Arabidopsis thaliana Col-0 (NP 001330047.1) AtMAMI LTIGA 5 Arabidopsis thaliana mt-0 (AJ486884.1) AtmMAM1 LTIGA 5 Arabidopsis thaliana sorbo (CAD31141.1) AtsMAM1 LTIGA 5 Arabidopsis thaliana Br-0 (1001 genomes 6904) AtbMAMI LSIGA 5 VACPS Brassica oleracea var. oleracea (XP 013618041.1) BooMAM1.1 5 Brassica napus (XP 013678219.1) BnMAM1.1 5 VACPS Brassica rapa (XP 009130133.1) BrMAM1.1 5 VACPS Eruca vesicaria subsp. sativa (AGS49163.1) EvsMAM LACPS 5 Arabidopsis thaliana Col-0 (NP 173285.2) AtIPMS1 5 HNIPS Arabidopsis thaliana Col-0 (NP 177544.1) AtIPMS2 HNIPS 5 Brassica napus (XM 013817468.2) BnMAM1.2 INIGS 5 Brassica rapa (XM 009138151.2) BrMAM1.2 5 INIGS Brassica rapa subsp. pekinensis (ACR10246.1) BrpMAM.1 INIGS 5 Raphanus sativus (XM 018606131.1) RsMAM1.2 LNLGS 5 5 Arabidopsis thaliana Ler-0 (O8VX04.1) AtMAM2 LNVAS Arabidopsis cebennensis (CAJ55509.1) AcMAMa LNVAS 5 Arabidopsis lyrata lyrata (XP 002872029.1) AllMAM2 LNVAS 5 Arabidopsis lyrata petraea (CAJ55506.1) AlpMAMa LNVAS 5 5 Eutrema salsugineum (XP 006394566.2) EsMAM2 LNVAS Camelina sativa (XP 010493409.1) CsMAM2.1 LNVAS 5 Camelina sativa (XP 010421098.1) CsMAM2.2 LNVAS 5 Camelina sativa (XP 010454580.1) CsMAMI 5 LNVAS 5 Boechera divaricarpa (CAJ55512.1) BdMAMa LNVAS Capsella rubella (XP 006289820.1) CrMAM2 LNVAS 5 Brassica oleracea var. oleracea (XP 013593685.1) BooMAM2 LNVAS 5 Brassica napus (XP 013730921.2) BnMAM2 LNVAS 5 Raphanus sativus (XP 018477323.1) RsMAM2 5 LNVAS Eutrema salsugineum (XP 006394567.1) EsMAM1 LNIAS 5 Brassica rapa (XM 009138149.2) BrMAM1.4 LNLAS 5 Brassica rapa subsp. pekinensis (ACR10248.1) BrpMAM.2 LNLAS 5 Brassica oleracea var. oleracea (XM_013763569.1) BooMAM1.2 FTLAS 5 Brassica rapa (XM 009146283.2) BrMAM1.3 FTLAS 5 Raphanus sativus (XP 018457526.1) RsMAM1.1 FTLAS 5 Arabidopsis lyrata lyrata (CAJ55517.1) AllMAMc.1 CCIAS 5 Arabidopsis lyrata subsp. lyrata (XP_020879218.1) AllMAM3.2 5 CCIAS Arabidopsis lyrata subsp. lyrata (EFH48290.1) AllMAMc.2 5 CCIAS Arabidopsis lyrata petraea (CAJ55508.1) AlpMAMc CCIAS 5 Camelina sativa (XP 019083909.1) CsMAM3.3 5 CCIAS Capsella rubella (XP 006289994.1) CrMAMI CCIAS 5 Arabidopsis cebennensis (CAJ55511.1) AcMAMc CCIAS 5 Boechera divaricarpa (CAJ55514.1) BdMAMc CCIAS 5 Camelina sativa (XP 010493411.1) CsMAM3.1 5 CCIAS Camelina sativa (XP 010454582.1) CsMAM3.7 CCIAS 5 Capsella rubella (XM 006289411.2) CrMAM3.2 CCVAG 5 Camelina sativa (XM 010473736.2) CsMAM3.4 GGFAG 5 Camelina sativa (XM 010418504.2) CsMAM3.5 GGFAG 5 Capsella rubella (XM 006301203.2) CrMAM3.3 IGFAG 5 Camelina sativa (XM 010430647.2) CsMAM3.6 IGFAG 5 Boechera divaricarpa (CAJ55513.1) BdMAMb IGFAA 5 Arabidopsis lyrata lyrata (XP 002872030.1) AllMAM3.1 5 LGFAA Arabidopsis lyrata subsp. petraea (CAJ55507.1) AlpMAMb LGFAT 5 Arabidopsis cebennensis (CAJ55510.1) AcMAMb IGFAT 5 Arabidopsis thaliana Col-0 (NP 197693.1) AtMAM3 MGFAA 5 Arabidopsis thaliana Br-0 (1001 genomes 6904) AtbMAM3 5 MGFAA Arabidopsis thaliana Ler-0 (1001 genomes 7213) AtlMAM3 MGFAA 5 Arabidopsis thaliana sorbo (AJ486943.1) AtsMAM3 MGFAA 5 Camelina sativa (XP 010421099.1) CsMAM3.2 TGFAA 5 Camelina sativa (XP_010493410.1) CsMAM3.8 TGFAA 5 Capsella rubella (XP 006290200.1) CrMAM3.1 5 TGFAA

1		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36 37	38	39	40	41	42	43 4	44 45	46	47	48	49	50 5	51 5	2 53	54	55	56	57
AtMAM1	1		100,00	99,41	95,45	92,11	92,11	91,32	85,85	86,05	82,09	87,82	85,32	75,55	79,49	79,53	79,96	79,61	79,84	79,65	73,59	79,06	75,73	77,60	77,80	77,21	77,80	79,02	77,76	75,49	76,67	73,92	75,98	69,85	77,56	77,56	76,97 77	7,17 76,9	7 79,33	75,59	77,17	75,83	72,05	71,65 70,	67 71,	71 72,62	2 72,82	65,94	60,89 6	ô0,95 6	0,75 76,	32 75,'	93 76,22	45,31	44,70
AtmMAM1	2	0		99,41	95,45	92,11	92,11	91.32	85.85	86.05	82.09	87.82	85.32	75,55	79,49	79,53	79,96	79.61	79.84	79.65	73,59	79.06	75,73	77.60	77.80	77.21	77.80	79.02	77,76	75,49	76.67	73.92	75,98	69.85	77,56	77,56	76.97 77	7.17 76.9	7 79.33	75,59	77.17	75.83	72.05	71.65 70.	67 71.	71 72.62	2 72.82	65,94	60.89 F	60.95 F	0.75 76	32 75.	.93 76.22	45.31	44,70
AteMAM1	2	3	2		05.26	01.01	01 01	01 12	86.05	86.05	91.90	97.92	85.32	75.55	70 /0	70.53	80.15	70.61	80.04	70.94	73 77	70.26	75.73	78.00	78 10	77.60	79 10	70.02	78.15	75.60	76.86	74 12	76.17	70.22	77.76	77.76	77 17 77	7 36 77 1	7 70.53	75.70	77.36	75.83	72.24	71.85 70	87 72	10 72.62	72.87	65.94	0.80 6	60.05 0	0.75 76	52 76	13 76.41	45.31	44.70
					33,20	00.00	00.00	00.00	07,00	07,00	01,00	07,02	00,02	70,00	00.00	10,00	00,10	70,01	70.00	70.00	70,00	70,20	74.05	70,00	70,70	70.40	70,70	10,02	70,10	75,00	70,00	79,00	75,17	0,22	75.70	75.00	75.00 74		70,00	74.44	75.70	74,00	74.00	70,07 70,	47 74	72,02	72,02	05,04	00,00 0	0,00 0.	10,00 75	2 70,	05 75.0	40,01	++,/0
AtMAM2	4	23	23	24		93,69	93,69	92,90	87,03	87,23	82,87	88,41	86,69	76,65	80,66	80,12	81,09	79,41	79,26	79,06	73,22	/8,4/	74,95	78,59	/8,/8	/8,19	/8,/8	80,00	/8,/4	/5,10	/6,4/	73,92	/5,59	69,85	/5,/9	75,98	75,20 74	4,61 /4,4	1 //,56	(4,41	75,79	74,66	/1,06	70,67 70,4	4/ /1,	1 /1,46/	/ /1,65/	65,35	61,28 6	51,54 6	1,34 /5,3	34 74,5	15 75,24	44,69	43,93
AIIMAM2	5	40	40	41	32		99,21	96,84	88,80	88,61	84,84	90,37	88,45	77,57	81,45	81,73	82,06	80,63	78,91	78,71	72,73	77,73	74,41	78,04	78,24	77,65	78,24	80,43	77,80	74,76	76,52	73,78	75,44	69,54	76,62	76,82	76,03 75	5,64 75,4	4 78,19	73,48	75,05	74,31	59,94	69,16 68,	96 70,	j9 71,51	/ 71,71	65,03	60,97 6	51,22 6	1,02 75,1	39 75,0	JO 75,68	45,00	44,55
AlpMAMa	6	40	40	41	32	4		96,84	89,00	88,80	85,04	90,37	88,65	77,76	81,64	81,93	82,24	80,23	79,10	78,91	72,91	77,93	74,61	78,04	78,24	77,65	78,24	80,43	77,80	74,56	76,32	73,58	75,24	69,54	76,62	76,82	76,03 75	5,64 75,4	4 78,39	73,48	75,05	74,31	59,94	69,16 68,	96 70,	78 71,51	(71,71	65,03	60,97 6	61,42 6	1,22 75,	00 74,	61 75,49	45,16	44,70
AcMAMa	7	44	44	45	36	16	16		88,02	87,82	83,86	89,39	87,87	76,84	80,66	80,75	81,31	79,84	78,12	77,93	71,82	76,76	74,22	77,45	77,65	77,06	77,65	80,23	77,41	74,56	75,93	73,19	75,44	69,54	75,83	76,03	75,25 74	4,85 74,6	6 77,60	73,08	74,66	74,12	69,55	68,76 68,	57 70,	59 71,32	2 71,51	64,83	61,17 F	60,83 F	0,63 74,	22 73,	83 74,90	44,69	44,24
CsMAM2 1	8	72	72	71	66	57	56	61		97.42	92.06	93.45	92.13	77.39	81.45	80.94	80.93	78 54	78.52	78.32	72 18	77 15	73.63	76.67	76.86	76.27	76.86	76.91	77 67	73 39	75.34	71.82	74 07	69 17	75.25	75 44	75.64 75	583 76.0	76.62	72 69	73.92	72 94	59 17	68.38 68	18 70	61 71.07	7 7126	64.82	59.88 F	60 79 F	0 79 73	87 73	28 74 07	45.62	44.55
Colline III 2.1	0	74	71	71	65	50	57	62	12		02.96	02.95	02.01	77.20	01.45	00.04	00.75	70.74	70.10	70.01	72.00	77 72	72.62	77.45	77.65	77.06	77.65	77.60	70 46	72.20	75.54	70.01	74.66	60.54	74.05	75.05	75.64 76	02 76.0	77.41	72.00	74.10	72.52	50.17	03 00 03	10 70	41 71 6F	5 71 0/	65.42	60.67	61.20 (1 20 74	07 72	10 74 46	45.62	44.55
CSIMAMIZ.2	9	11	11	71	05	50	57	02	15		92,00	93,05	92,91	77,59	01,45	00,94	80,75	70,74	79,10	70,91	75,09	71,15	75,05	77,45	77,05	77,00	77,05	77,09	70,40	75,59	75,54	12,21	74,00	09,54	74,00	75,05	75,04 70	0,05 70,2	5 11,41	12,09	74,12	75,55	59,17	00,30 00,	10 70,	71,05	7 1,04	05,42	00,07 0	71,39 0	1,39 14,0	11 13,5	10 74,40	45,02	44,00
CSMAM1	10	91	91	92	87	11	76	82	40	36		89,09	87,99	73,53	//,34	77,01	11,20	/8,31	/5,64	/5,44	69,29	/4,0/	/5,56	73,14	/3,33	/2,/5	73,33	72,99	73,91	70,45	72,02	68,88	72,02	66,79	/2,10	72,30	72,69 73	3,08 73,2	3 /4,26	69,74	70,78	70,00	56,60	65,81 66,1	00 67,	36 70,757	/ /0,/5/	65,11	59,96 6	10,20 6	J,20 69,7	/4 69,7	16 /0,5/	44,20	43,73
BdMAMa	11	62	62	62	59	49	49	54	33	31	55		92,32	78,12	82,23	82,51	81,87	80,31	80,27	80,08	73,82	78,91	75,20	78,82	79,02	78,43	79,02	78,86	79,05	74,17	76,32	73,19	75,24	70,09	75,83	76,03	76,62 76	6,42 76,2	3 78,59	73,87	74,90	74,12	59,96	69,17 68,	77 71,3	20 72,43	72,62	66,21	61,84 6	51,98 6	1,78 75,0	J5 74,7	26 74,66	45,78	45,17
CrMAM2	12	75	75	75	68	59	58	62	40	36	61	39		76,56	80,54	79,84	79,70	78,47	78,40	78,21	72,10	76,85	73,35	76,37	76,56	75,98	76,56	76,61	77,95	72,51	74,46	72,32	73,98	69,29	75,15	75,34	75,73 75	5,34 75,3	4 77,10	72,02	72,99	72,66	59,09	68,3 <mark>1</mark> 68,	11 70,	53 70,66	5 70,85	64,44	59,92 6	30,43 6	0,24 72,	21 71,6	32 72,82	45,48	44,57
BooMAM2	13	133	133	133	127	122	121	126	123	123	144	119	128		93,15	87,22	87,82	75,46	75,41	75,23	74,95	75,41	71,01	72,79	72,98	72,43	73,35	72,66	72,56	69,72	70,83	67,71	70,28	69,33	72,19	72,38	73,11 72	2,19 72,0	1 73,11	70,53	71,32	71,14	64,94	64,21 63,	84 65,	19 68,49	68,67	62,92	57,95 5	58,04 5	7,86 68,	50 68,	13 69,53	43,60	42,88
BnMAM2	14	105	105	105	99	95	94	99	95	95	116	91	100	37		91,73	84,89	79,18	79,34	79,14	73,14	79,34	74,66	76,56	76,76	76,17	77,15	76,41	76,32	73,29	74,46	71,15	73,59	68,37	75,93	76,13	77,10 75	5,93 75,7	3 76,91	74,17	75,00	74,80	58,24	67,45 67,	06 68,	69 72,20	72,39	66,67	61,24 F	61,49 F	1,30 71,	98 71,	60 73,06	45,16	44,39
RsMAM2	15	104	104	104	101	93	92	98	97	97	117	89	103	69	42		84.40	79.22	79.96	79,76	73.31	79,96	75.05	76,77	76.97	76.38	77,17	76.62	76,68	73.67	74.85	72,30	73.97	68.88	76,13	76.33	77.32 75	5.94 75.7	4 76.53	74.36	75.59	75.00	58.32	67.52 66.	93 68.	77 71.65	5 71.84	65,74	60.67 F	61.90 F	1.71 71	96 71	.57 73.83	45.31	45,17
EeMAM2	16	107	107	106	101	96	95	100	102	103	122	97	109	66	81	83		80.41	79 44	79.25	77.88	79.25	74 39	76.59	76 78	76.22	76.97	76.45	75.80	72.52	73.64	70.65	72 90	70.02	75.23	75.42	75.23 74	167 744	75.98	72.05	72.66	72 47	57.60	66.85 66	85 68	22 69.81	1 70.00	62.92	58.07 F	59.10 F	9 10 71	46 70	90 72 8F	44 29	43.86
E-MAMA	17	104	104	104	105	00	101	102	100	100	100	100	110	124	107	106	105	00,11	77.10	77.00	70.06	76.44	75.04	75.72	75.02	75.24	75.02	75.00	75.00	71.00	70.05	70.10	72.52	66.01	74.74	74.00	74.54 72	72 72 5	75.60	70.55	72.10	74.10	0.00	60.00 60	50 60	76 75 64	75.04	60.00	62,20 (65 10 (4 00 71	60 74	04 72.00	44.52	44.96
ESIMAWIT	17	104	104	104	105	99	101	105	109	100	100	100	110	134	107	100	105		11,19	11,00	70,90	70,41	15,54	75,75	75,95	75,54	75,95	75,20	75,00	71,29	72,05	70,12	75,55	00,91	74,71	74,90	74,51 75	5,15 15,5	75,09	72,00	75,19	74,12	09,00	09,09 00,	00,	75,04	75,04	00,00	03,29 0	15,19 0	+,99 71,0	72 71,0	74 75,05	44,00	44,00
BOOMAM1.1	18	103	103	102	106	108	107	112	110	107	124	101	111	134	105	102	110	117		99,80	90,61	92,28	87,52	76,27	/6,4/	/5,88	/6,6/	75,69	/4,/1	/1,/6	/3,53	70,39	72,96	67,58	76,08	76,27	/6,6/ /6	5,08 75,2	/ //,06	73,92	74,95	74,95	/0,45	69,86 69,1	08 68,	/5 /0,02/	/0,21/	63,01	57,06 5	18,43 5	3,43 72,2	21 71,8	52 72,90	45,00	45,02
BnMAM1.1	19	104	104	103	107	109	108	113	111	108	125	102	112	135	107	103	111	118	1		90,42	92,08	87,33	76,08	76,27	75,69	76,47	75,49	74,51	71,57	73,33	70,39	72,76	67,40	76,08	76,27	76,47 75	5,88 76,0	3 76,86	73,73	74,76	74,76	70,45	69,86 69,	08 68,	/5 70,02/	2 70,21	63,01	57,06 5	58,43 5	8,43 72,0	J2 71,4	43 72,71	45,00	45,02
BrMAM1.1	20	145	145	144	147	150	149	155	153	148	168	144	154	138	148	146	121	160	51	52		86,37	80,85	70,07	70,26	69,71	70,44	69,53	68,80	66,42	67,88	64,96	66,91	66,36	69,89	70,07	70,44 69	9,71 69,8	9 70,44	67,70	68,67	68,67	65,03	64,48 63,	75 63,4	45 64,98	65,16	58,11	52,89 5	53,83 5	4,01 66,7	30 65,	76 67,70	42,48	42,21
BjIPMS1	21	107	107	106	110	114	113	119	117	114	132	108	119	134	106	102	111	121	39	40	74		86,34	76,27	76,47	75,88	76,67	75,69	75,49	71,96	73,53	70,20	72,76	67,58	75,49	75,69	76,27 75	5,29 75,4	76,27	74,12	75,34	75,15	70,84	70,25 69,3	28 68,	75 69,83	3 70,02	62,43	56,87 5	57,84 5	7,65 71,	ô2 71,'	23 73,49	45,16	44,70
EvsMAM	22	124	124	124	128	131	130	132	135	135	120	127	137	158	130	127	137	121	63	64	104	69		73,37	73,57	72,98	73,77	72,19	71,99	70,22	72,19	68,24	72,89	66,67	74,07	74,26	74,07 73	3,48 73,4	3 74,26	71,79	73,03	73,23	58,64	67,85 68,	05 67,	32 69,88	3 70,08	63,84	58,22 5	57,34 5	7,14 67,	72 67,	52 69,22	43,44	43,68
AIIMAMc 1	23	114	114	112	109	112	112	115	119	115	137	108	121	148	120	118	125	124	121	122	164	121	135		99.40	98.61	99.20	93.85	88.47	83.73	85.71	82.34	83.04	75,14	80.00	80,20	80.00 79	9.80 79.8	81.58	78.53	79.37	77.98	70.24	69.84 69.4	44 70.	89 69.57	7 69.77	64.55	59,49 5	59.33 F	9.13 72	92 72	.33 74.41	44.06	42.37
AIIMAM3 2	24	113	113	111	108	111	111	114	118	114	136	107	120	147	110	117	124	123	120	121	163	120	134	3		99.20	99.40	94.05	89.07	84 13	86 31	82.74	83.43	75.51	80.20	80.40	80.20 80	0.00 80.0	8178	79 13	79.96	78 17	70.83	70.04 70	04 71	49 69 77	7 69.96	64.95	59.49 F	59.33 F	9 13 73	12 72	53 74.61	44 38	42.68
	24	110	110	444	444	444	444	447	404	117	120	110	100	150	100	100	107	106	100	104	100	100	107	7		55,20	00.01	02.45	00.47	02.72	05,31	02.02	00,40	74.77	70.60	70.00	70.60 70	70.4	01,10	70.50	70.27	77.50	70.04	60.44 60	44 70	00 60.10	60.20	65.24	50.94	50.60 1	0 40 70	52 74	04 74.00	44.06	40.07
AIIWAWC.2	23	110	110	114	400	114	114	117	121	117	139	110	123	150	122	120	127	120	125	124	100	123	137	1	4	-	30,01	33,45	00,47	03,75	00,71	00,20	02,04	74,11	79,00	19,00	19,00 18	0,41 75,4	01,19	70,00	79,57	77,50	70,24	09,44 09,4	44 70,	09,19	09,30	03,34	59,04 5	19,00 5	3,40 72,	71,2	74,02	44,00	42,57
AIPMAMC	20	113	113	111	108	111	111	114	118	114	130	107	120	145	117	116	123	123	119	120	162	119	133	4	3	0		94,25	88,87	84,13	86,31	82,54	83,23	/5,32	80,20	80,40	80,20 80	0,00 80,0	81,78	79,13	79,96	18,57	/0,63	69,84 69,	84 /1,	19 69,961	/ /0,16/	64,75	59,49 5	J9,13 5'	3,93 73,5	52 72,8	32 75,00	44,53	42,83
AcMAMc	27	107	107	107	102	100	100	101	118	114	138	108	120	149	121	119	126	127	124	125	167	124	141	31	30	33	29		86,31	81,94	83,93	80,36	80,31	72,78	78,26	78,46	78,06 77	7,87 77,6	7 79,05	76,39	77,03	76,04	59,11	68,32 68,	12 70,	36 69,05	/ 69,25/	64,03	58,98 5	59,21 5	9,01 72,7	/3 72,1	13 73,62	43,28	42,21
BdMAMc	28	113	113	111	108	113	113	115	113	109	132	106	112	149	121	118	129	127	129	130	171	125	142	58	55	58	56	69		84,49	86,68	82,31	84,66	76,78	77,14	77,34	77,53 77	7,34 77,3	4 80,52	78,31	79,16	77,76	75,73	74,90 74,3	27 75,	/8 68,48	68,68	67,56	61,76 6	j2,45 6	2,24 74,5	50 73,9	30 73,12	43,59	42,68
CsMAM3.1	29	125	125	124	127	129	130	130	136	136	151	132	141	165	137	134	147	147	144	145	184	143	151	82	80	82	80	91	78		94,43	86,48	82,64	76,07	75,49	75,69	75,10 74	4,51 74,5	1 77,08	77,58	78,61	75,45	59,25	68,65 68,3	25 67,	J2 65,38	65,57	60,79	55,58 5	55,56 5	5,36 69,1	<u>96</u> 69,7	37 70,28	43,75	43,15
CsMAM3.7	30	119	119	118	120	120	121	123	126	125	143	121	131	159	131	128	141	139	135	136	176	135	141	72	69	72	69	81	67	28	-	89,46	84,42	77,37	76,88	77,08	76,48 76	6,48 76,4	3 78,66	78,97	80,00	76,83	70,44	69,64 69,3	25 69,	90 67,31	67,50	62,38	56,95 5	56,75 5	6,55 71,/	54 70,	75 71,65	43,91	43,30
CsMAM3.3	31	133	133	132	133	134	135	137	144	142	159	137	142	176	148	141	157	153	151	151	192	152	161	89	87	84	88	99	89	68	53		79,09	72,36	73,72	73,91	73,52 73	3,72 73,73	2 75,30	73,61	74,26	72,28	56,27	65,48 65,4	48 66,	53 66,02	2 66,21	65,62	59,88 f	60,33 F	0,13 67,	19 66,	40 67,72	42,16	41,41
CrMAM1	32	123	123	122	125	126	127	126	133	130	143	127	134	162	136	133	145	135	139	140	182	140	138	86	84	88	85	100	77	88	79	106		84.83	74.95	75.15	75.54 75	5.15 75.1	5 78.11	78,13	78,77	79.92	69.98	69.18 68.3	39 69.	84 68.29	9 68.48	63.55	59.06 F	57.68 5	7.49 69	35 68.	76 70.33	43.15	41.77
CrMAM2.2	33	164	164	162	164	166	166	166	168	166	181	163	168	169	173	169	164	180	177	178	185	177	181	134	132	136	133	147	124	120	122	149	81	10004000	69.94	70.13	70.87 70	13 70.5	72 73	74.21	75.00	74.95	56.36	65.61 65	23 67	16 61 70	61 97	57.65	53.60 F	52.90 F	271 64	33 63	59 65 OF	40.95	39.64
	24	114	114	440	107	110	110	100	100	100	140	100	107	103	400	103	107	100	100	100	105	105	101	104	100	100	100	110	145	12.5	147	122	107	460	00,04	00.60	06.00	0.05 04.6	00.47	02.50	04.50	00.04	73.64	70.00 70.	20 07,	00 70.02	70.42	64.26	50,00 0,	E7.04 1	7.74 70	70 70	10 72.07	40,00	44.45
AIIMAM3.1	34	114	114	113	123	119	119	123	120	128	142	123	127	151	123	121	132	129	122	122	105	120	132	101	100	103	100	110	115	124	117	133	127	102		99,00	90,22 92	2,05 91,0	0 88,47	83,50	84,52	82,34	(3,01	12,82 12,	22 12,	18 10,231	10,43	04,30	08,32 0	17,94 D	1,14 12,1	8 72,	19 13,81	43,00	44,15
AlpMAMb	35	114	114	113	122	118	118	122	125	127	141	122	126	150	122	120	131	128	121	121	164	124	131	100	99	102	99	109	114	123	116	132	126	161	2		96,61 92	2,05 91,6	5 88,47	83,50	84,52	82,34	73,81	73,02 72,4	42 72,	28 70,43	/ 70,62/	64,55	58,51 5	58,13 5	7,94 72,9	38 72,3	39 74,07	43,82	44,31
AcMAMb	36	117	117	116	126	122	122	126	124	124	139	119	124	146	117	115	132	130	119	120	162	121	132	101	100	103	100	111	113	126	119	134	124	157	19	17	93	3,64 93,24	4 88,47	83,10	83,93	82,94	73,41	72,62 71,	83 71,	38 70,62	2 70,82	65,15	58,51 5	58,53 5	8,33 73,	18 72,3	39 74,07	43,97	44,46
AtMAM3	37	116	116	115	129	124	124	128	123	122	137	120	126	151	123	122	135	134	122	123	166	126	135	102	101	104	101	112	114	129	119	133	126	161	40	40	32	99,2	88,67	83,50	84,13	82,34	72,82	72,02 71,	43 70,	39 70,04	4 70,23	64,75	58,71 5	58,33 5	7,94 73,	18 72,	58 74,66	43,44	43,61
AtsMAM3	38	117	117	116	130	125	125	129	122	121	136	121	126	152	124	123	136	135	121	122	165	125	135	102	101	104	101	113	114	129	119	133	126	159	42	42	34	4	88,47	83,30	83,93	82,34	72,82	72,02 71,4	43 70,	89 70,04	4 70,23	64,75	58,51 5	58,13 5	7,74 73,	18 72,	58 74,66	43,44	43,61
BdMAMb	39	105	105	104	114	111	110	114	119	115	131	109	117	146	118	119	128	124	117	118	162	121	131	93	92	95	92	106	98	116	108	125	111	147	58	58	58	57 5	3	87,08	88,29	84,72	73,41	72,82 72,	62 71,	68 70,82	2 71,01	65,35	59,69 F	58,73 5	8,53 72,	98 72,	39 74,26	43,12	43,15
CsMAM3.2	40	124	124	123	130	135	135	137	139	138	154	133	143	160	132	130	149	140	133	134	177	132	143	108	105	108	105	119	108	113	106	133	110	138	83	83	85	83 8	4 65		96,79	89,18	73,75	73,15 72,	95 71.	20 66,73	3 66,93	63,00	58,30 E	56,31 F	6,11 71	43 70.	.83 72.92	43,28	43,30
CsMAM3.8	41	116	116	115	123	127	127	129	133	132	149	128	138	156	128	124	146	137	128	129	172	126	137	104	101	104	101	116	104	108	101	130	107	134	78	78	81	80 8	1 59	16		90.60	74.00	73 40 73	00 71	06 67.96	6 68 16	63.47	58.97 5	57 40 F	7 20 72	48 71	88 74 1F	43.84	4 43 70
CHAM2 1	12	102	102	102	120	121	121	120	120	125	152	122	140	157	120	197	147	122	120	120	172	107	126	111	110	112	109	101	111	124	117	140	101	124	90	90	96	00 0	77	54	47		74.00	72.20 72	0.0	96 67.70	67.00	62.07	50 50 5	57.20 F	7.00 70	10 60	70 72.27	12,75	12.61
	42	123	140	123	123	151	450	152	150	155	100	152	457	100	123	127	177	152	120	12.5	102	140	150	150	147	115	140	121	447	124	140	140	101	104	122	100	124	407 40	7 424	424	420	120	14,00	00.45 05	72 04	CE CA 04	07,30	62.04	57,07	50.00	7,00 70,	10 03,7	07 67.50	40,75	40,01
CSMAM3.4	43	142	142	141	147	153	153	155	150	150	108	152	157	190	162	160	1/3	153	151	151	192	149	159	150	147	150	148	150	11/	155	149	170	151	180	133	132	134	13/ 13	134	131	130	130	1/5	99,15 95,	/3 81,	15 64,011	64,20	63,81	57,97 5	18,28 5	3,07 69,0	18 08,2	2/ 07,59	41,85	41,81
CsMAM3.5	44	144	144	143	149	157	157	159	160	160	172	156	161	194	166	164	177	157	154	154	195	152	163	152	151	154	152	160	121	158	153	174	155	184	137	136	138	141 14	1 137	134	133	134	4	94,	87 80,	30 63,42	63,62	63,18	57,56 5	j8,49 5	3,28 68,6	57 67,8	37 67,19	41,54	41,50
CsMAM3.6	45	149	149	148	150	158	158	160	161	161	171	158	162	196	168	167	177	160	158	158	199	157	162	154	151	154	152	161	124	160	155	174	159	186	140	139	142	144 14	4 138	135	135	136	20	24	82,	28 63,23	63,42	62,97	57,14 5	56,39 5	6,18 67, ⁵	37 67,4	47 66,40	41,22	41,34
CrMAM3.3	46	144	144	142	145	150	149	150	149	150	162	146	150	189	160	158	170	159	160	160	201	160	166	147	144	147	146	150	117	162	152	169	152	176	141	140	142	147 14	7 143	144	145	151	87	91	84	65,56	65,76	65,69	59,63 5	58,79 5	8,58 69,	48 69,/	J8 68,97	42,41	41,81
BnMAM1.2	47	141	141	141	147	147	147	148	149	146	148	142	152	173	144	146	163	123	155	155	194	156	153	157	156	159	155	160	162	179	169	174	163	209	153	152	151	154 154	4 150	171	165	166	185	188 1	89 1	77	99,80	84,10	70,92 6	64,66 6	4,46 64,	85 64,	27 66,80	43,82	43,53
BrMAM1.2	48	140	140	140	146	146	146	147	148	145	148	141	151	172	143	145	162	122	154	154	193	155	152	156	155	158	154	159	161	178	168	173	162	208	152	151	150	153 15	3 149	170	164	165	184	187 1	88 1	76 1		83,94	70,78 F	64,53 F	4,33 65,	05 64,	47 66,99	43,97	43,68
BroMAM 1	49	173	173	173	176	178	178	179	178	175	172	171	181	201	170	173	198	155	189	189	230	192	179	179	177	174	178	182	157	198	190	165	183	227	180	179	176	178 17	3 175	185	183	185	173	176 1	77 1	64 70	9 80		80,79 7	74.65 7	4.41 61	17 60	76 61.58	39.03	38.34
ReMAM1.0	50	201	201	201	100	201	201	200	205	201	201	105	206	230	200	201	226	195	222	222	261	222	211	207	207	204	207	210	197	227	220	105	200	251	212	212	212	211 04	2 206	211	20.0	210	203	205 0	07 1	95 146	6 147	02	-	75.24	5.00 56	46 56	06 57.24	26.66	35.02
D-114111.2	50	201	400	201	199	201	201	100	100	105	107	100	200	2007	100	100	220	103	040	040	201	225	211	207	207	204	207	210	107	221	220	195	200	201	213	212	200	210 21	200	211	200	210	100	100 0		07 470	477	100	102	5,24 17	0.50 50,5	22 50,0	02 57.54	30,00	25.44
BrMAM1.4	51	198	198	198	195	197	196	199	198	195	197	192	201	221	196	192	218	1/3	212	212	253	215	212	205	205	202	206	206	181	224	218	190	212	252	212	211	209	210 21	208	218	213	214	199	198 2	1	1/6/		108	103	9	5,50 57,3	25 56,8	57,51	35,16	35,11
BrpMAM.2	52	199	199	199	196	198	197	200	198	195	197	193	202	228	197	193	218	174	212	212	252	216	213	206	206	203	207	207	182	225	219	191	213	253	213	212	210	212 21	3 209	219	214	215	200	199 2	09 1	18 177	178	109	104	2	57,0	J3 56,F	53 57,31	35,01	34,95
BooMAM1.2	53	121	121	120	126	126	128	132	133	132	154	127	142	172	144	143	153	145	142	143	185	145	164	137	136	139	134	138	127	152	144	166	156	193	138	137	136	136 13	5 137	144	139	151	154	156 1	60 1	52 181	180	193	219	213	214	98,	19 88,91	44,84	44,24
BrMAM1.3	54	123	123	122	128	128	130	134	136	135	157	131	145	174	146	145	156	148	145	146	188	147	165	140	139	142	137	141	130	155	148	170	159	197	141	140	140	139 13	9 140	147	142	153	158	160 1	62 1	j4 184	4 183	195	221	215	216	9	88,12	45,47	43,93
RsMAM1.1	55	122	122	121	127	125	126	129	133	131	151	130	140	167	139	134	146	134	139	140	178	136	157	130	129	132	127	134	136	151	144	164	151	189	133	132	132	129 12	9 131	137	131	140	164	166 1	70 1	57 171	170	194	218	215	216	56	60	45,94	45,48
AtIPMS1	56	350	350	350	354	352	351	354	348	348	356	347	350	379	351	350	371	355	352	352	390	351	362	358	356	358	355	363	361	360	359	369	365	398	360	359	358	362 36	2 364	363	360	360	371	373 3	75 3	68 359	358	389	406	413	414 3	53 3	49 346		86,28
AtIPMS2	57	355	355	355	360	356	355	358	356	356	359	352	357	385	357	352	375	354	353	353	393	355	361	370	368	370	367	371	368	365	364	375	375	408	358	357	356	362 36	2 365	364	362	362	373	375 3	76 3	73 362	2 361	394	412	414	415 3	58 3	60 350	87	
sectors and sectors and	10000	2000	1000000	100000000	Support	1000	100000	STANA ST	1000000	Sector 1	1000 C	10000	CHARACTER .	1000000	-COMMINS		NICONST.	Section 2	Second Sec.	3000000	130622-012	1000000	311525553	201202023	51593 GM	20100000	1000000	1000000	511525645-	1000000	Surveyora:	Street and	Second Second	200000	STREET, ST	and the second se	1000 CC	NOTICE STREET	11 C 11 C 12 C 12 C 12 C 12 C 12 C 12 C		STREET, ST	10000000	CHARGE STREET	S100.000	1999 (J. 1999)			A CONTRACTOR OF						4	4















Supplementary Figure legends

Supplementary Figure S1. Alignment of 57 MAM and 2 IPMS full protein sequences. According to *A. thaliana* MAM1 numbering, only Leu186, Thr257, Ile258, Gly259 and Ala290 residues are shown.

Supplementary Figure S2. Matrix from the alignment of MAM and IPMS enzyme sequences. Upper part indicates sequence similarity in percentage and the lower part shows differences between the protein sequences. Two MAM sequences have been removed from the matrix, as the comparison indicated low sequence similarity due to poor quality of the sequence data.

Supplementary Figure S3. LC-MS traces of homomethionine (HM), dihomomethionine (DHM), trihomomethionine (TriHM), tetrahomomethionine (TetraHM), pentahomomethionine (PentaHM) and hexahomomethionine (HexaHM). A representative sample of MAM1 and MAM3 containing strains as well as an empty vector control are shown. For each compound, the pure sample is shown in the top panel.

Supplementary Figure S4. LC-MS traces of heptahomomethionine (HeptaHM), homoleucine (HL) and homophenylalanine (HPhe). A representative sample of MAM1 and MAM3 containing strains as well as an empty vector control are shown. For each compound, the pure sample is shown in the top panel.

Supplementary Figure S5. Homology model of MAM1 from *A. thaliana*. (yellow) superimposed on the crystal structure of *N. meningitis* IPMS (green). Only the $(\beta/\alpha)_8$ catalytic barrel is shown. The RMSD value is 0.26 Å.

Supplementary Figure S6. Protein amino acids monitored in this study. Each graph shows levels of one amino acid in the media of *E. coli* strains expressing MAM variants and an empty vector control. The mean of all cultures is indicated by the red line. ANOVA was used to investigate changes in the individual amino acids between the cultures. p-values are shown in upper right corner of each graph. Data represents average and standard deviation of three biological replicates each grown in three technical replicates.

Supplementary Figure S7. Produced chain elongated amino acids were grouped according to how many methylene groups were added to the methionine, phenylalanine or leucine structures (one, two or three and above). Bars represents the percentage of each group of products relative to the total production within each culture. Data represents average and standard deviation of three biological replicates each grown in three technical replicates.

Supplementary Figure S8. Glucosinolate analysis in *A. thaliana* ecotype Col-0 and knockout mutants mam1 and mam3. Glucosinolates (GLS) were grouped into aromatic (2PE) GLSs, indole GLSs and short chain (SC – one to three elongation rounds) and long chain (LC – four elongation rounds and above) aliphatic GLSs. Data represents average and standard deviation of 3-7 biological replicates.

Supplementary Figure S9. Protein levels in *E. coli* strains expressing the chain elongation pathway genes, A) *BCAT4*, B) *MAM1*, C) *LSU1*, D) *MAM3*, E) *SSU3*, F) *IPMS2* and G) *IPMDH1* and H) *E. coli* housekeeping gene *ICD*. A-G are normalized the ICD, while the ICD is not normalized. Different colours indicate individual peptides within each protein. Data represents average and standard deviation of three biological replicates.

Supplementary Tables

Supplementary Table S1. List of primers used in this study. Lower case letters denotes the USER

tail used for cloning. Uracils are marked in blue. Mutated nucleotides are marked in red.

Name	Sequence	Description
MAM1_fwd	ggcttaauATGCATCACCACCACCATCACAACTATGTGCGTGTATTC	MAM1 forward primer
BCAT4_rev	ggtttaauTCAGCCCTGGCGGTCAAT	BCAT4 reverse primer
MAM3_fwd	ggcttaauATGCATCACCACCACCATCACGCTGAGTCCAAAAAGGTGGC	MAM3 forward primer
MAM3_rev	acaaaattauTTCTAGAGGGGTTATACAACAGCGGAAATC	MAM3 reverse primer
IPMS2_fwd	ggcttaauATGCATCACCACCACCATCACATGGAGTCTTCGATTCTCA	IPMS2 forward primer
IPMS2_rev	acaaaattauTTCTAGAGGGGTCAGGCAGGGACTTCGTTG	IPMS2 reverse primer
L186_fwd	acatctactaguGACATTCACATGAAATATAAG	Fusion primer for L186-mutant
L186M_rev	actagtagatguGAATACCATTATCCTTGGCCTC	Fusion primer for L186M-mutant
T257/G259_fwd	acggtagggauCAACATGCCACATGAATACGG	Fusion primer for T257-mutant
T257N_rev	atccctaccguATCACCGATGTTCACCACCGTAA	Fusion primer for T257N-mutant
T257G_rev	atccctaccguATCACCGATGCCCACCACCGTAA	Fusion primer for T257G-mutant
T257V_rev	atccctaccguATCACCGATGACCACCACCGTAA	Fusion primer for T257V-mutant
T257D_rev	atccctaccguATCACCGATGTCCACCACCGTAA	Fusion primer for T257D-mutant
T257C_rev	atccctaccguATCACCGATGCACACCACCGTAA	Fusion primer for T257C-mutant
T257S_rev	atccctaccguATCACCGATGCTCACCACCGTAA	Fusion primer for T257S-mutant
G259P_rev	atccctaccguATCTGGGATGGTCACCACCGTAA	Fusion primer for G259P-mutant
G259A_rev	atccctaccguATCGGCGATGGTCACCACCGTAA	Fusion primer for G259A-mutant
A290S_fwd	acgatgttgtcguCAGCGTTCATTGTCACAACGAC	Fusion primer for A290S-mutant
A290T_fwd	acgatgttgtcguCACCGTTCATTGTCACAACGAC	Fusion primer for A290T-mutant
A290G_fwd	acgatgttgtcguCGGCGTTCATTGTCACAACGAC	Fusion primer for A290G-mutant
A290_rev	acgacaacatcguCAATTCCAGGGGTGTTTGCTTTG	Fusion primer for A290-mutant
GA_rev	atccctaccguATCGGCGATGCCCACCACCGTAA	Fusion primer for T257G/G259A-mutant

Supplementary Table S2. Transitions and response factors used to quantify levels of chain elongated amino acids. Response factors of methionine- and leucine-derived products were reported in (20).

Amino acid	Q1	Q3	CE	Internal standard	Q1	Q3	Response factor
	180.1	91.1 ^{Qt}	-22	13C,15N-Phe	176.2	129.2	1.61
HPhe	180.1	134.1	-8				
	180.1	117.1	-13				
HM	164.2	70.3 ^{Qt}	-16	13C,15N-Val	124.1	77.2	0.35
рнм	178.2	84.2 ^{Qt}	-14	13C,15N-Phe	176.2	129.2	1.05
DIIM	178.2	132.1	-10				
ТеіНМ	192.2	98.2 ^{Qt}	-14	13C,15N-Phe	176.2	129.2	1.25
1111111	192.2	146.1	-9				
TetraHM	206.2	112.2 ^{Qt}	-13	13C,15N-Phe	176.2	129.2	0.91
ictianivi	206.2	160.1	-10				
PentaHM	220.3	126.2 ^{Qt}	-16	13C,15N-Phe	176.2	129.2	0.41
I CittaIIIvi	220.3	174.1	-10				
HevoHM	234.4	140.2 ^{Qt}	-16	13C,15N-Phe	176.2	129.2	0.36
пслани	234.4	188.1	-11				
HontoHM	248.2	188.1 ^{Qt}	-10	13C,15N-Phe	176.2	129.2	n.d.
пертани	148.2	154.1	-16				
HL	146.2	100.1	10	13C,15N-Phe	176.2	129.2	0.88
DHL	160.2	114.1	-10	13C,15N-Phe	176.2	129.2	1.00*
TriHL	174.2	128.1	-10	13C,15N-Phe	176.2	129.2	1.00*

*Response factors for DHL and TriHL were assumed to be 1.00. CE = collision energy. Q = quadrupole. Qt = quantifier transition

Supplemental Table S3: Transitions used for Selected Reaction Monitoring (SRM) for targeted proteomics on peptides of methionine chain elongation pathway proteins. Retention times and parent ion to fragment ion transitions are given. All peptides were selected in Q1 as the double-charged ions $[M+H]^{2+}$ and fragment ions in Q3 as single-charged ions $[M+H]^{+}$. Collision energies (CE) for natural non-labelled (light) and isotopically labelled (heavy) peptides were identical.

				Light p	eptide	Heavy p	peptide	
				Q1	Q3	Q1	Q3	CE
Protein name	AGI code	Peptide	RT	$[M+H]^{2+}$	$\left[M+H ight]^+$	$[M+H]^{2+}$	$\left[M+H ight]^+$	[eV]
BCAT4	At3g19710	TGEETLAAK	1.60	460.25	761.42	464.25	769.42	-13
			1.60	460.25	818.44	464.25	826.44	-15
			1.60	460.25	632.38	464.25	640.38	-14
		LYETLSDIQTGR*	8.30	698.36	776.4	703.36	786.4	-19
			8.30	698.36	990.53	703.36	1000.53	-26
			8.30	698.36	1119.57	703.36	1129.57	-23
		SITNYCPVWIPLAEAK	18.70	931.49	927.54	935.49	935.54	-3
			18.70	931.49	1123.67	935.49	1131.67	-29
			18.70	931.49	628.38	935.49	636.38	-41
		GNVVSTPTIAGTILPGVTR	16.50	927.03	529.32	932.03	539.32	-29
			16.50	927.03	642.4	932.03	652.4	-28
MAM1	At5g23010	SLGFNDIQFGCEDGGR*	13.60	886.39	897.36	891.39	907.36	-31
			13.60	886.39	1025.42	891.39	1035.42	-33
			13.60	886.39	404.2	891.39	414.2	-41
		DGEQSPGGSLTPPQK	2.50	749.37	981.55	753.37	989.55	-23
			2.50	749.37	1068.58	753.37	1076.58	-25
			2.50	749.37	469.29	753.37	477.29	-30
		STYEILSPEDIGIVK	17.00	832.45	957.54	836.45	965.54	-22
			17.00	832.45	870.51	836.45	878.51	-25
			17.00	832.45	1070.62	836.45	1078.62	-24
		SGNASLEEVVMALK	17.50	724.38	918.51	728.38	1126.63	-24
			17.50	724.38	1118.63	728.38	1039.59	-24
			17.50	724.38	1031.59	728.38	926.51	-23
MAM3	At5g23020	GESLMDGVYTK	6.70	600.29	813.4	604.29	821.4	-19
			6.70	600.29	1013.51	604.29	1021.51	-16
			6.70	600.29	682.35	604.29	690.35	-19
		ALVVNGAEISSEK	5.70	658.86	934.46	662.86	942.46	-20
			5.70	658.86	1033.53	662.86	1041.53	-20
			5.70	658.86	820.42	662.86	828.42	-21
		SGNAPLEEVVMALK	18.70	729.39	1128.65	733.39	1136.65	-21
			18.70	729.39	918.51	733.39	926.51	-25
			18.70	729.39	588.4	733.39	596.4	-23
		STYEILSPEDVGIVK*	15.50	825.44	943.52	829.44	951.52	-23
			15.50	825.44	856.49	829.44	864.49	-23
			15.50	825.44	1056.61	829.44	1064.61	-25
		DGEQSPGAALTPPQK	3.40	748.38	469.29	752.38	477.29	-32
			3.40	748.38	372.24	752.38	380.24	-41

			3.40	748.38	979.57	752.38 987.57	7 -24
IPMS2	At1g74040	GTYEIMSPEEIGLER*	15.40	889.94	1102.53	894.94 1112.53	3 -28
			15.40	889.94	942.5	894.94 952.5	5 -32
IPMI-LSU1	At4g13430	FILDGEMPSYLQAK*	16.90	806.42	806.45	810.42 814.45	5 -26
			16.90	806.42	937.5	810.42 945.5	5 -24
			16.90	806.42	1123.56	810.42 1131.56	5 -24
		VWMDVYALPVPGAGGK	18.50	830.44	682.4	834.44 690.4	4 -21
			18.50	830.44	486.28	834.44 494.28	3 -37
			18.50	830.44	261.17	834.44 269.17	7 -49
IPMI-SSU3	At3g58990	LGSFALNGLPK	12.60	558.83	712.45	562.83 720.45	5 -19
			12.60	558.83	1003.57	562.83 1011.57	7 -18
			12.60	558.83	641.41	562.83 649.41	-17
		EDGSSLLINHTTR	3.90	721.87	854.49	726.87 864.49	-29
			3.90	721.87	967.58	726.87 977.58	3 -29
			3.90	721.87	741.41	726.87 751.41	-28
		NCVATGEIFPLESEVR*	15.10	910.95	829.45	915.95 839.45	5 -30
			15.10	910.95	976.52	915.95 986.52	2 -30
			15.10	910.95	490.27	915.95 500.27	-37
IPMDH1	At5g14200	LSDAILLGAIGGYK*	17.00	695.91	891.54	699.91 899.54	-19
			17.00	695.91	778.46	699.91 786.46	5 -20
			17.00	695.91	1004.63	699.91 1012.63	3 -22
		AGSLEGLEFDFK	14.20	656.83	855.44	660.83 863.44	-20
			14.20	656.83	984.48	660.83 992.48	3 -18
			14.20	656.83	685.33	660.83 693.33	3 -17
		IEDAVVDALNK	6.05	593.83	944.52	597.83 952.52	2 -17
			6.05	593.83	659.39	597.83 667.39	9 -17
			6.05	593.83	758.45	597.83 766.45	5 -17
ICD	JW1122	GPLTTPVGGGIR*	6.37	562.83	655.40	567.83 665.40) -20
			6.37	562.83	857.49	567.83 867.49	-21
			6.37	562.83	756.44	567.83 766.44	-19

*= peptides represented in Figure 8.

Supplemental Table S4: Pairwise t-test of the methionine levels from media of *E. coli* strains expression the chain elongation pathway with 18 different MAM variants and an empty vector control. p-values shown.

	Empty																	
	vector	MAM1	MAM3	IPMS2	L186M	T257N	T257G	T257V	T257D	T257C	T257S	G259P	G259A	A290S	A290T	A290G	GA	GAG
MAM1	0.1316	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
MAM3	0.7101	0.2507	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
IPMS2	0.0254	0.0004	0.5510	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
L186M	0.3535	0.0103	0.5755	0.0023	-	-	-	-	-	-	-	-	-	-	-	-	-	-
T257N	0.2301	0.0088	0.1192	0.2755	0.0372	-	-	-	-	-	-	-	-	-	-	-	-	-
T257G	0.8806	0.1727	0.8245	0.0178	0.4355	0.1784	-	-	-	-	-	-	-	-	-	-	-	-
T257V	0.9379	0.1136	0.6532	0.0305	0.3152	0.2609	0.8196	-	-	-	-	-	-	-	-	-	-	-
T257D	0.3792	0.0199	0.2139	0.1591	0.0752	0.7432	0.3045	0.4223	-	-	-	-	-	-	-	-	-	-
T257C	0.6634	0.2773	0.9491	0.0087	0.6195	0.1055	0.7753	0.6080	0.1920	-	-	-	-	-	-	-	-	-
T257S	0.5230	0.3757	0.7885	0.0051	0.7698	0.0700	0.6245	0.4740	0.1332	0.8379	-	-	-	-	-	-	-	-
G259P	0.1362	0.0040	0.0655	0.4266	0.0185	0.7637	0.1024	0.1569	0.5307	0.0572	0.0366	-	-	-	-	-	-	-
G259A	0.0043	4.9e-05	0.0016	0.4823	0.0003	0.0773	0.0029	0.0053	0.0383	0.0013	0.0007	0.1385	-	-	-	-	-	-
A290S	0.4230	0.4693	0.6657	0.0033	0.8977	0.0494	0.5140	0.3799	0.0974	0.7125	0.8695	0.0251	0.0005	-	-	-	-	-
A290T	0.1735	0.0057	0.0862	0.3536	0.0254	0.8680	0.1323	0.1985	0.6218	0.0758	0.0492	0.8930	0.1075	0.0342	-	-	-	-
A290G	0.0920	0.8519	0.1836	0.0002	0.4347	0.0054	0.1229	0.0786	0.0126	0.2048	0.2851	0.0024	2.8e-05	0.3639	0.0035	-	-	-
GA	0.8826	0.0993	0.6039	0.0357	0.2834	0.2909	0.7659	0.9444	0.4632	0.5604	0.4326	0.1776	0.0064	0.3438	0.2232	0.0681	-	-
GAG	0.7299	0.0666	0.4745	0.0552	0.2058	0.3888	0.6206	0.7891	0.5911	0.4364	0.3272	0.2475	0.0106	0.2541	0.3053	0.0446	0.8432	-
GAM	0.3673	0.0189	0.2059	0.1656	0.0718	0.7602	0.2943	0.4096	0.9821	0.1847	0.1278	0.5454	0.0403	0.0931	0.6377	0.0119	0.4498	0.5758