

Supplementary Information

Supplementary Table 1. Synthetic hexaploid lines and their corresponding diploid and tetraploid parents used in the study

		Male parent	
		AS2386 (DD) - C26 <i>Ae. tauschii</i>	AS2399 (DD) - C30 <i>Ae. tauschii</i>
Female parent	PI377655 (AABB) <i>T. turgidum</i> ssp. <i>dicoccum</i>	C66 (AABBDD)	C65 (AABBDD)
	Langdon (AABB) <i>T. turgidum</i> ssp. <i>durum</i>	C44 (AABBDD)	C45 (AABBDD)

Supplementary Table 2. Number of raw reads in the 240 RNA-seq samples

		Diploid - AS2386	Diploid - AS2399	SHW - C44	SHW - C45	SHW - C65	SHW - C66	Tetraploid - Langdon	Tetraploid - PI377655
Pistil-1DAA	Rep1	22,195,307	21,995,116	33,587,073	26,493,898	38,641,474	26,548,645	28,846,234	28,035,524
	Rep2	22,995,789	34,757,108	36,490,086	33,720,903	39,157,764	23,082,570	44,131,554	22,652,205
	Rep3	24,015,698	22,989,427	91,812,896	23,633,788	27,469,412	31,711,344	26,122,325	22,785,314
Boot	Rep1	76,018,937	32,301,846	28,027,166	38,784,598	18,707,397	38,612,808	33,243,732	24,941,487
	Rep2	26,200,871	73,864,787	21,492,555	26,939,056	61,995,968	20,344,851	45,296,952	25,427,653
	Rep3	29,151,714	68,049,299	28,500,457	85,145,293	69,852,158	22,442,149	27,178,086	23,280,574
Glume	Rep1	35,420,234	29,310,601	20,759,066	28,314,129	47,565,899	28,268,183	38,976,192	64,828,969
	Rep2	21,937,111	23,713,143	22,781,410	47,640,557	20,144,197	44,869,236	27,482,753	22,573,351
	Rep3	29,713,083	21,744,437	23,737,425	26,490,383	21,575,767	31,696,463	40,205,086	23,904,763
Hypocotyl	Rep1	30,449,989	20,003,076	13,082,000	48,991,348	18,179,165	18,007,903	28,016,934	38,735,285
	Rep2	22,841,340	31,214,263	23,833,152	51,412,571	27,737,105	29,903,001	42,518,094	27,349,705
	Rep3	63,882,306	46,891,825	50,655,072	28,343,485	51,303,621	22,989,560	39,910,639	40,895,942
Palea+Lemma	Rep1	24,328,003	32,518,917	24,198,386	42,344,790	20,249,452	23,162,717	64,847,457	33,799,385
	Rep2	26,014,180	21,748,599	22,482,334	30,774,636	25,410,801	24,318,988	25,346,626	20,559,596
	Rep3	27,805,863	21,900,549	21,547,690	41,084,241	29,369,761	23,520,086	22,848,870	40,133,310
Pistil-AM	Rep1	26,023,695	28,445,422	56,573,952	27,251,070	24,266,368	24,290,980	53,144,692	24,637,191
	Rep2	23,690,579	20,529,663	12,878,054	23,573,721	26,393,617	24,437,509	30,271,276	23,713,978
	Rep3	20,806,267	27,419,849	25,902,215	24,955,332	27,162,721	23,635,128	38,392,332	32,237,698
Root	Rep1	37,598,774	28,541,828	33,567,318	26,045,053	25,478,138	19,511,358	34,691,430	26,340,471
	Rep2	29,137,833	25,129,915	23,934,237	35,683,705	29,225,962	21,364,532	21,883,804	24,330,645
	Rep3	47,832,348	25,090,283	22,864,680	30,691,902	21,624,952	26,808,534	25,119,702	28,174,617
Shoot	Rep1	27,411,093	23,796,164	30,077,914	25,784,399	27,149,920	35,503,678	42,150,240	23,856,393
	Rep2	29,526,120	23,787,924	23,346,192	25,126,541	40,080,997	19,545,212	54,426,481	25,778,462
	Rep3	27,553,375	12,778,098	53,706,831	28,990,179	48,394,047	34,000,995	36,586,301	24,547,842
Anther	Rep1	14,858,969	12,068,339	13,332,346	12,464,913	15,245,079	14,566,281	14,138,343	12,871,028
	Rep2	13,950,637	14,561,991	12,961,043	13,591,105	11,329,218	14,192,473	14,466,506	12,874,863
	Rep3	13,939,729	13,903,778	12,948,472	14,120,579	13,776,126	13,739,453	12,189,781	14,738,894
Pistil-AI	Rep1	13,188,605	13,449,612	13,036,625	12,154,908	13,265,009	13,370,423	13,956,148	13,240,572
	Rep2	12,789,103	13,009,865	12,653,047	12,378,022	12,666,519	13,168,331	13,237,777	15,109,353
	Rep3	11,175,795	14,047,307	13,584,399	13,336,772	12,082,013	6,573,063	13,008,756	11,463,936

Pistil-1DAA: pistil-one day after anthesis; Pistil-AM: pistil-when anthers are at mature stage; Pistil-AI: pistil-when anthers are at immature stage; Boot: head at boot stage

Supplementary Table 3. Number of reads in the 240 RNA-seq samples, after processing

		Diploid - AS2386	Diploid - AS2399	SHW - C44	SHW - C45	SHW - C65	SHW - C66	Tetraploid - Langdon	Tetraploid - PI377655
Pistil-1DAA	Rep1	16,652,462	15,620,498	23,790,476	18,114,304	26,722,162	18,910,673	21,160,261	20,875,899
	Rep2	15,274,606	24,308,623	27,552,871	22,883,456	26,607,670	16,101,400	32,282,843	16,014,445
	Rep3	17,596,827	16,943,904	70,743,378	16,474,019	19,708,725	21,376,446	18,355,411	15,236,838
Boot	Rep1	57,664,218	24,949,933	21,275,022	29,714,612	13,089,654	30,169,811	23,571,404	17,661,315
	Rep2	19,408,624	57,391,546	15,926,482	20,617,391	47,873,378	14,793,083	34,287,497	18,371,225
	Rep3	20,664,589	53,646,495	20,195,131	64,951,442	49,579,406	15,987,495	19,319,412	17,171,614
Glume	Rep1	26,815,121	20,940,544	15,246,336	19,648,878	32,319,338	21,431,871	29,463,422	48,193,103
	Rep2	16,181,955	17,665,911	17,013,063	34,431,917	14,395,762	34,300,068	19,643,543	16,772,106
	Rep3	23,384,600	15,494,944	16,957,425	18,430,477	15,674,851	22,514,609	28,535,092	18,511,746
Hypocotyl	Rep1	22,561,521	14,100,352	10,041,404	37,561,278	13,827,431	13,993,188	19,525,603	27,837,920
	Rep2	16,526,306	22,602,975	17,221,309	40,381,040	20,276,202	21,450,701	30,098,228	20,226,843
	Rep3	48,387,770	34,862,966	36,242,751	21,403,064	35,854,302	16,338,510	28,766,799	29,606,341
Palea+Lemma	Rep1	18,391,019	25,039,738	17,712,620	29,284,744	14,637,765	17,059,434	48,637,322	24,787,679
	Rep2	20,019,127	15,967,411	16,328,130	21,710,695	18,812,481	17,763,568	17,905,772	14,222,274
	Rep3	19,870,649	16,053,756	16,023,215	32,167,434	21,649,321	17,532,475	17,107,285	28,181,077
Pistil-AM	Rep1	18,349,055	20,387,882	39,204,701	19,597,028	17,808,171	18,540,363	39,515,015	17,642,079
	Rep2	17,009,153	14,338,346	9,774,662	17,003,537	18,099,276	16,707,667	20,147,366	16,541,649
	Rep3	14,373,624	19,829,020	19,493,466	18,377,313	19,459,379	17,142,187	28,539,125	23,726,105
Root	Rep1	25,851,418	21,188,494	24,812,414	18,371,284	19,203,581	13,541,267	26,718,856	19,765,758
	Rep2	21,390,326	18,620,533	17,297,014	26,998,387	22,692,101	15,503,742	15,431,234	17,525,916
	Rep3	33,999,451	17,916,134	15,909,748	21,996,230	15,535,210	19,776,405	19,374,245	19,934,284
Shoot	Rep1	19,523,100	18,255,513	22,491,360	18,934,613	19,607,143	27,386,269	30,091,216	16,814,046
	Rep2	22,614,844	17,088,763	17,308,713	17,897,686	28,082,616	14,874,879	38,629,216	18,534,622
	Rep3	21,063,835	10,026,717	38,010,200	21,020,090	34,583,788	24,084,686	27,829,956	17,347,074
Anther	Rep1	10,862,366	8,457,261	10,832,242	9,653,328	12,421,104	10,966,326	10,320,422	10,231,104
	Rep2	11,112,928	11,739,559	9,546,590	10,147,261	9,136,176	11,468,430	11,543,432	10,230,761
	Rep3	10,378,299	9,800,090	9,542,973	11,388,733	9,912,320	9,921,095	9,810,303	11,785,351
Pistil-AI	Rep1	9,854,619	11,066,191	10,647,010	9,158,324	10,770,855	9,972,559	10,392,686	10,512,209
	Rep2	9,304,179	9,562,473	9,243,986	10,093,944	10,334,726	9,781,472	10,698,688	11,338,157
	Rep3	8,967,274	10,234,854	11,120,788	9,712,338	9,793,567	4,829,128	9,814,128	9,472,780

Pistil-1DAA: pistil-one day after anthesis; Pistil-AM: pistil-when anthers are at mature stage; Pistil-AI: pistil-when anthers are at immature stage; Boot: head at boot stage

Supplementary Table 4. Summary of proportion of uniquely mapped and multi-mapped reads

Genotype	Source material	Tissue	Rep	Uniquely mapped reads (%)	Multi-mapped (%)	Too many multi-mapped* (%)	Total multi-mapped ^s (%)
AS2386	Diploid parent	Anther	1	83.07	13.69	1.22	14.91
AS2386	Diploid parent	Anther	2	84.01	13.21	1.19	14.40
AS2386	Diploid parent	Anther	3	82.94	13.49	1.32	14.81
AS2386	Diploid parent	Glume	1	84.42	12.72	0.53	13.25
AS2386	Diploid parent	Glume	3	83.45	13.74	0.50	14.24
AS2386	Diploid parent	Glume	2	85.43	11.07	1.15	12.22
AS2386	Diploid parent	Boot	3	88.18	8.95	0.36	9.31
AS2386	Diploid parent	Boot	2	87.34	9.74	0.75	10.49
AS2386	Diploid parent	Boot	1	88.09	9.32	0.38	9.70
AS2386	Diploid parent	Hypocotyl	1	85.23	11.11	1.21	12.32
AS2386	Diploid parent	Hypocotyl	3	87.49	9.46	0.58	10.04
AS2386	Diploid parent	Hypocotyl	2	85.63	10.90	0.95	11.85
AS2386	Diploid parent	Palea+Lemma	3	85.55	10.33	0.98	11.31
AS2386	Diploid parent	Palea+Lemma	1	86.50	10.11	0.90	11.01
AS2386	Diploid parent	Palea+Lemma	2	86.34	10.64	0.67	11.31
AS2386	Diploid parent	Pistil-1DAA	3	87.59	7.47	2.24	9.71
AS2386	Diploid parent	Pistil-1DAA	2	85.98	7.95	3.05	11.00
AS2386	Diploid parent	Pistil-1DAA	1	89.04	7.23	1.33	8.56
AS2386	Diploid parent	Pistil-AM	3	87.70	7.84	1.83	9.67
AS2386	Diploid parent	Pistil-AM	1	86.76	7.94	2.51	10.45
AS2386	Diploid parent	Pistil-AM	2	87.66	7.85	1.66	9.51
AS2386	Diploid parent	Pistil-AI	3	83.79	13.42	0.54	13.96
AS2386	Diploid parent	Pistil-AI	2	83.12	13.82	0.61	14.43
AS2386	Diploid parent	Pistil-AI	1	82.82	13.86	0.61	14.47
AS2386	Diploid parent	Root	5	88.36	6.68	2.19	8.87
AS2386	Diploid parent	Root	4	88.78	6.64	1.99	8.63
AS2386	Diploid parent	Root	2	89.52	6.83	0.93	7.76
AS2386	Diploid parent	Shoot	2	89.12	8.15	0.31	8.46
AS2386	Diploid parent	Shoot	1	86.94	9.44	0.88	10.32
AS2386	Diploid parent	Shoot	3	86.90	10.25	0.51	10.76
AS2399	Diploid parent	Anther	4	83.23	14.42	0.57	14.99
AS2399	Diploid parent	Anther	2	81.54	14.89	0.93	15.82
AS2399	Diploid parent	Anther	3	80.38	13.59	1.65	15.24
AS2399	Diploid parent	Glume	3	83.82	13.01	0.60	13.61
AS2399	Diploid parent	Glume	2	85.70	10.47	1.05	11.52
AS2399	Diploid parent	Glume	1	83.42	13.20	0.74	13.94
AS2399	Diploid parent	Boot	3	88.17	9.14	0.39	9.53
AS2399	Diploid parent	Boot	1	87.08	9.79	0.93	10.72
AS2399	Diploid parent	Boot	2	86.15	11.28	0.34	11.62
AS2399	Diploid parent	Hypocotyl	1	83.53	12.81	1.17	13.98
AS2399	Diploid parent	Hypocotyl	3	85.57	11.38	0.67	12.05
AS2399	Diploid parent	Hypocotyl	2	83.78	12.60	0.97	13.57
AS2399	Diploid parent	Palea+Lemma	1	85.94	11.05	0.37	11.42

AS2399	Diploid parent	Palea+Lemma	2	86.17	10.13	0.81	10.94
AS2399	Diploid parent	Palea+Lemma	3	86.84	9.74	0.71	10.45
AS2399	Diploid parent	Pistil-1DAA	1	86.10	7.47	3.64	11.11
AS2399	Diploid parent	Pistil-1DAA	3	88.03	7.38	2.18	9.56
AS2399	Diploid parent	Pistil-1DAA	2	85.31	7.91	3.71	11.62
AS2399	Diploid parent	Pistil-AM	2	84.95	8.02	4.04	12.06
AS2399	Diploid parent	Pistil-AM	1	85.55	7.82	3.55	11.37
AS2399	Diploid parent	Pistil-AM	3	86.51	7.62	3.24	10.86
AS2399	Diploid parent	Pistil-AI	2	82.28	13.75	0.89	14.64
AS2399	Diploid parent	Pistil-AI	1	83.05	13.89	0.52	14.41
AS2399	Diploid parent	Pistil-AI	3	83.54	13.72	0.50	14.22
AS2399	Diploid parent	Root	1	88.70	6.39	2.29	8.68
AS2399	Diploid parent	Root	4	89.31	7.42	0.70	8.12
AS2399	Diploid parent	Root	3	88.88	6.47	2.20	8.67
AS2399	Diploid parent	Shoot	2	84.25	12.07	0.78	12.85
AS2399	Diploid parent	Shoot	1	83.29	13.83	0.56	14.39
AS2399	Diploid parent	Shoot	3	87.57	9.57	0.53	10.10
C44	SHW	Anther	1	82.15	13.41	0.83	14.24
C44	SHW	Anther	6	81.42	13.70	0.90	14.60
C44	SHW	Anther	8	82.04	13.12	1.31	14.43
C44	SHW	Glume	3	84.89	11.03	0.96	11.99
C44	SHW	Glume	2	85.48	10.13	1.10	11.23
C44	SHW	Glume	1	84.42	11.73	0.94	12.67
C44	SHW	Boot	1	88.37	8.29	0.53	8.82
C44	SHW	Boot	2	88.02	8.53	0.79	9.32
C44	SHW	Boot	3	87.33	9.08	0.67	9.75
C44	SHW	Hypocotyl	1	85.67	10.72	0.68	11.40
C44	SHW	Hypocotyl	3	85.35	10.25	1.24	11.49
C44	SHW	Hypocotyl	2	86.52	9.25	1.12	10.37
C44	SHW	Palea+Lemma	3	85.77	10.87	0.61	11.48
C44	SHW	Palea+Lemma	1	85.34	10.63	0.77	11.40
C44	SHW	Palea+Lemma	2	85.40	11.01	0.58	11.59
C44	SHW	Pistil-1DAA	2	88.49	6.82	1.83	8.65
C44	SHW	Pistil-1DAA	1	87.50	7.20	2.17	9.37
C44	SHW	Pistil-1DAA	3	89.60	6.85	0.82	7.67
C44	SHW	Pistil-AM	1	86.18	7.82	2.70	10.52
C44	SHW	Pistil-AM	2	89.61	7.02	0.61	7.63
C44	SHW	Pistil-AM	3	86.58	7.16	3.25	10.41
C44	SHW	Pistil-AI	4	83.76	13.04	0.63	13.67
C44	SHW	Pistil-AI	3	83.18	13.26	0.70	13.96
C44	SHW	Pistil-AI	2	83.64	13.00	0.63	13.63
C44	SHW	Root	1	88.52	7.28	0.66	7.94
C44	SHW	Root	3	86.41	7.23	2.84	10.07
C44	SHW	Root	2	88.69	7.08	0.96	8.04
C44	SHW	Shoot	2	86.75	9.31	0.89	10.20
C44	SHW	Shoot	3	85.68	10.24	0.89	11.13
C44	SHW	Shoot	1	84.31	12.06	1.02	13.08

C45	SHW	Anther	2	81.86	13.66	0.75	14.41
C45	SHW	Anther	5	83.46	12.90	0.61	13.51
C45	SHW	Anther	1	82.71	13.29	0.83	14.12
C45	SHW	Glume	3	78.84	17.61	0.63	18.24
C45	SHW	Glume	1	83.85	12.27	0.64	12.91
C45	SHW	Glume	2	84.55	11.29	0.88	12.17
C45	SHW	Boot	2	86.66	10.34	0.44	10.78
C45	SHW	Boot	3	87.99	9.03	0.38	9.41
C45	SHW	Boot	1	85.51	11.40	0.45	11.85
C45	SHW	Hypocotyl	1	87.90	8.51	0.59	9.10
C45	SHW	Hypocotyl	2	88.68	7.93	0.41	8.34
C45	SHW	Hypocotyl	3	86.47	10.05	0.55	10.60
C45	SHW	Palea+Lemma	3	84.51	11.99	0.82	12.81
C45	SHW	Palea+Lemma	2	84.89	10.65	0.93	11.58
C45	SHW	Palea+Lemma	1	83.48	12.61	0.72	13.33
C45	SHW	Pistil-1DAA	3	87.12	7.54	2.15	9.69
C45	SHW	Pistil-1DAA	2	84.16	7.72	4.57	12.29
C45	SHW	Pistil-1DAA	1	85.30	7.78	3.53	11.31
C45	SHW	Pistil-AM	2	83.85	7.56	5.34	12.90
C45	SHW	Pistil-AM	1	84.61	7.65	4.52	12.17
C45	SHW	Pistil-AM	3	88.15	7.36	1.66	9.02
C45	SHW	Pistil-AI	3	83.19	13.41	0.55	13.96
C45	SHW	Pistil-AI	2	83.13	13.24	0.67	13.91
C45	SHW	Pistil-AI	1	83.14	13.14	0.75	13.89
C45	SHW	Root	3	88.71	7.37	0.98	8.35
C45	SHW	Root	2	88.25	6.91	1.04	7.95
C45	SHW	Root	1	88.48	7.43	0.94	8.37
C45	SHW	Shoot	2	85.61	10.46	0.82	11.28
C45	SHW	Shoot	1	84.08	11.55	1.30	12.85
C45	SHW	Shoot	3	86.77	9.35	0.81	10.16
C65	SHW	Anther	4	84.09	13.10	0.34	13.44
C65	SHW	Anther	1	84.15	13.09	0.41	13.50
C65	SHW	Anther	3	83.91	12.89	0.46	13.35
C65	SHW	Glume	2	83.86	12.11	1.00	13.11
C65	SHW	Glume	3	82.30	13.63	1.03	14.66
C65	SHW	Glume	1	83.43	11.71	1.12	12.83
C65	SHW	Boot	1	87.09	9.56	0.42	9.98
C65	SHW	Boot	2	86.95	9.86	0.59	10.45
C65	SHW	Boot	3	85.03	11.52	0.68	12.20
C65	SHW	Hypocotyl	2	84.61	11.08	1.53	12.61
C65	SHW	Hypocotyl	1	85.58	11.20	0.65	11.85
C65	SHW	Hypocotyl	3	85.84	9.95	1.13	11.08
C65	SHW	Palea+Lemma	2	86.60	9.52	1.10	10.62
C65	SHW	Palea+Lemma	1	84.49	11.18	1.18	12.36
C65	SHW	Palea+Lemma	3	83.38	12.70	1.11	13.81
C65	SHW	Pistil-1DAA	1	85.14	7.65	3.90	11.55
C65	SHW	Pistil-1DAA	2	86.35	7.68	2.74	10.42

C65	SHW	Pistil-1DAA	3	88.30	7.43	1.53	8.96
C65	SHW	Pistil-AM	2	87.42	7.94	1.65	9.59
C65	SHW	Pistil-AM	1	84.54	7.55	4.73	12.28
C65	SHW	Pistil-AM	3	82.00	7.80	6.72	14.52
C65	SHW	Pistil-AI	3	83.41	13.12	0.58	13.70
C65	SHW	Pistil-AI	1	82.74	13.60	0.66	14.26
C65	SHW	Pistil-AI	2	82.81	13.24	0.73	13.97
C65	SHW	Root	2	90.02	6.63	0.87	7.50
C65	SHW	Root	3	87.81	7.23	2.04	9.27
C65	SHW	Root	1	89.31	6.99	1.13	8.12
C65	SHW	Shoot	1	78.86	17.40	1.12	18.52
C65	SHW	Shoot	2	82.96	12.59	1.33	13.92
C65	SHW	Shoot	3	84.72	11.39	0.88	12.27
C66	SHW	Anther	1	83.57	13.15	0.43	13.58
C66	SHW	Anther	2	83.69	13.32	0.40	13.72
C66	SHW	Anther	4	83.65	12.96	0.53	13.49
C66	SHW	Glume	3	78.74	17.81	0.70	18.51
C66	SHW	Glume	2	86.57	10.20	0.36	10.56
C66	SHW	Glume	1	85.17	11.16	0.76	11.92
C66	SHW	Boot	2	86.07	10.54	0.64	11.18
C66	SHW	Boot	1	86.61	10.58	0.37	10.95
C66	SHW	Boot	3	85.73	10.93	0.58	11.51
C66	SHW	Hypocotyl	2	83.79	12.08	1.29	13.37
C66	SHW	Hypocotyl	1	81.67	14.51	0.74	15.25
C66	SHW	Hypocotyl	3	81.80	13.30	1.86	15.16
C66	SHW	Palea+Lemma	2	84.62	11.27	1.00	12.27
C66	SHW	Palea+Lemma	3	84.10	12.39	0.82	13.21
C66	SHW	Palea+Lemma	1	83.95	12.33	0.87	13.20
C66	SHW	Pistil-1DAA	1	84.88	7.46	4.28	11.74
C66	SHW	Pistil-1DAA	2	86.41	7.71	2.82	10.53
C66	SHW	Pistil-1DAA	3	84.97	7.83	3.82	11.65
C66	SHW	Pistil-AM	3	87.19	7.54	2.42	9.96
C66	SHW	Pistil-AM	2	84.45	7.91	4.20	12.11
C66	SHW	Pistil-AM	1	87.26	7.42	2.51	9.93
C66	SHW	Pistil-AI	1	83.61	13.13	0.66	13.79
C66	SHW	Pistil-AI	3	82.76	13.70	0.62	14.32
C66	SHW	Pistil-AI	2	82.43	13.73	0.69	14.42
C66	SHW	Root	1	86.17	7.16	1.01	8.17
C66	SHW	Root	3	88.51	6.99	1.62	8.61
C66	SHW	Root	2	88.62	6.77	1.76	8.53
C66	SHW	Shoot	3	84.61	11.53	0.73	12.26
C66	SHW	Shoot	1	86.57	9.85	0.46	10.31
C66	SHW	Shoot	2	83.72	12.81	0.83	13.64
Langdon	Tetraploid parent	Glume	1	84.25	11.86	0.44	12.30
Langdon	Tetraploid parent	Glume	2	83.44	11.69	0.81	12.50
Langdon	Tetraploid parent	Glume	3	82.89	12.83	0.71	13.54
Langdon	Tetraploid parent	Boot	2	84.90	12.05	0.32	12.37

Langdon	Tetraploid parent	Boot	1	85.75	10.48	0.55	11.03
Langdon	Tetraploid parent	Boot	3	85.56	10.63	0.68	11.31
Langdon	Tetraploid parent	Hypocotyl	2	83.77	11.69	1.18	12.87
Langdon	Tetraploid parent	Hypocotyl	3	85.22	11.13	0.58	11.71
Langdon	Tetraploid parent	Hypocotyl	1	86.27	9.27	1.15	10.42
Langdon	Tetraploid parent	Palea+Lemma	1	84.15	12.03	0.48	12.51
Langdon	Tetraploid parent	Palea+Lemma	3	86.68	9.32	0.94	10.26
Langdon	Tetraploid parent	Palea+Lemma	2	84.25	11.48	0.75	12.23
Langdon	Tetraploid parent	Pistil-1DAA	2	87.76	7.15	2.01	9.16
Langdon	Tetraploid parent	Pistil-1DAA	1	87.10	7.13	2.59	9.72
Langdon	Tetraploid parent	Pistil-1DAA	3	85.99	7.57	2.76	10.33
Langdon	Tetraploid parent	Pistil-AM	2	85.70	7.61	3.21	10.82
Langdon	Tetraploid parent	Pistil-AM	1	88.66	7.02	1.21	8.23
Langdon	Tetraploid parent	Pistil-AM	3	89.36	7.08	0.58	7.66
Langdon	Tetraploid parent	Root	3	89.37	6.96	0.74	7.70
Langdon	Tetraploid parent	Root	1	89.54	7.11	0.50	7.61
Langdon	Tetraploid parent	Root	2	88.60	7.46	0.68	8.14
Langdon	Tetraploid parent	Shoot	2	80.25	15.64	0.99	16.63
Langdon	Tetraploid parent	Shoot	1	82.92	11.06	1.57	12.63
Langdon	Tetraploid parent	Shoot	3	84.79	11.67	0.53	12.20
Langdon	Tetraploid parent	Anther	5	82.93	13.31	0.48	13.79
Langdon	Tetraploid parent	Anther	2	82.21	13.42	0.56	13.98
Langdon	Tetraploid parent	Anther	3	82.88	13.22	0.48	13.70
Langdon	Tetraploid parent	Pistil-AI	1	81.58	12.61	1.28	13.89
Langdon	Tetraploid parent	Pistil-AI	2	82.75	12.36	1.07	13.43
Langdon	Tetraploid parent	Pistil-AI	4	83.08	12.35	0.96	13.31
PI377655	Tetraploid parent	Glume	3	85.34	11.69	0.32	12.01
PI377655	Tetraploid parent	Glume	1	86.14	10.32	0.49	10.81
PI377655	Tetraploid parent	Glume	2	86.42	9.48	1.11	10.59
PI377655	Tetraploid parent	Boot	1	83.87	11.71	0.45	12.16
PI377655	Tetraploid parent	Boot	3	86.20	9.42	1.59	11.01
PI377655	Tetraploid parent	Boot	2	82.08	14.53	0.53	15.06
PI377655	Tetraploid parent	Hypocotyl	3	85.68	9.90	1.09	10.99
PI377655	Tetraploid parent	Hypocotyl	1	85.28	10.56	1.20	11.76
PI377655	Tetraploid parent	Hypocotyl	2	83.98	12.25	1.03	13.28
PI377655	Tetraploid parent	Palea+Lemma	1	82.16	14.07	0.88	14.95
PI377655	Tetraploid parent	Palea+Lemma	3	83.28	13.25	0.67	13.92
PI377655	Tetraploid parent	Palea+Lemma	2	83.56	12.51	0.95	13.46
PI377655	Tetraploid parent	Pistil-1DAA	1	88.36	7.28	1.43	8.71
PI377655	Tetraploid parent	Pistil-1DAA	3	85.35	7.71	3.20	10.91
PI377655	Tetraploid parent	Pistil-1DAA	2	80.77	7.50	7.75	15.25
PI377655	Tetraploid parent	Pistil-AM	3	89.17	7.32	0.61	7.93
PI377655	Tetraploid parent	Pistil-AM	1	84.80	7.72	3.87	11.59
PI377655	Tetraploid parent	Pistil-AM	2	86.22	7.93	2.56	10.49
PI377655	Tetraploid parent	Root	4	88.54	7.42	1.01	8.43
PI377655	Tetraploid parent	Root	1	88.59	7.10	1.01	8.11
PI377655	Tetraploid parent	Root	2	88.70	7.36	0.82	8.18

PI377655	Tetraploid parent	Shoot	1	80.87	14.33	1.23	15.56
PI377655	Tetraploid parent	Shoot	2	84.28	11.30	0.95	12.25
PI377655	Tetraploid parent	Shoot	3	85.13	10.55	1.13	11.68
PI377655	Tetraploid parent	Anther	4	83.37	13.09	0.53	13.62
PI377655	Tetraploid parent	Anther	2	83.73	12.73	0.50	13.23
PI377655	Tetraploid parent	Anther	3	83.55	13.07	0.41	13.48
PI377655	Tetraploid parent	Pistil-AI	2	83.38	12.94	0.55	13.49
PI377655	Tetraploid parent	Pistil-AI	4	83.16	12.42	0.93	13.35
PI377655	Tetraploid parent	Pistil-AI	3	82.77	13.02	0.78	13.80

**Too many multi-mapped reads imply reads mapping to more than 10 loci \$Total multi-mapped implies the sum of multi-mapped and too many multi-mapped reads*

Pistil-1DAA: pistil-one day after anthesis; Pistil-AM: pistil-when anthers are at mature stage; Pistil-AI: pistil-when anthers are at immature stage; Boot: head at boot stage.

Supplementary Table 5. Number of triads biased towards the AB and D subgenomes in the parental level of expression and the SHW background

SHW	Parents/ SHW*	Pistil-1DAA		Boot		Pistil-AM		Anther		Pistil-AI		Glume		Hypocotyl		Palea+Lemma		Root		Shoot	
		AB biased	D biased	AB biased	D biased	AB biased	D biased	AB biased	D biased	AB biased	D biased	AB biased	D biased	AB biased	D biased	AB biased	D biased	AB biased	D biased	AB biased	D biased
C44	SHW	6,886 (-2.7577)	3,556 (1.1739)	5,069 (-2.7606)	2,992 (1.2135)	3,860 (-3.7535)	1,572 (1.8123)	3,484 (-2.5037)	1,975 (1.5327)	5,243 (-2.5754)	2,477 (1.1562)	4,940 (-2.988)	2,244 (1.5222)	3,704 (-4.3743)	640 (2.6087)	5,166 (-2.9745)	2,330 (1.4397)	4,963 (-3.5897)	1,902 (1.5716)	3,167 (-4.2085)	1,376 (2.1535)
	Parents	1,471 (-1.7018)	5,626 (2.1351)	700 (-3.2717)	6,839 (1.889)	2,203 (-1.29)	3,784 (2.2471)	865 (-2.3239)	6,234 (2.4059)	1,047 (-1.7311)	1,0365 (1.5026)	2,357 (-2.1738)	7,044 (1.7993)	471 (-3.1401)	6,160 (2.554)	1,310 (-2.3041)	6,448 (2.3956)	1,053 (-2.4667)	12,714 (1.5124)	1,071 (-2.6505)	3,907 (3.6611)
C45	SHW	3,286 (-1.4999)	2,875 (1.413)	3,666 (-1.2864)	3,790 (1.233)	3,008 (-1.5487)	2,617 (1.4366)	2,064 (-1.8394)	1,730 (1.7007)	2,788 (-1.3753)	2,396 (1.3264)	815 (-3.2174)	735 (3.1225)	1,632 (-2.153)	1,723 (1.8929)	1,565 (-2.2685)	1,527 (2.1279)	2,765 (-1.5269)	2,984 (1.3928)	795 (-3.0994)	786 (2.9369)
	Parents	1,963 (-1.5472)	9,476 (1.6018)	1,369 (-1.9462)	13,604 (1.3177)	2,550 (-1.3416)	5,608 (1.7844)	1,000 (-2.1385)	5,575 (2.3361)	920 (-1.9668)	10,495 (1.4122)	2,614 (-1.8089)	5,881 (2.0119)	1,216 (-2.0073)	7,301 (2.0876)	1,985 (-1.8371)	8,586 (2.1801)	824 (-2.5347)	8,122 (2.0916)	1,221 (-2.157)	1,830 (4.6597)
C65	SHW	2,941 (-1.5634)	2,899 (1.4843)	1,957 (-1.8329)	2,163 (1.6844)	1,426 (-2.2148)	1,392 (2.1096)	1,927 (-1.9912)	1,576 (1.971)	3,343 (-1.171)	3,177 (1.1735)	3,281 (-1.599)	3,104 (1.5195)	2,308 (-1.6095)	2,591 (1.5255)	3,423 (-1.4091)	3,362 (1.3694)	3,293 (-1.3203)	3,674 (1.2486)	881 (-3.1496)	826 (3.0063)
	Parents	1,184 (-2.4306)	11,041 (1.401)	1,760 (-1.2221)	13,878 (1.3188)	1,645 (-1.941)	9,476 (1.4874)	1,092 (-2.2004)	4,402 (2.2806)	988 (-1.9739)	10,086 (1.4445)	1,853 (-2.0502)	3,764 (2.3942)	1,042 (-2.3845)	5,907 (1.864)	1,188 (-2.2121)	8,547 (2.1358)	738 (-2.5328)	9,590 (1.9212)	1,155 (-2.1834)	6,387 (2.3872)
C66	SHW	2,038 (-1.8335)	2,513 (1.6338)	2,478 (-1.4125)	3,422 (1.3084)	2,809 (-1.4906)	3,392 (1.3367)	1,841 (-2.0856)	1,740 (1.9145)	2,367 (-1.3552)	2,976 (1.2564)	1,051 (-2.8733)	1,090 (2.7251)	1,584 (-1.9159)	2,208 (1.7135)	1,348 (-2.2346)	1,633 (2.0951)	1,754 (-1.8702)	2,457 (1.6176)	793 (-3.1758)	890 (2.9798)
	Parents	1,274 (-2.0341)	11,153 (1.4293)	478 (-3.5611)	12,944 (1.3496)	1,496 (-1.7724)	9,125 (1.5867)	1,115 (-2.1407)	5,667 (2.1912)	1,099 (-1.7060)	10,128 (1.5192)	2,279 (-1.9382)	7,264 (1.7225)	512 (-3.3352)	5,597 (2.1047)	950 (-2.5973)	7,344 (2.2196)	817 (-2.7019)	13,208 (1.4689)	808 (-3.1095)	9,978 (1.991)

Pistil-1DAA: pistil-one day after anthesis; Pistil-AM: pistil-when anthers are at mature stage; Pistil-AI: pistil-when anthers are at immature stage; Boot: head at boot stage.

*Parents: Parental level of expression; SHW: Synthetic hexaploid wheat.

The number of triads showing significant bias towards the AB and D subgenomes in the SHW and parental expression levels (in-silico SHW scenario) are summarized in this table. The values in the brackets in each cell represent the average value of the magnitude of HEB in the particular SHW-tissue scenario i.e., $\frac{1}{n} \sum_{i=1}^n \log_2 \left(\frac{RPKM_D}{RPKM_{AB}} \right)$, where n is the number of triads showing significant bias towards the specific subgenome, and $RPKM_D$ and $RPKM_{AB}$ represent the expression values from the D and AB subgenomes, respectively.

Supplementary Table 6. Summary of tissue specificity of homoeologues constituting the triads in the four SHW lines

Homoeologue tissue specificity	Number of triads (absolute values)				Relative percentage*			
	C44	C45	C65	C66	C44	C45	C65	C66
All homoeologues not tissue specific ¹	12,751	13,368	13,241	13,391	69.5	72.8	72.1	72.9
All homoeologues same tissue specificity ²	1,556	1,938	1,868	1,798	8.5	10.6	10.2	9.8
D tissue specific, A and B not tissue specific ³	1204	381	399	394	6.6	2.1	2.2	2.1
B tissue specific, A and D not tissue specific ³	516	476	495	523	2.8	2.6	2.7	2.8
A tissue specific, B and D not tissue specific ³	473	422	482	481	2.6	2.3	2.6	2.6
A and B same tissue specificity, D other tissue specificity ⁴	119	137	98	99	0.6	0.7	0.5	0.5
A and B same tissue specificity, D not tissue specific ⁵	351	227	245	228	1.9	1.2	1.3	1.2
A and D same tissue specificity, B other tissue specificity ⁴	115	153	168	158	0.6	0.8	0.9	0.9
A and D same tissue specificity, B not tissue specific ⁵	259	263	277	277	1.4	1.4	1.5	1.5
B and D same tissue specificity, A other tissue specificity ⁴	114	156	169	167	0.6	0.8	0.9	0.9
B and D same tissue specificity, A not tissue specific ⁵	269	259	293	279	1.5	1.4	1.6	1.5
All homoeologues showing varied tissue specificity ⁶	630	577	622	562	3.4	3.1	3.4	3.1
Total	18,357	18,357	18,357	18,357	100.0	100.0	100.0	100.0

¹All three homoeologues of the triads are broadly expressed without any tissue specificity; ²All three homoeologues show expression specificity to the same tissue;

³One of the three homoeologues is tissue specific and the other two are broadly expressed; ⁴Two of the three homoeologues show expression specificity in the same tissue and the third homoeologue shows expression specificity in another tissue; ⁵Two of the three homoeologues show expression specificity in the same tissue and the third homoeologue is broadly expressed; ⁶All homoeologues showed varied tissue specificity or wider expression. *Percentage of triads relative to the total number of triads (18,357).

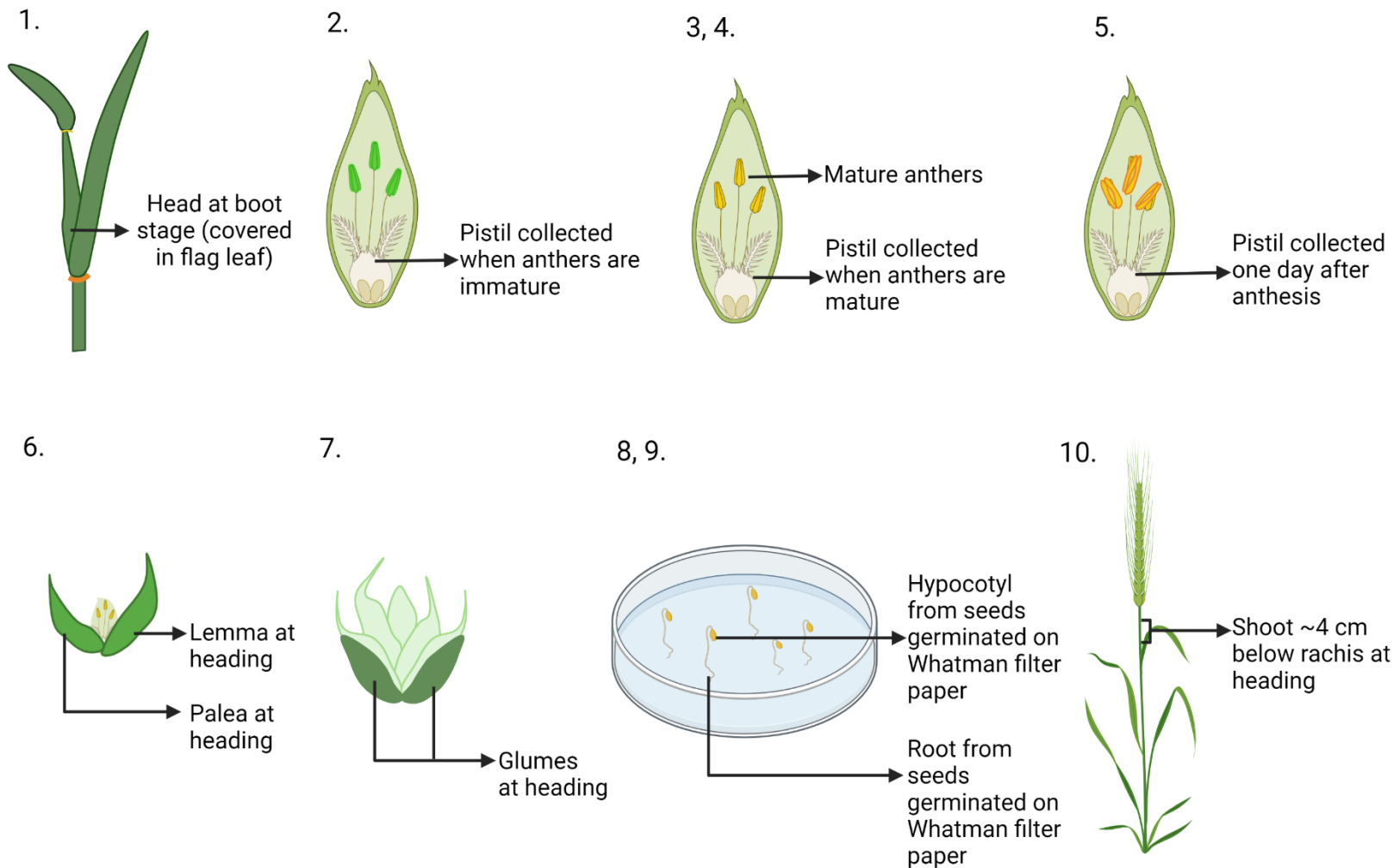
Supplementary Table 7. Summary of the number of triads with varied tissue specificity of homoeologues and expression bias patterns across the ten tissues in the four SHW lines

SHW	Homoeologues showing tissue specificity in triads	Bias pattern	Pistil-1DAA	Pistil-AI	Palea+Lemma	Pistil-AM	Root	Shoot	Anther	Boot	Glume	Hypocotyl
C44	A,B,D	Total	13	23	6	18	653	24	600	140	14	65
C44	A,B,D	AB-bias	5	6	1	5	244	6	236	33	5	16
C44	A,B,D	D-bias	7	2	2	1	125	6	143	32	4	6
C44	A,B,D	UN-biased	1	15	3	12	284	12	221	75	5	43
C44	A and B	Total	16	20	6	20	219	15	77	49	8	40
C44	A and B	AB-bias	9	3	1	2	59	4	17	3	1	8
C44	A and B	D-bias	2	2	0	1	13	2	3	3	1	3
C44	A and B	UN-biased	5	15	5	17	147	9	57	43	6	29
C44	A and D	Total	14	21	4	11	146	29	72	37	12	28
C44	A and D	AB-bias	7	4	2	2	41	6	29	7	5	4
C44	A and D	D-bias	3	4	1	2	42	7	18	9	1	3
C44	A and D	UN-biased	4	13	1	7	63	16	25	21	6	21
C44	B and D	Total	19	11	7	10	134	28	84	47	10	33
C44	B and D	AB-bias	4	2	1	4	46	5	27	6	4	7
C44	B and D	D-bias	8	5	2	1	33	7	26	7	2	3
C44	B and D	UN-biased	7	4	4	5	55	16	31	34	4	23
C44	A only	Total	60	80	59	82	231	92	176	112	72	100
C44	A only	AB-bias	6	12	8	5	57	10	34	8	8	13
C44	A only	D-bias	11	19	8	16	16	15	9	16	13	4
C44	A only	UN-biased	43	49	43	61	158	67	133	88	51	83
C44	B only	Total	77	78	47	71	266	78	188	90	60	140
C44	B only	AB-bias	20	10	9	9	51	8	27	13	6	17
C44	B only	D-bias	11	14	4	14	38	15	25	6	11	13
C44	B only	UN-biased	46	54	34	48	177	55	136	71	43	110
C44	D only	Total	158	225	116	163	241	189	204	159	121	164
C44	D only	AB-bias	104	181	76	110	114	85	100	72	91	98
C44	D only	D-bias	20	4	8	9	33	31	30	20	6	7
C44	D only	UN-biased	34	40	32	44	94	73	74	67	24	59
C45	A,B,D	Total	58	33	21	8	838	52	527	268	10	123
C45	A,B,D	AB-bias	16	2	3	0	178	6	159	43	2	24
C45	A,B,D	D-bias	17	2	7	4	236	5	146	64	1	23
C45	A,B,D	UN-biased	25	29	11	4	424	41	222	161	7	76
C45	A and B	Total	25	21	8	10	127	37	37	50	6	43
C45	A and B	AB-bias	7	4	1	3	33	5	13	7	2	12
C45	A and B	D-bias	3	1	1	1	17	6	8	6	1	8
C45	A and B	UN-biased	15	16	6	6	77	26	16	37	3	23
C45	A and D	Total	25	22	10	5	157	51	46	57	5	38
C45	A and D	AB-bias	3	5	2	2	28	8	9	11	0	9
C45	A and D	D-bias	9	3	0	1	52	12	14	16	0	11
C45	A and D	UN-biased	13	14	8	2	77	31	23	30	5	18
C45	B and D	Total	24	14	9	5	165	38	39	61	6	54

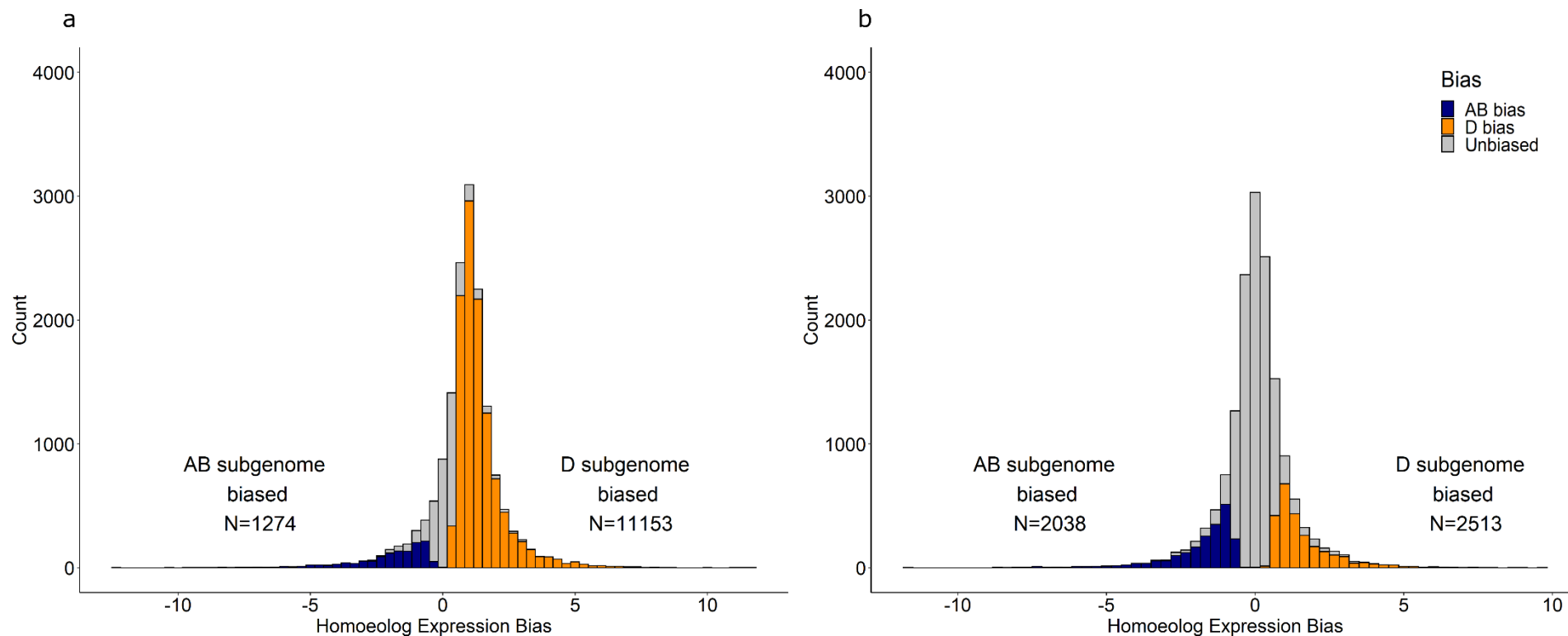
C45	B and D	AB-bias	6	2	2	1	24	3	8	8	0	3
C45	B and D	D-bias	4	2	3	3	64	9	15	14	0	15
C45	B and D	UN-biased	14	10	4	1	77	26	16	39	6	36
C45	A only	Total	89	81	78	61	199	99	110	124	42	114
C45	A only	AB-bias	15	8	13	7	36	8	31	29	5	17
C45	A only	D-bias	15	20	14	13	40	10	11	22	7	14
C45	A only	UN-biased	59	53	51	41	123	81	68	73	30	83
C45	B only	Total	86	80	81	53	237	130	99	135	34	126
C45	B only	AB-bias	18	8	3	8	42	13	18	20	0	26
C45	B only	D-bias	14	20	18	9	43	13	14	29	4	15
C45	B only	UN-biased	54	52	60	36	152	104	67	86	30	85
C45	D only	Total	69	64	76	50	218	105	86	105	52	104
C45	D only	AB-bias	6	15	9	11	30	11	9	14	10	11
C45	D only	D-bias	19	9	12	6	61	14	33	26	9	22
C45	D only	UN-biased	44	40	55	33	127	80	44	65	33	71
C65	A,B,D	Total	82	22	10	15	856	53	468	237	8	117
C65	A,B,D	AB-bias	19	2	1	4	189	3	141	27	2	29
C65	A,B,D	D-bias	16	4	4	2	251	6	107	41	1	21
C65	A,B,D	UN-biased	47	16	5	9	416	44	220	169	5	67
C65	A and B	Total	22	11	6	13	142	38	33	33	9	36
C65	A and B	AB-bias	6	3	1	3	38	3	12	6	1	10
C65	A and B	D-bias	4	2	0	1	25	6	7	4	3	7
C65	A and B	UN-biased	12	6	5	9	79	29	14	23	5	19
C65	A and D	Total	34	25	10	8	181	41	48	57	4	37
C65	A and D	AB-bias	5	1	2	3	37	4	9	10	1	10
C65	A and D	D-bias	8	4	3	0	59	12	24	10	1	11
C65	A and D	UN-biased	21	20	5	5	85	25	15	37	2	16
C65	B and D	Total	32	19	8	10	192	33	44	68	6	50
C65	B and D	AB-bias	5	4	1	2	35	5	8	8	1	4
C65	B and D	D-bias	11	2	1	3	83	11	21	13	1	18
C65	B and D	UN-biased	16	13	6	5	74	17	15	47	4	28
C65	A only	Total	88	97	81	54	221	117	120	173	45	133
C65	A only	AB-bias	15	8	8	6	50	16	28	34	4	23
C65	A only	D-bias	10	27	17	7	46	17	13	31	12	31
C65	A only	UN-biased	63	62	56	41	125	84	79	108	29	79
C65	B only	Total	100	84	68	67	244	106	110	137	63	125
C65	B only	AB-bias	14	12	10	7	46	10	26	21	6	30
C65	B only	D-bias	9	16	15	5	55	6	10	20	14	20
C65	B only	UN-biased	77	56	43	55	143	90	74	96	43	75
C65	D only	Total	78	75	55	52	224	94	94	128	51	101
C65	D only	AB-bias	9	12	9	9	38	11	10	19	11	23
C65	D only	D-bias	17	12	10	7	67	17	34	27	11	20
C65	D only	UN-biased	52	51	36	36	119	66	50	82	29	58
C66	A,B,D	Total	65	26	11	15	781	29	503	254	5	109
C66	A,B,D	AB-bias	13	6	0	1	118	3	123	30	1	26
C66	A,B,D	D-bias	16	3	3	7	184	6	136	56	2	16
C66	A,B,D	UN-biased	36	17	8	7	479	20	244	168	2	67

C66	A and B	Total	24	24	10	6	120	29	36	33	6	39
C66	A and B	AB-bias	9	2	1	1	27	4	13	4	1	8
C66	A and B	D-bias	1	2	1	1	18	4	7	3	1	5
C66	A and B	UN-biased	14	20	8	4	75	21	16	26	4	26
C66	A and D	Total	23	22	9	17	156	32	48	73	11	44
C66	A and D	AB-bias	4	3	1	3	20	1	11	13	6	4
C66	A and D	D-bias	4	3	2	2	42	9	21	20	0	11
C66	A and D	UN-biased	15	16	6	12	94	22	16	40	5	29
C66	B and D	Total	27	20	10	13	174	34	39	69	8	52
C66	B and D	AB-bias	4	2	1	3	23	3	11	5	0	3
C66	B and D	D-bias	12	2	3	2	49	4	18	15	1	16
C66	B and D	UN-biased	11	16	6	8	102	27	10	49	7	33
C66	A only	Total	100	95	61	68	205	107	111	126	53	130
C66	A only	AB-bias	10	7	9	6	34	10	31	20	5	18
C66	A only	D-bias	20	23	10	14	30	11	12	20	7	18
C66	A only	UN-biased	70	65	42	48	141	86	68	86	41	94
C66	B only	Total	116	85	46	58	229	110	113	135	52	144
C66	B only	AB-bias	25	10	2	6	41	12	24	15	3	18
C66	B only	D-bias	12	25	10	10	32	11	16	28	4	24
C66	B only	UN-biased	79	50	34	42	156	87	73	92	45	102
C66	D only	Total	83	86	44	55	211	84	81	121	38	93
C66	D only	AB-bias	11	25	4	7	19	9	7	19	11	15
C66	D only	D-bias	20	8	4	12	54	22	25	17	3	19
C66	D only	UN-biased	52	53	36	36	138	53	49	85	24	59

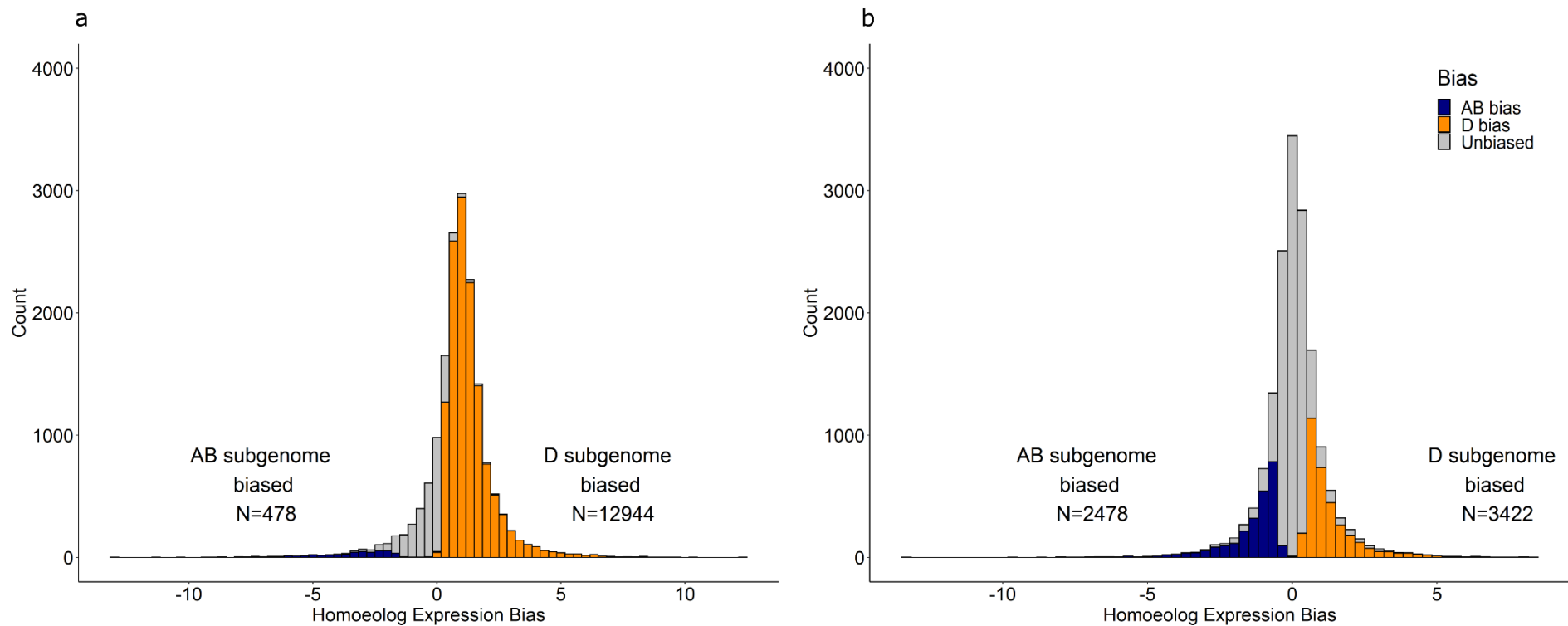
Pistil-1DAA: pistil-one day after anthesis; Pistil-AM: pistil-when anthers are at mature stage; Pistil-AI: pistil-when anthers are at immature stage; Boot: head at boot stage.



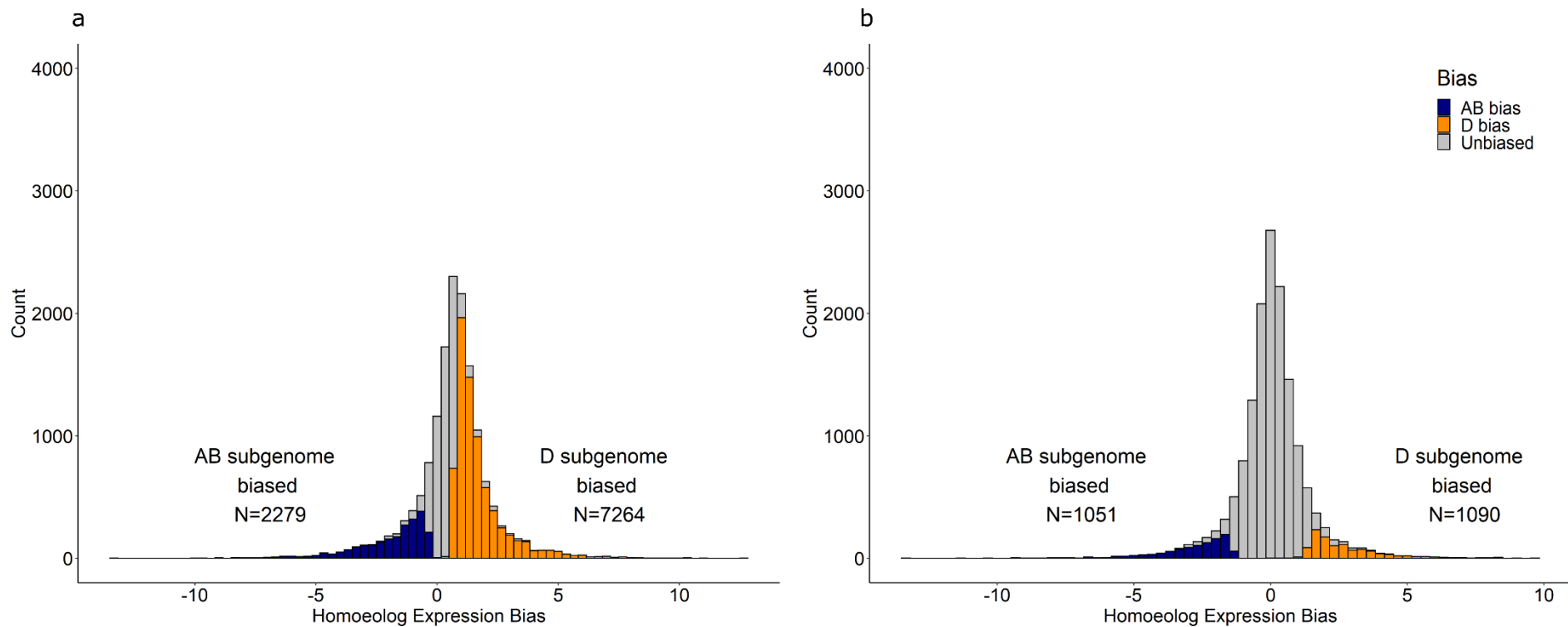
Supplementary Figure 1. Pictorial representation of the ten different tissues used in the study. (1) Head at boot stage; (2) Pistil when anthers are green and immature; (3) Mature anthers; (4) Pistil when anthers are mature; (5) Pistil-one day after anthesis; (6) Palea+Lemma; (7) Glumes; (8) Hypocotyl; (9) Root; (10) Shoot. Figure created with Biorender.com.



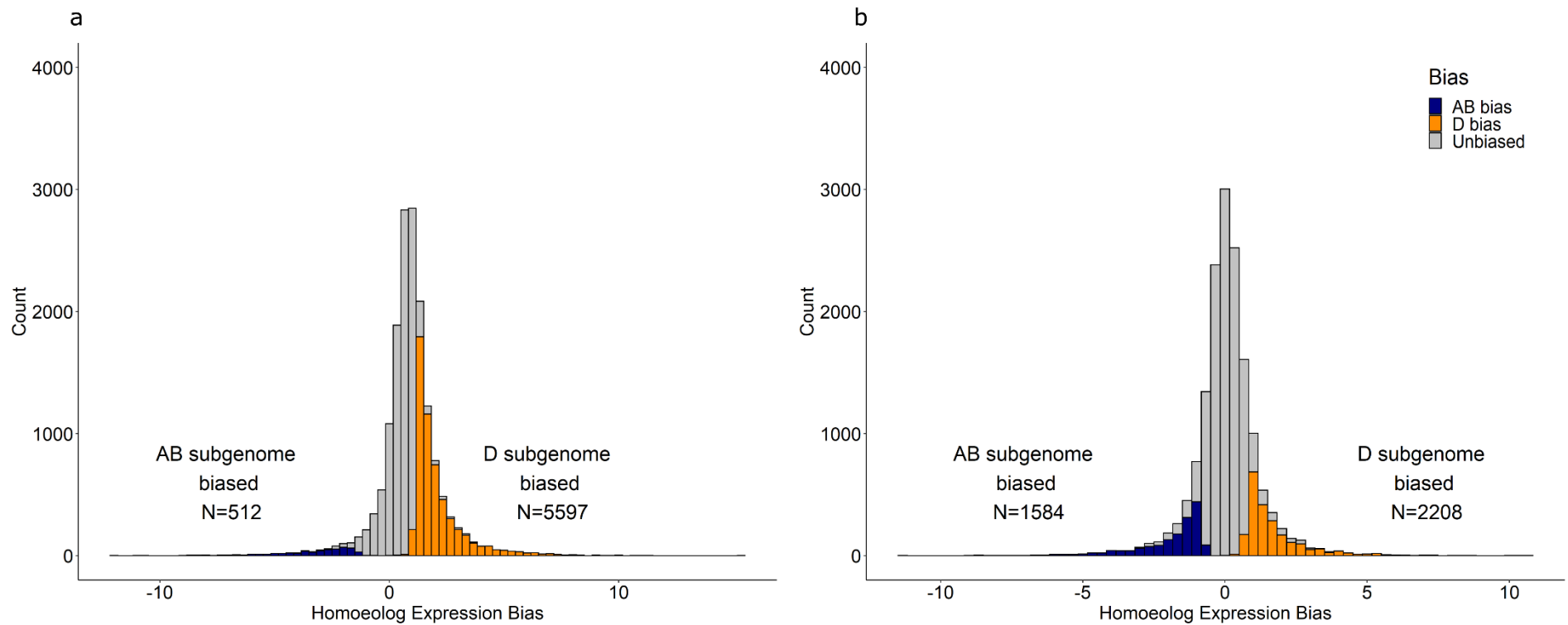
Supplementary Figure 2. Distribution of homoeologue expression bias in pistil-one day after anthesis of SHW-C66. (a) Comparison of the expression bias of triads towards AB and D genomes of tetraploid (PI377655) and diploid (AS2386) parents; (b) Comparison of the expression bias of triads towards AB and D subgenomes of SHW-C66.



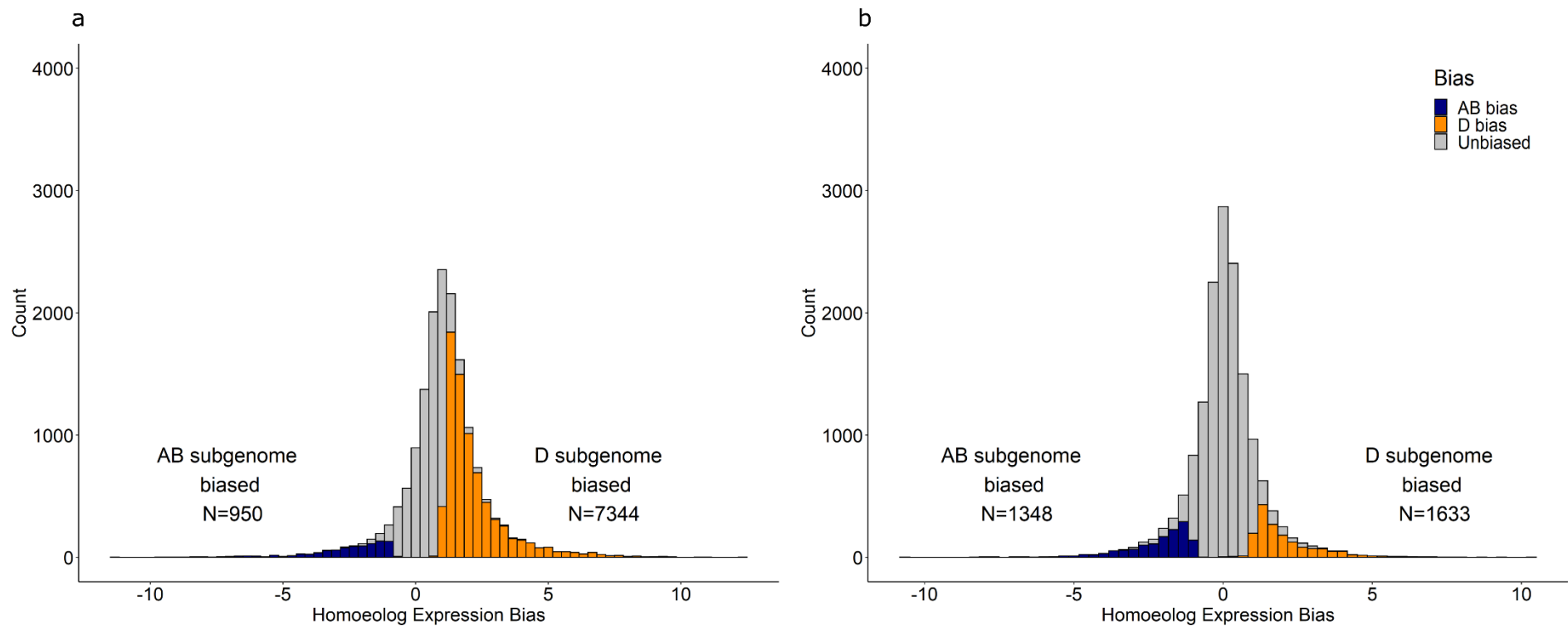
Supplementary Figure 3. Distribution of homoeologue expression bias in head collected at boot stage of SHW-C66. (a) Comparison of the expression bias of triads towards AB and D genomes of tetraploid (PI377655) and diploid (AS2386) parents; (b) Comparison of the expression bias of triads towards AB and D subgenomes of SHW-C66.



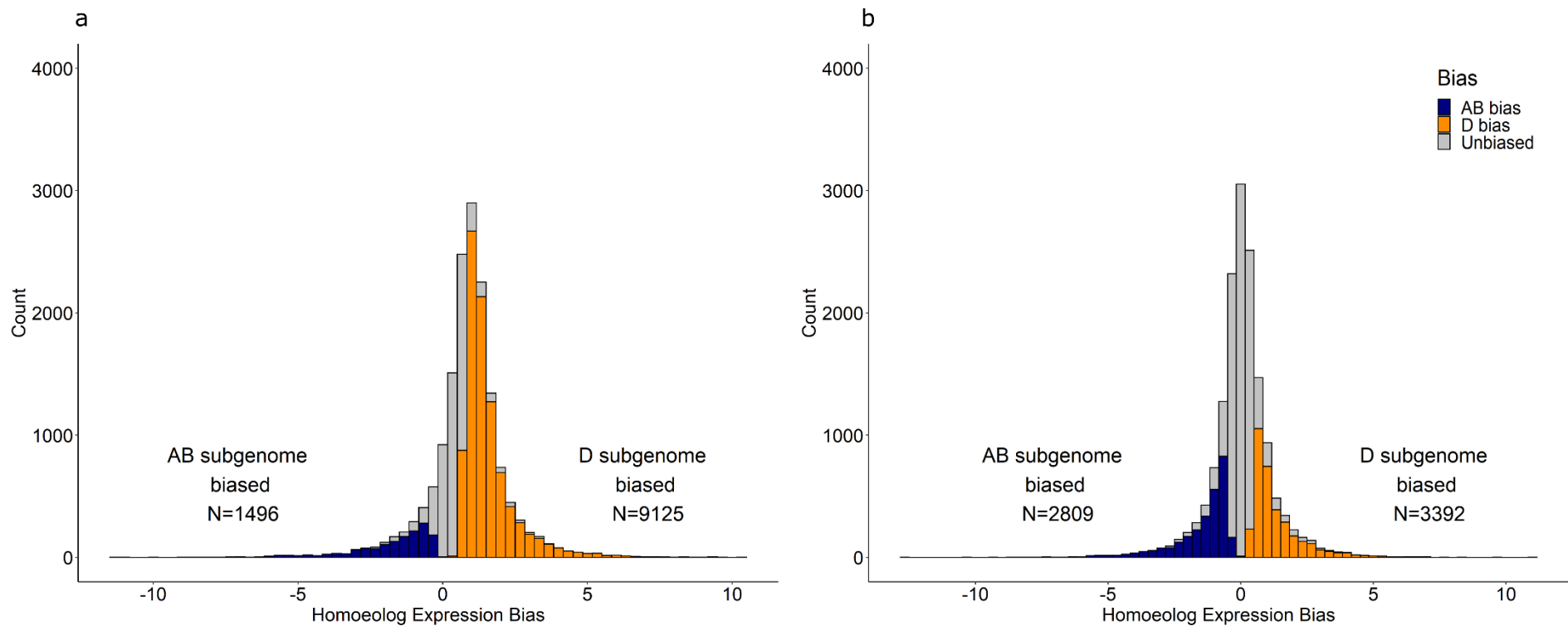
Supplementary Figure 4. Distribution of homoeologue expression bias in glume of SHW-C66. (a) Comparison of the expression bias of triads towards AB and D genomes of tetraploid (PI377655) and diploid (AS2386) parents; (b) Comparison of the expression bias of triads towards AB and D subgenomes of SHW-C66.



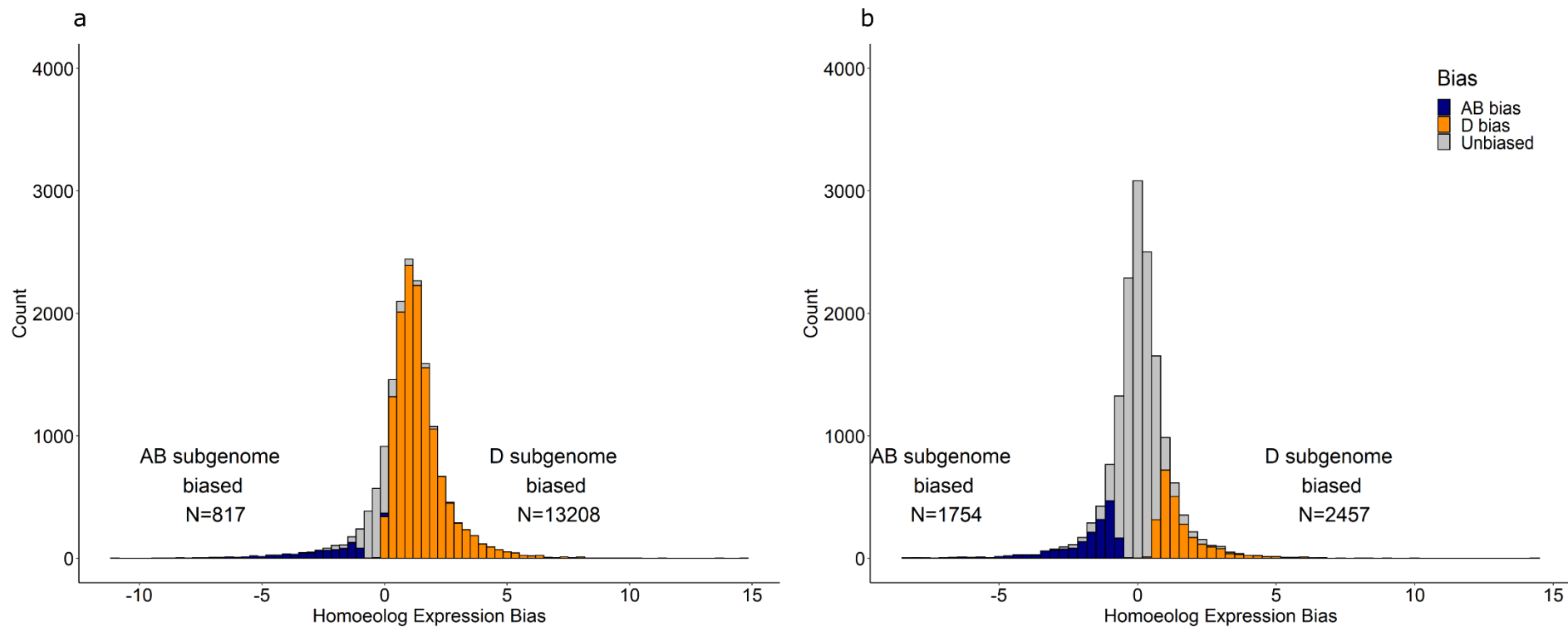
Supplementary Figure 5. Distribution of homoeologue expression bias in hypocotyl of SHW-C66. (a) Comparison of the expression bias of triads towards AB and D genomes of tetraploid (PI377655) and diploid (AS2386) parents; (b) Comparison of the expression bias of triads towards AB and D subgenomes of SHW-C66.



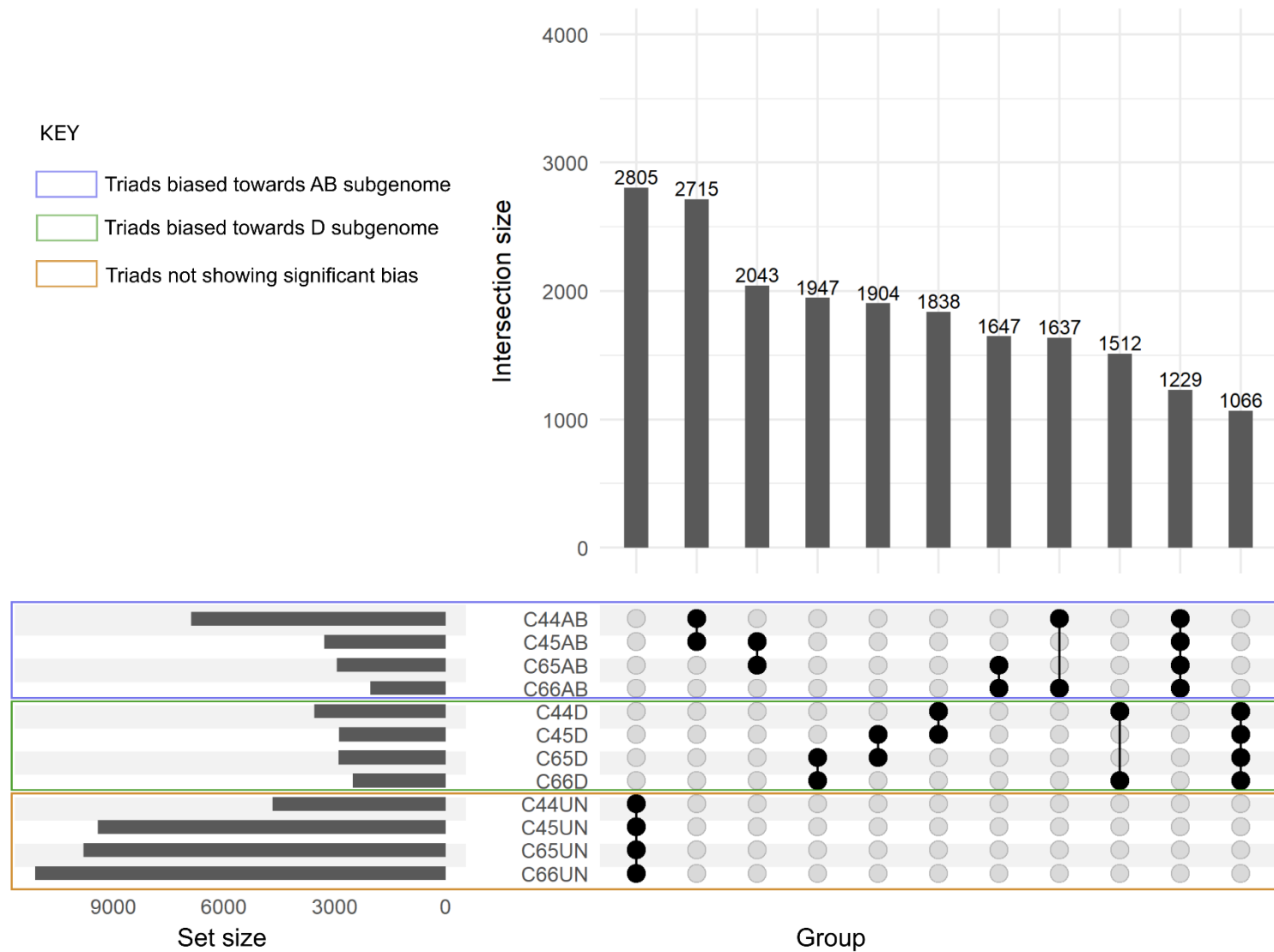
Supplementary Figure 6. Distribution of homoeologue expression bias in palea+lemma of SHW-C66. (a) Comparison of the expression bias of triads towards AB and D genomes of tetraploid (PI377655) and diploid (AS2386) parents; (b) Comparison of the expression bias of triads towards AB and D subgenomes of SHW-C66.



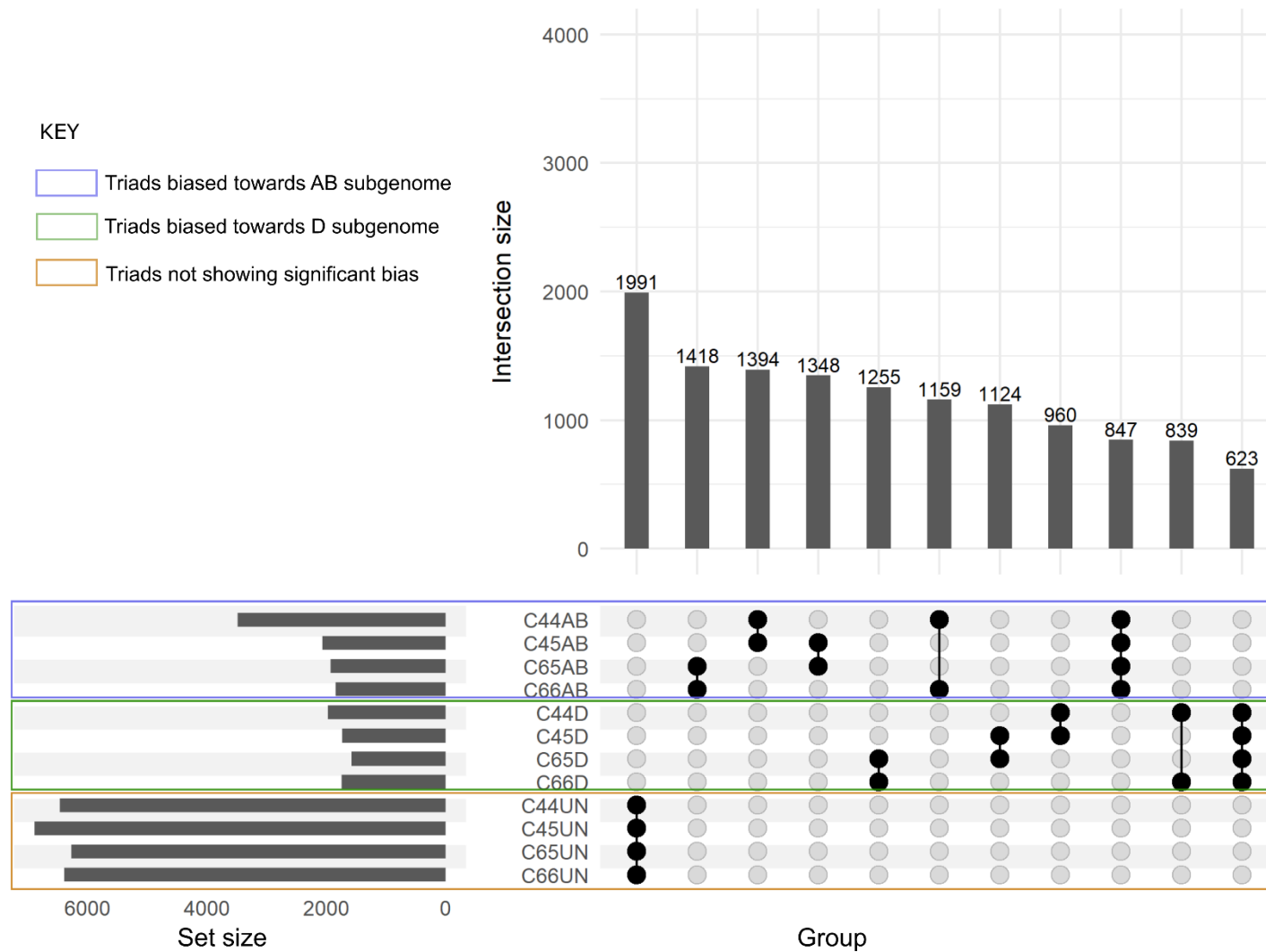
Supplementary Figure 7. Distribution of homoeologue expression bias in pistil (collected when anthers were mature) of SHW-C66. (a) Comparison of the expression bias of triads towards AB and D genomes of tetraploid (PI377655) and diploid (AS2386) parents; (b) Comparison of the expression bias of triads towards AB and D subgenomes of SHW-C66.



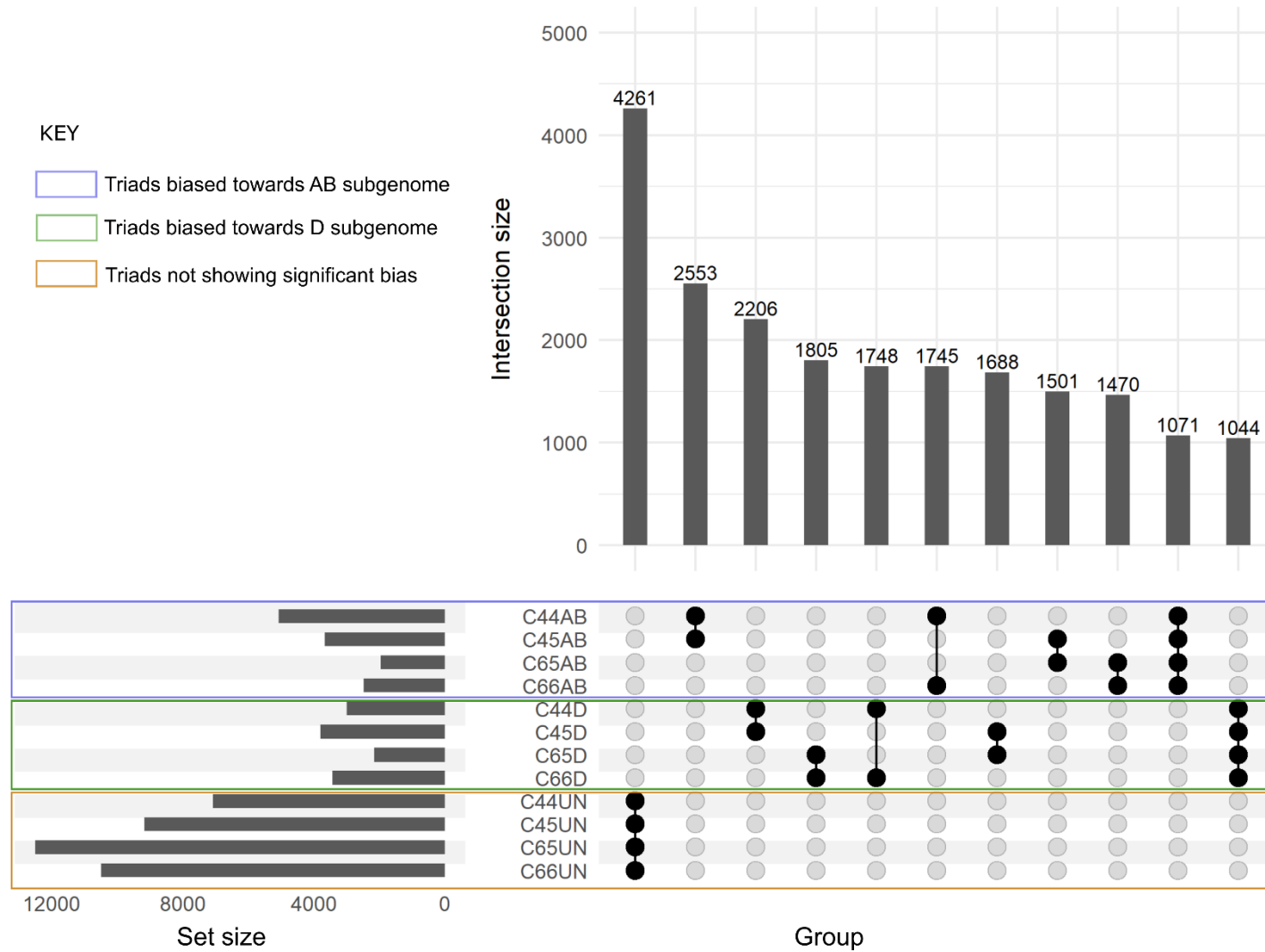
Supplementary Figure 8. Distribution of homoeologue expression bias in root of SHW-C66. (a) Comparison of the expression bias of triads towards AB and D genomes of tetraploid (PI377655) and diploid (AS2386) parents; (b) Comparison of the expression bias of triads towards AB and D subgenomes of SHW-C66.



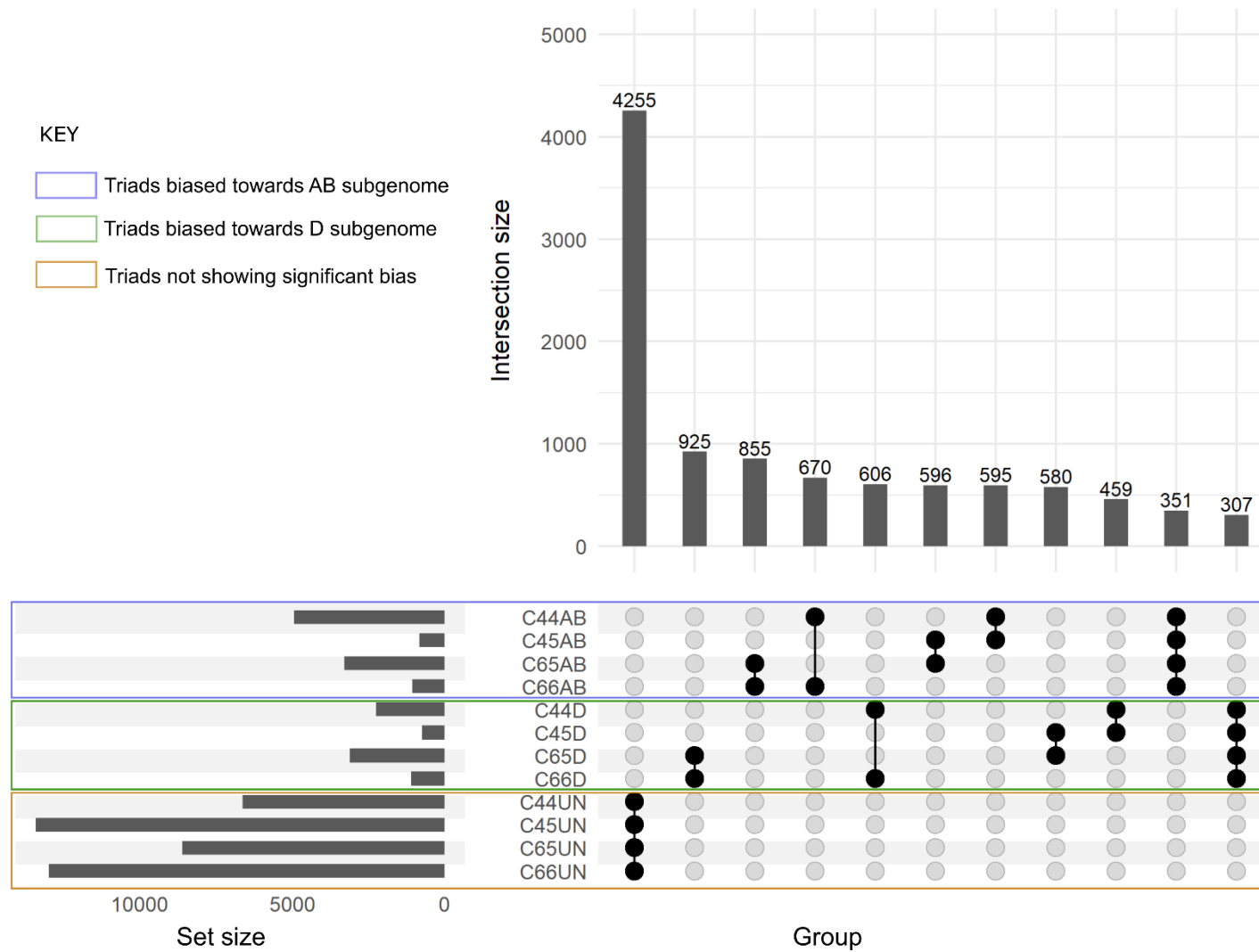
Supplementary Figure 9. Subsets of triads showing similar expression patterns across all four SHW lines in pistil-one day after anthesis.



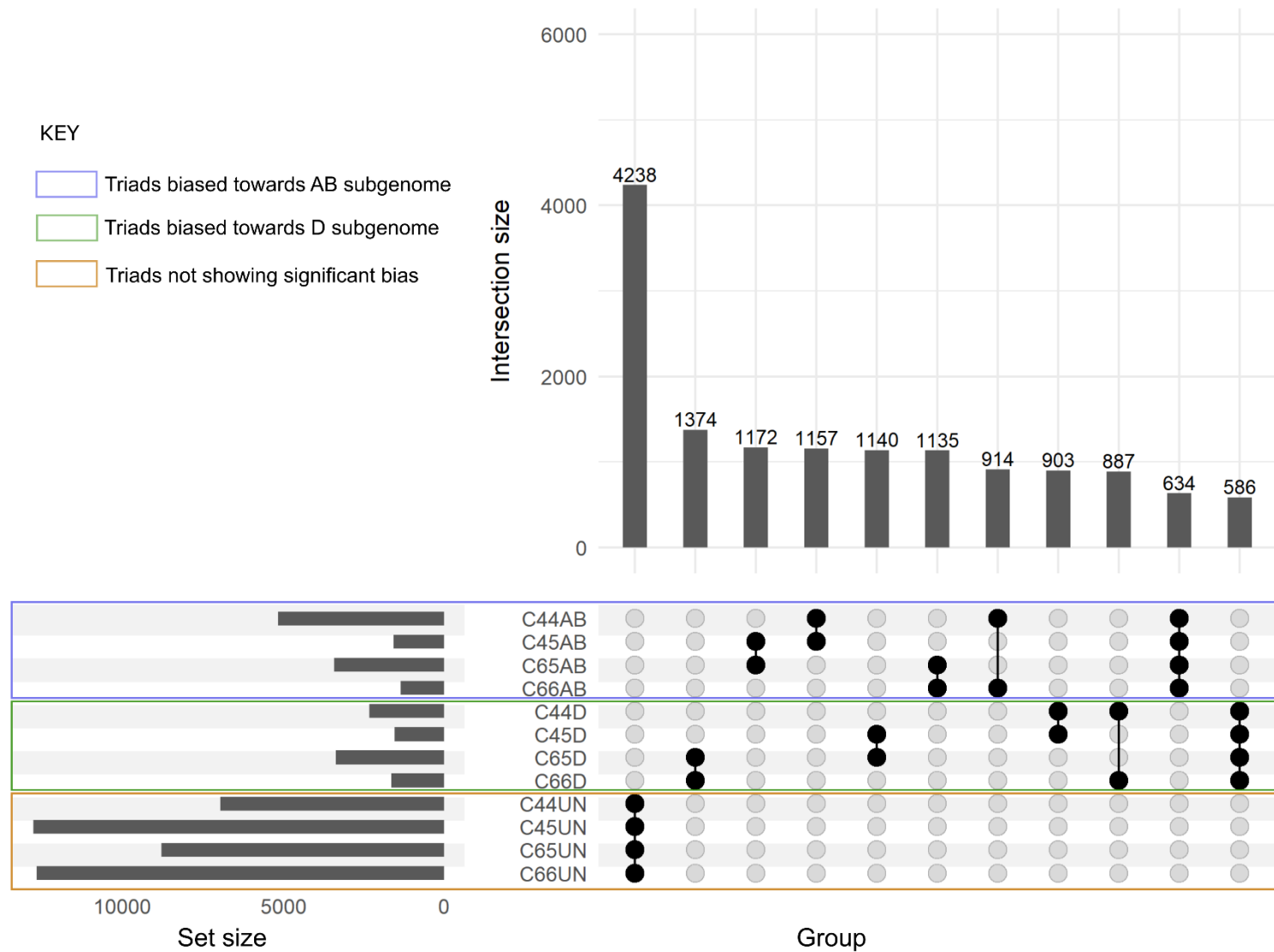
Supplementary Figure 10. Subsets of triads showing similar expression patterns across all four SHW lines in mature anther.



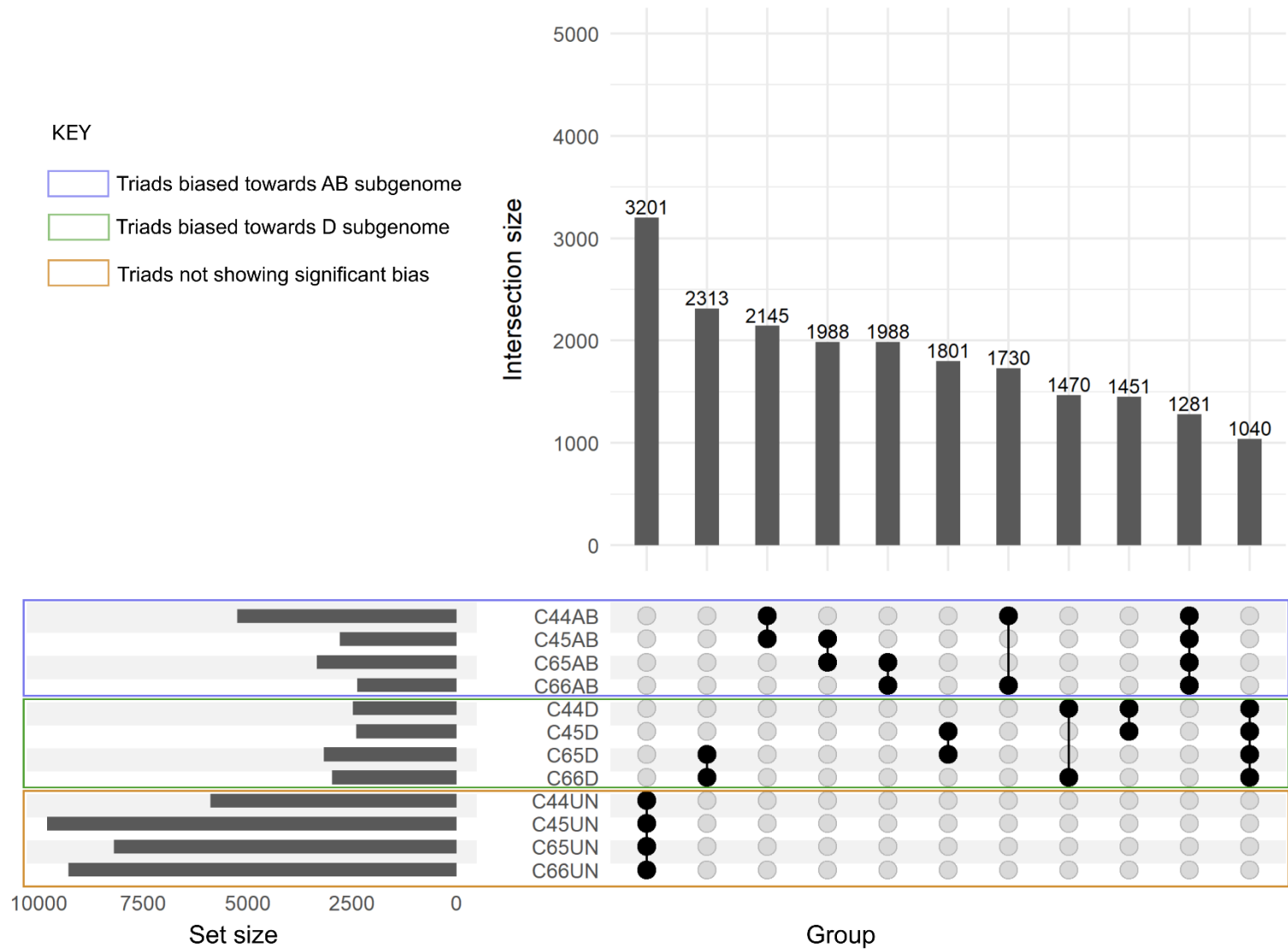
Supplementary Figure 11. Subsets of triads showing similar expression patterns across all four SHW lines in head collected at boot stage.



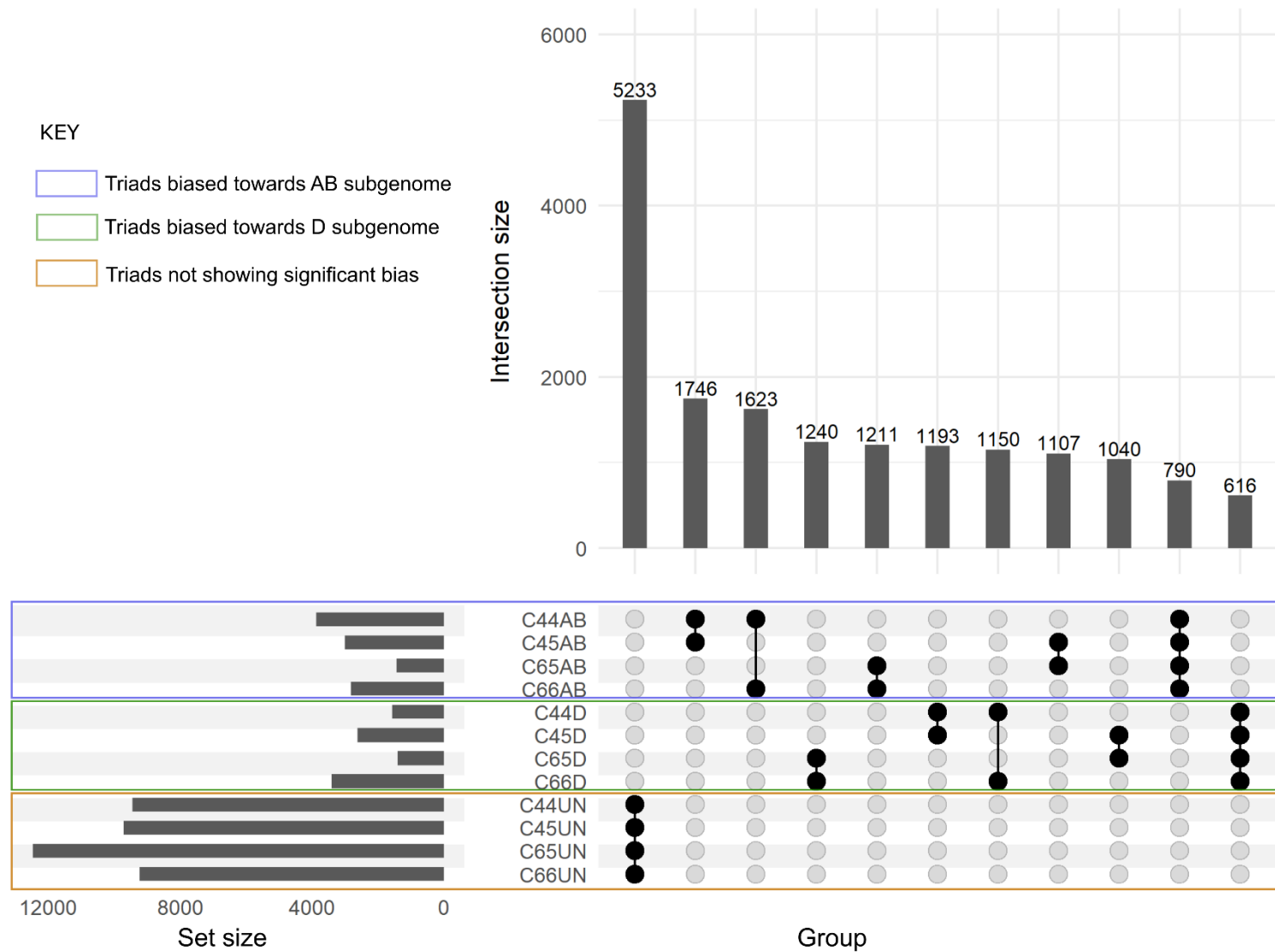
Supplementary Figure 12. Subsets of triads showing similar expression patterns across all four SHW lines in glume.



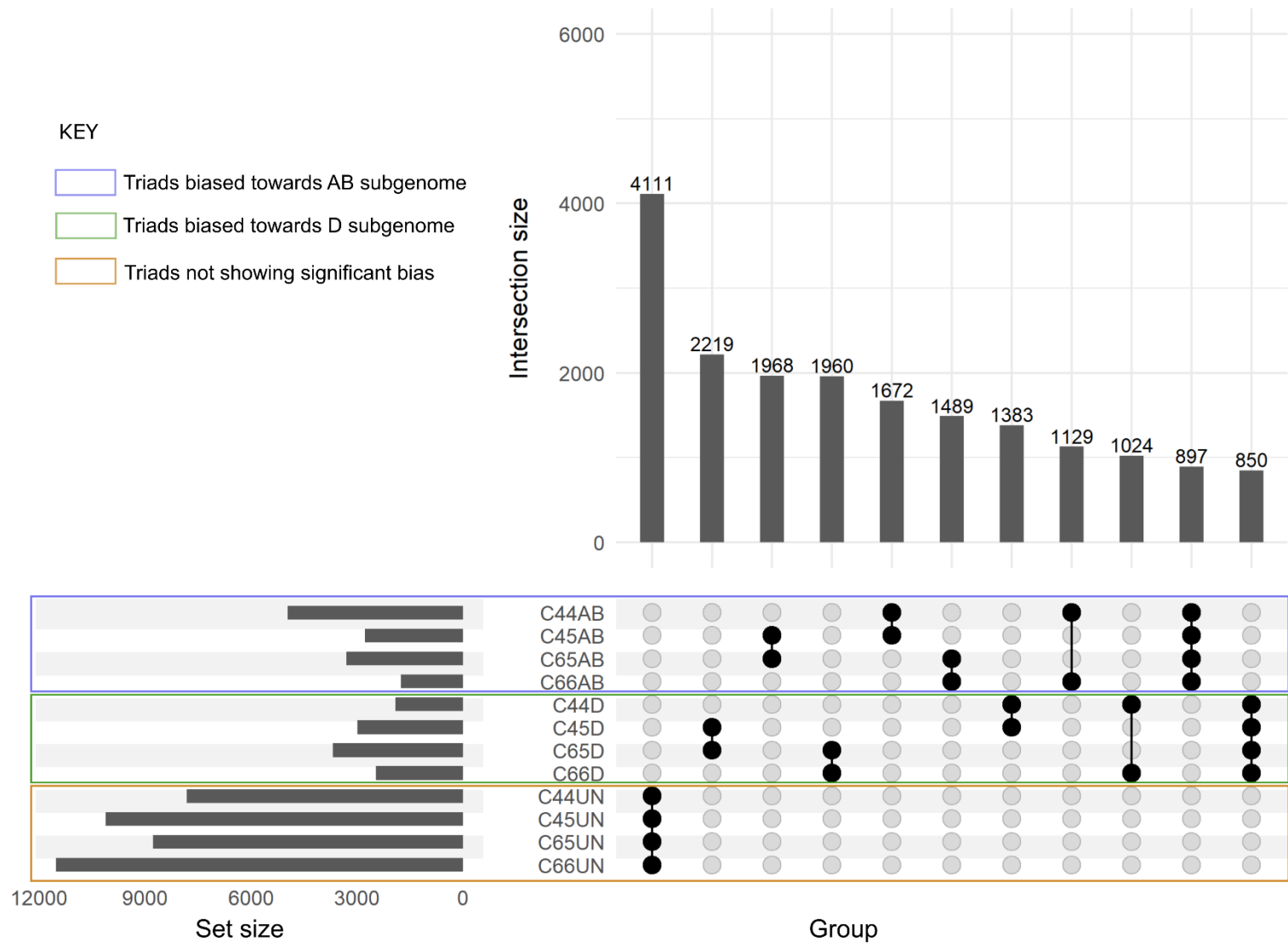
Supplementary Figure 14. Subsets of triads showing similar expression patterns across all four SHW lines in palea+lemma.



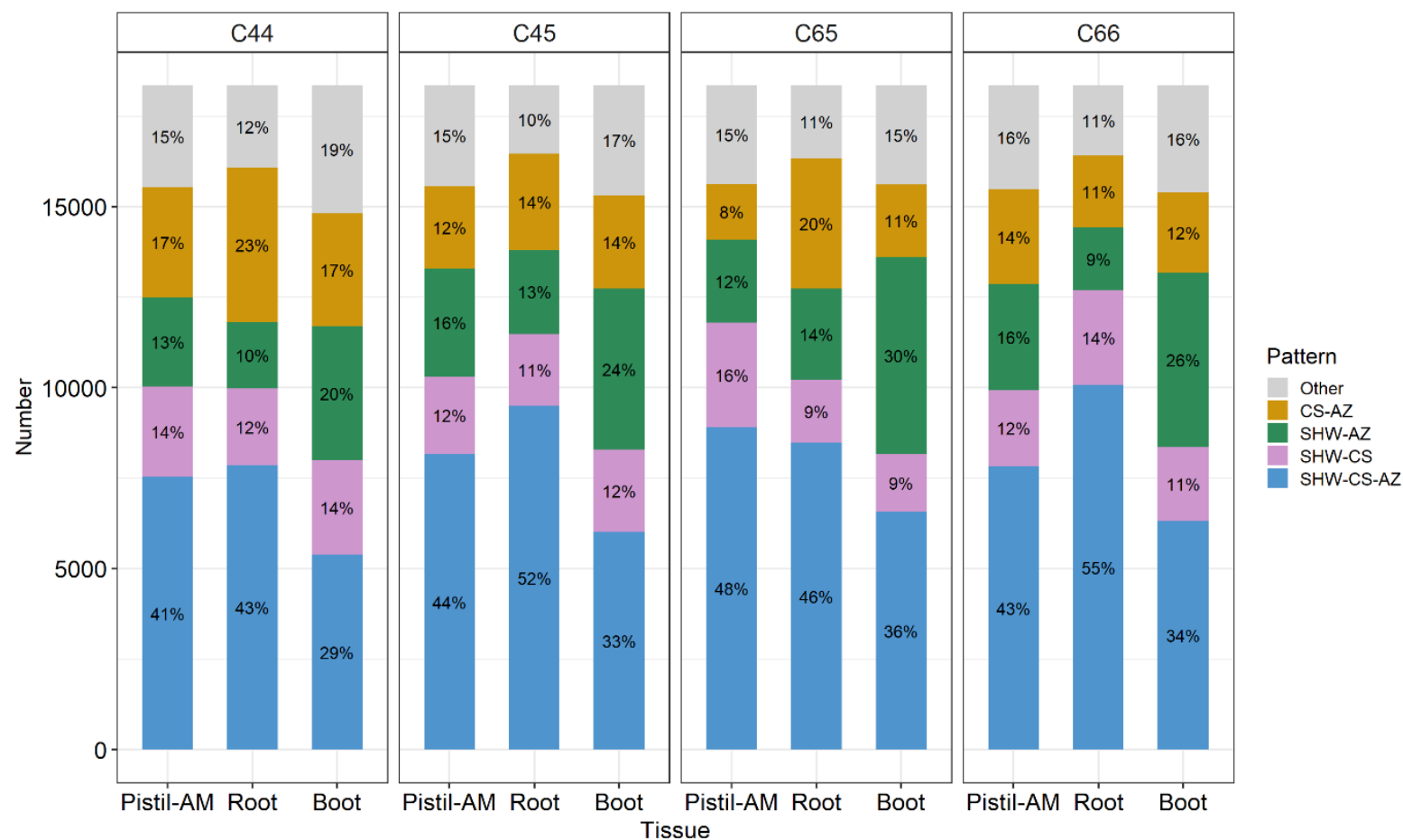
Supplementary Figure 15. Subsets of triads showing similar expression patterns across all four SHW lines in pistil-when anthers are green and immature.



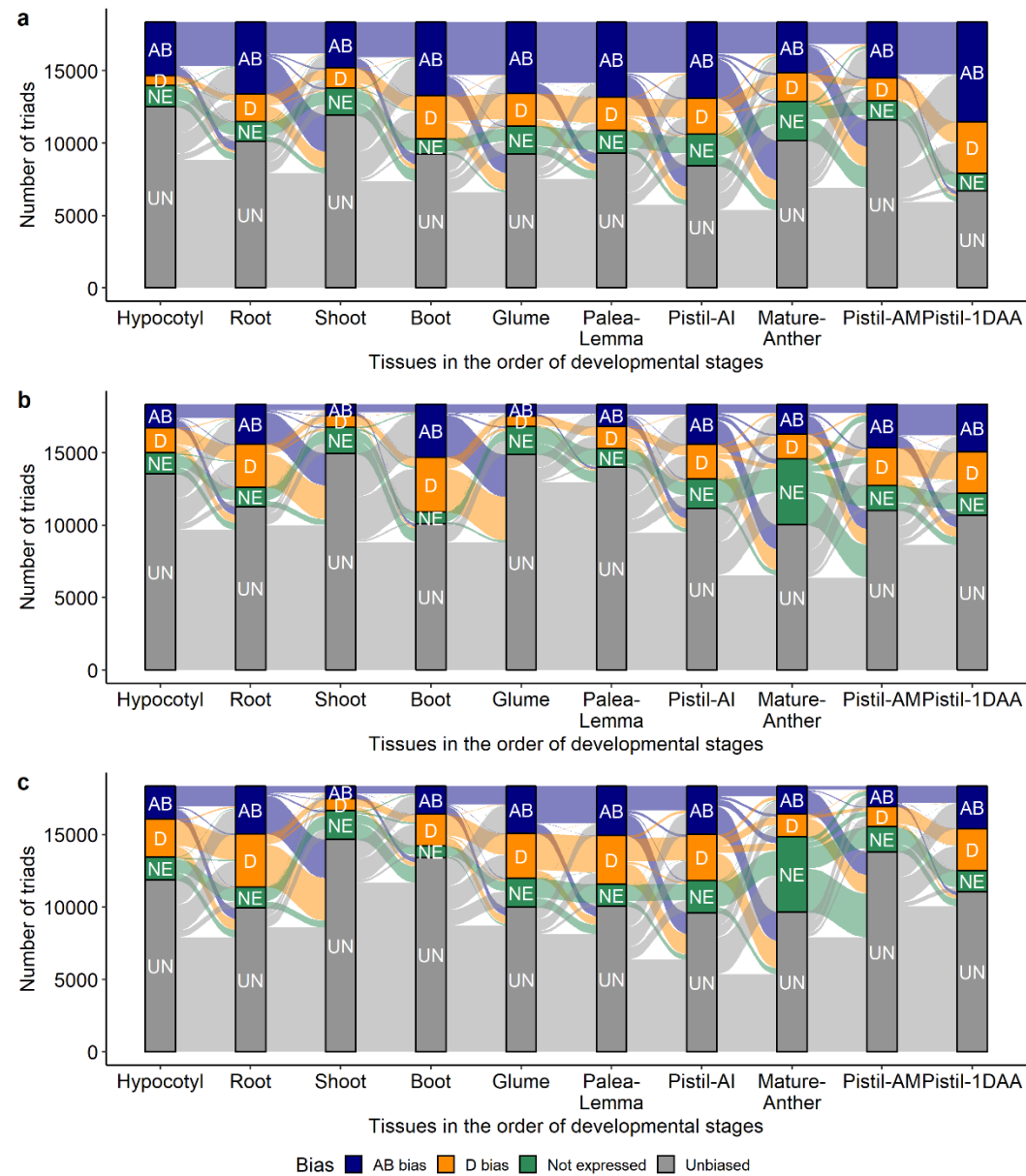
Supplementary Figure 16. Subsets of triads showing similar expression patterns across all four SHW lines in pistil-when anthers are yellow and just prior to dehiscence.



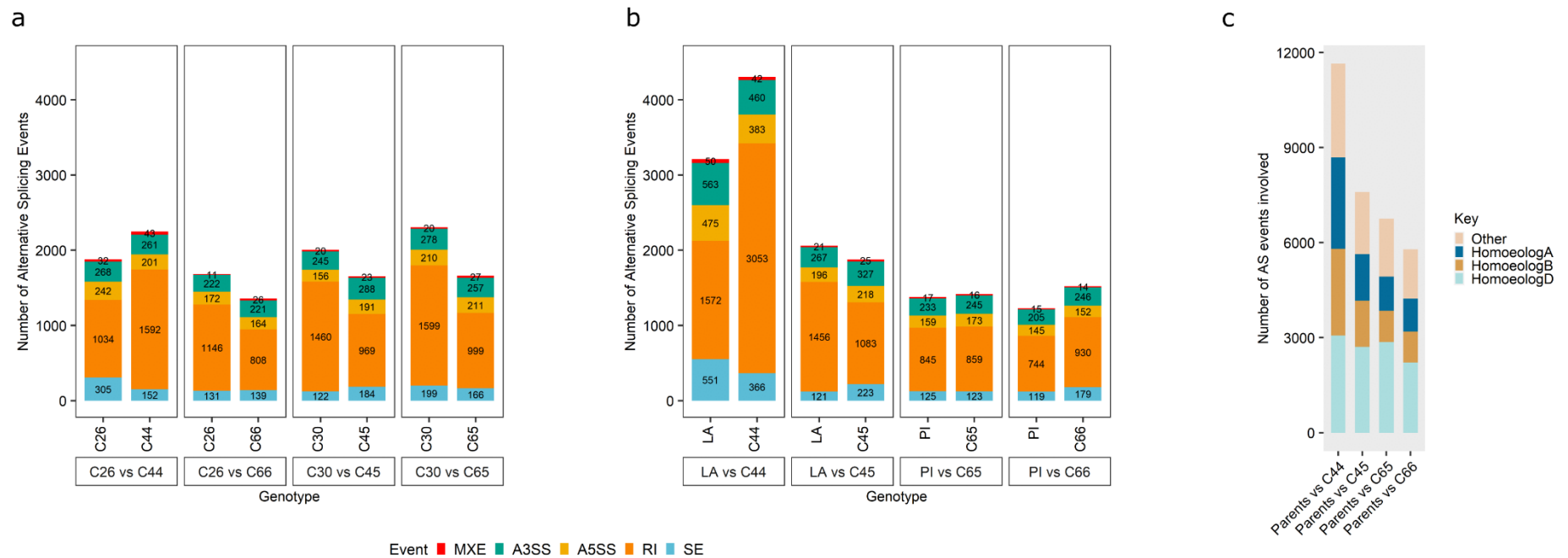
Supplementary Figure 17. Subsets of triads showing similar expression patterns across all four SHW lines in root.



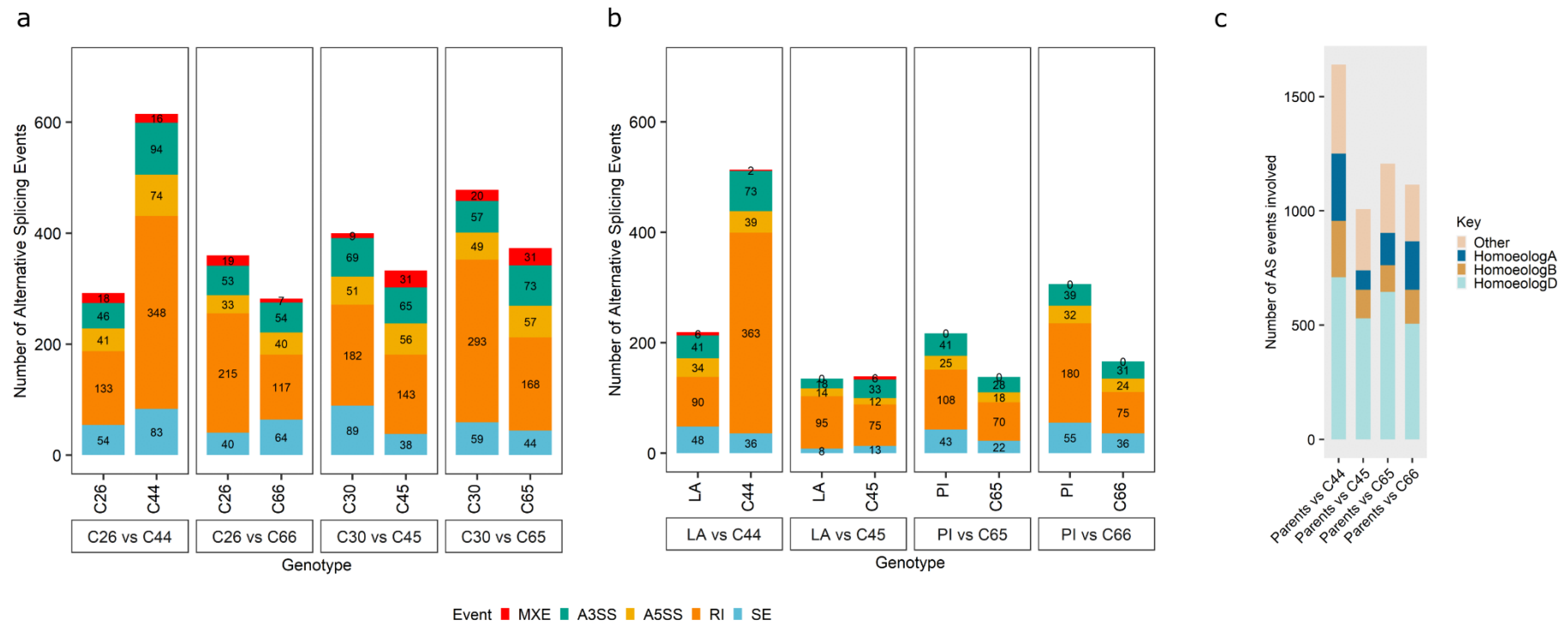
Supplementary Figure 18. The proportion of triads showing varied bias patterns between the SHWs (C44, C45, C65, C66), the landrace Chinese Spring and cultivar Azhurnaya. The different patterns represent the following: CS-AZ - triads showing similar pattern in Chinese Spring and Azhurnaya and not in the SHW line; SHW-AZ - triads showing reversal of bias in Azhurnaya to the same observed in SHW; SHW-CS - triads showing similar pattern in SHW and Chinese Spring and not in Azhurnaya; SHW-CS-AZ - triads showing similar patterns in SHW, Chinese Spring and Azhurnaya.



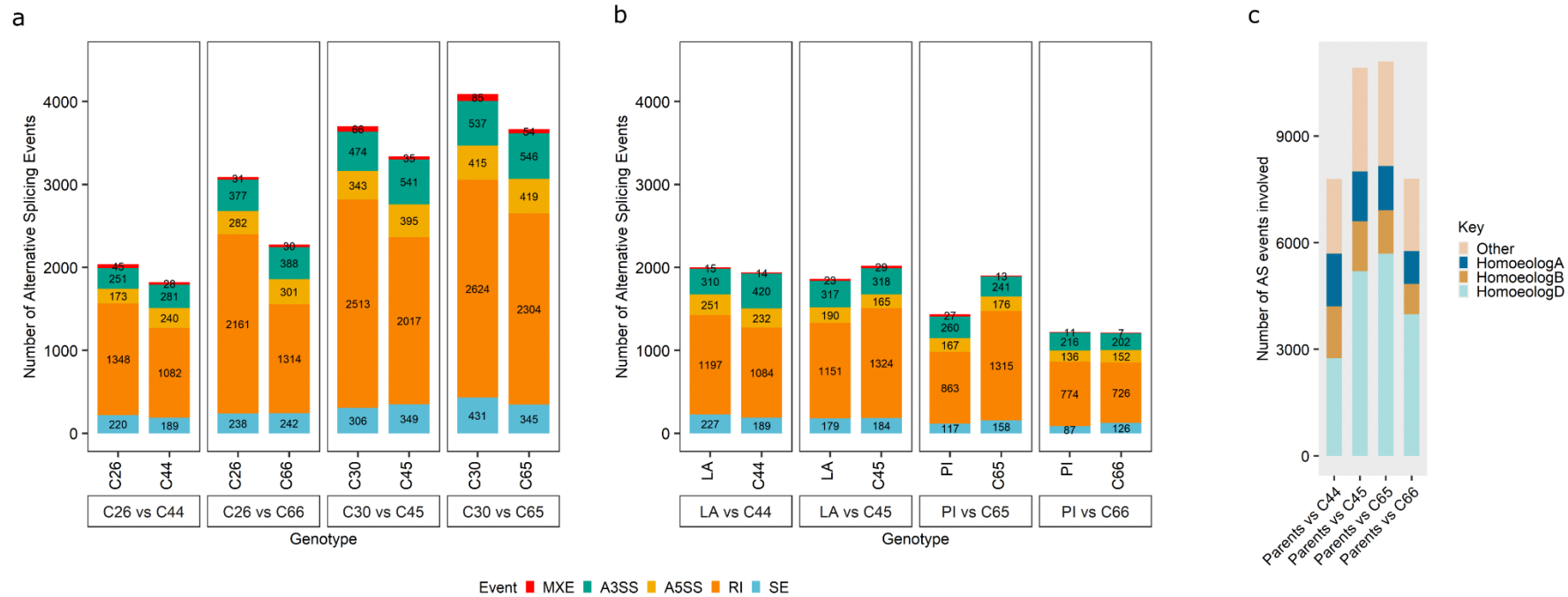
Supplementary Figure 19. Alluvial plots representing the expression bias trends of the triads across the tissues in the (a) SHW-C44 (b) SHW-C45 and (c) SHW-C65. AB bias (AB), represented by navy blue bars: triads significantly biased towards the AB subgenome; D bias (D), represented by dark orange bars: triads significantly biased towards the D subgenome; Not expressed (NE), represented by green bars: the homoeologues of the triads are not expressed; Unbiased (UN), represented by gray bars: no significant expression bias observed.



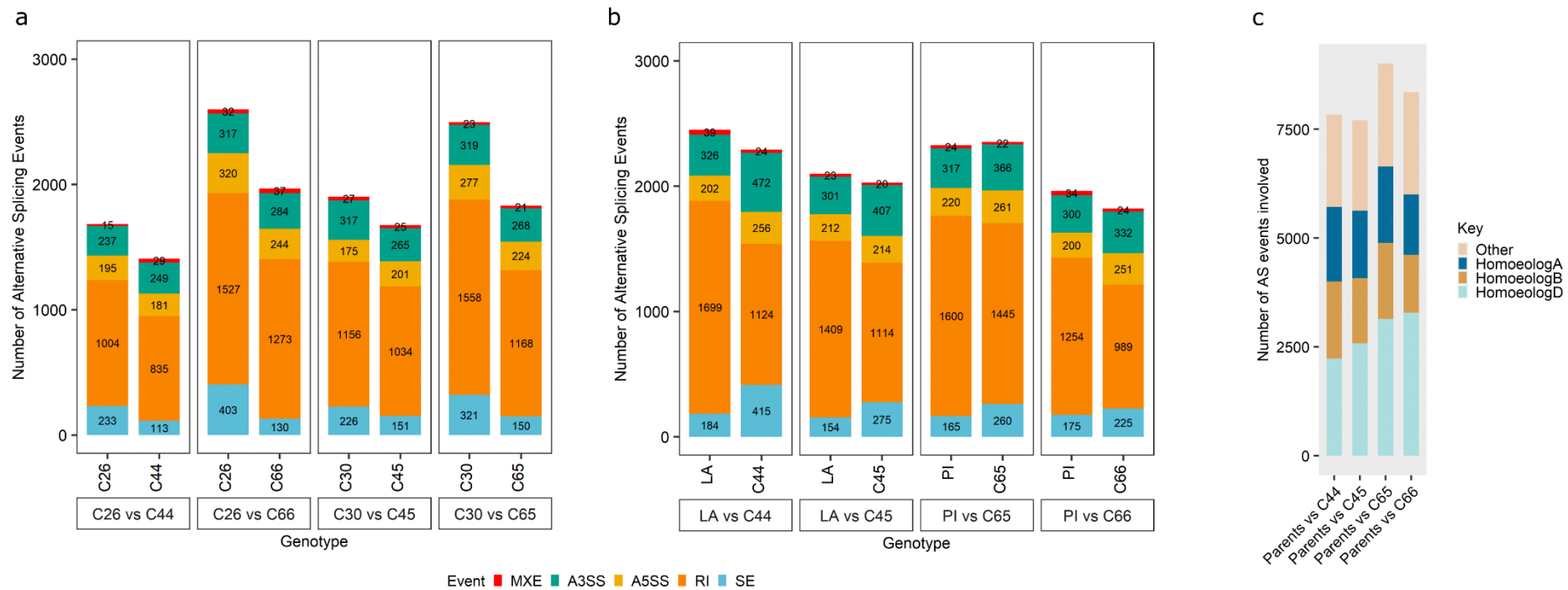
Supplementary Figure 20. Number of alternative splicing events detected in the Diploid/Tetraploid parent vs SHW comparison in pistil-one day after anthesis.



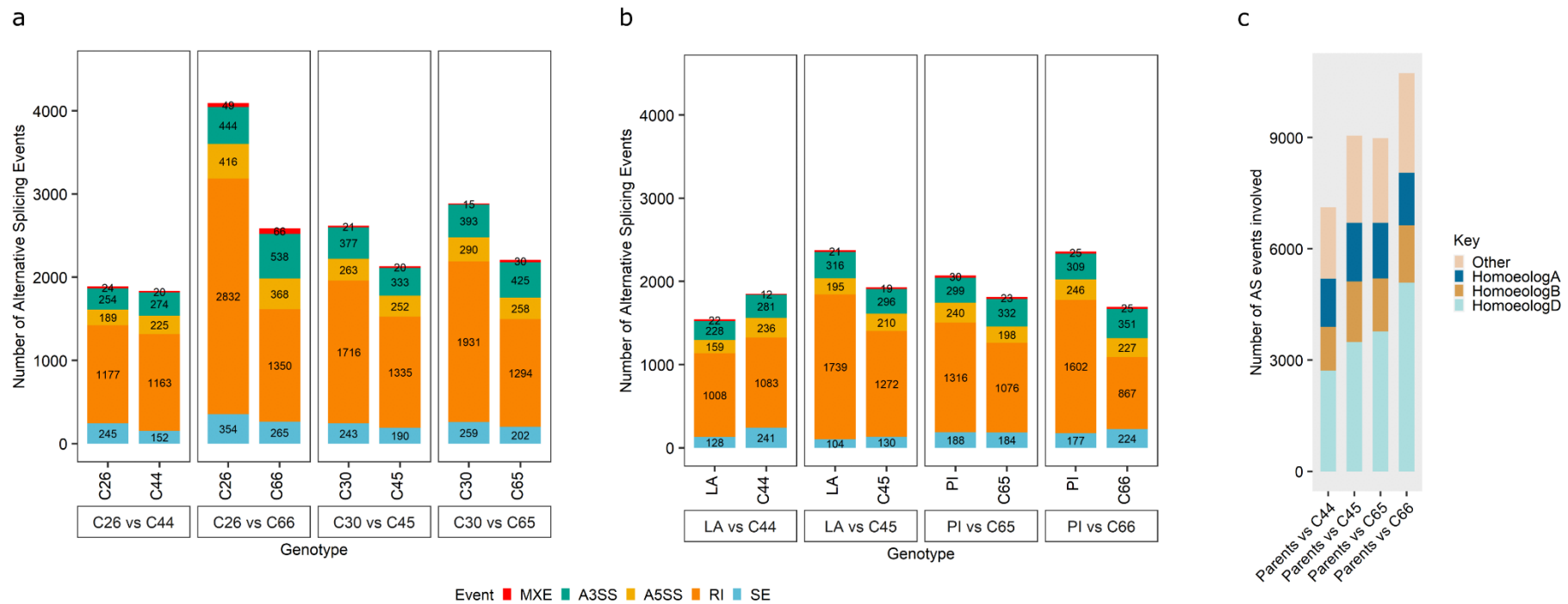
Supplementary Figure 21. Number of alternative splicing events detected in the Diploid/Tetraploid parent vs SHW comparison in mature anther.



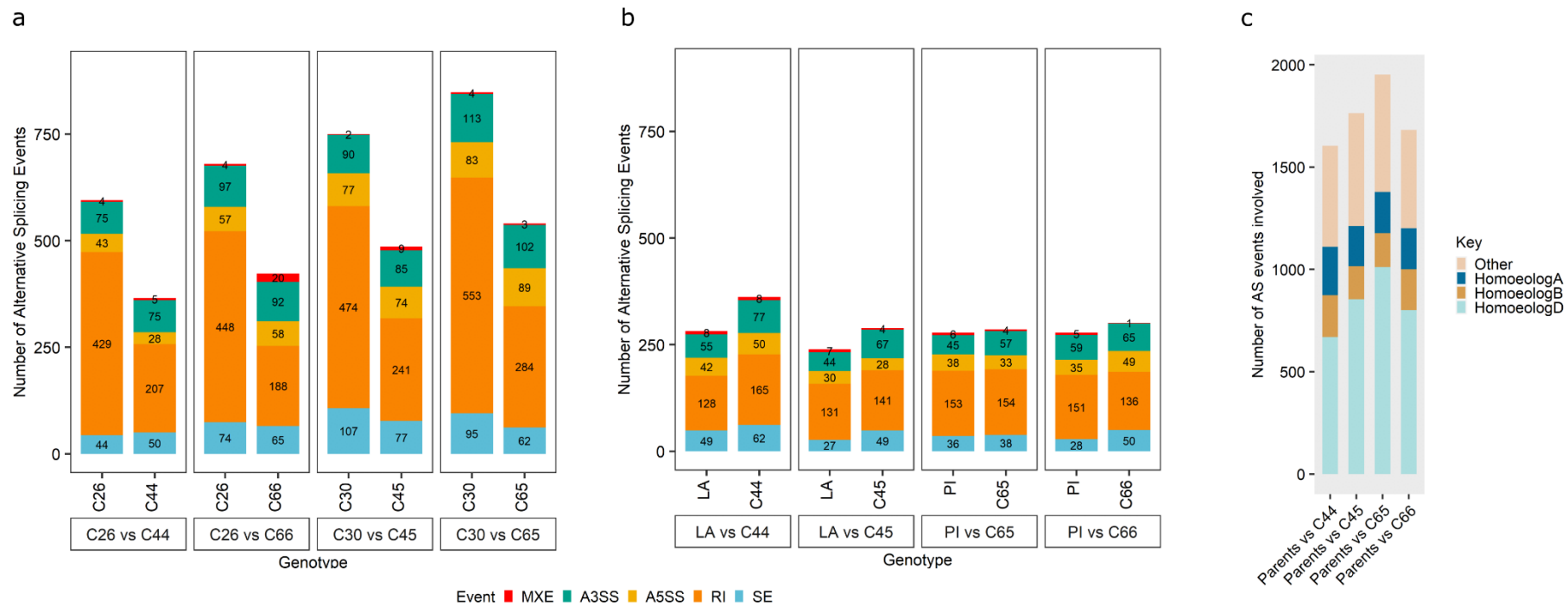
Supplementary Figure 22. Number of alternative splicing events detected in the Diploid/Tetraploid parent vs SHW comparison in head at boot stage.



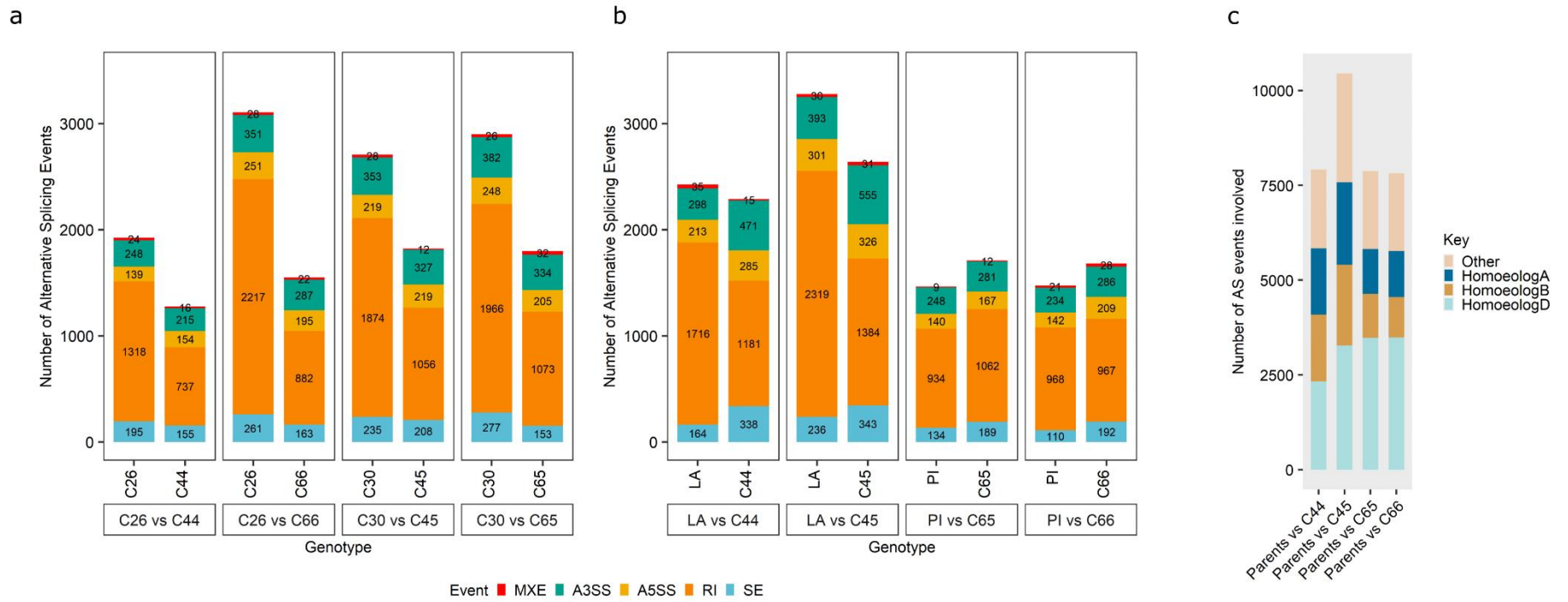
Supplementary Figure 23. Number of alternative splicing events detected in the Diploid/Tetraploid parent vs SHW comparison in glume.



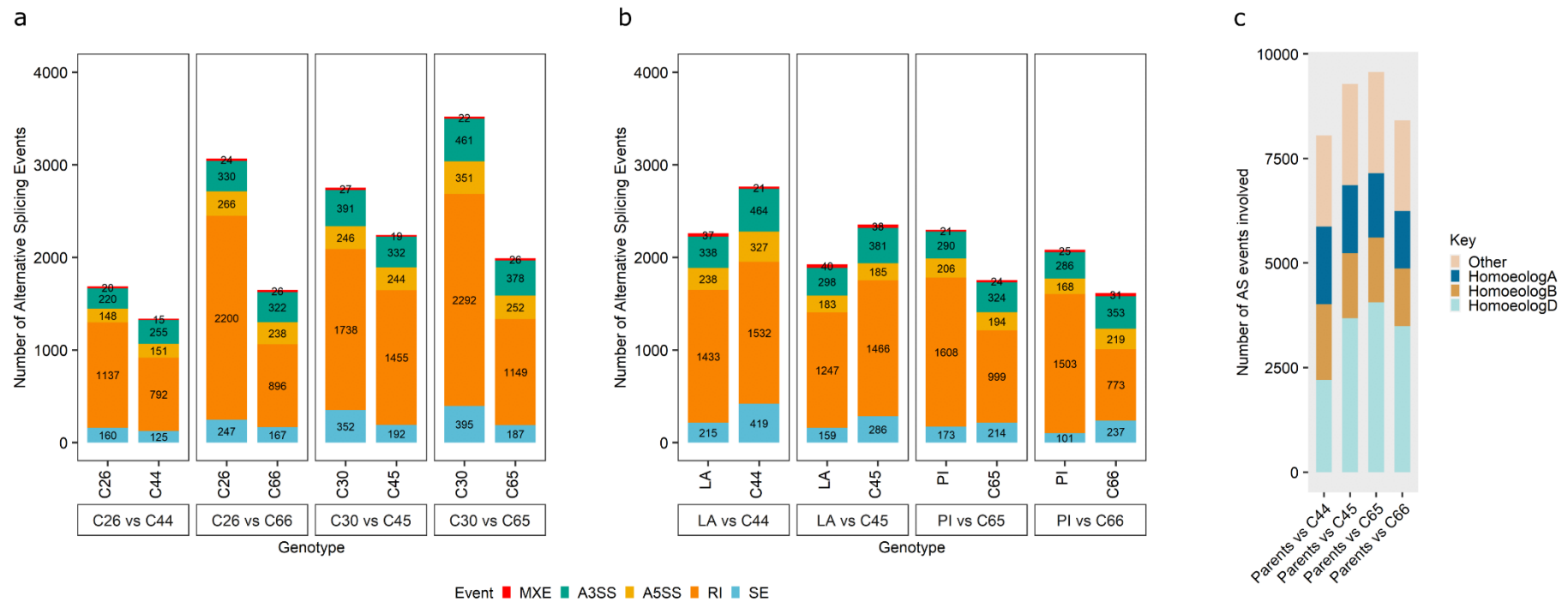
Supplementary Figure 24. Number of alternative splicing events detected in the Diploid/Tetraploid parent vs SHW comparison in hypocotyl.



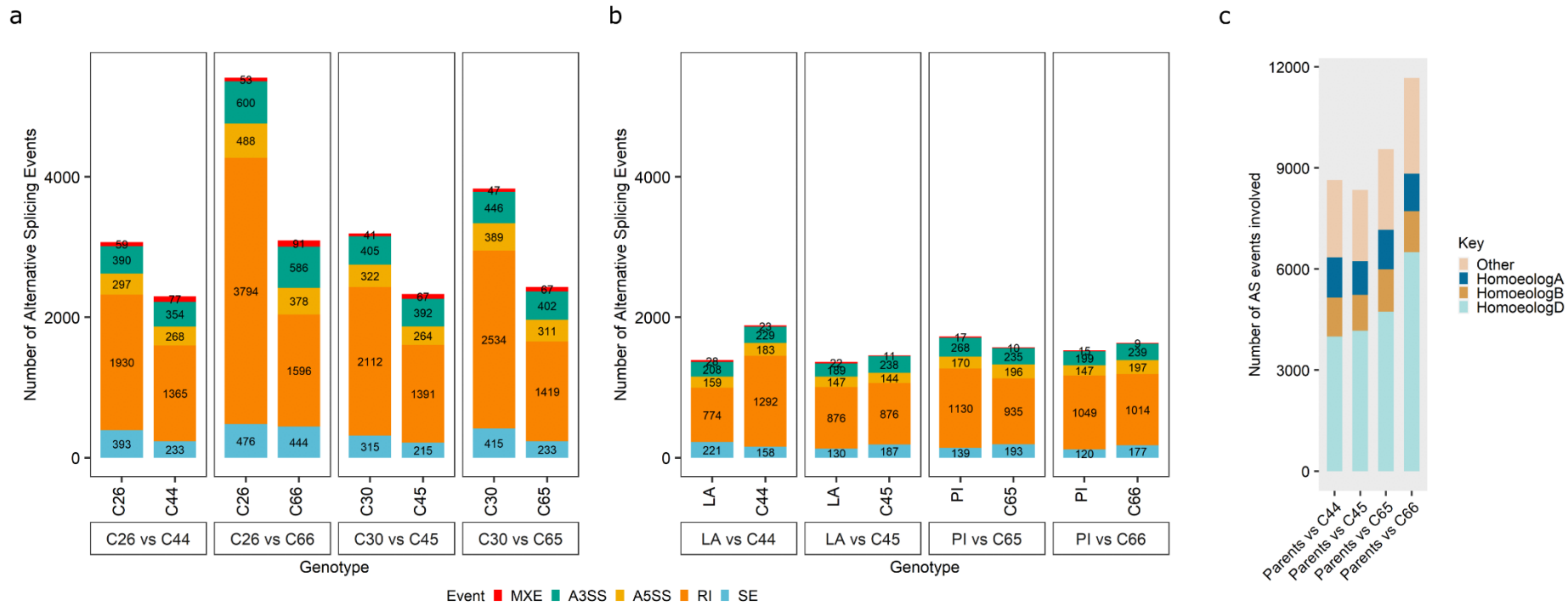
Supplementary Figure 25. Number of alternative splicing events detected in the Diploid/Tetraploid parent vs SHW comparison in pistil-when anthers are green and immature.



Supplementary Figure 26. Number of alternative splicing events detected in the Diploid/Tetraploid parent vs SHW comparison in pistil-when anthers are yellow and just prior to dehiscence.



Supplementary Figure 27. Number of alternative splicing events detected in the Diploid/Tetraploid parent vs SHW comparison in palea+lemma.



Supplementary Figure 28. Number of alternative splicing events detected in the Diploid/Tetraploid parent vs SHW comparison in root.