

GENETICS

Supporting Information

<http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.114.165548/-/DC1>

Chromosomal Evolution and Patterns of Introgression in *Helianthus*

Jessica G. Barb, John E. Bowers, Sebastien Renaut, Juan I. Rey,
Steven J. Knapp, Loren H. Rieseberg, and John M. Burke

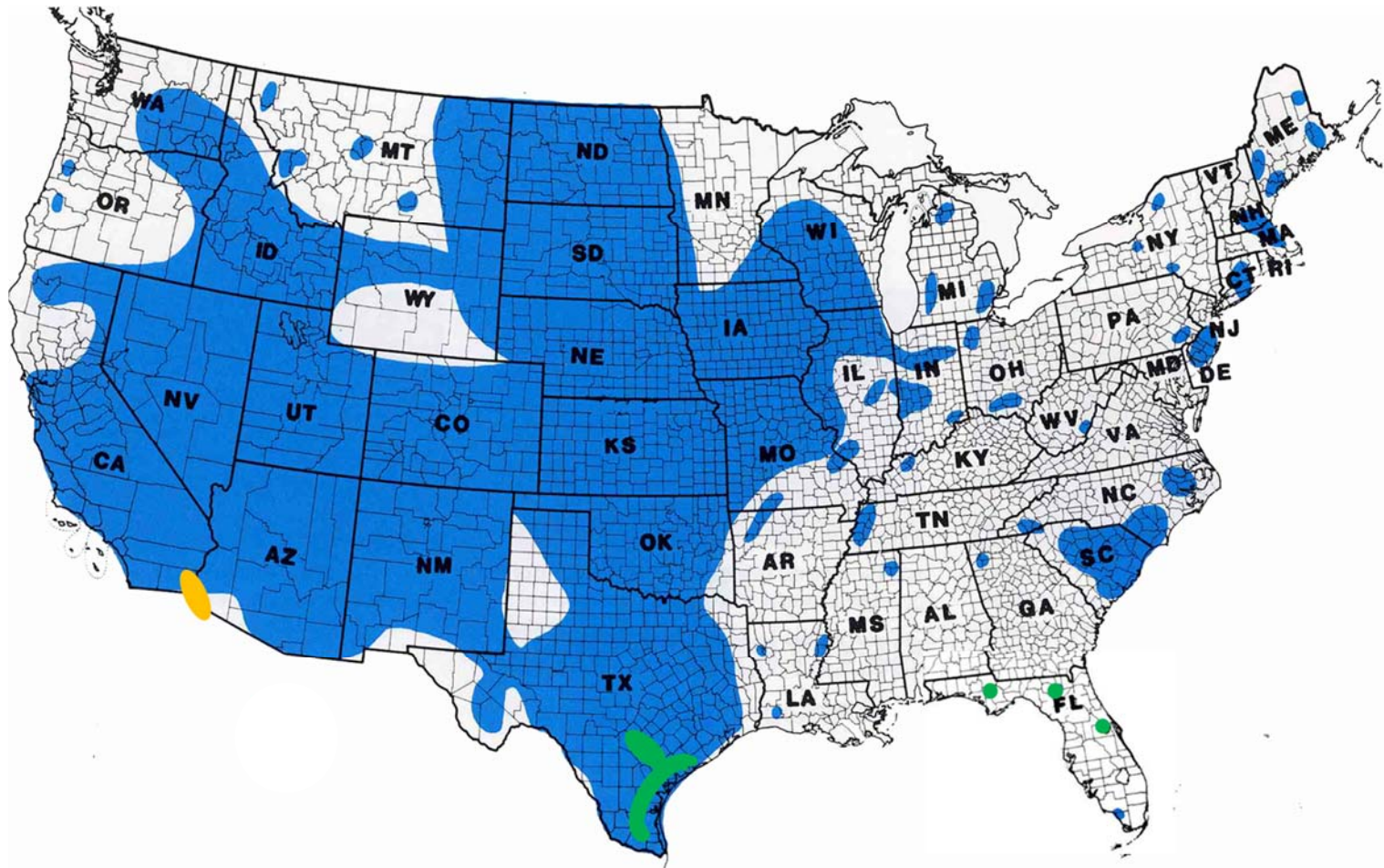


Figure S1 General distribution of wild *Helianthus annuus* (blue), *H. argophyllus* (green), and *H. niveus* ssp. *tephrodes* (orange) in the United States. Adapted from Rogers *et al.* 1982. Please note that the distribution of *H. annuus* and *H. niveus* ssp. *tephrodes* both extend southward into Mexico.

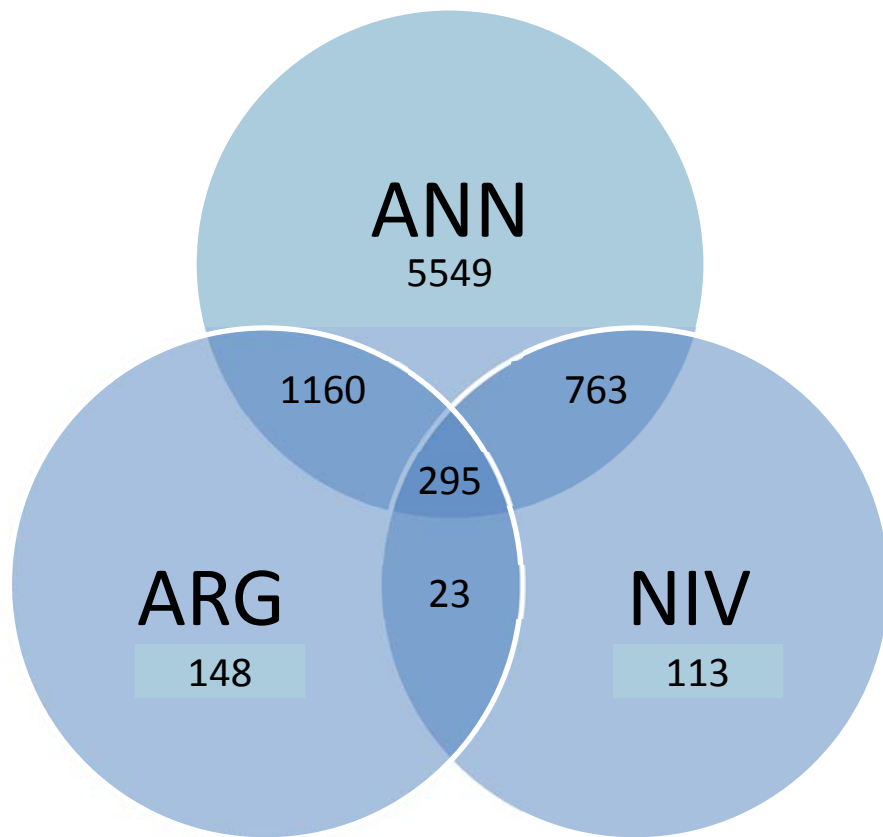


Figure S2 SNP markers mapped in *Helianthus annuus* (ANN), *H. argophyllus* (ARG), and *H. niveus* ssp. *tehprodes* (NIV).

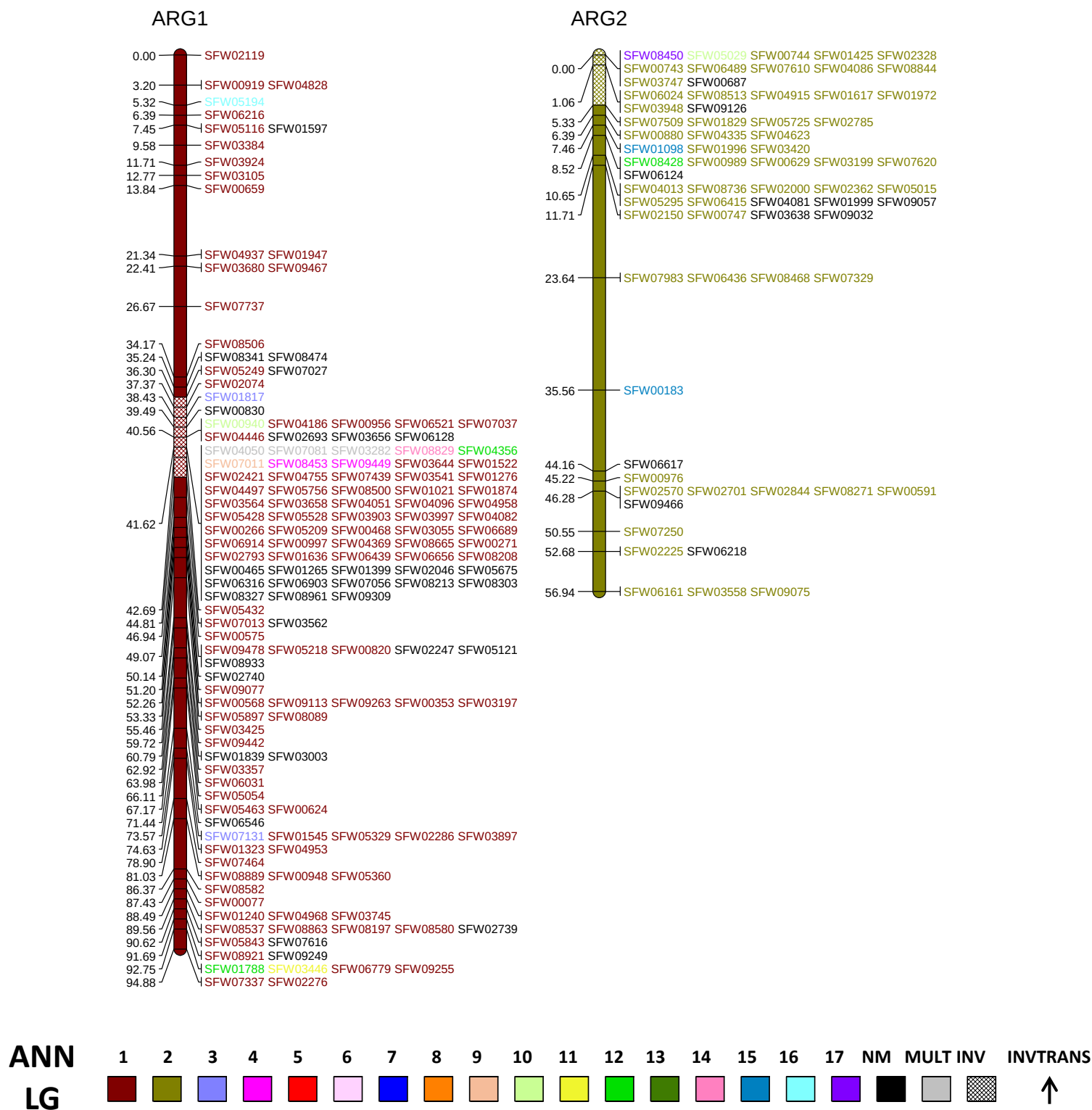
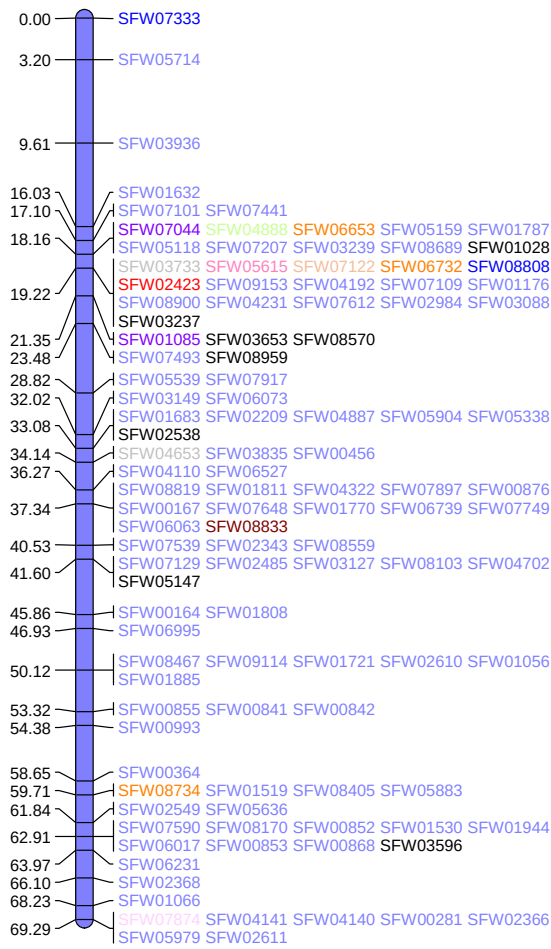
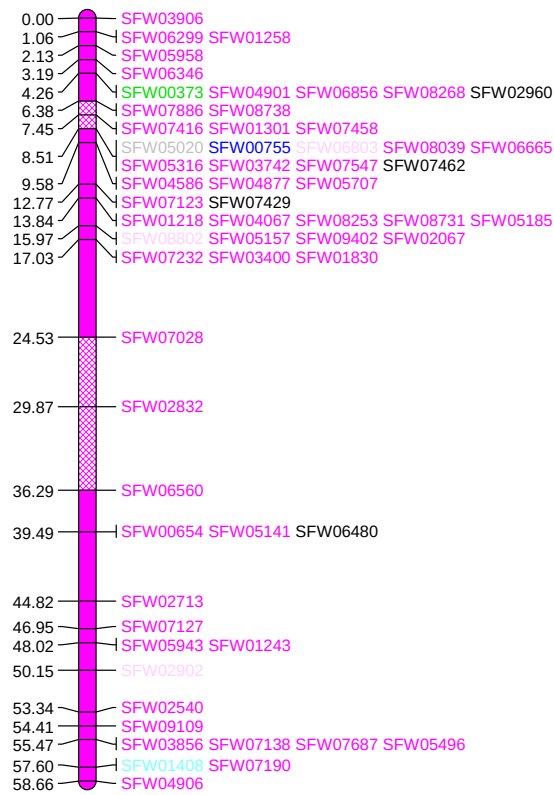


Figure S3 Genetic linkage maps of *Helianthus argophyllus* (ARG) and *H. niveus* ssp. *tephrodes* (NIV). ARG and NIV linkage groups (LGs) are labeled and color coded based on macrosynteny with *H. annuus* chromosomes ANN1-17 (Bowers *et al.* 2012) (see Figure 1 for details). SNP markers are colored corresponding to where they were mapped on the ANN consensus map (ANN LGs 1-17). SNP markers and LGs shaded in gray (MULT) are markers or regions of markers that are mapped to multiple ANN LGs not including that particular ARG or NIV LG, respectively. SNP markers shaded in black (NM) were not mapped in ANN. INV/cross hatch regions indicate inverted regions relative to ANN. Arrows indicated translocated regions that are also inverted.

ARG3



ARG4



ANN
LG

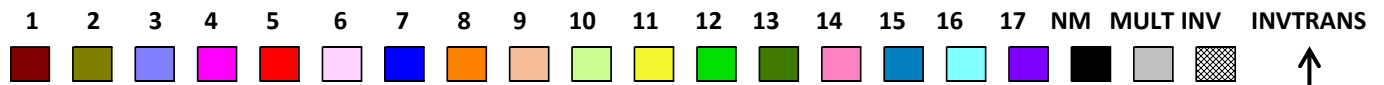
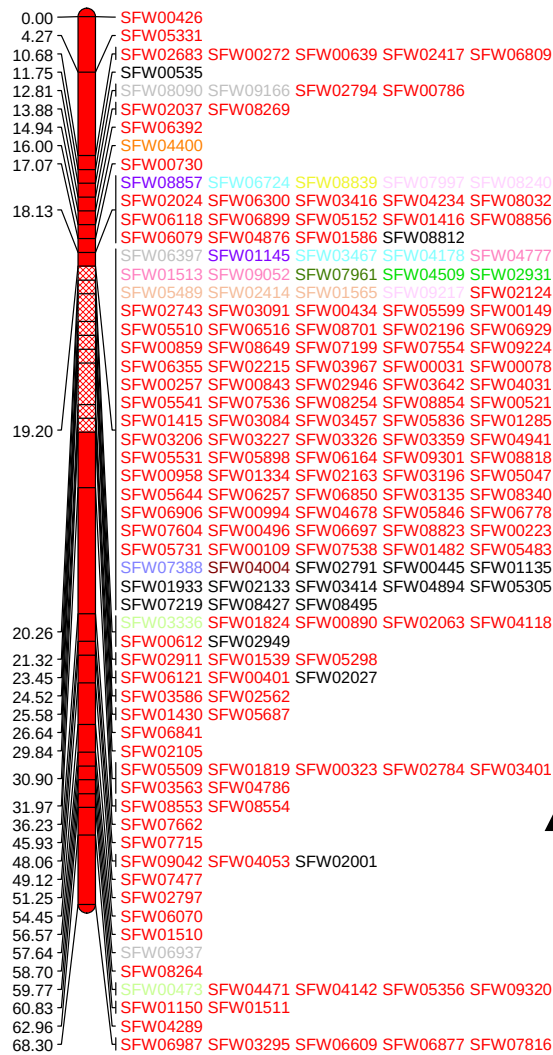
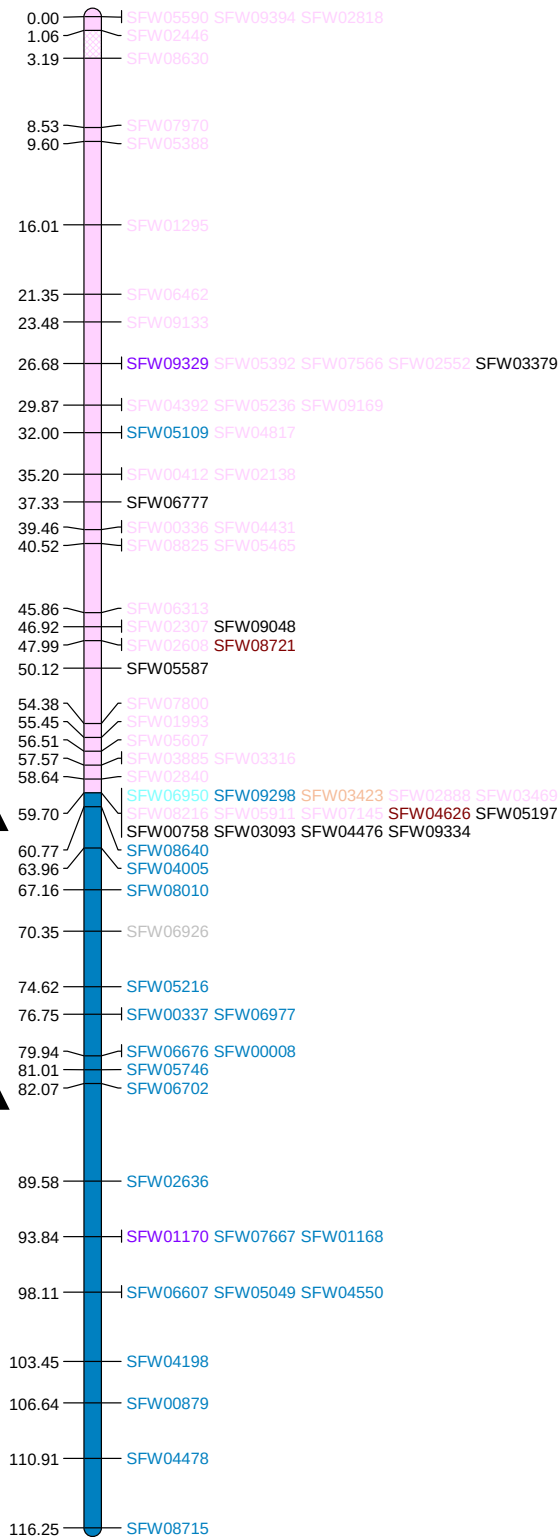


Figure S3 continued

ARG5



ARG6/15



ANN
LG

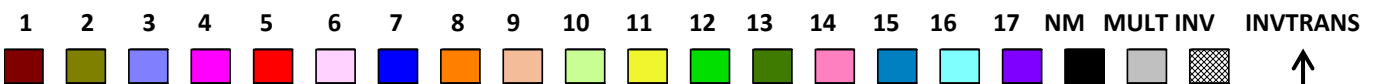
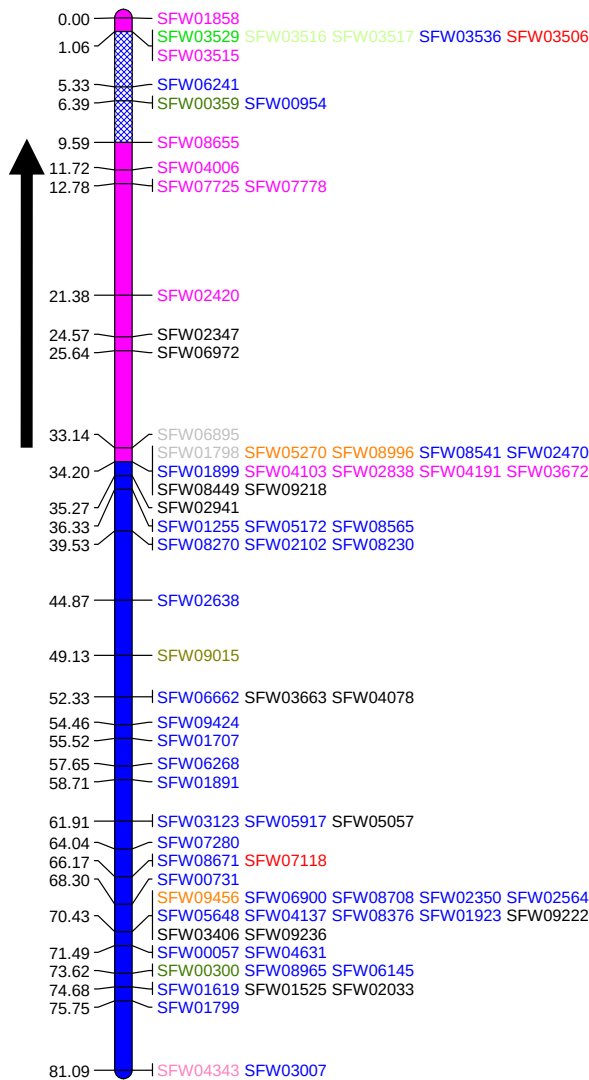


Figure S3 continued

ARG4/7



ARG8

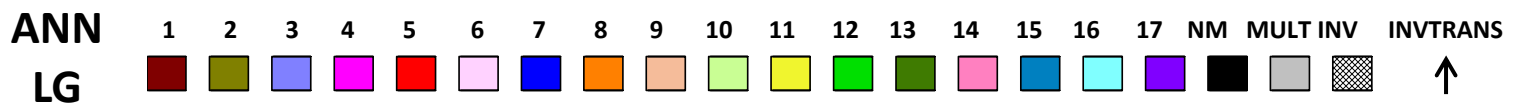
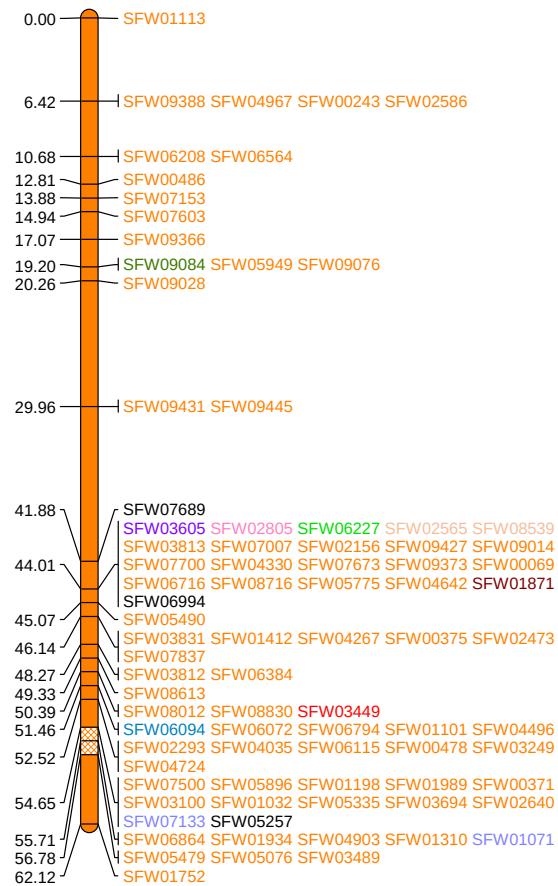
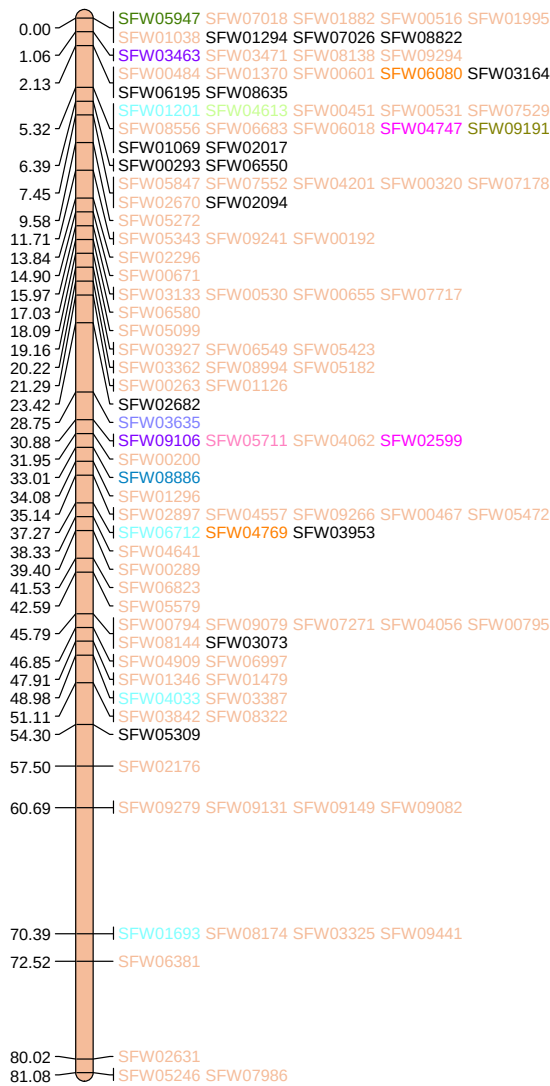


Figure S3 continued

ARG9



ARG10

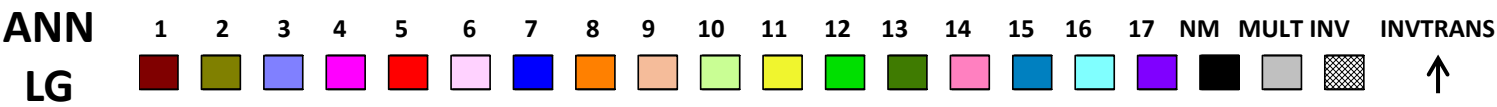
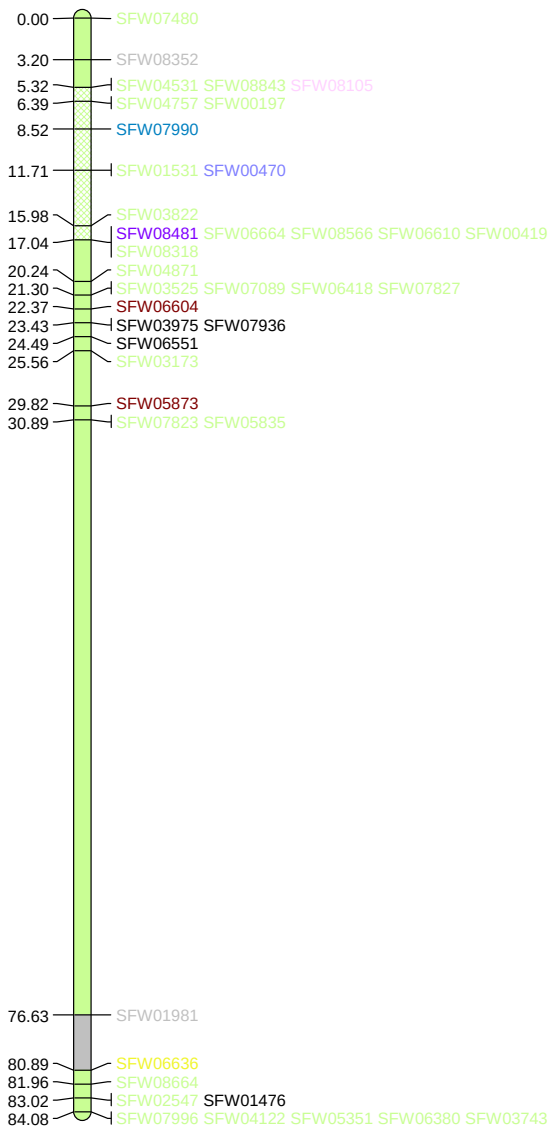


Figure S3 continued



ANN
LG

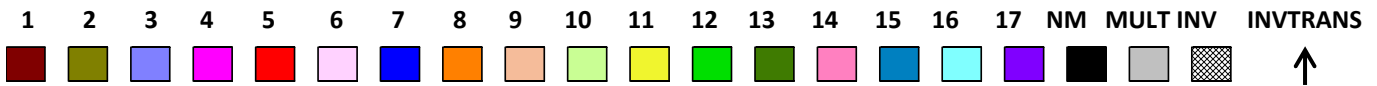
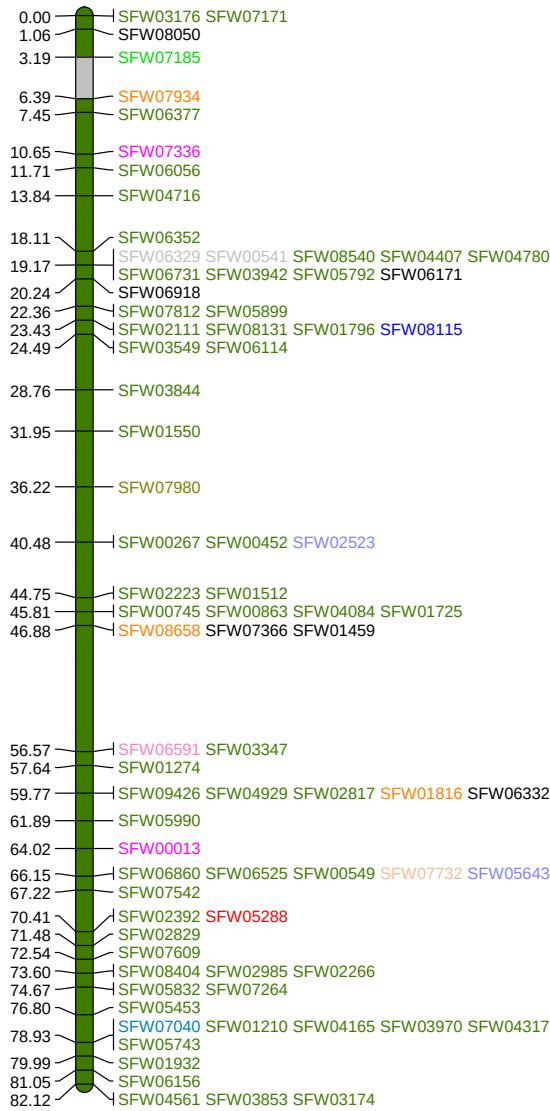
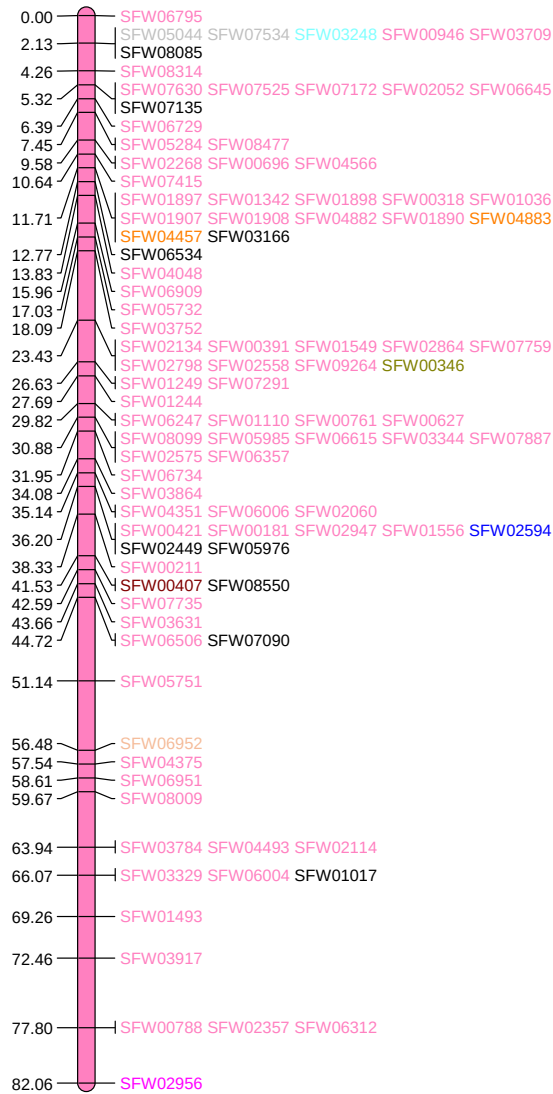


Figure S3 continued

ARG13



ARG14

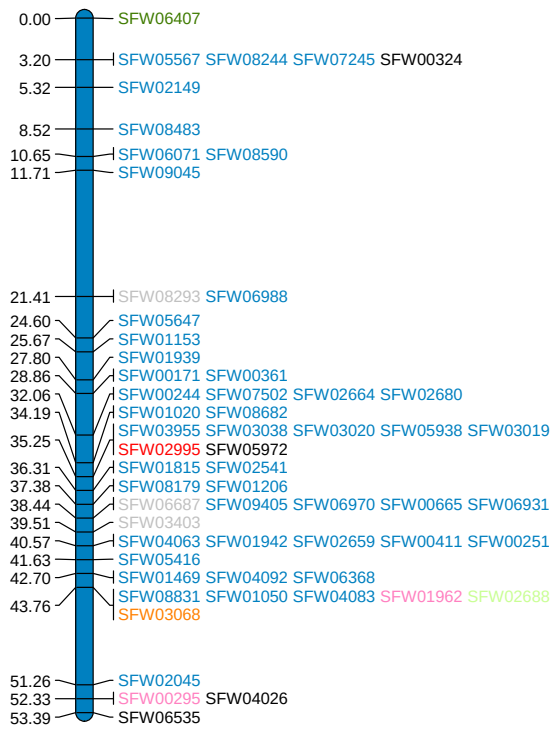


ANN
LG



Figure S3 continued

ARG15



ARG16/12

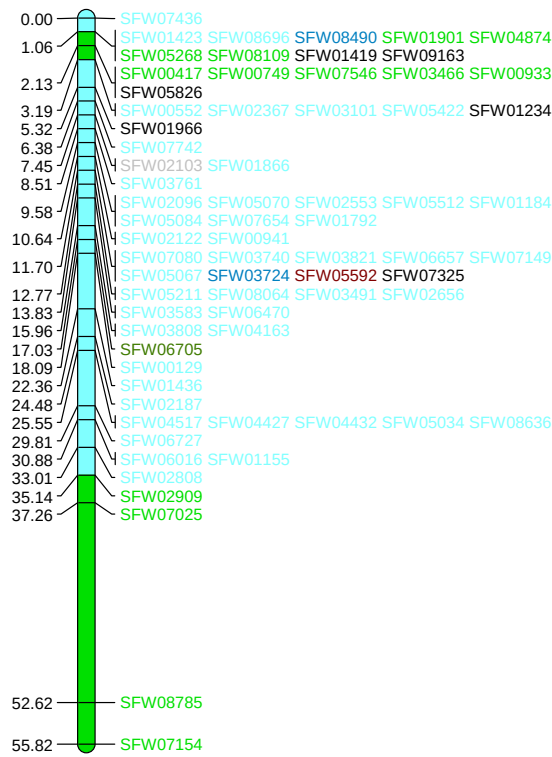


Figure S3 continued

ARG17

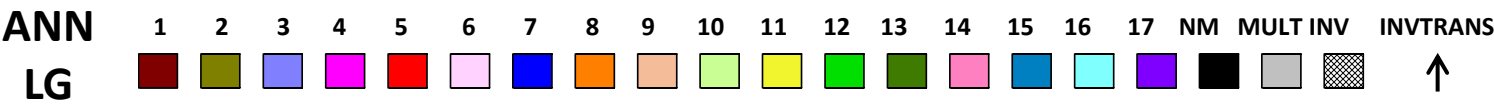
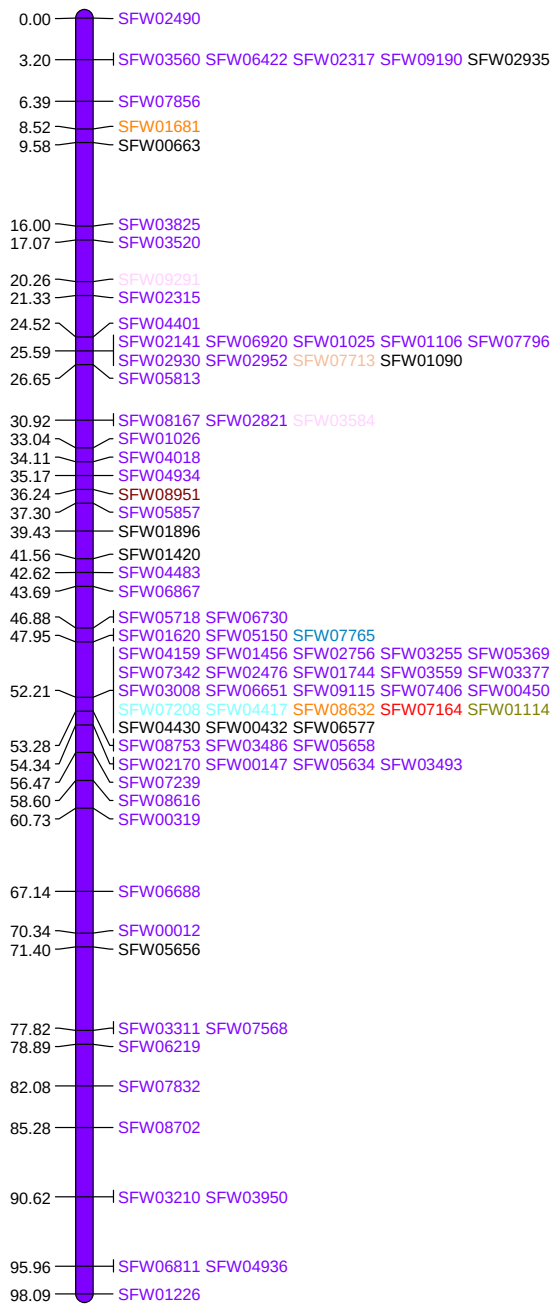


Figure S3 continued

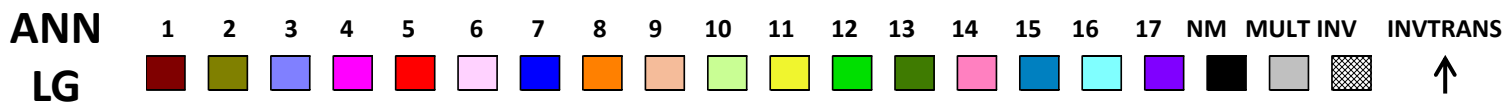
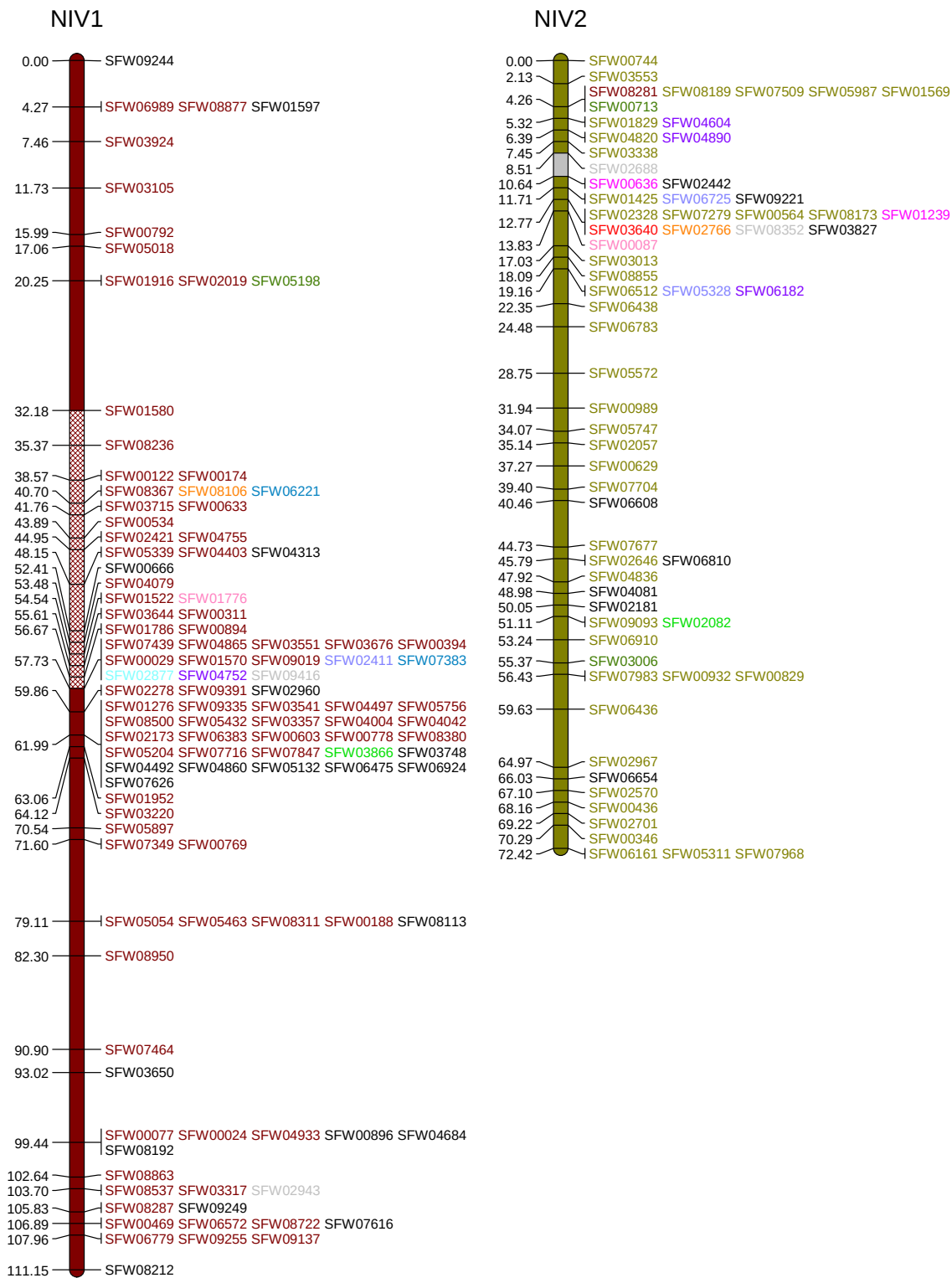


Figure S3 continued

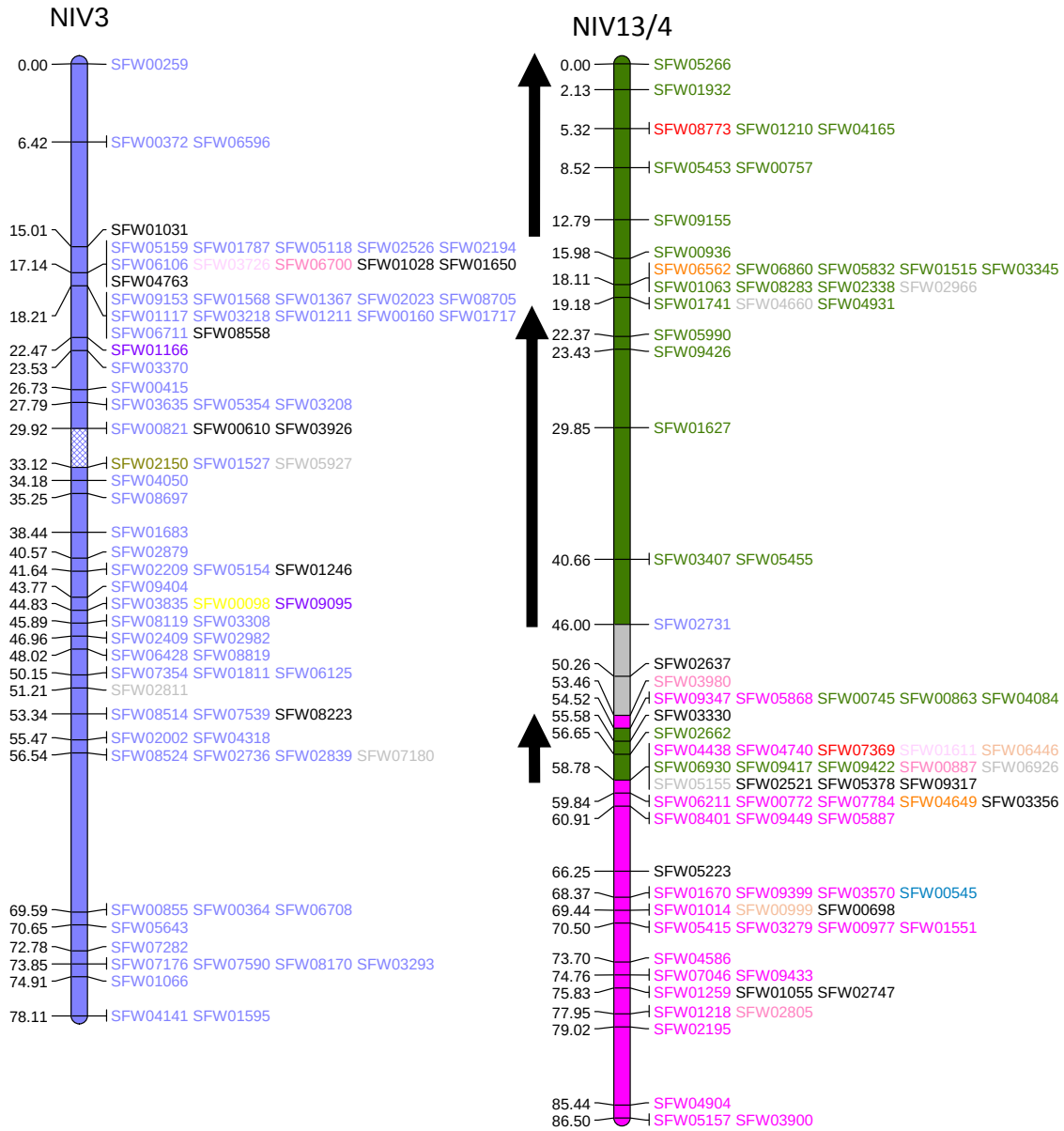
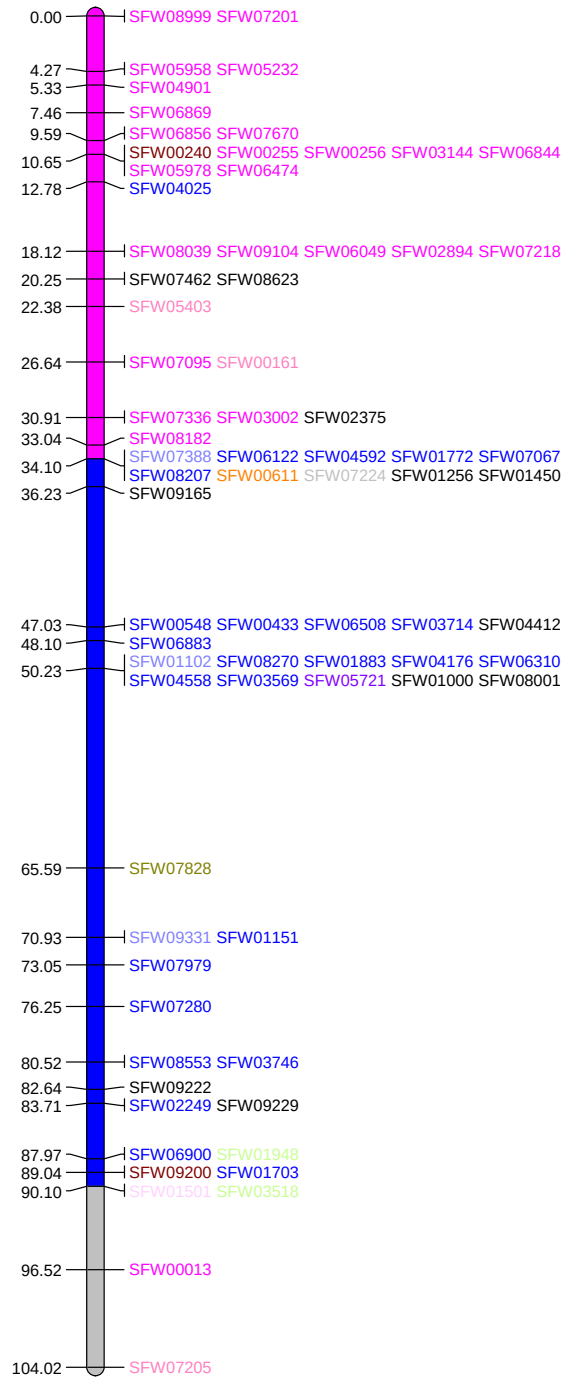
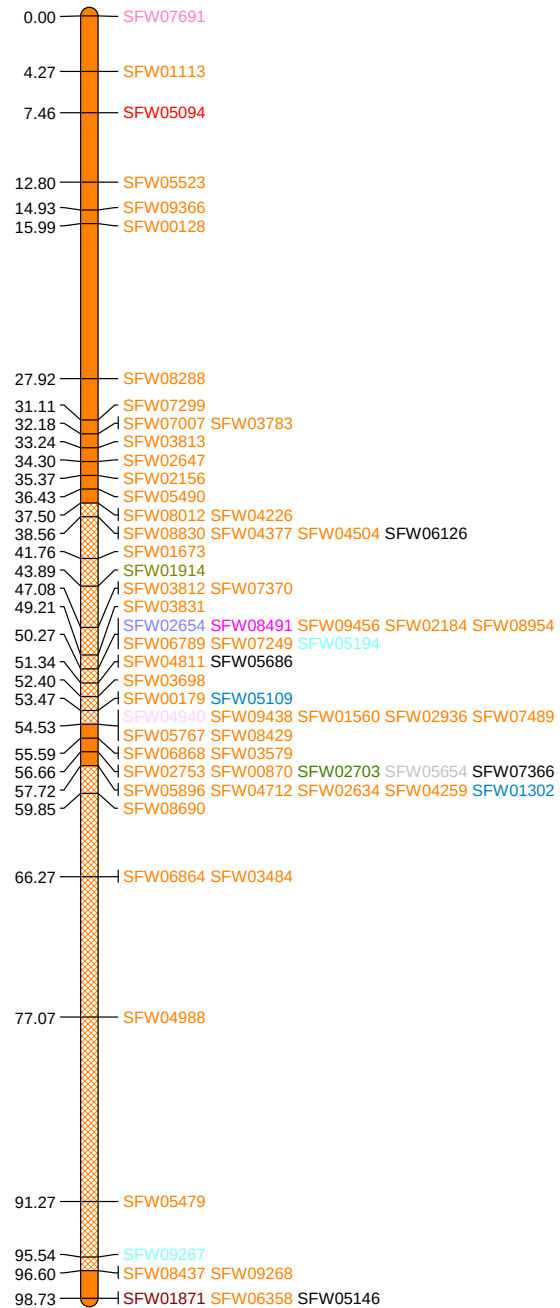


Figure S3 continued

NIV4/7



NIV8



ANN
LG



Figure S3 continued

NIV13



NIV14

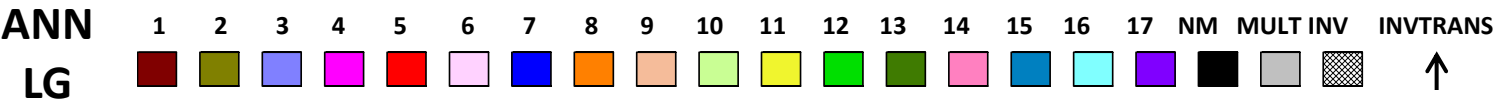
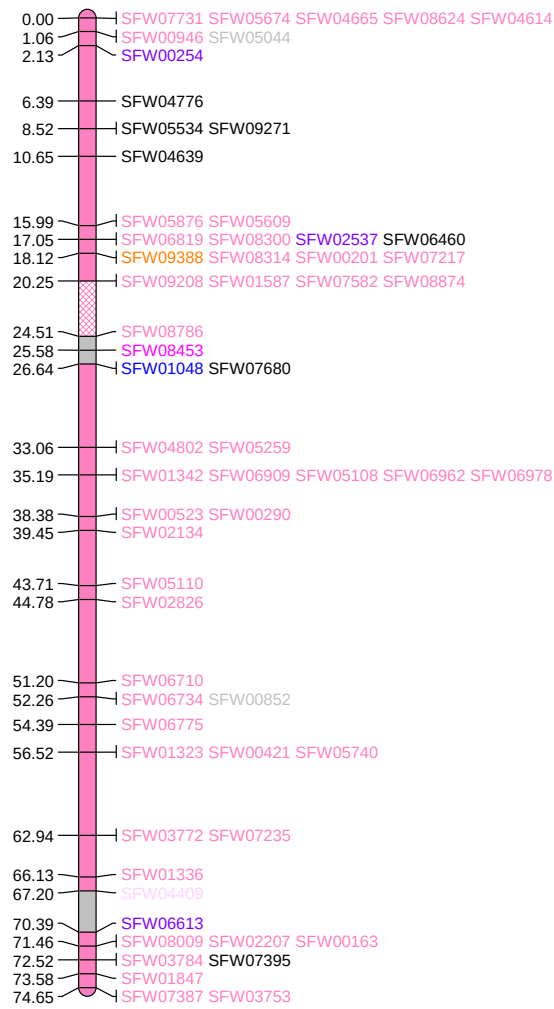


Figure S3 continued

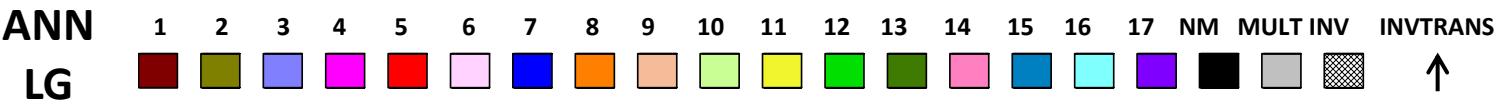
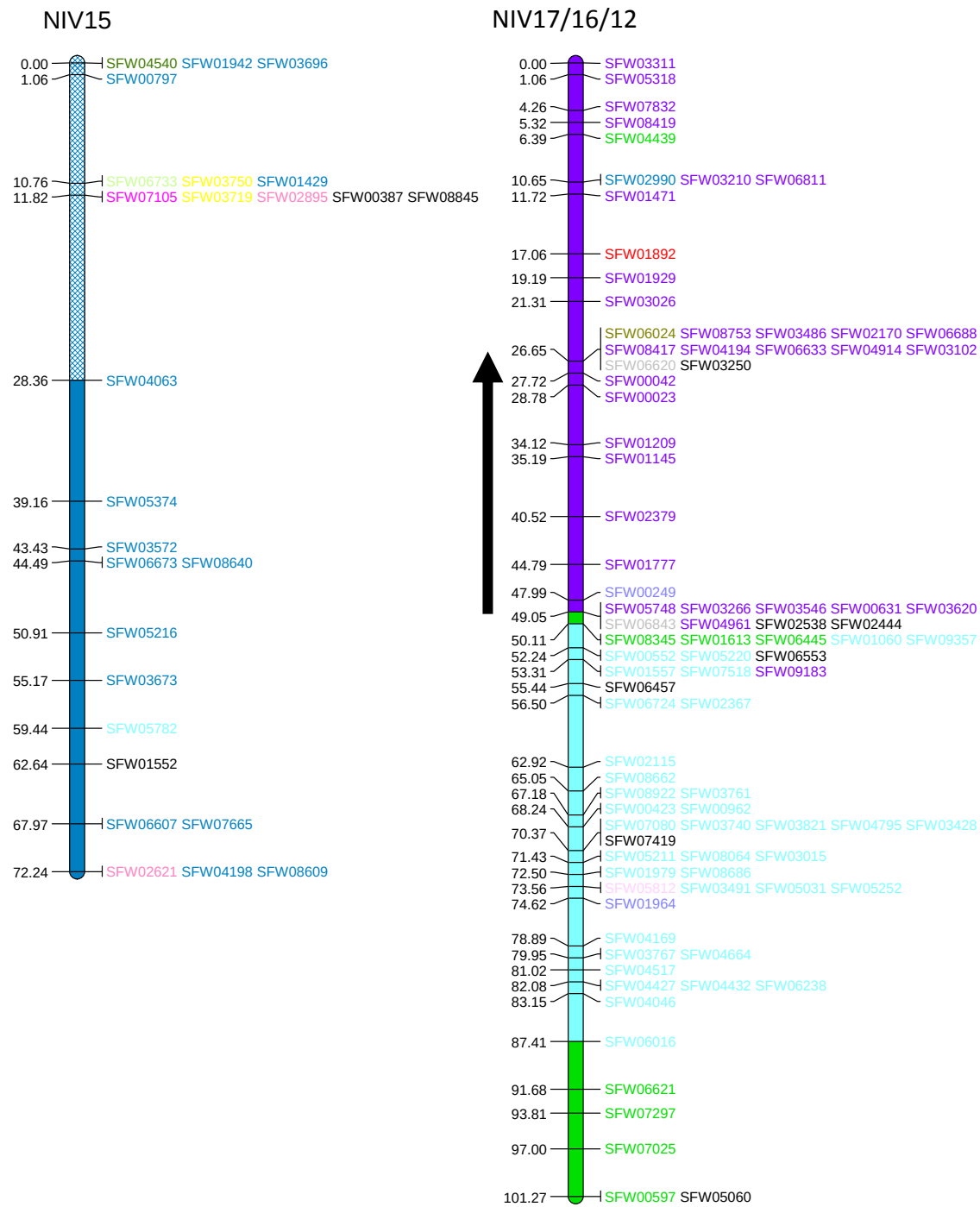


Figure S3 continued

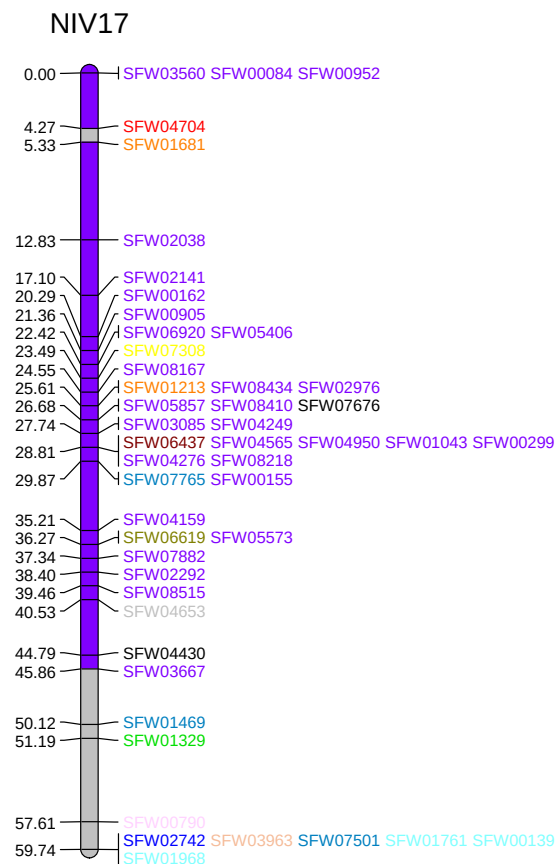


Figure S3 continued

Figure S4 Genetic maps of *Helianthus argophyllus* (ARG) and *H. niveus* ssp. *tephrodes* (NIV) compared to a consensus *H. annuus* (ANN) map (Bowers *et al.* 2012). Color coding and chromosome nomenclature follow Figure 1. ARG and NIV markers are color coded to represent the LG that they were mapped to on the ANN consensus map. ANN markers are color coded to represent the LG that they were mapped to on the ARG and NIV maps, respectively. Markers colored in black (NM) were not mapped on the ANN consensus map. Markers colored in gray (MULT) were mapped to multiple LGs in ANN, but not to that particular LG in ARG or NIV, respectively. Homologous markers are connected by lines. Inverted segments are indicated with cross hatching. Synteny and collinearity were assumed in regions of conflicting data, and markers violating synteny or collinearity in these regions were identified (bold, underlined). Marker names have been abbreviated (SFW = S). Only ANN markers mapped in ARG or NIV are included in this figure.

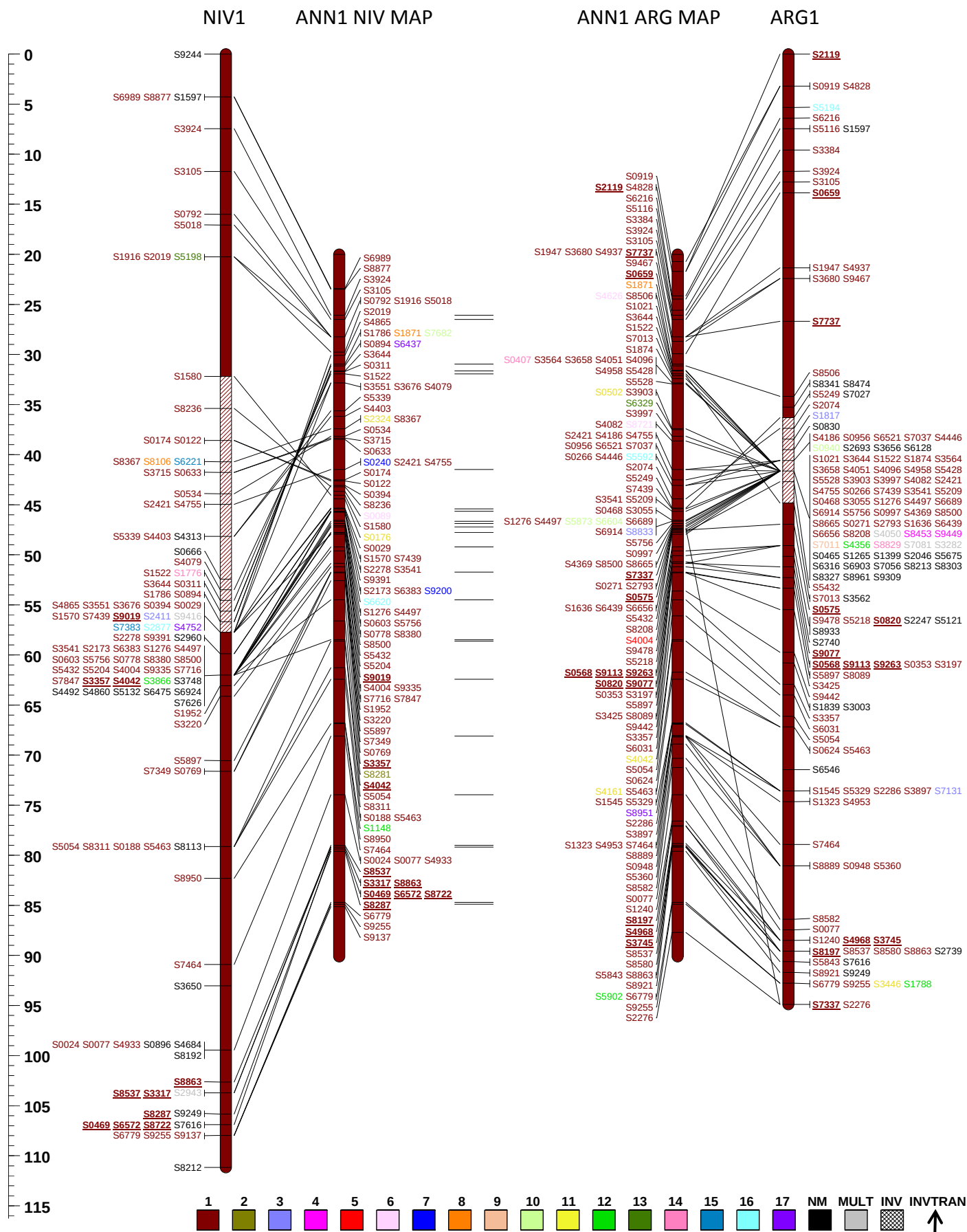


Figure S4 continued

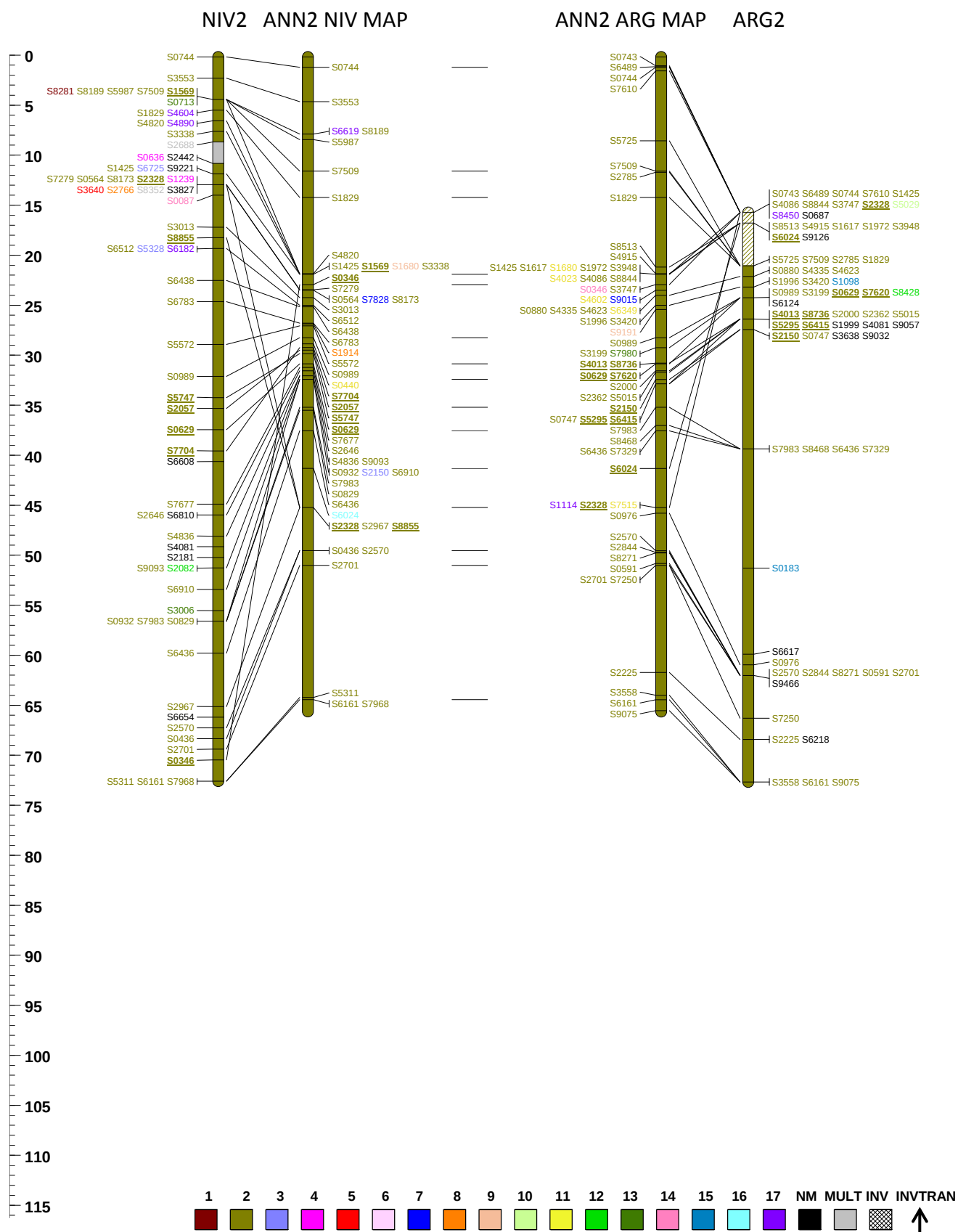


Figure S4 continued

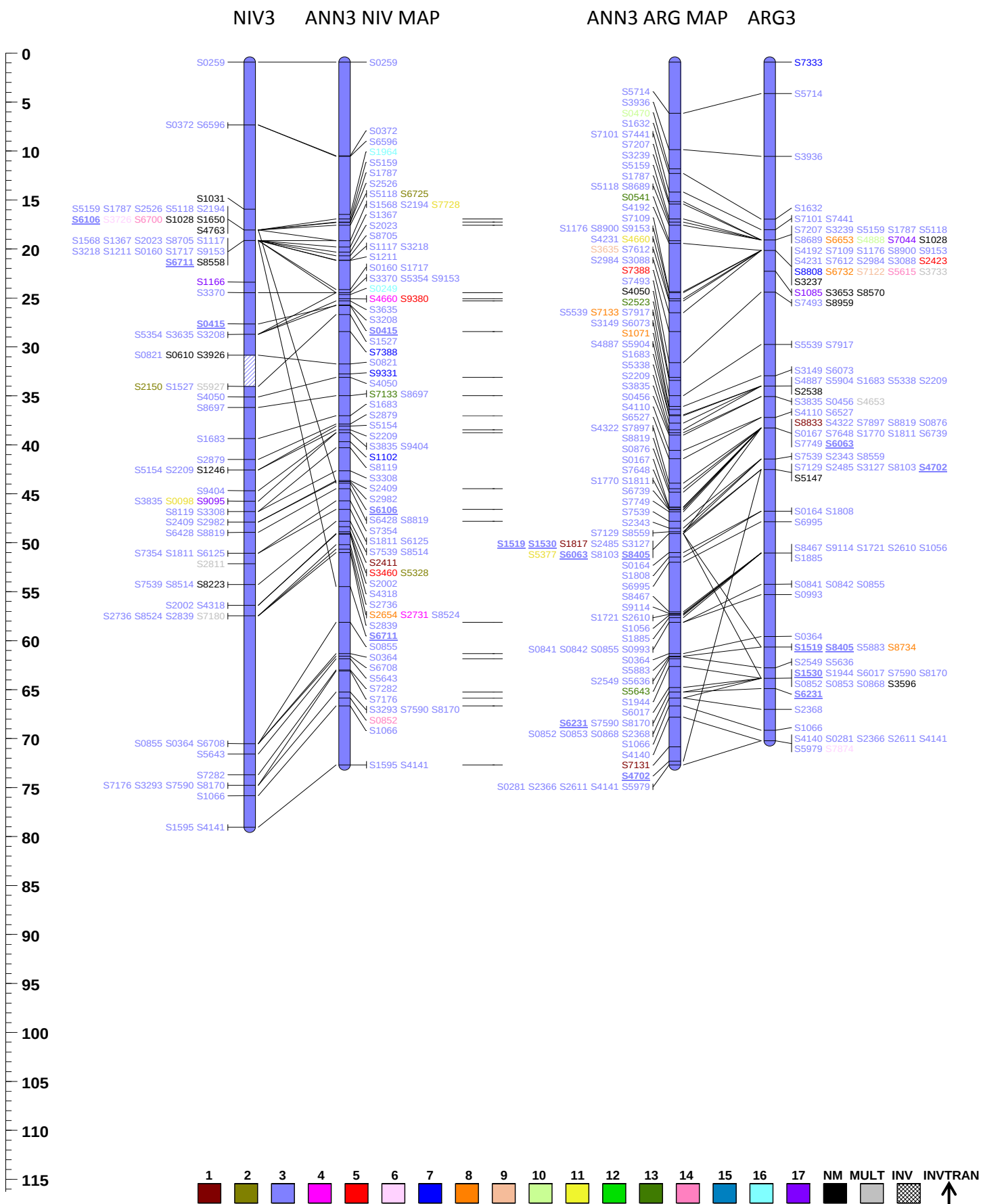


Figure S4 continued

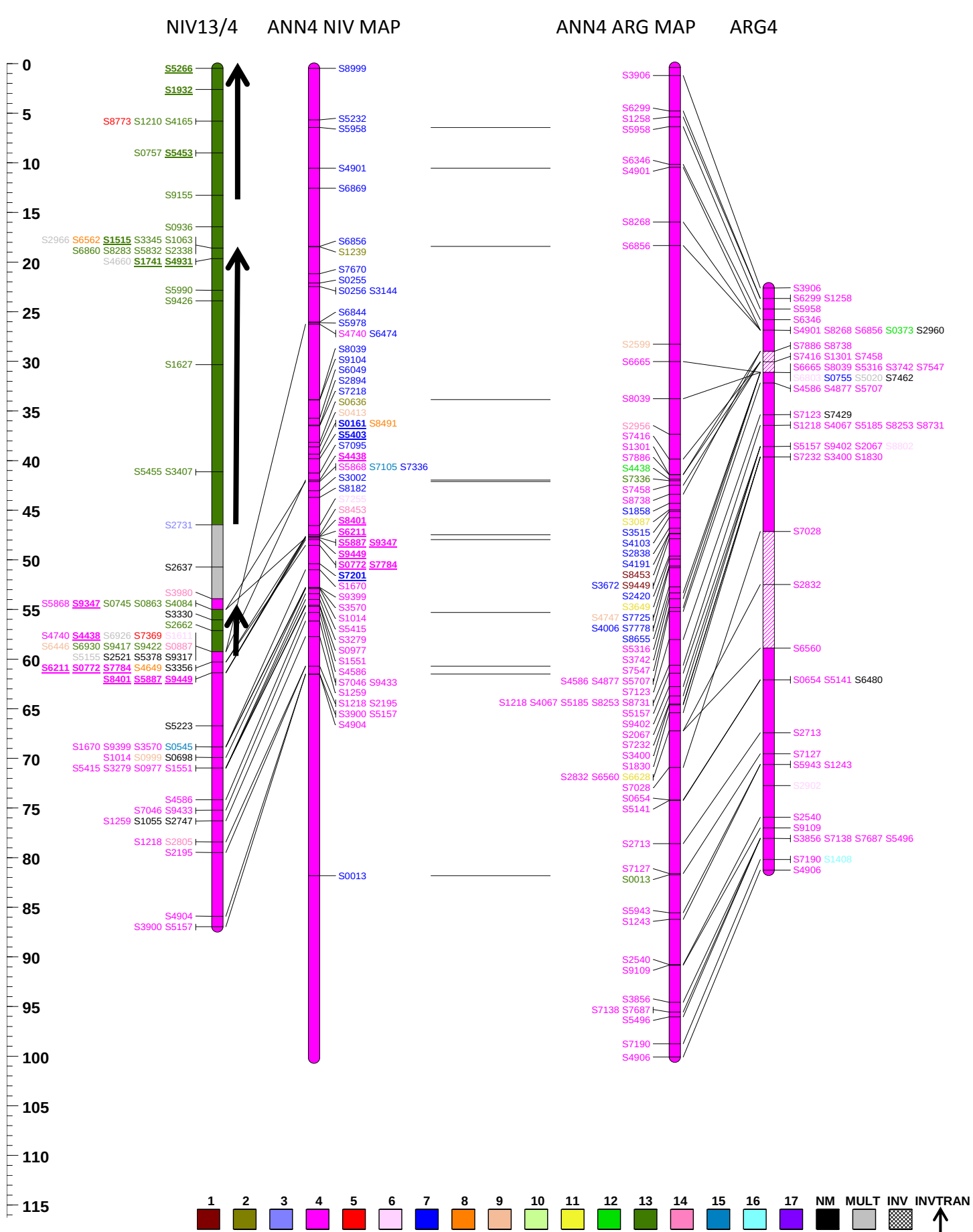
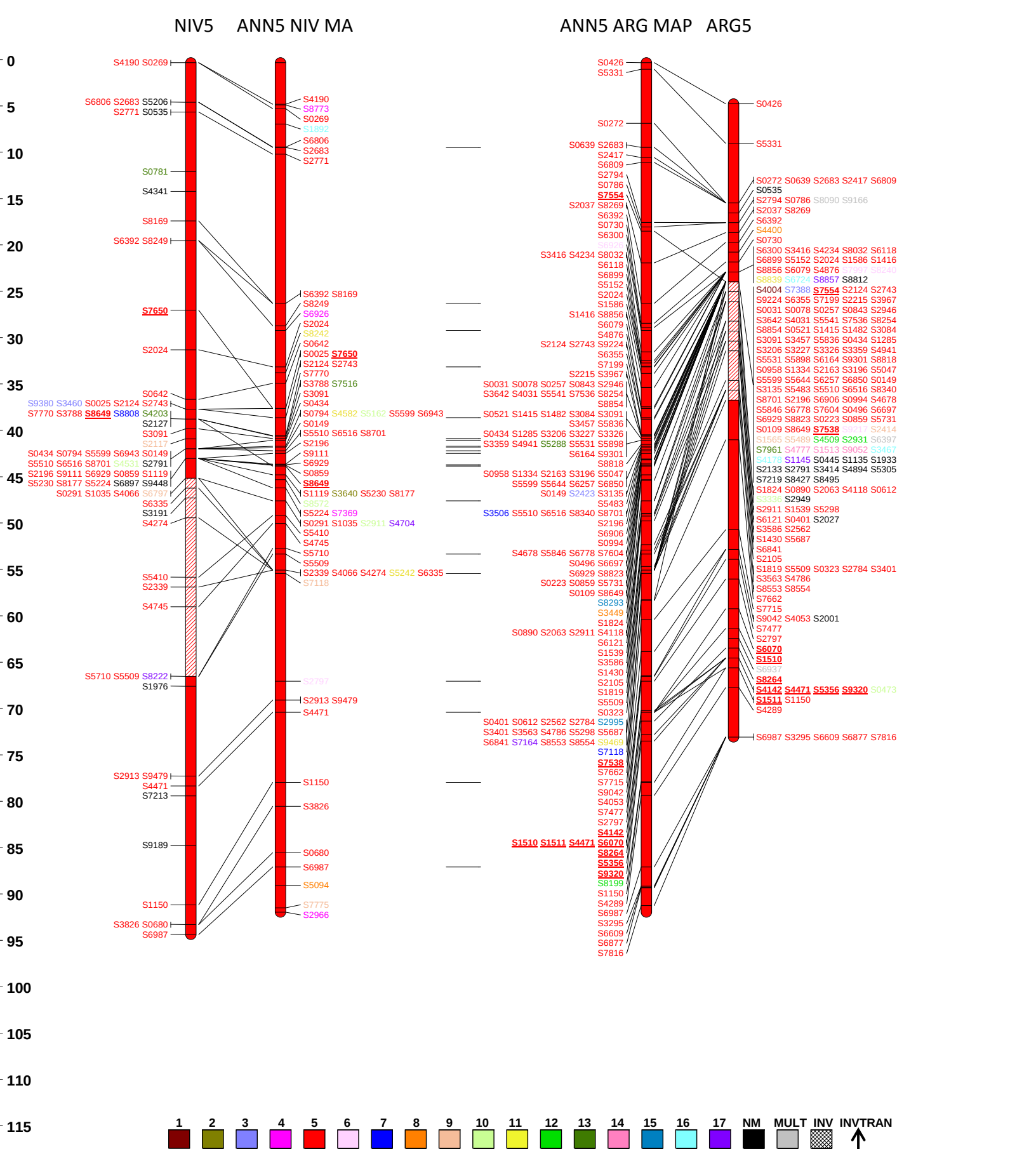


Figure S4 continued



NIV6/15 ANN6 NIV MAP

ANN6 ARG MAP

ARG6/15

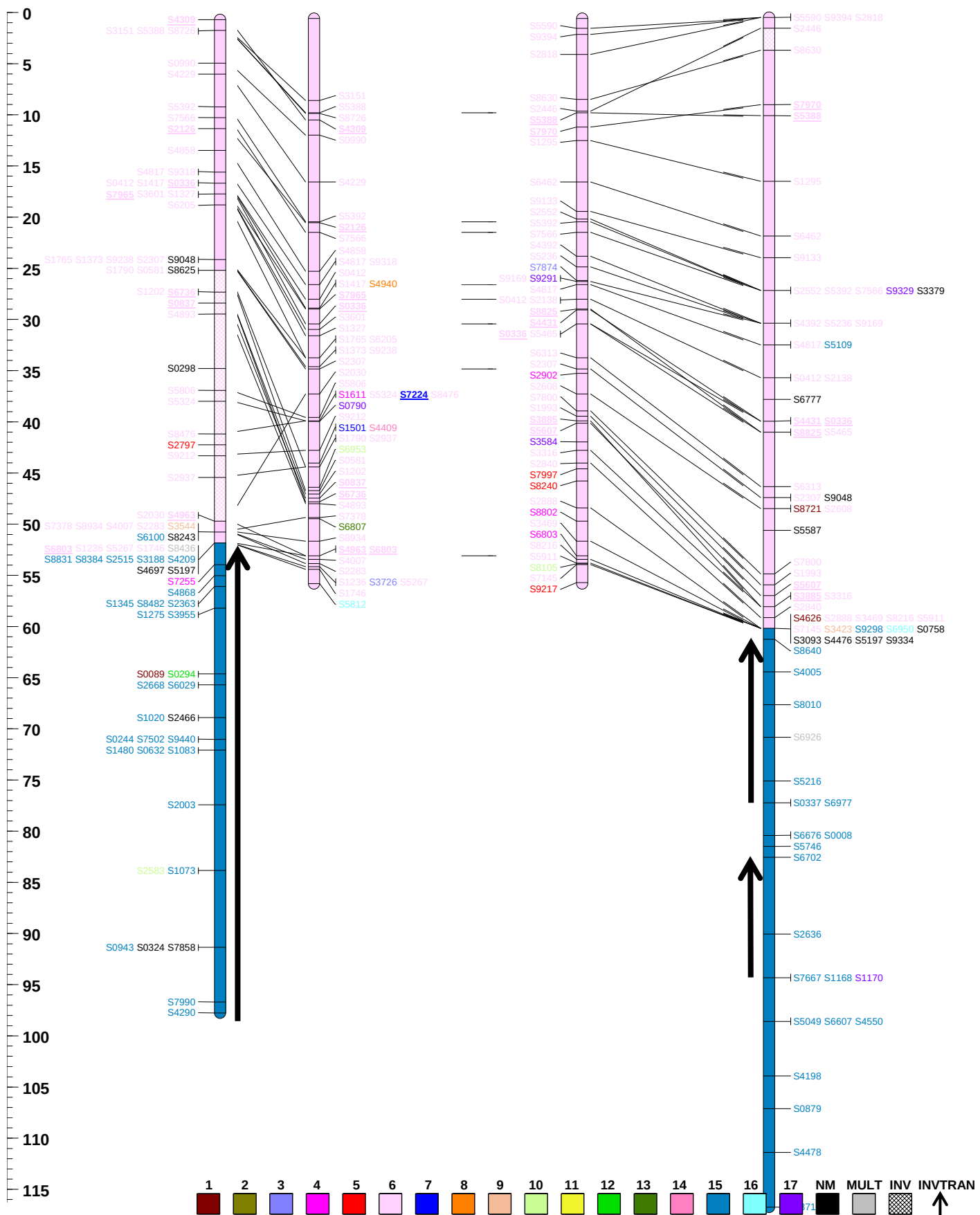


Figure S4 continued

ANN7 ARG MAP ARG4/7

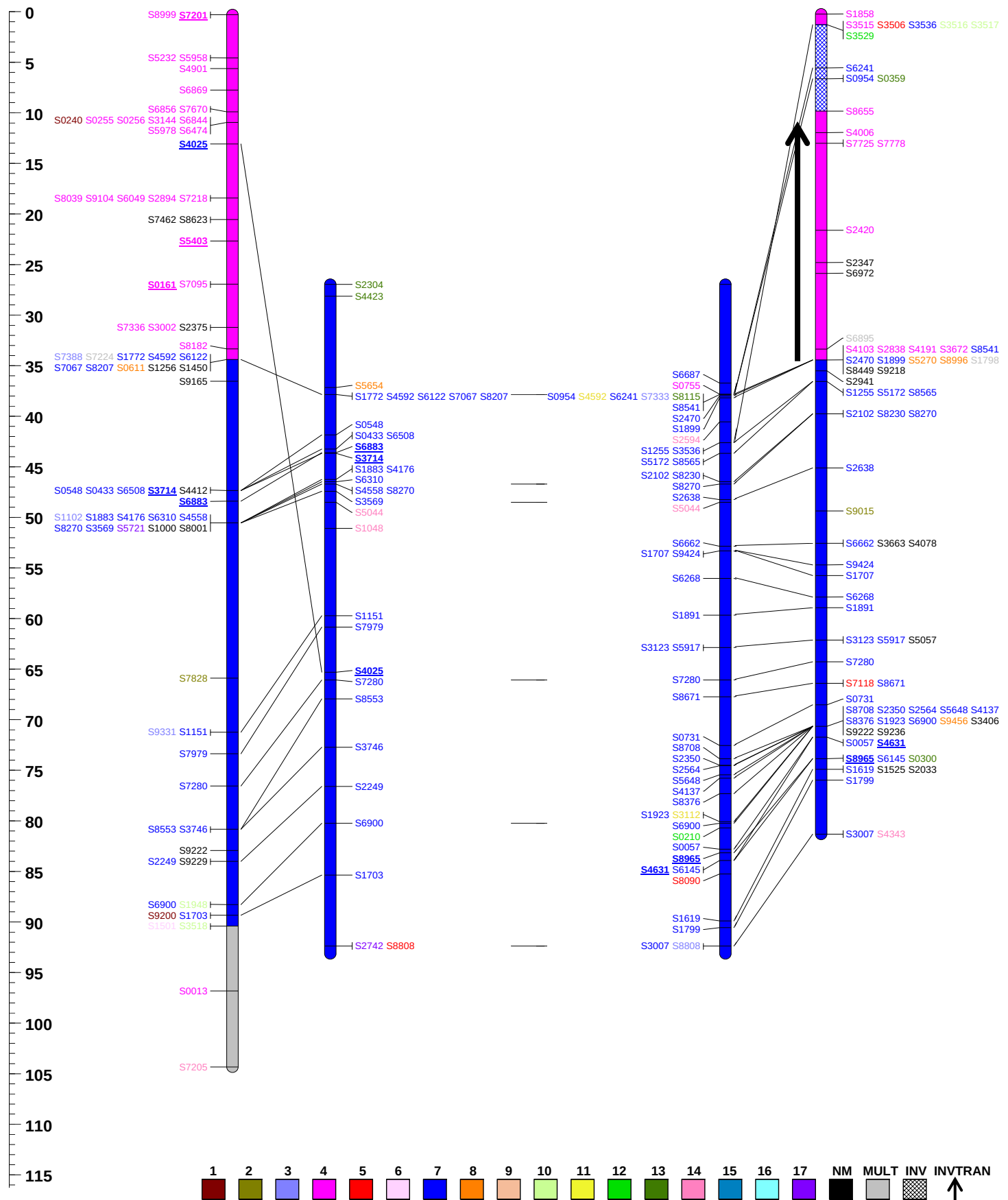


Figure S4 continued

NIV9 ANN9 NIV MAP

NN9 ARG MAP ARG9

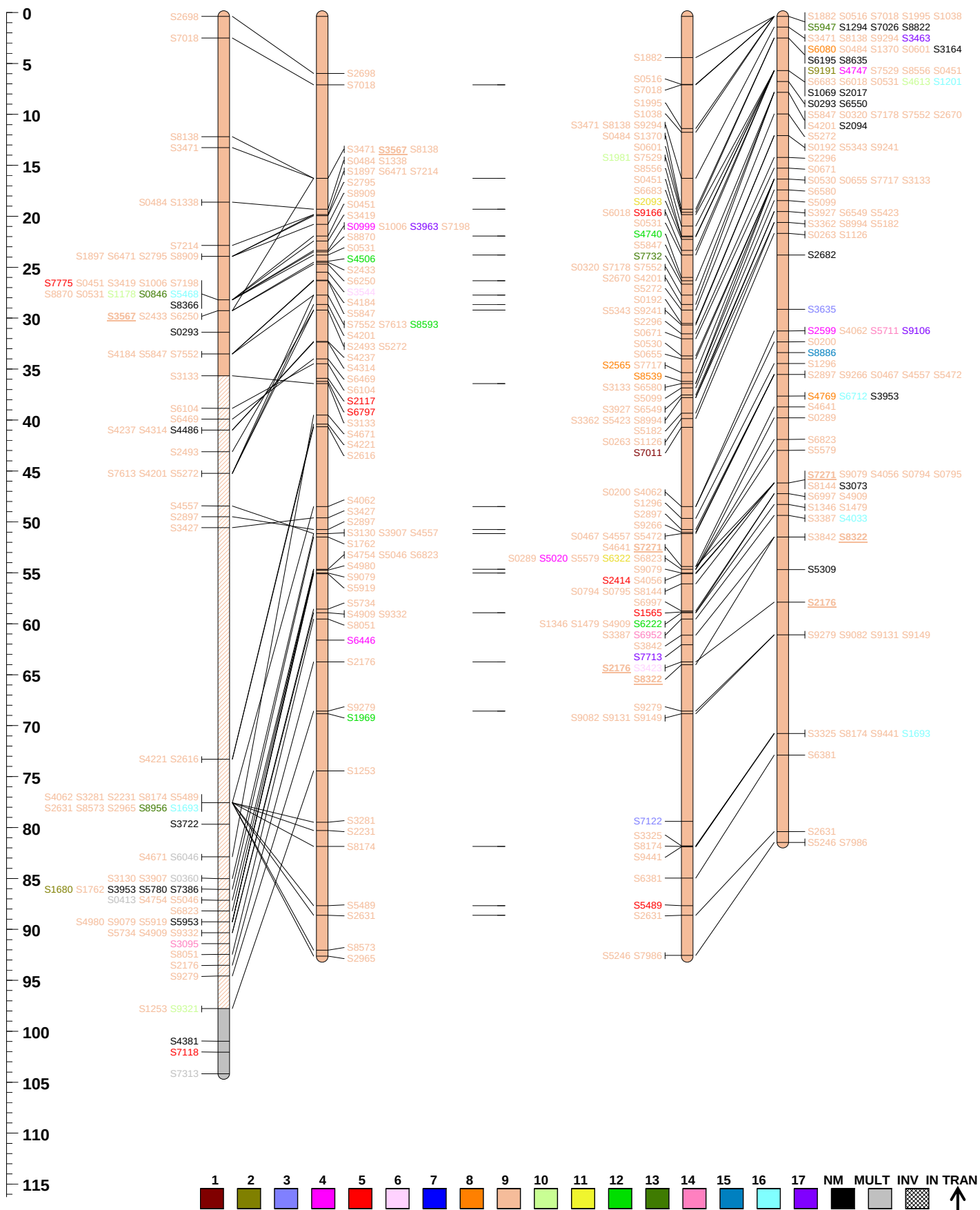


Figure S4 continued

NIV10 ANN10 NIV MAP

ANN10 ARG MAP

ARG10

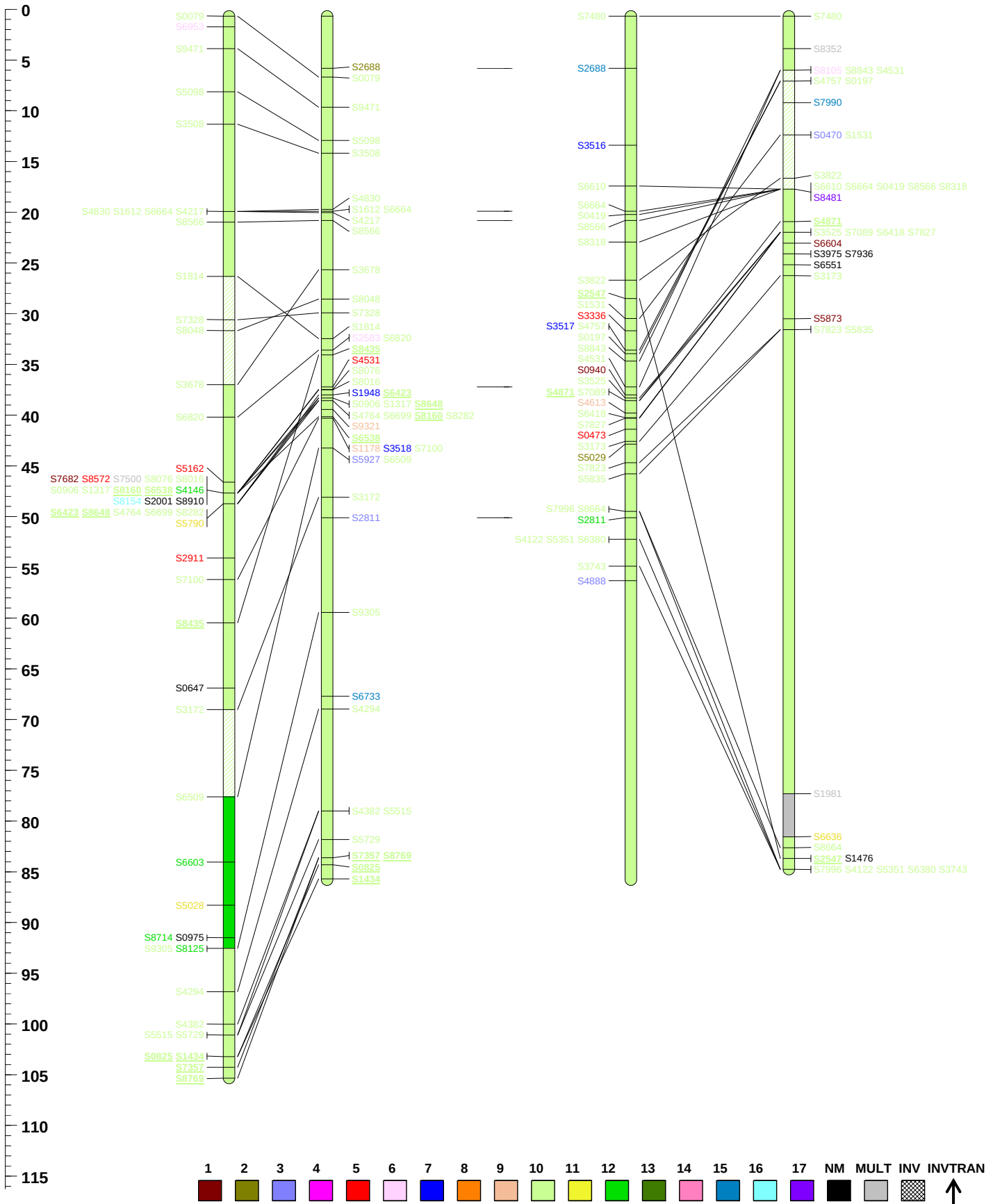


Figure S4 continued

ANN11 ARG MAP ARG11

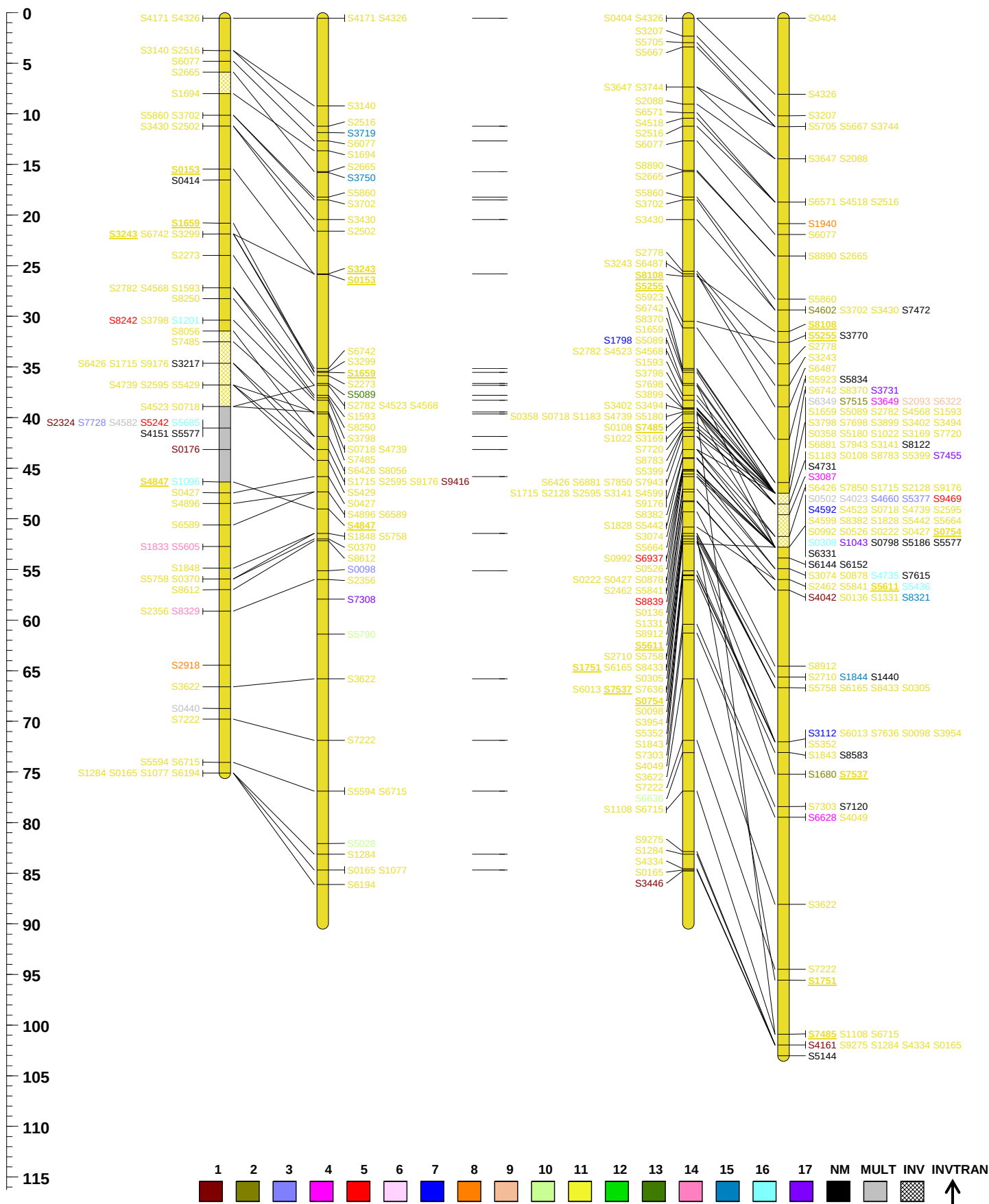


Figure S4 continued

ANN12 ARG MAP ARG12/16

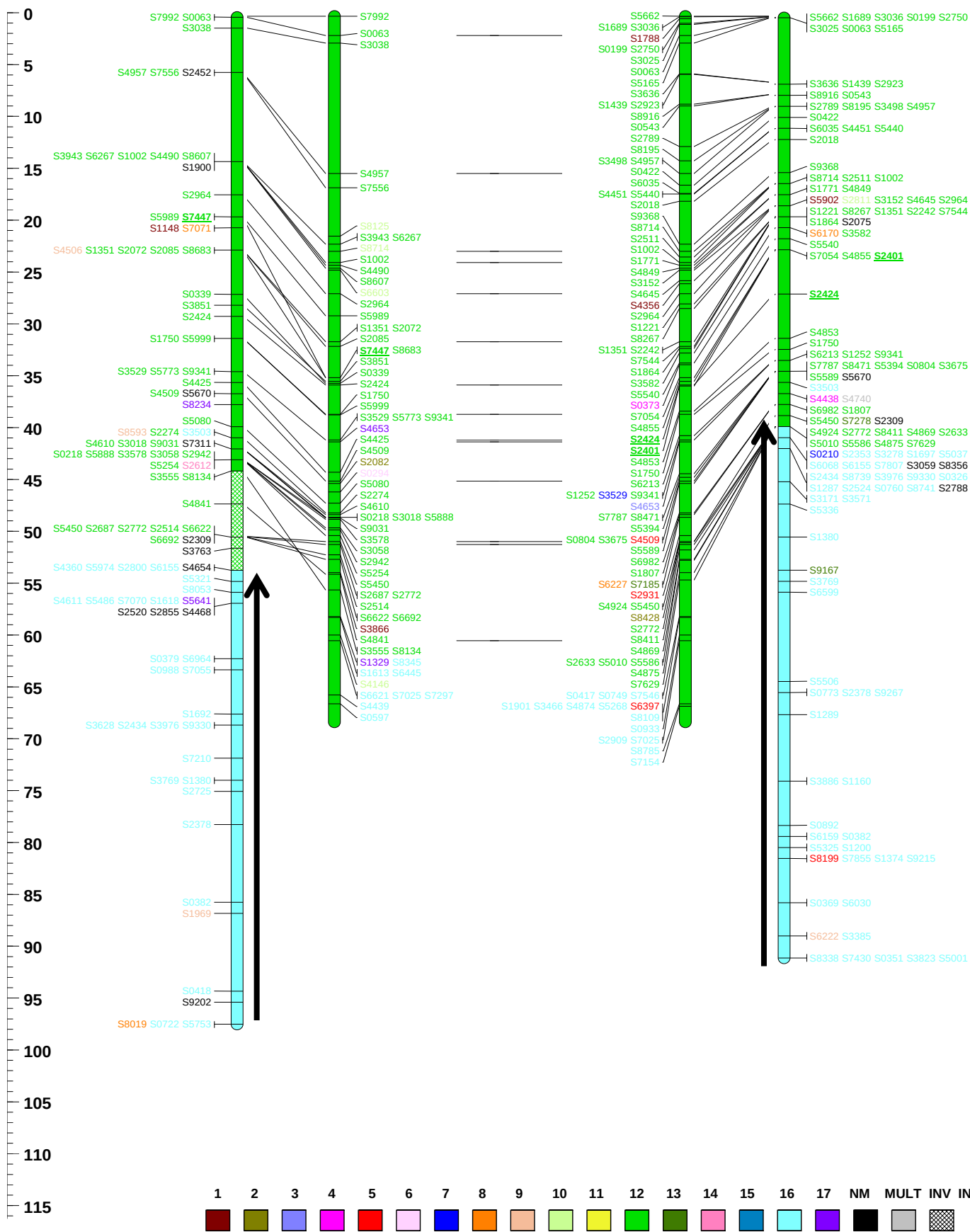
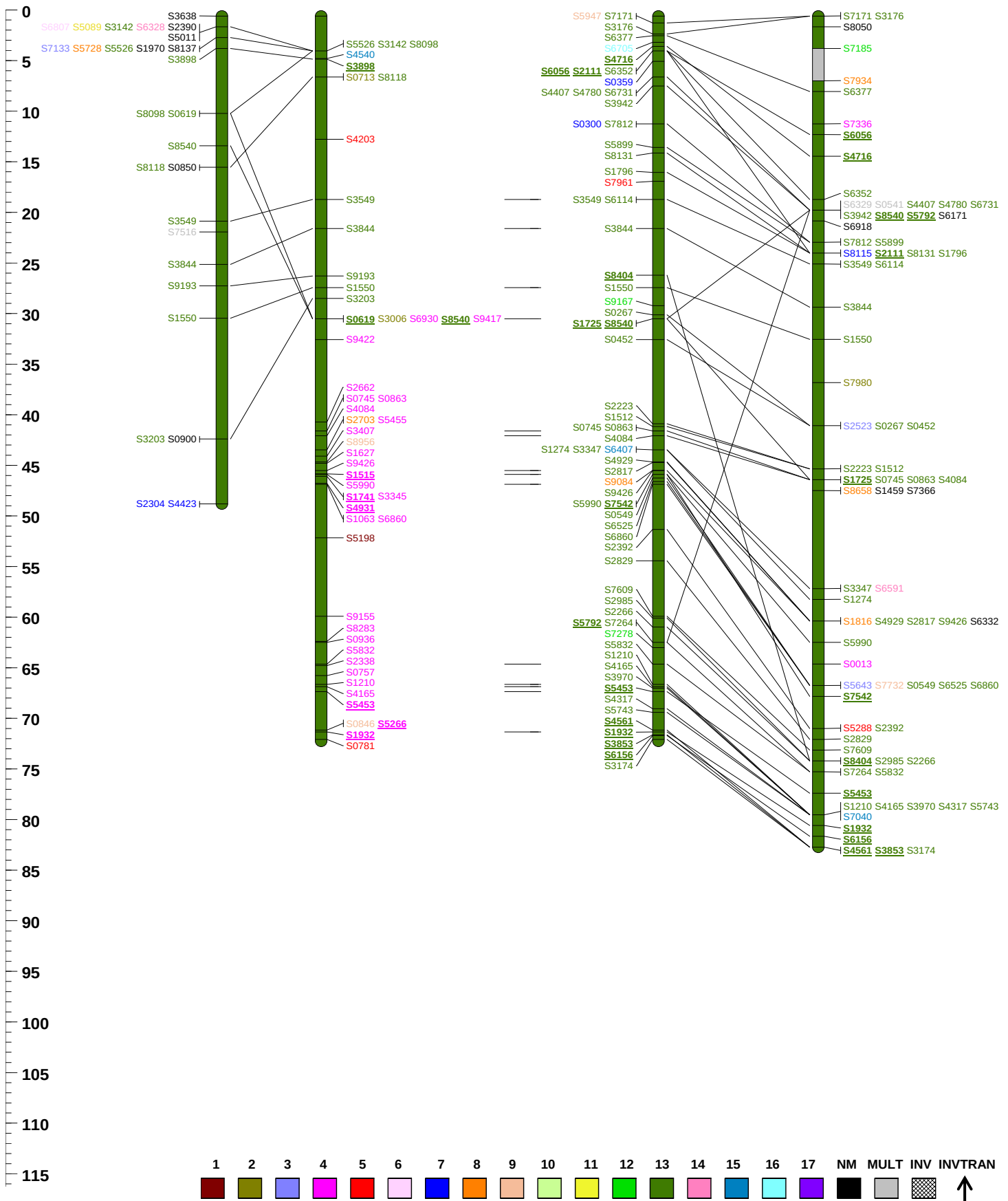


Figure S4 continued

NIV13 ANN13 NIV MAP

ANN13 ARG MAP

ARG13



NIV14 ANN14 NIV MAP

ANN14 ARG MAP ARG14

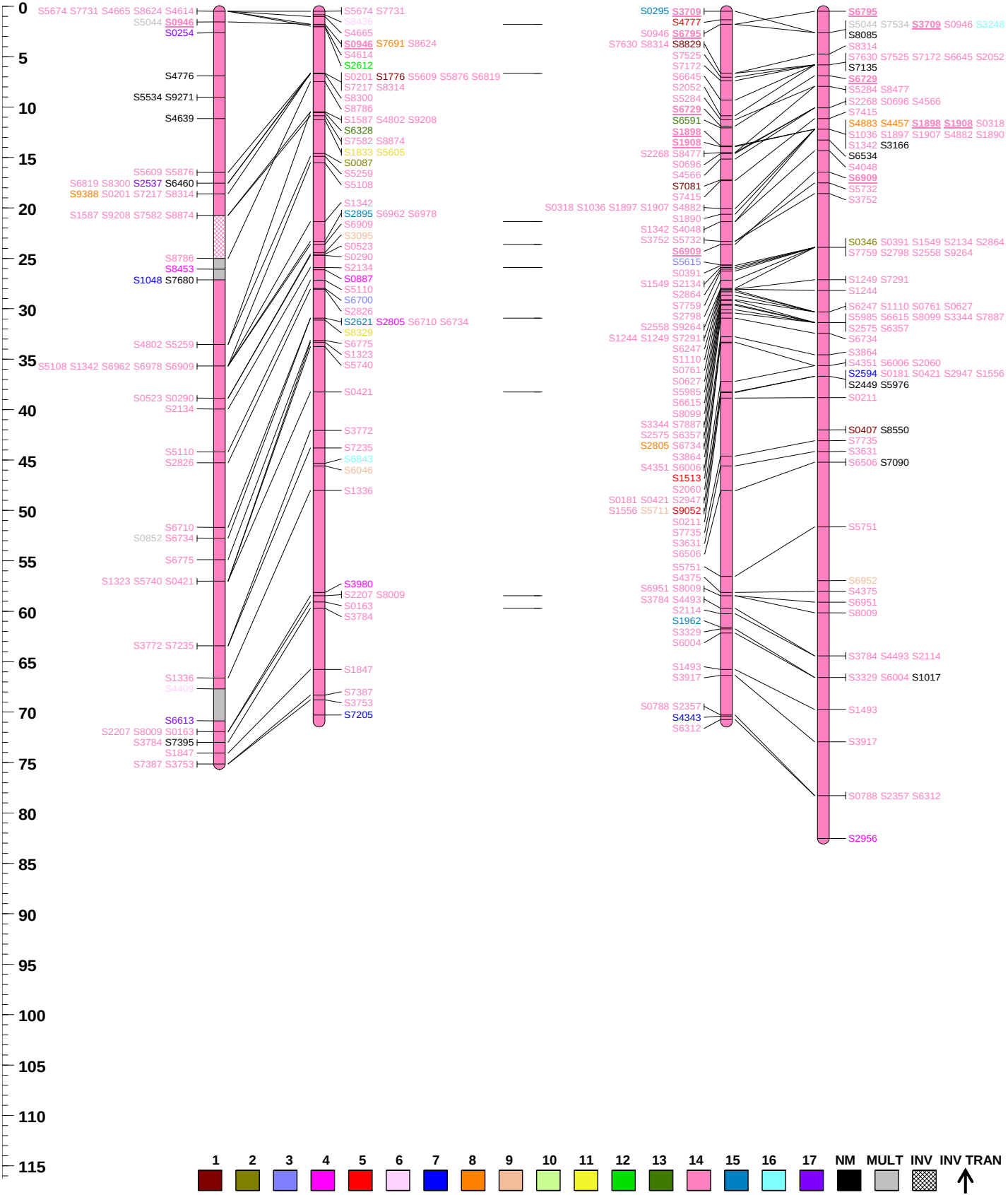
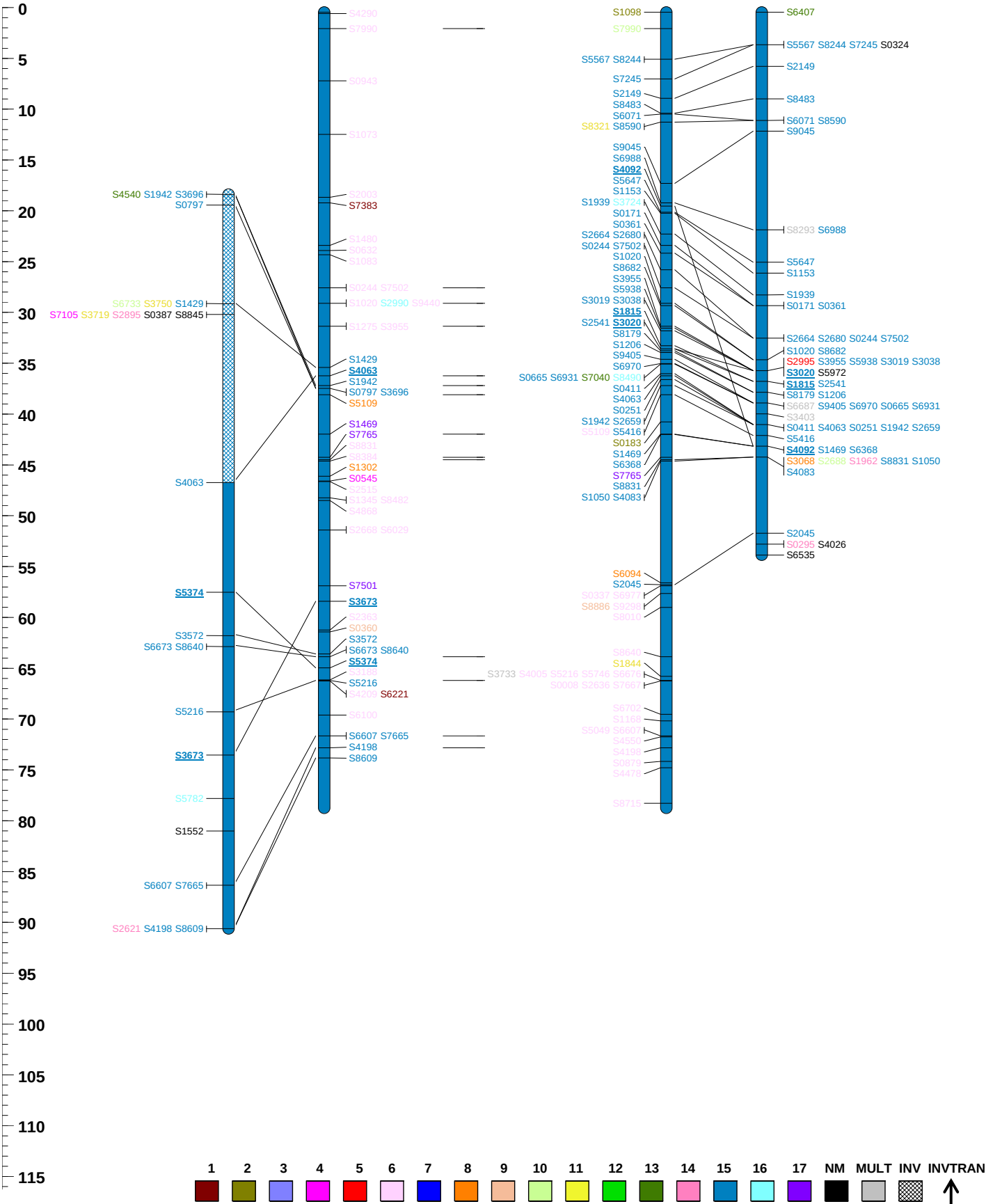


Figure S4 continued

NIV15 ANN15 NIV MAP

ANN15 ARG MAP ARG15



NIV17/16/12 ANN16 NIV MAP

ANN16 ARG MAP ARG16/12

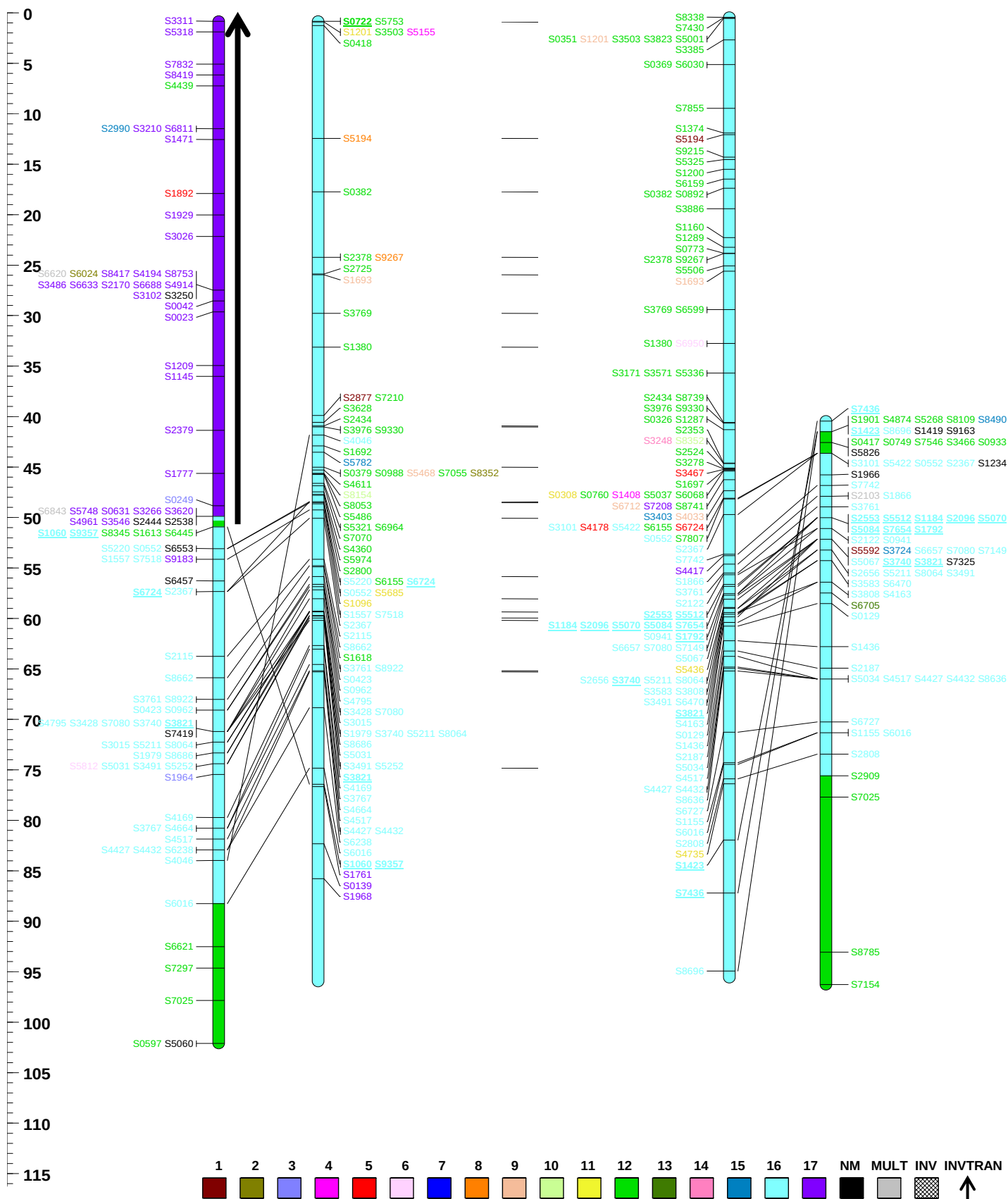


Figure S4 continued

NIV17 ANN17 NIV MAP

ANN17 ARG MAP ARG17

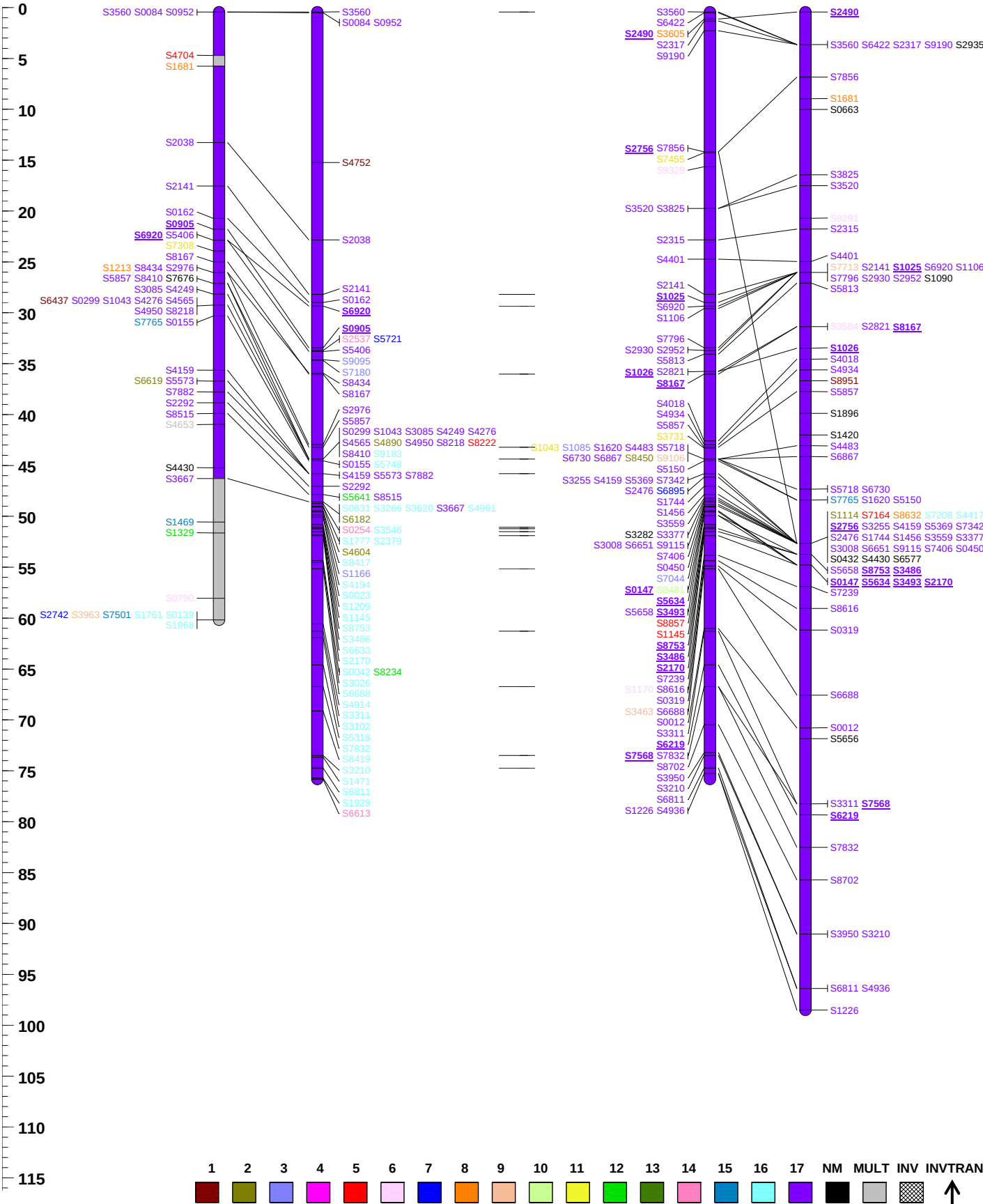


Figure S5 Genetic maps of *Helianthus argophyllus* (ARG) and *H. niveus* ssp. *tephrodes* (NIV) compared to a consensus *H. annuus* (ANN) map (Bowers *et al.* 2012). Only the 295 SNP markers mapped in all three species are included. Color coding and chromosome nomenclature follow Figure 1. ARG and NIV markers are color coded to represent the LG that they were mapped to on the ANN consensus map. ANN markers are color coded to represent the LG that they were mapped to on the ARG and NIV maps, respectively. Markers colored in black (NM) were not mapped on the ANN consensus map. Markers colored in gray (MULT) were mapped to multiple LGs in ANN, but not to that particular LG in ARG or NIV, respectively. Homologous markers are connected by lines. Inverted segments are indicated with cross hatching. Synteny and collinearity were assumed in regions of conflicting data, and markers violating synteny or collinearity in these regions were identified (bold, underlined). Marker names have been abbreviated (SFW = S). Only ANN markers mapped in ARG or NIV are included in this figure.

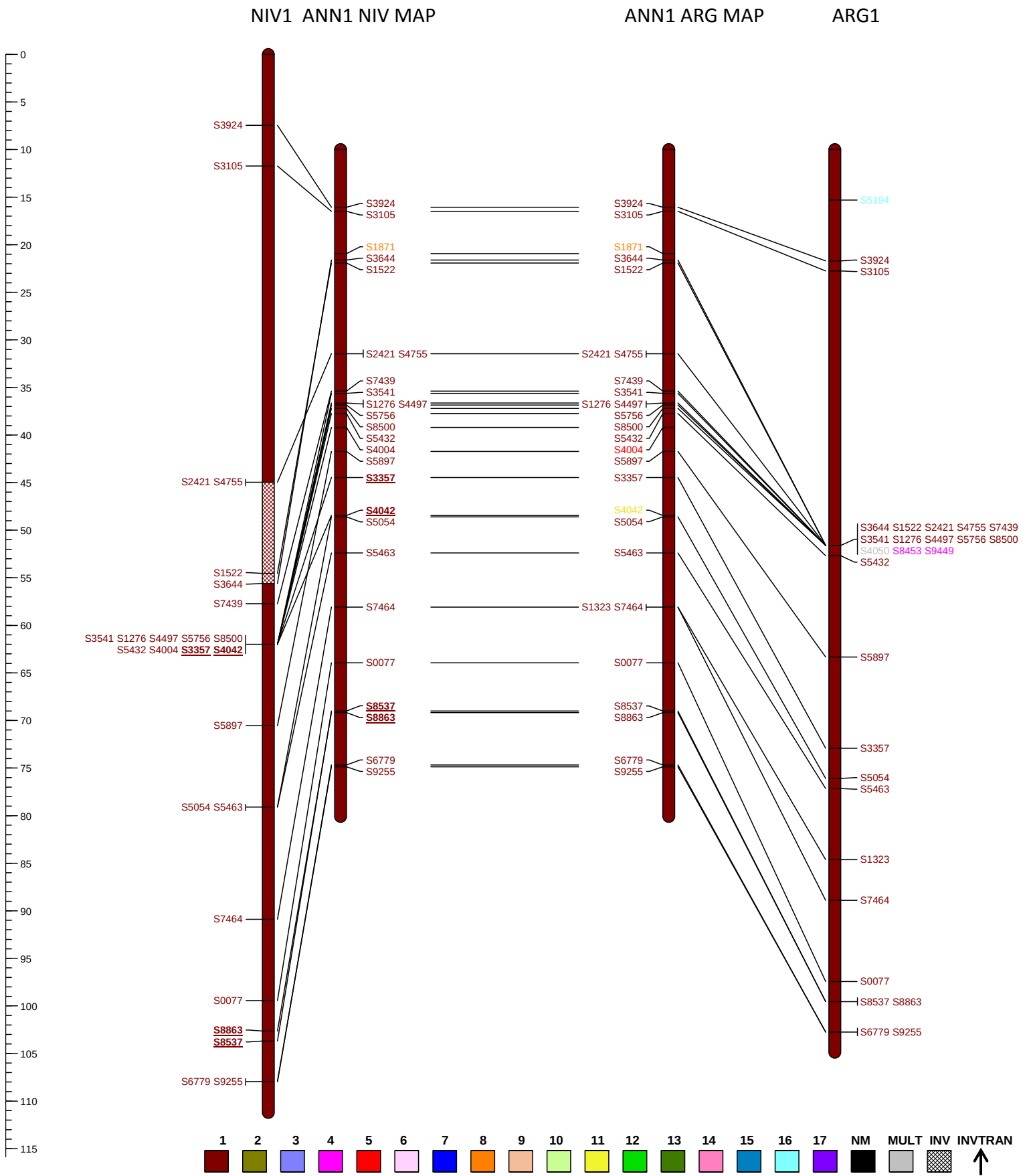


Figure S5 continued

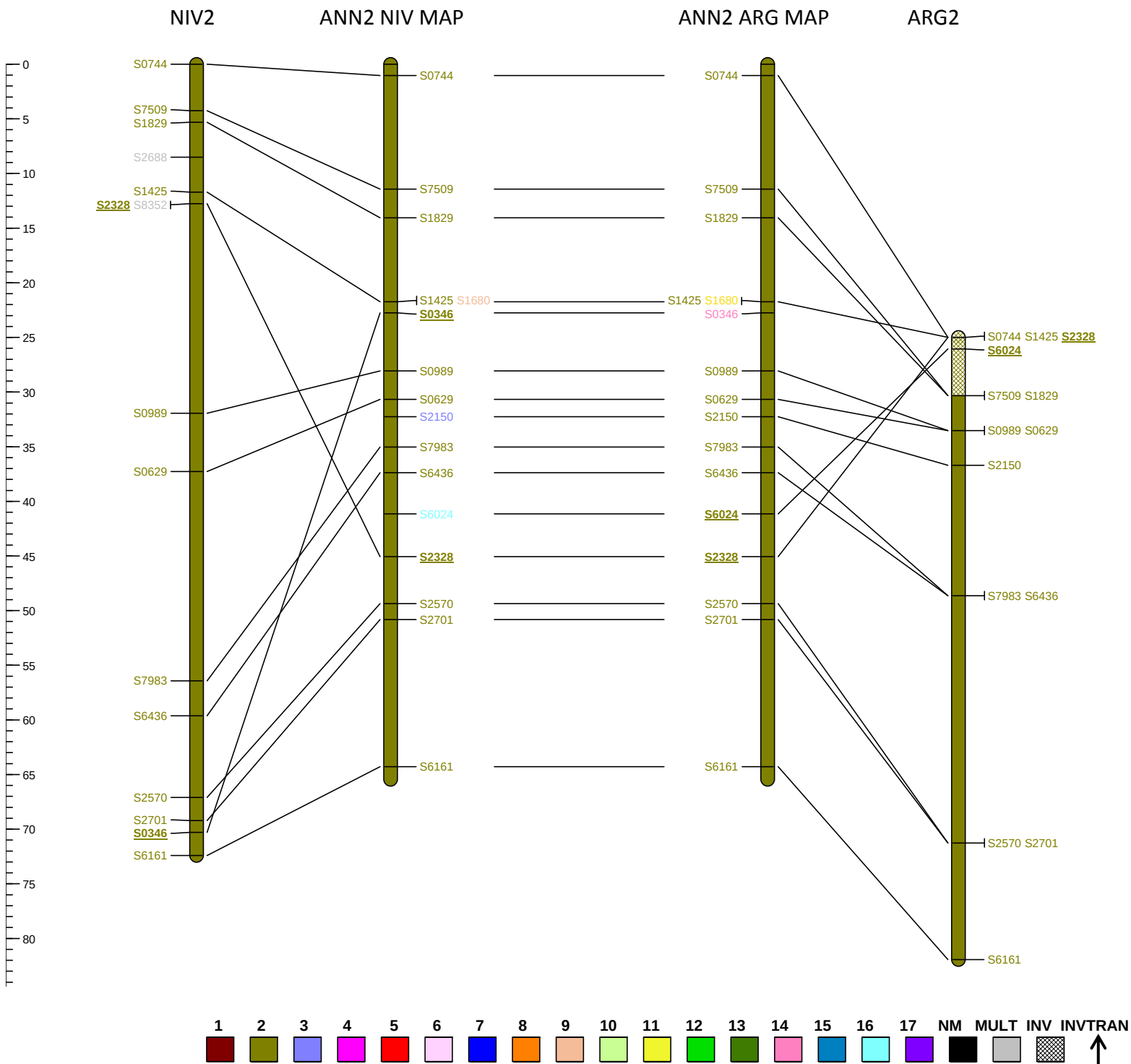


Figure S5 continued

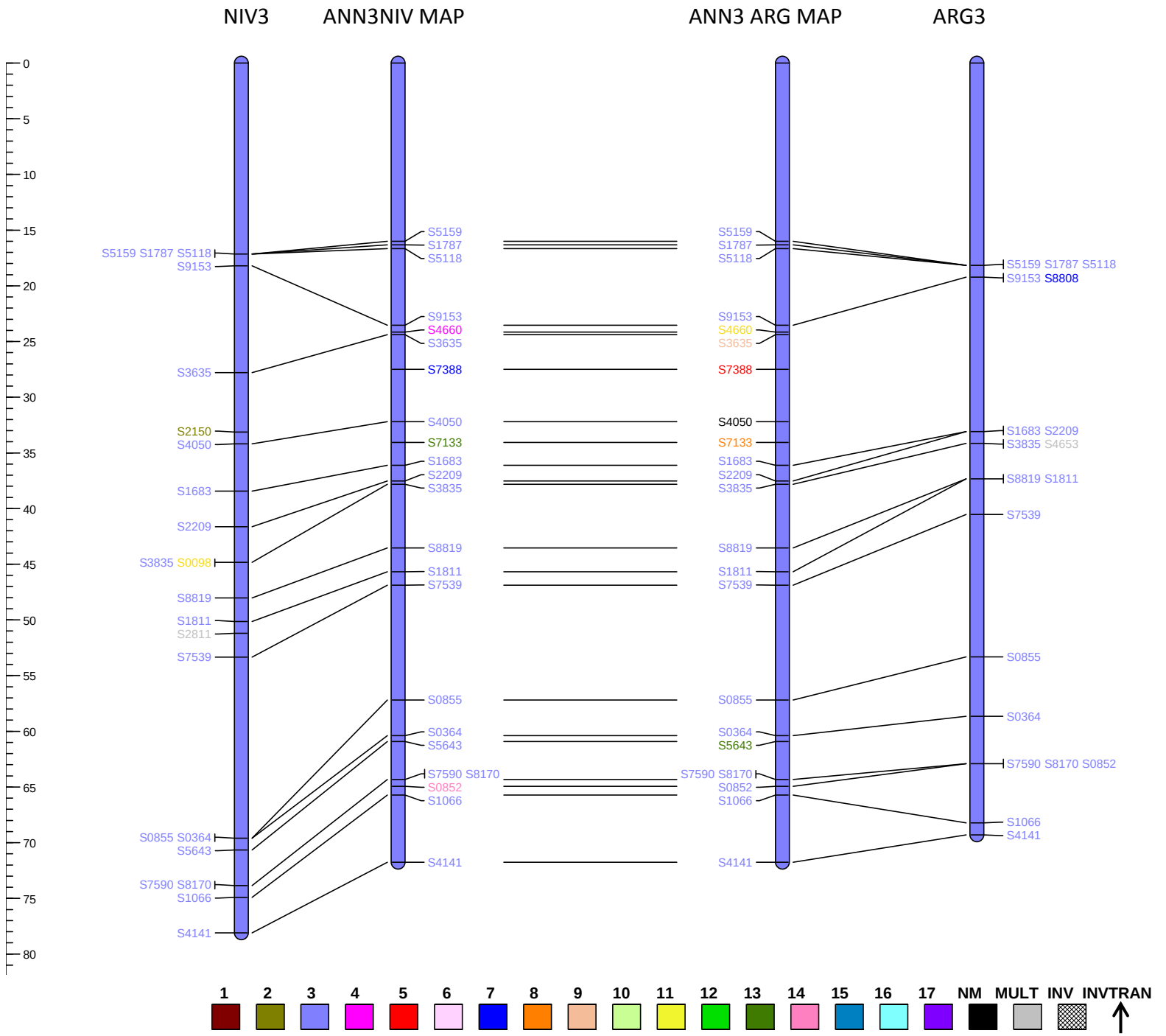


Figure S5 continued

NIV13/4

ANN4 NIV MAP

ANN4 ARG MAP

ARG4

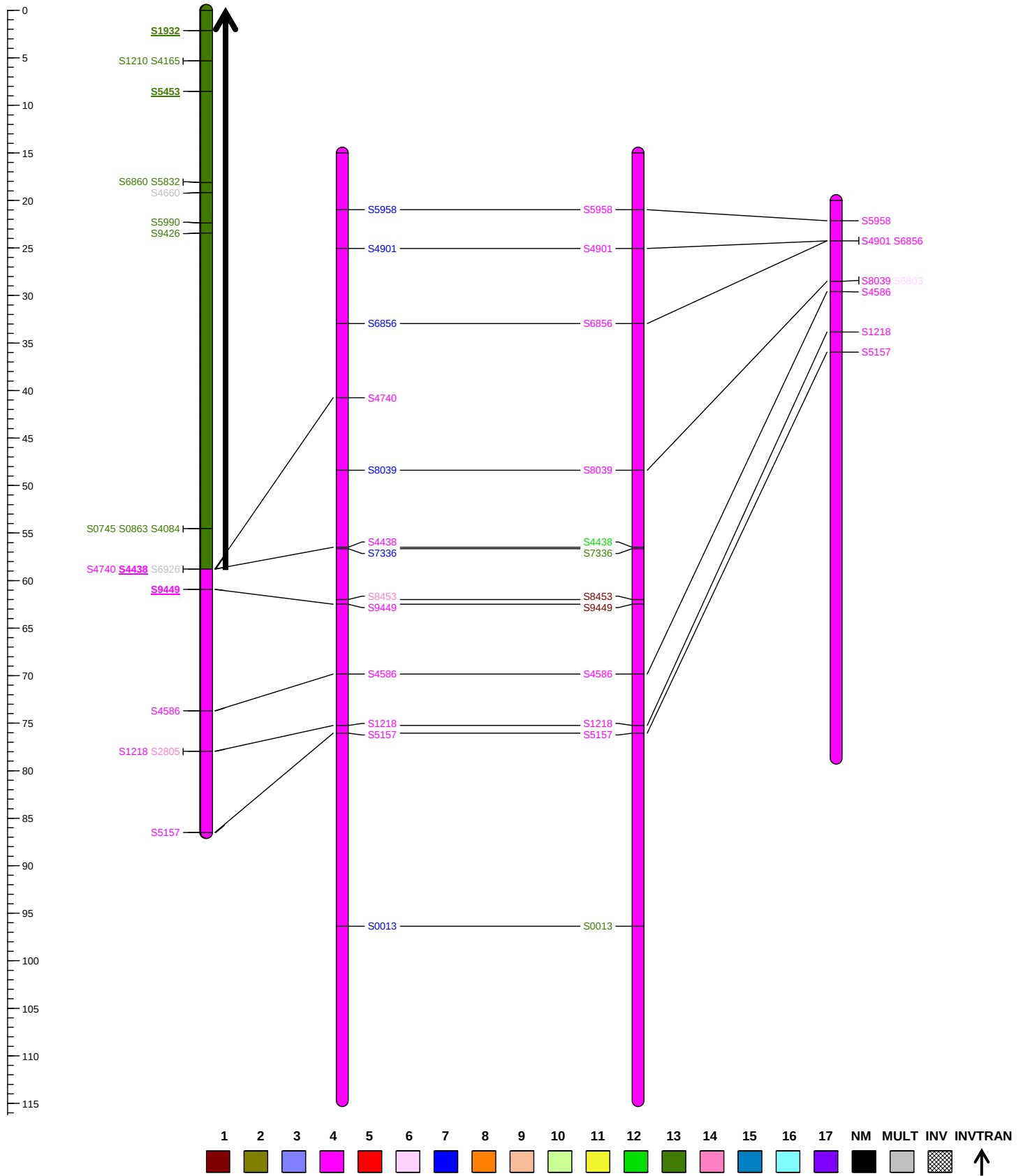


Figure S5 continued

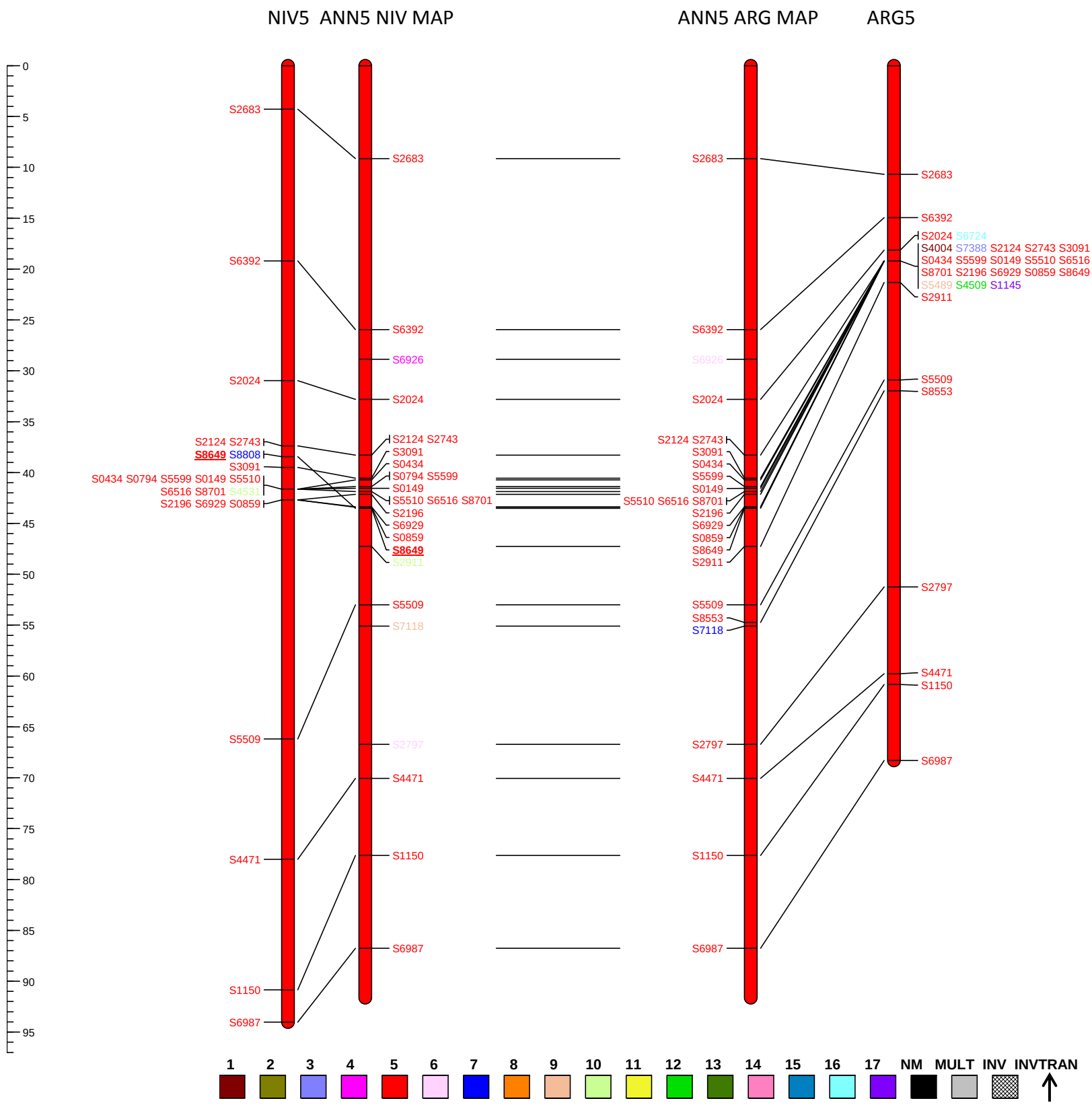


Figure S5 continued

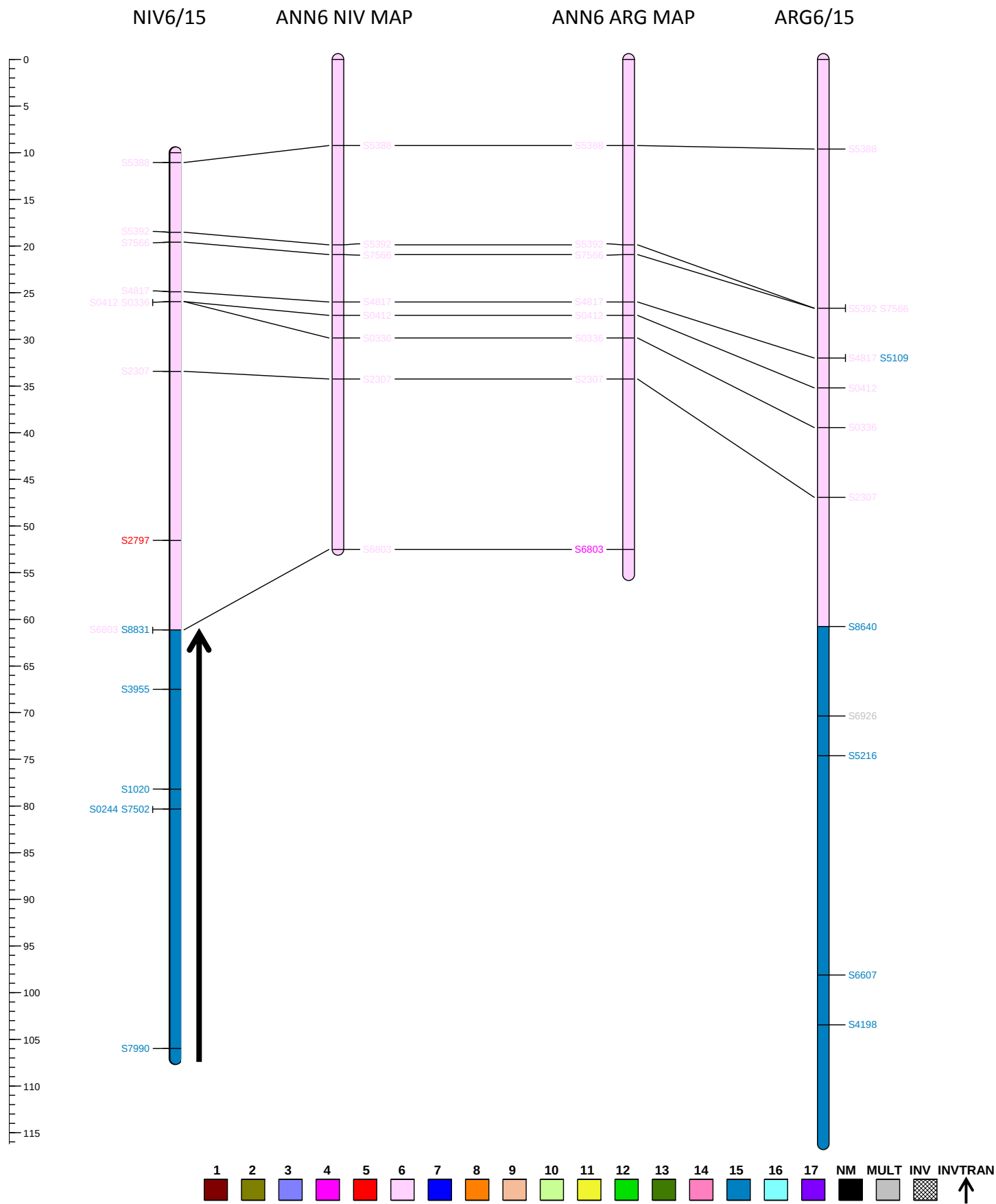


Figure S5 continued

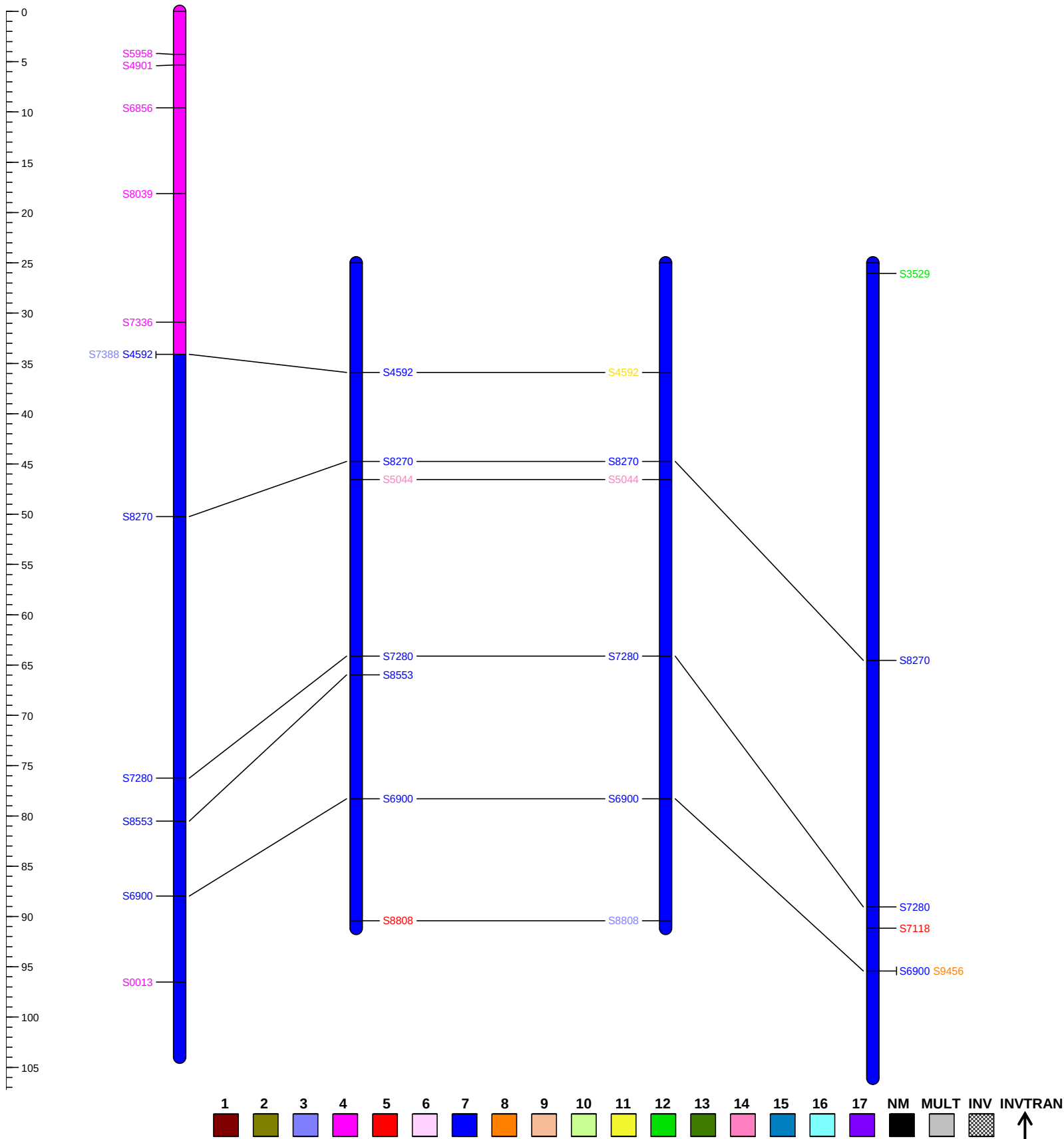


Figure S5 continued

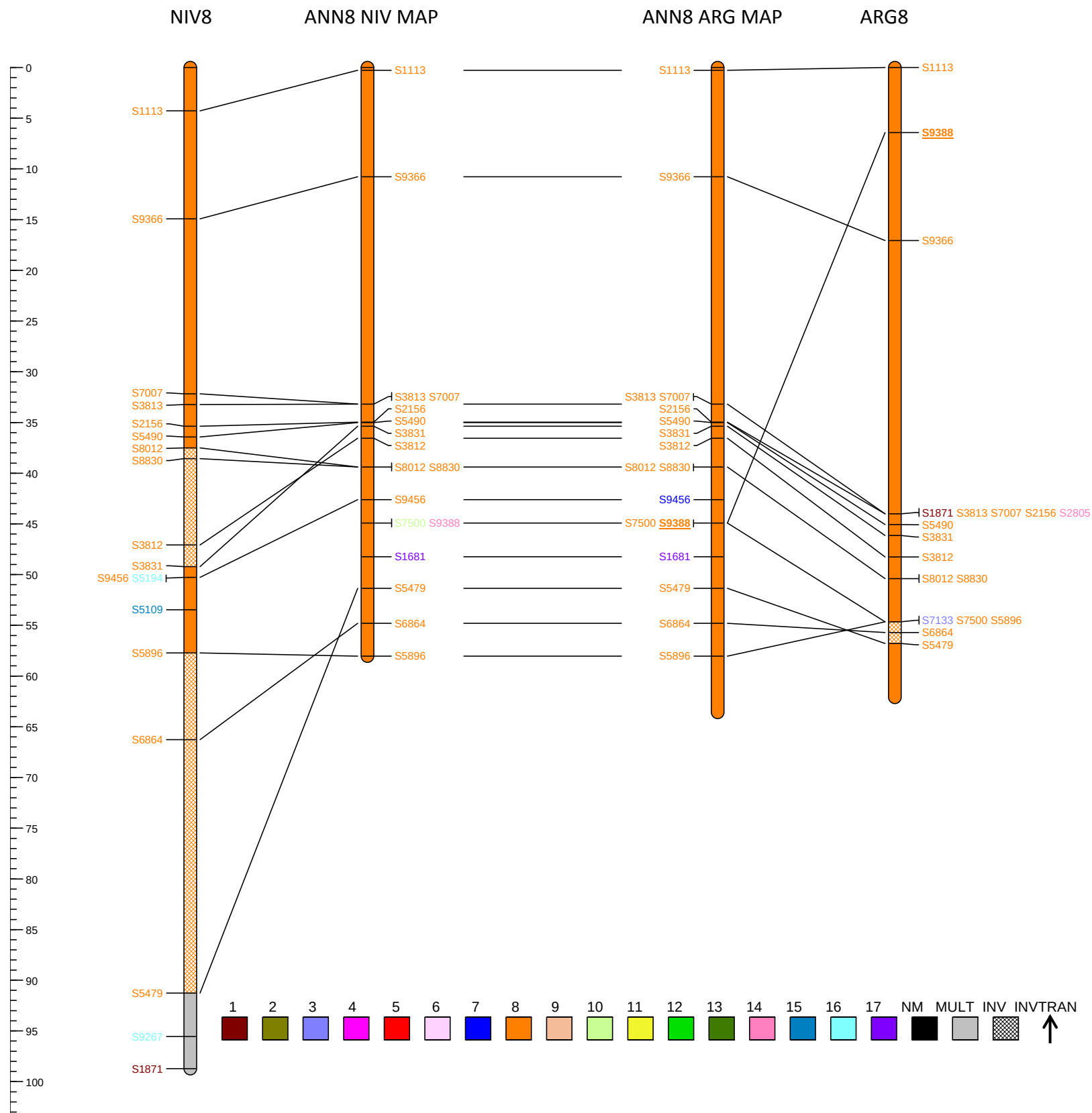


Figure S5 continued

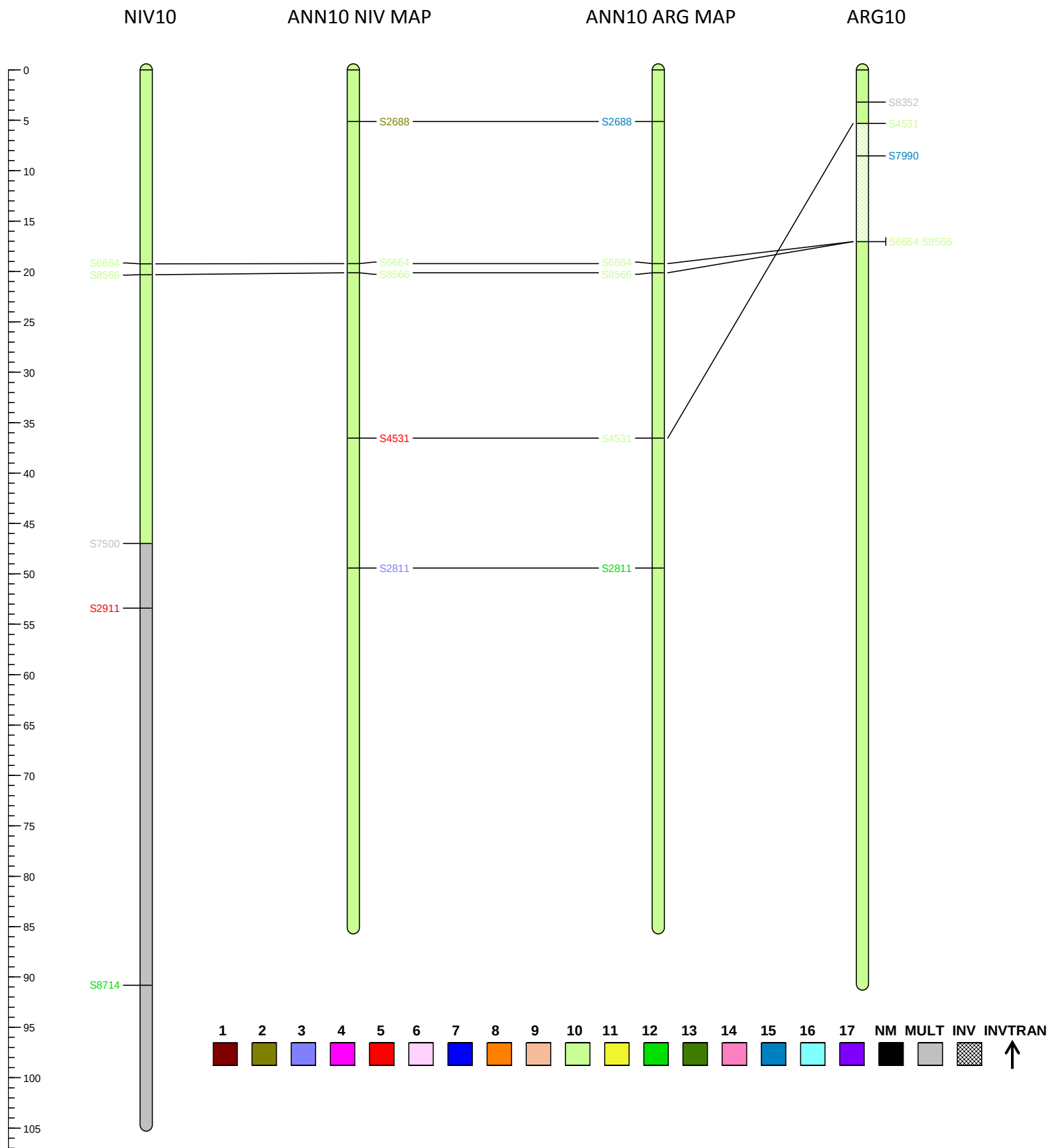


Figure S5 continued

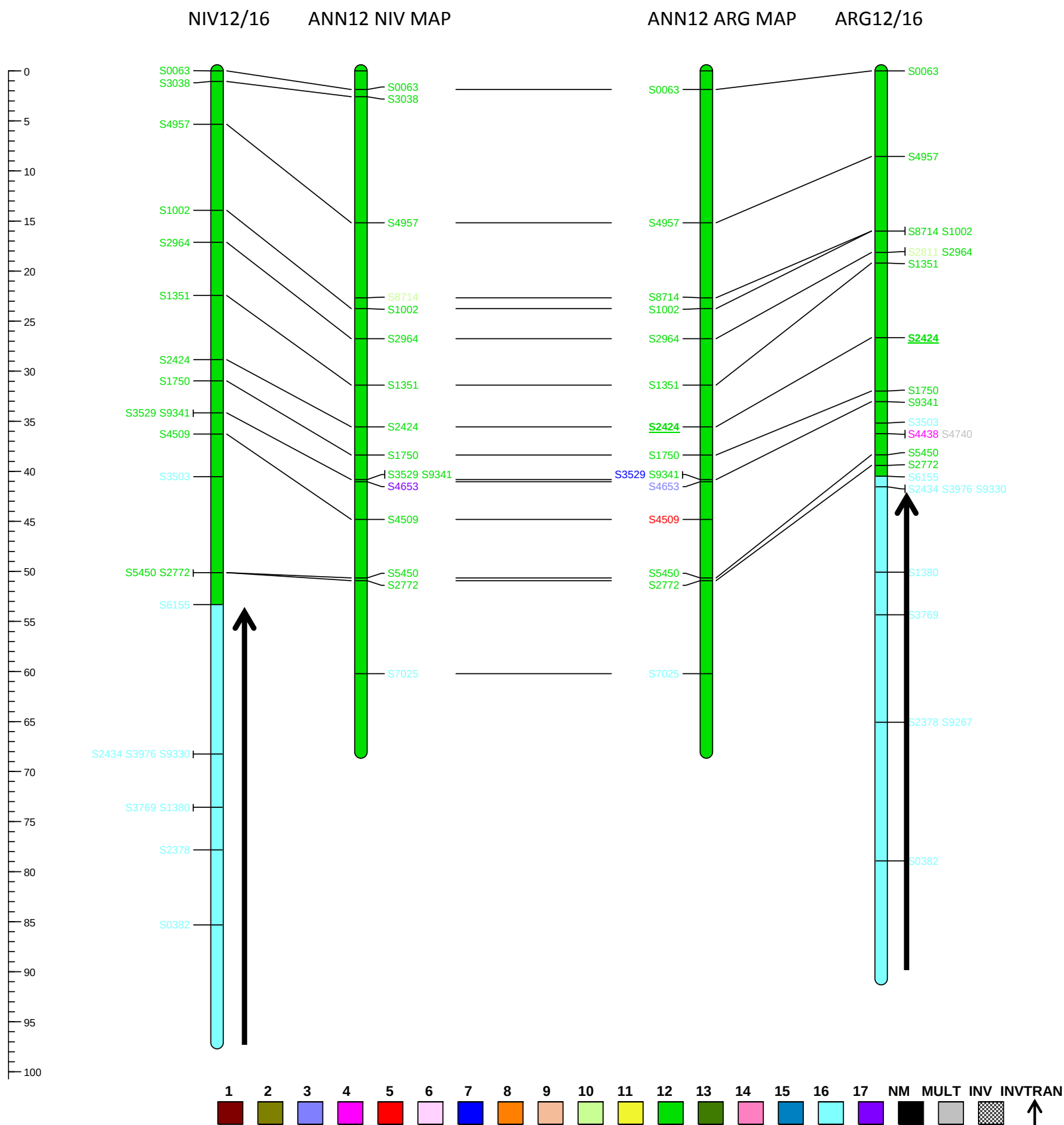


Figure S5 continued

NIV13

ANN13 NIV MAP

ANN13 ARG MAP

ARG13

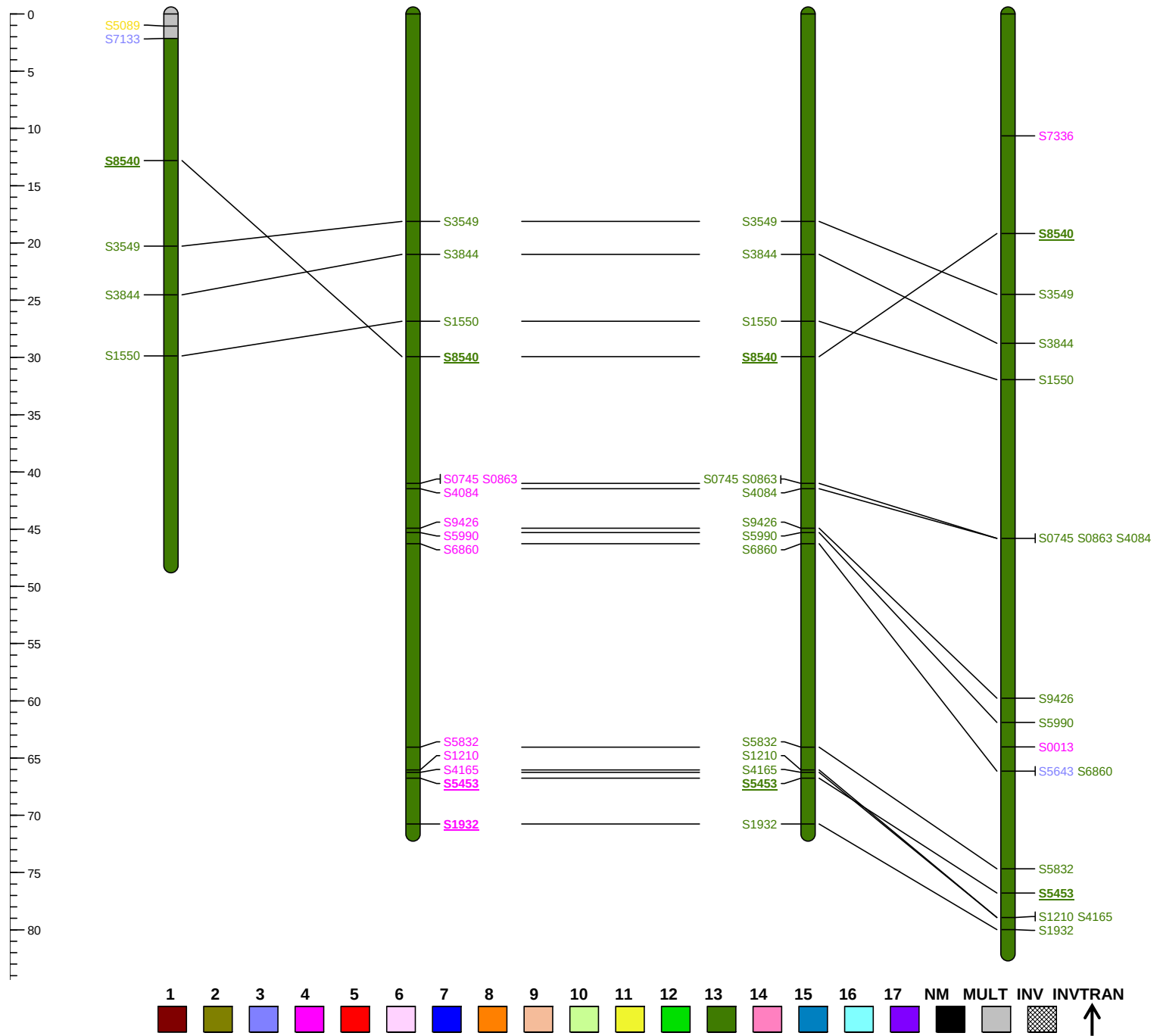


Figure S5 continued

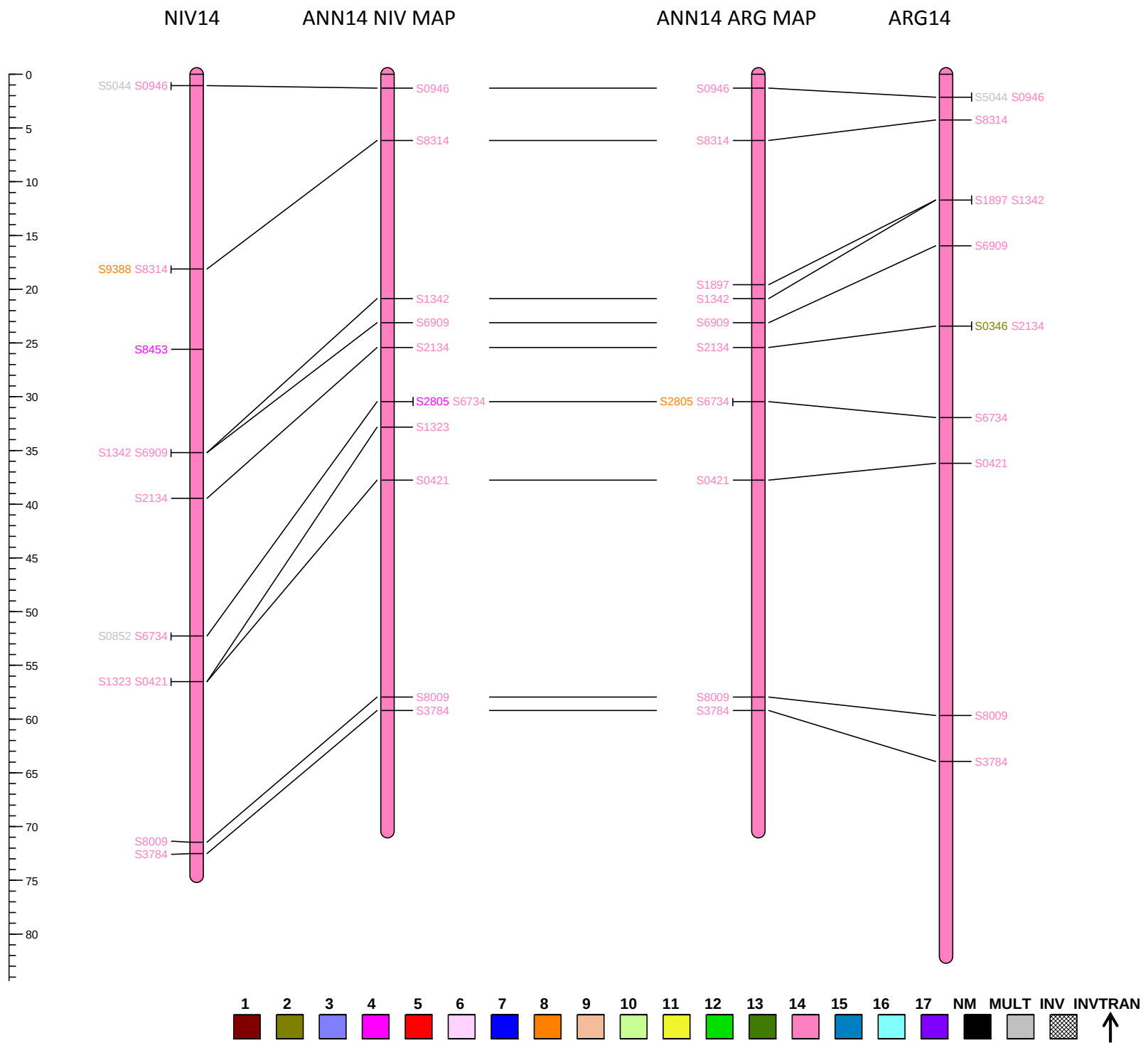


Figure S5 continued

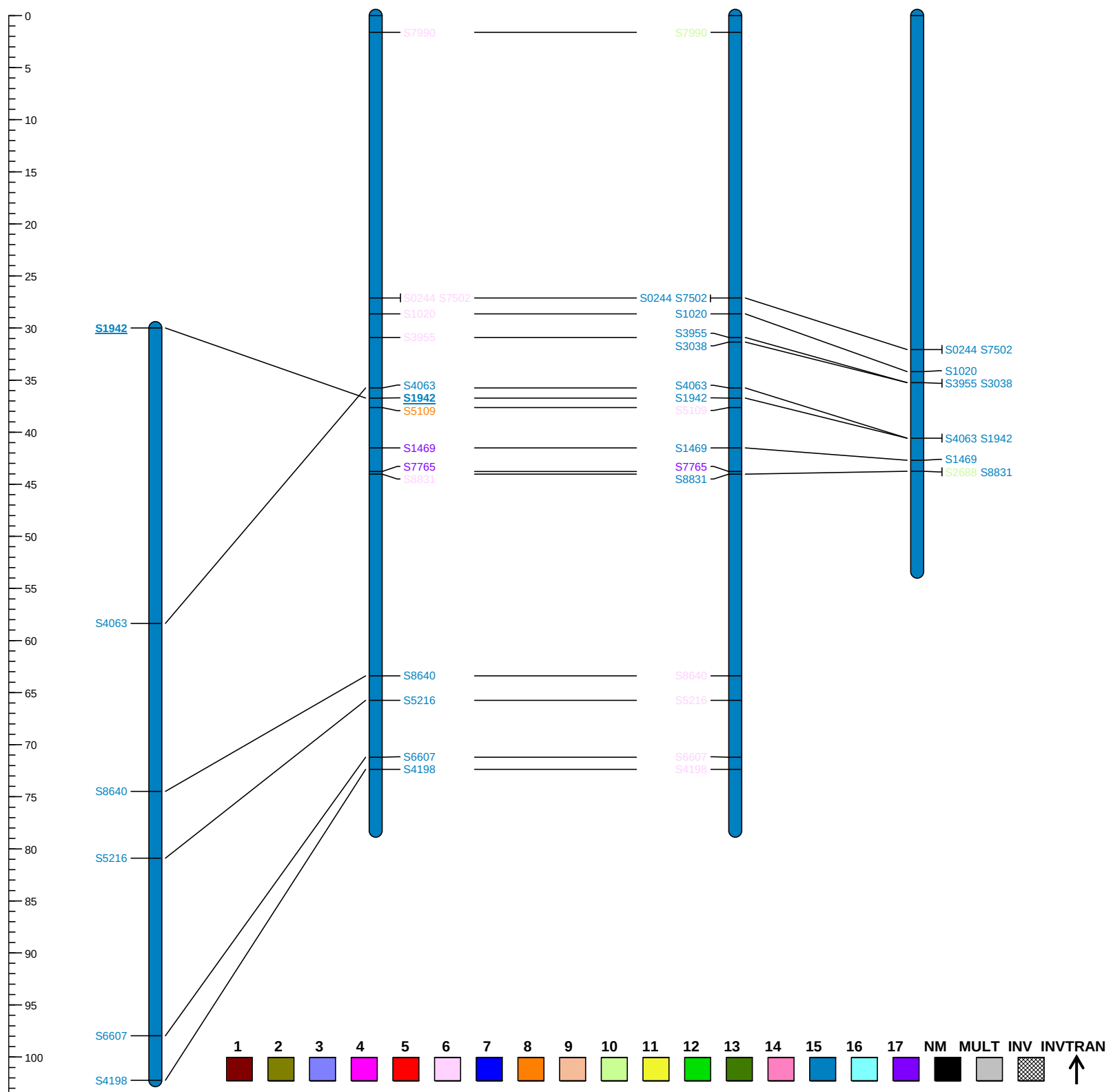


Figure S5 continued

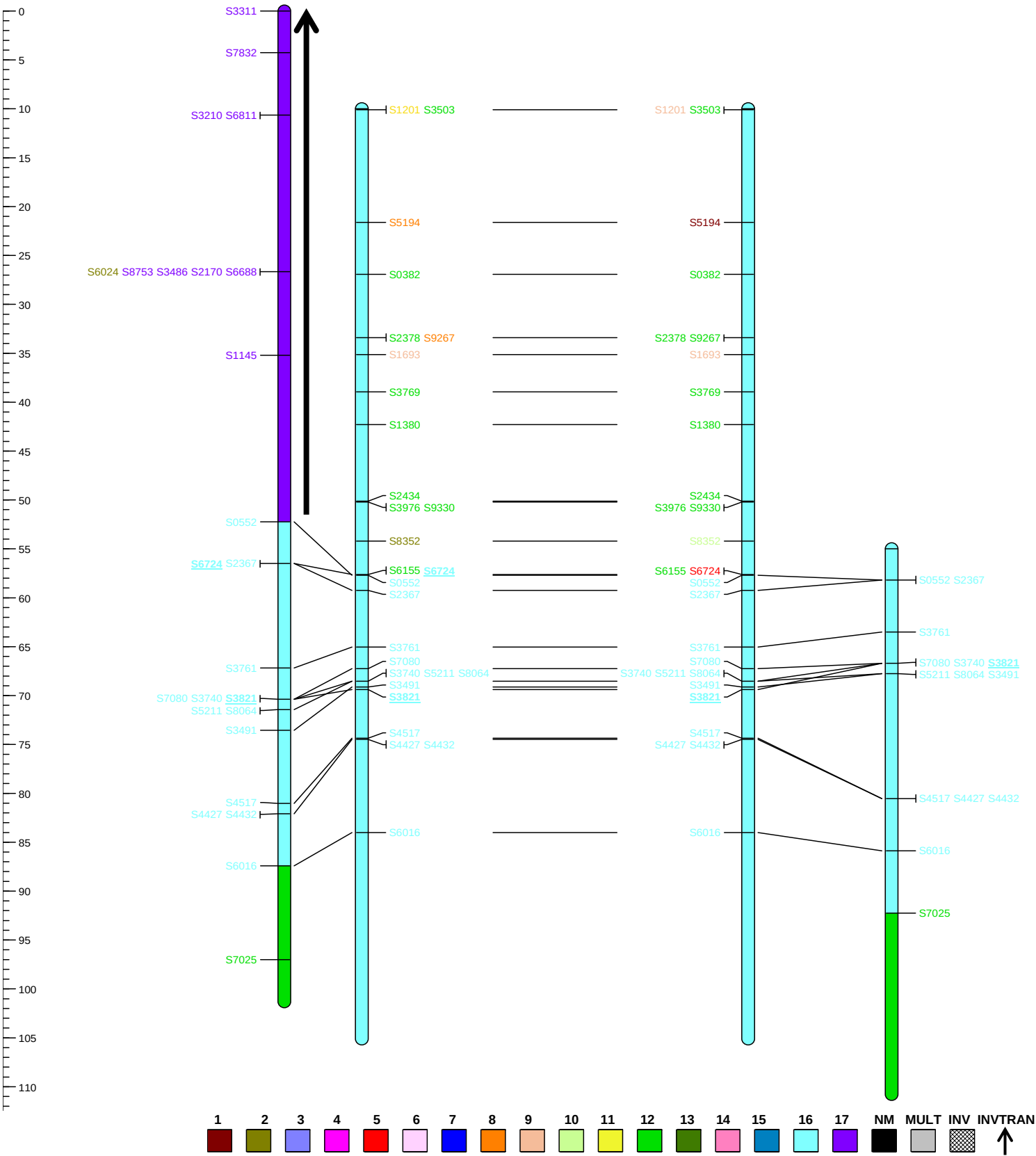


Figure S5 continued

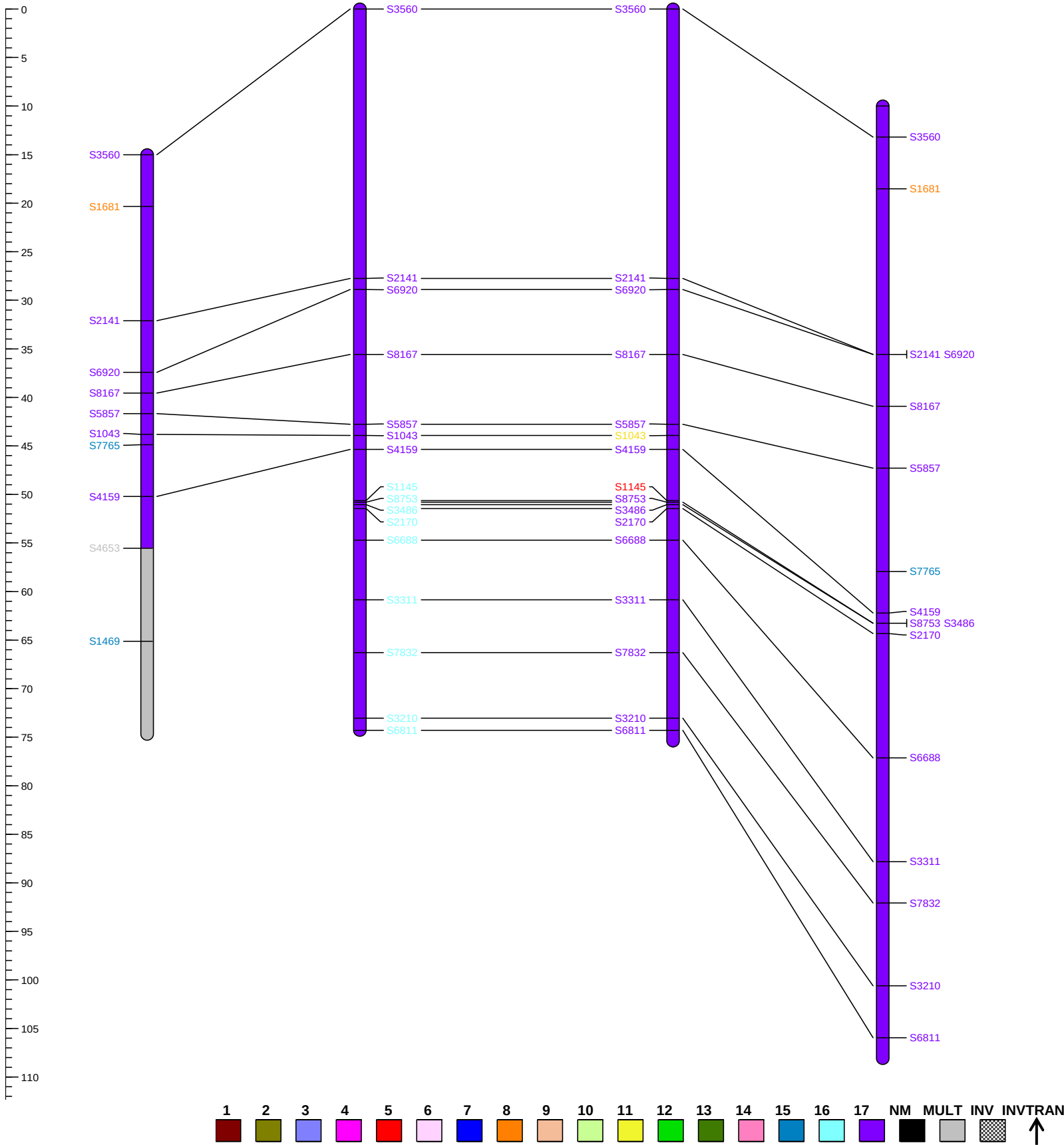


Figure S5 continued

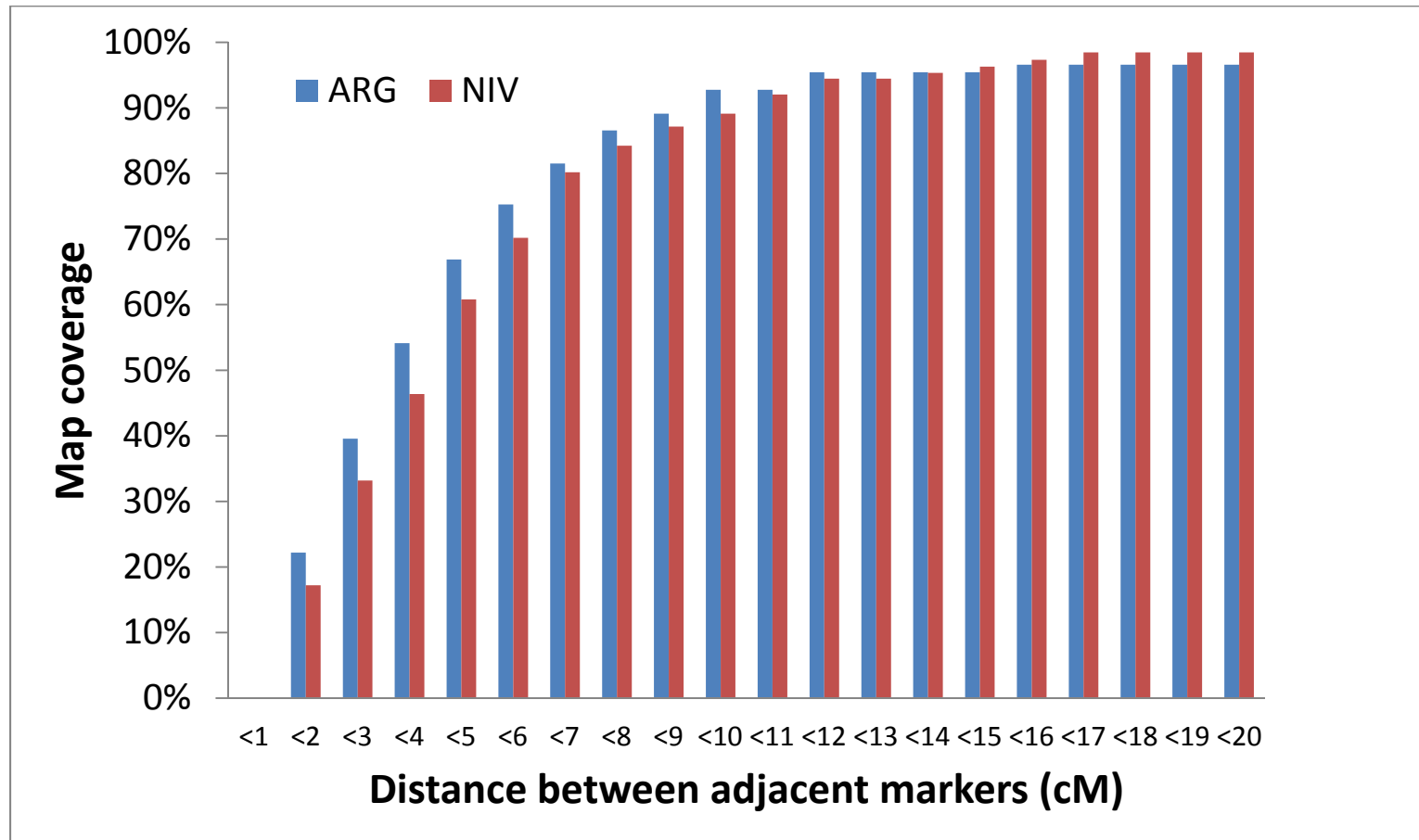


Figure S6 Distance (cM) between adjacent markers for the genetic maps of *Helianthus argophyllus* (ARG) and *H. niveus* ssp. *tephrodes* (NIV).

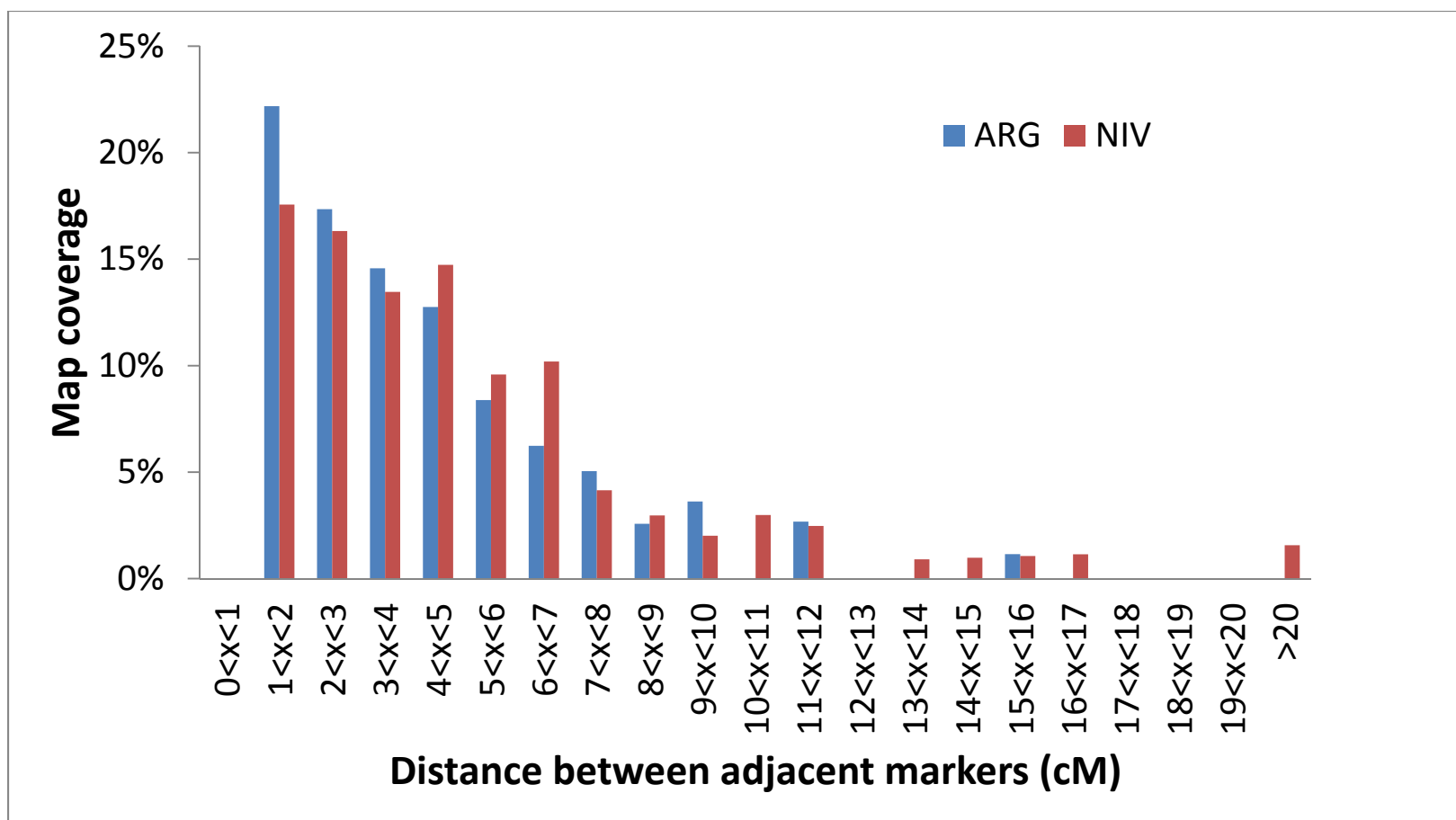


Figure S7 Distance (cM) between adjacent markers for the genetic maps of *Helianthus argophyllus* (ARG) and *H. niveus* ssp. *tephrodes* (NIV).

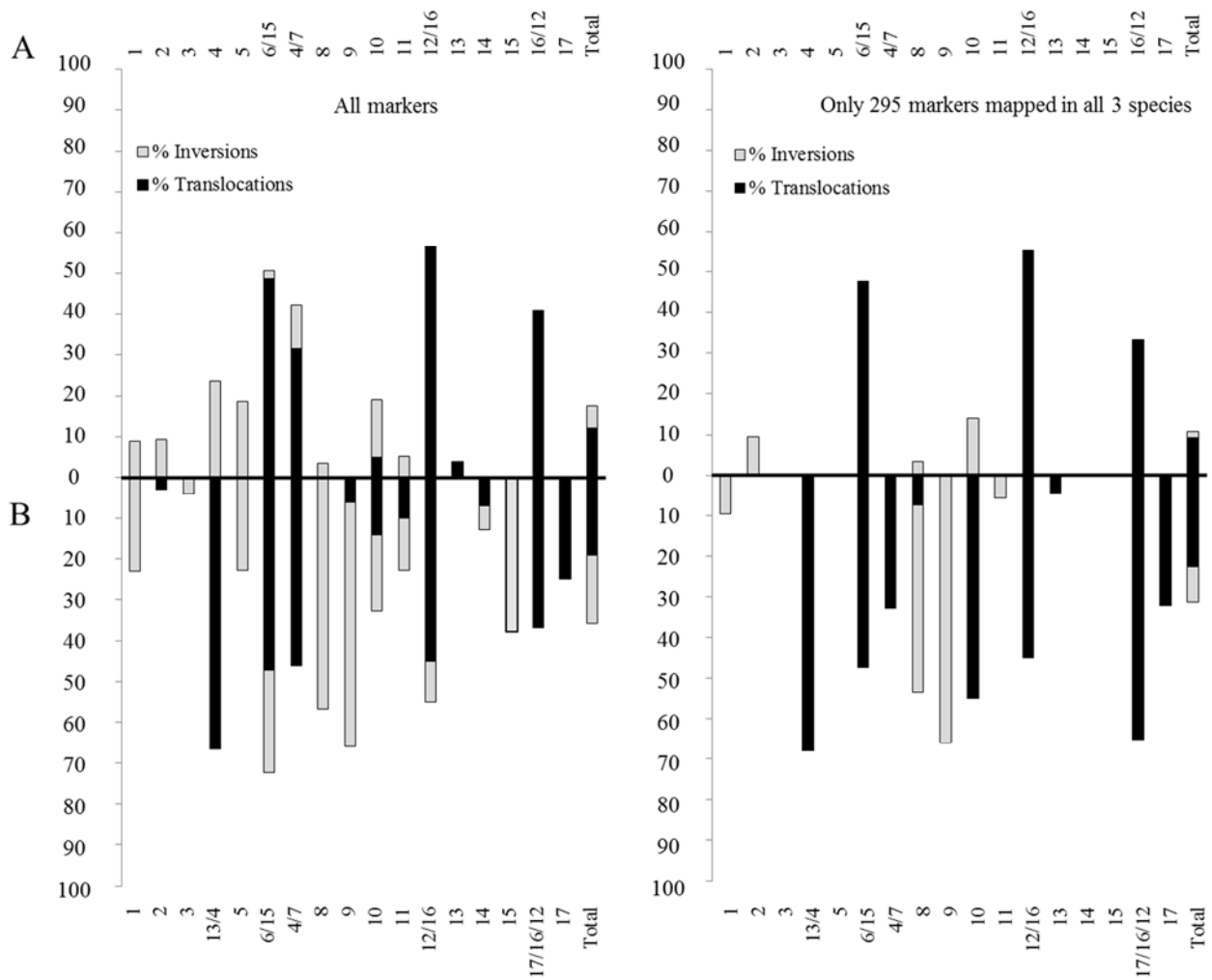


Figure S8 Chromosomal rearrangements in *Helianthus argophyllus* (ARG) and *H. niveus* ssp. *tephrodes* (NIV) relative to *H. annuus* (ANN). The percentage of ARG (A) and NIV (B) LGs that are translocated or inverted relative to the ANN consensus map (Bowers *et al.* 2012) based on the species-pair sets of markers (left panel) mapped in ANN and ARG and ANN and NIV, respectively and also the set of 295 markers mapped in all three species (right panel).

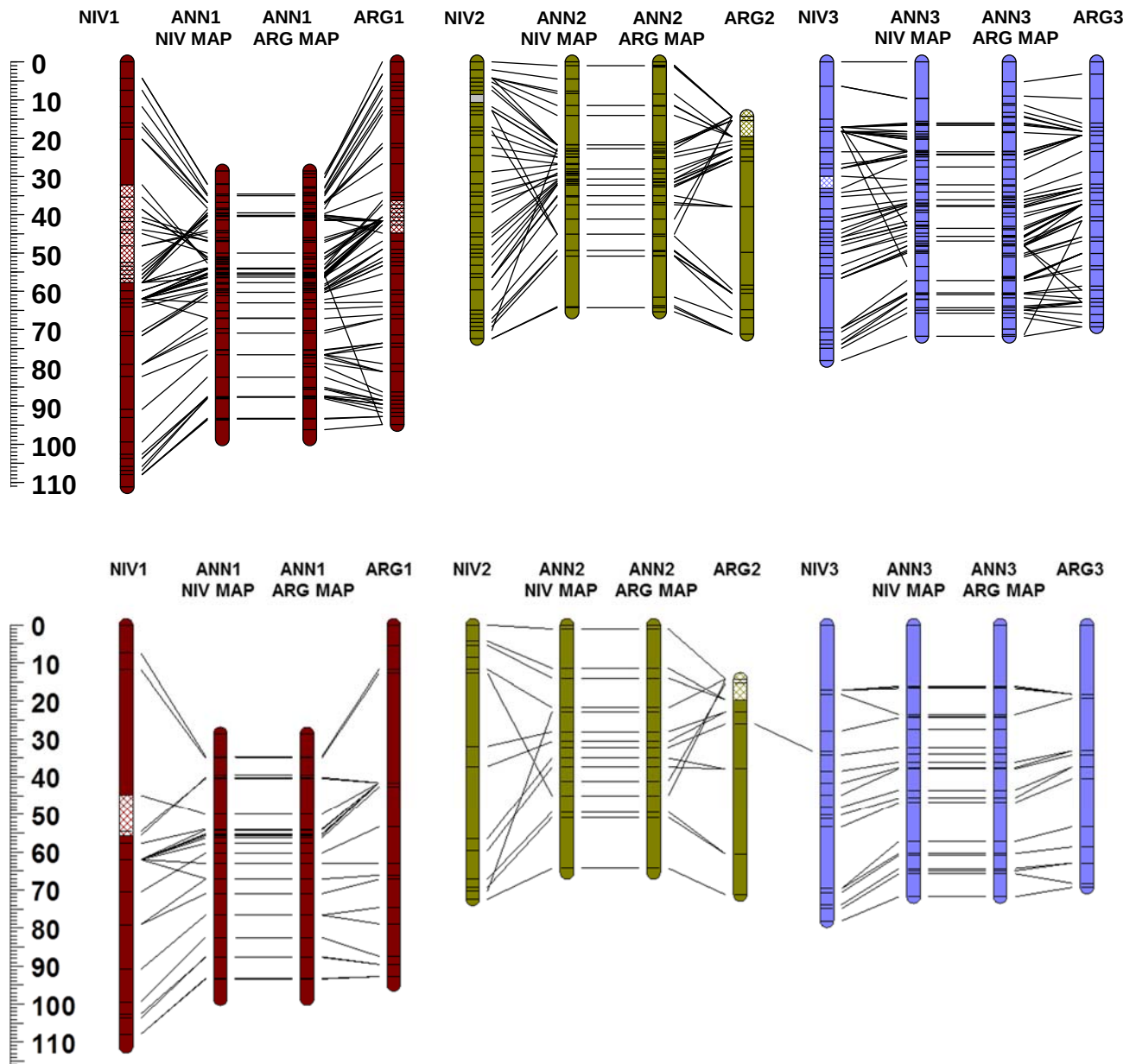


Figure S9 A side-by-side vertical comparison of the comparative mapping of *H. argophyllus* (ARG) and *H. niveus* ssp. *tephrodes* (NIV) relative to *H. annuus* (ANN) based on the species-pair marker sets (top panel) and the set of 295 markers mapped in all three species (bottom panel). Color coding and chromosome nomenclature follow Figure 1. LGs colored in gray (MULT) were mapped to multiple LGs in ANN, but not to the corresponding LG in ARG or NIV, respectively. Homologous markers are connected by lines. Inverted segments are indicated with cross hatching. Arrows indicate translocated regions that are also inverted. Only ANN markers mapped in ARG or NIV are included in this figure.

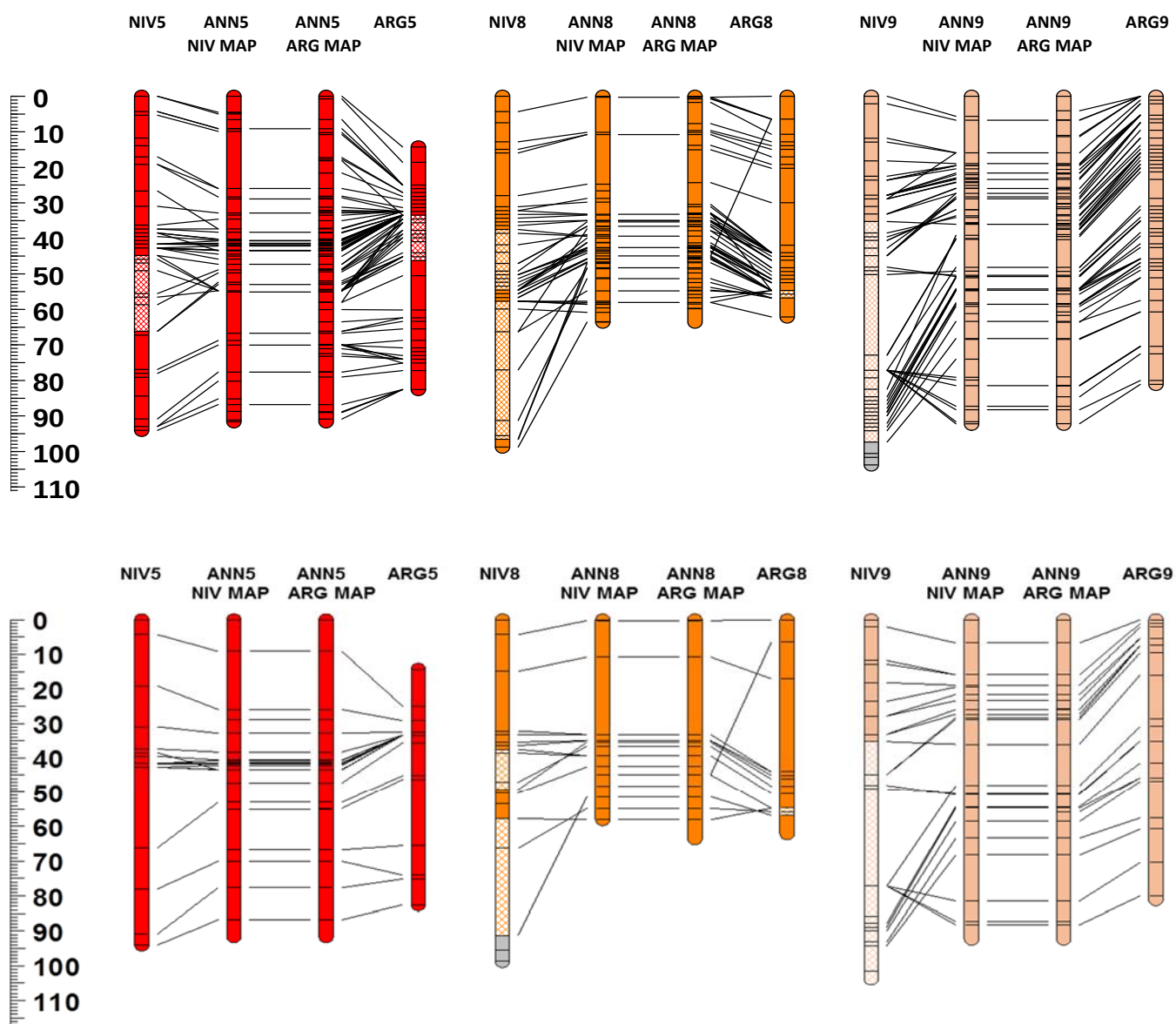


Figure S9 continued

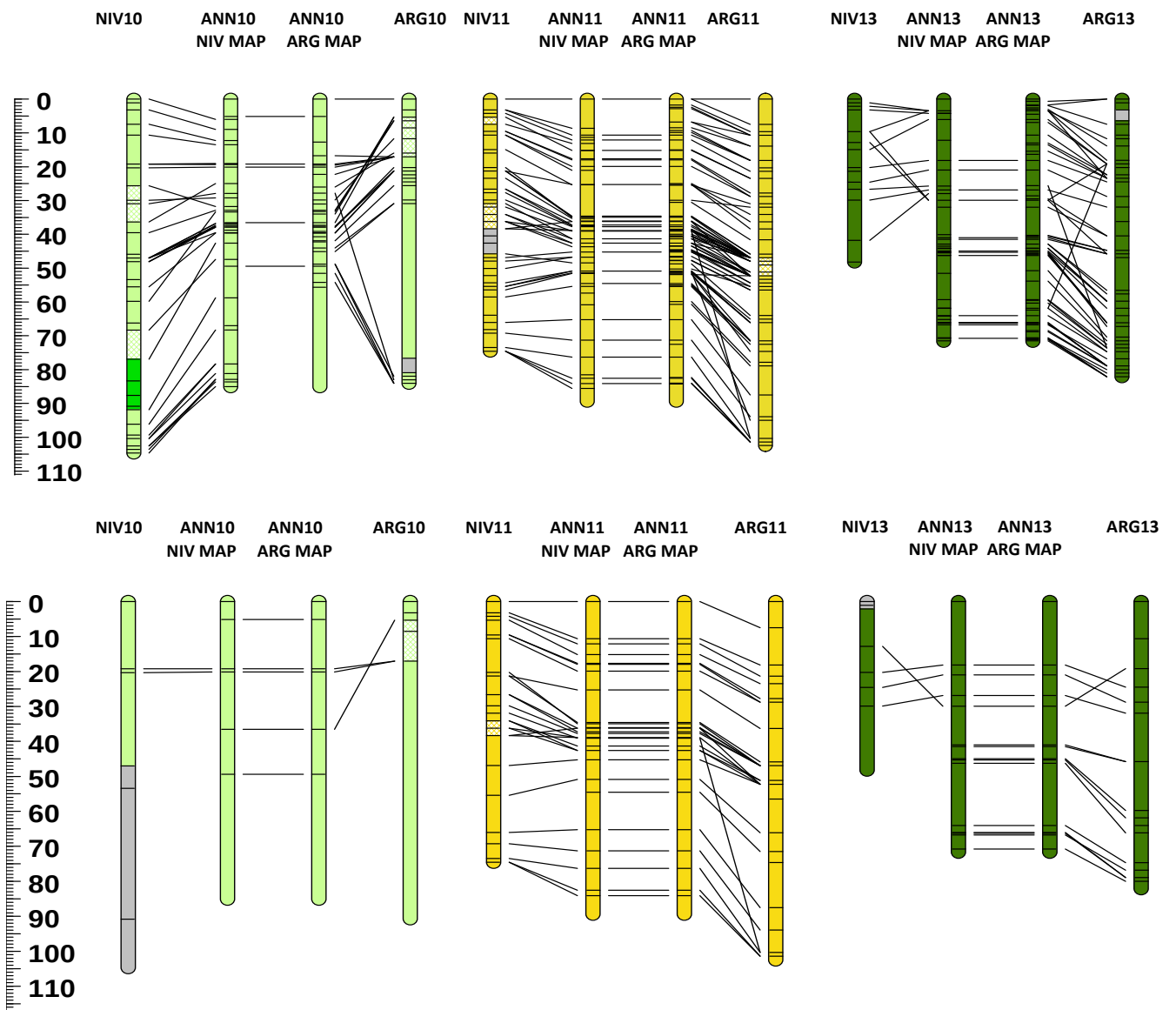


Figure S9 continued

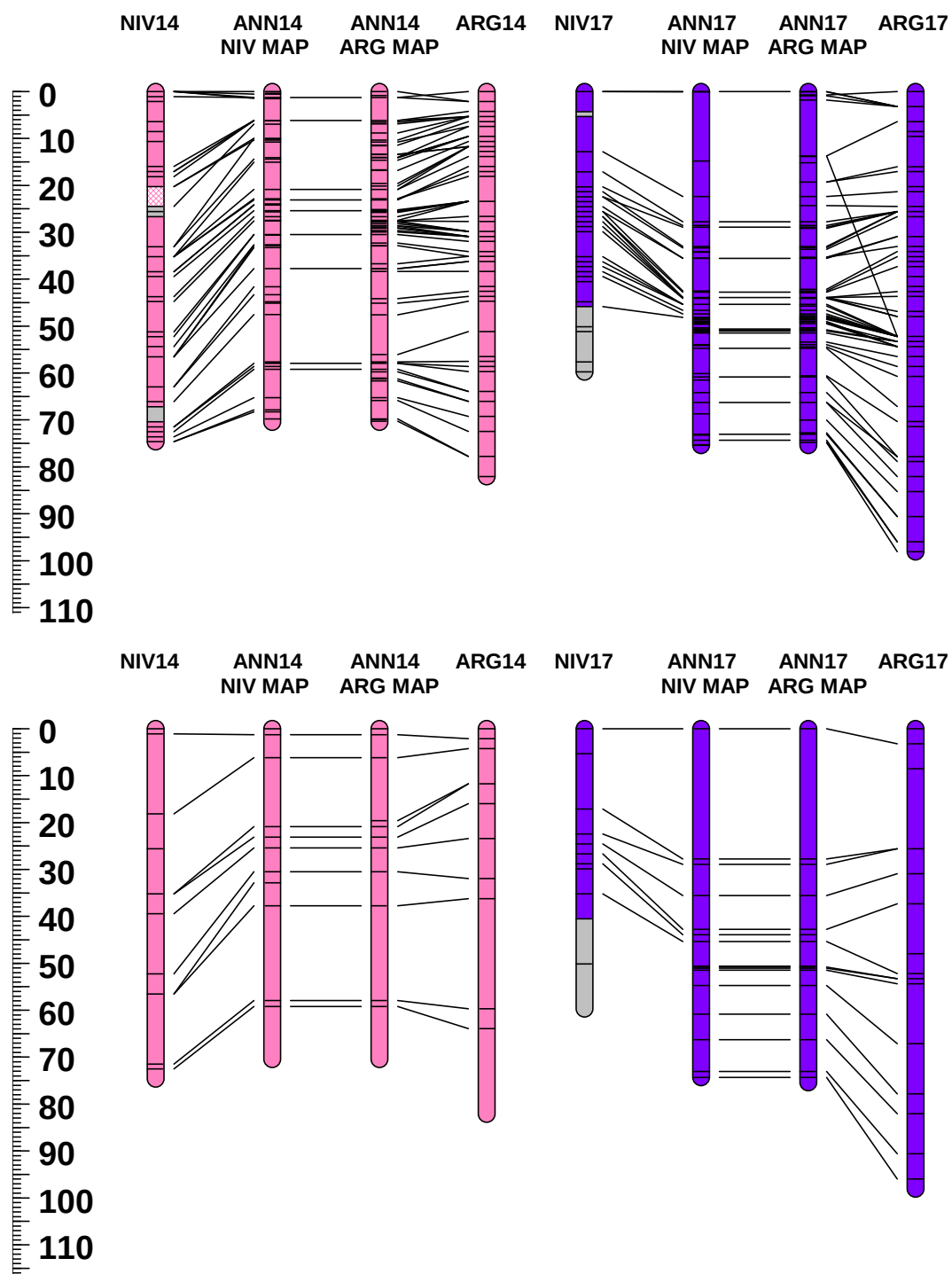


Figure S9 continued

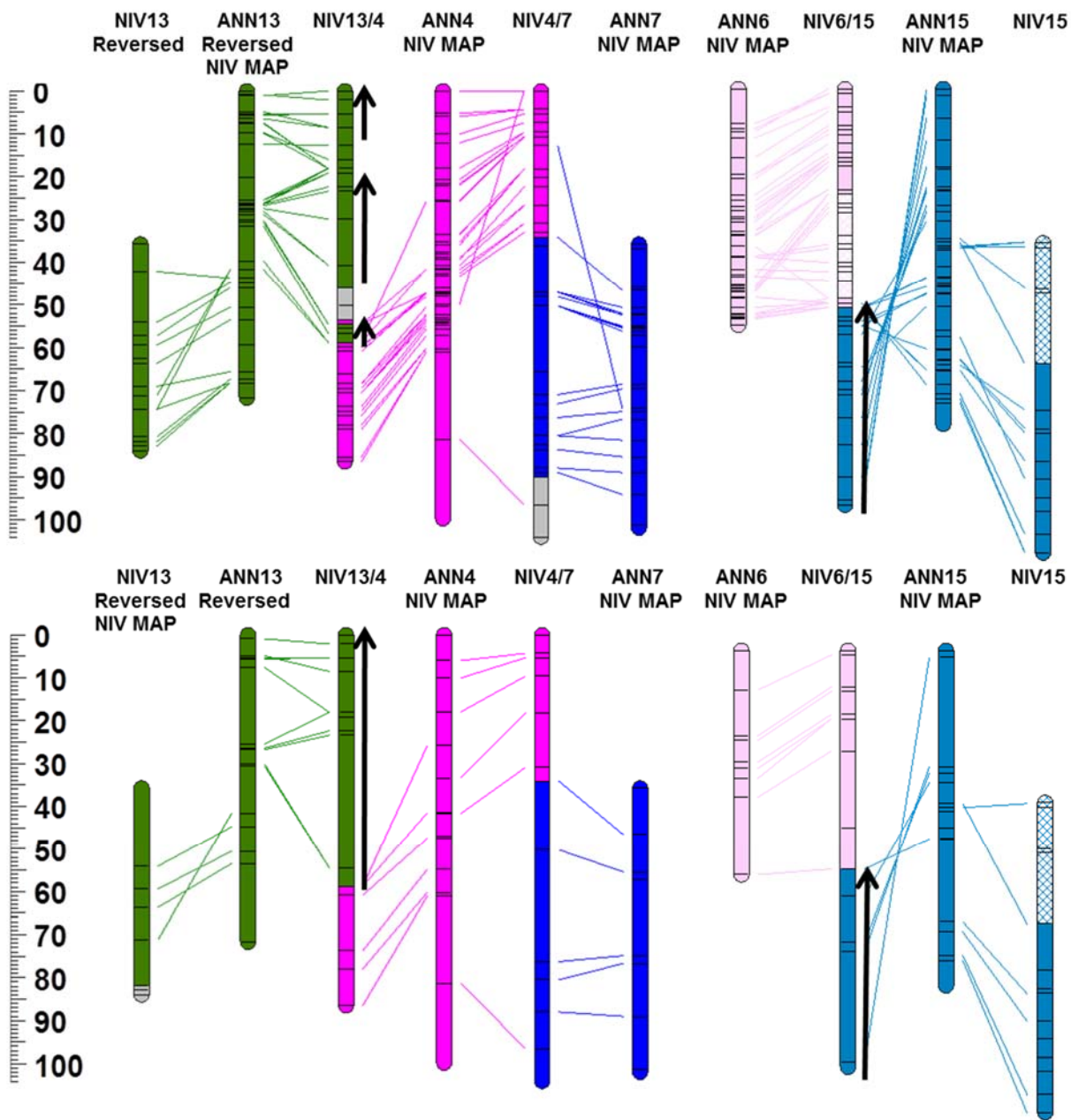


Figure S9 continued

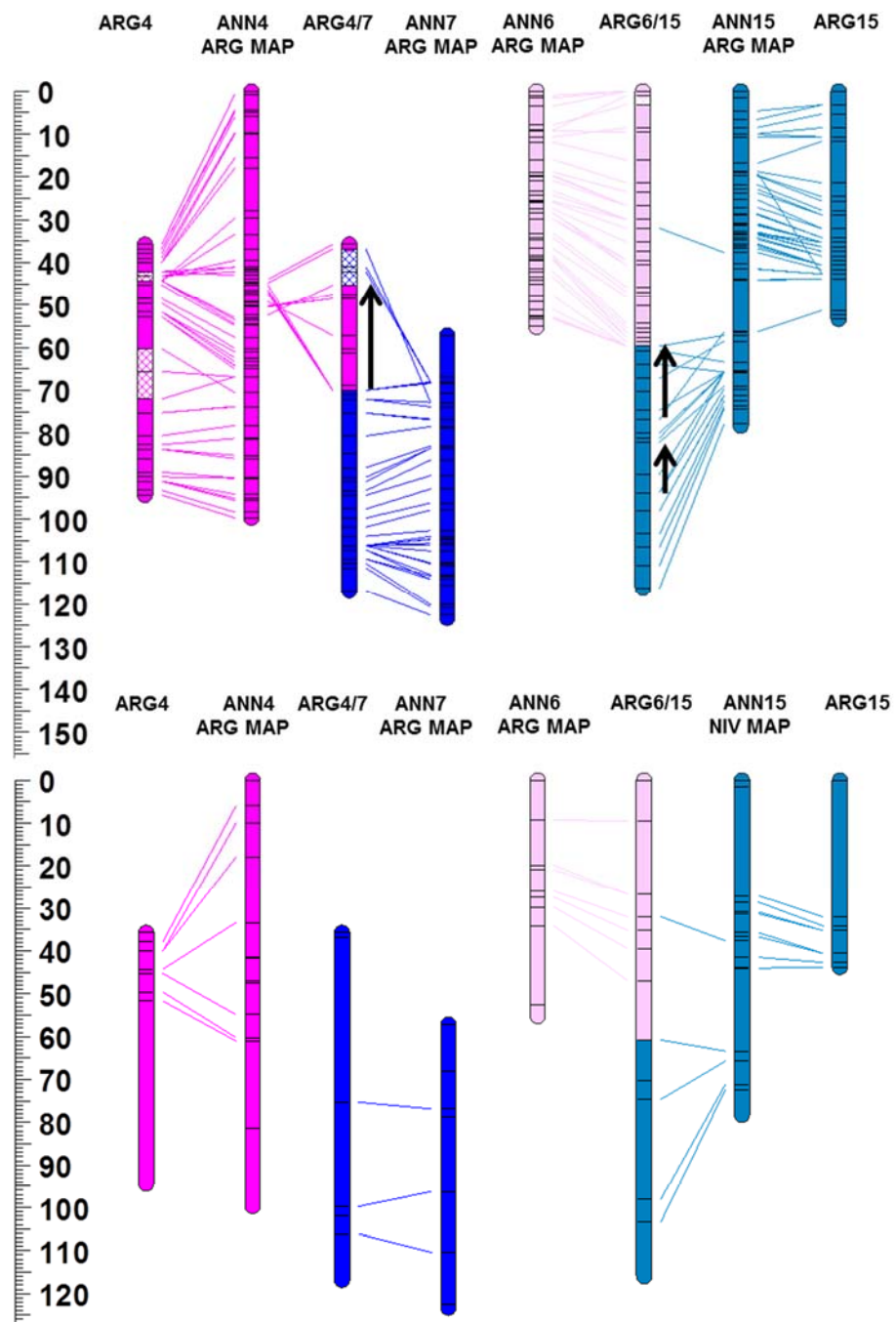


Figure S9 continued

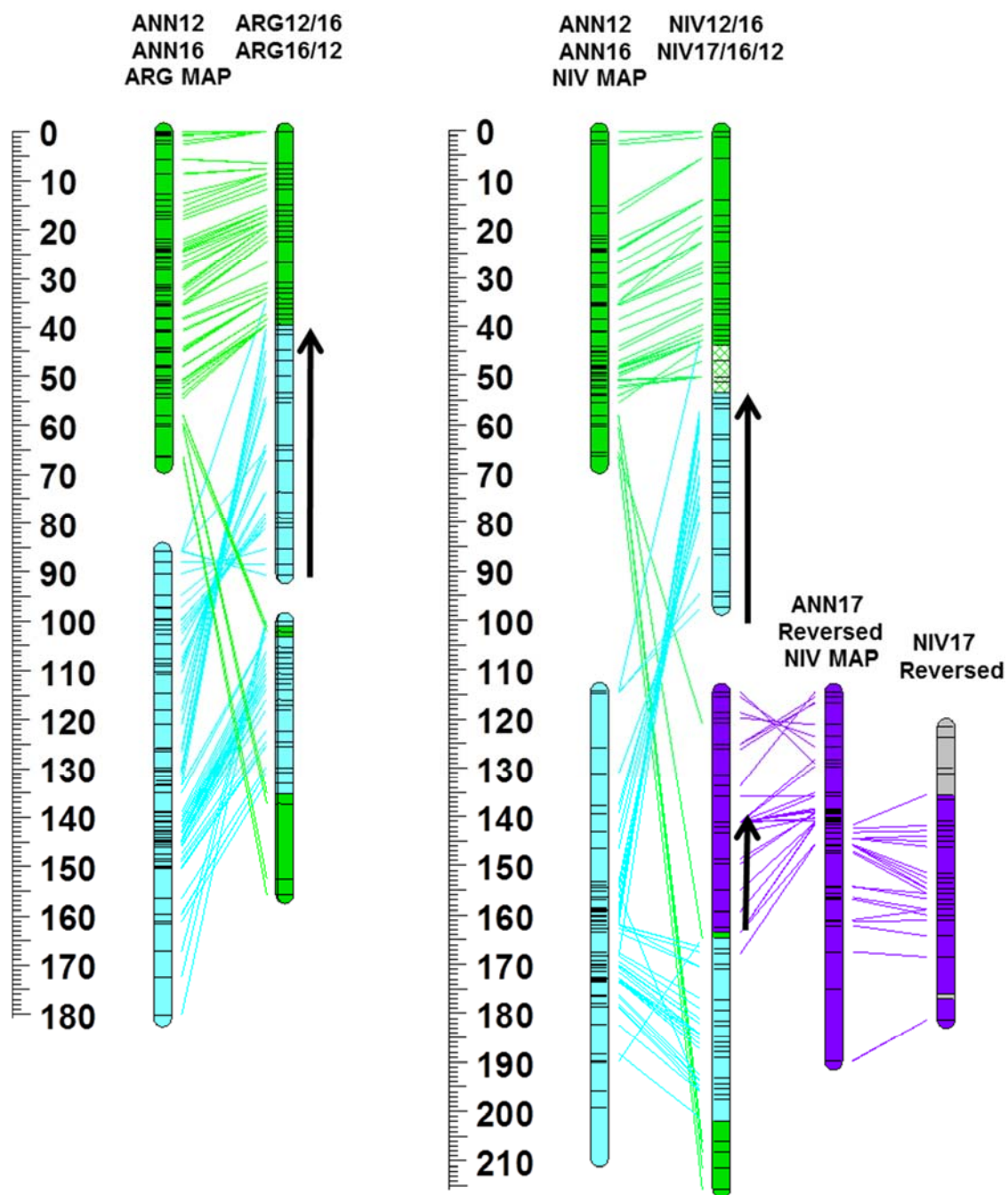


Figure S9 continued

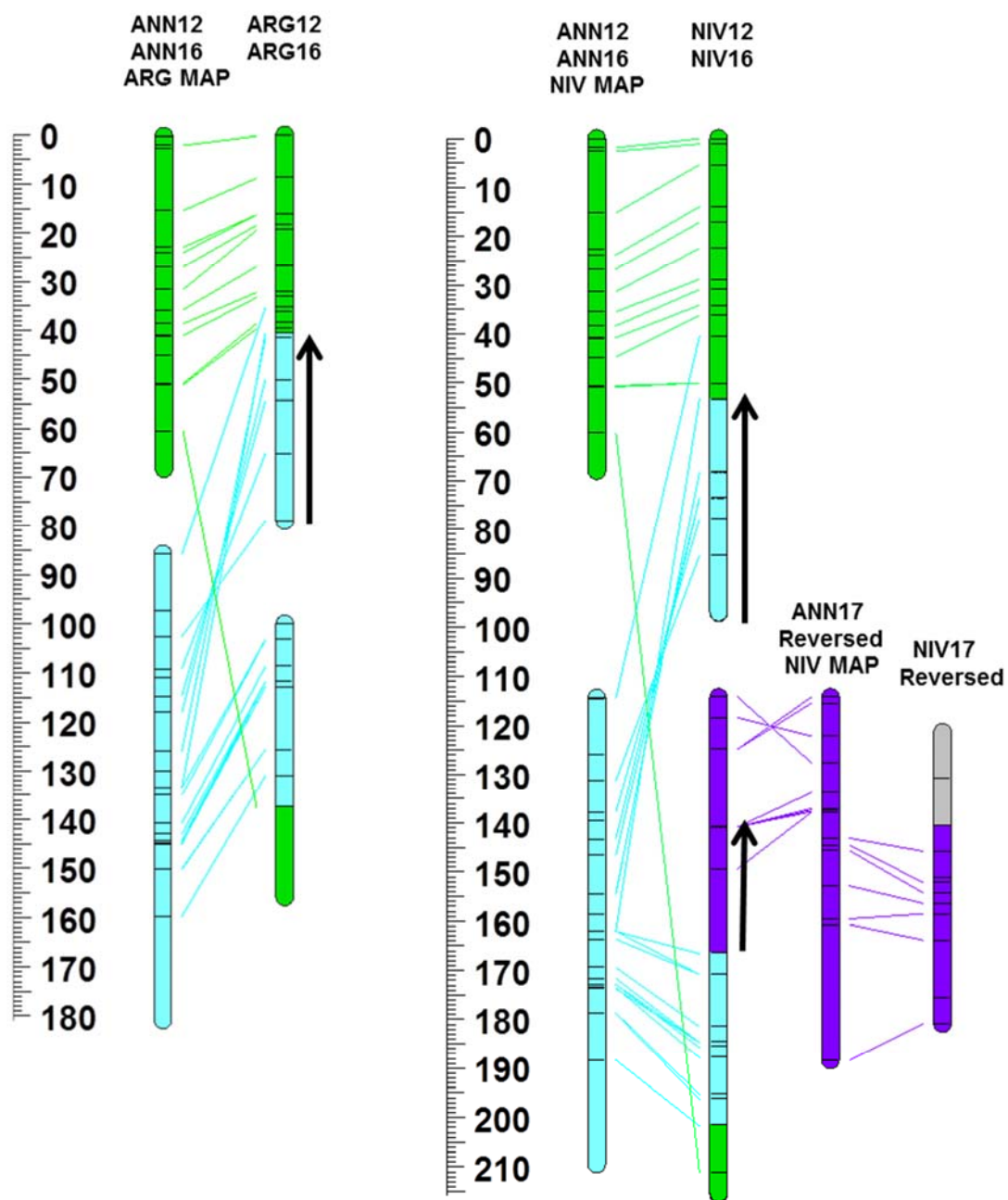


Figure S9 continued

Figure S10 Comparative map of *Helianthus argophyllus* (ARG) and *H. niveus* ssp. *tephrodes* (NIV). Color coding and chromosome nomenclature follow Figure 1. ARG and NIV markers are color coded to represent the LG that they were mapped to in the other species. Markers colored in black (NM) were not mapped in the other species. Markers colored in gray (MULT) were mapped to multiple LGs in the other species, but not to the corresponding LG in ARG or NIV, respectively. Homologous markers are connected by lines. Inverted segments are indicated with cross hatching. Synteny and collinearity were assumed in regions of conflicting data and markers violating synteny or collinearity in these regions were identified (bold, underlined). Markers ending with an asterisk were mapped in ARG and NIV but not in ANN.

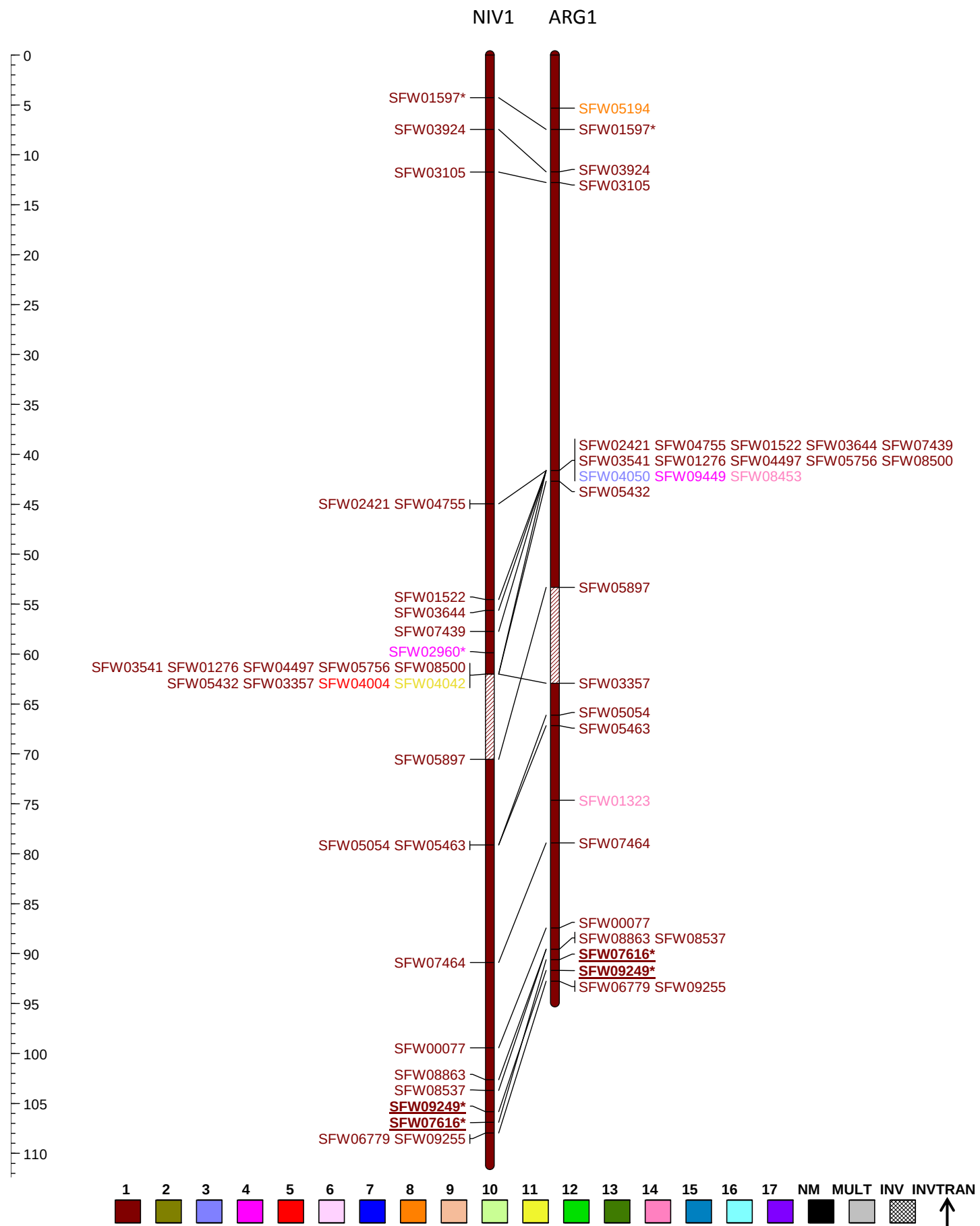


Figure S10 continued

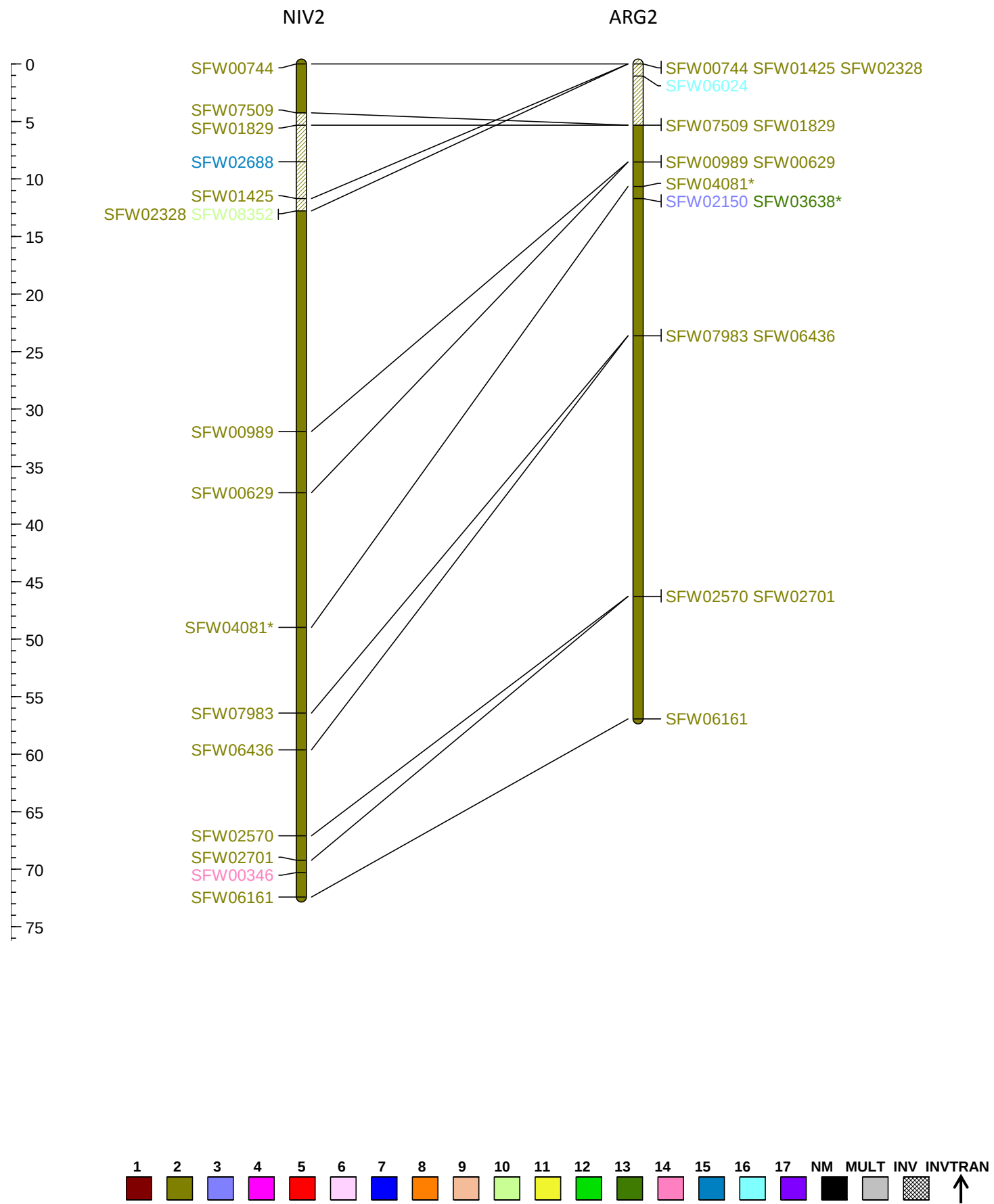
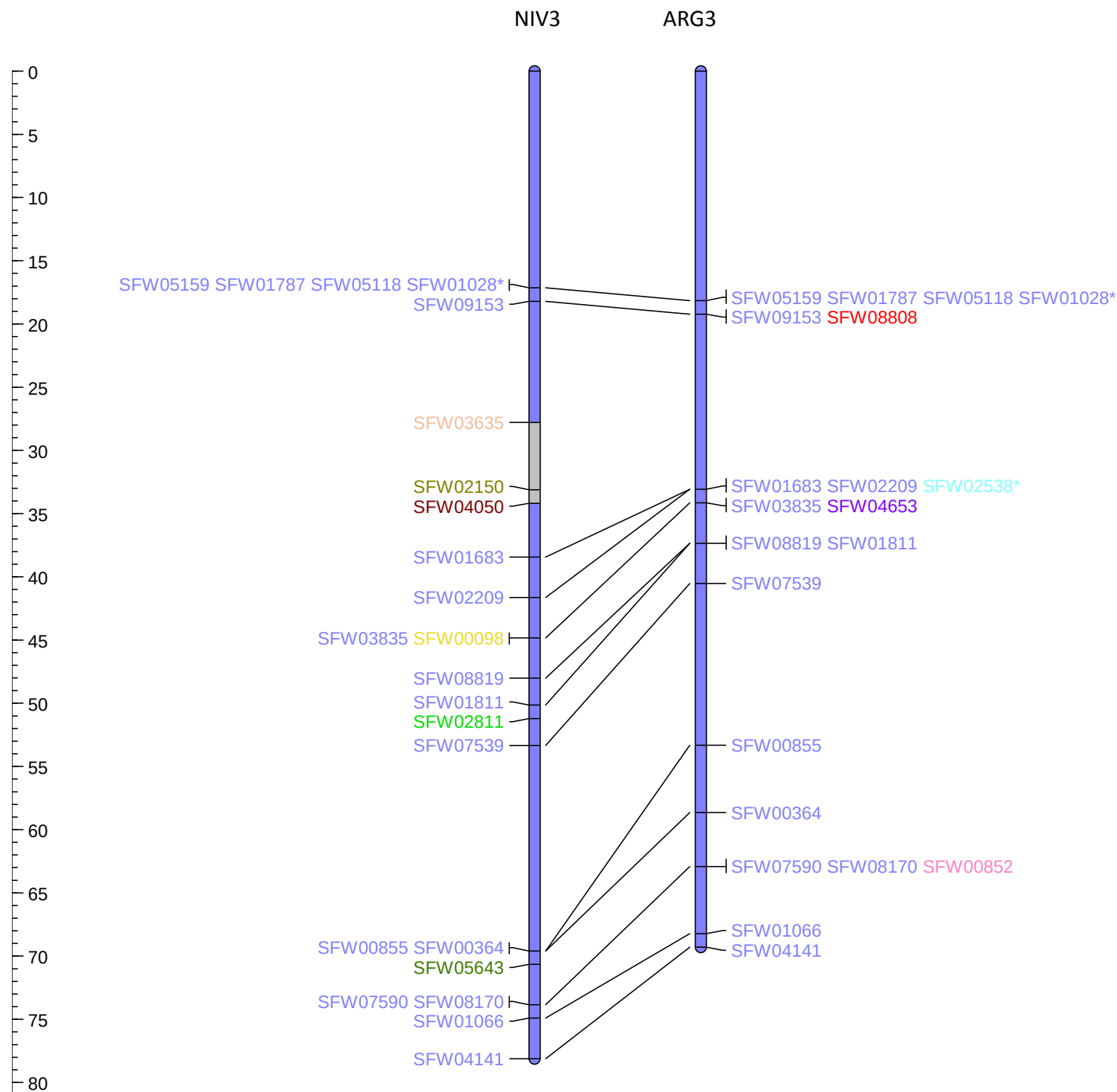
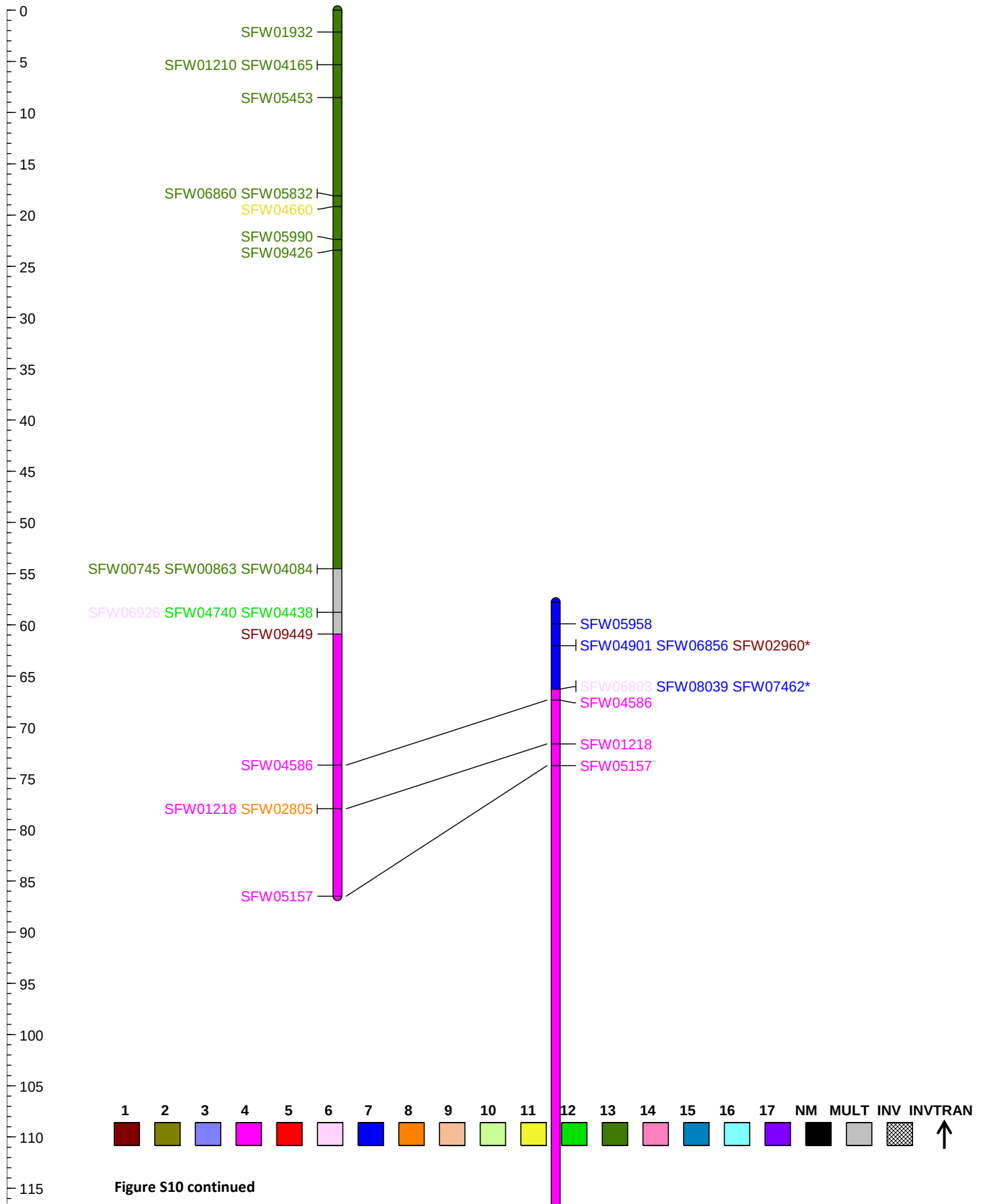


Figure S10 continued



NIV13/4

ARG4



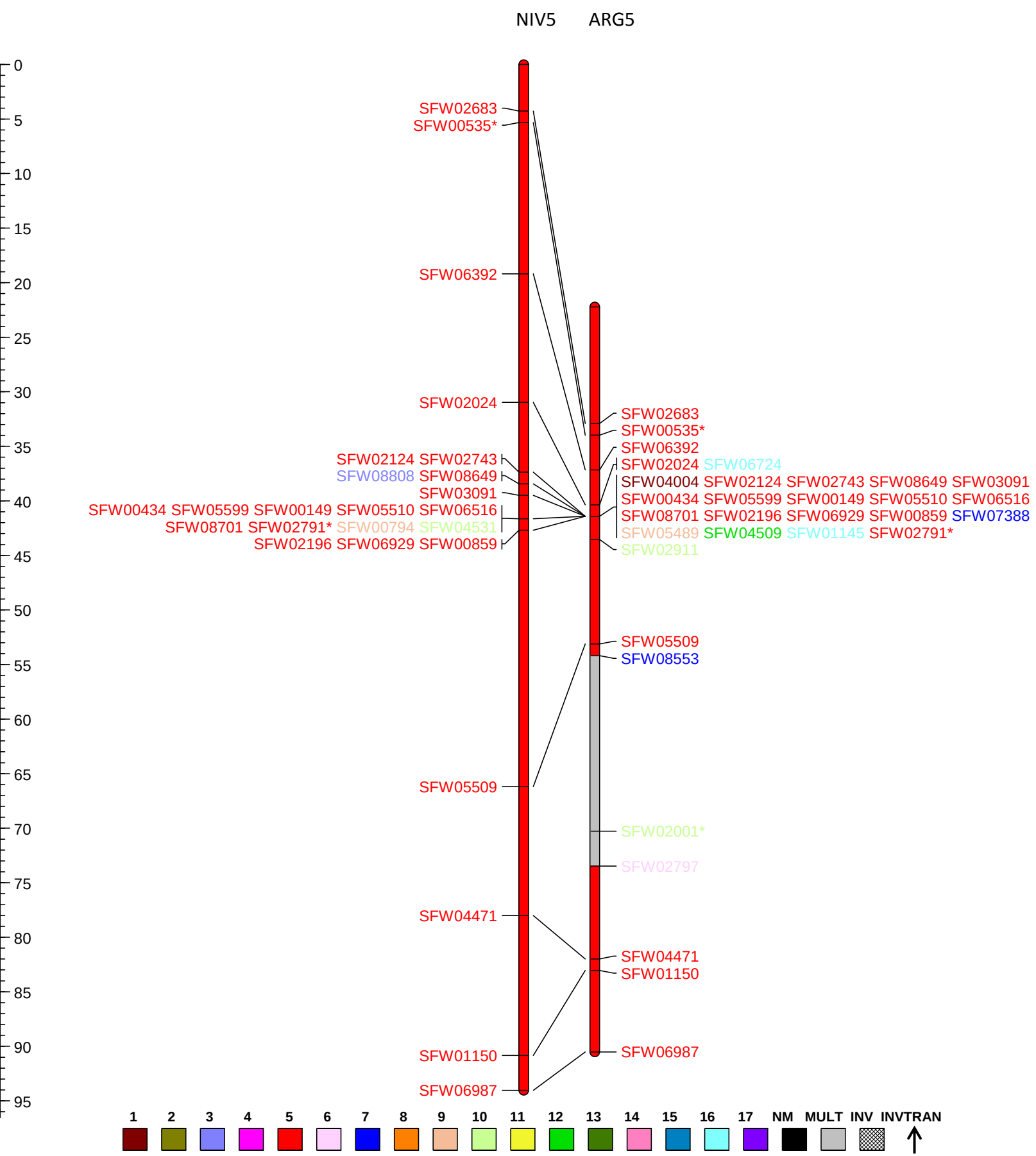


Figure S10 continued

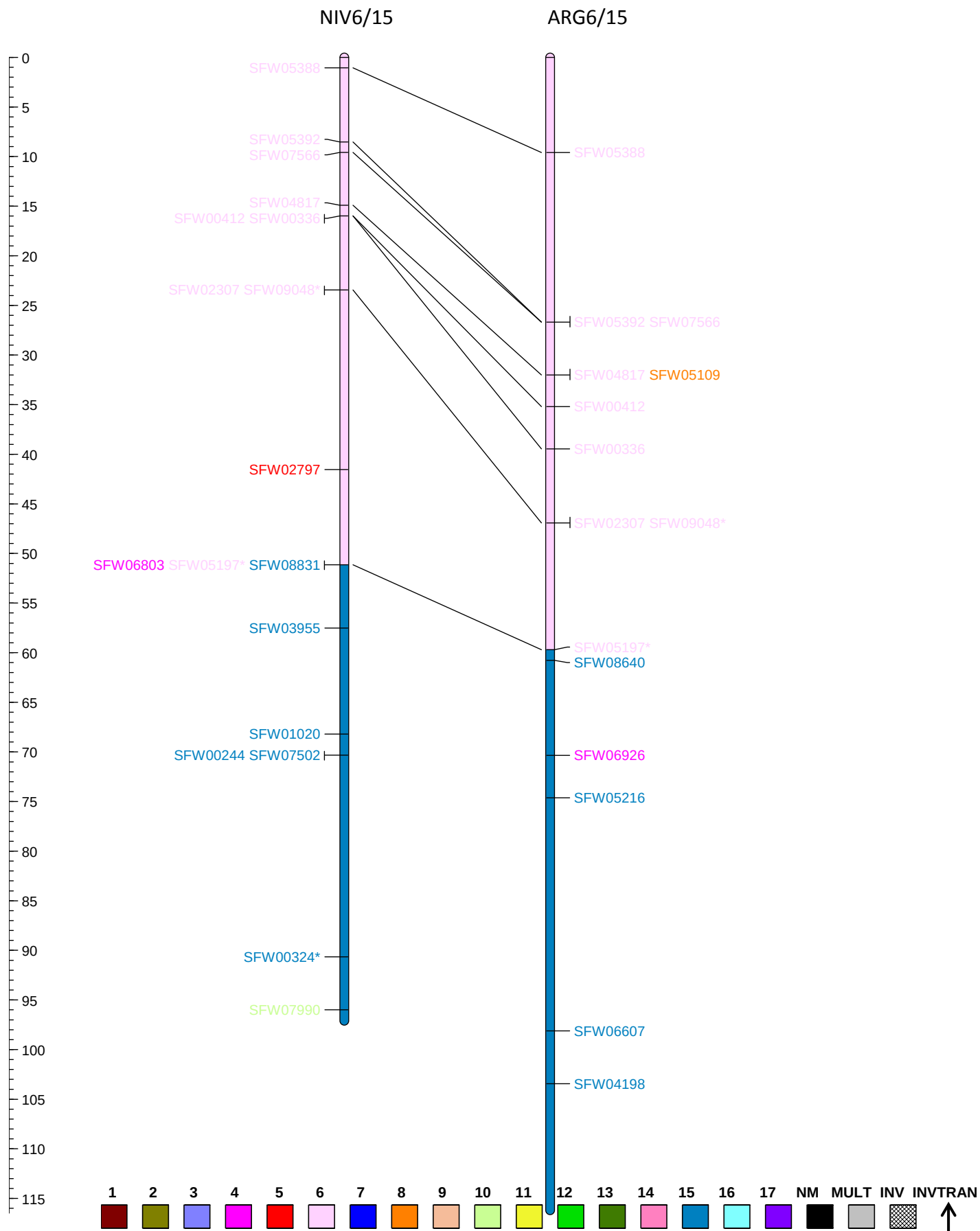


Figure S10 continued

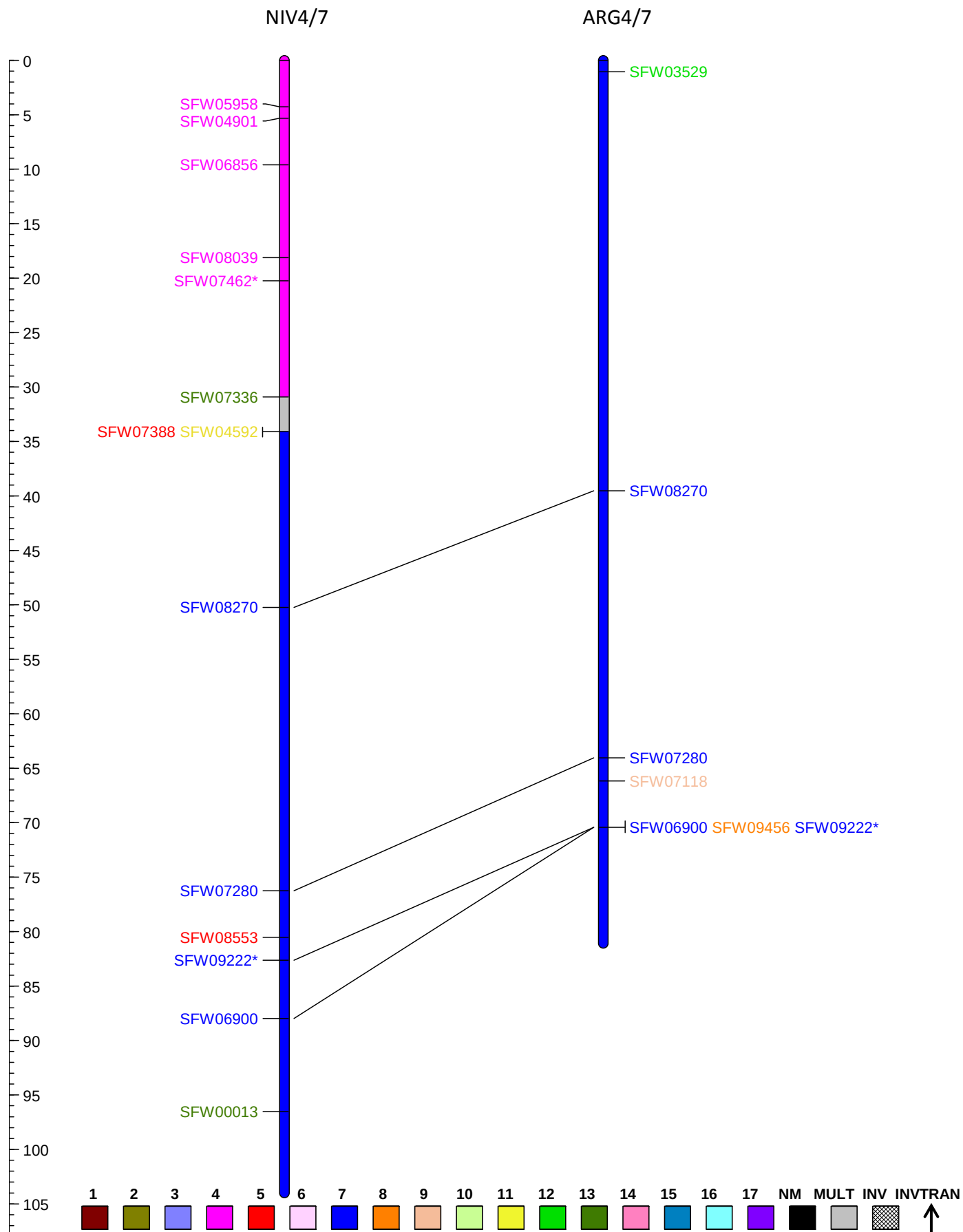


Figure S10 continued

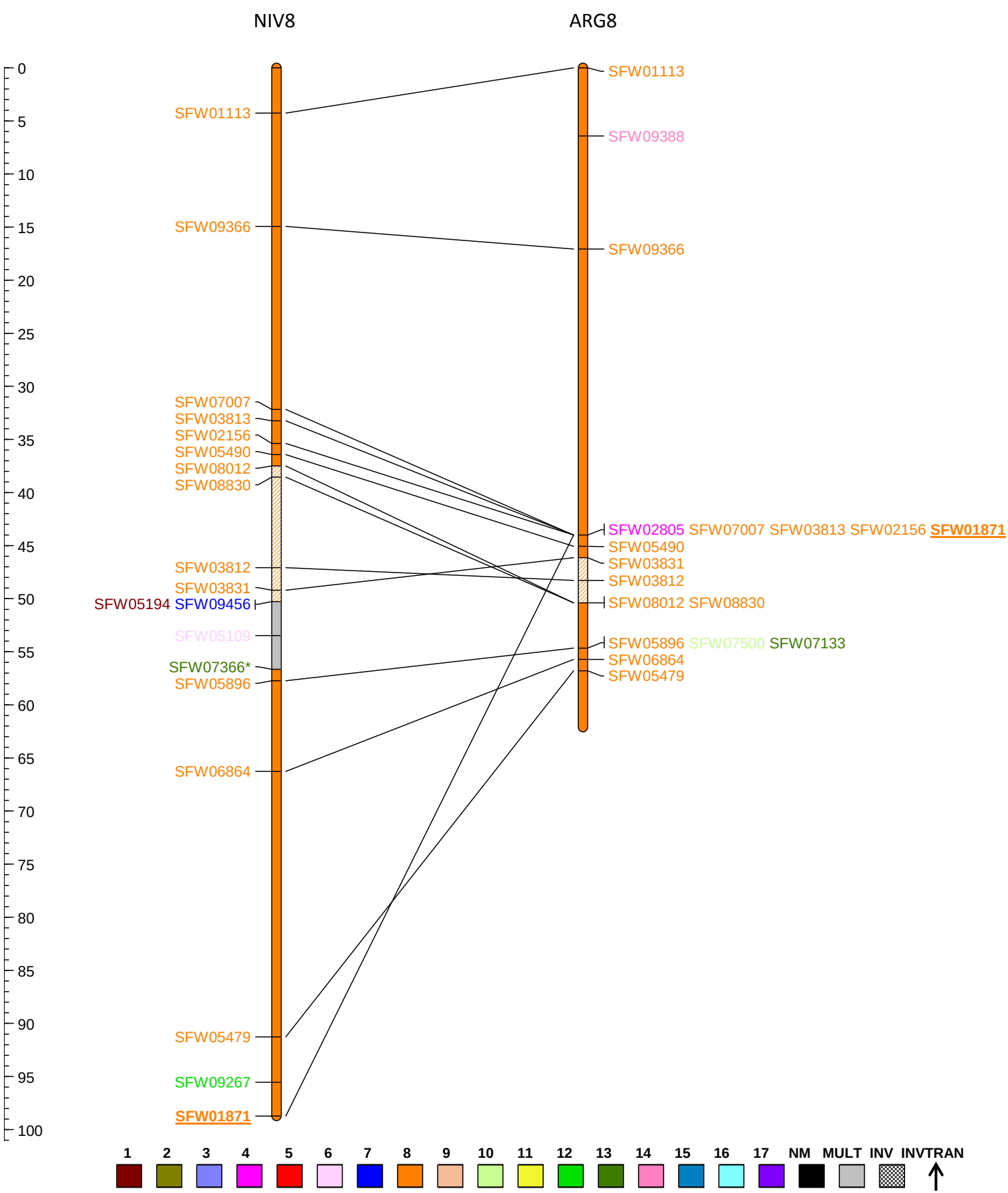


Figure S10 continued

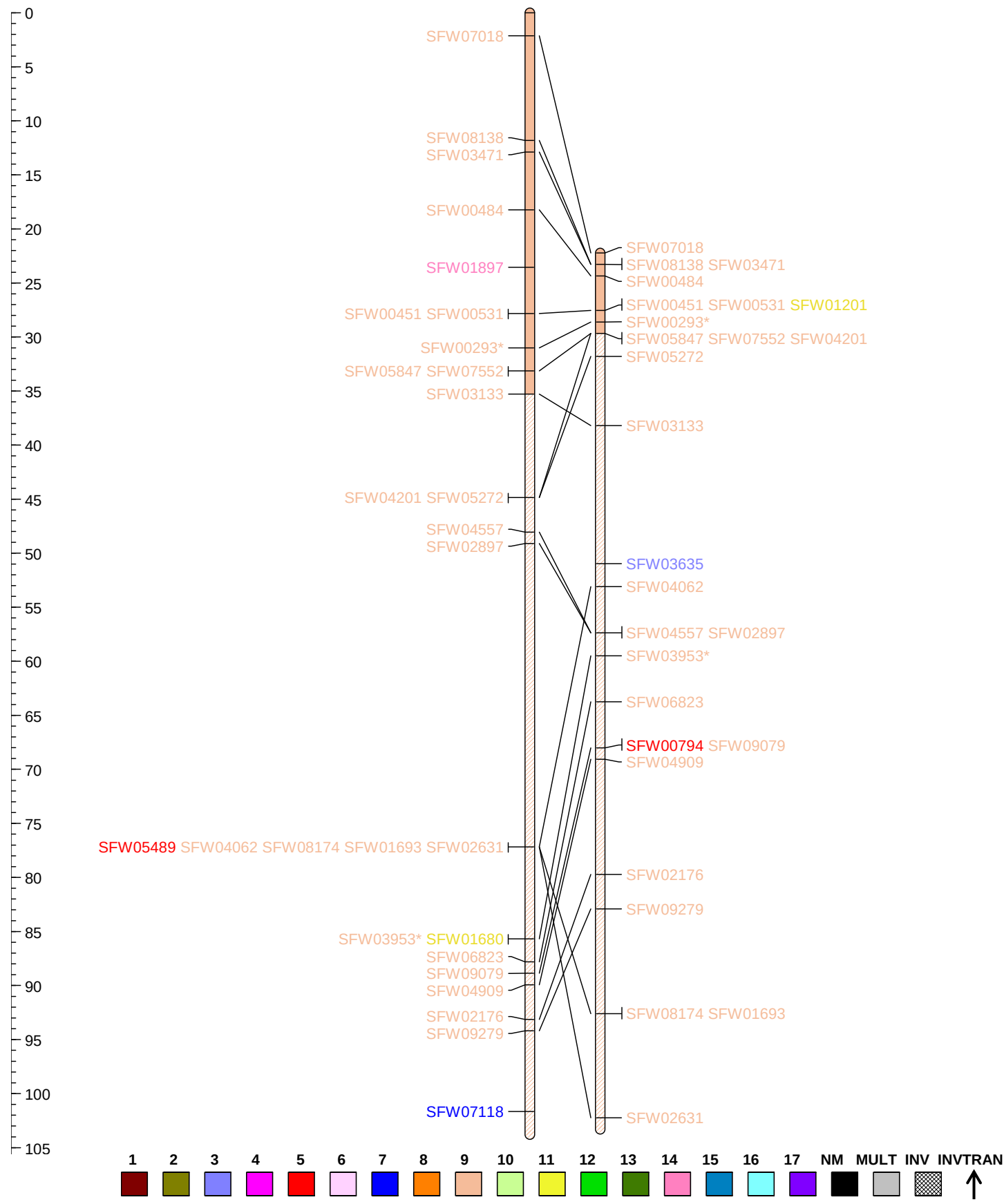


Figure S10 continued

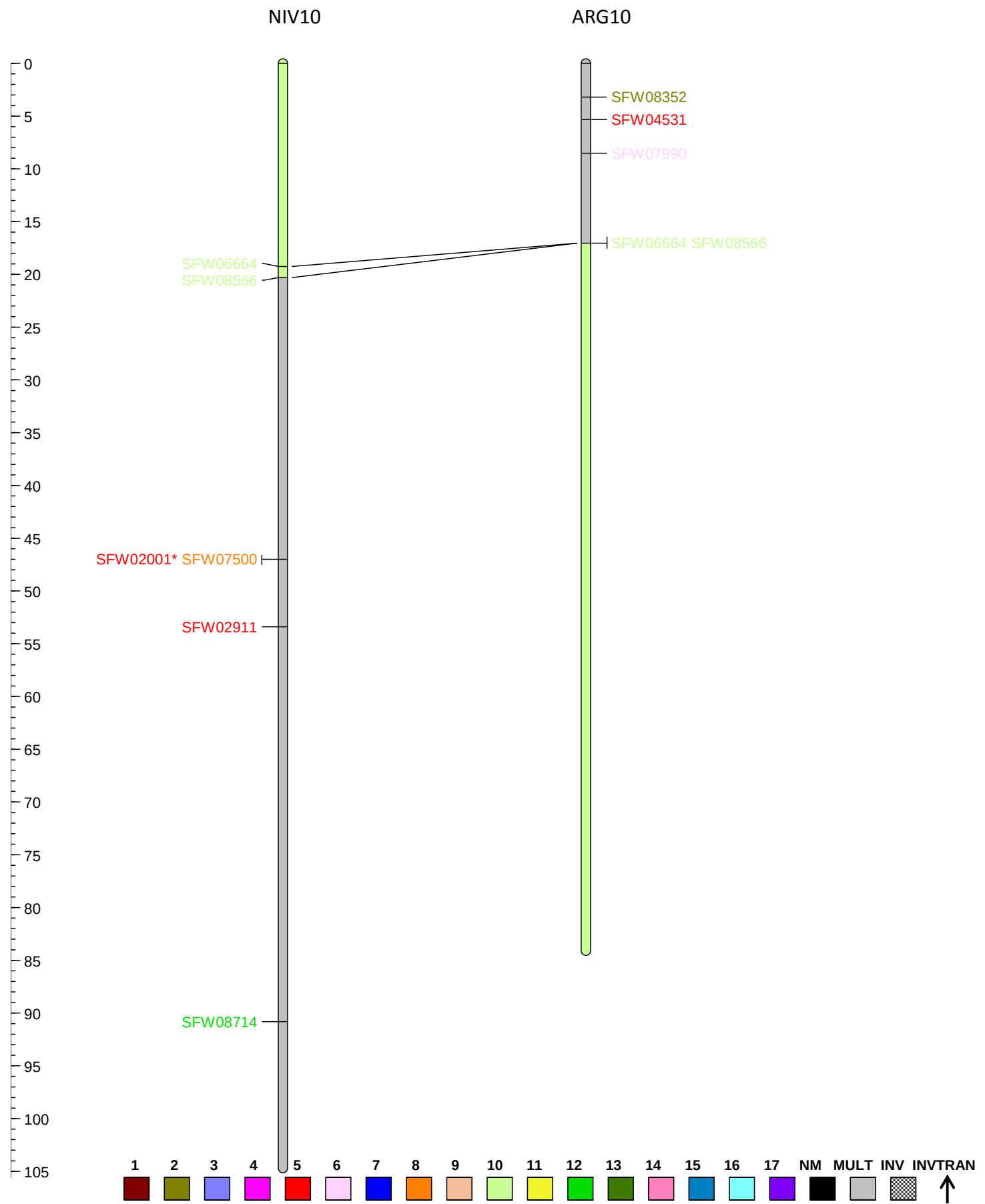


Figure S10 continued

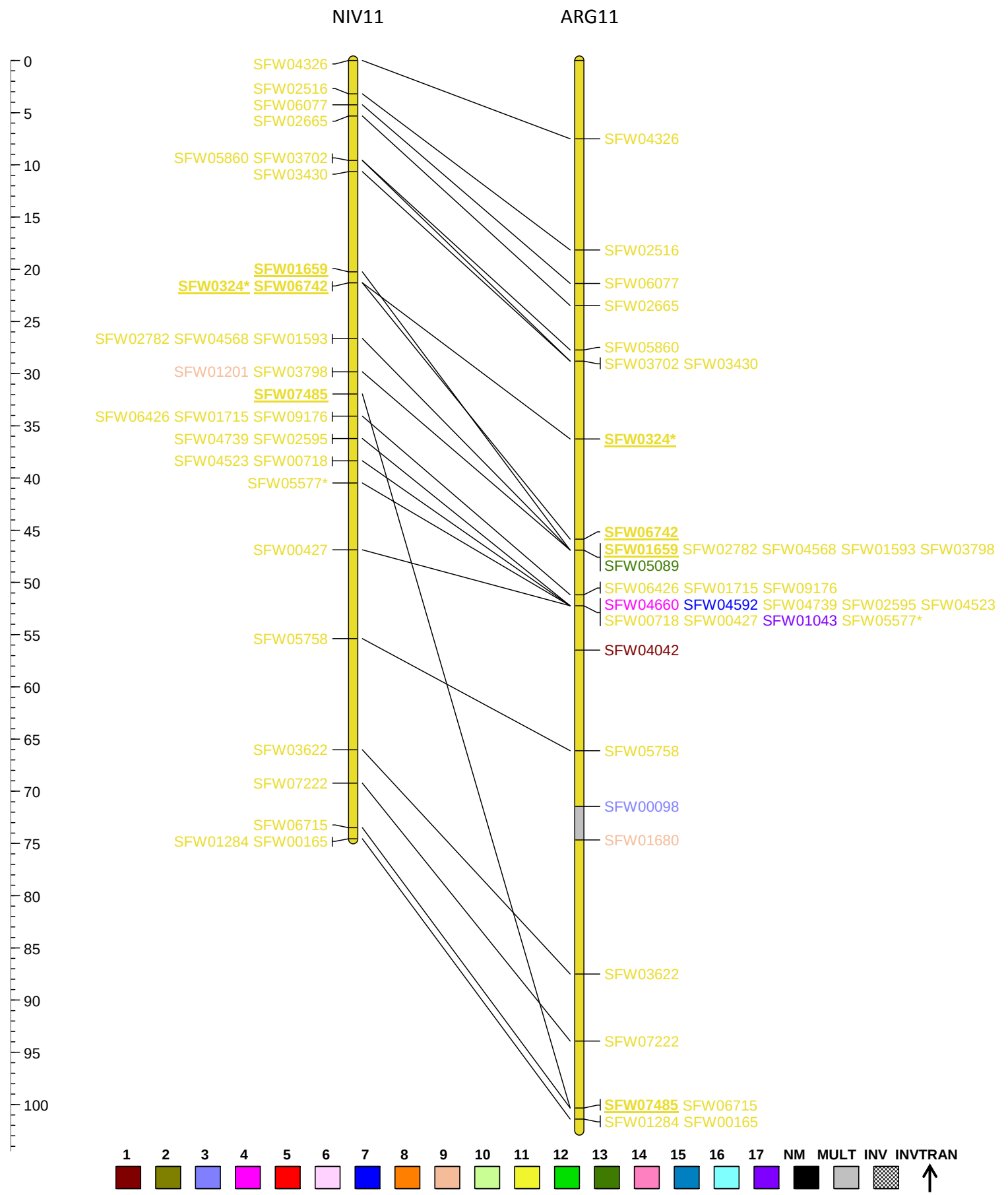
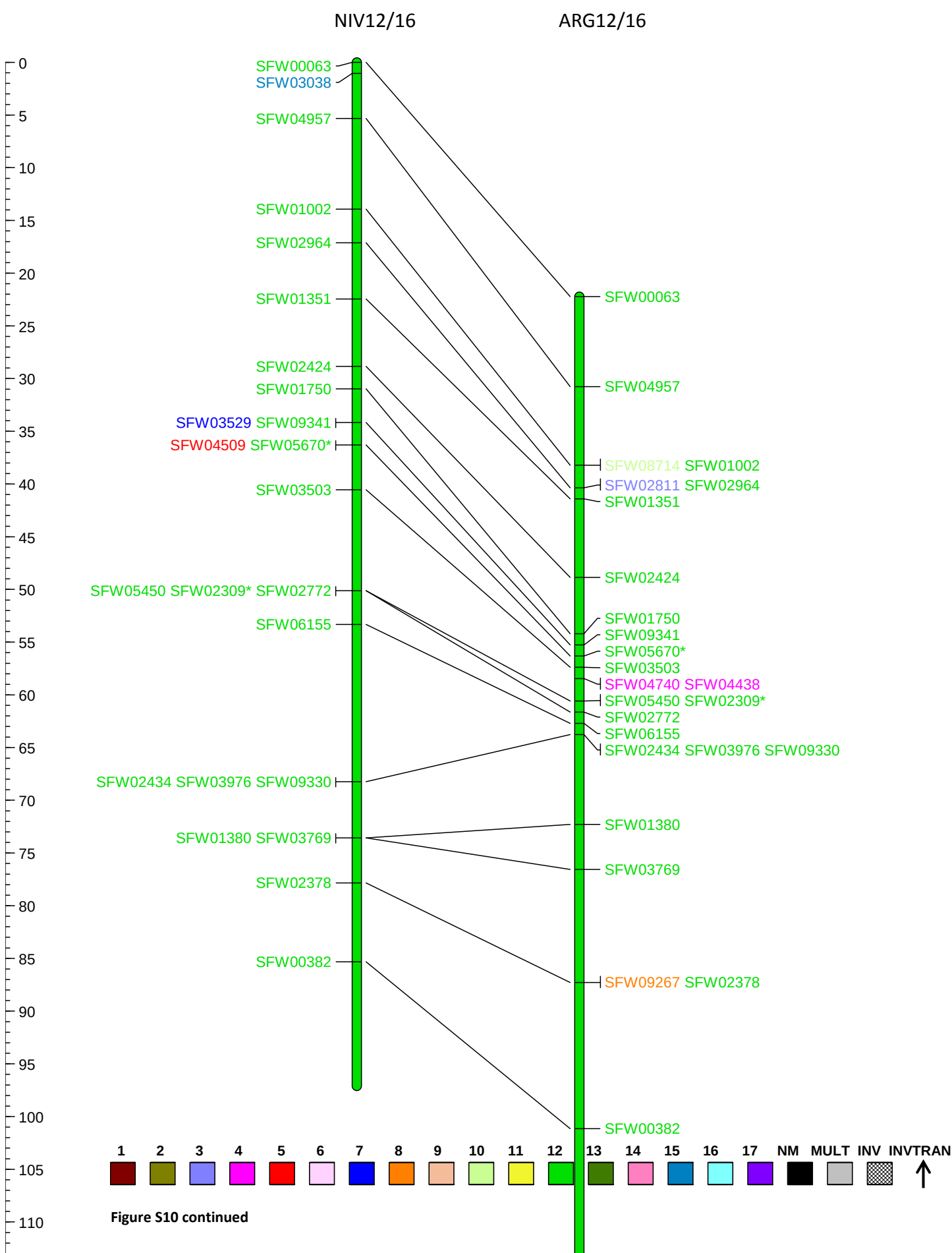


Figure S10 continued



NIV13

ARG13

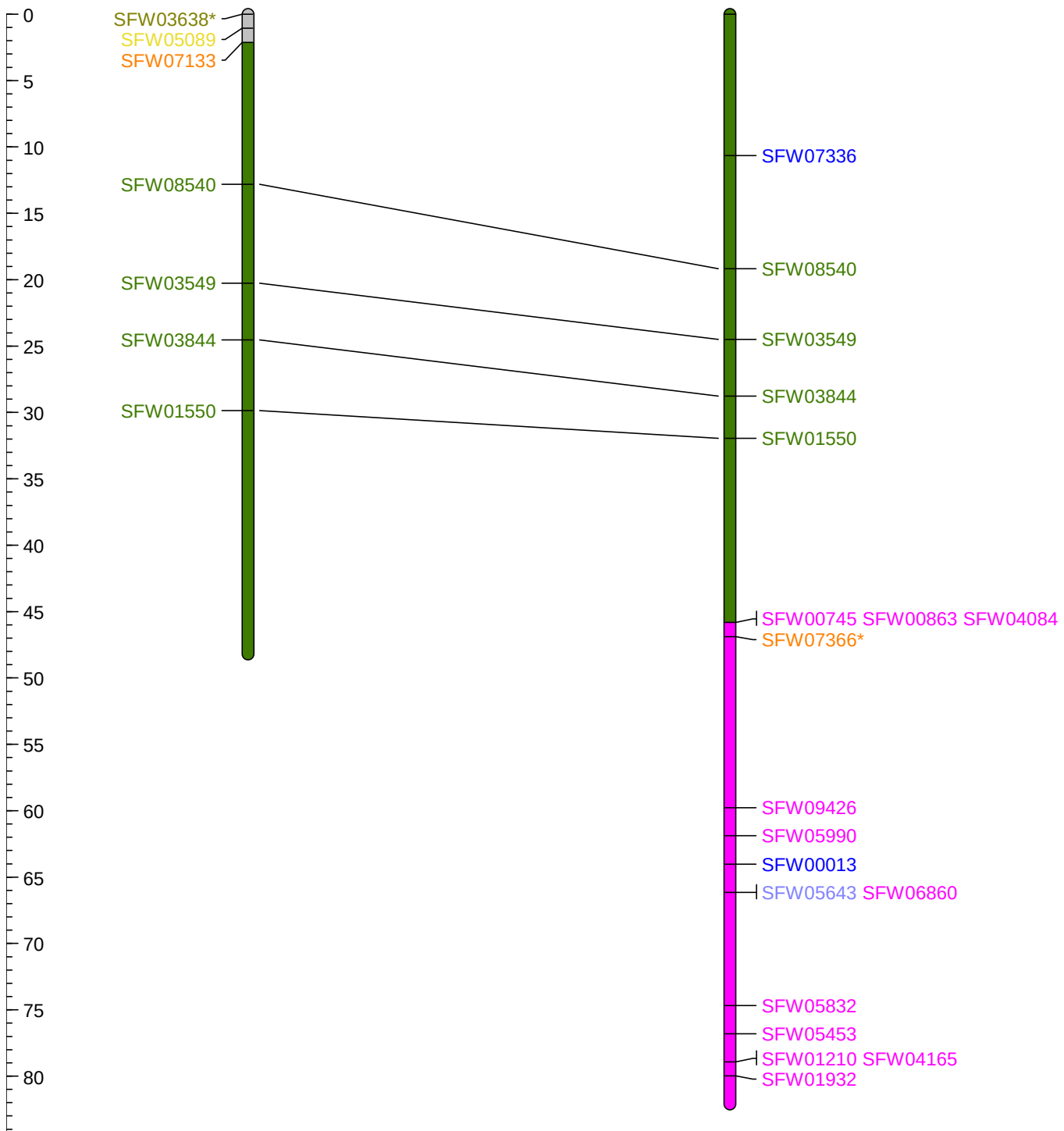


Figure S10 continued

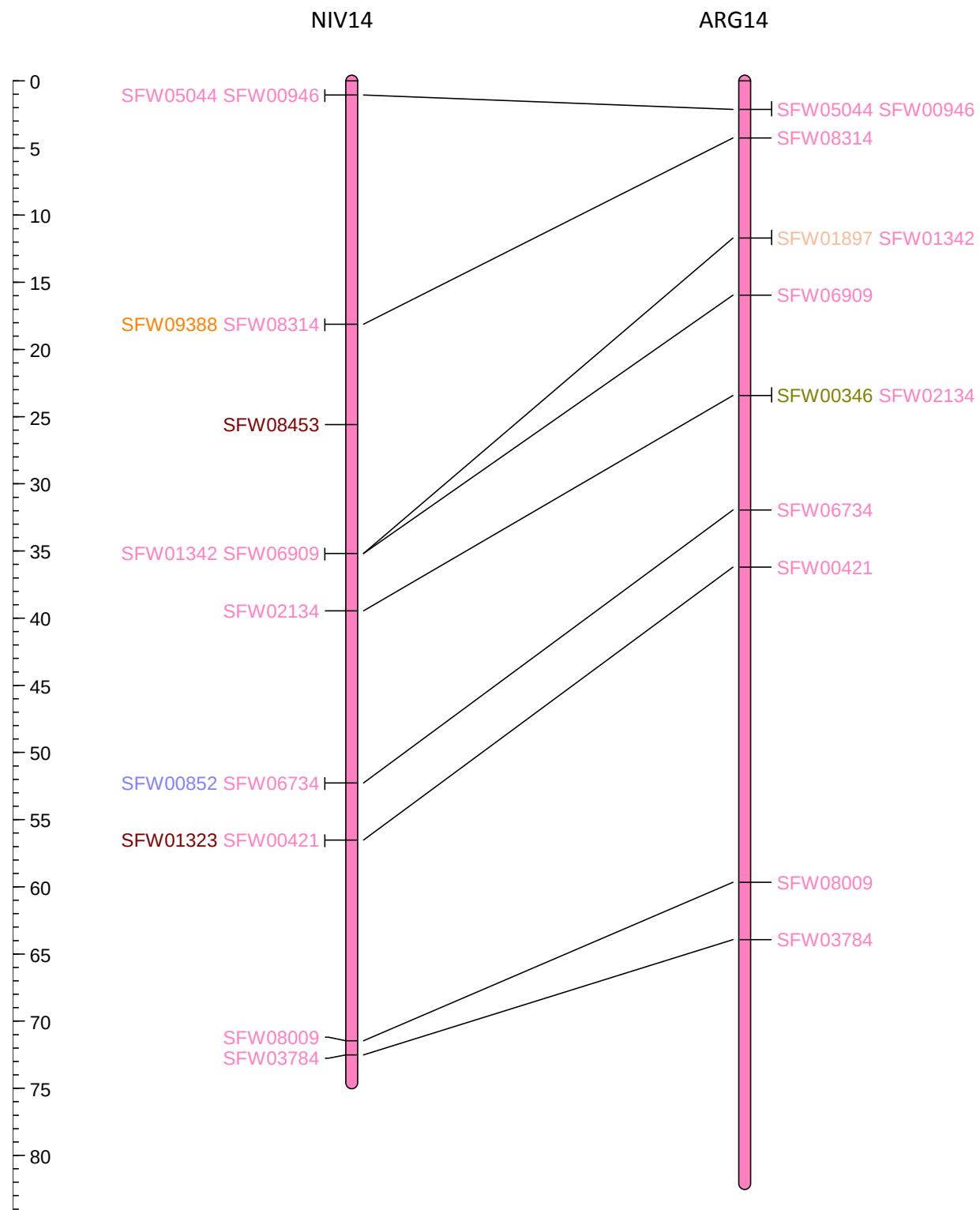


Figure S10 continued

NIV15

ARG15

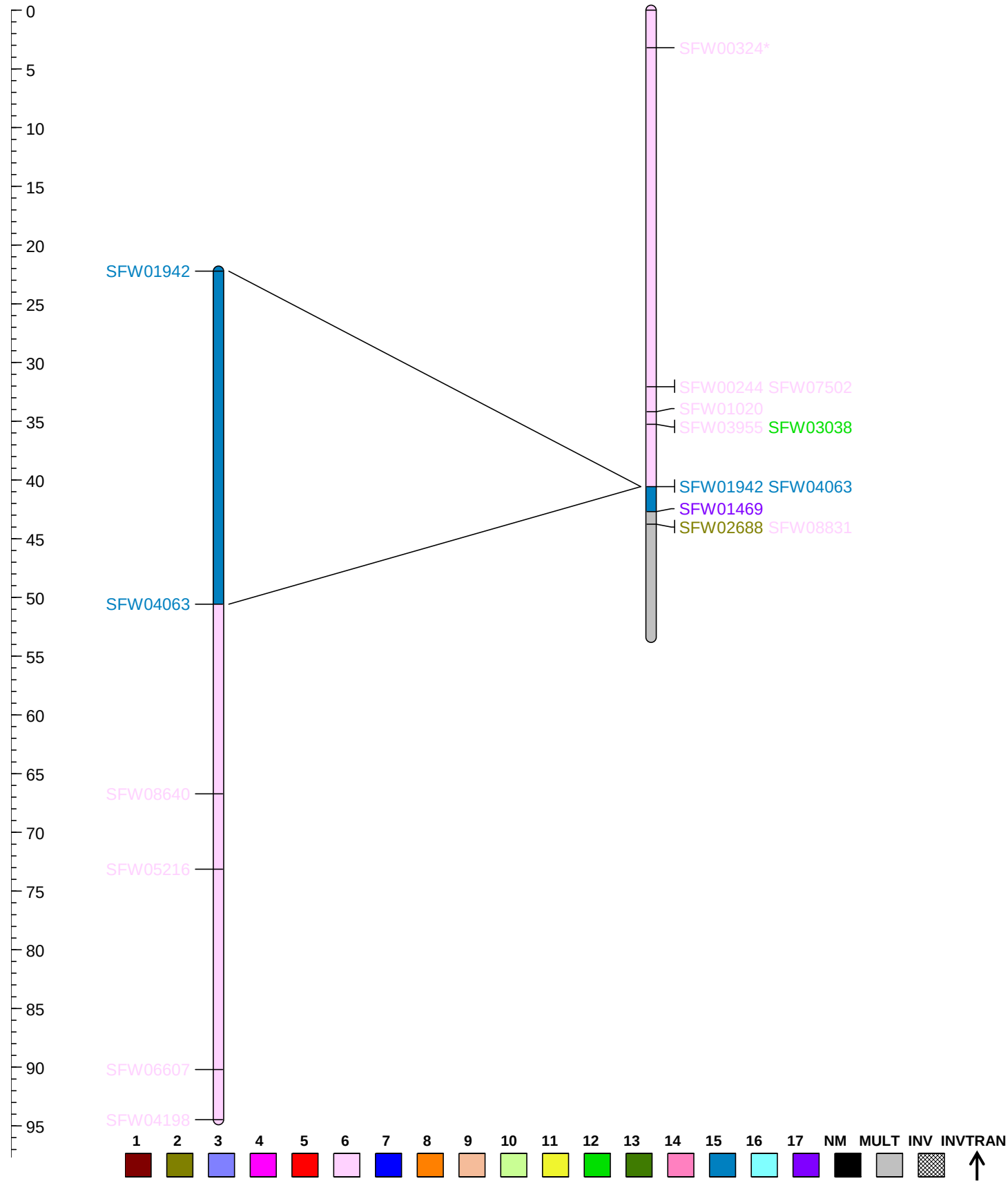


Figure S10 continued

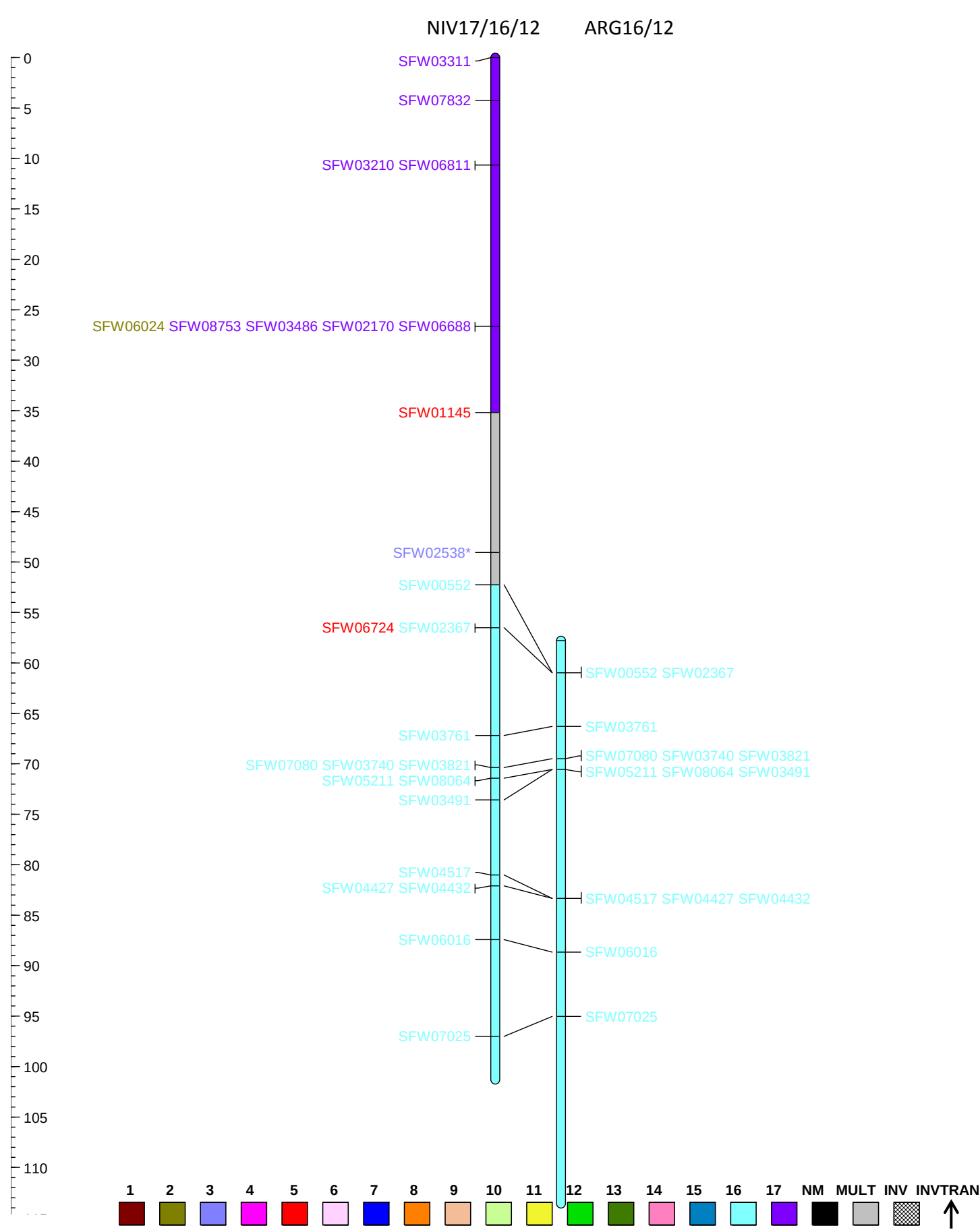
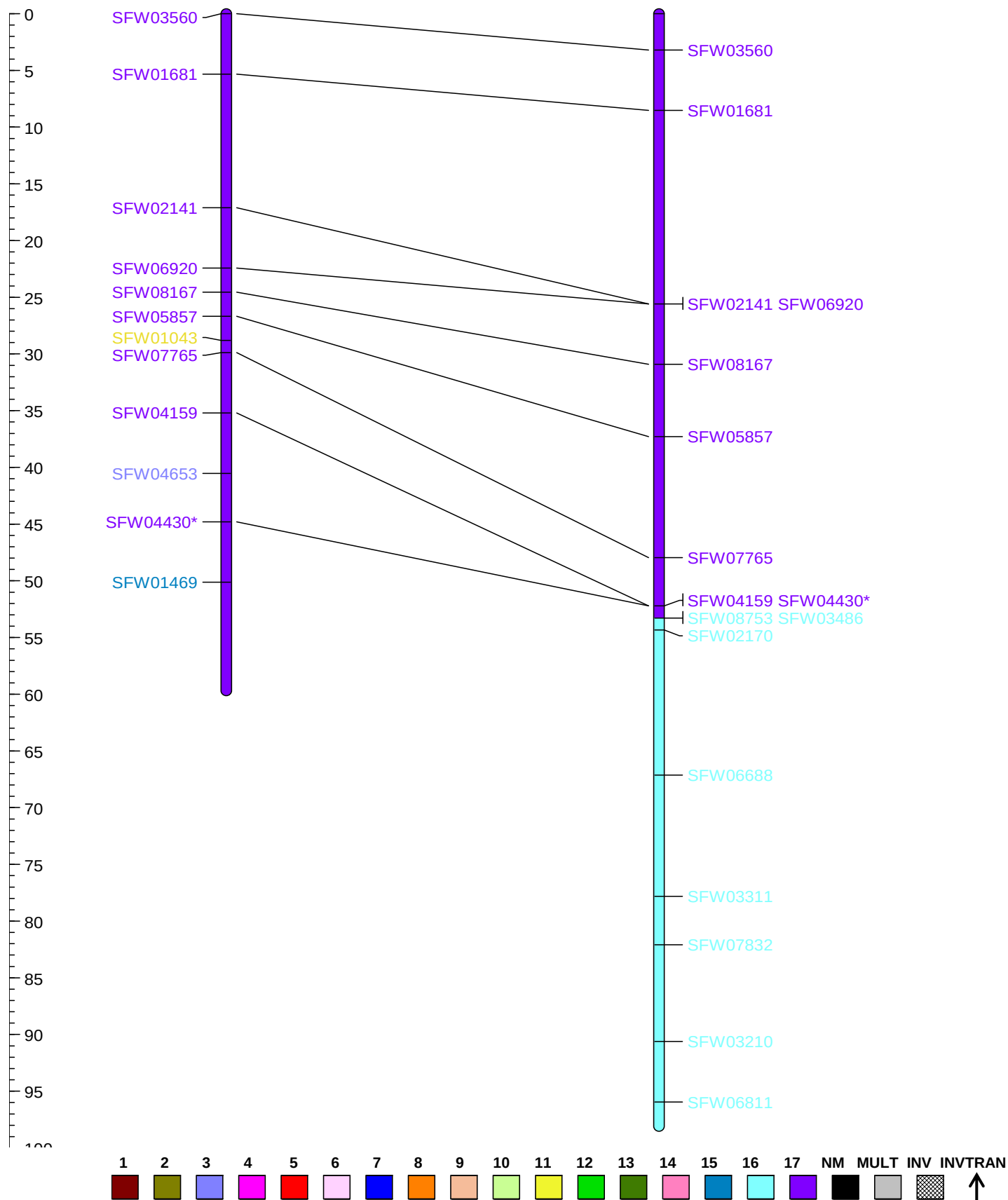
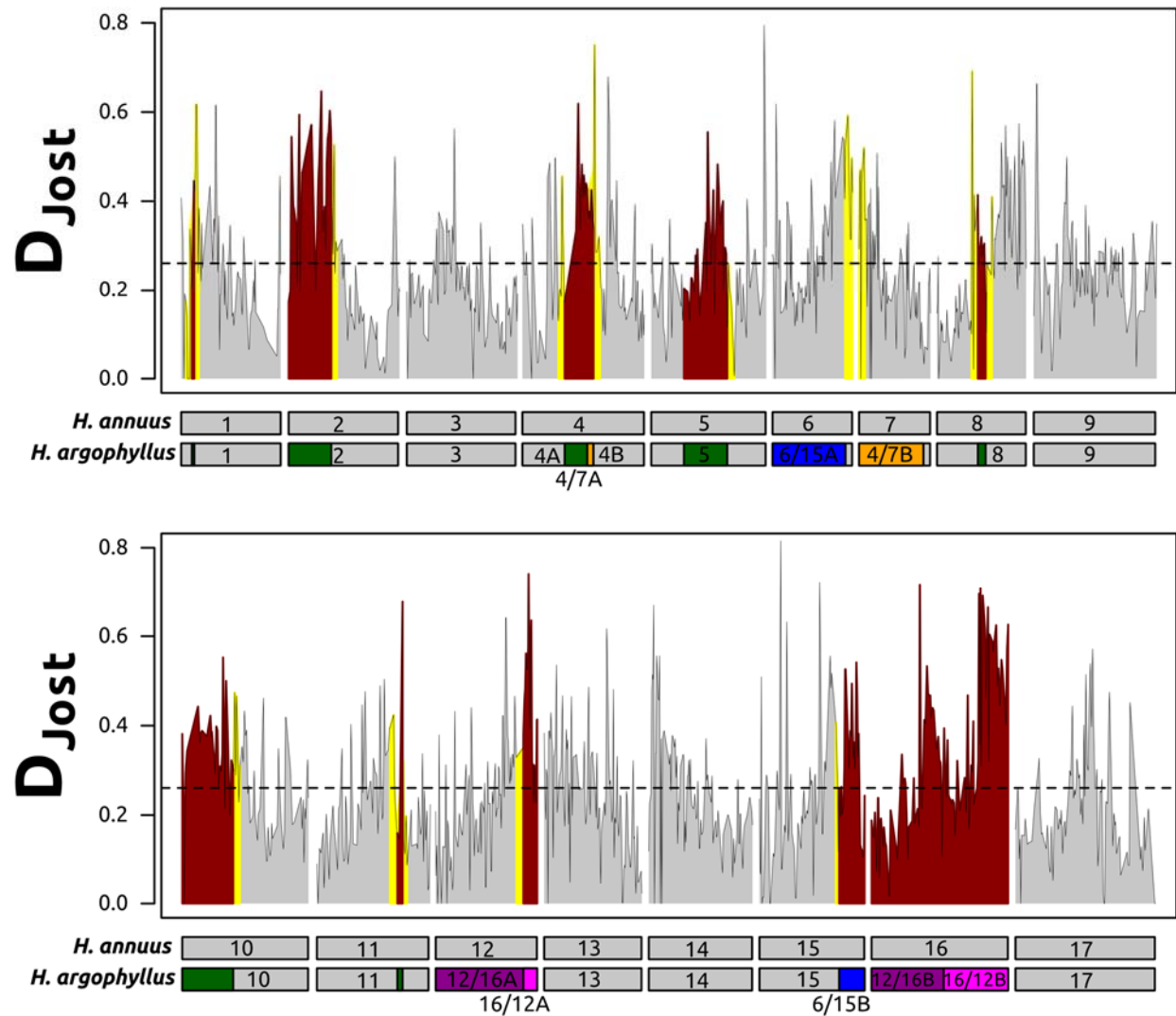


Figure S10 continued

NIV17

ARG17





Linkage groups (chromosomes)

Figure S11 Genome-wide divergence (D) between *Helianthus annuus* (ANN) and *H. argophyllus* (ARG) in syntenic and rearranged regions of the genome. Syntenic portions of the genome are colored in gray, rearranged portions are in red, and the 5 cM regions neighboring the rearrangements are in yellow. Linkage groups in ANN and their corresponding location in ARG are pictured below the x-axis. Inverted chromosomal segments are pictured in green, while translocated segments in ARG are in blue, orange, light purple, or dark purple.

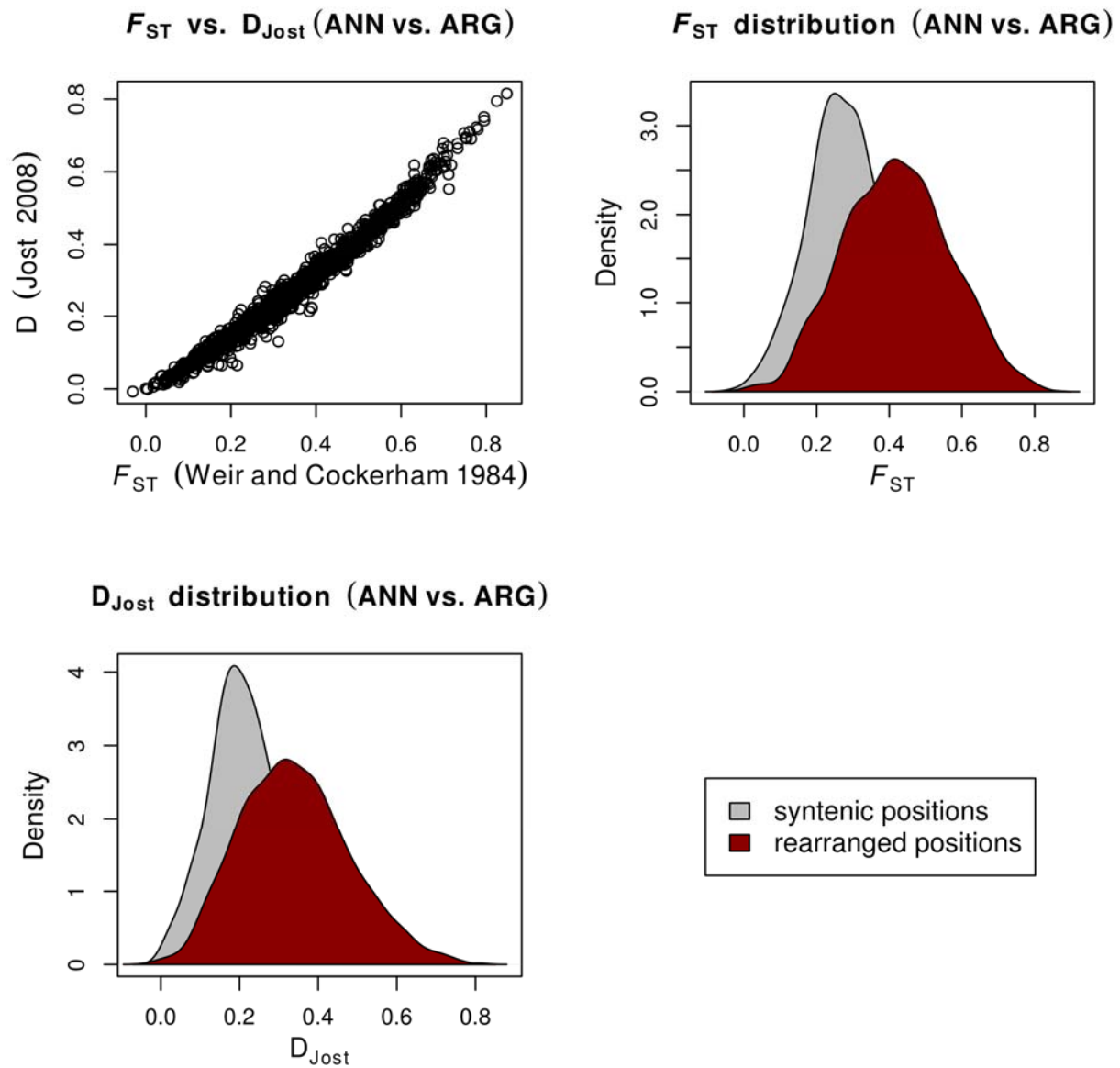


Figure S12 Comparison of the F_{ST} and D values: (A) correlation of the F_{ST} and D values, distribution of F_{ST} (B) and D (C) between *Helianthus annuus* (ANN) and *H. argophyllus* (ARG) in the syntenic and rearranged regions of the genome.

Table S1 Map statistics of the genetic maps of *Helianthus argophyllus* (ARG) and *H. niveus* ssp. *tephrodes* (NIV) and their comparison to the *H. annuus* (ANN) consensus map.

ARG	1	2	3	4	5	6/15	4/7	8	9	10	11	12/16	13	14	15	16/12	17	Total
Map length (cM)	94.9	56.9	69.3	58.7	68.3	116.2	81.1	62.1	81.1	84.1	102.5	90.7	82.1	82.1	53.4	55.8	98.1	1337.3
Number of markers	151	68	112	61	186	75	76	84	111	40	141	128	80	97	59	70	87	1626
Average distance between 2 markers (cM)	2.0	3.8	2.4	2.3	2.1	2.9	2.6	2.8	2.1	4.2	2.6	2.1	2.2	2.2	2.2	2.2	2.5	2.4
Maximum distance between 2 markers (cM)	7.5	11.9	6.4	7.5	9.7	7.5	8.6	11.9	9.7	45.7	8.6	8.6	9.7	6.4	9.7	15.4	6.4	45.7
# of inverted segments	1	1	0	2	1	1	1	1	0	1	1	0	0	0	0	0	0	10
# of translocated segments	0	0	0	0	0	1	2	0	0	1	0	1	1	0	0	2	0	8
% of markers not mapped in ANN	21%	16%	7%	7%	9%	12%	17%	4%	14%	10%	11%	5%	8%	9%	7%	9%	10%	10%
NIV	1	2	3	13/4	5	6/15	4/7	8	9	10	11	12/16	13	14	15	17/16/12	17	Total
Map length (cM)	111.2	72.4	78.1	86.5	94.0	97.1	104.0	98.7	103.8	104.7	74.6	97.1	48.2	74.6	72.2	101.3	59.7	1478.2
Number of markers	109	66	81	82	71	86	75	68	85	55	67	96	27	62	26	90	48	1194
Average distance between 2 markers (cM)	3.0	1.9	2.5	2.8	3.0	2.4	3.6	3.0	2.8	3.5	2.1	2.4	3.7	2.5	5.6	2.4	2.3	2.7
Maximum distance between 2 markers (cM)	11.9	5.3	13.1	10.8	9.7	7.5	15.4	14.2	45.7	8.6	5.3	8.6	11.9	6.4	16.5	6.4	7.5	22.7
# of inverted segments	1	0	1	0	1	1	0	2	1	2	1	1	0	1	1	0	0	13
# of translocated segments	0	1	0	3	0	1	2	0	1	1	1	1	0	2	0	3	2	18
% of markers not mapped in ANN	18%	12%	11%	12%	15%	10%	15%	6%	11%	7%	6%	11%	26%	11%	12%	8%	4%	11%

Table S2 Marker colocalization in the genetic maps of *Helianthus argophyllus* (ARG) and *H. niveus* ssp. *tephrodes* (NIV).

ARG	1	2	3	4	5	6/15	4/7	8	9	10	11	12/16	13	14	15	16/12	17	Total
Markers	151	68	112	61	186	75	76	84	111	40	141	128	80	97	59	70	87	1626
Positions	48	16	30	26	33	42	32	23	41	21	41	45	39	39	25	26	40	567
Positions with 1 marker	25	4	10	12	17	26	18	10	18	12	16	16	21	23	11	14	29	282
Postions with 2+ markers	23	12	20	14	16	16	14	13	23	9	25	29	18	16	14	12	11	285
% of markers cosegregating w/ 1+ markers	83.4	94.1	91.1	80.3	90.9	65.3	76.3	88.1	83.8	70.0	88.7	87.5	73.8	76.3	81.4	80.0	66.7	81.0
Maximum # of markers cosegregating at a single position	58	12	16	9	98	14	12	21	12	6	26	10	9	12	7	9	23	21
Average # of colocalizing markers per position	5.5	5.3	5.1	3.5	10.6	3.3	4.1	5.7	4.4	3.1	5.0	4.1	3.4	4.6	3.4	4.7	5.3	4.8
NIV	1	2	3	13/4	5	6/15	4/7	8	9	10	11	12/16	13	14	15	17/16/12	17	Total
Markers	109	66	81	82	71	86	75	68	85	55	67	96	27	62	26	90	48	1194
Positions	38	40	32	32	33	41	31	34	38	31	38	42	14	32	15	43	28	562
Positions with 1 marker	18	29	14	16	20	22	13	20	22	24	20	20	8	14	8	27	18	313
Postions with 2+ markers	20	11	18	16	13	19	18	14	16	7	18	22	6	18	7	16	10	249
% of markers cosegregating w/ 1+ markers	83.5	56.1	82.7	80.5	71.8	74.4	82.7	70.6	74.1	56.4	70.1	79.2	70.4	77.4	69.2	70.0	62.5	72.4
Maximum # of markers cosegregating at a single position	26	9	12	14	10	12	10	8	11	13	7	8	6	5	5	12	7	10
Average # of colocalizing markers per position	4.6	3.4	3.7	4.1	4.1	3.4	3.6	3.4	3.9	4.4	2.7	3.5	3.2	2.9	3.0	3.9	3.3	3.6

Table S3 Length (cM) of the syntenic segments (SS), inverted segments (INV), translocated segments (TRANS), and inverted translocated segments (TRANS/INV) by linkage group (LG) for the genetic maps of *Helianthus argophyllus* (ARG) and *H. niveus* ssp. *tephrodes* (NIV) relative to the *H. annuus* (ANN) consensus map.

Species	LG	Segment type	Segment #	Start point (cM)	End point (cM)	Segment length (cM)
NIV	1	SS	1	0	32.18	32.18
NIV	1	INV	1	32.18	57.73	25.55
NIV	1	SS	2	57.73	111.15	53.42
ARG	1	SS	1	0	36.3	36.3
ARG	1	INV	1	36.3	44.81	8.51
ARG	1	SS	2	44.81	94.9	50.09
NIV	2	SS	1	0	8.51	8.51
NIV	2	TRANS	1	8.51	10.64	2.13
NIV	2	SS	2	10.64	72.42	61.78
ARG	2	INV	1	0	5.33	5.33
ARG	2	SS	1	5.33	56.9	51.57
NIV	3	SS	1	0	29.92	29.92
NIV	3	INV	1	29.92	33.12	3.2
NIV	3	SS	2	33.12	78.11	44.99
ARG	3	SS	1	0	69.3	69.3
NIV	13/4	TRANS/INV	1	0	12.79	12.79
NIV	13/4	TRANS	1	12.79	18.11	5.32
NIV	13/4	TRANS/INV	2	18.11	46	27.89
NIV	13/4	TRANS	2	46	53.46	7.46
NIV	13/4	SS	1	53.46	54.52	1.06
NIV	13/4	TRANS/INV	3	54.52	58.78	4.26
NIV	13/4	SS	2	58.78	86.5	27.72
ARG	4	SS	1	0	6.38	6.38
ARG	4	INV	1	6.38	8.51	2.13
ARG	4	SS	2	8.51	24.53	16.02
ARG	4	INV	2	24.53	36.29	11.76
ARG	4	SS	3	36.29	58.7	22.41
NIV	5	SS	1	0	44.82	44.82
NIV	5	INV	1	44.82	66.19	21.37
NIV	5	SS	2	66.19	94.03	27.84
ARG	5	SS	1	0	19.2	19.2
ARG	5	INV	1	19.2	31.97	12.77
ARG	5	SS	2	31.97	68.3	36.33
NIV	6/15	SS	1	0	24.5	24.5
NIV	6/15	INV	1	24.5	49.01	24.51
NIV	6/15	SS	2	49.01	51.15	2.14
NIV	6/15	TRANS	1	51.15	97.06	45.91
ARG	6/15	SS	1	0	1.06	1.06
ARG	6/15	INV	1	1.06	3.19	2.13
ARG	6/15	SS	2	3.19	59.7	56.51
ARG	6/15	TRANS/INV	1	59.7	76.75	17.05
ARG	6/15	TRANS	1	76.75	82.07	5.32
ARG	6/15	TRANS/INV	2	82.07	93.84	11.77
ARG	6/15	TRANS	2	93.84	116.3	22.46
NIV	4/7	TRANS	1	0	34.1	34.1
NIV	4/7	SS	1	34.1	90.1	56
NIV	4/7	TRANS	2	90.1	104.02	13.92
ARG	4/7	TRANS	1	0	1.06	1.06
ARG	4/7	INV	1	1.06	9.59	8.53
ARG	4/7	TRANS/INV	1	9.59	34.2	24.61
ARG	4/7	SS	1	34.2	81.1	46.9
NIV	8	SS	1	0	37.5	37.5
NIV	8	INV	1	37.5	54.53	17.03
NIV	8	SS	2	54.53	57.72	3.19
NIV	8	INV	2	57.72	96.6	38.88
NIV	8	SS	3	96.6	98.73	2.13
ARG	8	SS	1	0	54.64	54.64
ARG	8	INV	1	54.64	56.78	2.14
ARG	8	SS	2	56.78	62.1	5.32
NIV	9	SS	1	0	35.27	35.27
NIV	9	INV	1	35.27	97.39	62.12
NIV	9	TRANS	1	97.39	103.78	6.39
ARG	9	SS	1	0	81	81
NIV	10	SS	1	0	25.65	25.65

Table S3 continued.

Species	LG	Segment type	Segment #	Start point (cM)	End point (cM)	Segment length (cM)
NIV	10	INV	1	25.65	36.32	10.67
NIV	10	SS	2	36.32	68.34	32.02
NIV	10	INV	2	68.34	76.94	8.6
NIV	10	TRANS	1	76.94	91.88	14.94
NIV	10	SS	3	91.88	104.66	12.78
ARG	10	SS	1	0	5.32	5.32
ARG	10	INV	1	5.32	17.04	11.72
ARG	10	SS	2	17.04	76.63	59.59
ARG	10	TRANS	1	76.63	80.89	4.26
ARG	10	SS	3	80.89	84.1	3.21
NIV	11	SS	1	0	5.32	5.32
NIV	11	INV	1	5.32	7.45	2.13
NIV	11	SS	2	7.45	30.89	23.44
NIV	11	INV	2	30.89	38.34	7.45
NIV	11	TRANS	1	38.34	45.79	7.45
NIV	11	SS	3	45.79	74.55	28.76
ARG	11	SS	1	0	46.91	46.91
ARG	11	INV	1	46.91	52.23	5.32
ARG	11	SS	2	52.23	102.5	50.27
NIV	12/16	SS	1	0	43.74	43.74
NIV	12/16	INV	1	43.74	53.32	9.58
NIV	12/16	TRANS/INV	1	53.32	97.09	43.77
ARG	12/16	SS	1	0	39.42	39.42
ARG	12/16	TRANS/INV	1	39.42	90.7	51.28
NIV	13	SS	1	0	48.2	48.2
ARG	13	SS	1	0	3.19	3.19
ARG	13	TRANS	1	3.19	6.39	3.2
ARG	13	SS	2	6.39	82.1	75.71
NIV	14	SS	1	0	20.25	20.25
NIV	14	INV	1	20.25	24.51	4.26
NIV	14	TRANS	1	24.51	26.64	2.13
NIV	14	SS	2	26.62	67.2	40.58
NIV	14	TRANS	2	67.2	70.39	3.19
NIV	14	SS	3	70.39	74.65	4.26
ARG	14	SS	1	0	82.1	82.1
NIV	15	INV	1	0	28.36	28.36
NIV	15	SS	1	28.36	72.24	43.88
ARG	15	SS	1	0	53.6	53.6
NIV	17/16/12	TRANS/INV	1	0	49.05	49.05
NIV	17/16/12	TRANS	1	49.05	50.11	1.06
NIV	17/16/12	SS	1	50.11	87.41	37.3
NIV	17/16/12	TRANS	2	87.41	101.27	13.86
ARG	16/12	SS	1	0	1.06	1.06
ARG	16/12	TRANS	1	1.06	3.19	2.13
ARG	16/12	SS	2	3.19	35.14	31.95
ARG	16/12	TRANS	2	35.14	55.18	20.04
NIV	17	SS	1	0	4.27	4.27
NIV	17	TRANS	1	4.27	5.33	1.06
NIV	17	SS	2	5.33	45.86	40.53
NIV	17	TRANS	2	45.86	59.74	13.88
ARG	17	SS	1	0	98.1	98.1

Table S4 Length (cM) of the rearranged segments (INV & TRANS), inverted segments (INV), translocated segments (TRANS), and inverted & translocated segments (TRANS/INV) between *Helianthus argophyllus* (ARG) and *H. niveus* ssp. *tephrodes* (NIV) relative to the *H. annuus* (ANN) consensus map.

	Avg. length of all rearranged segments	Avg. length of all INV	Maximum length of INV	Minimum length of INV	Avg. length of all TRANS	Maximum length of TRANS	Minimum length of TRANS
ARG	11.12	7.03	12.77	2.13	14.83	51.28	1.06
NIV	16.69	18.84	62.12	2.13	15.53	43.77	1.06

Table S5 Genome coverage (%) of the genetic maps of *Helianthus argophyllus* (ARG) and *H. niveus* ssp. *tephrodes* (NIV) based on the 295 SNP markers mapped in cultivated sunflower (*Helianthus annuus*), ARG, and NIV.

ARG	1	2	3	4	5	6/15	4/7	8	9	10	11	12/16	13	14	15	16/12	17	Total
	61.8	60.2	73.8	23.7	84.4	60.5	7.9	48.0	98.9	16.5	91.7	87.1	84.4	46.8	21.5	61.0	94.6	62.4
NIV	1	2	3	13/4	5	6/15	4/7	8	9	10	11	12/16	13	14	15	17/16/12	17	Total
	63.4	100.0	78.0	61.6	70.4	76.9	63.5	70.3	95.9	7.2	100.0	87.9	62.0	95.7	60.7	95.8	83.8	73.9