

Table 1 Suppl. Primer sequences used for semi-quantitative PCR of candidate genes.

Gene	Sequence
<i>HvGAPDH</i>	5'-CGTTCATCACCACCGACTAC-3' 5'-CAGCCTTGTCCTTGTCAGTG-3'
<i>HvHRGP</i>	5'-GGAACATATCCTTCATGGTGG-3' 5'-CACCTCCAGGAATATCAAGC-3'
<i>HvARR12</i>	5'-CCAGCTCAAGGAAACAGGAG-3' 5'-GGAGTCTGTAAGTTCCTCAC-3'
<i>HvPip</i>	5'-GGCAGGTGTTTGGCTTCATG-3' 5'-GTGCAGTCATCATCTCCAC-3'
<i>HvDI19-2</i>	5'-AGTTACTTCAAGATGCAACG-3' 5'-CGATGGCTCAGCCACAGGC-3'
<i>HvC4H</i>	5'-TGTACACCTGCGTCGACTGC-3' 5'-CCGAGAACACACCAATAACC-3'
<i>HvADC</i>	5'-GGAACATATCCTTCATGGTGG-3' 5'-CACCTCCAGGAATATCAAGC-3'
<i>HvPRP</i>	5'-GCTCTGCAGGTGGCGATCAAG-3' 5'-CCATGATGGTCTTCTTGATGGG-3'

Table 2 Suppl. Barley orthologs identified within the QTG region on chromosome 1H. *At* - *Aegilops tauschii*, *Tu* - *Triticum urartu*, *Os* - *Oryza sativa*, *Bd* - *Brachypodium distachyon*, *Hv* - *Hordeum vulgare*, *Do* - *Dichanthelium oligosanthes*.

Gene	Gene function	Gene model/EST	E-value/identity
<i>AtARR12</i>	two-component response regulator	AK376525	0.0/96 %
<i>AtbHLH13</i>	transcription factor bHLH13	EMT04182.1	0.0/96 %
<i>TuMAPK</i>	MAP kinase phosphatase with leucine-rich repeats protein 1	EMS52742.1	0.0/86 %
<i>AtRLK</i>	receptor-like protein kinase 2	EMT01559.1	0.0/94 %
<i>OsYUCCA5</i>	indole-3-pyruvate monooxygenase	XP_015634157.1	1e-155/72 %
<i>AtABCC9</i>	ABC transporter C family member 9	EMT27565.1	0.0/94 %
<i>HvPip</i>	proline iminopeptidase	AK372041	0.0/99 %
<i>TuRPT3</i>	root phototropism protein 3	EMS51026.1	0.0/97 %
<i>TuPPK1</i>	phosphatidylinositol-4-phosphate 5-kinase 1	EMS61702.1	0.0/95 %
<i>AtBEL-1</i>	homeobox BEL1-like	EMT11923.1	7e-77/87 %
<i>HvDI19-2</i>	dehydration-induced 19 homolog 2	AK252258.1	0.0/99 %
<i>AtPEPCK</i>	phosphoenolpyruvate carboxylase 1	EMT14603.1	0.0/86 %
<i>AtTMKL1</i>	kinase-like protein	EMT27558.1	2e-78/67 %
<i>AtRPH8A</i>	disease resistance protein RPH8A	EMS51588.1	0.0/78 %
<i>BdCBR1</i>	carbonyl reductase [NADPH] 1	XP_003564994.1	1e-106/76 %
<i>AtMTL13</i>	methyltransferase-like protein 13	EMT14674.1	4e-79/79 %
<i>TuABCC13</i>	ABC transporter C family member 13	EMS58693.1	9e-121/83 %
<i>HvHRGPL</i>	hydroxyproline-rich glycoprotein-like	MLOC_66121.2	0.0/99 %
<i>AtCO1</i>	cytoplasmic aconitate hydratase	EMT03129.1	1e-122/75 %
<i>AtABCC10</i>	ABC transporter C family member 10	EMT21953.1	0.0/87 %
<i>AtPK2</i>	serine/threonine-protein kinase	EMS67775.1	0.0/94 %
<i>BdRUNKEL</i>	serine/threonine-protein kinase RUNKEL	XP_014755217.1	0.0/90 %
<i>AtVPS18</i>	vacuolar sorting-associated protein 18-like protein	EMT32396.1	2e-68/72 %
<i>AtWAK3</i>	wall-associated receptor kinase 3	EMT22123.1	6e-80/68 %
<i>TuRPP13</i>	disease resistance RPP13-like protein 4	EMS65671.1	0.0/77 %
<i>AtCYP450</i>	cytochrome P450 76C4	EMT05061.1	2e-180/90 %
<i>TuAOXL</i>	aldehyde oxidase-like protein	EMS64922.1	0.0/94 %
<i>DoAAMT10</i>	aluminum-activated malate transporter 10	OEL13872.1	0.0/67 %
<i>HvCP-MII</i>	serine carboxypeptidase II	CAA70815.1	1e-153/85 %
<i>HvRLKs</i>	receptor-like kinase	AAD44031.1	0.0/98 %
<i>TuUGT85A3</i>	UDP-glycosyltransferase 85A3	EMS52500.1	0.0/96 %
<i>TueIF3e</i>	eukaryotic translation initiation factor 3 subunit E	EMS48036.1	0.0/99 %
<i>AtPK</i>	putative serine/threonine-protein kinase receptor	EMT11316.1	0.0/94 %
<i>TuPRM1</i>	disease resistance protein RPM1	EMT18740.1	0.0/85 %

Table 3 Suppl. Barley orthologs identified within the QTG region on chromosome 2H. *At* - *Aegilops tauschii*, *Tu* - *Triticum urartu*, *Os* - *Oryza sativa*, *Bd* - *Brachypodium distachyon*, *Hv* - *Hordeum vulgare*, *Zm* - *Zea mays*.

Gene	Gene function	Gene model/EST	E-value/identity
<i>TuCKL7</i>	casein kinase I-like 2	EMS55588.1	1e-89/67 %
<i>BdRKS1</i>	G-type lectin S-receptor-like serine/threonine-protein kinase	XP_010228733.1	0.0/84 %
<i>HvADC</i>	arginine decarboxylase	MLOC_52374.1	0.0/95 %
<i>ZmPPR-817</i>	pentatricopeptide repeat (PPR)-containing protein	ACN62066.1	0.0/73 %
<i>HvHRGP</i>	hydroxyproline-rich glycoprotein	AK362809	0.0/99 %
<i>TuLURP1</i>	late up-regulation in response to Hpa	EMS64353.1	1e-82/94
<i>AtFEI1</i>	LRR receptor-like serine/threonine-protein kinase	EMT33046.1	1e-96/99 %
<i>HvPRP</i>	proline-rich family protein	AK359091	0.0/99 %
<i>TuWRKY</i>	WRKY transcription factor	ABN43183.1	4e-47/78 %
<i>AtNAK</i>	Serine/threonine-protein kinase NAK	EMT20587.1	6e-123/97 %
<i>AtPI4Ks</i>	phosphatidylinositol 4-kinase type 2-beta	EMT28909.1	0.0/93 %
<i>AtSMG1</i>	serine/threonine-protein kinase SMG1	EMT02085.1	0.0/74 %
<i>AtE3UPL10</i>	E3 ubiquitin-protein ligase SINA-like 10	EMT30213.1	6e-122/95 %
<i>BdNTR1</i>	NRT1/ PTR FAMILY 4.3-like	XP_003579814.1	3e-124/87 %
<i>TuULK4</i>	serine/threonine-protein kinase ULK4	EMS46352.1	0.0/97
<i>TuPER57</i>	peroxidase 57	EMS35728.1	3e-149/96 %
<i>AtPPA1</i>	soluble inorganic pyrophosphatase 1	EMT33816.1	2e-64/99 %
<i>AtPOT7</i>	potassium transporter 7	JAT44902.1	5e-104/85 %

Table 4 Suppl. Barley orthologs identified within the QTG region on chromosome 7H. *At* - *Aegilops tauschii*, *Ta* - *Triticum aestivum*, *Tu* - *Triticum urartu*, *Os* - *Oryza sativa*, *Bd* - *Brachypodium distachyon*, *Hv* - *Hordeum vulgare*, *Ga* - *Gossypium arboreum*, *Zm* - *Zea mays*, *Gs* - *Glycine soja*

Gene	Gene function	Gene model/EST	E-value/identity
<i>TuRPM1</i>	disease resistance protein RPM1	EMS63672.1	1e-53/70
<i>TaHSP70</i>	heat shock protein 70	AFD04130.1	0.0/97
<i>AtSMG1</i>	serine/threonine-protein kinase	EMT02085.1	1e-69/74
<i>AtPSKR2</i>	phytosulfokine receptor 2	EMT21082.1	4e-124/80
<i>BdPPR</i>	pentatricopeptide repeat-containing protein	XP_014755207.1	0.0/93 %
<i>HvC4H</i>	cinnamate-4-hydroxylase	AHJ61295.1	7e-161/98
<i>GaCYP450</i>	cytochrome P450	KHG02507.1	9e-139/92 %
<i>HvHDG</i>	hydroxysteroid dehydrogenase	AK362483	2e-44/88 %
<i>OsBGL5</i>	glucan endo-1,3-beta-glucosidase 5	LOC4346582	1e-42/66 %
<i>HvHRGPL</i>	hydroxyproline-rich glycoprotein-like	MLOC_53136.1	0.0/99 %
<i>TaDFR</i>	dihydroflavonol-4-reductase	LOC100125685	6e-8/71 %
<i>ZmG3Pp</i>	glycerol 3-phosphate permease	NP_001148138.2	1e-119/45 %
<i>GsLRR</i>	receptor-like serine/threonine-protein kinase	KHN47452.1	8e-161/95 %
<i>AtCRRK25</i>	cysteine-rich receptor-like protein kinase 25	EMT15732.1	4e-63/71 %
<i>TuHERK1</i>	receptor-like protein kinase HERK 1	EMS58126.1	2e-69/77 %
<i>AtSUVH1</i>	histone-lysine N-methyltransferase, H3 lysine-9 specific	EMT20222.1	4e-8/29 %
<i>AtERF1</i>	ethylene-responsive transcription factor 1	EMT22348.1	3e-31/90 %
<i>TuSHV3</i>	glycerophosphoryl diester phosphodiesterase 1	EMS62136.1	2e-47/49 %
<i>TuSKOR</i>	potassium channel	EMS48431.1	1e-137/78 %
<i>AtUCOQ4</i>	ubiquinone biosynthesis COQ4-like protein	EMT10501.1	0.0/83 %

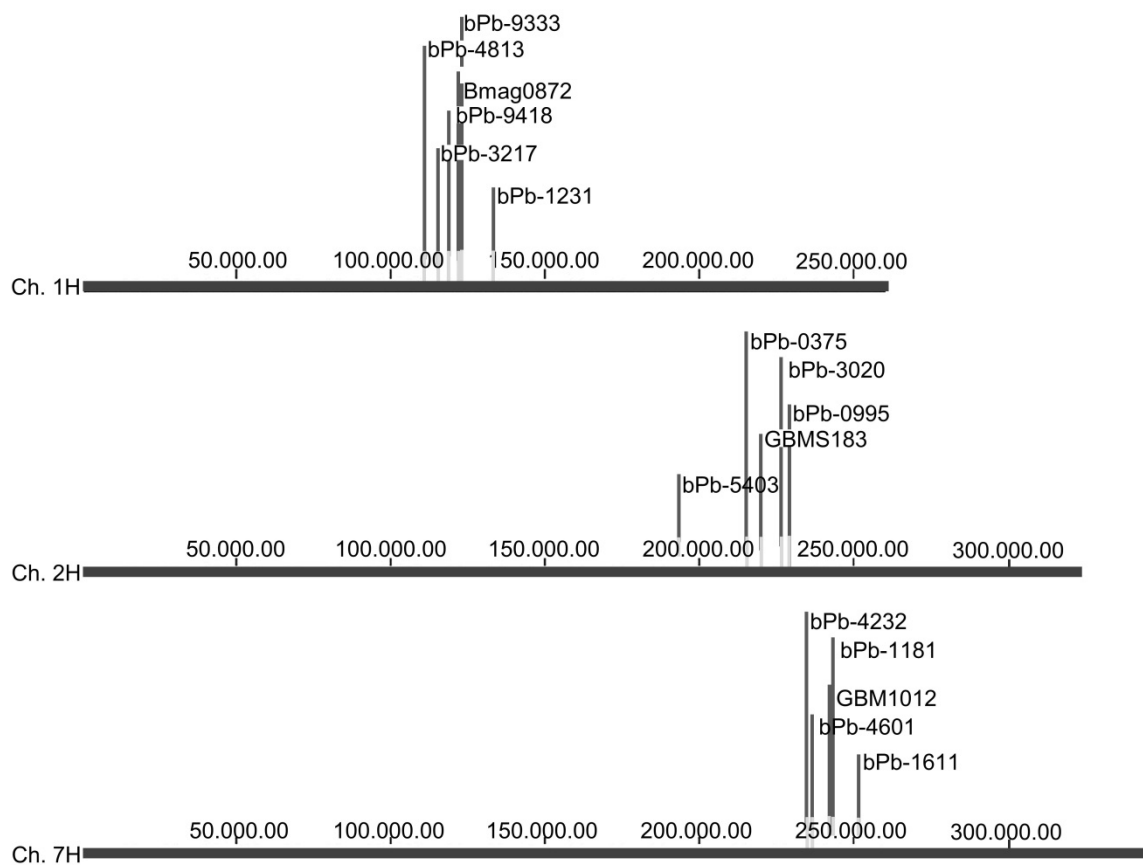


Fig. 1 Suppl. *In silico* mapping of molecular markers significantly associated with proline accumulation and osmotic potential and their closely linked markers to the consensus sequence of chromosomes 1H, 2H, and 7H.