

Figure S1 Detection of 49 bp deletion in *trnL-UAA* intron in lowland and upland switchgrass. Alamo and Kanlow represented the southern and northern lowland ecotypes, respectively. While Dacotah represented a typical upland ecotype. "M" indicated the molecular weight standard with 1 kb DNA Ladder (Axygen Biosciences, Union City, CA)

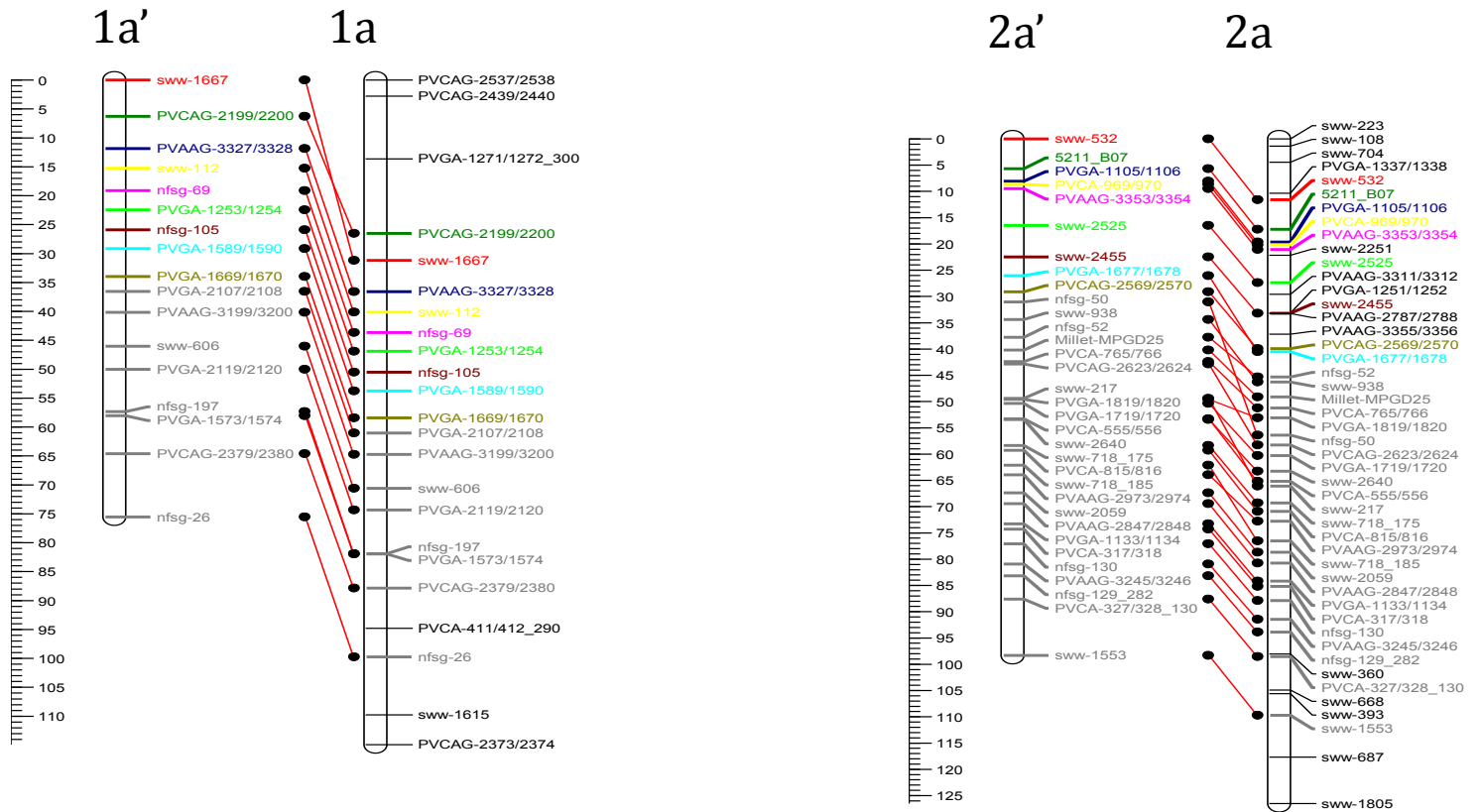
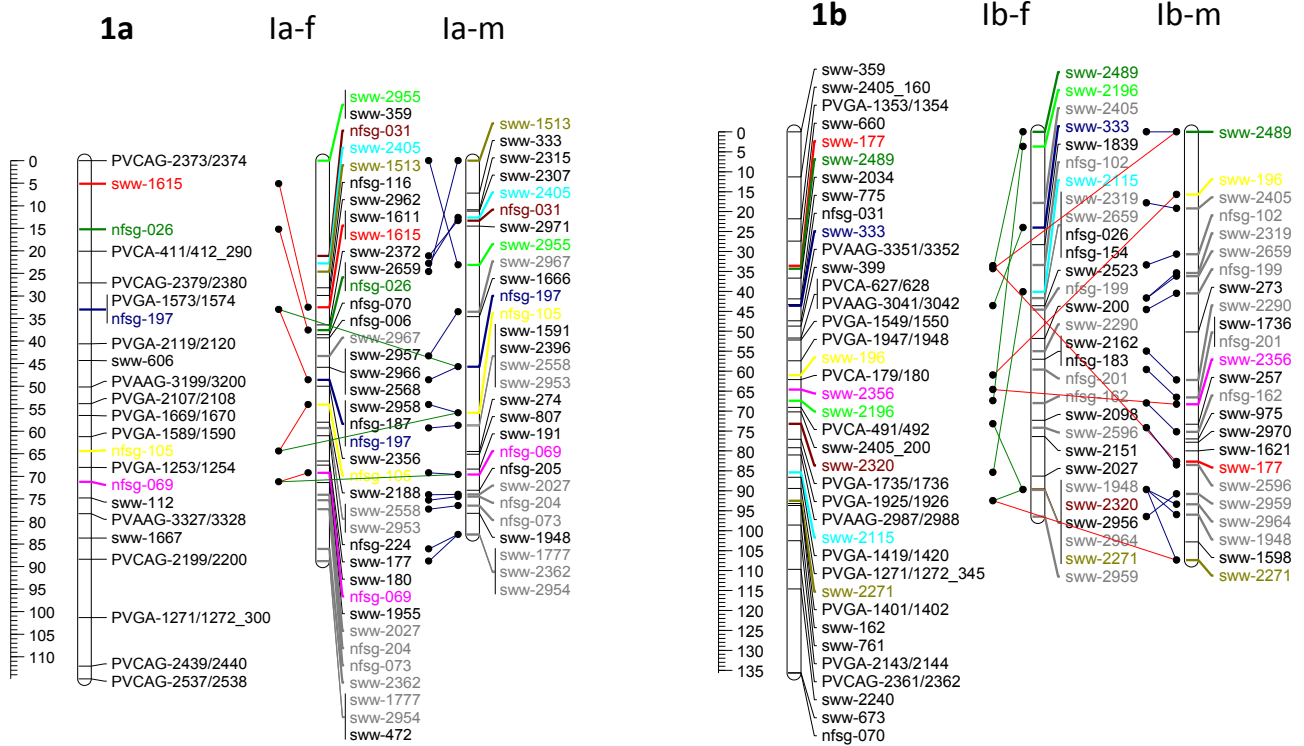


Figure S2 Collinerity between the initial and final framework linkage maps. Here only linkage groups (LGs) 1a and 2a are shown as the representatives of all LGs. The LG number of initial framework map is indicated by a quote symbol. All loci mapped with the same markers across LGs are highlighted with matching colors

Figure S3



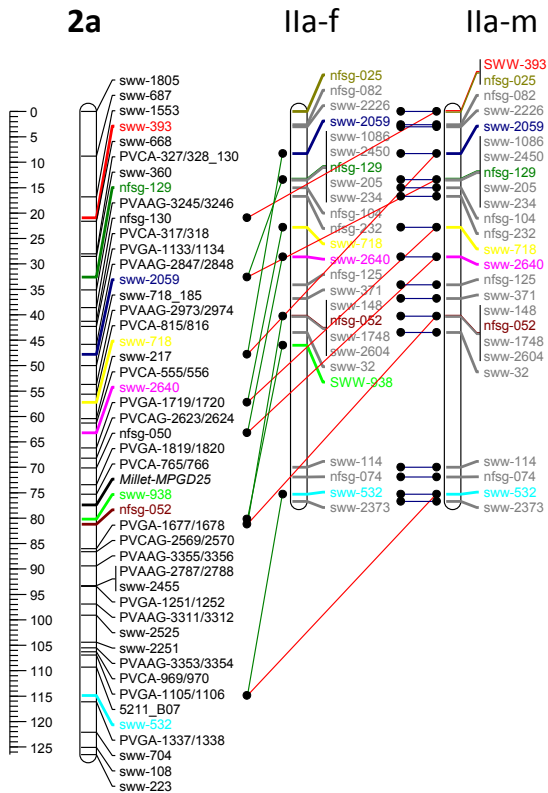
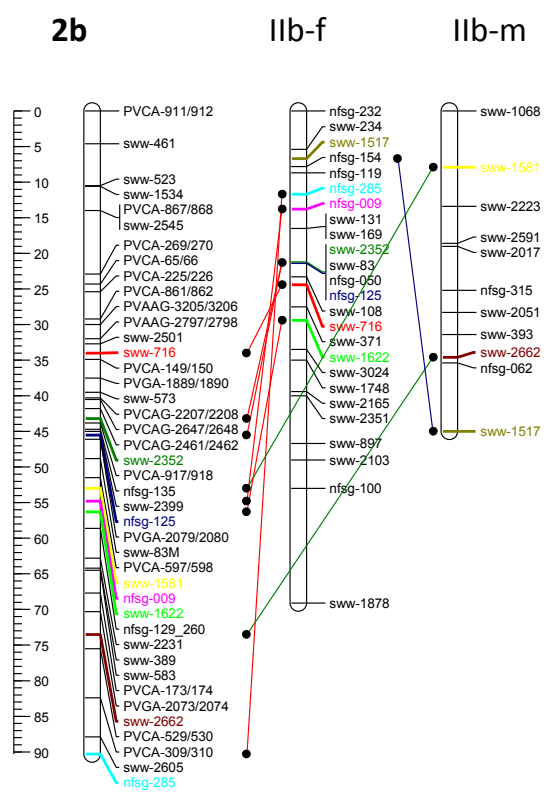


Figure S3-Continued



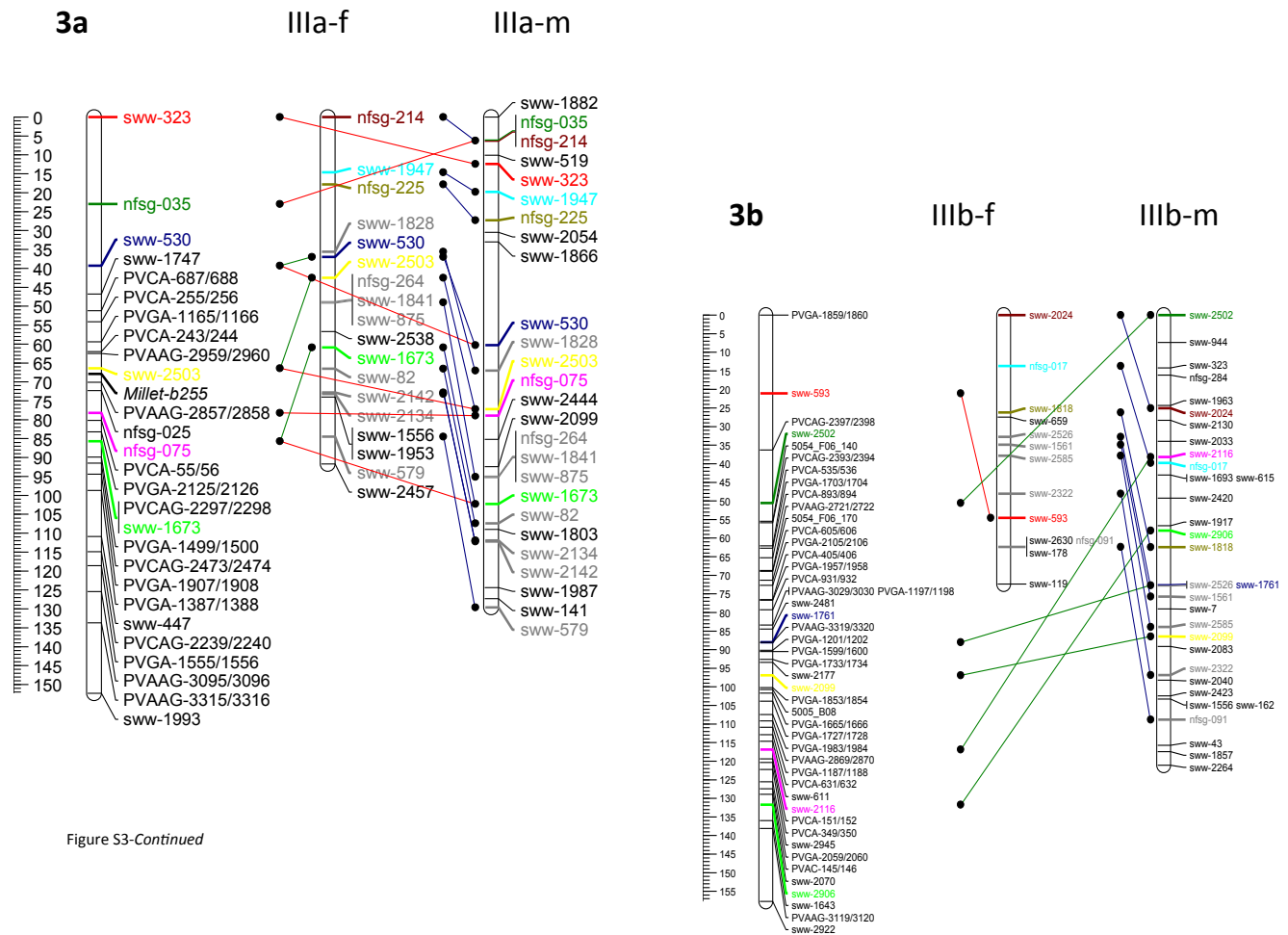


Figure S3-Continued

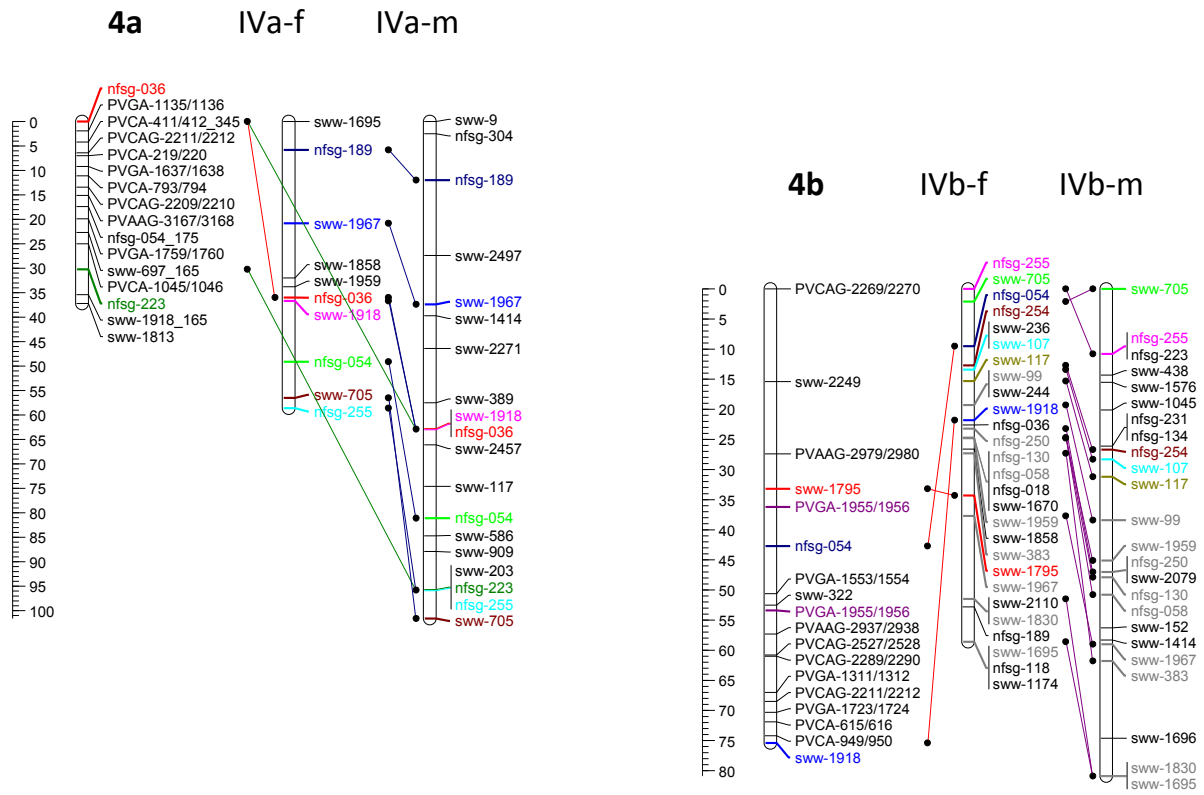


Figure S3-Continued

5a

Va-f

Va-m

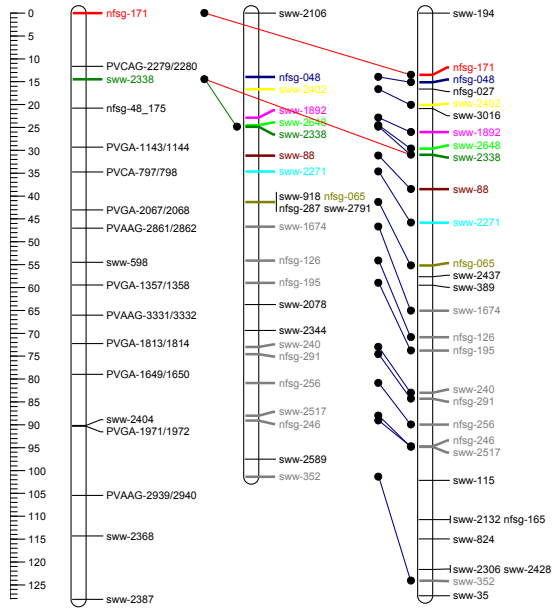
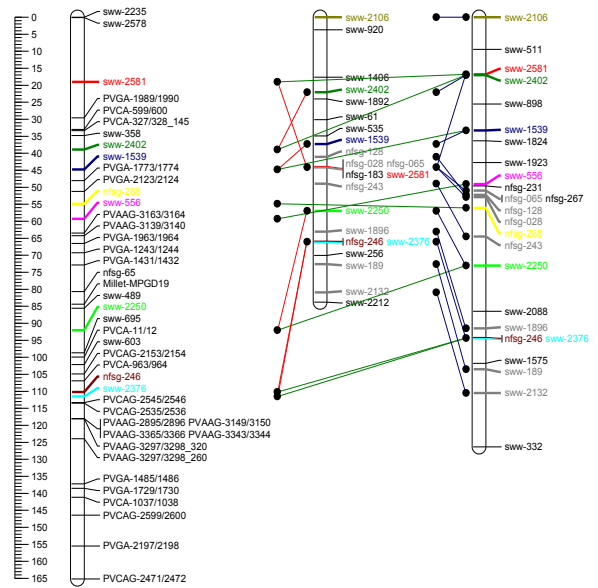


Figure S3-Continued

5b

Vb-f

Vb-m



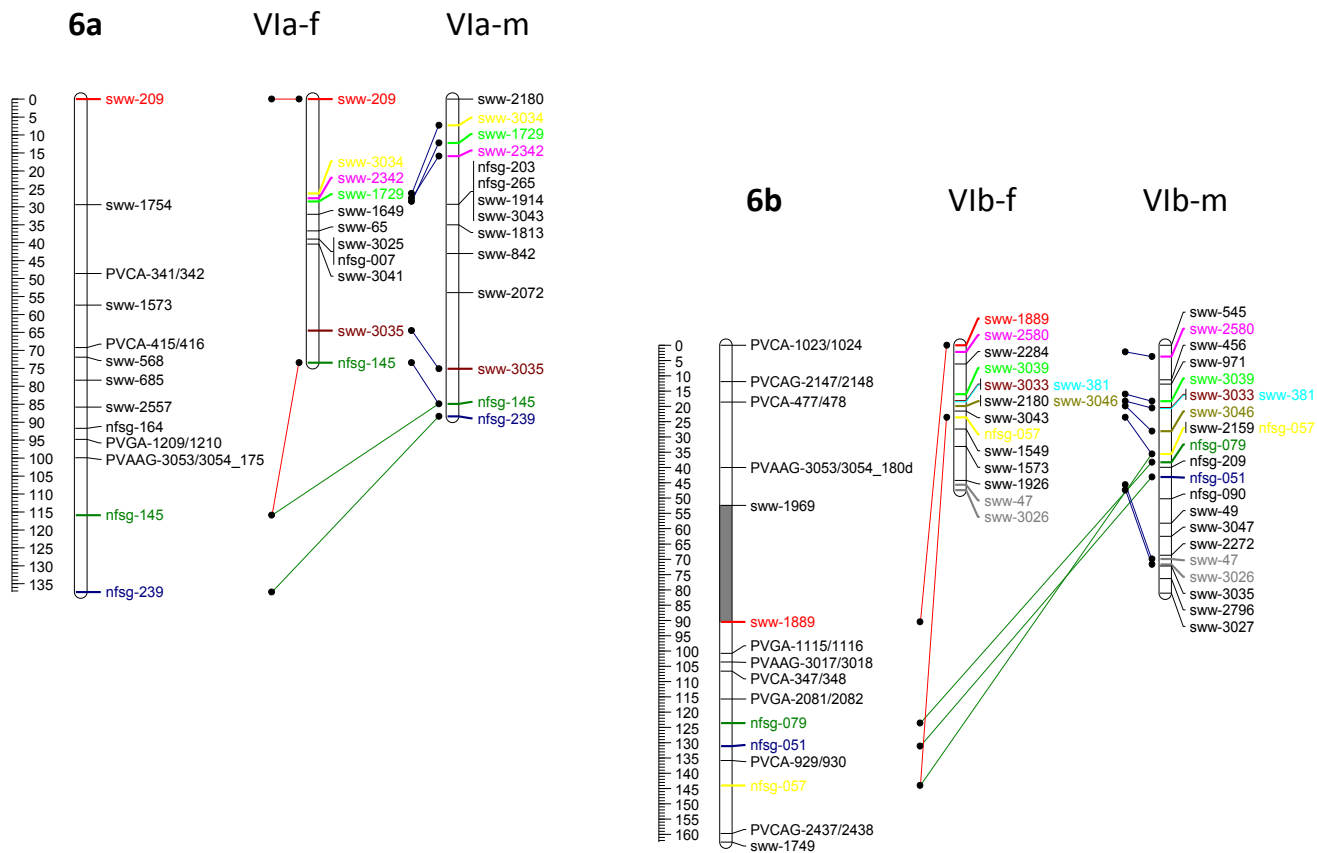


Figure S3-Continued

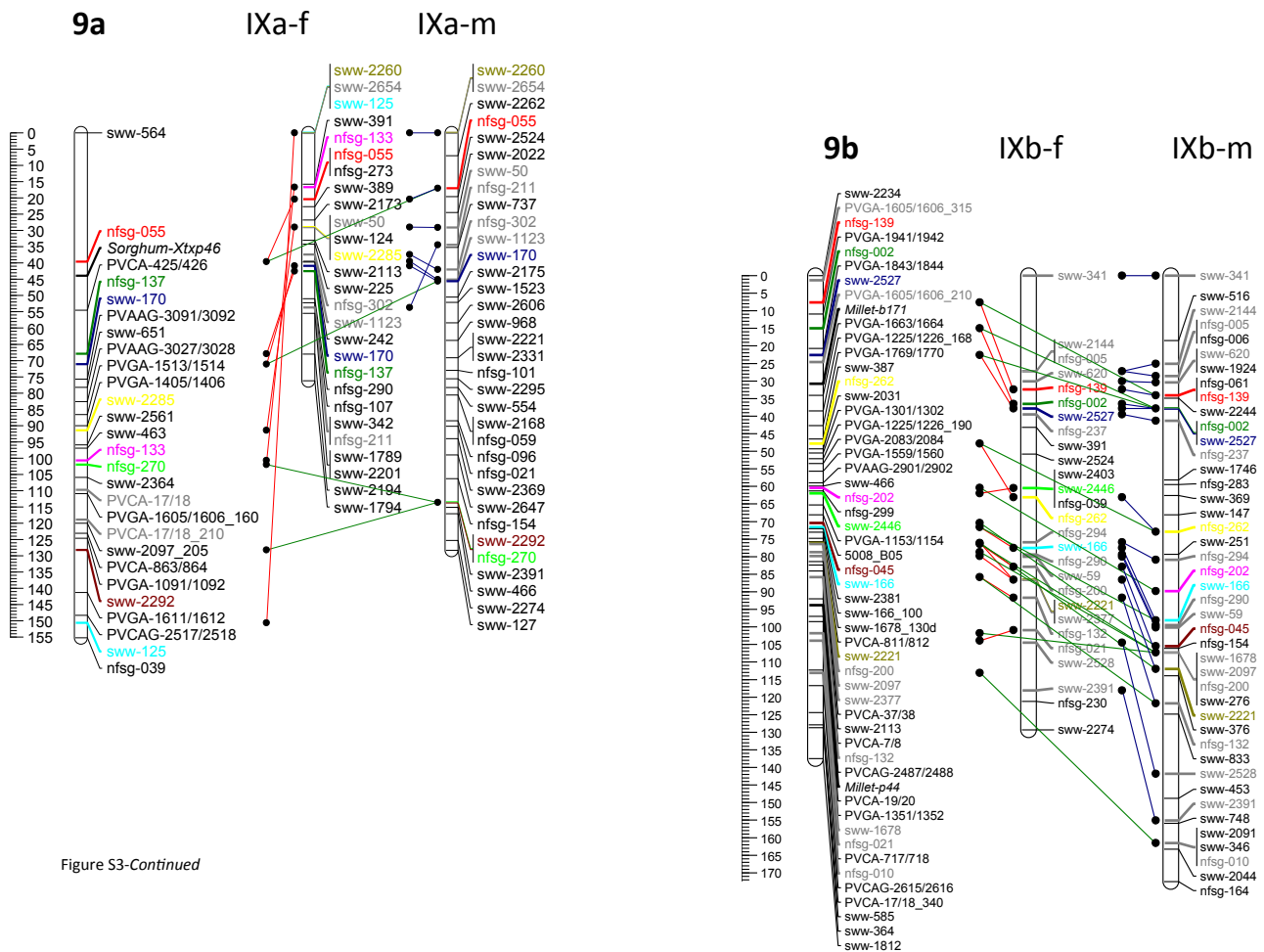


Figure S3-Continued

Figure S3 Collinearity between this and published linkage map (Okada *et al.* 2010). The names of linkage groups (LGs) in this study are indicated with Arabic numbers in bold, and the designation of LGs and two subgenomes ('a' and 'b') is consistent with the reference map (Okada *et al.* 2010). The letter 'f' and 'm' at the end of reference LGs (Roman number) denotes female and male parent maps, respectively. To compare the two maps, the duplicated loci amplified from same markers in reference map and the band sizes were removed. All loci mapped with the same markers across LGs are highlighted with matching colors.

File S1

Raw Genotyping Data

File S1 is available for download at <http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.111.001503/-/DC1>.

Table S1 Expected progeny phenotypes and segregation ratios for disomic and tetrasomic inheritance in a selfed population of a tetraploid switchgrass plant

Inheritance mode	Marker scoring types	Genotypes of two bands observed ^a	Theoretical genotypes of selfed progeny ^b	Expected selfed progeny band pattern	Expected progeny ratio
Disomic		<i>AB</i>	<i>1AA, 2AB, 1BB</i>	a:ab:b	1:2:1
Tetrasomic	co-dominant	<i>ABBB</i>	<i>(1AABB,2ABBB),1BBBB</i>	ab:b	3:1
		<i>AABB</i>	<i>1AAAA,(8AAAAB,18AABB,8ABBB),1BBBB</i>	a:ab:b	1:34:1
		<i>AAAB</i>	<i>1AAAA,(2AAAAB,1AABB)</i>	a:ab	1:3
Disomic		<i>A_</i>	<i>(1AA, 2A_), 1_ _</i>	presence:absence	3:1
Tetrasomic	dominant	<i>A_ _ _</i>	<i>(1AA_ _ ,2A_ _ _),1_ _ _ _</i>	presence:absence	3:1
		<i>AA_ _</i>	<i>(1AAAA,8AAA_ ,18AA_ _ ,8A_ _ _),1_ _ _ _</i>	presence:absence	35:1
		<i>AAA_</i>	<i>(1AAAA,2AAA_ ,1AA_ _)</i>	presence:absence	all presence

^a Italicized capital letters represent genotypes.

^b The genotypes in parenthesis produce the same gel banding phenotypes.

Table S2 Detection of redundancy among published primers (Tobias *et al.* 2006, 2008; Wang *et al.* 2011) using bl2seq basic local alignment search tool (BLAST) (NCBI, Bethesda, MD)

Marker ID of Wang <i>et al.</i> (2011)	Marker ID of Okada <i>et al.</i> (2010)	SSR type	% Read (similarity)	Read length (bp)	E value	Bit score ^b
PVGA-1225/1226	NFSG005	gSSR	100	21	9.00E-08	39.9
PVGA-1901/1902	NFSG006	gSSR	100	22	6.00E-08	41.7
PVGA-1643/1644	NFSG066	gSSR	100	21	4.00E-09	39.9
PVGA-1419/1420	NFSG102	gSSR	100	20	2.00E-10	38.1
PVGA2-1329/1330	NFSG136	gSSR	100	20	7.00E-09	38.1
	NFSG249	gSSR	100	20	5.00E-08	39.9
PVGA-1669/1670	NFSG187	gSSR	100	21	4.00E-08	39.9
PVGA-1627/1628	NFSG215	gSSR	100	21	2.00E-09	38.9
PVGA-1657/1658	NFSG243	gSSR	100	21	1.00E-08	30.7
PVGA-1867/1868	SWW2864	eSSR	100	20	2.30E-08	39.9
PVGA-2035/2036	SWW2881	eSSR	100	21	4.00E-08	39.9
PVGA-1295/1296	SWW2954	eSSR	100	21	7.00E-09	38.8
PVCAG-2245/2246	SWW3033	eSSR	100	21	2.10E-09	30.7
PVGA6-1793/1794	SWW2839	eSSR	76	16	4.00E-06	38.8
PVGA5-1697/1698	sww2845	eSSR	100	21	1.41E-09	38.8
PVCA- 985/986	SWW3043	eSSR	100	18	8.10E-07	38.1
sww1 ^a	4821_A04	eSSR	100	20	2.00E-09	38.1
sww842	4934_H04	eSSR	100	20	1.00E-09	38.1
SWW35	No reverse sequence hit in GenBank	eSSR				
NFSG028	Redundant with NFSG027	gSSR				

^a The last four primer pairs are the comparison of primer pairs from same research group (Tobias *et al.* 2006, 2008; Okada *et al.* 2010)

^b Note the bit score represents the normalized value that can be used to compare alignment scores from different searches

Table S3 Presentation of identical bridge markers in the linkage groups (LGs) of this map and a previous study (Okada *et al.* 2010)

LGs in this study	Corresponding LGs and subgenome designation of Okada <i>et al.</i> 2010	No. of bridge markers	LGs and alternate subgenome designation of Okada <i>et al.</i> 2010	No. of bridge markers
1a	Ia	5	Ib	0
1b	Ib	10	Ia	5
2a	IIa	8	IIb	2
2b	IIb	8	IIa	1
3a	IIIa	6	IIIb	1
3b	IIIb	7	IIIa	0
4a ^a	IVa	4	IVb	1
4b	IVb	3	IVa	2
5a	Va	3	Vb	0
5b	Vb	8	Va	2
6a	VIa	3	VIb	1
6b	VIb	4	VIa	0
7a	VIIa	4	VIIb	0
7b	VIIb	0	VIIa	0
8a	VIIIa	4	VIIIb	0
8b	VIIIb	3	VIIIa	0
9a	IXa	8	IXb	1
9b	IXb	16	Ixa	2
Total		102		15

^aTwo bridge markers (nfs-054 and sw-1918) were shared by both LG 4a and 4b.

Table S4 A list of switchgrass markers and their corresponding nine chromosomes of foxtail millet by BlastN analysis in Phytozome v7.0

Chr. of foxtail millet	Switchgrass markers	Total
I	nfsg-026,nfsg-105,nfsg-197,PVAAG-2987/2988,PVAAG-3327/3328,PVAAG-3351/3352,PVCA-179/180,PVCA-411/412,PVCA-627/628,PVCAG-2199/2200,PVCAG-2379/2380,PVCAG-2439/2440,PVCAG-2537/2538,PVGA-1253/1254,PVGA-1271/1272,PVGA-1353/1354,PVGA-1573/1574,PVGA-1669/1670,PVGA-1735/1736,PVGA-1925/1926,PVGA-1947/1948,PVGA-2119/2120,sww-112,sww-1615,sww-162,sww-1667,sww-177,sww-196,sww-2115,sww-2196,sww-2240,sww-2271,sww-2320,sww-2405,sww-2489,sww-333,sww-359,sww-606,sww-660,sww-673	40
II	PVCA-529/530,5211_B07,Millet-MPGD25,nfsg-050,nfsg-052,nfsg-125,nfsg-129,nfsg-130,nfsg-285,PVAAG-2787/2788,PVAAG-2797/2798,PVAAG-2847/2848,PVAAG-3205/3206,PVAAG-3245/3246,PVAAG-3311/3312,PVAAG-3353/3354,PVAAG-3355/3356,PVCA-173/174,PVCA-269/270,PVCA-309/310,PVCA-317/318,PVCA-327/328,PVCA-555/556,PVCA-597/598,PVCA-765/766,PVCA-815/816,PVCA-861/862,PVCA-867/868,PVCA-911/912,PVCA-917/918,PVCA-969/970,PVCAG-2207/2208,PVCAG-2461/2462,PVCAG-2569/2570,PVCAG-2623/2624,PVGA-1105/1106,PVGA-1133/1134,PVGA-1337/1338,PVGA-1677/1678,PVGA-1719/1720,PVGA-1819/1820,PVGA-2079/2080,sww-108,sww-1553,sww-1581,sww-1622,sww-1805,sww-217,sww-223,sww-2231,sww-2251,sww-2352,sww-2455,sww-2501,sww-2525,sww-2545,sww-2640,sww-2662,sww-360,sww-389,sww-393,sww-461,sww-523,sww-532,sww-573,sww-583,sww-668,sww-704,sww-716,sww-718,sww-938	71
III	5005_B08,5054_F06,Millet-b255,nfsg-025,nfsg-035,nfsg-075,PVAAG-2721/2722,PVAAG-2869/2870,PVAAG-2959/2960,PVAAG-3095/3096,PVAAG-3119/3120,PVAAG-3315/3316,PVAAG-3319/3320,PVCA-151/152,PVCA-405/406,PVCA-55/56,PVCA-631/632,PVCA-687/688,PVCA-893/894,PVCA-931/932,PVCAG-2239/2240,PVCAG-2297/2298,PVCAG-2393/2394,PVCAG-2473/2474,PVGA-1115/1116,PVGA-1187/1188,PVGA-1197/1198,PVGA-1201/1202,PVGA-1665/1666,PVGA-1703/1704,PVGA-1727/1728,PVGA-1957/1958,PVGA-1983/1984,PVGA-2059/2060,PVGA-2105/2106,PVGA-2125/2126,sww-1643,sww-1673,sww-1761,sww-1993,sww-2070,sww-2177,sww-2481,sww-2502,sww-2503,sww-2906,sww-2922,sww-2945,sww-323,sww-447,sww-530,sww-593,sww-611	53
IV	PVCA-1045/1046,nfsg-036,nfsg-054,PVAAG-3167/3168,PVCA-219/220,PVCA-615/616,PVCA-793/794,PVCA-949/950,PVCAG-2269/2270,PVCAG-2527/2528,PVGA-1311/1312,PVGA-1553/1554,PVGA-1637/1638,PVGA-1723/1724,PVGA-1759/1760,PVGA-1955/1956,sww-1795,sww-697	18
V	PVCA-1037/1038,Millet-MPGD19,nfsg-048,nfsg-065,nfsg-246,PVAAG-2861/2862,PVAAG-2895/2896,PVAAG-2939/2940,PVAAG-3139/3140,PVAAG-3149/3150,PVAAG-3331/3332,PVCA-11/12,PVCA-797/798,PVCAG-2153/2154,PVCAG-2197/2198,PVCAG-2279/2280,PVCAG-2471/2472,PVCAG-2535/2536,PVCAG-2545/2546,PVGA-1143/1144,PVGA-1243/1244,PVGA-1963/1964,PVGA-1989/1990,PVGA-2123/2124,sww-1539,sww-2235,sww-2338,sww-2368,sww-2376,sww-2387,sww-2402,sww-2404,sww-2578,sww-2581,sww-358,sww-598,sww-603	37
VI	PVCA-1023/1024,nfsg-145,nfsg-164,nfsg-239,PVAAG-3017/3018,PVAAG-3053/3054,PVCA-341/342,PVGA-1209/1210,sww-1754,sww-1889,sww-1969,sww-209,sww-2557,sww-568,sww-685	16
VII	Millet-MPGD17,PVCAG-2163/2164,PVCAG-2389/2390,PVCAG-2503/2504,PVGA-1869/1870,sww-1394,sww-1742,sww-2532	8
VIII	5048_B06,nfsg-034,nfsg-112,nfsg-219,PVAAG-2961/2962,PVAAG-3181/3182,PVCA-541/542,PVCAG-2187/2188,PVGA-1149/1150,PVGA-1275/1276,PVGA-1627/1628,sww-123,sww-1862,sww-2443	14
IX	5008_B05,Millet-b171,Millet-p44,nfsg-010,nfsg-039,nfsg-055,nfsg-132,nfsg-133,nfsg-200,nfsg-202,nfsg-262,nfsg-270,PVAAG-2901/2902,PVAAG-3027/3028,PVAAG-3091/3092,PVCA-17/18,PVCA-19/20,PVCA-37/38,PVCA-425/426,PVCA-7/8,PVCA-811/812,PVCA-863/864,PVCAG-2517/2518,PVCAG-2615/2616,PVGA-1091/1092,PVGA-1135/1136,PVGA-1153/1154,PVGA-1301/1302,PVGA-1351/1352,PVGA-1405/1406,PVGA-1513/1514,PVGA-1605/1606,PVGA-1611/1612,PVGA-1663/1664,PVGA-1843/1844,PVGA-1941/1942,PVGA-2083/2084,Sorghum-Xtxp46,sww-125,sww-166,sww-1678,sww-170,sww-1812,sww-2031,sww-2097,sww-2113,sww-2221,sww-2234,sww-2285,sww-2292,sww-2364,sww-2377,sww-2381,sww-2446,sww-2561,sww-364,sww-387,sww-463,sww-466,sww-564,sww-585,sww-651	62
Grand total		319