Supplemental Tables

Table S1. Genetic markers used for genetic mapping

Primer name	Forward primer (5'->3')	Tm (℃)	Comment product size(bp)
M4-F	ACCAGCAGACAGTTGTTATG	56	DNA marker
M4-R	AACTCAGTGTGCGGATTC		
M2425-2F	TCTTCATCTCTTCCTAAGTG	55	DNA marker
M2425-2R	AACCTCCTTGTGATGTATT		
M2526-F	AACTAGAAGCCAGAATCTAACG	56	DNA marker
M2526-R	GGTCTTACCAACAAGTCATACC		
M28-F	TTGGCATCATCATCTTAGCA	56	DNA marker
M28-R	ACCATCAATGTCCCAGTTC		
M71-20-F	GTAACCATTGTCTAA-GCCGAAAG	55	DNA marker
M71-20-R	TAAGCTACCAGAACCAAAC-CAAC		
M71-21-1F	CCCTCGGTTTGTATTATTCCTTC	55	DNA marker
M71-21-1R	TCCGCCATGTGTGTATTTGTGAC		
M71-28-3F	GGCTGCTCGATCACAATCACAAC	55	DNA marker
M71-28-3R	CACGAC-CAAACTGAAATCCCCAC		
M64-16-F	ATGGCAAAGTTAA-GAGGTATATCAG	55	DNA marker
M64-16-R	TTATGTGGCACAC-TCTGTTACTCC		
MG64-15-F	AAACACACCTTGAAATTAG-TAAGC	55	DNA marker
MG64-15-R	GAAGGTTTATGGTGGTTTCCGCG		
MG64-17-F	TAAGTAAGAAAC-CTACTTATTCTCCG	55	DNA marker
MG64-17-R	GTTTGACAACCTCCCTAG-TATAAA		
MG64-17-1F	ACAACGTCTCTGCCAGTGCGATC	55	DNA marker
MG64-17-1R	ACCGTTGTTGAGCTACTTGTT		
MG64-17-2F	TTATTCCTTGTCCCAATCGACAC	55	DNA marker
MG64-17-2R	TGGGATAAACATGCAACGCAC		
M64-17-F	CCATCTTGAGTTTGTATTGTG-CATT	55	DNA marker

M64-17-R	AGCACCAGCACTAATGAAA-TAAAGG		
SNP48-F	ACTGTCAACCTCCAAAAAC-CAAA	56	SNP marker
SNP48-R	GGGGTGGGGGATTCAGACTT		
M4950-1F	TAACTGATGCGATCTAATGA-TAGGG	58	DNA marker
M4950-1R	GGTAATGCGAGAATTTCCACAA		
M4950-2F	GATAAGGTAAGGCTTTGTGTACG	58	DNA marker
M4950-2R	GAGTTTTAGTTGATGGCGGATA		
M50-F	GCAAGAAAGTACCACCCAGAT	58	DNA marker
M50-R	AGAAGTCAAGGGATTCAACGT		
M32-F	ATCGCTTCAAAAATCACCA	51	DNA marker
M32-R	AAAGGCTTTAACAACTCCG		
M152-F	TTGATTGGAGTTAAGGGTGGT	54	DNA marker
M152-R	CGTGAGGTCTATAAGGAGGGT		
M236-F	AGCCAAAGCAAGTTCAAAT	52	DNA marker
M236-R	ACAGAAGCCACAACACAAA		

Table S2. Primers used in this study

Primer name	Forward primer (5'->3')
pBI-OAC-C3-F	AGAACACGGGGGACTCTAGAATGAATACTCAAGGA-GAATCATCAACTACT
pBI-OAC-C3-R	GATCGGGGAAATTCGAGCTCTTATGCCTTCCGGA-TACTACTCTGCTG
pBI-OAC-C4-F	AGAACACGGGGGACTCTAGAATGAATACTCAAGGA-GAATCATCTTC
pBI-OAC-C4-R	GATCGGGGAAATTCGAGCTCTTATTCTCCGGA-GAAACATTTTCC
pBI-OE3-C4-pro-moter-F	ACCATGATTACGCCAAGCTTGTCGACATGAA-TACTCAAGGAGAATCATCTTC
pBI-OE3-C4-pro-moter-R	GATCGGGGAAATTCGAGCTCCTGA-TATACAGGCGAATTCAGAAC
pBI-OE3-C4-gene-F	ATTACGCCAAGCTTGTCGACGGCAAAAGTTAGATTAC-GAAAATACC
pBI-OE3-C4-gene-R	CTCCTTGAGTATTCATGTCGACATTTGATG
qPCR-C4-F	GAAGATACTCGCAAAAACTTCATTGA
qPCR-C4-R	TTCGAGAAAACAACAATGGCAATT
qPCR-PVY-CP-F	ACACCAGTGAGGGCTAGRGA
qPCR-PVY-CP-R	GTGGTGTGCCTCTCTGTGTT
Semi-qPCR-C3-F	GCGAACCTGAGCACCAAGAC
Semi-qPCR-C3-R	TCCGCAGGAAAATGTGATGGTA
Semi-qPCR-C4-F (MG64-17-1F)	ACAACGTCTCTGCCAGTGCGATC
Semi-qPCR-C4-R (MG64-17-1R)	ACCGTTGTTGAGCTACTTGTT
Ef1α-F	ATTGGAAACGGATATGCTCCA
Ef1α-R	TCCTTACCTGAACGCCTGTCA

Table S3. Statistical results from the potato BC-SNP map

Chromo-some	Length of linkage group (cM)	Interval numbers	No. of mark-ers	Mean marker intervals (cM)	Max Marker interval (cM)
1	129.92	17	22	5.91	29.62
2	81.25	23	27	3.01	14.67
3	79.80	20	31	2.57	18.97
4	86.14	11	21	4.10	27.96
5	85.33	10	17	5.02	17.1
6	67.97	8	11	6.18	16.74
7	69.65	15	31	2.25	13.83
8	65.43	14	18	3.63	16.76
9	52.80	6	9	5.87	31.97
10	68.08	9	11	6.19	27.94
11	68.14	15	23	2.96	15.14
12	64.31	12	16	4.02	13.52
Total	918.82	13	237		
Average	76.57	160	19.75	6.3	

Table S4. Position and sequence of 6 tightly linked SNPs markers

Name	Superscaf-fold	Size	Position	Sequence
sol-cap_snp_c2_22070	PGSC0003DMB000000439	101	chromosome 9 46389432-46389532	AATCTACATCATCTGAG-TGAATTTCTAGCTGGTAA-GCGCGCTGATGGTCC[A/C]AAA-GAAGCTCTTCAAATTCTG-GACATTGTTTTGAGA-GAGCTTTCGATCAA
sol-cap_snp_c2_20640	PGSC0003DMB000000020	101	chromosome 9 48863726-48863826	CGGACCCATT-GTCGCGCTGACCCACCCGAT-TATAACGAGAATCTG-GATTA[C/T]ATGCGCCCCGAG-TAG-TTTCCCTCCTCCACCCATGAA-TAACCCGTGAGGTC
sol-cap_snp_c2_40086	PGSC0003DMB000000020	101	chromosome 9 49152274-49152374	GAACAGATCCTTCAA-GCATCCTCATTGAATATCAAC-GATCAATCAGGTGA[T/C]AGA-GAGATGTGCGCGTTTACATATTT-GAGGATGAATCCTGAC-CTATTCCA
sol-cap_snp_c2_40079	PGSC0003DMB000000690	101	chromosome 9 49247381-49247481	GACGTAGTTGTCAT-ACCAGCTGGCGTTCCAAGAAA-GCCTGGTATGACACG[G/A]GAC-GACTTGTTCAACATTAATGCTAA-TATTGTGAAAGGCTTGGTT-GAGGC
sol-cap_snp_c2_40085	PGSC0003DMB000000020	101	chromosome 9 49152340-49152440	TTGTTT-GCGTCTTTTCCTTCTTTCATTTTCT TCACGAAGGCAAC-GAATCG[T/C]CTCCAGTTATCAG-GATGGAATAGGTCAGGAT-TCATCCTCAAATATGTAAA
sol-cap_snp_c2_48042	PGSC0003DMB000000339	101	chromosome 9 51381163-51381263	CTGAGGAA-TATACTCATTATTTTT-GCCAAACTCAATCCTGGTATAA-GATA[C/T]GTG-CAAGGGATGAATGAAGTATTGG CTCCACTATTCTATGTATTCAG-GAA

Table S5. ELISA results for 5 recombinants

Clones	ODA405				Average	Clones
	Rep1	Rep 2	Rep 3	Rep 4		
40-3	0.061	0.046	0.103	0.020	0.058±0.035	R
143-6	3.246	3.169	3.269	3.170	3.214±0.051	S
Re1	3.490	3.520	3.543	3.245	3.449±0.138	S
Re2	4.000	3.434	3.234	3.228	3.474±0.363	S
Re3	0.045	0.043	0.036	0.041	0.041±0.004	R
Re4	0.112	0.035	0.011	0.119	0.069±0.054	R
Re5	0.089	0.171	0.012	0.010	0.071±0.076	R

*40-3 indicates *S. chacoense* accession 40-3, the resistant parent; 143-6 indicates *S. berthaultii* accession143-6, the susceptible parent.

Table S6. Functional annotation of 6 genes in the interval defined by fine mapping

Gene	Conserved domain	Length (bp)
C1	No conserved domain	5638
C2	Oxidoreductase	2198
C3	TIR-NBS-LRR	3940
C4	TIR-NBS-LRR	4167
C5	No conserved domain	549
C6	No conserved domain	3359

Table S7. Distribution of *Ry*$_{chc}$ homologs in 13 wild accessions of *S. chacoense*

	Copy number	No. of clones sequenced
S. chacoense accession40-3	15	57
CHC39-7	20	75
C545	8	74
M6	5	24
CHC524-8	6	41
CHC524-8-1	4	24
CHC524-8-2	6	48
CHC54-1	20	71
CHC54-2	18	53
CHC54-3	8	36
CHC55-1	20	78
CHC55-2	10	60
CHC55-3	20	63
SUM	160	704

Table S8. Genotyping of *Ry*$_{chc}$ in potato accessions with 3 molecular markers

Name	Genotype			Phenotype
	M71-20	MG64-17	M64-17	
S. chacoense accession40-3	+	+	+	R
S. berthaultii accession143-6	–	–	–	S
C545	+	+	+	R
M6	+	+	+	R
CHC39-7	+	+	–	R
CHC524-8-1	+	+	+	R
CHC524-8-2	+	+	+	R
CHC524-8-3	+	+	+	R
CHC54-1	–	–	–	S
CHC54-2	–	–	–	S
CHC54-3	–	–	–	S
CHC55-1	+	–	–	S
CHC55-2	+	–	–	S
CHC55-3	+	–	–	S
Eesteling	+	–	–	S
03P74-16	+	–	–	S
06P13-6	+	–	–	S
07HE077-3	+	–	–	S
11FF28-9	–	–	–	S
392625-1	+	–	–	S
393140-2	+	–	–	S
Agata	+	–	–	S
Da	–	–	–	S
F70021-2	+	–	–	S
HB0211-1	+	–	–	S
Monalisa	+	–	–	S
MPI 63.6131.63	+	–	–	S
NEA20008	+	–	–	S
Pepo418	+	–	–	S
Riviera	–	–	–	S
S.punae	+	–	–	S
T0035-1	+	–	–	S

W2	+	–	–	S
Дельфин	+	–	–	S
E10	–	–	–	S
E3	–	–	–	S
AC142	+	–	–	S

* –/+, absence/presence of the indicated molecular marker.

Supplemental Figures

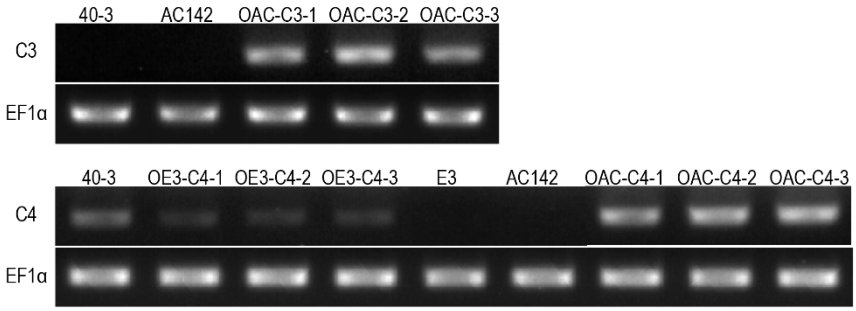


Figure S1. Expression analysis of *C3* and *C4* using semi-quantitative RT-PCR.

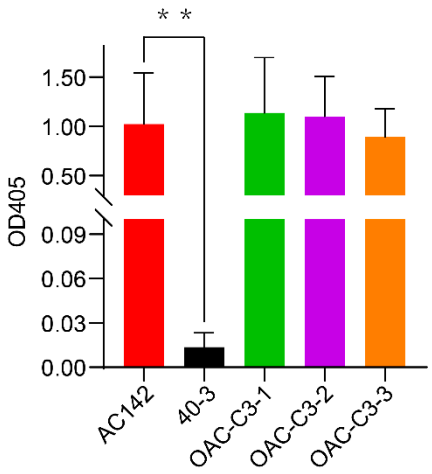


Figure S2. Phenotyping of PVY^{O} resistance in *C3* transgenic lines. The phenotypic characterizations were performed with ELISAs. 40-3 indicates the resistant parent, *S. chacoense* accession 40-3. ELISA (ODA405) <0.1 indicates that the plants were resistant. ELISA (ODA405) >0.1 indicates that the plants were susceptible. Data are presented as mean values ± SE. ** indicates a statistically significant difference ($P < 0.01$) relative to AC142, as determined with a Student's t-test.



Figure S3. Phenotype of non-inoculated leaves of E3 transgenic strains approximately 1 month after virus inoculation.

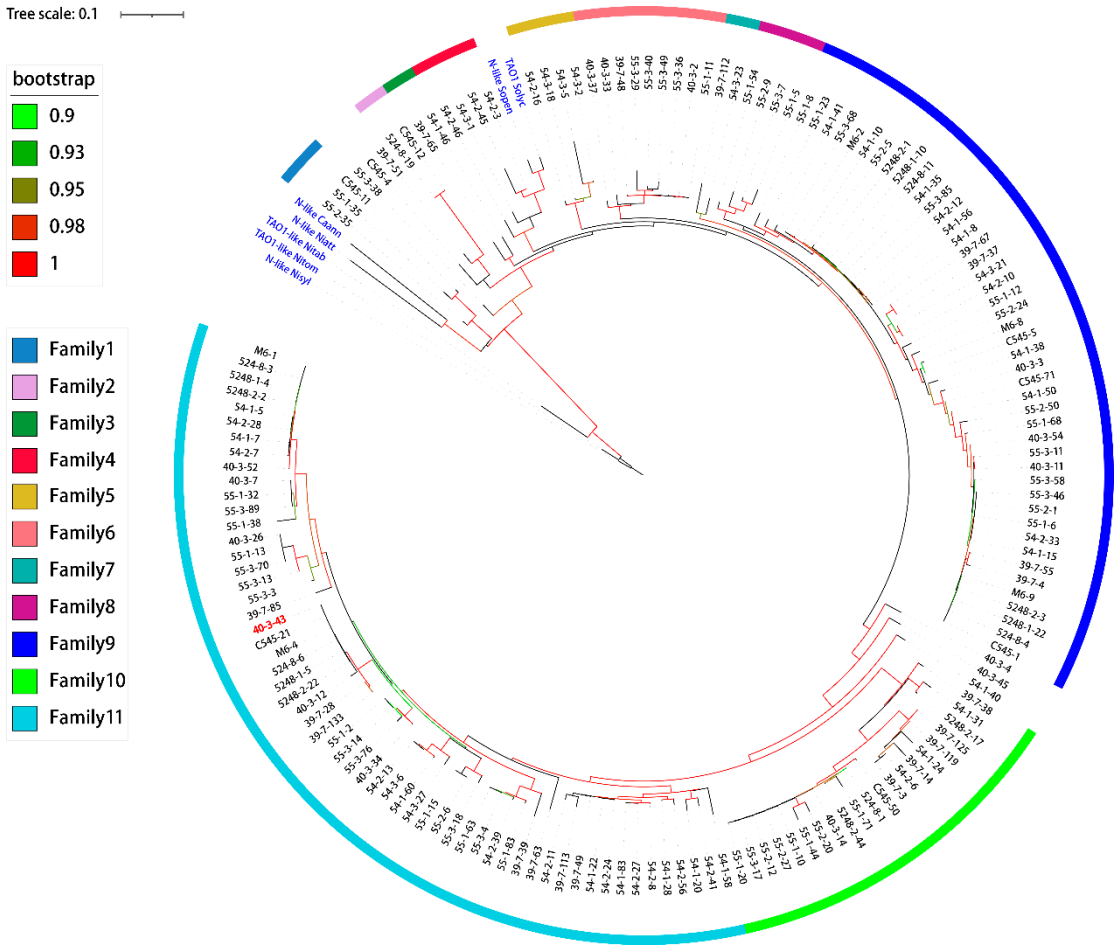


Figure S4. Phylogeny of *Ry*$_{chc}$ homologs. A maximum likelihood (ML) phylogenetic tree was constructed for 13 diverse wild accessions of *S. chacoense*. Seven *Ry*$_{chc}$ homologs from other species (indicated in red) were used as outgroups. These seven homologs are *N-like_Caann* from pepper, *TAO1_Solyc* and *N-like_Sopen* from tomato, and *N-like_Niatt*, *N-like_Nisyl*, *TAO1-like_Nitab* and *TAO1-like_Nitom* from tobacco. The fragment of *Ry*$_{chc}$ is indicated with red.

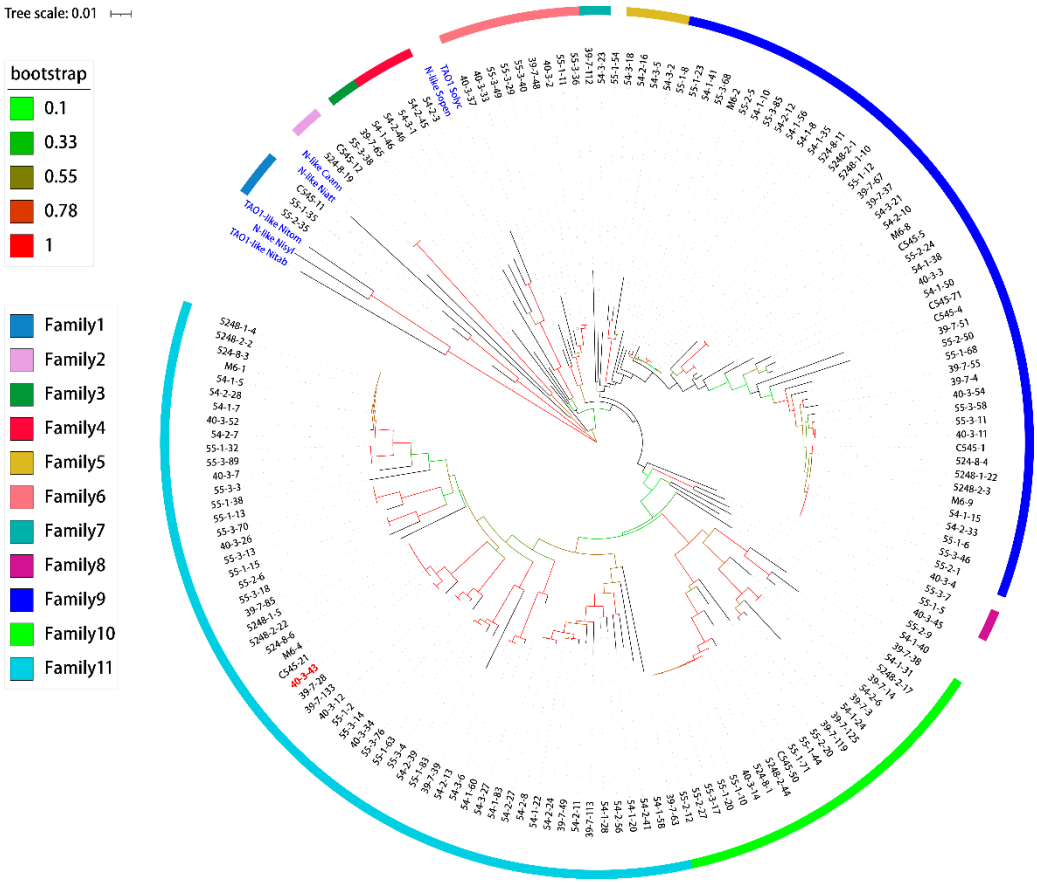


Figure S5. Phylogeny of *Ry*$_{chc}$ homologs. A neighbor-joining (NJ) phylogenetic tree was constructed for 13 diverse wild accessions of *S. chacoense*. Seven *Ry*$_{chc}$ homologs from other species (indicated with blue) were used as outgroups. These seven homologs are *N-like_Caann* from pepper, *TAO1_Solyc* and *N-like_Sopen* from tomato, and *N-like_Niatt*, *N-like_Nisyl*, *TAO1-like_Nitab* and *TAO1-like_Nitom* from tobacco. The fragment of *Ry*$_{chc}$ is indicated with red.

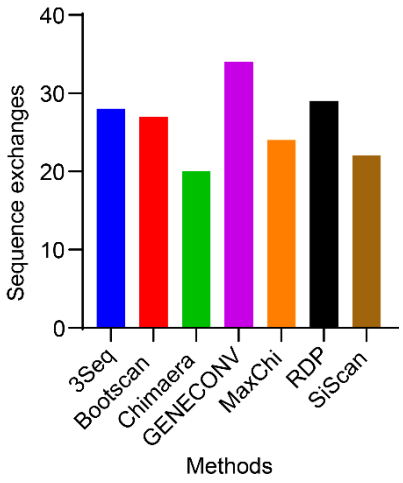


Figure S6. Sequence exchange in Family 11.

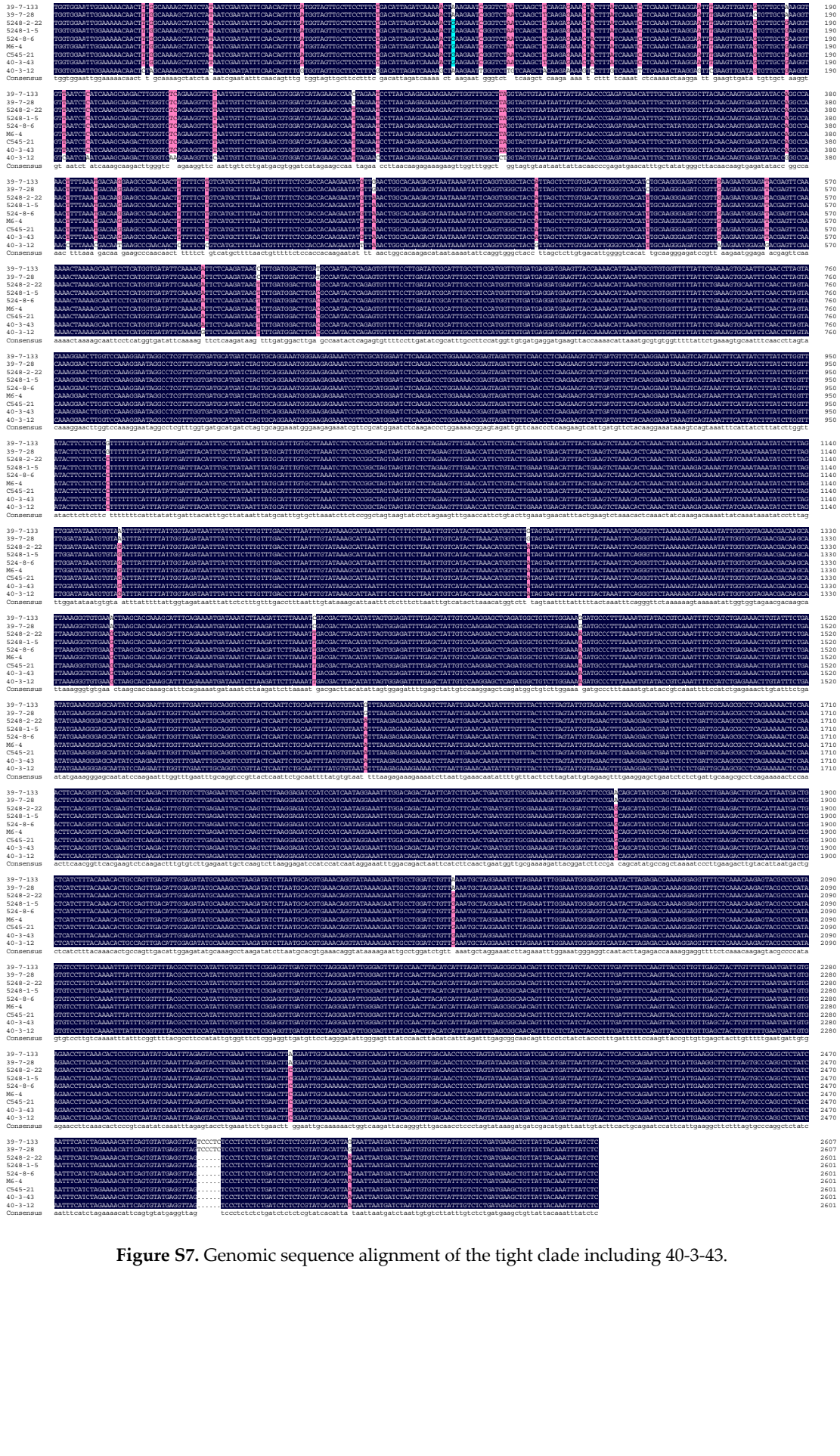


Figure S7. Genomic sequence alignment of the tight clade including 40-3-43.

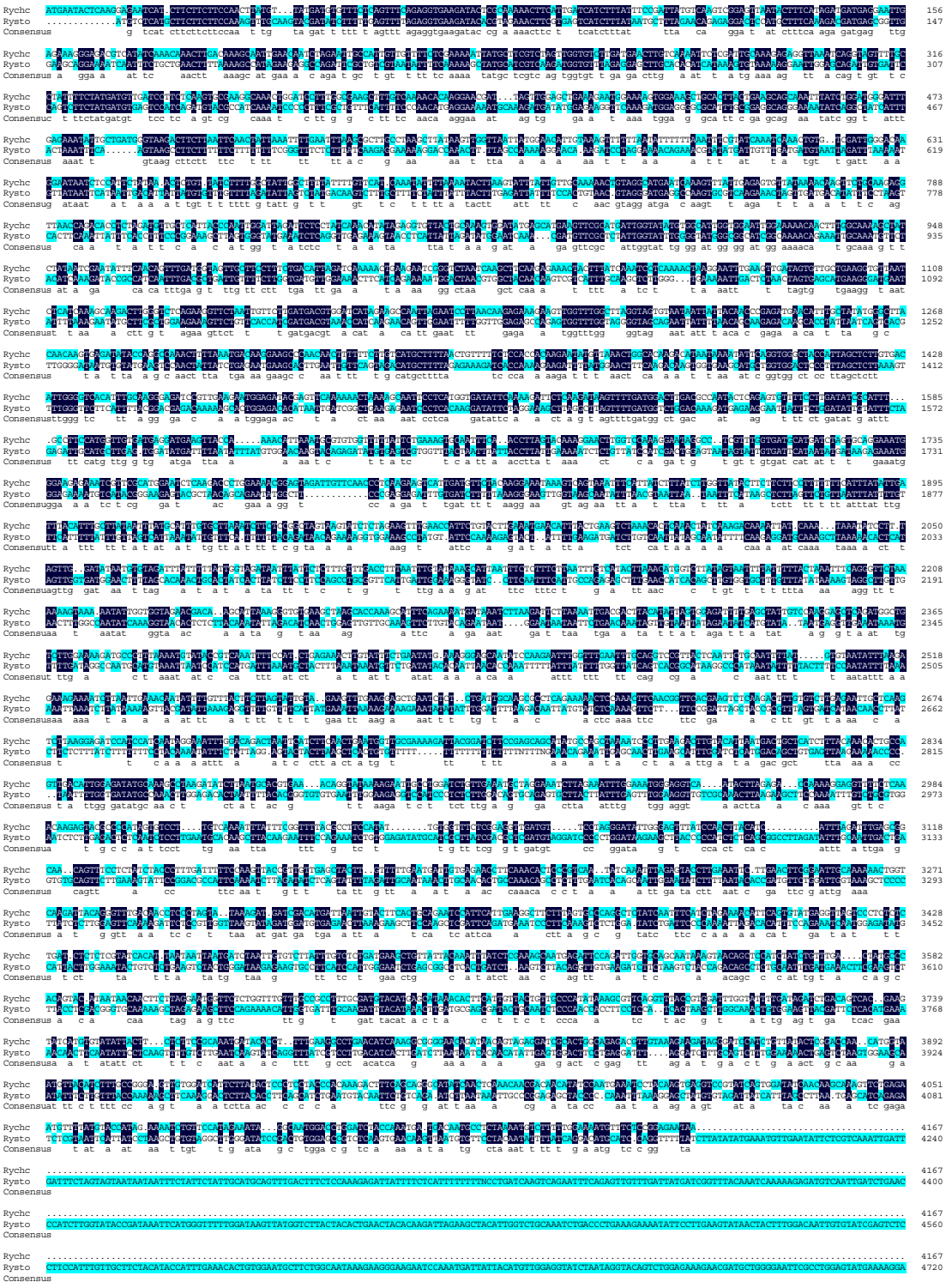


Figure S8. Genomic sequence alignment of *Ry*$_{chc}$ and *Ry*$_{sto}$.