Table S2. Core *Psa* genes under positive selection.

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| --- | --- | --- | --- | --- | --- |
| **Gene ID**1 | **Annotation**  | **LRT P**2 | **M8 ω3** | **BEB PSS**4 | **Subcellular localization** |
| IYO\_24570 | Predicted metal-dependent hydrolase  | 3.41E-06 | 999.0 | 2 (0) | Cytoplasmic |
| IYO\_26080 | Coenzyme PQQ synthesis protein F | 1.69E-05 | 999.0 | 4 (4) | Periplasmic |
| IYO\_04335 | Conserved uncharacterized protein CreA  | 1.80E-05 | 999.0 | 3 (2) | Cytoplasmic membrane |
| IYO\_15110 | Threonine efflux protein  | 3.63E-05 | 999.0 | 3 (2) | Cytoplasmic membrane |
| IYO\_08380 | Pantothenate synthetase PanC | 2.49E-04 | 999.0 | 2 (1) | Cytoplasmic |
| **IYO\_21565** | Flagellar P-ring protein FlgI | 7.43E-04 | 129.6 | 1 (1) | Periplasmic |
| **IYO\_18505** | Manganese transport protein MntH | 1.29E-03 | 777.2 | 2 (0) | Cytoplasmic membrane |
| IYO\_22505 | Phosphoglycolate phosphatase | 1.52E-03 | 337.5 | 1 (1) | Cytoplasmic |
| IYO\_12100 | Acyl carrier protein AcpP | 2.63E-03 | 999.0 | 1 (0) | Cytoplasmic |
| IYO\_09985 | Phospholipase D | 2.65E-03 | 999.0 | 1 (0) | Cytoplasmic membrane |
| **IYO\_01585** | Hypothetical protein | 2.89E-03 | 999.0 | 7 (1) | Unknown |
| IYO\_03380 | Exodeoxyribonuclease V gamma chain | 3.10E-03 | 67.2 | 1 (0) | Cytoplasmic membrane |
| IYO\_19810 | Sarcosine oxidase SolA | 3.19E-03 | 999.0 | 1 (0) | Cell wall |
| IYO\_12435 | Soluble lytic murein transglycosylase | 3.20E-03 | 999.0 | 1 (1) | Periplasmic |
| **IYO\_12210** | Oxidoreductase | 5.36E-03 | 999.0 | 1 (0) | Cytoplasmic |
| **IYO\_09020** | Group 1 glycosyltransferase | 6.14E-03 | 6.1 | 3 (0) | Cytoplasmic |
| IYO\_16285 | Outer membrane efflux protein | 9.06E-03 | 999.0 | 1 (1) | Outer membrane |

1 Boldface genes have positively selected sites with unique polymorphisms in the outbreak clade

2 Probability values for the likelihood ratio test (LRT) for comparisons between M7 and M8

3 ω = 999 indicates the rate of synonymous substitution = 0

4 Bayes Empirical Bayes determination of positively selected sites (BEB PSS) with posterior probabilities > 0.75; the number of BEB PSS with probabilities > 0.95 shown parenthetically.