Supplementary Table 1

Oligonucleotides used in this study.

Oligonucleotide	Sequence	Size	
		WT	Mutant
1062-1	ATGAAAATGATGAGAAAAACATTGTTGGC	457	
1062-2	GCTAAAGTTACGTGCTGAAACGTTCTTGATAATGTTCTGGGTTGTAGC		
1062-3	GCTACAACCCAGAACATTATCAAGAACGTTTCAGCACGTAACTTTAGC	447	
1062-4	TTACAGGTCGACTAAAATTGTCTTAGTCG		
1062-5	AAACTCGGACAACAGATCCG	2757	904
1062-6	ATCCTCATGATAGAGCCTGC		
2864-1	ATGGCTCTTTTACATAAACCTTCATTGC	341	
2864-2	GTAGCCGTAGTTCTTGGTAATCATCGTCACCATTGTGATTAGCAATC		
2864-3	GATTGCTAATCACAATGGTGACGATGATTACCAAGAACTACGGCTAC	341	
2864-4	TTACTTACGACGACGCCACATTGC		
2864-5	TCGATGAACTTAGGTGAAACG	2595	682
2864-6	GTTTATTATGACTCGAAAAGCC		
576-1	ATGAGCAAGGAAACATTTGATAGC	500	
576-2	CCAAATACGAAGATATCCCAATCTCGTATGTTGGACCATTAGTGTG		
576-3	CACACTAATGGTCCAACATACGAGATTGGGATATCTTCGTATTTGG	465	
576-4	TTAAACTGCGATTTCACCGCC		
576-5	TAAAGTCAGCCAACAGGAAGC	2028	965
576-6	GCTGATCTTAGCTAGATTTGC		
2984fd1	ATGGAAAACTTCAAACATCTAC		
2984rev1	TTAAAATGCTTCTTCGAGCG		
2985fd1	GTGGACATCAATCTAGACATTC		
2985rev1	AATAGCCATTGATTCAAAGGC		
2986fd1	ATGAAAAAGTTAATCGCACTAGGC		
2986rev1	TTAATCACGACGACCTATAAGC		
2987fd1	ATGATTCGTCATATTCTACTG		
2987rev1	TTACAAGGAGTAATCAAACAC		
2994fd1	ATGGGCACTTGGTCGAAAG		
2994rev1	TCAACTTAAATGGCTCTTTG		
2995fd1	ATGAGTGAAAAAGTGAAAGTAGC		
2995rev1	TTAAATGTCTAACGTCAGTTCTTG		
2996fd1	ATGAATTACGATGAGTTTAACC		
2996rev1	TTACGTGCGTGGTTCAGATAG		
tas2984fd2	ATCTTAGAAGCGGGTGCTGC		
tas2984fd3	CTCACATGGATTTCATTATCG		
tas2984rev2	CGCTTCTTGATAAGAACAGG		
tas2995fd2	ATCGAACTGCCAGTCATTCC		

Supplementary Table 2

Proteomic analysis of 56 spots present in LGP32 and/or Δ*vsm* ECP.

Sample	**Score**	**Hit/submitted**	**Intensity**	**ORF**	**Product**	**MW/pI**
Δ*vsm*	4,24E+08	24/124	72%	VSA1062	Metalloprotease	101/4,6
Δ*vsm*	1,88E+04	16/250	35%	VSA1096	Conserved hypothetical protein	40/5,9
Δ*vsm*	1,58E+07	22/197	50%	VS1430	ABC transporter	36/5,4
Δ*vsm*	5,25E+03	10/162	30%	VS2427	Conserved hypothetical protein	36/5,9
Δ*vsm*	6,31E+13	39/130	76%	VS2864	Conserved hypothetical protein	94/4,6
Δ*vsm*	4,51E+06	19/250	27%	VS2048	Alanine dehydrogenase	39/5,2
LGP32	8,00E+06	16/246	44%	**VS1267**	Metalloprotease	66/5,5
LGP32	1,19E+06	16/250	39%	**VS1267**	Metalloprotease	66/5,5
LGP32	1,66E+07	16/100	56%	**VS1267**	Metalloprotease	66/5,5
LGP32	9,21E+05	15/147	43%	VS1430	ABC transporter	36/5,4
LGP32	1,54E+06	16/108	55%	VS1430	ABC transporter	36/5,4
LGP32	2,49E+05	24/250	54%	VS1430	ABC transporter	36/5,4
LGP32	1,73E+10	29/163	60%	VSA576	Conserved hypothetical protein	74/5,3
Both	2,52E+04	13/222	51%	VSA205	ABC transporter: Substrate-binding protein precursor; phosphate uptake	28/5,7
Both	5,93E+04	15/250	25%	VS1661	Hypothetical protein	58/5,3
Both	8,46E+07	28/250	45%	VSA576	Conserved hypothetical protein	74/5,3
Both	2,40E+06	18/89	67%	VSA310	Outer membrane protein	35/4,4
Both	5,64E+07	17/68	78%	VS1068	hypothetical protein	36/4,2
Both	6,28E+04	16/239	47%	VS1055	Lysine-arginine-ornithine-binding periplasmic protein	28/5,4

					precursor	
Both	4,67E+06	19/250	33%	VSA1211	ABC-type sugar transport system, periplasmic component	48/5,9
Both	5,25E+03	10/162	30%	VS2427	Conserved hypothetical protein	37/5,9
Both	1,34E+06	16/250	39%	VS9	Putative amino-acid ABC transporter-binding protein patH precursor	27/5
Both	9,7E+04	12/170	45%	VSA395	Outer membrane protein OmpA	37/4,4
Both	1,47E+07	15/243	19%	VS861	Long-chain fatty acid transport protein precursor	45/4,5