

Supplementary Information

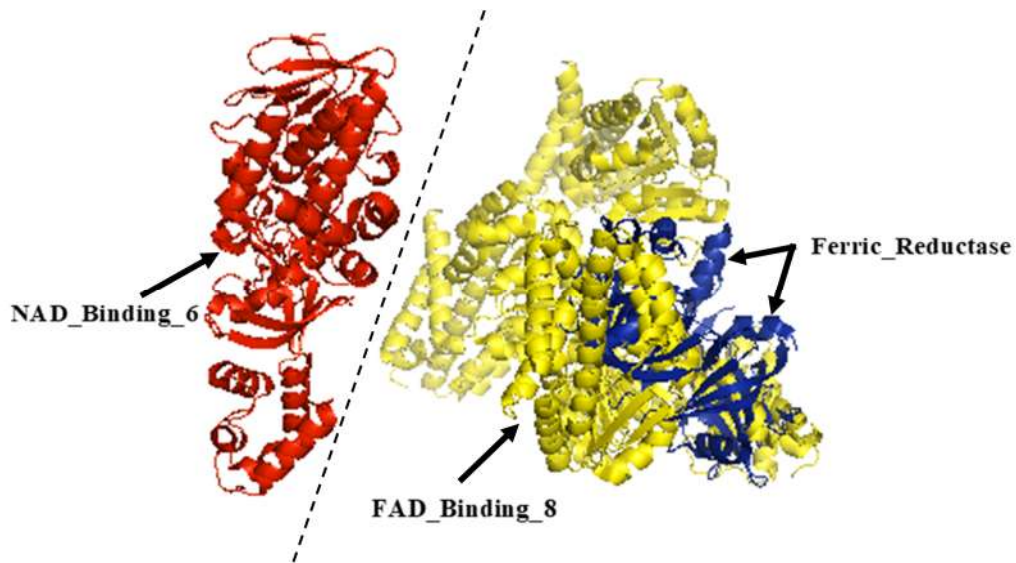
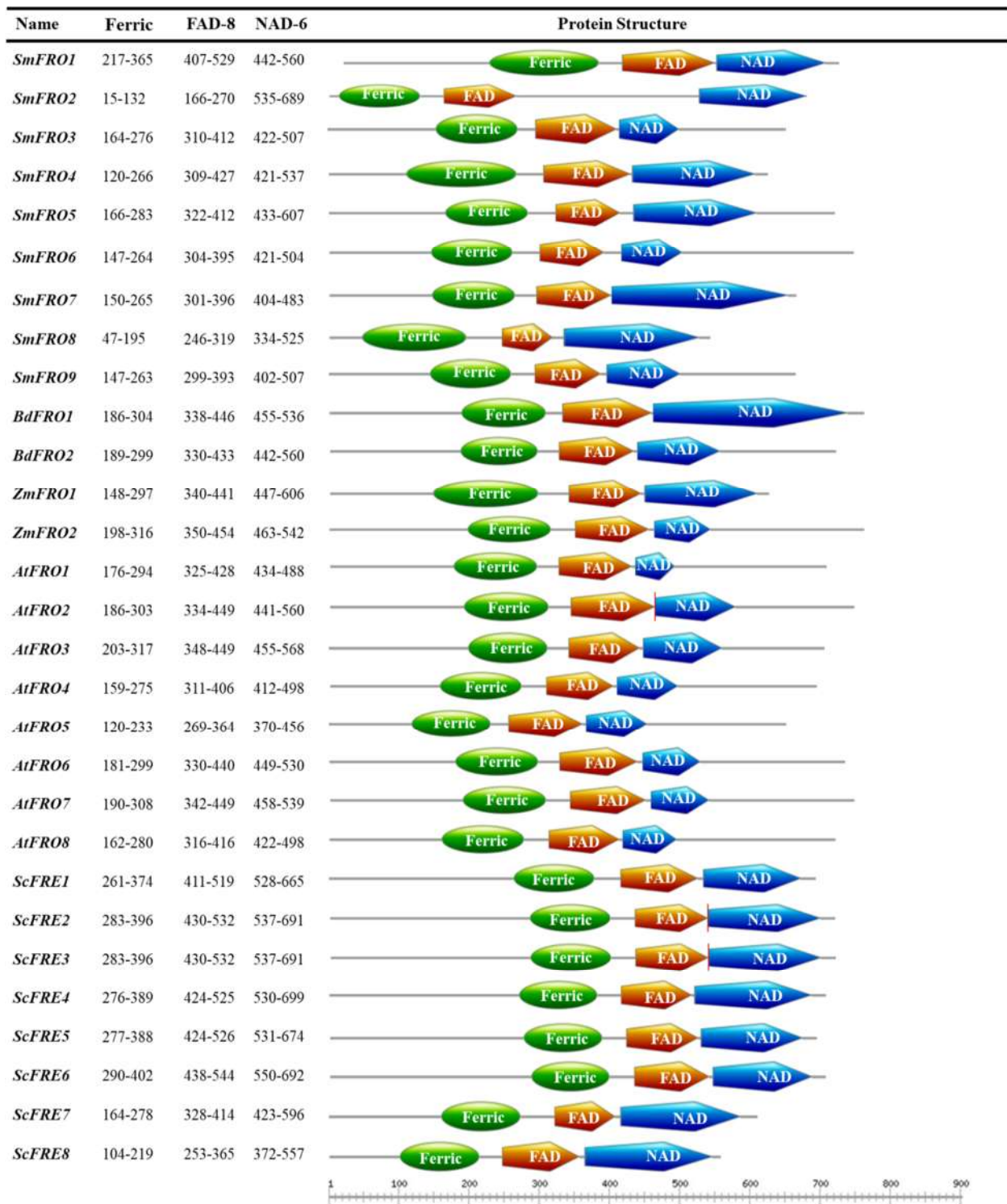


Figure S1. 3D general representation of functional domains, Red represents NAD_binding_6 domain, the Yellow represents the FAD_binding_8 domain and the Blue represents the Ferric_Reductase domain. Moreover, the Ferric_reductase and FAD_bing_8 domains (Blue+Yellow) are more highly conserved domains which are closer to each other in FRO gene families.



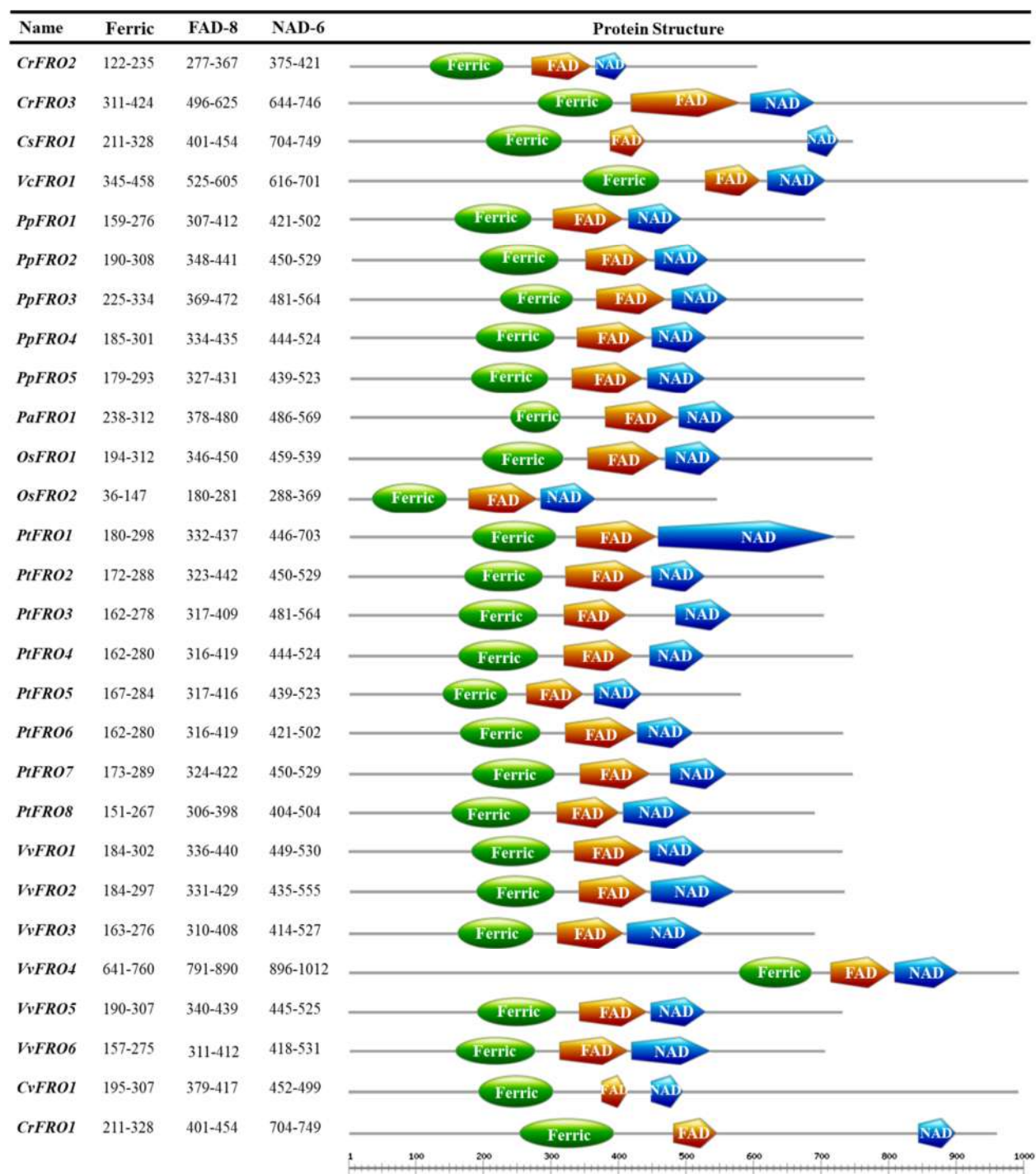


Figure S2. The Structure of the FRO proteins, Numbers indicate amino acid position of the corresponding conserved domains. The green, orange and blue ovals and pentagons indicate the Ferric means (Ferric-reductase), FAD means (FAD-binding-8), and NAD means (NAD-binding-6 domain), respectively, the scale bar represents the number of amino acids coded by each gene.

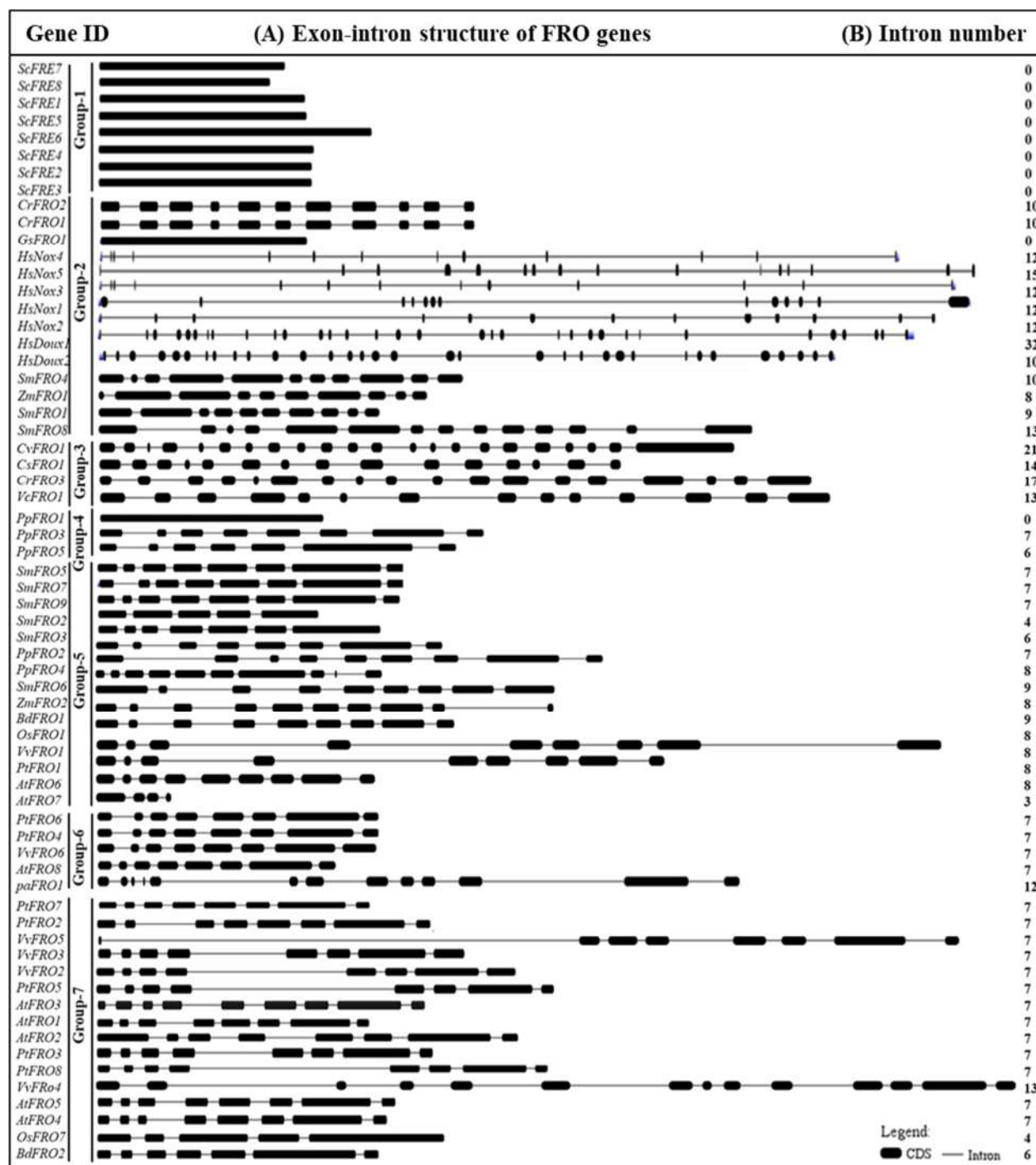
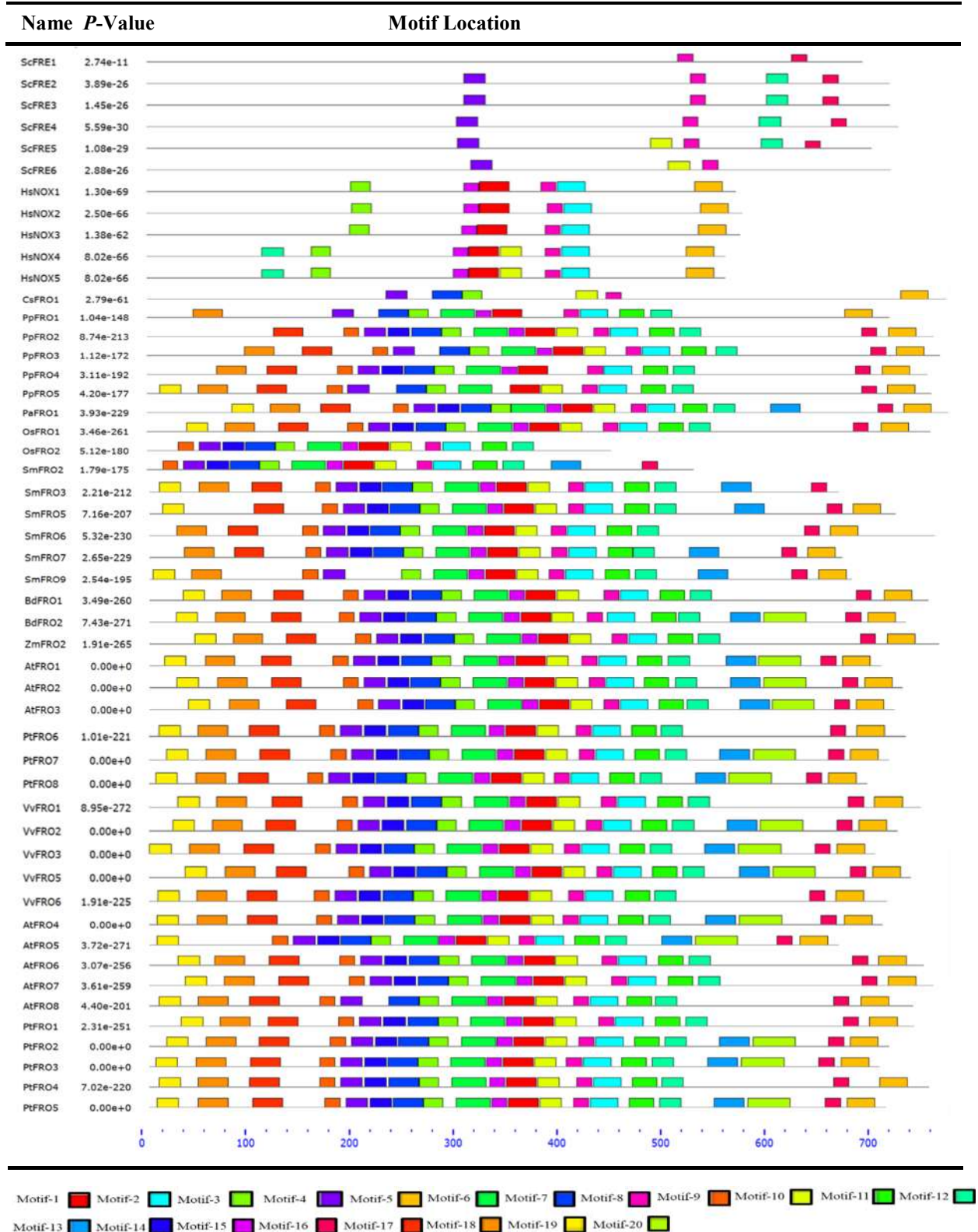


Figure S3. The exon/intron structures of FRO family genes. The structure of individual *FRO* gene was obtained through the Gene Structure Display Server (<http://gsds.cbi.pku.edu.cn>) by aligning the coding or cDNA sequences with their corresponding genomic DNA sequence. Black boxes represent exons and black lines represent introns. (B) represents intron numbers of each gene contained.

Site of amino acids and motif location of FROs protein



Schematic diagram of amino acid motifs of FRO, s proteins

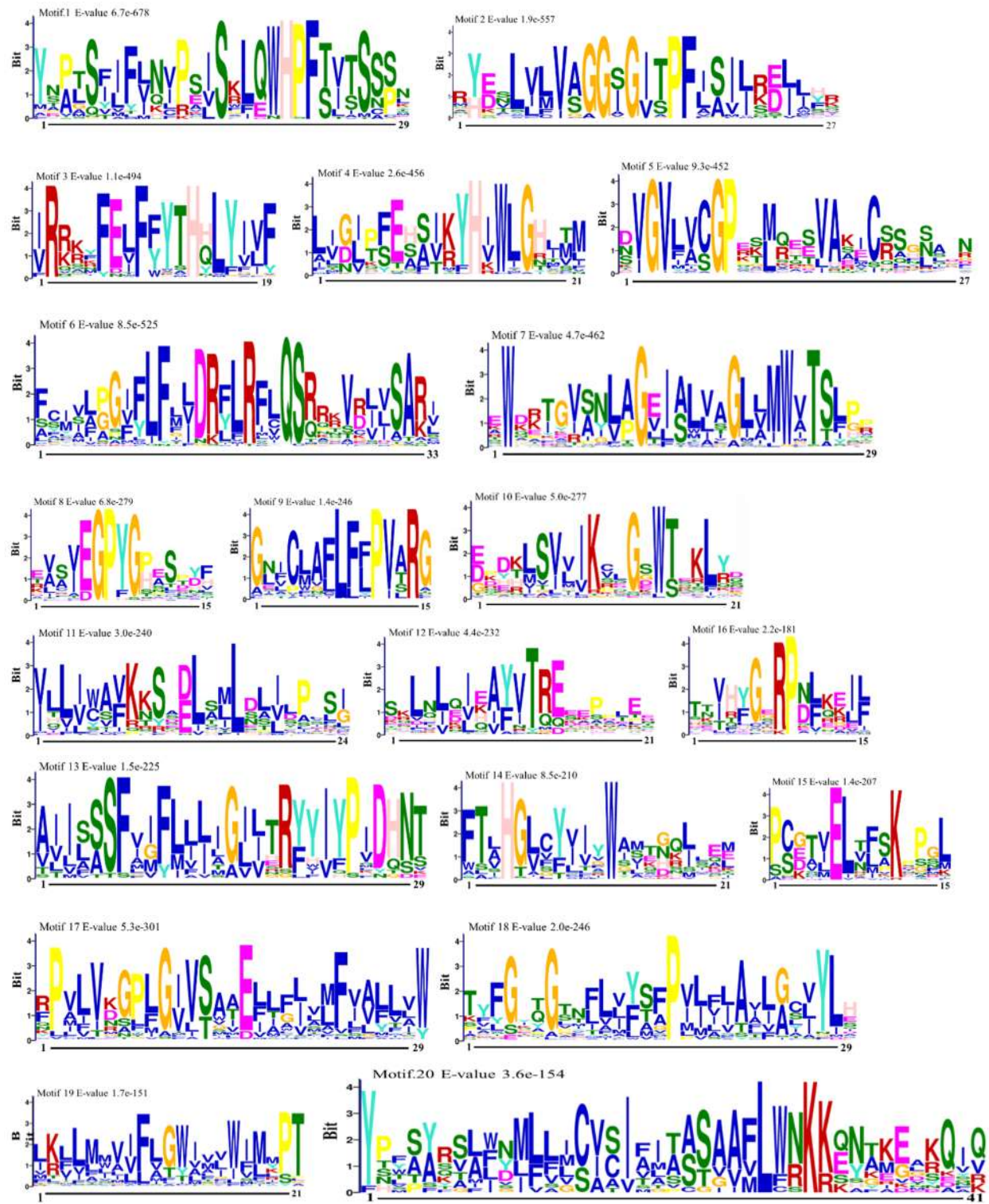


Figure S4. Phylogenetic relationships and schematic diagram of amino acid motifs of FRO, s proteins. The number of nodes represent the bootstrap value.

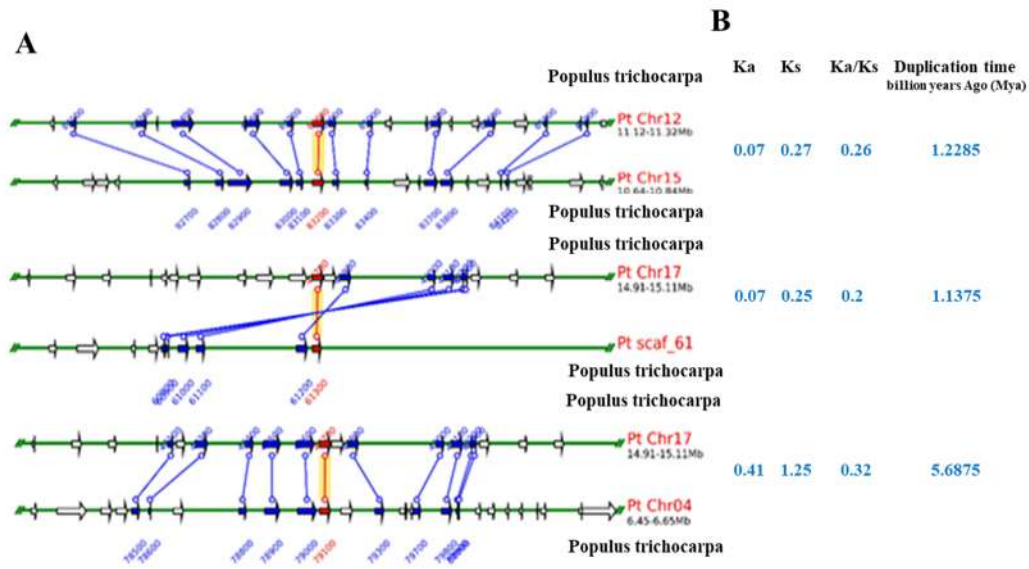


Figure S5. The non-synonymous (Ka) and synonymous (Ks) were estimated for the paralogous gene pairs of FRO family genes. Genome Duplication Database, Divergence time (T, million years ago, Mya) for each paralogous gene pair was calculated using the average Ks of λ substitutions of *Populus trichocarpa* per synonymous sites per year as $T = Ks/2\lambda$ ($\lambda = 9.1 \times 10^{-9}$)

Supplementary Tables

Table S1. Detail of Plant Genomes Analyzed in This Study

Species	Genome size (Mbp)	Database
<i>Homo sapiens</i>	3400	http://asia.ensembl.org/Homo_sapiens/Info/Index
<i>Arabidopsis thaliana</i>	157	http://www.arabidopsis.org/
<i>Oryza sativa</i>	430	http://rice.plantbiology.msu.edu/index.shtml
<i>Zea mays</i>	2,400	http://www.maizesequence.org/index.html
<i>Brachypodium distachyon</i>	355	http://www.phytozome.net/brachy.php
<i>Selaginella moellendorffii</i>	110	http://genome.jgipsf.org/Selmo1/Selmo1.home.html
<i>Populus trichocarpa</i>	500	http://genome.jgi-psf.org/Poptr1_1/Poptr2_2.home.html
<i>Vitis vinifera</i>	500	http://www.genoscope.cns.fr/externe/GenomeBrowser/Vitis/
<i>Physcomitrella patens</i>	500	http://genome.jgi-psf.org/Phypa1_1/Phypa1_1.home.html
<i>Volvox carteri</i>	140	http://genome.jgi-psf.org/Volca1/Volca1.info.html
<i>Coccomyxa subellipsoidea C-169</i>	48.82	http://genome.jgipsf.org/Coc_C169_1/Coc_C169_1.home.html
<i>Chlamydomonas reinhardtii</i>	120	http://genome.jgi-psf.org/Chlre4/Chlre4.info.html
<i>Chlorella variabilis NC64</i>	46.15	http://genome.jgi-psf.org/ChlNC64A_1/ChlNC64A_1.home.html
<i>Picea abies</i>	20,480	http://congenie.org/start
<i>Saccharomyces cerevisiae</i>	12	http://www.yeastgenome.org/download-data
<i>Galdieria sulphuraria</i>	13.7	http://genomics.msu.edu/galdieria/

The detail information about physiochemical characteristics of FRO Gene families

Gene name	Gene locus ID	CDS length	PI	M.W (KDa)	pIs	Ii	Ai	Major amino acids	GRAY
SmFRO1	e_gw1.0.1110.1	2136	711	80.96	8.96	44.51	82.88	L (9.6%), A (8.3%), S (7.6)	-0.122
SmFRO2	e_gw1.39.66.1	1590	529	60.33	9.54	36.32	102.63	I (9.8%), L (9.1%), V (7.8%)	0.209
SmFRO3	e_gw1.45.93.1	1992	663	74.93	9.59	35.68	105.44	L (12.2%), A (8.1%), V (8.0%)	0.337
SmFRO4	estExt_fgenes1_pm	1878	625	71.59	9.27	38.37	90.59	L (9.3%), V (8.3%), G (6.6%)	-0.024
SmFRO5	estExt_fgenes2_pg	2157	718	80.32	9.30	40.55	105.58	L (11.1%), A (9.9%), I (8.2%)	0.291
SmFRO6	estExt_fgenes2_pg	2271	756	84.38	8.74	39.68	108.28	L (13.2%), V (8.7%), S (7.7%)	0.399
SmFRO7	estExt_Genewise1	2004	667	74.65	9.43	39.45	107.06	L (11.7%), V (10.2%), S (8.1%)	0.349
SmFRO8	fgenes1_pm	1628	542	61.89	9.43	39.25	94.78	L (10.7%), V (8.1%), A (7.2%)	0.160
SmFRO9	gw1.9.156.1	2028	676	76.91	9.26	42.02	103.98	L (10.2%), V (8.3%), I (8.3%)	0.270
BdFRO1	Bradi5g11147.1	2253	758	81.68	7.01	38.74	104.17	L (12%), A (10.7%), G (8.8%)	0.410
BdFRO2	Bradi5g19150.1	2187	735	80.15	9.15	40.28	102.45	L (12.9%), A (8.8%), S (8.8%)	0.330
ZmFRO1	GRMZM2G089291-T01	2517	624	71.15	9.36	41.81	93.24	L (9.3%), V (8.2%), I (6.9%)	0.090
ZmFRO2	GRMZM2G068557-T01	2926	760	84.04	7.93	41.44	103.91	L (12.4%), A (9.3%), V (9.6%)	0.398
AtFRO1	AT1G01590.1	2642	704	79.60	9.56	41.78	105.04	L (10.9%), S (10.8%), V (7.7%)	0.311
AtFRO2	AT1G01580.1	2635	725	81.50	9.37	39.61	101.81	L (11.3%), S (10.6%), I (9.1%)	0.253
AtFRO3	AT1G23020.1	2154	717	80.93	9.79	38.06	106.03	L (12.0%), S (11.2%), I (8.8%)	0.328
AtFRO4	AT5G23980.1	2337	699	80.25	9.44	39.86	101.86	L (12.0%), S (9.9%), V (7.6%)	0.183
AtFRO5	AT5G23990.1	1974	657	74.89	8.94	42.62	94.73	L (10.2%), S (10.2%), V (7.6%)	0.098
AtFRO6	AT5G49730.1	2675	738	83.45	7.94	37.76	113.37	L (13.1%), S (8.8%), V (8.7%)	0.431
AtFRO7	AT5G49740.1	2640	747	84.12	6.82	35.17	112.52	L (13.0%), V (9.4%), S (9.0%)	0.432
AtFRO8	AT5G50160.1	2520	728	83.23	9.58	47.28	110.05	L (13.0%), I (8.5%), S (7.8%)	0.281
PtFRO1	Potri.001G079000.1	2190	729	81.80	6.68	39.45	112.78	L (13.3%), S (8.9%), V (8.4%)	0.417
PtFRO2	Potri.004G079100.1	2118	705	79.45	9.34	43.35	101.53	L (11.5%), S (11.2%), I (8.4%)	0.243
PtFRO3	Potri.004G079200.1	2091	696	79.30	9.30	41.66	104.48	L (12.5%), S (9.2%), V (7.3%)	0.314
PtFRO4	Potri.012G084800.1	2232	743	83.14	9.48	47.71	112.45	L (12.8%), S (10.0%), V (7.3%)	0.394

PtFRO5	Potri.014G088000.1	2109	702	78.44	9.64	34.56	107.22	L (13.0%), S (9.8%), I (8.3%)	0.334
PtFRO6	Potri.015G083200.1	2169	722	81.10	9.43	47.48	107.76	L (12.7%), S (10.4%), I (8.2%)	0.296
PtFRO7	Potri.017G142700.1	2121	706	79.09	9.10	45.01	104.55	L (12.2%), S (10.9%), I (7.8%)	0.328
PtFRO8	Potri.017G142800.1	2058	685	78.05	9.29	41.95	105.58	L (12.8%), S (8.9%), V (7.4%)	0.311
VvFRO1	GSVIVT01023105001	2483	735	83.33	6.24	44.62	113.57	L (13.5%), S (8.4%), V (8.0%)	0.455
VvFRO2	GSVIVT01026991001	2325	714	79.56	9.68	40.87	106.90	L (13.0%), S (10.5%), I (7.6%)	0.277
VvFRO3	GSVIVT01026993001	2264	693	77.42	9.45	40.82	107.89	L (14.1%), S (10.4%), I (6.9%)	0.306
VvFRO4	GSVIVT01028873001	3617	1178	130.07	9.41	37.52	107.21	L (12.7%), S (9.8%), A (8.2%)	0.475
VvFRO5	GSVIVT01028874001	2184	727	81.90	9.02	41.68	104.06	L (12.8%), S (10.0%), V (7.0%)	0.295
VvFRO6	GSVIVT01007662001	2342	703	79.79	9.34	47.48	106.09	L (12.5%), S (8.5%), I (8.2%)	0.290
OsFRO1	LOC_Os04g36720.1	1440	525	65.7481	9.34	48.28	110.32	L (11.8%), S (11.6%), A (9.1%)	0.252
OsFRO7	LOC_Os04g48930.1	2277	759	48.4685	9.72	57.52	95.07	L (13.8%), V (10.3%), A(10.1%)	0.060
ScFRE1	YLR214W(FRE1)	2061	686	78.877	9.49	52.16	91.77	L (9.3%), S (9.1%), V (7.6%)	0.448
ScFRE2	YKL220C (FRE2)	2136	711	80.0722	9.21	30.33	94.21	L (10.0%), A (7.9%), S (7.0%)	0.129
ScFRE3	YOR381W(FRE3)	2136	711	80.5892	6.66	35.83	94.75	L (10.3%), A (7.6%), G (7.0%)	0.152
ScFRE4	YNR060W(FRE4)	2160	719	82.0153	9.26	30.27	94.02	L (10.4%), A (8.1%), I (7.0%)	0.044
ScFRE5	YOR384W(FRE5)	2085	694	80.2923	8.83	37.32	96.37	L (10.8%), I (7.2%), K (6.9%)	0.025
ScFRE6	YLL051C (FRE6)	2139	712	81.9892	9.06	33.75	103.65	L (11.7%), I (9.4%), S (8.7%)	0.153
ScFRE7	YOL152W(FRE7)	1863	620	70.9053	8.86	42.47	97.60	L (9.5%), I (9.0%), S (8.7%)	0.102
ScFRE8	YGL160W(FRE8)	1713	570	65.8400	8.88	43.99	102.46	I (10.0%), S (9.3%), L (12.5%)	-0.040
HsNOX1	ENSP00000362057	1695	564	64.8710	8.79	39.69	89.70	L (10.1%), S (8.0%), F (7.4%)	0.022
HsNOX2	ENSP00000367851	1713	570	65.3359	8.90	34.69	93.72	V (7.4%), L (10.0%), F (6.8%)	0.049
HsNOX3	ENSP00000159060	1707	568	64.9349	8.28	41.18	92.39	L (10.9%), A (7.7%), S (7.2%)	0.089
HsNOX4	ENSP00000263317	1656	578	64.1022	8.94	45.56	89.53	L (12.3%), S (7.8%), F(6.7%)	-0.081
HsNOX5	ENSP00000260364	1665	554	64.1022	8.94	45.56	89.53	L (12.3%), S (7.8%), F (6.7%)	-0.081
HsDUOX1	ENSP00000317997	4656	1551	177.235	8.12	47.83	88.56	L (11.6%), R(7.9%), S (7.5)	-0.190
HsDUOX2	ENSP00000267837	4670	1548	175.364	8.02	46.85	89.68	L (11.8%), G (7.0%), S (6.8%)	-0.148
CvFRO1	estExt_fgenes3_pg	3364	1123	123.931	9.69	48.36	88.76	A (11.6%), L (10.9%), G (8.4%)	0.073
CrFRO2	Cre03.g188400.t1.1	1863	620	67.6035	6.54	40.95	90.37	A (12.7%), L (9.5%), G (8.1%)	0.102
CrFRO3	Cre04.g227400.t1.2	3264	1087	114.566	9.85	44.41	88.39	A (15.3%), L (10.2%), (9.1%)	0.215
CsFRO1	estExt_Genemark1	2322	773	85.2232	7.69	43.80	106.64	L (15.5%), A (10.0%), G (8.2%)	0.290
VcFRO1	Vocar20008902m	2994	998	107.129	9.95	48.36	91.57	L (12.6%), S (11.3%), A (11.2%)	0.129
PpFRO1	Pp1s14_322V6.1	2157	718	80.8249	9.28	41.18	111.45	L (11.8%), I (8.2%), V (7.9%)	0.384
PpFRO2	Pp1s39_125V6.1	2286	761	85.1266	6.71	38.11	102.48	L (12.9%), S (8.5%), V (7.9%)	0.229
PpFRO3	Pp1s54_173V6.1	2304	767	85.6383	9.03	42.48	94.05	V (8.6%), A (8.1%), L (9.1%)	0.163
PpFRO4	Pp1s663_3V6.1	2268	755	84.7296	8.54	39.70	103.02	L (12.2%), S (8.6%), V (7.9%)	0.302
PpFRO5	Pp1s90_3V6.	2283	760	84.5003	8.76	38.48	100.26	L (11.6%), V (9.6%), G (8.0%)	0.274
PaFRO1	MA_76199g0010	2328	775	87.8788	9.35	38.05	103.59	L (12.4%), S (9.4%) V (7.5%),	0.157

Table S2. Abbreviations: MW, molecular weight; Pl, protein length; pIs, isoelectric point; Ii, index instability; Ai, aliphatic index; GRAVY, grand average of hydropathicity; (A, Ala; P, Pro; S, Ser; G, Gly; L, Leu;N, ASN; T,Thr).The data source of each specie is list in table 2, whereas the information about protein was taken from ExPASy (<http://web.expasy.org/protparam/>)

Table S3. Motif sequences identified by MEME tools

Motif	Sites	Width	E-value	Multilevel consensus sequence
1	43	29	6.7e-678	YNPTSIFVNCPSISKLQWHPFTVTSSPN
2	43	27	1.9e-557	RYENLVMVAGGIGITPFISIIRDIIYR
3	44	19	1.1e-494	IRKRYFELFYTHHLYIVF
4	44	21	2.6e-456	LIDIPFEHSIKYHIWLGHMMM
5	41	27	9.3e-452	DVGVLVCGPEKMQUEEVAKECRSHNADN
6	38	33	8.5e-525	FCMVLPGIFLFMIDRFLRFCQSRKVDIVSARC
7	38	29	4.7e-462	EWDRGTGVANLAGEIALVAGLVMWVTSLPP
8	50	15	6.8e-279	EVCVEGPGYPESDYF
9	37	15	1.4e-246	GNICMAFLFFPVARG
10	41	21	5.0e-277	DDDKMSVVIKCQGDWTQKLYD
11	38	24	3.0e-240	VHLICAVKKSDDLCLDLIDPQSI
12	44	21	4.4e-232	SQLNLQIEAYVTREEEPDTE
13	20	29	1.5e-225	AISSSFVMFMLIIGHITRYIYPIDHNT
14	33	21	8.5e-210	FTAHGLCYIYWAMTNQIQEM
15	42	15	1.4e-207	PCDTVELNFSKPPGL
16	41	15	2.2e-181	TNVHYGCRPNFKEIF
17	33	29	5.3e-301	RPVLVDGPLGIVSAAEFLFIMMFVALLVW
18	33	29	2.0e-246	TYFGYQGTNFLVYSFPMMFIAVLGCVYLH
19	30	21	1.7e-151	LKFLMMVIFLGMVWIMMPT
20	14	41	3.6e-154	YPYSYRSAWNMLLMCVCIATASAAFLWNKKQNTKEDKQIQ

Table-S4: Genomic Information of FRO genes

Gene Name	Translation ID	Sequence Position	Full length Chr	Chr	Orientation
<i>VvFRO1</i>	GSVIVT01023105001	22531017-22539454	22702307	12	Forward
<i>VvFRO2</i>	GSVIVT01026991001	18754824-18759433	20304914	15	Reverse
<i>VvFRO3</i>	GSVIVT01026993001	18731174-18734997	20304914	15	Reverse
<i>VvFRO4</i>	GSVIVT01028873001	17920090-17930273	22053297	16	Reverse
<i>VvFRO5</i>	GSVIVT01028874001	17911251-17919834	22053297	16	Reverse
<i>VvFRO6</i>	GSVIVT01007662001	10745402-10748530	17126926	17	Forward
<i>PaFRO1</i>	MA_76199g0010	18853-25876	33200	18	Forward
<i>OsFRO1</i>	LOC_Os04g36720.1	22182599-22186943	35502694	4	Forward
<i>OsFRO2</i>	LOC_Os04g48930.1	29178862-29181665	35502694	4	Reverse
<i>ZmFRO1</i>	GRMZM2G089291_T01	88970062-88974958	307041717	1	Reverse
<i>ZmFRO2</i>	GRMZM2G068557_T01	46785444-46790374	244442276	2	Reverse
<i>BdFRO1</i>	Bradi5g11147.1	14832325-14837374	28563423	5	Reverse
<i>BdFRO2</i>	Bradi5g19150.1	22305120-22308896	28563423	5	Reverse
<i>CrFRO1</i>	Cre03.g188300.t1.1	5747176-5751750	9200000	3	Forward
<i>CrFRO2</i>	Cre03.g188400.t1.1	5753406-5758534	9200000	3	Forward
<i>CrFRO3</i>	Cre04.g227400.t1.2	3355079-3363615	4000000	4	Forward
<i>SmFRO1</i>	e_gw1.0.1110.1	3570486-3573210	6,951,972	Sca_0	Forward
<i>SmFRO2</i>	e_gw1.39.66.1	1077630-1079463	1,708,524	Sca_39	Forward
<i>SmFRO3</i>	e_gw1.45.93.1	1271397-1273747	1,506,775	Sca_45	Reverse
<i>SmFRO4</i>	estExt_fgenes1_pm	237856-240422	266977	Sca_7	Reverse
<i>SmFRO5</i>	estExt_fgenes2_pg	1890551-1893253	3,093,912	Sca_10	Reverse
<i>SmFRO6</i>	estExt_fgenes2_pg	1191056-1194130	1,266,795	Sca_59	Forward
<i>SmFRO7</i>	estExt_Genewise1.	1893670-1896353	3,093,912	Sca_10:	Reverse
<i>SmFRO8</i>	fgenes1_pm	59562-61662	235874	Sca_101	Forward
<i>SmFRO9</i>	gw1.9.156.1	889190-891684	3150000	Sca_9	Forward
<i>VcFRO1</i>	Vocar20008902m	13806643-13818846	14100000	Sca_1	Reverse
<i>CsFRO1</i>	estExt_Genemark1.C_30426	2251468-2257154	3000000	Sca_3	Forward
<i>CvFRO1</i>	estExt_fgenes3_pg.C_60163	1277608-1284529	2000000	Sca_6	Reverse

Table-S4: Genomic Information of genes Cont.....

Gene Name	Translation ID	Sequence Position	Full length Chr	Chr	Orientation
<i>ScFRE1</i>	YLR214W (FRE1)	568567-570627	1078177	12	Forward
<i>ScFRE2</i>	YKL220C (FRE2)	9091-11226	666816	11	Reverse
<i>ScFRE3</i>	YOR381W (FRE3)	1055545-1057680	1091291	15	Forward
<i>ScFRE4</i>	YNR060W (FRE4)	739951-742110	784333	14	Forward
<i>ScFRE5</i>	YOR384W (FRE5)	1061564-1063648	1091291	15	Forward
<i>ScFRE6</i>	YLL051C (FRE6)	37333-39471	1078177	12	Reverse
<i>ScFRE7</i>	YOL152W (FRE7)	40748-42610	1091291	15	Forward
<i>ScFRE8</i>	YGL160W (FRE8)	239347-241407	1078177	12	Forward
<i>AtFRO1</i>	AT1G01590.1	214150 - 217734	30427671	1	Forward
<i>AtFRO2</i>	AT1G01580.1	209208 - 213080	30427671	1	Forward
<i>AtFRO3</i>	AT1G23020.1	209208 - 213080	30427671	1	Forward
<i>AtFRO4</i>	AT5G23980.1	8097978 - 8101330	26975502	5	Reverse
<i>AtFRO5</i>	AT5G23990.1	8105565 - 8108590	26975502	5	Reverse
<i>AtFRO6</i>	AT5G49730.1	20201037 - 20204595	26975502	5	Reverse
<i>AtFRO7</i>	AT5G49740.1	20205302 - 20208777	26975502	5	Reverse
<i>AtFRO8</i>	AT5G50160.1	20415764 - 20418847	26975502	5	Forward
<i>PtFRO1</i>	Potri.001G079000.1	6257724 - 6264650	48367220	1	Reverse
<i>PtFRO2</i>	Potri.004G079100.1	6550267 - 6553701	23188140	4	Reverse
<i>PtFRO3</i>	Potri.004G079200.1	6557306 - 6561136	23188140	4	Reverse
<i>PtFRO4</i>	Potri.012G084800.1	11220313 - 11224179	14929429	12	Forward
<i>PtFRO5</i>	Potri.014G088000.1	6946787 - 6951800	17716633	14	Reverse
<i>PtFRO6</i>	Potri.015G083200.1	10742214 - 10745893	15134944	15	Forward
<i>PtFRO7</i>	Potri.017G142700.1	15005978 - 15009498	14661173	17	Reverse
<i>PtFRO8</i>	Potri.017G142800.1	15009803 - 15013806	14661173	17	Reverse
<i>PpFRO1</i>	Pp1s14_322V6.1	13113522 - 13118092	19500000	6	Forward
<i>PpFRO2</i>	Pp1s39_125V6.1	480603 - 485383	17500000	11	Reverse
<i>PpFRO3</i>	Pp1s54_173V6.1	1325642 - 1330056	5300000	27	Reverse
<i>PpFRO4</i>	Pp1s663_3V6.1	7326760 - 7332442	16500000	16	Forward
<i>PpFRO5</i>	Pp1s90_3V6.1	22657 - 27233	17800000	9	Reverse

Table S5. The cis-elements regulatory elements in the promoter region of OsFRO1& OsFRO7 gene

Cis-elements	Core sequences	Functions of the cis-elements	Position Strand
LOC_Os04g48930 (OsFRO1)			
ABRE	AGTACGTGGC	cis-acting element involved in the abscisic acid responsiveness	1255+
GC-motif	AGCGCGGCC	Unknown	1200+
P-box	CCTTTTG	gibberellin-responsive element	1375+
Skn-1-motif	GTCAT	cis-acting regulatory element required for endosperm expression	720+
Sp1	GGGCGG	light responsive element	358-
Sp1	GGGCGG	light responsive element	1141+
Motif-IIb	CCGCCGCGCT	abscisic acid responsive element	1200-
TATA -box	TACAAAA	core promoter element around -30 of transcription start	716-
Plant-Ap-2-Like	CGCGCCGG	Unknown	198+
LOC_Os04g36720 (OsFRO7)			
P-box	CCTTTTG	gibberellin-responsive element	86-
Skn-1-motif	GTCAT	cis-acting regulatory element required for endosperm expression	425+
TATA -box	TACAAAA	core promoter element around -30 of transcription start	384_
GC-motif	GCCGCGCG	Unknown	1200+

Table. S6: The detailed list of primers used for expression analysis

Primers used for semi-quantitative RT-PCR analysis.			
Gene	Primer (5'→3')	Product size	Exon No
<i>OsFRO1 Forward</i>	ATTGTGACAGGCATAGAACTCG	333 bp	1
<i>OsFRO1 Reverse</i>	GACTGGAAAGAAGACAGGAACG		
<i>OsFRO7 Forward</i>	GCCTGCTAATGTGGGTGAC	273 bp	1
<i>OsFRO7 Reverse</i>	GGAGACTTGCTGGCTTTGA		
<i>OsActin1 Forward</i>	CAGCACATTCCAGCAGATGT	198 bp	2
<i>OsActin1 Reverse</i>	TAGGCCGGTTGAAAAC TTG		
Primers used for real-time qRT-PCR analysis			
Gene	Primer (5'→3')	Product size	Exon No
<i>OsFRO1 Forward</i>	TCCTGTTCTTTCCAGTCGC	284 bp	1
<i>OsFRO1 Reverse</i>	GTTCTTGTCATTTTCAGCATCT		
<i>OsFRO7 Forward</i>	CTGGCATTTTCACGTTGGC	271 bp	1
<i>OsFRO7 Reverse</i>	CGGAGACTTGCTGGCTTTG		
<i>OsActin1 Forward</i>	GTGGTCGCCCCCTCCTGAAAG	198 bp	2
<i>OsActin1 Reverse</i>	GGCTTAGCATTCTTGGGTCCG		