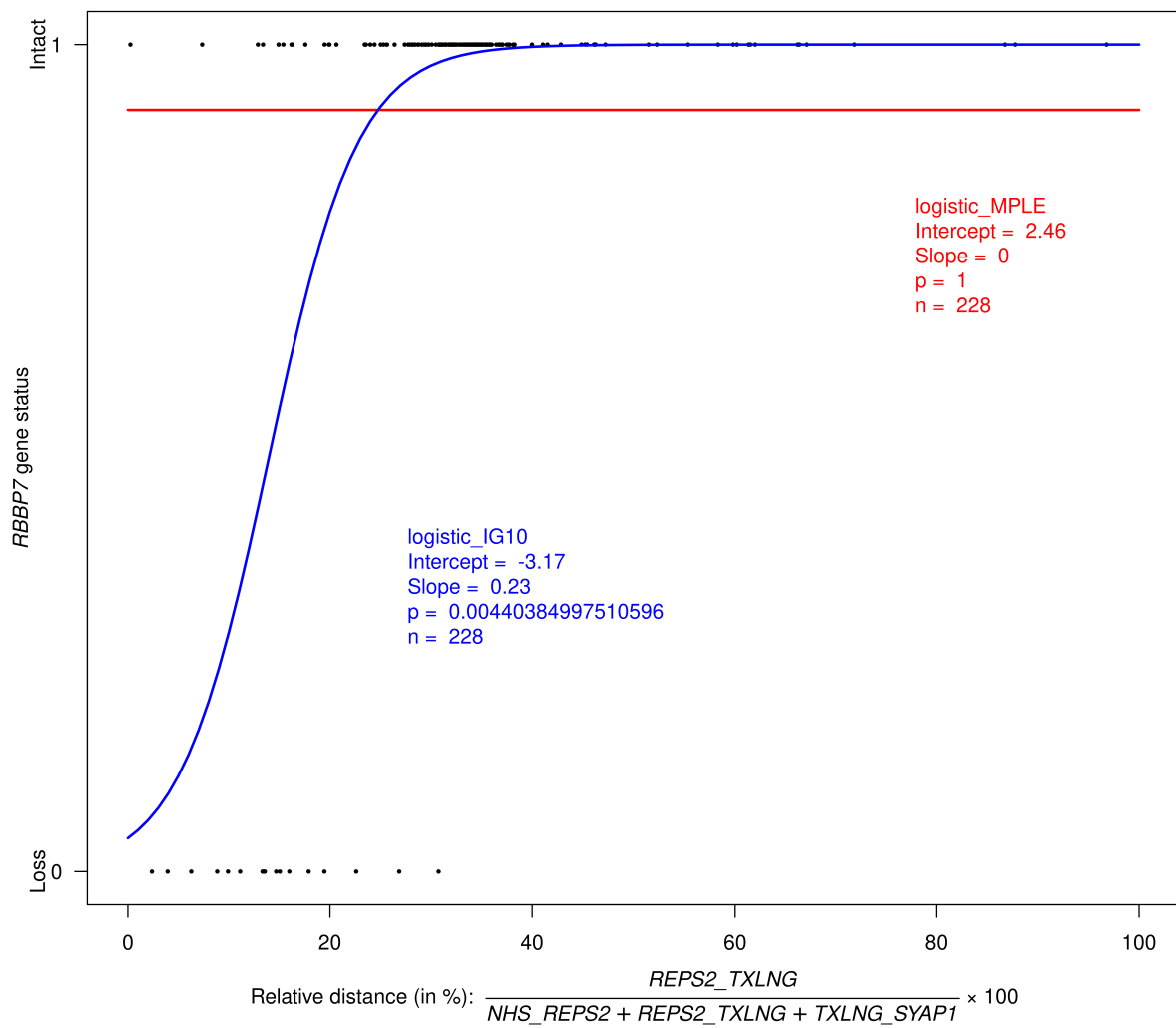


Figure 350: Phylogenetic_signal_of_deletion_plot.png

RBBP7_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
RBBP7	228	18	210	5	0.0044038499751059	1

Lastz Alignment evidence

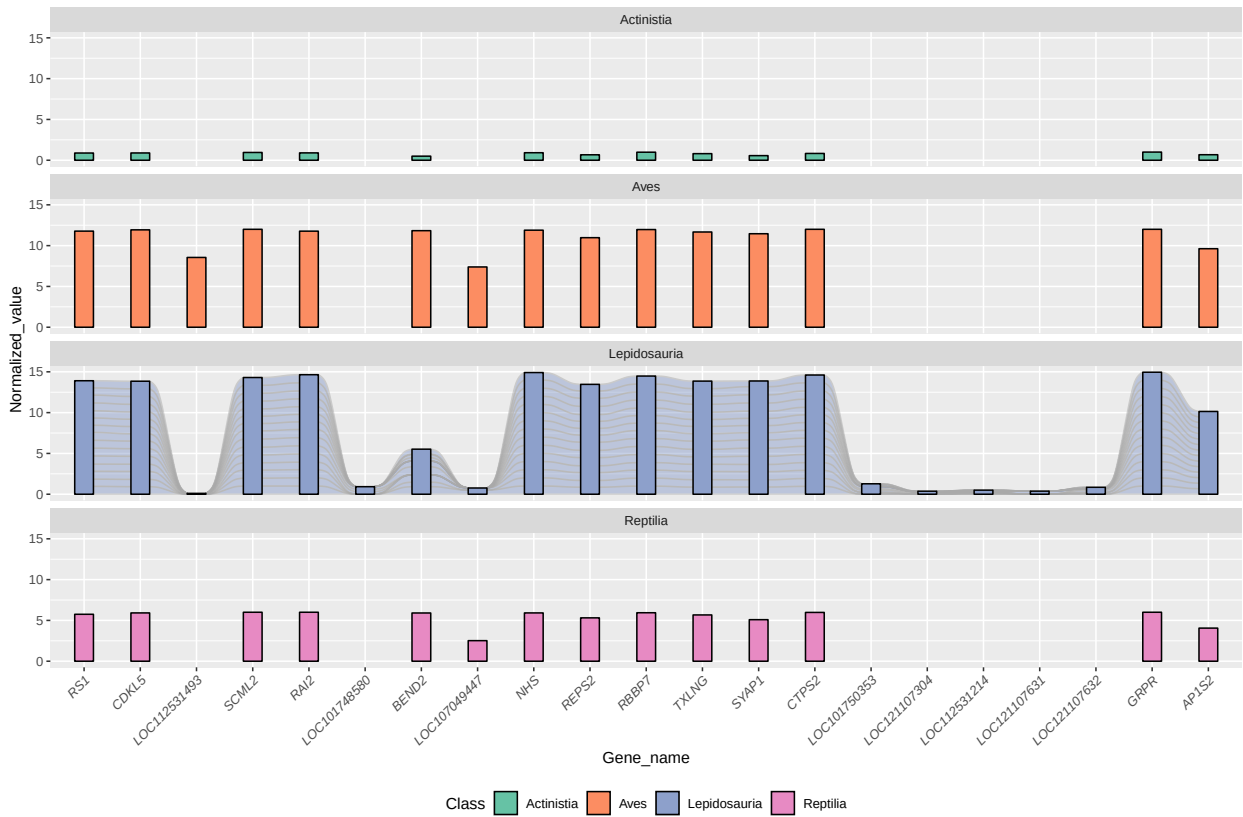


Figure 351: RBBP7.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Lastz gene tree

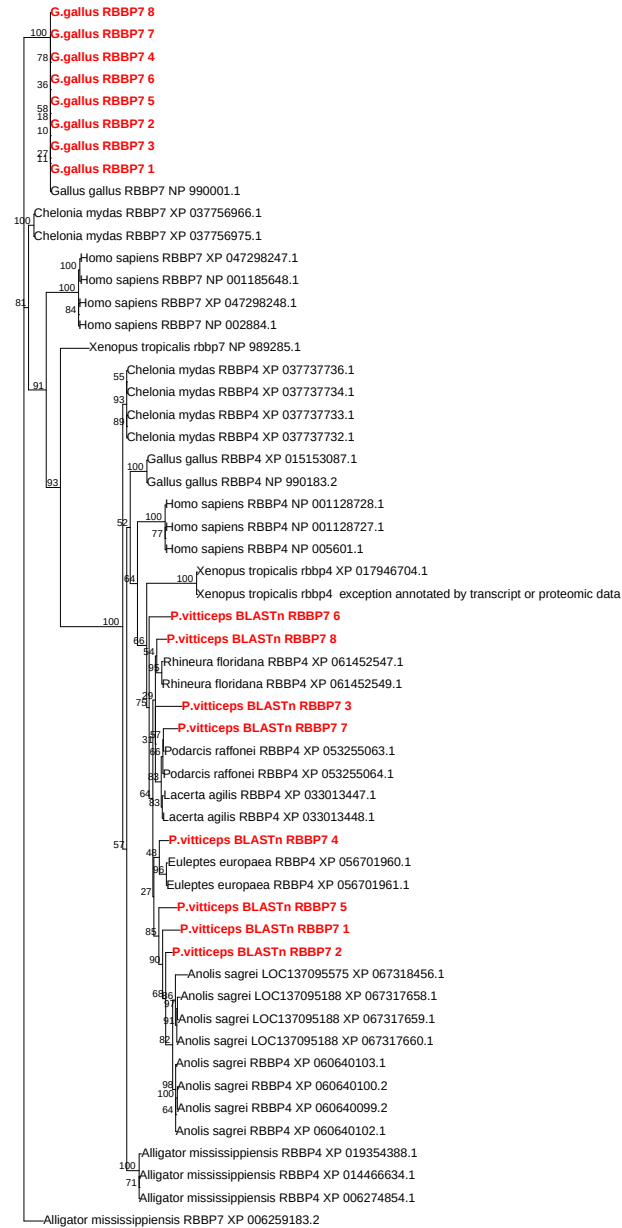


Figure 353: RBBP7.combined.mafft.aln.highlighted.pdf

Syntenic evidence

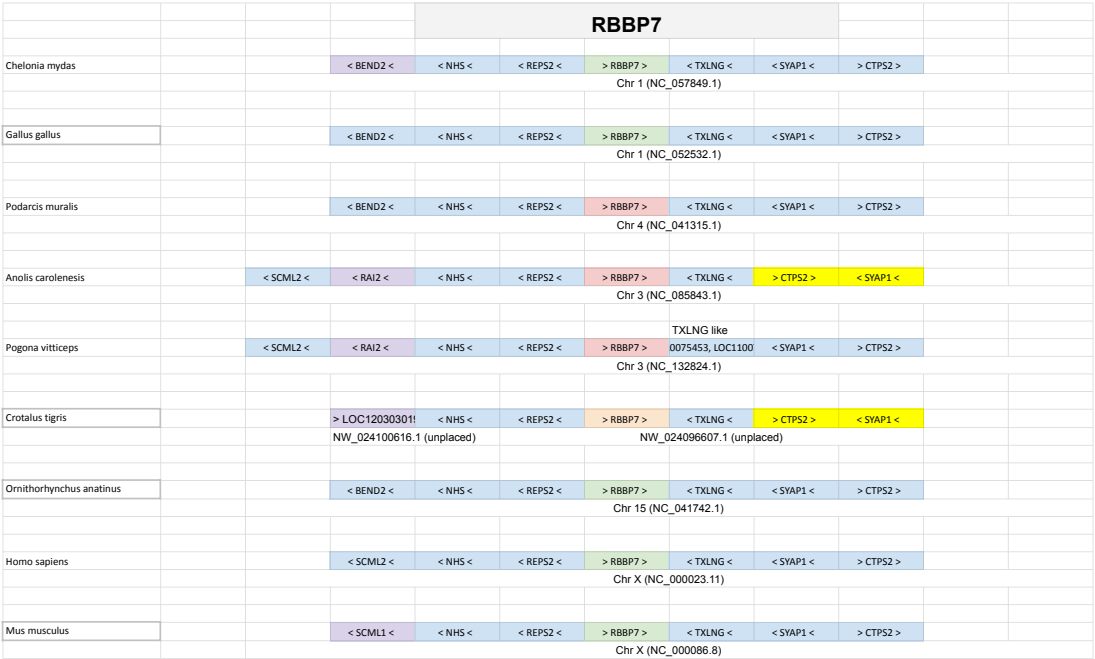


Figure 354: RBBP7.pdf

RBBP7.txt

Synteny analysis of RBBP7

We analyzed the synteny of RBBP7 in squamates and representative outgroups

→ . The RBBP7 syntenic block is largely conserved; however, in

→ Crotalus tigris and Anolis carolinensis, the orientation of the

→ flanking genes CTPS2 and SYAP1 is inverted compared to the conserved

→ pattern. In the synteny plots, red blocks indicate the absence of

→ RBBP7, green blocks mark its presence, light blue blocks represent

→ genes conserved across lineages, and light purple blocks denote

→ flanking genes with altered orientation.

Transcriptomic evidence *Pogona vitticeps*



Figure 355: RBBP7.png

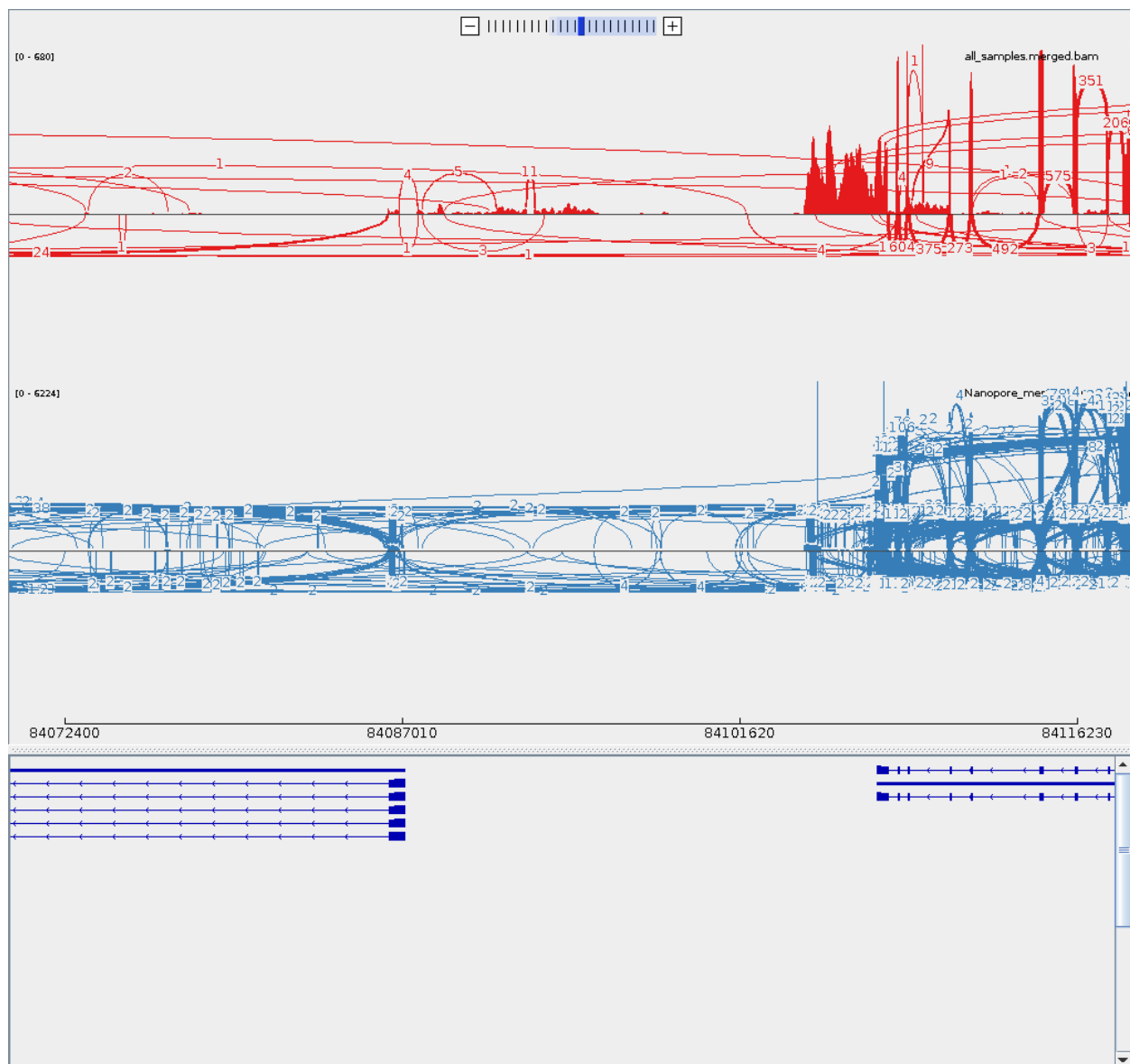


Figure 356: RBBP7_Shash.png

35 RIPPLY3

Assembly verification Evidence

Crotalus_tigris-PacBio

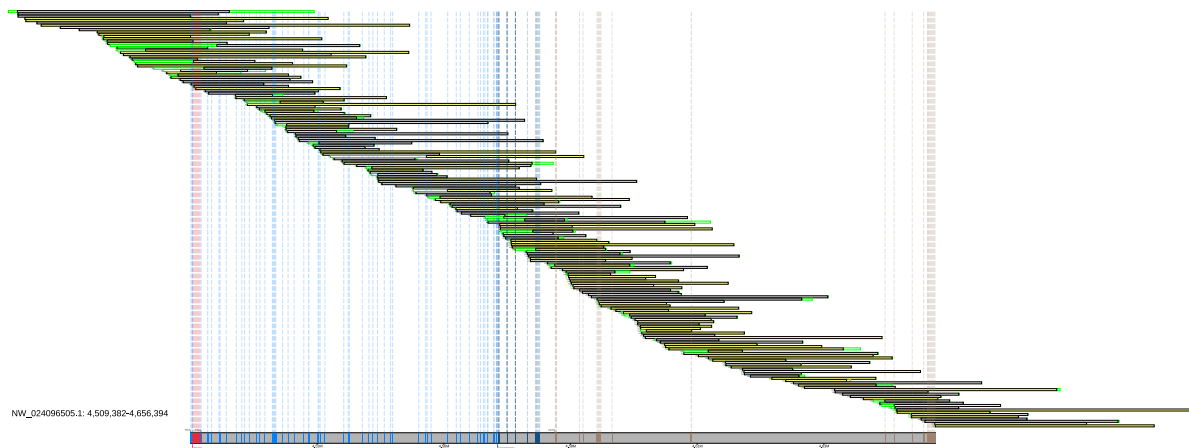


Figure 357: RIPPLY3:NW_024096505.1:4509382-4656394.pdf

Podarcis_muralis-PacBio

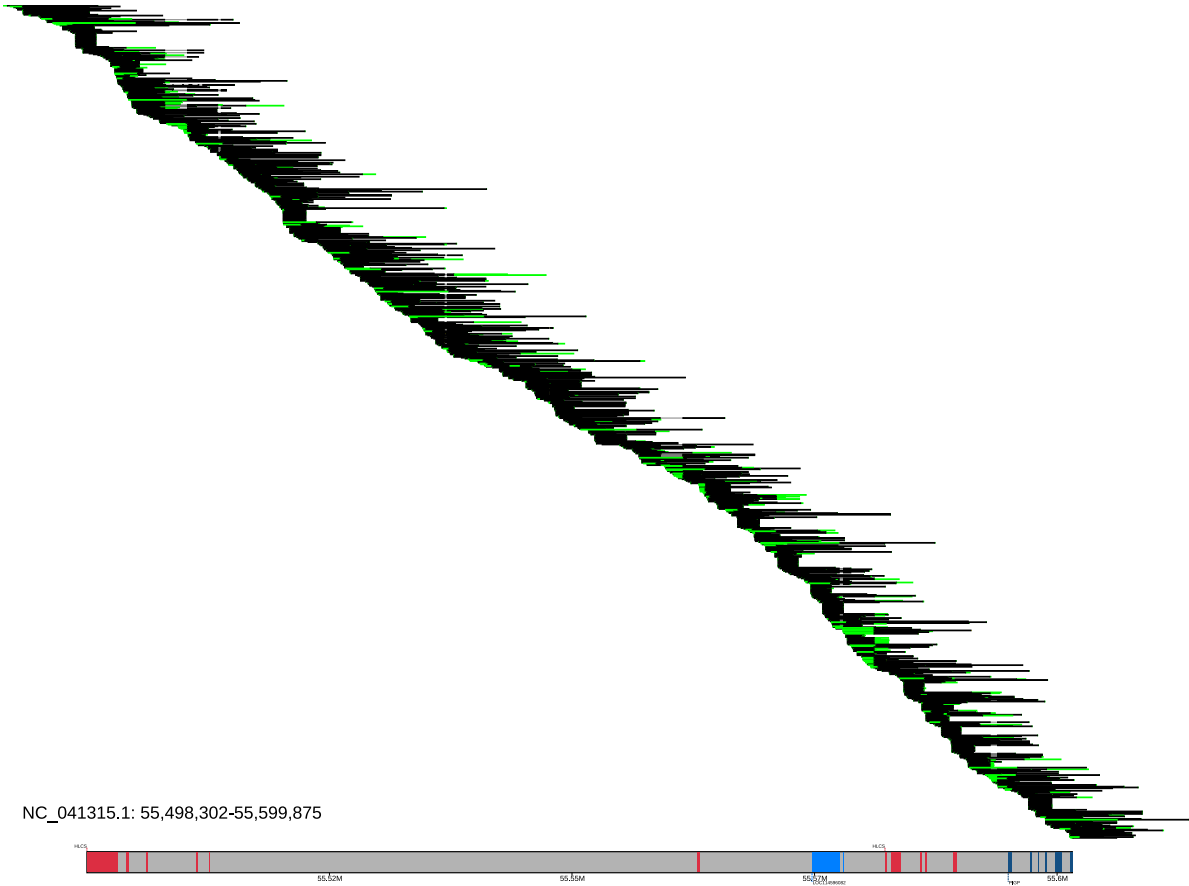


Figure 358: RIPPLY3:NC_041315.1:55498302-55599875.pdf

Pogona_vitticeps-Nanopore

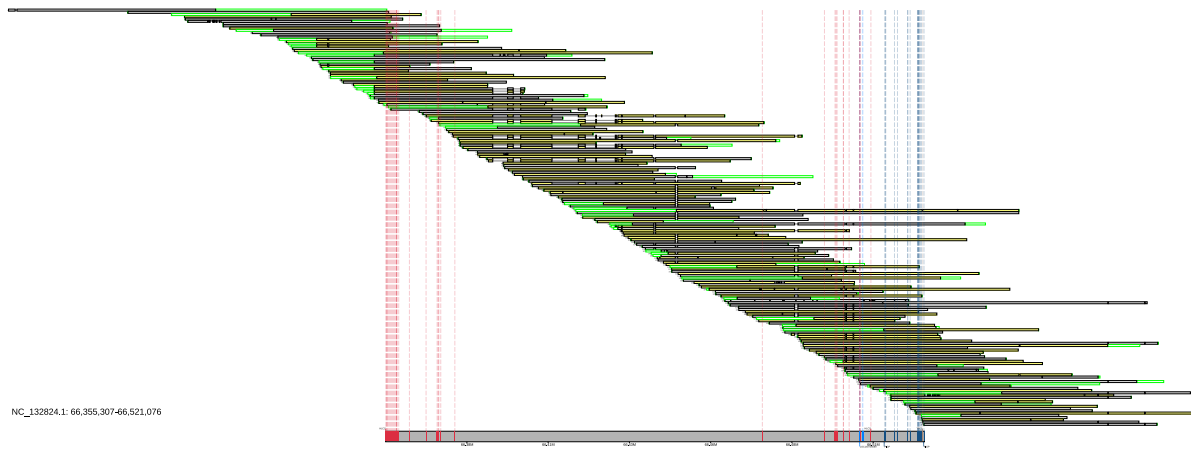


Figure 359: RIPPLY3:NC_132824.1:66355307-66521076.pdf

Important gene stats

RIPPLY3_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
RIPPLY3	6.870967742	56.0599 +/- 7.05223	4.35468 +/- 0.706374	54.4033 +/- 17.1297	No	Na

Intergenic distance phylogenetic signal evidence

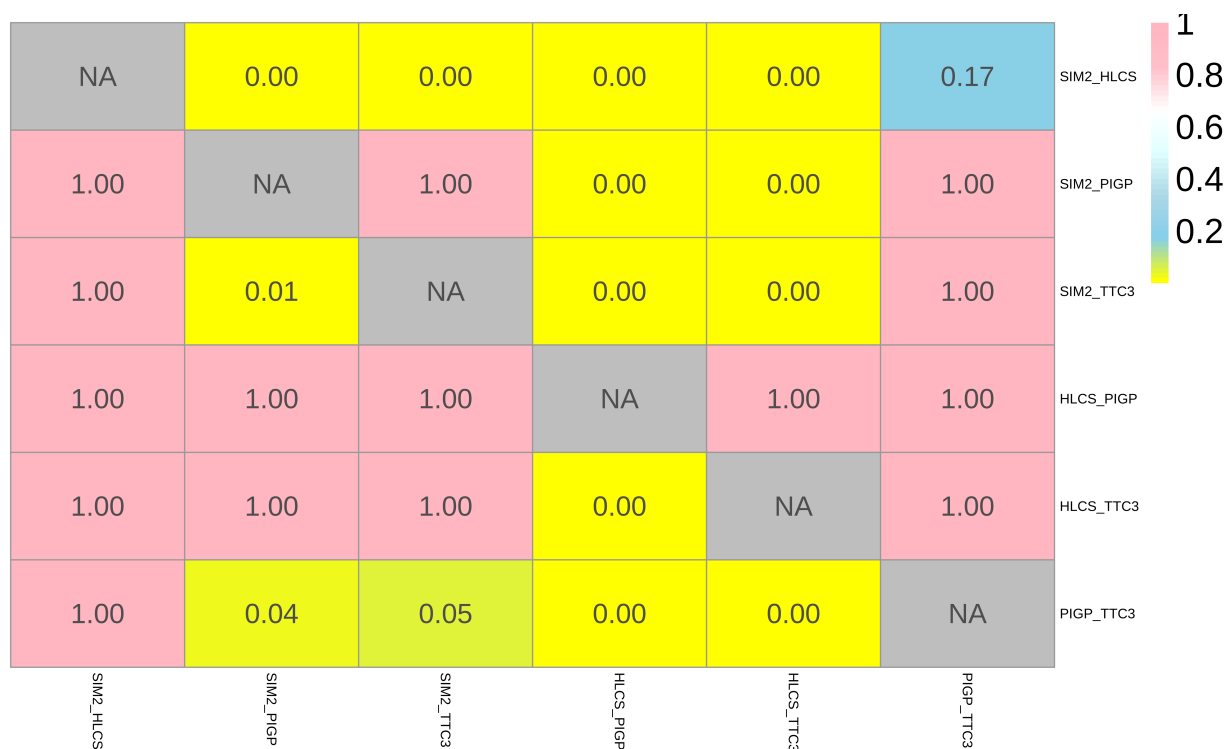


Figure 360: Heatmap_of_deletion_plot.png

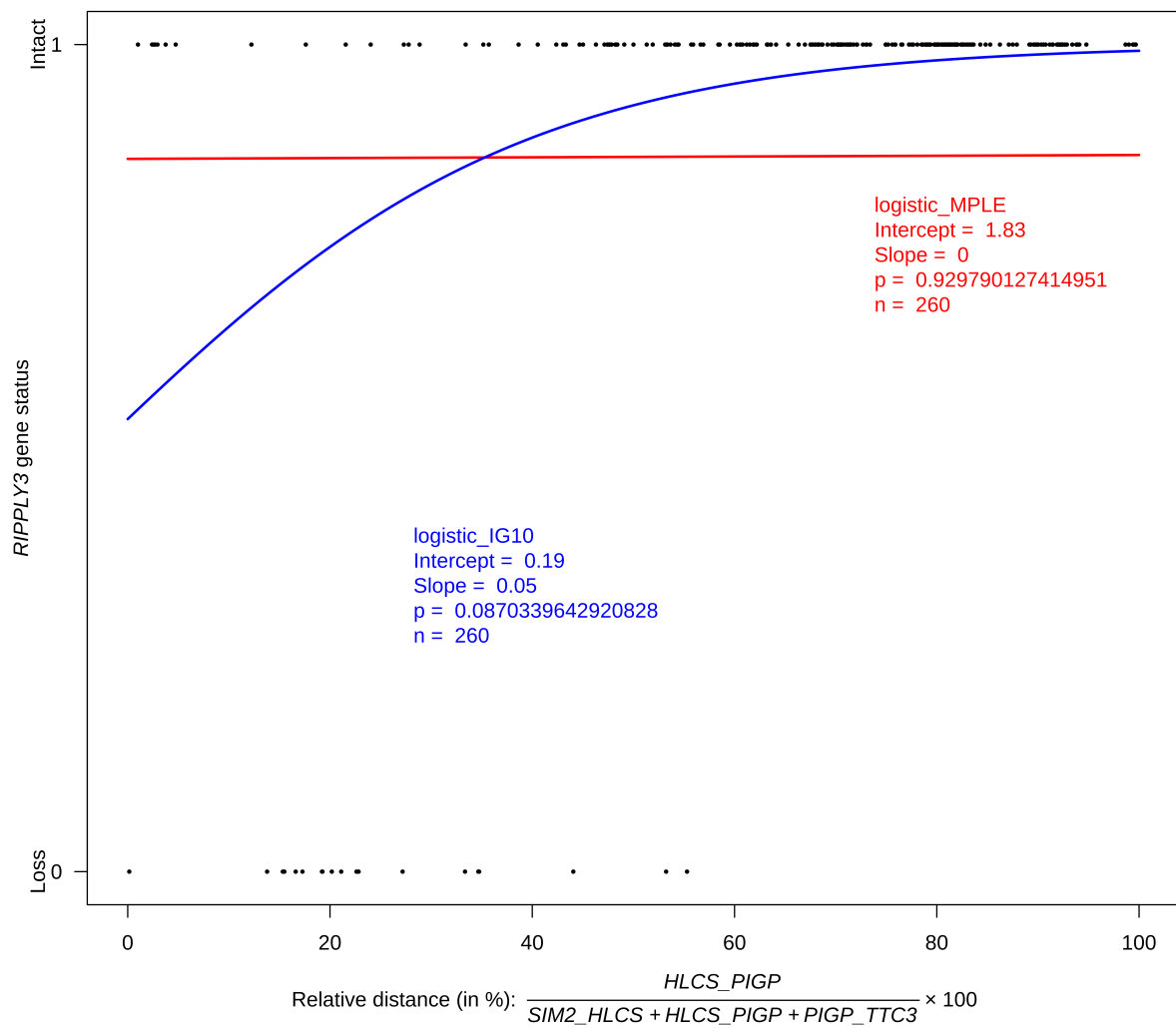


Figure 361: Phylogenetic_signal_of_deletion_plot.png

RIPPLY3_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
RIPPLY3	260	19	241	5	0.0870339642920828	0.929790127414951

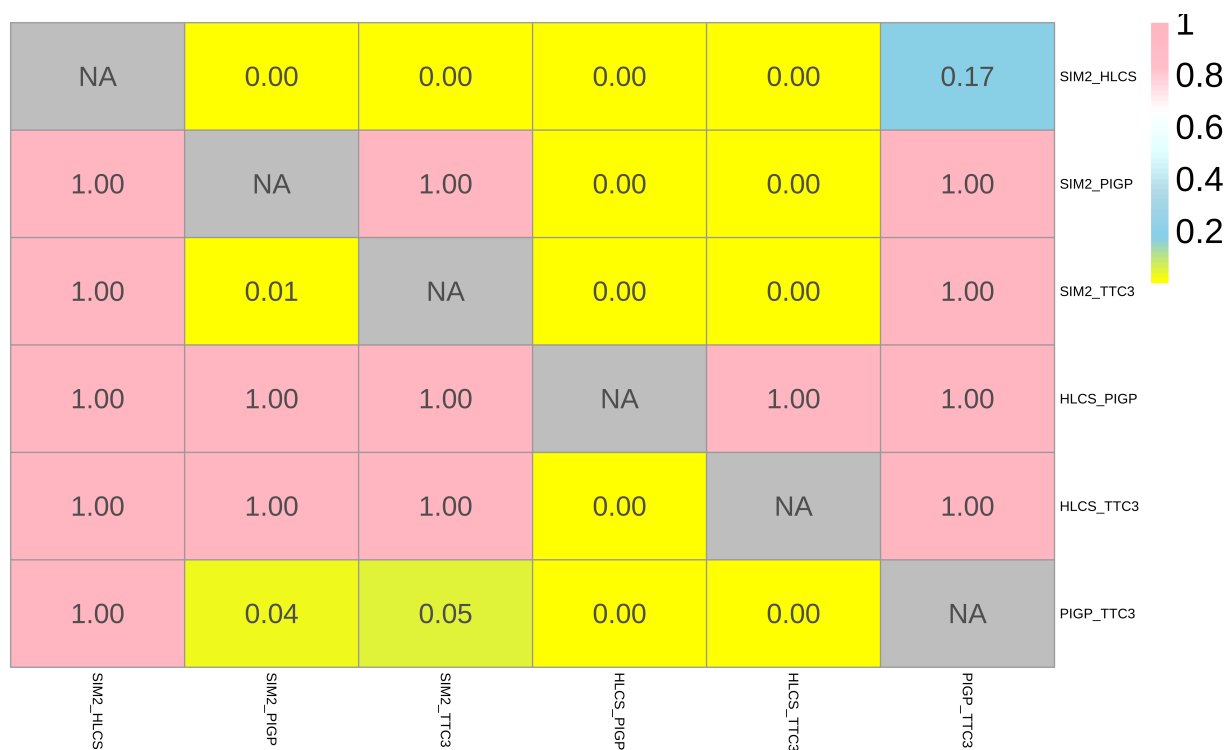


Figure 362: Heatmap_of_deletion_plot.png

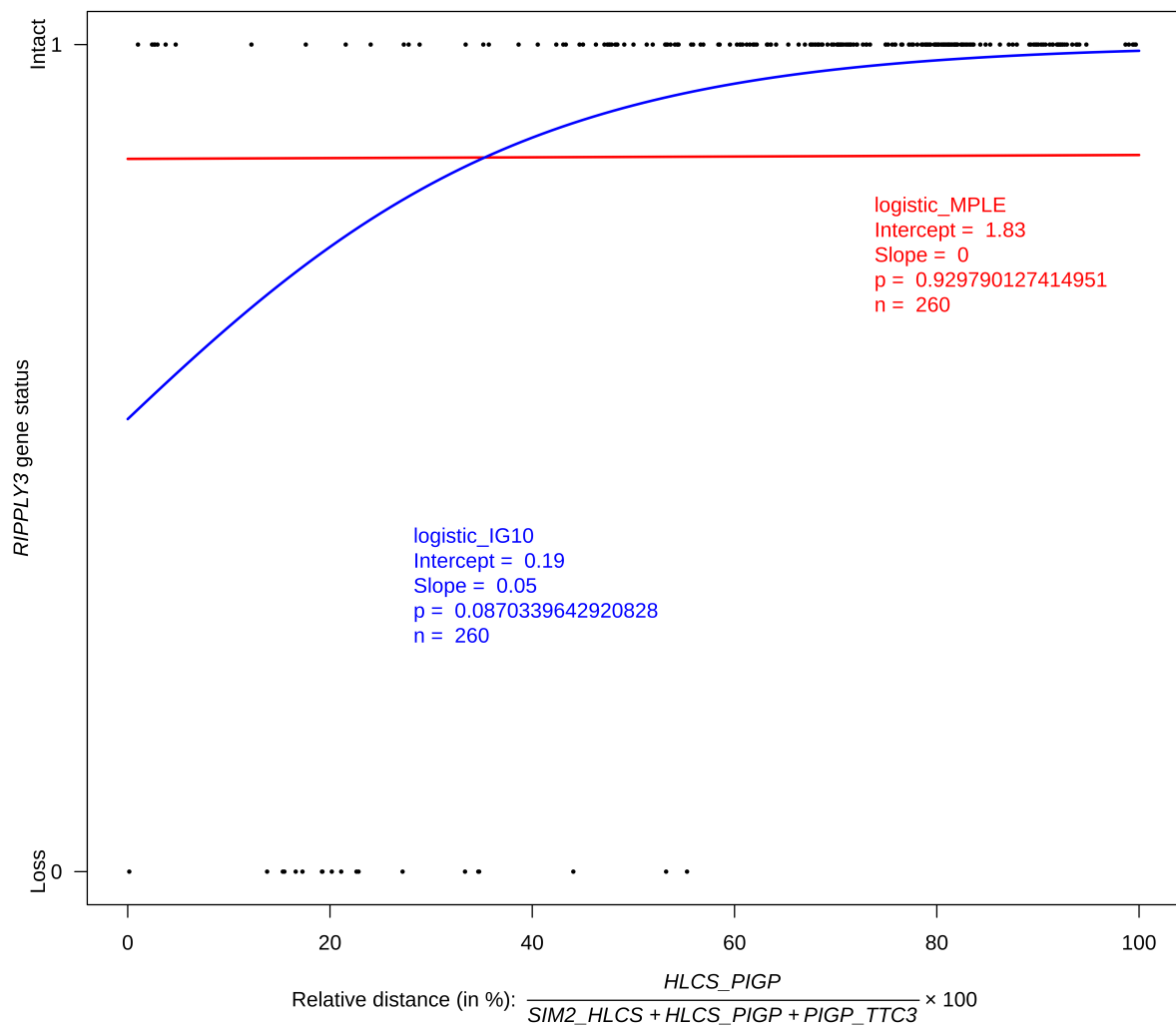


Figure 363: Phylogenetic_signal_of_deletion_plot.png

RIPPLY3_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
RIPPLY3	260	19	241	5	0.0870339642920828	0.929790127414951

Lastz Alignment evidence

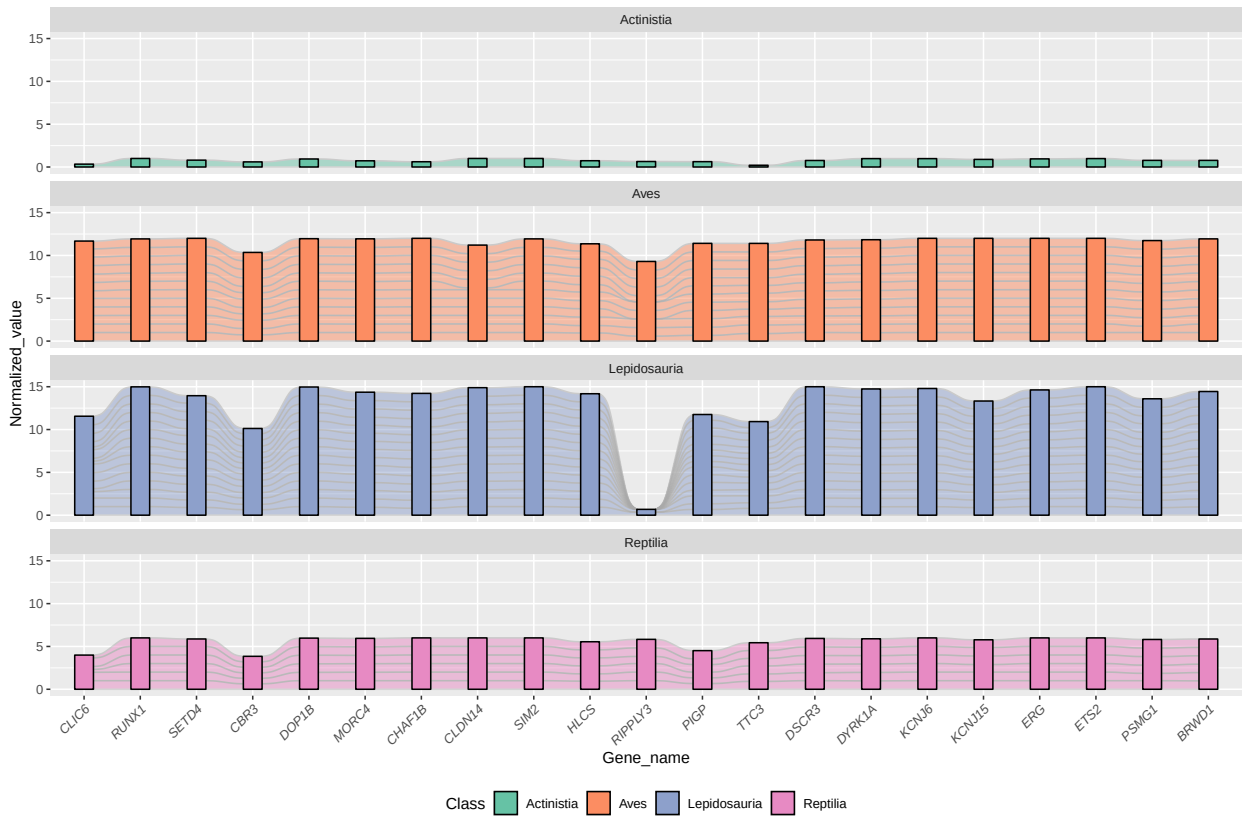


Figure 364: RIPPLY3.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

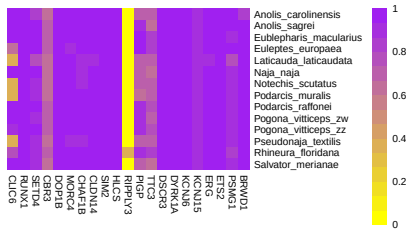


Figure 365: RIPPLY3.FS_Exonic.Final.Gallus_gallus.21_genes_heatmap.pdf

Syntenic evidence



Figure 366: RIPPLY3.pdf

RIPPLY3.txt

Synteny analysis of RIPPLY3

We analyzed the synteny of RIPPLY3 in squamates and representative outgroups. The RIPPLY3 syntenic block is conserved, with the exception of one flanking side in Ornithorhynchus anatinus. The expected flanking arrangement < CLDN14 < > SIM2 > < HLCS < is present on chromosome 17 (NC_041744.1) In the synteny plots, red blocks indicate the absence of RIPPLY3, green blocks mark its presence, light blue blocks represent genes conserved flank genes across lineages, and light purple blocks denote flanking genes with altered arrangement or orientation.

Transcriptomic evidence *Pogona vitticeps*

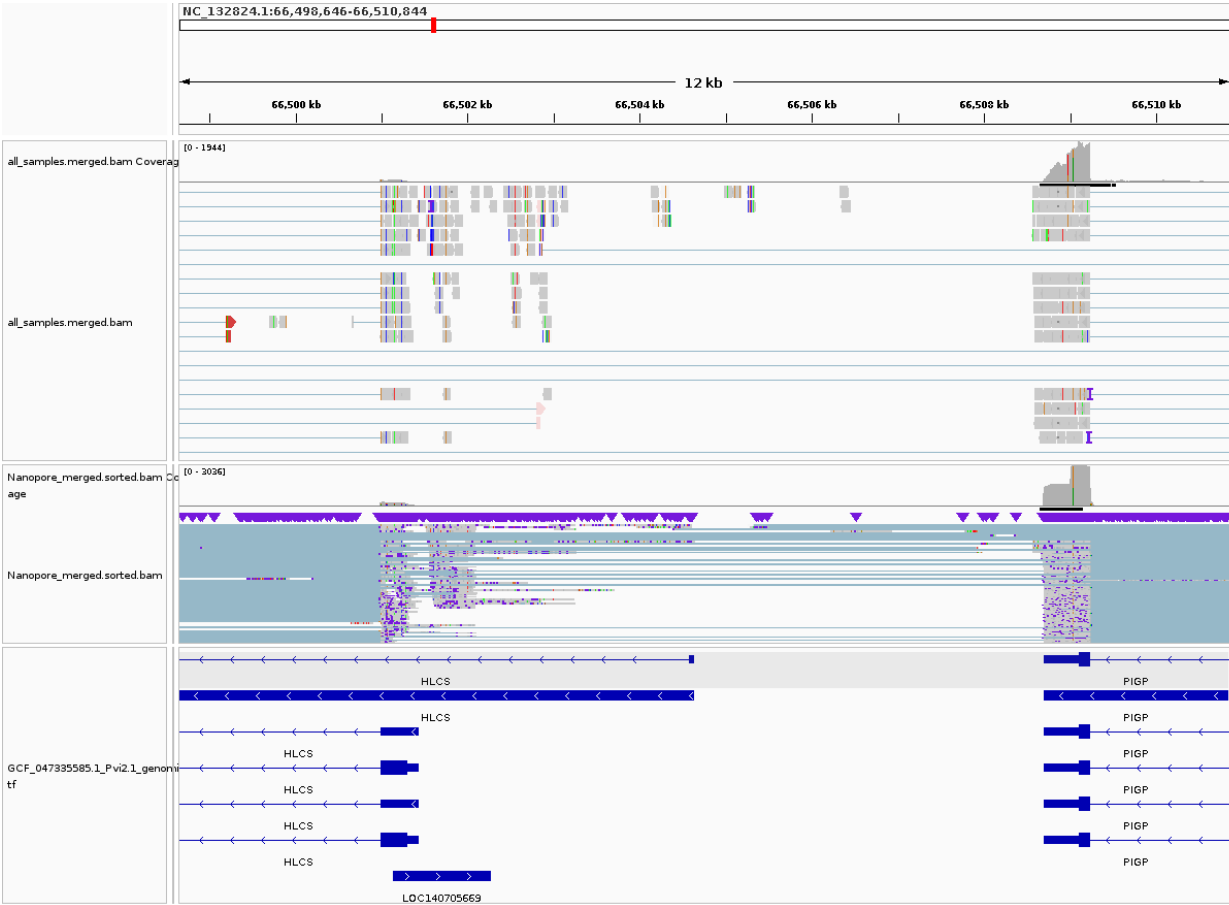


Figure 367: RIPPLY3.png

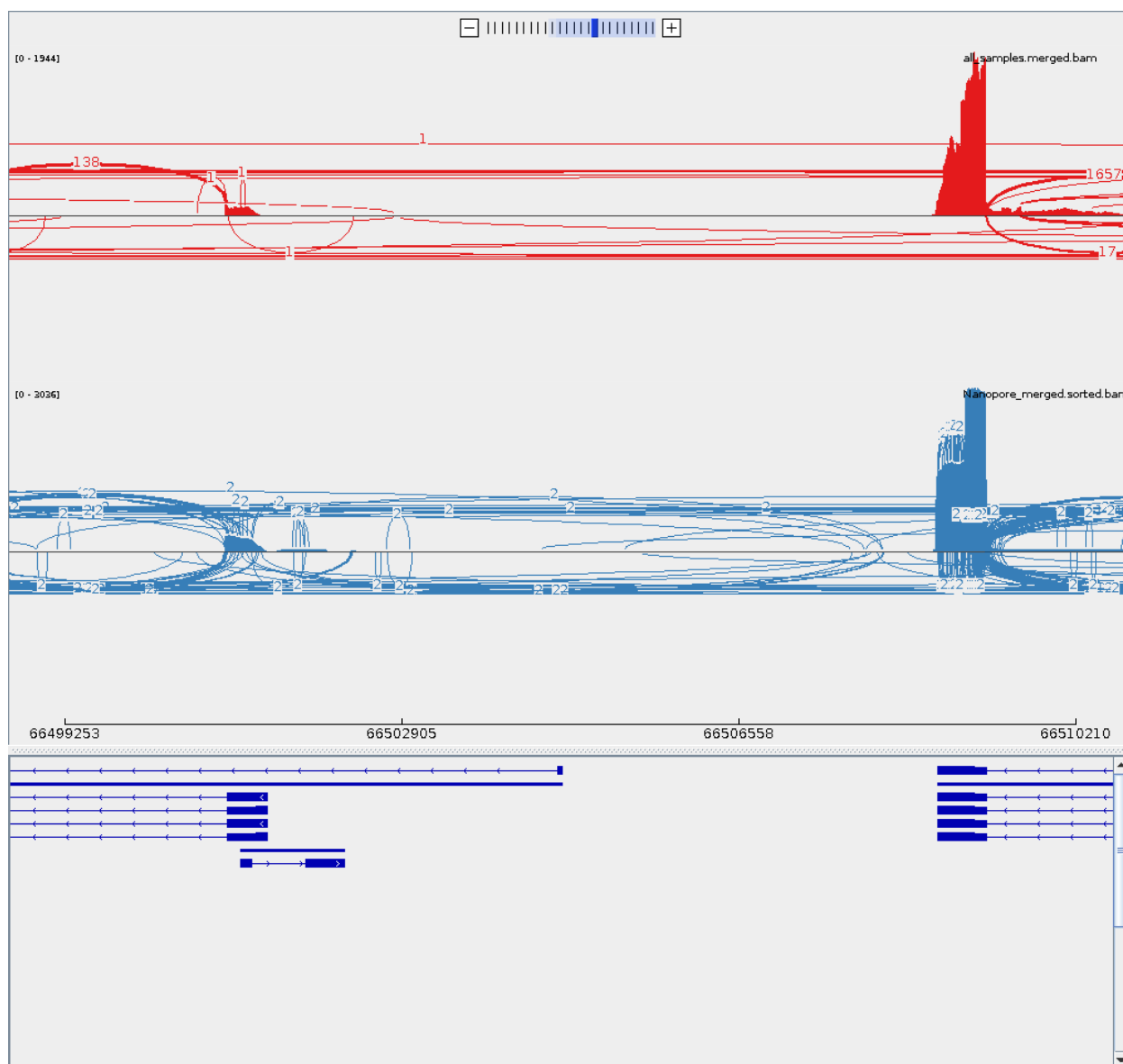


Figure 368: RIPPLY3_Sashimi.png

36 RUBCNL

Important gene stats

RUBCNL_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
RUBCNL	8.36	49.8711 +/- 4.09322	3.68856 +/- 0.235255	62.0166 +/- 15.1042	No	RUBCN;

Lastz Alignment evidence

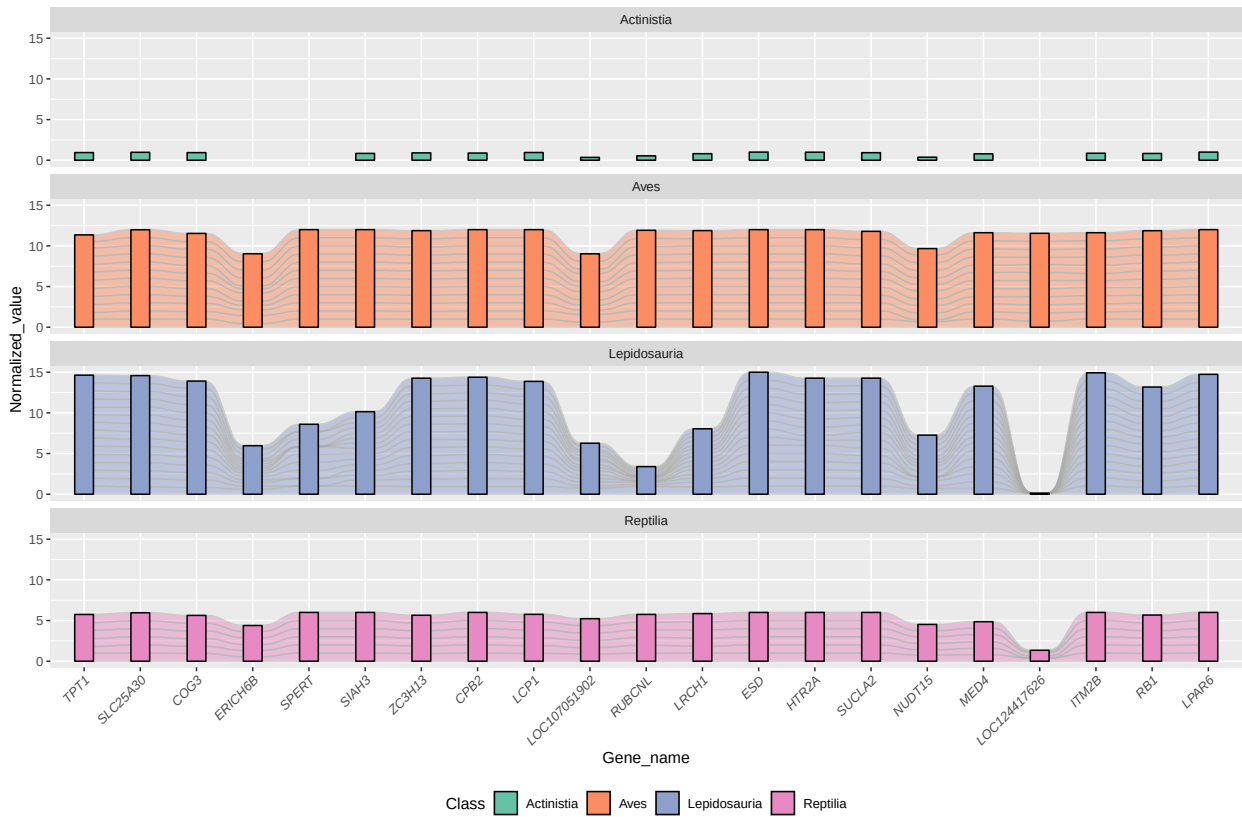


Figure 369: RUBCNL.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf



Figure 370: RUBCNL.FS_Exonic.Final.Gallus_gallus.21_genes_heatmap.pdf

Lastz gene tree

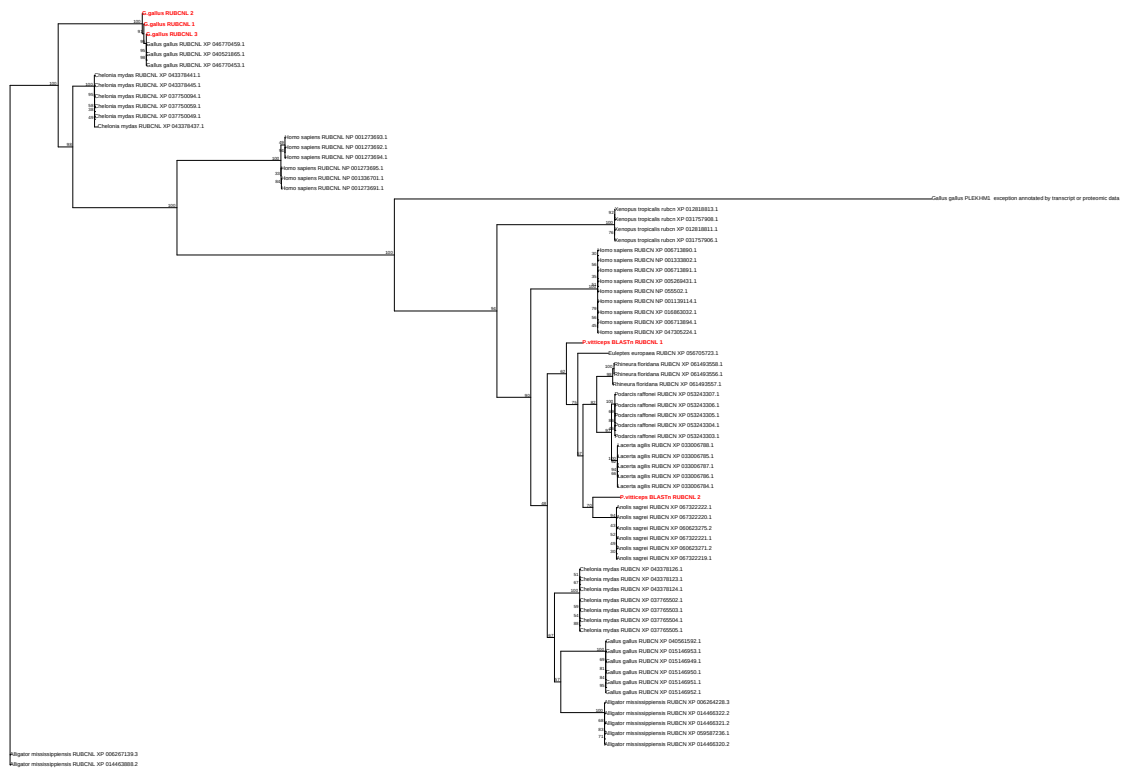


Figure 371: RUBCNL.combined.mafft.aln.highlighted.pdf

Syntenic evidence

	SIAH3, LCP1, LRCH1, RUBCNL																		
Chelonia mydas	> SUCIA2 >	< LOC11996020 >	> HTR2A >	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	> CPB2 >	> ZC3H13 >	> SIAH3 >	< CBP2 <	> ERICHBB >	< COG3 <					
	Chr 1 (NC_007948.1)																		
Gallus gallus	> SUCIA2 >	> HTR2A >	> ESD >	< LRCH1 <	> RUBCNL >	< LOC10050802 <	> LCP1 >	> CPB2 >	> ZC3H13 >	> SIAH3 >	< SIRT1 <								
	NC_023322.1																		
Podarcis muralis	> SUCIA2 >	< NPLRC3 <	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	> CPB2 >	< ZC3H13 <	> SIAH3 >	< COG3 <	< SIRT1 <	# same chromosome but on another side after skipping two genes						
	Chr 1 (NC_041311.1) Chr 3 (NC_041314.1) Chr 5 (NC_041316.1)																		
Anolis carolinensis	> SUCIA2 >	> HTR2A >	< NPLRC3 <	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	< p981 <	< sp9824 <	< drap18 <	> z3h13 >	< CPB2 <	> SIAH3 >	< COG3 <	< drap1 <	> ERICHBB >		
	Chr 1 (NC_085841.1) Chr 1 (NC_085841.1) Chr 1 (NC_128222.1) Chr 3 (NC_128224.1)																		
Pogona vitticeps	> SUCIA2 >	> HTR2A >	< NPLRC3 <	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	< p981 <	< sp9824 <	< drap18 <	> z3h13 >	< CPB2 <	> SIAH3 >	> z3h1 >	< sirt1 <	# same chromosome but after skipping genes		
	Chr 1 (NC_128222.1) Chr 1 (NC_128222.1) Chr 3 (NC_128224.1)																		
Crotalus tigris	> SUCIA2 >	> HTR2A >	< NPLRC3 <	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	< p981 <	< sp9824 <	< drap18 <	> z3h13 >	< CPB2 <	> SIAH3 >	< COG3 <	> ERICHBB >			
	NW_024007046.1 (unplaced) NW_024007046.1 (unplaced) NW_024008059.1 (unplaced) NW_024008059.1 (unplaced)																		
Oreodonhrychus sinuatus	> SUCIA2 >	< LOC103170481 >	> HTR2A >	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	> CPB2 >	> ZC3H13 >	> SIAH3 >	> ERICHBB >	< COG3 <						
	Chr 20 (NC_041747.1)																		
Homo sapiens	> SUCIA2 >	> HTR2A >	< HTR2A-AS1 <	> ESD >	< LRCH1 <	< FBXP5AF3 <	> UNCG0388 >	> RUBCNL >	< LRRC63 <	> LOC107884571 >	> LCP1 >	> CPB2 >	< CPB2-AS1 <	> ZC3H13 >	< LOC10370391 <	> SIAH3 >	< CPB2 <	> ERICHBB >	< COG3 <
	Chr 13 (NC_000313.12)																		
Mus musculus	> SUCIA2 >	< Gm41210 <	> HTR2A >	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	> CPB2 >	< Gm35679 <	> ZC3H13 >	< Gm41212 <	> SIAH3 >	< CPB2 <	< Gm35219 <	> ERICHBB >	< COG3 <		

Figure 372: RUBCNL.pdf

RUBCNL.txt

Synteny analysis of RUBCNL

The syntenic block for

RUBCNL shows evidence of both interchromosomal and intrachromosomal

→ rearrangements within squamates. In species such as

Anolis carolinensis and *Pogona vitticeps*, the flanking genes are located

→ on two different chromosomes, indicating a break in syntenly.

→ Furthermore, in lizards like

Podarcis muralis, the block appears to have also undergone an

→ intrachromosomal rearrangement, with flanking genes repositioned to

→ a different location on the same chromosome after skipping several

↪ intervening genes. The block is highly fragmented in the snake
Crotalus tigris, with genes located on multiple unplaced scaffolds.

In the synteny plots, red blocks indicate the absence of the target gene,
↪ while green blocks mark its presence. Light blue blocks represent
↪ flanking genes that are conserved across lineages, and light purple
↪ blocks denote instances where a different flanking gene is present.

37 SH2D1A

Important gene stats

SH2D1A_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
SH2D1A	17.50675676	52.2995 +/- 5.19917	3.89495 +/- 0.359204	74.7435 +/- 16.7247	Yes	Na

Intergenic distance phylogenetic signal evidence

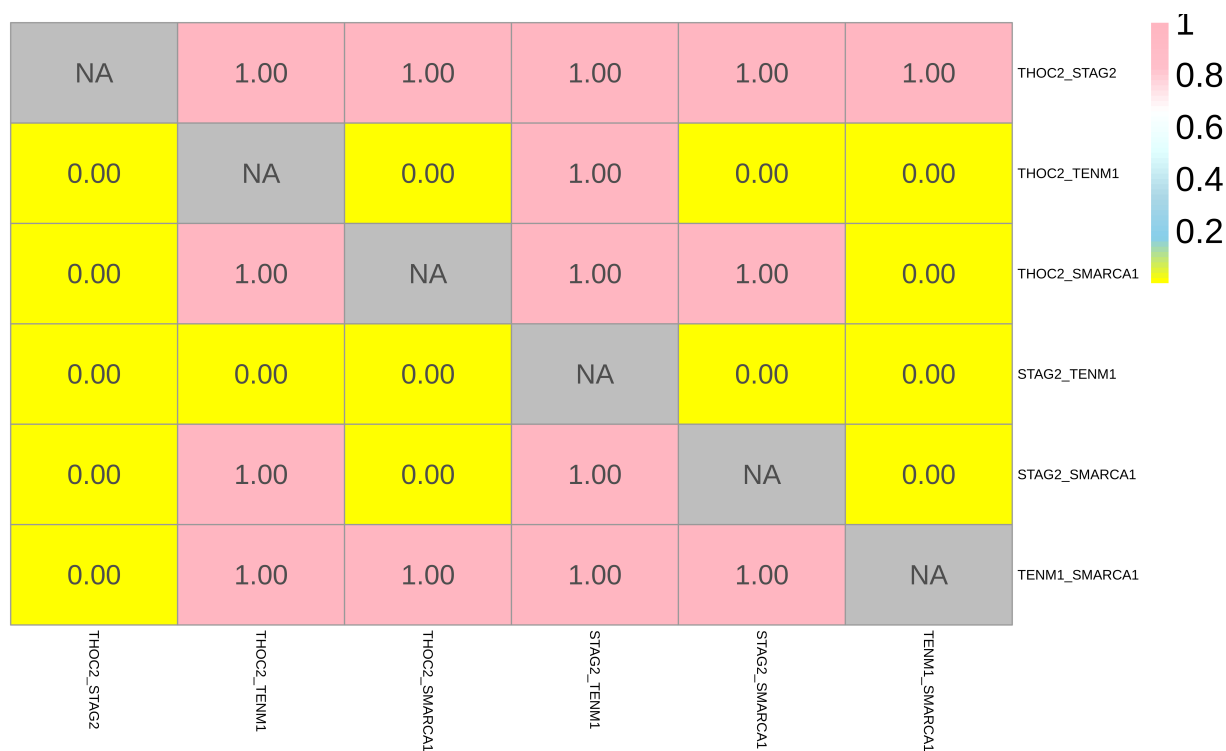


Figure 373: Heatmap_of_deletion_plot.png

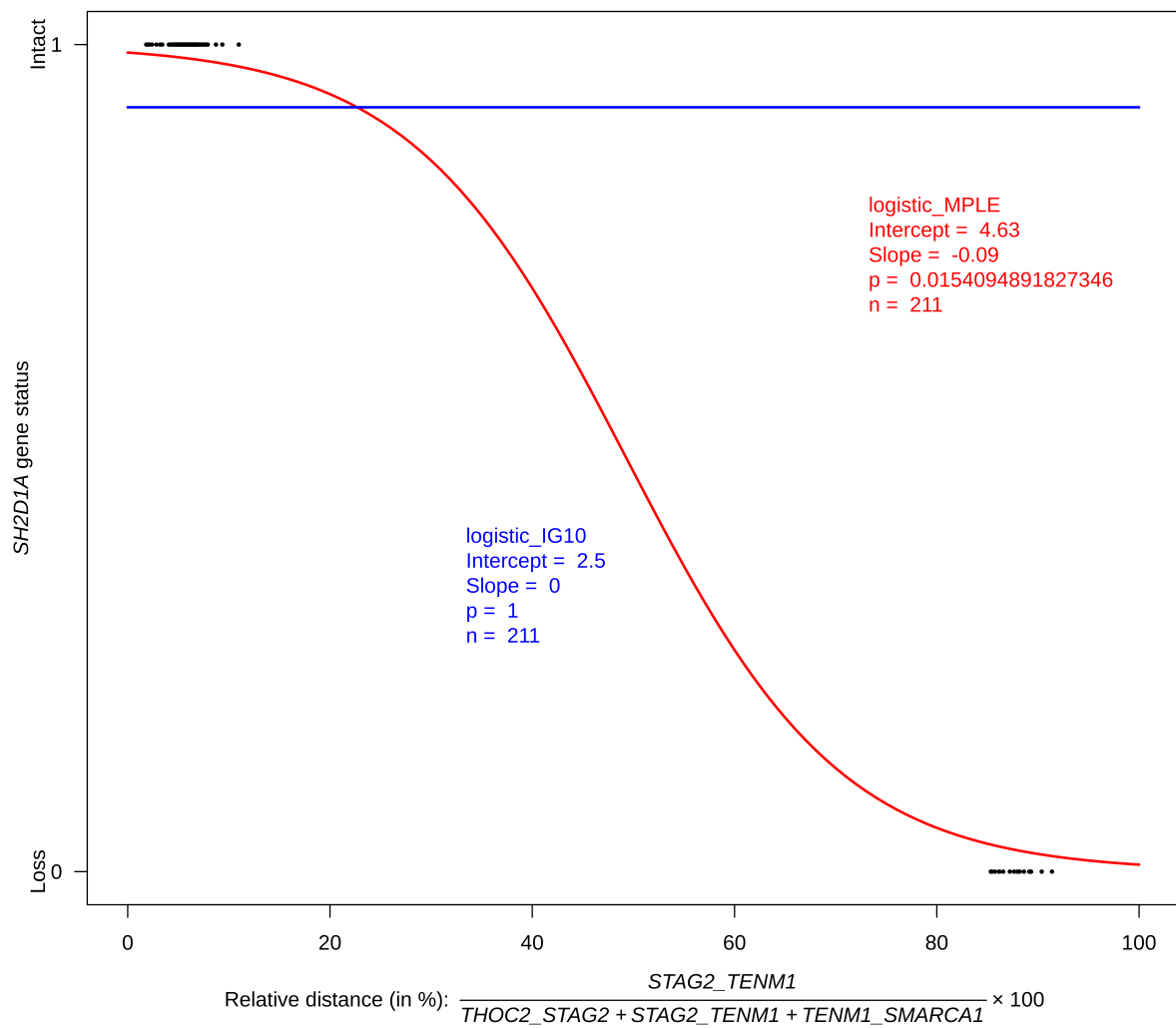


Figure 374: Phylogenetic_signal_of_deletion_plot.png

SH2D1A_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
SH2D1A	211	16	195	0	1	0.0154094891827346

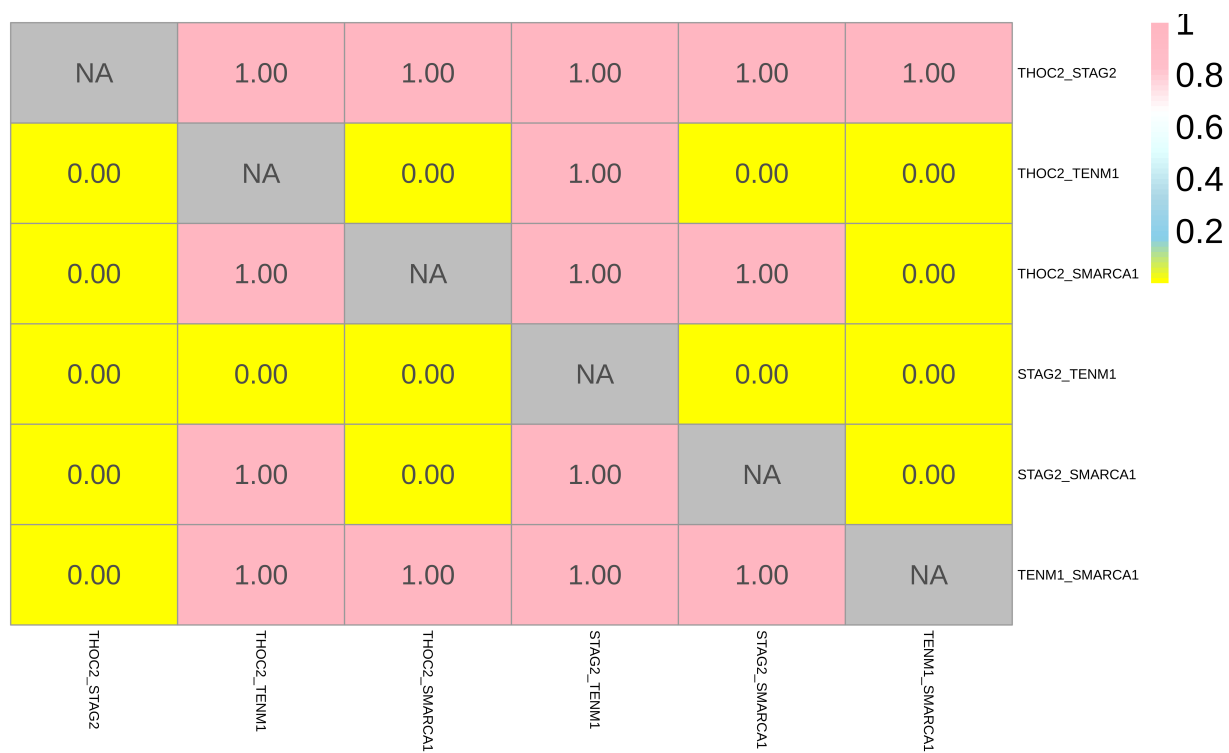


Figure 375: Heatmap_of_deletion_plot.png

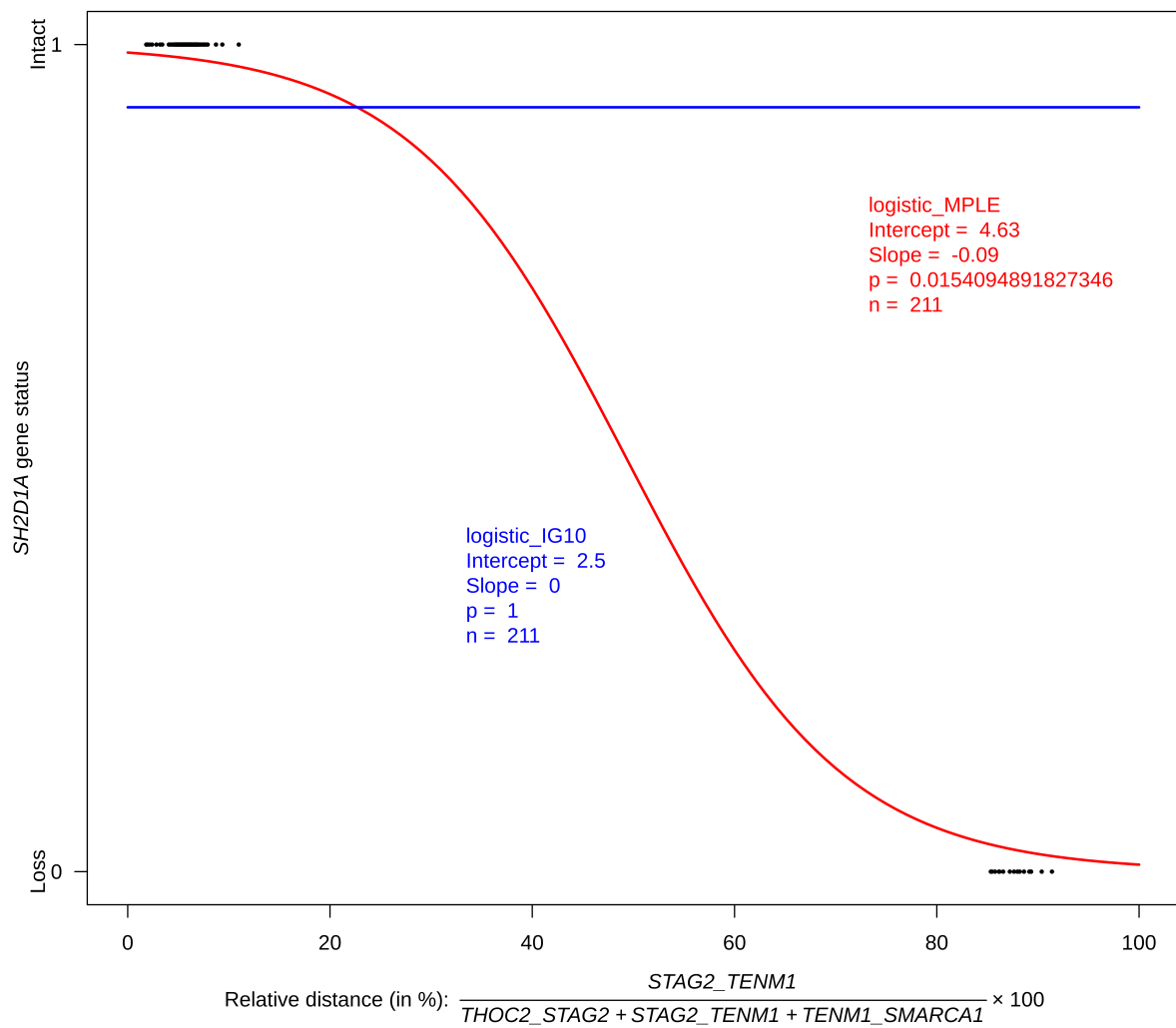


Figure 376: Phylogenetic_signal_of_deletion_plot.png

SH2D1A_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
SH2D1A	211	16	195	0	1	0.0154094891827346

Lastz Alignment evidence

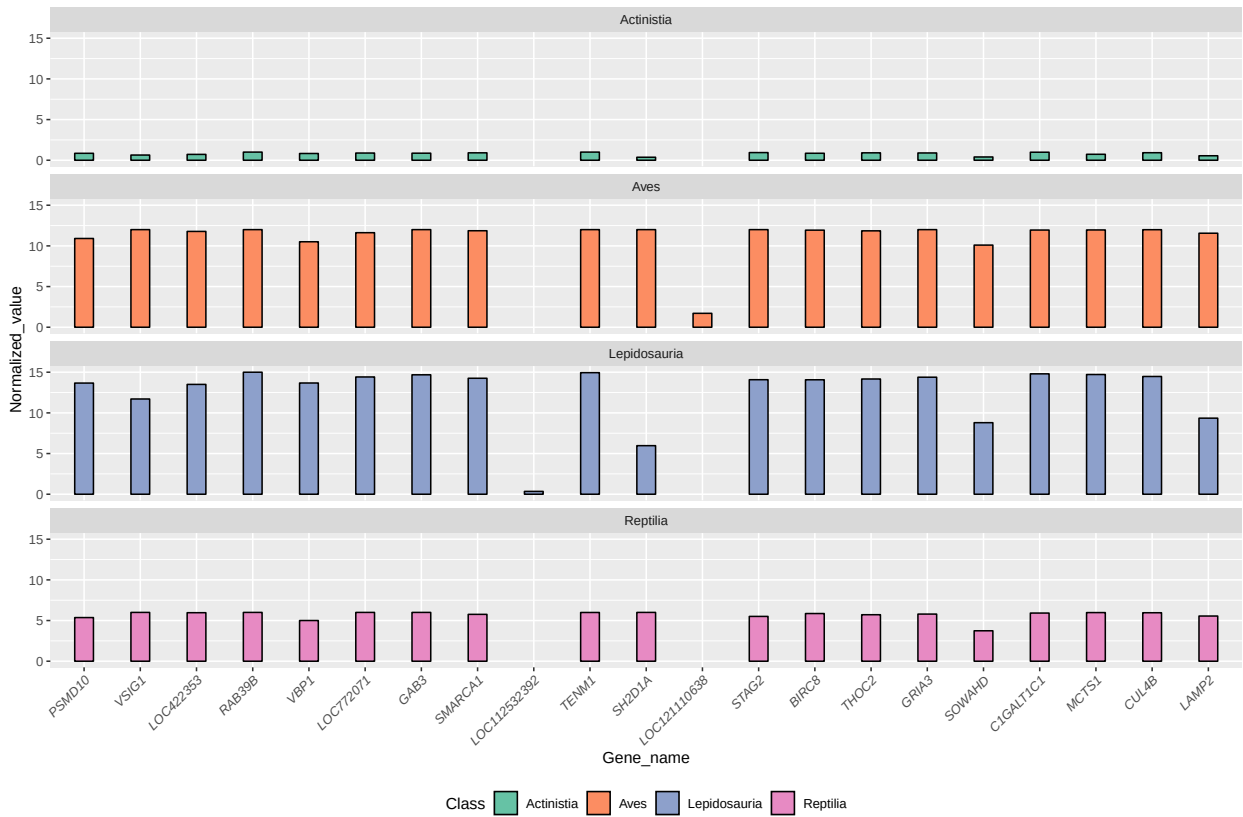


Figure 377: SH2D1A.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf



Lastz gene tree

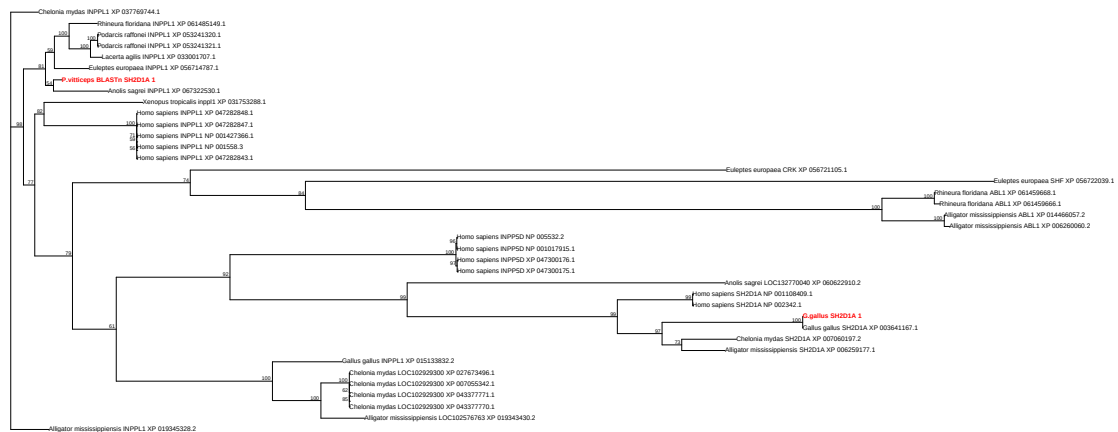


Figure 379: SH2D1A.combined.mafft.aln.highlighted.pdf

Syntenic evidence

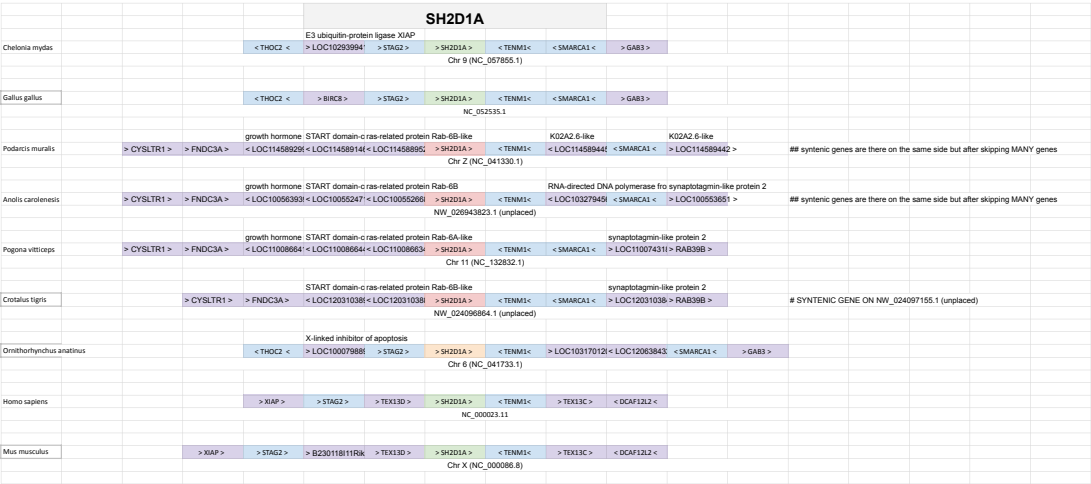


Figure 380: SH2D1A.pdf

SH2D1A.txt

Synteny analysis of SH2D1A

The SH2D1A syntenic block, which is relatively conserved in outgroups like
→ turtles and birds, shows evidence of intra chromosomal
→ rearrangements in squamates. In multiple lizard lineages, including
Podarcis muralis and Anolis carolinensis, the syntenic genes have been
→ transposed to a new location on the same chromosome after skipping a
→ large number of intervening genes. The rearrangement in the snake
Crotalus tigris, where the syntenic block has been fragmented across at
→ least two different unplaced scaffolds.

In the synteny plots, red blocks indicate the absence of the target gene,
→ while green blocks mark its presence. Light blue blocks represent
→ flanking genes that are conserved across lineages, and light purple
→ blocks denote instances where a different flanking gene is present.
→ A bright yellow color indicates a change in the gene's orientation.

38 SH2D2A

Assembly verification Evidence

Crotalus_tigris-PacBio

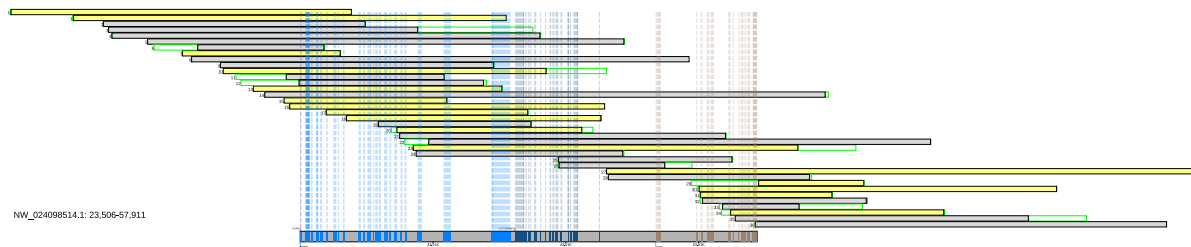


Figure 381: SH2D2A:NW_024098514.1:23506-57911.pdf

Podarcis_muralis-PacBio

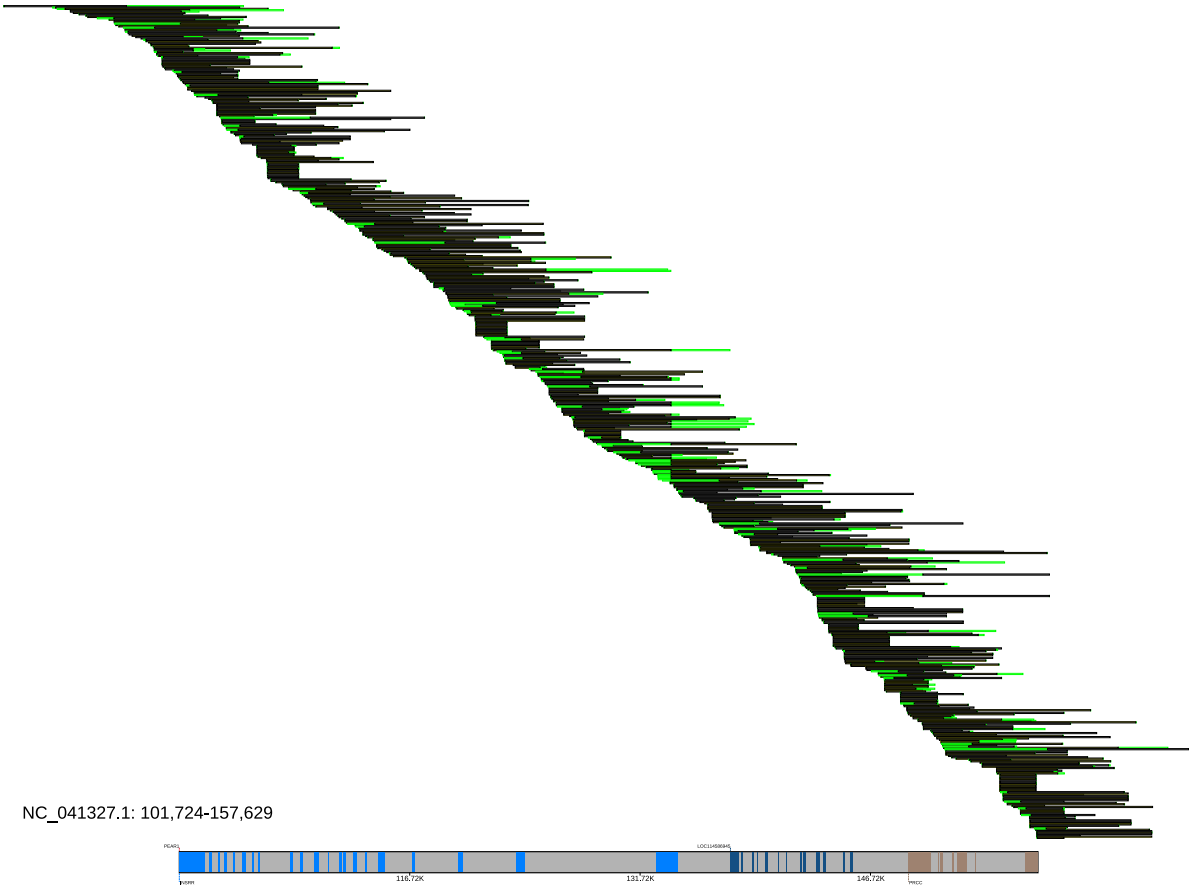


Figure 382: SH2D2A:NC_041327.1:101724-157629.pdf

Pogona_vitticeps-Nanopore

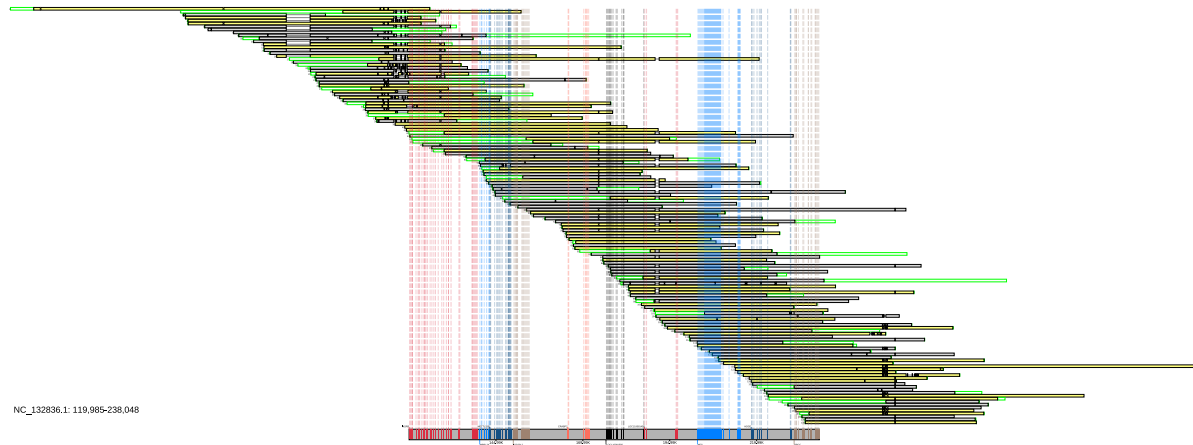


Figure 383: SH2D2A:NC_132836.1:119985-238048.pdf

Important gene stats

SH2D2A_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
SH2D2A	3.837837838	64.47 +/- 5.22718	4.48034 +/- 0.409953	63.5671 +/- 15.2581	Yes	Na

Intergenic distance phylogenetic signal evidence

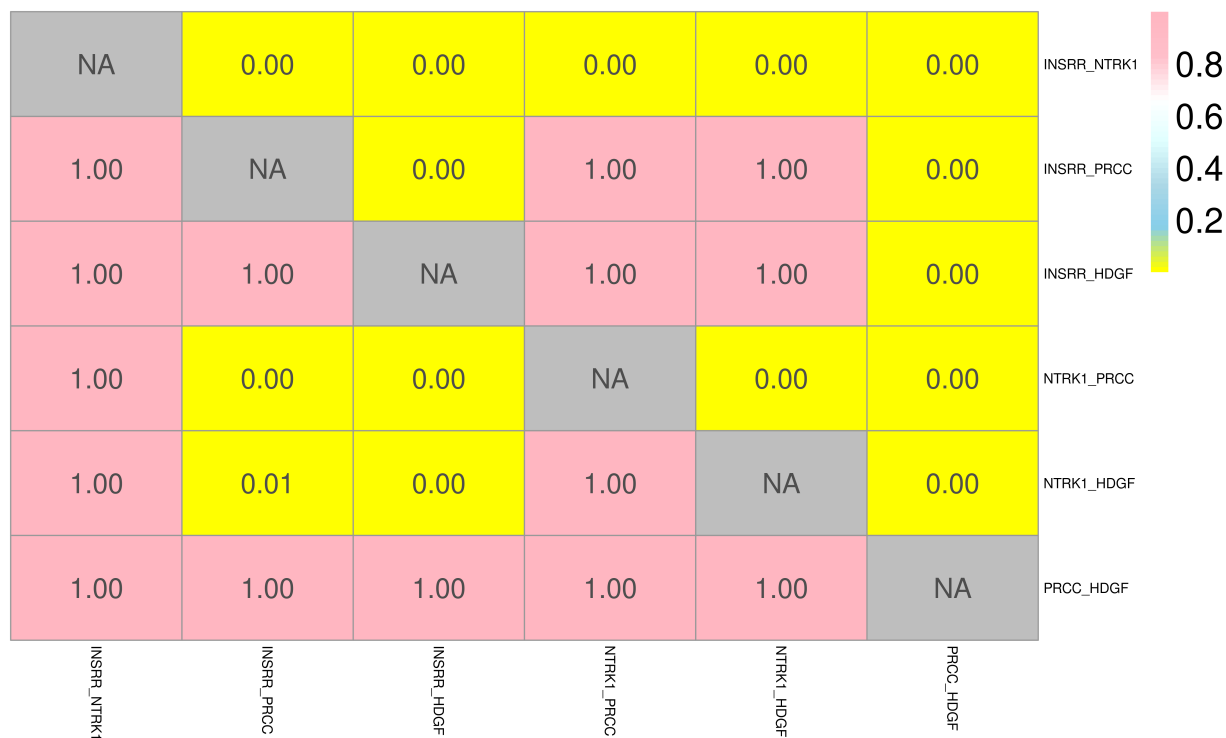


Figure 384: Heatmap_of_deletion_plot.png

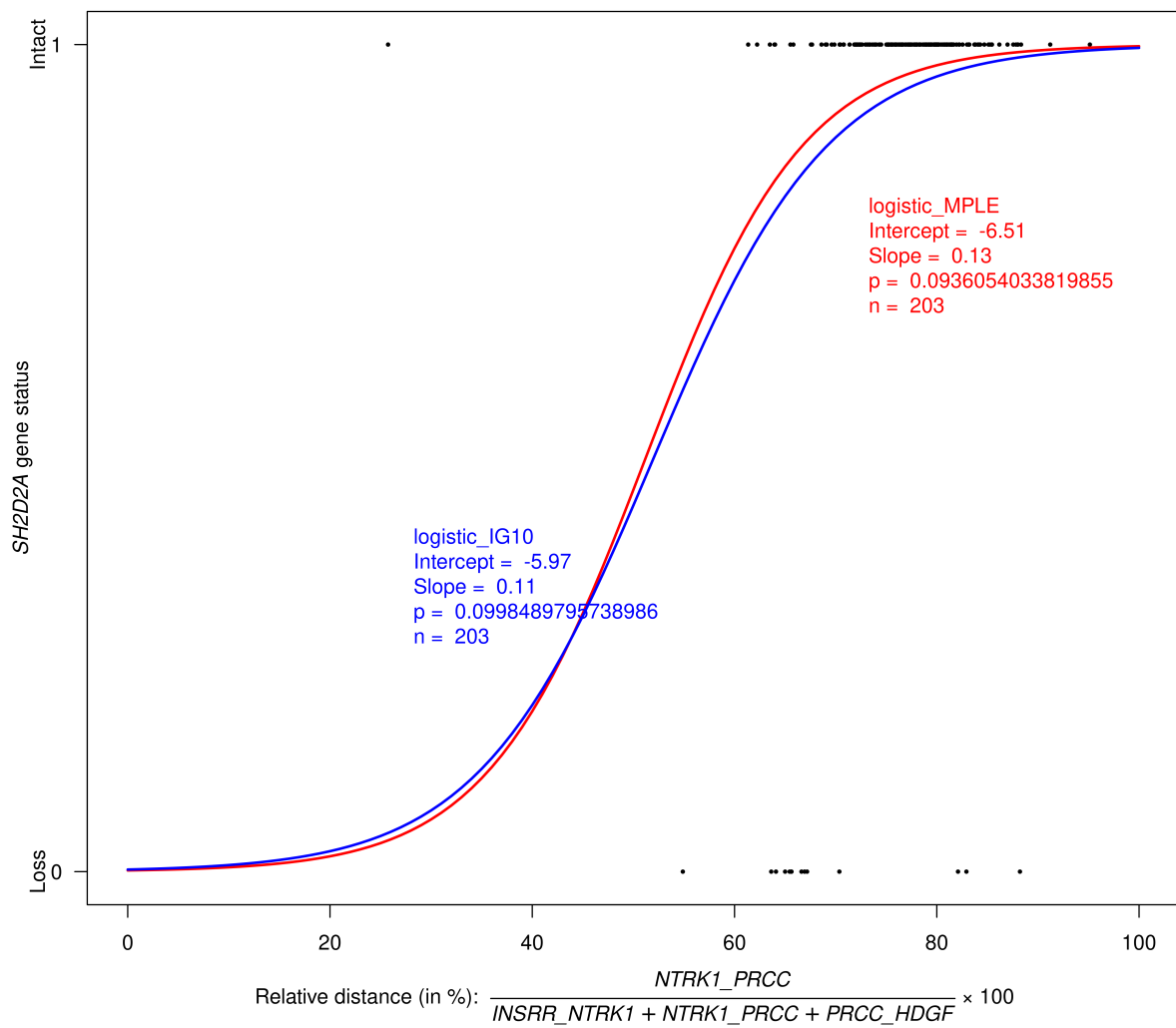


Figure 385: Phylogenetic_signal_of_deletion_plot.png

SH2D2A_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
SH2D2A	203	14	189	1	0.0998489795738986	0.0936054033819855

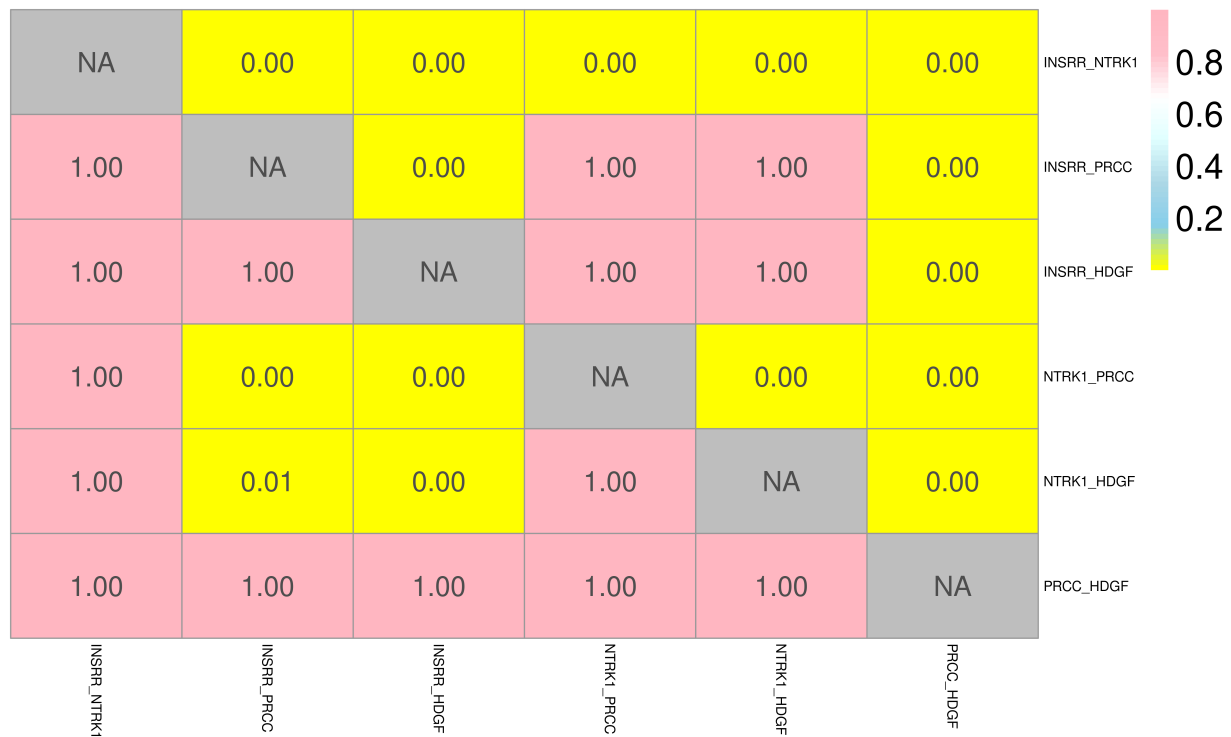


Figure 386: Heatmap_of_deletion_plot.png

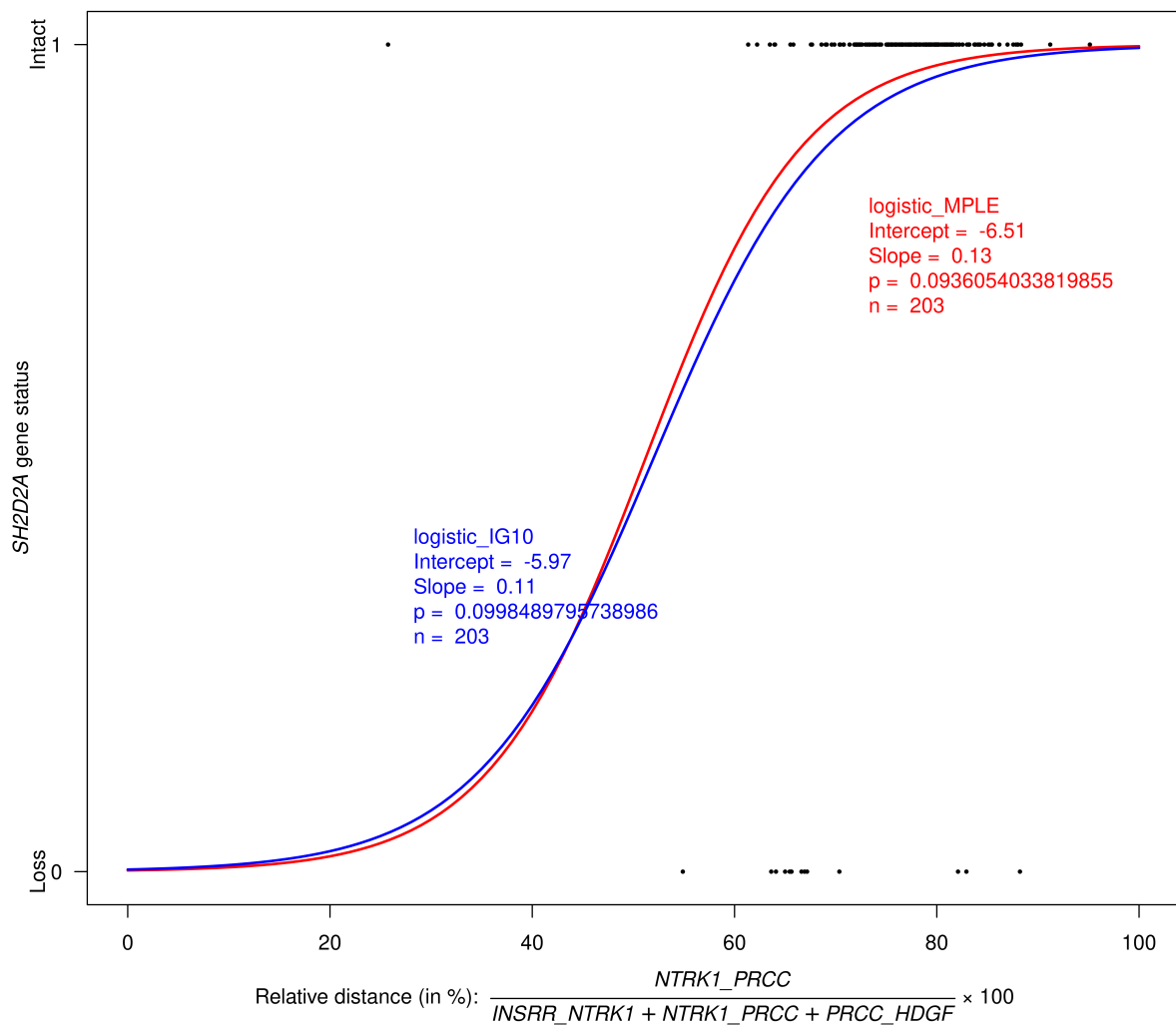


Figure 387: Phylogenetic_signal_of_deletion_plot.png

SH2D2A_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
SH2D2A	203	14	189	1	0.0998489795738986	0.0936054033819855

Lastz Alignment evidence

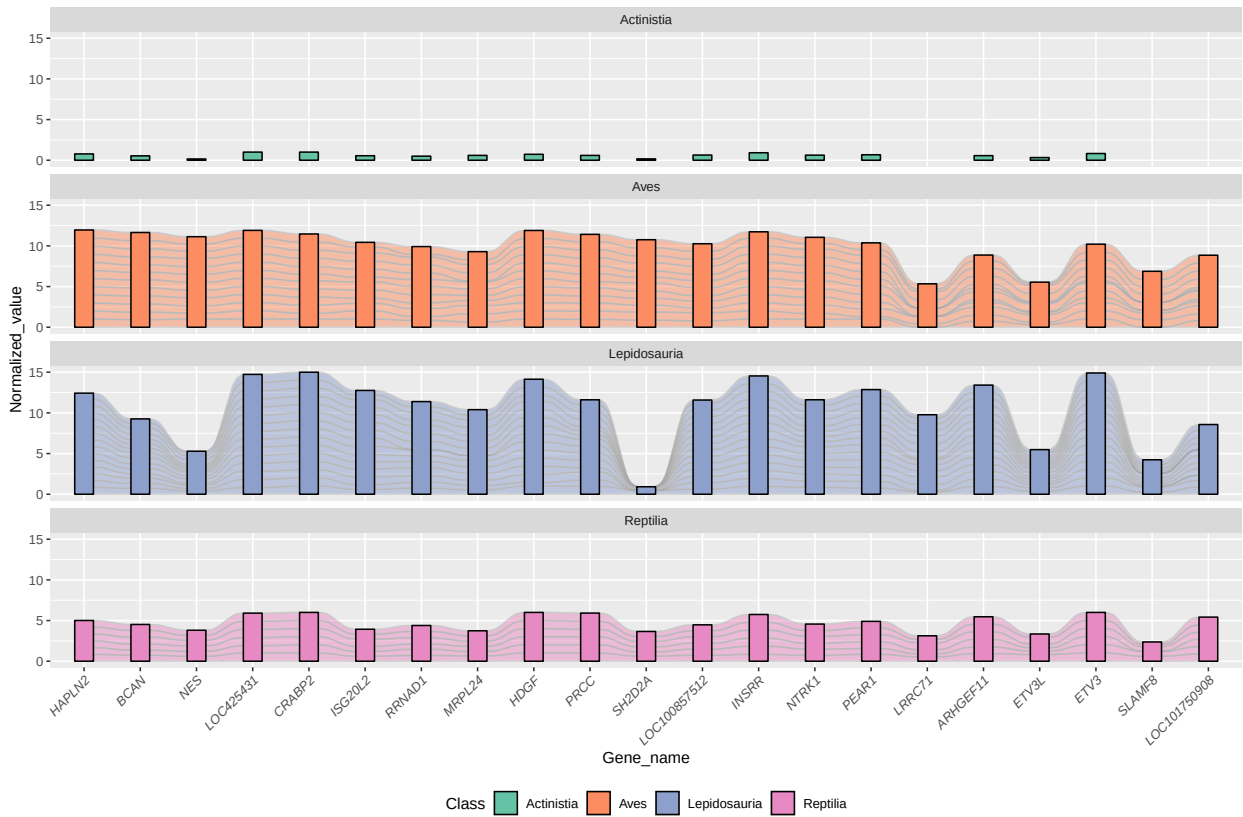


Figure 388: SH2D2A.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Syntenic evidence

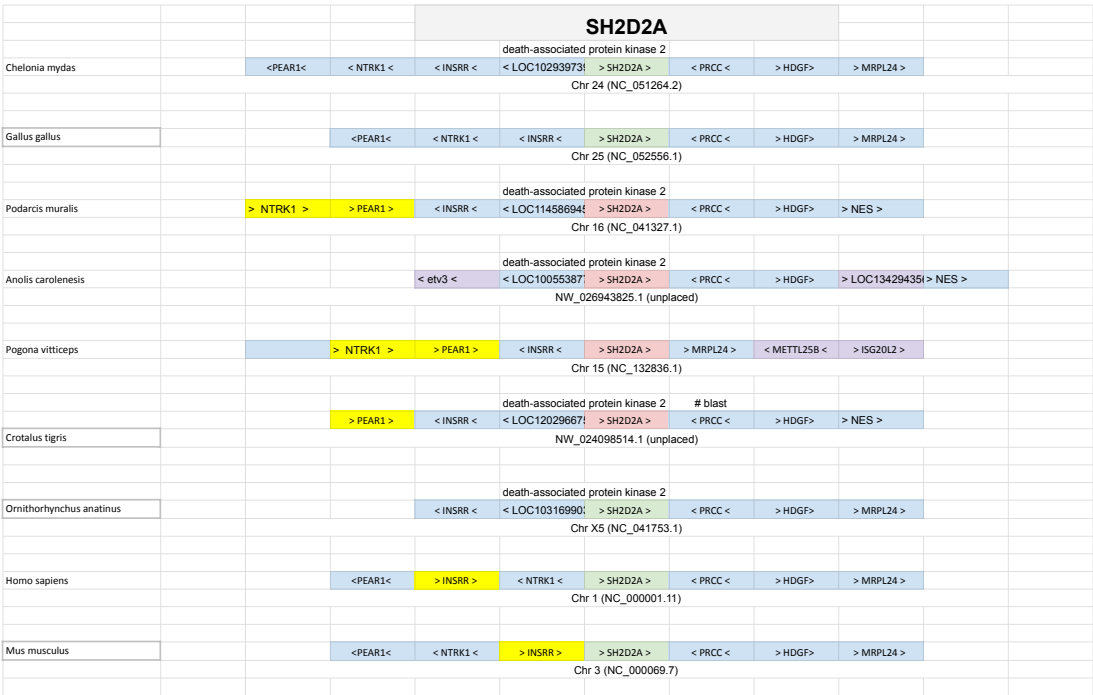


Figure 390: SH2D2A.pdf

SH2D2A.txt

Synteny analysis of SH2D2A

We analyzed the synteny of SH2D2A across squamates and representative outgroups. The syntenic block is largely conserved; however, the orientation of the flanking genes NTRK1 PEAR1 is altered in some species, as indicated by bright yellow boxes in the synteny plots. All other genes in the block maintain the conserved arrangement. In the synteny plots, red blocks indicate the absence of SH2D2A, green blocks mark its presence, light blue blocks represent genes conserved across lineages, and light purple blocks denote different flanking genes.

Transcriptomic evidence Pogona vitticeps



Figure 391: SH2D2A.png

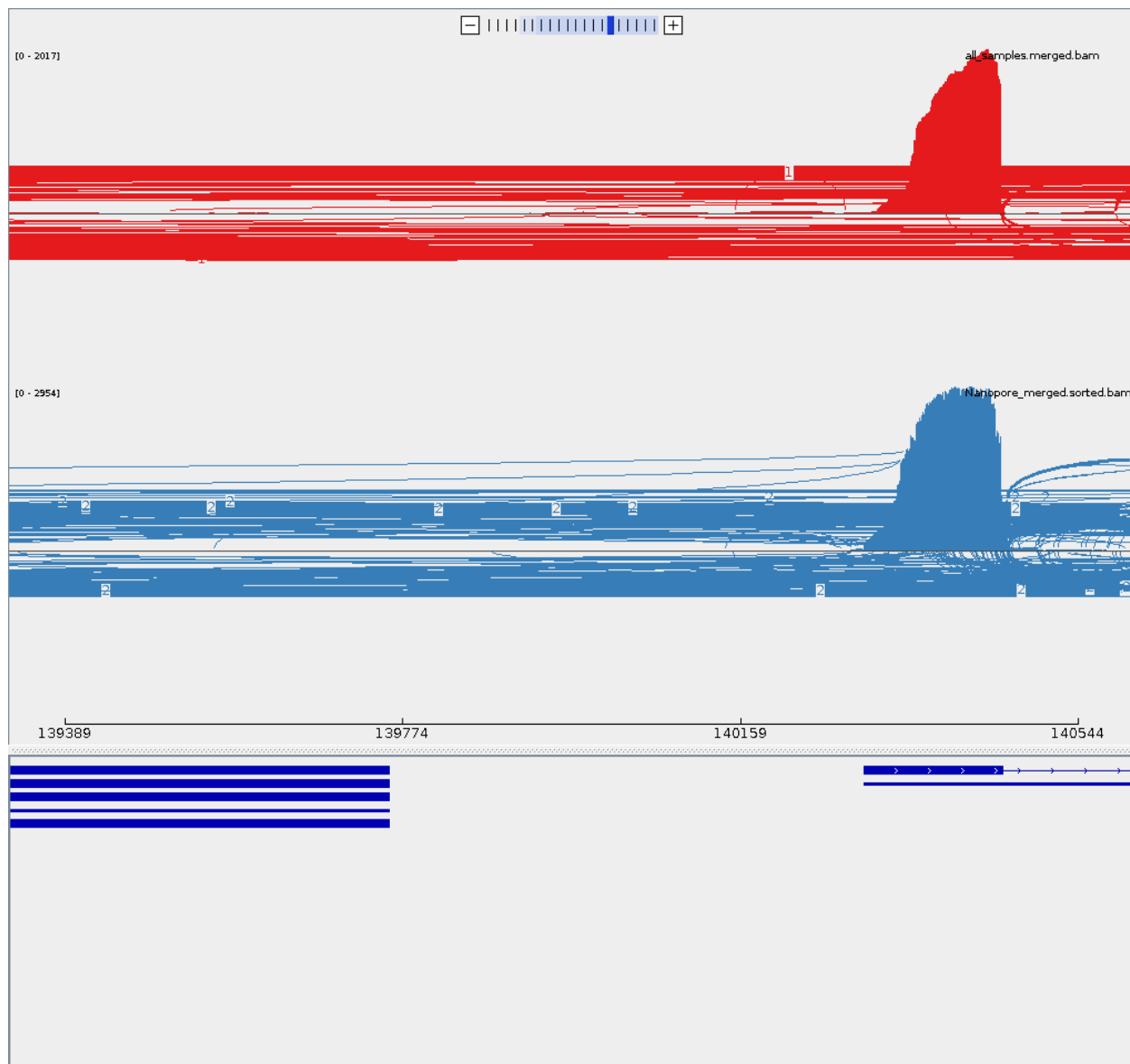


Figure 392: SH2D2A_Sashimi.png

39 SIAH3

Important gene stats

SIAH3_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
SIAH3	39.95437262	58.5165 +/- 4.94266	4.03715 +/- 0.370638	79.3318 +/- 11.6421	Yes	SIAH2;

Lastz Alignment evidence

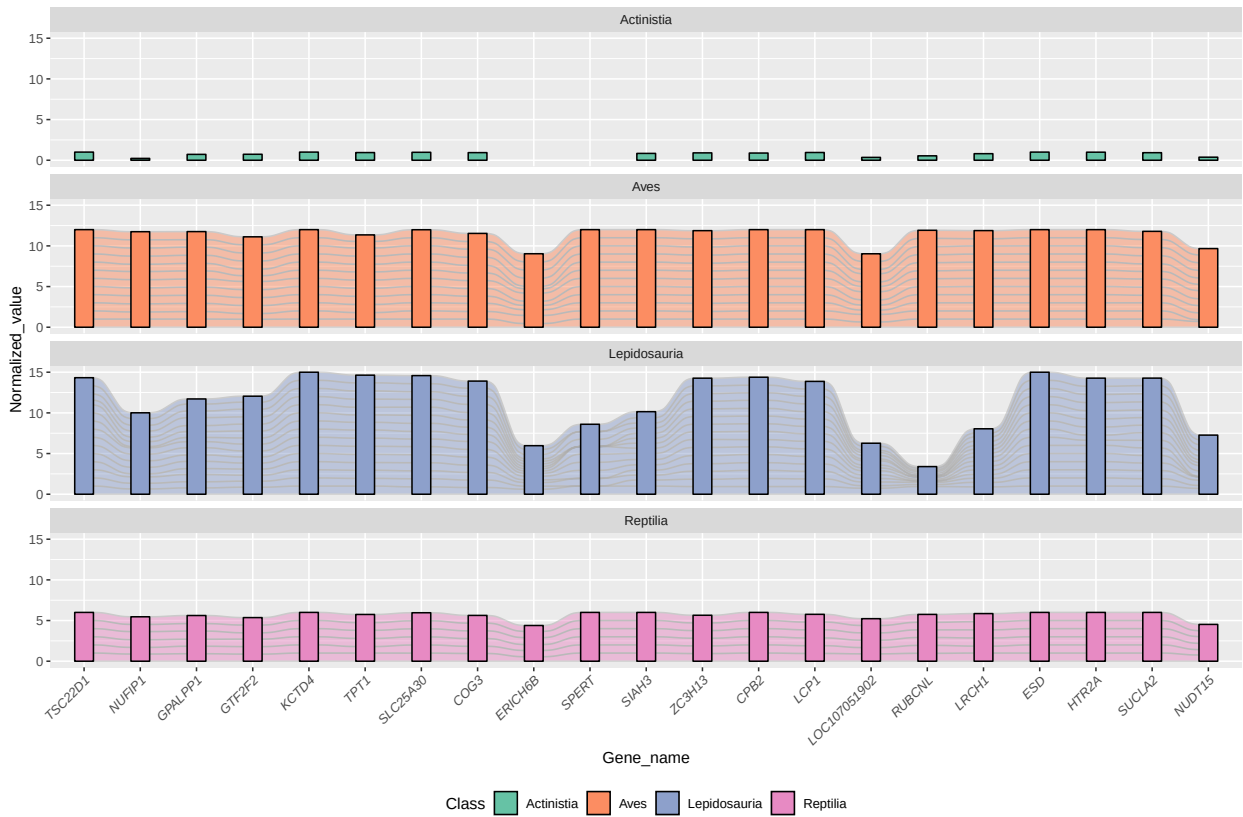


Figure 393: SIAH3.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Lastz gene tree



Figure 395: SIAH3.combined.mafft.aln.highlighted.pdf

Syntenic evidence

	SIAH3, LCP1, LRCH1, RUBCNL														
Chelonia mydas	> SUCIA2 >	< LOC11596522 >	> HTR2A >	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	> CPB2 >	> ZC3H13 >	> SIAH3 >	< CBP2 <	> ERICHBB >	< COG3 <	
	Chr 1 (NC_057948.1)														
Gallus gallus	> SUCIA2 >	> HTR2A >	> ESD >	< LRCH1 <	> RUBCNL >	< LOC101933892 <	> LCP1 >	> CPB2 >	> ZC3H13 >	> SIAH3 >	< SPRT <				
	NC_023322.1														
Podarcis muralis	> SUCIA2 >	< NPLRC3 <	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	> CPB2 >	< ZC3H13 <	> SIAH3 >	< COG3 <	< SPRT <	# same chromosome but on another side after skipping two genes		
	Chr 1 (NC_04131)		Chr 3 (NC_041314.1)				Chr 3 (NC_041314.1) #		Chr 5 (NC_041316.1)						
Anolis carolinensis	> SUCIA2 >	> HTR2A >	< NPLRC3 <	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	< p981 <	< sp9824 <	< dr9c18 <	> z3h13 >	< CPB2 <	> SIAH3 >	
	Chr 1 (NC_085841.1)		Chr 1 (NC_085841.1)				Chr 1 (NC_085841.1)		Chr 3 (NC_085841.1)		< COG3 <	< dr9c <	> ERICHBB >		
Pogona vitticeps	> SUCIA2 >	> HTR2A >	< NPLRC3 <	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	< p981 <	< sp9824 <	< dr9c18 <	> z3h13 >	< CPB2 <	> SIAH3 >	
	Chr 1 (NC_132822.1) #		Chr 1 (NC_132822.1)				Chr 1 (NC_132822.1)		Chr 3 (NC_132824.1)		> z3h1 >	< sp981 <	# same chromosome but after skipping genes		
Crotalus tigris	> SUCIA2 >	> HTR2A >	< NPLRC3 <	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	< p981 <	< sp9824 <	< dr9c18 <	> z3h13 >	< CPB2 <	> SIAH3 >	
	NW_02410010.1 (unplaced)		NW_024097046.1 (unplaced)				NW_024098059.1 (unplaced)		NW_024098059.1 (unplaced)		< COG3 <	> ERICHBB >			
Oreodonhrychus sinuatus	> SUCIA2 >	< LOC103170481 >	> HTR2A >	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	> CPB2 >	> ZC3H13 >	> SIAH3 >	> ERICHBB >	< COG3 <		
	Chr 20 (NC_041747.1)														
Homo sapiens	> SUCIA2 >	> HTR2A >	< HTR2A-AS1 <	> ESD >	< LRCH1 <	< FBXP5AF3 <	> UNCG3389 >	> RUBCNL >	< LRRC63 <	> LOC107884571 >	> LCP1 >	> CPB2 >	< CPB2-AS1 <	> ZC3H13 >	
	Chr 13 (NC_000313.12)														
Manus manul	> SUCIA2 >	< GH41210 <	> HTR2A >	> ESD >	< LRCH1 <	> RUBCNL >	< LRRC63 <	> LCP1 >	> CPB2 >	< GH41212 <	> SIAH3 >	< CBP2 <	< GH35219 <	> ERICHBB >	
	< COG3 <														

Figure 396: SIAH3.pdf

SIAH3.txt

Synteny analysis of SIAH3

The syntenic block for

SIAH3 shows evidence of both interchromosomal and intrachromosomal
 ↳ rearrangements within squamates. In species such as

Anolis carolinensis and *Pogona vitticeps*, the flanking genes are located
 ↳ on two different chromosomes, indicating a break in synten.
 ↳ Furthermore, in lizards like

Podarcis muralis, the block also appears to have undergone an
 ↳ intrachromosomal rearrangement, with flanking genes repositioned to
 ↳ a different location on the same chromosome after skipping several

↪ intervening genes. The block is highly fragmented in the snake
Crotalus tigris, with genes located on multiple unplaced scaffolds.

In the synteny plots, red blocks indicate the absence of the target gene,
↪ while green blocks mark its presence. Light blue blocks represent
↪ flanking genes that are conserved across lineages, and light purple
↪ blocks denote instances where a different flanking gene is present

40 SLC24A1

Assembly verification Evidence

Crotalus_tigris-PacBio

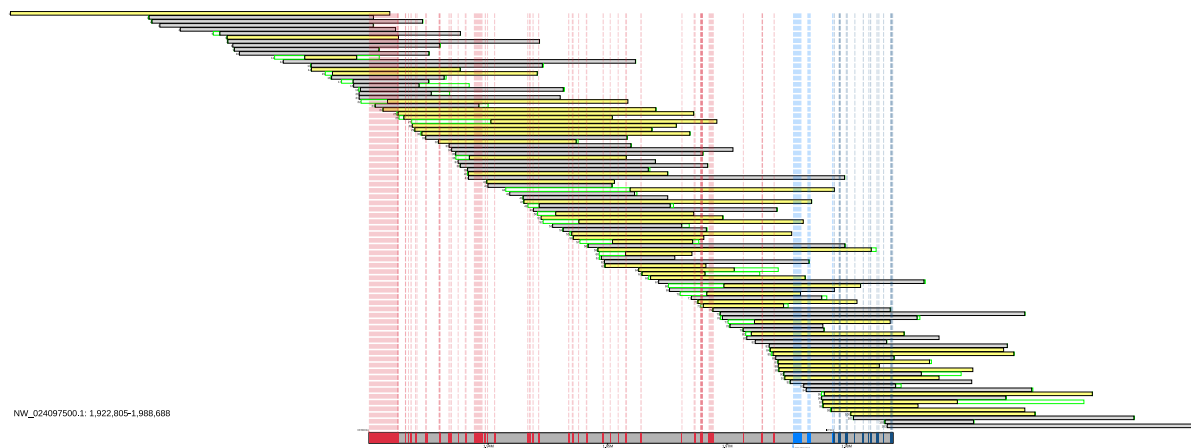


Figure 397: SLC24A1:NW_024097500.1:1922805-1988688.pdf

Podarcis_muralis-PacBio

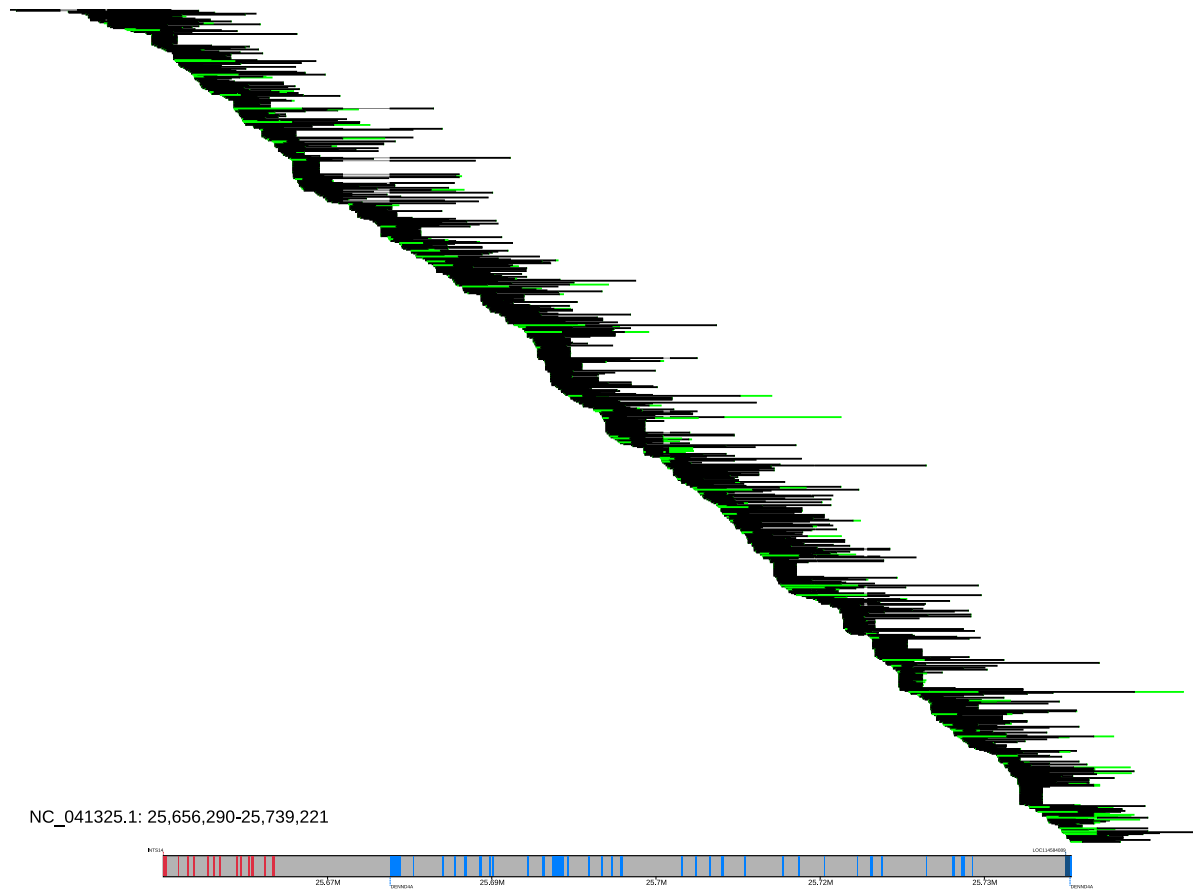


Figure 398: SLC24A1:NC_041325.1:25656290-25739221.pdf

Pogona_vitticeps-Nanopore

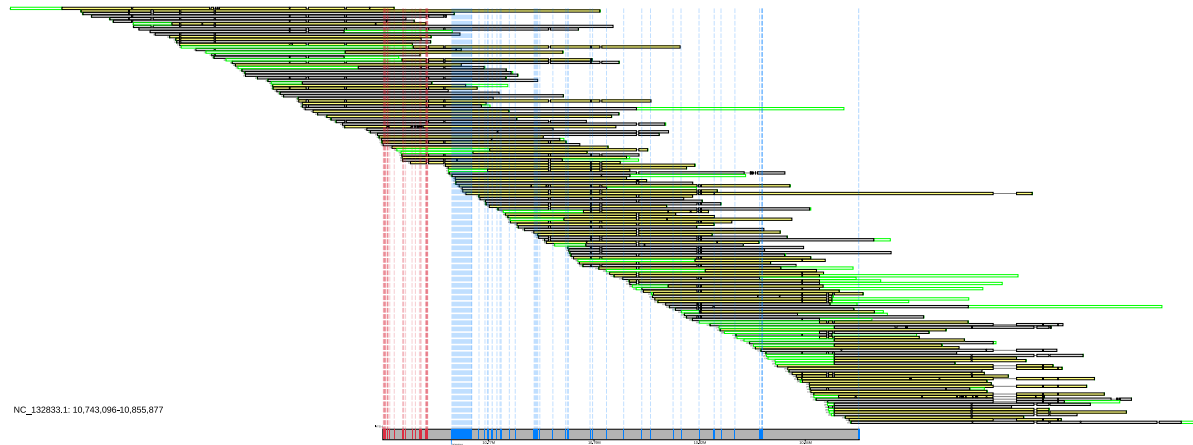


Figure 399: SLC24A1:NC_132833.1:10743096-10855877.pdf

Important gene stats

SLC24A1_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
SLC24A1	18.93939394	50.9563 +/- 3.2167	3.72741 +/- 0.251878	59.4598 +/- 18.5087	Yes	Na

Intergenic distance phylogenetic signal evidence



Figure 400: Heatmap_of_deletion_plot.png

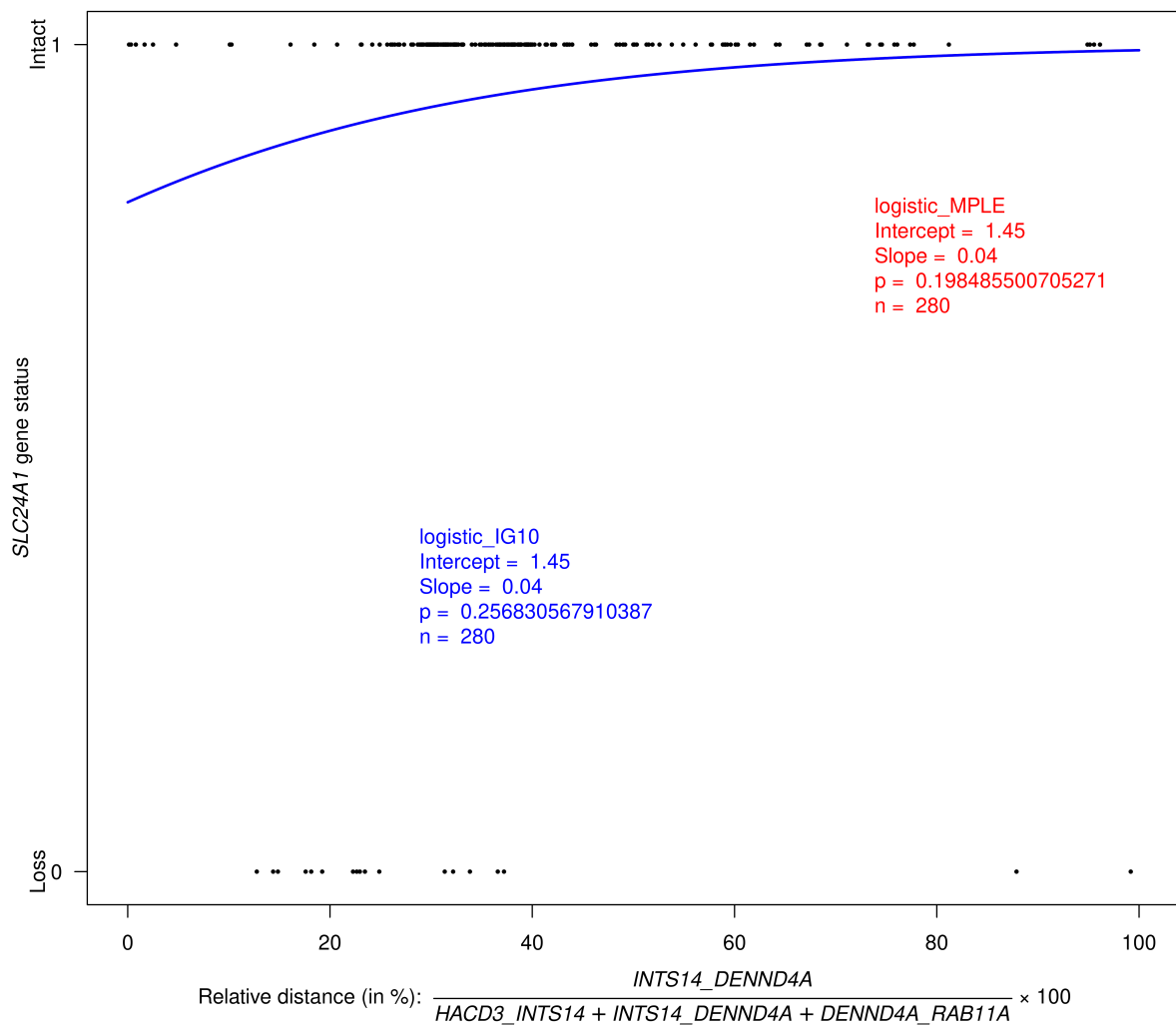


Figure 401: Phylogenetic_signal_of_deletion_plot.png

SLC24A1_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
SLC24A1	280	18	262	5	0.256830567910387	0.198485500705271

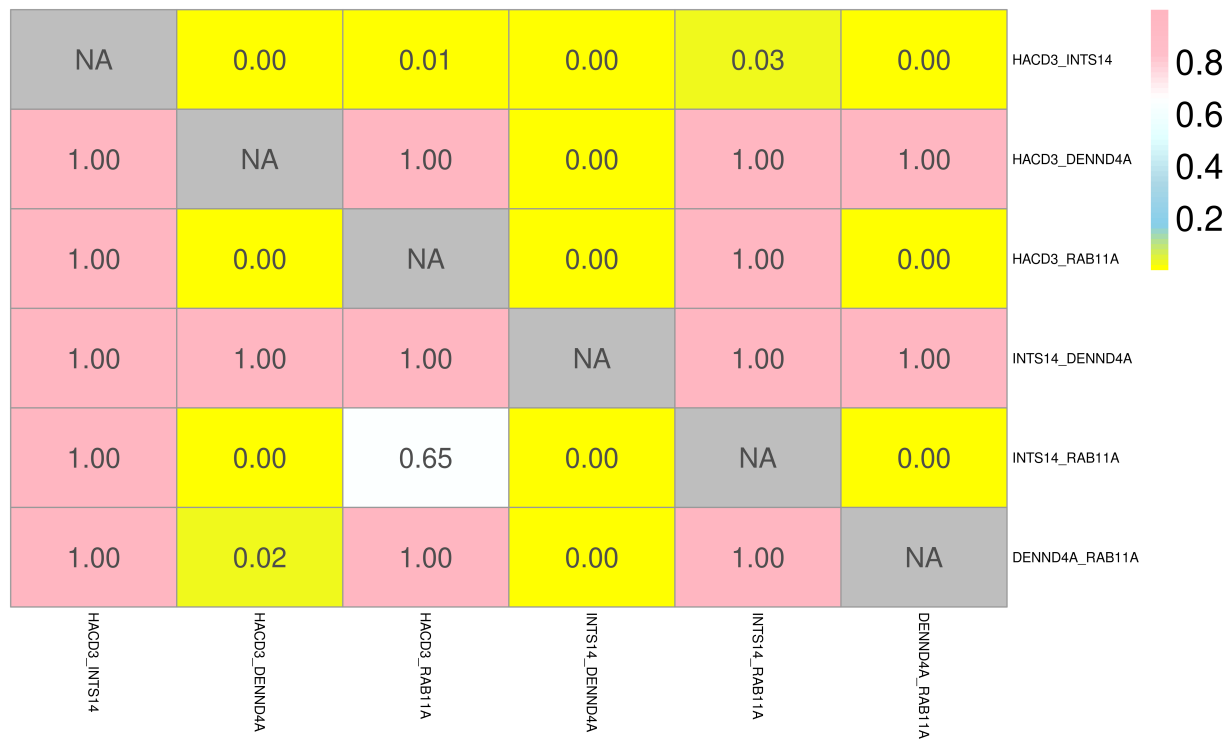


Figure 402: Heatmap_of_deletion_plot.png

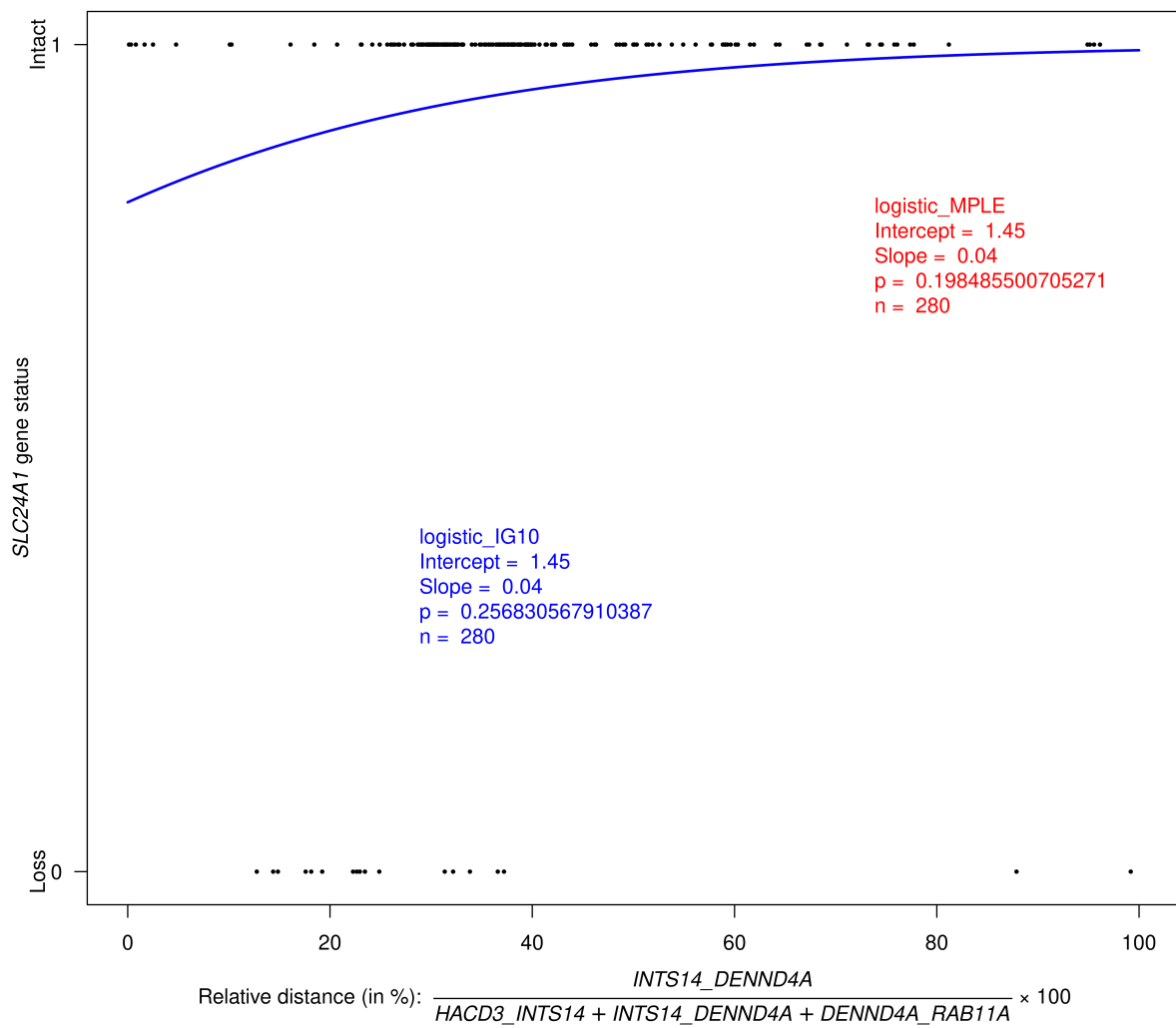


Figure 403: Phylogenetic_signal_of_deletion_plot.png

SLC24A1_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
SLC24A1	280	18	262	5	0.256830567910387	0.198485500705271

Lastz Alignment evidence

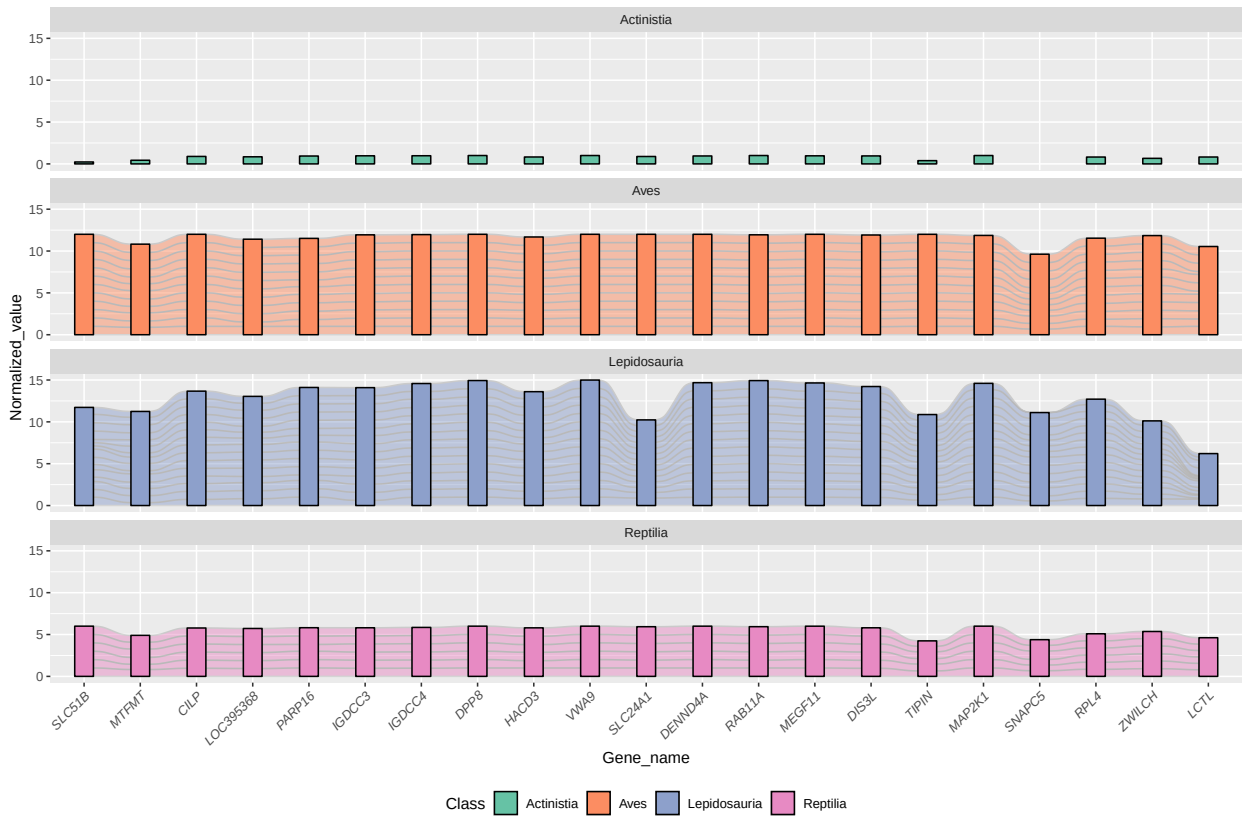


Figure 404: SLC24A1.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

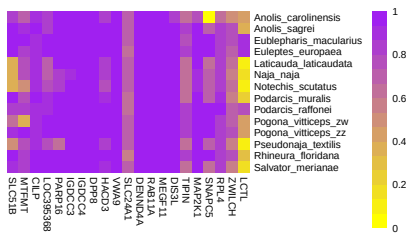


Figure 405: SLC24A1.FS_Exonic.Final.Gallus_gallus.21_genes_heatmap.pdf

Lastz gene tree

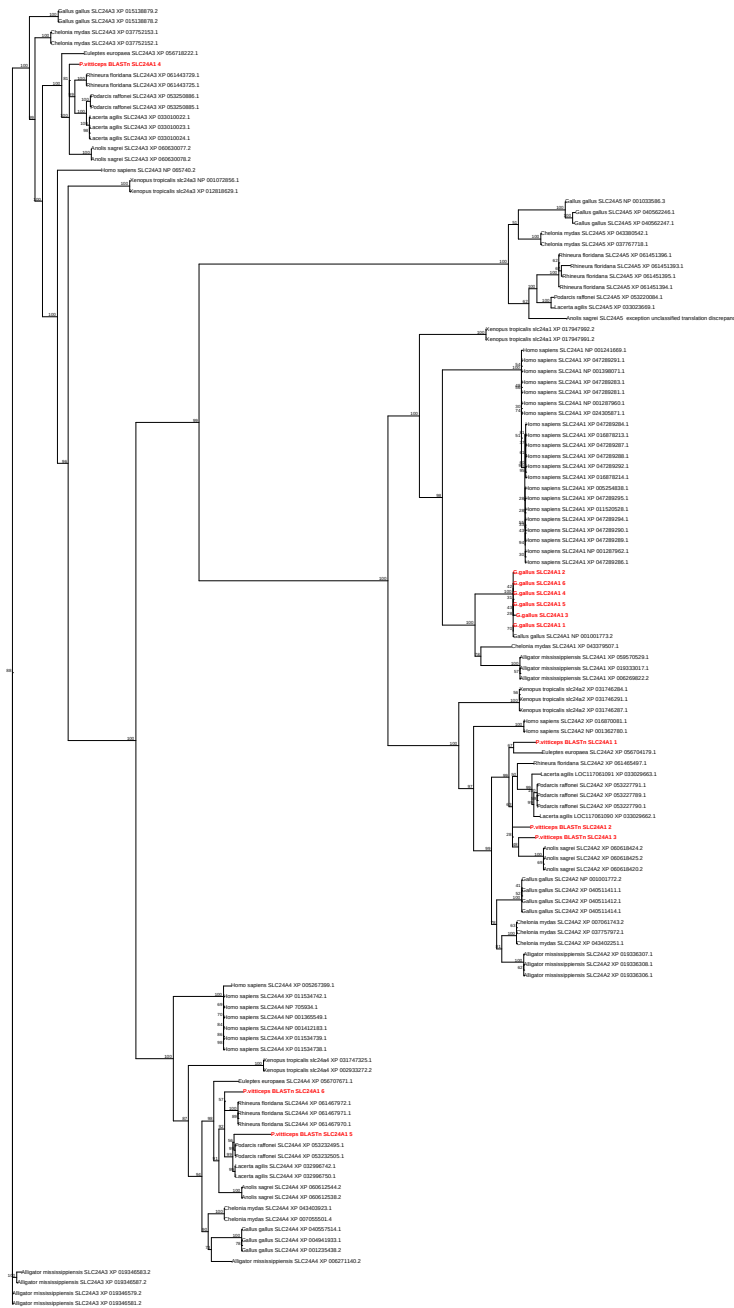


Figure 406: SLC24A1.combined.mafft.aln.highlighted.pdf

Syntenic evidence

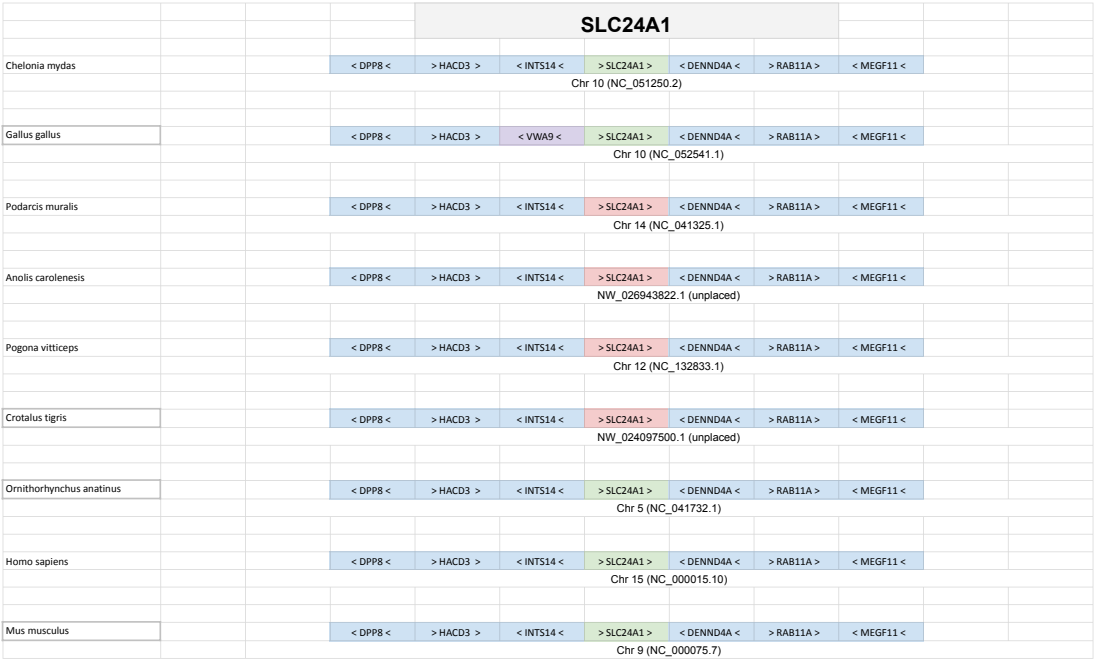


Figure 407: SLC24A1.pdf

SLC24A1.txt

Synteny analysis of SLC24A1

We analyzed the synteny of SLC24A1 across squamates and representative outgroups. The SLC24A1 syntenic block is conserved in all examined species. In the synteny plots, red blocks indicate the absence of SLC24A1, green blocks mark its presence, light blue blocks represent genes conserved across lineages, and light purple blocks denote different flanking genes.

Transcriptomic evidence Pogona vitticeps



Figure 408: SLC24A1.png

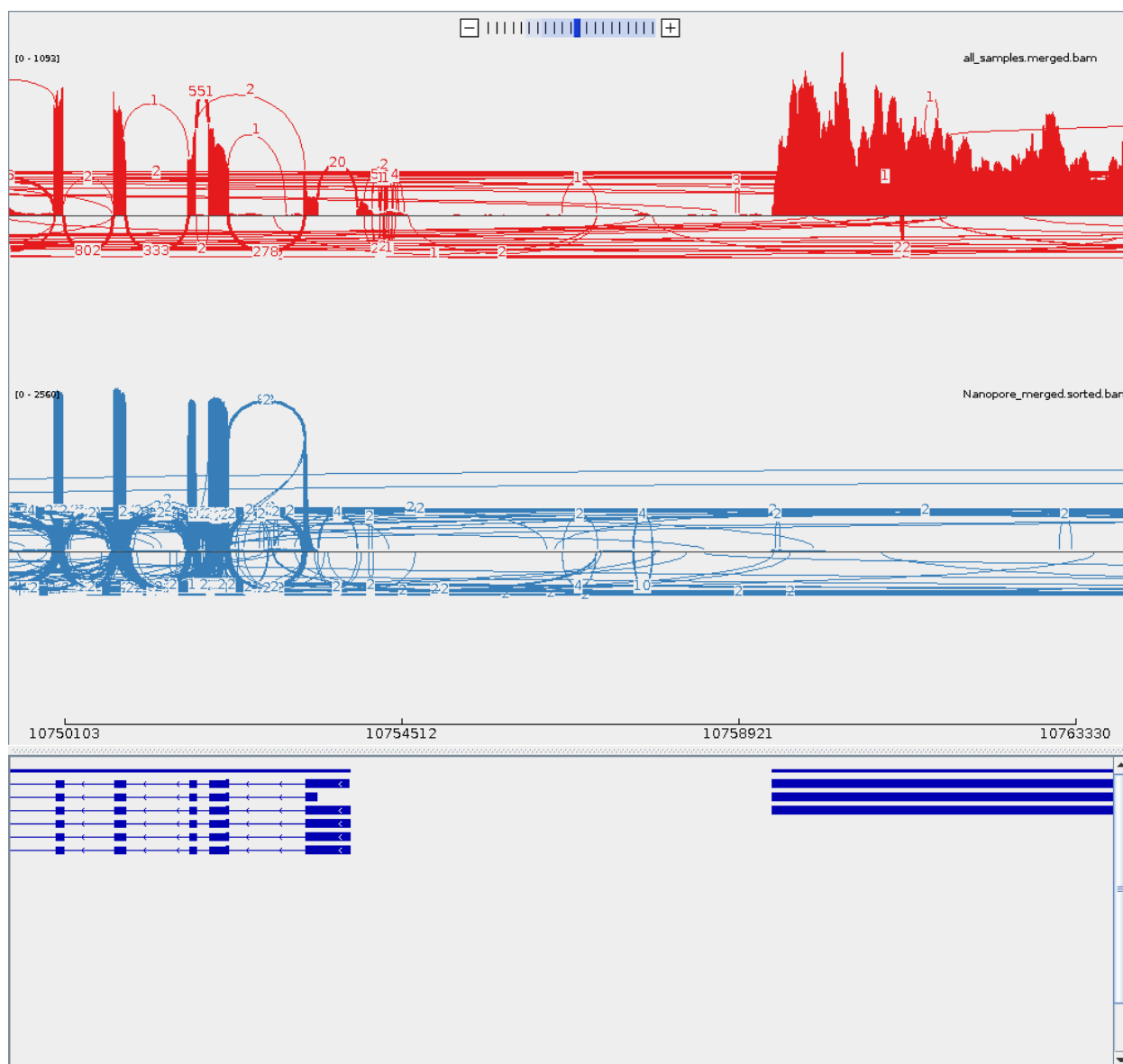


Figure 409: SLC24A1_Shash.png

41 SLC9A5

Assembly verification Evidence

Crotalus_tigris-PacBio

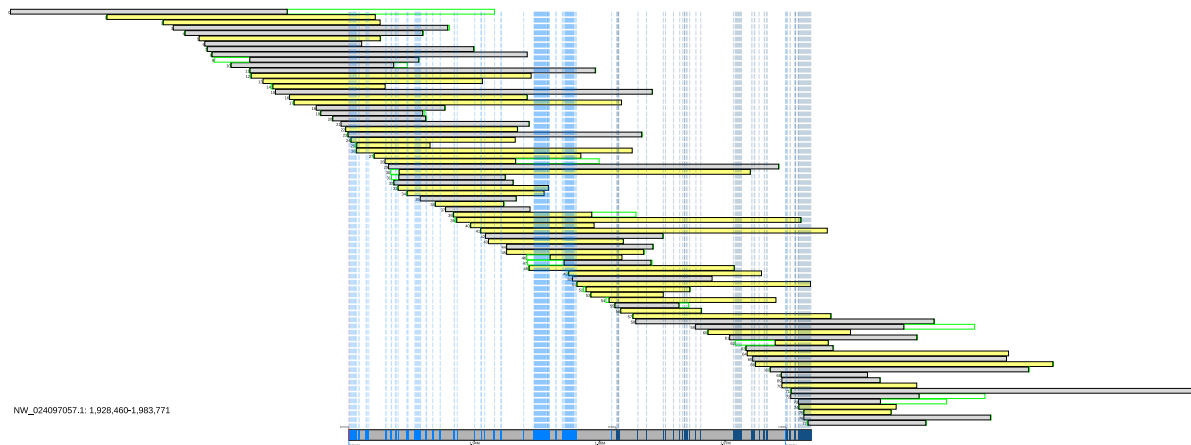


Figure 410: SLC9A5:NW_024097057.1:1928460-1983771.pdf

Podarcis_muralis-PacBio

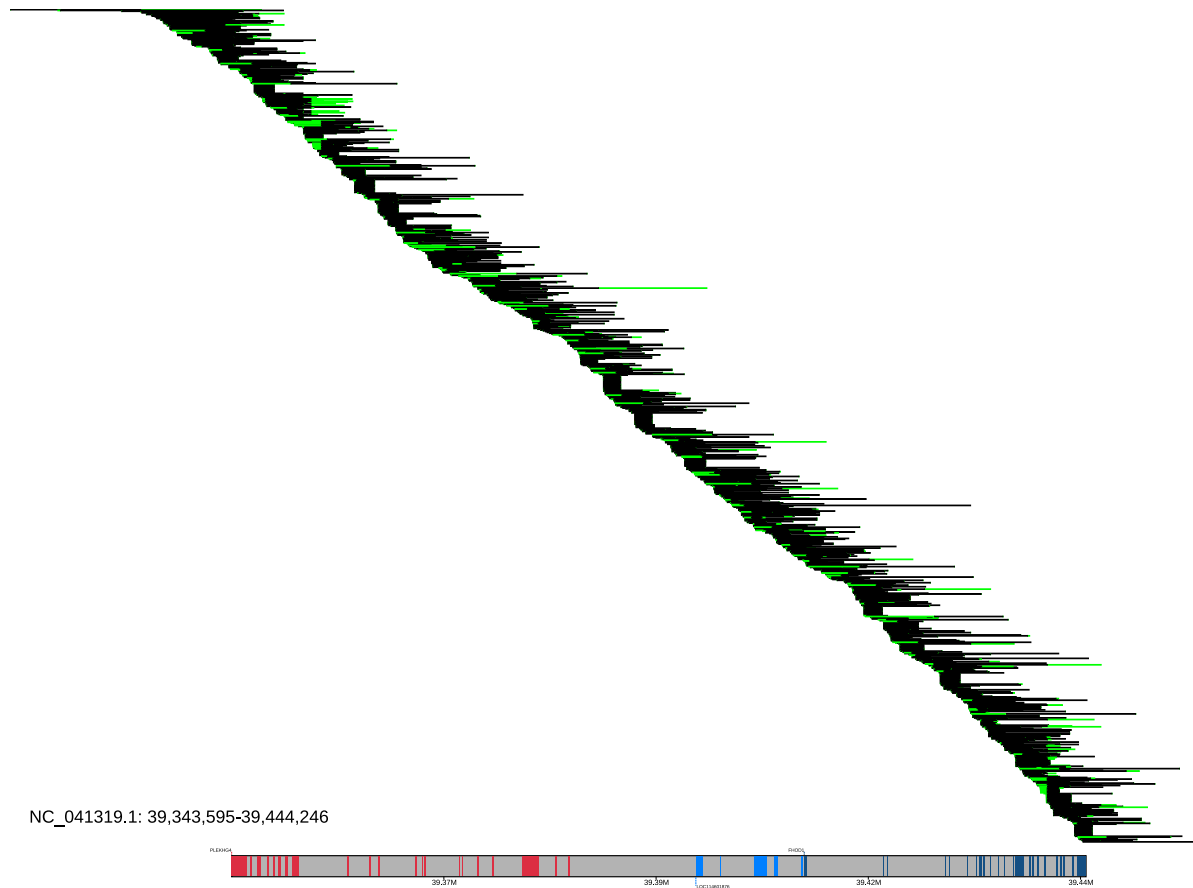


Figure 411: SLC9A5:NC_041319.1:39343595-39444246.pdf

Pogona_vitticeps-Nanopore

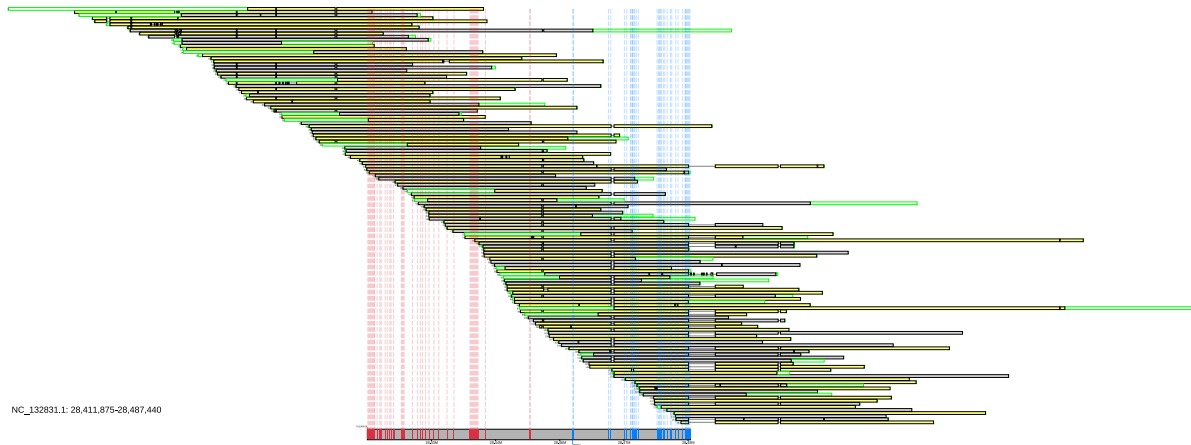


Figure 412: SLC9A5:NC_132831.1:28411875-28487440.pdf

Important gene stats

SLC9A5_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest_paralog (recovered using IQ-TREE)
SLC9A5	15.51515152	58.1247 +/- 3.47816	4.12677 +/- 0.27267	75.2257 +/- 15.0959	Yes	LOC132762995:Naja_naja SRR10428157.blast;Pogona_witticeps.ERR409938.blast;SLC9A3;

Intergenic distance phylogenetic signal evidence



Figure 413: Heatmap_of_deletion_plot.png

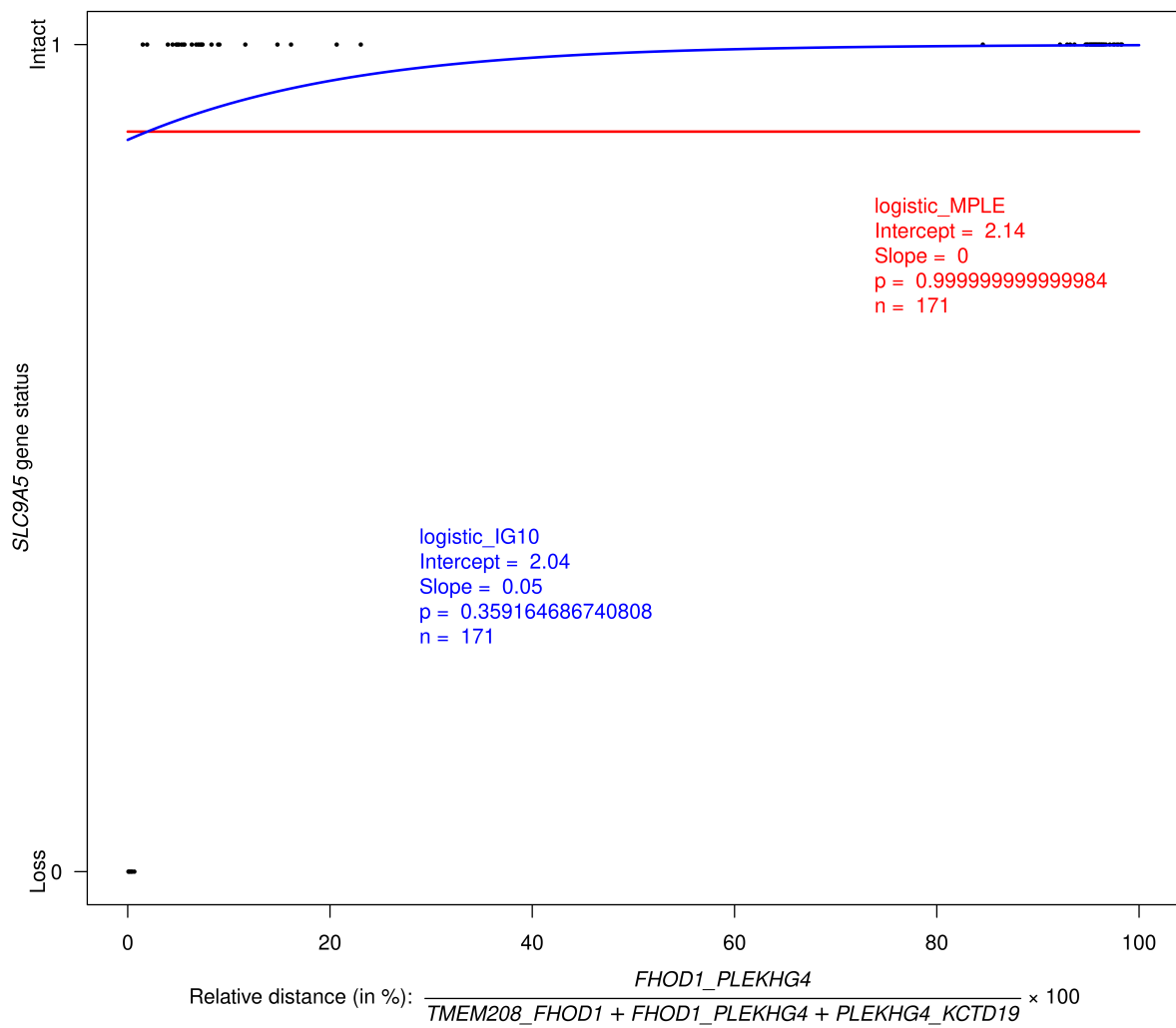


Figure 414: Phylogenetic_signal_of_deletion_plot.png

SLC9A5_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
SLC9A5	171	18	153	5	0.359164686740808	0.999999999999984

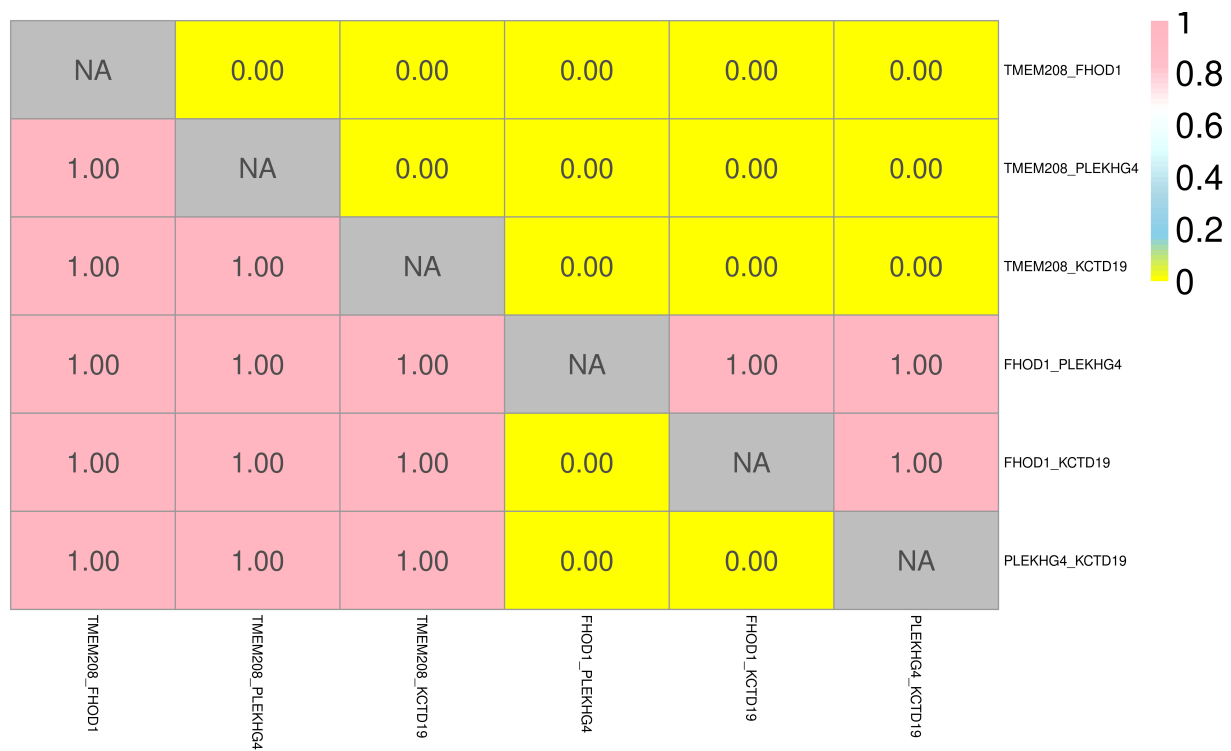


Figure 415: Heatmap_of_deletion_plot.png

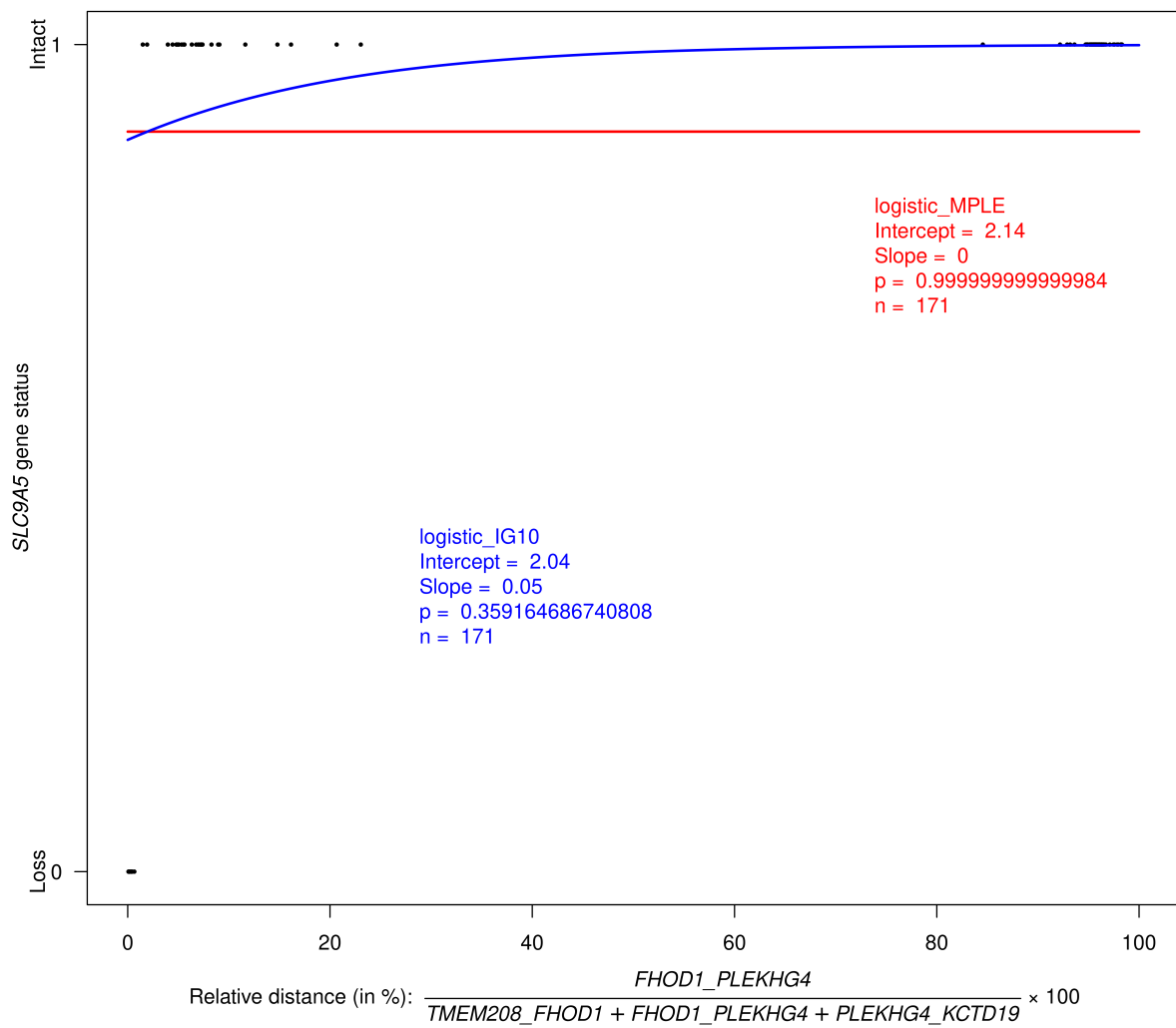


Figure 416: Phylogenetic_signal_of_deletion_plot.png

SLC9A5_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
SLC9A5	171	18	153	5	0.359164686740808	0.999999999999984

Lastz Alignment evidence

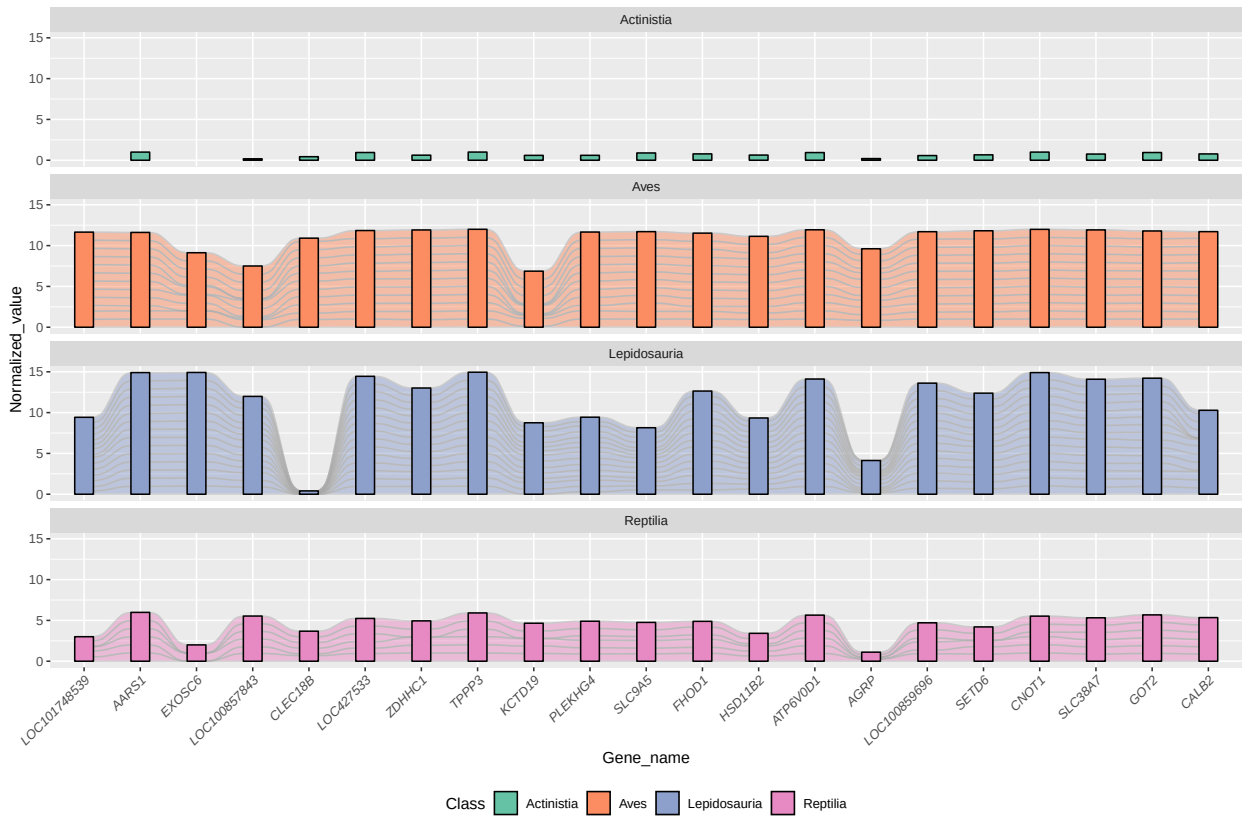


Figure 417: SLC9A5.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Lastz gene tree

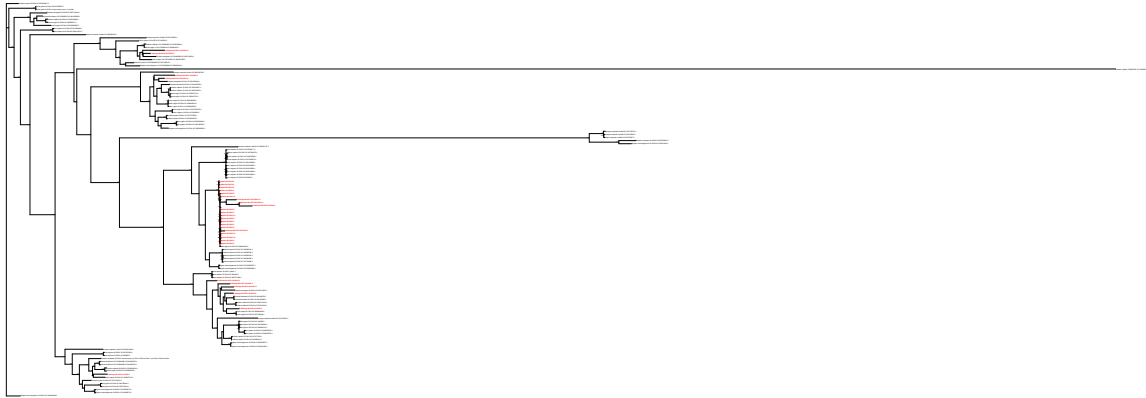


Figure 419: SLC9A5.combined.mafft.aln.highlighted.pdf

[illegible]

Figure 420: SLC9A5.pdf

SLC9A5.txt

Synteny analysis of SLC9A5

We analyzed the synteny of SLC9A5 across squamates and representative
 ↳ outgroups. The SLC9A5 syntenic block is conserved in all examined
 ↳ species. In the synteny plots, red blocks indicate the absence of
 ↳ SLC9A5, green blocks mark its presence, light blue blocks represent
 ↳ genes conserved across lineages, and light purple blocks denote
 ↳ different flanking genes.

Transcriptomic evidence *Pogona vitticeps*



Figure 421: SLC9A5.png

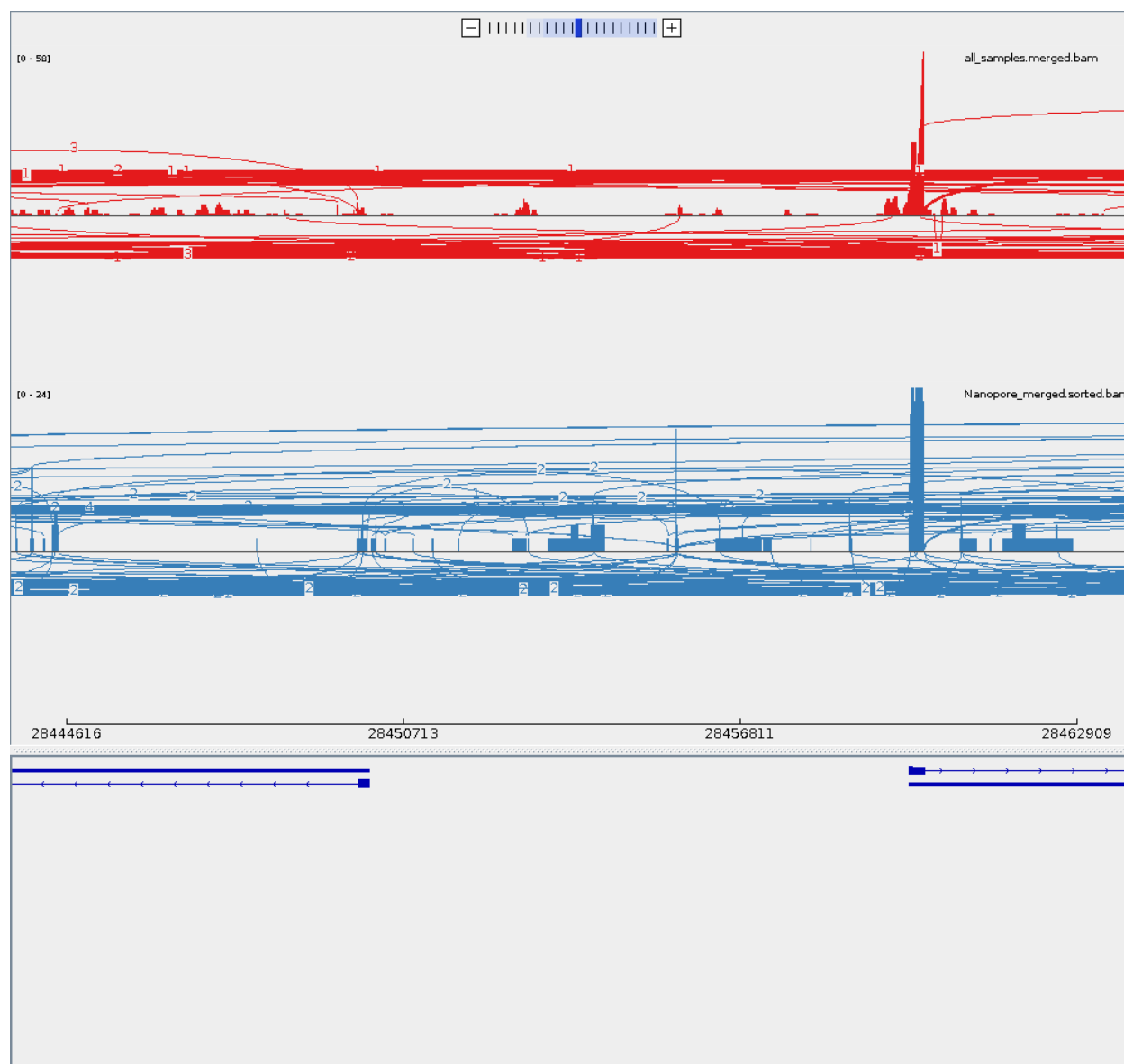


Figure 422: SLC9A5_Shash.png

42 SSTR4

Assembly verification Evidence

Crotalus_tigris-PacBio

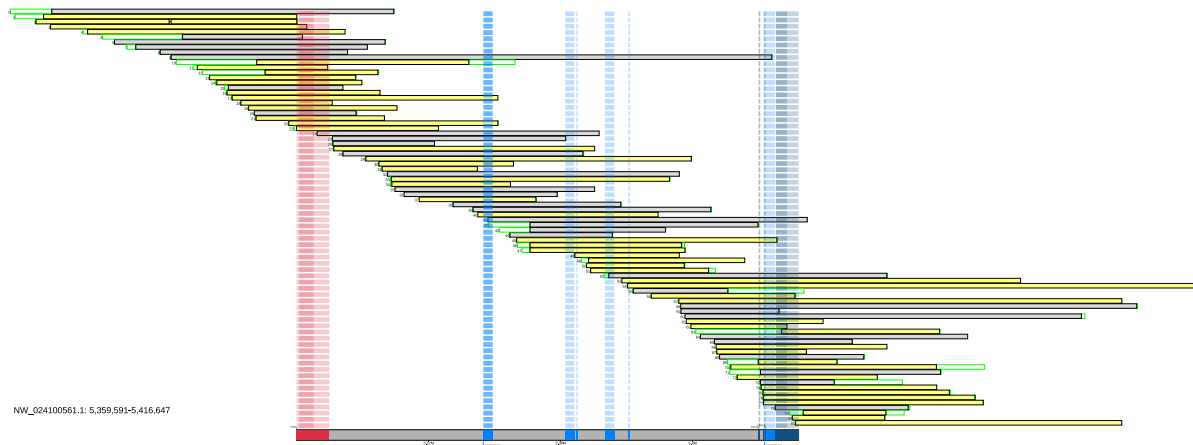


Figure 423: SSTR4:NW_024100561.1:5359591-5416647.pdf

Podarcis_muralis-PacBio

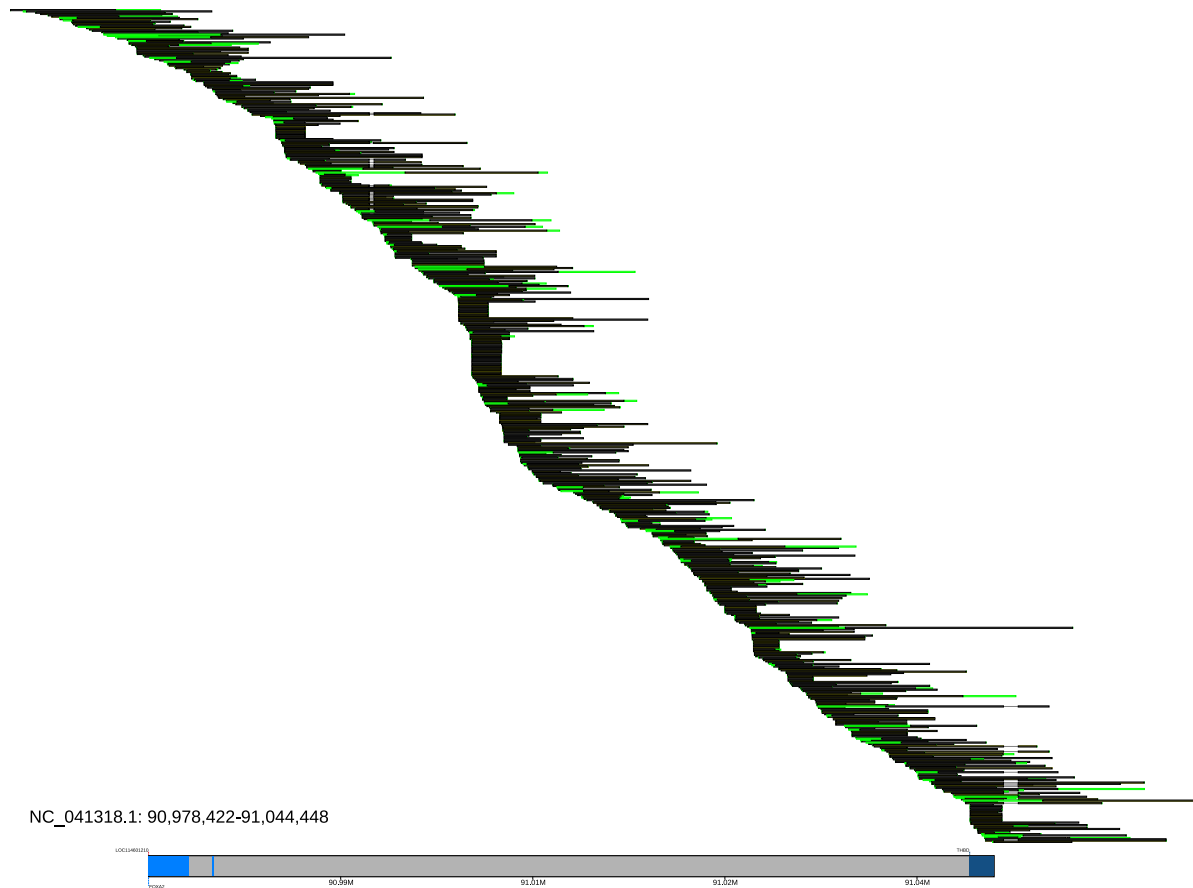


Figure 424: SSTR4:NC_041318.1:90978422-91044448.pdf

Pogona_vitticeps-Nanopore

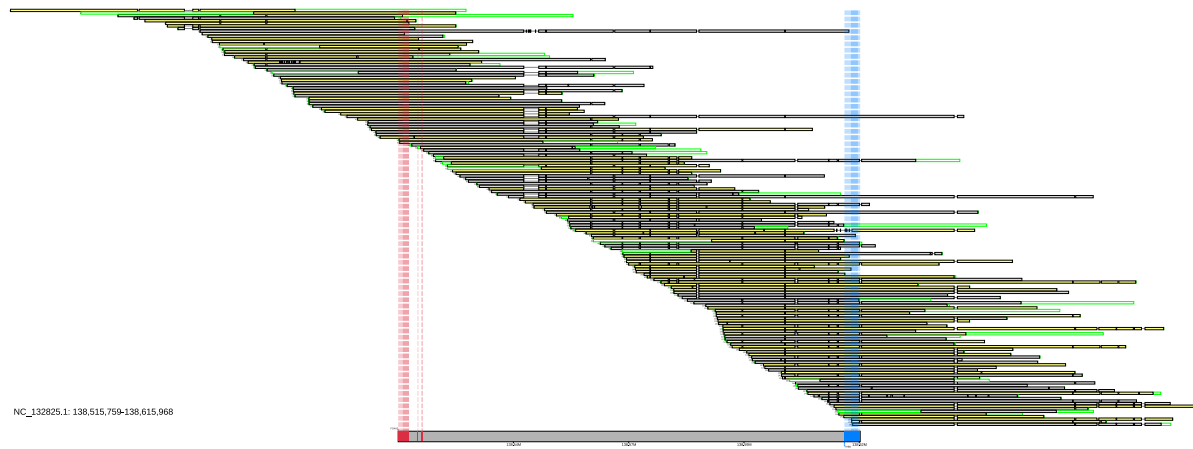


Figure 425: SSTR4:NC_132825.1:138515759-138615968.pdf

Important gene stats

SSTR4_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
SSTR4	77.3030303	64.7248 +/- 4.57964	4.64262 +/- 0.50583	78.4982 +/- 10.6112	Yes	SSTR1;

Intergenic distance phylogenetic signal evidence

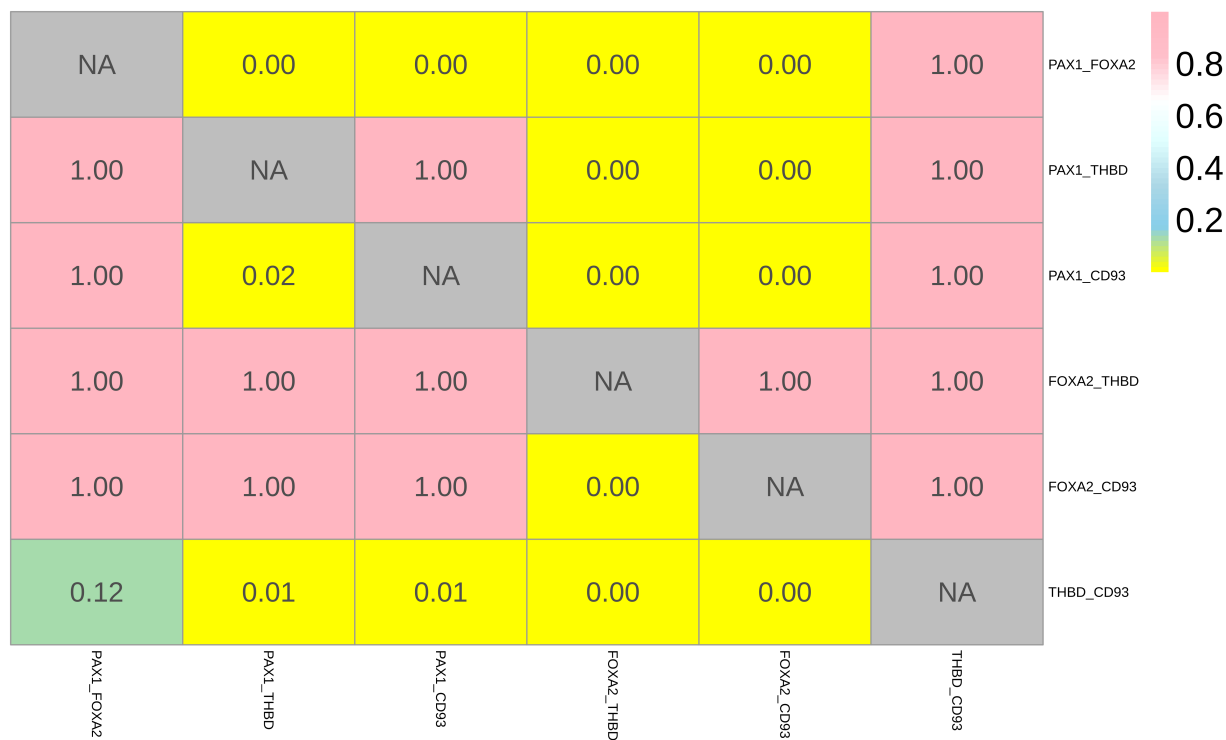


Figure 426: Heatmap_of_deletion_plot.png

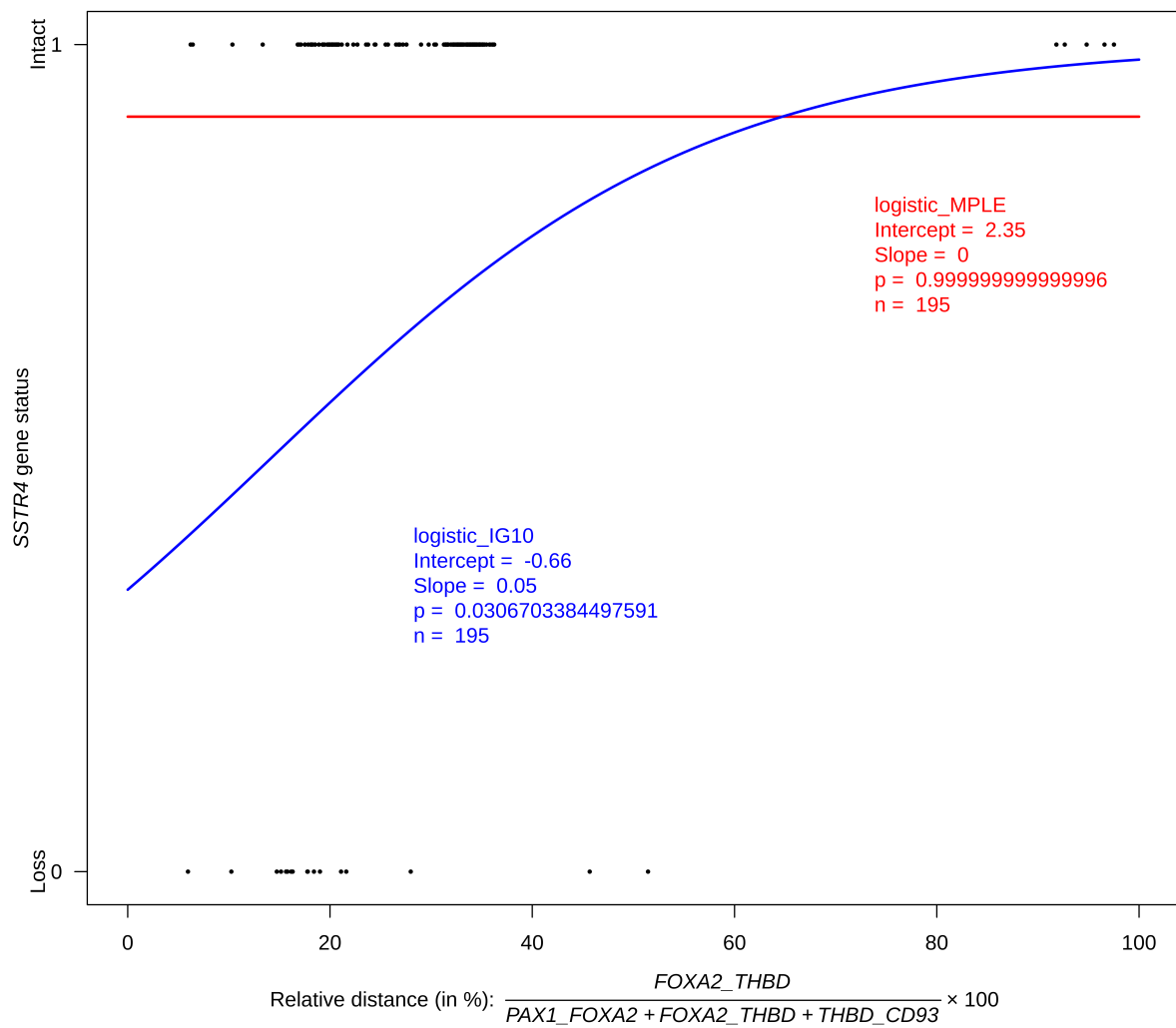


Figure 427: Phylogenetic_signal_of_deletion_plot.png

SSTR4_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
SSTR4	195	17	178	5	0.0306703384497591	0.999999999999996

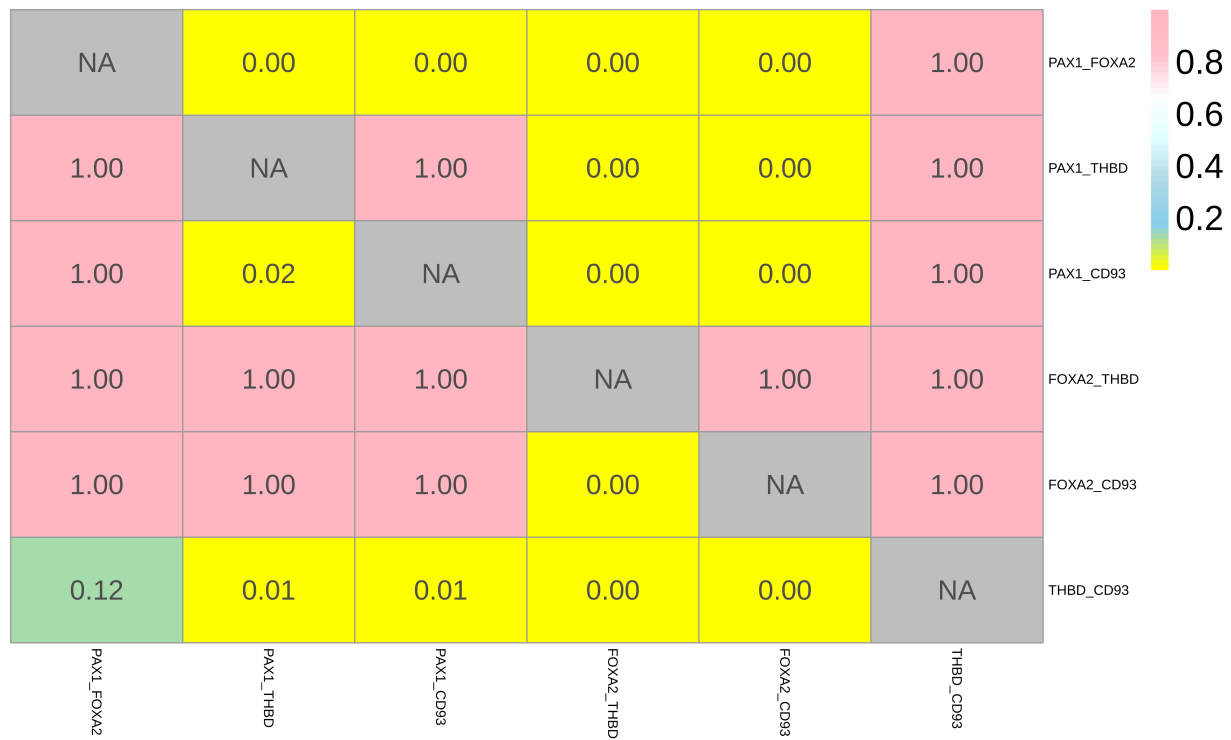


Figure 428: Heatmap_of_deletion_plot.png

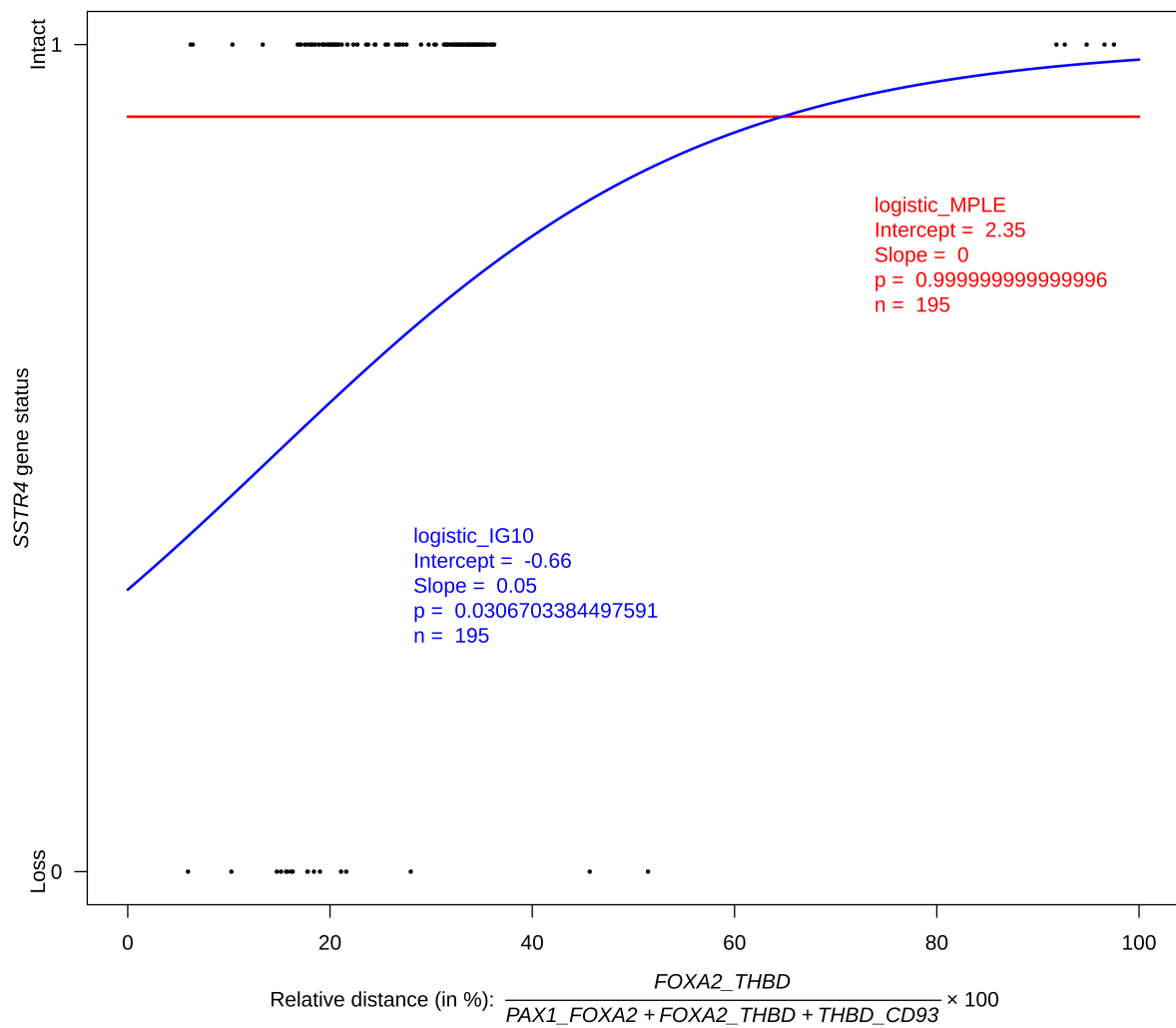


Figure 429: Phylogenetic_signal_of_deletion_plot.png

SSTR4_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
SSTR4	195	17	178	5	0.0306703384497591	0.999999999999996

Lastz Alignment evidence

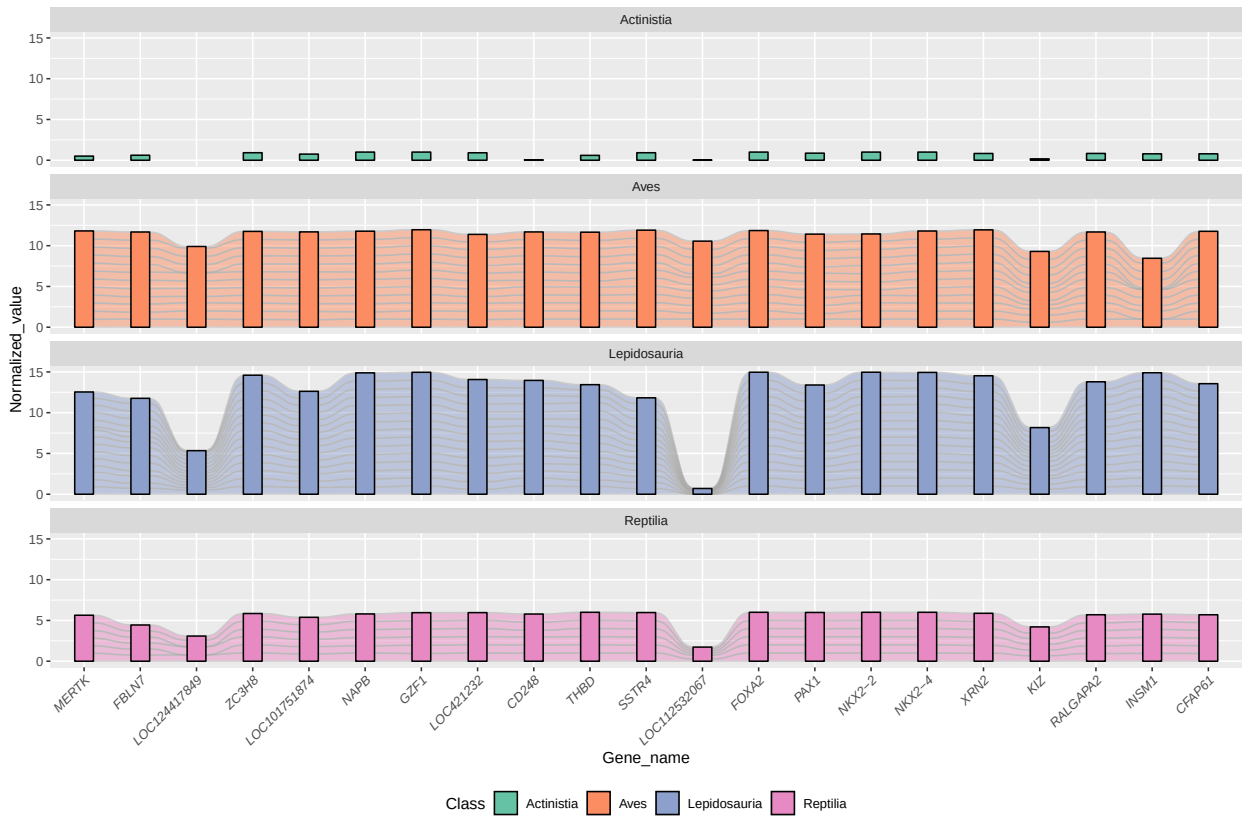


Figure 430: SSTR4.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

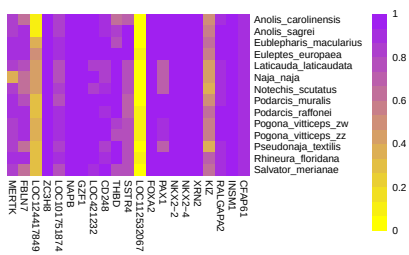


Figure 431: SSTR4.FS_Exonic.Final.Gallus_gallus.21_genes_heatmap.pdf

Lastz gene tree

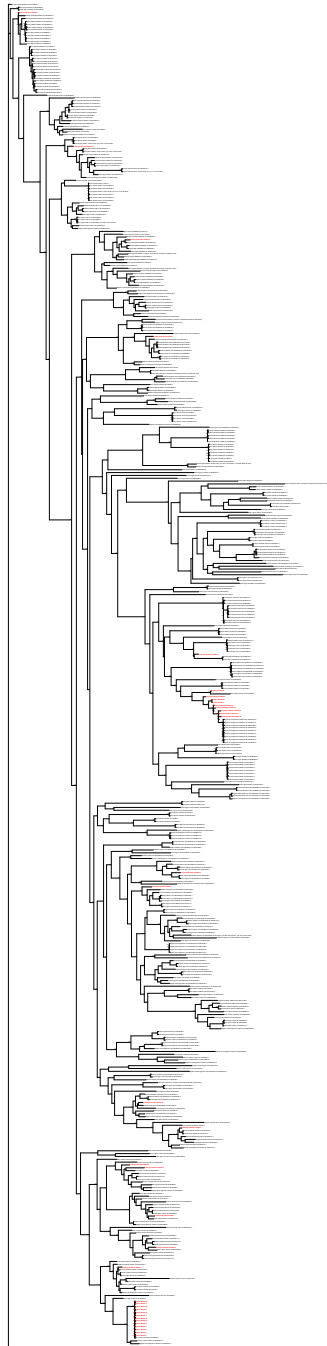


Figure 432: SSTR4.combined.mafft.aln.highlighted.pdf

Syntenic evidence

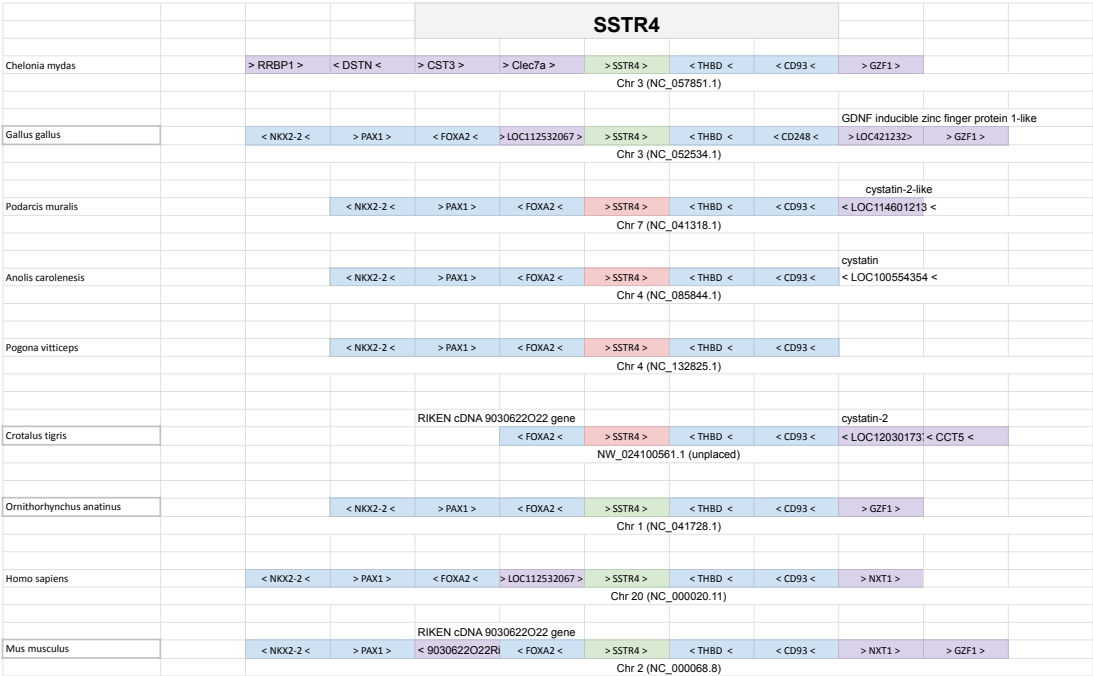


Figure 433: SSTR4.pdf

SSTR4.txt

Synteny analysis of SSTR4

We analyzed the synteny of SSTR4 across squamates and representative outgroups. The SSTR4 syntenic block is largely conserved, with the exception of one flanking side in Chelonia mydas. On this side, the expected flank < NKX2-2 < > PAX1 > < FOXA2 < is present after skipping several intervening genes, but in an inverted orientation compared to the conserved arrangement. In the synteny plots, red blocks indicate the absence of SSTR4, green blocks mark its presence, light blue blocks represent genes conserved across lineages, and light purple blocks denote different flanking genes.

Transcriptomic evidence Pogona vitticeps



Figure 434: SSTR4.png

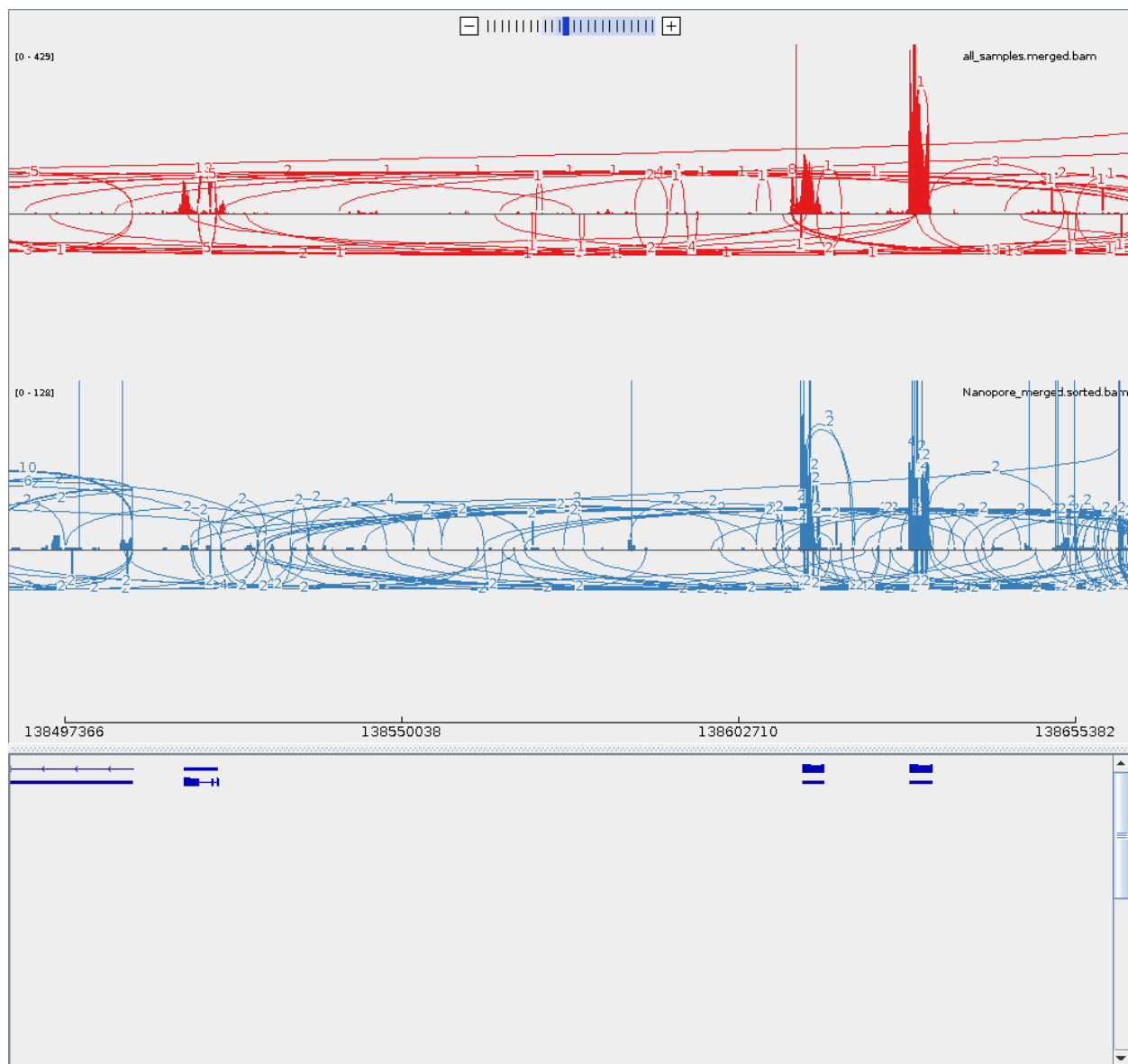


Figure 435: SSTR4_Shash.png

43 STAP1

Assembly verification Evidence

Crotalus_tigris-PacBio

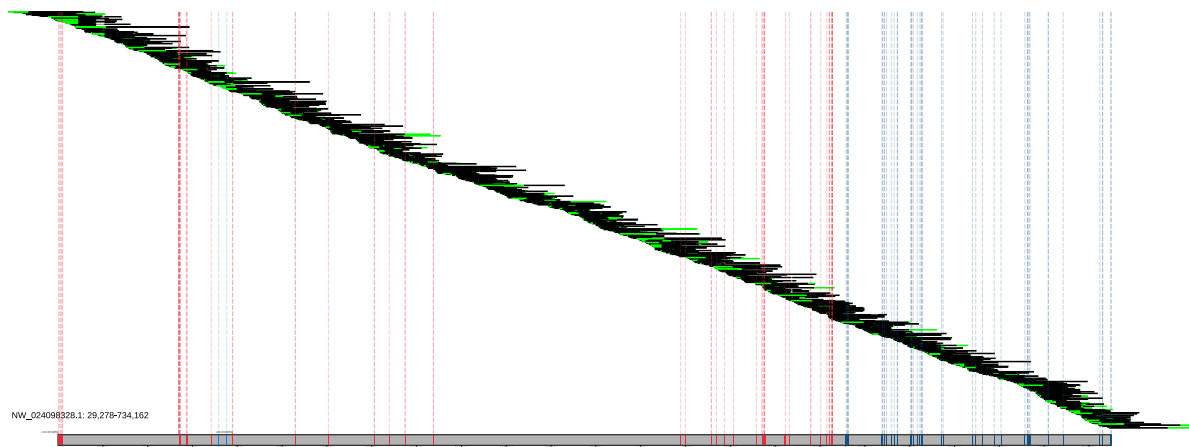


Figure 436: STAP1:NW_024098328.1:29278-734162.pdf

Podarcis_muralis-PacBio

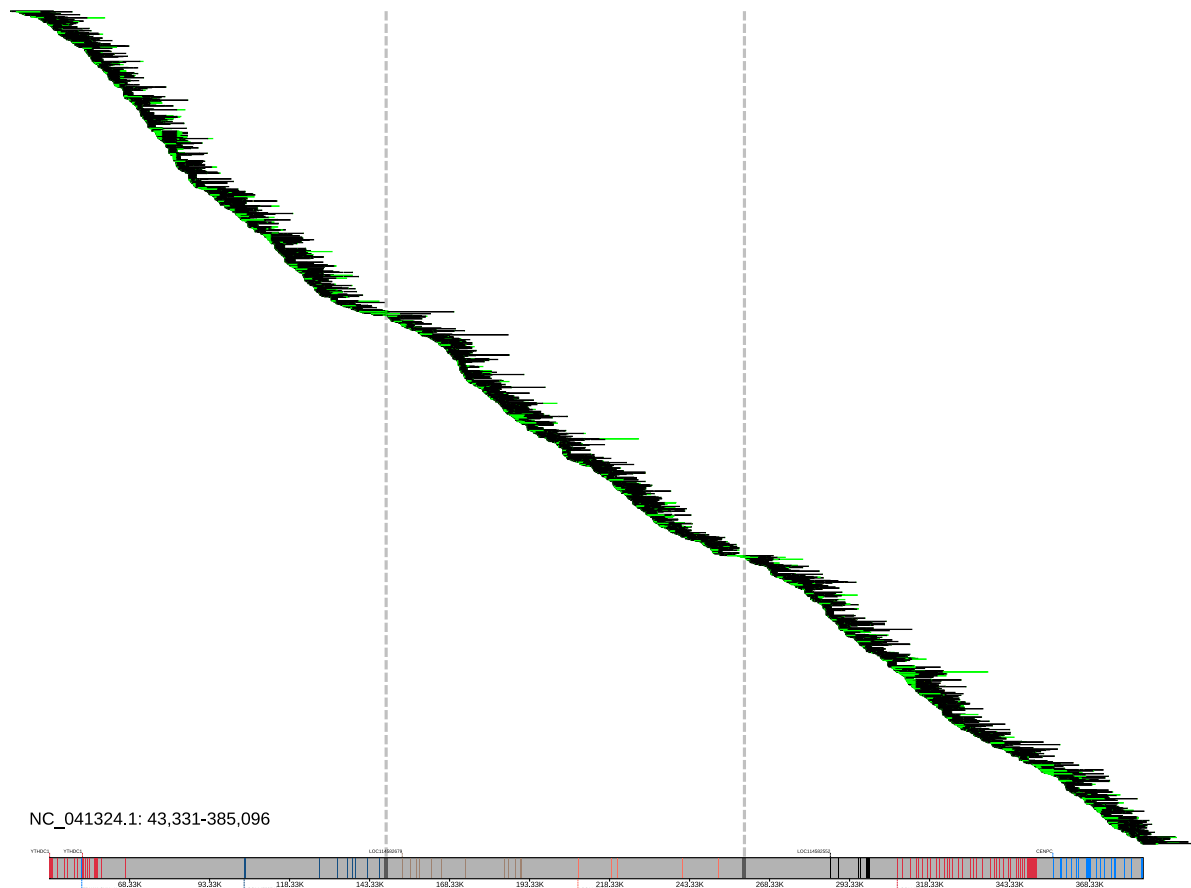


Figure 437: STAP1:NC_041324.1:43331-385096.pdf

Pogona_vitticeps-Nanopore

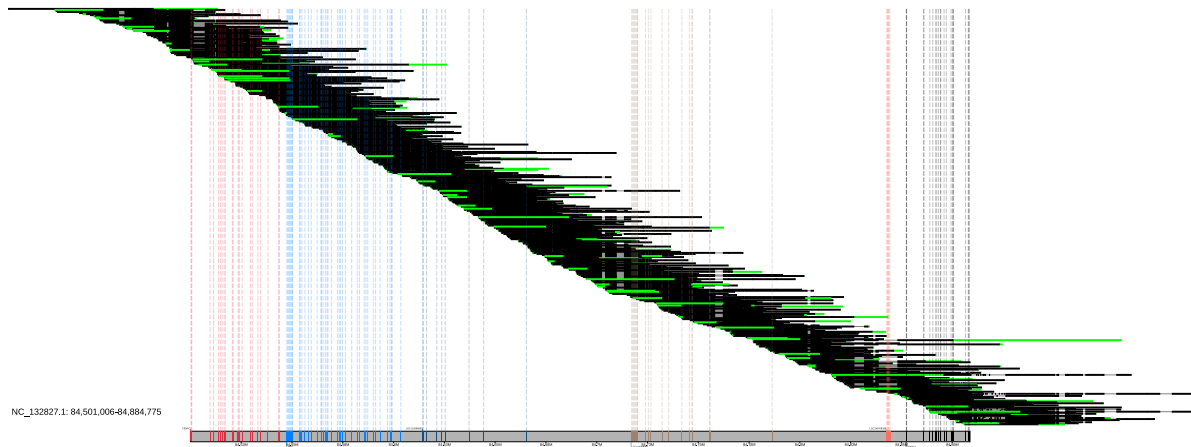


Figure 438: STAP1:NC_132827.1:84501006-84884775.pdf

Important gene stats

STAP1_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
STAP1	4.365217391	43.0135 +/- 2.76765	3.62437 +/- 0.164604	76.9943 +/- 15.3136	Yes	Na

Intergenic distance phylogenetic signal evidence

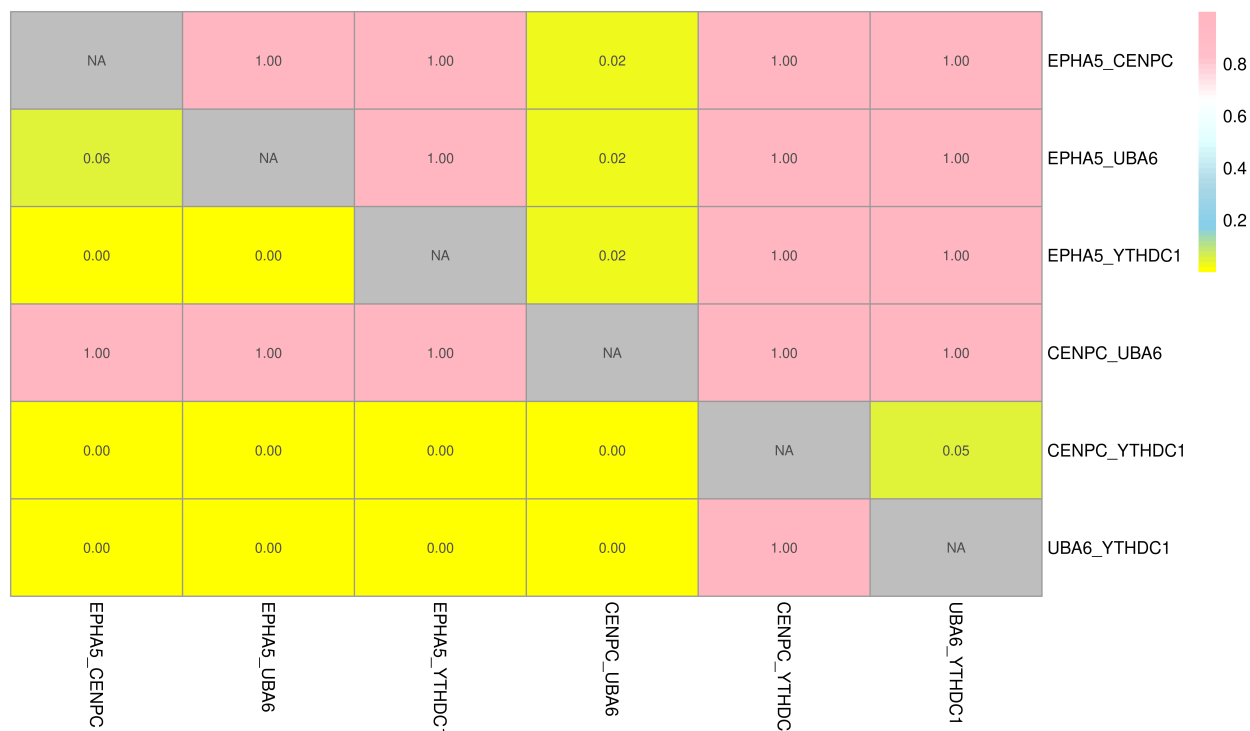


Figure 439: Heatmap_of_deletion_plot.png

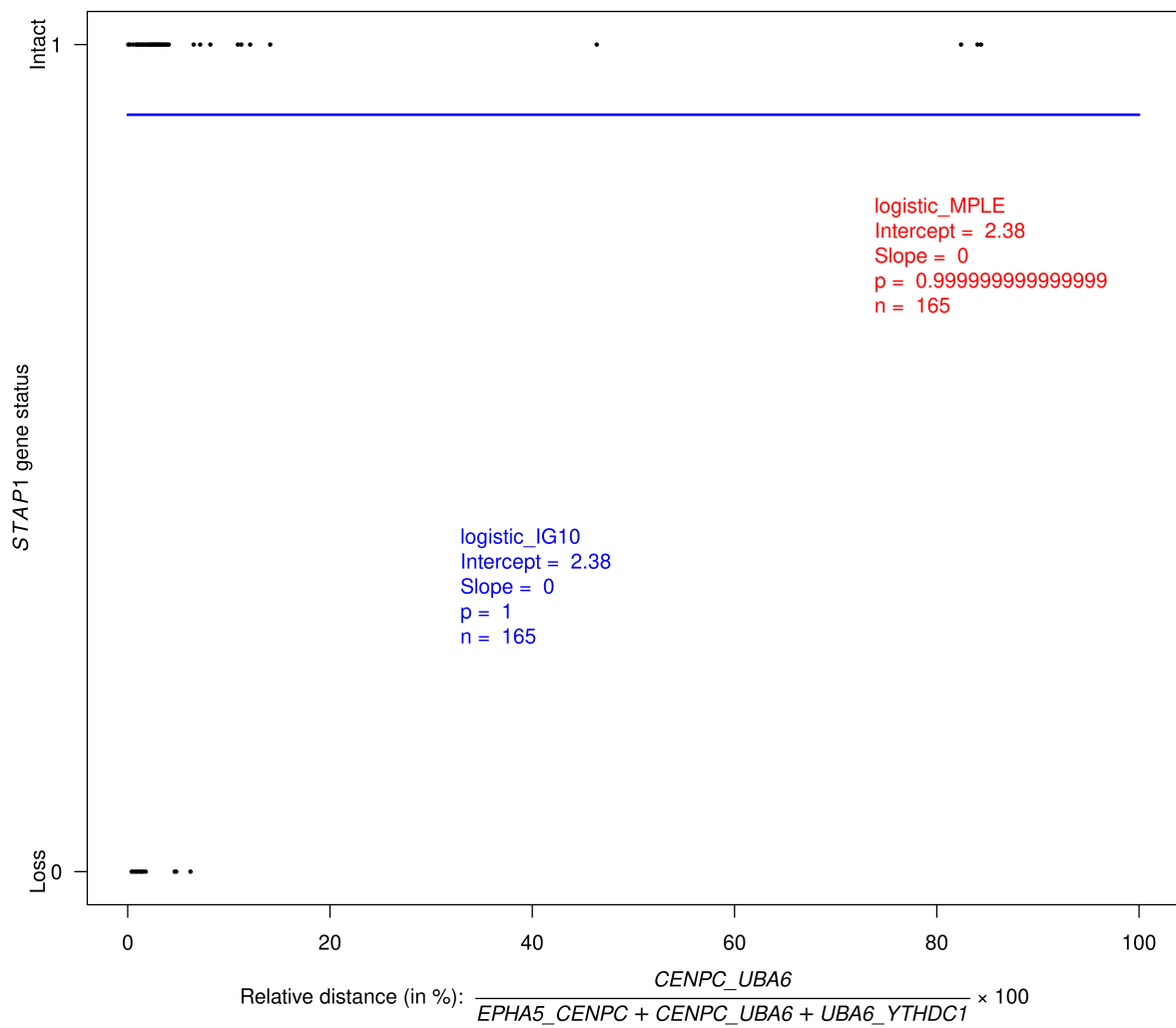


Figure 440: Phylogenetic_signal_of_deletion_plot.png

Lastz Alignment evidence

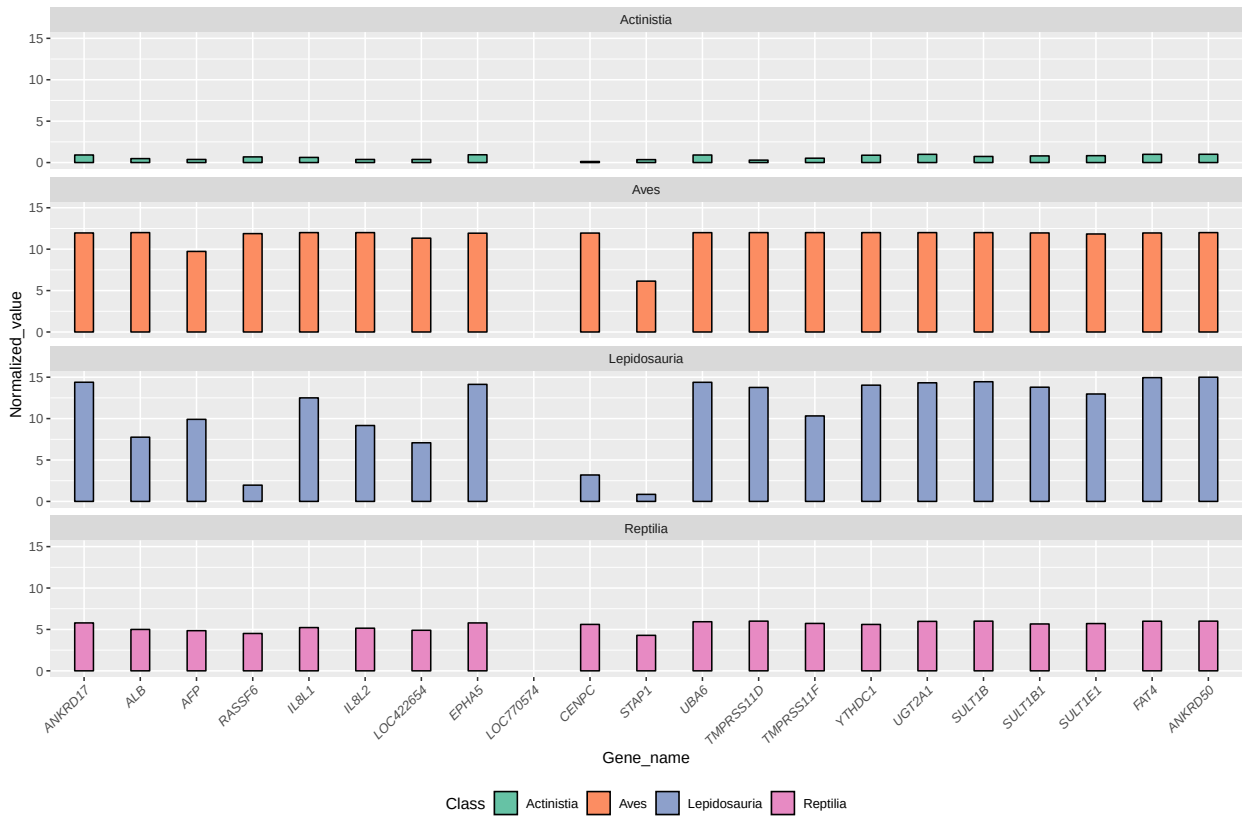


Figure 441: STAP1.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Syntenic evidence

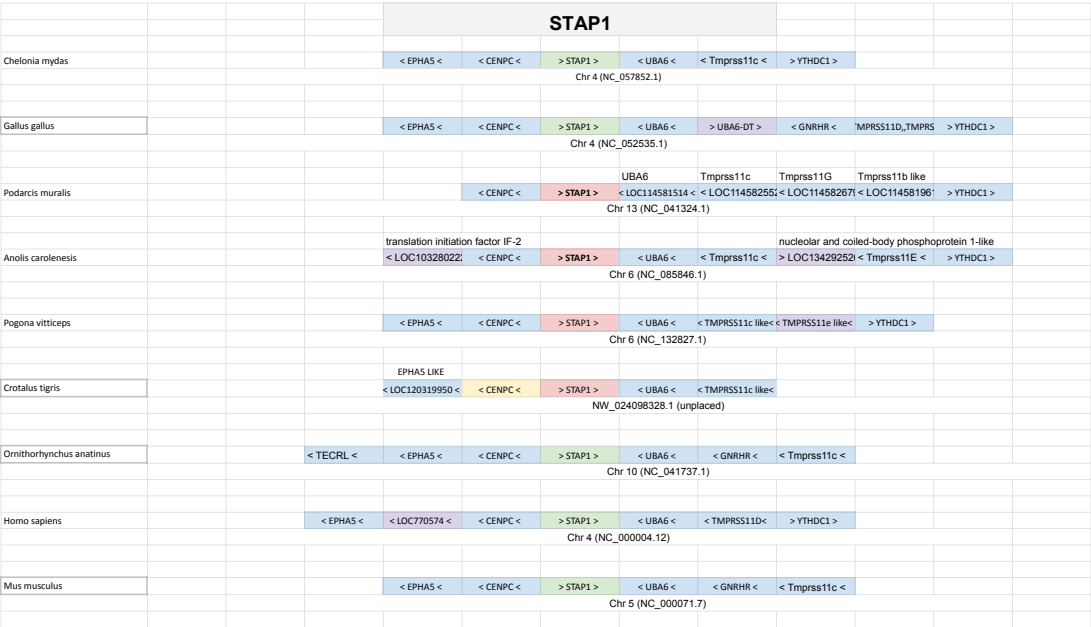


Figure 443: STAP1.pdf

STAP1.txt

Synteny analysis of STAP1

We analyzed the synteny of STAP1 across squamates and representative outgroups. The STAP1 syntenic block is conserved in all examined species. In the synteny plots, red blocks indicate the absence of STAP1, green blocks mark its presence, light blue blocks represent genes conserved across lineages, and light purple blocks denote different flanking genes.

Transcriptomic evidence *Pogona vitticeps*



Figure 444: STAP1.png

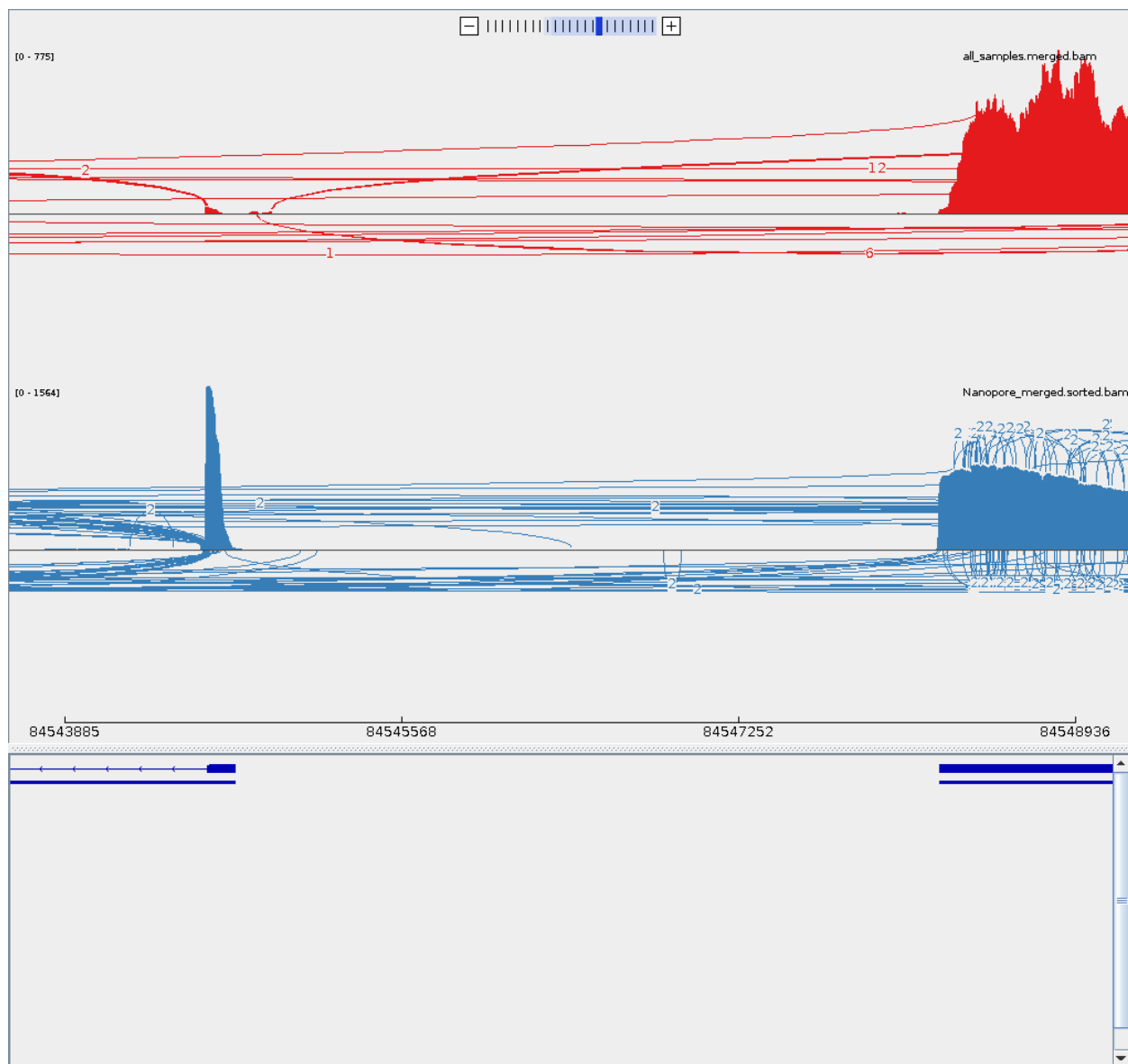


Figure 445: STAP1_Sashimi.png

44 STOML3

Important gene stats

STOML3_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
STOML3	33.55725191	50.6469 +/- 2.89453	3.69029 +/- 0.246395	76.4081 +/- 12.5648	Yes	LOC110082937;LOC116519176;LOC132763676;

Lastz Alignment evidence

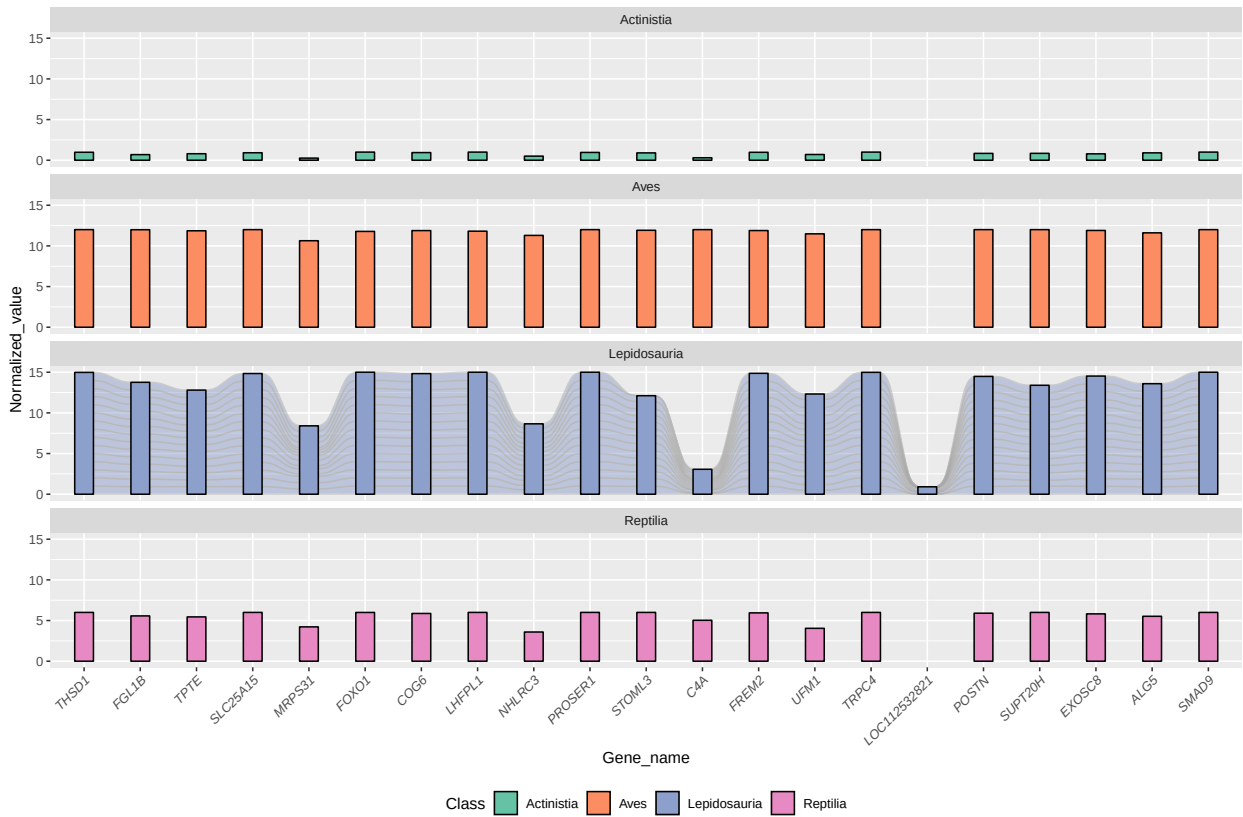


Figure 446: STOML3.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Lastz gene tree

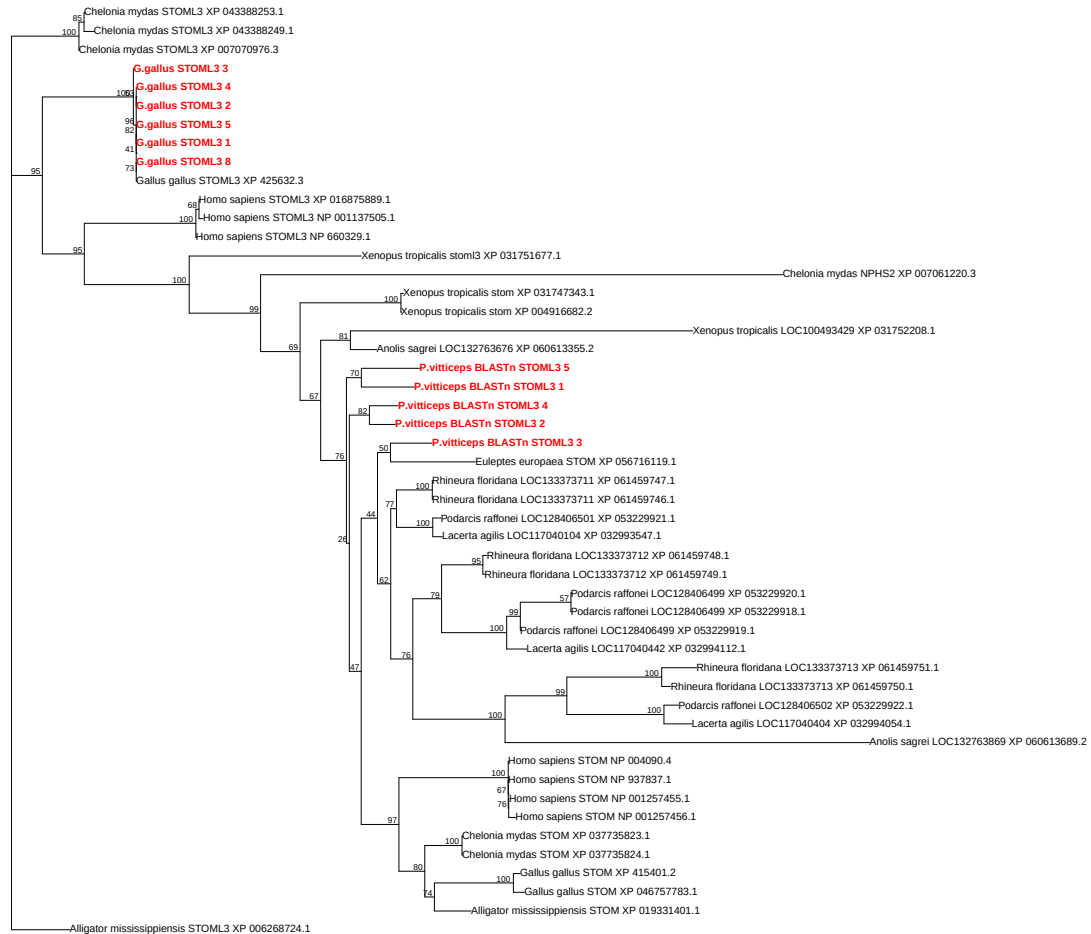


Figure 448: STOML3.combined.mafft.aln.highlighted.pdf

	FREM2, STOML3										
	complement C4										
<i>Chelonia mydas</i>	< POSTN <	< TRPC4 <	< LOC122463132	> UFM1 >	> FREM2 >	> LOC102944468	< STOML3 <	< PROSER1 <	> NHLRC3 >		
	Chr 1 (NC_057848.1)										
<i>Gallus gallus</i>	< POSTN <	< LOC112513821 <	< TRPC4 <	> UFM1 >	> FREM2 >	> CAA >	< STOML3 <	< PROSER1 <	> NHLRC3 >		
	NC_012512.1										
<i>Podarcis muralis</i>	< POSTN <	< TRPC4 <	> UFM1 >	> FREM2 >	< STOML3 <	> NHLRC3 >					
	Chr 17 (NC_041328.1)			Chr 8 (NC_041319.1)			Chr 1 (NC_04131 Chr 3 (NC_041314.1)				
<i>Anolis carolinensis</i>	< POSTN <	< TRPC4 <	> UFM1 >	> FREM2 >	< STOML3 <	< PROSER1 <	> NHLRC3 >	# PROSER1 and # NHLRC3 are present on the same chromosome but many genes apart			
	NW_026943819.1 (unplaced)										
<i>Pogona vitticeps</i>	< POSTN <	< TRPC4 <	> UFM1 >	> FREM2 >	< STOML3 <	< PROSER1 <	> NHLRC3 >	# PROSER1 and # NHLRC3 are present on the same chromosome but many genes apart!			
	Chr 2 (NC_132823.1)			Chr 8 (NC_132829.1)			Chr 1 (NC_132822.1)				
<i>Crotalus tigris</i>	< POSTN <	< TRPC4 <	> UFM1 >	> FREM2 >	< STOML3 <	< PROSER1 <	> NHLRC3 >	NW_024096970, NW_024097046.1 (unplaced)			
	NW_024097978, NW_024100094, NW_024100466.1 (unplaced)										
<i>Osmiahydnorhynchus anatinus</i>	< POSTN <	< TRPC4 <	> UFM1 >	> FREM2 >	> LOC114805871 <	< STOML3 <	> LOC114805871 <	> NHLRC3 >	< PROSER1 <		
	Chr 20 (NC_041747.1)										
<i>Homo sapiens</i>	< POSTN <	< TRPC4 <	> UFM1 >	> FREM2 >	< STOML3 <	< PROSER1 <	> NHLRC3 >				
	NC_000011.11										
<i>Mus musculus</i>	< POSTN <	< TRPC4 <	> UFM1 >	< Gm30735 <	> FREM2 >	< STOML3 <	< PROSER1 <	> NHLRC3 >			
	Chr 3 (NC_000069.7)										

Figure 449: STOML3.pdf

STOML3.txt

Synteny analysis of STOML3

The syntenic genes for STOML3 are located on multiple chromosomes,
 ↳ indicating an interchromosomal rearrangement. Additionally, one of
 ↳ the flanking genes also shows evidence of an intrachromosomal
 ↳ rearrangement.

In the synteny plots, red blocks indicate the absence of the target gene,
 ➔ while green blocks mark its presence. Light blue blocks represent
 ➔ flanking genes that are conserved across lineages, and light purple
 ➔ blocks denote instances where a different flanking gene is present.

45 SUV39H2

Assembly verification Evidence

Crotalus_tigris-PacBio

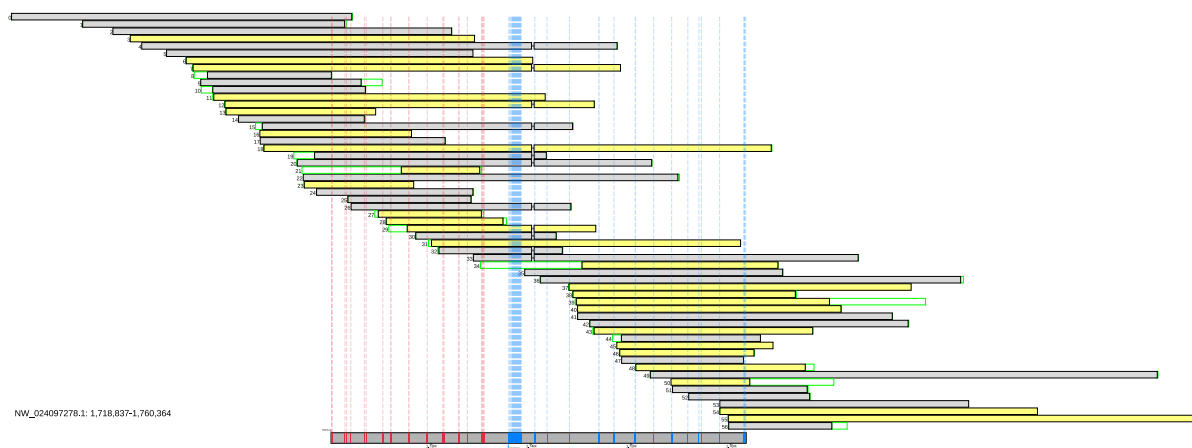


Figure 450: SUV39H2:NW_024097278.1:1718837-1760364.pdf

Podarcis_muralis-PacBio

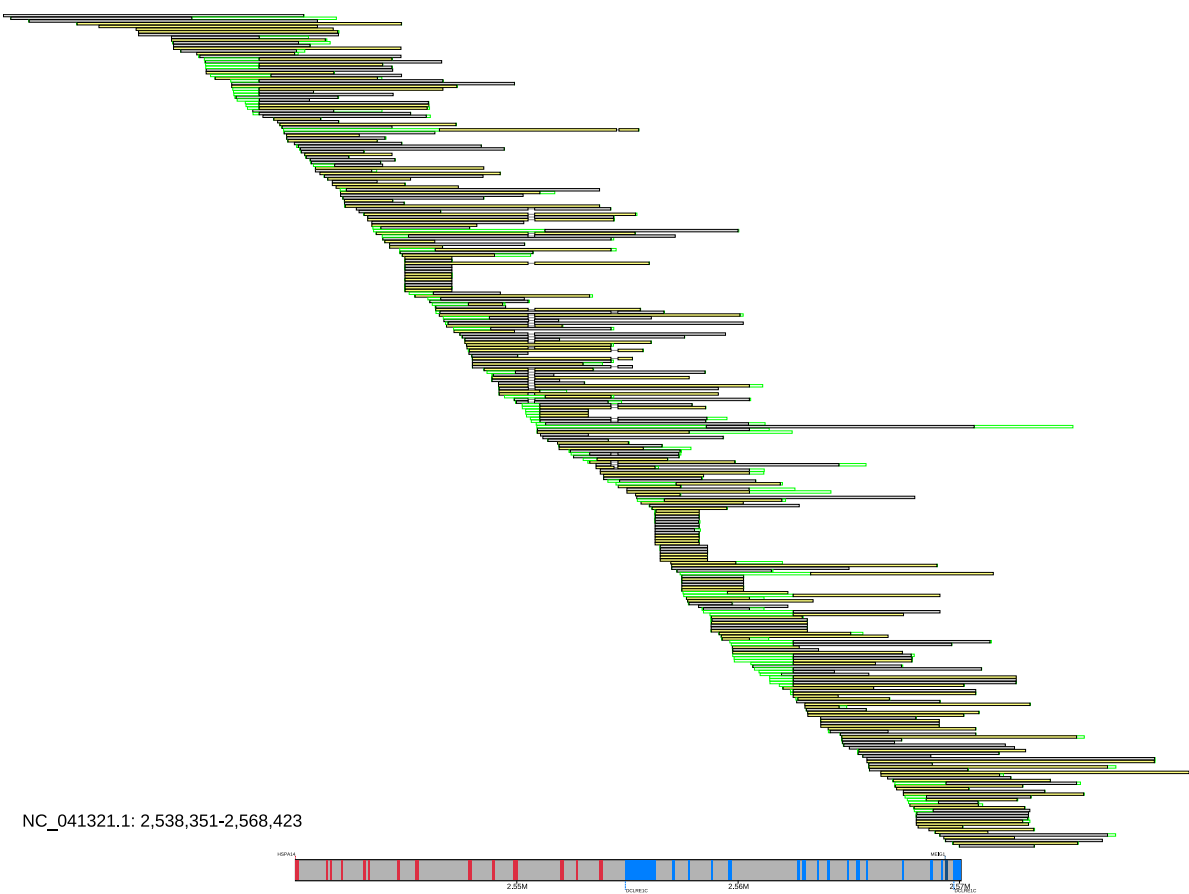


Figure 451: SUV39H2:NC_041321.1:2538351-2568423.pdf

Pogona_vitticeps-Nanopore

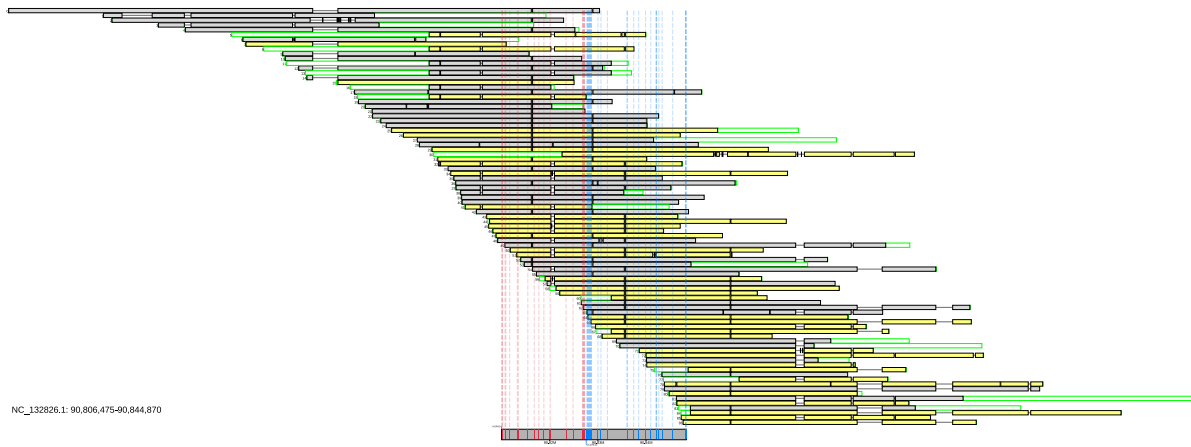


Figure 452: SUV39H2:NC_132826.1:90806475-90844870.pdf

Important gene stats

SUV39H2_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
SUV39H2	23.98473282	42.617 +/- 2.81379	3.95263 +/- 0.471771	81.6558 +/- 11.6191	Yes	SUV39H1;

Intergenic distance phylogenetic signal evidence

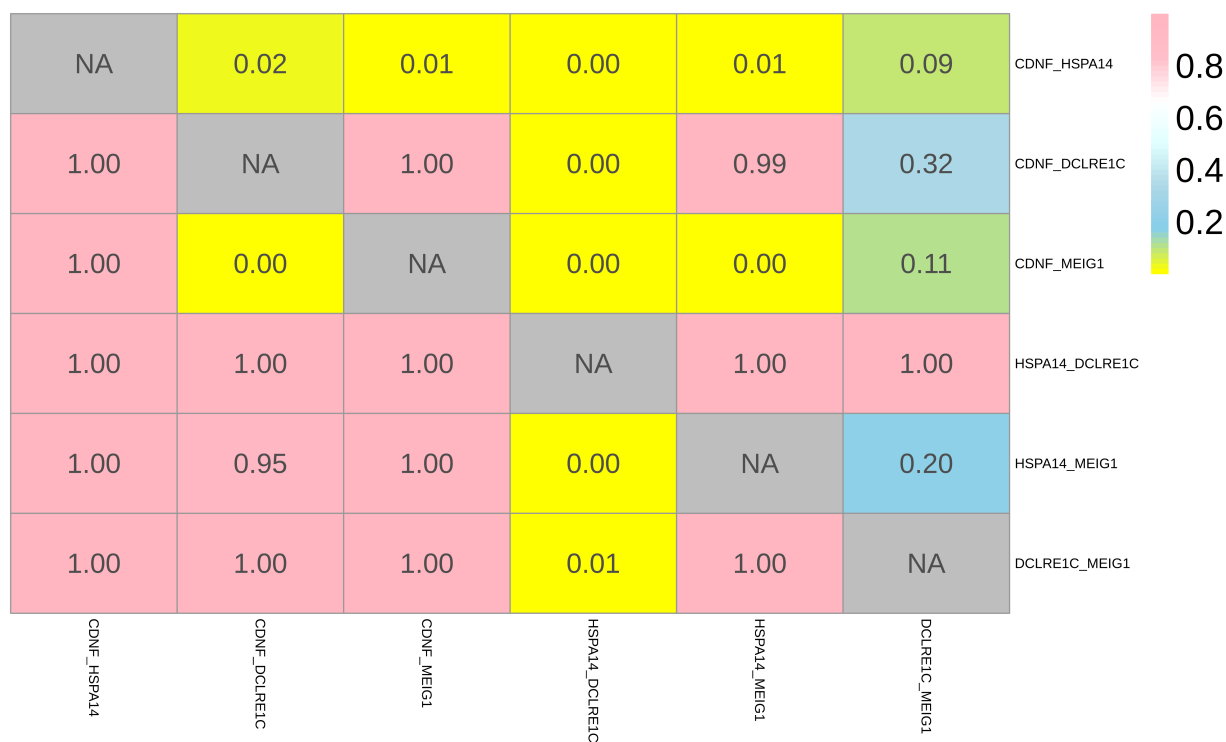


Figure 453: Heatmap_of_deletion_plot.png

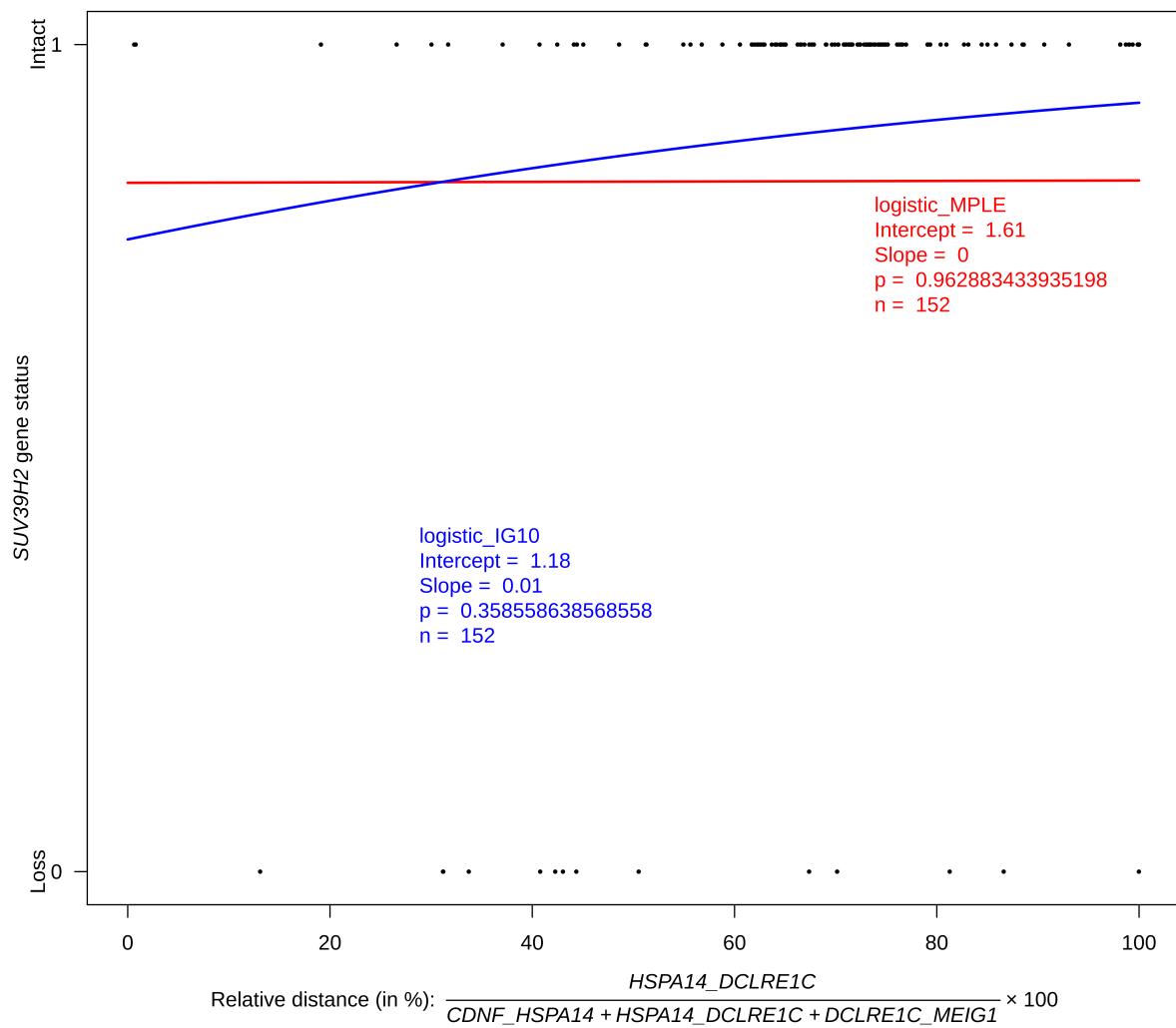


Figure 454: Phylogenetic_signal_of_deletion_plot.png

SUV39H2_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
SUV39H2	152	14	138	5	0.358558638568558	0.962883433935198



Figure 455: Heatmap_of_deletion_plot.png

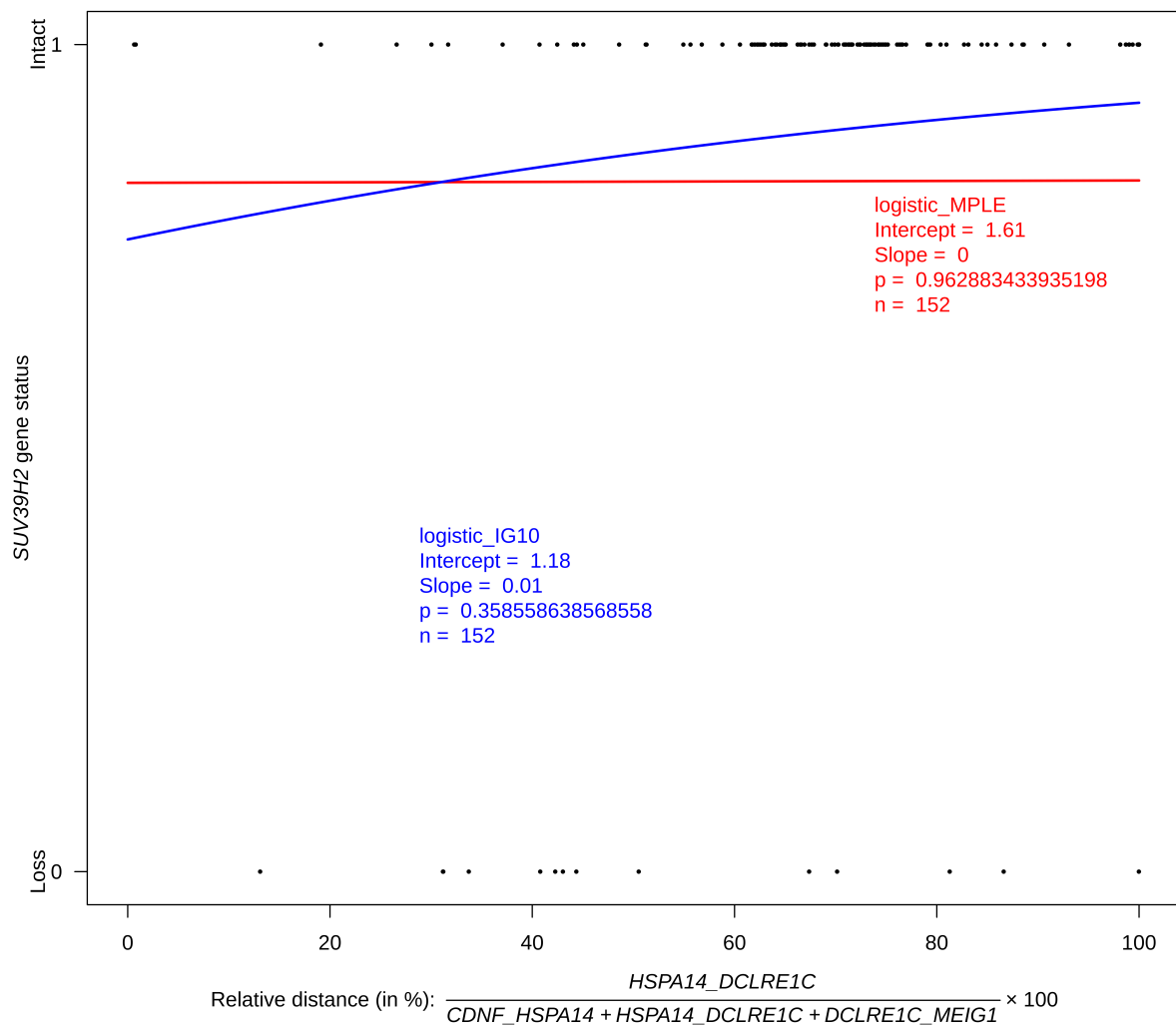


Figure 456: Phylogenetic_signal_of_deletion_plot.png

SUV39H2_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
SUV39H2	152	14	138	5	0.358558638568558	0.962883433935198

Lastz Alignment evidence

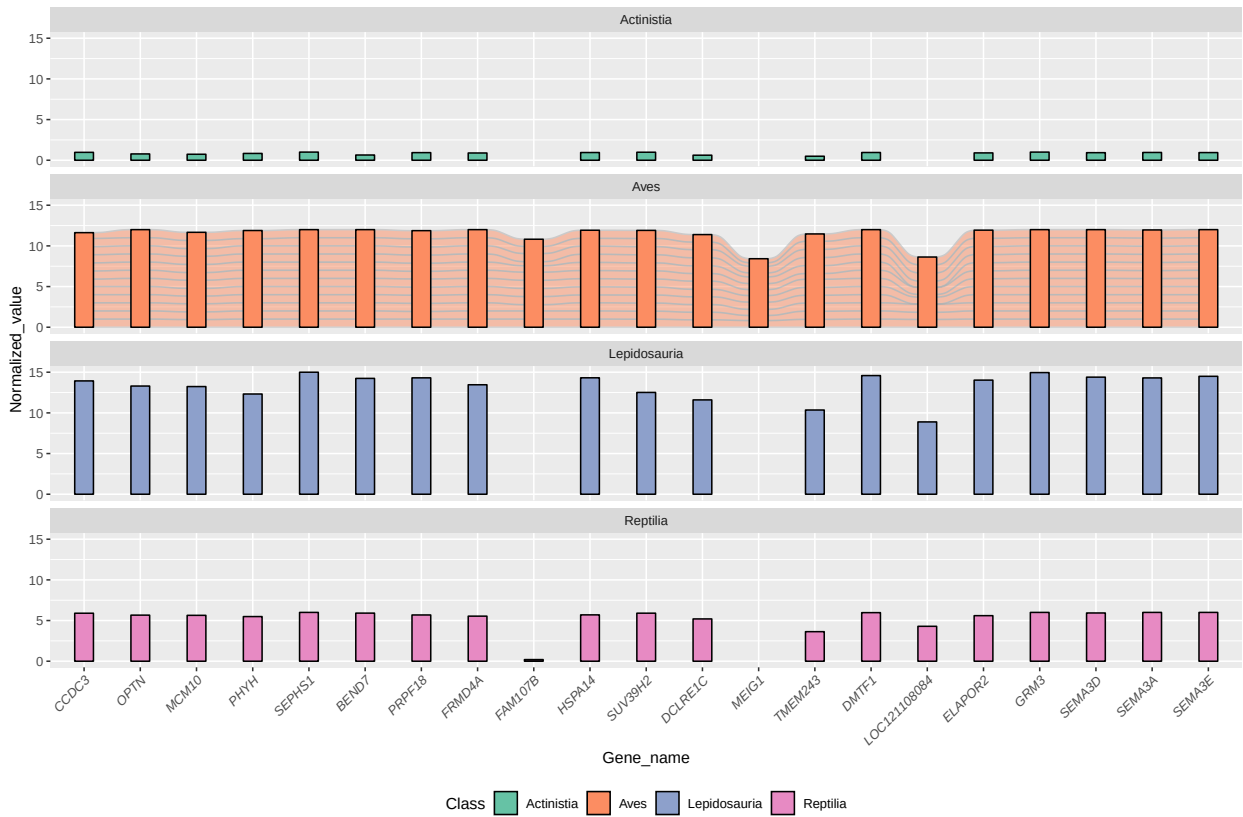


Figure 457: SUV39H2.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Lastz gene tree

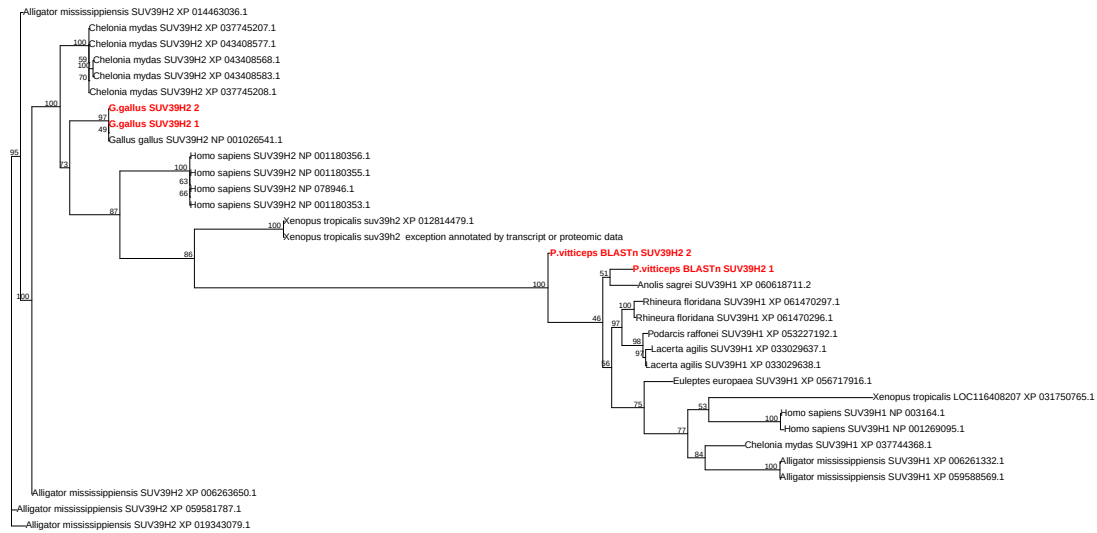


Figure 459: SUV39H2.combined.mafft.aln.highlighted.pdf

Syntenic evidence



Figure 460: SUV39H2.pdf

SUV39H2.txt

Synteny analysis of SUV39H2

We analyzed the synteny of SUV39H2 across squamates and representative outgroups. The SUV39H2 syntenic block is mostly conserved, with minor variations in some lineages. In the synteny plots, red blocks indicate the absence of SUV39H2, green blocks mark its presence, light blue blocks represent genes conserved across lineages, and light purple blocks denote different flanking genes.

Transcriptomic evidence Pogona vitticeps



Figure 461: SUV39H2.png

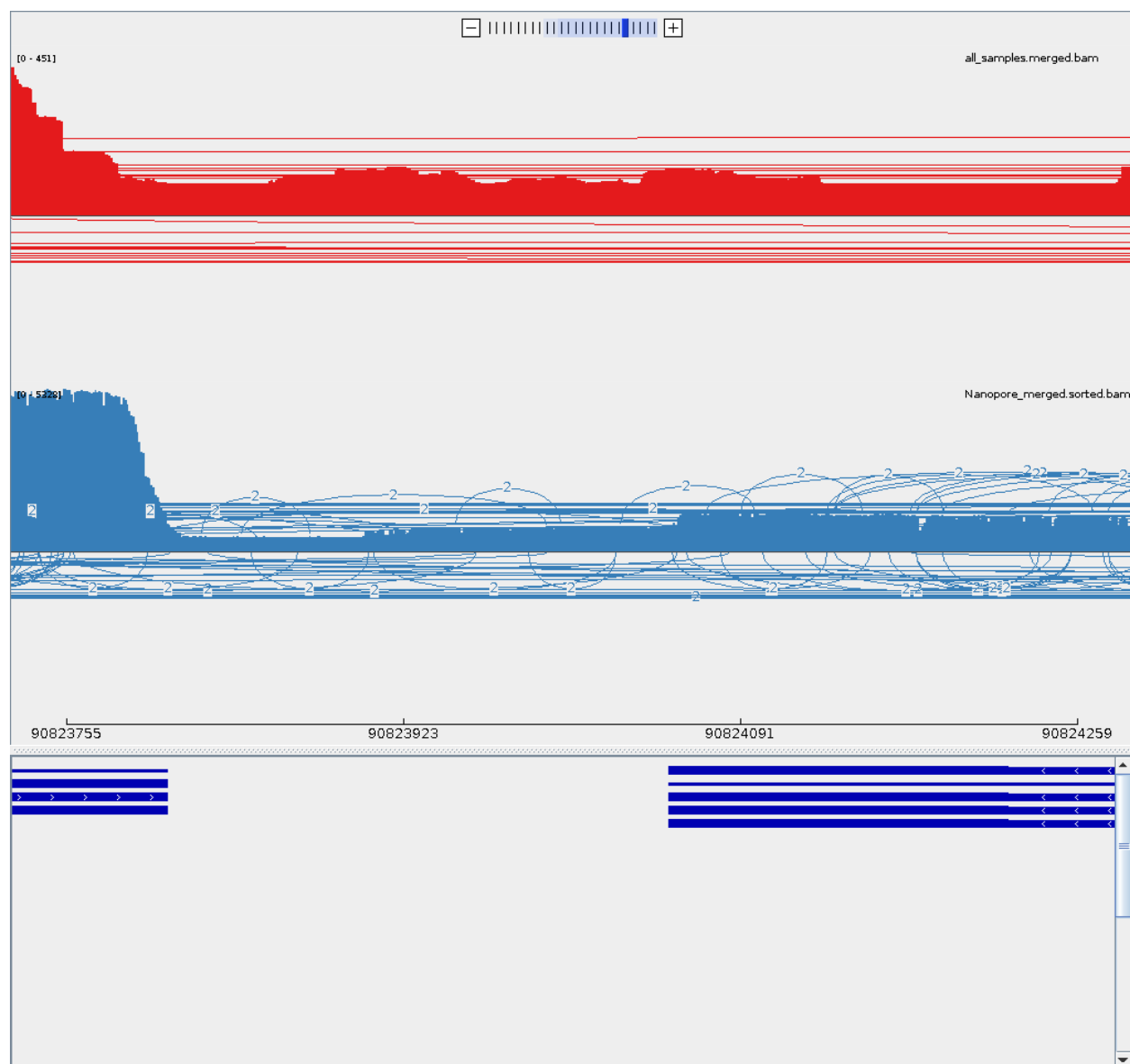


Figure 462: SUV39H2_Sashimi.png

46 TBC1D14

Assembly verification Evidence

Crotalus_tigris-PacBio

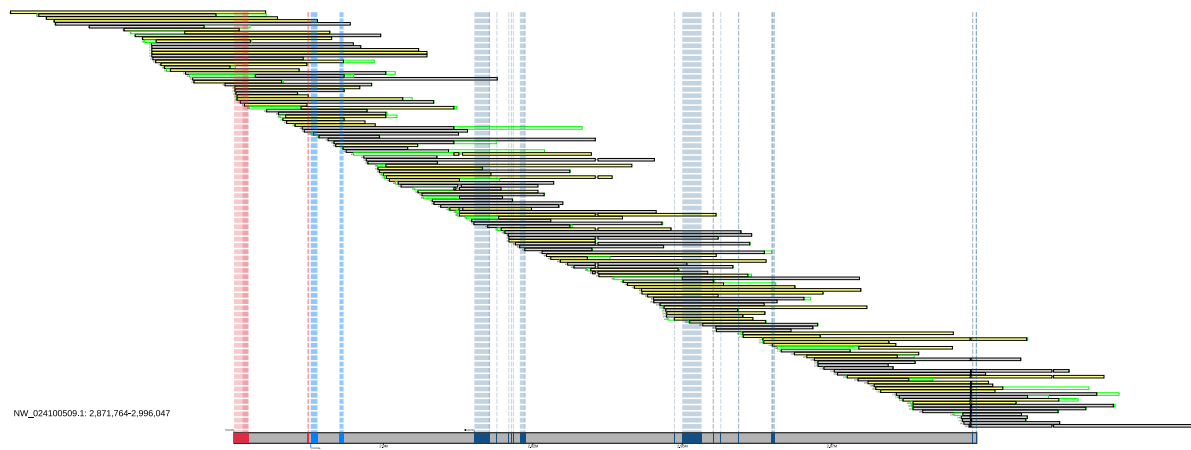


Figure 463: TBC1D14:NW_024100509.1:2871764-2996047.pdf

Podarcis_muralis-PacBio

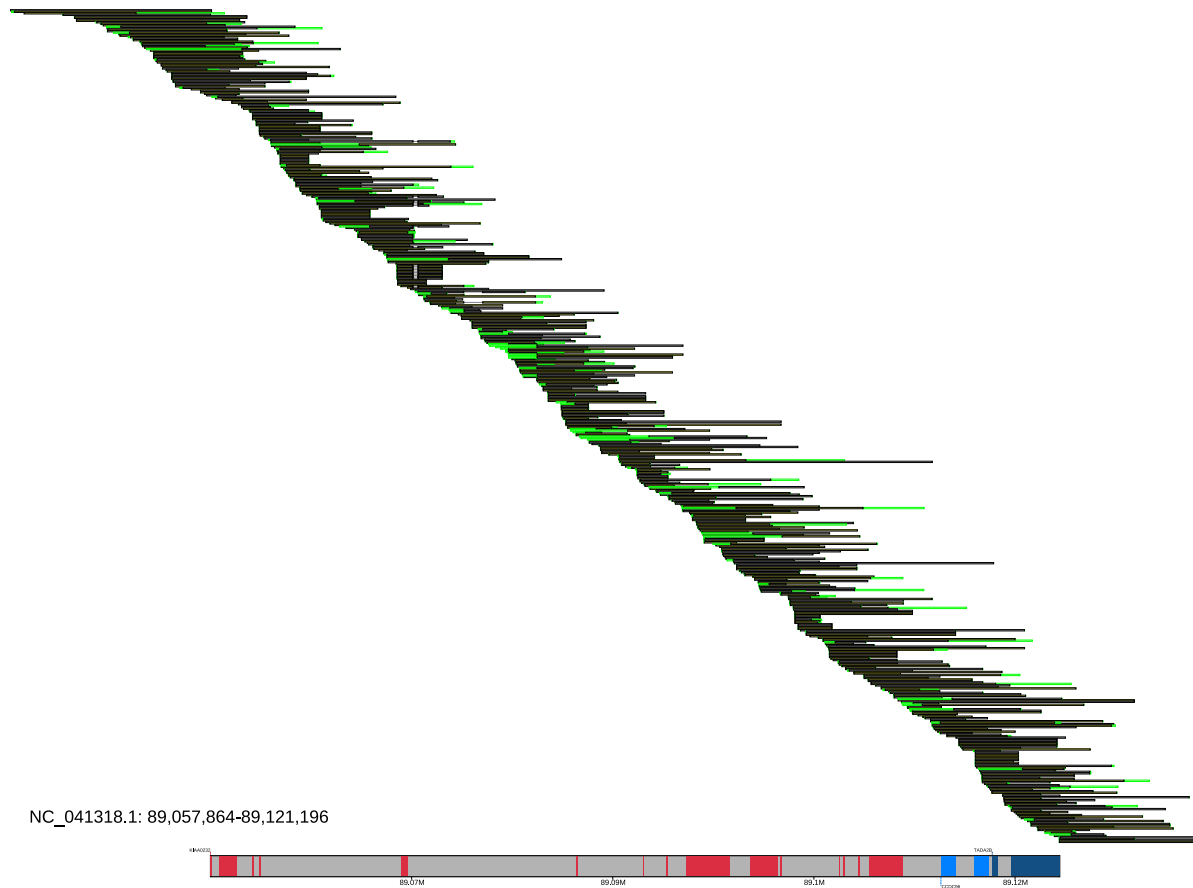


Figure 464: TBC1D14:NC_041318.1:89057864-89121196.pdf

Pogona_vitticeps-Nanopore

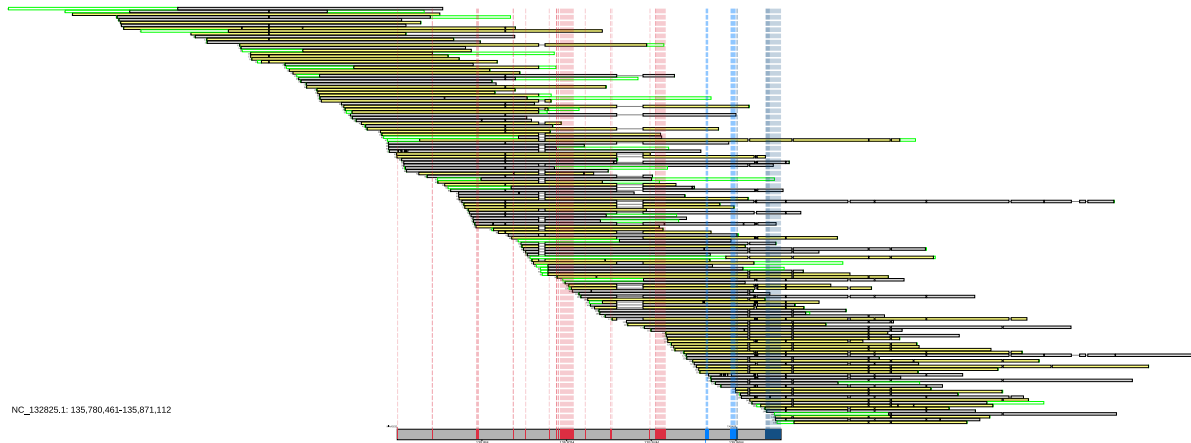


Figure 465: TBC1D14:NC_132825.1:135780461-135871112.pdf

Important gene stats

TBC1D14_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
TBC1D14	22.97718631	50.496 +/- 5.69818	3.84368 +/- 0.331527	70.0982 +/- 12.6112	Yes	Na

Intergenic distance phylogenetic signal evidence

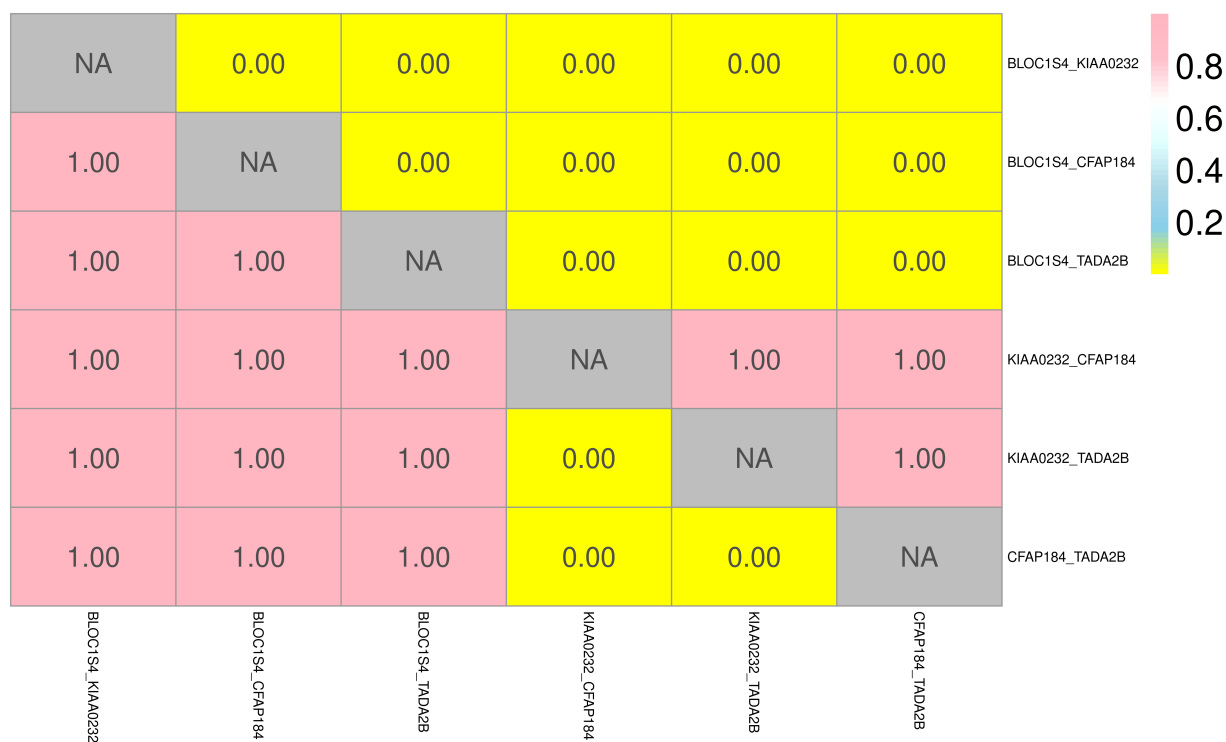


Figure 466: Heatmap_of_deletion_plot.png

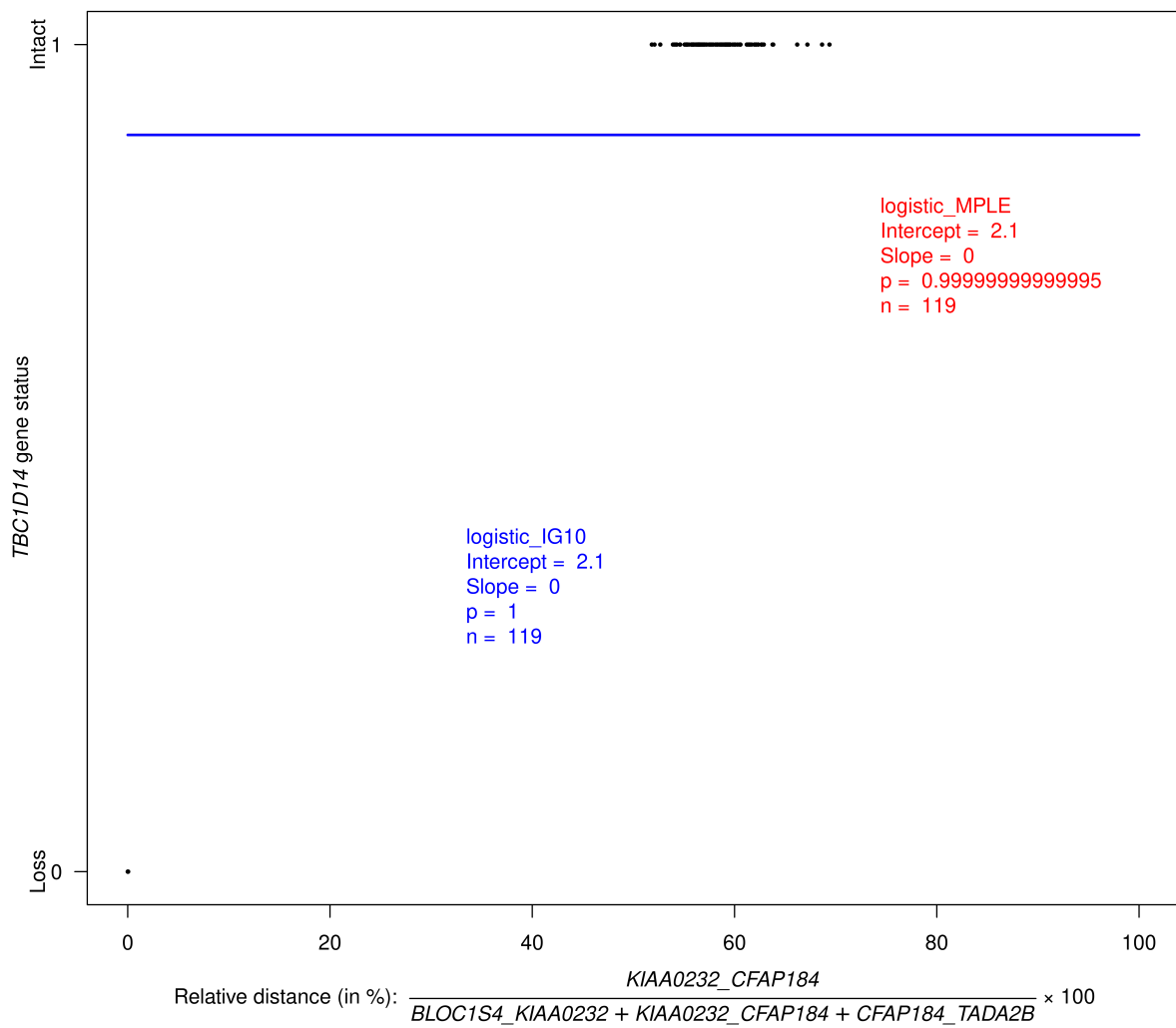


Figure 467: Phylogenetic_signal_of_deletion_plot.png

TBC1D14_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
TBC1D14	119	13	106	5	1	0.999999999999995

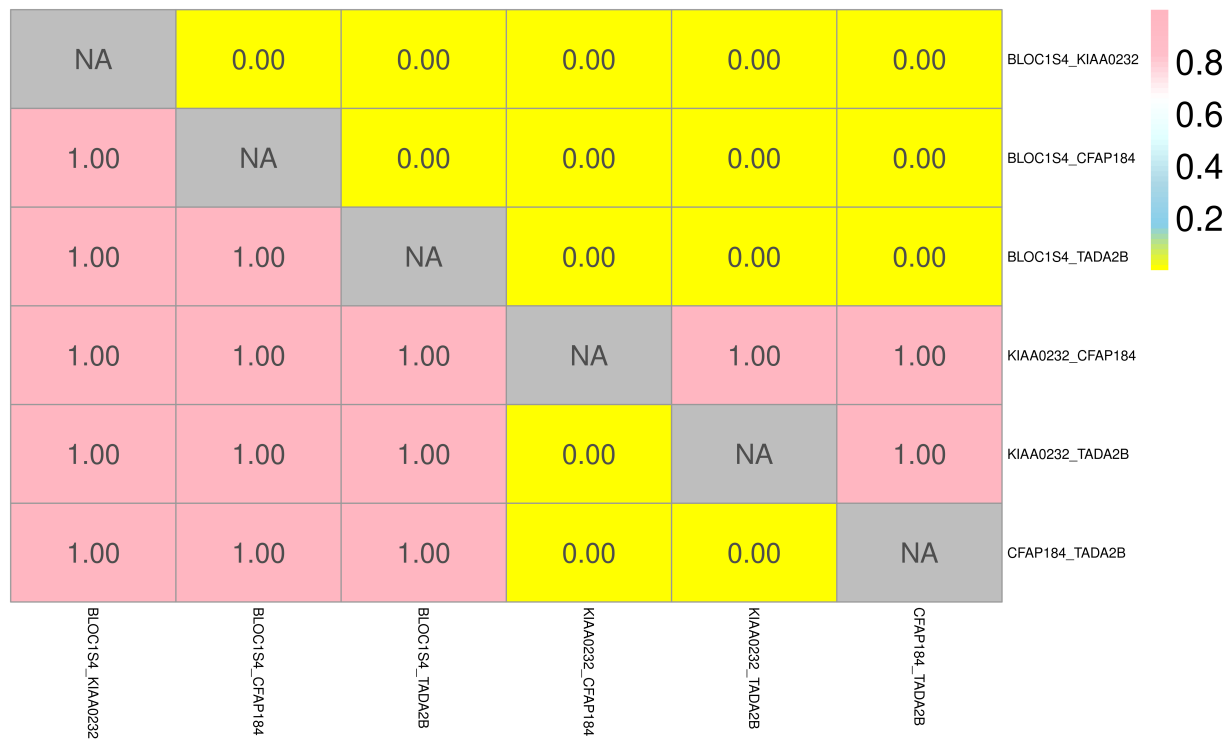


Figure 468: Heatmap_of_deletion_plot.png

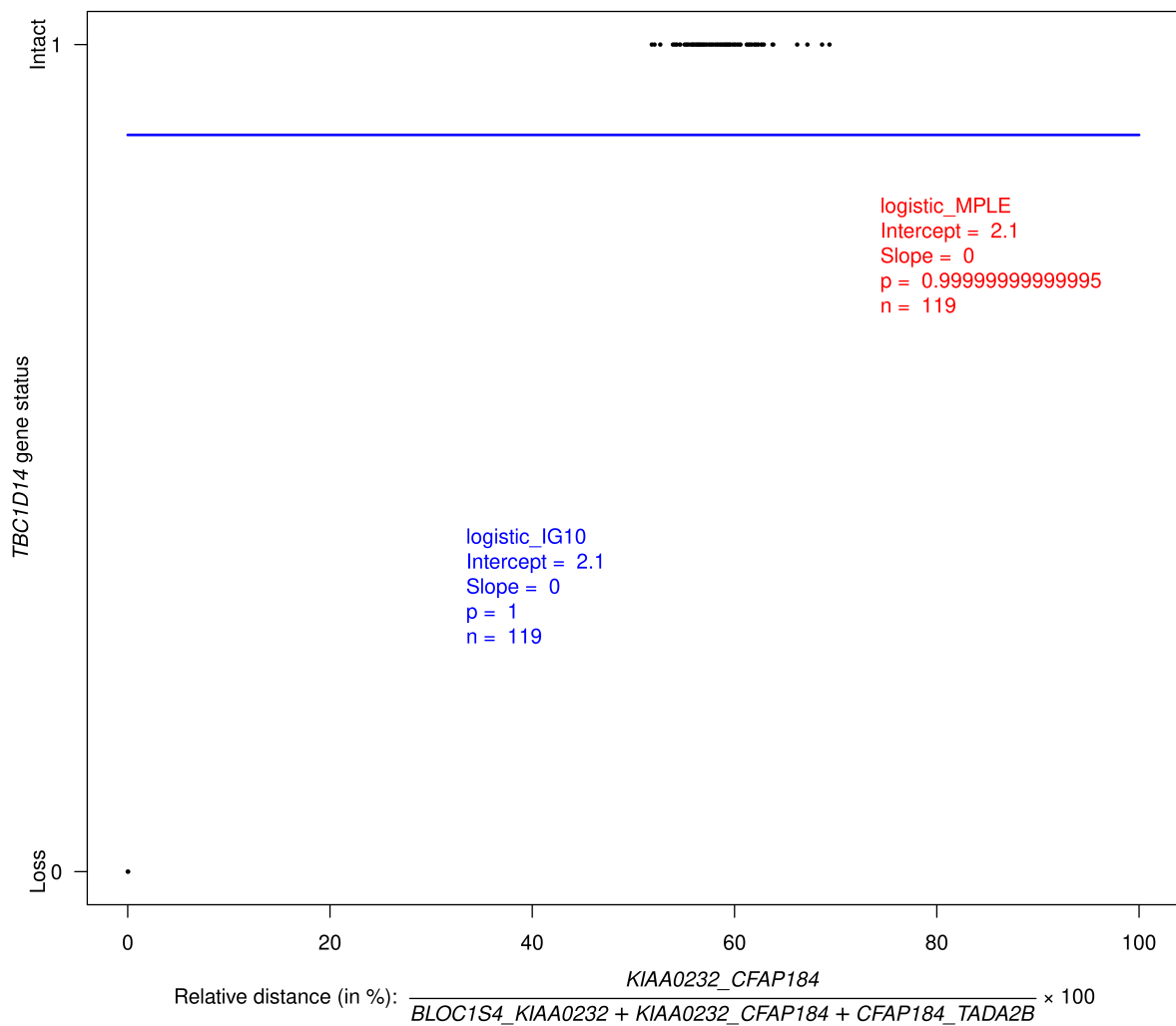


Figure 469: Phylogenetic_signal_of_deletion_plot.png

TBC1D14_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
TBC1D14	119	13	106	5	1	0.999999999999995

Lastz Alignment evidence

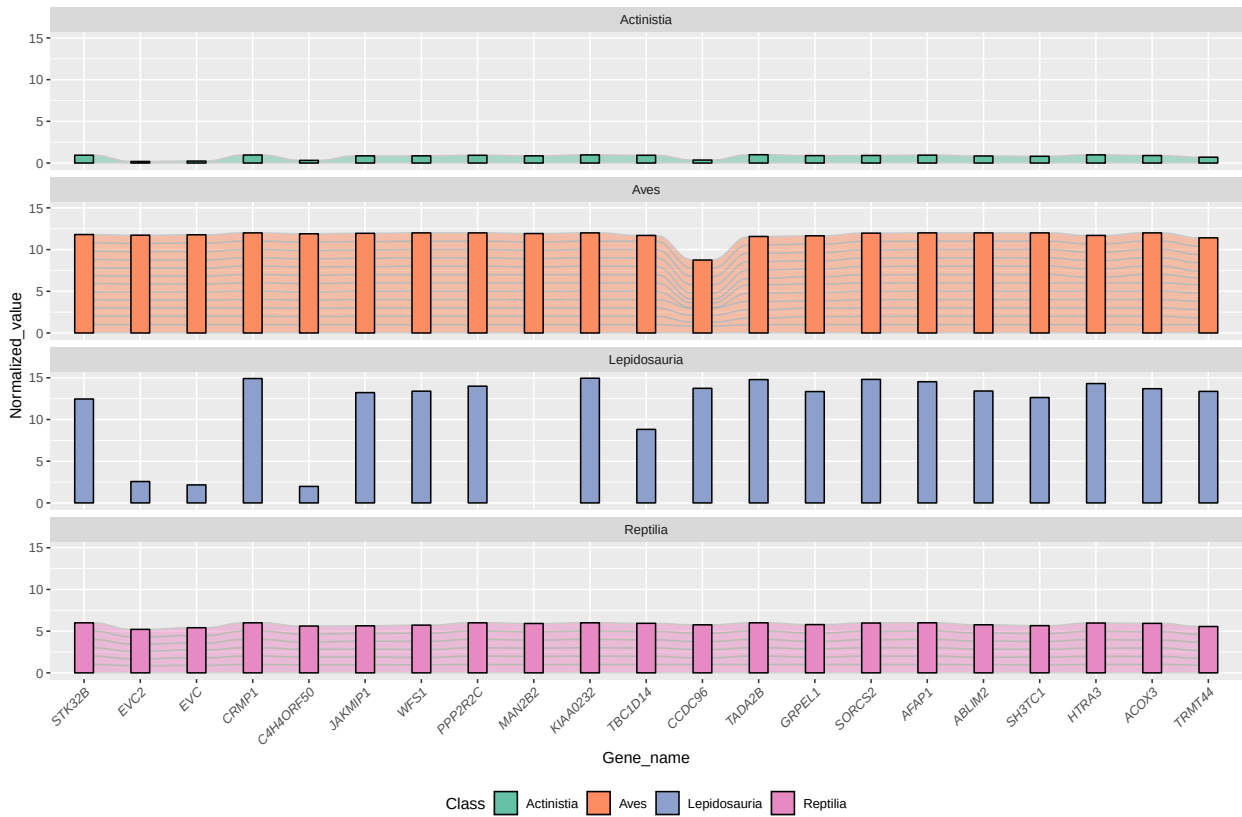


Figure 470: TBC1D14.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

Lastz gene tree

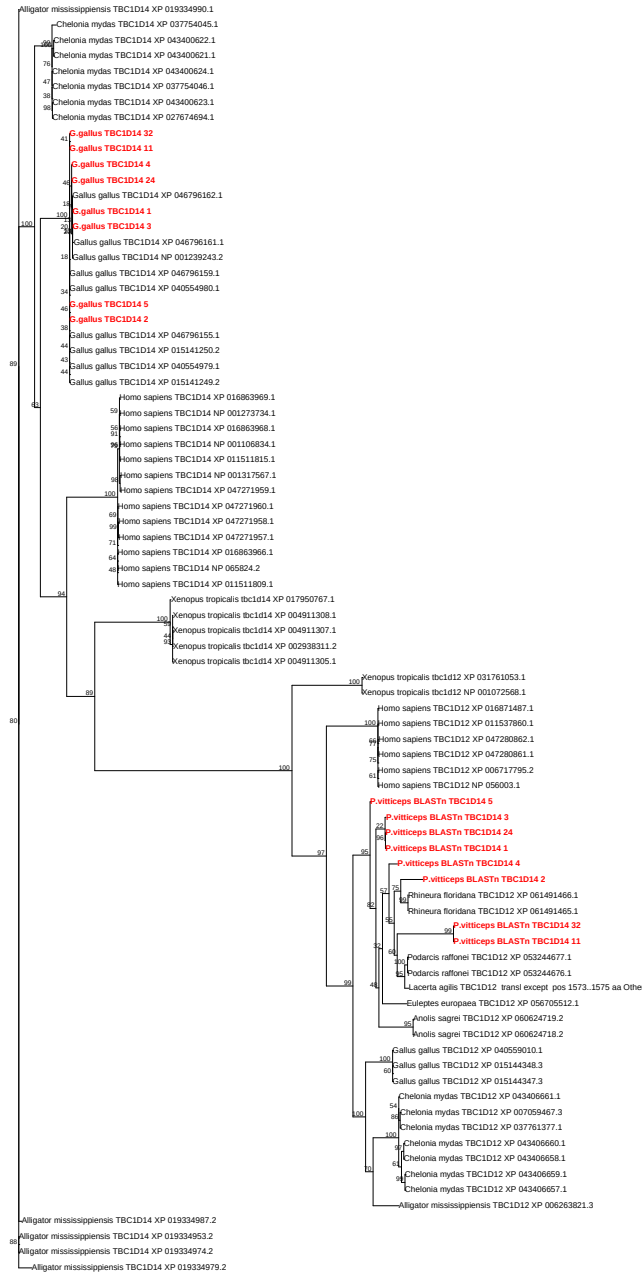


Figure 472: TBC1D14.combined.mafft.aln.highlighted.pdf

Syntenic evidence

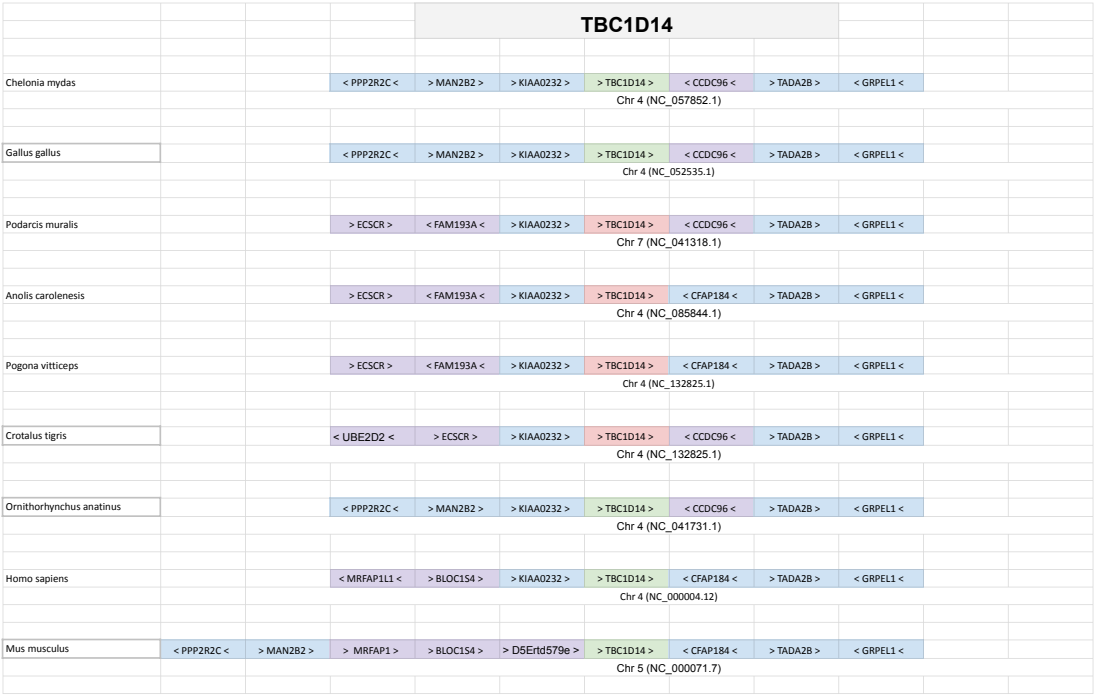


Figure 473: TBC1D14.pdf

TBC1D14.txt

Synteny analysis of TBC1D14

We analyzed the synteny of TBC1D14 across squamates and representative outgroups. The TBC1D14 syntenic block is mostly conserved, with minor variations in some lineages. In the synteny plots, red blocks indicate the absence of TBC1D14, green blocks mark its presence, light blue blocks represent genes conserved across lineages, and light purple blocks denote different flanking genes.

Transcriptomic evidence Pogona vitticeps

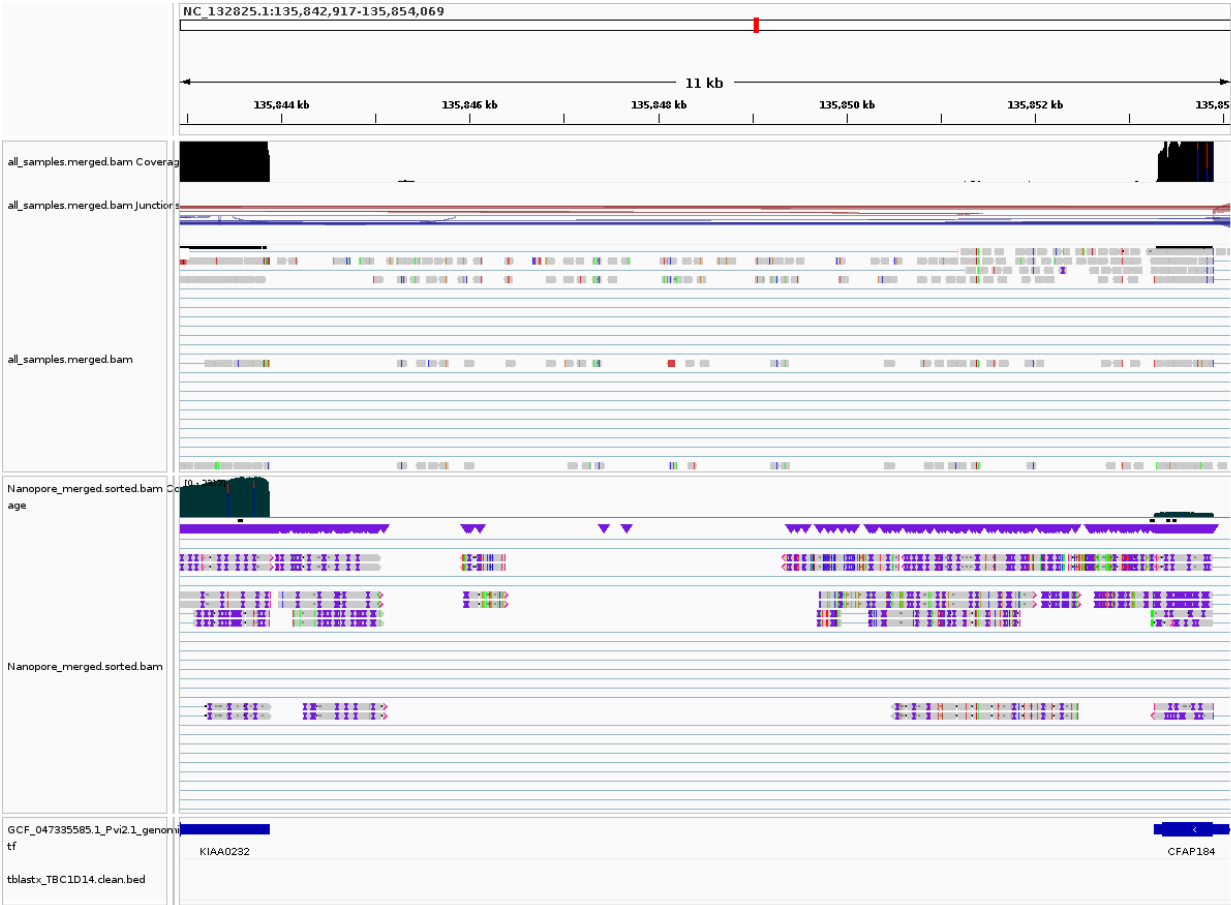


Figure 474: TBC1D14.png

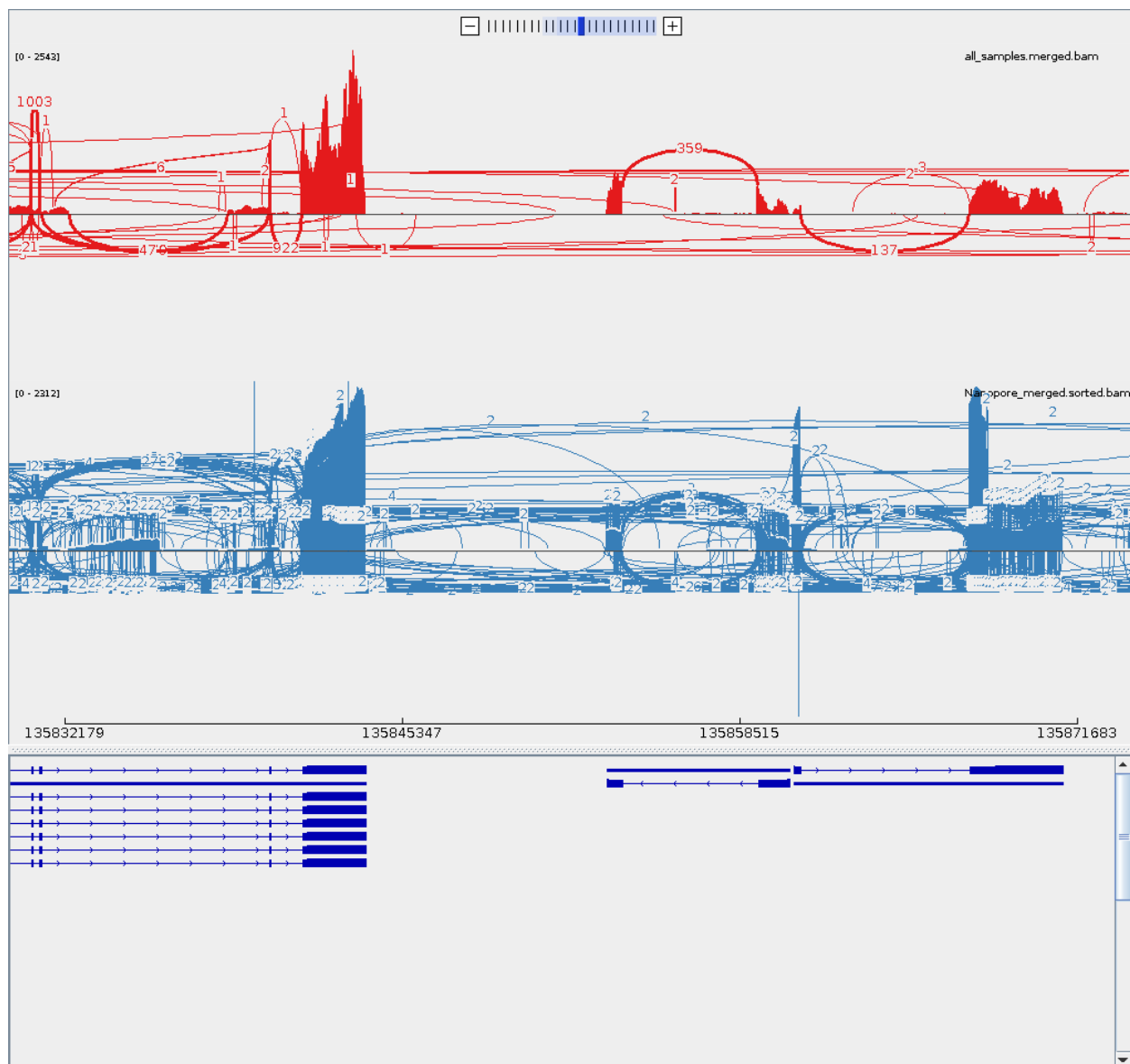


Figure 475: TBC1D14_Sashimi.png

47 TMEM273

Assembly verification Evidence

Crotalus_tigris-PacBio

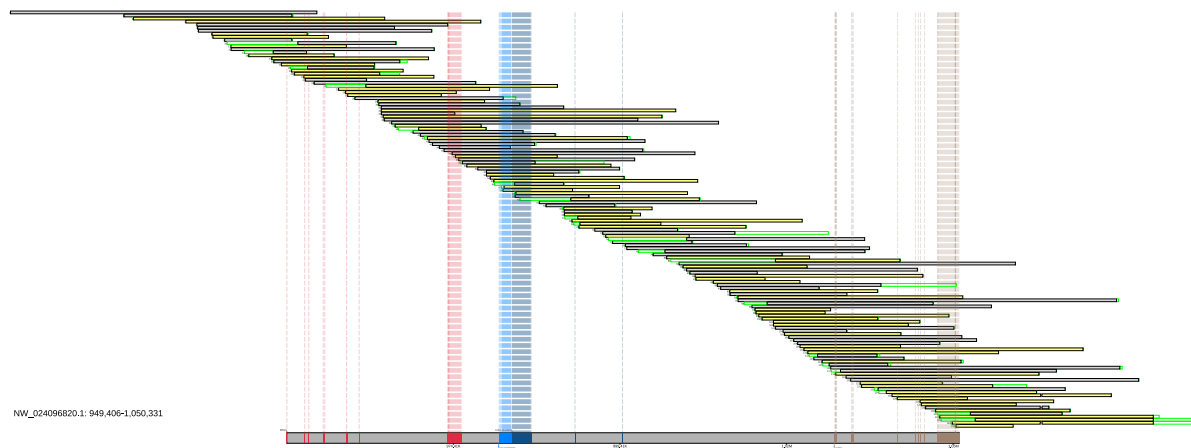


Figure 476: TMEM273:NW_024096820.1:949406-1050331.pdf

Podarcis_muralis-PacBio

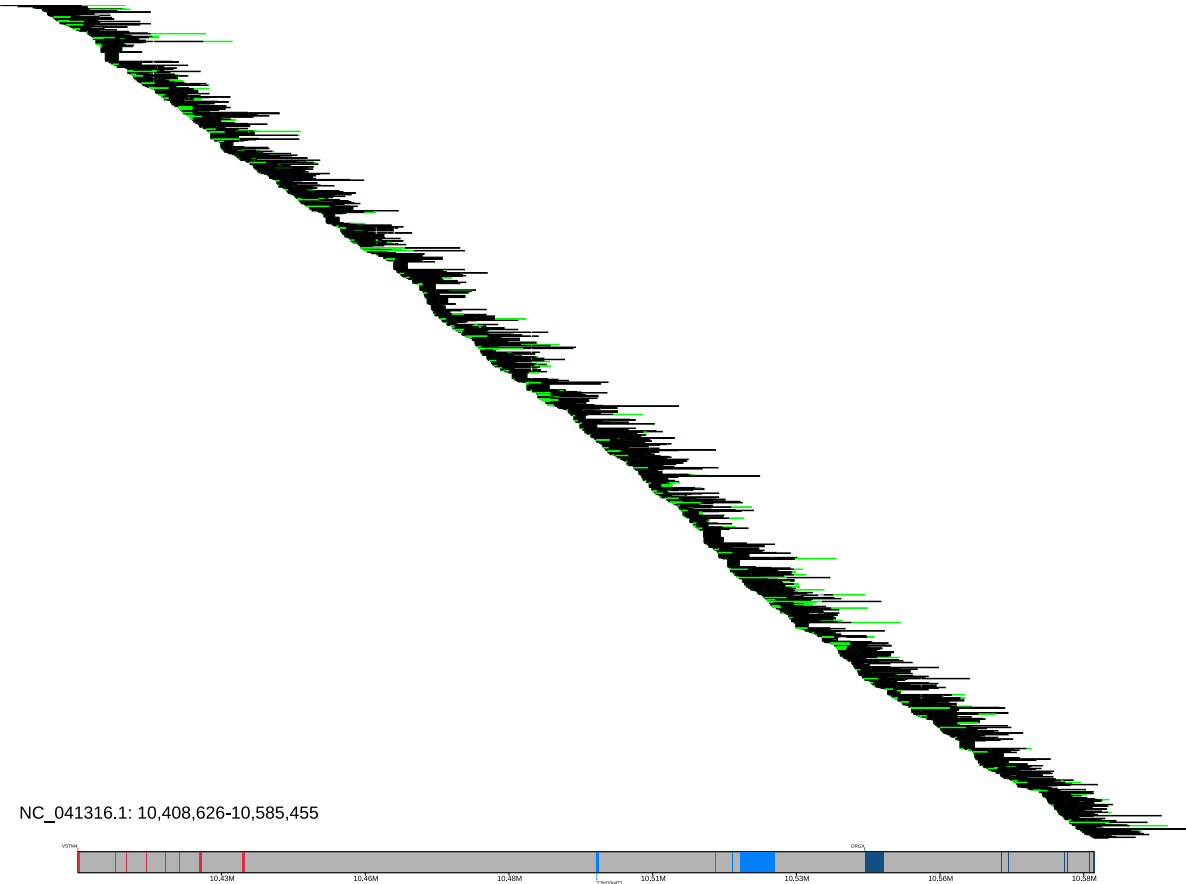


Figure 477: TMEM273:NC_041316.1:10408626-10585455.pdf

Pogona_vitticeps-Nanopore

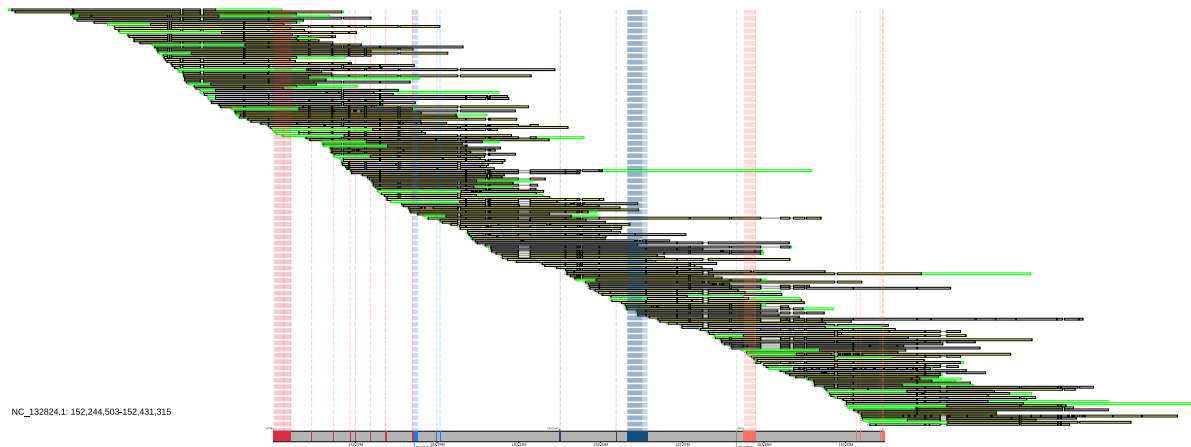


Figure 478: TMEM273:NC_132824.1:152244503-152431315.pdf

Important gene stats

TMEM273_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
TMEM273	12.87878788	47.8148 +/- 6.95776	3.73348 +/- 0.478687	40.081 +/- 12.3672	No	Na

Intergenic distance phylogenetic signal evidence

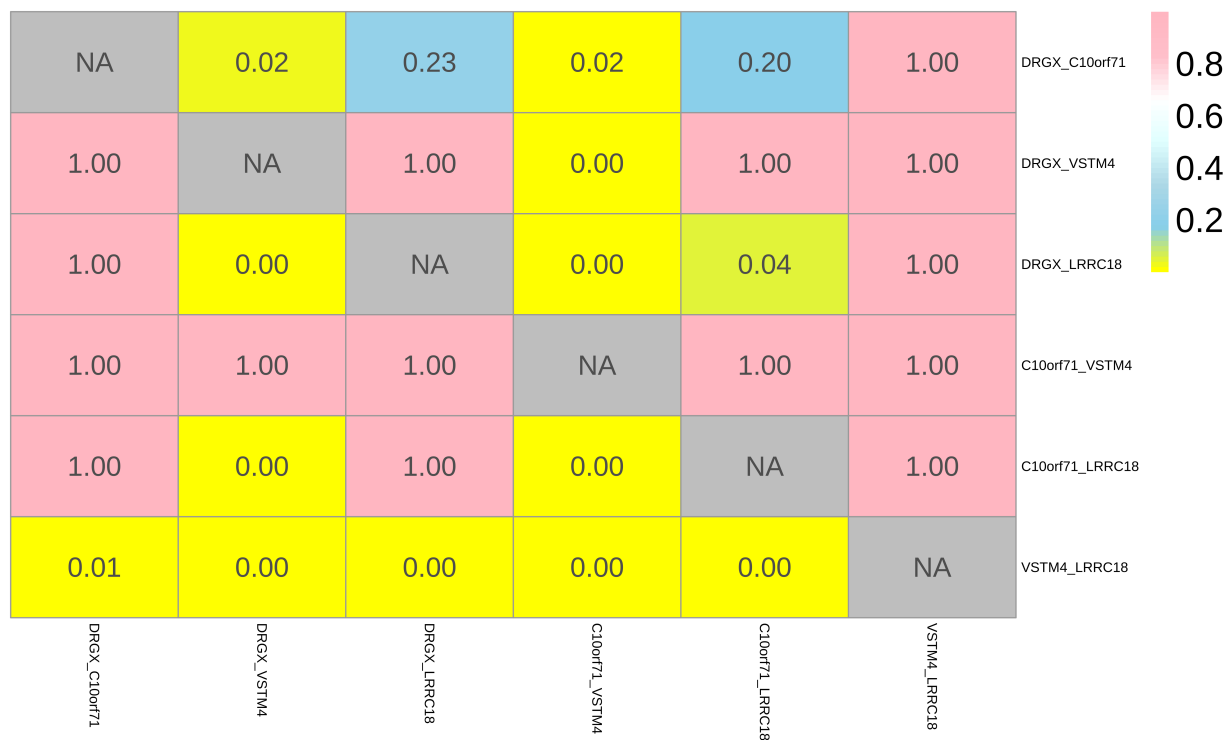


Figure 479: Heatmap_of_deletion_plot.png

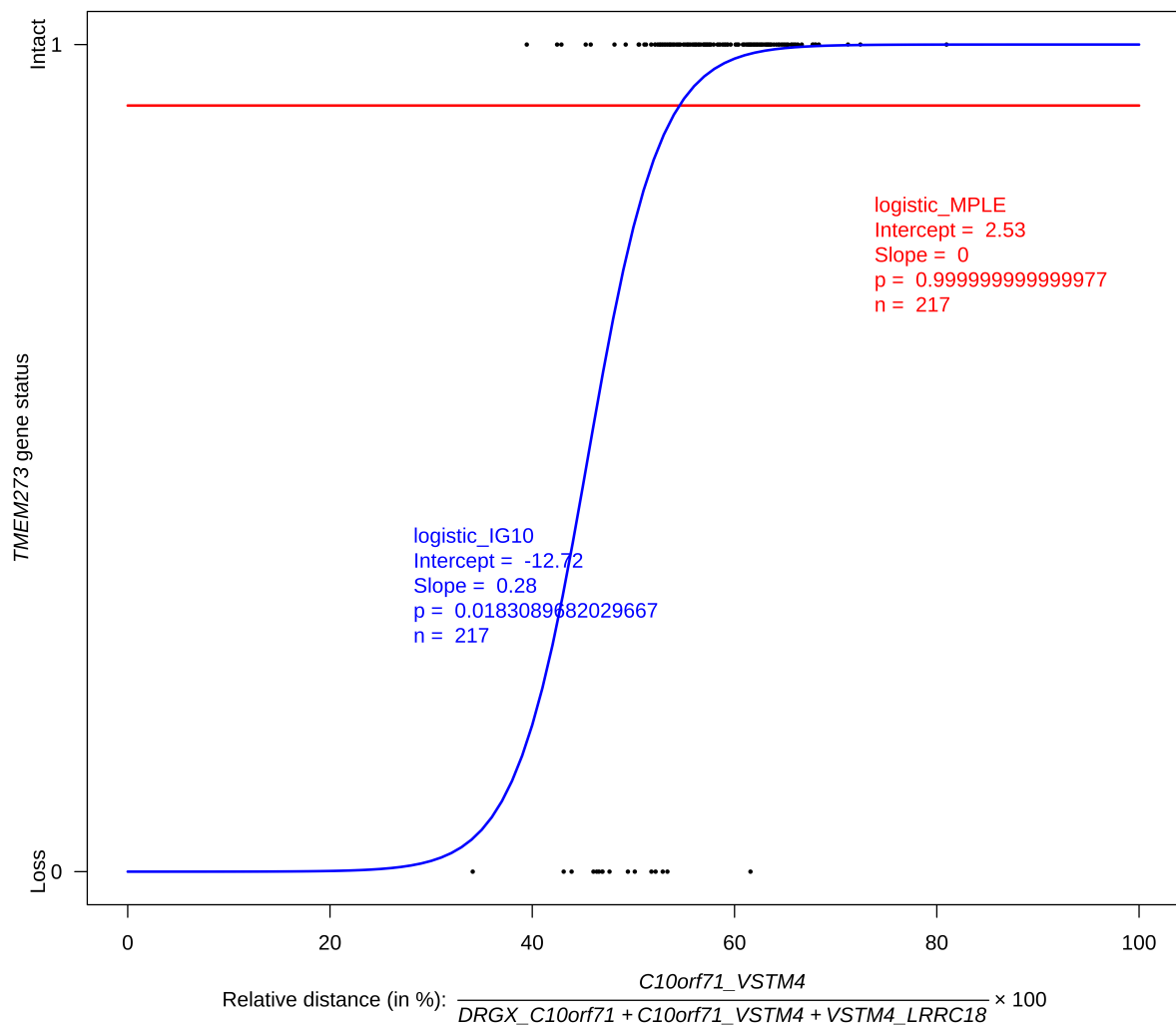


Figure 480: Phylogenetic_signal_of_deletion_plot.png

TMEM273_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
TMEM273	217	16	201	5	0.0183089682029667	0.999999999999977

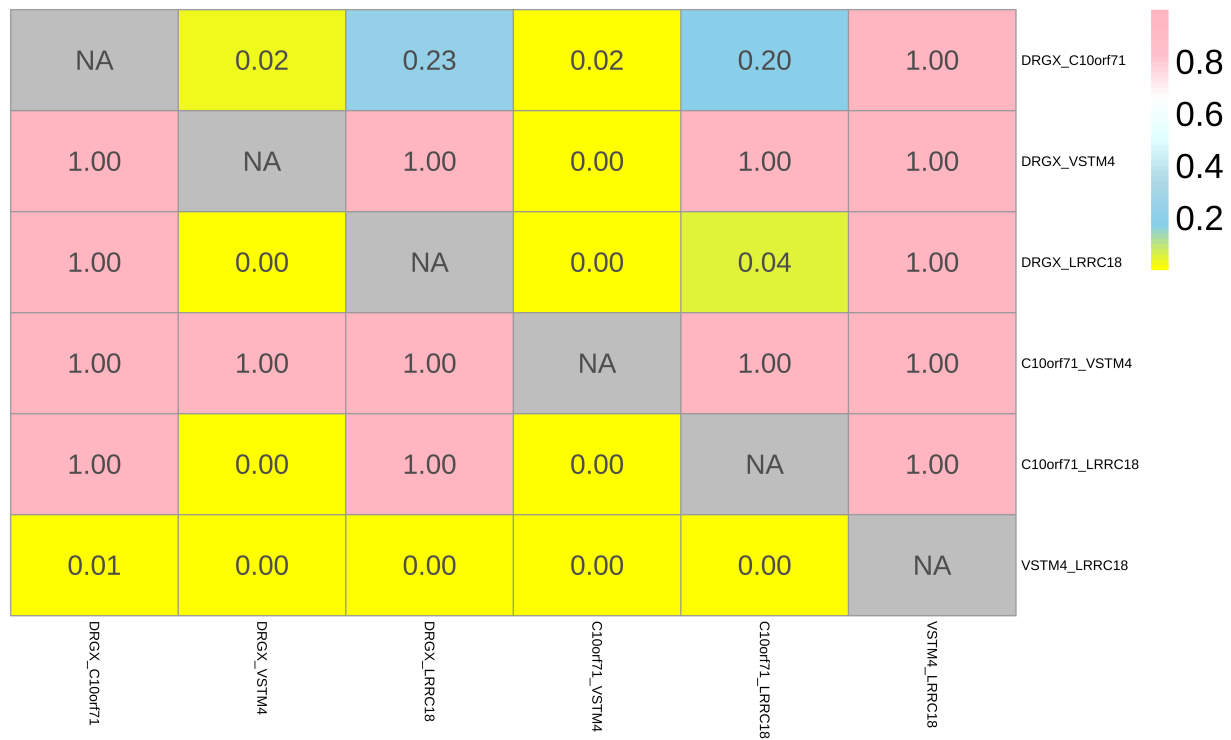


Figure 481: Heatmap_of_deletion_plot.png

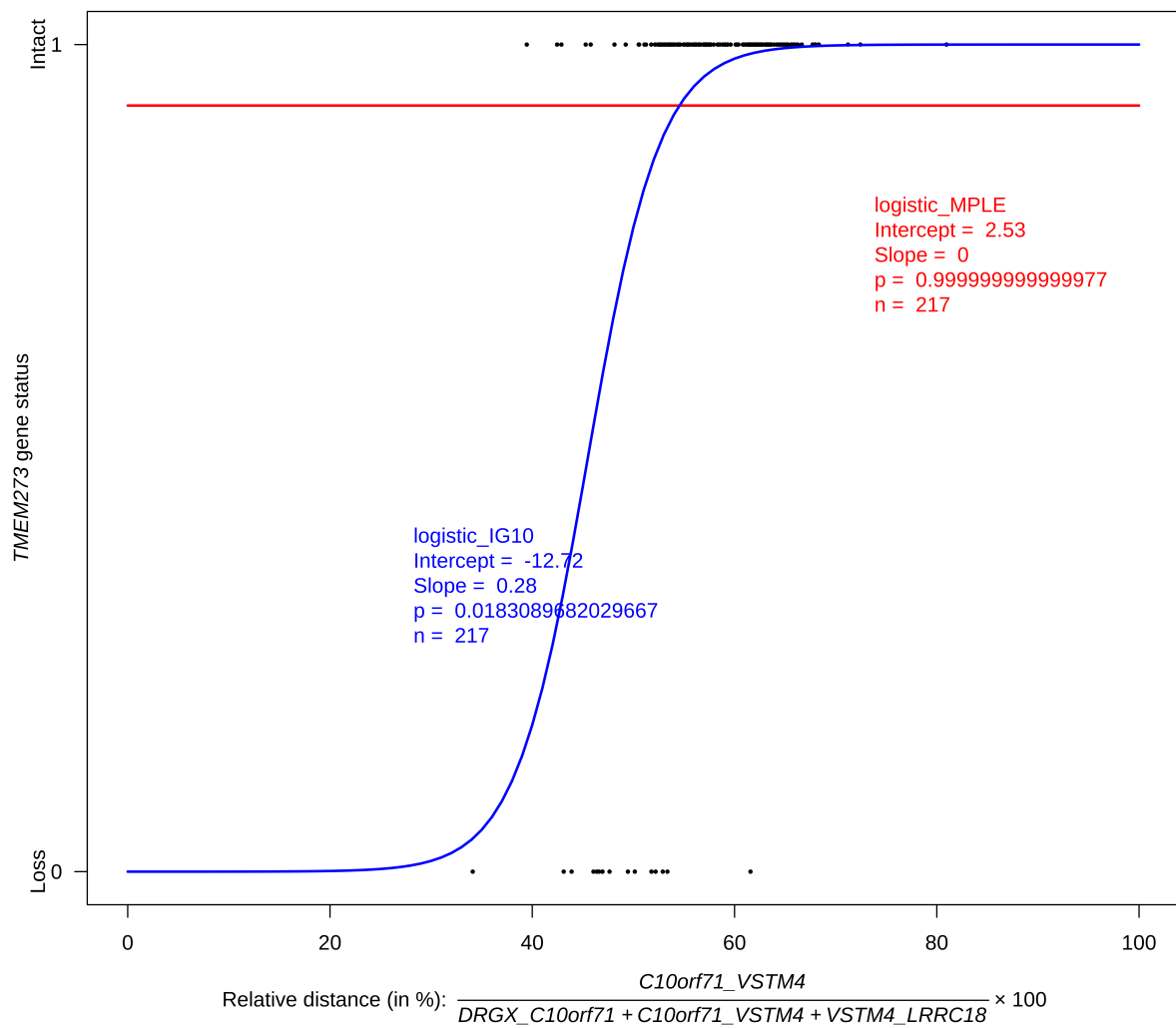


Figure 482: Phylogenetic_signal_of_deletion_plot.png

TMEM273_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
TMEM273	217	16	201	5	0.0183089682029667	0.999999999999977

Syntenic evidence

				C10orf128/TMEM273						
Chelonia mydas		> ERCC6 >	> DRGX >	< C10orf71 <	> C10orf128 >	> VSTM4 >	> LRRC18 >	< WDFY4 <		
					Chr 7 (NC_057853.1)					
Gallus gallus		> ERCC6 >	> DRGX >	< C10orf71 <	> C10orf128 >	> VSTM4 >	> LRRC18 >	< WDFY4 <		
					Chr 6 (NC_052537.1)					
Podarcis muralis		> ERCC6 >	> DRGX >	< C10orf71 <	> C10orf128 >	> VSTM4 >	> LRRC18 >	< WDFY4 like <		
					Chr 5 (NC_041316.1)					
Anolis carolinensis		> ERCC6 >	> DRGX >	< C10orf71 <	> C10orf128 >	> VSTM4 >	> LRRC18 >	< mapk8 <		
					Chr 3 (NC_085843.1)					
Pogona vitticeps		> ERCC6 >	> DRGX >	< C10orf71 <	> C10orf128 >	> VSTM4 >	> LRRC18 >	< WDFY4 <		
					Chr 3 (NC_132824.1)					
Crotalus tigris		> ERCC6 >	> DRGX >	< LOC120309951 <	> C10orf128 >	> VSTM4 >	< WDFY4 <	< HHAT <		
					cardiac-enriched FHL2-interacting protein-like NW_024096820.1 (unplaced)					
Ornithorhynchus anatinus		> ERCC6 >	> DRGX >	< C10orf71 <	> C10orf128 >	> VSTM4 >	> LRRC18 >	< WDFY4 <		
					Chr 3 (NC_041730.1)					
Homo sapiens		> ERCC6 >	> LOC112532694 >	> DRGX >	< C10orf71 <	> C10orf128 >	> FAM170B >	> VSTM4 >	> LRRC18 >	< WDFY4 <
					Chr 10 (NC_000010.11)					
Mus musculus		> ERCC6 >	> DRGX >	< 3425401B19R1 <	> C10orf128 >	> VSTM4 >	> LRRC18 >	< WDFY4 <		
					Chr 14 (NC_000080.7)					

Figure 483: TMEM273.pdf

TMEM273.txt

Synteny analysis of TMEM273

We analyzed the synteny of TMEM273 across squamates and representative outgroups. The TMEM273 syntenic block is mostly conserved, with minor variations in some lineages. In the synteny plots, red blocks indicate the absence of TMEM273, green blocks mark its presence, light blue blocks represent genes conserved across lineages, and light purple blocks denote different flanking genes.

Transcriptomic evidence Pogona vitticeps



Figure 484: TMEM273.png

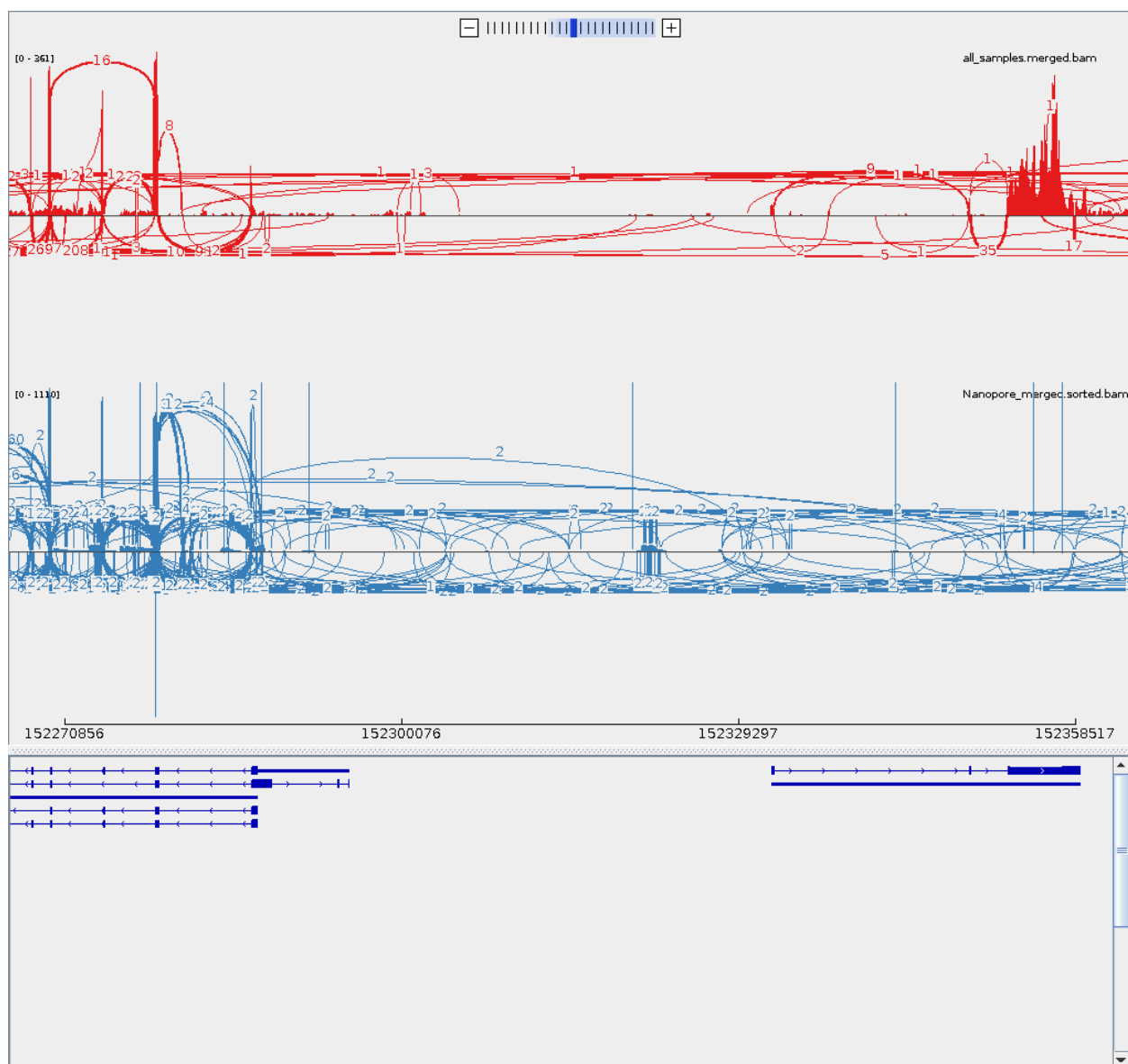


Figure 485: TMEM273_Sashimi.png

48 TNIP2

Important gene stats

TNIP2_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
TNIP2	3.350649351	57.8278 +/- 7.3046	4.42899 +/- 0.586119	60.6134 +/- 14.6202	No	Na

Lastz Alignment evidence

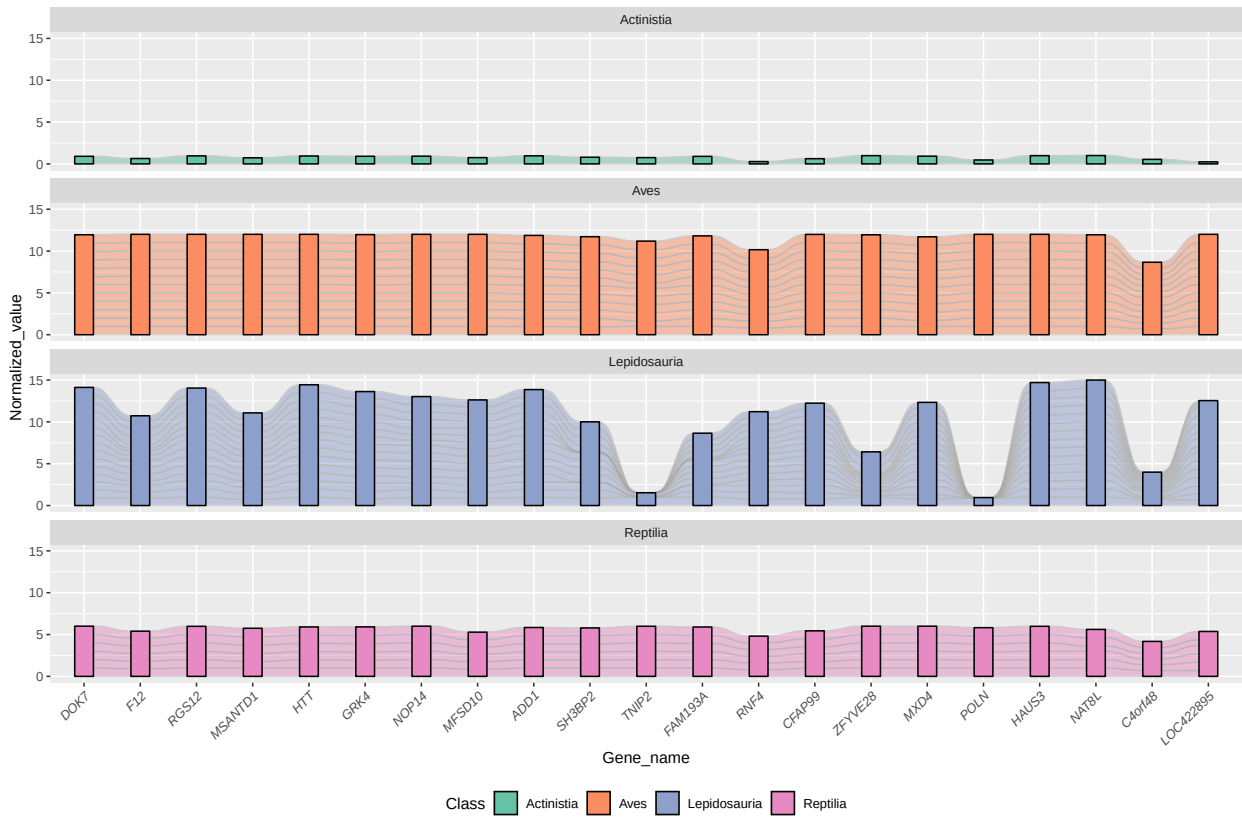


Figure 486: TNIP2.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

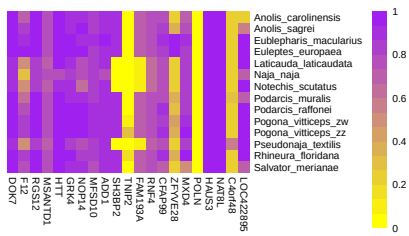


Figure 487: TNIP2.FS_Exonic.Final.Gallus_gallus.21_genes_heatmap.pdf

Lastz gene tree

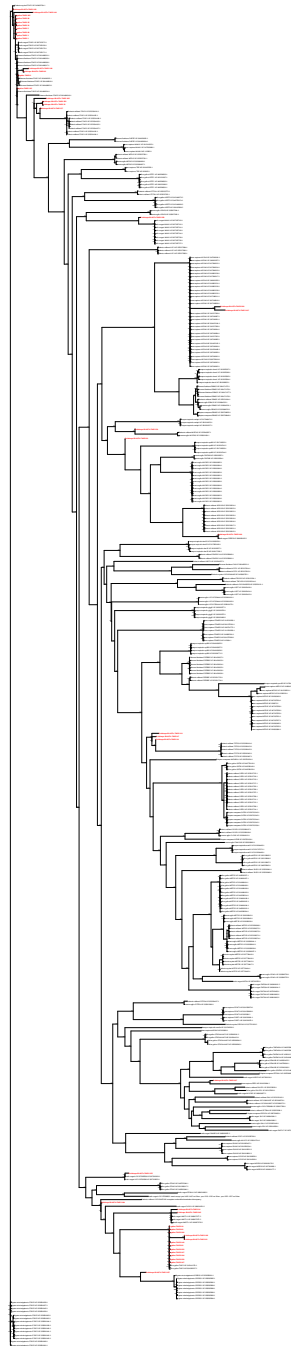


Figure 488: TNIP2.combined.mafft.aln.highlighted.pdf

49 UNKL

Important gene stats

UNKL_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
UNKL	23.60606061	55.8052 +/- 9.46216	4.11594 +/- 0.540491	64.352 +/- 13.4657	Yes	UNK;

Intergenic distance phylogenetic signal evidence

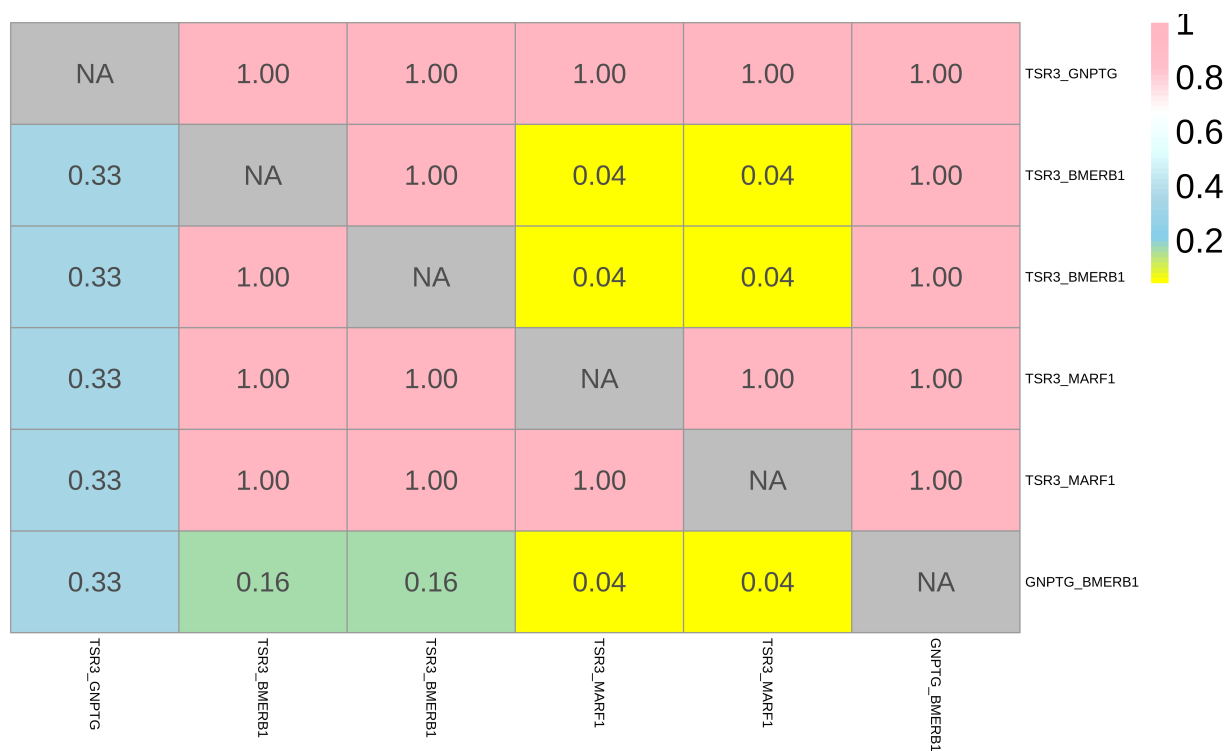


Figure 489: Heatmap_of_deletion_plot.png

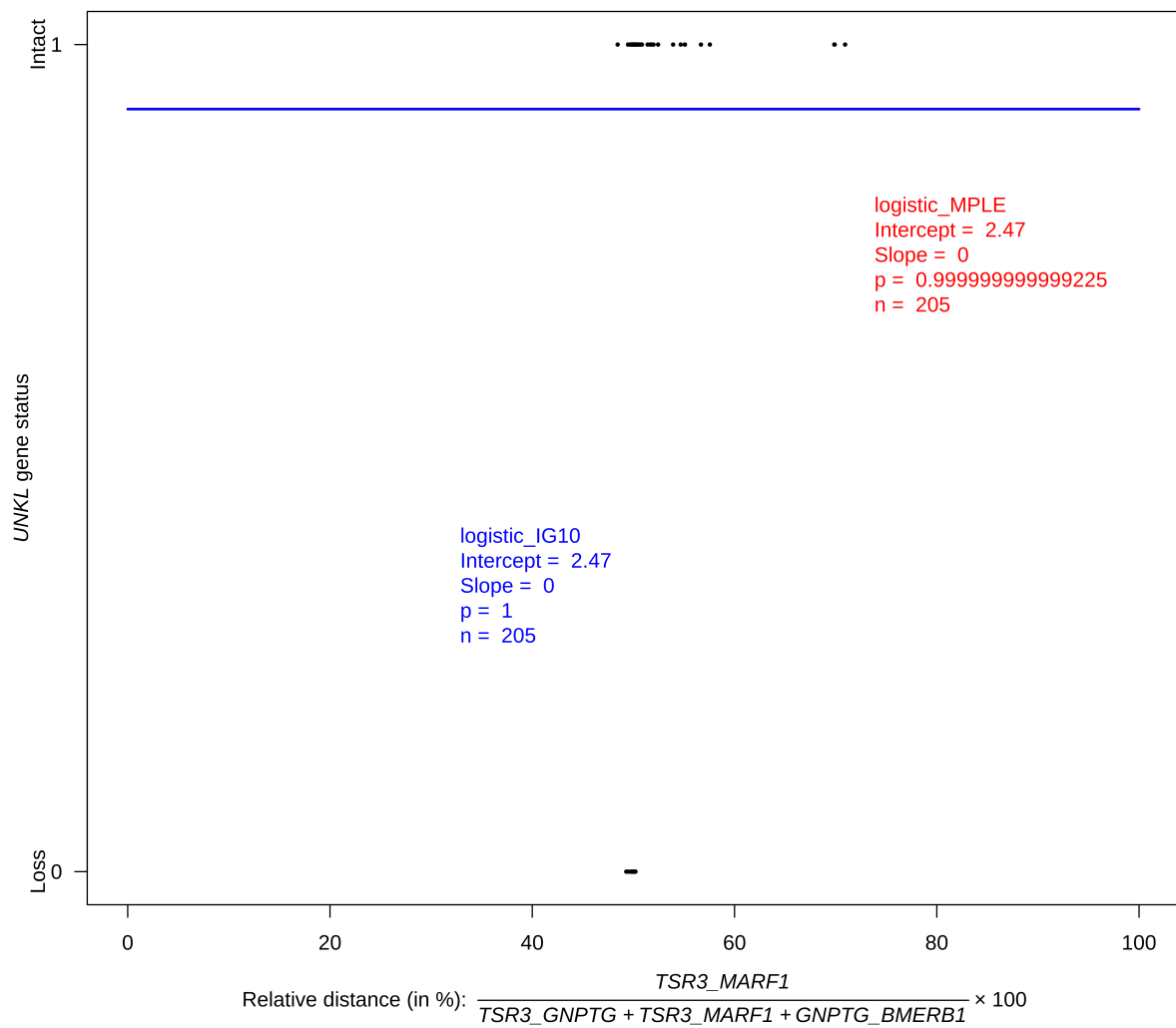


Figure 490: Phylogenetic_signal_of_deletion_plot.png

UNKL_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
UNKL	207	16	191	3	1	0.999999999999225

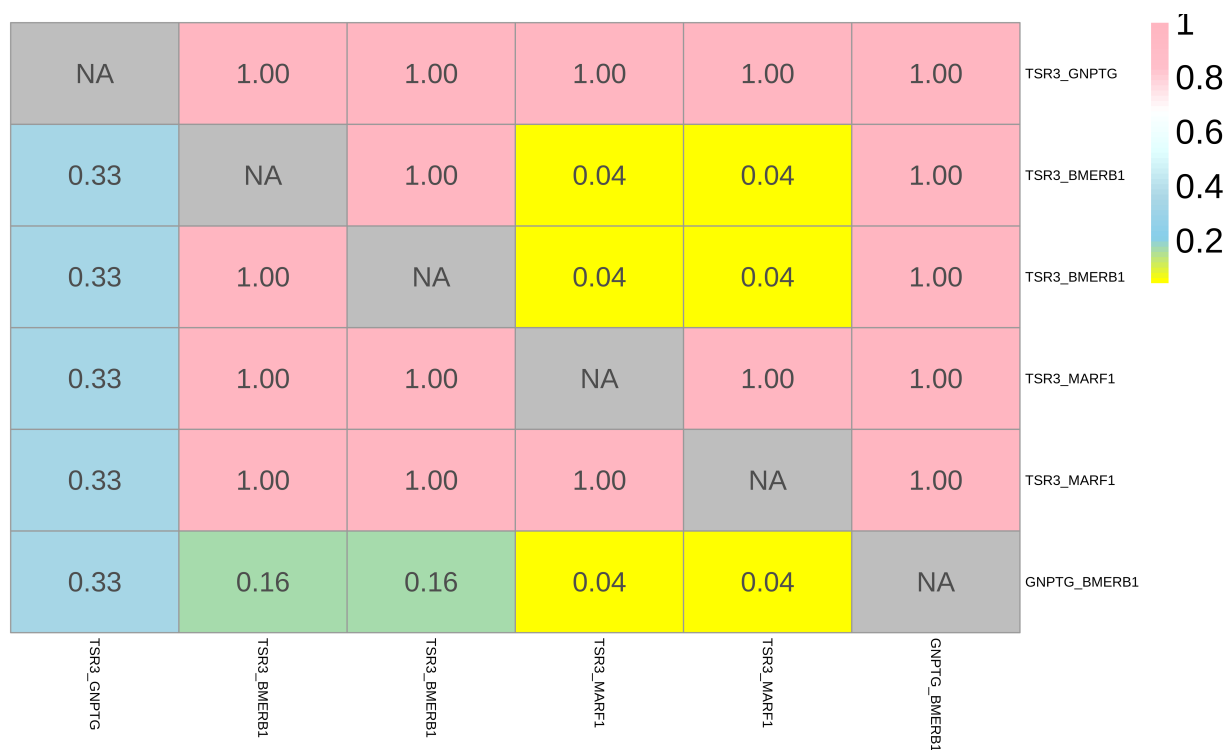


Figure 491: Heatmap_of_deletion_plot.png

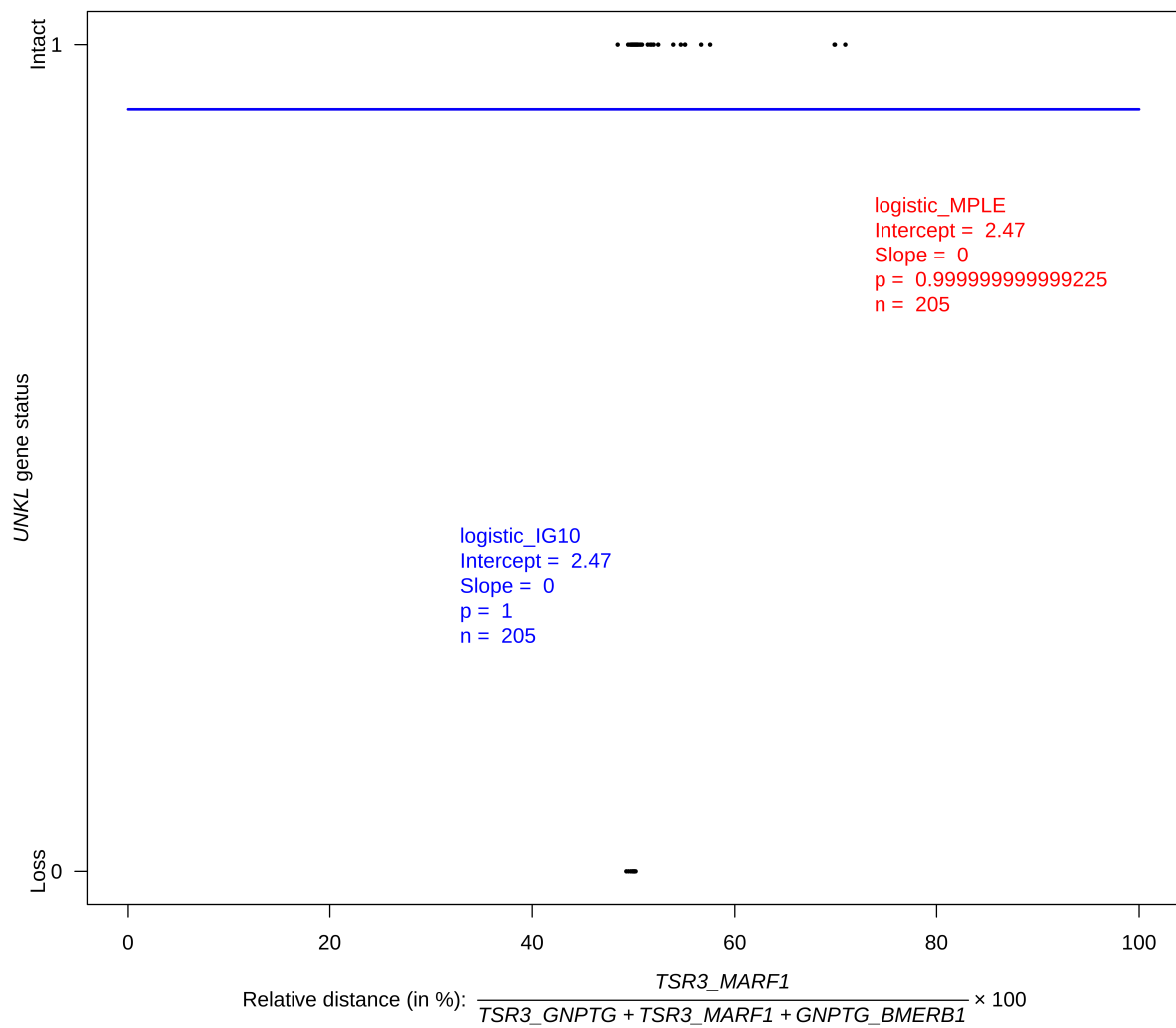


Figure 492: Phylogenetic_signal_of_deletion_plot.png

UNKL_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
UNKL	207	16	191	3	1	0.999999999999225

Lastz Alignment evidence

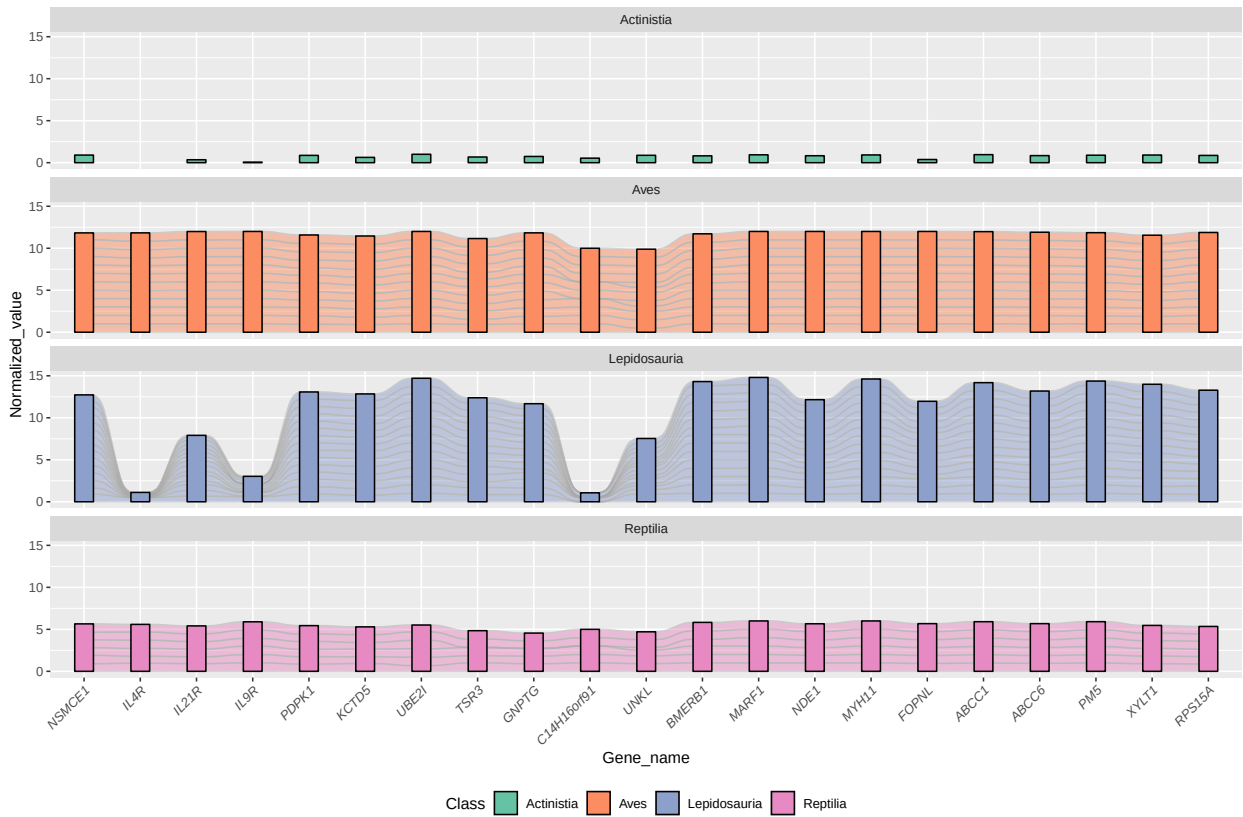


Figure 493: UNKL.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

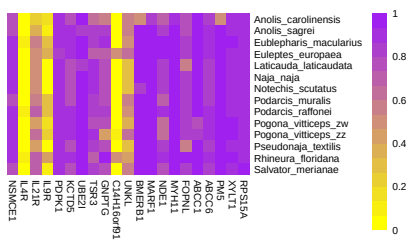


Figure 494: UNKL.FS_Exonic.Final.Gallus_gallus.21_genes_heatmap.pdf

Lastz gene tree

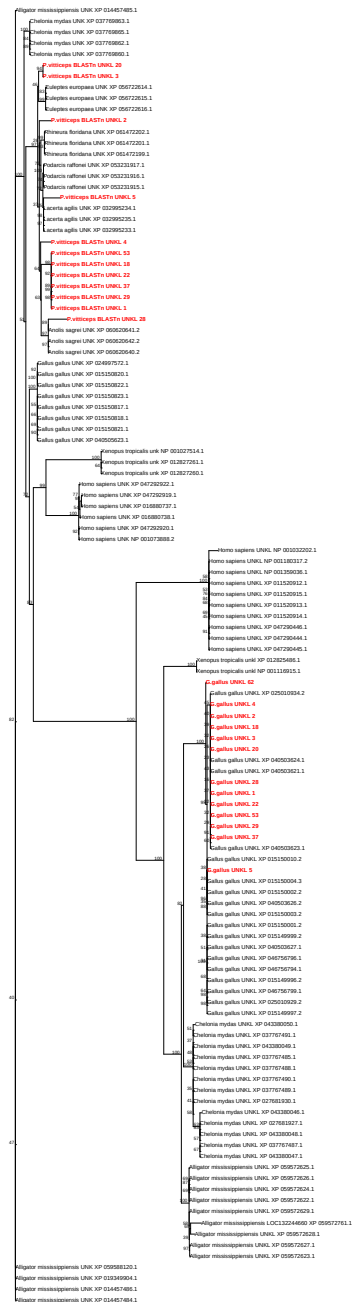


Figure 495: UNKL.combined.mafft.aln.highlighted.pdf

				UNKL					
Chelonia mydas	< TSR3 <	> GNPTG >	> C14H16orf91 >	> UNKL >	## Chromosome end				
			Chr 10 (NC_051250.2)						
Gallus gallus	< TSR3 <	> GNPTG >	> C14H16orf91 >	> UNKL >	> BMERB1 >	< MARF1 <	> NDE1 >		
			Chr 14 (NC_052545.1)						
Podarcis muralis	> KCTD5 >	> UBE2I >	> GNPTG >	> UNKL >	C16orf45-like		von Willebrand factor (vWF) type D domain		
			Chr 14 (NC_041325.1) ##		> LOC11458444 >	< MARF1 <	< LOC11458444 <	< ABCD6 <	
						Chr 14 (NC_041325.1) ##		## same chromosome but far off	
Anolis carolinensis	> UBE2I >	< TSR3 <	> GNPTG >	> UNKL >	> BMERB1 >	< MARF1 <	< ABCD6 <	## same chromosome but far off	
		NW_026943824.1 (unplaced) ##			NW_026943824.1 (unplaced) ##				
		chromosome end							
Pogona vitticeps	> UBE2I >	< TSR3 <	> GNPTG >	> UNKL >	> BMERB1 >	< MARF1 <	< LOC140702531 <	## Same chromosome but BmerB1 flank present on opposite side	
		Chr 13 (NC_132834.1)							
		vWD							
Crotalus tigris	> UBE2I >	< TSR3 <	> GNPTG >	> UNKL >	> BMERB1 >	< MARF1 <	< LOC120315652 <		
		NW_024097152.1 (unplaced)			NW_024097414.1 (unplaced)				
Omithorhynchus anatinus	> PTXA >	> CLCN7 >	> PERCCI <	> C14H16orf91 >	> UNKL >	> TSR3 >	< BAIAP3 <	< UBE2I <	
		Chr 21 (NC_041748.1)							
Homo sapiens	> CCDC154 >	> PERCCI <	> UQCC4 >	> UNKL >	< GNPTG <	> TSR3 >	< BAIAP3 <		
		Chr 16 (NC_000016.10)							
Mus musculus	> CCDC154 >	> PERCCI <	> UQCC4 >	> UNKL >	< GNPTG <	> TSR3 >	< BAIAP3 <		
		Chr 17 (NC_000083.7)							

Figure 496: UNKL.pdf

UNKL.txt

Synteny analysis of UNKL

The UNKL syntenic block, which is relatively conserved in outgroups has
 ↳ undergone significant rearrangements in squamates. In lizard species
 ↳ such as
Podarcis muralis and *Anolis carolinensis*, the block has been transposed to
 ↳ a distant location on the same chromosome.

The rearrangement is more complex in the lizard *Pogona vitticeps*, which
 ↳ shows evidence of an inversion, with a flanking gene appearing on
 ↳ the opposite side of the chromosome. In the snake *Crotalus tigris*,
 ↳ the synteny is even more disrupted, with the gene block fragmented
 ↳ across at least two different unplaced scaffolds.

In the synteny plots, red blocks indicate the absence of the target gene,
→ while green blocks mark its presence. Light blue blocks represent
→ flanking genes that are conserved across lineages, and light purple
→ blocks denote instances where a different flanking gene is present.
→ A bright yellow color indicates a change in the gene's orientation.

50 UTS2B

Assembly verification Evidence

Crotalus_tigris-PacBio

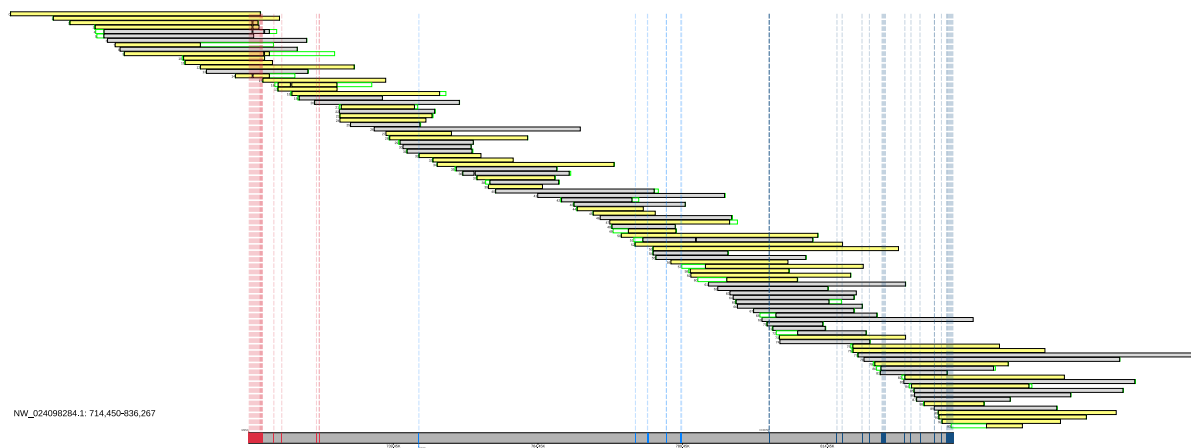


Figure 497: UTS2B:NW_024098284.1:714450-836267.pdf

Podarcis_muralis-PacBio

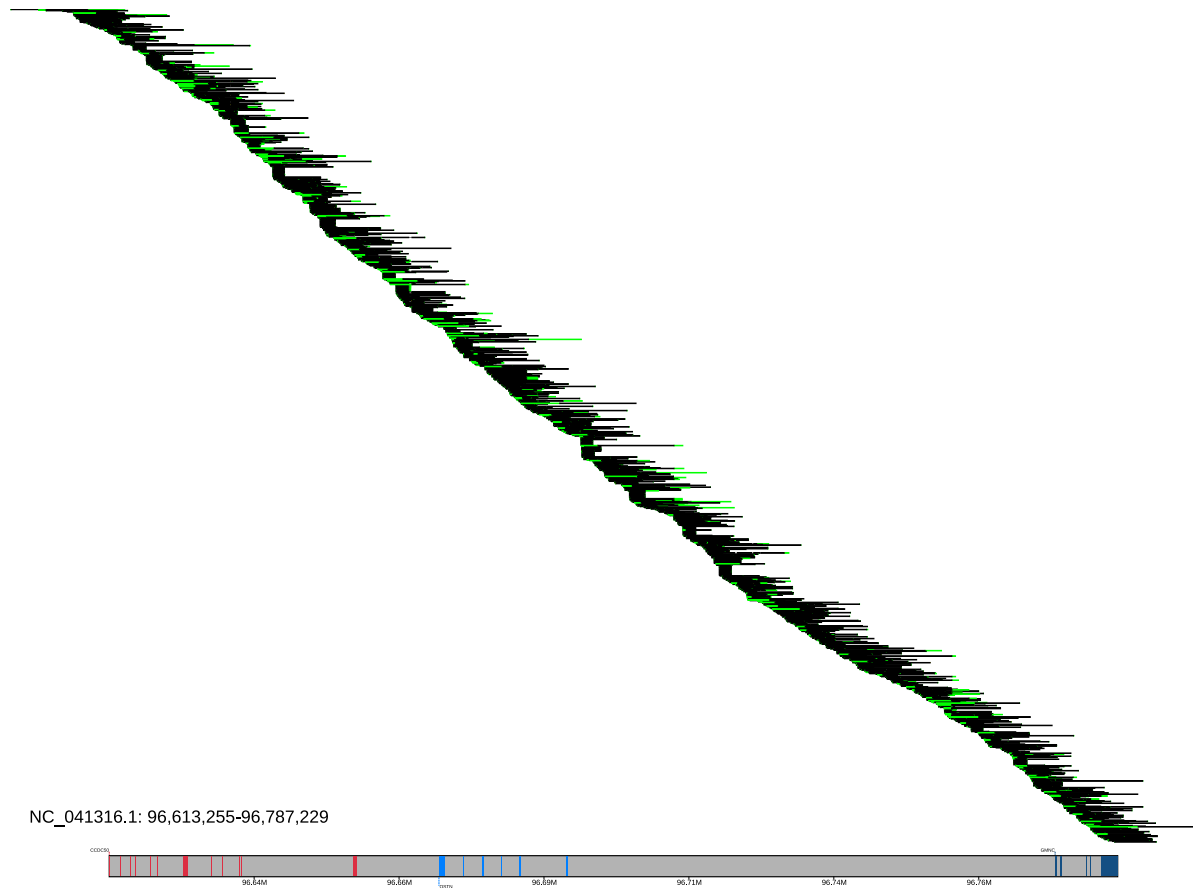


Figure 498: UTS2B:NC_041316.1:96613255-96787229.pdf

Pogona_vitticeps-Nanopore



Figure 499: UTS2B:NC_132824.1:273103737-273329574.pdf

Important gene stats

UTS2B_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
UTS2B	8.763636364	44.2954 +/- 5.49736	3.43598 +/- 0.268995	59.0309 +/- 11.663	No	Na

Intergenic distance phylogenetic signal evidence

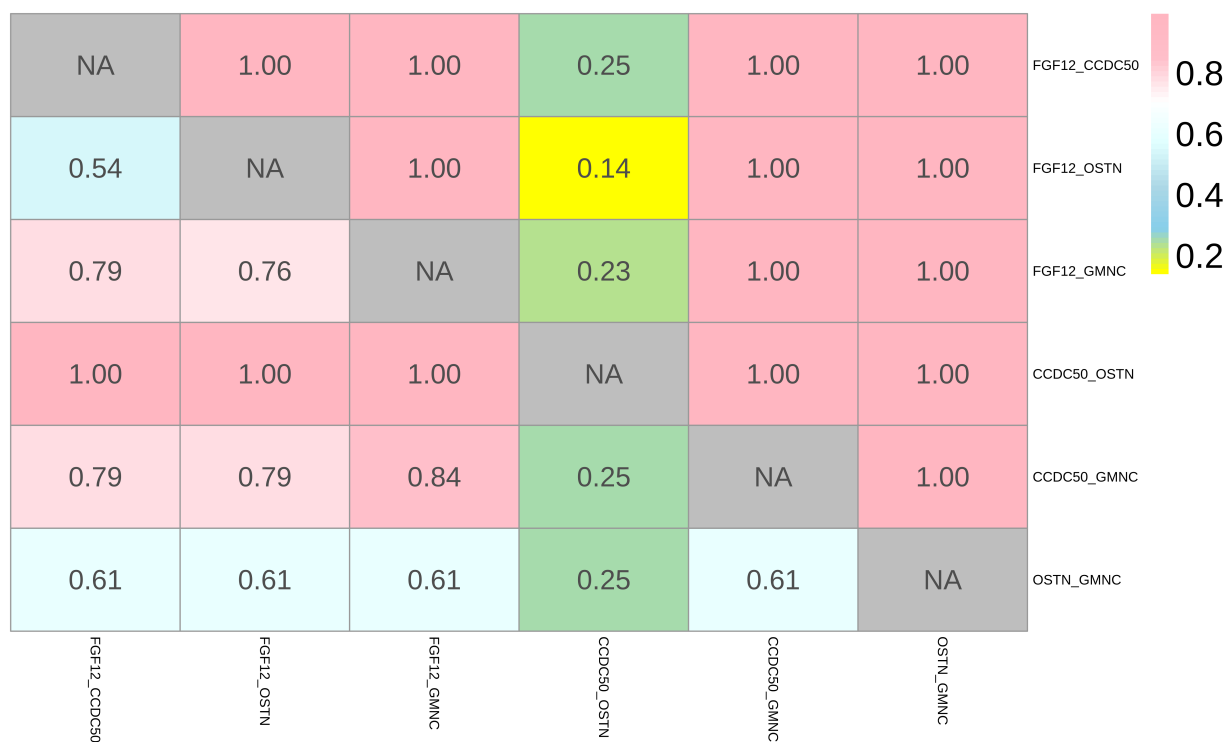


Figure 500: Heatmap_of_deletion_plot.png

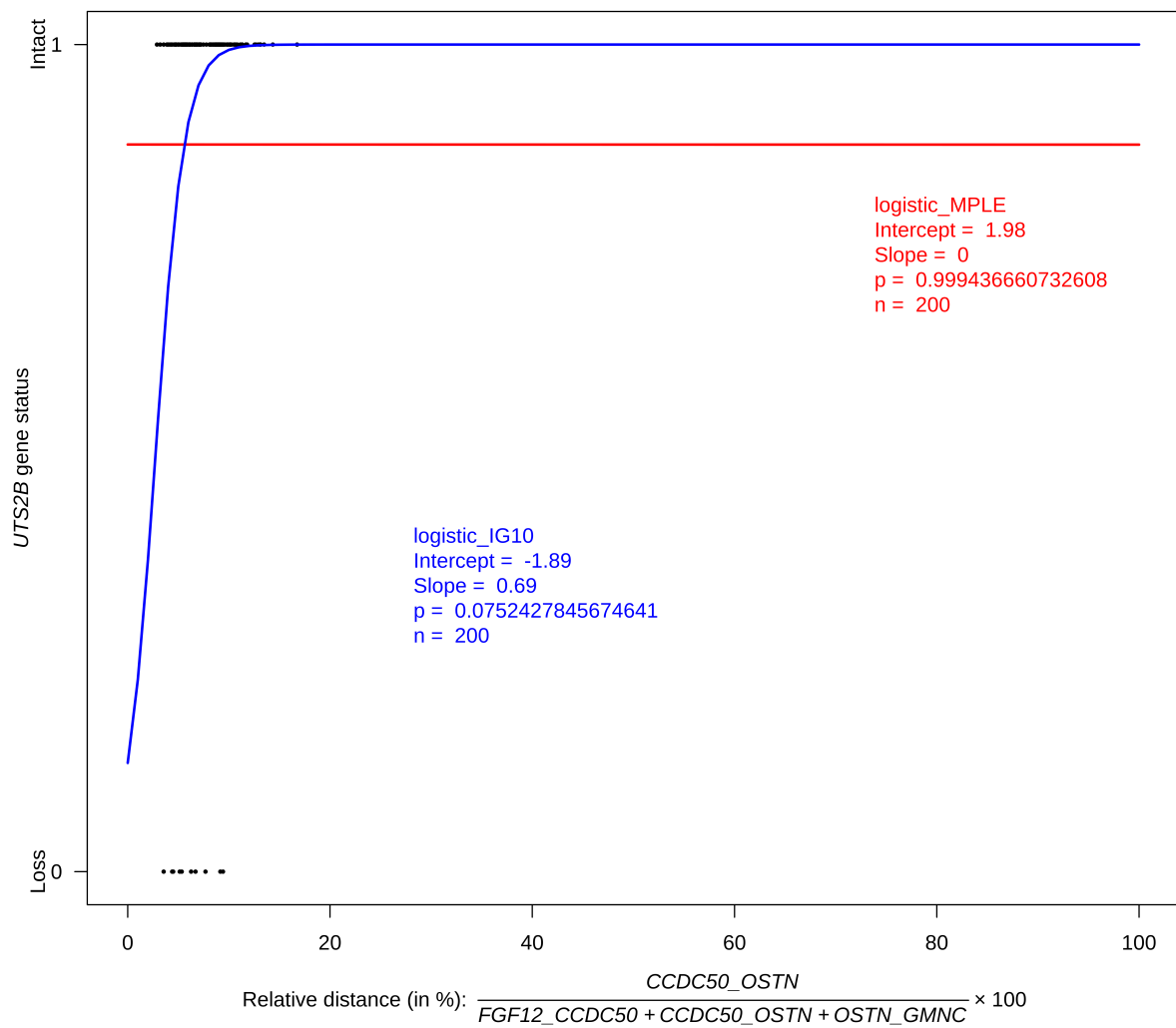


Figure 501: Phylogenetic_signal_of_deletion_plot.png

UTS2B_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
UTS2B	200	10	190	0	0.0752427845674641	0.999436660732608

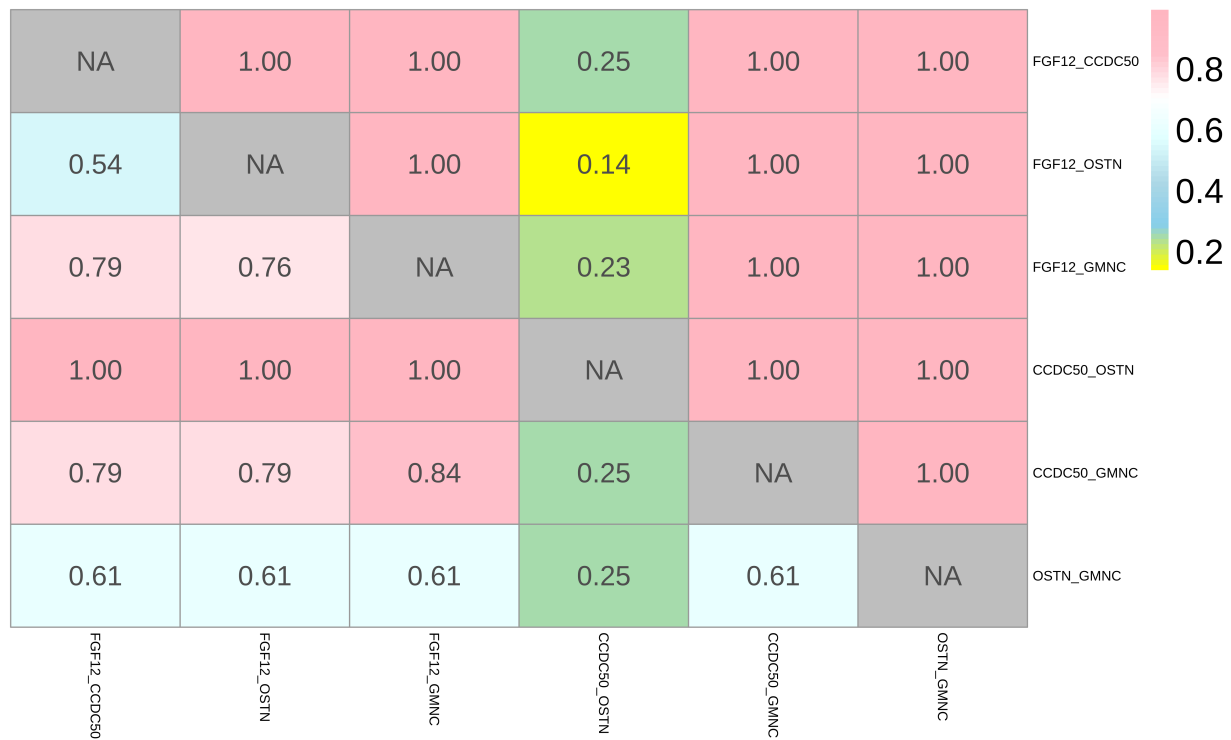


Figure 502: Heatmap_of_deletion_plot.png

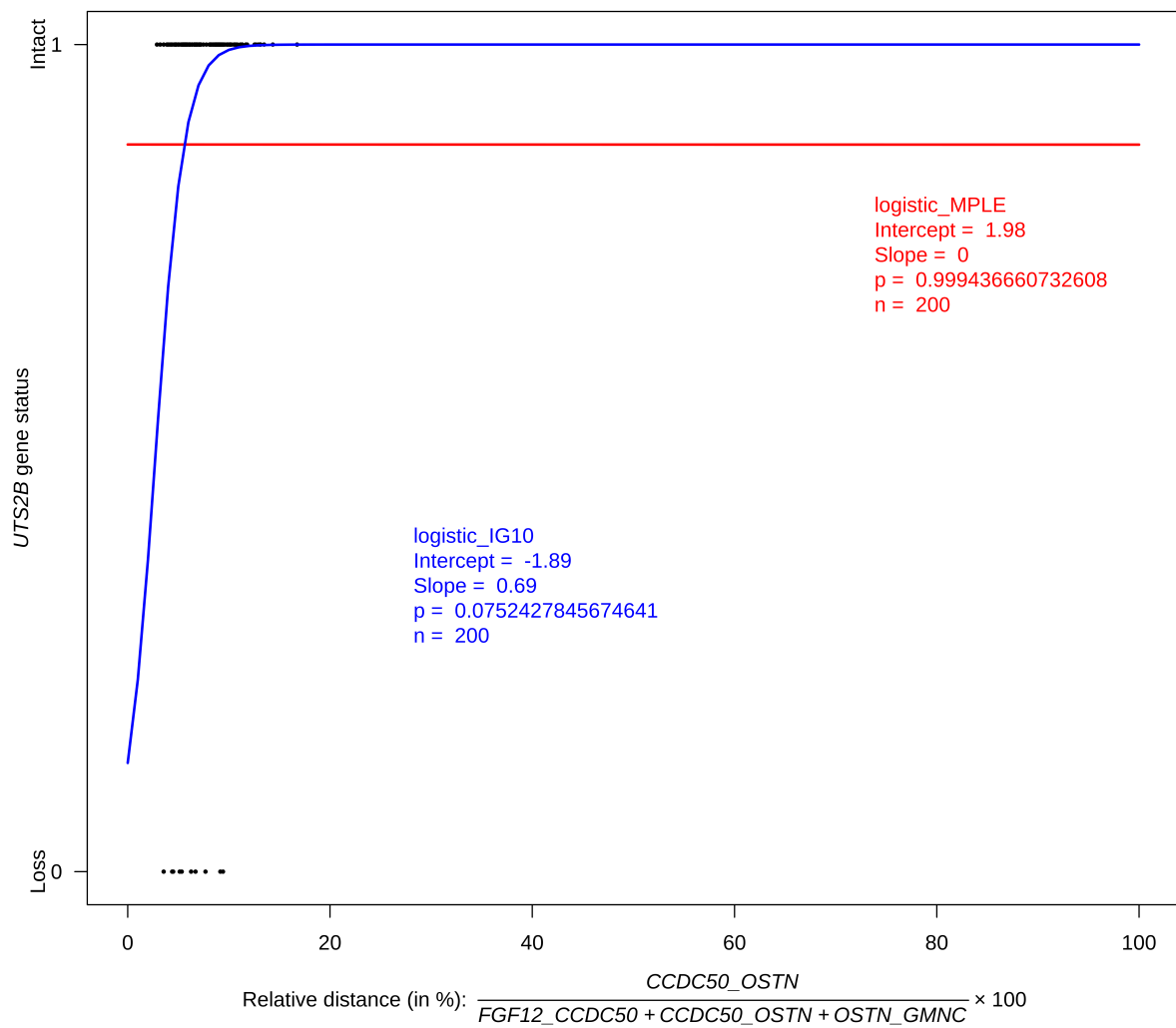


Figure 503: Phylogenetic_signal_of_deletion_plot.png

UTS2B_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
UTS2B	200	10	190	0	0.0752427845674641	0.999436660732608

Lastz Alignment evidence

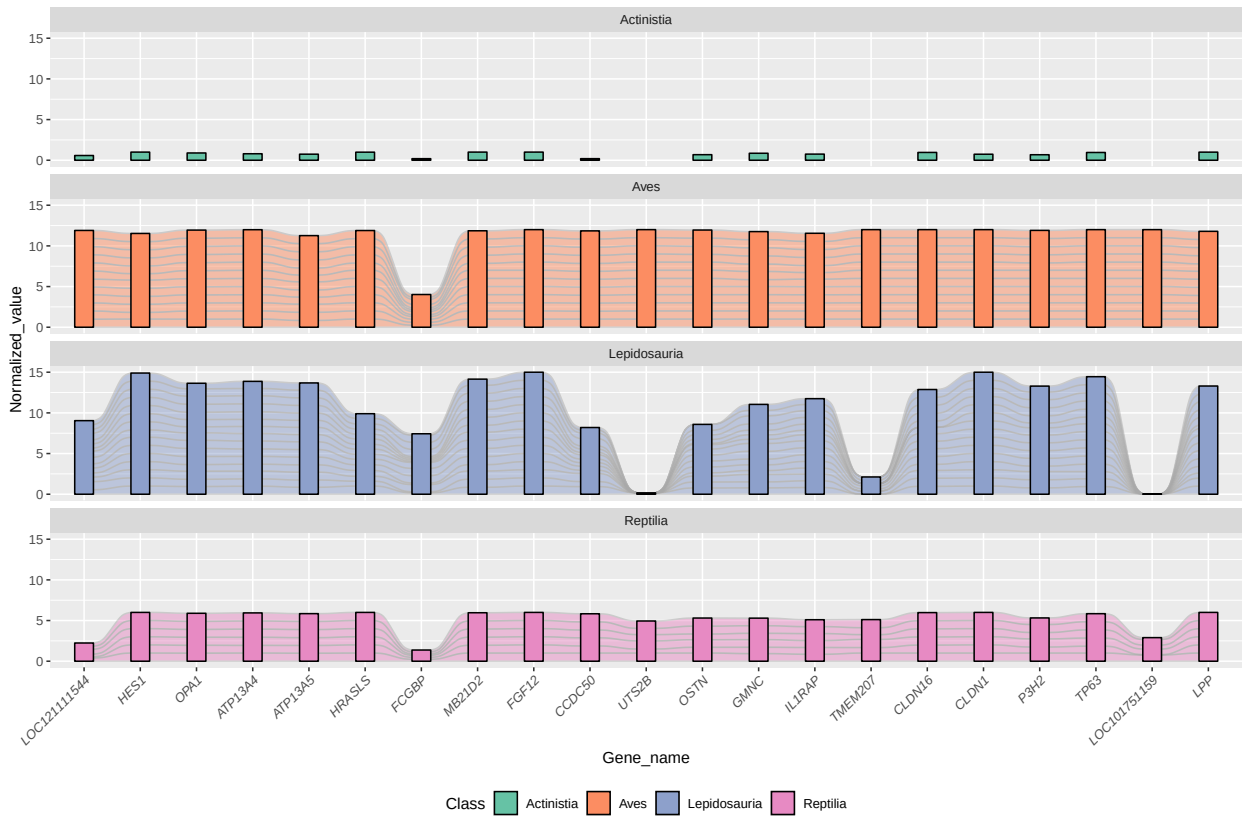
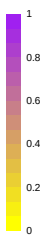


Figure 504: UTS2B.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf



Syntenic evidence

					UTS2B				
Chelonia mydas		> MB21D2 >	> FGF12 >	< CCDC50 <	> UTS2B >	> OSTN >	> GMNC >	< IL1RAP <	
					Chr 9 (NC_057855.1)				
Gallus gallus		> MB21D2 >	> FGF12 >	< CCDC50 <	> UTS2B >	> OSTN >	> GMNC >	< IL1RAP <	
					NC_052540.1				
Podarcis muralis		> MB21D2 >	> FGF12 >	< CCDC50 <	> UTS2B >	< OSTN <	> GMNC >	< IL1RAP <	
					Chr 5 (NC_041316.1)				
Anolis carolinensis		> IL1RAP >	> MB21D2 >	> FGF12 >	> UTS2B >	< IL1RAP <	> LOC103282167 >	< cldn16 <	
					Chr 3 (NC_085843.1)				
Pogona vitticeps		> MB21D2 >	> FGF12 >	< CCDC50 <	> UTS2B >	> OSTN >	> GMNC >	< IL1RAP <	
					NC_132824.1				
Crotalus tigris				< CCDC50 <	> UTS2B >	< OSTN <	> GMNC >	< IL1RAP <	
					NW_024098284.1 (unplaced)				
Ornithorhynchus anatinus		> MB21D2 >	> FGF12 >	< CCDC50 <	> UTS2B >	> OSTN >	> GMNC >	< IL1RAP <	
					Chr 7 (NC_041734.1)				
Homo sapiens		> MB21D2 >	> FGF12 >	< PYDC2 <	< CCDC50 <	> UTS2B >	> OSTN >	> GMNC >	< IL1RAP <
					NC_000003.12				
Mus musculus		> MB21D2 >	> FGF12 >	< CCDC50 <	> UTS2B >	> OSTN >	> GMNC >	< IL1RAP <	
					Chr 16 (NC_000082.7)				

Figure 506: UTS2B.pdf

UTS2B.txt

Synteny analysis of UTS2B

We analyzed the synteny of UTS2B across squamates and representative
 ↳ outgroups. The UTS2B syntenic block is conserved in all examined
 ↳ species; however, the orientation of the flanking gene OSTN is
 ↳ altered in *Podarcis muralis* and *Crotalus tigris*. In the synteny
 ↳ plots, red blocks indicate the absence of UTS2B, green blocks mark
 ↳ its presence, light blue blocks represent genes conserved across
 ↳ lineages, and light purple blocks denote different flanking genes.

Transcriptomic evidence *Pogona vitticeps*



Figure 507: UTS2B.png

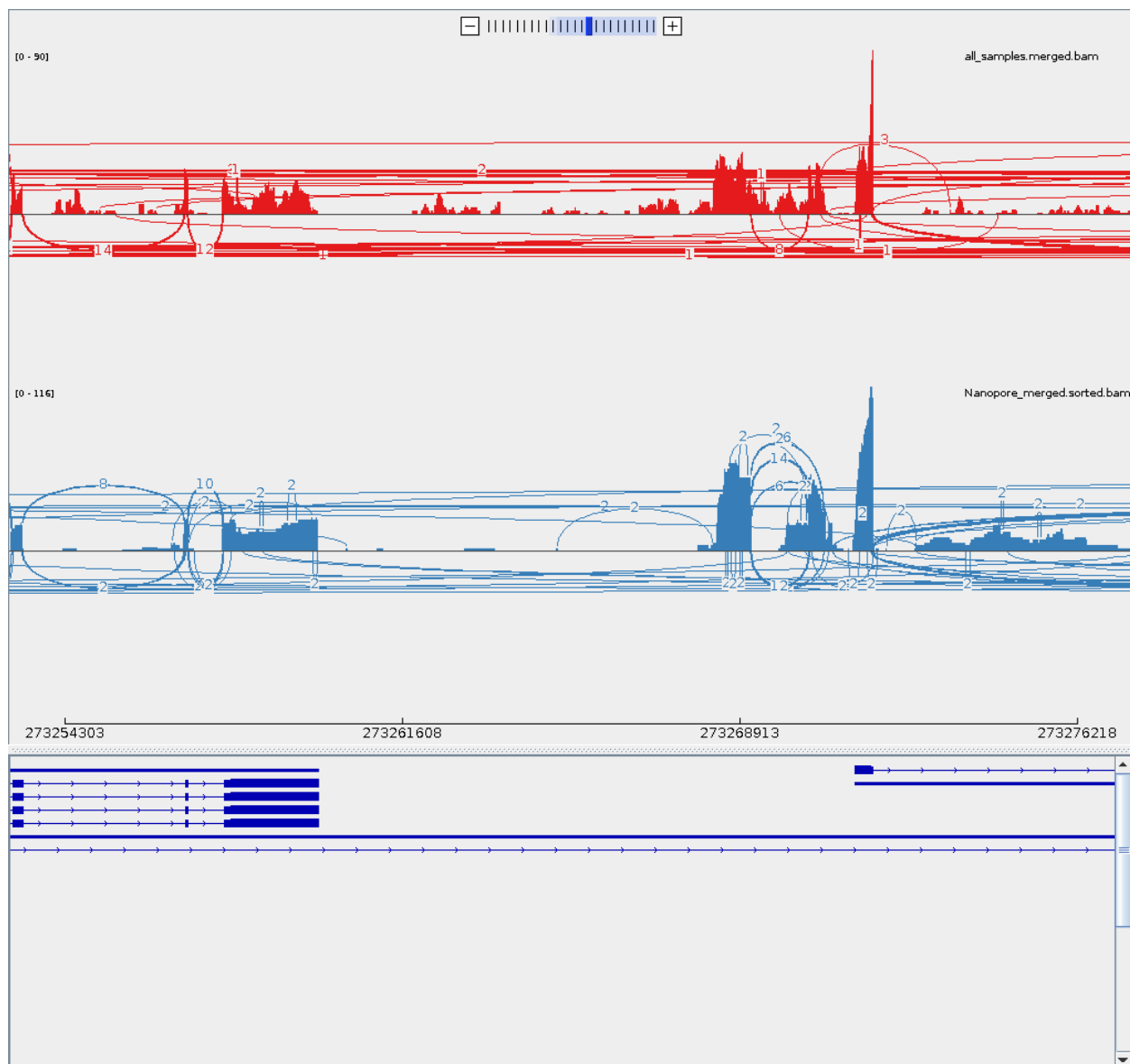


Figure 508: UTS2B_Sashimi.png

51 WNT2

Assembly verification Evidence

Crotalus_tigris-PacBio

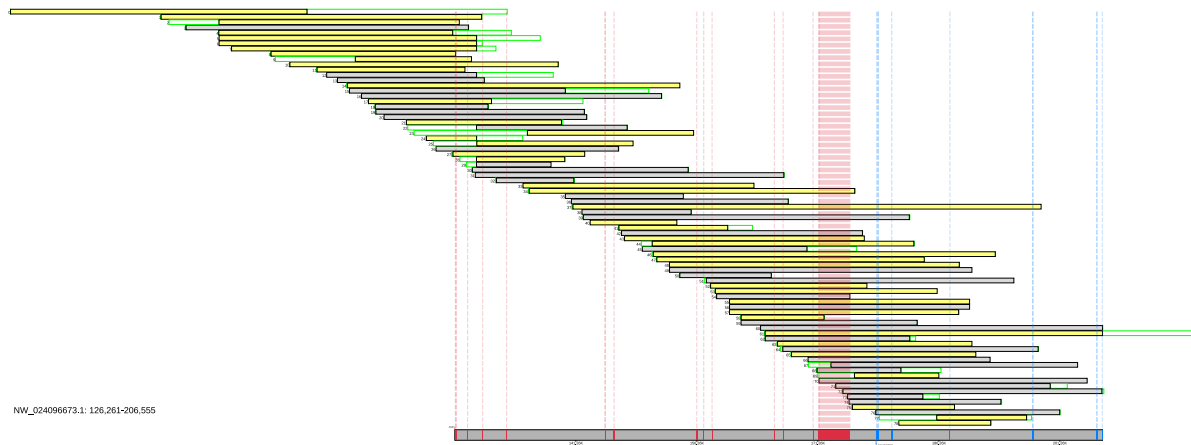


Figure 509: WNT2:NW_024096673.1:126261-206555.pdf

Podarcis_muralis-PacBio

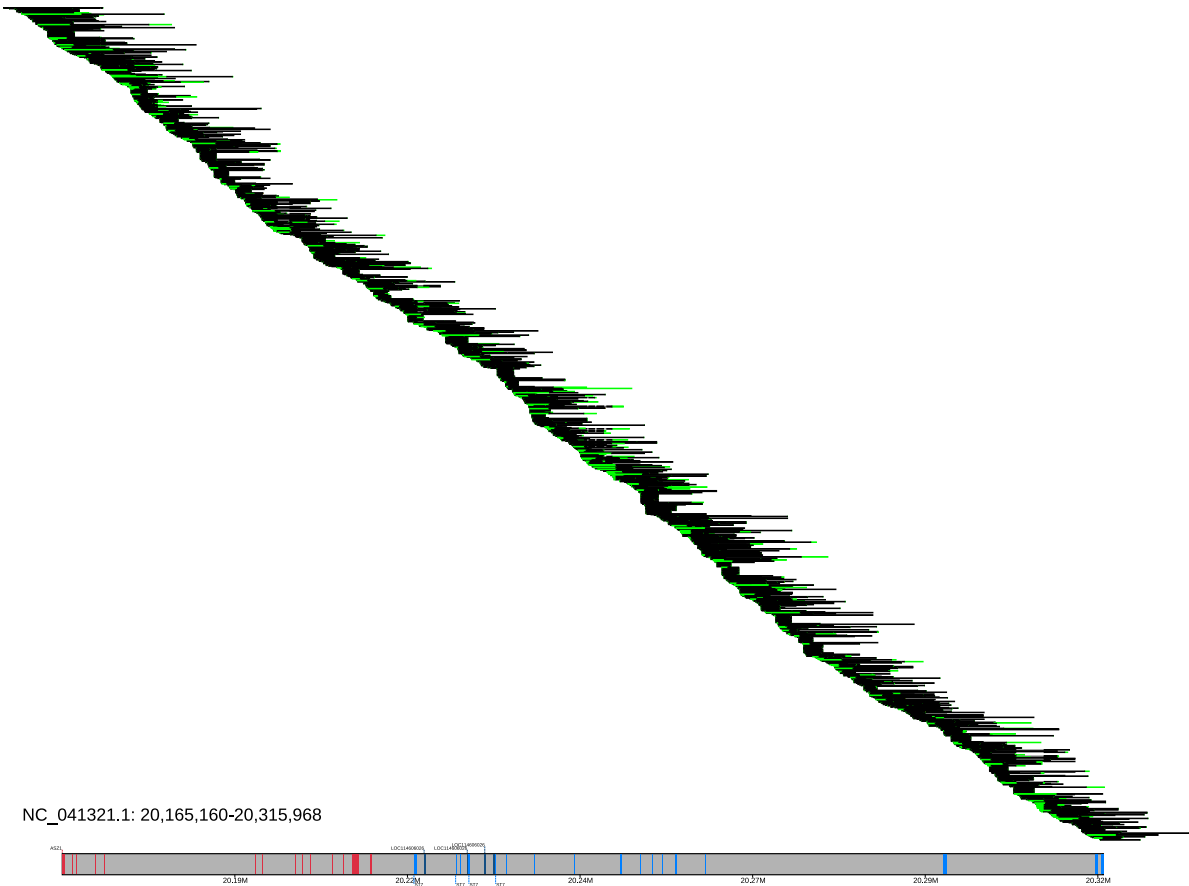


Figure 510: WNT2:NC_041321.1:20165160-20315968.pdf

Pogona_vitticeps-Nanopore

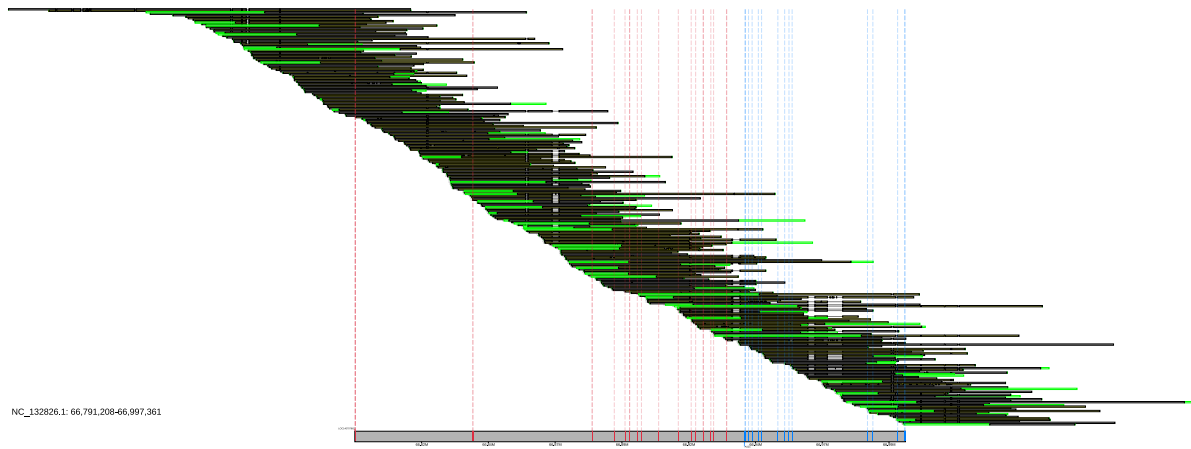


Figure 511: WNT2:NC_132826.1:66791208-66997361.pdf

Important gene stats

WNT2_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
WNT2	72.12547529	56.9025 +/- 4.12475	4.06383 +/- 0.369824	79.3658 +/- 12.1512	Yes	Anolis_sagrei SRR30050337.blast;Pogona_vitticeps ERR409938.blast;WNT2B;

Intergenic distance phylogenetic signal evidence

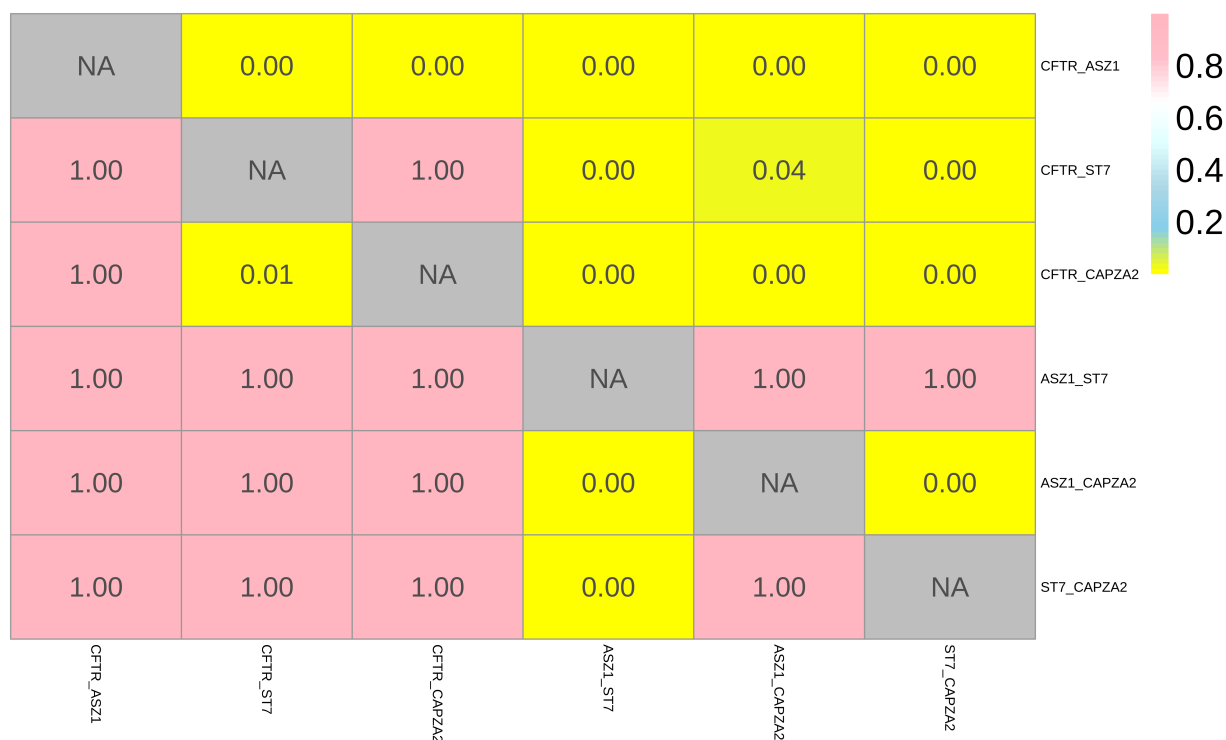


Figure 512: Heatmap_of_deletion_plot.png

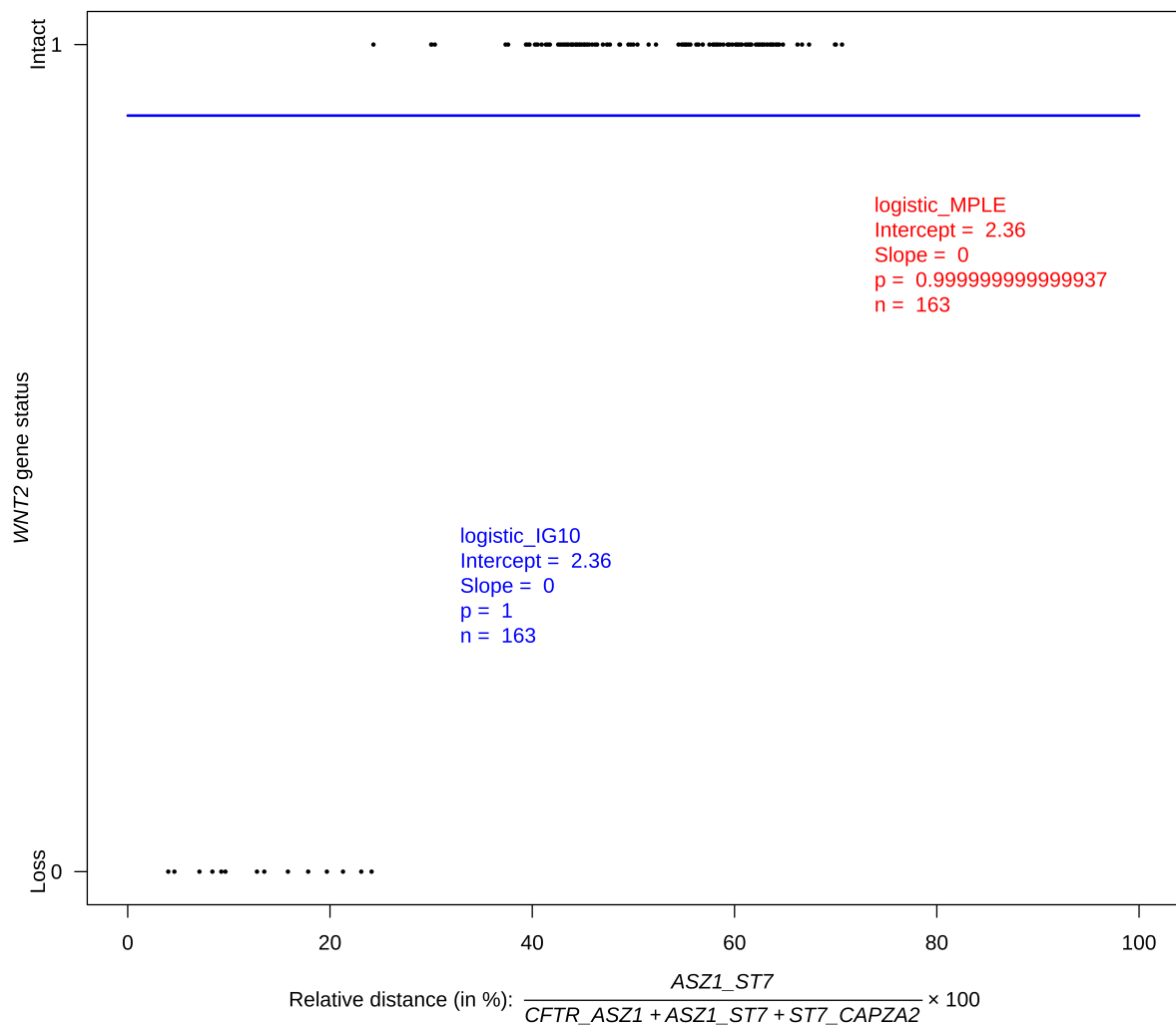


Figure 513: Phylogenetic_signal_of_deletion_plot.png

WNT2_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
WNT2	163	14	149	5	1	0.999999999999937

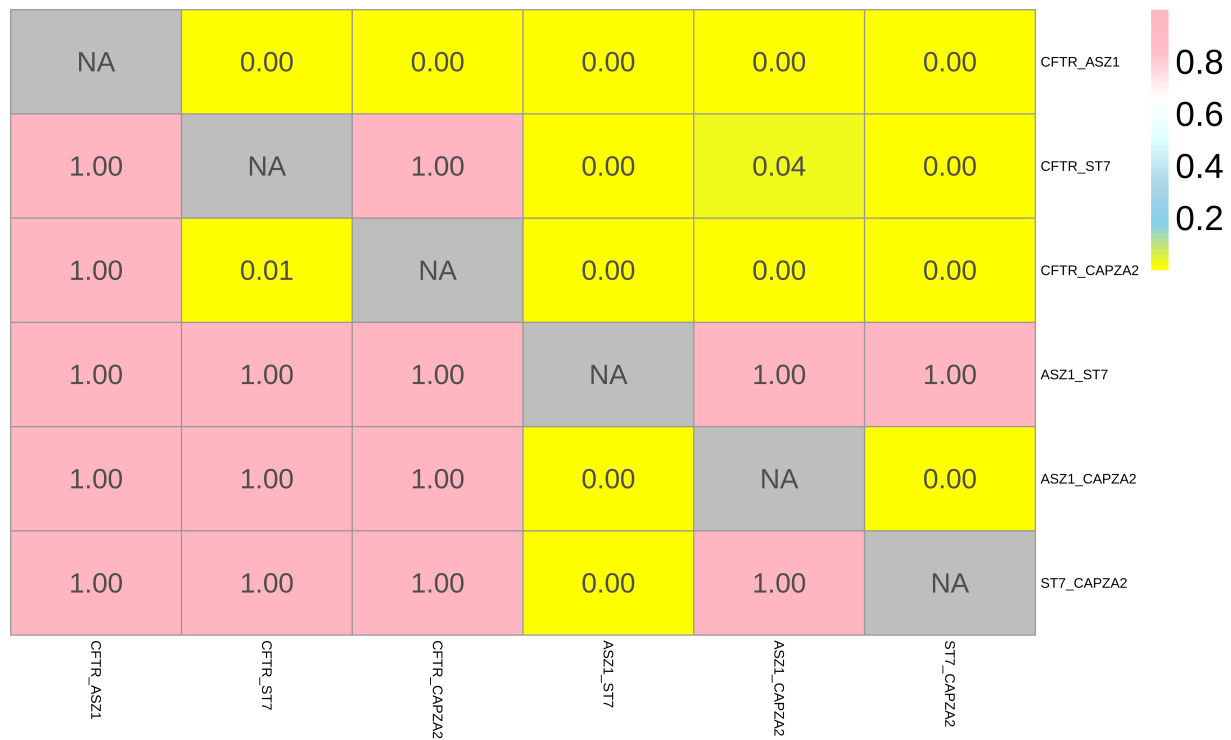


Figure 514: Heatmap_of_deletion_plot.png

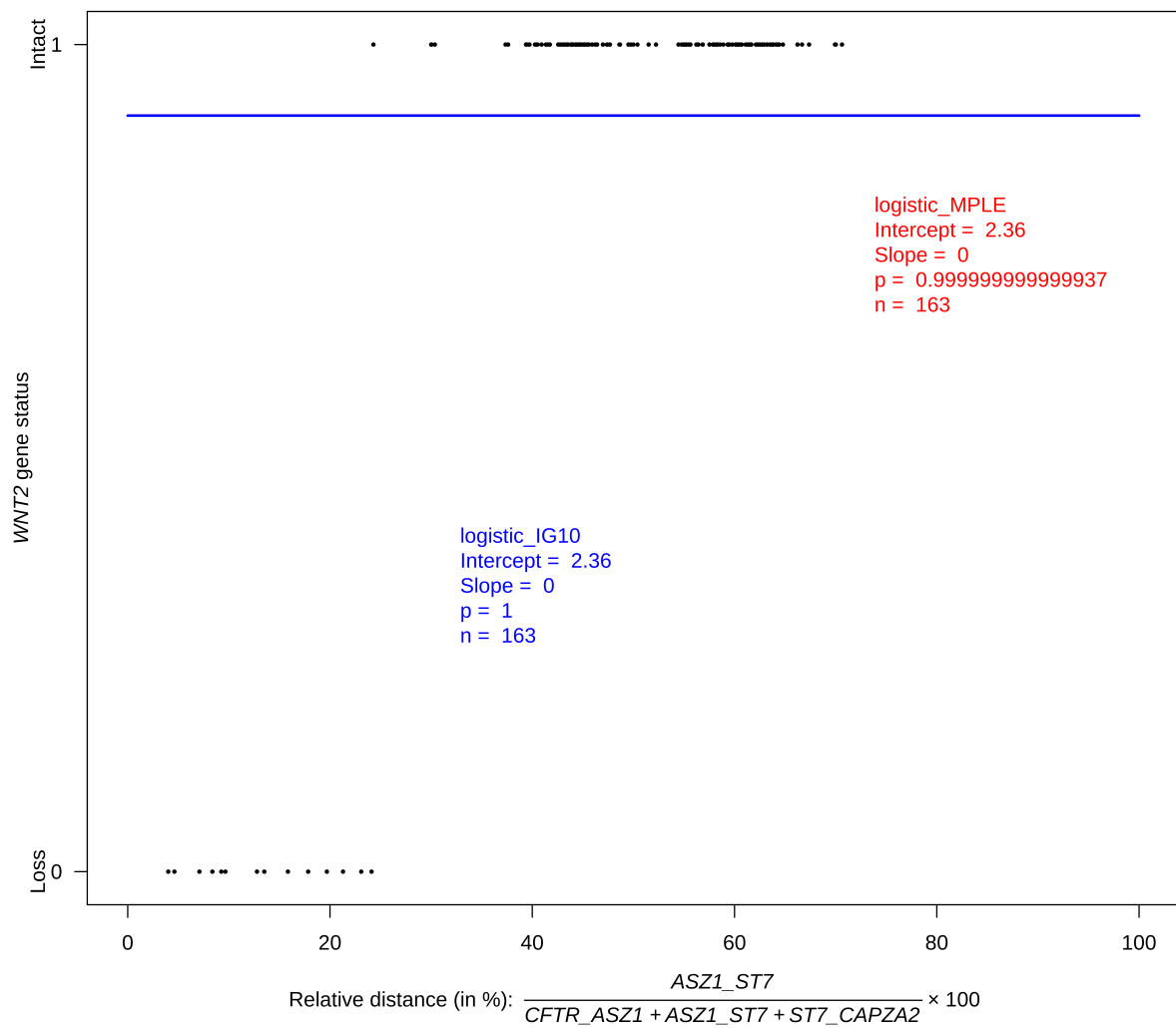


Figure 515: Phylogenetic_signal_of_deletion_plot.png

WNT2_pvals_summary.tsv

Gene	Total_Species	Squamates	Non_Squamates	Sig_Pvals_Count	IG10_Pval	MPLE_Pval
WNT2	163	14	149	5	1	0.999999999999937

Lastz Alignment evidence

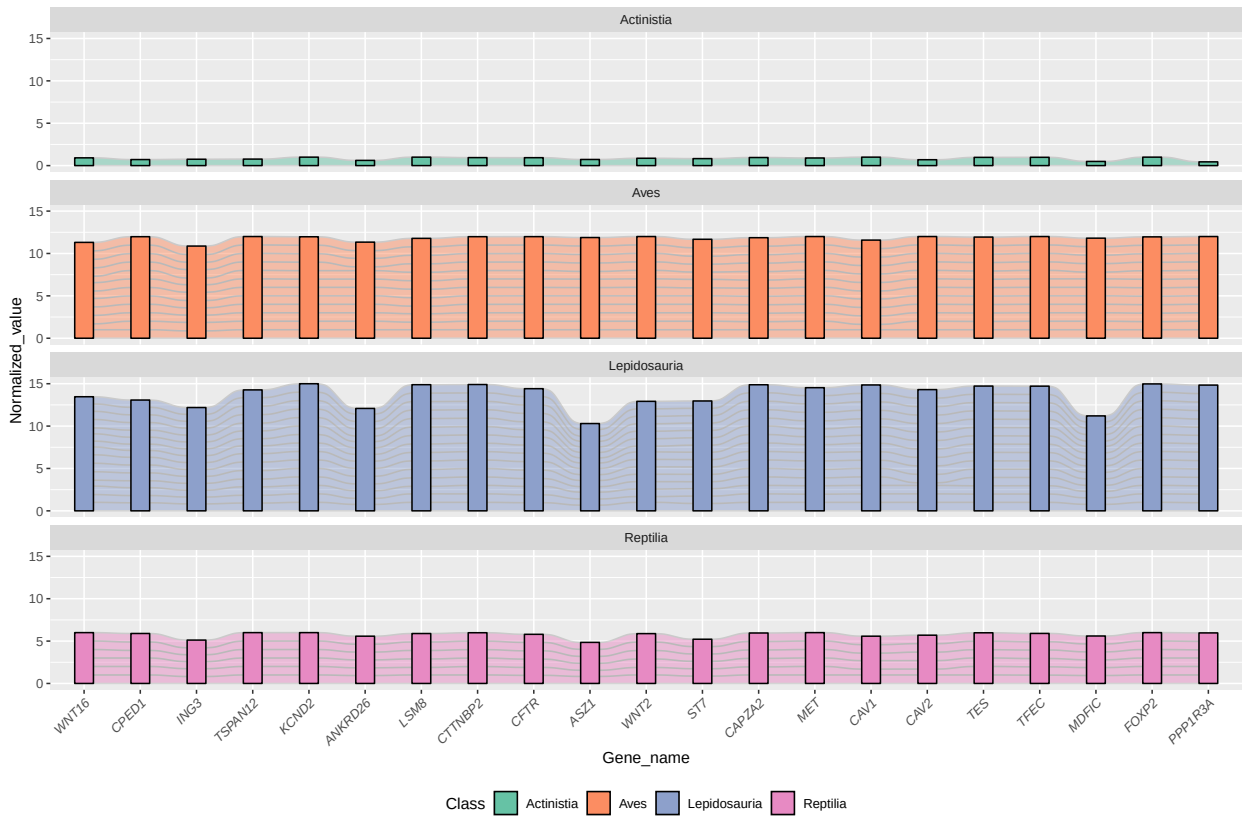


Figure 516: WNT2.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

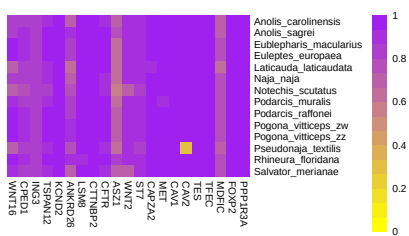


Figure 517: WNT2.FS_Exonic.Final.Gallus_gallus.21_genes_heatmap.pdf

Lastz gene tree



Figure 518: WNT2.combined.mafft.aln.highlighted.pdf

Syntenic evidence

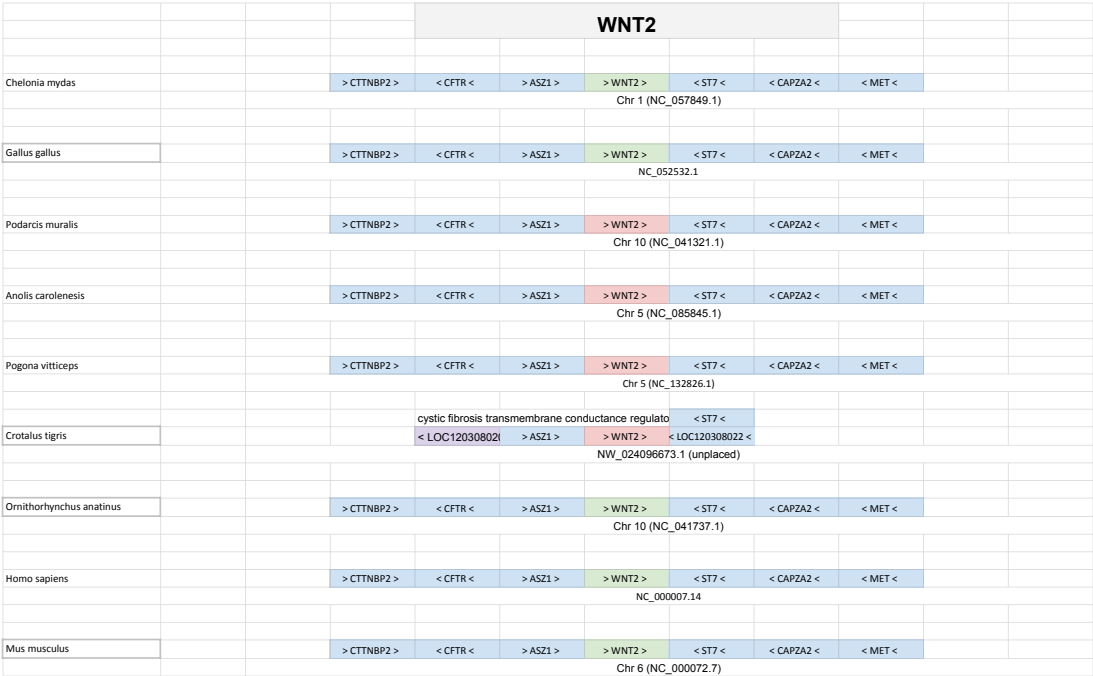


Figure 519: WNT2.pdf

WNT2.txt

Synteny analysis of WNT2

We analyzed the synteny of WNT2 across squamates and representative outgroups. The WNT2 syntenic block is conserved in all examined species. In the synteny plots, red blocks indicate the absence of WNT2, green blocks mark its presence, light blue blocks represent genes conserved across lineages, and light purple blocks denote different flanking genes.

Transcriptomic evidence *Pogona vitticeps*



Figure 520: WNT2.png

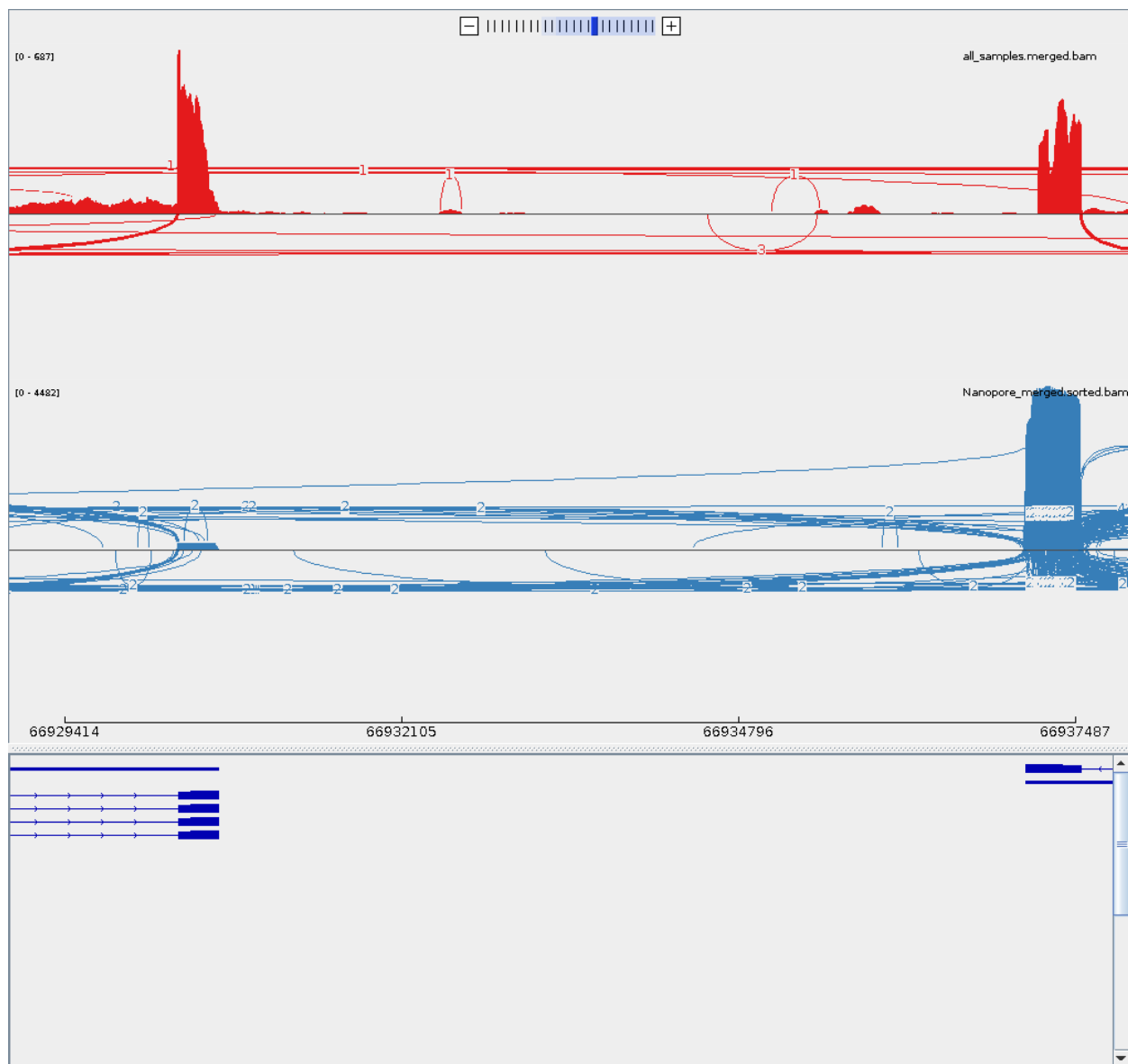


Figure 521: WNT2_Sashimi.png

52 YBX3

Important gene stats

YBX3_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
YBX3	18.6490566	61.6475 +/- 3.35013	5.41117 +/- 0.616257	75.7669 +/- 16.9572	Yes	YBX1;

Lastz Alignment evidence

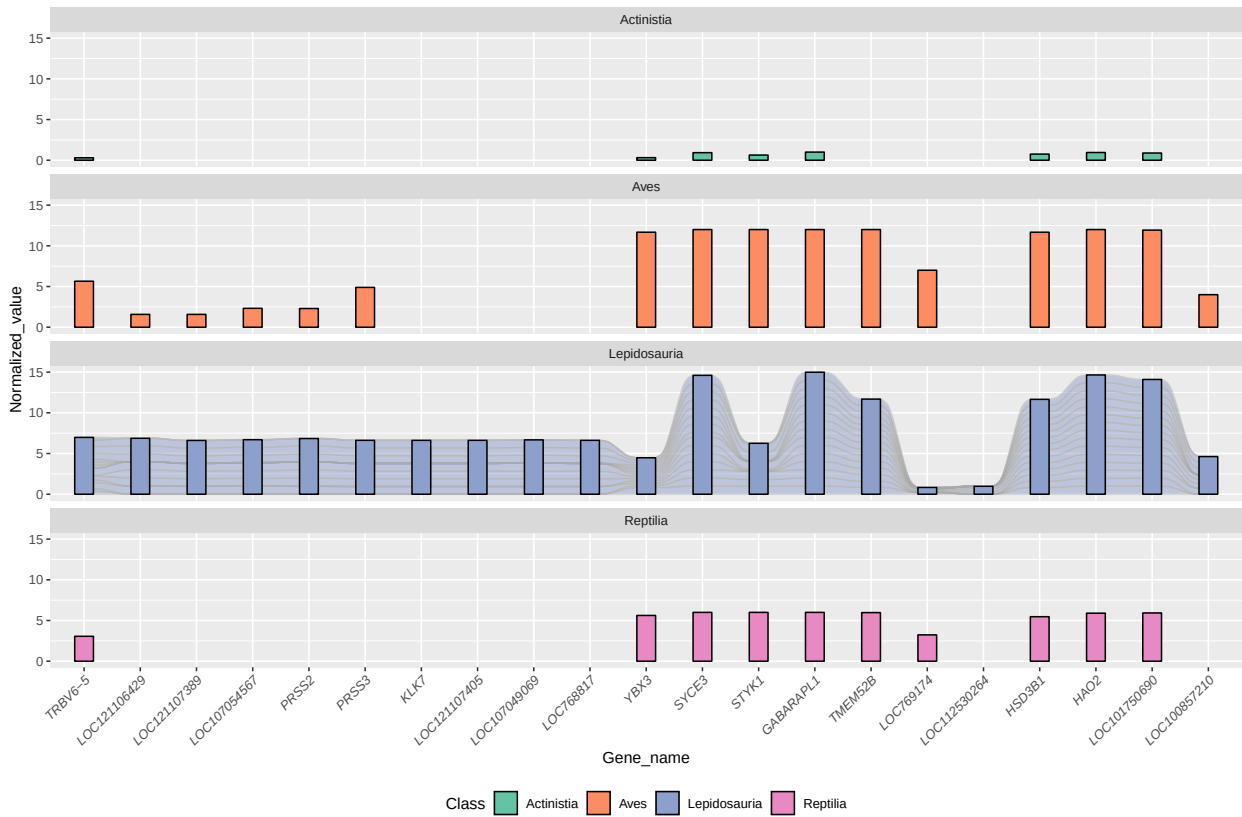


Figure 522: YBX3.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf



Lastz gene tree

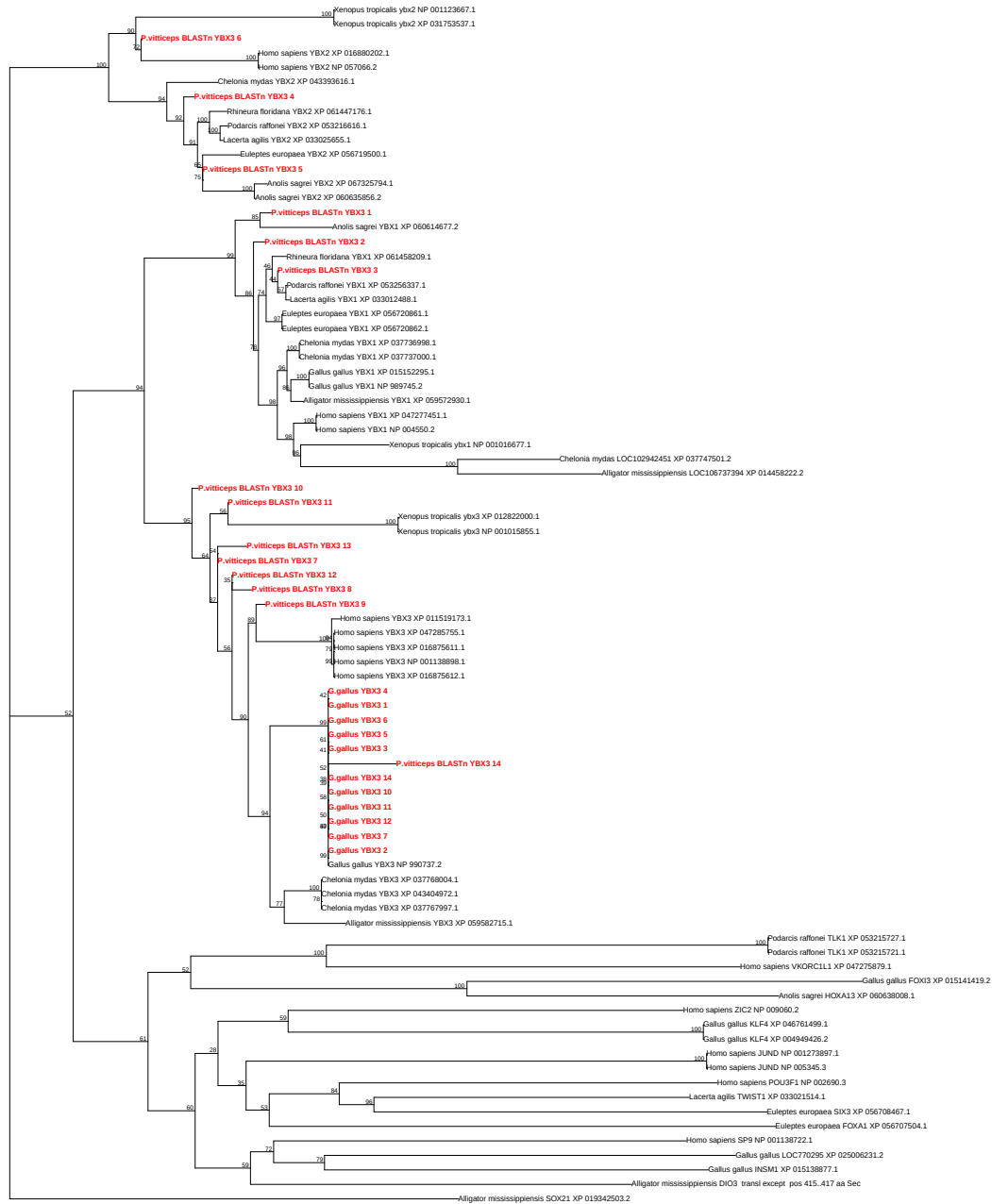


Figure 524: YBX3.combined.mafft.aln.highlighted.pdf

Orthofinder genetree

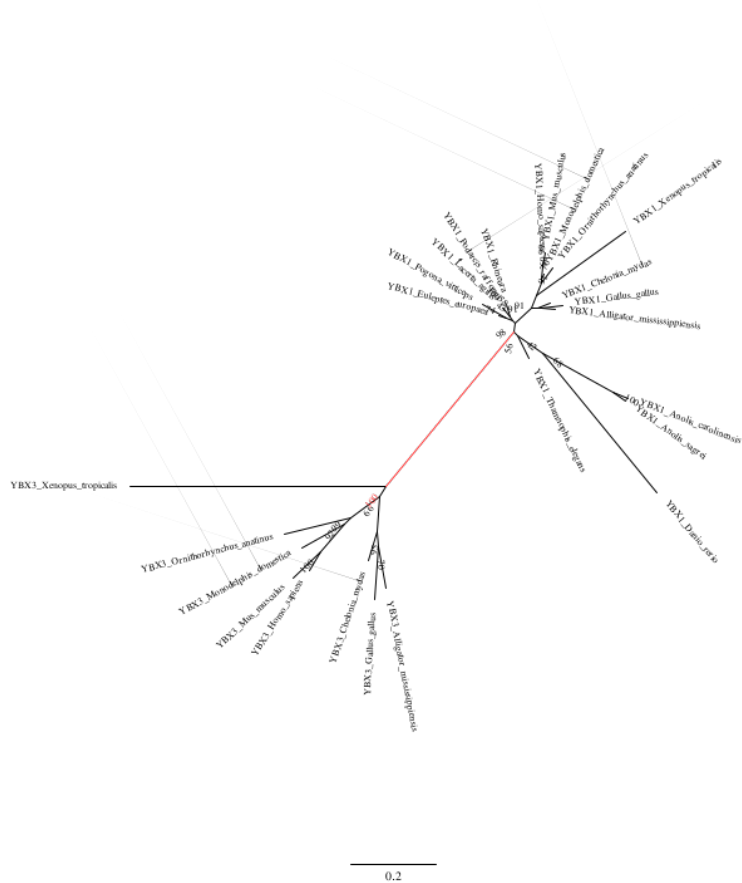


Figure 525: YBX1_2_3.PRANK.aln.contree.png

Syntenic evidence

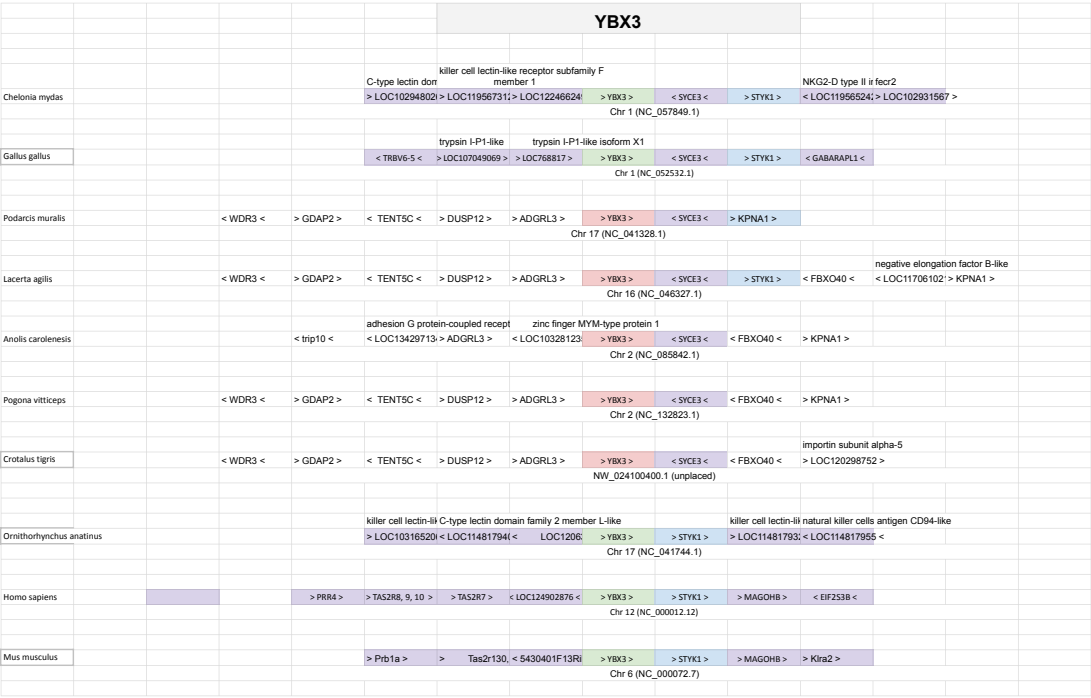


Figure 526: YBX3.pdf

YBX3.txt

Synteny analysis of YBX3

The analysis of the YBX3 gene reveals a significant interchromosomal
→ rearrangement in squamates when compared to outgroup species like
→ turtles and birds. In the syntenic plots, red blocks indicate the
→ absence of the target gene, while green blocks mark its presence.
→ Light blue blocks represent flanking genes that are conserved across
→ lineages, and light purple blocks denote instances where a
→ different flanking gene is present.

53 ZNF438

Crotalus_tigris-PacBio

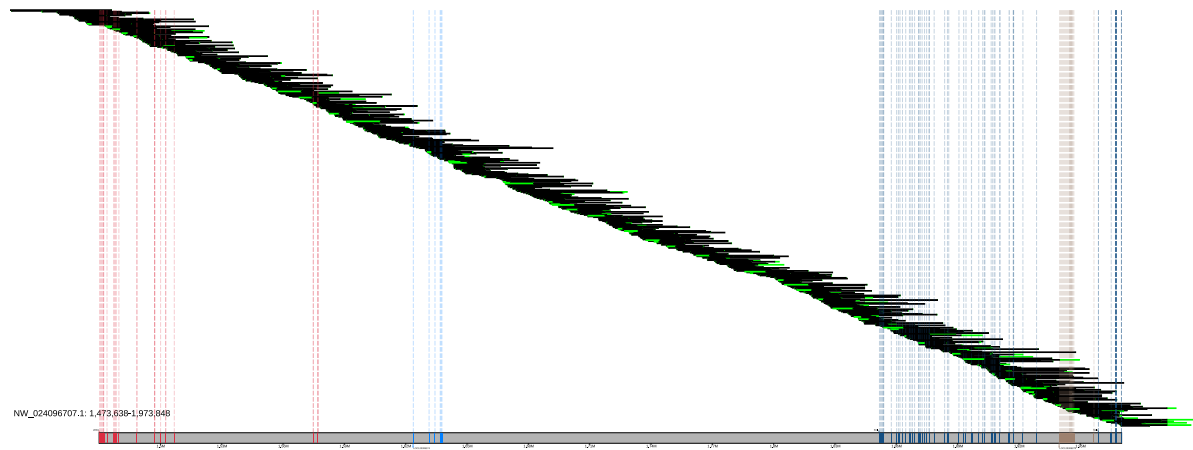


Figure 527: ZNF438:NW_024096707.1:1473638-1973848.pdf

Podarcis_muralis-PacBio

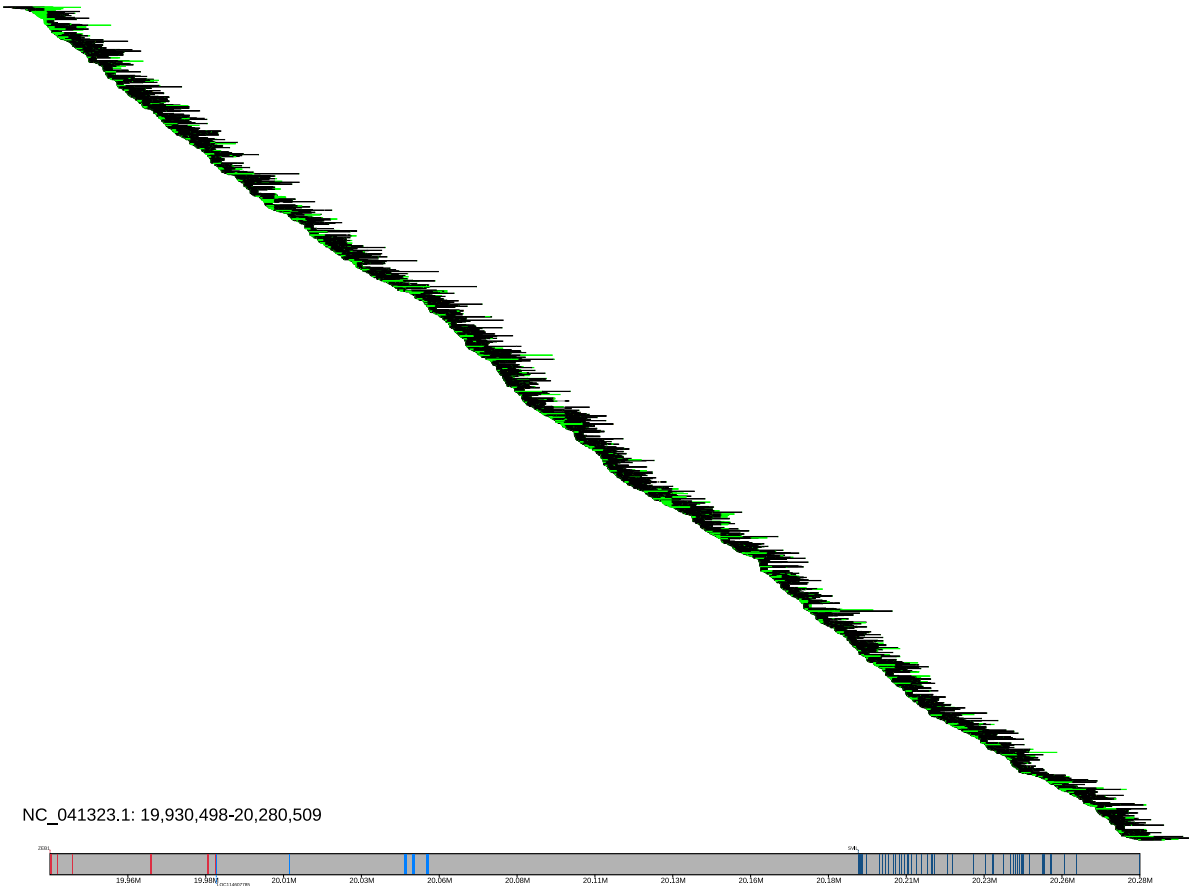


Figure 528: ZNF438:NC_041323.1:19930498-20280509.pdf

Pogona_vitticeps-Nanopore

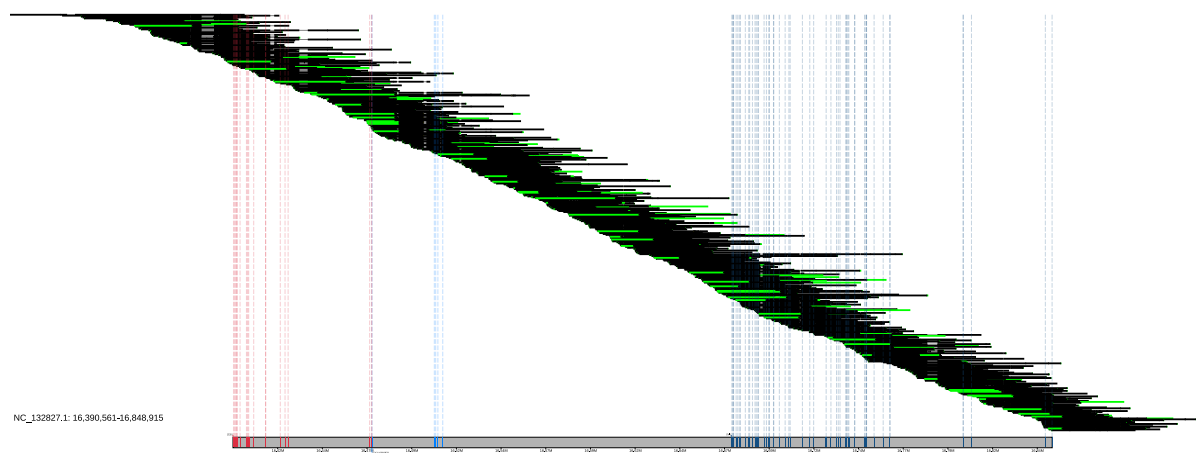


Figure 529: ZNF438:NC_132827.1:16390561-16848915.pdf

Important gene stats

ZNF438_Important_stats.tsv

Gene	Genome Blast Coverage	GC-Content (mean)	GC-Stretch (mean)	Sequence identity with Human ortholog (mean)	Paralogs status (Ensembl)	Closest paralog (recovered using IQ-TREE)
ZNF438	1.845454545	48.4148 +/- 7.16021	3.74957 +/- 0.33933	66.1018 +/- 11.7142	No	Na

Intergenic distance phylogenetic signal evidence

Lastz Alignment evidence

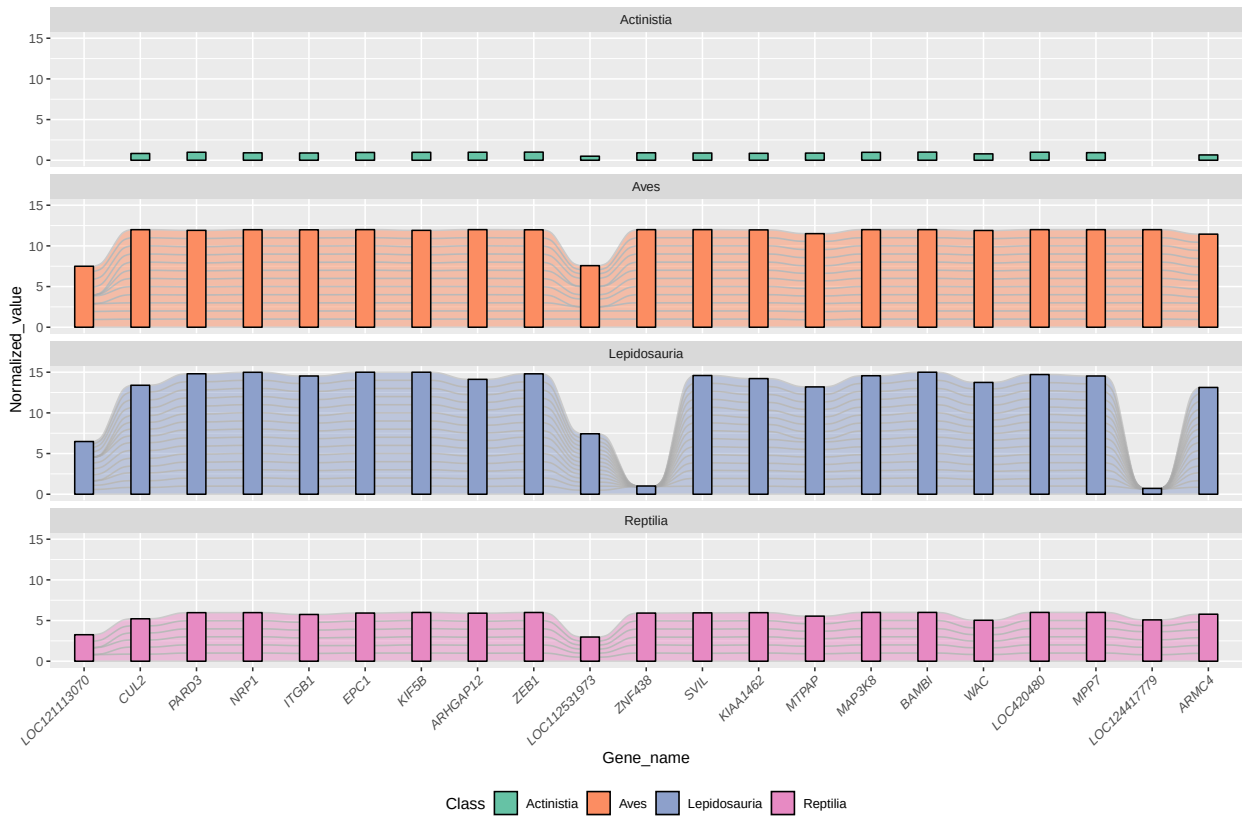


Figure 530: ZNF438.FS_Exonic.Final.Gallus_gallus.21_genes_alluvial.pdf

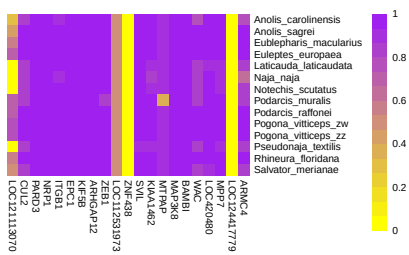


Figure 531: ZNF438.FS_Exonic.Final.Gallus_gallus.21_genes_heatmap.pdf

Lastz gene tree

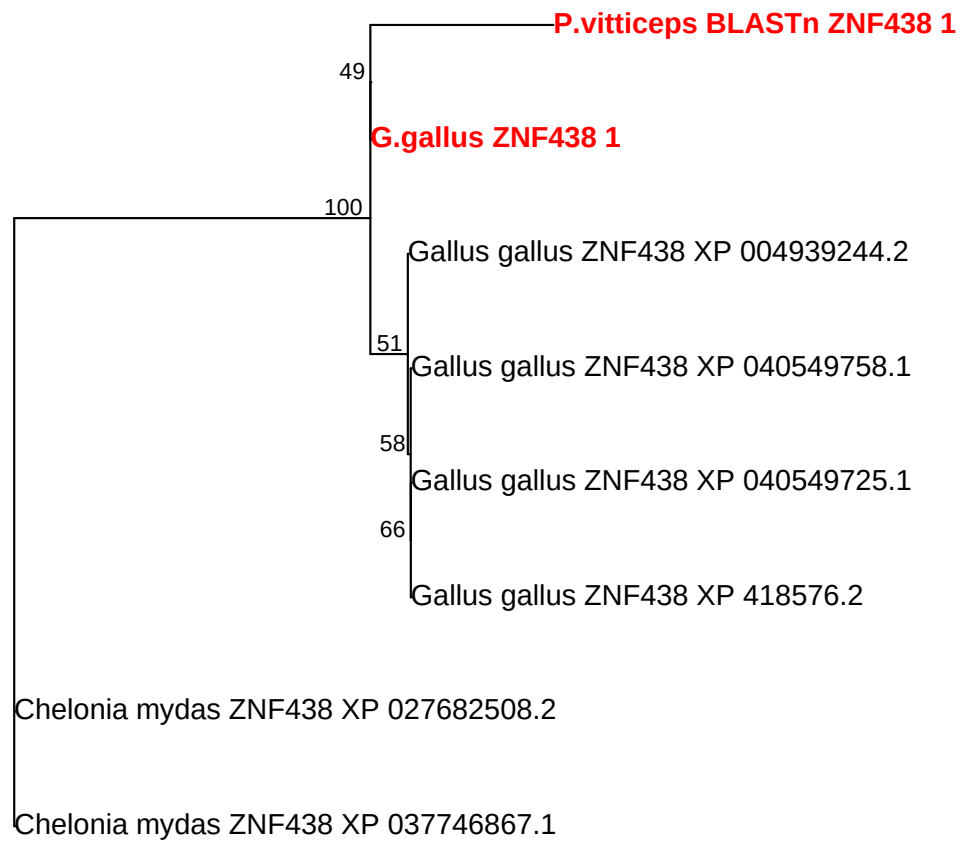


Figure 532: ZNF438.combined.mafft.aln.highlighted.pdf

Syntenic evidence

	ZNF438									
Chelonia mydas	> KIF5B >	> ARHGAP1 >	< ZEB1 <	> ZNF438 >	< SVIL <	< JCAD <	< MTPAP <			
	Chr 2 (NC_057850.1)									
Gallus gallus	> KIF5B >	> ARHGAP1 >	< ZEB1 <	> ZNF438 >	< SVIL <	< JCAD <	< MTPAP <	< MAP3K8 <		
	NC_052533.1									
Podarcis muralis	> KIF5B >	> ARHGAP1 >	LOC114607077	> LOC114607785 >	< ZEB1 <	> ZNF438 >	< SVIL <	< JCAD <	< MTPAP <	
	Chr 12 (NC_041323.1)									
Anolis carolinensis	> KIF5B >	> ARHGAP1 >	< ZEB1 <	> ZNF438 >	< SVIL <	< JCAD <	< MTPAP <			
	Chr 6 (NC_085846.1)									
Pogona vitticeps	> KIF5B >	> ARHGAP1 >	LOC110082878 >	< ZEB1 <	> ZNF438 >	< SVIL <	< JCAD <	< MTPAP <		
	chr5(NC_132827.1)									
Crotalus tigris	> KIF5B >	> ARHGAP1 >	< ZEB1 <	> ZNF438 >	< SVIL <					
	NW_024096707.1 (unplaced)									
Ornithorhynchus anatinus	> KIF5B >	> ARHGAP1 >	< ZEB1 <	> ZNF438 >	< SVIL <	< LOC120638788 <	< JCAD <	< MTPAP <	> MAP3K8 >	
	Chr 13 (NC_041740.1)									
Homo sapiens	> KIF5B >	> ARHGAP1 >	< ZEB1 <	> ZNF438 >	< SVIL2P <	< MAP3K8 <	> MTPAP >			
	NC_000010.11									
Mus musculus	> KIF5B >	> ARHGAP1 >	< ZEB1 <	> ZNF438 >	< SVIL <	< JCAD <	< MTPAP <			
	Chr 18 (NC_000084.7)									

Figure 533: ZNF438.pdf

ZNF438.txt

Synteny analysis of ZNF438

We analyzed the synteny of ZNF438 across squamates and representative outgroups. The ZNF438 syntenic block is conserved in all examined species. In the synteny plots, red blocks indicate the absence of ZNF438, green blocks mark its presence, light blue blocks represent genes conserved across lineages, and light purple blocks denote different flanking genes.

Transcriptomic evidence *Pogona vitticeps*

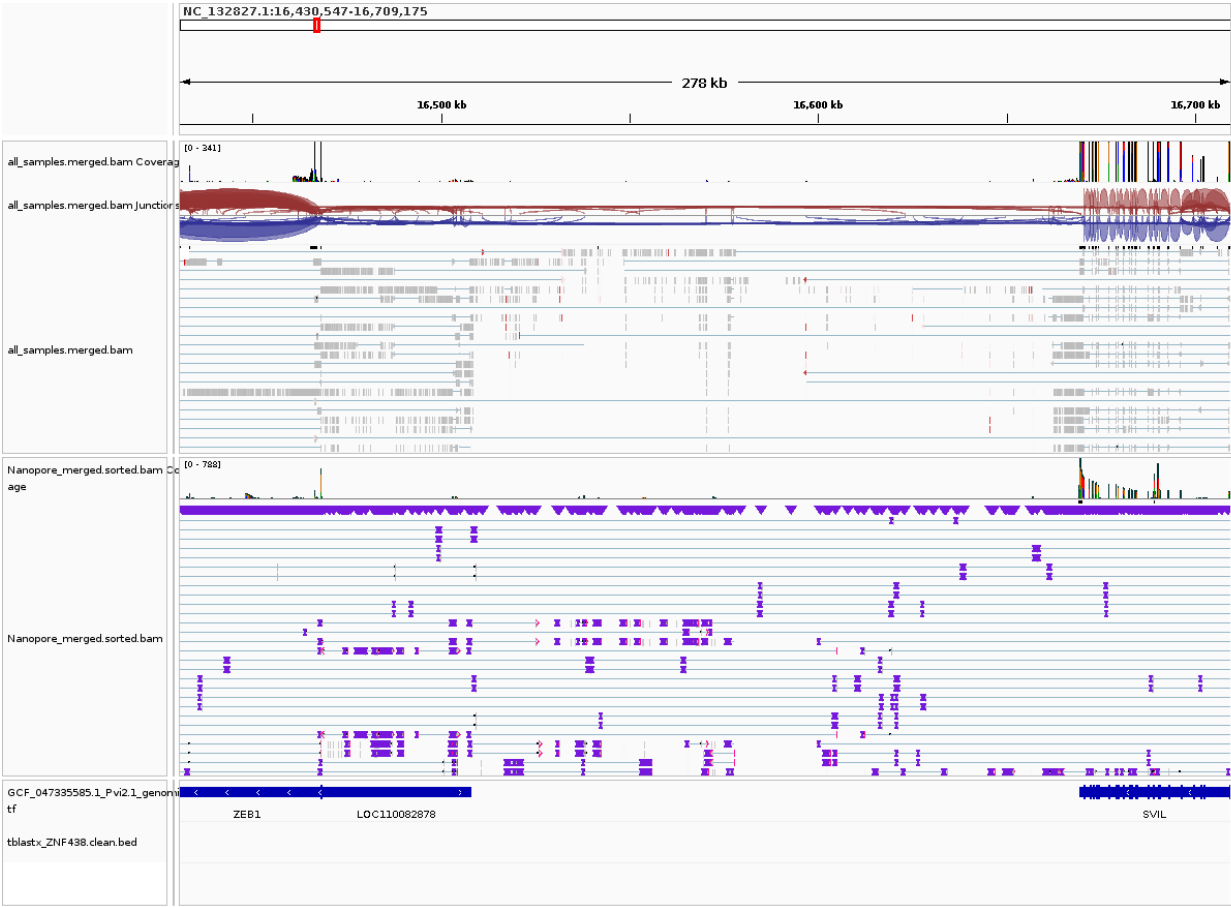


Figure 534: ZNF438.png

