

			1111122222	2222222222	2222233333	3333333333	3333344444
	3444444556	6666666679	0333400468	8888888999	9999900000	0011112233	3333414555
	7345667351	2256788809	6669424121	1378899012	5667744456	6755573711	1167394189
	3265476314	0398403958	8035356281	7511567432	9271637842	6303671735	6779204087
PMEN3	CCTAAACCAC	TTTGCGACAA	AGACGCAATC	TCGGAAGTGT	TGTAAAACGT	CTGCCTCTGG	TTGTGTTAAC
9A/1	.....	.....	.CGTATGGCT	CTAACGACTC	CACTGGCAAC	TCATTCTCAA	AATCACCGGT
9V/5	.....	.....	.CGTA-GGCT	CTAAC.ACTC	CACTGGCAAC	TCATTCTCAA	AATCACCGGT
9V/6	.....	.....	.CGTATGGCT	CTAAC.ACTC	CACTGGCAAC	TCATTCTCAA	AATCACCGGT
PMEN1	TTCTGGAAGT	GACATATTGG	G.....	.....	.....	.....	.....

  

	4555555555	5555555555	5555666666	6666666666	6777777777	7777777777	7788888899
	8233444457	7788889999	9999113344	4445559999	9000000011	1111111222	2215888923
	7556235985	7902771234	5569172334	4480032388	9011223324	4467778134	4655699347
	3640074361	8383486903	3760086510	3681337647	9824692350	3640392932	5870639581
PMEN3	TTGTACGTTT	GGTTAAAGCA	CGTCCTATAC	ATTGATTAAA	CTTAATCATC	ACGTTAGGCA	AAGCGATGGC
9A/1	CCACGTAGCC	AACGCCGAGC	ATCATCCCTT	TCGATCCCTT	TCCCTCACGT	GAACCTAATT	GGT.....
9V/5	CCACGTAGCC	AACGCCGAGC	ATCATCCCTT	TCGATCCCTT	TCCCTCACGT	GAACCTAATT	GGT.....
9V/6	CCACGTAGCC	AACGCCGAGC	ATCATCCCTT	TCGATCCCTT	TCCCTCACGT	GAACCTAATT	GGT.....
PMEN1	.....	.....	.....	.....	.....	.....	...TAGCTAA

**Figure S3. Variable site output showing the PMEN3 putative import region 4 and flanking regions.** Regions from the genomes of the PMEN1 reference strain, the PMEN3 reference strain and the PMEN3 ancestral representatives, 9A/1, 9V/5 and 9V/6 are shown. Numbers indicate variable site positions within the alignment. Periods (".") indicate bases identical to the PMEN3 reference at a given site. Dashes ("-") indicate missing bases at a given site. Red brackets indicate the putative imported region.