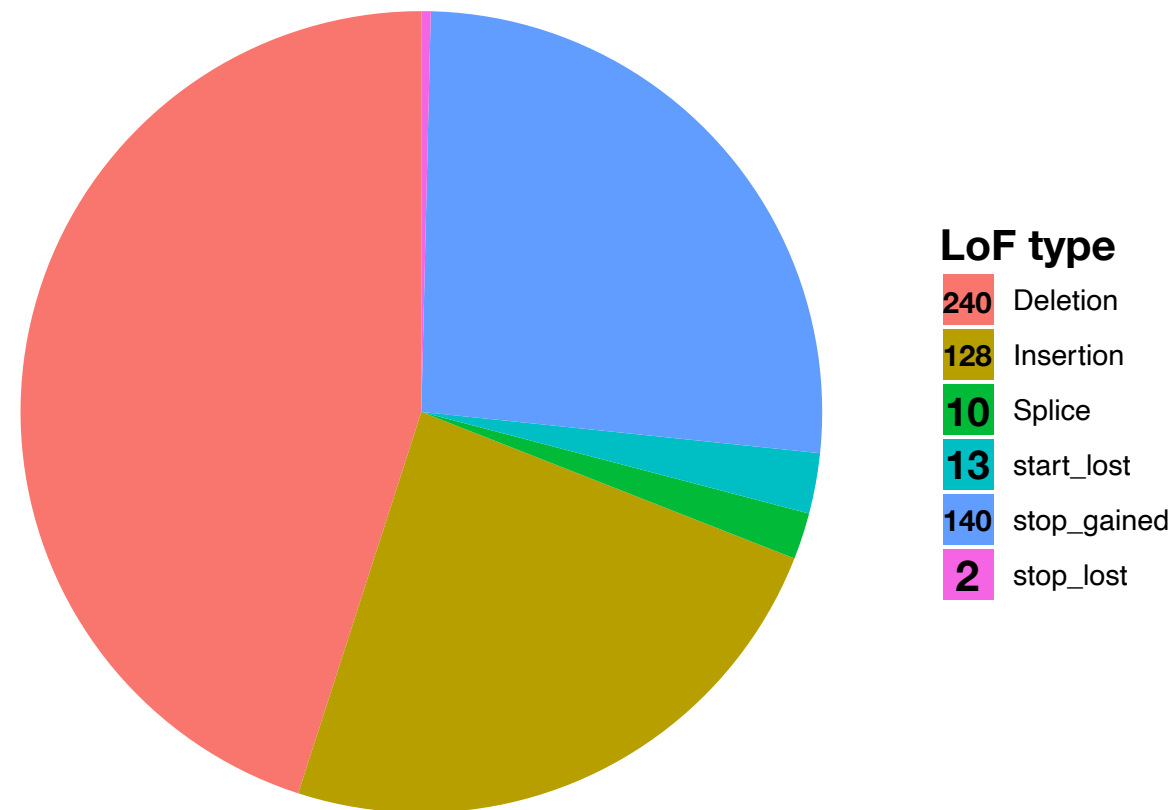
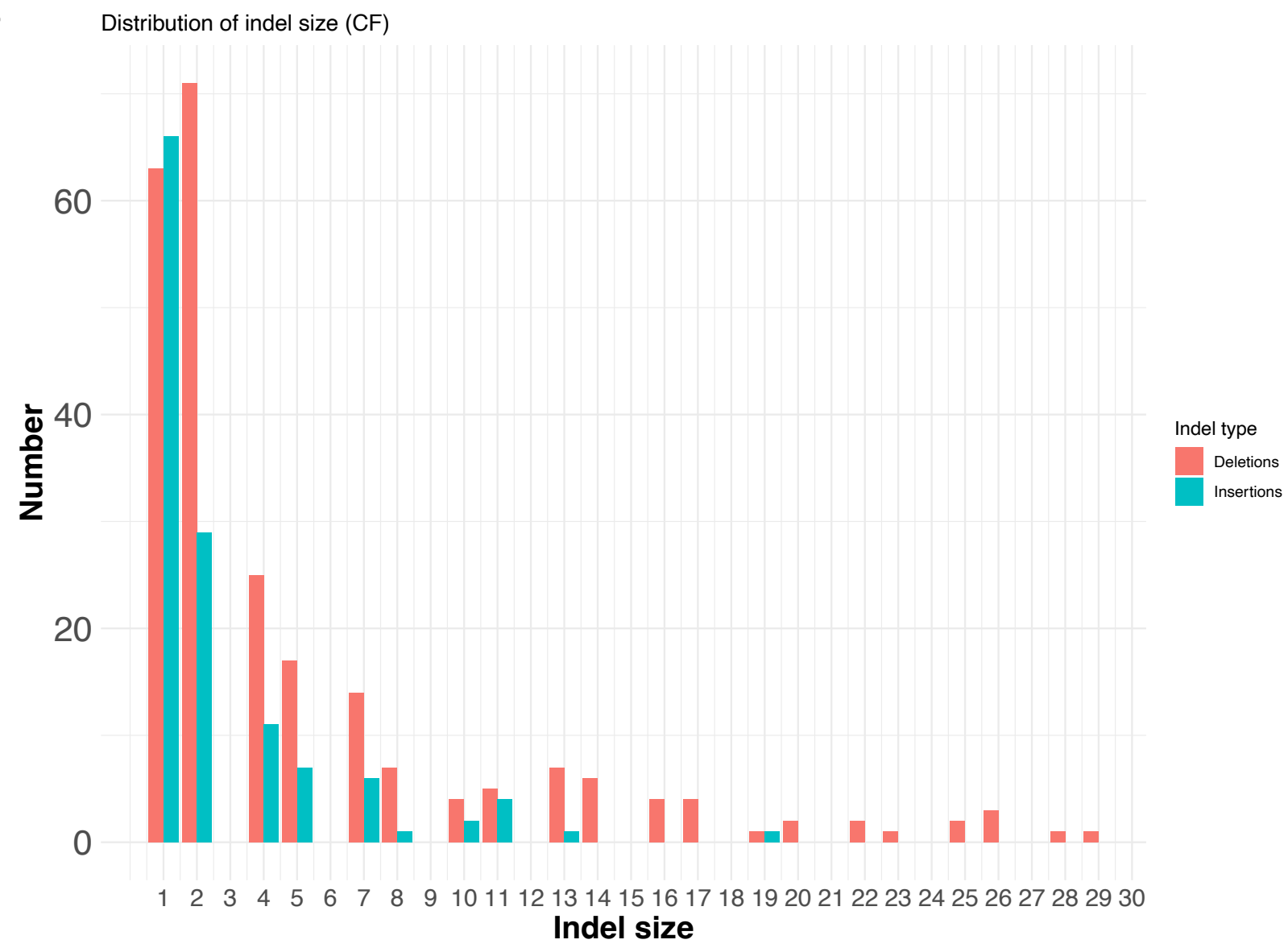


A**B****Fig. S1**

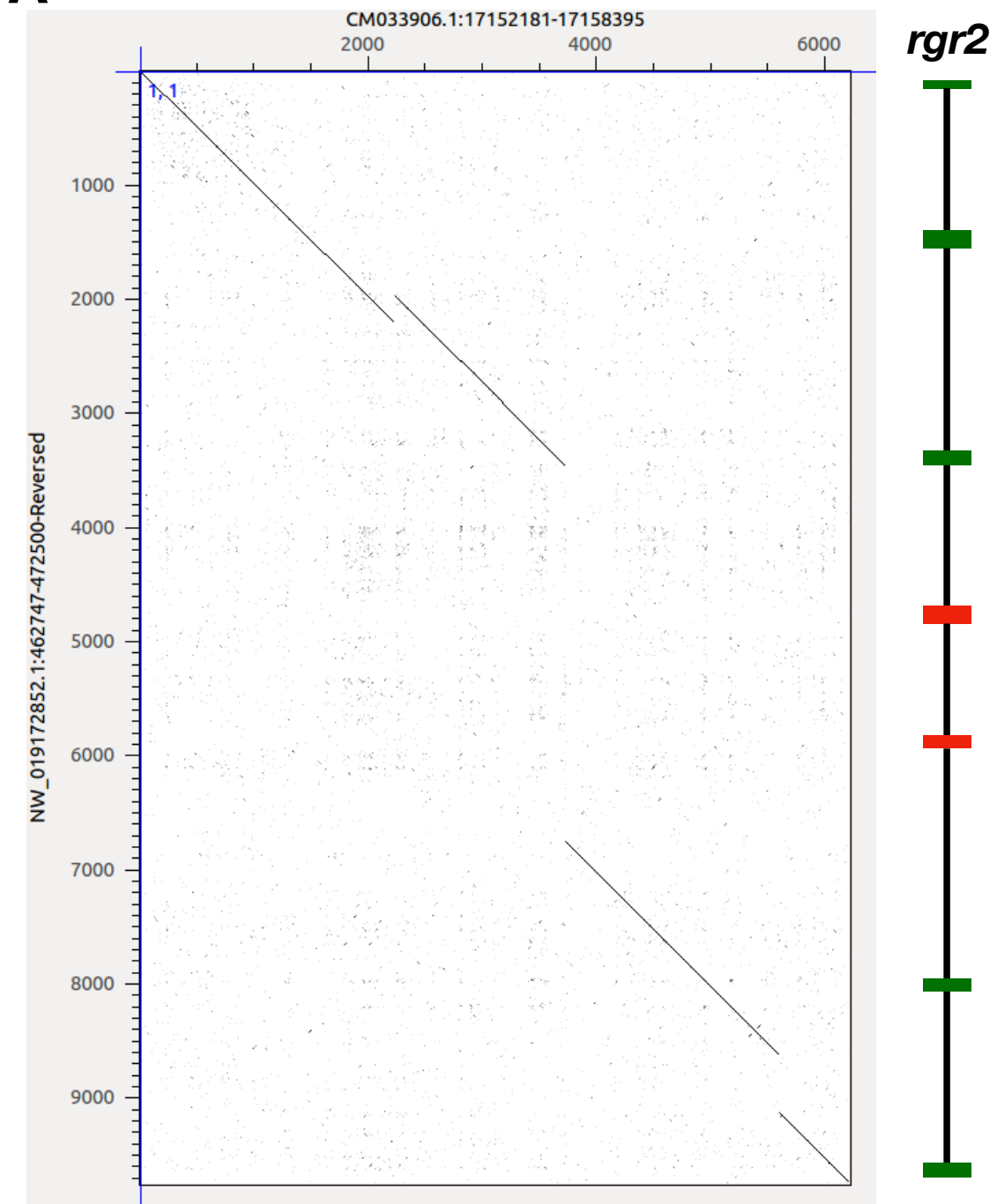
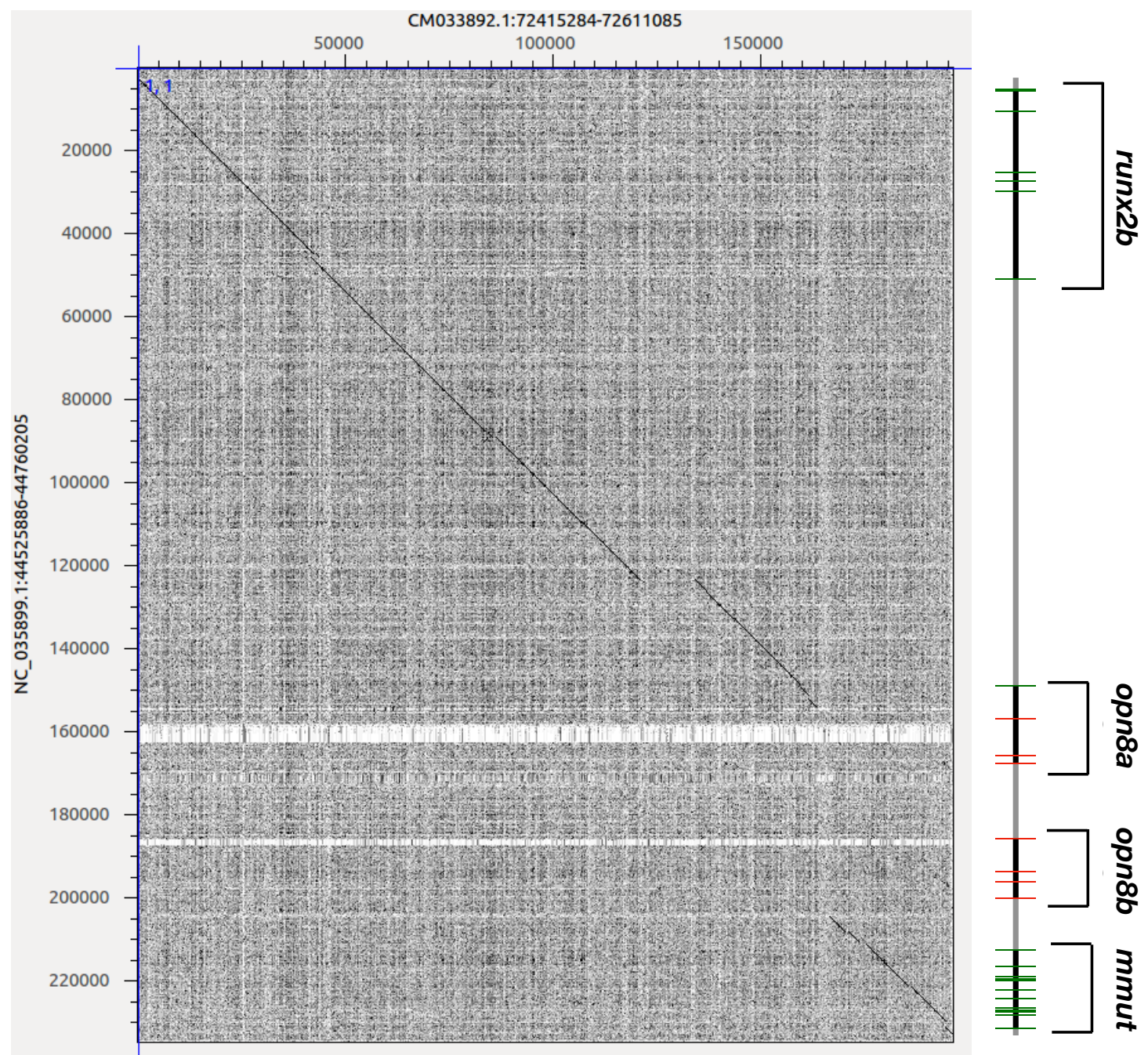
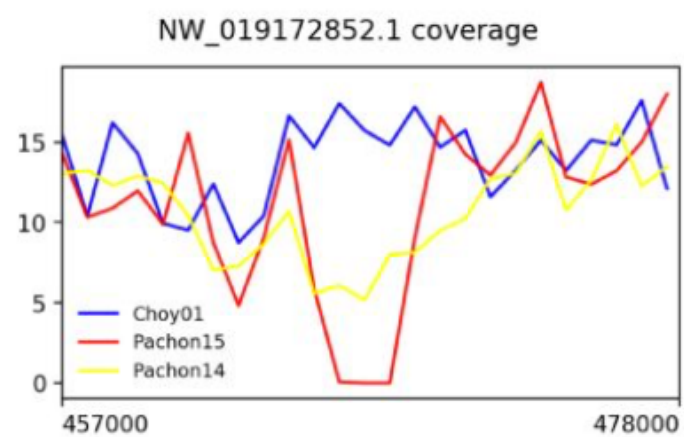
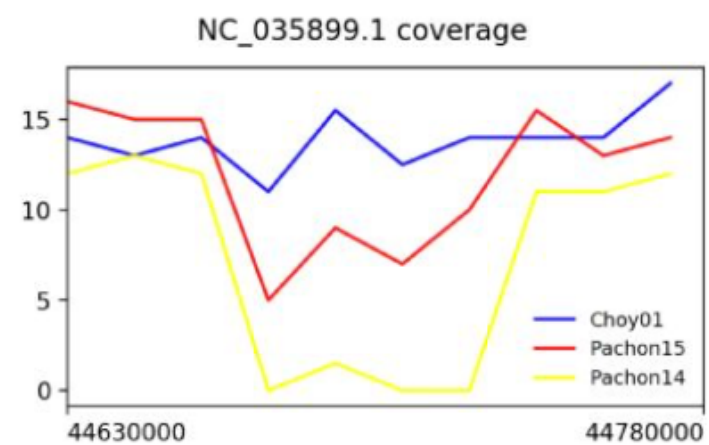
A**B****C****D**

Fig. S2

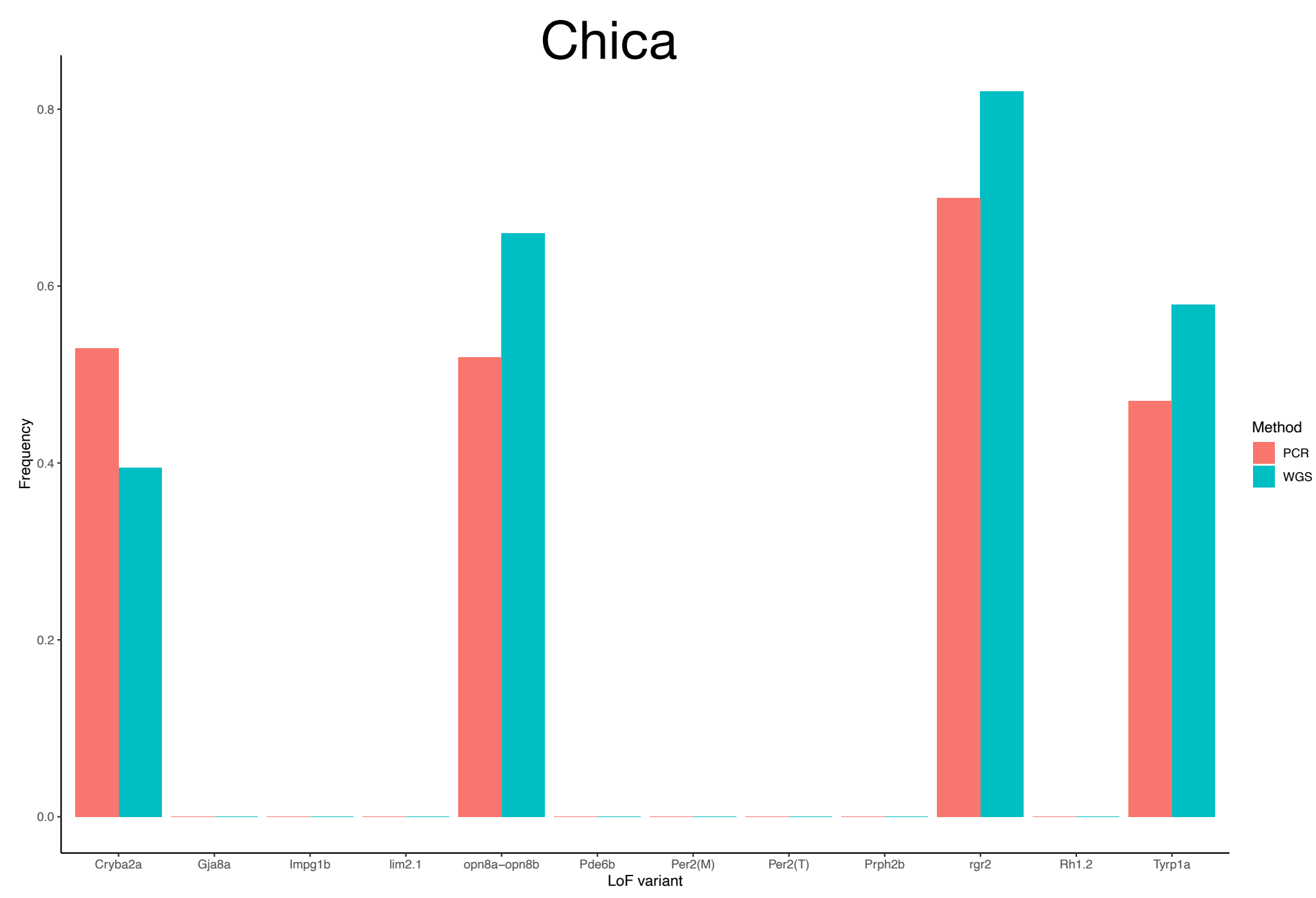
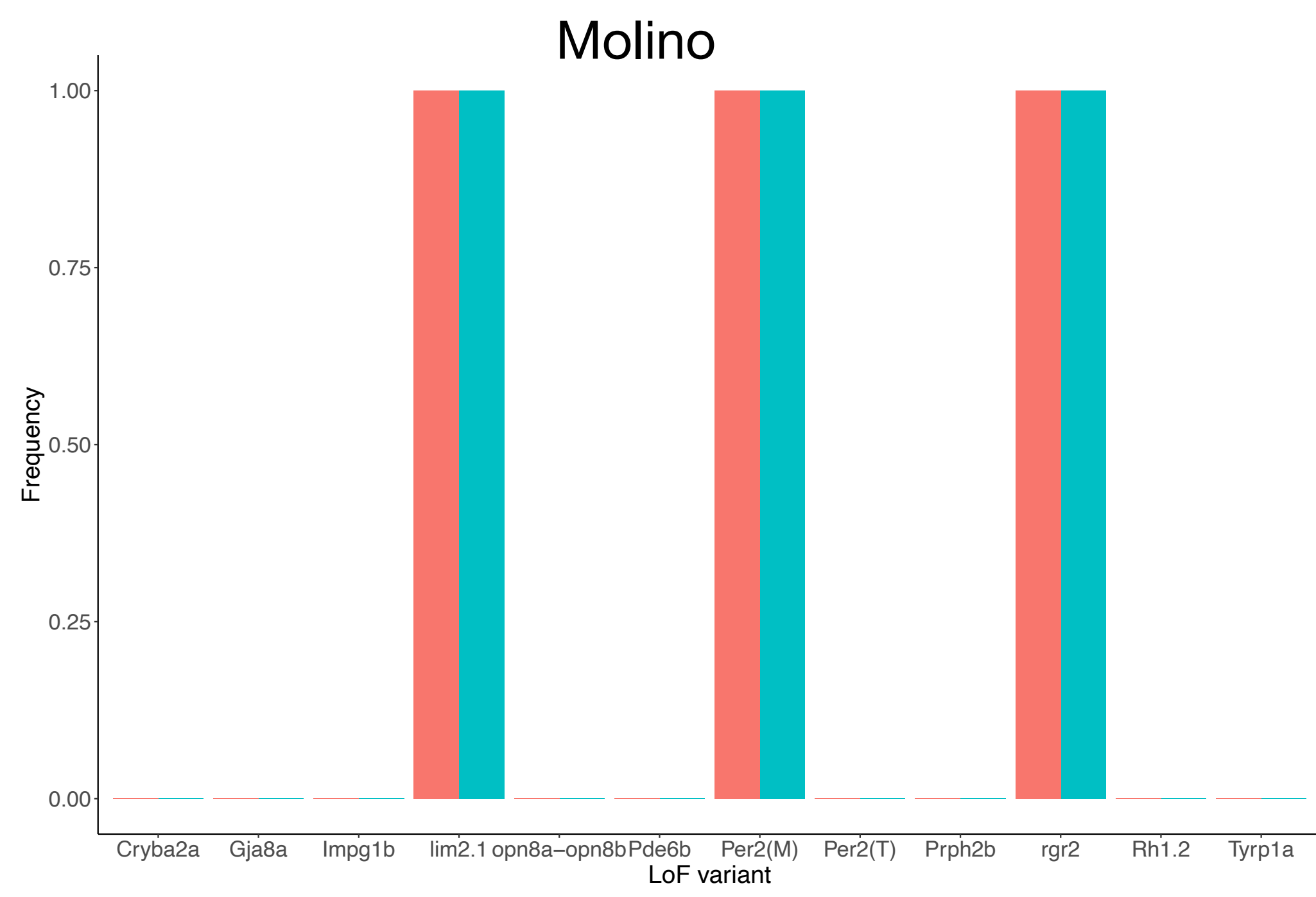
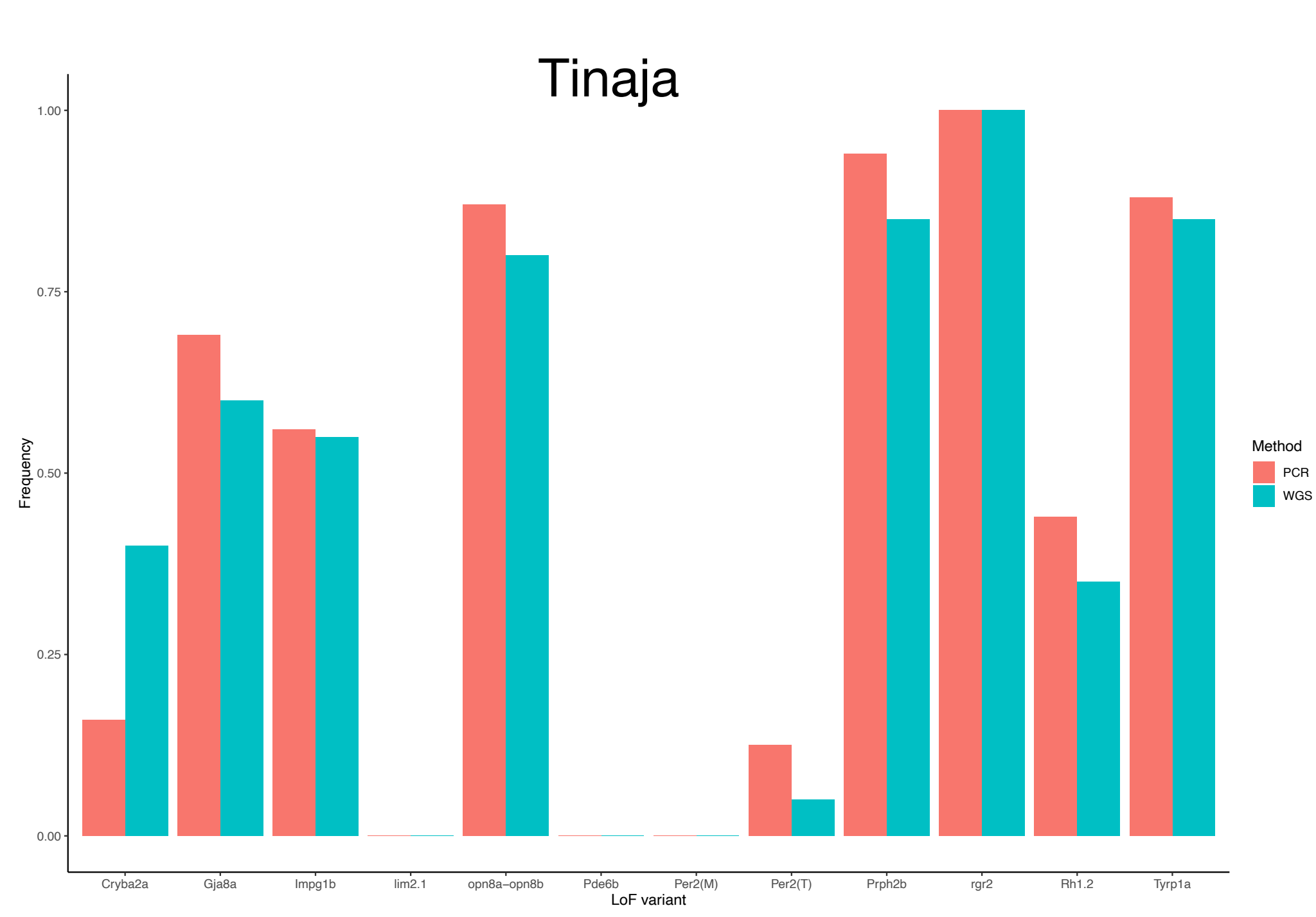
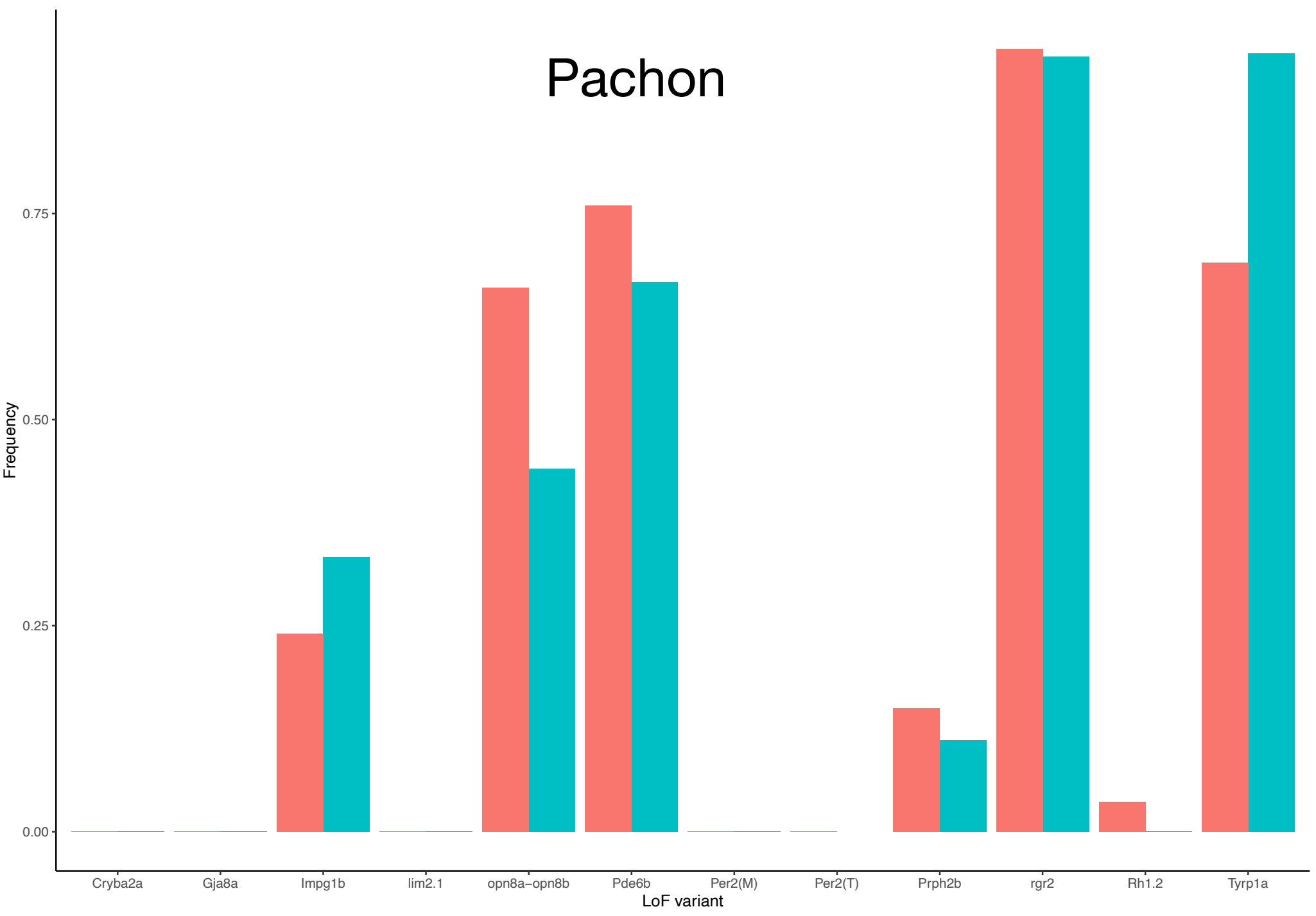


Fig. S3



— SL
— ED

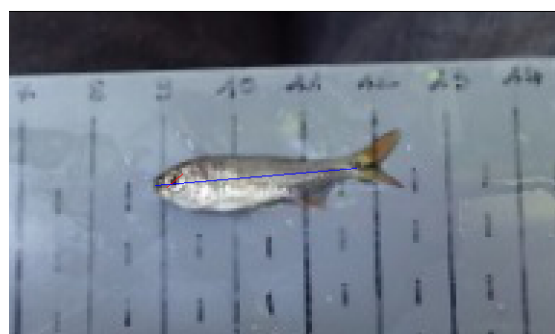
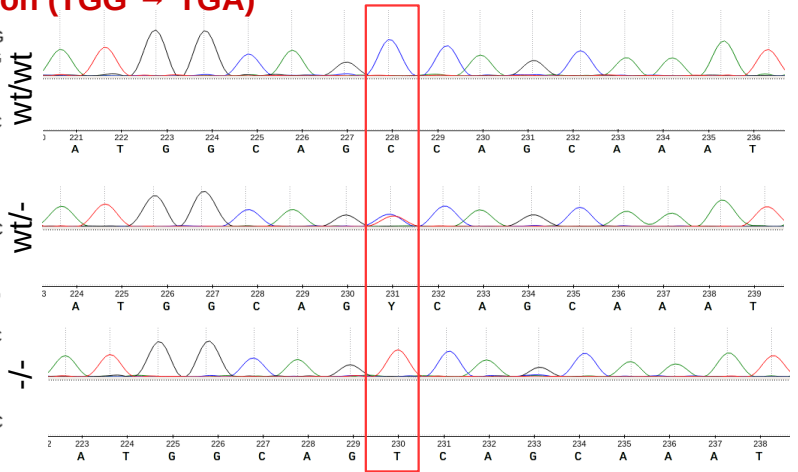


Fig. S4

rh1.2

Stop codon (TGG → TGA)

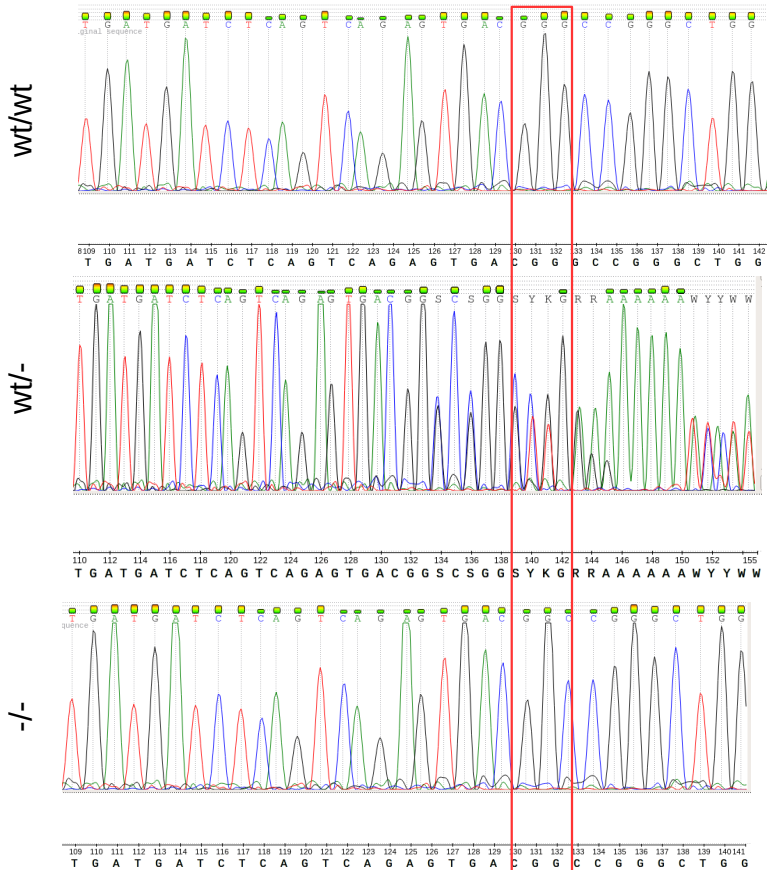
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TCAATGCCTTTACGCTCCACGTCACTATCGAGACCAGAAGCTGAGGACTCCG
CTCAACTACATCCTGCTGAATCTGGCCACAGCCAACCTTTTCATGGTGATTGGC
GGTTTTACCACCACCATGTACACAGCCCTGCATGGCTACTTCATCTTTGGCCAT
GCTGGCTGCAACTTGAAGGATTCTTCGCCACTCTCGGTGGTGAGATCTCGCT
TTGGTCACTGGTGGTCTTCTGCTGGAAAGGTGGATGGTGGTCTGCAAGCCTC
TCAAACCTTTCTGCTTCCGCCAGATCCACGCTGCCTCGGAGTGGGCTTTTCT
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ATCCCTGAGGGCTTACAGTGCTCTTGCAGGAGTCACTACTACACCGAAAAGTCC
TCATCTCTTCAACGAGTCTTCTGTCATCTACATGTTGCGGTTCACTTCACCAT
CCCGCTGACCGTCATCAGCTTTTGTACACCTGGCTGCTCTGCACAGTCAAGG
CAGCGGCGGCGCGCAGCAGGAGTCTGAGACTACGAGAGGGCAGAGCGAG
AGGTCAACCGCATGGTCTGTCATGATGATCGTGGCGTTCCTTATTGCTGCTGC
CATACGCAAGCATTGCTGGTACATCTTACACATCCCGGAATCGTCGTCAAC
CCCCTCTTCATGACCAATCCCTCTTCTTCCGCAAGAGCTCAACGCTCTACAA
CCCTGTAATCTACGCTGTCATGAACAAGCCGTTCAAGAGACTGCATGATCCGCA
CCATCTGCGGTGGCGAGAATCCGTTTGAGAAAGCCGATGAGTCCACCACTCC
AGCTCTCCAAGACGGAAG**CCTCCTCTGTCTCCAGT**TCAGTTTCTCTCTGA
ATAA



tyrp1a

1bp deletion

ACGTTTCTTTAAATAACAAAGTTTAATAATTGCCAAAGTTTAAAGCAA
CATATAAACTAATGTTTTAGTCTCTATT**GACCTCTGTGACATTG**
AGTACTGAACCTTATTGTATCTATTGTTATTAATAAAAGTAAATACTAATAG
CATAATTCTAATAAATGATATGATTTTTCTCCAGCCCGGCC**G**TCAC
CTGACTGAGATCATCACCATCGCTGTGGTAGCAGCCCTCATCGTGGT
GGCGGTCTATCTTTGCCATCACCAGTGCGCCGTCCGCTCCAAAACG
TACAAGATGGACGGCCGTAGCCGCTGCTCGGAGAA**CAGTACCAGC**
GCTACGATGATCACGACAGACACAGCGACAAGACCCAGTCTGTGGTT
TAAACCACTGGTGTAGAAAACCAACCACTGCCCTCTATCTCTCAG



pde6b

11bp deletion

GAGTCCTAATGAGTGGGTGGAAAATTGGATAAAATTTAATAGGAATAAAATGAT
TTTTAAAGACTGTGCACTCTTGTGATGCGTGTGTTGGTGATTTCTCCAGCC
CAT**GATGGACCGAAACAAGCAGCAG**ACCTTCCCAAGC**TTCAGTGGCG**TTT
ATAGACTT**CGTCTGCACTTTCGTCTACAAGGT**ATTCTCAGCGTTTCTATATT
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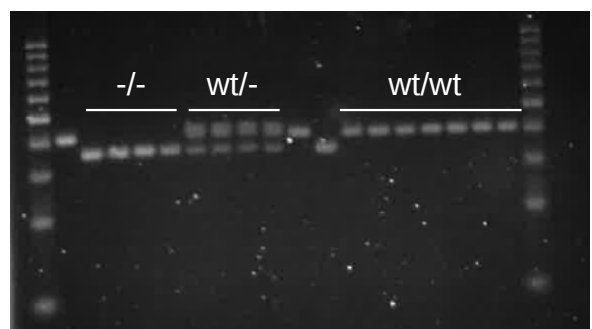


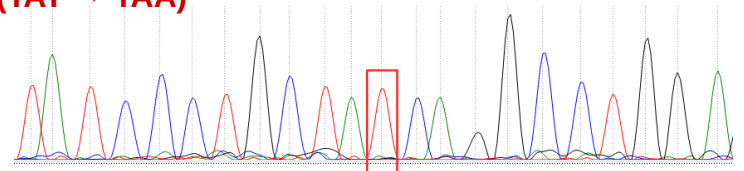
Fig. S5

cryba2a

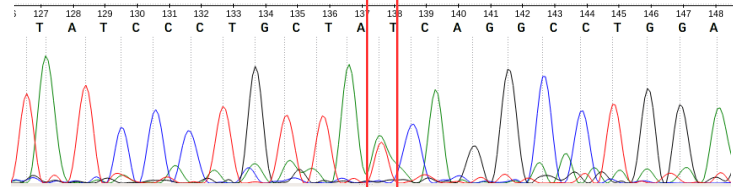
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CCAGCTGGGTGGGTTATGAGTATCCAGAGCACCAGGGCCAGCAGTT
CATCCTGGAGAAGGGGAGACTATCCCTGTTACAGGCCTGGAGTGGC
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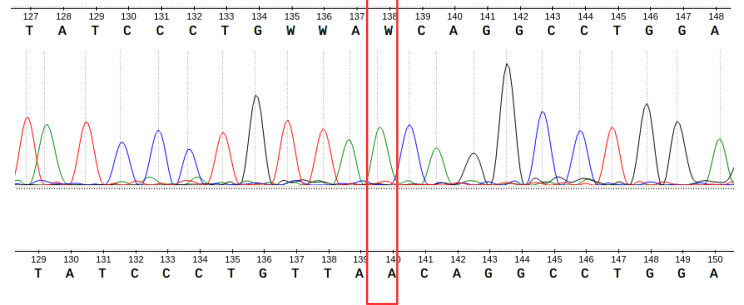
wt/wt



wt/-



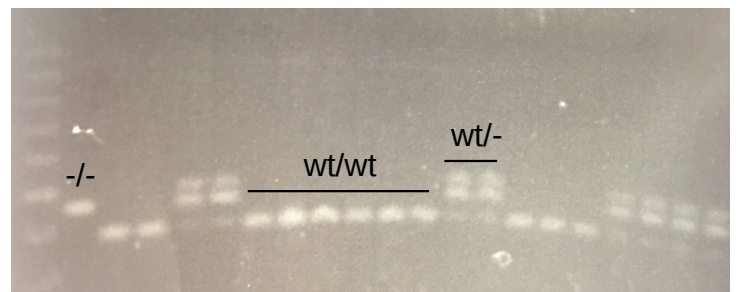
-/-



imp1b

13bp insertion

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GCCTAAATGGGGGACCTGTGAAATCCTAGCANNNNNNNNNNNNGGCCATGGAGCCACTTGACAG
GTACCTCCATACTGATCAGGTTTTTTTATATACAGCTTCGGAAAAATTAAGAGACCGATTCTGAATC
GGTTTCTCTGATTTGCTATTATAGTTTATGTTGAGTAAATGAACATTGTTTATCTATAAAGTAC



gja8a

16bp deletion

CTTAGGTAATATTTAGAGGAAGTGAACGAACACTCGACTGTGATTGGCCGCGTTTGGC
TCACGGTGCTCTTCATCTTCCGATTCTGATTCTGGGCACGGCGGCGGAGTTCTGCTG
GGGCGACGAACAGTCCGATTACGTGTGTAACACCAGCAGCCTGGTGTGAGAAATGT
TTGTACGATGAAGCTTCCCTATCTCTCATTCCGGCTTTGGGTTCTCGAGATCATCT
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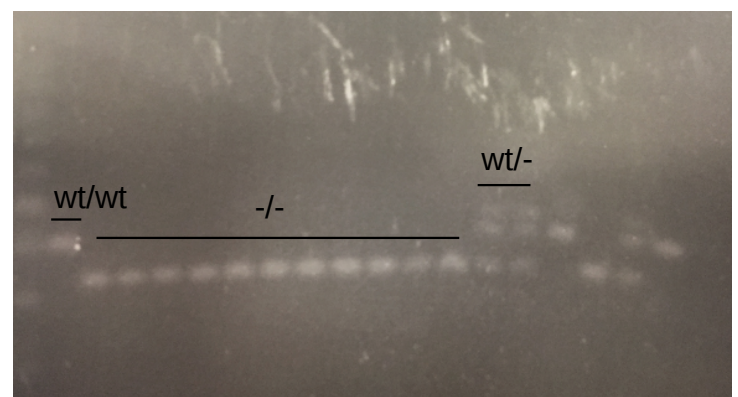
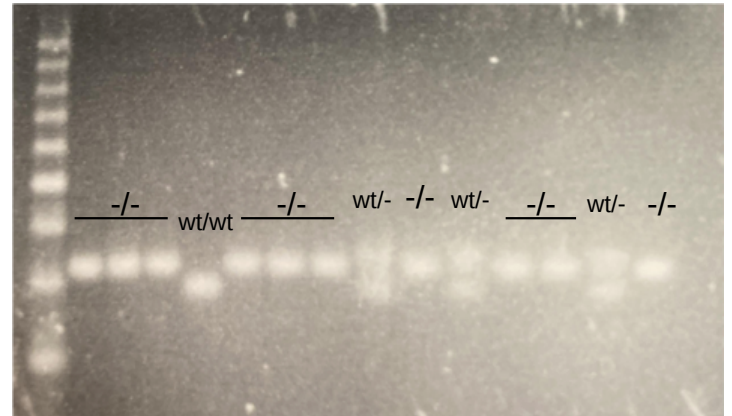


Fig. S5

zgc:153441

2bp insertion

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TCCTTGATCAGTTACAGGCAGAGCAAACCTAGCCAACGTTCTGTTCCACAGAGAGCTCTCACGGCGGATCAAA
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TACCTGCTGTCCTCTCCTGCCATCCTCCTCATGAAGACCCGAGGAGGAGCTCAGACTACCATTTACTG
CACCATCACTGAGGAGCTGGAAAAATACAATGGCTGTTACTTTAGGTAAGTTCATAAAAAATCCAAAGTGA
GTATATATTTATACAGTTTACAAAAAATTAAGATACCACTTAAAAATGCTAAGCTTTTTTGTGGCTTGTGACC
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AAAAATAAAAGCATTTTATGATAATGATCTTTGCATCTTTGGTAATGGCAGTGAAGCTGATGGAGCC
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AAGAAGAG



prph2b

Stop codon (AAG → TAG)

GTGGATCAACAACAAAGTAACAAAGGAAGATTCTGAGGGCATGAAAAAAGAGATCAGA
TTATAGGTCATTGATTAATTAGGTTAGGTCCAAGTCCAAGTTTAAACAAATAGACTGCAGATATT
ACCAATCCATCATTTTTTATTTTGTGTTTATTTGATAAACAGATAGCAGATATGGTGGACTGA
AGTACCTGACAACCTCTTTGGAGACCTTGAGAAACCCAGAGAACCAGAAAGCAGAGTGAG
GGTTGGCTGCTGGAGAGAGTGTGAAGGAGACCATGTCTGGCATCATGGAGAAGATCAAGACC
TTTGGCAAGGGCAACCAAGGTGGAGGGGGAGGGGGCAAGAGCTCCTGCCACAAGCTGAGATGA
TCACACCTTTAACTTTGGGACTGTAAAGCTTAATTGAGAGAGAACAATAAATTAAGTTATTCTC
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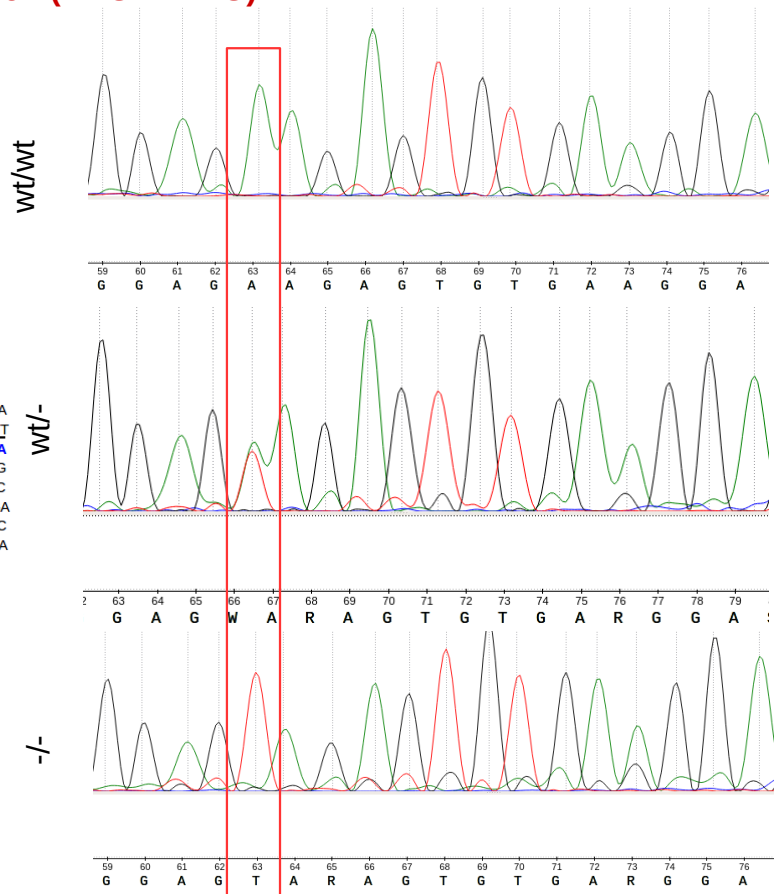
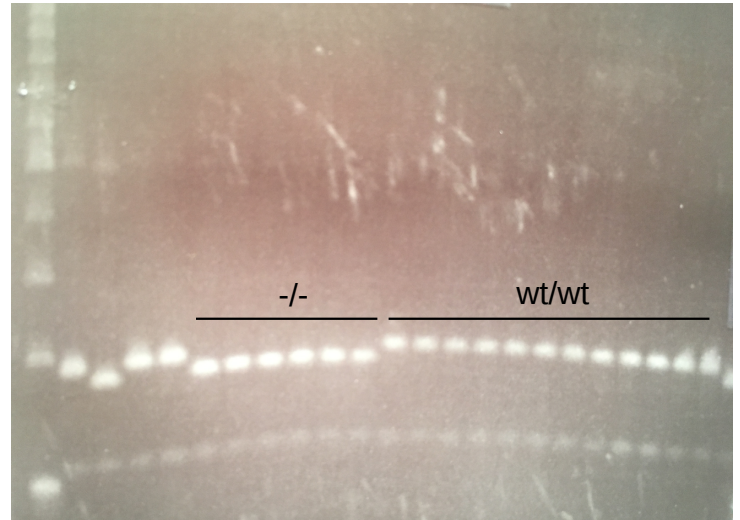


Fig. S5

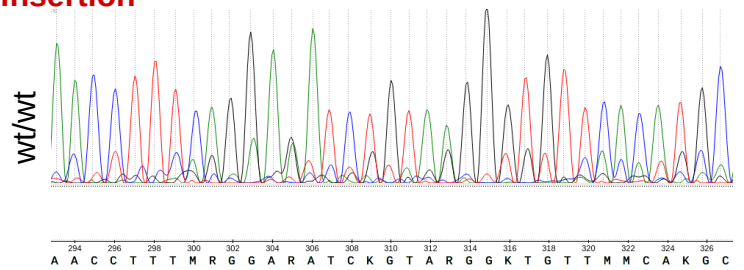
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TGTGTGCAGGCTTTTCGTGTTCTTGGCCATGGCTGTGTACACGGGGTAACATGAATATTAC
GGTAAGCGCTACGGCAGCTTTCCTCTCTGGTCTACATCATCGGTGGTGGCGGGTGGT
CTCACCTTCTTTTCAGGTAGGCTACCTCCTCCGCACACAACCGCCCAAGTGAAGAGTACTCT
CTGTCTGATATTTTATATCTTTATATTGATTGTTTAAAGCTGAATGTGCTTCTCTGCTCTTCT
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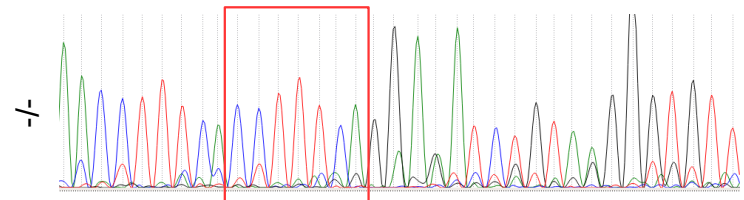


Per2 (E14) 7bp insertion

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CTGTACATGACCTTTTGGTCAGCATCTTTCATTAGAATTTCTCATCACCATTTTCTTTACATTA
GGGCACAAAAATCGGACTTGTCAATATAACATTTCAATATAAAGATTTTAAAGAAAAACATTGT
AAATAAAATTGAAAAATGGAAGCACCCATTTAAAGATTAAATACTTTATATTAATGACAGATT
CCATACCACTCTCATGTTTCAGGGCCCTACATTCTTAAATAGTTATCTACTACTCCAGCACTGT
TTGTATAGAGCATGATGAATAAGTGTCTGTGTTTCTACAGAGAACCTTTCACTTTTCAAGGA
GATCTGTAAGGTTGTCATGCAGAGAAGAACAGGAGCAGCAGACCAGAAAGGCTCCAGGCG
AGTAAGTCCATAGATAAGATTCCATATTCATGTGCTTAGATATCTGTCTGTGATAAAGGTGTC
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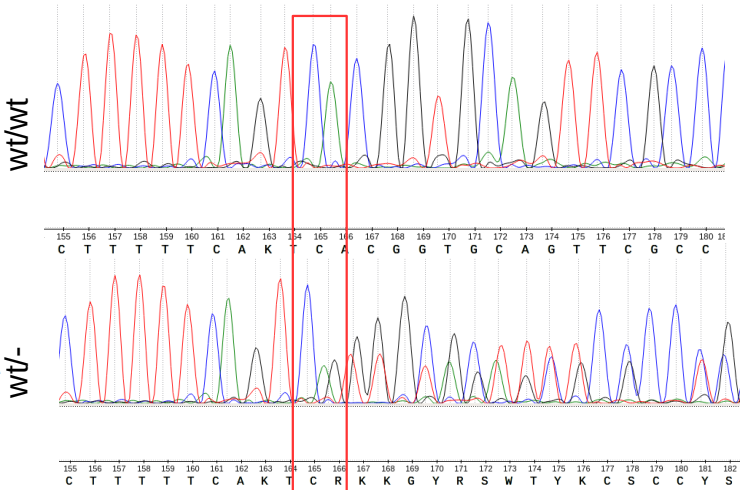


No heterozygous detected



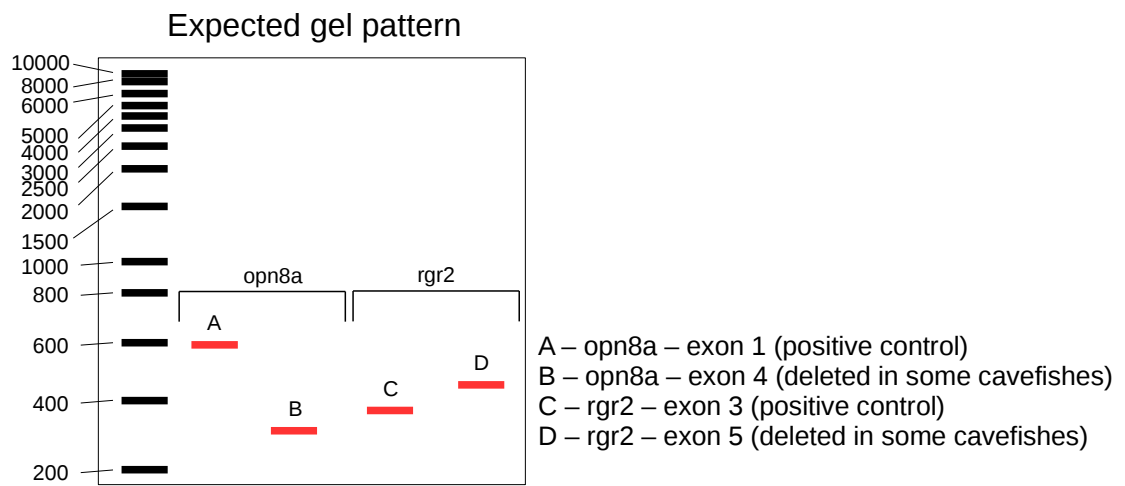
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CCTCAAAGCCCATGGAACAGAGCTGAGGGAGGCGCAGTCACGGAGCTCCACCCCTCAGTC
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GCTCAACCTGCTGAGCTGAGGAGAGAGCAACCGTCTATGGAGAGACAGGACAGCTCGGCGC
CCTCTACTGGAGCTCAGGGGAACACAGCACTGCAGCAGAGAAGACTCTGGCCAAGACTGAC
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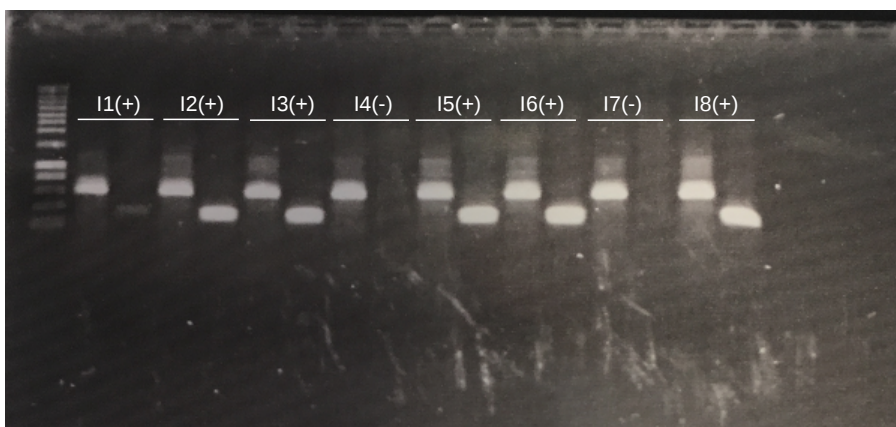


No deleted homozygous detected

Fig. S5

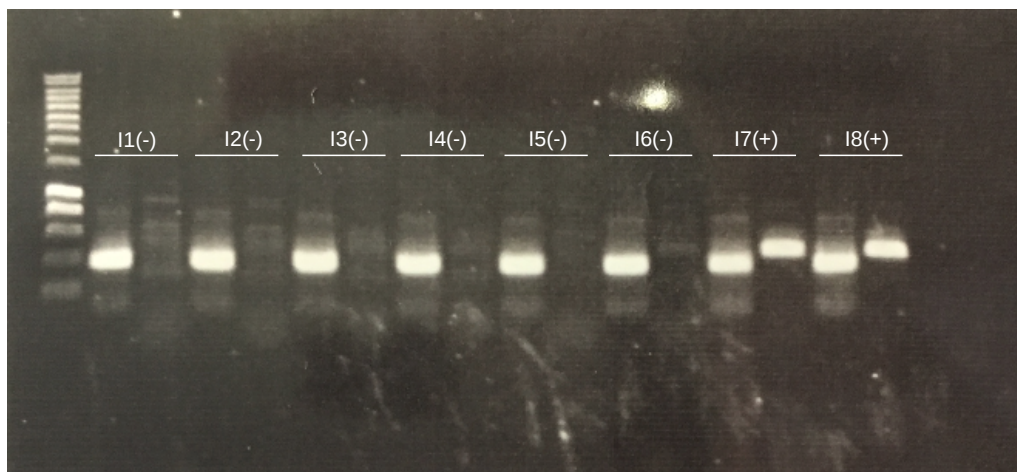


opn8



- I1 – PCF3-A4 (Chica)
- I2 – PCF3-B4 (Chica)
- I3 – PCF3-C4 (Chica)
- I4 – PCF3-D4 (Chica)
- I5 – PCF3-E4 (Chica)
- I6 – PCF3-F4 (Chica)
- I7 – PCF3-G4 (Chica)
- I8 – PCF3-G4 (Chica)

rgr2



- I1 – PCF1-A8 (Escondido)
- I2 – PCF1-B8 (Escondido)
- I3 – PCF1-C8 (Escondido)
- I4 – PCF1-D8 (Escondido)
- I5 – PCF1-E8 (Escondido)
- I6 – PCF1-F8 (Escondido)
- I7 – PCF1-G8 (Sabinos)
- I8 – PCF1-H8 (Sabinos)

Fig. S5

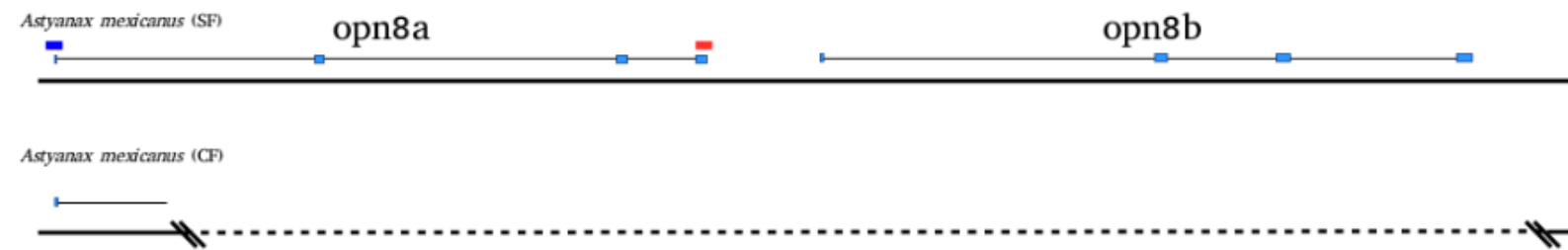
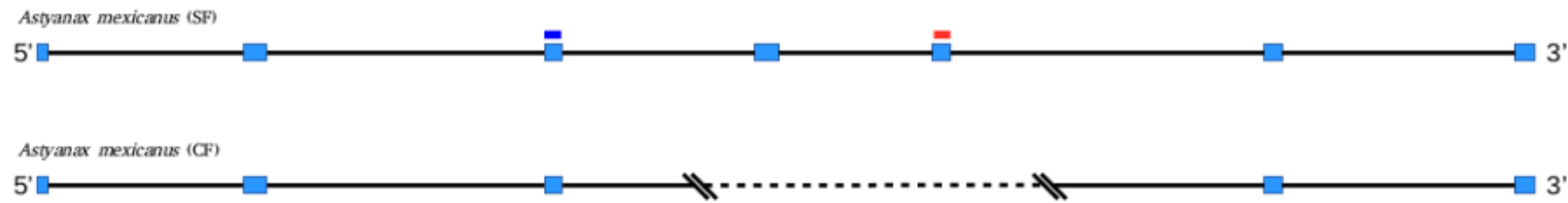
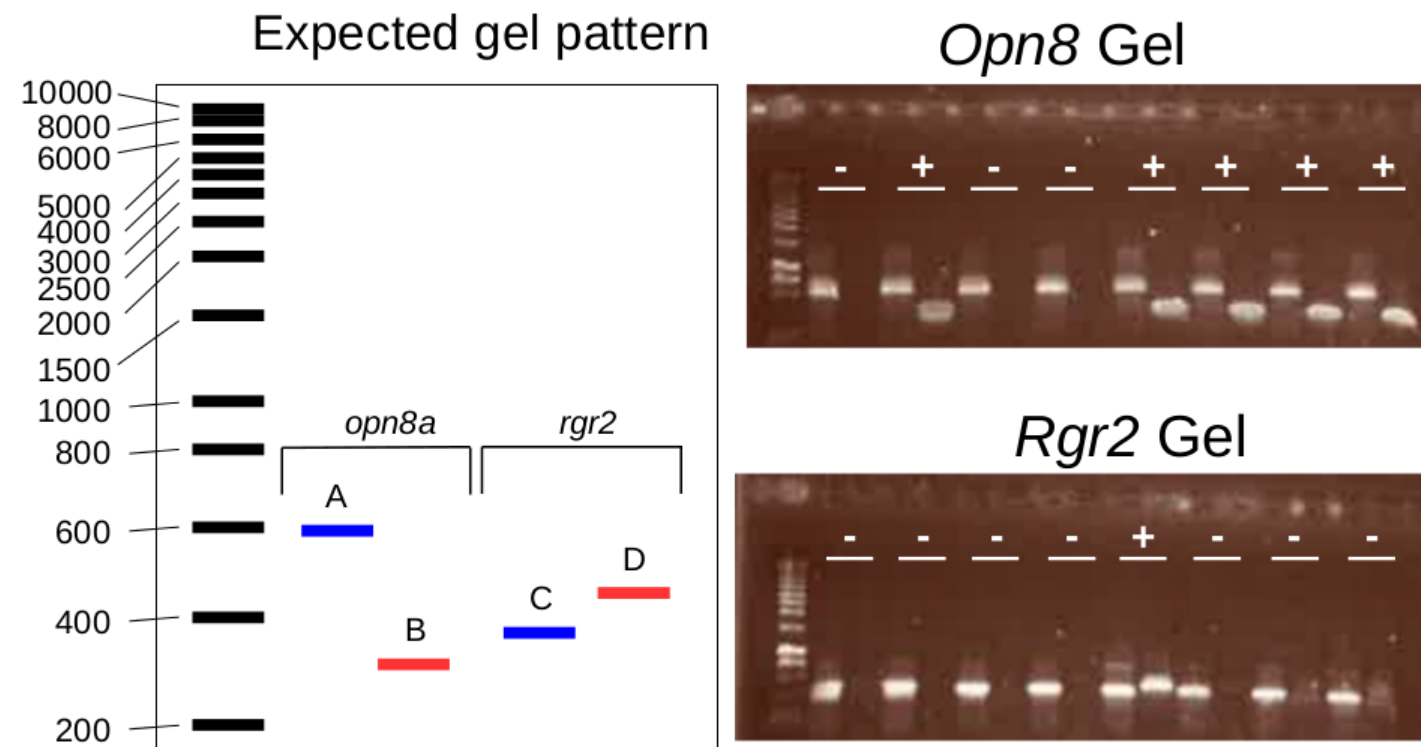
A*opn8**rgr2***B**

Fig. S6

A - 335 *Danio rerio* orthologous genes - GO Biological Process GeneRIF Predicted Z-score

Index	Name	P-value	Adjusted p-value	Z-score	Combined score
1	eye_photoreceptor_cell_differentiation_(GO:0001754)	0.00003454	0.01899	-2.65	27.22
2	peripheral_nervous_system_neuron_development_(GO:0048935)	0.00003454	0.01899	-1.79	18.41
3	cellular_response_to_UV_(GO:0034644)	0.0001474	0.02026	-3.53	31.13
4	response_to_UV_(GO:0009411)	0.0001474	0.02026	-2.95	26.07
5	eye_photoreceptor_cell_development_(GO:0042462)	0.0001474	0.02026	-2.68	23.66
6	retinal_rod_cell_development_(GO:0046548)	0.0001474	0.02026	-2.65	23.40
7	retinal_cone_cell_differentiation_(GO:0042670)	0.0001474	0.02026	-2.65	23.40
8	photoreceptor_cell_development_(GO:0042461)	0.0001474	0.02026	-1.80	15.88
9	retinal_cone_cell_development_(GO:0046549)	0.0005780	0.04542	-2.69	20.07
10	phosphatidylinositol_metabolic_process_(GO:0046488)	0.0005780	0.04542	-2.07	15.45
11	phosphatidylinositol_biosynthetic_process_(GO:0006661)	0.0005780	0.04542	-2.06	15.33
12	opsin_transport_(GO:0036372)	0.0005780	0.04542	-2.03	15.17
13	photoreceptor_cell_differentiation_(GO:0046530)	0.0005780	0.04542	-1.76	13.13
14	protein_prenylation_(GO:0018342)	0.0005780	0.04542	-1.75	13.05
15	lymphocyte_differentiation_(GO:0030098)	0.002072	0.1266	-2.98	18.40
16	regulation_of_photoreceptor_cell_differentiation_(GO:0046532)	0.002072	0.1266	-2.41	14.89
17	retinal_metabolic_process_(GO:0042574)	0.002072	0.1266	-2.39	14.75
18	pineal_gland_development_(GO:0021982)	0.001997	0.1266	-1.82	11.32
19	response_to_glucocorticoid_(GO:0051384)	0.006745	0.3710	-3.15	15.73
20	mitochondrial_fusion_(GO:0008053)	0.006745	0.3710	-2.52	12.62
21	T_cell_differentiation_(GO:0030217)	0.05190	0.9665	-4.84	14.33
22	cGMP_metabolic_process_(GO:0046068)	0.05190	0.9665	-4.30	12.73
23	cGMP_biosynthetic_process_(GO:0006182)	0.05190	0.9665	-4.17	12.35
24	cortisol_metabolic_process_(GO:0034650)	0.01979	0.9665	-2.59	10.17
25	melanosome_transport_(GO:0032402)	0.05190	0.9665	-3.15	9.32

B - 335 *Danio rerio* orthologous genes - Phenotype GeneRIF Predicted Z-score

Index	Name	P-value	Adjusted p-value	Z-score	Combined score
1	eye_photoreceptor_cell_differentiation	0.00003454	0.008444	-474.39	4873.65
2	retinal_outer_plexiform_layer	0.00003454	0.008444	-329.22	3382.27
3	rhodopsin_metabolic_process	0.00003454	0.008444	-320.03	3287.78
4	photoreceptor_cell	0.00003454	0.008444	-210.00	2157.44
5	photoreceptor_cell_morphogenesis	0.00003454	0.008444	-133.26	1369.05
6	optomotor_response	0.00003278	0.008444	-14.67	151.47
7	basal_protein_localization	0.0001474	0.01272	-494.30	4361.01
8	eye_photoreceptor_cell	0.0001474	0.01272	-472.82	4171.46
9	eye_photoreceptor_cell_development	0.0001474	0.01272	-472.19	4165.91
10	cellular_response_to_UV	0.0001474	0.01272	-442.20	3901.37
11	retina_layer_formation	0.0001474	0.01272	-331.21	2922.09
12	retinal_cone_cell_differentiation	0.0001474	0.01272	-328.83	2901.08
13	retinal_photoreceptor_layer	0.0001474	0.01272	-324.86	2866.07
14	photoreceptor_cell_development	0.0001474	0.01272	-201.00	1773.33
15	retinal_rod_cell	0.0001474	0.01272	-133.01	1173.45
16	retinal_rod_cell_development	0.0001474	0.01272	-84.01	741.17
17	pineal_complex	0.0001474	0.01272	-49.23	434.37
18	regulation_of_circadian_rhythm	0.0005780	0.03141	-558.18	4161.71
19	circadian_regulation_of_gene_expression	0.0005780	0.03141	-449.86	3354.08
20	rod_bipolar_cell	0.0005780	0.03141	-406.88	3033.68
21	retinal_cone_cell_development	0.0005780	0.03141	-343.55	2561.50
22	protein_prenylation	0.0005780	0.03141	-226.91	1691.78
23	protein_farnesylation	0.0005780	0.03141	-216.21	1612.06
24	photoreceptor_cell_differentiation	0.0005780	0.03141	-190.00	1416.62
25	protein_geranylgeranylation	0.0005780	0.03141	-150.69	1123.50

C - 243 *Homo sapiens* orthologous genes

GO biological process / Disease	Database	Raw p-value	Adj. p-value	Genes
visual perception (GO:0007601)	DAVID	1.5E-04	1.9E-01	<i>ABCA4, CRYBA2, CYP4V2, IMPG1, LRIT3, NRL, PRPH2, PDE6B, RLBP1, RHO, WFS1</i>
retinitis pigmentosa	ClinVar 2019	3.5E-5	9.2E-4	<i>PRPH2, ABCA4, SAG, RHO, NRL, PDE6B, RLBP1</i>
retinitis pigmentosa	OMIM	3.8E-4	8.7E-3	<i>ABCA4, SAG, RHO, NRL, PDE6B,</i>

Table S1