Table 1 Suppl. Materials used in this study. Data from previously published sequences in the GenBank (http://www.ncbi.nlm.nih.gov) are showed by *bold*.

Materials	GenBank	Genome	Coding	tRNA	rRNA	GC [%]	Genome size [bp]
Pseudoroegneria libanotica (Hackel) D.R. Dewey	KX822019	St	76	30	4	38.35	135026
Aegilops speltoides Tausch var. *ligustica* (Savign.) Fiori.	**KJ614405**	S	76	25	4	38.31	135660
Aegilops tauschii Coss.	**KJ614412**	D	76	25	4	38.34	135568
Hordeum jubatum L.	**KM974741**	H	76	29	4	38.24	136826
Hordeum vulgare L. subsp. *vulgare*	**EF115541**	I	75	30	4	38.32	136462
Secale cereale L.	**KC912691**	R	75	28	4	38.30	135604
Triticum monococcum L.	**LC005977**	A^m	76	23	4	38.27	136886
Triticum urartu Tumanian *ex* Gandilyan	**KJ614411**	A	76	27	4	38.28	136865
Bromus vulgaris (Hook.) Shear	**KM974737**						

Table 2 Suppl. Distribution of cpSSRs loci in the coding genes of *P. libanotica.* The cpSSRs located in the introns are *underlined*.

Gene	SSR number	Coding region	(Base)$_{repeats}$	SSR number	Location
rpoC2	6	24862-29301	(T)$_8$	1	27190-27197
			(A)$_8$	3	27330-27337, 27431-27438, 27453-27460
			(AT)$_5$	1	25613-25612
			(AT)$_4$	1	25723-25730
ndhF	5	101515-103734	(A)$_8$	4	101555-101562, 102225-102232, 103143-103150, 103284-103291
			(T)$_9$	1	101771-101779
ycf3	5	41820-43809	(T)$_8$	1	<u>42668-42675</u>
			(A)$_8$	2	<u>43654-43661</u>, <u>43664-43671</u>
			(TCCT)$_3$	1	<u>42568-42579</u>
			(CCATA)$_3$	1	43441-43455
matK	3	1684-3222	(A)$_9$	1	2230-2238
			(A)$_8$	1	2540-2547
			(A)$_{11}$	1	2608-2618
atpF	2	32622-33988	(A)$_9$	1	<u>33216-33224</u>
			(A)$_8$	1	<u>33483-33490</u>
infA	2	76306-76647	(T)$_{10}$	2	76613-76622, 76631-76640
ndhD	2	106825-108327	(A)$_8$	1	107914-107921
			(AATA)$_3$	1	107027-107038
rpl16	2	77765-79231	(A)$_{19}$	1	<u>79184-79202</u>
			(TG)$_4$	1	<u>78425-78432</u>
rps14	2	36203-36514	(T)$_9$	1	36426-36434
			(T)$_8$	1	36502-36509
rps4	2	44818-45423	(T)$_9$	1	45319-45327
			(T)$_8$	1	45390-45397
ccsA	1	105691-106659	(A)$_8$	1	106216-106223
clpP	1	67773-68423	(TA)$_4$	1	67773-68423
ndhA	1	111124-113237	(T)$_{11}$	1	<u>112539-112549</u>
ndhB	1	85552-87796	(AG)$_4$	1	85894-85901
ndhH	1	113239-114420	(TC)$_5$	1	114005-114014
ndhK	1	48654-49391	(T)$_9$	1	49359-49367
petB	1	71359-72751	(A)$_8$	1	<u>71493-71500</u>
psaI	1	57481-57591	(AC)$_4$	1	57641-57648
psaJ	1	64747-64875	(T)$_8$	1	64866-64873
psbB	1	68918-70444	(T)$_8$	1	69651-69658
psbC	1	9613-11034	(G)$_8$	1	10186-10193
rpl22	1	80152-80601	(T)$_8$	1	80202-80209
rpoA	1	74373-75392	(A)$_8$	1	74404-74411
rpoC1	1	22609-24657	(AAT)$_4$	1	24313-24324
rps19	1	134700-134981	(A)$_8$	1	134708-134715

Table 3 Suppl. Variation of coding genes length [bp] in eight diploid *Triticeae* species.

| Gene	Region		*P. libanotica*	*A. speltoides*	*A. tauschii*	*H. jubatum*	*H. vulgare*	*S. cereale*	*T. monococcum*	*T. uratu*
petB	LSC	Exon1	6	699	699	6	6	699	648	699
		Intron	747	--	--	652	696	--	--	--
		Exon2	642	--	--	699	699	--	--	--
Total coding region length			648	699	699	705	705	699	648	699
petD	LSC	Exon1	8	525	525	8	8	525	477	525
		Intron	743	--	--	749	749	--	--	--
		Exon2	481	--	--	475	475	--	--	--
Total coding region length			489	525	525	483	483	525	477	525
rpl16	LSC	Exon1	402	273	273	29	29	270	225	273
		Intron	1056	--	--	540	540	--	--	--
		Exon2	9	--	--	232	232	--	--	--
Total coding region length			411	273	273	261	261	270	225	273
rpl2	IR	Exon1	432	498	498	432	432	429	431	498
		Intron	651	--	--	663	663	660	660	--
		Exon2	402	--	--	390	390	393	391	--
Total coding region length			834	498	498	822	822	822	822	498
rps12	IR	Exon1	30	273	273	29	29	270	225	273
		Intron	540	--	--	540	540	-	--	--
		Exon2	231	--	--	232	232	--	--	--
Total coding region length			261	273	273	261	261	270	225	273
infA	LSC	Exon	342	249	249	342	342	249	342	342
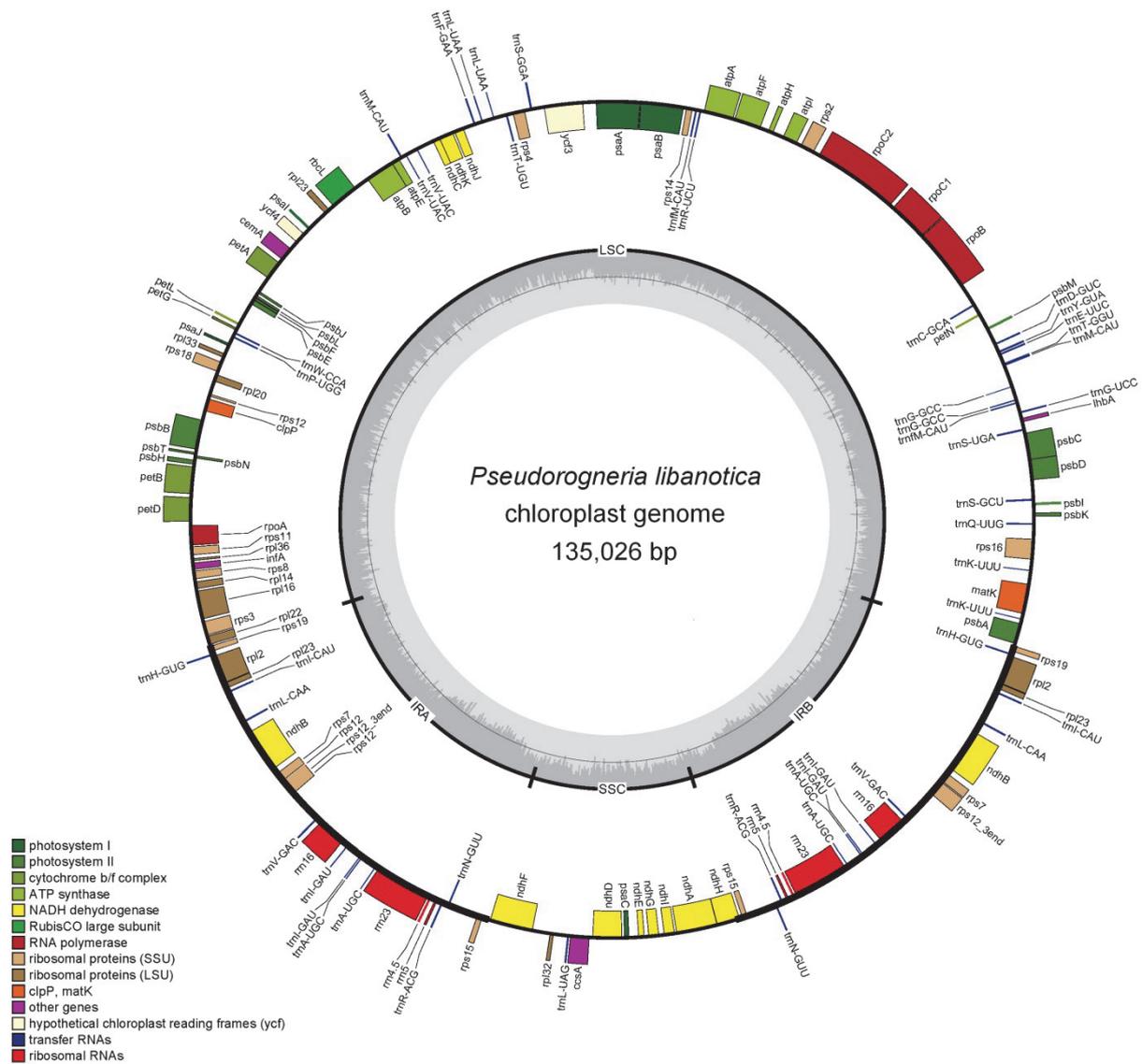
Fig. 1 Suppl. Gene map of the *P. libanotica* cp genome. Genes drawn inside the circle are transcribed clockwise, and those outside are counterclockwise. Genes belonging to different functional groups are marked with different colours. The *dark gray* in the inner circle corresponds to GC content, while the *ligh gray* corresponds to AT content.
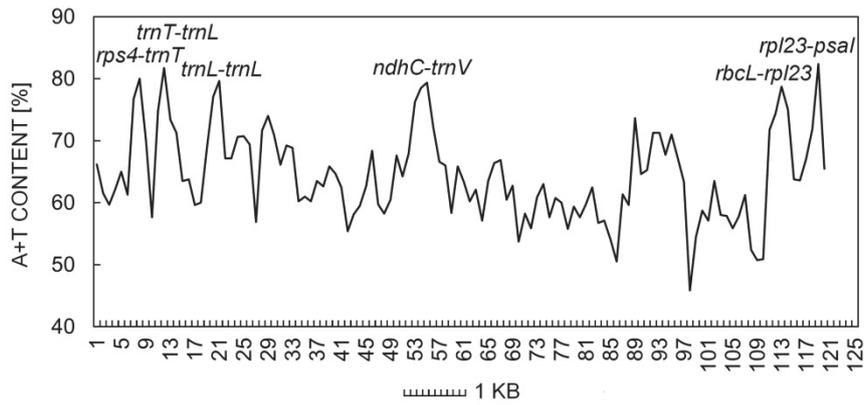
Fig. 2 Suppl. AT content exited in *rps4-ps*aI region of diploid *Triticeae* species. Each point is refers to the calculation of the percentage of AT content in every adjacent 100 nucleotides.
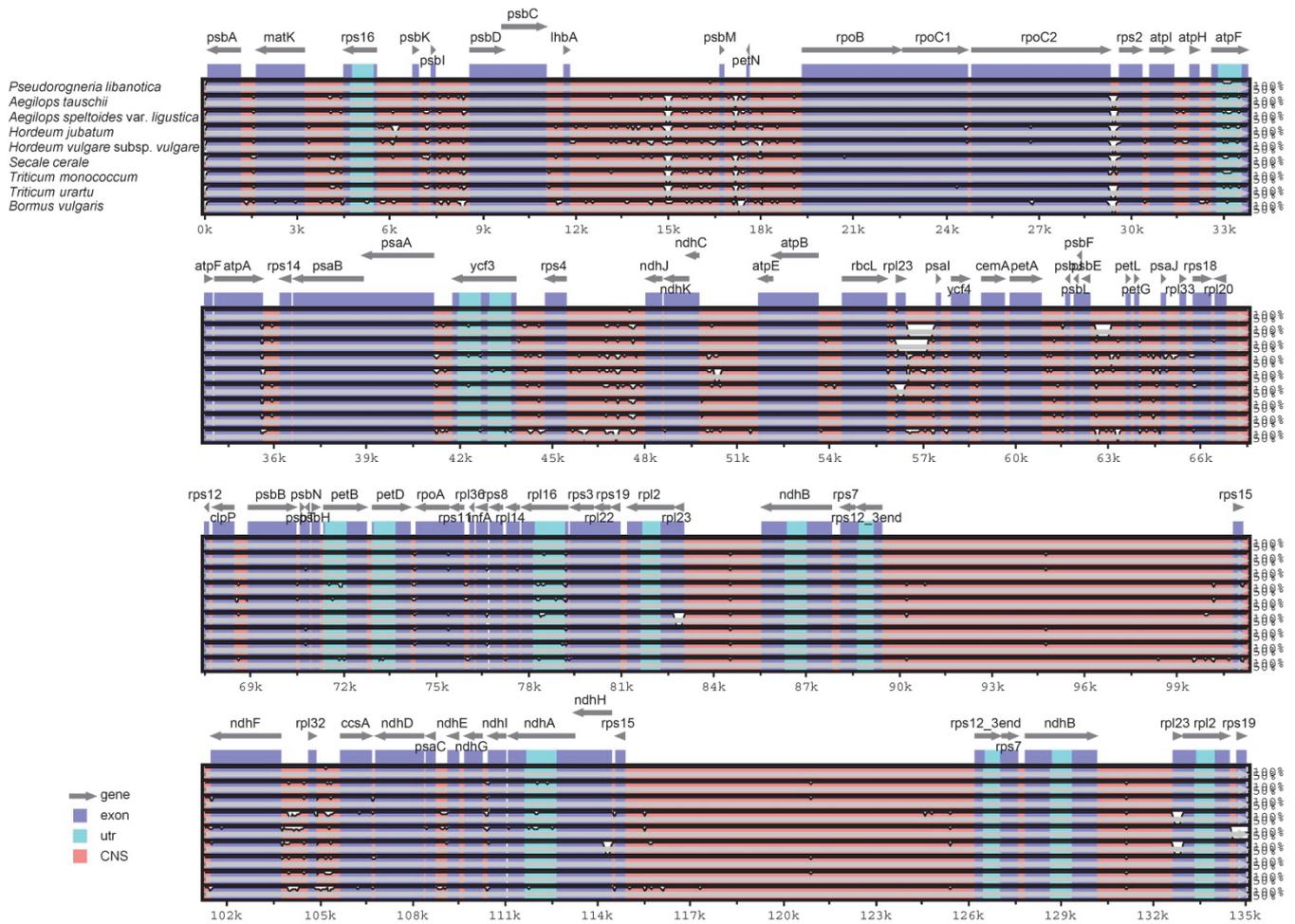

Fig. 3 Suppl. Nine cp genomes were aligned using *mVISTA* program. *Grey arrows* and *thick black lines* above the alignment indicate genes with their orientation. Genome regions as protein-coding exon, intron and conserved noncoding sequences (CNS) are marked by different colours .