

B73	MAEGSWTPTAELPLRQCPAVDDDLQVQVVEKCLGGGSAARRTGATATATATRDGSGVWSGKPCQRDRSGGWVAGFLMLANQALVTFVAVNCVGTNLVTFMS	99
mn2-m1	MAEGSWTPTAELPLRQCPAVDDDLQVQVVEKCLGGGSAARRTGATATATATRDGSGVWSGKPCQRDRSGGWVAGFLMLANQALVTFVAVNCVGTNLVTFMS	100
mn2-m2	MAEGSWTPTAELPLRQCPAVDDDLQVQVVEKCLGGGSAARRTGATATATATRDGSGVWSGKPCQRDRSGGWVAGFLMLANQALVTFVAVNCVGTNLVTFMS	99
mn2-710B	MAEGSWTPTAELPLRQCPAVDDDLQVQVVEKCLGGGSAARRTGATATATATRDGSGVWSGKPCQRDRSGGWVAGFLMLANQALVTFVAVNCVGTNLVTFMS	100
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B73	VVMRLDNADAANKANNWAGTTYVFSIVGALVSDSYWGRYKACTIEQLIFLAGLVELAVACHVFLDKSCHFGGGGGGRQEHCRPPTTAQSLVVFVSIYQI	198
mn2-m1	VVMRLDNADAANKANNWAGTTYVFSIVGALVSDSYWGRYKACTIEQLIFLAGLVELAVACHVFLDKSCHFGGGGGGRQEHCRPPTTAQSLVVFVSIYQI	199
mn2-m2	VVMRLDNADAANKANNWAGTTYVFSIVGALVSDSYWGRYKACTIEQLIFLAGLVELAVACHVFLDKSCHFGGGGGGRQEHCRPPTTAQSLVVFVSIYQI	198
mn2-710B	VVMRLDNADAANKANNWAGTTYVFSIVGALVSDSYWGRYKACTIEQLIFLAGLVELAVACHVFLDKSCHFGGGGGGRQEHCRPPTTAQSLVVFVSIYQI	200
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B73	ALGNAYQPAVTTFGADQFDETDARERRSKAFFGYFFVANNLGGVLAVTALAYMEDEGQWVLAFWIATAAALLGFLFAVGTIRYRHFVPSGNVAVSVC	298
mn2-m1	ALGNAYQPAVTTFGADQFDETDARERRSKAFFGYFFVANNLGGVLAVTALAYMEDEGQWVLAFWIATAAALLGFLFAVGTIRYRHFVPSGNVAVSVC	299
mn2-m2	ALGNAYQPAVTTFGADQFDETDARERRSKAFFGYFFVANNLGGVLAVTALAYMEDEGQWVLAFWIATAAALLGFLFAVGTIRYRHFVPSGNVAVSVC	298
mn2-710B	ALGNAYQPAVTTFGADQFDETDARERRSKAFFGYFFVANNLGGVLAVTALAYMEDEGQWVLAFWIATAAALLGFLFAVGTIRYRHFVPSGNVAVSVC	300
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B73	QVVVAAVRNRVRACVRAQDMYDPTDGDREKKGVRKVMVHTPEYRCLDKAAVIKDPASAEHFEPAAGQPQGHSSSKPNPWRCLTLTOVEELKCILRLVPI	396
mn2-m1	QVVVAAVRNRVRACVRAQDMYDPTDGDREKKGVRKVMVHTPEYRCLDKAAVIKDPASAEHFEPAAGQPQGHSSSKPNPWRCLTLTOVEELKCILRLVPI	397
mn2-m2	QVVVAAVRNRVRACVRAQDMYDPTDGDREKKGVRKVMVHTPEYRCLDKAAVIKDPASAEHFEPAAGQPQGHSSSKPNPWRCLTLTOVEELKCILRLVPI	396
mn2-710B	QVVVAAVRNRVRACVRAQDMYDPTDGDREKKGVRKVMVHTPEYRCLDKAAVIKDPASAEHFEPAAGQPQGHSSSKPNPWRCLTLTOVEELKCILRLVPI	400
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B73	WLCSTLYSTYSQMSVVFIEQACIMDDSLSKLTIPPAGMDVFEILGVTAQVFIYRFCIVRVMAHISHEPTELQRMGTGLVISAAMVASGVVEQQRLARA	496
mn2-m1	WLCSTLYSTYSQMSVVFIEQACIMDDSLSKLTIPPAGMDVFEILGVTAQVFIYRFCIVRVMAHISHEPSSRGWAGS.....	476
mn2-m2	WLCSTLYSTYSQMSVVFIEQACIMDDSLSKLTIPPAGMDVFEILGVTAQVFIYRFCIVRVMAHISHEPTELQRMGTGLVISAAMVASTRPAALSASSGR	496
mn2-710B	WLCSTLYSTYSQMSVVFIEQACIMDDSLSKLTIPPAGMDVFEILGVTAQVFIYRFCIVRVMAHISHEPTELQRMGTGLVISAAMVASGVVEQQRLARA	500
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B73	TAGVDASSLSILNQIPQYLLIGASEVFMVYTMTEFFNDQLEPLRLSLGSAMSVASMSAGSFASLLVTLVMAITCRGGRPGWIPODLNKGHVDFPFYLI	596
mn2-m1	476
mn2-m2	SRSTC.....	501
mn2-710B	TAGVDASSLSILNQIPQYLLIGASEVFMVYTMTEFFNDQLEPLRLSLGSAMSVASMSAGSFASLLVTLVMAITCRGGRPGWIPODLNKGHVDFPFYLI	600
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B73	AALNAVDLLAFVVFAPRYRPAVPIIHGEDETGGVEKQDAEECI	640
mn2-m1	476
mn2-m2	501
mn2-710B	AALNAVDLLAFVVFAPRYRPAVPIIHGEDETGGVEKQDAEECI	644

Fig. S4 Multiple amino acid sequence alignment of *mn2-m1*, *mn2-m2*, *mn2-710B* and B73. The red, yellow and blue boxes indicate missense mutations in three mutants (*mn2-m1*, *mn2-m2*, *mn2-710B*), two mutants (*mn2-m1* and *mn2-710B*), and one mutant (*mn2-710B*) compared to wild type inbred line B73, respectively. The red and blue lines indicate the two different MFS (Major Facilitator Superfamily) regions, respectively.