

Table S1. Amino acid (%) of bHLH protein in *Oryza sativa* subsp. Japonica cv. Nipponbare

Proteins	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V
OsbHLH056	6.1	4.5	4.5	5.3	2.0	3.6	6.9	6.1	2.0	4.0	11.7	5.7	2.8	2.8	4.5	13.4	5.7	0.4	2.0	6.1
OsbHLH057	12.1	4.3	3.1	5.1	2.0	5.9	8.2	5.1	0.8	2.7	6.6	8.2	3.1	3.5	12.1	6.6	4.3	1.2	0.8	4.3
OsbHLH058	27.3	0.0	0.0	2.6	0.0	2.6	0.0	5.2	3.9	1.3	2.6	3.9	2.6	3.9	18.2	3.9	5.2	3.9	5.2	7.8
OsbHLH059	8.9	5.1	3.4	8.9	2.1	3.4	7.2	8.9	1.3	3.0	10.6	8.1	1.3	3.4	8.9	5.1	3.8	1.3	0.4	5.1
OsbHLH062	5.3	7.9	6.0	4.5	1.1	5.7	8.7	6.0	3.4	3.0	9.8	4.9	1.1	2.3	8.3	6.8	6.8	0.4	1.5	6.4
OsbHLH063	6.3	7.1	4.4	4.8	0.8	6.3	8.7	5.6	1.6	2.8	9.9	4.8	3.2	1.6	11.9	8.3	5.6	0.8	0.8	4.8

A=Alanine, R=Arginine, N=Asparagine, D=Aspartic Acid, C=Cysteine, Q= Glutamine, E=Glutamic Acid, G= Glycine, H=Histidine, I=Isoleucine, L=Leucine, K=Lysine, M=Methionine, F= Phenylalanine, P=Proline, S=Serine, T=Threonine, W=Tryptophan, Y=Tyrosine, V=Valine

Table S2. Physico-chemical properties of different bHLH proteins in *Oryza sativa*

Protein	MW (kDa)	pI	No. of AA	+ve AA	-ve AA	Instability index	Aliphatic index	GRAVY	Extinction coefficients
OsbHLH056	26961.53	5.60	247	25	30	44.59	85.26	-0.290	13200
OsbHLH057	27873.70	5.88	256	32	34	65.33	61.13	-0.655	19730
OsbHLH058	7896.08	8.12	77	3	2	53.54	65.06	0.194	22460
OsbHLH059	25592.97	5.15	236	31	38	41.38	76.53	-0.565	18240
OsbHLH062	29686.27	6.77	265	34	35	62.87	73.92	-0.824	11460
OsbHLH063	27890.48	5.70	252	30	34	66.48	69.68	-0.800	14105

Table S3. Top threading template (OsbHLH059)

Protein Name	Rank	PDB Hit	Normalised Z score
Osbhlh059	1.	7f2fA	1.05
	2.	6f1tX	1.11
	3.	ln1w	2.40
	4.	6z91A	1.07
	5.	7f2f	1.94
	6.	7OgtB	1.05
	7.	7f2f	2.57
	10.	1am9A	1.29

Note: Rank 8 and 9 Template Z score below 1

Table S4. Top threading template (OsbHLH058)

Protein Name	Rank	PDB Hit	Normalised Z score
Osbhlh058	1.	2nbiA	1.08
	2.	6x87X	1.11
	3.	2nbiA	1.16
	4.	2mk0A	1.06
	5.	5yfpE	1.14
	6.	4ntqA	1.05
	7.	3j9aA	1.06
	8.	7jjvA	1.06
	9.	2tmaA	1.00
	10.	2mf8A	1.00

Table S5. Top threading template (OsbHLH056)

Protein Name	Rank	PDB Hit	Normalised Z score
Osbhlh056	1.	1am9A	1.23
	2.	7wood	1.13
	3.	6g11	2.42
	6.	7f2f	1.79
	8.	7f2f	2.67
	9.	1am9A	1.29

Table S6. Top threading template (OsbHLH063)

Protein Name	Rank	PDB Hit	Normalised Z score
Osbhlh063	1.	1n1w	2.42
	2.	6f1tX	1.33
	3.	7f2f	1.85
	4.	7b6zA	1.20
	5.	7f2f	2.46
	6.	5yz0C	1.21
	7.	7t92C	1.02
	8.	5gnjG	1.55
	9.	5nnvA	1.16
	10.	1nkp	2.39

Rank 4,5,7 and 10 Template Z score below 1

Table S7. Top threading template (OsbHLH057)

Protein Name	Rank	PDB Hit	Normalized Z score
Osbhlh057	2.	7f2fA	1.09
	4.	1n1w	2.25
	5.	7f2f	1.93
	6.	6z91A	1.08
	7.	7f2f	2.52
	8	5gnjA	1.35
	10	7wood	1.25

Rank 1,3 and 9 Template Z score below 1

Table S8. Top threading template (OsbHLH062)

Protein Name	Rank	PDB Hit	Normalised Z score
Osbhlh062	1.	1n1w	2.44
	2.	6f1tX	1.28
	3.	7f2f	1.82
	4.	7b6zA	1.25
	5.	7f2f	2.64
	6.	5h64B	1.20
	7.	7s7bB	1.08
	8.	5gnjG	1.43
	9.	5yz0C	1.17
	10.	1nkp	2.42

Table S9. Sub-cellular localisation of the 6 bHLH proteins using Deeplock2.0

Protein	Subcellular localization	Probability score
OsbHLH059	Nucleus	0.925
OsbHLH057	Nucleus	0.6413
OsbHLH056	Nucleus	0.8956
OsbHLH063	Nucleus	0.8864
OsbHLH057	Nucleus	0.9102
OsbHLH062	Nucleus	0.8421

Table S10. The InterPro families and domains of the 6 bHLH proteins

Protein name (Uniprot ID)	Source Database	Family	InterPro family description	Domain	InterPro domain description
OsbHLH059 (Q6ZGM4)	INTERPRO	Transcription factor ILR3-like (40-236) AA acid	This family represents a group of plant transcription factors, including ILR3 (also known as AtbHLH105) and its closest homologues bHLH34, bHLH104 and bHLH115 from Arabidopsis	Myc-type, basic helix-loop-helix (bHLH) domain (66-123)AA	This conserved domain, which is present in a variety of eukaryotic proteins, is likely a sequence-specific DNA-binding protein that functions as a transcription factor. It has 40–50 amino acid residues. This domain is thought to consist of two amphipathic helices connected by a variable-length linker region that could take the form of a loop (Kato et al.1992). Protein dimerisation is mediated by this 'helix-loop-helix' (HLH) domain.
Osbhlh058 (Q60EM5)	INTERPRO	Transcription factor ILR3-like. (10-77) AA acid	ILR3 (also known as AtbHLH105) and its closest Arabidopsis homologues, bHLH34, bHLH104, and bHLH115, are among the transcription factors for plants that make up this family (Gao2020). These transcription factors can form homo- and heterodimers and are involved in the direct activation of the production of bHLH38, bHLH39, bHLH100, and bHLH101, which positively regulate Fe homeostasis.	None	–

OsbHLH056 (Q0JFZ0)	INTERPRO	NONE	–	Myc-type, basic helix- loop-helix (bHLH) domain (68-125) AA acid	Same as for protein OsbHLH059
OsbHLH063 (Q10KL8)	INTERPRO	NONE	–	Myc-type, basic helix- loop-helix (bHLH) domain (36-86) AA	Same as for protein OsbHLH059
OsbHLH057 (Q6Z5B8)	INTERPRO	Transcription factor ILR3- like	Same as OsbHLH058-59	Myc-type, basic helix- loop-helix (bHLH) domain (92-143) AA	Same as for protein OsbHLH059
OsbHLH062 (Q69V10)	INTERPRO	NONE	–	Myc-type, basic helix- loop-helix (bHLH) domain (35-85) AA	Same as for protein OsbHLH059

Table S11. Super family description of 6 bHLH protein

Protein name (Uniprot ID)	Source Database	Homologous Superfamily	Superfamily description
OsbHLH059 (Q6ZGM4)	INTERPRO	Helix-loop-helix DNA-binding domain superfamily	This conserved domain, which is present in a variety of eukaryotic proteins, is likely a sequence-specific DNA-binding protein that functions as a transcription factor. It has 40–50 amino acid residues. This domain is thought to consist of two amphipathic helices connected by a variable-length linker region that could take the form of a loop. The proteins mentioned below include this 'helix-loop-helix' (HLH) domain, which mediates various protein dimerisation.
Osblh058 (Q60EM5)	INTERPRO	None	–
OsbHLH056 (Q0JFZ0)	INTERPRO	Helix-loop-helix DNA-binding domain superfamily (65-142) AA	Same description as in protein osbHLH059
OsbHLH063 (Q10KL8)	INTERPRO	Helix-loop-helix DNA-binding domain superfamily (32-111) AA	Same description as in protein osbHLH059
OsbHLH057 (Q6Z5B8)	INTERPRO	Helix-loop-helix DNA-binding domain superfamily (32-111) AA	Same description as in protein osbHLH059
OsbHLH062 (Q69V10)	INTERPRO	Helix-loop-helix DNA-binding domain superfamily (31-109) AA	Same description as in protein osbHLH059