

## A multi-component prime-boost vaccination regimen with a consensus MOMP antigen enhances *Chlamydia trachomatis* clearance.

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Provisional

1 **A multi-component prime-boost vaccination regimen with a**  
2 **consensus MOMP antigen enhances *Chlamydia trachomatis***  
3 **clearance.**  
4

5 Running title: Prime-boost regimens against *C. trachomatis*.

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20 **Keywords:** *Chlamydia trachomatis*, consensus, mosaic, prime-boost regimens, Adenovirus-  
21 vector vaccines, MVA-vector vaccines, DNA vaccines.

22

23 **Abstract**

24 Background: A vaccine for *Chlamydia trachomatis* is of urgent medical need. We explored  
25 bioinformatic approaches to generate an immunogen against *C. trachomatis* that would  
26 induce cross-serovar T cell responses as (i) CD4<sup>+</sup> T cells have been shown in animal models  
27 and human studies to be important in chlamydial protection, and (ii) antibody responses may  
28 be restrictive and serovar-specific.

29 Methods: A consensus antigen based on over 1,500 MOMP sequences provided high epitope  
30 coverage against the most prevalent *C. trachomatis* strains *in silico*. Having designed the T  
31 cell immunogen, we assessed it for immunogenicity in prime-boost regimens. This consensus  
32 MOMP transgene was delivered using plasmid DNA, Human Adenovirus-5 (HuAd5) or  
33 modified vaccinia Ankara (MVA) vectors with or without MF59® adjuvanted recombinant  
34 MOMP protein.

35 Results: Different regimens induced distinct immune profiles. The DNA-HuAd5-MVA-  
36 Protein (DAMP) vaccine regimen induced a cellular response with a Th1 biased serum  
37 antibody response, alongside high serum and vaginal MOMP-specific antibodies. This  
38 regimen significantly enhanced clearance against intravaginal *C. trachomatis* serovar D  
39 infection in both BALB/c and B6C3F1 mouse strains. This enhanced clearance was shown to  
40 be CD4<sup>+</sup> T cell dependent. Future studies will need to confirm the specificity and precise  
41 mechanisms of protection.

42 Conclusions: A *C. trachomatis* vaccine needs to induce a robust cellular response with broad  
43 cross-serovar coverage and a heterologous prime-boost regimen may be an approach to  
44 achieve this.

45

Provisional

## 46 Introduction

47 Genital chlamydial infection is the most common cause of bacterial sexually transmitted  
48 diseases (STDs) worldwide, accounting for more than 90 million cases of STDs globally each  
49 year (WHO, 2001). Over US\$3 billion is spent annually on an estimated 4 million reported  
50 clinical cases of genital chlamydial infections in the US alone (CDC, 2010), thus  
51 development of a vaccine against *Chlamydia trachomatis* represents a significant public  
52 health priority. A promising vaccine antigen of *C. trachomatis* is the major outer membrane  
53 protein (MOMP). The MOMP antigen has been used in a range of previous pre-clinical  
54 vaccine studies with a mixture of encouraging (Pal et al., 2001;Farris et al., 2010) and  
55 disappointing results (Igietseme and Murdin, 2000;Sun et al., 2009). This may reflect the  
56 high level of amino acid variability in the MOMP antigen, the basis for *C. trachomatis*  
57 serotypes (Yuan et al., 1989).

58  
59 New bioinformatic approaches have been developed to account for amino acid diversity and  
60 aid in the design of immunogens to induce cross-serovar T cell responses: these include the  
61 design of mosaic or conserved antigen sequences. Mosaic vaccine antigens are designed with  
62 the intent to be used in polyvalent combinations to optimise the coverage of potential T cell  
63 epitopes (Fischer et al., 2007), for example HIV mosaic antigens increased the breadth and  
64 potency of vaccine elicited immune responses (Barouch et al., 2010), conferring protective  
65 responses in non-human primate models (Barouch et al., 2013). Consensus vaccine antigens  
66 rely on a single centralised antigen designed to reduce sequence distances between the  
67 vaccine and circulating strains by using the most common amino acid at each position of the  
68 protein (Gaschen et al., 2002). By reducing the genetic differences between the vaccine and  
69 the primary isolate, consensus antigens can increase the breadth of immune response (Eugene  
70 et al., 2013).

71  
72 Here we computationally design and *in silico* assess both consensus and mosaic MOMP  
73 antigens for broad T cell coverage against the *C. trachomatis* genital serovars D-K, for the  
74 reasons that (a) chlamydial infections in both animal models and humans suggest a strong  
75 protective role for CD4<sup>+</sup> Th1-biased immune responses (Su and Caldwell, 1995;Li et al.,  
76 2008;Farris et al., 2010) and (b) that these may be supplemented by MOMP specific  
77 antibodies able to mediate antibody-dependent cellular cytotoxicity (ADCC) (Moore et al.,  
78 2002).

79  
80 We assess the quantity and quality of the antibody and cellular response to MOMP following  
81 different prime-boost combinations using DNA vaccines, recombinant viral vectors and  
82 protein-in-adjuvant formulations (McKay et al., 2014). Both DNA and recombinant viral  
83 vectors preferentially induce cellular immunity (Tregoning and Kinnear, 2014) and subunit  
84 proteins humoral immunity: the use of different prime boost combinations can be tailored to  
85 influence the phenotype of both arms of induced adaptive immunity. DNA vaccine vectors,  
86 human Adenovirus 5 and MVA viral vectors have already entered phase I clinical trials,  
87 showing safety and tolerability (Hayton et al., 2014;Nilsson et al., 2015). Research groups  
88 have reported enhanced T cell induction through heterologous prime-boost vaccination  
89 strategies in a range of disease models (including tuberculosis (McShane et al., 2001), HIV  
90 (Hanke et al., 1998), HPV (van der Burg et al., 2001) and Ebola (Sullivan et al., 2000)) but  
91 these strategies have yet to be comprehensively investigated for *C. trachomatis*.

92

93 We demonstrate that different vaccination regimens when used to deliver the same MOMP  
94 antigen via differing platforms can be configured to induce distinct immune outcomes. We  
95 further investigate which distinct MOMP-specific immune responses are required for  
96 enhanced *C. trachomatis* clearance following genital challenge in mice. We observe that a  
97 regimen using DNA-HuAd5-MVA-Protein (DAMP) vaccines reduced bacterial load early  
98 after infection regardless of mouse strain used, and that this enhanced clearance while  
99 dependent upon CD4<sup>+</sup> T cell responses may have been augmented by induced MOMP-  
100 specific antibody responses.

101

## 102 **Material and Methods**

### 103 **Bioinformatic antigen design**

104 1,464 serovar E *ompA* sequences, surveyed from a total of 5,026 *C. trachomatis* strains  
105 isolated in 33 distinct geographic regions from five continents were compared (Nunes et al.,  
106 2010). Phylogenetic analysis was based on the protein sequence alignment derived from  
107 (Nunes et al., 2010), and the maximum likelihood tree was created using FastTree (Price et  
108 al., 2009) using default settings; the figure was generated using Rainbow Tree  
109 ([www.hiv.lanl.gov](http://www.hiv.lanl.gov)). 49 distinct *ompA* variants were present within the serovar E sequences,  
110 and were used in the *in silico* generation of the consensus MOMP (Con E) antigen sequence  
111 for the experimental studies. The generated consensus and mosaic antigens were assessed for  
112 their coverage against different Chlamydia MOMP variants using the Epitope Coverage  
113 Assessment Tool EPICOVER. Full bioinformatic tool settings, a detailed description of the  
114 method, and consensus and mosaic antigen sequence information is provided in the  
115 Supplemental Methods and Materials (Supplementary File 1).

116

### 117 **Plasmid, viral vectors and recombinant protein**

118 Mammalian codon optimised MOMP Con E antigen was synthesised by GeneArt (Invitrogen,  
119 UK) and cloned into pcDNA3.1 (Invitrogen, UK). Con E was homologously recombined into  
120 the E1 and E3 deleted HuAd5 genome plasmid, pAL1112 (kindly provided by Prof. Gavin  
121 Wilkinson, Cardiff University). Con E was recombined into the MVA pox vector by the Viral  
122 Vector Core Facility, The Jenner Institute (University of Oxford, UK). *E. coli* codon  
123 optimised Con E expressed at too low a yield in BL21 *E. coli*, and as such a recombinant  
124 MOMP matching *C. trachomatis* from serovar D/UW/Cx expressed in BL21 *E. coli* was  
125 used.

126

### 127 **Chlamydia**

128 *C. trachomatis* serovar D (strain UW-3/Cx) was provided by Dr. Frank Follmann (Statens  
129 Serum Institut) and propagated in McCoy cells as described previously (Scidmore, 2005).  
130 Chlamydial EBs were harvested, purified and quantified as described in (Scidmore, 2005),  
131 and stored at -80°C in SPG buffer (Sucrose/Phosphate/Glutamic acid: 0.2 M sucrose, 20 mM  
132 sodium phosphate and 5 mM glutamic acid).

133

### 134 **Mice immunisations and infections**

135 Female 6-8 weeks old, BALB/c mice (Harlan, Stornoway, UK) and female 6-8 weeks old  
136 B6C3F1 mice (Charles River, Italy) were kept in specific-pathogen-free conditions in  
137 accordance with the UK Home Office guidelines. All work was approved by the Imperial  
138 College Ethical Review Process (ERP) Committee. Mice received immunisations at three-  
139 week intervals (Table 1). DNA vaccinations were at 10 µg doses, intramuscularly into the  
140 hind quadriceps muscle in a volume of 50 µl with electroporation. Electroporation was with 5  
141 mm electrodes at the immunisation site using an ECM 830 Square Wave Electroporation  
142 System (BTX), with three pulses of 100 V each, followed by three pulses of the opposite  
143 polarity with each pulse ( $P_{ON}$ ) lasting 50 ms and an interpulse ( $P_{OFF}$ ) interval of 50 ms. All  
144 HuAd5 and MVA vaccinations were at dosages of  $10^7$  PFU and  $10^6$  PFU respectively.  
145 rMOMP was administered at a dose of 10 µg in a 1:1 mixture with MF59® (an oil-in-water  
146 emulsion adjuvant) (Novartis, Sienna, Italy) in a final volume of 50 µl for intramuscular  
147 immunisations. Because of the multi-component immunisation regime, vehicle and vector-  
148 alone controls were not included to reflect reduce, replace and refinement practice. Seven  
149 days prior to intravaginal infection, mice were injected subcutaneously with 2mg of DMPA  
150 (Depo-Provera, Pfizer). For intravaginal infections, purified *C. trachomatis* D/UW-3/Cx EBs  
151 were dissolved in SPG buffer to a concentration of  $4 \times 10^7$  IFU/ml, mice were anaesthetised,  
152 and 10 µl of the EB solution pipetted into the mouse vagina. The optimal infective dose of  
153  $4 \times 10^5$  IFU of *C. trachomatis* D/UW-3/Cx EBs per mouse was previously determined by Dr.  
154 Frank Follmann, SSI (unpublished data) and consistent with (O'Connell et al., 2011; Picard et  
155 al., 2012). Furthermore, bacterial clearance profiles were consistent between naïve BALB/c  
156 and B6C3F1 mice at this infective dose (Fig S2). Unfortunately *C. trachomatis* E/Bour could  
157 not be propagated to a high enough infectious titre for intravaginal infection.

158

### 159 **Intravaginal *C. trachomatis* load quantification**

160 Vaginal swabs were obtained at 3, 7, 10 and 14 days after infection. Swabs were vortexed  
161 with glass-beads in 500 µl SPG buffer and stored at  $-80^{\circ}\text{C}$  until analysis. Infectious load was  
162 determined as described in (Hansen et al., 2008). Inclusions were visualised by staining with  
163 polyclonal rabbit anti-MOMP serum (provided by Dr. Frank Follmann, SSI), followed by an  
164 Alexa 594-conjugated goat anti-rabbit H+L (Life Technologies, UK).

165

### 166 **Mice sampling**

167 Tail bleeds were collected before regimen, and two weeks post each immunisation. Blood  
168 was collected and centrifuged at 1,000 g for 10 min. The serum was harvested and stored at -  
169  $20^{\circ}\text{C}$ . To assess IFN- $\gamma$  T cell responses, lymphocyte cultures from spleens were prepared as  
170 described previously (McKay et al., 2014). Vaginal lavage was performed at the same time  
171 points as tail bleeds, using three 25 µl washes/mouse with sterile Phosphate buffered saline  
172 (PBS) that were later pooled. Lavage samples were incubated with protease inhibitor (Roche  
173 Diagnostics, Germany) before centrifuging at 1,000 g for 10 min. The fluid supernatant from  
174 these samples was harvested and stored at  $-20^{\circ}\text{C}$ .

175

### 176 **Semi-quantitative MOMP-specific ELISA, avidity assay, and MOMP-specific IFN- $\gamma$** 177 **ELISpot**

178 A semi-quantitative immunoglobulin ELISA protocol described previously (Badamchi-Zadeh  
179 et al., 2015) was followed. The avidity indices of serum samples were determined by their  
180 antibody-antigen binding resistance to 8 M urea. Serum samples were pre-diluted to give an  
181 OD<sub>450 nm</sub> readout between 1.0 and 1.5 in an ELISA and were added to MOMP antigen coated  
182 plates. Plates were then washed three times with either PBS-T or 8 M urea in PBS-T, before  
183 incubating with anti-mouse IgG-HRP. Samples were developed with TMB as described  
184 above. The avidity index was calculated as the percentage of urea treated OD<sub>450 nm</sub>/ PBS-T  
185 OD<sub>450 nm</sub>. IFN- $\gamma$  ELISpot assays (Mabtech, UK) were carried out on mouse splenocytes as to  
186 manufacturer's instructions.

187

## 188 **Depletion of CD4<sup>+</sup> T-cells**

189 Mice were depleted of CD4<sup>+</sup> T-cells by the i.p. route with injections of 500  $\mu$ g monoclonal  
190 anti-mouse CD4 IgG2b (clone GK1.5) (BioXcell, Cat: BE0003-1) on days -1 and +1 with  
191 respect to day of challenge being day 0. The depletion of CD4<sup>+</sup> T cells was verified by FACS  
192 analysis on murine PBMC, splenocytes and vaginal tissue on day +2 using anti-CD3e PE,  
193 anti-CD4 APC and anti-CD8a eFluor605NC antibodies (All BD Biosciences, UK).

194

## 195 **Statistical Analysis**

196 All statistical analyses were carried out using Prism 6.0 (GraphPad, USA). Normality of the  
197 data distribution was assessed using the Kolmogorov Smirnov normality test. For non-  
198 parametric data the Kruskal-Wallis test with Dunn's multiple comparison post-test was used  
199 to compare more than two groups, or the two-tailed Mann-Whitney test to compare two  
200 groups. For parametric data, a one-way ANOVA was used for multiple comparisons, with  
201 Bonferroni's multiple comparison post-test for comparison of specific groups. P<0.05 was  
202 considered significant (\* p<0.05, \*\* p<0.01 and \*\*\* p<0.001).

203

## 204 **Results**

### 205 **Design and cross-serovar coverage assessment of consensus and mosaic MOMP** 206 **antigens**

207 The worldwide prevalence of specific urogenital *C. trachomatis* serovars has not been fully  
208 characterised. A literature review (PubMed) identified 13 publications describing the country  
209 or regional serovar-specific prevalence (Lan et al., 1995;Morre et al., 2000;Suchland et al.,  
210 2003;Yamazaki et al., 2005;Gao et al., 2007;Suarkia et al., 2007;Banda et al., 2008;Hafner  
211 et al., 2008;Donati et al., 2009;Petrovay et al., 2009;Smelov et al., 2009;Gallo Vaulet et al.,  
212 2010;Papadogeorgakis et al., 2010). In 10 out of the 13 *C. trachomatis* serovar surveys  
213 published, serovar E emerged as the most prevalent (Fig 1A). MOMP is a lead vaccine  
214 antigen candidate for *C. trachomatis*, and with worldwide MOMP sequence data available  
215 (Nunes et al., 2010) for the differing genital serovars (D-K, Da, Ia, and Ja) it was possible to  
216 bioinformatically perform MOMP based immunogen design. We found sequences within all  
217 serovars to be conserved, with only sporadic amino acid substitutions (Fig 1B). From our  
218 phylogenetic analyses, *C. trachomatis* has quite distant species, but high levels of  
219 conservation within a serovar. Thus this kind of phylogenetic profile lends itself more  
220 towards a consensus antigen design approach as opposed to a single mosaic antigen design  
221 (Fischer et al., 2007). Based on 49 published serovar E sequence variants (Nunes et al., 2010)



222 we generated a novel MOMP consensus sequence (Con E), which fully matched the solution  
223 for a single mosaic and was identical to the circulating *C. trachomatis* strain E-Bour, as well  
224 as to 8 additional partial MOMP protein sequences from a wide variant of geographic origins  
225 (Nunes et al., 2010). Using a single consensus antigen the potential epitope coverage of the E  
226 serovar led to extremely high coverage (~95%) (Fig 1C). For even broader coverage, our  
227 analyses suggest multiple mosaic antigens may be more appropriate (Fig 1C and  
228 Supplementary File 1).

229

### 230 **Differences in humoral and cellular immunogenicity of *C. trachomatis* MOMP vaccines** 231 **following intramuscular multi-component prime-boost regimen screen**

232 The immunogenicity of the consensus MOMP antigen was assessed in BALB/c mice  
233 immunised in multi-component prime-boost regimens with DNA (D), HuAd5 (A), MVA (M)  
234 and protein with the oil-in-water emulsion adjuvant MF59® (P) vaccines (Table 1). The  
235 MF59® adjuvant has been demonstrated to induce IL-5 and IL-10 responses to the MOMP  
236 antigen and was therefore used as a comparator to the more Th1 skewing DNA and viral  
237 vector approaches (Knudsen et al., 2016). Serum and vaginal washes were sampled two  
238 weeks after final immunisation. The highest MOMP-specific serum IgG concentrations were  
239 observed after the PPP regimen (mean + SEM = 1.27 +/- 0.16 mg/ml) and the lowest from the  
240 DDD regimen (mean + SEM = 15.4 +/- 2.54 µg/ml) (Fig 2A). Protein (+ MF59®)  
241 immunisation significantly increased MOMP-specific serum IgG concentrations compared to  
242 prime-boost regimen without two protein boosts. MOMP-specific vaginal IgG concentrations  
243 were measured following the multi-component prime-boost regimens (Fig 2B). The PPP  
244 regimen induced significantly higher MOMP-specific vaginal IgG than DDDAM, DDDA,  
245 DDDM, DDD, AM or the naïve group ( $p \leq 0.05$ ). MOMP-specific IgA was not detectable in  
246 the sera or vaginal washes following any of the prime-boost regimens (data not shown).

247

248 Viral vector vaccines have been shown to induce high and long lasting cytophilic, Th1  
249 skewed, antibody responses (Douglas et al., 2010). A correlate for Th1 and Th2 skewing of  
250 the immune response in mice is the antigen-specific IgG2a to IgG1 ratio. MOMP-specific  
251 serum IgG2a and IgG1 concentrations were measured by ELISA, and their ratios calculated  
252 (Fig 2C). The highest MOMP-specific serum IgG2a:IgG1 ratio was induced following the  
253 DAMP regimen (mean = 14.2), with the lowest ratio induced following PP (+ MF59®)  
254 vaccination (mean = 0.0036). There was a significant statistical difference in the IgG2a:IgG1  
255 ratios between DAMP and PPP ( $p \leq 0.005$ ) and DAMP and PP ( $p \leq 0.0005$ , one-way  
256 ANOVA with Bonferroni's multiple comparison post-test). Protein only vaccine regimens  
257 induced Th2-biased immune environments indicated by IgG2a:IgG1 ratios of less than 1  
258 caused by high IgG1 concentrations. Vaccine regimens with a vector-based vaccine prime  
259 consistently induced a Th1-biased, cytophilic antibody response as indicated by IgG2a:IgG1  
260 ratios of greater than 1.

261

262 To differentiate and qualitatively evaluate the humoral responses an avidity assay was  
263 performed (Fig 2D). All protein free regimens had mean avidity indices of <30%, with the  
264 DAMP and PP regimens also having low mean avidity indices. Regimens involving two  
265 protein boosts all had avidity indices >40%, with the APP regimen inducing MOMP-specific  
266 serum IgGs with the highest avidity (mean = 51.8%).

267

268 T cell responses were assessed one week after the final immunisation. MOMP specific IFN-  
269  $\gamma$ + T cell responses as assessed by ELISpot were induced by all prime-boost regimens, with  
270 the DDD and AM regimens inducing the strongest T cell responses (a median of 504 and 502  
271 SFU/10<sup>6</sup> splenocytes respectively, Fig 2E). T cell responses induced by the DDD and AM  
272 regimens were significantly higher than those induced in the PP regimen ( $p \leq 0.05$ ). From  
273 this we conclude that there were significant differences in both the quantity and quality of the  
274 antibody and cellular response following the different regimens.

275

### 276 **Multi-component prime-boost regimens induce analogous immunogenicity profiles in** 277 **both BALB/c and B6C3F1 mice**

278 As we wished to test the effect of altering the immune response on Chlamydial protection, the  
279 following groups were chosen for further investigation as they gave distinct, skewed immune  
280 responses in the BALB/c screen: AM and DDD (T cell, low antibody), PPP (Th2 skewed  
281 antibody, no Th1 T cells), and DAMP (Th1 skewed antibody and T cell). These vaccine  
282 regimens induced comparable responses in B6C3F1 mice as they did in BALB/c mice for  
283 MOMP-specific serum IgG concentrations (Fig 3A), MOMP-specific vaginal IgG  
284 concentrations (Fig 3B), MOMP-specific serum IgG2a to IgG1 ratios (Fig 3C), and MOMP  
285 specific IFN- $\gamma$  T cell responses (Fig 3D).

286

### 287 **The DAMP vaccine regimen enhances the clearance of *C. trachomatis*, regardless of** 288 **mouse strain, and is CD4<sup>+</sup> T dependent**

289 Immunised BALB/c mice were challenged with *C. trachomatis* D/UW-3/Cx intravaginally.  
290 The DAMP regimen significantly reduced chlamydial IFU per swab at day 3 after challenge  
291 (median = 354 IFU/swab) compared to unvaccinated controls (median = 22,688 IFU/swab)  
292 (DAMP: \*  $p = 0.0359$ , 2-tailed Mann-Whitney test) (Fig 4A). There were no statistical  
293 differences at the later sampling points of 7, 10 and 14 days (data not shown) after challenge  
294 reflecting the natural clearance of *C. trachomatis* in mice. The DDD, AM, and PPP regimens  
295 did not significantly reduce chlamydial shedding at any time points sampled after challenge  
296 in BALB/c mice.

297

298 Immunised B6C3F1 mice were challenged with *C. trachomatis* D/UW-3/Cx intravaginally.  
299 Similar to BALB/c mice, the DAMP vaccination regimen significantly reduced chlamydial  
300 IFU per swab at day 3 after challenge (median = 6,531 IFU/swab) compared to unvaccinated  
301 controls (median = 34,788 IFU/swab) (\*  $p = 0.0303$ , 2-tailed Mann-Whitney test) in  
302 B6C3F1s (Fig 4B). In addition, the PPP regimen significantly reduced chlamydial IFU per  
303 swab at day 3 after challenge (median = 8,095 IFU/swab) compared to unvaccinated controls  
304 (median = 34,788 IFU/swab) (\*  $p = 0.0451$ , 2-tailed Mann-Whitney test) (Fig 4B). There  
305 were no statistical differences at the later sampling points of day 7, day 10 or day 14 after  
306 challenge, and consistent with this challenge model, there was no oviduct pathology observed  
307 (hydrosalpinx) in challenged BALB/c or B6C3F1 mice (data not shown). Of the four tested  
308 prime-boost regimens, only the DAMP regimen consistently enhanced the clearance of  
309 intravaginal *C. trachomatis*.

310

311 We assessed the mechanism of the vaccine-induced enhanced clearance. Monoclonal  
312 antibodies were used to deplete CD4<sup>+</sup> T cells in DAMP vaccinated and unvaccinated control  
313 B6C3F1 mice prior to intravaginal challenge. There was no difference between the DAMP  
314 immunised CD4<sup>+</sup> depleted groups and the naïve CD4<sup>+</sup> depleted group in chlamydial loads,  
315 indicating that the DAMP vaccine induced enhanced clearance is CD4<sup>+</sup> T cell dependent (Fig  
316 4C).

317

## 318 Discussion

319 New bioinformatic strategies have been developed as an approach to elicit broad immune  
320 responses against the more intractable antigenically variable pathogens, such as *C.*  
321 *trachomatis*. Two such approaches, consensus and mosaic, were used to design a MOMP  
322 antigen(s) to provide broad cellular cross-serovar coverage. We performed phylogenetic  
323 analyses revealing *C. trachomatis* MOMP to have quite distant species but high levels of  
324 amino acid conservation within a serovar. This phylogenetic structure lends itself more  
325 towards a consensus-based antigen design as opposed to a mosaic-based approach (Fischer et  
326 al., 2007). Therefore a single consensus MOMP antigen (Con E), constructed from variant  
327 sequences of the most common *C. trachomatis* serovar, was used. Nevertheless, combining  
328 the Con E antigen with additional mosaic antigens (that we have designed (Supplementary  
329 Materials)) would provide complementary coverage to all other serovars. This would be a  
330 well-justified approach to theoretically achieve comprehensive coverage of all serovars in  
331 one vaccine, with no loss of coverage of the E serovar (Fig 1C), however assessing these  
332 additional antigens immunologically was out of the scope of this initial study.

333

334 Having designed our broad-coverage T cell immunogen, we then assessed its  
335 immunogenicity using a range of prime-boost regimens. Few multi-component prime-boost  
336 vaccine regimens have been tested for the generation of immune responses against  
337 Chlamydia (Brown et al., 2012), with the majority focussing on homologous prime-boost  
338 strategies (Pal et al., 2005; Schautteet et al., 2011). The use of different vectors within prime-  
339 boost regimen can help to avoid anti-vector immunity and improve vaccine-elicited immune  
340 responses. Previous uses of DNA vaccines expressing Chlamydia transgenes have not been  
341 adjuvanted by electroporation as in this study (Dong-Ji et al., 2000; Penttila et al., 2004), and  
342 only one previous use of an adenovirus-vectored vaccine against *Chlamydia muridarum*  
343 (expressing CPAF) has been reported (Brown et al., 2012).

344

345 Following an initial screen of eleven prime-boost regimens, four immunologically distinct  
346 regimens were assessed in both BALB/c and B6C3F1 mice. The AM, DDD, PPP and DAMP  
347 regimens showed no mouse-strain specific discrepancies in the humoral or cellular responses  
348 induced. Of these four regimens, only the DAMP vaccination regimen enhanced the  
349 clearance of intravaginal *C. trachomatis*, regardless of mouse strain. This enhanced  
350 chlamydial clearance afforded by the DAMP vaccination regimen was dependent on CD4<sup>+</sup> T  
351 cells, as shown by CD4<sup>+</sup> T cell depletion following vaccination. Previous chlamydia vaccine  
352 studies in mice have also revealed a role for CD4<sup>+</sup> T cells in their protection, including in the

353 liposomal delivery of rMOMP (Hansen et al., 2008) and the subcutaneous delivery of CTH1  
354 (Olsen et al., 2010).

355

356 The importance of IFN- $\gamma$  *in vivo* to chlamydia control has been demonstrated previously  
357 (Cotter et al., 1997; Ito and Lyons, 1999). In this respect it appears somewhat surprising that  
358 the DDD and AM regimens, inducing stronger T cell IFN- $\gamma$  responses than DAMP, failed to  
359 show any evidence for enhanced clearance. However, a distinct characteristic of the DAMP  
360 vaccination regimen was the co-induction of significantly higher levels of MOMP-specific  
361 IgG2a (with a high IgG2a/IgG1 ratio). This was in spite of the use of the protein adjuvant  
362 MF59®, which has previously been shown to skew T cell responses against MOMP towards  
363 IL-5 and IL-10 (Knudsen et al., 2016); this may be explained by the order of immunisations,  
364 with the initial MOMP antigen exposures in the context of DNA and viral vector delivery  
365 skewing the response, as the protein-adjuvant boosted regimens resulted in a strong IgG1  
366 bias. Chlamydial-specific IgG2a antibody concentrations have previously correlated with  
367 protection in animal studies (Pal et al., 2001). Thus although enhanced clearance was  
368 dependent upon CD4 T cell responses, these data suggest induced IgG2a responses may have  
369 played a contributory role in the enhanced clearance of *C. trachomatis* infection. In this  
370 respect, EB opsonisation by IgG isotypes is known to affect the uptake of chlamydia into  
371 cells (Peterson et al., 1997). EB opsonisation with a high IgG1 and low IgG2a anti-MOMP  
372 polyclonal sera has been shown to enhance infection of a cell line through the FcRn mediated  
373 uptake of these IgG-coated EBs, suggesting a negative role for MOMP-specific IgG1  
374 antibodies (Armitage et al., 2014). The IgG2a isotype by contrast mediates effector functions  
375 including antibody-dependent cellular cytotoxicity (ADCC), with evidence suggesting this  
376 effector function may facilitate the early clearance of a chlamydial infection (Moore et al.,  
377 2002), furthermore ADCC is associated with enhanced antigen presentation with the potential  
378 to amplify CD4 T cell responses (Rafiq et al., 2002). Collectively, these suggest that the anti-  
379 MOMP IgG isotype may have a contributory role in the protection observed from the DAMP  
380 regimen, though without a DAM comparator arm this would require further investigation.

381

382 We cannot rule out that the DAMP vaccination regimen itself is in fact lowering the  
383 establishment of infection, and thus resulting in the lower IFU observed, as our earliest  
384 sampling point is day 3 after challenge. Moreover, we cannot exclude the possibility that non-  
385 specific effects of the vaccine components in the DAMP regimen may impact general T-cell  
386 function. Future work should assess the potential non-specific immunologic effects of  
387 antigen-delivery by viral vectors alongside adjuvantation during prime-boost vaccinations.

388

389 In this study we undertook a bioinformatic approach to generate an immunogen that would  
390 induce cross-serovar Chlamydial T cell responses. We have revealed a capability to induce an  
391 array of MOMP-specific immune responses, both cellular and humoral, using four differing  
392 MOMP-based vaccine modalities in multi-component prime-boost regimens. The comparison  
393 of the same antigen by different modalities gives us insight into the distinct immune profiles  
394 induced by these vaccines. Based on our focus of developing vaccine candidates to progress  
395 towards clinical testing we opted to use *C. trachomatis* for our challenged studies, rather than  
396 the more conventional use of *C. muridarum* that is pathogenic in mice. Though *C.*  
397 *trachomatis* is not a natural pathogen of mice, it has been argued that that intravaginal  
398 infection with *C. trachomatis* mimics in many ways both the course and outcome of infection

399 in most women as asymptomatic and self-limiting (Lyons et al., 2005). In this context, the  
400 observed significant reduction in shedding following DAMP vaccination observed 3 days  
401 post infection is particularly encouraging given rapid natural clearance in naïve animals. We  
402 would anticipate a greater impact on *C. trachomatis* clearance in transcervical infection  
403 models, in non-human primate models, and in humans, where the infection is slow to clear  
404 and/or may establish chronic infection and this will form the focus of our future studies.

#### 405 **Conflict of Interest Statement:**

406 The authors declare no commercial or financial conflict of interest.

407

#### 408 **Author Contributions:**

409 AB, PM, BK, GB, AW performed the experiments; AB, PM, JT & RS designed the studies;  
410 AN, JG, FF provided data sources. AB& JT wrote the paper.

411

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415

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424

425

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635

636 **Table 1. Multi-component prime-boost vaccine regimens.**

637 In vaccine regimen nomenclature, D represents DNA (+ electroporation), A represents  
 638 HuAd5, M represents MVA, and P represents recombinant MOMP protein adjuvanted with  
 639 MF59®.

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Regimen	d0	d21	d42	d63	d84
<b>DDDAM</b>	DNA	DNA	DNA	HuAd5	MVA
<b>DDDA</b>	DNA	DNA	DNA	HuAd5	
<b>DDDM</b>	DNA	DNA	DNA	MVA	
<b>DDD</b>	DNA	DNA	DNA		
<b>AM</b>	HuAd5	MVA			
<b>DAMP</b>	DNA	HuAd5	MVA	Protein	
<b>AMPP</b>	HuAd5	MVA	Protein	Protein	
<b>DDPP</b>	DNA	DNA	Protein	Protein	
<b>APP</b>	HuAd5	Protein	Protein		
<b>PPP</b>	Protein	Protein	Protein		
<b>PP</b>	Protein	Protein			

655 **Figure 1. Global *C. trachomatis* serovar prevalence, phylogeny and theoretical epitope**  
 656 **coverage of consensus and mosaic MOMP antigens.**

657 (A) The serovar prevalence of *C. trachomatis* worldwide compiled from a literature review  
 658 and represented in descending prevalence at global locations. (B) A phylogenetic maximum  
 659 likelihood tree based on the *ompA* sequence alignments derived from (Nunes et al., 2010) was  
 660 created using FastTree and the graphic generated by Rainbow Tree. (C) Potential epitope  
 661 coverage against all serovars (total) and individual serovars (serovars D-K) were analysed for  
 662 a monovalent Con E antigen, Con E and Con F antigens, 2 mosaic antigens, a Con E antigen  
 663 and a mosaic antigen, three mosaic antigens and a Con E antigen with 2 additional mosaic  
 664 antigens using EPICOVER. Mean 9-mer coverage presented against individual and total  
 665 combined serovars D to K, with exact (red), off-by-1 (orange) and off-by-2 (yellow) epitope  
 666 matching.

667 **Figure 2. Antibody and cellular responses following multi-component prime-boost**  
 668 **vaccination regimens.**

669 BALB/c mice (n = 8 per group) were intramuscularly immunised in various prime-boost  
 670 regimens, with sera and vaginal wash collected two weeks after final boost. MOMP-specific  
 671 IgG concentrations were measured in serum (A) and vaginal washes (B), expressed as the

672 mean + SEM concentrations. (C) Serum MOMP-specific IgG2a and IgG1 isotype  
673 concentrations were measured by ELISA, and the mean + SEM IgG2a:IgG1 ratios plotted.  
674 The dotted line indicates the IgG2a:IgG1 ratio of 1, demonstrating Th1-skewing above this  
675 line or Th2-skewing below it. (D) Serum antibody avidity was measured by MOMP-specific  
676 IgG ELISA with non-reducing (H<sub>2</sub>O) and reducing (8 M urea) washes after sample addition.  
677 Results are shown as percentage (%) change in binding ( $\frac{\text{reducing OD } 650}{\text{non-reducing OD}} \times 100$ ). IgG  
678 concentrations, avidities and IgG2a:IgG1 ratio represented as group means and SEM. (E)  
679 Vaccinated BALB/c mice (n = 8 per group) were sacrificed one-week post-final  
680 immunisation and splenocytes assessed by IFN- $\gamma$  ELISpot for MOMP-reactive T cells  
681 stimulated by a peptide pool consisting of 15-mers overlapping by 11 amino acids. Data  
682 expressed as group medians (+ interquartile range) (SFU/million antigen stimulated cells). \*  
683  $p \leq 0.05$  (yellow), \*\*  $p \leq 0.005$  (orange), \*\*\*  $p \leq 0.0005$  (red) and \*\*\*\*  $p \leq 0.0001$  (dark red)  
684 by one-way ANOVA with Bonferroni's multiple comparison post-test on logged values (A-  
685 D) and by Kruskal-Wallis with Dunn's multiple comparison test (E).

686 **Figure 3. Prime-boost vaccine regimens induce comparable immune responses in both**  
687 **BALB/c and B6C3F1 mouse strains.**

688 MOMP-specific IgG concentrations were measured in serum (A) and vaginal washes (B) for  
689 both BALB/c and B6C3F1 vaccinated mice (n = 8 per group), expressed as individual  
690 concentrations with bars representing the means. (C) Serum MOMP-specific IgG2a and IgG1  
691 isotype concentrations were measured by ELISA for both BALB/c and B6C3F1 vaccinated  
692 mice (n = 5-8 per group), and individual points and bars representing the means IgG2a:IgG1  
693 ratios plotted. The dotted line indicates the IgG2a:IgG1 ratio of 1, demonstrating Th1-  
694 skewing above this line or Th2-skewing below it. (D) Splenocytes were assessed by IFN- $\gamma$   
695 ELISpot for MOMP-reactive T cells stimulated by a peptide pool consisting of 15-mers  
696 overlapping by 11 amino acids for both vaccinated BALB/c and B6C3F1 mice. Data  
697 expressed as individual values with bars representing group medians (+ interquartile range)  
698 (SFU/million antigen stimulated cells).

699 **Figure 4. The DAMP vaccine regimen enhances the clearance of intravaginal *C.***  
700 ***trachomatis* in BALB/c and B6C3F1 mice, in a CD4<sup>+</sup> T cell dependent manner.**

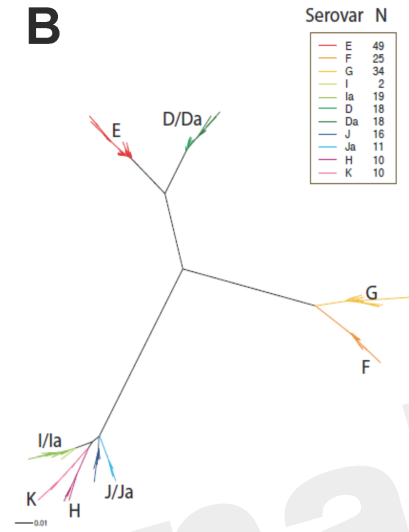
701 Six weeks after the final vaccination and 1 week after 2 mg/mouse subcutaneous Depo-  
702 Provera treatment, BALB/c and B6C3F1 mice (n = 7 to 10 per group) were infected  
703 intravaginally with  $4 \times 10^5$  IFU of *C. trachomatis* D/UW-3/Cx. The vaginal vault of mice were  
704 sampled using individual swabs at day 3 ((A) BALB/c; (B) B6C3F1) after challenge, and  
705 vaginal Chlamydial loads quantified by infection assay and immunofluorescent microscopy.  
706 The fold reduction in median Chlamydial load compared to naïve BALB/c (A) and B6C3F1  
707 (B) mice at day 3 after infection is also represented. (C) B6C3F1 mice (n = 8 per group) were  
708 immunised with the DAMP regimen or left unvaccinated and subsequently depleted of CD4<sup>+</sup>  
709 T cells by i.p. injections of 500  $\mu$ g/mouse of anti-mouse CD4 monoclonal antibody (clone  
710 GK1.5) on days -1 and +1 with respect to day of challenge day 0. *C. trachomatis* load was  
711 measured in the vaginal vault at day 3 after infection. Individual and median values are  
712 represented. \*  $p \leq 0.05$ , \*\*  $p \leq 0.01$ , \*\*\*  $p \leq 0.001$ , 2-tailed Mann-Whitney U test.

# Figure 1

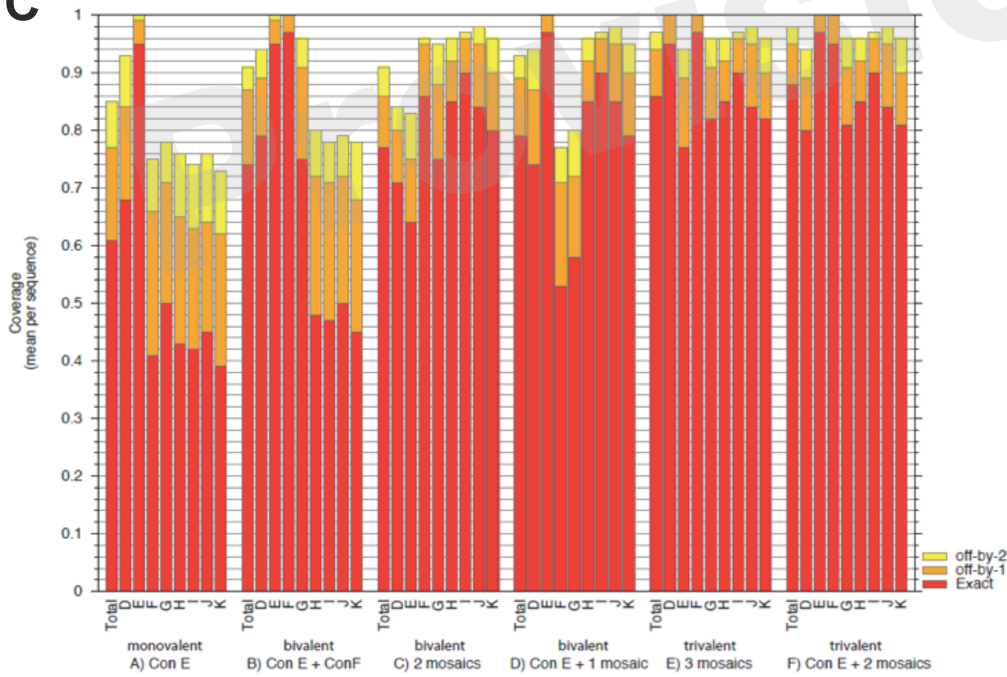
**A**



**B**



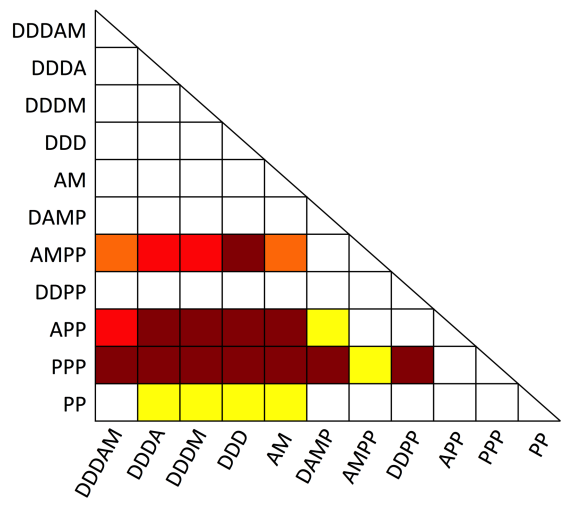
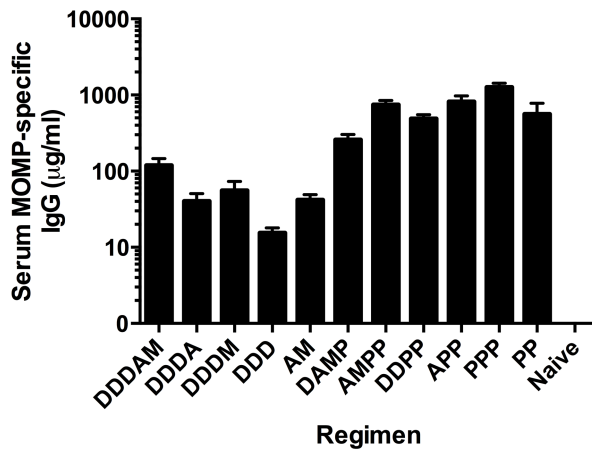
**C**



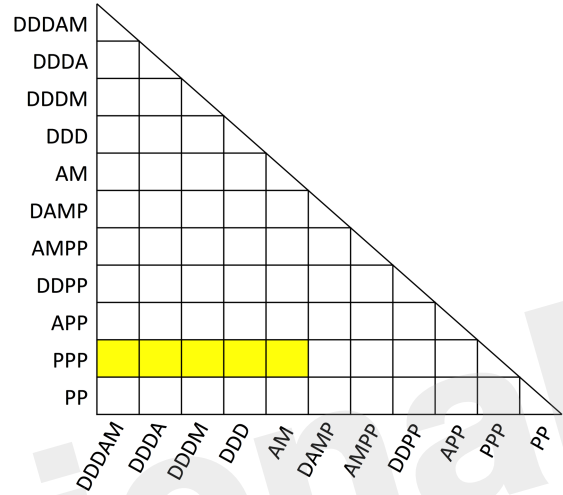
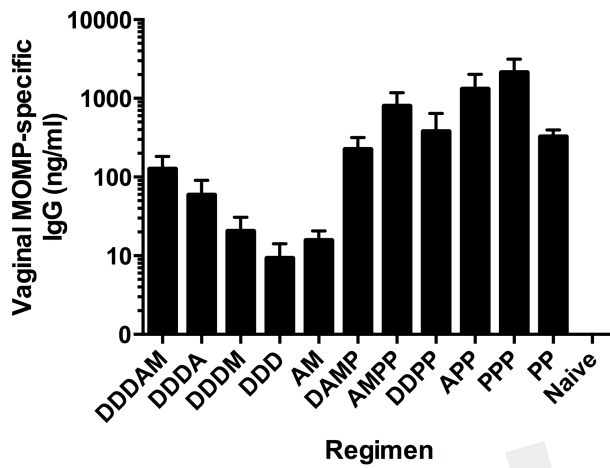
**Figure 2**

Figure 02.TIFF

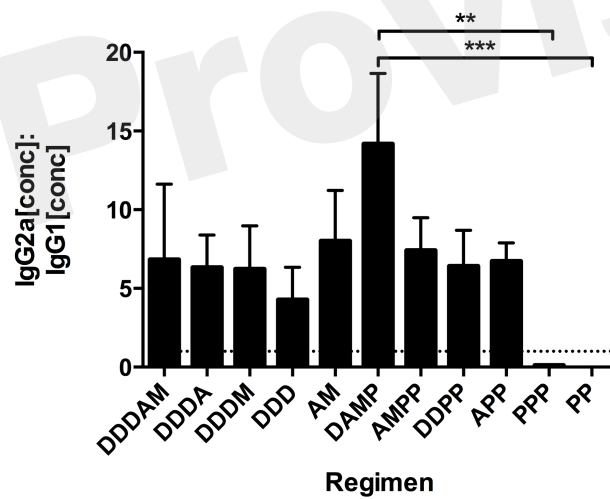
**A**



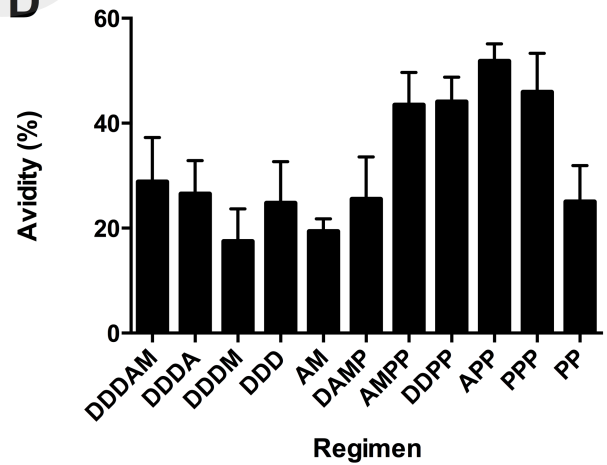
**B**



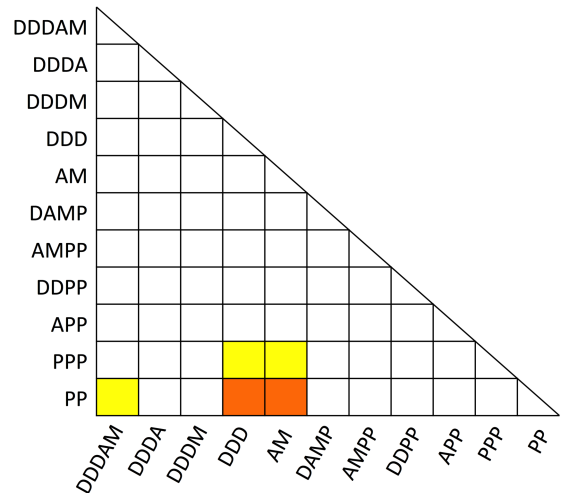
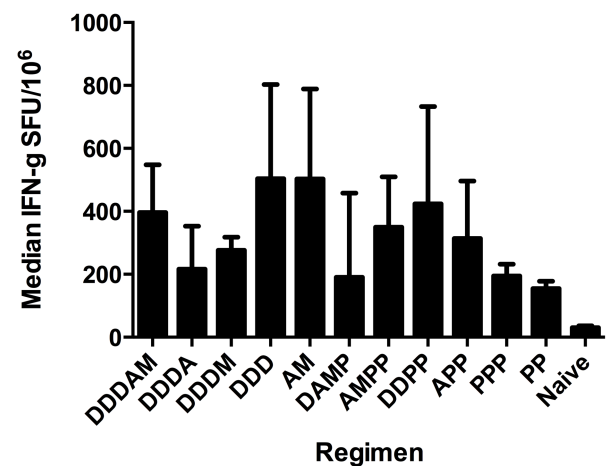
**C**



**D**

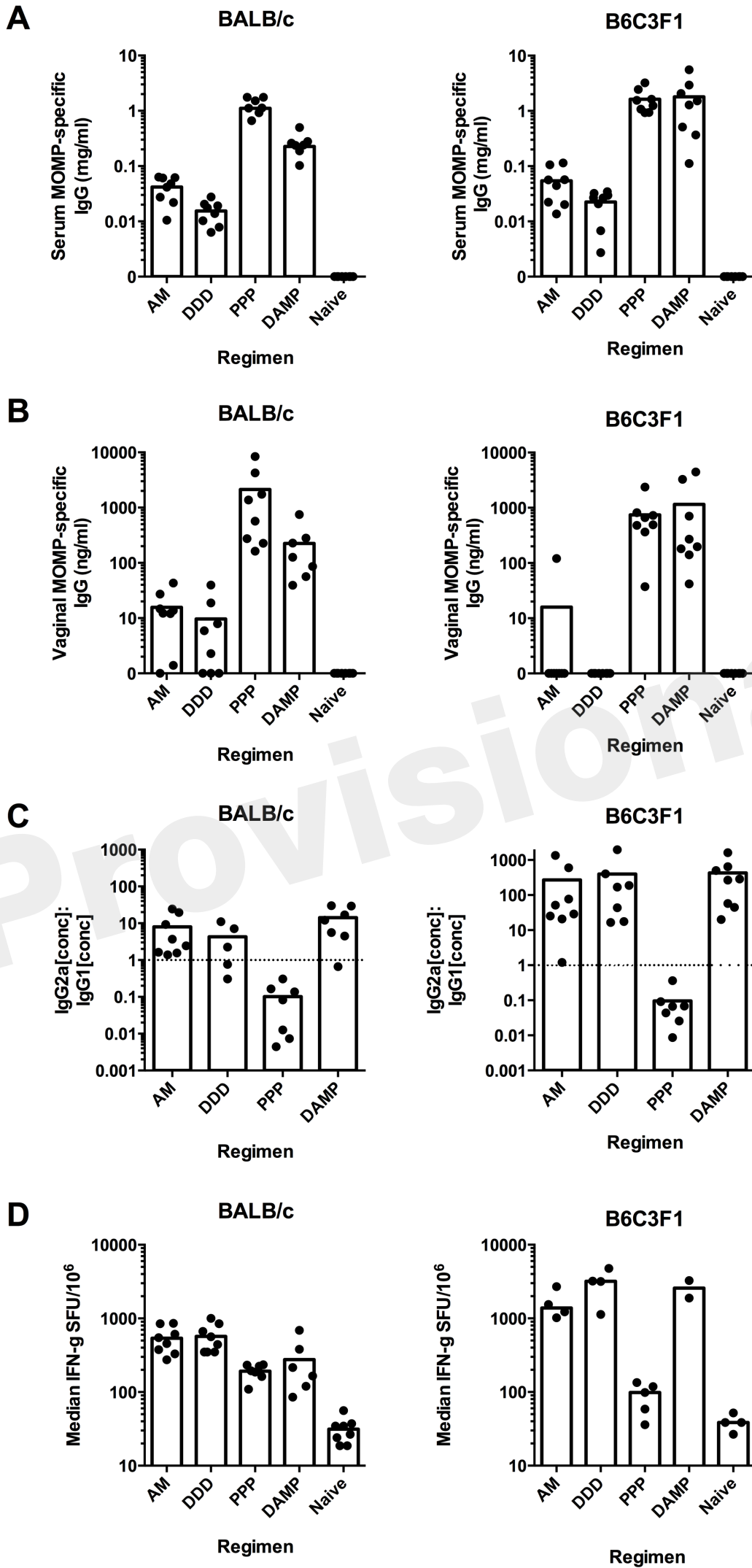


**E**



**Figure 3**

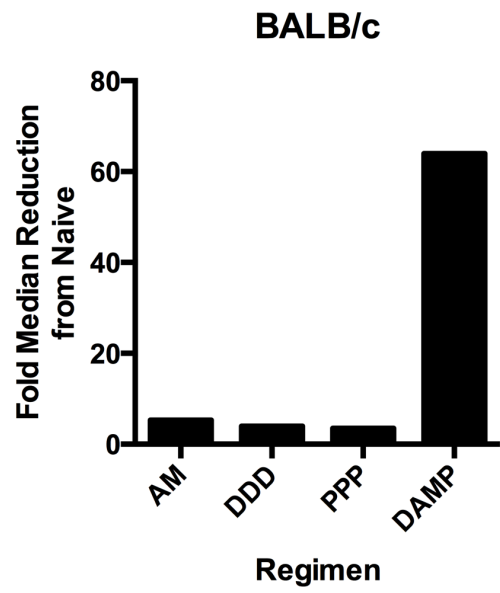
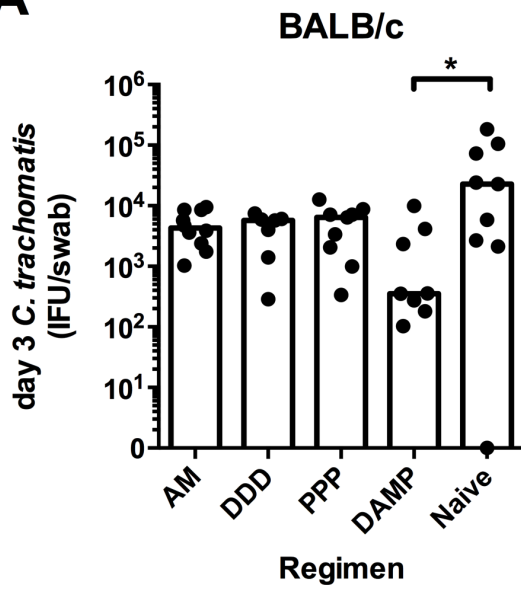
Figure 03.TIFF



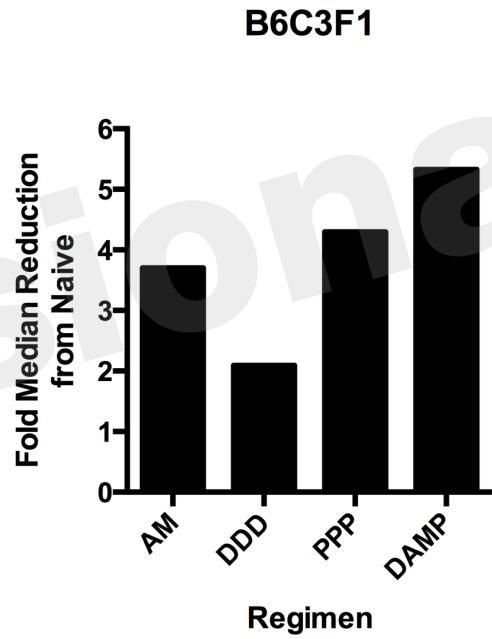
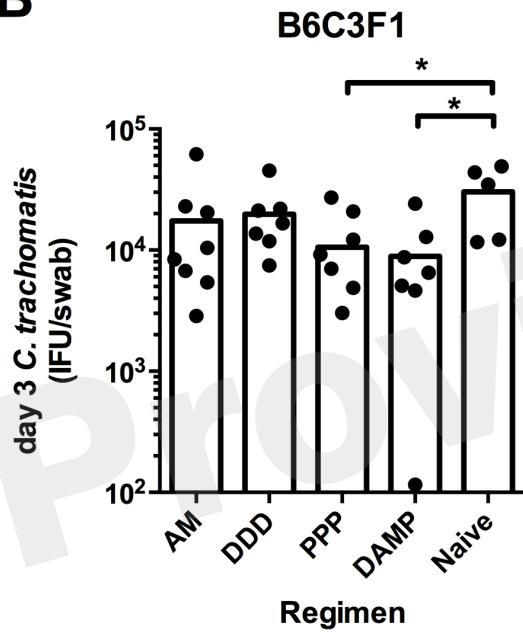
**Figure 4**

Figure 04.TIFF

**A**



**B**



**C**

