Table S1. Primers used for identifying barley dwarfing alleles

Gene	Primer name	Marker type	Sequence 5'→3'	Target mutation	Target allele identification	Literature source
HvGA20ox2	Identification of *sdw1.c* and *sdw1.ins*					
	MC40861P3F	InDel	tatggcgtgaccaaaggttc	64 (+GTTA)	No PCR - *sdw1.a* or *sdw1.e* 247 bp - *sdw1.c*, 410 bp - *sdw1.ins*	[4]
	MC40861P4R		caccaatccaccacgaaga			
	Program: 94 °C – 3 min 30 sec; 37 cycles (94 °C – 45 sec, 54 °C – 45 sec, 72 °C – 1 min); 72 °C – 7 min					
	dCsdw1.c-F	dCAPS	cgtgaccaaaggttcctgtcc	64 (+GTTA)	No PCR - *sdw1.a* or *sdw1.e* HpaII: CCGG[2] 276 bp – *sdw1.ins* 113 bp (site is absent) – *sdw1.c*	Present study
	dCsdw1.c-R		attgctgaggcggccatgtta**c**c[1]			
	Program: 94 °C – 3 min 30 sec; 37 cycles (94 °C – 45 sec, 61 °C – 45 sec, 72 °C – 30 sec); 72 °C – 7 min					
	Identification of *sdw1.d*					
	Hv20ox2-F	CAPS	cgctgattaactgggacaca	1665 G→A	No PCR - *sdw1.a* or *sdw1.e* HaeIII: GGCC 194 bp (site is absent)	[6, 24]
	Hv20ox2-R		gttcgctcgttaggaagcag			
	Program: 94 °C – 3 min 30 sec; 8 cycles (94 °C – 45 sec, 59 °C with a 0.5 °C stepdown per 1 cycle – 1 min 30 sec, 72 °C – 1 min); 30 cycles (94 °C – 45 sec, 55 °C – 45 sec, 72 °C – 45 sec); 72 °C – 7 min					
HvBrI1	Identification of *uzu1.a*					
	–	dCAPS	gaaatggagaccattggcaagatcaa**g**c	2612 A→G	BstHHI: GCGC 265 + 29 bp (site is available)	[16]
	–		ccttgcctccagattctcatcaac			
	Program: 94 °C – 3 min 30 sec; 8 cycles (94 °C – 45 sec, 67 °C with a 0.5 °C stepdown per 1 cycle – 1 min 30 sec, 72 °C – 1 min); 30 cycles (94 °C – 45 sec, 63 °C – 45 sec, 72 °C – 45 sec); 72 °C – 7 min					
HvDep1	Identification of *ari-e.GP*					
	dCari-e.GP-F	dCAPS	agcagcaccaattctctcgtaa	1508 (+A)	FokI: CATCC 154 bp (site is absent)	Present study
	dCari-e.GP-R		caagcagaacgtgagactgg**a**t	*Fok*I: CATCC		
	Program: 94 °C – 3 min 30 sec; 37 cycles (94 °C – 45 sec, 60 °C – 45 sec, 72 °C – 30 sec); 72 °C – 7 min					

[1] Underlined are nucleotides changed in the primers (compared to the original gene sequence) for creating dCAPS markers.

[2] Instead of these restriction enzymes, their isoschisomers HpaII (BsiSI, HapII, MspI), HaeIII (BshFI, BsnI, BspANI, BsuRI), BstHHI (AspLEI, CfoI, Hin6I, HinP1I, HspAI), FokI (BseGI, BstF5I, BtsCI) can be used.

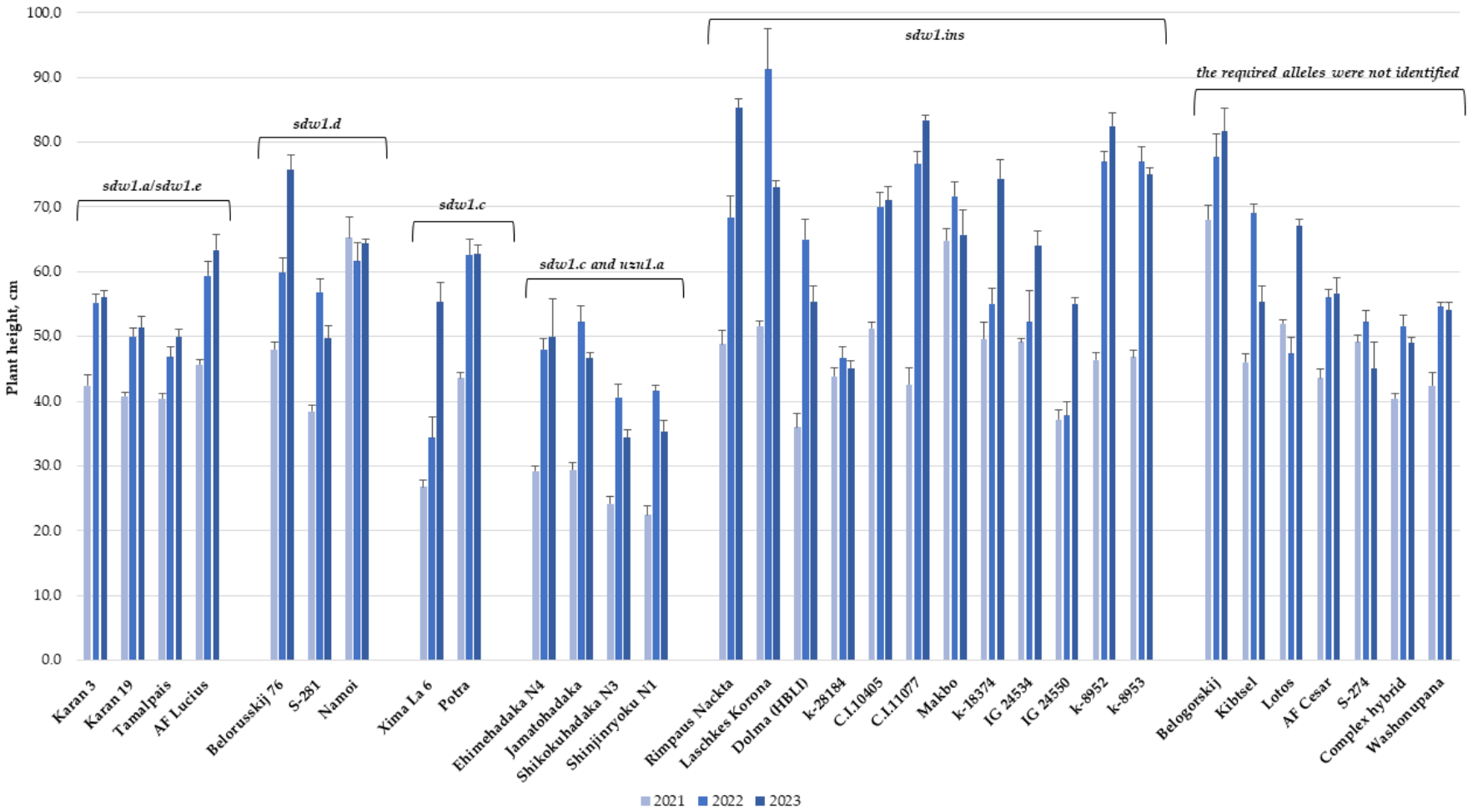

Figure S1. Variation in height of barley accessions in 2021-2023.

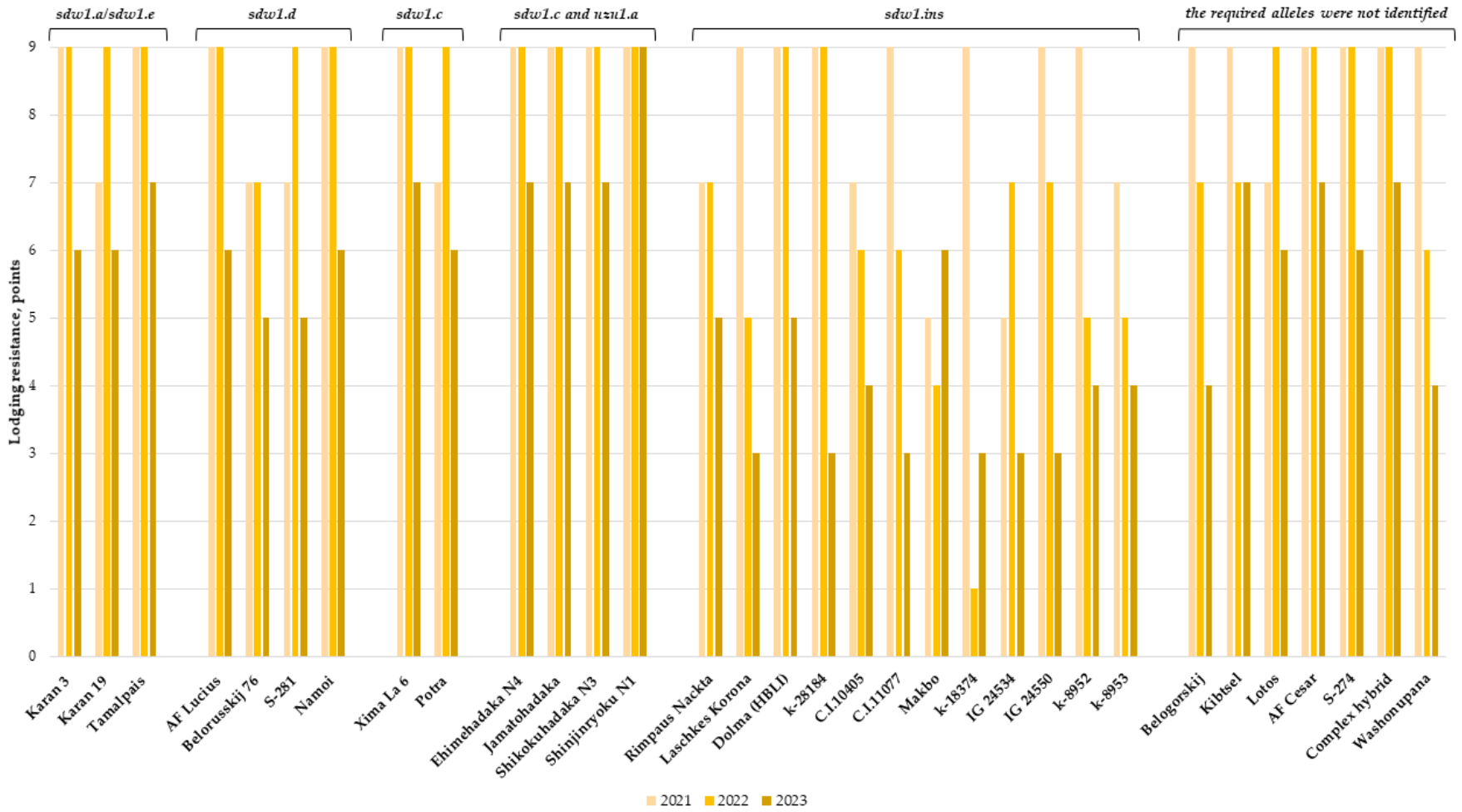

Figure S2. Variation in lodging resistance of barley accessions in 2021-2023 (9 points - high lodging resistance, 5 - average resistance, 1 – lodging).

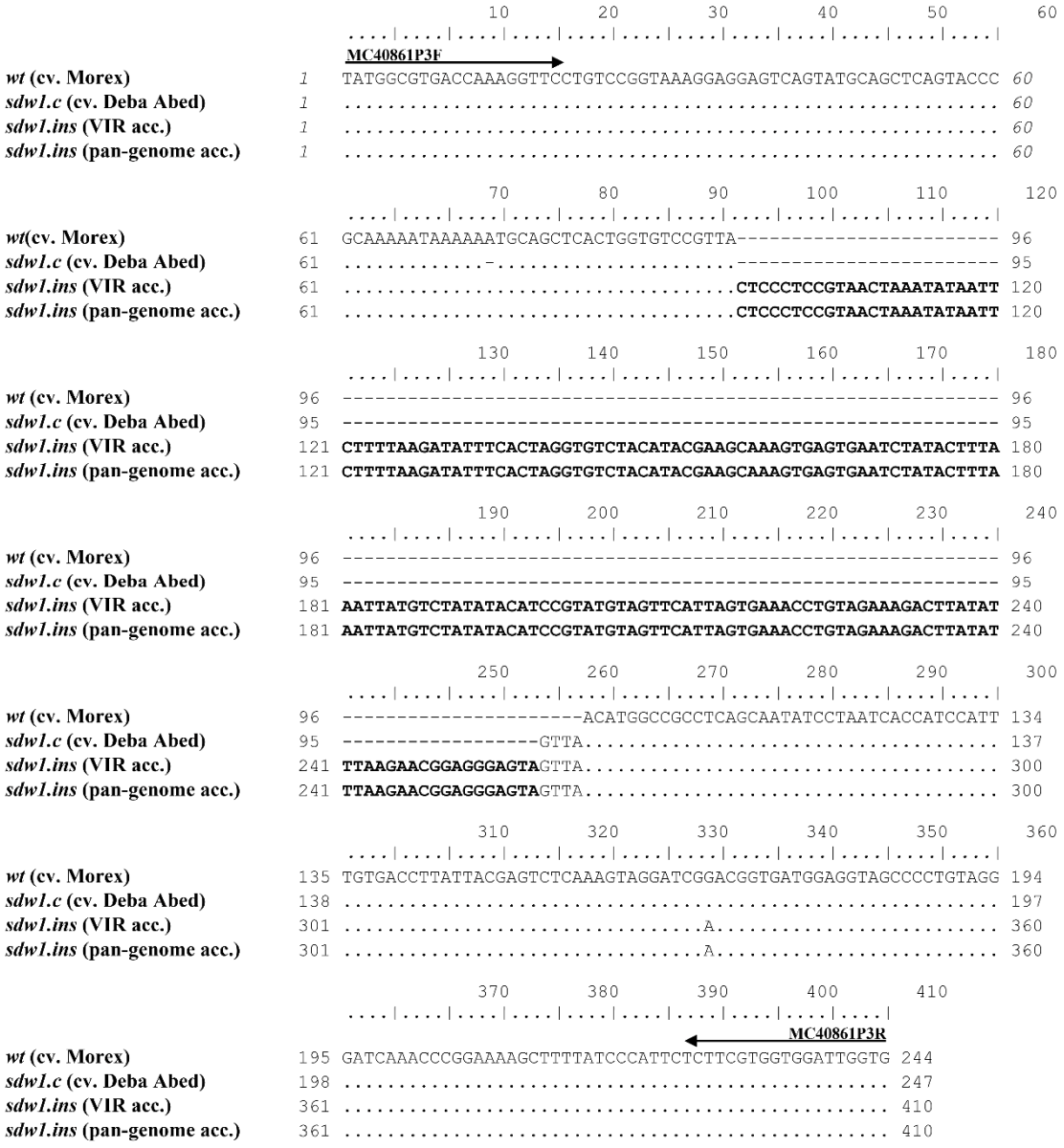

Figure S3. Sequence alignment of PCR-products flanked by the MC40861P3F/R primers. The sequences homologous to the Thalos_2 transposon are highlighted in bold. VIR accessions are Dolma, Makbo, Rimpaus Nackta, C.I.10405 and k-8953; pan-genome accessions are HOR8148, HOR10350 and HOR13821 with the same sequences.