Table S1. Individual values and means with corresponding standard errors (SEM)of six growth parameters of *Triticum aestivum* genotype Bolal 2973 and *Triticum urartu* genotype PI662222 grown in high-B (10 mM Boron) growth conditions and the control (3.1 µM Boron) (n=3). Significance of the effects of genotype, treatment and genotype-treatment interaction (G×T) obtained from two-way ANOVA are indicated as **** for $p < 0.0001$; *** for $p < 0.001$; ** for $p < 0.01$; * for $p < 0.05$, and ns for $P \geq 0.05$ (not significant).

Trait	Genotype	Bolal 2973 (*T. aestivum*)				PI662222 (*T. urartu*)				*P* value		
	Treatment	Rep 1	Rep 2	Rep 3	Mean ± SEM	Rep 1	Rep 2	Rep 3	Mean ± SEM	G×T	Genotype (G)	Treatment (T)
Shoot Length (cm)	Control	42.500	35.000	40.000	39.17 ± 2.20	21.000	22.000	23.000	22.00 ± 0.58	**	****	*
	10 mM Boron	30.000	27.000	28.000	28.33 ± 0.88	25.500	25.000	21.000	23.83 ± 1.42			
Root Length (cm)	Control	24.500	28.000	26.000	26.17 ± 1.01	21.000	26.000	24.000	23.67 ± 1.45	ns	ns	**
	10 mM Boron	18.000	21.000	13.500	17.50 ± 2.18	16.500	19.500	15.000	17.00 ± 1.32			
Shoot Fresh Weight (g)	Control	0.474	0.514	0.502	0.497 ± 0.01	0.111	0.164	0.189	0.155 ± 0.02	ns	***	ns
	10 mM Boron	0.526	0.430	0.190	0.382 ± 0.10	0.133	0.110	0.069	0.104 ± 0.02			
Root Fresh Weight (g)	Control	0.106	0.195	0.120	0.140 ± 0.03	0.075	0.063	0.146	0.095 ± 0.03	ns	ns	ns
	10 mM Boron	0.062	0.090	0.050	0.067 ± 0.01	0.105	0.096	0.044	0.082 ± 0.02			
Shoot Dry Weight (g)	control	0.061	0.053	0.046	0.0533 ± 0.004	0.014	0.021	0.023	0.0193 ± 0.003	ns	***	ns
	10 mM Boron	0.067	0.056	0.035	0.0526 ± 0.009	0.025	0.020	0.013	0.0193 ± 0.003			
Root Dry Weight (g)	control	0.015	0.009	0.009	0.0110 ± 0.002	0.004	0.005	0.009	0.0060 ± 0.002	ns	**	ns
	10 mM Boron	0.008	0.007	0.006	0.0070 ± 0.001	0.006	0.007	0.004	0.0056 ± 0.001			

Table S2. Results of quality estimate of reference genome alignment statistics and sequencing data of *T. urartu* (Tu) leaves grown under high-B (10 mM B) growth conditions in comparison to the control treatment (3.1 μM B).

Parameters/ Sample	Tu_Control	Tu_high-B_Treatment	Parameters/ Sample	Tu_Control	Tu_high-B_Treatment
Total Clean Reads (M)	56.06	79.2	Uniquely Gene Mapping Ratio (%)	36.34	36.64
Total Clean Bases (Gb)	5.61	7.92	Total Gene Number	26602	27981
Clean Reads Q20 (%)	96.23	96.76	Known Gene Number	25520	26809
Clean Reads Q30 (%)	87.61	89.67	Novel Gene Number	1082	1172
Total Genome Mapping Ratio (%)	12.60	12.15	Total Transcript Number	29378	30744
Uniquely Genome Mapping Ratio (%)	4.30	4.02	Known Transcript Number	25695	27025
Total Gene Mapping Ratio (%)	68.05	70.34	Novel Transcript Number	3683	3719