

1 **Supplementary Table 2: Gene expression of A66.1 cells treated with CSP2, MAbs and**
2 **CSP2 plus MAbs**
3 S2a. Differentially expressed genes comparing CSP2-treated and untreated A66.1 cells two
4 minutes after incubation. Genes that exhibited a > 2.5 fold increase are shown. Hypothetical
5 genes, which are not included, are shown in supplementary Table 3.

SEQ_ID	FUNCTION	Fold change
SP_2207080700002076	competence protein ComF, putative	66.6
SP_1266080700001180	DNA processing protein DprA, putative	53.1
SP_0954080700000884	competence protein CeiA	45.5
SP_0955080700000885	competence protein CeiB	42.2
SP_2208080700002077	helicase, putative	39.6
SP_2201080700002070	choline binding protein D	38.4
SP_1908080700001793	single-strand DNA-binding protein	34.8
SP_2051080700001932	competence protein CglC	32.6
SP_2052080700001933	competence protein CglB	29.5
SP_2050080700001931	competence protein CglD	28.7
SP_1808080700001696	type IV prepilin peptidase, putative	28.2
SP_2049080700001930	hypothetical protein	26.5
SP_0957080700000887	ABC transporter, ATP-binding protein	26.2
SP_2053080700001934	competence protein CglA	25.9
SP_0042080700000038	competence factor transporting ATP-binding/permease protein ComA	24.7
SP_0014080700000014	transcriptional regulator ComX1	22.6
SP_0978080700000908	competence protein CoiA	19.6
SP_2236080700002101	putative sensor histidine kinase ComD	19.1
SP_1945080700001829	hypothetical protein	18.1
SP_1717080700001609	ABC transporter, ATP-binding protein	15.5
SP_1941080700001825	competence damage-inducible protein A	15.5
SP_1988080700001872	immunity protein, putative	14.1
SP_2235080700002100	response regulator ComE	10.6
SP_1088080700001010	DNA repair protein RadC	10.2
SP_0043080700000039	competence factor transport protein ComB	10.0
SP_1987080700001871	ABC transporter, ATP-binding protein	9.8
SP_0544080700000510	immunity protein BlpX	8.2
SP_1809080700001697	transcriptional regulator	7.8
SP_1714080700001606	GntR family transcriptional regulator	7.3

SP_0529080700000496	BlpC ABC transporter	7.2
SP_0030080700000027	competence-induced protein Ccs16	7.2
SP_1110080700001031	bifunctional riboflavin kinase/FMN adenylyltransferase	6.7
SP_0545080700000511	immunity protein BlpY	6.5
SP_0524080700000491	BlpT protein, fusion	5.0
SP_0047080700000043	phosphoribosylaminoimidazole synthetase	5.0
SP_0942080700000874	IS1381 transposase protein A	4.6
SP_0046080700000042	amidophosphoribosyltransferase	4.2
SP_1089080700001011	glutamine amidotransferase, class I	4.1
SP_1729080700001620	truncated IS1381 transposase	4.1
SP_0540080700000506	BlpN protein	4.0
SP_1310080700001221	IS1381 transposase protein A	3.8
SP_0048080700000044	phosphoribosylglycinamide formyltransferase	3.7
SP_0528080700000495	peptide pheromone BlpC	3.6
SP_2206080700002075	ribosomal subunit interface protein	3.5
SP_1812080700001700	tryptophan synthase subunit beta	3.4
SP_1894080700001780	sucrose phosphorylase	3.3
SP_0021080700000020	deoxyuridine 5'-triphosphate nucleotidohydrolase	3.3
SP_0044080700000040	phosphoribosylaminoimidazole-succinocarboxamidesynthase	3.3
SP_1898080700001784	alpha-galactosidase	3.2
SP_0053080700000049	phosphoribosylaminoimidazole carboxylase catalytic subunit	3.1
SP_2186080700002055	glycerol kinase	3.1
SP_1857080700001744	cation efflux system protein	2.9
SP_0368080700000344	cell wall surface anchor family protein	2.9
SP_0045080700000041	phosphoribosylformylglycinamide synthase, putative	2.9
SP_0054080700000050	phosphoribosylaminoimidazole carboxylase ATPase subunit	2.8
SP_1811080700001699	tryptophan synthase subunit alpha	2.8
SP_1927080700001811	IS1381 transposase protein A	2.7
SP_1813080700001701	N-(5'-phosphoribosyl)anthranilate isomerase	2.7
SP_2142080700002017	ROK family protein	2.6
SP_2158080700002030	L-fucose isomerase	2.6
SP_1086080700001008	IS1381 transposase protein B	2.6
SP_2240080700002105	spspoJ protein	2.6
SP_1980080700001864	cmp-binding-factor 1	2.5
SP_0541080700000507	bacteriocin BlpO	2.5
SP_2035080700001917	3-keto-L-gulonate-6-phosphate decarboxylase	2.5

1 S2b. Differentially expressed genes comparing CSP2-treated and untreated A66.1 cells two
 2 minutes after incubation. Genes that exhibited a > 2.5 fold decrease in expression are shown.
 3 Hypothetical genes, which are not included, are shown in supplementary Table 3.

SEQ ID	FUNCTION	Fold change
SP_1821080700001709	LacI family sugar-binding transcriptional regulator	3.1
SP_1171080700001090	HAD superfamily hydrolase	2.9
SP_0985080700000913	regulatory protein, putative	2.9
SP_1294080700001208	chromosome condensation/ camphor resistance protein CrcB	2.8
SP_1182080700001101	lactose phosphotransferase system repressor	2.8
SP_2119080700001996	transcriptional regulator, putative	2.8
SP_1115080700001036	transcriptional regulator MutR, putative	2.7
SP_1249080700001164	guanosine 5'-monophosphate oxidoreductase	2.6
SP_0012080700000012	hypoxanthine-guanine phosphoribosyltransferase	2.6

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1 S2c. Differentially expressed genes comparing CSP2- and CSP2 plus 1E2 (ms IgG₁ to PPS3)-
2 treated A66.1 cells two minutes after incubation. Genes that exhibited a > 2.5 fold decrease in
3 expression are shown. Hypothetical genes, which are not included, are shown in supplementary
4 Table 3.

SEQ_ID	FUNCTION	Fold change
SP_0729080700000677	cation transporter E1-E2 family ATPase	6.3
SP_0727080700000675	transcriptional repressor, putative	6.2

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1 S2d. Differentially expressed genes comparing CSP2- and CSP2 plus 1E2 (ms IgG₁ to PPS3)-
2 treated A66.1 cells eight minutes after incubation. Genes that exhibited a > 2.5 fold decrease in
3 expression are shown. Hypothetical genes, which are not included, are shown in supplementary
4 Table 3.

SEQ_ID	FUNCTION	Fold change
SP_1249080700001164	guanosine 5'-monophosphate oxidoreductase	2.8

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1 S2e. Differentially expressed genes comparing 1E2 (ms IgG₁ to PPS3)-treated and untreated
2 A66.1 cells at bacterial growth of OD₄₀₅: 0.032. Genes that exhibited a > 2.5 fold decrease in
3 expression are shown. Hypothetical genes, which are not included, are shown in supplementary
4 Table 3.

SEQ_ID	FUNCTION	Fold change
SP_0082080700000077	cell wall surface anchor family protein	5.9
SP_0395080700000368	transcriptional regulator, putative	2.6
SP_0396080700000369	PTS system, mannitol-specific IIA component	2.6
SP_2150080700002024	ornithine carbamoyltransferase	2.5
SP_0090080700000084	ABC transporter, permease protein	2.5

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1 S2f. Differentially expressed genes comparing control MAb 31B12 (ms IgG₁to PPS8)-treated
2 and untreated A66.1 cells at bacterial growth at OD₄₀₅: 0.032. Genes that exhibited a > 2.5 fold
3 decrease in expression are shown. Hypothetical genes, which are not included, are shown in
4 supplementary Table 3.

SEQ_ID	FUNCTION	Fold change
SP_1809080700001697	transcriptional regulator	2.9
SP_1294080700001208	chromosome condensation/camphor resistance protein CrcB	2.7
SP_0082080700000077	cell wall surface anchor family protein	2.7
SP_0641080700000599	serine protease	2.6

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