

**Table S1.** Primers used for RT-qPCR analysis.

<b>Gene</b>	<b>transcript ID</b>	<b>Forward primer</b>	<b>Reverse primer</b>
<i>OsMRP15</i>	<i>OS06T0158900</i>	GATACAATCTAGACCCCCTTG	CAACAAGTGAATCCAATCCCTG
<i>OsGSTU34</i>	<i>OS10T0395400</i>	GATGAGCCCGTTCACGAT	AACTTGTCATCTATGTAGGCGG
<i>OsMATE3</i>	<i>OS01T0766000</i>	TGGCTTGCTCTGCTCTATATG	GATGAGGAACTGGAAGATCTCC
<i>OsMATE34</i>	<i>OS08T0562800</i>	GAGTTGCACTTCAAACACTCAT	CTCCTTGTAAGAGAGGTTTGGT
<i>OsActin-1</i>	<i>Os03T0718100</i>	GAGTATGATGAGTCGGGTCCAG	ACACCAACAATCCCAAACAGAG

**Table S2.** Physiochemical property of MATE proteins.

Plant species	gene	Accession No / ID /AGI code	Chr	Exon count	MW (KDa)	A.A	PI	AI	II	GRAVY
<i>Vitis vinifera</i>	VvMate1	XP_002282932.1	12	8	54.90	504	8.38	127.72	24.67	0.809
<i>Vitis vinifera</i>	VvMATE2	XP_002282907.1	12	8	54.41	506	6.99	133.95	23.91	0.887
<i>Medicago truncatula</i>	MtMATE1	ACX37118.1	5	9	54.89	504	6.50	128.85	23.53	0.859
<i>Brassica rapa</i>	BrTT12	ACJ36213.1	7	8	55.17	507	8.36	124.02	28.40	0.752
<i>Arabidopsis thaliana</i>	AtTT12	At3g59030.1	3	8	55.15	507	8.36	120.18	30.21	0.745
<i>Fragaria ananassa</i>	FaTT12	AUA60209.1			55.01	506	5.51	126.01	27.69	0.806
<i>Malus domestica</i>	MdMATE1	ADO22709.1/ GU064953.1	9	7	55.12	505	6.52	125.70	25.28	0.799
<i>Malus domestica</i>	MdMATE2	ADO22711.1/ GU064955	17	7	55.97	514	6.99	123.72	24.37	0.761
<i>Oryza sativa</i>	OsMATE55	LOC_Os12g42130.1	12	8	54.10	500	6.32	128.36	25.35	0.848
<i>Oryza sativa</i>	OsMATE15	LOC_Os03g37640.1	3	7	53.62	500	6.52	119	32.30	0.763
<i>Oryza sativa</i>	OsMATE13	LOC_Os03g37470.1	3	6	37.35	350	7.52	120.97	23.60	0.881
<i>Raphanus sativus</i>	RsMATE2	MF360948	5	7	55.04	505	5.18	117.80	27.62	0.708
<i>Oryza sativa</i>	OsMATE14	LOC_Os03g37490.1	3	7	55.79	520	5.24	114.21	30.58	0.731
<i>Oryza sativa</i>	OsMATE12	LOC_Os03g37411.1	3	7	53.84	500	6.98	114.52	30.51	0.702
<i>Oryza sativa</i>	OsMATE34	LOC_Os08g44870.1	8	3	51.60	489	5.6	116.93	32.79	0.746
<i>Oryza sativa</i>	OsMATE7	LOC_Os02g57570.1	2	2	38.74	363	4.72	110.06	32.98	0.528
<i>Solanum lycopersicum</i>	Slmate /MTP77	AAQ55183.1	3	7	55.17	506	5.89	119.13	21.64	0.650
<i>Medicago truncatula</i>	MtMATE2	ADV04045.1	1	7	54.52	501	5.68	126.45	27.82	0.785
<i>Arabidopsis thaliana</i>	AtFFT	At4g25640	4	7	53.22	488	6.13	120.88	33.84	0.798
<i>Raphanus sativus</i>	RsMATE8	MF360954	8		53.37	490	6.89	119.80	31.51	0.792
<i>Vitis vinifera</i>	VvAM3	ACN91542.1	16	6	53.85	493	6.53	116.06	28.46	0.678
<i>Vitis vinifera</i>	VvAM1	ACN88706.1	16	7	53.50	489	5.89	118.12	24.07	0.725
<i>Oryza sativa</i>	OsMATE3	LOC_Os01g56050.1	1	8	51.58	484	9.58	119.94	30.64	0.728
<i>Oryza sativa</i>	OsMATE16	LOC_Os03g42830.1	3	8	51.83	477	8.93	117.80	26.65	0.76
<i>Oryza sativa</i>	OsMATE39	LOC_Os10g11860.1	10	8	50.22	464	8.82	117.16	30.09	0.806
<i>Raphanus sativus</i>	RsMATE3	MF360949	3		56.48	519	5.34	112.76	27.96	0.812
<i>Oryza sativa</i>	OsMATE33	LOC_Os08g43654.1	8	3	56.17	522	6.71	116.07	37.06	0.698
<i>Oryza sativa</i>	OsMATE9	LOC_Os03g08900.1	3	8	52.96	489	6.97	117.89	26.69	0.775
<i>Oryza sativa</i>	OsMATE31	LOC_Os08g37432.1	8	8	52.55	489	6.09	123.25	22.92	0.802
<i>Oryza sativa</i>	OsMATE35	LOC_Os09g29284.1	9	8	51.97	482	9	117.97	40.07	0.730
<i>Oryza sativa</i>	OsMATE48	LOC_Os11g03484.1	11	4	36.14	329	5.09	114.98	38.61	0.652
<i>Oryza sativa</i>	OsMATE51	LOC_Os12g03200.1	12	6	33.89	311	5.08	116.62	39.96	0.648
<i>Oryza sativa</i>	OsMATE47	LOC_Os11g03240.1	11	8	54.68	497	6.36	117.89	38.93	0.689
<i>Oryza sativa</i>	OsMATE 52	LOC_Os12g03230.1	12	7	54.68	497	6.36	117	38.93	0.689
<i>Oryza sativa</i>	OsMATE49	LOC_Os11g03500.1	11	9	54.24	495	6.33	115.78	32.01	0.606
<i>Oryza sativa</i>	OsMATE53	LOC_Os12g03260.1	12	8	55.44	507	6.01	116.13	30.83	0.615
<i>Arabidopsis thaliana</i>	AtFRD3	At3g08040	3	12	55.95	526	9.63	114.70	29.83	0.613
<i>Raphanus sativus</i>	RsMATE7	MF360953	7		48.11	451	5.9	117.07	36.64	0.598

The MATE transporter genes were denominated systematically based on their physical locations on the chromosomes of rice. The MW (Molecular weight in kiloDaltons), A.A (Number of amino acids), PI (isoelectric point), AI (aliphatic index), II (instability index), and GRAVY (GRAND average of Hydropathicity Index) were computed using the ExPASy Compute pI/ Mw tool ([http:// web.expasy.org/cgi-bin/protparam](http://web.expasy.org/cgi-bin/protparam); accessed on 30 August 2020).

Table S3: The Differentially conserved motif of MATE gene family

<b>MOTIF</b>	<b>PROTEIN SEQUENCE</b>	<b>LENGHT</b>
<b>MEME-1</b>	PLLAITILLNSIQPVLSGVAVGSGWQALVAYVNLGCYYJIGJPJGCLLGF	50
<b>MEME-2</b>	GFAYGIMLGMASALETLCGQAYGAKQYHMLGVYLQRS	37
<b>MEME-3</b>	CKETWTGFSWKAFTGJWAFVKLSLASAVMLCLEJWYNQILVLJTGLLKNA	50
<b>MEME-4</b>	EIALDSJSICMNINGWEMMISLGFNAAISVRVSNELGAGHPRAAKFSVFV	50
<b>MEME-5</b>	KGIWWGMIIGTLLQTLILLFJTARTBWNKEVEEASERLKKW	41
<b>MEME-6</b>	IAAAAGTFALGLIPQJFAYAINFPLQKFLQAQSKVNPLAYI	41
<b>MEME-7</b>	YGLSFVTQAFVGHJGALELAAASJASTVIQ	30
<b>MEME-8</b>	JLLPJYWFATPJLIALGQSPE	21
<b>MEME-9</b>	RDYLAYJFTSDKEVIDAVSDL	21
<b>MEME-10</b>	HVLLSWLVVYVLGLGLLGAAL	21
<b>MEME-11</b>	RLVAWESKKLWRIAGPSIFVS	21
<b>MEME-12</b>	TLSFSWWJJVAAQLAYIVFSP	22

**Table S4.** Similarity index and identity.

OsMATE	OTHER MATE	Similarity index	IDENTITY
OsMATE 34	MTP77/ SIMATE	51	52.74
	MtMATE2	51	52.67
	AtFFT	55	56.99
	RsMATE8	54	55.21
	VvAM3	54	54.56
	VvAM1	54	52.51
	RsMATE3	42	44.77
OsMATE 7	MTP77	41	59.68
	MtMATE2	39	56.23
	AtFFT	42	61.39
	RsMATE8	42	60.66
	VvAM3	39	57.19
	VvAM1	39	57.52
	RsMATE3	31	43.41
OsMATE33	RsMATE3	50	50.97
	MTP77/ SIMATE	44	46.04
	MtMATE2	46	47.37
	AtFFT	44	47.63
	RsMATE8	45	47.23
	VvAM3	44	45.92
	VvAM1	44	46.31
OsMATE39	RsMATE3	46	47.08
	MTP77/ SIMATE	41	41.34
	MtMATE2	41	41.99
	AtFFT	40	41.34
	RsMATE8	40	40.69
	VvAM3	41	41.34
	VvAM1	41	40.91
OsMATE16	RsMATE3	51	50.22
	MTP77/ SIMATE	44	44.73
	MtMATE2	45	45.49
	AtFFT	46	47.20
	RsMATE8	46	46.34
	VvAM3	46	46.02
	VvAM1	46	45.24
OsMATE 3	RsMATE3	47	51.58
	MTP77/ SIMATE	44	46.51
	MtMATE2	42	45.03
	AtFFT	43	47.45
	RsMATE8	44	46.07
	VvAM3	43	45.24
	VvAM1	43	44.26

Sequence identity was analyzed using Clustal Omega multiple sequence analysis  
<https://www.ebi.ac.uk/Tools/msa/clustalo/>; accessed on 21 August 2020

**Table S5:** The basic information about MATE protein localization.

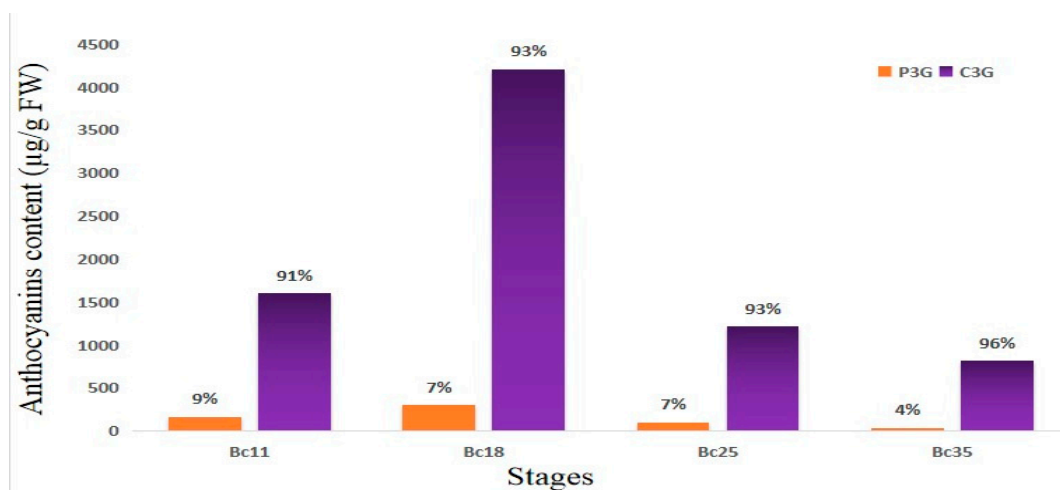
Proteins	plas	vacu	ER	GOLG	Cyto	chlo	mito
VvMate1 T12	6	4		3	1		
VvMATE2	2	9		3			
MtMATE1	7	5	1	1			
BrTT12	8	3	1	2			
AtTT12	6	4	1	3			
FaTT12	6	5	1	2			
MdMATE1	6	5		3			
MdMATE2	6	4	1	3			
OsMATE55	7	4	1	2			
OsMATE15	6	4	2	2			
OsMATE13	4	10					
RsMATE2	7	4	1	2			
OsMATE14	6	4	1	2	1		
OsMATE12	8	3	2	1			
OsMATE34	6	5	1	1	1		
OsMATE7	6.5	1	4		4	1	1
SIMATE/MTP77	9	4	1				
MtMATE2	9	4	1				
AtFFT	13	1					
RsMATE8	8	2	1	3			
VvAM3	6	4	1	3			
VvAM1	9	2	1	2			
OSMATE3	11	1	1			1	
OSMATE16	1	10		2	1		
OSMATE39	6	6		1	1		
RsMATE3	7	4		3			
OsMATE33	12	2					
OSMATE9	9	4	1				
OsMATE31	11	1	2				
OSMATE35	3	6	1	3	1		
OSMATE48	10	1	2		1		
OSMATE51	9	2	2		1		
OsMATE47	11	1	2				
OsMATE52	11	1	2				
OsMATE49	11	1	2				
OsMATE53	13	1					
AtFRD3	3	8		2	1		
RsMATE7	5	4	3			2	

Subcellular localization prediction using <https://wolfsort.hgc.jp/>; accessed on 8 September 2021. plas, vacu, ER, Golg, Cyto, Chlo, mito represent respectively plasma membrane protein, vacuole, endoplasmic reticulum, golgi apparatus, chloroplast and mitochondria.

**Table S6:** Expression pattern of anthocyanin biosynthesis and transporter genes based on fold-change levels in Bc and Wc.

gene groups	gene_ID	Gene name	Log2FC	Log2FC	Log2FC
			Bc11/Wc11	Bc18/Wc18	Bc25/Wc25
<b>Transporter genes</b>	Os06g0158900	OsABCC15/ MRP15	5.29***	-1.19***	-0.35*
	Os10g0395400	OsGSTU34/GST	9.37***	12.47***	9.57***
	<a href="#">Os01g0766000</a>	OsMate3	-1.49*	-0.78*	-0.32*
	<a href="#">Os02g0821600</a>	Mate7	-0.95*	0.00	0.00
	<a href="#">Os03g0626700</a>	Mate16	4.29*	0.57*	0.55*
	<a href="#">Os08g0550200</a>	Mate 33	0.00	-3.97*	-2.28*
	<a href="#">Os08g0562800</a>	Mate 34	9.21***	6.43***	3.98***
	<a href="#">Os10g0195000</a>	OsSTA240/ MATE39	0.00	-3.23*	-3.81***
<b>Phenylalanine pathway</b>	Os02g0627100	OsPAL1/ OsPAL	7.12 ***	2.81 ***	2.01 ***
	Os05g0320700	C4H2/ OsC4H	2.90 ***	2.99 ***	1.24 *
	Os02g0177600	4CL3/Os4CL	3.78 ***	2.49 ***	1.30 *
<b>Structural genes</b>	Os11g0530600	CHS/ OsCHS	9.20 ***	9.33 ***	7.21 ***
	Os03g0819600	gh1/ OsCHI	4.58 ***	2.23 ***	1.76 ***
	Os04g0662600	OsF3H-1/OsF3H	7.37 ***	8.71 ***	7.16 ***
<b>Anthocyanin pathway</b>	Os10g0320100	OsF3'H	8.09 ***	8.38 ***	7.59 ***
	Os03g0367200	OsCYP75A11/ OsF3'5'H	0.00	2.17 *	4.15 *
	Os01g0633500	Rd/OsDFR	9.49 ***	11.65 ***	11.76 ***
<b>Structural genes</b>	Os01g0372500	OsANS	10.06 ***	11.58 ***	5.59 ***
	Os03g0259400	OsLAR	5.75 *	2.43 *	3.20 ***
	Os04g0630800	OsANR	-0.05 *	1.18 *	2.38 ***
<b>Decorating genes</b>	Os06g0192100	UGT/Os3GT	3.62 ***	5.25***	2.44 ***
	Os08g0157500	ROMT9/Os3'MT	0.57 *	0.05 *	0.63 *
	Os04g0557800	PI/OSB1	0.00	-4.04 *	-2.23 *
<b>Regulatory genes</b>	Os04g0557500	Kala4/OSB2	8.65 ***	10.59 ***	9.98 ***
	Os06g0205100	C/OsCI	0.00	0.00	-1.23 *
	Os03g0410000	OsMyb3/Kala 3	3.94 *	5.06 ***	4.18 ***
	Os02g0682500	OsWD40-50 /OsWD40	0.99 *	3.69 ***	2.26 ***

(\*\*\*) The difference is significant between black and white caryopsis; (\*) the difference is not significant between black and white caryopsis; The fold change with positive and negative values represents upregulated and downregulated genes.

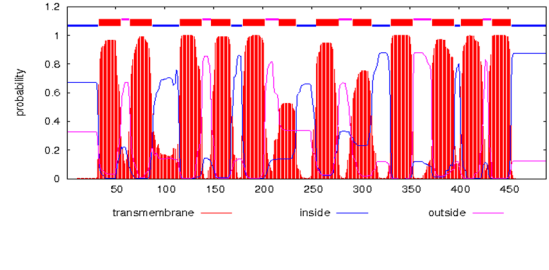
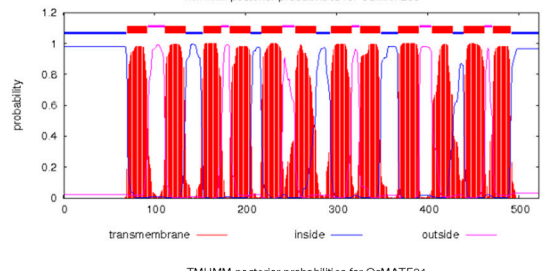
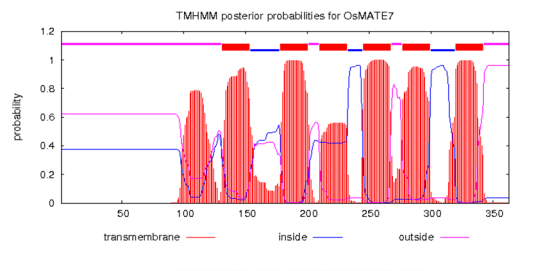
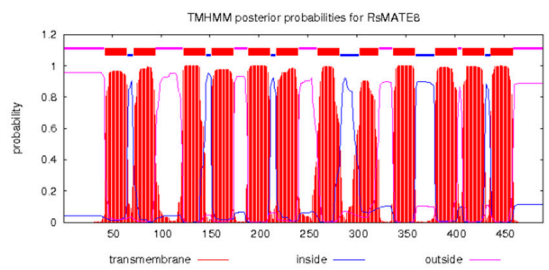
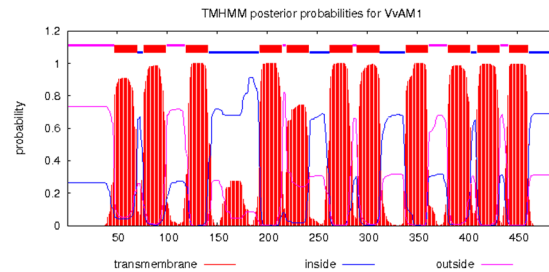
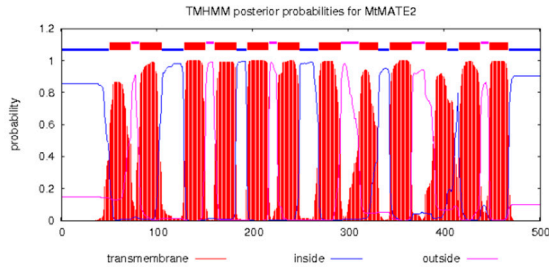
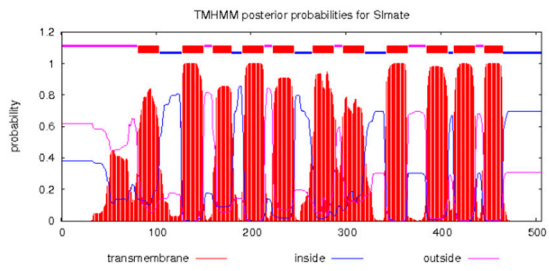


**Figure S1.** Anthocyanin quantification in black rice caryopsis at different stages; FW, fresh weight; Bc, Black caryopsis; the numbers after Bc in the graph represent days after flowering; P3G, Peonidin-3-O-glucoside in orange bar; C3G, cyanidin-3-O-glucoside; DAF, days after flowering; the number above each bar represents the relative percentage of C3G and P3G in TAC.

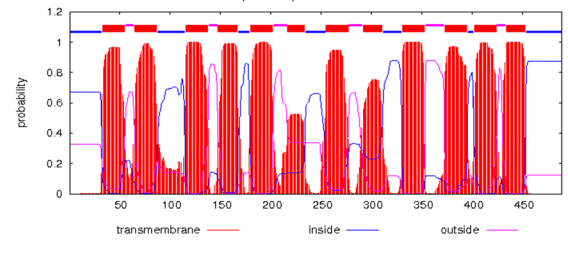
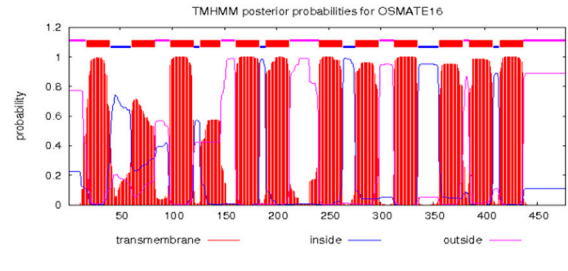
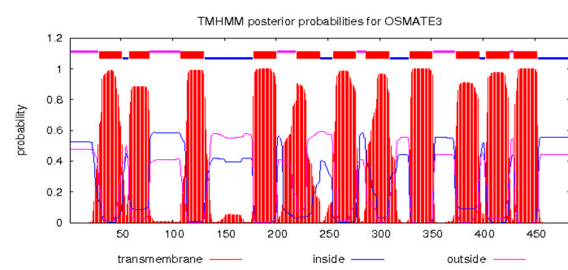
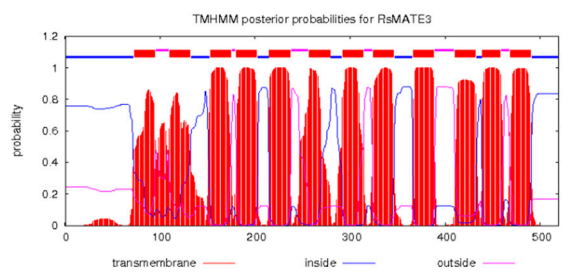
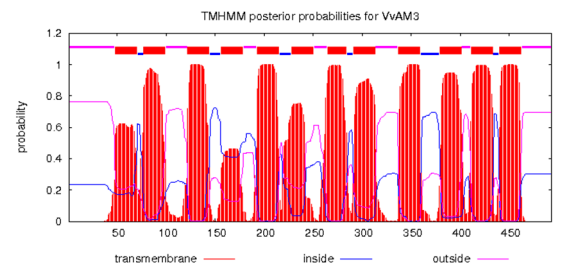
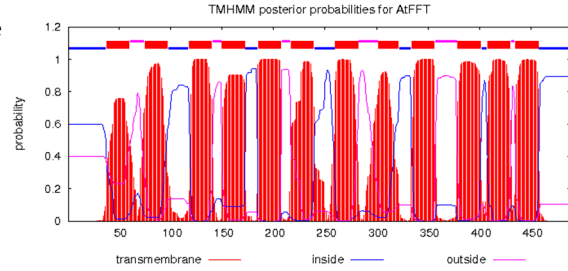




**Figure S2.** Secondary structures of the 6 rice MATEs proteins and 7 anthocyanin MATEs-like proteins predicted by SOPMA. The  $\alpha$ -helix, extended strand,  $\beta$ -turn, and random coil are denoted as the longest (blue), medium long (dark red), short (green), and the shortest (pink) vertical bars, respectively.

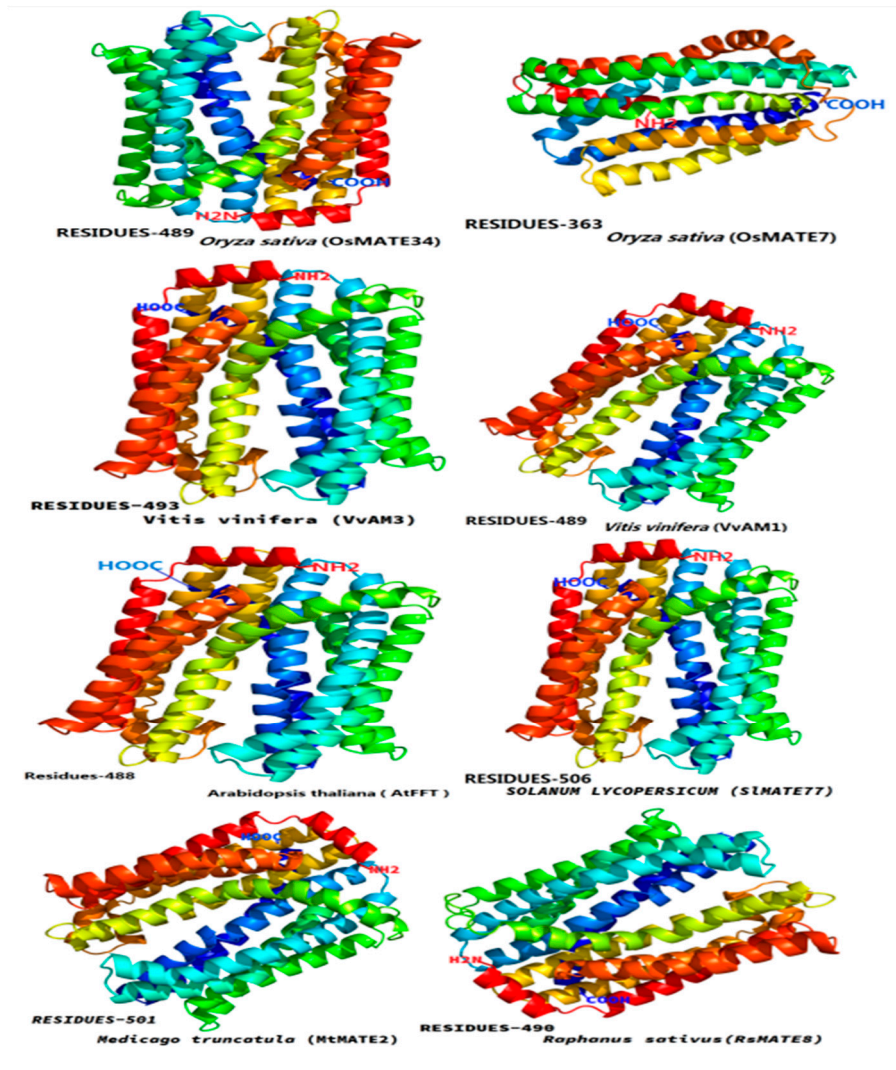


1e



rmind

using the TMHMM2 program.



**Figure S4.** Comparison of the three-dimensional configuration of two putative OsMATEs and six anthoMATEs.