

Supplementary Materials

Supplemental figures

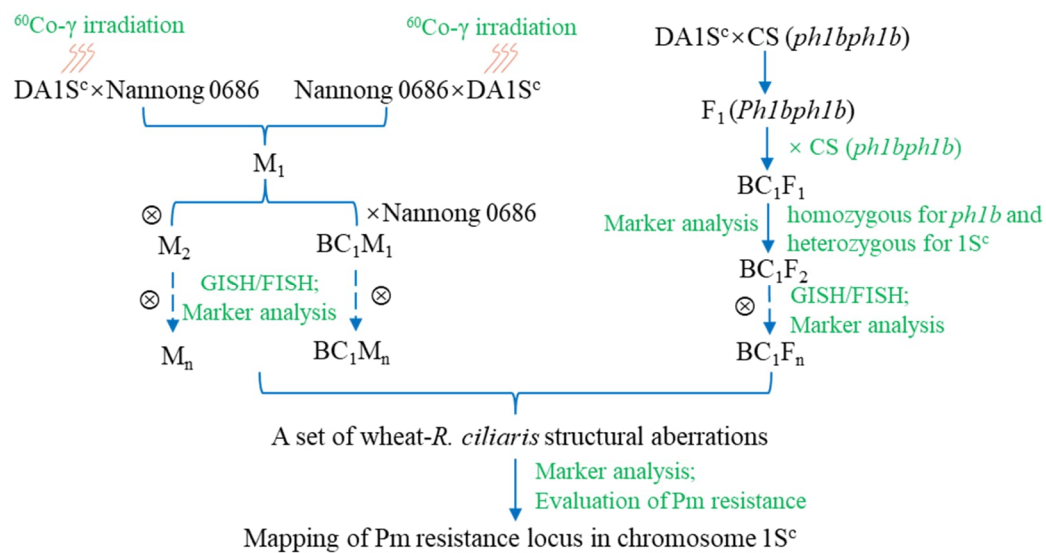


Fig. S1 Technical routes for developing a set of wheat-*R. ciliaris* structural aberrations.

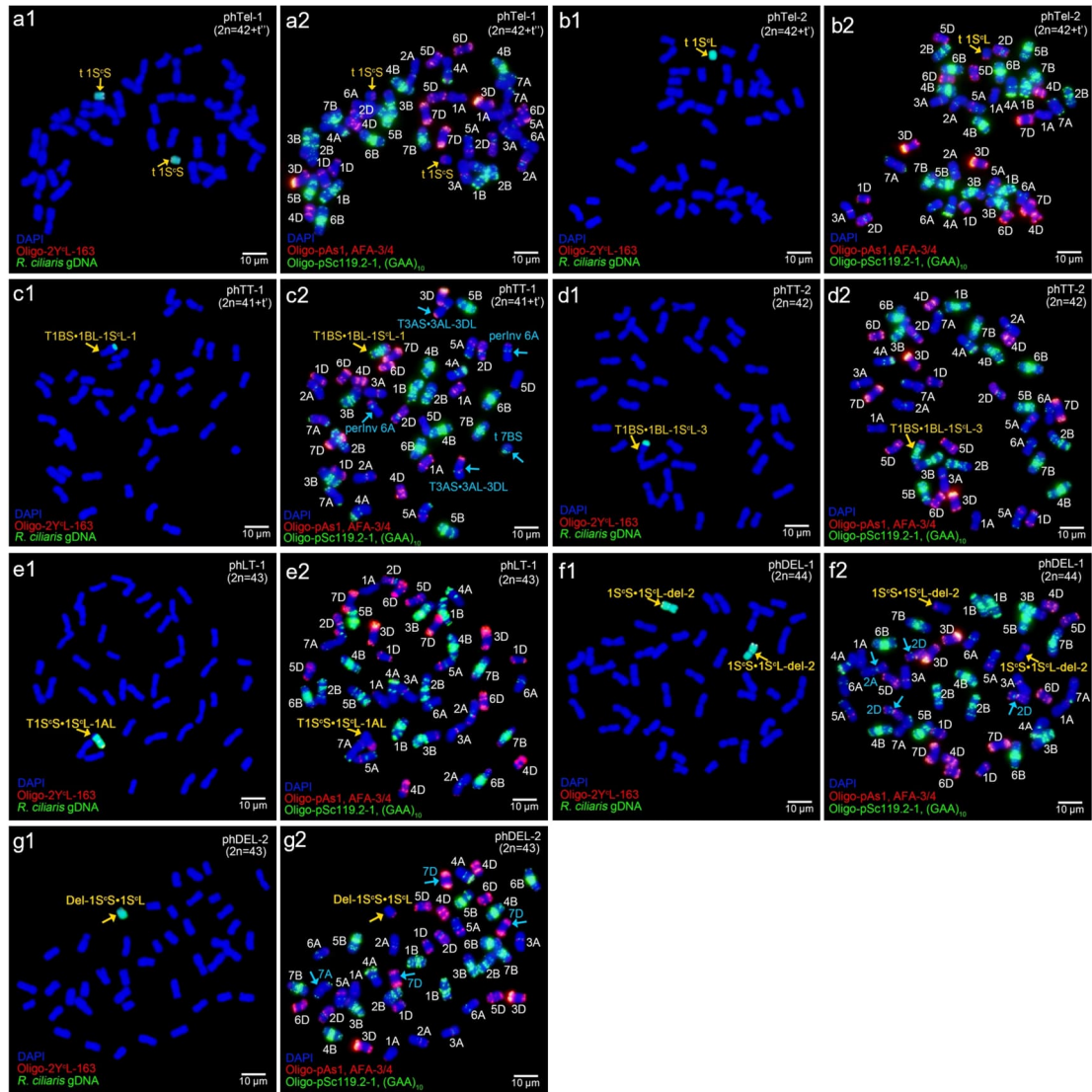


Fig. S2 Sequential GISH/FISH analysis of seven structural aberrations induced by CSph1b mutant. **a1 and a2:** phTel-1 (Dt 1S^cS). **b1 and b2:** phTel-2 (Mt 1S^LL). **c1 and c2:** phTT-1 (T1BS•1BL-1S^LL-1). **d1 and d2:** phTT-2 (T1BS•1BL-1S^LL-3). **e1 and e2:** phLT-1 (T1S^cS•1S^LL-1AL). **f1 and f2:** phDEL-1 (1S^cS•1S^LL-del-2). **g1 and g2:** phDEL-2 (Del-1S^cS•1S^LL). For each aberration, left was GISH and FISH analysis using *R. ciliaris* gDNA (green) and oligo-2Y^L-163 (red) as probes, right was FISH analysis using modified ONPM#4 as probes. Chromosomes were counterstained with DAPI (blue). Yellow arrows indicate alien translocation chromosomes. Blue arrows indicate structural aberrations of wheat chromosomes. Bars = 10 μm.

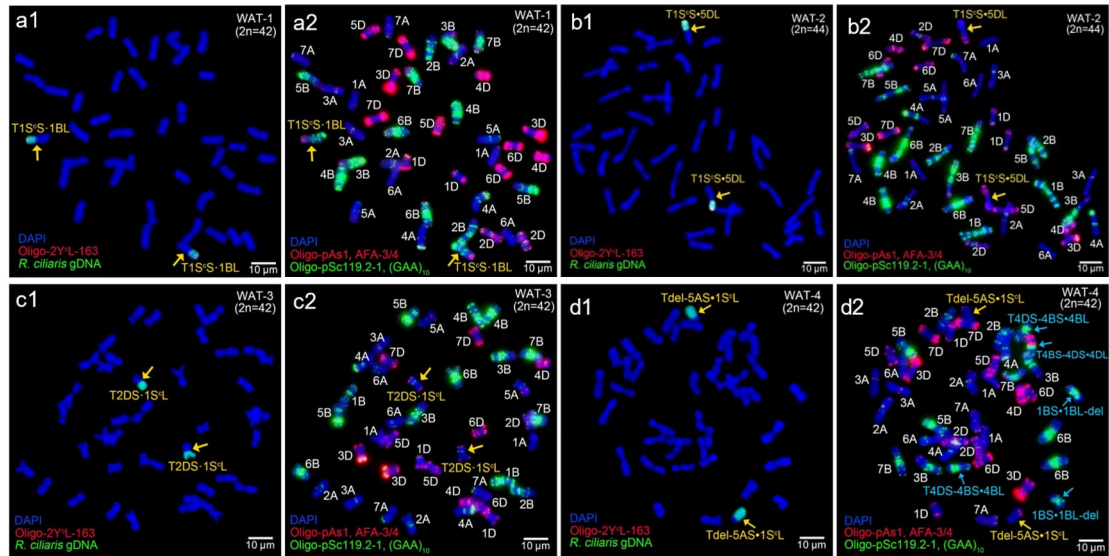


Fig. S3 Sequential GISH/FISH analysis of four wheat-*R. ciliaris* whole-arm translocation lines induced by irradiation.

a1 and a2: WAT-1 (T1S^cS•1BL). **b1 and b2:** WAT-2 (T1S^cS•5DL). **c1 and c2:** WAT-3 (T2DS•1S^cL). **d1 and d2:** WAT-4 (T2DS•1S^cL). For each translocation line, left was GISH and FISH analysis using *R. ciliaris* gDNA (green) and oligo-2Y^L-163 (red) as probes, right was FISH analysis using modified ONPM#4 as probes. Chromosomes were counterstained with DAPI (blue). Yellow arrows indicate alien translocation chromosomes. Blue arrows indicate structural aberrations of wheat chromosomes. Bars = 10 μm.

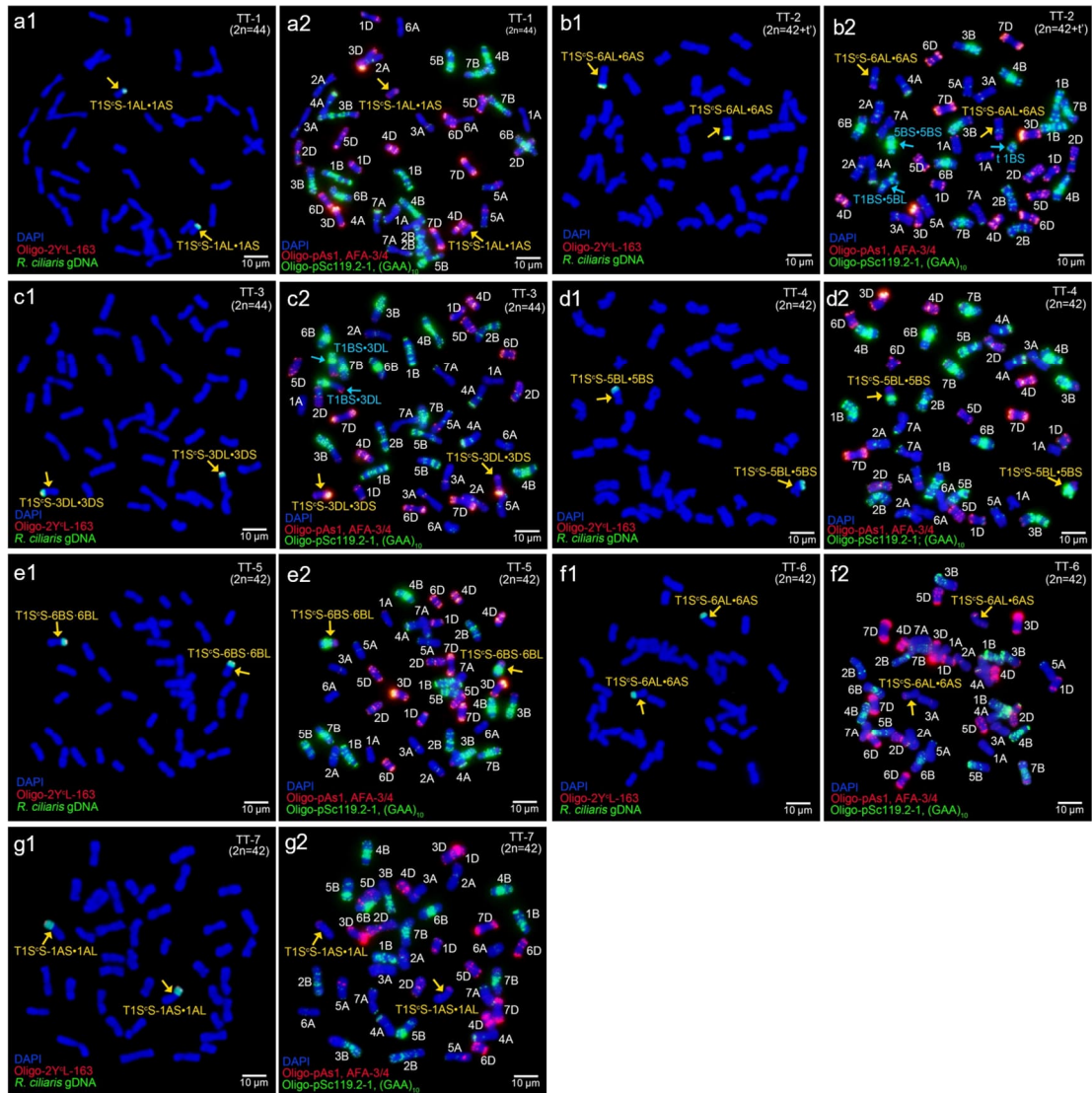


Fig. S4 Sequential GISH/FISH analysis of seven wheat-*R. ciliaris* 1S^cS terminal translocation lines induced by irradiation.

a1 and a2: TT-1 (T1S^cS-1AL•1AS). **b1 and b2:** TT-2 (T1S^cS-6AL•6AS). **c1 and c2:** TT-3 (T1S^cS-3DL•3DS). **d1 and d2:** TT-4 (T1S^cS-5BL•5BS). **e1 and e2:** TT-5 (T1S^cS-6BS•6BL). **f1 and f2:** TT-6 (T1S^cS-6AL•6AS). **g1 and g2:** TT-7 (T1S^cS-1AS•1AL). For each translocation line, left was GISH and FISH analysis using *R. ciliaris* gDNA (green) and oligo-2Y^cL-163 (red) as probes, right was FISH analysis using modified ONPM#4 as probes. Chromosomes were counterstained with DAPI (blue). Yellow arrows indicate alien translocation chromosomes. Blue arrows indicate structural aberrations of wheat chromosomes. Bars = 10 μm.

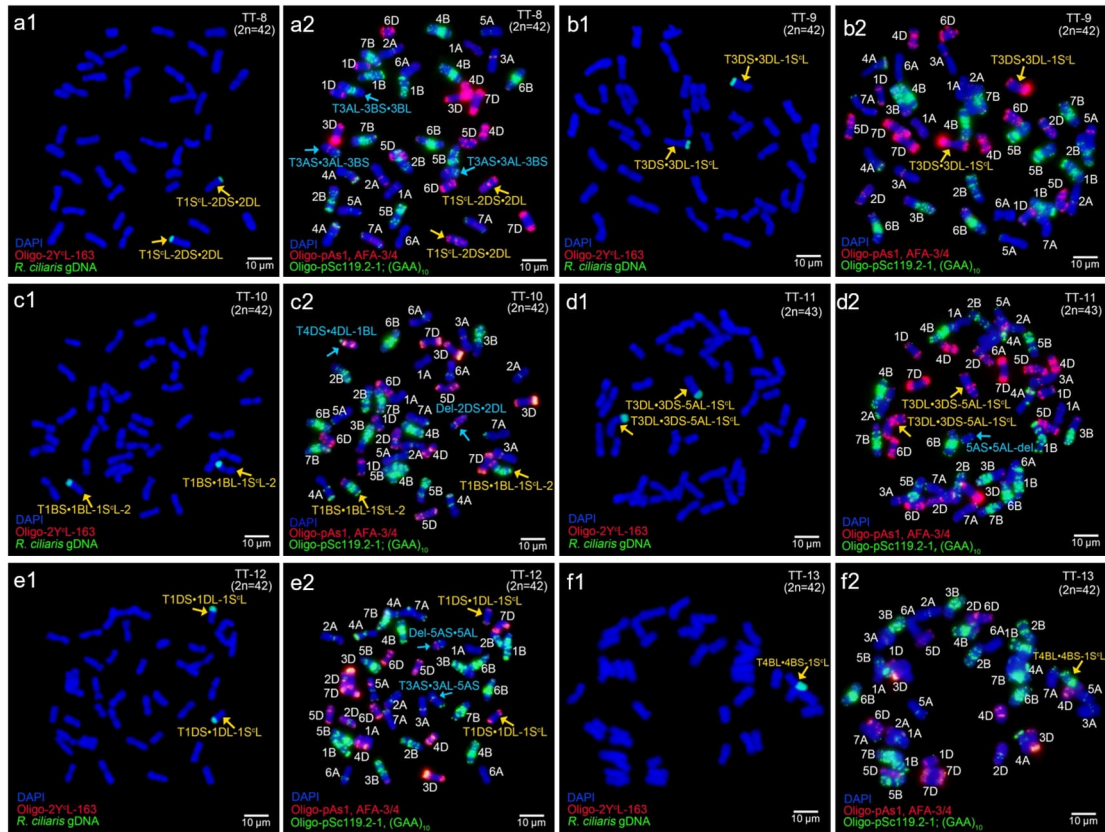


Fig. S5 Sequential GISH/FISH analysis of six wheat-*R. ciliaris* 1S^L terminal translocation lines induced by irradiation.

a1 and a2: TT-8 (T2DL•2DS-1S^L). **b1 and b2:** TT-9 (T3DS•3DL-1S^L). **c1 and c2:** TT-10 (T1BS•1BL-1S^L-2). **d1 and d2:** TT-11 (T3DL•3DS-5AL-1S^L). **e1 and e2:** TT-12 (T1DS•1DL-1S^L). **f1 and f2:** TT-13 (T4BL•4BS-1S^L). For each translocation line, left was GISH and FISH analysis using *R. ciliaris* gDNA (green) and oligo-2Y^L-163 (red) as probes, right was FISH analysis using modified ONPM#4 as probes. Chromosomes were counterstained with DAPI (blue). Yellow arrows indicate alien translocation chromosomes. Blue arrows indicate structural aberrations of wheat chromosomes. Bars = 10 μm.

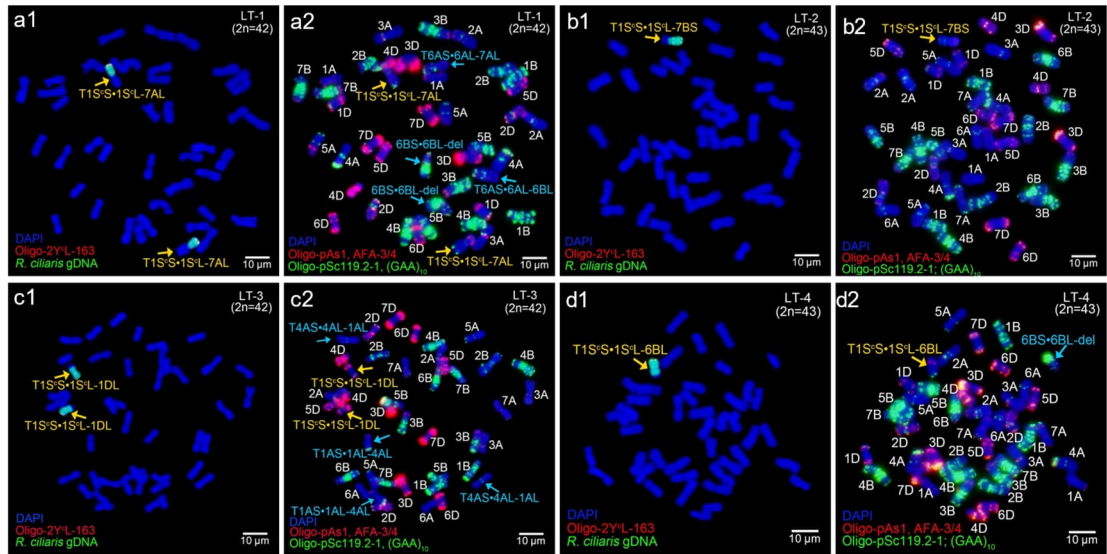


Fig. S6 Sequential GISH/FISH analysis of four wheat-*R. ciliaris* large-fragment translocation lines induced by irradiation.

a1 and a2: LT-1 (T1S^cS•1S^cL-7AL). **b1 and b2:** LT-2 (T1S^cS•1S^cL-7BS). **c1 and c2:** LT-3 (T1S^cS•1S^cL-1DL). **d1 and d2:** LT-4 (T1S^cS•1S^cL-6BL). For each translocation line, left was GISH and FISH analysis using *R. ciliaris* gDNA (green) and oligo-2Y'L-163 (red) as probes, right was FISH analysis using modified ONPM#4 as probes. Chromosomes were counterstained with DAPI (blue). Yellow arrows indicate alien translocation chromosomes. Blue arrows indicate structural aberrations of wheat chromosomes. Bars = 10 μm.

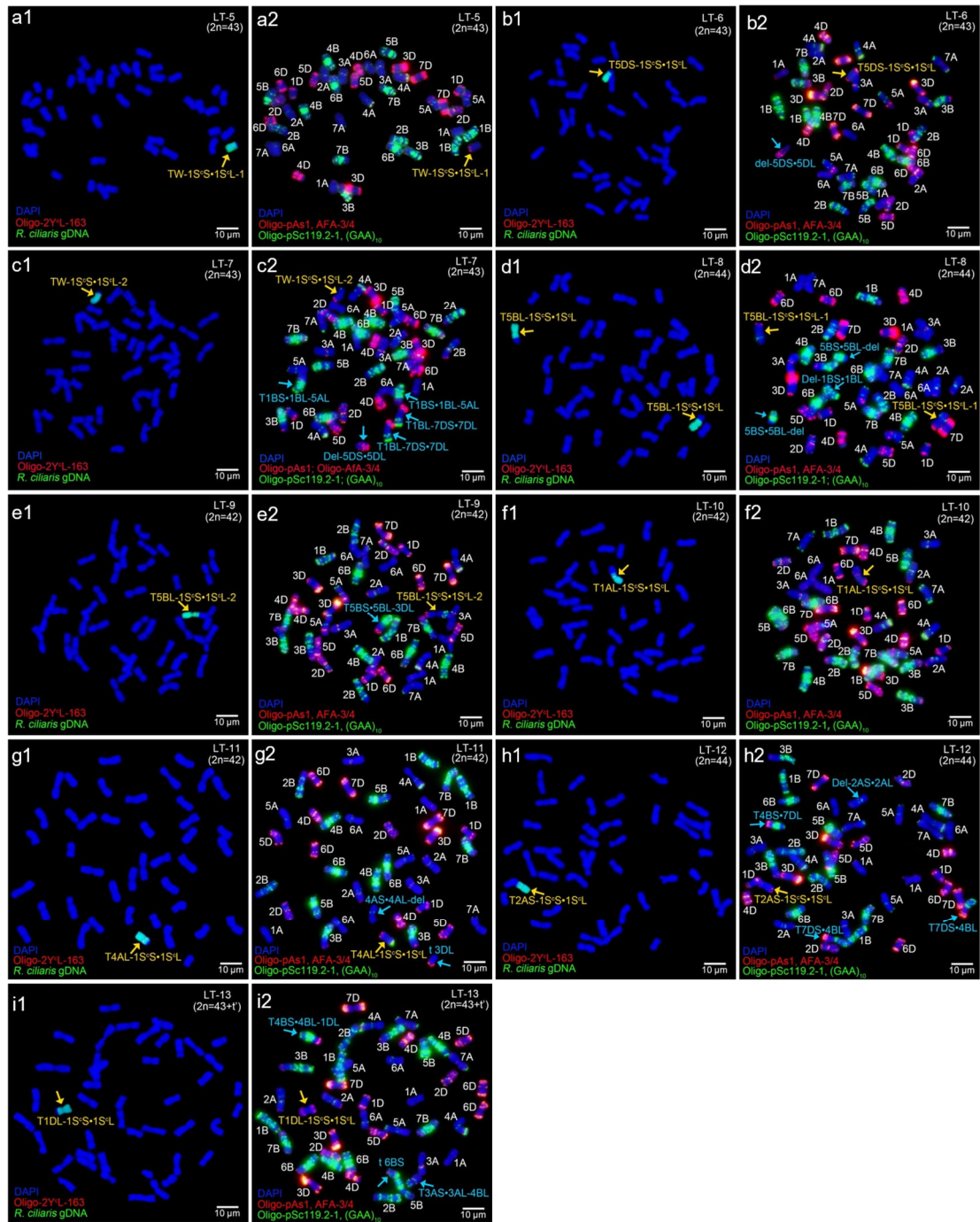


Fig. S7 Sequential GISH/FISH analysis of nine wheat-*R. ciliaris* large-fragment translocation lines induced by irradiation.

a1 and a2: LT-5 (TW-1S'S•1S'L-1). **b1 and b2:** LT-6 (T5DS-1S'S•1S'L). **c1 and c2:** LT-7 (TW-1S'S•1S'L-2). **d1 and d2:** LT-8 (T5BL-1S'S•1S'L-1). **e1 and e2:** LT-9 (T5BL-1S'S•1S'L-2). **f1 and f2:** LT-10 (T1AL-1S'S•1S'L). **g1 and g2:** LT-11 (T4AL-1S'S•1S'L). **h1 and h2:** LT-12 (T2AS-1S'S•1S'L). **i1 and i2:** LT-13 (T1DL-1S'S•1S'L). For each translocation line, left was GISH and FISH analysis using *R. ciliaris* gDNA (green) and oligo-2Y'L-163 (red) as probes, right was FISH analysis using modified ONPM#4 as probes. Chromosomes were counterstained with DAPI (blue). Yellow arrows indicate alien translocation chromosomes. Blue arrows indicate structural aberrations of wheat chromosomes. Bars = 10 μm.

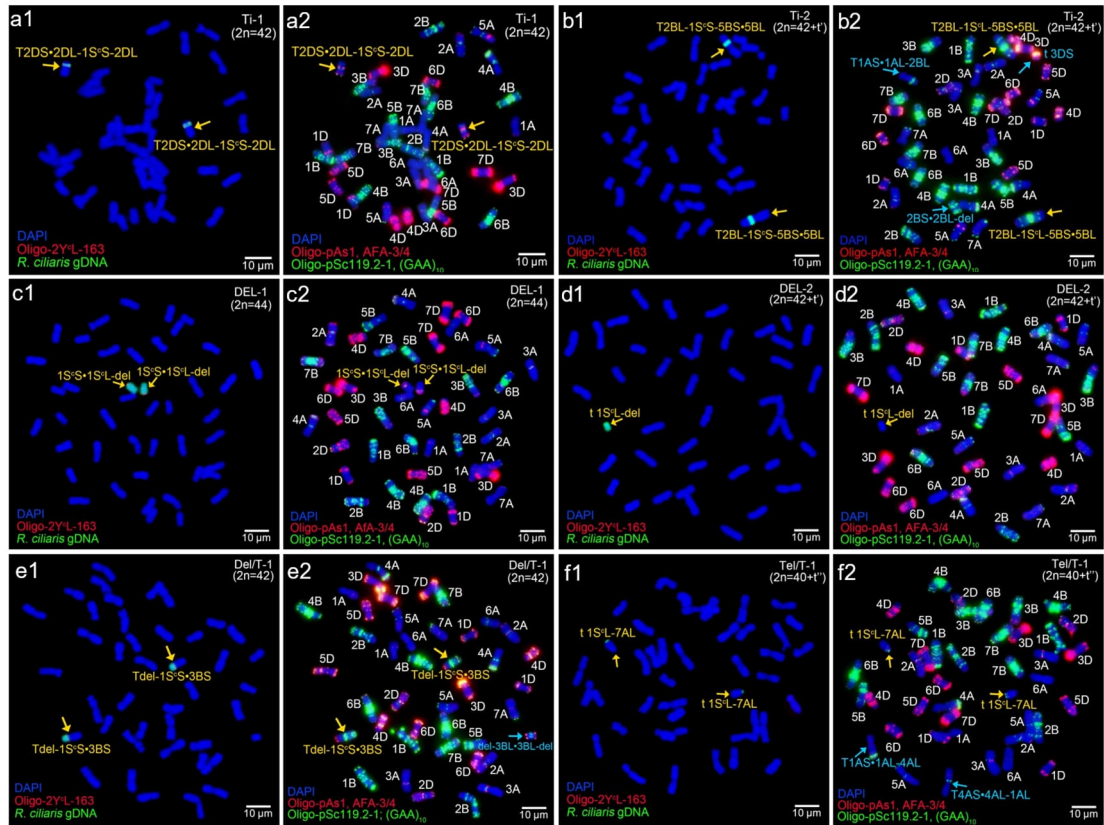


Fig. S8 Sequential GISH/FISH analysis of two wheat-*R. ciliaris* interstitial translocation lines, two chromosome deletion lines, one deletion/translocation lines and one telosomic/translocation line induced by irradiation.

a1 and a2: Ti-1 (T2DS•2DL-1ScS-2DL). **b1 and b2:** Ti-2 (T2BL-1S^cS-5BS•5BL). **c1 and c2:** DEL-1 (1S^cS•1S^cL-del-1). **d1 and d2:** DEL-2 (t 1S^cL-del). **e1 and e2:** Del/T-1 (Tdel-1S^cS•3BS). **f1 and f2:** Tel/T-1 (t 1S^cL-7AL). For each line, left was GISH and FISH analysis using *R. ciliaris* gDNA (green) and oligo-2Y^L-163 (red) as probes, right was FISH analysis using modified ONPM#4 as probes. Chromosomes were counterstained with DAPI (blue). Yellow arrows indicate alien translocation chromosomes. Blue arrows indicate structural aberrations of wheat chromosomes. Bars = 10 μm.

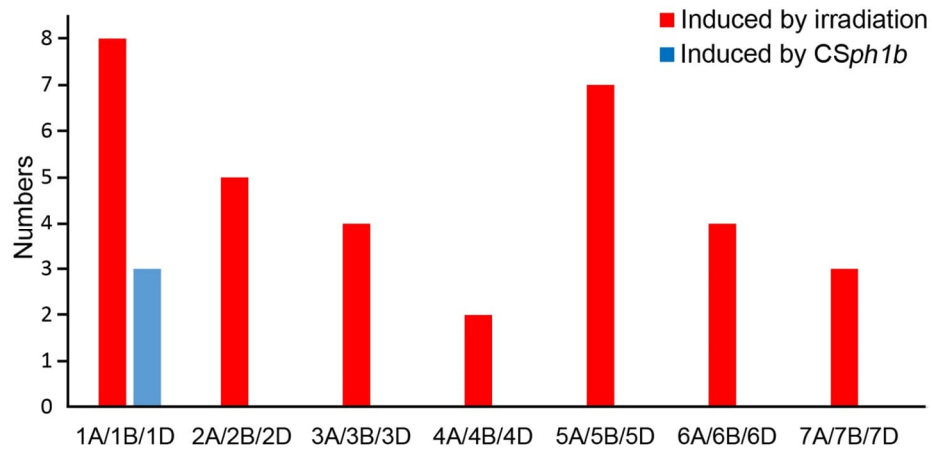


Fig. S9 Number of translocation lines with different homoeologous groups of wheat chromosomes. The x-axis represents the 7 homoeologous groups of wheat, the y-axis represents the number of translocation lines. The red and blue bar represent translocation lines induced by irradiation and *CSph1b* mutant, respectively.

Supplemental tables

Table S1 Information of 111 1S^c diagnostic markers.

Marker_ID	Primer_F	Primer_R	Location_1E (Mb)	Location_1A (Mb)	Location_1B (Mb)	Location_1D (Mb)	Location_1R (Mb)	Specific amplicon (s) on chromosome (s)
CMH2-3	GAGTGCATGCCTTCGGTTTA	TACTGTGGGCTCGCTTGAT	1.62	1.16	1.20	0.04	-	1B, 1S ^c
CMH4-1	GTCGAAAGCCTGTTGATGCA	GTCGACTAACCCCTTCCAGCT	1.72	1.21	1.41	0.07	-	1A, 1S ^c
CMH6-2	CATCAGCTGCCTTGACAAAA	GGTCATGGATGGTTTCAAGG	1.80	1.34	1.51	0.17	17.33	1S ^c
CMH10-1	GATGCGCTCTTGGAAGGTAA	AGAACCAACTGAGCGAGCAT	11.59	8.11	46.55	5.87	-	1S ^c
CMH11-2	GAAGATGGGCCAAGAGAACA	TCGACCAATCTCTGCACAGT	12.80	8.53	8.78	5.96	14.22	1A, 1B, 1D, 1S ^c
CMH14-1	CGTCAAGGAGTTCGAGAAGG	GAACCTGCCAAATGTCCTCC	16.63	8.99	9.22	6.76	15.82	1A, 1B, 1D, 1S ^c
CMH16-1	CGCACAATGATTCAGCTTCC	TTGAAATGTGTGGGGCCATC	18.25	9.58	9.60	7.20	16.53	1S ^c
CMH18-2	GCCAACAAGAACCTGCACAG	GTGACTCAGGGCTCTAACGA	20.71	10.92	10.59	8.29	28.12	1B, 1D, 1S ^c
CMH22-1	AAGGGGTCGGTCTTCTATGG	GGCATCGAGGAGAGCATTTG	24.54	12.13	13.28	9.84	-	1S ^c
CMH23-1	AAACTGGTTGAAAGCGCGTA	AGGCCGAGGAAAATGCTACT	26.33	12.96	14.91	10.16	9.89	1S ^c
CMH24-1	GCAGAGAAGAAACGGTCGAC	GTTCAACCAGGGATGGCAAG	27.34	13.05	15.58	10.27	13.39	1D, 1S ^c
CMH26-1	CCATTCAAGTGCTCGTCCAG	TTCCAGTGCCTCCGTCATAG	29.29	13.53	16.01	10.78	13.58	1A, 1S ^c
CMH28-1	GCATTCCTCGAACCAGCTTA	GGTAGTGAAGCGGACGAAAG	30.05	13.58	16.16	10.81	13.73	1A, 1B, 1D, 1S ^c
CMH29-1	TTTGATCACGTACACAGCGC	CGTGTCTTGCTCTCAGTCT	33.48	15.21	17.74	11.95	20.87	1A, 1B, 1D, 1S ^c
CINAU963	TTCGAGGAAGGGTCTGATCC	GGATCCAACCAAACTATCTGCT	34.14	15.58	18.55	12.38	20.21	1S ^c
CMH35-1	CAGCCGATCTTGCCGTGC	AGGCGCTCTCCATGTTCTT	37.30	18.81	25.98	17.30	24.03	1A, 1B, 1S ^c
CMH36-1	ATCCCTTCCACGTGTAAGCA	GAGGCCTCTTGAATTGCTCG	37.84	20.15	26.45	17.89	24.33	1A, 1B, 1S ^c
CMH40-1	CGTGCTTCTGTAGACGGT	AACATGATACCAACCTTGACCA	42.32	22.92	30.66	20.80	905.49	1D, 1S ^c
CMH41-1	TGGTCTACAATTCGCCCTCT	AGACTTCTGGGTGGCGG	43.02	23.23	34.05	21.52	32.71	1S ^c
CMH49-1	GCCCACGCTGCTATTGTG	GAGCTGGCTAATGGAGAGGT	50.85	26.40	43.96	26.35	38.46	1A, 1S ^c
CMH51-1	CATGGGCTGCTCATTGTTCA	TGAAACACCCCAAACAGTACT	52.99	27.85	44.55	27.03	38.78	1A, 1B, 1S ^c

CMH56-1	CAACAAGGGTCTTCAGGCAC	CCTGAAGGTTGAAGCTGGT	56.49	30.76	47.89	29.97	41.80	1A, 1B, 1D, 1S ^c
CMH67-1	CTGGCTACCTGGCTCATC	TGCCGTGAGAAATCTTGTGTG	62.81	35.55	58.75	37.40	48.57	1A, 1B, 1D, 1S ^c
CINAU940	GAGCATGTCTGAGTTGGAGT	CCCCTATGAAGCCCAAAACG	65.08	38.56	62.38	39.65	56.19	1A, 1S ^c
CINAU956	TCTGAGAGATCCTTGCTCGC	ATCAAAATCCATGGTACCAGGT	65.32	38.84	62.49	40.03	52.88	1S ^c
CMH78-1	GAACCCGAACAGATGGAAGC	CTACCTCCCCGTGTCATTCA	69.20	41.67	65.17	42.85	58.16	1A, 1D, 1S ^c
CMH81-1	TCTCTGAGCATGCTTGTGTC	TAAGCCTCCGAACAATGGGT	71.17	-	-	44.50	-	1D, 1S ^c
CMH83-1	ACTACCACGTCCATCTGCTC	GCCCGGGATGTACGTGAT	72.22	44.52	68.51	-	62.31	1S ^c
CMH84-1	CAAACGCTCTGTCTTGCAT	TGAGGGCTTCATATCGTCGT	73.29	46.66	69.74	47.71	-	1D, 1S ^c
CMH86-1	GGGTCTCTGCAGCCAATTT	GCCCTGAGTCCAAGGAGAAG	74.30	48.36	71.31	49.42	62.93	1D, 1S ^c
CMH91-1	GTGTGCACCATAGGAAAGGC	ATCTGTGGAAGCTCATGGGG	77.34	51.65	75.59	52.80	70.00	1A, 1B, 1D, 1S ^c
CMH92-1	TGAAGATGATGCTCCAAAACGG	ATGTATTCGATTGCCAGCCG	77.42	51.70	75.66	52.81	70.05	1A, 1B, 1D, 1S ^c
CMH93-2	GGATGTCGAGAAAGCACGTT	TGAGTTTCTCCTCCTCCTCTC	77.55	51.84	76.08	53.15	70.19	1S ^c
CMH94-2	CCCCATACCCCATCATCCTC	CAAGTCCCCGAATGTCTCCT	78.85	-	-	55.61	72.54	1A, 1D, 1S ^c
CMH95-1	CCACCACCACTTCGTCATCT	CCTCCTTGATCTCTGCTGCT	79.11	54.75	89.42	55.82	73.46	1S ^c
CMH96-2	GAGCAAGCGACAGACTAGGA	AAGATCCCTGGCCTTGTTGT	79.19	54.98	89.75	55.91	-	1B, 1S ^c
CMH102-2	CCAATCGTTCAAAGTGGGCA	ACCGGAATGTCATTTTGGGT	84.60	56.86	97.76	59.13	-	1S ^c
CMH103-2	GGTTGTCAAATGGGAAGGAGT	CTCCTCAGCCTTCACGAGT	85.03	56.53	97.15	58.89	75.91	1S ^c
CMH105-2	CTGCTGACTTCAACCCTGTC	AGAACACACTGAGGCTTCGA	88.43	60.69	101.48	62.83	100.41	1A, 1B, 1D, 1S ^c
CMH106-1	AGCCGAAGTTAGATCCTTGACT	TCAAATGGACAACGTGCTGG	88.92	61.20	101.95	63.17	103.58	1B, 1S ^c
CMH109-1	GGAAATAGTCGTGTGCAGGG	CCCATCGCCAATTTCTCCAG	89.22	61.42	102.80	63.50	-	1A, 1B, 1D, 1S ^c
CMH111-1	TGCTGTTGTGAATGTATGCCA	CCAACGCATGCCCTTGATAT	90.11	62.34	105.01	65.15	715.45	1S ^c
CMH114-1	GATGGCCTTGAACCTCTGCG	CCCCACTACCATCATGCTCT	90.83	63.20	106.03	65.79	-	1S ^c
CMH117-1	CGCCTCTTCTTCCACGATTG	CGGCGTCCTTGATCTTGTTT	91.01	63.38	106.32	65.99	101.87	1A, 1S ^c
CMH118-2	CAAAGCCTGTTGTTGCCCTA	GCGGGGAGGGATTACAGATA	91.54	63.85	106.92	66.21	107.73	1S ^c
CMH126-1	TCCTTGACCTGCATCTCCTG	GTCCCTCAGATGCTCCAGTC	96.26	68.20	114.47	70.20	113.25	1B, 1D, 1S ^c
CMH129-1	GGGCTTCATCTTCATCCGTG	AGCTGCTCGTCTGGTTCAT	97.84	70.09	116.85	72.30	115.46	1D, 1S ^c

CMH137-1	CCGAAAGCACTTAACAACATCTC	ATGGCGGAATTCAGAGGTCT	103.99	76.37	124.05	77.59	121.27	1S ^c
CMH139-2	GCTGAATTGCTGGTGGACTT	AGGCATCTGGAGCTTATATT	104.18	76.79	124.32	77.47	122.24	1B, 1S ^c
CMH142-1	GTGCTTCACGTGGTAAATCAC	GTCCTGGTTTCTTGAAGCG	105.24	78.85	125.32	78.84	123.54	1D, 1S ^c
CMH148-1	TGAGTGAGCGCTTGACAGAG	TCATTGCACCTGGGTCATCT	108.05	110.97	127.21	80.57	125.16	1S ^c
CMH149-1	GGGGAATGCATTGGAGTAGC	TTTTCCGATAGTCATTCAAGAA	110.62	98.72	130.12	82.15	128.96	1B, 1S ^c
CMH151-1	GGTACCCCGACGACATCAA	CCTTCCCTGGCCTTTCCTTG	111.56	100.25	136.46	82.35	144.11	1B, 1S ^c
CMH155-1	CAGGAGCGGAAGAGAAGAGA	GCTCCCTTACCGTCGATGAT	112.28	100.74	137.56	83.12	-	1A, 1B, 1S ^c
CMH158-1	ATCACGAAGCAATGCATGGC	GAGGAGTGCTTGAAGAGGGA	114.47	82.03	144.00	88.37	658.48	1B, 1D, 1S ^c
CMH159-1	TTCGGATGCACTCTCCCATT	CTTCTCCAAGCGCTCCAATC	114.89	82.64	144.93	89.11	139.64	1B, 1D, 1S ^c
CMH162-1	GGACCTTCGATGCATGGTA	CTCGGTGCTTGGTTCAACAA	116.29	86.30	147.61	90.92	-	1B, 1S ^c
CMH163-2	AGGTCAAGAAGGTGCTACAGA	GATGAGCTTCTTGACGAGCG	116.31	86.32	148.05	90.94	-	1B, 1D, 1S ^c
CMH164-1	GAAAACGCACGCTCCCTTAT	TGGAGAGCAATGAAGTGGGA	117.24	87.33	148.65	92.29	-	1S ^c
CMH166-1	GCGCTTTTCAATAAAGTTGGCT	CCTCGGCCTATTTTGCTTACC	119.19	113.34	165.06	111.22	178.06	1A, 1B, 1D, 1S ^c
CINAU939	AAACCCCAATGCAATCGGAC	GCAGGCAGGTTCTTAGCAAT	120.45	108.06	166.86	109.96	176.64	1A, 1S ^c
CMH170-3	ACCAGGGAAGAGAGAGACCA	ACGTGGCAATGGATTTTCGAG	121.61	109.30	168.52	107.71	174.04	1S ^c
CINAU1799	AGTCCCGGTAAAGAAATCAAAG	TTCCACAAACTCCTGAAGCC	122.24	103.22	169.33	106.56	173.35	1A, 1B, 1S ^c
CINAU1778	CGCTTCAGTTTCAGGGATCA	CACCCTGTCAGCATGAAGTG	134.09	118.16	175.16	113.76	188.23	1S ^c
CINAU954	GTTTCAGGGAGGCTGCATTG	CCCGAGCACTCATTAACAACC	145.17	134.59	189.93	123.59	205.46	1A, 1B, 1D, 1S ^c
CINAU947	TGGAGCACTGGGTTATGGTT	GCTCTGAAC TTGCTCCAGATG	146.74	137.04	193.24	125.82	208.05	1B, 1S ^c
CINAU930	AAGAACGGCGAGCCCAAG	TCCGCCATGTAGCTAATCGT	155.24	150.34	197.43	145.10	233.25	1A, 1S ^c
CINAU949	GTTAGACATTGGGGAGGGCA	ACATAAGTTTGCCACCCTCA	156.18	151.42	201.95	144.50	247.70	1S ^c
CINAU929	TTTGATTTCAGCCACAGTTCAA	CCTGAAGCCATCCATGCATC	161.26	157.12	216.04	140.61	920.39	1D, 1S ^c
CINAU1771	ATGGATGACAGCTTG GTTGA	CATCCTCAAGTGCTCGCATC	161.49	157.74	215.53	140.41	231.75	1A, 1S ^c
CINAU962	CTCTCCGTGGTAGCTGTG	AGTAGAAAGGCATGA ACTCCAC	162.85	169.16	216.58	139.92	243.44	1A, 1S ^c
CINAU1795	GCTGAGATTGTGGGAAACG	ACTCTGTGTGTTGCGTTCC	164.29	165.39	208.21	137.67	249.84	1S ^c
CINAU957	TTGCCTTCTACAACATTCCGA	TACCAATCTCTGCTGTCCCC	164.81	167.17	208.45	136.55	311.55	1A, 1S ^c

CINAU1699	GGTCTGTGGGGATTTC AATTCA	GGGCGTAAAAATTCCAAGGGG	216.93	227.43	255.64	-	315.78	1S ^c
CINAU893	AAGAAAGGAAGGCTGGAAGAG	GCTTCTGCCGCCATTA ACT	219.31	221.85	269.32	219.31	354.84	1S ^c
CINAU857	GGGCATGCTCTTTCAACGG	TCATTTTCCAAACACCCTCAGT	220.20	220.49	258.40	220.20	479.88	1D, 1S ^c
CINAU1698	TTGCTGGAGGAAGATGCTCT	TTGGGCCAATCTTGTCCTCT	222.98	233.97	247.26	222.98	-	1S ^c
CINAU1724	CAGTTGGTGCATTTTGATTTC AA	AGGAATCATCGTGCAACTCA	225.35	239.37	271.33	225.35	283.14	1A, 1B, 1D, 1S ^c
CINAU876	CCAAGTTGGGAGAGGGAGG	CTGAAGCAACGACGGGAATA	228.54	243.51	278.91	228.54	423.73	1A, 1B, 1D, 1S ^c
CINAU895	TCGTATACAATCAGTGCAGCT	TGGATGCCAGGTTGATATCTTAT	233.86	252.09	285.64	233.86	434.06	1S ^c
CINAU1677	TGAACCTTGAGAACTTTGACCC	TGTTCTTCTTGCTCTCCAGCTC	236.74	253.24	286.62	236.74	436.28	1A, 1B, 1D, 1S ^c
CINAU1730	TAGTTGGGGAGAAAGGACCG	CGCTGAAGGGCAAGTTAGAA	237.54	256.27	295.21	237.54	442.00	1A, 1B, 1D, 1S ^c
CINAU1744	ACATATCAGGGCGAAATTGAGC	TGTGTGTTTCCGTCGAACAA	248.95	270.77	309.13	248.95	366.98	1A, 1D, 1S ^c
CINAU1702	GGCATCATAACTAGGGCAAGG	TAGAAGGCCCTCACCCACTT	257.27	287.81	323.74	257.27	395.41	1D, 1S ^c
CINAU870	TGTTCCGTGGAGATATCTTCCA	GGAAGGCCATCTGAATCAATTAC	261.78	295.49	333.05	261.78	406.61	1A, 1B, 1D, 1S ^c
CINAU1685	GTTCATTTACTCGCCGGGAC	GAGTTGCTCCACAGAAGGCT	272.56	313.52	347.01	272.56	465.31	1A, 1B, 1D, 1S ^c
CINAU884	CAGTTCGCGCAAATCTACCA	CCGTTGGAAGTTTTCAGTTGC	274.42	315.58	374.48	274.42	466.99	1A, 1S ^c
CINAU855	TCTGCAAAGATCGATACAAGGT	CTGCAATTCTTGTCCTCCA	279.67	323.51	368.71	279.67	477.43	1S ^c
CINAU844	ACCAAGTAGTCAAGATGGTCGA	GCGTCAGTGGAGTTTGTAGA	279.81	324.19	368.16	279.81	477.29	1S ^c
CINAU841	ACGAGTTGCAAGGAAATGGAG	TGTCACGCTCCATCTCAAGA	305.62	358.57	394.01	305.62	526.93	1S ^c
CINAU866	TCCAATCATTGCGCCAAATCT	GCAGTGTC AAAAGTCCCTT	317.55	370.24	403.44	317.55	832.25	1S ^c
CINAU909	AGCAGCTTGAGAACTTGGT	TCCCGAGGTATCAAGACTGC	330.37	388.05	421.53	330.37	590.79	1B, 1S ^c
CINAU880	TGGCAATGTCTGTAGCCATC	GAACTCAAGCCGTGTCATGG	348.52	421.94	443.01	348.52	619.38	1S ^c
CINAU1717	ATGGATGCTGCACCTCCAT	TGTCGAACTGTTACATATTGCT	365.28	443.07	463.36	365.28	-	1A, 1B, 1D, 1S ^c
CINAU910	ATGTGCACTTTTCCAAGACCT	AAGAAACGGACCGGGGTAC	366.84	444.30	465.69	366.84	678.00	1D, 1S ^c
CINAU889	AGGGATCAAGTGGAGAGTGA	TGTTCCAGTTCGAGCAAGAC	367.93	445.02	467.18	367.93	678.77	1S ^c
CINAU1684	CTCTTCAGGAACAGCAACCG	TCACACCATTTGCTTCAGA	376.36	457.36	484.25	376.36	703.45	1D, 1S ^c
CINAU1733	CCCATCCGATAGCCTTCCAT	CCATTTTCAGCAAGTGTCCT	397.73	482.44	515.92	397.73	735.74	1A, 1D, 1S ^c
CINAU847	ATGGCTCCTTCACTACGAGC	ACGTTTCTGATCCAGCTCTATTG	400.69	484.61	519.58	400.69	745.81	1A, 1B, 1S ^c

<i>CINAU891</i>	AAGGCAGGGCTTTGTCAAAT	TGTTTGCCTGCTAGAAAGTCTTC	408.12	492.70	534.49	408.12	758.20	1A, 1S ^c
<i>CINAU1736</i>	ACTAGGGAGGAATCACATTGTTT	GCTGTGGGGCTAAACAAAGG	442.83	519.83	578.02	442.83	810.54	1A, 1S ^c
<i>CINAU900</i>	GGCTGTTCGTTTTGTGGACT	ATCAGCAGATCCCGTCAGAA	447.80	537.03	602.41	447.80	859.76	1B, 1S ^c
<i>CINAU1701</i>	TTGGATGTACTCAGTGGCCA	ACATCCCAAAGACGAACGGT	454.99	531.90	590.19	454.99	827.88	1D, 1S ^c
<i>CINAU1679</i>	GCGCGATTTTGTGTTTCAGG	CCATGAGTTCTCTGTGGTATGC	455.04	531.87	589.97	455.04	827.67	1B, 1S ^c
<i>CINAU1734</i>	CGAAAGTCTGACCTGAGTATGG	TGGCCTCCTTTCCAAGATG	464.74	521.01	579.46	464.74	903.57	1S ^c
<i>CINAU913</i>	GAGGAGCCAGCTGATATTTATGT	TGGTCATCTTCAGCACCGAA	466.07	541.72	611.47	466.07	840.56	1B, 1D, 1S ^c
<i>CINAU886</i>	GAACGAGATACTCACACTGCT	TTTGCTAAAAC TTCAGCCTCTTT	469.65	543.89	617.47	469.65	843.26	1B, 1S ^c
<i>CINAU873</i>	ATGATCCTCTCCTCATCCGA	CGTGAAACAACAGAAGCCAC	487.92	555.55	643.14	487.92	837.04	1A, 1B, 1D, 1S ^c
<i>CINAU902</i>	ATCCATGGCGCTTCAGATAG	GACCAGAGGAGGAAGGCG	503.70	566.31	660.56	503.70	891.60	1A, 1B, 1D, 1S ^c
<i>CINAU874</i>	GAAAGCATTCCTCAACCCC	AGAAGAGTCAAGTCCACCAGA	527.11	581.59	678.32	527.11	921.55	1A, 1B, 1D, 1S ^c
<i>CINAU1749</i>	TTCACTTCGACCCCTGCTTC	CTCGAACTGCTTGGGAGAAC	550.75	595.65	694.48	550.75	937.88	1S ^c

Notes: The red font represents the flanking markers of *PmRc1* locus; the dotted line represents the position of centromere; "-" represents markers that failed to be anchored.

Table S2 Four different types of the 1S^c diagnostic markers.

Type	Specific amplicon (s) on chromosome (s)	Number of markers	Percentage
Type I	1S ^c	35	31.50%
Type II	1A, 1S ^c	13	11.70%
	1B, 1S ^c	12	10.80%
	1D, 1S ^c	13	11.70%
	Total	38	34.20%
Type III	1A, 1B, 1S ^c	6	5.40%
	1A, 1D, 1S ^c	4	3.60%
	1B, 1D, 1S ^c	6	5.40%
	Total	16	14.40%
Type IV	1A, 1B, 1D, 1S ^c	22	19.80%
Total		111	

Table S3 Information of the 1S^c bin map.

Bin name	Number of markers	Bin length (Mb)	Average physical distance between markers (Mb)
1S ^c S-1	3	6.70	2.23
1S ^c S-2	5	15.93	3.19
1S ^c S-3	3	5.69	1.90
1S ^c S-4	4	7.68	1.92
1S ^c S-5	4	10.95	2.74
1S ^c S-6	6	20.33	3.39
1S ^c S-7	5	8.56	1.71
1S ^c S-8	3	2.38	0.79
1S ^c S-9	9	12.27	1.36
1S ^c S-10	12	22.91	1.91
1S ^c S-11	5	4.84	0.97
1S ^c S-12	9	40.50	4.50
1S ^c S-13	3	4.85	1.62
1S ^c S-14	2	26.43	13.22
Cnetromere	0	20.00	-
1S ^c L-1	5	16.94	3.39
1S ^c L-2	5	26.17	5.23
1S ^c L-3	2	14.06	7.03
1S ^c L-4	4	25.54	6.39
1S ^c L-5	2	31.24	15.62
1S ^c L-6	7	75.25	10.75
1S ^c L-7	1	5.20	5.20
1S ^c L-8	1	21.07	21.07
1S ^c L-9	1	19.84	19.84
1S ^c L-10	3	14.57	4.86
1S ^c L-11	3	18.89	6.30
1S ^c L-12	1	17.03	17.03
1S ^c L-13	2	43.12	21.56
1S ^c L-14	1	14.43	14.43
1S ^c S_average	5.21	13.57	2.60
1S ^c L_average	2.71	24.92	9.18
1S ^c _average	3.83	19.25	4.98
Maximum	12	75.25	21.56
Minimum	0	2.38	0.79
1S ^c S_total	73	190	
1S ^c L_total	38	343	
1S ^c _total	111	553	

Table S4 Pm resistance evaluation of the 16 structural aberrations involving 1S^c.

Name of the lines	Material	Year	Generation	Genotype	Number of individuals	Pm infection types
	CS	2020-2021	-		6	3.08±0.44
	CS	2021-2022			6	3.75±0.69
	IK	2020-2021	-		6	6.75±0.47
	IK	2021-2022			6	7.66±0.55
	Nannong 0686	2020-2021	-		6	2.58±1.59
	Nannong 0686	2021-2022			6	3.16±1.17
	IK- <i>R. ciliaris</i> amphiploid	2020-2021	-		6	8.16±0.55
	IK- <i>R. ciliaris</i> amphiploid	2021-2022			6	8.41±0.34
	DA1S ^c	2020-2021	-		6	1.08±0.53
	DA1S ^c	2021-2022			6	1.41±0.67
TT-1	T1S ^c S-1AL•1AS	2020-2021	M ₄	1Sc(+)	9	4.72±1.65
				1Sc(-)	16	4.46±1.67
TT-1	T1S ^c S-1AL•1AS	2021-2022	M ₅	1Sc(+)	15	4.53±0.74
				1Sc(-)	18	4.66±1.5
TT-3	T1S ^c S-3DL•3DS	2020-2021	M ₄	1Sc(+)	11	4.77±1
				1Sc(-)	12	4.83±0.98
TT-3	T1S ^c S-3DL•3DS	2021-2022	M ₅	1Sc(+)	24	5.64±1.59
				1Sc(-)	22	5.27±1.44
TT-4	T1S ^c S-5BL•5BS	2020-2021	M ₄	1Sc(+)	13	5.61±1.49
				1Sc(-)	16	5.12±1.69
TT-4	T1S ^c S-5BL•5BS	2021-2022	M ₅	1Sc(+)	18	6.5±1.11
				1Sc(-)	24	5.16±1.98*
TT-5	T1S ^c S-6BS•6BL	2020-2021	M ₄	1Sc(+)	17	4.85±1.55
				1Sc(-)	20	4.97±1.57
TT-5	T1S ^c S-6BS•6BL	2021-2022	M ₅	1Sc(+)	22	5.68±1.83
				1Sc(-)	23	6.06±1.74
TT-7	T1S ^c S-1AS•1AL	2020-2021	M ₄	1Sc(+)	16	1.59±0.83**
				1Sc(-)	13	3.53±1.15
TT-7	T1S ^c S-1AS•1AL	2021-2022	M ₅	1Sc(+)	46	1.85±1**
				1Sc(-)	32	4.17±1.56
WAT-1	T1S ^c S•1BL	2020-2021	BC ₁ M ₃	1Sc(+)	23	2.52±1.23**
				1Sc(-)	10	5.5±1.51
WAT-1	T1S ^c S•1BL	2021-2022	BC ₁ M ₄	1Sc(+)	46	2.58±1.11**
				1Sc(-)	20	5.02±1.56
WAT-3	T2DS•1S ^c L	2020-2021	M ₄	1Sc(+)	16	4.72±1.5
				1Sc(-)	17	4.88±1.41
WAT-3	T2DS•1S ^c L	2021-2022	M ₅	1Sc(+)	27	5.18±1.36
				1Sc(-)	25	5.04±1.76

LT-5	TW-1S ^c S•1S ^c L-1	2020-2021	M ₄	1Sc(+)	17	4.58±1.36
				1Sc(-)	13	4.88±1.09
LT-5	TW-1S ^c S•1S ^c L-1	2021-2022	M ₅	1Sc(+)	24	4.95±1.53
				1Sc(-)	20	5.07±1.22
Ti-1	T2DS•2DL-1S ^c S-2DL	2020-2021	M ₄	1Sc(+)	12	4.2±1.42
				1Sc(-)	11	4.72±1.78
Ti-1	T2DS•2DL-1S ^c S-2DL	2021-2022	M ₅	1Sc(+)	16	4.12±1.56
				1Sc(-)	22	4.09±1.84
LT-6	T5DS-1S ^c S•1S ^c L	2020-2021	M ₄	1Sc(+)	12	4.5±1
				1Sc(-)	10	4.45±0.9
LT-6	T5DS-1S ^c S•1S ^c L	2021-2022	M ₅	1Sc(+)	22	5.15±1.26
				1Sc(-)	17	5.52±1.42
LT-7	TW-1S ^c S•1S ^c L-2	2020-2021	M ₄	1Sc(+)	11	3.18±1.36**
				1Sc(-)	19	4.47±1.5
LT-7	TW-1S ^c S•1S ^c L-2	2021-2022	M ₅	1Sc(+)	14	2.82±1.44**
				1Sc(-)	23	4.71±1.71
LT-8	T5BL-1S ^c S•1S ^c L-1	2020-2021	M ₄	1Sc(+)	12	3.2±1.28**
				1Sc(-)	11	4.86±1.12
LT-8	T5BL-1S ^c S•1S ^c L-1	2021-2022	M ₅	1Sc(+)	30	3.18±1.84**
				1Sc(-)	30	5.31±1.77
LT-9	T5BL-1S ^c S•1S ^c L-2	2020-2021	M ₄	1Sc(+)	7	2±1.22**
				1Sc(-)	15	4.1±1.25
LT-9	T5BL-1S ^c S•1S ^c L-2	2021-2022	M ₅	1Sc(+)	14	2.32±1.18**
				1Sc(-)	20	4.3±1.86
Del/T-1	Tdel-1S ^c S•3BS	2020-2021	M ₄	1Sc(+)	17	2.35±1.78**
				1Sc(-)	8	4.31±2.17
Del/T-1	Tdel-1S ^c S•3BS	2021-2022	M ₅	1Sc(+)	34	2.55±1.29**
				1Sc(-)	23	4.21±1.39
LT-12	T2AS-1S ^c S•1S ^c L	2020-2021	M ₄	1Sc(+)	12	2.79±1.26**
				1Sc(-)	14	4.46±1.52
LT-12	T2AS-1S ^c S•1S ^c L	2021-2022	M ₅	1Sc(+)	22	3.47±1.23**
				1Sc(-)	23	5.15±1.6
LT-13	T1DL-1S ^c S•1S ^c L	2020-2021	M ₄	1Sc(+)	11	2.18±1.15**
				1Sc(-)	15	4.56±1.84
LT-13	T1DL-1S ^c S•1S ^c L	2021-2022	M ₅	1Sc(+)	18	3.8±1.75**
				1Sc(-)	26	5.84±1.59

Table S5 Known Pm resistance genes located on homoeologous group 1 chromosomes of Triticeae species.

Gene	Original species	Chromosomal localization	Physical localization	Reference
<i>Pm3a-3t</i>	<i>Triticum aestivum</i>	1AS	4.497-4.503 Mb (<i>Pm3b</i>)	Yahiaoui et al. 2004
<i>Pm8</i>	<i>Secale cereale</i>	1RS	<i>Pm3</i> locus	Lu et al. 2013
<i>Pm17</i>	<i>S. cereale</i>	1RS	<i>Pm3</i> locus	Singh et al. 2018
<i>Pm24</i>	<i>T. aestivum</i>	1DS	38.780-38.789 Mb	Lu et al. 2020
<i>Pm10</i>	<i>T. aestivum</i>	1D	Not determined	Tosa et al. 1987
<i>Pm25</i>	<i>T. aestivum</i>	1A	Not determined	Shi et al. 1997
<i>Pm28</i>	<i>T. aestivum</i>	1B	Not determined	Peusha et al. 2000
<i>Pm32</i>	<i>Aegilops speltoides</i>	1S ^s S	Not determined	Hsam et al. 2003
<i>Pm39</i>	<i>T. aestivum</i>	1BL	Not determined	Lillemo et al. 2003
<i>Pm67</i>	<i>Haynaldia villosa</i>	1VS	Not determined	Zhang et al. 2020
<i>Pm223899</i>	<i>T. aestivum</i>	1AS	4.505-5.336 Mb	Li et al. 2018
<i>MIHLT</i>	<i>T. aestivum</i>	1DS	<i>Pm24</i> locus	Wang et al. 2015
<i>PmBN418</i>	<i>S. cereale</i>	1RS	<i>Pm3</i> locus	Xu et al. 2021
<i>PmCn17</i>	<i>S. cereale</i>	1RS	<i>Pm3</i> locus	Ren et al. 2009
<i>PmSESY</i>	<i>S. sylvestre</i>	1RL	717.89-721.70 Mb	He et al. 2021