Interleukin 10 controls the balance between tolerance, pathogen elimination and immunopathology in birds.

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Abstract

Effective mucosal immunity in the intestine involves a fine balance between tolerance of the microbiome, recognition and elimination of pathogens, and inflammatory tissue injury. The anti-inflammatory cytokine IL10 regulates these processes in the intestines of mice and humans; the anti-inflammatory activity of IL10 is also conserved in birds. To determine the function of IL10 in avian mucosal immunity, we generated germ line modifications of the chicken *IL10* locus to abolish or reduce IL10 expression. *In vitro* analysis of macrophage response to lipopolysaccharide confirmed the loss of IL10 protein expression, the lack of dosage compensation in heterozygotes, and prevention of autocrine inhibition of nitric oxide production in homozygous IL10 knockout macrophages. IL10-deficiency significantly altered the composition of the caecal microbiome, but unlike IL10-deficient mice and humans, IL10-deficient chickens did not exhibit spontaneous colitis. Following experimental challenge with *Salmonella enterica* serovar Typhimurium or *Campylobacter jejuni* in IL10-deficient chickens, enhanced clearance of the pathogens was associated with elevated transcription of pro-inflammatory genes and increased infiltration of inflammatory cells into gut mucosa. In IL10-deficient chickens challenged with the parasite *Eimeria tenella,* pathogen clearance was accelerated but caecal lesions were more severe and weight gain was compromised. Neither the heterozygous IL10 knockout nor a homozygous IL10 enhancer mutation had a major effect on pathogen clearance or inflammation in any of the challenge models. Our findings highlight the intrinsic compromise in mucosal immune response and have important implications for the development of strategies to combat avian and zoonotic pathogens in poultry.

Introduction

Elimination of potential pathogens by the innate and acquired immune systems involves an intrinsic compromise between host protection and tissue injury that requires mechanisms to control the nature, magnitude, duration and specificity of effector pathways. A key component of specificity is the capacity to distinguish between pathogens and the commensal microbiome, and nowhere is this challenge more pressing than in the intestine. The anti-inflammatory cytokine, interleukin 10 (IL10), has long been recognized as an essential feedback regulator of intestinal inflammation in mammals (reviewed in [1]). IL10-deficient mice generated by homologous recombination developed spontaneous enterocolitis [2]. Subsequent studies revealed that components of the intestinal microbiome were essential to development of pathology and determined the extent and location of lesions [3]. In humans, homozygous mutations in genes encoding IL10 or its receptor, IL10RA, have been associated with early-onset inflammatory bowel disease [1].

In mammals, IL10 is produced by both myeloid and T and B lymphoid cells following activation by immune stimuli [1, 4], with subtle differences between mice and humans [5]. In the specific context of the intestine, conditional deletion of the *IL10* and *IL10RA* genes in mice indicated that production of the ligand by macrophages was not required for pathology, consistent with T cells being the major source of intestinal IL10 [6, 7]. By contrast, macrophage-specific deletion of the *IL10RA* gene encoding the IL10 receptor was sufficient to elicit spontaneous colitis in mice [8-10]. The contribution of IL10 to feedback modulation of host defense is not restricted to the gut. There have been countless studies of the impact of IL10 deficiency in mouse parasite, bacterial, fungal and viral disease models (reviewed in [4]). The primary focus of these studies has been on the mitigation of immunopathology by IL10, with less attention given to pathogen elimination. By contrast to studies in mice, analysis of the quantitative importance of IL10 in other species has been largely correlative. Both ligand and receptor are conserved in vertebrates, and zebrafish has been discussed as a model for understanding

71 IL10 biology [11]. Here we focus on the chicken, both a model vertebrate and an economically
72 important livestock species.

73 The original cloning and sequencing of chicken *IL10* cDNA and genomic DNA [12] described
74 the immunomodulatory activity of the recombinant protein on T cell production of interferon-
75 gamma (IFNγ), its regulated expression in T cells and macrophages *in vitro*, and increased
76 mRNA expression during parasite (*Eimeria maxima*) infection. Like the mammalian transcript,
77 chicken *IL10* mRNA contains multiple copies of the AUUUA instability motif in the 3'-
78 untranslated region (UTR). We and others have provided evidence that quantitative variation
79 in IL10 production may contribute to inter-individual or inter-breed variation in infectious
80 disease susceptibility in chickens [13-17]. To test this hypothesis directly, and more generally
81 to determine the conservation of IL10 biological function across vertebrates, we have
82 generated germ line modifications of the chicken *IL10* locus that abolish or reduce IL10
83 expression. We describe the lack of dosage compensation in heterozygous mutation, and
84 present evidence that the reduced expression of IL10 leads to increased pathogen clearance
85 at the expense of increased inflammation.

86 **Results**

87 **Generation of IL10-deficient chickens**

88 The emergence of CRISPR/Cas9 technology and the ability to culture, cryopreserve,
89 genetically modify and subsequently transfer chicken primordial germ cells (PGCs) into sterile
90 surrogate host embryos has expedited the analysis of gene function in the chick (Figure 1A;
91 [18-21]). We used this approach to edit the *IL10* locus in chicken PGCs and create two
92 independent lines of IL10-deficient chickens (Figure 1). We first created an IL10 knockout
93 (IL10KO) line by introducing a premature in-frame stop codon in exon 1 of the *IL10* gene in
94 chicken PGCs, 75 bp downstream of the start codon (C26>*; Figure 1B and D, and SI
95 Appendix, Figure S1). To generate a potential expression hypomorph, we created an IL10-

96 Enhancer knockout (IL10EnKO) line by deleting a 533-bp genomic fragment encompassing a
97 non-coding sequence located approximately 2.3-2.8 kb upstream of the *IL10* transcription start
98 site, in chicken PGCs (Figure 1B-C and SI Appendix, Figure S2). This sequence was targeted
99 based upon alignment of sequences from multiple avian species that identified a core of 300
100 bp with conservation around 85%, containing perfectly conserved motifs for known
101 transcriptional regulators, including AP1, FOXP3 and members of the NFAT/ETS family (SI
102 Appendix, Figure S3). The size and species conservation of this element resembles the well-
103 characterized intronic enhancer of the *Csf1r* locus [22].

104 To create IL10KO and IL10EnKO chickens, male PGCs carrying the desired biallelic edit in
105 *IL10* exon 1 or in the putative *IL10* enhancer region (as validated by PCR and DNA
106 sequencing; Figure 1C-D and SI Appendix, Figure S4) were injected into iCaspase9 sterile
107 surrogate host embryos, in which a chemically inducible caspase 9 protein is expressed from
108 the PGC-specific *DAZL* locus, together with a GFP reporter [23]. Embryos were treated with
109 the iCaspase9 activation chemical AP20187, incubated to hatch, and the resulting chicks were
110 raised to sexual maturity under specified pathogen-free (SPF) conditions at the National Avian
111 Research Facility (NARF). Mating of the iCaspase9 surrogate host cockerels to Rhode Island
112 Red (RIR) hens generated 100% IL10KO or IL10EnKO heterozygous (HET) offspring in the
113 first generation (G1; Figure 1A; see SI Appendix, Table S1 for detailed G1 bird numbers).
114 Upon sexual maturity, G1 HET birds were intercrossed to generate the second generation
115 (G2) of IL10KO and IL10EnKO wildtype (WT), HET and homozygous (HOM) birds for
116 analyses. Both lines produced WT, HET and HOM offspring at a 1:2:1 mendelian ratio (see SI
117 Appendix, Table S1 for detailed G2 bird numbers).

118 **Confirmation of the IL10 mutation in bone marrow-derived macrophages**

119 Chicken bone marrow-derived macrophages (BMDMs) cultured in recombinant macrophage
120 colony-stimulating factor respond to bacterial lipopolysaccharide (LPS) by secreting IL10 that
121 can be detected by ELISA [24]. The autocrine function of IL10 in this assay was demonstrated

122 by the addition of neutralizing anti-IL10 antibody, which amplified the expression of nitric oxide
123 synthase (NOS2) and production of nitric oxide [24]. Figure 2A confirms the release of IL10
124 by LPS-stimulated BMDMs derived from WT embryos and the complete absence of detectable
125 IL10 release by BMDMs derived from IL10KO HOM embryos. The absence of IL10 was
126 associated with a significant increase in nitric oxide production that was not additive with the
127 impact of added anti-IL10 antibody (Figure 2B). Since IL10 mediates feedback control it is
128 conceivable that the loss of one functional allele could be compensated by increased
129 expression from the other allele. However, we found that expression of IL10 was reduced by
130 up to 50% in BMDMs derived from IL10KO HET embryos, with a corresponding partial impact
131 on nitric oxide production (Figure 2A-B). The impact of the IL10EnKO HOM mutation was
132 more variable between samples in both assays, but consistent with a partial expression
133 hypomorph (Figure 2A-B).

134 **Loss of IL10 does not lead to spontaneous immunopathology**

135 The IL10KO and IL10EnKO chicken lines were created and raised under SPF conditions in
136 the NARF SPF avian facility. Close monitoring of the WT, HET and HOM birds over several
137 months in that environment did not reveal any health issues or adverse phenotypes. The
138 IL10KO and IL10EnKO edits did not significantly affect the post-hatch growth of HET and HOM
139 birds compared to their respective WT controls (Figure 3A-B), although IL10EnKO HET and
140 HOM hens were overall heavier than IL10EnKO WT controls (Figure 3B). Regular gross post-
141 mortem examination of tissues and histopathological analyses of the gastrointestinal tract over
142 several months (using a semiquantitative scoring system [25]) revealed no evidence of
143 intestinal pathology in IL10KO HOM and IL10EnKO HOM birds compared to WT controls
144 (Figure 3C). These results are in contrast with the early onset colitis and failure to thrive
145 phenotypes observed in IL10-deficient mouse models in both conventional and SPF
146 environments [2, 9, 26, 27].

147 Spontaneous colitis in *Il10*$^{-/-}$ mice is associated with and dependent upon dysbiosis in the
148 intestinal microbiome [28-30]. We compared the caecal microbiome of IL10KO WT and HOM
149 birds at 4 weeks of age using 16S rDNA V3-V4 hypervariable amplicon sequencing as
150 described [31, 32]. The caecal microbiome of both genotypes was dominated by the phylum
151 *Firmicutes* (SI Appendix, Figure S5A) and the most abundant genera were *Lactobacillus* and
152 *Faecalibacterium* (SI Appendix, Figure S5B). Linear discriminant analysis (LDA) Effect Size
153 (LEfSe) analysis showed enrichment of the phylum *Firmicutes* and the genera
154 *Defluviitaleaceae_UCG-011* and *Paludicola* in the IL10KO HOM group, while the phylum
155 *Bacteroidota* and the genera *Alistipes* and *UCG_008* were enriched in the WT group (SI
156 Appendix, Figure S5C). Principal component analyses showed clear separation of the
157 microbial communities based on beta diversity (SI Appendix, Figure S5D, R^2 = 0.25, *P* =
158 0.017). These findings confirm that mucosal IL10 regulates the composition of the chicken
159 microbiome.

160 To evaluate a potential environmental impact on the phenotype of IL10-deficient birds, a
161 cohort of IL10KO WT and HOM birds was hatched and raised in the NARF conventional avian
162 facility. IL10KO HOM birds remained healthy in that environment as they aged. Post-growth
163 hatch rates were comparable between IL10KO WT and HOM hens, with the exception of a
164 marginal effect on growth that resolved with age (Figure 3D); there was also no evidence of
165 overt intestinal pathology in IL10KO HOM birds compared to WT controls (Figure 3E). Cellular
166 infiltration scores were however significantly higher in the duodenum and proximal colon of
167 both IL10KO WT and HOM birds raised in the conventional facility as opposed to the SPF
168 environment (Figure 3F).

169 Two important differences exist between the IL10KO mouse and chicken models. Firstly, the
170 birds are outbred. Most mouse studies are conducted on an inbred background and the impact
171 of the *IL10* mutation is strain-specific [27]. Secondly, chickens in the NARF conventional avian
172 facility are routinely immunised against major avian pathogens (SI Appendix, Table S2). The

173 original analysis of IL10-deficient mice revealed little impact on T cell-dependent antibody
174 responses [2]. We measured antibody titres in 29-weeks old IL10KO WT and HOM birds
175 raised in the NARF conventional facility for 7 of the pathogens that the birds were vaccinated
176 against (SI Appendix, Figure S6): avian encephalomyelitis virus (AEV), chicken anaemia virus
177 (CAV), duck adenovirus (the agent of egg drop syndrome, EDS), infectious bursal disease
178 virus (IBDV), infectious bronchitis virus (IBV), infectious laryngotracheitis virus (ILTV), and
179 Newcastle disease virus (NDV). The administration schedule, nature and delivery mode of
180 these vaccines is summarised in SI Appendix, Table S2**.**

181 Statistical analyses revealed differences in vaccine response between IL10KO WT and HOM
182 birds. Antibody titres to AEV and IBDV were significantly lower in IL10KO HOM birds
183 compared to WT controls, whereas those to EDS and IBV were significantly higher in IL10KO
184 HOM birds compared to WT controls (SI Appendix, Figure S6). AEV and IBDV vaccination
185 were carried out with live vaccines delivered in the drinking water, whereas EDS and the last
186 dose of IBV vaccination were done with inactivated vaccines given by intramuscular injection
187 (SI Appendix, Table S2). Antibody titres to CAV, ILTV and NDV were not significantly different
188 between IL10KO HOM birds and WT controls (SI Appendix, Figure S6).

189 **The impact of IL10 deficiency on the response to enteric bacterial infection**

190 *Campylobacter jejuni* (*C. jejuni*) and non-typhoidal *Salmonella* are zoonotic diarrhoeal
191 pathogens of global importance [33]. Breed-specific pathology associated with *C. jejuni*
192 infection in chickens was associated with relatively low caecal *IL10* mRNA [34]. Similarly, IL10-
193 deficient C57BL/6J mice exhibited severe inflammation in the caecum and colon upon *C. jejuni*
194 infection, whereas congenic wild-type mice were persistently colonised in the absence of gut
195 pathology [35]. A similar outcome was reported in IL10-deficient mice infected with *Salmonella*
196 Typhimurium (*S*. Typhimurium) [36].

197 To study the role of IL10 during *Campylobacter* infection in chickens, two cohorts of 20 IL10KO
198 WT, HET or HOM chickens obtained from the NARF SPF avian facility were inoculated at 14
199 days-old with 10^2 colony forming units (CFU) *C. jejuni* strain M1 and analysed 1- and 2-weeks
200 post-infection. The dose of strain M1 used is the lowest needed to achieve reliable caecal
201 colonisation [37]. In the first cohort, colonisation of the caeca by *C. jejuni* in IL10KO HOM birds
202 was significantly lower at 1-week post-infection, with a median of 4.8 $\log_{10}$ CFU g^{-1} compared
203 to >9 $\log_{10}$ CFU g^{-1} in WT birds Figure 4A). However, this was not sustained and by 2-weeks
204 post-infection all groups had caecal colonisation at >9 $\log_{10}$ CFU g^{-1} (Figure 4A). In the second
205 cohort, median counts were not statistically different between IL10KO WT and HOM birds at
206 1-week post-infection, but caecal colonisation decreased by ~2 $\log_{10}$ CFU g^{-1} in IL10KO HOM
207 birds at 2-weeks post-infection relative to WT birds (Figure 4A). The IL10KO HET birds did
208 not differ significantly from WT in either cohort (Figure 4A). Histopathological analysis revealed
209 that the caecal mucosa of IL10KO HOM birds presents with significantly increased numbers
210 of lymphocytes and plasma cells, admixed with infiltrating heterophils, when compared to WT
211 and IL10KO HET birds in both cohorts (SI Appendix, Figures S7 and S8). To confirm the
212 apparent hyperinflammatory response in IL10KO HOM birds, we used multiplex quantitative
213 reverse transcriptase-PCR (qRT-PCR) to measure expression of immunity-related genes in
214 the caecum, as described [38]. In both cohorts we detected large increases in expression of
215 pro-inflammatory cytokines, chemokines and other effectors, notably *Nos2*, in the IL10KO
216 HOM caecum relative to WT (Figure 4B).

217 To test the role of IL10 in response to *Salmonella* infection, groups of 20 IL10KO WT, HET or
218 HOM chickens were inoculated at 14 days-old with 10^8 CFU *S*. Typhimurium strain ST4/74
219 nal^R [39]. The impact of lack of IL10 on bacterial burden in caecum, liver and spleen was
220 marginal at 1 week, but by 2 weeks the majority of IL10KO HOM birds had eliminated the
221 pathogen, whereas WT birds retained bacteria in both caecum and spleen (Figure 4C).
222 Enhanced lymphoplasmacytic and heterophil infiltration was observed in the ileum and

223 caecum of IL10KO HOM compared to WT or IL10KO HET birds at both intervals after *S*.
224 Typhimurium infection (SI Appendix, Figure S9). As observed following the *C. jejuni* challenge,
225 analysis of inflammatory gene expression by multiplex qRT-PCR revealed a substantial
226 increase in response in the IL10KO HOM birds relative to WT (Figure 4D). Volcano plots
227 showing the direction and magnitude of gene expression differences detected between
228 IL10KO WT and HOM birds following bacterial infection are shown in SI Appendix, Figures
229 S10 and S11. In summary, the absence of IL10 leads to a sustained increase in inflammation
230 in response to enteric bacterial infection that is also associated with more effective clearance.

231 **The impact of IL10 deficiency on the outcome of enteric protozoan infection**

232 *Eimeria tenella* (*E. tenella*) is one of ten protozoan parasite species that can cause coccidiosis
233 in chickens [40]. *Eimeria* infection of chickens induces a robust IFNγ-driven immune response
234 with evidence of higher IL10 expression associated with increased susceptibility [12, 41].
235 Following an initial titration, an infectious dose of 7000 sporulated *E. tenella* oocysts per bird
236 was set as the standard challenge, as this induced measurable phenotypes in pathology,
237 performance, and parasite replication in the absence of overt disease in WT birds. Oral
238 challenge with this or a mock dose was administered to cohorts of 10 IL10KO HOM and
239 IL10EnKO HOM chickens and corresponding WT and HET controls on day 21 post-hatch. The
240 outcomes are shown in Figure 5**.** Average parasite replication was determined by quantitative
241 PCR (qPCR) as the ratio of parasite genomes detected per host genome in total caecal tissue
242 collected six days post-infection. Parasite burden was almost ablated in IL10KO HOM and
243 significantly reduced in IL10EnKO HOM chickens compared to their respective WT controls,
244 whereas HET mutations had no significant effect in either case (Figure 5A-B). Histology
245 confirmed reduced parasite replication in IL10KO HOM chickens, with dense populations of
246 late-stage gametocytes observable in WT caecal tissues and correspondingly very sparse
247 numbers in IL10KO HOM chickens (Figure 5C-D). This selective reduction of parasite burden
248 in IL10KO HOM chickens was associated with a significant increase in caecal lesion score

249 and a substantial reduction in body weight gain over the 6-day challenge interval (Figure 5E
250 and G). By contrast, both IL10KO HET and IL10EnKO HOM and HET (each anticipated to
251 reduce IL10 expression) showed reduced caecal lesion scores and had no effect on body
252 weight gain compared to their respective WT controls (Figure 5E-H).

253 To better characterise the differences in pathology, performance and parasite replication
254 detected between IL10KO WT and HOM chickens, we undertook a time course study,
255 analysing parasite burden by qPCR at 0-, 2-, 4-, 6-, 8- and 10-days post-infection. In parallel,
256 excreted oocysts per gram (OPG) were counted in litter samples collected from IL10KO WT
257 and HOM groups during the period of peak oocyst excretion at 7-, 8- and 9-days post-infection.
258 Figure 6A confirms the greatly reduced *E. tenella* replication in IL10KO HOM, that was
259 reflected in corresponding reduced excretion of oocysts (Figure 6B). Lesions associated with
260 *E. tenella* infection were accelerated in IL10KO HOM chickens compared to WT (Figure 6C).
261 The adverse impact of IL10KO HOM on body weight gain was sustained to day 8 and showed
262 signs of recovery by day 10 (Figure 6D), likely due to complete pathogen elimination (Figure
263 6A). Consistent with the mild inflammatory cell infiltration in IL10KO HOM birds noted in Figure
264 5D, inflammatory gene expression was elevated in the caecum prior to challenge (Day 0). The
265 greatest difference in IL10KO HOM birds relative to WT was detected on day 6, during the
266 period of peak pathology (Figure 6C and E). Volcano plots showing the direction and
267 magnitude of gene expression differences detected between IL10KO WT and HOM birds
268 following *E. tenella* infection are shown in SI Appendix, Figure S12, highlighting genes
269 associated with inflammation (*Il6*) and lysosomes (*Hps5*). Transcription of genes associated
270 with movement of molecules across membranes (*Pkd2l1, Abcg2*) and tubulin production
271 (*Tubat*) was lower in IL10KO HOM birds 6 days post-infection.

272 **Discussion**

273 An intrinsic compromise exists between effective host defence leading to pathogen elimination
274 and the induction of immune-mediated pathology. The central importance of IL10 in mediating
275 this balance has been studied extensively in the mouse, notably in the context of parasite
276 infections [1, 4, 5, 11, 42]. The regulatory function of IL10 is especially important in preventing
277 inappropriate responses to the intestinal microbiome with the potential to drive spontaneous
278 enterocolitis [2, 8, 10, 27]. Here we have generated two *IL10* mutations in the chicken genome,
279 a definitive knockout and a putative enhancer mutation. Notwithstanding the development of
280 robust technologies based upon CRISPR/Cas9, the development of models of immune
281 deficiency in chickens remains time consuming and logistically challenging, and relatively few
282 informative mutations have been generated [20, 43]. The enhancer mutation was intended to
283 generate a quantitative impact on IL10 expression to model selection for reduced expression
284 in production lines of birds. Based upon the mouse *Il10*$^{-/-}$ phenotype, we also anticipated a
285 possible severe post-hatch failure to thrive due to spontaneous colitis in IL10KO HOM chicks.
286 An unexpected outcome was the discovery that the IL10KO in chicken is not dosage
287 compensated, therefore the HET provides a second model of the impact of reduced
288 expression. In overview, neither the IL10KO HET nor the IL10EnKO HOM had a large effect
289 on pathogen clearance or inflammation in either of the challenge models, indicating that IL10
290 biology is not highly sensitive to changes in expression of the magnitude that has been
291 detected in individual lines of commercial broilers and layers [14, 44, 45].

292 Detailed analysis of the IL10KO HOM birds in SPF or conventional avian facilities revealed no
293 evidence of spontaneous intestinal inflammation or compromised body weight gain, and only
294 a small and inconsistent effect on specific antibody responses to routine live or inactivated
295 vaccines. Since spontaneous colitis in mice depends upon resident enteric bacteria [3], it is
296 possible that the difference compared to the rodent models lies in the nature of the chicken
297 intestinal microbiome [46], in which case the changes that we observed in the microbiome of

298 IL10KO HOM chicks may serve to mitigate potential spontaneous intestinal pathology. In any
299 case, the results indicate that deletion of IL10 from the genome or selection in favour of low
300 IL10 expression alleles [14, 17, 44, 45] need not necessarily affect production traits.

301 In both the bacterial challenge models, and in the *Eimeria* challenge, the response of IL10KO
302 HOM bird highlights for the first time in a non-rodent species the compromise between
303 pathogen elimination and pathology. Accelerated pathogen clearance is associated with
304 increased inflammatory gene expression and local inflammation, and in the case of *Eimeria*,
305 reduced body weight gain. The models we have chosen are not lethal and there is effective
306 pathogen clearance even in WT birds. Findings with *Campylobacter* in IL10KO HOM birds are
307 consistent with elevated intestinal inflammation in a broiler breed with relatively low IL10
308 expression, albeit a significant reduction in caecal colonisation relative to breeds with higher
309 IL10 expression was not observed [34]. While the caecal load of *C. jejuni* was markedly
310 reduced in IL10KO HOM birds at most intervals examined, some inconsistency existed in the
311 timepoints when the reduction reached statistical significance between cohorts, likely as a
312 consequence of inter-animal variation. This is typical of *C. jejuni* colonisation in chickens,
313 where bacterial population structures have been reported to be variable and unpredictable
314 [47]. Similar variation between time intervals, birds and repeated experiments has been
315 reported when evaluating vaccines against *C. jejuni* colonisation (e.g. [48, 49]). In mammals,
316 *Salmonella* has been reported to gain a competitive advantage from intestinal inflammation,
317 both owing to availability of tetrathionate that *Salmonella* can uniquely use as a respiratory
318 electron acceptor [50] and remodelling of the indigenous microbiota [51]. It is unclear if
319 *Salmonella* derives the same benefits during colonisation of the avian intestine and the counts
320 of viable bacteria recovered from the caeca of WT and IL10KO HOM birds can only be
321 interpreted as the balance of bacterial growth and killing.

322 Our results with *Eimeria* are relevant to commercial studies aimed at targeting IL10 to mitigate
323 disease. Coccidiosis has been estimated to exert costs in excess of £10 billion every year to

324 the chicken production industry [52], with *E. tenella* among the most common and pathogenic
325 species [53, 54]. Feeding neutralizing anti-IL10 antibody to chickens during *Eimeria* infection
326 was reported to mitigate reduced body weight gain (BWG) but had an inconsistent impact on
327 parasite replication and pathology [55, 56]. Similarly, feeding antibody to IL10 receptor 2 (but
328 not receptor 1) reduced lost BWG, but had no effect on oocyst shedding [57]. Feeding
329 chickens genetically modified corn (*Zea mays*) expressing IL10 improved BWG and reduced
330 oocyst shedding and caecal lesions [58]. These results are consistent with the phenotypes
331 associated with a reduction, rather than complete absence, of IL10 observed here.

332 Given the excessive inflammatory activation we observed in non-lethal infections, and the
333 literature in mice, IL10KO HOM birds or hypomorphs might be hyper-sensitive to more virulent
334 bacterial infections and viral pathogens, such as avian influenza, that can elicit a cytokine
335 storm. On the other hand, they may be primed for a more rapid and effective response. These
336 possibilities can now be tested using the models we have developed.

337 **Materials and Methods**

338 **Animals**

339 All chicken lines used in this study were bred and maintained at the National Avian Research
340 Facility (NARF), University of Edinburgh, under UK Home Office Establishment Licence and
341 in compliance with the Animals (Scientific) Procedures Act (ASPA) 1986. All regulated
342 procedures were approved by local ethical review committees and carried out by UK Home
343 Office Personal Licence holders under UK Home Office Project Licences 70/8528 and
344 PP9565661 (creation and maintenance of genetically altered chicken lines), PCD70CB48
345 (*Campylobacter* and *Salmonella* challenges performed at the Moredun Research Institute)
346 and PDAAD5C9D (*Eimeria* challenges performed at the Royal Veterinary College). Animals
347 were humanely culled in accordance with Schedule 1, ASPA 1986.

348 The Rhode Island Red (RIR) line was maintained as a closed outbred population in the NARF
349 specified pathogen-free (SPF) avian facility. The CSF1R-eGFP line [59] was created and
350 maintained on a Hy-Line background in the NARF conventional avian facility by HOM x HOM
351 crosses; CSF1R-eGFP fertile eggs were used for PGC derivation. The iCaspase9 line [23]
352 was created and maintained on a RIR background in the NARF SPF avian facility by crossing
353 iCaspase9 HET cockerels to RIR hens; iCaspase9 fertile eggs were used as hosts for PGC
354 injection. The IL10KO and IL10EnKO lines were created in the NARF SPF avian facility and
355 maintained on a mixed Hy-Line / RIR background by crossing iCaspase9 surrogate host
356 cockerels carrying gene-edited PGCs (generation G0) to RIR hens to produce the first
357 generation (G1) of IL10KO HET and IL10EnKO HET chickens (see SI Appendix, Table S1 for
358 detailed G1 bird numbers); the second generation (G2) of IL10KO and IL10EnKO chickens
359 was obtained by crossing G1 HET cockerels to G1 HET hens from each line, resulting in WT,
360 HET and HOM offspring (see SI Appendix, Table S1 for detailed G2 bird numbers).

361 **Chicken PGC derivation and culture**

362 PGC lines were derived from blood collected from CSF1R-eGFP HOM embryos at
363 Hamburger-Hamilton (HH) stage 16 and expanded in FAOT medium as previously described
364 [60]. A W-chromosome-specific PCR [61] was used to determine the sex of the PGC lines.
365 PGC lines were tested for *Mycoplasma* contamination by PCR using primers specific for
366 *Mycoplasma synoviae* (MS; Myco5_14713A and Myco3_14709) and *Mycoplasma*
367 *gallisepticum* (MG; Myco5_14712 and Myco3_14709); see SI Appendix, Table S3 for primer
368 sequences.

369 **CRISPR plasmid, guide RNAs and ssODN donor**

370 Guide RNAs (gRNAs) were designed using CHOPCHOP [62] and CRISPOR [63] and cloned
371 into the High Fidelity CRISPR/Cas9 plasmid HF-PX459 V2.0 [64] as described previously [65].
372 A gRNA (ggIL10_exon1_g3) and a 143-bp single-stranded oligonucleotide DNA (ssODN;

373 IL10_exon1_HDRoligo2; IDT Ultramer™ DNA Oligonucleotide) containing a STOP codon
374 (TAG) and AvrII restriction site (CCTAGG), were used to edit *IL10* exon 1. Two gRNAs
375 (IL10_enhancer_guide1 and IL10_enhancer_guide2) were used in combination to delete the
376 *IL10* putative enhancer region. See SI Appendix, Table S4 for gRNA and ssODN sequences.

377 **PGC transfection and screening**

378 To edit *IL10* exon 1, 200,000 CSF1R-eGFP male PGCs were transiently transfected with 1.5
379 µg gRNA plasmid ggIL10_exon1_g3 and 10 pmol ssODN IL10_exon1_HDRoligo2. To delete
380 the *IL10* putative enhancer region, 200,000 CSF1R-eGFP male PGCs were transiently
381 transfected with 1.0 µg gRNA plasmid IL10_enhancer_guide1 and 1.0 µg gRNA plasmid
382 IL10_enhancer_guide2. Transient transfections were performed with Lipofectamine 2000
383 (Invitrogen), followed by treatment with 0.4 µg/mL puromycin to enrich for transfected PGCs,
384 as previously described [64]. Bulk PGC populations were screened by PCR to confirm the
385 presence of the desired IL10KO or IL10EnKO edits. Single-cell clonal populations were
386 subsequently expanded as previously described [64] and screened by PCR and sequencing.
387 Primers IL10_Exon1_F4 and IL10_Exon1_R4 were used to amplify a 1826-bp fragment
388 encompassing *IL10* exon 1, followed by digestion with AvrII to identify PGCs carrying the
389 IL10KO edited allele (SI Appendix, Figure S4A); primers IL10_Exon1_F1 and IL10_Exon1_R1
390 were subsequently used to sequence the *IL10* exon 1 fragment. Primers IL10-Enhancer_F2
391 and IL10_Enhancer_R2 were used to amplify and sequence a fragment encompassing the
392 *IL10* putative enhancer region (SI Appendix, Figure S4C). See SI Appendix, Table S3 for
393 primer sequences and expected fragment sizes. PGCs were transfected and cultured under
394 SPF conditions and regularly tested for mycoplasma contamination, as described above.

395 **Generation of surrogate host chickens and establishment of the IL10KO and IL10EnKO**
396 **lines under SPF conditions**

397 Male PGCs carrying the desired IL10KO or IL10EnKO biallelic edits were injected into
398 iCaspase9 embryos at HH stage 16, together with the iCaspase 9 activator AP20187 (Takara
399 Bio) as previously described [23], to create surrogate host cockerels carrying IL10KO HOM or
400 IL10EnKO HOM germ cells (G0 founders); all manipulations were performed under SPF
401 conditions in the NARF SPF avian facility. G0 founders were hatched and raised to sexual
402 maturity in negative pressure isolators and released to floor pens at 22 weeks. The SPF status
403 of the G0 founders was externally assessed at three timepoints (10-, 20- and 30-weeks post-
404 hatch) by screening for 17 different pathogens (Sci-Tech Ireland; SI Appendix, Table S5).

405 G0 founder cockerels were bred to RIR hens to produce the first generation (G1) of IL10KO
406 HET and IL10EnKO HET chickens (see SI Appendix, Table S1 for detailed G1 bird numbers);
407 the second generation (G2) of IL10KO and IL10EnKO chickens was obtained by crossing G1
408 HET cockerels to G1 HET hens, resulting in IL10KO and IL10EnKO WT, HET and HOM
409 offspring (see SI Appendix, Table S1 for detailed G2 bird numbers). All G1 and G2 chicks
410 were genotyped by PCR using genomic DNA extracted from chorioallantoic membrane or 4-
411 µL blood samples as previously described [23]. Primers IL10_Exon1_F1 and IL10_Exon1_R1
412 were used to amplify a 246-bp fragment encompassing *IL10* exon 1, followed by digestion
413 with AvrII to identify the IL10KO WT and edited alleles (SI Appendix, Figure S4B). Primers
414 IL10-Enhancer_F2 and IL10_Enhancer_R2 were used to amplify the IL10EnKO WT and
415 edited alleles (SI Appendix, Figure S4D). Primers LTR_U3_F, 235_F and 235_R were used
416 to amplify the CSF1R-eGFP WT and transgenic alleles. See SI Appendix, Table S3 for primer
417 sequences and expected fragment sizes. The SPF status of G1 and G2 chickens was verified
418 at point of lay (20-24 weeks) and at end of life (around 40 weeks).

419 **Animal monitoring, post-mortem examination and histopathological analyses under**
420 **SPF and conventional conditions**

421 All IL10KO and IL10EnKO chicks hatched in the NARF SPF avian facility were closely
422 monitored for signs of reduced growth, health issues, adverse phenotypes or unexpected
423 behaviours. All chicks were weighed daily in the first week post-hatch and twice a week until
424 four weeks; a small cohort of G2 IL10KO and IL10EnKO chicks was subsequently weighed
425 weekly, up to a maximum of 30 weeks. Post-mortem examination of one WT and one HOM
426 bird from both IL10KO and IL10EnKO lines was performed monthly from 16 to 40 weeks, with
427 a particular focus on the gastrointestinal tract. Tissue samples from the proximal colon, ileum
428 and duodenum were collected for histopathological analyses at all timepoints and scored in a
429 blinded manner using a semiquantitative scoring system [25] to grade the extent of destruction
430 of normal mucosal architecture (0-3), the presence and degree of cellular infiltration (0-3), the
431 extent of muscle thickening (0-3), the presence or absence of crypt abscesses (0-1), and the
432 presence or absence of goblet cell depletion (0-1), for a maximum possible score of 11.

433 In addition to animals raised in the NARF SPF avian facility, a single cohort of IL10KO chicks
434 was hatched in the NARF conventional avian facility and closely monitored as described
435 above. Post-mortem examination of one WT and one HOM IL10KO birds was performed
436 monthly from 10 to 50 weeks, with a particular focus on the gastrointestinal tract. Tissue
437 samples from the proximal colon, duodenum and caecum were collected for histopathological
438 analyses and scored as described above.

439 **Generation of bone marrow-derived macrophage from chicken embryos**

440 Bone marrow cells were isolated from the tibias and femurs of Day 18 embryos (by pooling
441 three embryos of the same genotype per sample) by flushing the bone marrow through a 40
442 µm cell strainer with RPMI-1640 medium (Sigma R5886) supplemented with 10% fetal bovine
443 serum ultra-low IgG (Gibco 011-90035M), 2 mM L-glutamine (Gibco 25030081) and 0.1X

444 penicillin/streptomycin (Gibco 15140122) using a syringe and blunt needle. Bone marrow cells
445 were washed, resuspended at $1x10^6$ cells/mL in supplemented RPMI-1640 medium, seeded
446 at 1 mL per well in 6-well plates or 150 µL per well in 96-well plates, and cultured for 7 days
447 at 41°C, 5% CO_2 in the presence of 200 ng/mL colony stimulating factor-1 (CSF-1) to induce
448 formation of bone marrow-derived macrophages (BMDM). Cell culture supernatants were
449 subsequently used for capture ELISA and nitric oxide assay, as detailed below.

450 **Detection of IL10 by capture ELISA**

451 On day 7 of culture, BMDMs cultured in 6-well plates were stimulated with 0.5 µg/mL
452 lipopolysaccharide (LPS from *E. coli* O55:B5; Sigma L2880) for 2 hours at 41°C, 5% CO_2 to
453 induce IL10 expression; supernatants were then harvested and IL10 protein levels were
454 measured by capture ELISA, as described previously [24]. Briefly, assay plates were coated
455 with 3 µg/mL capture antibody (ROS-AV164; [24]) incubated overnight at 4°C, washed and
456 blocked. Plates were then incubated with recombinant IL10 standards or 50 µl of 10-fold
457 diluted cell culture supernatants, followed by incubation with 1 µg/mL biotinylated detection
458 antibody (ROS-AV163; [24]) and then incubation with Pierce™ High Sensitivity Streptavidin-
459 HRP (1:5000; Thermo Fisher Scientific, cat #34028), before adding 1-Step™ TMB ELISA
460 Substrate Solution (Thermo Fisher Scientific, cat #21130) and then sulfuric acid stop solution.
461 Absorbance was measured at 450 nm (550 nm as a reference) in a SpectraMax 250
462 microplate spectrophotometer system (Molecular Devices, Sunnyvale, CA, USA). Data were
463 fitted with GraphPad Prism 7.0 using a second-order polynomial (quadratic) model; statistical
464 significance was calculated using two-tailed unpaired t tests.

465 **Nitric oxide assay**

466 On day 7 of culture, BMDMs cultured in 96-well plates were stimulated with 0.5 µg/mL LPS in
467 the presence or absence of 2.5 µg/mL neutralizing anti-IL10 antibody (ROS-AV163; [24]) for
468 24 hours at 41°C, 5% CO_2; supernatants were then harvested and nitrite levels were

469 measured by Griess assay, according to the manufacturer's instructions (Promega G2930);
470 absorbance was measured at 550 nm. Statistical significance was calculated using two-tailed
471 unpaired t tests.

472 **Response to vaccination**

473 IL10KO WT and HOM chicks hatched and raised in the NARF conventional avian facility were
474 vaccinated following the routine vaccination schedule in place in the facility (SI Appendix,
475 Table S2). One-mL blood samples were collected from the brachial vein of 29-weeks old hens
476 and sent fresh to Sci-Tech Ireland for antibody titre measurements by ELISA. Statistical
477 significance was calculated using Mann-Whitney U tests.

478 **Microbiome analysis**

479 Caecal contents were harvested from 4-weeks old IL10KO WT and HOM chicks raised in the
480 NARF SPF avian facility. DNA isolation, amplification of the V3-V4 region of the 16S rDNA
481 gene and pair-end sequencing were performed as described previously [32]. Raw reads were
482 quality assessed using fastQC, and the DADA2 plugin in QIIME2 was used to generate an
483 ASVs table against the SILVA138 database. Alpha diversity and weighted uniFrac distances
484 were calculated using the Phyloseq package, while Bray-Curtis metrics were generated using
485 the vegan package. PERMANOVA (Bray-Curtis) analysis was conducted to test for significant
486 effects of the group on overall microbiome community composition. LEfSe analysis was
487 performed to identify differentially abundant phyla and genera between both groups using a
488 linear discriminant analysis (LDA) score equal to 4 as a threshold value. P values were
489 declared significant at $P < 0.05$. The sequencing data have been deposited in the European
490 Nucleotide Archive (ENA) at EMBL-EBI under accession number PRJEB71960.

491 **Bacterial strains**

492 *Campylobacter jejuni* strain M1 was used as the minimum number of viable bacteria required
493 for reliable intestinal colonisation of chickens has been defined [37]. Strain M1 was grown on
494 charcoal cefoperazone deoxycholate agar (CCDA) at 41 °C for 48 hours in a microaerophilic
495 atmosphere (90 % N_2, 5 % CO_2 and 5 % O_2). For challenge, 10 mL of Mueller Hinton broth
496 was inoculated with single colonies and incubated for 16 hours with shaking at 41 °C in the
497 same atmosphere. Prior to inoculation, bacteria were confirmed to have spiral morphology
498 and to be motile by phase contrast microscopy. Cultures were diluted in phosphate-buffered
499 saline (PBS) based on a standard curve of colony-forming units (CFU/mL) relative to optical
500 density at 600 nm and inocula were retrospectively confirmed by plating serial ten-fold
501 dilutions onto CCDA. A spontaneous nalidixic acid-resistant mutant of *Salmonella enterica*
502 serovar Typhimurium strain 4/74 was used, as its colonisation kinetics are well defined in
503 chickens [39]. This was cultured on Luria Bertani (LB) agar containing 20 µg/mL nalidixic acid
504 at 37 °C overnight and a single colony was transferred to LB broth with nalidixic acid and
505 incubated at 37 °C with shaking for 20 hours. 100 µL of this culture was used for inoculation
506 and the number of viable bacteria given was determined retrospectively by plating serial ten-
507 fold dilutions onto LB agar.

508 **Experimental infection of chickens**

509 Animal experiments using *Campylobacter* or *Salmonella* were conducted at the Moredun
510 Research Institute. Birds were provided with access to water and irradiated feed based on
511 vegetable protein *ad libitum*. Groups of 20 to 22 birds of each genotype (IL10KO WT, HET,
512 HOM) were wing-tagged for identification and separately housed in biosafety level 2 facilities
513 from day 7 of age in colony cages. At 14 days of age, birds were inoculated by oral gavage
514 with 100 µL of bacterial suspension. In two separate trials with *C. jejuni*, birds were inoculated
515 with $1x10^2$ CFU of strain M1. In a single trial with *S.* Typhimurium, birds were inoculated with
516 $1x10^8$ CFU of strain 4/74 nal^R. At 7 days post-inoculation, half of the birds in each group were

517 euthanised by cervical dislocation. The remainder of the birds were euthanised at 14 days
518 post-inoculation. On post-mortem examination, samples from the ileum and the distal end of
519 the caecum were stored in RNA*later*® or fixed in 10% neutral-buffered formalin for
520 histopathology. The contents of the caeca were pooled at the bird level, homogenised in PBS,
521 and ten-fold serial dilutions cultured on CCDA at 41 °C in a microaerophilic atmosphere to
522 enumerate CFU/g of *C. jejuni* or MacConkey agar containing 20 µg/mL nalidixic acid at 37 °C
523 aerobically to enumerate CFU/g of *Salmonella*.

524 **Histopathology**

525 Formalin-fixed tissue samples were embedded in paraffin, sectioned, mounted on glass slides,
526 and stained by haematoxylin-eosin (HE) staining. Histopathological analyses were performed
527 by a certified veterinary pathologist blind to the genotype of individuals and the inoculum.
528 Samples of ileum and caecum were assessed for the presence of lymphoplasmacytic and
529 heterophil infiltration on a scale of 0 to 5 (where infiltration is 0 normal, 1 slight, 2 mild, 3
530 moderate, 4 marked or 5 severe).

531 **RNA extraction and multiplex PCR**

532 Caecal tissue samples in RNA*later*® were homogenised with a hand-held tissue homogeniser
533 and RNA was extracted using RNeasy kit following the instructions from the manufacturer
534 (QIAGEN). The concentration and integrity of the RNA were respectively analysed using a
535 NanoDrop microvolume spectrophotometer and TapeStation automated electrophoresis
536 system. Reverse transcription, preamplification and high-throughput quantitative PCR (qPCR)
537 for avian immune-related transcripts and reference genes were performed as previously
538 described using a 96.96 Dynamic Array IFC for Gene Expression ([38]; Standard BioTools,
539 San Francisco, CA, United States).

540 **Parasites**

541 Animal experiments using *Eimeria* were conducted at the Royal Veterinary College, using
542 chicks hatched at the NARF SPF avian facility. All chickens were provided with access to
543 water and ammonia fumigated feed based on vegetable protein *ad libitum*. The *Eimeria tenella*
544 Houghton (H) reference strain was used [66]. Parasites were passaged by oral inoculation of
545 specified pathogen-free Lohmann Valo chickens, purified and prepared for use as described
546 elsewhere [54]. At 21 days post-hatch, chicks were weighed and infected by oral inoculation
547 with 7000 sporulated *E. tenella* oocysts or mock-infected using sterile water. Group sizes
548 (minimum eight to ten per group) were determined following dose titration in IL10KO and
549 IL10EnKO HET chickens using power calculations with alpha set at 0.05 and power at 80%.
550 At the desired timepoint, birds were culled and whole blood was collected for serum. Caeca
551 were collected, scored for severity of infection [67] and preserved using RNAlater (Invitrogen).
552 Total genomic DNA (gDNA) was extracted from thawed complete caeca stored in RNAlater
553 from all studies. Caeca were homogenised in Buffer ATL using a TissueRuptor homogenizer
554 (Qiagen, Hilden, Germany) and then digested overnight at 56 °C in Buffer ATL and proteinase
555 K, prior to extraction using the Qiagen DNeasy Blood and Tissue DNA Kit according to
556 manufacturer's instructions.

557 Quantitative PCR for assessment of *E. tenella* genome copy number was performed as
558 previously described [68]. Briefly, gDNA extracted from caecal tissue was used as template
559 for qPCR targeting *E. tenella* (RAPD-SCAR marker Tn-E03-116, primers F: 5'-
560 TCGTCTTTGGCTGGCTATTC-3', R: 5'-CAGAGAGTCGCCGTCACAGT-3'), normalised
561 against the number of chicken tata-binding protein (TBP) genomic copies detected (F: 5'-
562 TAGCCCGATGATGCCGTAT-3', R: 5'-GTTCCCTGTGTCGCTTGC-3'). Quantitative PCR
563 was performed in 20 µL reactions in triplicate containing 10 µL 2 × SsoFast EvaGreen
564 Supermix (Bio-Rad, Hercules, CA, USA), 1 µL of primers (F: 3 µM, R: 3 µM), 8 µL of molecular
565 biological grade water (Invitrogen) and 1 µL of gDNA, or water as negative control. Hard-

566 shelled 96-well reaction plates (Bio-Rad) were sealed with adhesive film (Bio-Rad) and loaded
567 into a Bio-Rad CFX qPCR cycler. Reactions were heated to 95°C for 2 min, prior to 40 cycles
568 consisting of 95°C for 15 s then 60°C for 30 s with a fluorescence reading taken after each
569 cycle. Melting curve analysis was performed for 15 s at 95°C, before cooling to 65°C for 60 s,
570 then heating to 95°C in 0.5°C increments for 0.5 s. Absolute quantification was performed
571 against a standard curve generated using serially diluted plasmid DNA containing the
572 amplicon of interest (EtenSCAR or ChickenTBP), to generate a standard curve ranging from
573 10^6 to 10^1 genome copies per mL. Parasite genome copy number was normalised by division
574 with host (chicken) genome copy number.

575 **Statistical analyses**

576 Minitab Statistical Software was used to analyse IL10 protein levels and nitric oxide production
577 in BMDMs using two-tailed unpaired t tests, growth curves were analysed using two-tailed
578 unpaired t tests or one-way ANOVA with Bonferroni multiple comparison tests, and
579 histopathological scores were analysed using Mann-Whitney U tests or Kruskal-Wallis tests.
580 Analysis of bacterial counts, histopathology, and heatmaps was performed with GraphPad
581 Prism software version 10.2.0. Data from multiplex RT-qPCR was analysed with GenEx6
582 software. The distribution of data was analysed by D'Agostino-Pearson and Shapiro-Wilk
583 normality tests. *Eimeria* replication and chicken body weight gain during parasite infection
584 were analysed using one-way ANOVA with Tukey's multiple comparison tests, and differences
585 in lesion scores were tested by Kruskal-Wallis with Dunn's multiple comparison tests. Bacterial
586 counts and histopathology scores were analysed by Mann-Whitney U tests or Kruskal-Wallis
587 tests. Fold change in transcript abundance was analysed by t tests using normalised data.

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599 **Author Contributions**

600 Designed research: AP, DPB, DAH, DM, FT, KB, KW, MJM, MPS, RCT
601 Performed research: AAA, DPB, DM, GSA, JJO, KB, LG, LT, MV, RCT, ZW
602 Contributed new reagents/analytic tools: MJM
603 Analysed data: AAA, DB, DPB, DAH, DM, JDP, LG, LV, MJM, MPS, RCT, ZW
604 Wrote the paper: DPB, DAH, DM, FT, MJM, MPS, RCT
605 Secured funding: AP, DPB, DAH, DM, FT, KB, KW, MJM, MPS

606 **Competing Interests**

607 MJM is inventor on patent application WO 2020074915 for the iCaspase9 surrogate host
608 chicken; the University of Edinburgh is the applicant. The other authors declare no competing
609 interests.

610 **Data Availability Statement**

611 All study data are included in the article and/or SI Appendix. IL10KO and IL10EnKO edited
612 PGCs (HET and HOM) are cryopreserved and available to researchers under MTA.

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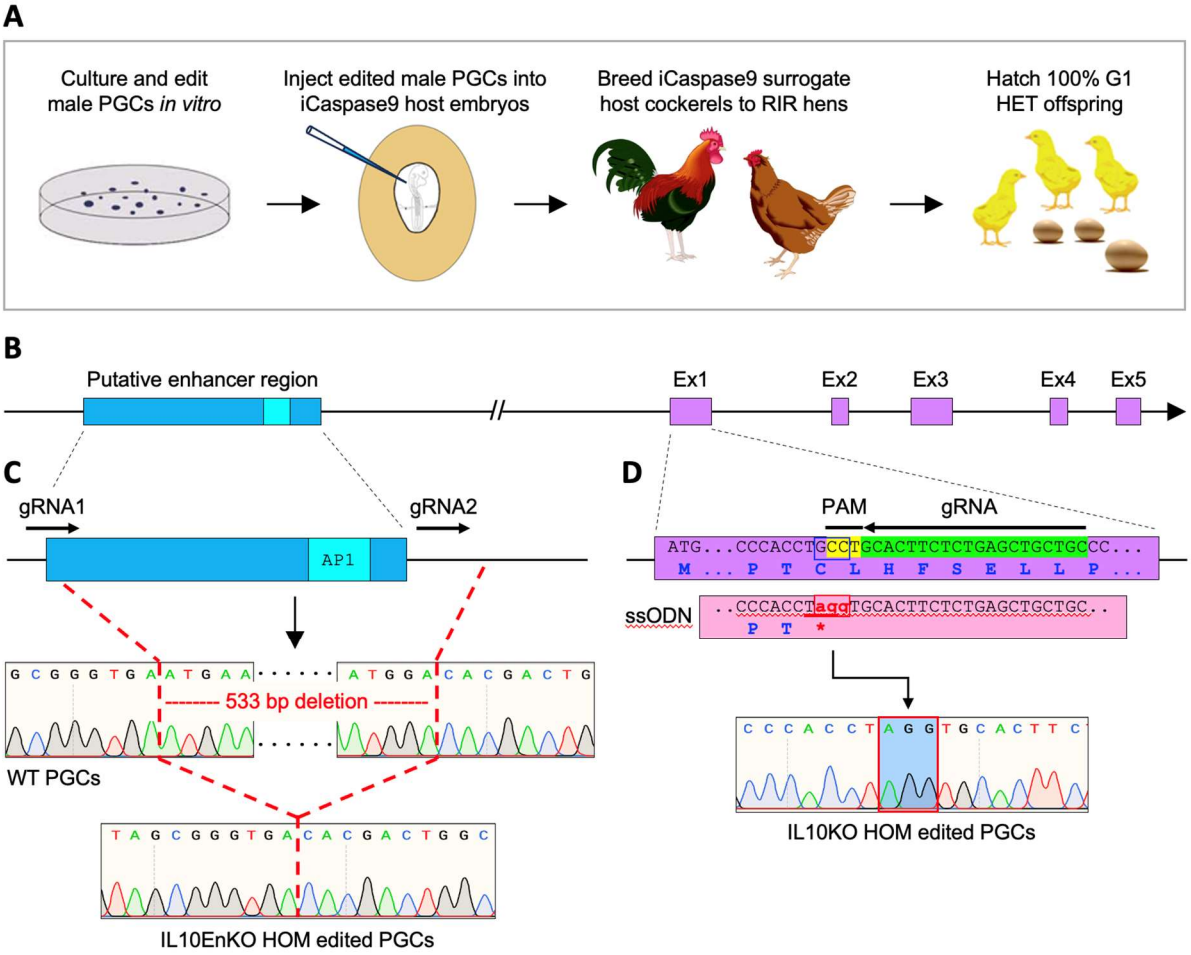


Figure 1: **IL10KO and IL10EnKO editing strategies. A**: Schematic of the pipeline used to create gene-edited chickens using embryonic PGCs and the iCaspase9 sterile surrogate host line. Male PGCs carrying the desired biallelic (HOM) edits were injected into iCaspase9 sterile surrogate host embryos to create IL10KO and IL10EnKO chickens. Upon sexual maturity, surrogate host cockerels were bred to RIR hens, resulting in 100% IL10KO HET or IL10EnKO HET offspring in the first generation (G1). **B**: Schematic of the *IL10* locus depicting the *IL10* putative enhancer region and the five *IL10* exons (Ex1 to Ex5). **C**: IL10EnKO HOM PGCs were created by deleting a 533-bp fragment encompassing the *IL10* putative enhancer region, using two gRNAs; DNA sequencing confirmed the biallelic deletion. **D**: IL10KO HOM PGCs were created using one gRNA and a 143-bp repair template (ssODN) to modify three nucleotides in *IL10* exon 1 (red, lowercase), thus introducing a premature in-frame stop codon in the *IL10* gene (underlined, *); DNA sequencing confirmed the biallelic edit.

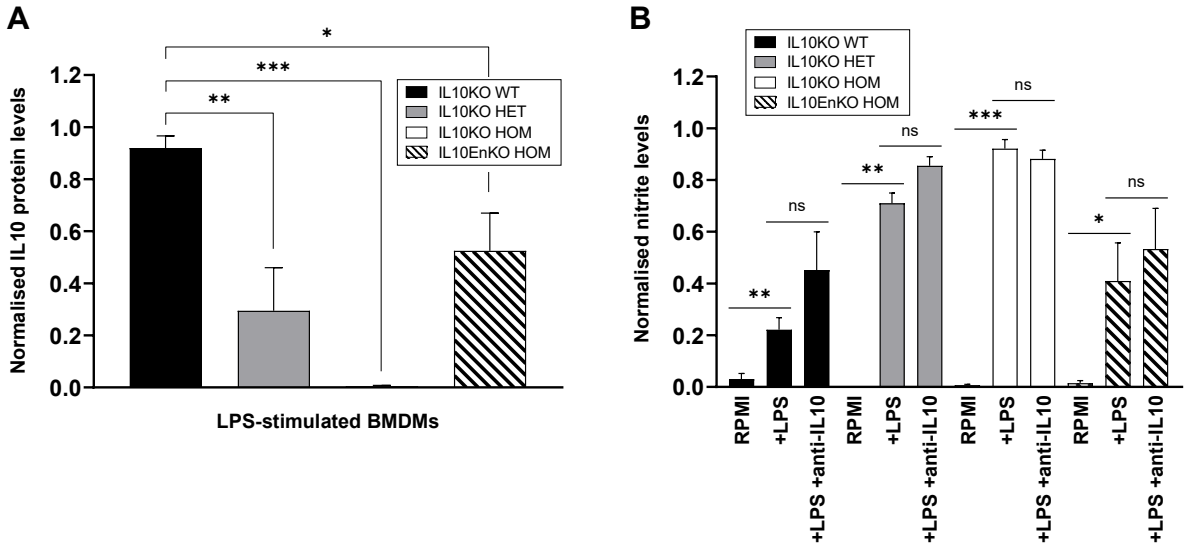


Figure 2: Confirmation of the IL10 mutation in bone marrow-derived macrophages. A: IL10 protein levels were measured by capture ELISA for LPS-stimulated BMDMs derived from Day 18 IL10KO WT (n=4), HET (n=2), HOM (n=4) and IL10EnKO HOM (n=4) embryos. Two independent experiments were performed and protein levels were normalised against the highest IL10KO WT value for each experiment and then combined. LPS treatment induced IL10 production in IL10KO WT BMDMs, but not in IL10KO HOM BMDMs; intermediate levels of IL10 were detected in IL10KO HET and IL10EnKO HOM BMDMs; IL10 expression in non-LPS induced samples was negligeable (<0.015; not shown). **B**: Nitric oxide production was assessed by measuring nitrite levels using Griess assay for LPS-stimulated BMDMs derived from Day 18 IL10KO WT (n=6), HET (n=2), HOM (n=7) and IL10EnKO HOM (n=6) embryos, in the absence or presence of neutralizing anti-IL10 antibody ROS-AV163 (anti-IL10). Three independent experiments were performed and nitrite levels were normalised against the highest IL10KO HOM nitrite value for each experiment before being combined. A significant increase in nitrite levels was observed in the absence of IL10 in LPS-stimulated IL10KO HOM BMDMs; nitrite levels were also significantly increased in LPS-stimulated IL10KO HET and IL10EnKO HOM BMDMs. Addition of neutralizing anti-IL10 antibody did not significantly affect nitrite levels in LPS-stimulated BMDMs, independently of the IL10 genotype. Note that each BMDM sample was derived from three pooled embryos of the same genotype. Data displayed as mean with SE. Statistical significance calculated using two-tailed unpaired t tests; *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$, ns: not significant.

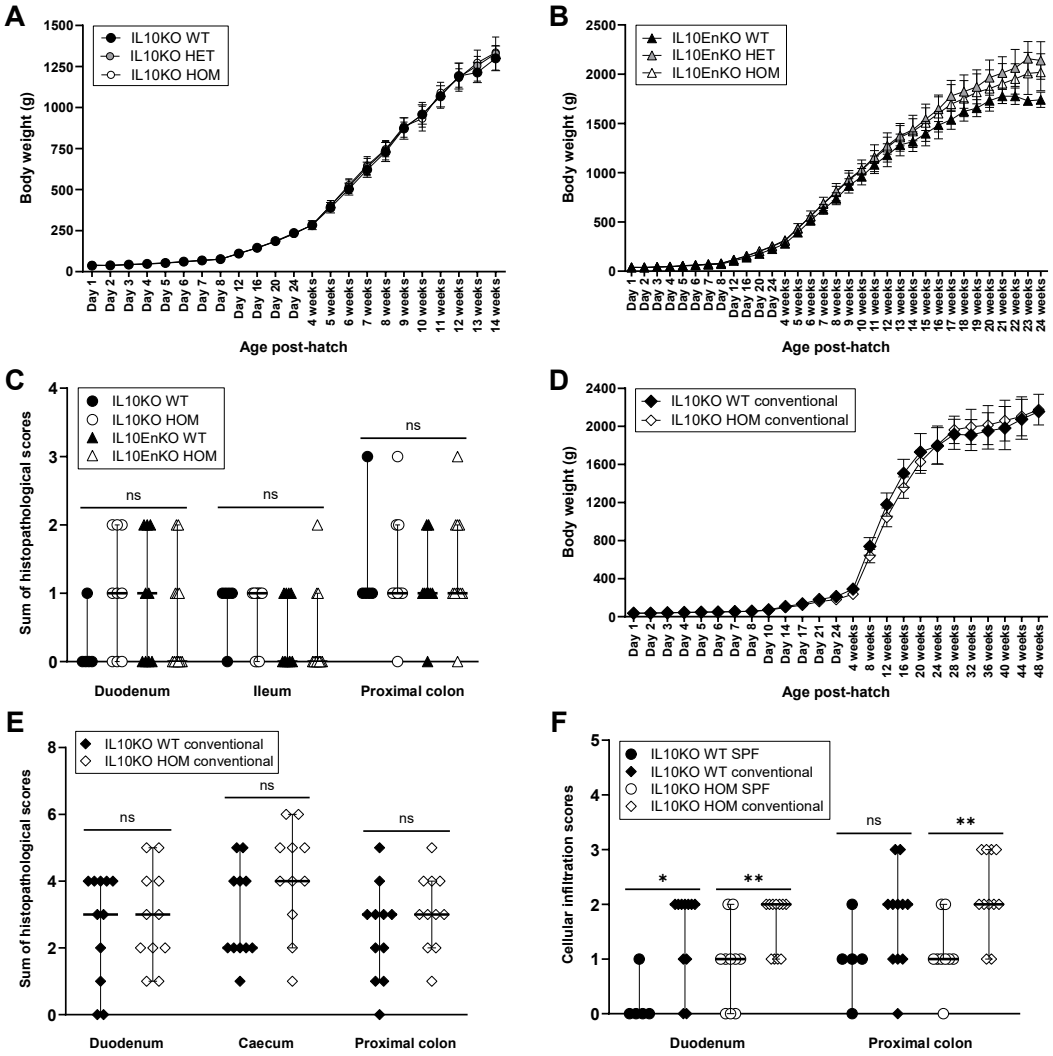


Figure 3: Growth curves and histopathological analyses of the gastrointestinal tract of IL10-deficient chickens in SPF and conventional facilities. A: Growth curves for IL10KO WT (n=3 to 8), HET (n=11 to 16) and HOM (n=2 to 4) hens raised in the NARF SPF facility, from hatch to 14 weeks. No significant weight differences were observed between genotypes at any timepoint ($P > 0.05$). **B**: Growth curves for IL10EnKO WT (n=2 to 4), HET (n=7 to 11) and HOM (n=5 to 11) hens raised in the NARF SPF facility, from hatch to 24 weeks. IL10EnKO HET and HOM hens were overall heavier than WT controls but this was statistically significant only between day 8 and day 24 ($P < 0.05$). **C**: Sums of histopathological scores for IL10KO WT (n=5) and HOM (n=9), and for IL10EnKO WT (n=9) and HOM (n=11) birds raised in the NARF SPF facility; tissue samples were collected at regular intervals from 16 to 40 weeks post-hatch. No significant differences were observed between genotypes for the tissues analysed. **D**: Growth curves for IL10KO WT (n=2 to 10) and HOM (n=5 to 15) hens raised in the NARF conventional facility, from hatch to 48 weeks. IL10KO HOM hens were significantly smaller than WT controls from 3 to 19 weeks post-hatch ($P < 0.05$), but this difference resolved with age. **E**: Sums of histopathological scores for IL10KO WT and HOM birds (n=11 in each group) raised in the NARF conventional facility; tissue samples were collected at regular intervals from 10 to 50 weeks post-hatch. No significant differences were observed between genotypes for the tissues analysed. **F**: Cellular infiltration scores for IL10KO WT and HOM birds raised in the NARF SPF and conventional facilities (same bird numbers as in C and E). Cellular infiltration scores were overall significantly higher for IL10KO WT and HOM birds raised in the conventional facility. Maximum possible sums of scores for data in C and E = 11; score range for data in F = 0 to 3. Data displayed as mean with SD (A, B and D) or as median with 95% confidence interval (C, E and F). Statistical significance calculated using one-way ANOVA with Bonferroni multiple comparison tests (A-B), Kruskal-Wallis test (C), two-tailed unpaired t tests (D), or Mann-Whitney U tests (E, F); *$P < 0.05$, **$P < 0.01$, ns: not significant.

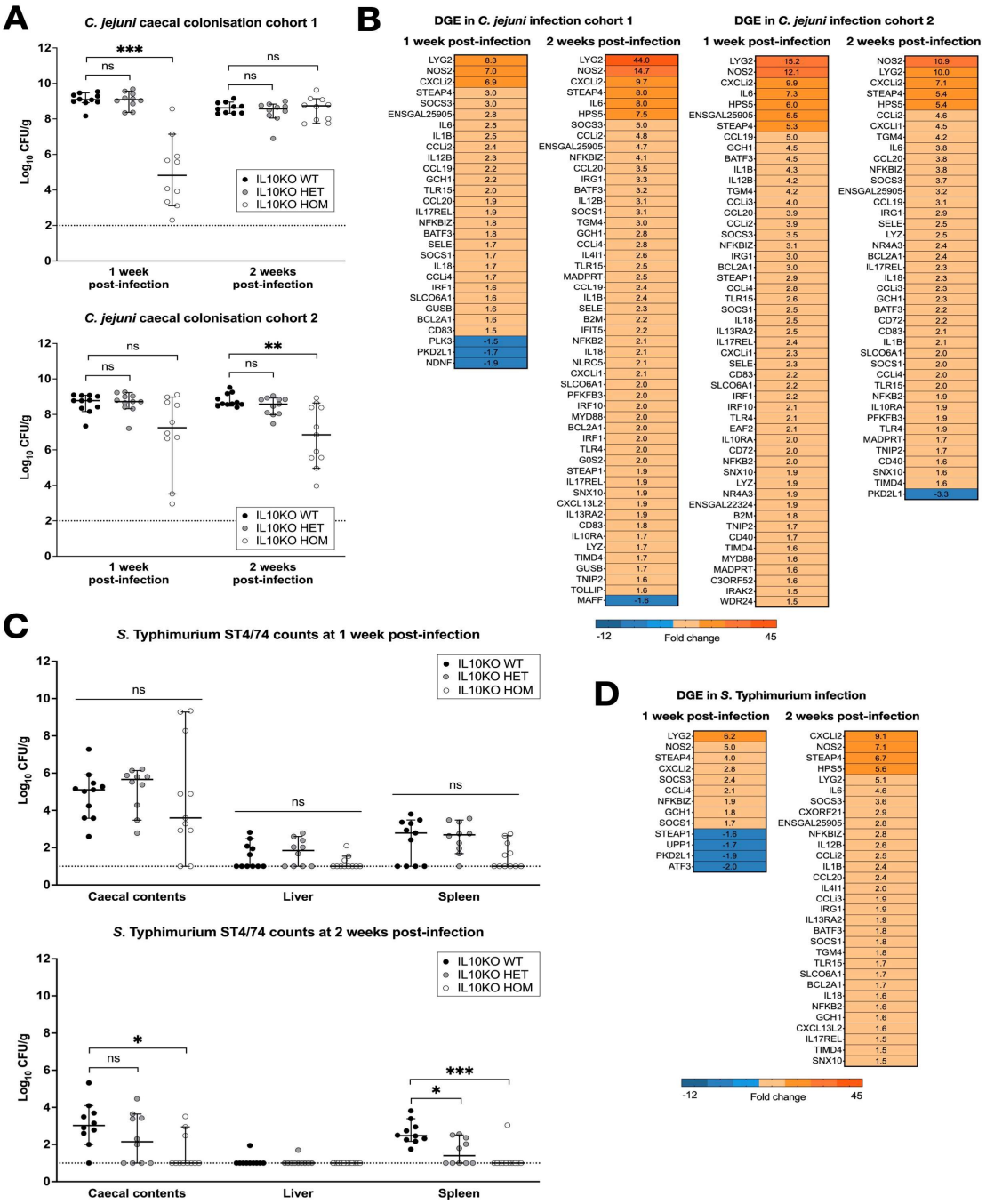


Figure 4: Net replication of *C. jejuni* and *S.* Typhimurium in the caeca of IL10KO WT, HET and HOM chickens and immune responses to infection. A: Caecal burden of *C. jejuni* strain M1 in IL1KO WT, HET and HOM chickens at 1- and 2-weeks post-inoculation in two separate trials. **B**: Heat map of differentially transcribed genes measured by multiplex qRT-PCR in the caeca of IL10KO HOM chickens in relation to IL10KO WT birds at 1- and 2-weeks post-inoculation in two separate trials. An increase in the expression of pro-inflammatory genes was consistently observed in both studies. **C**: Burden of S. Typhimurium strain ST4/74 in the caeca, liver and spleen of IL10KO WT, HET and HOM chickens at 1- and 2-weeks post-inoculation (single trial). **D**: Heat map of differentially transcribed genes in the caeca of IL10KO WT and HOM chickens 1- and 2-weeks post-inoculation with ST4/74. All group sizes: n=10 or 11. Bacterial colonisation shown as median with 95% confidence interval; dotted line shows limit of detection for each study (A, C). Statistical significance calculated using one-way ANOVA with Kruskal-Wallis test followed by Dunn's multiple comparison tests; *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$, ns: not significant.

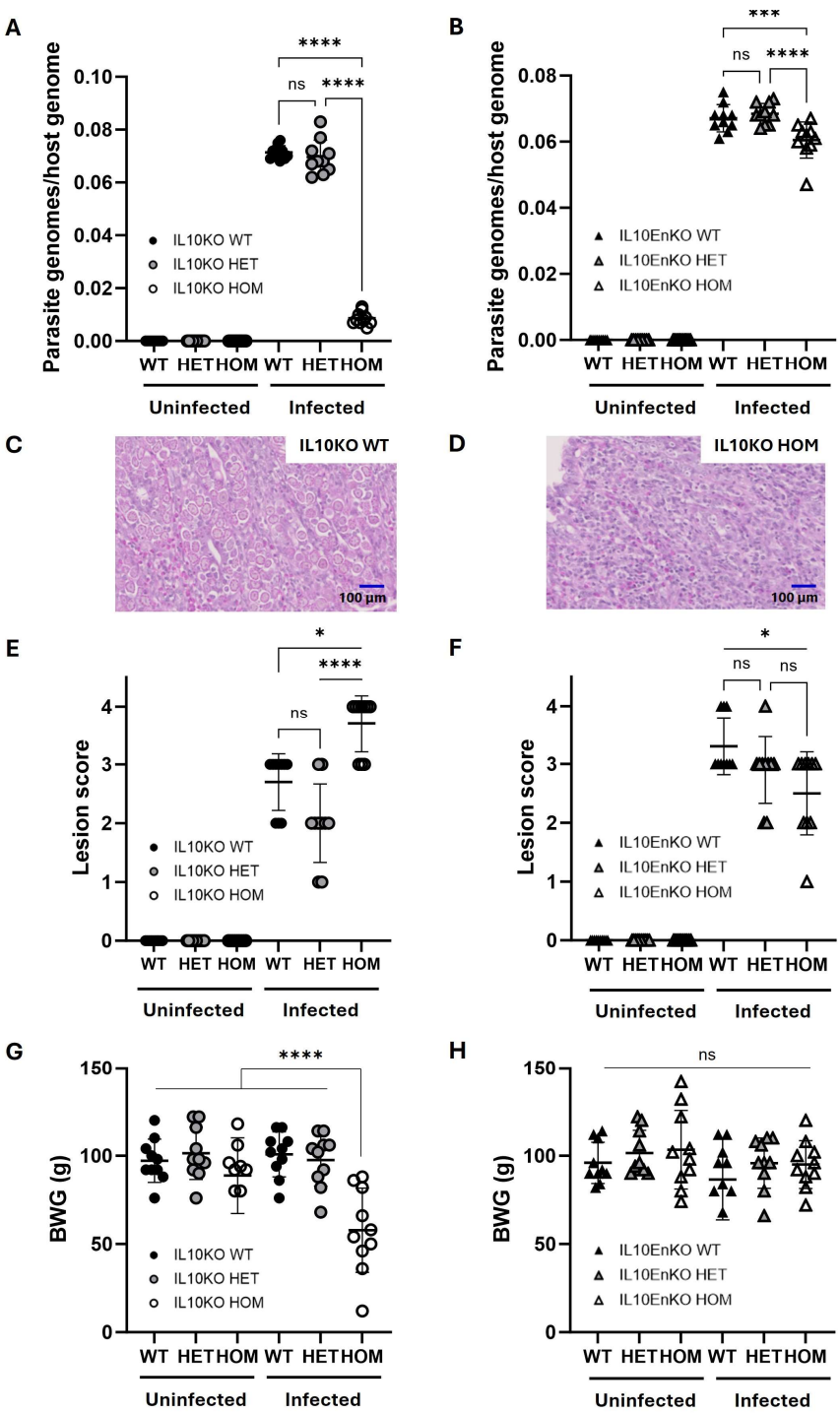
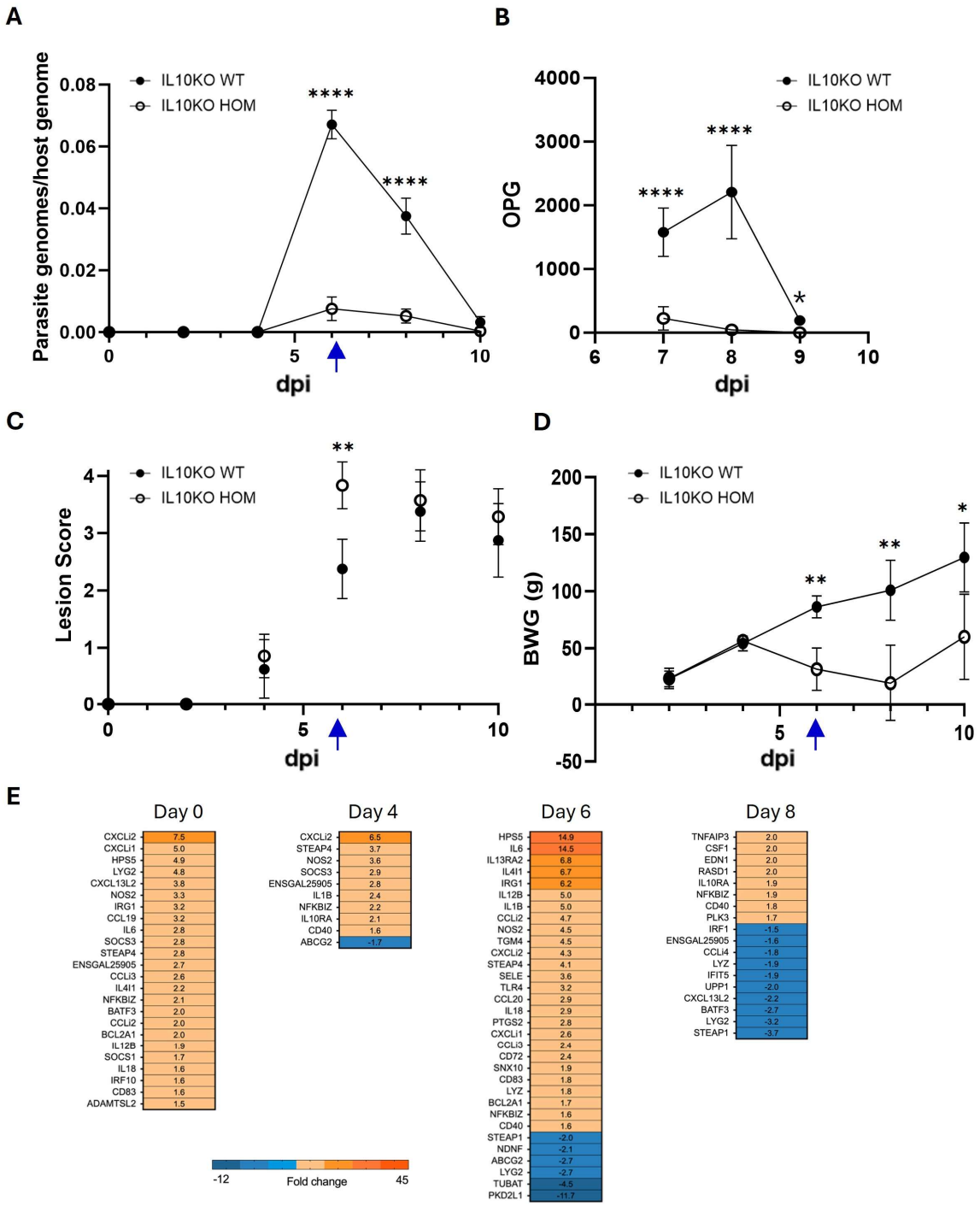


Figure 5: *Eimeria tenella* replication and impact on host pathology and performance in WT, HET and HOM G2 populations of IL10KO and IL10EnKO chickens. A-B: Parasite replication calculated as parasite genomes per host genome detected by quantitative PCR in genomic DNA extracted from caecal tissue six days post-infection (dpi). **C-D**: Haematoxylin and eosin stained caecal tissues collected from IL10KO WT and HOM chickens six days post *Eimeria tenella* infection. Numerous gametocytes are visible in the IL10KO WT line (C); gametocytes are largely absent in the IL10KO HOM line (D). **E-F**: Parasite-associated pathology measured as caecal lesion scores six dpi. **G-H**: Bodyweight gain (BWG) over six days from time of challenge to sampling. All group sizes: n=10. Statistical significance calculated using one-way ANOVA with Tukey's multiple comparison tests (A-B, G-H) or Kruskal-Wallis with Dunn's multiple comparison tests (E-F); *$P < 0.05$, ***$P < 0.001$, ****$P < 0.0001$, ns: not significant.



991
992
993 **Figure 6: *Eimeria tenella* infection time course in IL10KO WT and HOM chickens. A**: Parasite
994 replication calculated as parasite genomes per host genome detected by quantitative PCR in genomic
995 DNA extracted from caecal tissue. **B**: Oocysts per gram (OPG) litter. **C**: Parasite-associated pathology
996 measured as caecal lesion scores. **D**: Bodyweight gain (BWG) over ten days from time of challenge to
997 final sampling. **E:** Heat map of differentially transcribed genes in the IL10KO HOM caeca relative to
998 IL10KO WT chickens 0-, 4-, 6- and 8-days post-infection (dpi). 48 chicks per group, eight culled from
999 each group per timepoint. Statistical significance calculated using mixed-effects model (REML) with
1000 Tukey's multiple comparison tests (A, D), two-way ANOVA with Šídák's multiple comparison tests (B),
1001 or Mann-Whitney U tests (C); **P* < 0.05, ***P* < 0.01, ****P* < 0.001, *****P* < 0.0001, ns: not significant.
1002 Blue arrows indicate the time of sampling in the comparative phenotyping study (Figure 5).
1003