

INDELS	GeneID	Synonyms	Position	MAH104 (-)	CAM84 (I)	896 (I)	CAM20 (II)	574 (II)	67608 (I)	M189 (I)	213G (I)	619 (III)	CAM87 (III)	CAM86 (III)	CAM38 (III)	841 (III)	MapK10 Product	Maa104 Product	
	MapK10-0028c (1B4)	MAP0028c:MAV_1453:MAA1951	30	1.37	0.66	0.86	0.91	0.80	0.85	0.77	1.33	2.63	1.21	1.22	hypothetical protein		transposase		
	MapK10-0036 (1B2)	MAP0036:MAV_0042:MAA3298	40	0.83	1.23	0.99	0.83	0.42	1.80	1.09	1.09	1.07	1.10	1.15	0.98	hypothetical protein	NLP/Pf0 family protein		
	MapK10-0066 (1C18)	MAP0066:MAV_0073:MAA3208	71	0.93	0.99	1.04	0.82	0.40	1.16	1.41	1.04	1.01	1.09	1.12	hypothetical protein		DJ-1/PfpJ family protein		
	MapK10-0071 (1C23)	chbB:MAP0071:MAV_0079:MAA3203	76	1.29	0.78	0.94	1.02	0.85	0.82	0.60	0.98	1.64	3.72	1.77	1.16	1.16	DnaB	replicative DNA helicase	
	MapK10-0072c (1C24)	MAP0072c:MAV_0080:MAA3202	77	1.25	0.93	0.82	1.02	0.81	0.87	0.89	3.43	1.86	1.18	1.14	hypothetical protein		hypothetical protein		
	MapK10-0073c (1D1)	MAP0073c:MAV_0081:MAA3201	78	1.15	0.86	0.98	0.91	0.73	0.78	0.82	2.87	1.73	1.38	1.29	hypothetical protein		hypothetical protein		
	MapK10-0074 (1D2)	MAP0074:MAV_0082:MAA3200	79	1.13	0.86	1.02	0.92	1.04	1.02	1.04	2.91	1.57	1.00	0.96	hypothetical protein		transcriptional regulator, TetR family protein		
	MapK10-0075 (1D3)	MAP0075:MAV_0083:MAA3199	80	1.14	0.71	1.16	1.02	0.47	0.66	1.07	3.03	1.83	1.25	1.44	hypothetical protein		hypothetical protein		
	MapK10-0076 (1D4)	rrmL4_1:MAP0076:MAV_0084:MAA3198	81	1.18	0.60	0.88	0.87	0.73	0.83	1.08	2.74	1.50	1.73	1.50	1.07	WmpL4_1	putative transport protein MmpL4		
	MapK10-0077 (1D5)	MAP0077:MAV_0085:MAA3197	82	1.20	0.66	0.92	1.13	0.60	0.63	1.40	1.10	1.39	0.99	0.87	hypothetical protein		hypothetical protein		
	MapK10-0078 (1D6)	MAP0078:MAV_0086:MAA3196	83	1.31	0.81	1.03	1.04	0.54	0.75	0.84	0.68	2.06	1.37	1.00	hypothetical protein		hypothetical protein		
	MapK10-0079 (1D7)	MAP0079:MAV_0087:MAA3195	84	1.20	0.83	1.04	0.87	0.66	0.96	1.41	1.32	2.85	1.60	0.81	1.11	hypothetical protein		oxidoreductase, short chain dehydrogenase/reductase family protein	
	MapK10-0080c (1D8)	MAP0080c:MAV_0088:MAA3194	85	1.08	0.82	0.96	1.41	0.54	0.59	0.90	1.08	1.24	3.27	1.58	1.18	1.17	hypothetical protein	hypothetical protein	
	MapK10-0081 (1D9)	MAP0081:MAV_0089:MAA3193	86	1.13	0.92	1.16	0.97	0.78	0.68	1.05	3.32	1.65	1.30	1.19	hypothetical protein		FAD binding domain protein		
	MapK10-0082 (1D10)	MAP0082:MAV_0092:MAA3192	87	0.99	0.92	1.13	0.76	0.35	1.41	1.13	2.87	1.47	1.04	0.75	hypothetical protein		transcriptional regulator, Crp/Fnr family protein		
	MapK10-0083c (1D11)	MAP0083c:MAV_0091:MAA3191	88	1.27	0.87	0.91	0.97	1.02	1.12	0.88	2.54	1.67	0.98	0.88	hypothetical protein		hypothetical protein		
	MapK10-0084c (1D12)	MAP0084c:MAV_0093:MAA3190	89	1.12	0.97	0.86	0.90	0.82	0.88	0.77	2.33	1.51	1.02	1.10	hypothetical protein		hypothetical protein		
	MapK10-0085c (1D13)	lysR:MAP0085c:MAV_0094:MAA3189	90	1.06	0.87	1.10	0.99	0.90	0.85	1.08	2.82	1.35	1.10	0.98	LysR		integral membrane protein DUF6		
	MapK10-0086 (1D14)	MAP0086:MAV_0095:MAA3188	91	0.99	0.89	0.99	0.95	0.54	0.82	0.86	0.88	0.92	2.46	1.37	1.05	1.11	hypothetical protein		hypothetical protein
	MapK10-0087 (1D15)	MAP0087	92	0.39	1.24	0.78	1.06	0.51	0.74	0.56	0.78	1.30	3.07	1.55	1.01	1.04	hypothetical protein		hypothetical protein
	MapK10-0088 (1D16)	MAP0088:MAV_0096:MAA3187	93	0.97	0.86	0.91	1.00	0.73	0.77	0.72	0.78	1.27	3.69	1.94	1.09	1.12	hypothetical protein		hypothetical protein
	MapK10-0089 (1D17)	MAP0089:MAV_0097:MAA3187	94	1.12	0.85	0.98	1.02	1.07	1.07	1.11	4.05	1.74	1.16	1.18	hypothetical protein		phosphothioicin N-acetyltransferase		
	MapK10-0090c (1D18)	MAP0090c:MAV_0098:MAA3186	95	1.02	0.73	0.96	0.91	0.69	0.92	1.37	3.09	1.96	1.04	1.00	hypothetical protein		hypothetical protein		
	MapK10-0091c (1D19)	MAP0091c:MAA3185	96	1.48	0.75	1.19	1.11	0.70	0.70	0.62	2.99	1.23	1.15	1.12	hypothetical protein		hypothetical protein		
	MapK10-0092 (1D20)	MAP0092:MAV_0100:MAA3184	97	1.10	0.80	0.96	0.97	0.74	0.77	0.94	2.82	1.60	0.97	1.12	hypothetical protein		hypothetical protein		
	MapK10-0093 (1D21)	MAP0093:MAA3183	98	1.09	0.72	0.81	0.88	0.70	0.69	1.00	3.01	1.85	1.23	1.23	hypothetical protein		hypothetical protein		
	MapK10-0094 (1D22)	MAP0094	99	0.14	0.78	0.90	1.14	0.56	0.94	1.00	1.24	3.34	1.71	1.04	1.03	hypothetical protein		hypothetical protein	
	MapK10-0095c (1D23)	nucl_1:MAP0095c	100	0.12	0.64	0.80	1.05	0.82	0.75	0.69	1.00	2.77	1.77	1.09	0.90	1.00	NADH dehydrogenase subunit I		
	MapK10-0096c (1D24)	MAP0096c	101	0.09	0.81	0.90	1.11	0.83	0.76	0.57	0.92	1.29	3.33	1.82	1.19	1.00	hypothetical protein		hypothetical protein
	MapK10-0097c (1E1)	MAP0097c	102	0.05	0.85	0.89	0.82	0.75	0.81	0.94	3.34	1.89	1.12	1.14	hypothetical protein		hypothetical protein		
	MapK10-0098c (1E2)	MAP0098c	103	0.03	0.73	0.87	0.87	0.69	0.68	0.83	3.42	1.80	1.00	1.04	hypothetical protein		hypothetical protein		
	MapK10-0099 (1E3)	MAP0099	104	0.05	0.95	0.85	0.88	0.55	0.55	0.52	1.57	1.01	0.98	0.98	hypothetical protein		hypothetical protein		
	MapK10-0100 (1E4)	MAP0100	105	0.05	0.68	0.84	0.81	0.70	0.81	0.80	3.21	1.74	1.14	1.06	hypothetical protein		hypothetical protein		
	MapK10-0101 (1E5)	MAP0101	106	0.11	0.70	0.89	0.97	0.64	0.65	0.59	2.74	1.49	0.93	0.96	hypothetical protein		hypothetical protein		
	MapK10-0102 (1E6)	MAP0102	107	0.08	0.67	0.88	0.91	0.67	0.81	1.06	2.70	1.81	1.52	1.02	1.01	0.91	hypothetical protein		hypothetical protein
	MapK10-0103c (1E7)	MAP0103c	108	0.17	0.71	0.80	0.90	0.63	0.65	0.63	0.82	1.35	3.48	1.60	1.11	1.07	hypothetical protein		hypothetical protein
	MapK10-0124 (1F4)	MAP0124:MAA3166	130	0.95	1.20	1.14	0.83	0.41	1.81	1.17	0.89	0.85	1.01	0.93	hypothetical protein		hypothetical protein		
	MapK10-0128c (1F8)	MAP0128c:MAV_0122:MAA3162	134	1.06	0.96	0.90	1.03	0.78	0.85	0.91	0.28	0.86	0.93	0.96	1.10	hypothetical protein		hypothetical protein	
	MapK10-0148c (1G4)	MAP0148c:MAA3142	155	1.11	0.87	1.19	1.10	1.42	1.18	1.12	1.00	1.09	1.68	1.06	hypothetical protein		hypothetical protein		
	MapK10-0168c (1G24)	MAP0168c:MAV_0161:MAA3125	175	1.00	0.91	1.04	0.94	0.39	1.99	1.42	0.77	1.13	0.90	0.73	hypothetical protein		hypothetical protein		
	MapK10-0174 (1H6)	MAP0174:MAV_0168:MAA3120	181	1.03	0.93	1.12	1.16	0.29	1.04	1.11	0.48	0.90	0.92	0.99	hypothetical protein		hypothetical protein		
	MapK10-0210c (1H19)	pirC:MAP0210c:MAV_0207:MAA3084	220	1.09	1.04	0.95	2.16	1.03	1.42	1.24	1.02	0.89	0.97	1.00	PirG		Erp protein		
	MapK10-0253 (1K14)	MAP0253	286	0.90	0.66	0.90	0.42	0.62	0.68	0.91	1.52	1.10	1.02	1.13	hypothetical protein		hypothetical protein		
	Maa104-0258 (14H8)	MAV_0258:MAA3036	271	5.40			0.74				0.22						hypothetical protein		
	Maa104-0259 (14H7)	MAV_0259:MAA3035	272	27.98		0.72	0.85				0.39	0.94		1.28	0.64		hypothetical protein		
	Maa104-0261 (14H6)	MAV_0260:MAA3034	273	12.73							8.60						hypothetical protein		
	Maa104-0261 (14H5)	MAV_0261:MAA3033	274	35.22							13.76						hypothetical protein		
	Maa104-0270 (14H8)	MAV_0270:MAA3024	283	3.00	0.60	1.01	1.35	1.01	0.36	0.72	0.97	0.93	0.73	0.75	0.78	0.80	acetyltransferase, gnat family protein		
	Maa104-0295 (14H10)	MAV_0295:MAA3004	303	14.23			1.14				0.35						hypothetical protein		
	MapK10-0281 (1L18)	MAP0281:MAV_0327:MAA2974	335	1.04	0.71	0.80	0.35	0.46	0.91	1.13	3.32	1.74	1.21	1.05	hypothetical protein		hypothetical protein		
	MapK10-0282c (1L19)	MAP0282c	336	0.13	0.69	0.84	0.91	0.53	0.52	0.89	3.32	1.57	1.26	1.05	hypothetical protein		hypothetical protein		
	MapK10-0282c-0283c (1L20)	MAP0282c-0283c	337	0.18	0.71	0.83	0.92	0.60	0.72	0.82	3.33	1.60	1.03	1.12			hypothetical protein		
	MapK10-0330 (14H3)	MAV_0330:MAA2970	342	11.85		2.61											hypothetical protein		
	Maa104-0331 (14H2)	MAV_0331:MAA2869	343	6.07							0.33						hypothetical protein		
	INDEL1	Maa104-0339 (14G23)	352	2.04			0.44	10.29	14.81	18.48	9.97	10.00	12.18	9.22	6.79		transcriptional regulator, GmrR family protein		
	MapK10-0362c (1P5)	MAP0362c:MAV_0415:MAA2893	428	1.04	1.02	0.92	0.79	0.33	1.08	1.12	0.98	0.98	0.99	1.07	0.89	hypothetical protein		hypothetical protein	
	MapK10-0363 (1P6)	MAP0363:MAV_0416:MAA2892	429	0.96	1.01	1.04	1.05	0.36	1.77	1.30	0.28	0.83	1.02	1.07	0.97	hypothetical protein		GaB/Yey domain protein	
	MapK10-0415 (2B10)	MAP0415:MAV_0470:MAA2948	483				0.92	0.22	0.57	0.65							hypothetical protein		
	Maa104-0485 (14G6)	MAV_0485:MAA2834	496	20.28	2.61		0.75										hypothetical protein		
	MapK10-0486c (2E9)	MAP0486c:MAV_0580:MAA2752	588				0.89	0.81	0.38	0.86	1.09						Lamb/YcsF family protein		
	MapK10-0538c (2G13)	MAP0538c:MAV_0632:MAA2700	641	0.80	0.94	1.03	0.66	0.91	0.38	0.99	1.55	0.58	1.47	1.05	1.09	0.73	hypothetical protein		
	Maa104-0690 (14E23)	MAV_0690:MAA2647	700	9.76		0.69											hypothetical protein		
	Maa104-0697 (																		

	MapK10-0861 (3E3)	MAP0861	1,053	0.57	0.73	1.42	0.24	0.51	0.51	1.23	2.99	1.64	1.05	1.10	hypothetical protein			
	MapK10-0862 (3E4)	MAP0862	1,054	0.15	0.65	0.73	1.36	1.34	0.65	0.58	0.82	1.57	4.37	1.67	1.01	1.11	hypothetical protein	
	MapK10-0863 (3E5)	MAP0863	1,055	0.63	0.68	0.81	1.29	0.92	0.66	0.74	1.51	3.80	1.76	1.25	1.21	EpA		
	MapK10-0864 (3E6)	MAP0864	1,056	0.03	0.63	0.84	0.85	0.89	0.70	0.55	0.81	1.39	3.61	1.90	1.05	1.10	hypothetical protein	
	MapK10-0865 (3E7)	MAP0865	1,057	0.03	0.63	0.75	0.86	0.90	0.67	0.53	0.71	1.07	4.25	1.82	1.09	1.12	hypothetical protein	
	MapK10-0865-0866 (3E8)	MAP0865-0866	1,058	0.10	0.64	0.93	0.90	0.82	0.80	0.68	0.73	0.98	3.31	1.90	1.05	1.18		
	MapK10-0866 (3E9)	MAP0866	1,059	0.09	0.67	0.89	0.99	0.79	0.78	0.78	0.78	0.94	1.74	1.11	1.11	hypothetical protein		
	MapK10-1036 (3L12)	rvuC:MAP1036:MAV_3475:MAA0084	1,244	0.78	0.85	1.58	0.84	0.74	1.09	1.35	0.26	0.99	1.50	1.07	1.01	Holliday junction resolvase crossover junction endonuclease RuvC		
	MapK10-3459 (12M)	MAV_3459:MAA0099	1,261	2.16	2.46		0.79								hypothetical protein			
	MapK10-3380 (12I0)	MAV_3380:MAA0172	1,342	1.93			1.32			5.53					hypothetical protein			
	MapK10-3379 (12I1)	MAV_3379:MAA0173	1,343	2.14	0.82	0.90	1.45	1.09	0.16	0.23	0.18	0.56	0.40	0.28	0.25	1.74	AnsC-family protein transcriptional regulator MntJ protein	
	MapK10-1230-1231 (4D16)	MAP1230-1231	1,453	0.23	0.66	0.88	1.24	1.34	1.04	0.69	0.89	1.69	4.72	2.63	1.47	1.51		
	MapK10-1231 (4D17)	gmaA:MAP1231	1,454	0.15	0.72	0.81	1.02	1.34	0.85	0.59	0.85	3.88	1.83	1.24	1.20	GmdA		
	MapK10-1232 (4D18)	epaA:MAP1232	1,455	0.08	0.67	0.83	0.99	1.92	0.75	0.51	0.83	3.85	1.76	1.25	1.14	hypothetical protein		
	MapK10-1233 (4D19)	MAP1233	1,456	0.22	0.66	0.85	0.90	2.30	0.57	0.63	0.95	1.83	5.06	1.46	1.38	1.07	hypothetical protein	
	MapK10-1234 (4D20)	MAP1234	1,457	0.24	0.72	0.70	0.91	1.32	0.57	0.53	0.72	1.42	3.70	1.63	1.14	1.23	hypothetical protein	
	MapK10-1235 (4D21)	MAP1235	1,458	0.44	0.61	0.89	0.84	1.24	0.59	0.58	0.80	1.75	4.74	1.62	1.37	1.24	hypothetical protein	
	MapK10-1236 (4D22)	trc:MAP1236c	1,459	0.49	0.68	1.07	0.60	0.71	0.48	0.82	1.35	3.85	1.52	1.26	1.22	Dtrc		
	MapK10-3270 (12I9)	MAV_3270:MAA0277	1,462	7.61	0.78	0.74	0.78	1.09	7.27	8.55	12.23	9.09	7.54	4.41	5.91	4.27	hypothetical protein	
	MapK10-3269 (12I0)	MAV_3269:MAA0278	1,463	13.25		0.69	11.67	17.53	21.76	28.50	11.22	12.08	9.48	6.56			NAD dependent epimerase/dehydratase family protein	
	MapK10-3268 (12I1)	MAV_3268:MAA0280	1,465	13.00		0.65	23.01	20.74	35.81	43.60	21.42	17.43	12.52	11.71			MtB protein	
	MapK10-3265 (12I2)	MAV_3265:MAA0281	1,466	10.29		0.46	10.14	12.96	14.52	21.28	12.05	12.35	8.38	6.82			hypothetical glycosyl transferase	
	MapK10-3262 (12I3)	MAV_3262:MAA0284	1,469	16.56		0.71	19.96	27.06	26.63	10.76	23.46	19.58	14.82	12.49			hypothetical glycosyl transferase	
	MapK10-3261 (12I4)	MAV_3261:MAA0285	1,470	18.26		0.55	25.25	17.16	20.19	20.19	16.21	14.69	11.40	8.62			methyltransferase MfC	
	MapK10-3260 (12I5)	MAV_3260:MAA0286	1,471	21.60		0.67	20.85	19.55	26.74	32.11	19.16	18.87	12.51	10.22			MfD protein	
	MapK10-3259 (12I6)	MAV_3259:MAA0287	1,472	10.93	1.19	1.06	10.07	9.97	6.93	7.69	5.43	9.25	4.95	4.70	4.06		dehydrogenase DhgA	
	MapK10-3258 (12I7)	MAV_3258:MAA0288	1,473	10.64		1.07	15.39	16.03	21.58	51.19	17.70	14.54	11.19	10.69			glycosyltransferase family protein 28	
	MapK10-3252 (12I12)	MAV_3252:MAA0294	1,479	5.58		0.75	10.26										daunorubicin resistance protein C	
	MapK10-1237 (4D23)	MAP1237:MAV_3251:MAA0294	1,480	0.80	0.78	0.90	1.17	0.79	0.91	0.55	0.78	1.29	3.00	1.44	0.99	1.10	DrtB	
	MapK10-1258c (4E21)	MAP1258c:MAV_3223:MAA0322	1,509	0.80	1.19	1.12	3.07	1.00	1.68	1.12	1.27	0.91	0.89	0.89	0.88	0.96	hypothetical protein	
	MapK10-3132 (12K1)	MAV_3132:MAA0409	1,605	1.51						7.14							GGDEF domain protein	
	MapK10-3096 (12K5)	MAV_3096:MAA0482	1,682	1.67	0.93	0.94	0.89		0.25	0.27	0.23	0.55	0.32	0.35	0.30		linear gamma-irradiation sensitive subunit D transposase, Mutator family protein	
	MapK10-3098 (12K10)	MAV_3098:MAA0500	1,700	6.17														
	MapK10-1433c (4M5)	MAP1433c:MAV_3039:MAA0499	1,699	1.15	0.88	0.99	1.01	0.96	0.99	0.97	0.81	0.34	0.17	0.33	0.18	0.24	3-ketosteroid-delta-1-dihydro-3-ketosteroid-delta-1-dihydrogenase	
	MapK10-1434 (4M6)	MAP1434:MAV_3037:MAA0501	1,701	1.13	0.76	0.91	1.17	0.96	1.08	0.75	0.96	0.24	0.16	0.17	0.13	0.16	hypothetical protein	
	MapK10-1435 (4M7)	MAP1435:MAV_3035:MAA0502	1,702	1.24	0.84	1.13	0.94	1.10	1.02	0.79	0.92	0.22	0.09	0.16	0.10	0.16	hypothetical protein	
	MapK10-1436c (4M8)	MAP1436c:MAV_3034:MAA0503	1,703	0.73	0.94	0.84	1.26	1.05	1.01	0.92	1.07	0.13	0.06	0.05	0.09	0.09	hypothetical protein	
	MapK10-1437c (4M9)	MAP1437c:MAV_3033:MAA0504	1,704	0.95	0.71	1.05	0.96	0.88	0.63	0.78	0.86	0.06	0.10	0.06	0.10	0.06	hypothetical protein	
	MapK10-1438c (4M10)	MAP1438c:MAV_3032:MAA0505	1,705	0.92	0.90	0.96	0.97	1.25	0.89	0.71	0.81	0.22	0.10	0.14	0.06	0.13	LpH	
	MapK10-2986 (12K14)	MAV_2986:MAA0534	1,728	1.29		0.86	1.24	1.06	3.01	2.98	2.98	2.98	2.98	2.98	2.98	2.98	2.98	hypothetical protein
	MapK10-2987 (12K15)	MAV_2987:MAA0535	1,740	3.14		1.47	1.48	1.47	7.01	18.44	16.24	8.03	5.38	7.24	5.10			oxidoreductase, Mutator family protein
	MapK10-2986 (12K16)	MAV_2986:MAA0536	1,741	5.99		1.47	1.48	1.47	9.33	13.25	23.39	51.08	15.14	11.35	9.96			lipoprotein
	MapK10-2995 (12K17)	MAV_2995:MAA0537	1,742	5.09		0.75	13.29	14.40	19.19	5.97	15.85	11.86	8.21	6.35				adenylate-forming enzyme
	MapK10-2994 (12K18)	MAV_2994:MAA0538	1,743	11.63		0.75	17.44	14.44	15.38	22.46	17.44	14.44	8.65	6.78				putative class I aldolase
	MapK10-2993 (12K19)	MAV_2993:MAA0539	1,744	1.63		1.43	14.40	19.82	22.54	34.57	16.11	11.56	8.42	6.14				amidohydrolase 2
	MapK10-2992 (12K20)	MAV_2992:MAA0540	1,745	14.54	0.96	0.89	0.35	11.73	10.94	13.17	11.59	11.03	9.19	6.54	5.12			transcriptional regulator, MarR family protein
	MapK10-2991 (12K21)	MAV_2991:MAA0541	1,746	16.56		0.34	21.25	21.47	24.34	38.93	21.26	13.65	12.73	10.65				tetracycline polymerase synthesis O-methyltransferase TcmP
	MapK10-2990 (12K22)	MAV_2990:MAA0542	1,747	6.04		0.72	19.00	26.00	45.42	26.69	14.42	16.04	16.05	16.05				oxidoreductase
	MapK10-2989 (12K23)	MAV_2989:MAA0543	1,748	13.07		0.32	17.64	29.92	31.40	41.34	26.18	18.19	16.26	12.29				arylsulfatase
	MapK10-2988 (12K24)	MAV_2988:MAA0544	1,749	12.88		0.30	16.68	24.40	23.92	20.78	12.38	16.11	13.53	9.68				ubiquinone/ubiquinol biosynthesis methyltransferases
	MapK10-2987 (12K25)	MAV_2987:MAA0545	1,750	14.41	0.80	0.80	17.59	18.56	38.30	1.52	24.31	16.04	13.94	9.99				NAD binding oxidoreductase
	MapK10-2986 (12L)	MAV_2986:MAA0546	1,751	14.98	1.12	1.12	13.57	17.44	24.44	2.87	15.71	12.72	19.72	13.73				protein export protein SecE, putative transcriptional regulator, TetR family protein
	MapK10-2985 (12L3)	MAV_2985:MAA0547	1,752	21.18	1.19	1.19	8.76	14.56	14.77	3.52	13.44	14.05	7.38	6.91				cytochrome P450
	MapK10-2984 (12L4)	MAV_2984:MAA0548	1,753	4.32	1.04	0.94	1.16	1.09	6.27	5.68	5.66	10.51	10.11	4.52	5.39	5.69		enoyl-CoA hydratase/isomerase
	MapK10-2982 (12L5)	MAV_2982:MAA0549	1,754	11.65	0.82	0.82	10.54	11.55	17.54	10.54	13.17	16.34	7.77	9.01	1.55			transcriptional regulator, TetR family protein
	MapK10-2981 (12L6)	MAV_2981:MAA0550	1,755	10.04		1.19	9.85	9.35	14.95	22.94	11.79	6.71	8.00	7.59				calB/cal family protein
	MapK10-2980 (12L7)	MAV_2980:MAA0551	1,756	6.57		1.19	9.45	11.65	16.14	32.48	15.25	10.37	10.01	7.57				clavulanic acid dehydrogenase
	MapK10-2979 (12L8)	MAV_2979:MAA0552	1,757	4.19		1.19	5.71	7.88	26.88	12.75	8.12	4.85	6.00	6.58				hypothetical protein
	MapK10-2978 (12L9)	MAV_2978:MAA0553	1,758	3.29		1.19	4.07	6.11	16.22	4.42	6.75	3.63	4.22	3.43				transposase, Mutator family protein
	MapK10-2976 (12L11)	MAV_2976:MAA0555	1,760	10.96	3.13	0.88	10.96											transposase, Mutator family protein
	MapK10-2973 (12L13)	MAV_2973:MAA0557	1,762	9.22		4.21												transposase, Mutator family protein
	MapK10-1484-1485 (4O11)	MAP1484-1485	1,782	1.00		0.89	0.81	0.78	0.22	0.14	0.10	0.20	0.10	0.22	0.16	0.20		
	MapK10-1484c (4O12)	MAP1484c:MAV_2952:MAA0577	1,783	0.98	0.95	0.96	1.07	0.82	0.27	0.14	0.10	0.29	0.11	0.20				

	MapK10-1741c (5J13)	MAP1741c:MAV_2507:MAA0993	2,234	0.95	0.97	1.00	1.00	1.10	0.11	0.07	0.04	0.13	0.07	0.11	0.08	0.08	hypothetical protein	universal stress protein family protein	
	MapK10-1742c (5J14)	MAP1742c:MAV_2506:MAA0994	2,235	0.83	0.98	1.01	0.90	0.80	0.13	0.07	0.07	0.15	0.07	0.11	0.08	0.09	hypothetical protein	universal stress protein family protein	
	MapK10-1743c (5J15)	MAP1743c:MAV_2505:MAA0995	2,236	0.94	1.01	0.91	0.96	0.76	0.13	0.09	0.06	0.16	0.07	0.11	0.07	0.10	hypothetical protein	hypothetical protein	
	MapK10-1744 (5J16)	MAP1744:MAV_2504:MAA0996	2,237	0.86	0.90	1.11	1.15	1.11	0.16	0.10	0.08	0.19	0.14	0.20	0.11	0.15	hypothetical protein	hypothetical protein	
	Maa104-2674 (12N5)	MAV_2674:MAA0835	2,078	14.38								11.49					hypothetical protein	hypothetical protein	
	Maa104-2682 (12O3)	MAV_2682:MAA0887	2,101	8.35	0.97	1.09	0.75	0.54	1.50	0.90	1.00	0.99		0.98	0.71	0.36	aromatic ring-opening dehydrogenase, catalytic LigB subunit	transcriptional regulator, TetR family protein	
	Maa104-2686 (12P9)	MAV_2686:MAA0882	2,126	8.04								0.50					hypothetical protein	hypothetical protein	
	Maa104-2619 (12P10)	MAV_2619:MAA0889	2,131	8.55								0.34					acyl-CoA dehydrogenase domain protein	acyl-CoA dehydrogenase domain protein	
	Maa104-2612 (12P16)	MAV_2612:MAA0895	2,137	85.15			42.38										diogenase large subunit	diogenase large subunit	
	Maa104-2609 (12P18)	MAV_2609:MAA0897	2,138	7.15	0.74	1.62	1.29		1.23	1.41	1.35	0.48	1.31	1.09	1.13	0.96	enoyl-CoA hydratase/isomerase family protein	enoyl-CoA hydratase/isomerase family protein	
	Maa104-2602 (12P24)	MAV_2602:MAA0903	2,145	38.66								16.02					putative hydrolase	putative hydrolase	
	Maa104-2600 (13A2)	MAV_2600:MAA0905	2,147	18.27			2.95										acyl-CoA dehydrogenase	acyl-CoA dehydrogenase	
	Maa104-2594 (13A8)	MAV_2594:MAA0911	2,153	7.95								3.33					monooxygenase, FAD-binding	monooxygenase, FAD-binding	
	Maa104-2518 (13D6)	MAV_2518:MAA0982	2,223	8.87			13.11										hypothetical protein	hypothetical protein	
	MapK10-1771c (5K19)	MAP1771c	2,267	0.16	0.94	1.29	0.97	1.51	2.22	1.64	2.42	1.76	2.11	3.58	0.88	1.56	hypothetical protein	hypothetical protein	
	MapK10-1781 (5L5)	bp1MAP1781:MAV_2465:MAA1034	2,277	0.90	1.04	0.97	1.08	0.85	0.94	1.21	1.18	1.12	3.65	1.07	1.04	0.95	LplI protein	LplI protein	
	MapK10-1782c (5L6)	MAP1782c:MAV_2464:MAA1035	2,279	1.00	0.79	0.94	1.02	1.04	1.17	0.61	1.09	1.09	3.51	1.65	1.12	1.01	hypothetical protein	cytochrome P450 family protein	
	MapK10-1785 (5L9)	MAP1785	2,282	0.15	0.75	0.89	0.99	1.98	0.95	1.65	1.28		1.16	3.38	1.26		hypothetical protein	hypothetical protein	
	MapK10-1788 (5L12)	MAP1788:MAV_2459:MAA1040	2,285	1.13	0.72	0.92	0.88	1.57	0.84	0.53	0.84	1.53	3.41	1.58	1.01	1.28	hypothetical protein	transcriptional regulator, TetR family protein	
	Maa104-2422 (13O22)	MAV_2422:MAA1073	2,326	2.00	0.80	0.86	1.23	0.92	1.45	1.34	1.51	2.10	4.89	3.04	1.92	1.85	nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	
	MapK10-1820 (5O20)	MAP1820:MAV_2417:MAA1075	2,327	1.61	0.87	0.82	1.32	1.25	1.17	1.19	1.12	2.02	4.17	2.31	1.41	1.55	hypothetical protein	hypothetical protein	
	Maa104-2419 (13O23)	MAV_2419:MAA1074	2,328	2.26	0.90	1.03	1.18	0.82	1.82	1.58	1.89	2.24	4.23	2.81	1.67	1.86	nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	
	MapK10-1821c (5O21)	MAP1821c:MAV_2421	2,329	1.18	0.75	0.86	1.25	1.23	0.71	0.84	0.92	1.38	3.61	1.68	1.11	1.15	hypothetical protein	hypothetical protein	
	MapK10-1868c (5O22)	efPA_1MAP1868c:MAV_2368:MAA1116	2,380	1.09	0.85	0.77	1.10	1.03	0.84	0.54	0.83	1.17	3.39	1.20	1.00	1.08	ElpA_1	transporter, major facilitator family protein	
	MapK10-1868c (5O21)	MAP1868c:MAA1117	2,381	1.25	0.78	0.86	0.80	0.98	0.93	0.68	1.05	1.28	2.95	1.38	0.97	1.14	hypothetical protein	hypothetical protein	
	MapK10-1870c (5O22)	MAP1870c:MAA1117	2,382	1.18	0.80	0.92	1.16	0.80	1.07	0.90	0.92	1.05	1.63	1.03	0.95	0.86	hypothetical protein	hypothetical protein	
	MapK10-1871c (5O23)	MAP1871c:MAV_2367:MAA1118	2,383	1.33	0.70	0.82	0.91	0.81	0.84	0.52	0.69	1.11	2.74	1.37	1.14	1.03	hypothetical protein	hypothetical protein	
	MapK10-1872c (5O24)	mbH_2MAP1872c:MAV_2366:MAA1119	2,384	1.04	0.70	0.87	1.12	1.52	1.09	0.48	1.09	1.38	3.52	2.48	1.18	1.56	MbHf_2	hypothetical protein	
	MapK10-1944c (6S27)	MAP1944c:MAV_2287:MAA1192	2,458	2.98	0.88	0.98	1.45	2.06	2.44	2.76	0.79	1.22	0.95	0.88	1.22	0.84	0.86	hypothetical protein	Head5/YnfY family protein
	Maa104-2258 (13E16)	MAV_2258:MAA1219	2,487	3.32								4.19					transposase, Mutator family protein	transposase, Mutator family protein	
	INDEL8(MAV10)	Maa104-2254 (13E19)	MAV_2254:MAA1222	2,490	6.68		0.64	5.96	8.58	12.32		7.53	6.23	6.40	4.83		hypothetical protein	hypothetical protein	
	INDEL9(MAV9)	Maa104-2223 (13F10)	MAV_2223:MAA1251	2,518	13.84			31.72	29.88	21.98	13.77	26.13	21.90	17.51	13.16		transposase, Mutator family protein	transposase, Mutator family protein	
		MapK10-2025c (6F9)	pcic:MAP2025c:MAV_2164:MAA1306	2,576	1.09	0.60	0.89	0.85	2.51	0.69	0.75	0.83	1.09	1.31	1.12	1.02	hypothetical protein	4-carboxymuconolactone decarboxylase domain protein	
		MapK10-2026 (6F10)	MAP2026:MAV_2162:MAA1307	2,578	0.99	0.70	0.79	0.81	1.61	0.73	0.52	0.60	2.04	3.69	1.70	1.06	1.02	hypothetical protein	serine/threonine-protein kinase PtkE
		MapK10-2027c (6F11)	MAP2027c	2,579	0.14	0.71	0.80	0.79	1.09	0.79	0.72	0.82	1.75	3.66	1.76	1.18	1.10	hypothetical protein	hypothetical protein
		MapK10-2028c (6F12)	MAP2028c	2,580	0.18	0.71	0.81	1.35	0.89	0.82	0.89	1.60	3.34	1.74	1.15	1.04	hypothetical protein	hypothetical protein	
		MapK10-2028c (6F13)	MAP2028c	2,581	0.31	0.66	0.80	0.79	1.28	0.76	0.70	0.84	1.34	2.87	1.60	1.12	1.12	hypothetical protein	hypothetical protein
		MapK10-2030 (6F14)	MAP2030:MAV_2159:MAA1311	2,584	1.26	0.61	0.88	0.85	1.20	0.77	0.51	0.61	1.24	2.87	1.71	1.03	1.09	hypothetical protein	cytochrome P450 superfamily protein
		MapK10-2031c (6F15)	MAP2031c:MAV_2158:MAA1312	2,585	1.04	0.63	0.77	1.06	1.15	1.04	0.62	0.87	1.66	4.03	1.97	1.15	1.20	hypothetical protein	serine/threonine-protein kinase
		MapK10-2038c (6F18)	MAP2038c	2,588	0.33	1.08	1.19	2.02	2.01	1.85	1.91	4.18	1.71	4.31	1.24	2.22	hypothetical protein	hypothetical protein	
		MapK10-IRNAmh-2086c (6HMAP-IRNAmh-2086c:MAV_2095:MAA1369)	2,647	1.26	0.70	0.92	1.00	1.06	1.11	0.70	0.86	1.46	3.00	1.62	1.23	1.21	1.21	hypothetical protein	hypothetical protein
		MapK10-2108 (6I21)	MAP2108	2,672	0.15	0.79	0.93	1.35	1.95	1.31	0.83	2.15	1.38	1.00	2.56	1.31	1.53	hypothetical protein	hypothetical protein
		MapK10-2151 (6K17)	MAP2151	2,721	0.34	0.65	0.87	0.93	2.50	0.80	0.58	0.91	1.80	3.92	1.97	1.22	1.36	hypothetical protein	hypothetical protein
		MapK10-2151:2152c (6K18)	MAP2151:2152c	2,722	0.17	0.61	0.81	1.24	2.61	0.67	0.61	0.75	2.57	4.04	1.17	1.25	1.16	hypothetical protein	hypothetical protein
		MapK10-2152c (6K19)	MAP2152c	2,723	0.30	0.65	0.81	0.83	1.57	0.79	0.68	0.92	1.88	3.73	2.02	1.12	1.24	hypothetical protein	hypothetical protein
		MapK10-2153 (6K20)	MAP2153	2,724	0.05	0.66	0.93	0.75	1.28	0.82	0.62	0.90	1.56	3.91	1.71	1.23	1.18	hypothetical protein	hypothetical protein
		MapK10-2154c (6K21)	MAP2154c	2,725	0.06	0.71	0.80	0.81	1.31	1.05	0.60	0.75	1.25	4.17	1.90	1.23	1.13	hypothetical protein	hypothetical protein
		MapK10-2154c (6K22)	Spt10:MAP2155	2,726	0.18	0.74	0.84	0.82	0.94	1.69	1.59	2.39	1.58	3.70	1.70	1.23	1.32	Spt10	hypothetical protein
		MapK10-2156 (6K23)	MAP2156	2,727	0.11	0.67	0.95	0.85	0.97	1.99	1.99	3.06	2.26	3.95	2.22	1.66	1.54	hypothetical protein	hypothetical protein
		MapK10-2157 (6K24)	MAP2157	2,728	0.22	0.75	1.73	1.11	2.20	1.57	1.80	1.58	3.22	1.76	4.65	1.53	1.34	hypothetical protein	hypothetical protein
		MapK10-2158 (6L11)	MAP2158	2,729	0.69	0.85	1.05	2.31	1.00	0.62	0.82	3.45	1.84	1.44	1.23	1.23	hypothetical protein	hypothetical protein	
		MapK10-2156 (6L9)	MAP2156:MAV_2018:MAA1437	2,737	0.88	0.85	1.13	0.89	1.05	1.79	1.34	1.83	0.36	1.29	1.36	1.10	1.23	hypothetical protein	RNA polymerase ECF-subfamily protein sigma factor
		Maa104-2008 (13G12)	MAV_2008:MAA1448	2,768	6.92		0.49	14.84	21.13	26.19	13.53	12.46	12.94	10.81	6.91		2,3-dihydroxybenzoate-AMP ligase	2,3-dihydroxybenzoate-AMP ligase	
		Maa104-2007 (13G13)	MAV_2007:MAA1449	2,769	7.12		0.89	11.68	14.69	21.15	48.73	20.54	13.85	14.30	11.95		phospho-2-dehydro-3-deoxyheptonate aldolase	phospho-2-dehydro-3-deoxyheptonate aldolase	
		Maa104-2006 (13G14)	MAV_2006:MAA1450	2,770	4.67		0.48	9.83	10.19	14.81	22.03	10.86	11.04	9.22	9.77		PPE family protein	PPE family protein	
		Maa104-2005 (13G15)	MAV_2005:MAA1451	2,771	6.16			27.73	28.89	46.91	136.35	29.84	26.00	21.18	21.55		PapA2 protein	PapA2 protein	
		Maa104-2004 (13G16)	MAV_2004:MAA1452	2,772	13.05			20.31	20.79	33.49	60.47	17.23	17.36	11.75	9.80		ABC-2 type transporter	ABC-2 type transporter	
		Maa104-2001 (13G18)	MAV_2001:MAA1454	2,774	3.76		0.56	13.87	11.58	16.64	7.59	9.15	7.91	6.73	5.57		hypothetical protein	hypothetical protein	
		Maa104-2000 (13G19)	MAV_2000:MAA1455	2,775	1.74		0.64	11.83	10.15	14.25	19.51	7.07	7.15	6.57	7.42		hypothetical protein	hypothetical protein	
		Maa104-1998 (13G20)	MAV_1998:MAA1456	2,776	3.72	0.44	0.94	5.07	5.87	5.74	5.98	6.84	3.10	3.57	2.92	2.10		PPE family protein	PPE family protein
		Maa104-1996 (13G21)	MAV_1996:MAA1457	2,777	9.10			8.08	8.05	11.17	22.44	11.85	5.98	6.34	6.06		hypothetical protein	hypothetical protein	
		Maa104-1995 (13G22)	MAV_1995:MAA1458	2,778	7.35		0.71	11.13	10.15	14.25	19.51	7.07	7.15	6.57	7.42		diarylate cyclase	diarylate cyclase	
		Maa104-1994 (13G23)	MAV_1994:MAA1459	2,779	2.45		0.69	12.87	14.60	20.91	13.23	9.13	9.51	8.98	5.45		hypothetical protein	hypothetical protein	
		Maa104-1993 (13G24)	MAV_1993:MAA1460	2,780	2.21			15.07	19.73	37.07	45.18	11.17	13.25	11.62	9.19		HspR protein	HspR protein	
		Maa104-1992 (13H1)	MAV_1992:MAA1461	2,781	8.70		1.04	13.87	22.75	29.90	1.67	12.05	14.48	11.81	11.19		hypothetical protein	hypothetical protein	
		Maa104-1990 (13H2)	MAV_1990:MAA1462	2,782	4.90			7.82	8.12	7.86	10.51	2.97	8.70	7.18	6.95	6.21		18 kDa	

	Mpk10-2577 (M18)	MAP2577	3.402	0.13	1.07	1.51	1.64	3.58	2.37	1.53	1.72	4.04	3.03	3.52	1.27	1.70	hypothetical protein
	Mpk10-2595 (N12)	MAP2595.MAV_1329.MAA2068	3.420	0.90	0.91	0.89	3.76	0.99	1.13	1.04	1.14	1.05	0.94	0.83	0.86	1.08	hypothetical protein
	Mpk10-2626 (7020)	MAP2626.MAV_1296.MAA2066	3.451	0.45	1.15	1.03	2.29	0.69	1.26	1.52	1.02	0.86	0.79	0.94	0.86	1.19	hypothetical protein
	Mpk10-2630c (7024)	MAP2630c.MAV_1292.MAA2100	3.458	0.91	1.07	0.95	2.24	1.26	1.20	1.10	1.06	0.96	1.09	1.04	0.95	1.01	hypothetical protein
	Mpk10-2681c (8E8)	MAP2681c	3.518	1.70	0.71	0.81	0.82	1.04	0.65	0.48	0.67	1.26	3.72	1.57	1.07	1.13	hypothetical protein
INDEL11(LSP Type I)	Mpk10-2704 (8E5)	MAP2704.MAV_1210.MAA2178	3.541	1.03	1.05	1.01	1.09	0.88	0.35	0.29	0.20	1.11	0.88	0.90	0.93	0.84	hypothetical protein
	Mpk10-2705 (8E21)	MAP2705	3.607	0.70	0.92	0.77	1.01	1.21	0.82	0.56	0.72	1.33	3.34	1.92	1.07	1.17	hypothetical protein
	Mpk10-2768c (8E22)	MAP2768c	3.608	0.12	0.75	0.92	1.01	1.04	0.82	0.60	0.58	1.38	4.24	1.82	1.12	1.15	hypothetical protein
	Mpk10-2768c-2769c (8E23)	MAP2768c-2769c	3.609	1.20	0.81	0.83	0.92	0.92	0.69	0.52	0.65	1.22	3.19	1.53	1.02	1.13	hypothetical protein
	Mpk10-2768c (8E24)	MAP2768c	3.610	1.14	0.85	0.79	0.99	1.14	0.82	0.68	0.80	1.40	3.35	1.77	1.07	1.20	hypothetical protein
Maa104-3533 (12H22)	Maa104-3533 (12H22)	MAV_3533.MAA0035	3.613														transposase
	Maa104-3535 (12H21)	MAV_3535.MAA0034	3.614														transposase, Mutator family protein
	Maa104-3648 (15D14)	MAV_3648.MAA4819	3.727														hypothetical protein
	Maa104-3798 (15C18)	MAV_3798.MAA4679	3.853														hypothetical protein
	Maa104-3955a (15B12)	MAV_3955a.MAA4497	4.081	1.45	0.85	0.87	0.91	1.22	0.99	0.71	0.89	1.35	3.28	1.44	0.91	1.20	nucleic acid hydrolase
INDEL12(MAV21)	Maa104-4125 (15B2)	MAV_4125.MAA4377	4.215	2.55													virulence factor Mce family protein
	Maa104-4128 (15B1)	MAV_4128.MAA4374	4.218	5.39													hypothetical protein
	Maa104-4130 (15A24)	MAV_4130.MAA4373	4.219	4.05													immunogenic protein MPT64
	Mpk10-3373 (9C10)	MAP3373	4.314	0.66	0.82	0.62	1.50	2.71	1.06	0.74	1.80	2.86	3.91	1.55	1.05	1.03	hypothetical protein
	Mpk10-3460c (10C1)	MAP3460c	4.411	0.63	0.80	0.93	1.04	2.10	0.48	0.35	0.26	1.36	1.15	0.92	1.00	0.93	hypothetical protein
INDEL13	Mpk10-3480 (10C21)	MAP3480	4.432	0.16	0.73	0.94	1.06	1.39	1.75	1.51	1.62	2.04	2.09	4.71	1.14	1.07	hypothetical protein
	Maa104-4351 (14P22)	MAV_4351.MAA4164	4.445	5.00													putative HT1-type transcriptional regulator
	Maa104-4353 (14P22)	MAV_4353.MAA4163	4.447	6.76													alpha-ketoglutarate-dependent isomerase
INDEL15(LSP Type II)	Mpk10-3584 (10G5)	MAP3584.MAV_5129.MAA3444	4.542	1.11	1.09	1.03	1.05	0.94	1.32	0.93	0.75	0.39	0.30	0.32	0.28	0.27	hypothetical protein
	Maa104-5108 (14K16)	MAV_5108.MAA3464	4.581	16.21													transcriptional regulator, ArsR family protein
	Maa104-5108 (14K18)	MAV_5108.MAA3466	4.583	11.24													phosphoenolpyruvate carboxylase
	Maa104-5181 (14L17)	MAV_5181.MAA3491	4.586	39.90													acetyl-CoA acyltransferase
	Maa104-5074 (14L23)	MAV_5074.MAA3497	4.592	31.63													citrate lyase
Mpk10-5026 (14N13)	Mpk10-5026 (14N13)	MAV_5026.MAA3538	4.630	22.13													hypothetical protein
	Mpk10-3537c (10J10)	MAP3537c.MAV_4973.MAA3589	4.684	1.11	1.11	0.98	2.09	1.20	0.92	0.88	0.82	1.33	0.91	0.81	0.92	1.00	MmpL11
	Mpk10-3730 (10N8)	MAP3730	4.785	0.02	0.74	0.74	0.88	1.31	0.68	0.62	0.72	1.42	4.09	2.31	1.20	1.29	hypothetical protein
	Mpk10-3731c (10N9)	MAP3731c	4.786	0.01	0.77	0.89	0.95	2.66	0.94	0.71	1.02	2.56	4.28	1.97	1.28	1.17	hypothetical protein
	Mpk10-3732c (10N10)	MAP3732c	4.787	0.01	0.73	0.76	0.91	2.03	0.90	0.44	0.84	3.02	4.52	2.13	1.28	1.18	hypothetical protein
Mpk10-3732c (10N11)	Mpk10-3732c (10N11)	MAP3732c	4.788	0.01	0.73	0.79	0.91	1.25	0.91	0.75	0.91	1.77	1.94	1.91	1.14	1.15	hypothetical protein
	Mpk10-3734c (10N12)	MAP3734c	4.789	0.02	0.72	0.85	0.97	1.32	0.89	0.53	0.74	1.51	3.87	1.89	1.11	1.14	hypothetical protein
	Mpk10-3735c (10N13)	MAP3735c	4.790	0.02	0.67	0.88	0.73	1.33	0.78	0.39	0.64	1.45	4.81	2.26	1.14	1.24	hypothetical protein
	Mpk10-3736c (10N14)	MAP3736c	4.791	0.07	0.85	0.78	0.82	0.66	0.69	0.63	0.68	3.29	1.63	1.01	1.06	hypothetical protein	
	Mpk10-3737 (10N15)	MAP3737	4.792	0.06	0.84	0.77	1.11	0.81	0.68	0.71	0.88	1.12	2.16	1.28	0.94	0.95	hypothetical protein
	Mpk10-3738c (10N16)	MAP3738c	4.793	0.03	0.91	0.89	1.09	1.28	0.81	0.71	0.65	1.39	3.38	2.19	1.14	1.15	hypothetical protein
	Mpk10-3738c (10N17)	MAP3738c	4.794	0.05	0.78	0.91	1.34	1.95	0.66	0.55	0.76	2.93	3.28	1.70	1.13	1.20	hypothetical protein
	Mpk10-3738c (10N18)	MAP3738c	4.795	0.07	0.83	0.89	1.06	1.16	0.99	0.77	1.06	2.12	3.62	1.70	1.13	1.11	hypothetical protein
	Mpk10-3740 (10N18)	MAP3740	4.796	0.02	0.81	0.97	0.83	1.33	0.92	0.72	0.87	1.90	2.42	1.46	1.01	1.05	hypothetical protein
	Mpk10-3741 (10N19)	MAP3741	4.797	0.02	0.75	0.89	0.88	1.18	0.90	0.67	0.93	1.52	2.55	1.63	1.08	1.15	hypothetical protein
	Mpk10-3742 (10N20)	MAP3742	4.798	0.01	0.74	0.77	0.90	1.24	0.79	0.53	0.66	1.31	2.91	1.73	1.03	1.07	hypothetical protein
	Mpk10-3743 (10N21)	MAP3743	4.799	0.01	0.77	0.92	0.98	1.16	0.93	0.69	0.80	1.64	3.00	1.80	1.15	1.15	hypothetical protein
	Mpk10-3744 (10N22)	MAP3744	4.800	0.03	0.73	0.73	0.82	1.08	0.88	0.43	0.60	1.43	4.00	1.96	1.10	1.12	hypothetical protein
	Mpk10-3745 (10N23)	MAP3745	4.801	0.02	0.74	0.80	0.84	0.99	0.86	0.53	0.70	1.64	3.82	1.75	1.08	1.23	hypothetical protein
	Mpk10-3746 (10N24)	MAP3746	4.802	0.03	0.79	0.77	0.85	1.25	0.67	0.51	0.71	1.26	4.29	2.31	1.31	1.27	hypothetical protein
	Mpk10-3747c (10D1)	MAP3747c	4.803	0.06	0.67	0.86	0.80	2.93	0.90	0.72	1.01	3.41	4.33	1.80	1.19	1.19	hypothetical protein
	Mpk10-3748c (10C2)	IS110.MAP3748c	4.804	0.04	0.71	0.92	0.83	2.03	0.97	0.78	0.80	2.24	3.20	1.68	1.13	1.08	IS110 transposase
	Mpk10-3749 (10D3)	MAP3749	4.805	0.24	0.73	0.89	0.77	1.33	1.09	0.61	0.86	1.79	3.51	1.73	1.07	1.08	hypothetical protein
	Mpk10-3750 (10D4)	mmrS1.MAP3750	4.806	0.14	0.66	0.84	0.62	1.32	1.03	0.49	0.75	1.43	3.80	1.77	1.11	1.21	MmrS1
	Mpk10-3751 (10D5)	mmrL4.5.MAP3751	4.807	0.28	0.73	0.78	0.85	0.92	0.85	0.57	0.78	1.14	3.91	1.65	0.98	1.03	MmrL4.5
Mpk10-3752 (10D6)	fadD28.MAP3752	4.808	0.15	0.65	0.83	0.87	1.04	0.90	0.60	0.84	1.41	3.89	1.78	1.12	1.24	acyl-CoA synthase	
Mpk10-3753 (10D7)	MAP3753	4.809	0.30	0.71	0.76	0.86	1.04	0.75	0.50	0.71	1.54	3.78	1.81	1.16	1.05	hypothetical protein	
Mpk10-3754 (10D9)	MAP3754	4.810	0.08	0.73	0.77	0.88	1.25	0.89	0.60	0.70	1.65	3.76	2.25	1.34	1.39	hypothetical protein	
Mpk10-3755 (10D9)	MAP3755	4.811	0.07	0.69	0.83	1.02	2.46	1.10	0.86	1.16	2.35	3.34	2.08	1.26	1.19	hypothetical protein	
Mpk10-3756c (10D10)	MAP3756c	4.812	0.05	0.63	0.75	0.90	2.58	1.01	0.52	0.89	2.51	3.93	2.24	1.23	1.21	hypothetical protein	
Mpk10-3757c (10D11)	MAP3757c	4.813	0.21	0.74	0.94	0.95	1.21	1.14	0.86	1.00	1.85	3.26	1.78	1.13	1.17	hypothetical protein	
Mpk10-3758c (10D12)	MAP3758c	4.814	0.30	0.70	0.79	0.92	1.15	0.87	0.75	0.87	1.62	3.87	1.69	1.14	1.14	hypothetical protein	
Mpk10-3758c (10D13)	MAP3758c.MAV_4319.MAA4197	4.815	1.65	0.63	0.79	0.99	1.17	0.71	0.43	0.54	1.46	1.90	1.48	1.19	1.16	hypothetical protein	
Mpk10-3760c (10D14)	MAP3760c	4.816	0.88	0.70	0.92	0.73	0.89	0.67	0.52	0.57	1.30	3.14	1.53	1.24	1.13	hypothetical protein	
Mpk10-3761c (10D15)	MAP3761c	4.817	0.52	0.72	0.81	0.84	1.00	0.88	0.54	0.79	1.42	3.54	1.73	1.16	1.13	hypothetical protein	
Mpk10-3762c (10D16)	MAP3762c	4.818	0.18	0.69	0.86	0.97	1.51	1.08	0.54	0.68	1.38	5.20	2.45	1.24	1.34	hypothetical protein	
Mpk10-3763c (10D17)	papA3.2.MAP3763c	4.819	0.08	0.77	0.84	0.83	2.74	0.92	0.61	0.73	3.42	4.07	1.86	1.12	1.10	PapA3.2	
Mpk10-3764c (10D18)	pls2.MAP3764c	4.820	0.11	0.86	1.00	0.77	1.65	1.05	0.92	1.05	1.96	1.58	1.45	1.02	1.21	Pls2	
Mpk10-3765 (10D19)	MAP3765	4.821	0.32	0.81	1.00	0.89	1.13	0.98	0.77	0.74	1.22	2.70	1.29	1.12	1.00	hypothetical protein	
Mpk10-3766 (10D20)	MAP3766	4.822															

MapK10-4333-4334 (12G16) MAP4333-4334  
MaapVT2-P2 (15D24) pVT2-P2

5,450 0.23 0.79 0.93 1.10 1.39 0.85 0.48 0.80 1.06 3.35 1.96 1.15 1.52  
5,472

putative relaxase