

Table 1 Suppl. The 30 known MATE transporters in plants.

Plant species	Name	Accession No. or AGI code	References
<i>Arabidopsis thaliana</i>	AtFFT	At4g25640	Thompson <i>et al.</i> 2010
<i>Arabidopsis thaliana</i>	AtTT12	At3g59030	Debeaujon <i>et al.</i> 2001
<i>Arabidopsis thaliana</i>	AtADS1	At4g29140	Sun <i>et al.</i> 2011
<i>Arabidopsis thaliana</i>	AtZF14	At1g58340	Burko <i>et al.</i> 2011
<i>Arabidopsis thaliana</i>	AtEDS5	At4g39030	Yamasaki <i>et al.</i> 2013; Serrano <i>et al.</i> 2013
<i>Arabidopsis thaliana</i>	AtFRD3	At3g08040	Roschzttardtz <i>et al.</i> 2011
<i>Arabidopsis thaliana</i>	AtMATE	At1g51340	Liu <i>et al.</i> 2009
<i>Arabidopsis thaliana</i>	AtALF5	At3g23560	Diener <i>et al.</i> 2001
<i>Arabidopsis thaliana</i>	AtDTX1	At2g04070	Li <i>et al.</i> 2002
<i>Brassica campestris</i>	BrTT12	ACJ36213	Chai <i>et al.</i> 2009
<i>Brassica oleracea</i>	BoMATE	AGU16976	Wu <i>et al.</i> 2014
<i>Eucalyptus camaldulensis</i>	EcMATE1	BAM68465	Sawaki <i>et al.</i> 2013
<i>Glycine max</i>	GmFRD3b	ACE89003	Rogers <i>et al.</i> 2009
<i>Glycine max</i>	GmMATE75	KRH20827	Liu <i>et al.</i> 2016
<i>Hordeum vulgare</i>	HvAACT1	BAF75822	Furukawa <i>et al.</i> 2007
<i>Medicago truncatula</i>	MtMATE1	ACX37118	Zhao <i>et al.</i> 2009
<i>Medicago truncatula</i>	MtMATE2	HM856605	Zhao <i>et al.</i> 2011
<i>Nicotiana tabacum</i>	NtMATE1	BAF47751	Shoji <i>et al.</i> 2009
<i>Nicotiana tabacum</i>	NtMATE12	BAF47752	Shoji <i>et al.</i> 2009
<i>Nicotiana tabacum</i>	Nt-JAT1	CAQ51477	Morita <i>et al.</i> 2009
<i>Secale cereale</i>	ScFRDL1	BAJ61741	Yokosho <i>et al.</i> 2010
<i>Secale cereale</i>	ScFRDL2	BAJ61742	Yokosho <i>et al.</i> 2010
<i>Solanum lycopersicum</i>	SIMATE	AAQ55183	Mathews <i>et al.</i> 2003
<i>Sorghum bicolor</i>	SbMATE	ABS89149	Magalhaes <i>et al.</i> 2007
<i>Triticum aestivum</i>	TaMATE1B	AFZ61900	Ryan <i>et al.</i> 2009
<i>Vitis vinifera</i>	VvAM3	ACN91542	Gomez <i>et al.</i> 2011& 2009
<i>Vitis vinifera</i>	VvMATE1	XP_002282932	Perez-Diaz <i>et al.</i> 2014
<i>Vitis vinifera</i>	VvMATE2	XP_002282907	Perez-Diaz <i>et al.</i> 2014
<i>Zea mays</i>	ZmMATE1	ACM47310	Maron <i>et al.</i> 2010

Table 2 Suppl. The basic information of MATE transporter families in rice (Ch, Cy, Er, Pl, and Va represent chloroplast, cytoplasm, endoplasmic reticulum, plasma membrane protein, and vacuole, respectively); pI - isoelectric point.

Gene name	Chromosome location	Amino acid number	Molecular size [kDa]	Transmembrane domain number	pI	Protein localization
OsMATE1	LOC_Os01g31980.2	502	53.54	10	5.47	Pl
OsMATE2	LOC_Os01g49120.1	491	52.98	12	6.71	Pl
OsMATE3	LOC_Os01g56050.1	484	51.58	11	9.58	Pl
OsMATE4	LOC_Os01g69010.1	566	58.27	7	9.23	Pl
OsMATE5	LOC_Os02g02980.1	532	56.94	8	9.02	Ch
OsMATE6	LOC_Os02g45380.1	549	57.83	11	7.06	Ch
OsMATE7	LOC_Os02g57570.1	363	38.74	6	4.72	Pl
OsMATE8	LOC_Os02g58620.1	1097	116.40	7	9.40	Pl
OsMATE9	LOC_Os03g08900.1	489	52.96	12	6.97	Cy
OsMATE10	LOC_Os03g11734.2	571	59.96	8	8.60	Va
OsMATE11	LOC_Os03g12790.1	644	65.79	10	6.50	Er
OsMATE12	LOC_Os03g37411.1	500	53.84	12	6.98	Pl
OsMATE13	LOC_Os03g37470.1	350	37.35	9	7.52	Va
OsMATE14	LOC_Os03g37490.1	520	55.79	12	5.24	Pl
OsMATE15	LOC_Os03g37640.1	500	53.62	12	6.52	Pl
OsMATE16	LOC_Os03g42830.1	477	51.83	12	8.93	Va
OsMATE17	LOC_Os03g62270.1	516	53.51	10	6.97	Cy
OsMATE18	LOC_Os03g64150.1	479	50.62	9	9.76	Pl
OsMATE19	LOC_Os04g30490.1	483	50.96	12	7.49	Pl
OsMATE20	LOC_Os04g48290.1	560	59.19	13	6.33	Va
OsMATE21	LOC_Os05g48040.1	500	53.49	11	6.99	Pl
OsMATE22	LOC_Os06g29844.1	490	52.05	12	6.07	Pl
OsMATE23	LOC_Os06g29900.1	110	11.49	0	4.27	Cy
OsMATE24	LOC_Os06g29950.1	495	54.09	8	8.92	Pl
OsMATE25	LOC_Os06g29994.1	479	51.12	12	8.16	Cy
OsMATE26	LOC_Os06g36330.1	568	58.87	10	6.82	Pl
OsMATE27	LOC_Os06g49310.1	483	51.96	9	6.32	Va
OsMATE28	LOC_Os07g01750.1	568	62.42	10	9.52	Pl
OsMATE29	LOC_Os07g31884.1	566	61.06	12	9.37	Pl
OsMATE30	LOC_Os07g33310.1	493	51.87	11	8.71	Pl
OsMATE31	LOC_Os08g37432.1	489	52.55	9	6.09	Cy
OsMATE32	LOC_Os08g43250.1	536	55.67	8	8.69	Ch
OsMATE33	LOC_Os08g43654.1	522	56.17	12	6.71	Pl
OsMATE34	LOC_Os08g44870.1	489	51.60	12	5.60	Pl
OsMATE35	LOC_Os09g29284.1	482	51.99	10	9.00	Pl
OsMATE36	LOC_Os09g35600.1	541	56.44	10	7.49	Ch
OsMATE37	LOC_Os09g37610.1	577	60.07	10	9.30	Ch
OsMATE38	LOC_Os10g11354.1	485	51.49	12	7.95	Cy
OsMATE39	LOC_Os10g11860.1	464	50.21	10	8.82	Va
OsMATE40	LOC_Os10g13940.1	537	57.72	9	6.43	Pl
OsMATE41	LOC_Os10g20350.1	392	41.32	8	8.37	Pl
OsMATE42	LOC_Os10g20380.1	202	22.05	4	9.30	Pl
OsMATE43	LOC_Os10g20390.1	324	33.91	4	9.28	Pl
OsMATE44	LOC_Os10g20450.1	477	50.73	10	8.77	Pl
OsMATE45	LOC_Os10g20470.1	486	51.44	12	8.60	Va
OsMATE46	LOC_Os10g37920.1	539	56.03	12	7.04	Pl
OsMATE47	LOC_Os11g03240.1	497	54.67	10	6.36	Pl
OsMATE48	LOC_Os11g03484.1	329	36.14	6	5.09	Cy
OsMATE49	LOC_Os11g03500.1	495	54.24	11	6.33	Pl
OsMATE50	LOC_Os12g01580.1	550	58.37	11	5.33	Ch
OsMATE51	LOC_Os12g03200.1	311	33.89	4	5.08	Pl
OsMATE52	LOC_Os12g03230.1	276	30.20	7	7.64	Va
OsMATE53	LOC_Os12g03260.1	507	55.44	12	6.01	Pl
OsMATE54	LOC_Os12g36660.1	431	45.33	6	9.19	Va
OsMATE55	LOC_Os12g42130.1	500	54.10	11	6.32	Pl



Fig. 1 Suppl. Motifs (shown as *colored boxes*) in the full length protein of the rice MATE family. The scale is used to estimate the length of a motif (unit: amino acid) on the *bottom*. The rice MATE proteins are listed according to the order of subfamilies C1 to C4 from a phylogenetic tree, and different subfamilies are highlighted in different colors: C1 in blue, C2 in orange, C3 in yellow, and C4 in green.