

Supplementary material of the manuscript published in *Vitis* 55, 165–171 (2016):

Identification, characterization and expression analysis of ERF transcription factor *VviERF073* and standardization of stable reference genes under salt stress in grape

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Supplementary Table 1

List of *Arabidopsis* homologous genes interacting with *VviERF073* (GSVIVP00028041001)

S. No.	<i>Vitis vinifera</i> genes/protein interacting with <i>VviERF073</i>	Homologous gene in <i>Arabidopsis thaliana</i>	Biological role
1	GSVIVG000033487001	XTR7 AT4G14130.1-P	XTR7 (Xyloglucan Endotransglycosylase 7); Catalyzes xyloglucan endo-hydrolysis and/ or endotransglycosylation
2	GSVIVG00014541001	AtCKX6 AT1G75450.1-P	CKX5 (Cytokinin Oxidase 5); cytokinin dehydrogenase
3	GSVIVG00028044001	ERS1 AT2G40940.1-P	ERS1 (Ethylene Response Sensor 1); ethylene binding / protein histidine kinase/ receptor
4	GSVIVG00016760001	MBF1C AT3G24500.1-P	MBF1C (Multiprotein Bridging Factor 1C); DNA binding / transcription coactivator
5	GSVIVG00002180001	EIN 4 AT3G04580.1-P	EIN4 (Ethylene Insensitive 4); ethylene binding / receptor
6	GSVIVG00037194001	AT2G46690.1-P	Auxin-responsive family protein; auxin-responsive family protein
7	GSVIVG00034466001	IAA19 AT3G15540.1-P	IAA19 (Indole-3-Acetic Acid Inducible 19); transcription factor
8	GSVIVG00031238001	AT2G36690.1-P	Oxidoreductase, 2OG-Fe(II) oxygenase family protein
9	GSVIVG00022326001	AT1G71090.1-P	Auxin efflux carrier family protein
10	GSVIVG00021917001	AT1G76680.2-P	OPR1; 12-oxophytodienoate reductase; Encodes a member of an alpha/ beta barrel fold family of FMN-containing oxidoreductases
11	GSVIVG00019364001	BRI1 AT4G39400.1-P	BRI1 (Brassinosteroid Insensitive 1); kinase
12	RD22-B <i>GSVIVG00016747001</i>	RD22 AT5G25610.1-P	RD22; nutrient reservoir; responsive to dehydration 22 (RD22) mediated by ABA
13	GSVIVG00031249001/ GSVIVG00031237001	AT2G44800/ AT4G10490	Oxidoreductase, 2OG-Fe(II) oxygenase family protein
14	GSVIVG00028908001/ GSVIVG00021916001/ GSVIVG00021911001/ GSVIVG00021908001	OPR2	Encodes one of two closely related 12-oxophytodienoic acid reductases
15	GSVIVG00023625001	GID1B	(GA INSENSITIVE DWARF1B); encodes a gibberellin (GA) receptor
16	GSVIVG00019408001	CPR5	CPR5 (Constitutive Expression of PR Genes 5); Regulator of expression of pathogenesis-related (PR) genes

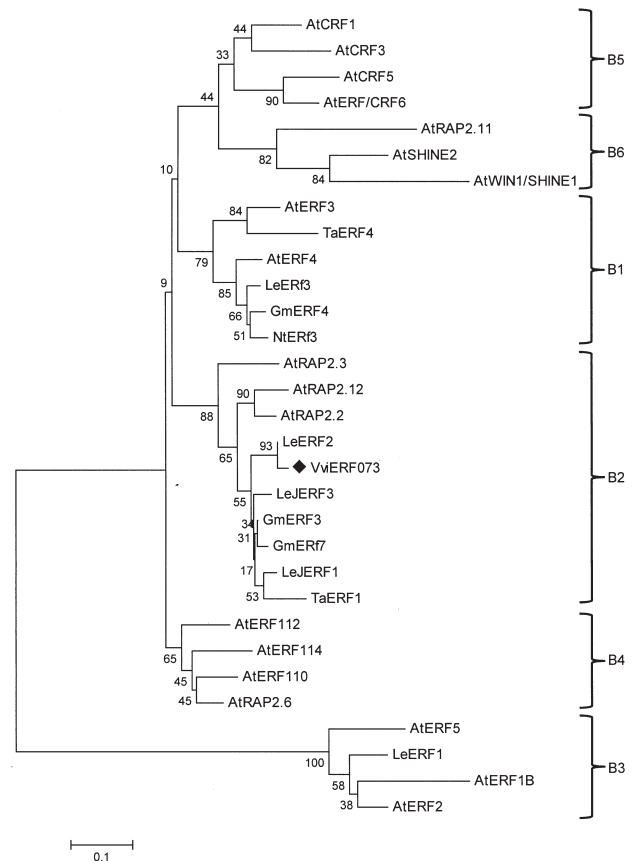
Supplementary Table 2

Details of candidate reference genes

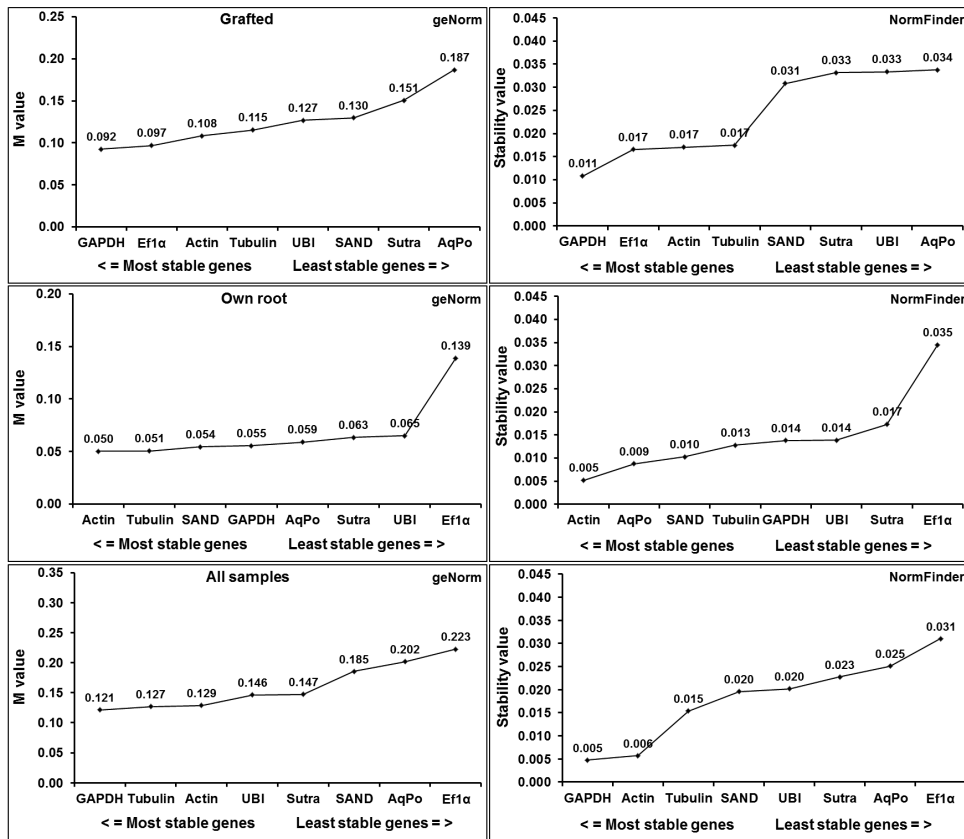
Gene name (abbreviation)	Primer sequence (5'-3')	PCR Efficiency	R ²
Glyceraldehyde 3-phosphate dehydrogenase (GAPDH)	F: TTC TCG TTG AGG GCT ATT CCA R: CCA CAG ACT TCA TCG GTG ACA	0.93	0.99
Actin 7/actin 2 (Actin)	F: CTT GCA TCC CTC AGC ACC TT R: TCC TGT GGA CAA TGG ATG GA	0.92	0.99
Aquaporin (AqPO)	F: TCC GCC AAG GAC TAT CAT GAC R: CGC AAT CAG AGC CCT GTA GAA	0.98	0.99
Elongation factor 1 α (EF1 α)	F: GAA CTG GGT GCT TGA TAG GC R: AAC CAA AAT ATC CGG AGT AAA AGA	1.0	0.99
Tubulin α 3/ α 5 chain (Tubulin)	F: CAG CCA GAT CTT CAC GAG CTT R: GTT CTC GCG CAT TGA CCA TA	1.0	0.98
SAND family protein (SAND)	F: CAA CAT CCT TTA CCC ATT GAC AGA R: GCA TTT GAT CCA CTT GCA GAT AAG	1.05	0.98
Sucrose transporter (Sutra)	F: GGA TAA CTT CCC TGC CTC AAT GA R: TTC TTG TAG CAG CTG AGA GGA TCA	0.96	0.99
Ubiquitine (UBI)	F: AGT AGA TGA CTG GAT TGG AGG T R: GAG TAT CAA AAC AAA AGC ATC G	0.97	0.99

1 TTCTTTCTGTGATCGAAGTCATTCTGAAGACTGAAGA
40 ATGTGTGGAGGTCTATCATCTCTGATTTCATACCTCGCAACCGGAACCCGCGGACCCA
1 M C G G A I I S D F I P R N R N R R D P
100 GCCCCAGACCTCTGGCCGACTCTTTCTTGCTAAACCCGATGGCTGTGAATACGATTTG
21 A P D L W P D S F F A K P D G C E Y D L
160 GGCCGCTTTAGCCAGAAGGGGCTTCTAATCTGAAAAGGTCTCAACCCATTTGGATGAT
41 G R F S Q K G L P N L K R S Q P I L D D
220 GAGCCAGAAGTGAAGCCGGCTAAGAGGGTGAGGAAGAATCTGTACAGGGGGATCCGGCAG
61 E P E V K P A K R V R K N L Y R G I R Q
280 CGTCCITGGGAAAATGGCCGCTGAGATTCTGATCCAGTAAAGGGGTTCCGGTTTGG
81 R P W G K W A A E I R D P S K G V R V W
340 CTCGGACCTTCAACACTGCGGAAGAAGCTGCGAGAGCTTACGACGAGGAGGCTCGGAAA
101 L G T F N T A E E A A R A Y D R E A R K
400 ATTCCGGGGAAGAAAGCAAAGTTAACTCCCAATGAAGACGATGACTACACTGAGAAT
121 I R G K K A K V N F P N E D D D Y T E N
460 CACCAAAATCACCGTCTCTACCAACTCGCTGGAATCCAATCCTTCTATTGTCAGCCC
141 H Q N H R A L P T R W N S N P S I C Q P
520 TATACCCCAAATTTCTCAAAAAGTTGGGTTTTGCTGATCACTTGAACAGATTGGAGCA
161 Y T P N F S K S L G F A D H L N Q I G A
580 TTCCCTCCAATGGGTTCAACACCGTTGGTCTATGAACGCTAACCCTGGTTGCTGTCACA
181 F P S N G F N T V G A M N A N P V A V T
640 ACCGAAGTGAATACGGCTCTGATTCGGAGTCTGTGATCCCTTCTCTGGATTGTGAAT
201 T E V K Y G S D S E S V Y P S S G L L N
700 TGCAATCAGAAAGCCTGTGTTGGGAAAGTGA AAAATCAGAAAGAGAACCAACAGAGACT
221 C N Q K A C V G K V K N Q K E N Q T E T
760 GTGACGGAAGCTGAGAAGGAGGAAATGGAAGTGCAGAAGCTGTCGGAGGAGCTAATGGCC
241 V T E A E K E E M E V Q K L S E E L M A
820 TATGAGTCGGTCATGAAGTTCTATCAGATCCCTATCTGACGGCAACTCAGCCGCGGT
261 Y E S V M K F Y Q I P Y L D G N S A A V
880 CCCAAGCTGCTCAGGAAAATGCTGGTGTCTGCGGTGGTGTGCCATGGAAAGCTCTTGG
281 P N A A Q E N A G A C G G A A M E A L W
940 AGCTTTGATGAATTTGAGTTGCTCTCAACCCACCTCAGCTGCTCTATAA
301 S F D E F A V A P Q P T S A A L *

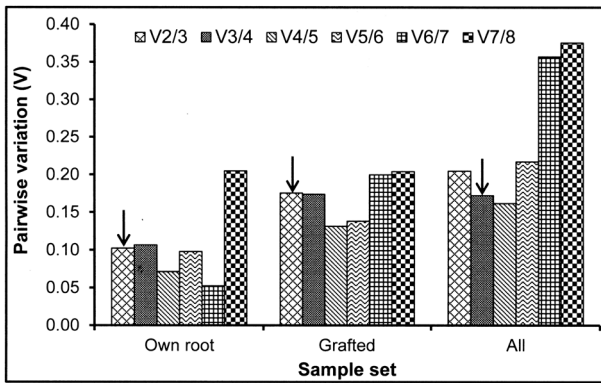
Supplementary Fig. 1: DNA sequence and deduced polypeptide sequence of *VviERF073*. The conserved ERF domain is shown with shaded background. Conserved N terminal sequence characteristic of B2 group is underlined.



Supplementary Fig. 2: Phylogeny analysis based on full length protein sequences. *VviERF073* grouped with ERF proteins of B2 group.



Supplementary Fig. 6: Expression stability and ranking of reference genes in different sample sets based on geNorm and NormFinder.



Supplementary Fig. 7: Pairwise variation of reference genes in different sample sets. Arrow indicates the optimal number of genes selected for data normalization.