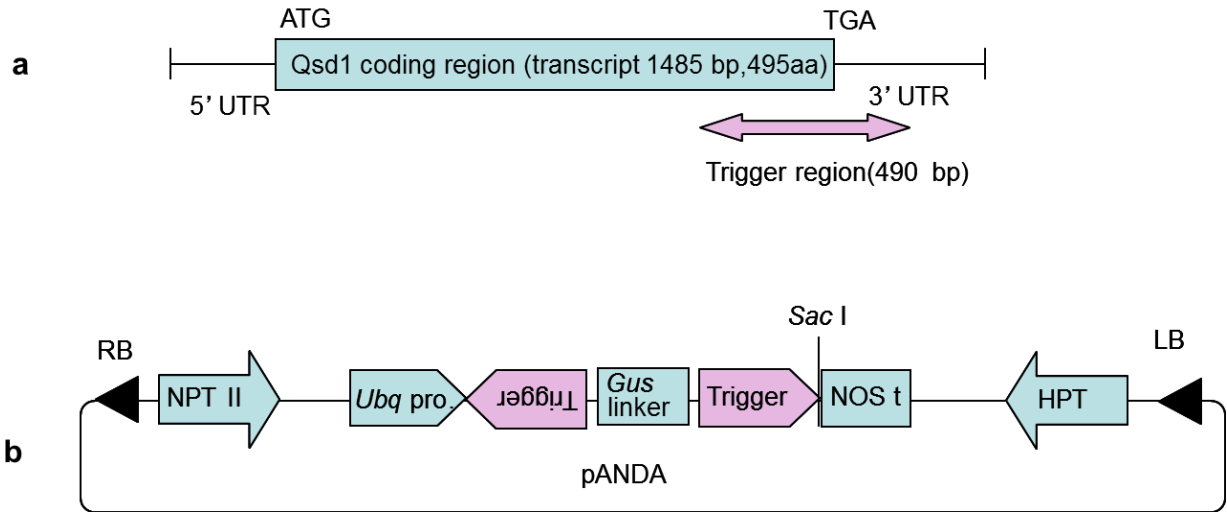
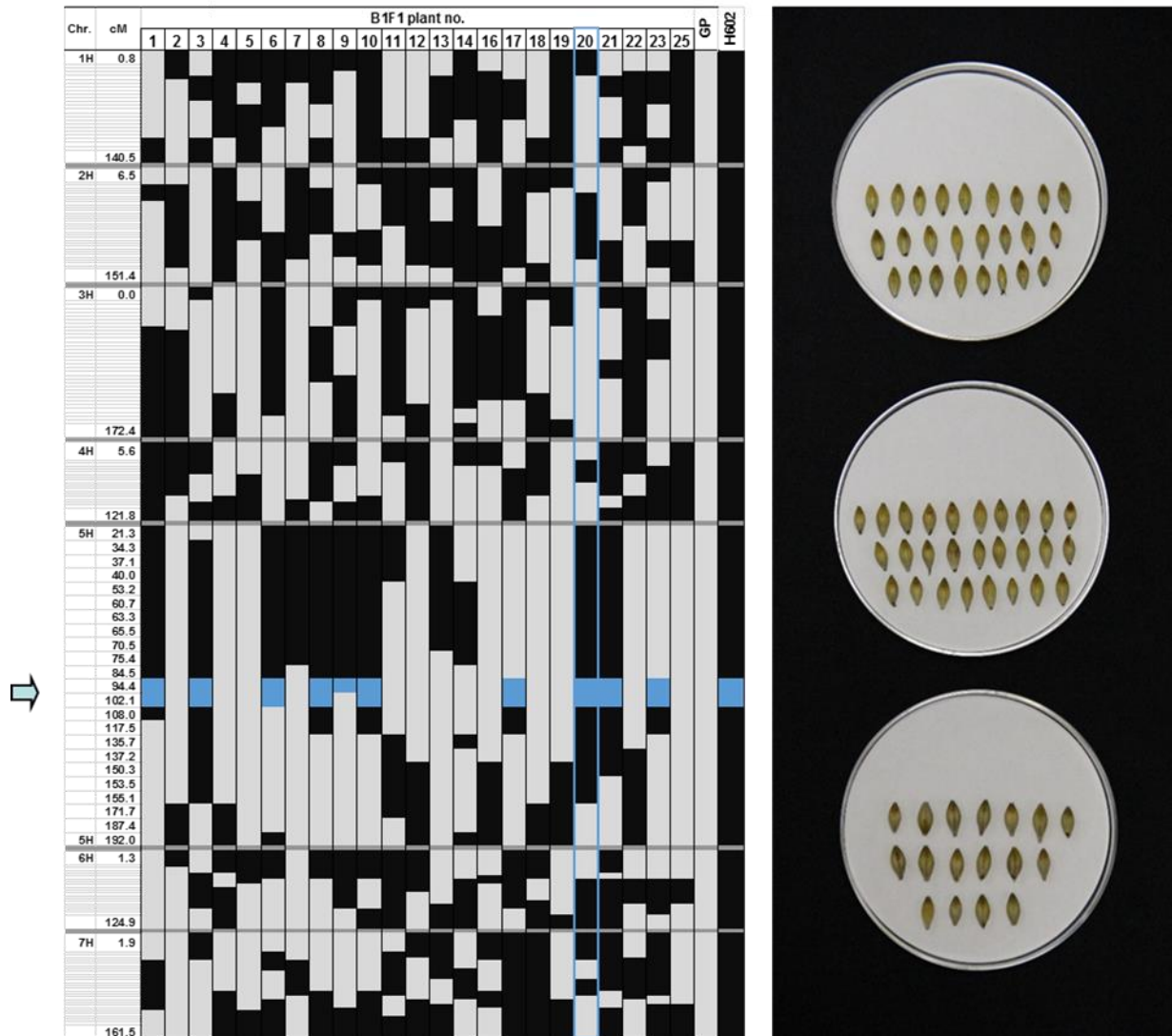


	10	20	30	40	50	60	
	ATGTCGTACAACAAGA	CCGCTCCATCACCGCCGAGACCA	TAAACCCCAAGGTC	CAAGATC			
1	M S Y N K T A S I T A E T I N P K V K I						20
	70	80	90	100	110	120	
	TTCGACTACGAGCCCTGCGGGGAGATCGCCAGGCACGCGAGCGGTTGGAGCAGGAGATG						
21	F D Y E P C G E I A R R H A E R L E Q E M						40
	130	140	150	160	170	180	
	GAGAAAGCCAGGTTCTCGCCCTTCCAGAGATTATACTGCAACCTTGGGAAACCT						
41	E K S P G S R P F P E I I Y C N L G N P						60
	190	200	210	220	230	240	
	CAGGCTCTCGGGCAGCGCCGATAAACCTTCTTGTGAGGTTATTTCTGTGTGACAAT						
61	Q A L G Q R P I T F F R E V I S L C D N						80
	250	260	270	280	290	300	
	CCAGCTCTCCTCGACAGAGATGAACCCGATGTTATTCAGTCCATGTGCCATAAATAGA						
81	P A L L H R D E T R M L F S P C A I N R						100
	310	320	330	340	350	360	
	GCGCGAAGATTATCGAGTCGATGCCCGAAGAACAACCGGTGCATATACCAACAGTCAG						
101	A R K I I E S M P G R N T G A Y T N S Q						120
	370	380	390	400	410	420	
	GGAAATCGAAGTTTGCAGAGCGGTTGCAAGTGGAAATCGCTGCAAGAGATGGTTTTCCA						
121	G I R S L R E A V A S G I A A R D G F P						140
	430	440	450	460	470	480	
	TCAAAGCCGGAAGACATCTTCTGACGGATGGAAGAGATTGAGGATCAATTTGAGTATG						
141	S R P E D I F L T D G A S S A I N L S M						160
	490	500	510	520	530	540	
	CAGATCTCATTAGGTCGAGAGATGGCATTATTGCCCCTTACCCGAATATCCATTA						
161	Q I L I R S Q E D G I L C P L P E Y P L						180
	550	560	570	580	590	600	
	TACTCGCGTCCATTACTTACTGATGGGACTATGGTACCGTACAATCTTAGCGAGGAT						
181	Y S A S I I L H G G T M V P Y N L S E D						200
	610	620	630	640	650	660	
	GGTATTGGGGCTTGAAGATTTTGGAAATAAGAGGTGCTTGGAGGAGCACGCATCGCA						
201	G D W G L E I F E V K R C L E E A R I A						220
	670	680	690	700	710	720	
	GGTTTGACTGTTCTGTGATGATGATATAAATCCCGGAAACCCAAACGGGACAGGTACTG						
221	G L T V R A M V I I N P G N P T G Q V L						240
	730	740	750	760	770	780	
	TCTGTCCAACCGAGGAGATAGTAAATTTGTGCGAAAGAAGGCTTGGTTATCCTT						
241	S V T N Q E E I V E F C R K E G L V I L						260
	790	800	810	820	830	840	
	GCCGATGAGGTATACCAAGATAATGTCTATGTGGAGGATAAGAAAGTCAATCTTCAAG						
261	A D E V Y Q D N V Y V E D R K F N S F K						280
	850	860	870	880	890	900	
	AAAAGTGCAGATCACTTGGGTGTCAGCAGAAATGACATCTCCATAGTGTCAATTCATCG						
281	K V A R S L G C D E N D I S I V S F H S						300
	910	920	930	940	950	960	
	GTTTCGATGGGTACTCTGGAGAATGTGGCAGAGAGGGGAGGCTACATGGAGATATGGT						
301	V S M G Y S G E C G R R G G Y M E I C G						320
	970	980	990	1000	1010	1020	
	TTTGGAGATGATGTGATGGGTGAGATTGCAAGGTGGCTTCTGTGACTCTTGGCCCAAC						
321	F G D D V M G E I R K V A S V T L C P N						340
	1030	1040	1050	1060	1070	1080	
	ACAAGTGGTCAAATTTACTAGCCTTGGAGATGGATCCACCAAAGTCAAGATGGTGT						
341	T N G Q I L T S L A M D P P K L G D G C						360
	1090	1100	1110	1120	1130	1140	
	TTCGAGGCTTTCATGGCTGAAAAGAAAGAAcCAGTACATCTTGGCCAAAGCGCCCAAG						
361	F E A F M A E K E E T S T S L A K R A K						380
	1150	1160	1170	1180	1190	1200	
	ACCTTGGTGAACGATTCAGCAGCCTGGAGGGAATGACCTGCAACAAAGTAAAGGGCGCA						
381	T L V N A F S S L E G M T C N K V E G A						400
	1210	1220	1230	1240	1250	1260	
	ATCTACGCCCTCCACGATCCATCTCCAGCAAGCGGCAACAAGCCGCAAGGCGGAG						
401	I Y A F P R I H L P A A A I K A A K A E						420
	1270	1280	1290	1300	1310	1320	
	GACaTGTCCCGAGACGTTCTACGCGTGGCGTCTTCTCGATGCCACCGGAATCGCGTTC						
421	D M S P D T F Y A C R L L D A T G I A V						440
	1330	1340	1350	1360	1370	1380	
	GTCCTGGCTCTGGATCCACGATCTCTGGCGCAACAAGCGGACCGGAGATGGCAT						
441	V P G S G F H Q I S G R N T A T G T W H						460
	1390	1400	1410	1420	1430	1440	
	ATCAGGTGACTATCCTTGTGCGCGAGGACAAAGATCGAGGCAATGATCGCGGCTCAAG						
461	I R C T I L V A E D K I E A M I A R L K						480
	1450	1460	1470	1480			
	GCCTCCACGAGTCTTCATGAAAGAGTTCCGCGACCCGAAAGCTGA						
481	A F H E S F M N E F R D R S *	495					

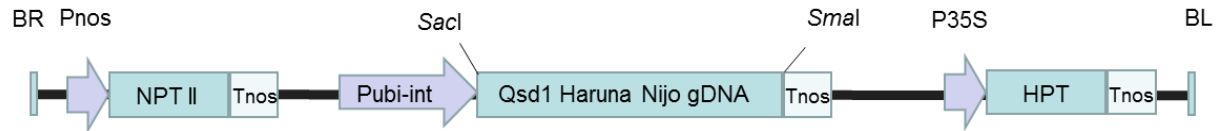
**Supplementary Fig. 1| Nucleotide and amino acid sequences of *qsdl* in dormant wild barley H602.**



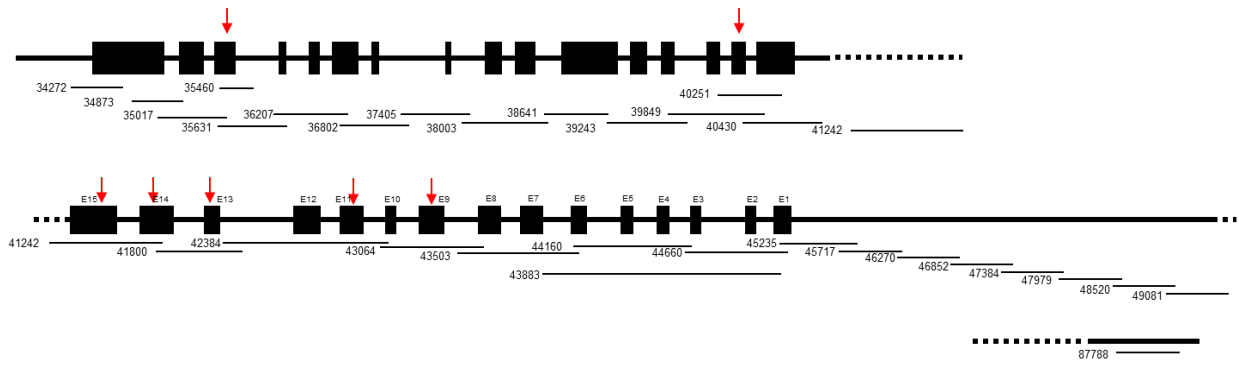
**Supplementary Fig. 2 | RNAi knockdown construct of *Qsd1*. a, Trigger region, b, RNAi trigger vector; pANDA.**



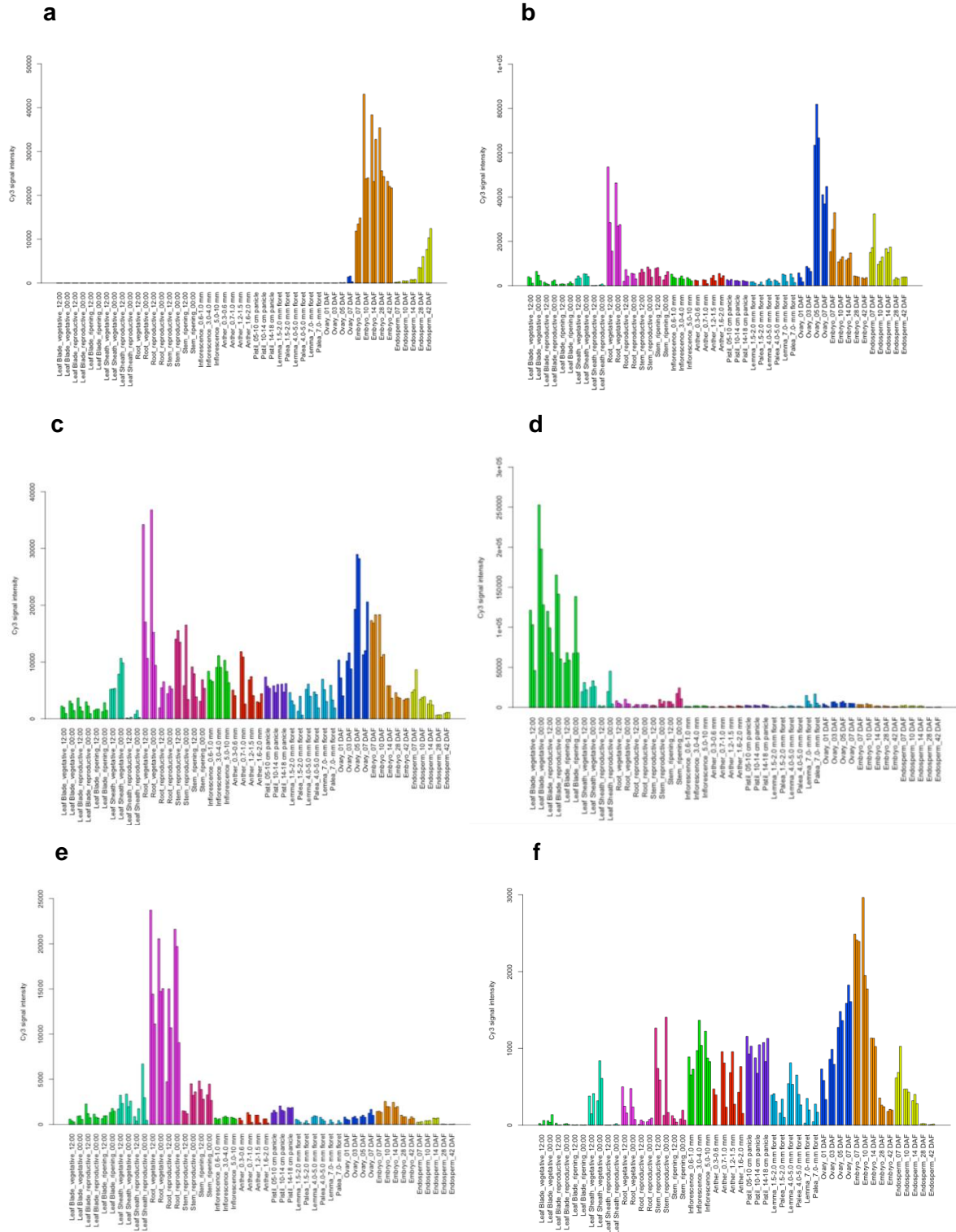
**Supplementary Fig. 3 | Genotyping and selection of B<sub>1</sub>F<sub>1</sub> plants derived from the cross between GP (Golden Promise: transformation efficient with less dormant allele *Qsd1/Qsd1*) and H602 (transformation inefficient with dormant allele *qsd1/qsd1*).** Left: Black box indicates heterozygous region of B<sub>1</sub>F<sub>1</sub> plants on the background of GP (gray box). *Qsd1* region is indicated by arrow in blue region of each plant. The B<sub>1</sub>F<sub>1</sub> plant No.20 (blue line) was self-pollinated to obtain a B<sub>1</sub>F<sub>2</sub> *qsd1/qsd1* homozygous plant (B<sub>1</sub>H<sub>602</sub>GP20-7). Right: Seed samples of B<sub>1</sub>H<sub>602</sub>GP20-7 (each spike for each Petri dish) show no germination after 35 d of 25°C dormancy reduction treatment.



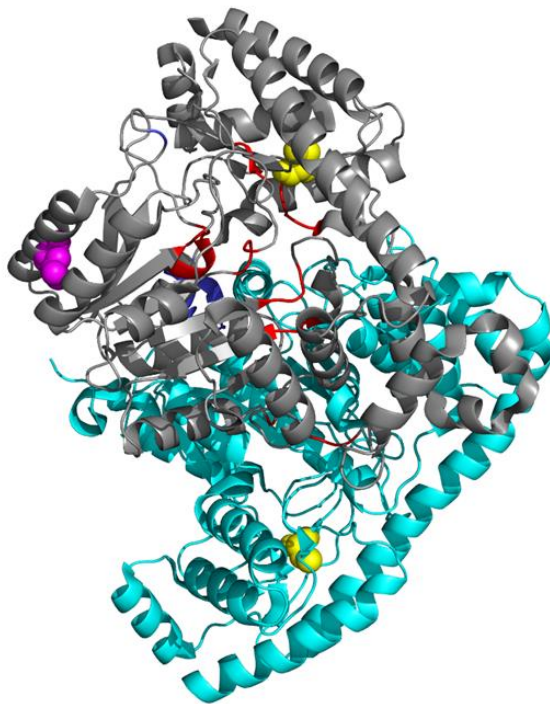
**Supplementary Fig. 4| T-DNA region of pBUH3.** Abbreviations are as follows: BR, right border; BL, left border; NPT II, neomycin; Phosphotransferase II; Pnos, nopaline synthase promoter; Tnos, 3' signal of nopaline synthase; P35S, 35S promoter; Pubi-int, maize ubiquitin promoter and the first intron; HPT, hygromycin phosphotransferase.



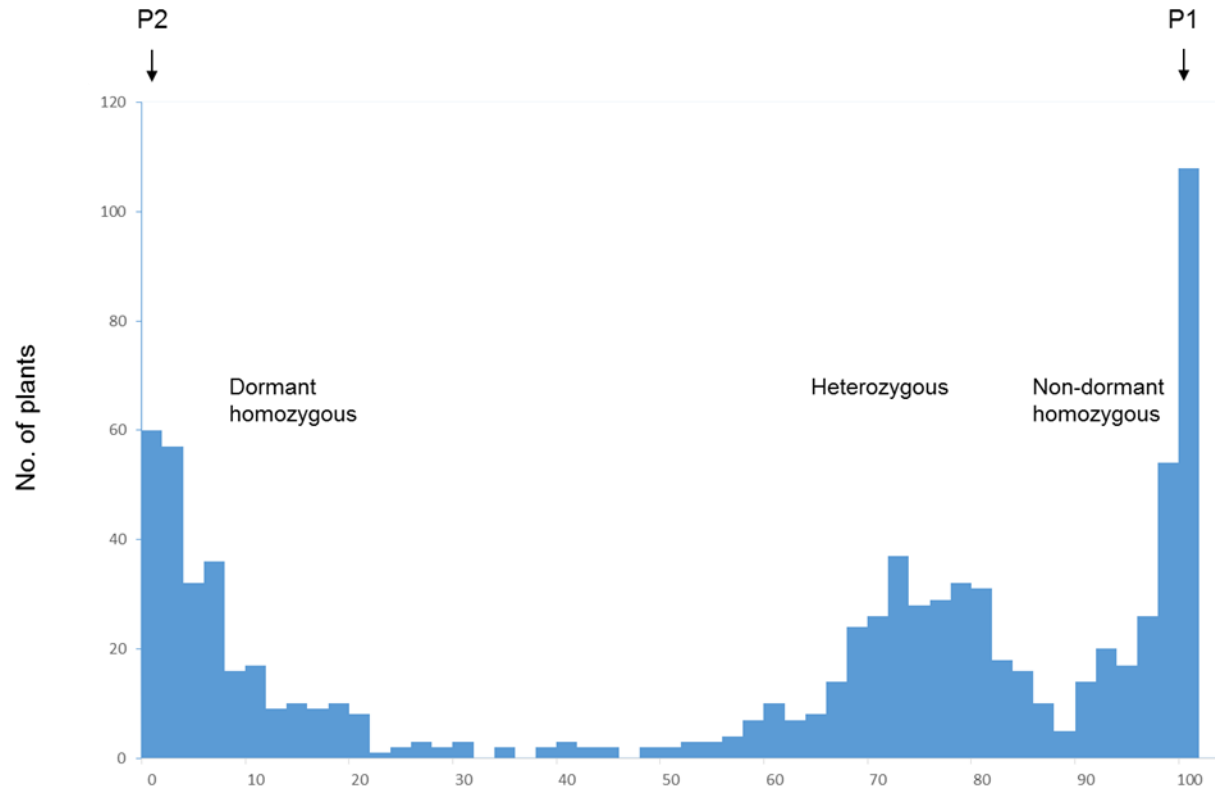
**Supplementary Fig. 5| PCR amplification at the region of *LC054176* (upper) and *Qsd1* (lower). Arrows indicate SNPs in exon between parents (Haruna Nijo and H602).**



**Supplementary Fig. 6 | Expression patterns of AlaAT rice orthologs.** Rice genes and barley orthologs in parenthesis of **a**, *Os09g043390* (*Qsd1*), **b**, *Os10g039050* (*Hv3*), **c**, *Os07g061780* (*Hv2*), **d**, *Os07g010830* (*Hv5*) and **e** and **f**, *Os10g039060* (*Hv4*). *Os10g039060* has two probes from full length cDNA AK119373 (e) and AK107029 (f) which might be derived from a different locus in RiceXPro<sup>23</sup>.

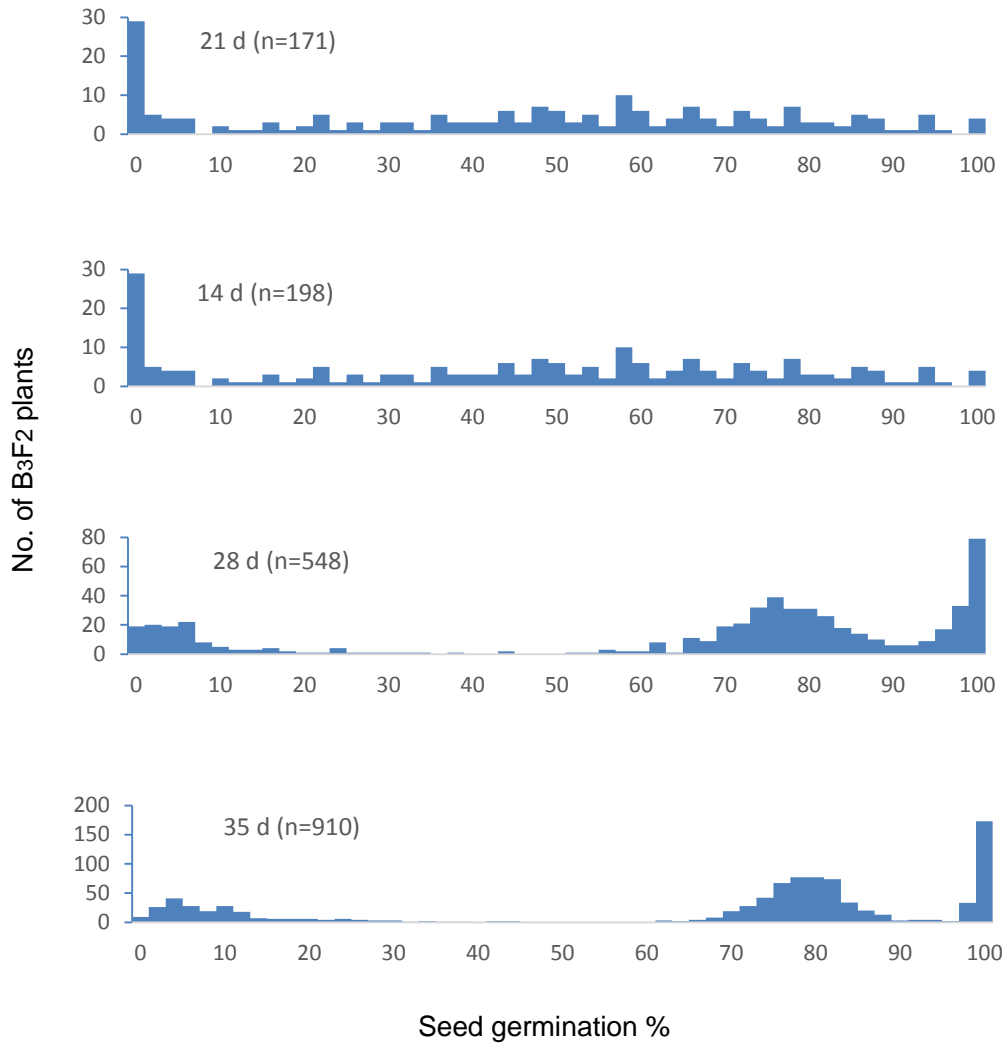


**Supplementary Fig. 7 | An *in silico* protein threaded model of QSD1 based on the crystal structure of AlaAT<sup>24</sup> (Hv3).** The model contains two subunits, coloured grey and cyan. The predicted position of the L214F substitution is shown in magenta. The NH<sub>2</sub>-terminus is shown in blue, the pyridoxal 5' phosphate binding pocket is in red, and cysteines are shown in yellow.

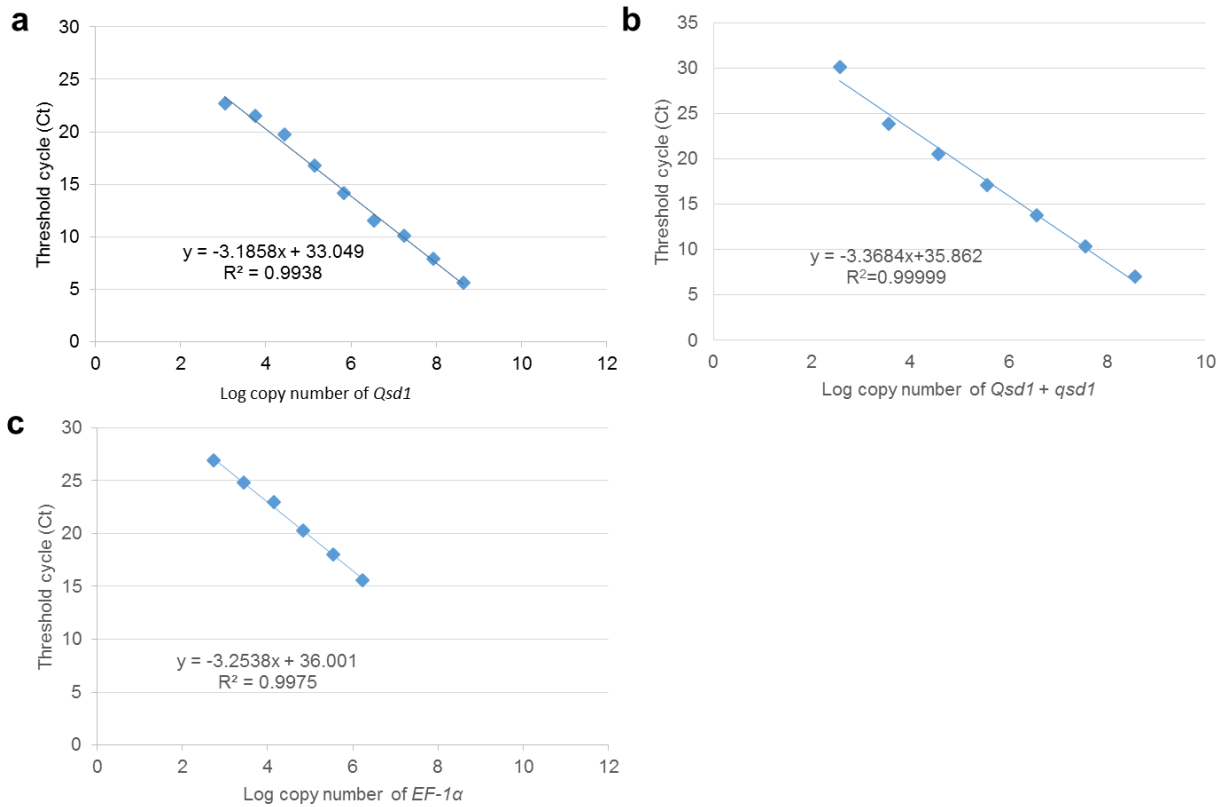


**Supplementary Fig. 8| Frequency distribution of seed germination % in F<sub>3</sub> plants (F<sub>4</sub> seeds) from the cross Haruna Nijo (P1)/H602 (P2) after 28 d treatment of dormancy reduction. *Qsd1/qsd1* is genotyped by dormant homozygous, heterozygous and non-dormant homozygous.**





**Supplementary Fig. 9| Frequency distributions of seed germination in F<sub>2</sub> plants (F<sub>3</sub> seeds) from the cross Haruna Nijo/H602 for time course treatments of dormancy reduction.**



**Supplementary Fig. 10| Log copy numbers for expression data.** Each figure represents the expression for **a**, *qsd1* (H602), **b**, *Qsd1* and *qsd1* for complementation experiment and **c**, *EF1-α* as a control. For primer sequences, see Supplementary Table 8.

**Supplementary Table 1| Primer information of markers for fine mapping of *Qsd1* region.**

Primer name	sequence ID	sequence L	sequence R
EST1	k01353*	GCAACCGTAGTCCTTGTGGT	GTGTGGCCTTTCAGGTGATT
EST2	k04618*	ATCAGGCATATGACCCAAGG	AGGGAAATGGTGCACAAGAC
EST3	NIASHv3083L11_R**	CCGCTCCCAAGAGTATTTT	GTTGCTAATCTCCCCGTTGT
EST4R	k00950*	ACTACAAAAGCCTTCCCCGT	TGCGAAACCATACCGTAACA
EST4F	FLOUba96g05_F	GTCCAATTCCCCACCACA	GCACGCAGCTCCTTGACA
EST5	NIASHv3013O02_F**	CAATCGCTCACTCTCCTCCT	TTCCGGTCTTGATGGAAAAC
EST6	CONTIG7699***	GTCGTCCTGAAGCAGATGGT	AACATGCACCCTACTTCAACG
EST7	NIASHv1145B20_R**	TACACTTCCGTGGCACAATC	GACGACGTGTACCTCGGCTA
EST8	NIASHv3118E04_R**	ATCACGGCAGGTGGTACAG	GTGTACCTCGGCTACGGCTA
EST9	NIASHv2005F14_F**	TTGCATTTCTGTTCTCCAGTG	CATGAGCTACTGCACGTTCC
EST10	NIASHv3091J11_F**	CGCCCAACTAGCTAAAAACAG	CGACAGCGACTTCACGTCT
EST11	rbah40i16****	GAGATCAATGACGTGCTCCA	TGGGGAAGTTGTGTTGGAAT
EST12	k03227*	TGATTGTTACGTTGCCTGGA	CATGCCACATAATGCAAAGG

\* Sato *et al.*<sup>13</sup>

\*\* bex-db (<http://barleyflc.dna.affrc.go.jp/bexdb/>)

\*\*\* HarvEST (<http://harvest.ucr.edu/>) barley assembly #32

\*\*\*\* Barley DB (<http://www.shigen.nig.ac.jp/barley/>)

**Supplementary Table 2 | Nucleotide polymorphisms in the *Qsd1* region.** Gene structures of *AK353915* and *LC054176* are tail-to-tail oriented to and separated only by 345 bp. Polymorphisms are indicated with E: exon and I: intron numbers and position refer to the Haruna Nijo BAC sequence (LC054174). NS show non synonymous amino acid change. Dormant and less-dormant parents used for QTL mapping<sup>9</sup> are compared.

			Gene structure of <i>LC054176</i>															Intergenic		Gene structure of <i>AK372829</i>																																																						
E:exon, I:intron			E3	I3	I3	I3	I5	E6	I6	I7	I7	I7	I8	I10	I10	E11	I11	I11	E12	I12	I13	I13	I13	I14	E15			E15	E15	E15	I14	I4	E14	I13	E13	I12	I12	E11	E9	I8	E8	I6	I5	I5	I3	I2	I2	I2	I2	I2	I1																							
Position on Haruna Nijo BAC clone LC054174			35654	35781	35812	36006	36032	36633	36795	36918	37510	37530	37762	377942	38684	38693	39301	39440	39451	39487	39558	39731	39954	40066	40086	40269	40272	40407	40947	41105	41169	41331	41480	41535	41641	41667	41771	41916	<b>42085</b>	42152	42521	<b>42850</b>	<b>43368</b>	43574	43654	44044	44295	44362	44675	44791	44846	44853	44870	44879	44909	44912	45025	45109																
<i>Qsd1/qsd1</i>	Acc. No.	Name	Non synonymous haplotype of <i>AK372829</i>																																																																							
<i>qsd1</i>	H602	Wild barley	T	G	C	C	T	A	T	A	T	T	C	C	C	T	T	T	C	T	T	C	T	T	G	T	C	T	T	C	T	T	G	T	---	C	T	T	G	T	G	---	C	G	---	A	T	CA	G	-	-	C	C	C	T	A	C	C	CT	A	C	A	G	T	A	TA	A	T	A					
<i>qsd1</i>	I765	Khanaqin 1	T	A	C	C	T	A	T	A	T	T	C	C	C	T	T	T	C	T	T	T	C	T	T	G	T	---	C	T	T	G	T	---	C	T	T	G	T	---	C	T	T	G	T	G	---	C	G	---	A	T	CA	A	-	-	C	C	C	T	A	C	C	CT	A	C	A	G	T	A	TA	A	T	A
<i>qsd1</i>	I767	Khanaqin 7	T	A	C	C	T	A	T	A	T	T	C	C	C	T	T	T	C	T	T	T	C	T	T	G	T	---	C	T	T	G	T	---	C	T	T	G	T	---	C	T	T	G	T	G	---	C	G	---	A	T	CA	A	-	-	C	C	C	T	A	C	C	CT	A	C	A	G	T	A	TA	A	T	A
<i>qsd1</i>	T602	Turkey 6	T	A	C	C	T	A	T	A	T	T	C	C	C	T	T	T	C	T	T	T	C	T	T	G	T	---	C	T	T	G	T	---	C	T	T	G	T	---	C	T	T	G	T	G	---	C	G	---	A	T	CA	A	-	-	C	C	C	T	A	C	C	CT	A	C	A	G	T	A	TA	A	T	A
<i>qsd1</i>	T615	Turkey 45	T	A	C	C	T	A	T	A	T	T	C	C	C	T	T	T	C	T	T	T	C	T	T	G	T	---	C	T	T	G	T	---	C	T	T	G	T	---	C	T	T	G	T	G	---	C	G	---	A	T	CA	A	-	-	C	C	C	T	A	C	C	CT	A	C	A	G	T	A	TA	A	T	A
<i>qsd1</i>	I626	Katana 1	C	A	T	C	C	A	T	G	C	G	T	C	T	C	C	---	C	C	T	C	A	C	C	G	C	CTT	C	T	C	C	G	A	G	GA	T	AAC	A	C	CA	A	C	A	T	C	C	A	A	T	TT	G	T	T	T	C	G	---	G	T	A													
<i>qsd1</i>	I622	H. E. S. 4	C	A	T	C	C	-	T	G	T	T	C	T	C	C	C	---	C	C	C	C	T	A	T	C	A	T	CTT	C	T	C	C	T	G	GA	C	T	AAC	A	C	AT	A	C	A	T	C	C	A	C	C	CT	G	T	T	T	C	G	---	G	T	A												
<i>qsd1</i>	C627	Mokussekko 3	C	A	T	C	C	A	T	G	T	T	C	T	C	C	C	---	C	C	C	C	T	A	T	C	A	T	CTT	T	T	C	C	T	G	GA	T	AAC	G	C	CA	A	C	A	T	C	C	A	C	T	CT	G	T	T	T	C	G	---	G	T	A													
<i>qsd1</i>		Steptoe	C	A	T	C	C	A	C	G	T	T	C	C	C	C	---	C	C	C	C	C	A	T	C	G	C	TTT	C	T	C	C	T	G	G	A	C	T	AAC	A	C	CA	A	C	A	T	C	G	C	C	CA	G	T	T	T	C	G	---	G	T	A													
<i>Qsd1</i>		Morex	C	A	T	G	C	-	T	G	T	T	C	T	C	C	C	---	C	C	C	C	T	A	T	C	A	T	CTT	C	C	C	C	T	G	GA	C	T	AAC	A	C	AT	A	C	A	T	G	C	A	C	C	CT	G	T	T	T	C	G	---	G	T	A												
<i>Qsd1</i>	J215	Ko A	C	A	T	G	C	-	T	G	T	T	C	T	C	C	C	---	C	C	C	C	T	A	T	C	A	T	CTT	C	C	C	C	T	G	GA	C	T	AAC	A	C	AT	A	C	A	T	G	C	A	C	C	CT	G	T	T	T	C	G	---	G	T	A												
<i>Qsd1</i>	U062	Russia 6	C	A	T	G	C	-	T	G	T	T	C	T	C	C	C	---	C	C	C	C	T	A	T	C	A	T	CTT	C	C	C	C	T	G	GA	C	T	AAC	A	C	AT	A	C	A	T	G	C	A	C	C	CT	G	T	T	T	C	G	---	G	T	A												
<i>Qsd1</i>	C649	Harbin 2-row	C	A	T	G	C	-	T	G	T	T	C	T	C	C	C	---	C	C	C	C	T	A	T	C	A	T	CTT	C	C	C	C	T	G	GA	C	T	AAC	A	C	AT	A	C	A	T	G	C	A	C	C	CT	G	T	T	T	C	G	---	G	T	A												
<i>Qsd1</i>	J247	Haruna Nijo	C	A	T	G	C	-	T	G	T	T	C	T	C	C	C	---	C	C	C	C	T	A	T	C	A	T	CTT	C	C	C	C	T	G	GA	C	T	AAC	A	C	AT	A	C	A	T	G	C	A	C	C	CT	G	T	T	T	C	G	---	G	T	A												
																				NS NS NS NS																																																						

**Supplementary Table 3| Degree of less-dormancy (% of germination) of mapping parents used for QTL detection and additive effects of *Qsd1* in each population<sup>9</sup>.**

Name	Accession No.	Allele	Non-synonymous SNP				Germination (%) after 25°C treatment		Additive effect of <i>Qsd1</i> allele (germination %)		Cross and <i>Qsd1</i> donor
			E14	E13	E11	E9	5w	10w	5w	10w	
Wild barley	H602	<i>qsd1</i>	T	G	C	C	0	0	15.8	26.5	J247/H602
Khanaqin 1	I765	<i>qsd1</i>	T	A	C	C	0	1	48.1	23.6	C649/I765
Khanaqin 7	I767	<i>qsd1</i>	T	A	C	C	0	0	46.2	42.5	C649/I767
Turkey 6	T602	<i>qsd1</i>	T	A	C	C	0	0	32.3	44.9	C649/T602
Turkey 45	T615	<i>qsd1</i>	T	A	C	C	0	0	29.8	45.7	C649/T615
Katana 1	I626	<i>qsd1</i>	C	A	T	C	12	24	13.1	10.6	C649/I626
H. E. S. 4	I622	<i>qsd1</i>	C	A	T	C	27	-	11.4	-	U602/I622
Mokussekkko 3	C627	<i>qsd1</i>	C	A	T	C	4	-	27.5	-	J215/C627
Ko A	J215	<i>Qsd1</i>	C	A	T	G	91	-	0	-	J215
Russia 6	U062	<i>Qsd1</i>	C	A	T	G	93	-	0	-	U062
Harbin 2-row	C649	<i>Qsd1</i>	C	A	T	G	100	100	0	0	C649
Haruna Nijo	J247	<i>Qsd1</i>	C	A	T	G	100	100	0	0	J247

**Supplementary Table 4| Association between haplotypes of non-synonymous SNPs in *Qsd1/qsdl* and average seed germination among 353 cultivated and 14 wild barley accessions.**

Non-synonymous SNP				Wild		Cultivated		Reference
E14	E13	E11	E9	%*	n	%*	n	
T	G	C	C	0.0	1			H602
T	A	C	C	1.5	4	5.5	4	
C	A	C	C			40.6	7	
C	A	T	C	0.0	6	56.2	235	
T	A	T	C	0.0	3	62.0	61	
C	A	C	G			80.1	17	
C	A	T	G			83.0	29	Haruna Nijo

\*Average germination % after 35 d of 25°C dormancy reduction treatment

**Supplementary Table 5| Primer information for polymorphism detection on *QsdI* region.**  
Position is based on the numbers from 3' end of Haruna Nijo BAC clone (LC054174).

Primer name	Position on BAC clone LC054174	Product size	Sequence L	Sequence R
34272	34272 - 34778	507	CCCGAAATCCCGTCTAGTCT	AAGATAGAAGCCGACCAAACC
34873	34873 - 35372	500	GTCCAATCCCCACCACA	GCACGCAGCTCCTTGACA
35017	35017 - 35698	698	CTTCTCCCCACGCTTACT	ACGAGCGAACCAATCTCCT
35460	35460 - 35974	515	CGTCCTATCCGTTTCCTGAG	TGGACAAGTTTCTTCAGATTCA
35631	35631 - 36300	670	GTCGTGCAACCCAATTCTT	TGCAAAGAATAATGTGTCTACCTTT
36207	36207 - 36836	656	TGGCTTGTTATAACACAGGTCTAT	ATATCTTTATGGCTGGGGACA
36802	36802 - 37446	671	GAAATGGCTGAGGAAGAAGG	AACTGAGTGAACTCAATCTGTGTATCT
37405	37405 - 38071	691	CATGATGTGCGGCACTAAC	TTGGGAGCAGAAAAGAACTG
38003	38003 - 38682	682	GAGCCTTTGTTGGTAGAGTTGC	CATGCATAAACAATGCGAATAGA
38641	38641 - 39330	690	TTGCCATCGCTTGTTACT	GAGATGGCCCTGAAGTTGAT
39243	39243 - 39935	693	CCAAACTTGCCATCTGCTC	CCCTTAGTTCCTCAGCATTGA
39849	39849 - 40530	690	ATGACCGTACGTATCCACTATTCA	CATCTGTCTTCGCGTAATCCT
40251	40251 - 40763	513	TTTGCTTTGTCACAGGTTG	AAAAGCCTTCCCCGTCTCTA
40430	40430 - 41086	657	TGGGCACTTTCAAGGTAATAA	CAAACTGAGGTCAATGTACCG
41242	41242 - 41866	625	GGGAGGCACTCACTCAGTACA	AGGGAATGACCTGCAACAAA
41800	41800 - 42337	538	GCTGCTGGGAGATGGATG	CCCCTGTTTCGCATACTTG
42384	42384 - 43138	755	TGCAGCAAAAGTCAACAAGG	TCGGAAAGAAGGCTTGGTTA
43064	43064 - 43656	593	CGCCCGCGTCACAAAACACTAC	GGTGGGACTATGGTATGGTGG
43503	43503 - 44194	692	ACGCACTCCCACTTTACACC	ATTGCAGTCCATGTGCCATA
43883	43883 - 45247	1364	CGCCACCTTAGCTAGCTCTC	ATGTCTTCCGGTCTTGATGG
44160	44160 - 44722	563	CTTCCGCGCTCTATTTATGG	CCAGAGGTGCGTCTTTCTTT
44660	44660 - 45294	635	GCTCTGGAAGTCTGGGTTGA	CAGCACAATCGCTCACTCTC
45235	45235 - 45835	601	GGGAGGAAGGAGGAGAGCTA	AAACATGCGTGGAGGTCAT
45717	45717 - 46366	649	CGATATAAATTATGCAAACATGACG	CGACAATCGTGAAGGTTTGAG
46270	46270 - 46923	653	CTCTCCTCCTTCGACACGAT	ATCCGCACCACACTACATCA
46852	46852 - 47504	652	GACGGTGAGCGAAGAAGG	CGAGGGGAGTAGTATACATCTAAAGC
47384	47384 - 48042	658	TCGTGCGGATGATAACCATA	CCAAGTCTTGCTGGGTTGTT
47949	47949 - 48639	690	CAGCGGAGGGTGAAACATAC	TACCGGACGACTGGACCTAC
48520	48520 - 49204	684	TTGGTTTCTCCACCTCTTG	GTCGAGGAGGCCGAACCTT
49081	49081 - 49742	661	CTACGCCCTCGGCCTCTT	GGCCGTAAGACCCCTGACC
87788	87788 - 88452	664	CAGATTGTTGCGGGGTTACTG	GAGAAACACACCGGTTGAAAA





**Supplementary Table 7| Information and annotation on amino acid sequences showing similarities to QSD1.**

Abbreviation	Species	ID	Annotation	Position	Remark
Hv1	<i>Hordeum vulgare</i>	gi 326520203 dbj BAK04026.1	predicted protein	chromosome 5HL	QSD1
Hv2	<i>Hordeum vulgare</i>	gi 326525020 dbj BAK07780.1	predicted protein	chromosome 2HS	
Hv3	<i>Hordeum vulgare</i>	gi 1703227 sp P52894.1 ALA2_HORVU	alanine aminotransferase	chromosome 1H?	AlaAT <sup>24</sup>
Hv4	<i>Hordeum vulgare</i>	gi 326491065 dbj BAK05632.1	predicted protein		
Hv5part	<i>Hordeum vulgare</i>	gi 326495904 dbj BAJ90574.1	predicted protein partial	chromosome 2H	
Os1	<i>Oryza sativa</i>	gi 115479309 ref NP_001063248.1		Os09g0433900	
Os2	<i>Oryza sativa</i>	gi 115481822 ref NP_001064504.1		Os10g0390500	
Os3	<i>Oryza sativa</i>	gi 297610424 ref NP_001064505.2		Os10g0390600	
Os4	<i>Oryza sativa</i>	gi 115473371 ref NP_001060284.1		Os07g0617800	
Os5	<i>Oryza sativa</i>	gi 115470235 ref NP_001058716.1		Os07g0108300	
Sb1	<i>Sorghum bicolor</i>	gi 242050886 ref XP_002463187.1	hypothetical protein	SORBIDRAFT_02g039340	
Sb2	<i>Sorghum bicolor</i>	gi 242039815 ref XP_002467302.1	hypothetical protein	SORBIDRAFT_01g023740	
Bd1	<i>Brachypodium distachyon</i>	gi 357158537 ref XP_003578159.1	PREDICTED: glutamate-glyoxylate aminotransferase 2-like		
Bd2	<i>Brachypodium distachyon</i>	gi 721610191 ref XP_010235387.1	PREDICTED: glutamate-glyoxylate aminotransferase 2-like isoform X2		
Bd3	<i>Brachypodium distachyon</i>	gi 357111762 ref XP_003557680.1	PREDICTED: glutamate-glyoxylate aminotransferase 2		
At1	<i>Arabidopsis thaliana</i>	gi 42562119 ref NP_173173.3	alanine aminotransferase		
At2	<i>Arabidopsis thaliana</i>	gi 14596229 gb AAK68842.1	alanine aminotransferase-like protein		
Mt1	<i>Medicago truncatula</i>	gi 357514319 ref XP_003627448.1 :39-524	alanine aminotransferase		
Mt2	<i>Medicago truncatula</i>	gi 357485703 ref XP_003613139.1 :9-475	glutamate-glyoxylate aminotransferase		

**Supplementary Table 8| qPCR primers and conditions for expression analysis of *Qsd1/qsd1*.**

Primer	Full length/partial cDNAs	Forward sequence (5'-3')	Reverse sequence (5'-3')	Annealing Temp (°C)	Fragment size (bp)
<i>Qsd1</i>	AK372829	AGGACAAGATCGAGGCAATG	ATAATTTGCAGGGAGCGAAG	60	98
<i>Qsd1/qsd1</i>	AK372829	CTCTTTGCCCAACACAAAT	GAATGCGTTCACCAAGGTCT	60	152
<i>HvEF-1α*</i>	L11740.1	GCCAGATCAGCAACGGTTAT	ATCTTGACGAACCCAGCATC	60	120

\* <http://www.ncbi.nlm.nih.gov/pubmed/815979>