

1 **During *Aspergillus* infection, neutrophil, monocyte-derived DC, and plasmacytoid DC**  
2 **enhance innate immune defense through CXCR3-dependent crosstalk**

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28 **Summary**

29 *Aspergillus fumigatus*, a ubiquitous mold, is a common cause of invasive aspergillosis (IA) in  
30 immunocompromised patients. Host defense against IA relies on lung-infiltrating neutrophils and  
31 monocyte-derived dendritic cells (Mo-DCs). Here, we demonstrate that plasmacytoid dendritic  
32 cells (pDCs), which are prototypically anti-viral cells, participate in innate immune crosstalk  
33 underlying mucosal antifungal immunity. *Aspergillus*-infected murine Mo-DCs and neutrophils  
34 recruited pDCs to the lung by releasing the CXCR3 ligands, CXCL9 and CXCL10, in a Dectin-  
35 1/Card9- and type I and III interferon-signaling dependent manner, respectively. During  
36 aspergillosis, circulating pDCs entered the lung in response to CXCR3-dependent signals. Via  
37 targeted pDC ablation, we found that pDCs were essential for host defense in the presence of  
38 normal neutrophil and Mo-DC numbers. Although interactions between pDC and fungal cells  
39 were not detected, pDCs regulated neutrophil NADPH oxidase activity and conidial killing.  
40 Thus, pDCs act as positive feedback amplifiers of neutrophil effector activity against inhaled  
41 mold conidia.

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43 **Keywords:** *Aspergillus fumigatus*, CXCR3, CXCL9, CXCL10, plasmacytoid DC, monocyte,  
44 neutrophil, dendritic cell, innate immunity, cytokine, lung, fungus, crosstalk

## 45 **Introduction**

46 *Aspergillus fumigatus* forms airborne spores (conidia) that humans typically clear in a silent  
47 and asymptomatic manner. Due to the growing number of humans that live in immune  
48 compromised states, *A. fumigatus* is the most common and lethal agent of mold pneumonia  
49 worldwide (Brown et al., 2012; Latge and Chamilos, 2019; Lionakis and Levitz, 2018; Tischler  
50 and Hohl, 2019). In humans and mice, sterilizing immunity against *A. fumigatus* conidia depends  
51 on the action of myeloid cells, primarily neutrophils, lung-infiltrating monocytes and monocyte-  
52 derived DCs (Mo-DCs), as well as alveolar macrophages; all lymphoid cells are redundant for  
53 host defense (Espinosa et al., 2014; Hohl et al., 2009; Latge and Chamilos, 2019; Mircescu et al.,  
54 2009). Phagocyte NADPH oxidase is central to fungal clearance, as evidenced by a 40-55%  
55 lifetime prevalence of IA in patients with chronic granulomatous disease (Marciano et al., 2015).  
56 Reactive oxygen species induce a regulated cell death process in neutrophil-engulfed conidia,  
57 and thereby protect the respiratory tract from tissue-invasive hyphae and fungal dissemination  
58 (Shlezinger et al., 2017).

59 Using targeted cell depletion strategies based on murine CCR2 promoter-dependent  
60 diphtheria toxin receptor (DTR) transgene expression (Espinosa et al., 2014; Hohl et al., 2009),  
61 recent studies implicated CCR2<sup>+</sup> inflammatory monocytes and Mo-DCs in sterilizing antifungal  
62 immunity, both by direct fungal killing and by regulating the lung inflammatory milieu  
63 (Espinosa et al., 2017; Espinosa et al., 2014). Since depletion of CCR2<sup>+</sup> cells diminished  
64 neutrophil antifungal activity, two models could explain these findings. First, CCR2<sup>+</sup> monocytes  
65 and Mo-DCs could release mediators that act directly on neutrophils to enhance antifungal  
66 effector functions. Second, CCR2<sup>+</sup> monocytes and Mo-DCs could mediate the recruitment or  
67 activation of a third cellular constituent that conditions the lung inflammatory milieu

68 independent of contributions from CCR2<sup>+</sup> monocytes and their derivatives. Here, we provide  
69 evidence for the second model and identify pDCs as a third leukocyte constituent that is essential  
70 for innate immune crosstalk and host defense against *A. fumigatus* in an otherwise immune  
71 competent host.

72 The mechanism by which pDCs contribute to antifungal immunity in the lung remains an  
73 open question. *In vitro*, human pDCs may spread over *A. fumigatus* hyphae to blunt fungal  
74 metabolic activity, and, in rare instances, undergo a cell death process that may result in  
75 extracellular traps (Loures et al., 2015; Ramirez-Ortiz et al., 2011). Mice treated with a mAb  
76 (i.e.,  $\alpha$ -PDCA-1/CD317) that primarily targets pDCs in the steady state, but likely targets  
77 additional leukocyte subsets under inflammatory conditions (Blasius et al., 2006), are susceptible  
78 to *A. fumigatus* challenge. In this study, we integrate pDCs into a model of innate immune  
79 crosstalk that is critical for defense against *A. fumigatus* in the lung. We found that fungus-  
80 infected Mo-DCs and neutrophils utilize Dectin-1/Card9 signaling to release CXCL9 and  
81 responded to type I and type III interferon signaling to release CXCL10. These CXCR3 ligands  
82 promoted pDC egress from the circulation into the infected lung. Lung CXCR3<sup>+</sup> pDCs enhanced  
83 neutrophil NADPH oxidase activity and fungal killing, preventing the formation of tissue-  
84 invasive hyphae and promoting sterilizing immunity. These findings integrate antifungal pDCs  
85 into a model of mucosal immune defense against inhaled molds.

## 86 **Results**

### 87 **Mo-DCs and neutrophils produce CXCL9 and CXCL10 during *A. fumigatus* infection**

88 To examine specific contributions of CCR2<sup>+</sup> monocytes and Mo-DCs to the lung  
89 inflammatory milieu during *A. fumigatus* challenge and to eliminate potential contributions of  
90 CCR2<sup>+</sup> NK cell and CD8<sup>+</sup> T cell subsets, we crossed the CCR2-diphtheria toxin receptor (DTR)  
91 transgene to Rag2<sup>-/-</sup> interleukin-2 receptor  $\gamma$  chain<sup>-/-</sup> mice. Lung homogenates of DT-treated  
92 CCR2-DTR<sup>+/-</sup> Rag2<sup>-/-</sup> interleukin-2 receptor  $\gamma$  chain<sup>-/-</sup> mice (CCR2-DTR<sup>+/-</sup> Rag2<sup>-/-</sup> Il2rg<sup>-/-</sup>)  
93 contained less CXCL10 (IP-10), CCL5 (RANTES), CCL17 (TARC), and CCL20 (MIP-3 $\alpha$ )  
94 compared to DT-treated non-transgenic Rag2<sup>-/-</sup> Il2rg<sup>-/-</sup> littermates at 36 h post-infection (pi), as  
95 measured in a cytokine array (Figures S1A and S1B).

96 Because a *CXCL10* polymorphism is implicated in IA susceptibility in hematopoietic cell  
97 transplant recipients (Fisher et al., 2017; Mezger et al., 2008), we measured lung levels of  
98 CXCL9 and CXCL10, both CXCR3 ligands, in naïve and in fungus-infected C57BL/6 mice. *A.*  
99 *fumigatus* challenge induced CXCL9 and CXCL10 expression in the lung, with a peak at 48 h pi  
100 (Figure 1A). To validate the multiplex array data, we ablated CCR2<sup>+</sup> monocytes and Mo-DCs in  
101 CCR2-DTR<sup>+/-</sup> Rag2<sup>-/-</sup> Il2rg<sup>-/-</sup> mice and observed a 50-70% reduction in lung CXCL9 and  
102 CXCL10 levels at 48 h pi (Figure S1C). Ablation of CCR2<sup>+</sup> monocytes and Mo-DCs in  
103 conventional CCR2-DTR<sup>+/-</sup> (CCR2 Depletor) mice that contain lymphoid lineage cells yielded  
104 nearly identical results (Figures 1B and 1C), consistent with the model that CCR2<sup>+</sup> myeloid cells  
105 represent a major cellular source of CXCR3 ligands during acute *A. fumigatus* infection.

106 To visualize hematopoietic cellular sources of CXCL9 and CXCL10, we generated chimeric  
107 mice (REX3 Tg  $\rightarrow$  C57BL/6) in which radiosensitive hematopoietic cells encoded RFP and BFP  
108 transgenes that were driven by the *Cxcl9* and *Cxcl10* promoters, respectively (Groom et al.,

109 2012). Following *A. fumigatus* challenge, Mo-DCs were the major cell type that expressed the  
110 RFP and BFP transgenes, consistent with the CCR2<sup>+</sup> cell ablation data in the CCR2-DTR<sup>+/-</sup>  
111 *Rag2<sup>-/-</sup>Il2rg<sup>-/-</sup>* and CCR2-DTR<sup>+/-</sup> backgrounds (Figures 1D, 1E and 1F). The majority of Mo-DCs  
112 produced CXCL9 and CXCL10 simultaneously, while a minority were positive only for  
113 CXCL10 (Figures 1E and 1F). Monocytes expressed primarily the CXCL10 transgene, while  
114 CXCL9 transgene expression was undetectable at baseline and during fungal infection.  
115 Neutrophils expressed both reporter transgenes during respiratory fungal infection, albeit with a  
116 lower frequency compared to Mo-DCs. pDCs, CD4<sup>+</sup> and CD8<sup>+</sup> T cells, and NK cells expressed  
117 very low levels of the reporter transgenes, respectively (Figures 1D-1F, S1D and 1E).

118 To ascertain that neutrophils contribute to CXCL9 and CXCL10 production, we generated  
119 BM chimera mice that enabled DT-induced neutrophil depletion (ROSA26-iDTR<sup>Mrp8-Cre</sup> →  
120 C57BL/6.SJL mice, neutrophil Deleter) and (non-Cre iDTR littermates → C57BL/6.SJL), and  
121 measured CXCL9 and CXCL10 levels following challenge with heat-killed swollen *A. fumigatus*  
122 conidia 48 h pi. This experimental set-up was utilized to eliminated potential differences in  
123 fungal growth observed in neutrophil depletion studies (Bonnett et al., 2006; Espinosa et al.,  
124 2014; Mehrad et al., 1999; Mircescu et al., 2009). Neutrophil-depleted mice exhibited  
125 significantly lower CXCL10 lung levels compared to non-depleted littermates, though CXCL9  
126 lung levels were similar (Figures 1G and 1H). Although CCR2<sup>+</sup> Mo-DCs were the major cellular  
127 source of CXCL9 and CXCL10 during acute *A. fumigatus* challenge, neutrophils contributed to  
128 CXCL10 production as well.

129 **Distinct signaling pathways promote CXCL9 and CXCL10 production by fungus-infected**  
130 **myeloid cells in the lung**

131 To examine whether fungal uptake by Mo-DCs and neutrophils drives CXCL9 and  
132 CXCL10 expression, we infected chimeric REX3 Tg → C57BL/6 mice with Alexa 633  
133 (AF633)-labeled conidia and compared RFP and BFP expression in fungus-engaged (AF633<sup>+</sup>)  
134 and bystander (AF633<sup>-</sup>) leukocytes. Fungus-engaged Mo-DCs and neutrophils had much higher  
135 levels of fluorescent transgene expression than corresponding bystander cells, indicating that  
136 fungal uptake promotes Mo-DC CXCL9 and CXCL10 production, neutrophil CXCL10  
137 production (Figures 2A-2E), and, to a lesser extent, monocyte CXCL9 production (Figures S2A,  
138 2B).

139 Dectin-1 is a major *A. fumigatus* recognition receptor by binding to  $\beta$ -glucan moieties that  
140 are exposed during conidial swelling, the first step in germination and hyphal formation (Brown  
141 et al., 2018; Hohl et al., 2005; Steele et al., 2005; Werner et al., 2009). Dectin-1 transduces  
142 signals via a cytoplasmic ITAM-like motif that, upon tyrosine phosphorylation, activates spleen  
143 tyrosine kinase and Card9 (Gross et al., 2006; Hsu et al., 2007a; Jhingran et al., 2015; Jia et al.,  
144 2014; Rogers et al., 2005). To determine whether Dectin-1/Card9 signaling mediates CXCL9  
145 and CXCL10 production, we infected gene-deficient mice and found that CXCL9, but not  
146 CXCL10 production, was significantly attenuated in both *Clec7a*<sup>-/-</sup> and *Card9*<sup>-/-</sup> mice (Figures  
147 2F-2G), directly linking fungal recognition by C-type lectin receptor signaling to CXCL9  
148 production in the lung.

149 Prior studies have demonstrated that CXCL10 expression can be induced in a variety of  
150 cells, including endothelial cells, keratinocytes, fibroblasts, mesangial cells, astrocytes,  
151 monocytes, and neutrophils by stimulation with IFN- $\alpha$ , IFN- $\beta$ , IFN- $\gamma$ , or LPS and in T cells by



152 antigen activation (Colvin et al., 2004; Luster and Ravetch, 1987; Ohmori and Hamilton, 1990;  
153 Qian et al., 2007). Since type I and type III interferon signaling are essential for host defense  
154 against *A. fumigatus* (Espinosa et al., 2017), we measured CXCL10 production in IFN-signaling  
155 deficient mice. Unlike CXCL9, lung CXCL10 levels were significantly reduced in *Ifnar1*<sup>-/-</sup> and  
156 in *Ifnlr*<sup>-/-</sup> mice (Figures 2F-2G), indicating that distinct upstream signals couple fungal  
157 recognition to CXCL9 and CXCL10 production during acute *A. fumigatus* infection.

158 Since  $\beta$ -glucan recognition and IFN signaling may impact the number of Mo-DCs and  
159 neutrophils in *A. fumigatus*-infected lungs (Jhingran et al., 2015; Jhingran et al., 2012; Werner et  
160 al., 2009), we sorted Mo-DCs and neutrophils from gene-deficient and wild-type mice and  
161 quantified *cxcl9* and *cxcl10* mRNA expression. Preliminary studies that measured *cxcl9* and  
162 *cxcl10* mRNA expression in Mo-DCs and neutrophils isolated from infected wild-type, *Clec7a*<sup>-/-</sup>,  
163 *Ifnar*<sup>-/-</sup>, and *Ifnlr*<sup>-/-</sup> mice supported the concept that  $\beta$ -glucan recognition and IFN signaling  
164 directly regulate *cxcl9* and *cxcl10* transcription, respectively (data not shown).

### 165 **CXCR3 is critical for survival and fungal clearance**

166 To assess the relevance of CXCR3 ligand production (Groom et al., 2012) for host  
167 outcomes, the survival of *Cxcr3*<sup>-/-</sup> mice was compared to *Cxcr3*<sup>+/+</sup> controls following *A.*  
168 *fumigatus* challenge. *Cxcr3*<sup>-/-</sup> mice were significantly more susceptible to challenge compared to  
169 controls (Figure 3A). The heightened susceptibility correlated with an increase in lung fungal  
170 burden (Figures 3B, S3A and S3B) and in lung tissue damage, as determined by comparisons of  
171 bronchoalveolar lavage fluid (BALF) lactate dehydrogenase (LDH) (Figure 3C) and albumin  
172 (Figure 3D) levels at 48 h pi or 72 h pi. These data linked *A. fumigatus*-triggered CXCL9 and  
173 CXCL10 production by Mo-DCs and neutrophils during acute *A. fumigatus* challenge to  
174 CXCR3-dependent protection and fungal clearance.

## 175 **CXCR3- and CCR2-dependent signals mediate pDC lung recruitment**

176 To define the cellular target of CXCR3 signaling, we measured CXCR3 expression on a  
177 wide range of leukocytes. Bone marrow (BM)-resident pDCs from naïve mice and lung pDCs  
178 from *A. fumigatus*-infected mice expressed CXCR3, unlike other myeloid cell subsets analyzed  
179 (Figure 4A). As expected, CD4<sup>+</sup> T cells, CD8<sup>+</sup> T cells and NK cells expressed CXCR3 (Figure  
180 S4A), but mice that lack the lymphoid lineage (*Rag2<sup>-/-</sup>Il2rg<sup>-/-</sup>*) did not exhibit heightened  
181 susceptibility to *A. fumigatus* challenge (Figure S4B), as reported previously (Espinosa et al.,  
182 2014).

183 On the basis of these results and published work (Ramirez-Ortiz et al., 2011), we  
184 hypothesized that CXCR3-dependent pDC trafficking is critical for innate antifungal immunity.  
185 In prior studies, we did not identify pDCs in lung cell suspensions due to the inclusion of  
186 collagenase type IV. This preparation method degraded a pDC epitope utilized for their  
187 identification (Figure S4C). Using a collagenase-free method to prepare single cell lung  
188 suspensions, we observed that pDCs started to infiltrate *A. fumigatus*-infected lungs at 48 h pi,  
189 with a peak at 72 h pi (Figure 4B). pDC lung infiltration followed the observed peak in lung  
190 CXCL9 and CXCL10 levels and the peak influx of CXCL9- and CXCL10-producing innate  
191 immune cells (Figures S4D-S4F). *Cxcr3<sup>-/-</sup>* mice exhibited a ~50% reduction in lung pDCs  
192 (Figure 4C), while the number of lung monocytes, Mo-DCs, and neutrophils were similar to  
193 control mice at 72 h pi (Figures S4G-S4I). CXCR3 surface expression was reduced on lung  
194 pDCs compared to circulating pDCs, consistent with the idea that CXCR3 surface expression is  
195 downregulated following engagement by CXCR3 ligands (Figure 4A). To examine whether  
196 CXCR3 acts in series or in parallel with other chemokine receptors to mediate pDC trafficking  
197 from the BM to the lung, we measured pDC surface expression of additional chemokine

198 receptors in the resting and fungus-infected state. Consistent with prior studies (Fujimura et al.,  
199 2015; Sawai et al., 2013; Serbina and Pamer, 2006; Swiecki et al., 2017), we found that CCR2 is  
200 expressed by lung-infiltrating pDCs (Figure 4D). pDC lung recruitment was attenuated by 60-  
201 70% in *Ccr2*<sup>-/-</sup> mice at 72 h pi compared to controls (Figure 4E). As expected (Hohl et al.,  
202 2009), lung monocyte and Mo-DC numbers were significantly reduced in *Ccr2*<sup>-/-</sup> mice (Figures  
203 S4J and S4K), while lung neutrophil accumulation was not affected (Figure S4L). In sum, these  
204 data indicate that CXCR3 and CCR2 both mediate pDC trafficking.

### 205 **Sequential CCR2- and CXCR3- dependent signals mediate pDC lung recruitment**

206 To determine at which steps CXCR3 and CCR2 regulate pDC trafficking, we generated  
207 mixed BM chimeric mice to compare the trafficking of congenically marked gene-deficient  
208 (*Cxcr3*<sup>-/-</sup> or *Ccr2*<sup>-/-</sup>) and gene-sufficient (*Cxcr3*<sup>+/+</sup> or *Ccr2*<sup>+/+</sup>) pDCs (Figure 5A). In one model,  
209 CXCR3 and CCR2 may act in parallel at the same trafficking step. In this scenario, the ratio of  
210 gene-knockout to gene-sufficient pDCs would be increased in the same compartment for both  
211 chemokine receptors, prior to the dependent trafficking step. In an alternate model, CXCR3 and  
212 CCR2 may act in series at different trafficking steps. In this scenario, the ratio of gene-deficient  
213 to gene-sufficient pDCs would be elevated in distinct compartments.

214 The ratio of *Cxcr3*<sup>-/-</sup> to *Cxcr3*<sup>+/+</sup> pDCs was elevated in the blood compared to the BM and  
215 lung compartments (Figures 5B and S4A), both during infection and at baseline (Figure 5B and  
216 Figure S5A). These data support a model in which CXCR3 primarily, but not exclusively,  
217 mediates pDCs trafficking from the circulation into the lung in *A. fumigatus*-infected mice. In  
218 contrast to pDCs, the ratio *Cxcr3*<sup>-/-</sup> to *Cxcr3*<sup>+/+</sup> neutrophils and monocytes was similar in all  
219 compartments analyzed, consistent with CXCR3-independent trafficking (Figure S5B-S5C).

220 The ratio of *Ccr2*<sup>-/-</sup> to *Ccr2*<sup>+/+</sup> pDCs was elevated in BM compared to the blood and lung  
221 under all conditions examined. These data are consistent with a CCR2-dependent defect in pDC  
222 exit from the BM during infection (Figure 5C) and in the steady state (Figure S5D). As  
223 anticipated, monocyte bone marrow egress was highly dependent on CCR2 (Figure 5SE), while  
224 neutrophil bone marrow was not (Figure S5F). In sum, these data show that CCR2- and CXCR3-  
225 dependent signals act in series to mediate pDC entry into the circulation and pDC egress from  
226 the circulation into the lung, respectively.

### 227 **Lung pDCs are essential for host defense against *A. fumigatus***

228 To link CXCR3 signaling to pDC-dependent antifungal immunity, our model would predict  
229 that the chemokine receptor, CXCR3, and its cellular target, the pDC, are both essential for  
230 innate antifungal immunity. To test this conjecture, we infected BDCA2-DTR<sup>+/-</sup> (pDC Deleter)  
231 mice in which pDCs are ablated at rest and under inflammatory conditions (Swiecki et al., 2010).  
232 Following DT treatment, pDCs were depleted fully in the steady state and at 72 h pi, while lung-  
233 infiltrating monocytes, Mo-DCs, neutrophils, and all other leukocyte subsets examined were not  
234 (Figures 6A-6E). In contrast to BDCA2-DTR<sup>+/-</sup> mice, CCR2-DTR<sup>+/-</sup> mice facilitated DT-induced  
235 ablation of pDCs in addition to other known CCR2<sup>+</sup> cells, i.e. monocytes, Mo-DCs, and NK cells  
236 (Figures S6A-6E) (Espinosa et al., 2014; Hohl et al., 2009).

237 To define the functional role of pDCs during *A. fumigatus* infection, we compared the  
238 mortality, lung LDH levels, lung fungal burden and histopathology in pDC-depleted mice and in  
239 littermate controls. pDC-depleted mice were more susceptible to *A. fumigatus* challenge than  
240 control mice (Figure 6F) and mortality correlated with greater lung damage, as measured by  
241 BAL fluid lactate dehydrogenase (LDH) levels (Figure 6G), an increased fungal burden  
242 following infection with two commonly used *A. fumigatus* isolates (Figures 6H and 6I), and a

243 failure to control fungal germination in the lung at 72 h pi (Figure 6J). Importantly, pDCs did not  
244 contribute to the production of CXCL9 and CXCL10 in the lung during *A. fumigatus* challenge,  
245 as predicted by prior data (Figures 6K and 6L). In sum, CXCR3<sup>+</sup> pDCs were essential for innate  
246 antifungal immunity in the lung after *A. fumigatus* challenge.

### 247 **Lung pDCs enhance neutrophil fungicidal activity**

248 To determine how pDCs shape innate antifungal immunity in the lung, we hypothesized that  
249 pDCs are critical for antifungal effector functions, since lung neutrophil and Mo-DC numbers  
250 were unaffected in pDC depleted mice. To test this hypothesis, we utilized the fluorescent  
251 *Aspergillus* reporter (FLARE) conidia that encode a dsRed viability fluorophore and are labeled  
252 with an Alexa Fluor 633 tracer (AF633). FLARE conidia enable us to distinguish live  
253 (DsRed<sup>+</sup>AF633<sup>+</sup>) and dead (DsRed<sup>-</sup>AF633<sup>+</sup>) conidia during cellular interactions with leukocytes  
254 with single-encounter resolution (Figure 7A). Using the FLARE strain, we quantified leukocyte  
255 conidial uptake and killing in pDC-depleted and littermate control mice. pDCs did not bind to or  
256 engulf *A. fumigatus* conidia, as measured by acquisition of AF633 fluorescence (Figures 7B and  
257 S7A). pDC ablation did not affect lung neutrophil fungal uptake at 72 h pi compared to lung  
258 neutrophils in pDC-sufficient controls (Figures 7C and 7D). However, the frequency of  
259 neutrophils that contained live conidia was substantially increased in pDC-depleted mice  
260 compared to control mice (Figures 7C and 7E). In other words, neutrophil-engulfed conidia were  
261 more likely to be killed in control mice than in pDC-depleted mice (Figures 7C and 7E). pDC  
262 ablation did not alter conidial uptake or significantly reduce conidial killing by monocytes and  
263 Mo-DCs at 72 h pi (Figures 7D and 7E). These findings indicate that pDCs enhanced neutrophil  
264 fungicidal activity.

265 Neutrophils generate reactive oxygen species (ROS) via NADPH oxidase as a primary  
266 effector mechanism against *A. fumigatus* (Marciano et al., 2015). Neutrophil NADPH oxidase  
267 induces a regulated cell death process in *A. fumigatus* conidia (Shlezinger et al., 2017). To  
268 determine whether pDCs regulate the neutrophil oxidative burst in *A. fumigatus*-infected mice,  
269 we measured neutrophil ROS production in pDC-depleted mice. The ROS median fluorescence  
270 intensity in ROS<sup>+</sup> lung neutrophils isolated from pDC-depleted mice was significantly reduced  
271 compared to ROS<sup>+</sup> neutrophils isolated from littermate control mice at 72 h pi (Figure 7E and  
272 7F). These data show that lung pDCs regulate neutrophil ROS generation during *A. fumigatus*  
273 challenge.

274 **Discussion**

275 Humans maintain lifelong sterilizing immunity to inhaled mold conidia. Breaches in the  
276 respiratory innate immune system lead to mold pneumonia, a life-threatening disease in patients  
277 with functional or numeric deficits in myeloid cell function, particularly with the loss of the  
278 antifungal properties of neutrophils. In this study, we demonstrate a three-cell circuit that  
279 involves pDCs, monocytes and derivative Mo-DCs, and neutrophils to regulate sterilizing  
280 immunity against *Aspergillus* conidia. This circuit acts as a feedforward amplification  
281 mechanism, by coupling fungal recognition and fungus-induced inflammation to CXCR3  
282 signaling-dependent pDC recruitment in the lung. pDCs regulate neutrophil ROS induction and  
283 fungal killing to mediate sterilizing immunity at the respiratory barrier.

284 Our data demonstrate that conidial uptake by lung-infiltrating monocytes and Mo-DCs  
285 triggered Dectin-1- and CARD9-dependent production of CXCL9 and type I and type III  
286 interferon signaling-dependent production of CXCL10; the latter process was readily detectable  
287 in neutrophils as well. The relative contribution of CXCL9 and CXCL10 and potential molecular  
288 redundancy with regard to downstream CXCR3-dependent processes during fungal infection  
289 remains an open question for future studies. Prior studies identified a polymorphism in the  
290 *Cxcl10* gene as a risk factor for IA in allogeneic hematopoietic cell transplant patients (Fisher et  
291 al., 2017; Mezger et al., 2008). In this cohort, patients with IA had higher CXCL10 serum levels  
292 than controls that did not develop IA, consistent with the idea that pulmonary fungal infection  
293 induces CXCL10, similar to findings in mice in this work. Furthermore, the high-risk haplotype  
294 was associated with reduced *Cxcl10* mRNA expression by immature DCs (iDCs) co-cultured  
295 with *Aspergillus* germlings compared to wild-type iDCs (Mezger et al., 2008). Thus, human  
296 iDCs and murine lung Mo-DCs both responded to *A. fumigatus* challenge by transcribing *Cxcl10*

297 mRNA. Although this process is generally regulated by IFN signaling in both mammalian  
298 species (O'Connell et al., 2019; Ohmori et al., 1993), a recent study by Rivera and colleagues  
299 defined essential roles for type I and type III, but not type II, IFNs in murine host defense against  
300 *A. fumigatus* (Espinosa et al., 2017). One model to account for these findings is that an early  
301 wave of type I interferon signaling, detected as early as 6 h pi in the lung and produced primarily  
302 by CCR2<sup>+</sup> lung-infiltrating monocytes and Mo-DCs (Espinosa et al., 2017), may drive CXCL10  
303 release in the lung in a paracrine or autocrine manner, as observed in this study. In accordance  
304 with this model, CXCL10 lung levels that peak at 48 h pi are dependent on type I and type III  
305 IFN receptor signal transduction in the *Aspergillus*-infected murine lung.

306 Although IFN-dependent and -independent stimuli can induce CXCL9 during microbial  
307 infection (Forero et al., 2019; Groom and Luster, 2011), previous studies have not directly linked  
308 C-type lectin receptor signaling to fungus-induced CXCL9 production. In murine models of  
309 experimental cryptococcosis with a wild-type or a recombinant vaccine strain that expresses  
310 human IFN- $\gamma$  fungal infection led to lung CXCL9 and CXCL10 production, though the identity  
311 of chemokine-producing cells was not investigated (Hole et al., 2016; Yamamoto et al., 2014). In  
312 this model, *Card9*<sup>-/-</sup> mice had lower lung CXCL9 levels than control mice. This finding was  
313 attributed to reduced lung infiltration of IFN- $\gamma$ -producing NK and CD4<sup>+</sup> T cells because  
314 *Cryptococcus*-stimulated BM-DCs failed to produce either cytokine *in vitro* (Yamamoto et al.,  
315 2014). In contrast, splenic and central nervous system (CNS)-resident Mo-DCs produced copious  
316 levels of CXCL9 and CXCL10 during murine cerebral malaria (Hirako et al., 2016). Because a  
317 significant fraction of CXCL9<sup>+</sup>CXCL10<sup>+</sup> splenic Mo-DCs contained hemozoin, a malarial  
318 pigment, this study supported the idea that microbial uptake regulated CXCR3 ligand release  
319 either directly or indirectly in infected cells. The authors provided evidence for indirect CXCL9



320 and CXCL10 regulation since their secretion was highly dependent on intact IFN- $\gamma$  receptor  
321 signaling. In the case of respiratory *A. fumigatus* infection, the dual regulation of CXCL9 by  
322 Dectin-1/Card9 and CXCL10 by type I and type III IFN signaling indicates both direct and  
323 indirect regulation of distinct CXCR3 ligands by a pathogen-associated molecular pattern  
324 receptor and soluble type I and type III IFNs.

325 CXCR3 ligands have been studied extensively in the context of CD4<sup>+</sup> and CD8<sup>+</sup> T cell  
326 trafficking in peripheral lymphoid and non-lymphoid tissues, in part due to high CXCR3  
327 expression on effector and memory T cell subsets, in contrast to naïve T cells (Qin et al., 2011).  
328 In draining LNs, antigen-activated and transferred DCs express CXCL9 and CXCL10 and  
329 thereby regulate the frequency of IFN- $\gamma$ <sup>+</sup> CD4<sup>+</sup> T cells, linking the CXCR3 signaling axis to the  
330 formation of effector Th1 cells (Groom et al., 2012). CXCR3 facilitated the entry of effector T  
331 cells into otherwise restricted sites, exemplified by CXCR3<sup>+</sup> CD8<sup>+</sup> T cells infiltration of the CNS  
332 or genital tract during murine malaria, West Nile virus, or herpes simplex virus 2 infection  
333 (Hirako et al., 2016; Nakanishi et al., 2009; Thapa and Carr, 2009; Thapa et al., 2008). During  
334 bacterial infection, a study reported that CXCR3 signaling regulated neutrophil influx to the  
335 infected cecum and thus controlled *Salmonella* extra-intestinal dissemination (Chami et al.,  
336 2017). In rodent models of viral (e.g., influenza virus or coronavirus) or chemical acute  
337 respiratory distress syndrome, CXCL10<sup>+</sup> lung-infiltrating neutrophils and CXCL9<sup>+</sup> macrophages  
338 mediated the recruitment of tissue-destructive CXCR3<sup>+</sup> neutrophils; this pathologic process was  
339 ameliorated in *Cxcr3*<sup>-/-</sup> or *Cxcl10*<sup>-/-</sup> mice (Ichikawa et al., 2013). During respiratory fungal  
340 challenge, we did not observe CXCR3 expression on lung-infiltrating neutrophils and neutrophil  
341 recruitment was unaffected in *Cxcr3*<sup>-/-</sup> mice compared to control mice. In more recent work in  
342 the *Salmonella* model, infected splenic macrophages reside in T cell-sparse granulomas but are

343 surrounded by mononuclear phagocytes that release CXCL9 and CXCL10 to recruit antigen-  
344 specific CXCR3<sup>+</sup> Th1 cells for bacterial containment (Goldberg et al., 2018). Thus, CXCR3  
345 ligands target both innate and adaptive immune cells in a highly context-dependent manner; this  
346 process can result in microbial containment or microbe-elicited tissue damage.

347 pDCs originate in the bone marrow (BM), circulate in the blood, and traffic to lymphoid  
348 and nonlymphoid tissues under homeostatic and inflammatory conditions (Fujimura et al., 2015;  
349 Sozzani et al., 2010; Swiecki et al., 2017). However, the mechanism that couples microbial  
350 recognition to pDC accumulation at peripheral sites has remained poorly understood. During  
351 respiratory fungal infection, neither CCR2<sup>+</sup> monocytes nor CCR2<sup>-</sup> neutrophils had the capacity  
352 to respond to CXCR3 ligands because these cells do not express CXCR3. Thus, the recruitment  
353 of lung-infiltrating monocytes and pDCs occurs via a pathway that bifurcated after the initial  
354 CCR2-dependent egress from the bone marrow reservoir. Although the precise cues that regulate  
355 the CXCR3-independent entry of circulating monocytes into the fungus-infected lung remain  
356 unknown, integrin-mediated mechanisms enable monocytic influx into hepatic foci of *Listeria*  
357 *monocytogenes* during systemic infection (Shi et al., 2010).

358 During other types of lung infections, e.g. influenza and RSV, pDCs traffic to the lungs and  
359 draining LNs of mice (Langlois and Legge, 2010; Smit et al., 2006; Wang et al., 2006) via  
360 pathways that are distinct compared to conventional DCs (Sawai et al., 2013; Sozzani et al.,  
361 2010). For example, pDC LN trafficking during murine influenza is regulated primarily by L-  
362 selectin (CD62L), with contributions from CXCR3 and CXCR4. Further pDC positioning within  
363 the LN is mediated by CCR7 and the release of pDC-derived CXCR3 ligands to enable the  
364 formation of clusters of pDCs that interact and activate cells of the adaptive immune system  
365 (Krug et al., 2002). In contrast, we did not observe pDC-dependent release of CXCL9 and

366 CXCL10 in the *Aspergillus*-infected lung, consistent with the model that pDC recruitment cues  
367 depends on heterologous myeloid cells. Beyond CXCR3, L-selectin, and CXCR4, the E-selectin  
368 ligands,  $\beta 1$  and  $\beta 2$  integrins, CCR5, CCR7, and the chemerin receptor ChemR23 have been  
369 implicated in pDC trafficking during states of inflammation (Diacovo et al., 2005; Kohrgruber et  
370 al., 2004; Sozzani et al., 2010; Vanbervliet et al., 2003; Wendland et al., 2007), though it has  
371 remained unclear how individual cues cooperate to guide distinct pDC trafficking steps, and  
372 what the relative strength of individual cues is for defined tissue destinations and types of  
373 inflammatory stimuli. The sequential requirements for CCR2 and CXCR3 signaling in distinct  
374 pDC trafficking steps during respiratory *A. fumigatus* infection provides a combinatorial model,  
375 in which a more general cue for myeloid cell bone marrow egress (i.e., CCR2 that acts on  
376 monocytes and pDCs) is combined with a more specific, pDC-targeted cue (i.e., CXCR3). The  
377 latter cue emanates primarily from CCR2<sup>+</sup> Mo-DCs that were not equipped to control fungal  
378 tissue invasion or license the full spectrum of neutrophil antifungal activity per se.

379 pDCs were functionally characterized as mediators of antiviral defense (Assil et al., 2019;  
380 Swiecki and Colonna, 2010). Recent studies have expanded their role to anti-bacterial (e.g.,  
381 *Legionella pneumophila*, *Chlamydia pneumoniae*, *Staphylococcus aureus*) (Ang et al., 2010;  
382 Crother et al., 2012; Parcina et al., 2013) and to anti-fungal defense (Ang et al., 2010; Hole et al.,  
383 2016). pDC-mediated antiviral responses are stimulated upon physical contact with infected cells  
384 (Assil et al., 2019). pDCs adhere to infected cells via  $\alpha_L\beta_2$  integrin/ICAM-1 interactions, during  
385 which viral RNA is transferred to pDCs, leading to IFN production via the nucleic acid sensor  
386 TLR7. This process activates type I IFN-dependent antiviral programs in infected tissues. During  
387 respiratory fungal infection, lung-infiltrating pDCs do not interact directly with *Aspergillus*  
388 conidia, but instead regulate neutrophils ROS induction. Our study does not exclude the

389 possibility that *Aspergillus*- or host cell-derived nucleic acids activate pDCs in the lung in situ.  
390 Prior work has demonstrated that *Aspergillus*-derived unmethylated CpG sequences can activate  
391 TLR9 signaling *in vitro* (Herbst et al., 2015; Ramirez-Ortiz et al., 2008). Alternatively, pDCs  
392 may recognize fungal Dectin-2/CLEC4N or Dectin-3/CLEC4E ligands (Loures et al., 2015;  
393 Maldonado and Fitzgerald-Bocarsly, 2017; Preite et al., 2018). In patients with systemic lupus  
394 erythematosus, neutrophil-derived extracellular traps (NETs) activate pDCs by releasing DNA-  
395 protein complexes, resulting in TLR9-dependent release of pathologic type I IFNs during  
396 autoimmunity (Garcia-Romo et al., 2011; Lande et al., 2011). While *A. fumigatus* conidia are  
397 poor inducers of NETosis, products of germination, specifically hyphae that are too large to be  
398 phagocytosed, are potent stimuli for NETosis (Bianchi et al., 2009; Bruns et al., 2010; Gibrat et  
399 al., 1989). Thus, pDC activation in the fungus-infected lung likely occurs by multiple, yet  
400 undefined mechanisms.

401 The molecular basis for pDC-neutrophil crosstalk represents an important area of future  
402 investigation. Two non-exclusive models are likely operative. First, pDCs may form direct  
403 contact with neutrophils after arriving at the site of infection. In this model, an individual pDC  
404 would interact with many neutrophils since neutrophils are ~100 times more prevalent in the  
405 lung at 48 h pi compared to pDCs. The relative paucity of pDCs, compared to other infiltrating  
406 myeloid cells (i.e., neutrophils, Mo-DCs), makes it unlikely that direct pDC-mediated  
407 fungistasis, observed at high effector to target cell ratios in the test tube, is physiologically  
408 significant in the fungus-infected lung (Loures et al., 2015; Maldonado and Fitzgerald-Bocarsly,  
409 2017). Second, either fungus-triggered or host cell-triggered pDC activation may result in the  
410 release of soluble mediators that boost neutrophil fungicidal activity. Previous studies have  
411 identified GM-CSF, type I IFN, and type III IFN as important regulators of neutrophil NADPH

412 oxidase activity during respiratory *A. fumigatus* and *B. dermatiditis* challenge (Espinosa et al.,  
413 2017; Hernandez-Santos et al., 2018; Kasahara et al., 2016). The development of pDC-restricted  
414 Cre-lox candidate gene deletion strategies is essential to test these candidates formally.

415 In this study, we uncover essential functions for pDCs in innate antifungal defense that  
416 cannot be compensated by the presence of other myeloid cells, including neutrophils, monocytes,  
417 and Mo-DCs. In fact, fungus-engaged Mo-DCs and neutrophils harness pDCs as a feedforward  
418 amplification mechanism to enhance innate antifungal activity in the lung by coupling fungal  
419 recognition and fungus-induced inflammation to the CXCR3 signaling-dependent recruitment of  
420 pDCs into the fungus-infected lung. In the lung pDCs regulate neutrophil ROS induction, a  
421 process that induces a regulated cell death process in mold conidia (Shlezinger et al., 2017). Our  
422 findings indicate that pDC recovery following administration of chemotherapy and in bone  
423 marrow transplant recipients may represent an important variable that affects infectious  
424 susceptibility not just to viral, but also to fungal pathogens. Recent studies in bone marrow  
425 transplant patients indicate that donor pDC reconstitution in the recipient is associated with  
426 favorable clinical outcomes, including non-relapse mortality from unrelated donors (Goncalves  
427 et al., 2015; Waller et al., 2019; Waller et al., 2014). These data raise the possibility that pDC  
428 recovery in bone marrow transplant patients may be important for controlling systemic fungal  
429 infections. Further studies to decipher the mechanistic role of pDCs in antifungal immunity is  
430 likely to inform strategies to harness these cells for prophylactic or therapeutic gain in vulnerable  
431 patient populations.

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443 Conceptualization, T.M.H., Y.G. and S.K.; Methodology, T.M.H., Y.G. and S.K.; Investigation,  
444 Y.G., S.K. A.J., B.Z., M.A.A., K.A.M.M, V.E., and A.R.; Writing – Original Draft, Y.G. and  
445 T.M.H.; Writing – Review & Editing, Y.G. and T.M.H.; Funding Acquisition, T.M.H.;  
446 Resources, A.D.L., V.E., and A.R.

447 **DECLARATION OF INTERESTS**

448 The authors declare no competing interests.

449 **Figure Legends.**

450 **Figure 1. CCR2<sup>+</sup> Mo-DCs and neutrophils produce CXCL9 and CXCL10 during A.**

451 ***fumigatus* challenge.**

452 (A-C) Lung CXCL9 and CXCL10 levels in (A) C57BL/6 mice (n = 5) at 0-72 h pi or (B-C) in  
453 DT-treated CCR2-DTR<sup>+/-</sup> and Non-Tg (CCR2-DTR<sup>-/-</sup>) littermates (n = 5) at 48 h pi with  $3 \times 10^7$   
454 CEA10 conidia.

455 (D) Representative plots of RFP (CXCL9) and BFP (CXCL10) expression in indicated lung  
456 leukocytes isolated from Rex3 Tg → C57BL/6.SJL BM chimeric mice at baseline (naïve, top  
457 row) and 48 h pi with  $3 \times 10^7$  CEA10 conidia (infected, bottom row). The blue and purple gates  
458 indicate the frequency of BFP<sup>+</sup> (CXCL9<sup>+</sup>) and BFP<sup>+</sup>RFP<sup>+</sup> (CXCL9<sup>+</sup> CXCL10<sup>+</sup>) cells,  
459 respectively.

460 (E) The graphs indicate the frequency of CXCL9<sup>-</sup> CXCL10<sup>+</sup> and CXCL9<sup>+</sup> CXCL10<sup>+</sup> neutrophils,  
461 monocytes, Mo-DCs, and pDCs and (F) the cellular identity of all CXCL9<sup>-</sup> CXCL10<sup>+</sup> (top) and  
462 CXCL9<sup>+</sup> CXCL10<sup>+</sup> lung leukocytes (bottom) at 48 h pi.

463 (G-H) Lung CXCL9 and CXCL10 levels in DT-treated ROSA26-iDTR<sup>Mrp8-Cre</sup> → C57BL/6.SJL  
464 (Neutrophil Deleter) or non-Cre iDTR littermates → C57BL/6.SJL (Control) BM chimeric  
465 mice (n = 10) at 48 h pi with  $3-4 \times 10^7$  heat-killed swollen CEA10 conidia. Data from 2  
466 independent experiments were pooled.

467 (A- C, G, H) Dots represent individual mice and data were presented as mean ± SEM. Statistical  
468 analysis: (A) Kruskal-Wallis test, timepoints compared to t = 0 h, (B, C, G, H) Mann-Whitney  
469 test. See also Figure S1.

470 **Figure 2. Fungal Uptake and Dectin-1/Card9 and IFN signaling regulate lung CXCL9 and**  
471 **CXCL10 levels during *A. fumigatus* infection.**

472 (A) Representative flow cytometry plots and bar graphs (B-E) that indicate the frequency of  
473 RFP<sup>+</sup> (CXCL9<sup>+</sup>; red bar in B-C), RFP<sup>-</sup> (CXCL9<sup>-</sup>; gray bar in B-C), BFP<sup>+</sup> (CXCL10<sup>+</sup>; blue bar, in  
474 D-E), and BFP<sup>-</sup> (CXCL10<sup>-</sup>; gray bar in D-E) bystander and fungus-engaged leukocytes isolated  
475 from (A, left column) naïve or (A, middle and right column, B-E) infected Rex3 Tg →  
476 C57BL/6.SJL BM chimeric mice (n = 7) with  $3 \times 10^7$  AF633-labeled CEA10 conidia. The solid  
477 black gates in (A) indicate bystander neutrophils, while the solid blue gates indicate fungus-  
478 engaged leukocytes. The dashed line in the black and blue gate indicate CXCL9<sup>+</sup> and CXCL9<sup>-</sup>  
479 (top quadrants) leukocytes, and CXCL10<sup>+</sup> and CXCL10<sup>-</sup> (bottom quadrants) leukocytes.  
480 (F) Lung CXCL9 and (G) CXCL10 levels in naïve wild-type (WT, n = 5) and in WT (n = 10),  
481 *Clec7a*<sup>-/-</sup> (n = 8), *Card9*<sup>-/-</sup> (n = 7), *Ifnar1*<sup>-/-</sup> (n = 9), and *Ifnlr*<sup>-/-</sup> (n = 9) mice 48 h pi with  $3 \times 10^7$   
482 CEA10 conidia. Data were pooled from 2 independent experiments.  
483 (B-G) Dots represent individual mice and data are presented as mean ± SEM. Statistical analysis:  
484 Mann-Whitney test. See also Figure S2.



485 **Figure 3. CXCR3 is critical for anti-*Aspergillus* defense.**

486 (A) Kaplan-Meier survival of C57BL/6 (n = 37) and *Cxcr3*<sup>-/-</sup> (n = 35) mice challenged with 4-8 ×

487 10<sup>7</sup> CEA10 conidia. Data from 3 experiments were pooled.

488 (B) Normalized lung fungal burden, (C) bronchoalveolar lavage fluid (BAL) LDH level, and (D)

489 BAL albumin levels in C57BL/6 and *Cxcr3*<sup>-/-</sup> mice 48 h pi with 3 × 10<sup>7</sup> CEA10 conidia. (A-D)

490 Dots represent individual mice and data were pooled from 2-4 experiments and presented as

491 mean ± SEM. Statistical analysis: Mann-Whitney test. See also Figure S3.

492 **Figure 4. CXCR3<sup>+</sup> pDCs traffic to *A. fumigatus*-infected lungs.**

493 (A) CXCR3 surface expression in BM (top row) and lung (bottom row) leukocytes isolated from

494 WT (black lines) or *Cxcr3*<sup>-/-</sup> mice (purple lines).

495 (B) Lung (blue filled dots) and BM (open black dots) pDC numbers at baseline and indicated

496 times pi with  $3 \times 10^7$  CEA10 conidia (n = 5).

497 (C) Lung pDC numbers in WT (open black dots) and *Cxcr3*<sup>-/-</sup> mice (open purple dots) at 72 h pi

498 (n = 10).

499 (D) CCR2 surface expression in BM and lung pDCs in WT (black lines) or *Ccr2*<sup>-/-</sup> mice (green

500 lines).

501 (E) Lung pDC numbers in WT (open black dots) and *Ccr2*<sup>-/-</sup> mice (open green dots) at 72 h pi (n

502 = 10).

503 (B, C, E) Data from 2-3 experiments were pooled and expressed as mean  $\pm$  SEM. Statistical

504 analysis: Mann-Whitney test. See also Figure S4.

505 **Figure 5. Sequential CCR2- and CXCR3-dependent signals mediate lung pDC recruitment.**

506 (A) Experimental scheme to generate mixed bone marrow chimeric mice and compare the

507 trafficking of *Cxcr3*<sup>-/-</sup>, *Ccr2*<sup>-/-</sup>, and WT pDCs during *A. fumigatus* infection.

508 (B, C) Relative frequencies of (B) *Cxcr3*<sup>-/-</sup> (open purple bars) and *Cxcr3*<sup>+/+</sup> (WT, open black

509 bars) and (C) *Ccr2*<sup>-/-</sup> (open green bars) and *Ccr2*<sup>+/+</sup> (WT, open black bars) pDCs in the BM,

510 blood, and lung of mixed BM chimeric mice 72 h pi. Data from 2-3 experiments were pooled

511 and expressed as mean ± SEM. Statistical analysis: Mann-Whitney test. See also Figure S5.

512 **Figure 6. pDCs are critical for anti-*Aspergillus* defense.**

513 (A) Representative flow cytometry plots of B220<sup>+</sup>Siglec-H<sup>+</sup> pDCs and (B) lung pDC, (C) lung  
514 monocyte, (D) lung Mo-DC, and (E) lung neutrophil numbers in DT-treated pDC Depleter mice  
515 (BDCA2-DTR; open red symbols) and non-Tg littermate controls (open black symbols) at 72 h  
516 pi with  $3 \times 10^7$  CEA10 conidia.

517 (F) Kaplan Meier survival of DT-treated pDC Depleter (n = 20) and non-Tg littermate control  
518 mice (n = 19) infected with  $3-6 \times 10^7$  CEA10 conidia.

519 (G) BAL LDH levels and (H) fungal burden of DT-treated pDC Depleter (open red symbols; n =  
520 6-18) or non-Tg littermates (Control, open black symbols; n = 6-17) at 72 h pi with  $3 \times 10^7$   
521 CEA10 conidia.

522 (I) Lung fungal burden at 72 h pi with  $3 \times 10^7$  Af293 conidia.

523 (J) Lung histopathology (top row, hematoxylin and eosin stain, scale bar 800 $\mu$ m; middle row,  
524 Gomori methenamine silver stain, scale bar 800 $\mu$ m; bottom row, GMS, scale bar 200 $\mu$ m) of DT-  
525 treated pDC Depleter (right column; n = 6) or non-Tg littermates (Control, left column; n = 6) at  
526 72 h pi with  $3 \times 10^7$  CEA10 conidia.

527 (K) Lung CXCL9 and (L) lung CXCL10 levels in DT-treated pDC Depleter mice (red symbols)  
528 and non-Tg littermate controls (black symbols) at 72 h pi with  $3 \times 10^7$  CEA10 conidia.

529 (B- L) Data were pooled from 2-3 independent experiments and expressed as mean  $\pm$  SEM.

530 Statistical analysis: Mann-Whitney test. See also Figure S6.

531 **Figure 7. Lung pDCs enhance neutrophil fungicidal activity.**

532 (A) Schematic of FLARE strain and changes in fluorescence emission following fungal uptake  
533 and killing by host leukocytes.

534 (B) AF633 fluorescence intensity in indicated lung leukocytes 72 h pi with FLARE (blue line) or  
535 AF633-unlabeled conidia.

536 (C) Representative plots that display dsRed and AF633 fluorescence intensity of lung neutrophils  
537 in DT-treated pDC Depletor (right panel) and non-Tg littermates (left panel) 72 h pi with  $3 \times 10^7$   
538 Af293 FLARE conidia. R1 denotes neutrophils that contain live conidia, R2 denotes neutrophils  
539 that contain killed conidia.

540 (D and E) The plots show neutrophil, monocyte, and Mo-DC (D) conidial uptake ( $R1 + R2$ )  $\pm$   
541 SEM and (E) conidial viability ( $R1 / (R1 + R2)$ )  $\pm$  SEM in indicated lung leukocytes isolated from  
542 DT-treated pDC Depletor (red symbols) and non-Tg littermates (black symbols) 72 h pi with  $3 \times$   
543  $10^7$  FLARE conidia.

544 (F) Representative plot and (G) mean  $\pm$  SEM neutrophil ROS production in cells isolated from  
545 DT-treated pDC Depletor (right panel) and non-Tg littermates (left panel) 72 h pi with  $3 \times 10^7$   
546 CEA10 conidia.

547 (C-E) Data from 2 experiments were pooled. (F, G) Data are representative of 2 experiments. (D,  
548 E, G) Dots represent individual mice and data are expressed as mean  $\pm$  SEM. Statistical analysis:  
549 Mann-Whitney test. See also Figure S7.

550 **STAR★METHODS**

551 **KEY RESOURCES TABLE**

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Antibodies		
APC Mouse anti-Mouse CD45.1 (clone A20)	BD Bioscience	Cat#558701; RRID: AB_1645214
PerCP-Cy <sup>TM</sup> 5.5 Mouse anti-Mouse CD45.2 (clone 104)	BD Bioscience	Cat#552950; RRID: AB_394528
APC-Cy <sup>TM</sup> 7 Rat anti-Mouse CD45 (clone 30-F11)	BD Bioscience	Cat#557659; RRID: AB_396774
PerCP-Cy <sup>TM</sup> 5.5 Rat anti-CD11b (clone M1/70)	BD Bioscience	Cat#550993; RRID: AB_394002
PE-Cy <sup>TM</sup> 7 Hamster anti-Mouse CD11c (clone HL3)	BD Bioscience	Cat#558079; RRID: AB_647251
BV 605 <sup>TM</sup> anti-mouse CD11c Antibody (clone N418)	BioLegend	Cat#117334; RRID: AB_117334
PE-Cy <sup>TM</sup> 7 Rat Anti-Mouse Ly-6C (clone AL-21)	BD Bioscience	Cat#560593; RRID: AB_1727557
FITC Rat anti-Mouse Ly-6G (clone 1A8)	BD Bioscience	Cat#551460; RRID: AB_394207
FITC Rat anti-Mouse CD45R/B220 (clone RA3-6B2)	BD Bioscience	Cat#553087; RRID: AB_394617
PE anti-mouse CD183 Antibody (clone CXCR3-173)	BioLegend	Cat#126505; RRID: AB_1027656
BV421 Rat Anti-Mouse Siglec-F (clone E50-2440)	BD Bioscience	Cat#562681; RRID: AB_2722581
BV605 Rat Anti-Mouse Siglec-H (clone 440c)	BD Bioscience	Cat#747673; RRID: AB_2744234
Purified Rat Anti-Mouse CD16/CD32 (clone 2.4G2)	BD Bioscience	Cat#553142; RRID: AB_394657
eFluor 450 NK1.1 Monoclonal Antibody (clone PK136)	eBioscience	Cat#48-5941-80; RRID: AB_2043878
eFluor 450 CD19 Monoclonal Antibody (clone eBio1D3)	eBioscience	Cat#48-0193-82; RRID: AB_2734905
Alexa Fluor 700, I-A/I-E Monoclonal Antibody (clone M5/114.15.2)	eBioscience	Cat#56-53-21; RRID: AB_494009
FITC Mouse IgG1 kappa Isotype Control	eBioscience	Cat#11-4714-42; RRID: AB_10596964
PE Rat IgG2a kappa Isotype Control	eBioscience	Cat#12-4321-42; RRID: AB_1518773
PerCP-Cyanine5.5 IgG Isotype Control	eBioscience	Cat#45-4888-80; RRID: AB_906260
APC Rat IgG2b kappa Isotype Control	eBioscience	Cat#17-4031-82; RRID: AB_470176
APC-eFluor 780 Rat IgG2b kappa Isotype Control	eBioscience	Cat#47-4031-80; RRID: AB_1272021

Alexa Fluor 700 Rat IgG2b kappa Isotype Control	eBioscience	Cat#56-4031-80; RRID: AB_837123
PE-Cyanine7 Rat IgG2a kappa Isotype Control	eBioscience	Cat#25-4321-82; RRID: AB_470200
eFluor 450 Rat IgG1 kappa Isotype Control	eBioscience	Cat#48-4301-82; RRID: AB_1271984
Cat#48-4301-82; RRID: AB_1271984	BioLegend	Cat#400649; RRID: N/A
Bacterial and Virus Strains		
AF293	Fungal genetics stock center	#A1100
AF293 ds-Red	(Jhingran et al., 2012)	N/A
CEA10 (also known as CBS144.89)	(Girardin et al., 1993)	Received from Robert A. Cramer
Chemicals, Peptides, and Recombinant Proteins		
Alexa Fluor 633 succinimidyl ester	Invitrogen	Cat#S12375
Collagenase IV	ThermoFisher Scientific	Cat#LS004189
RPMI-1640	RPMI-1640	21870092
Enrofloxacin	Bayer	Baytril 100
Voriconazole	Pfizer	N/A
Tween-20	Sigma	P9416
Protease Inhibitor Cocktail	Roche	Cat#11697498001
DNase I, Grade II	Sigma	Cat#10104159001
BCG albumin assay kit	Sigma	MAK124
isoflurane	Henry Schein Animal Health	Cat#29405
Diphtheria toxin (DT)	List Biological Laboratories	Cat#150
Paraformaldehyde, 32% Solution	ThermoFisher Scientific	Cat#50-980-495
CM-H <sub>2</sub> DCFDA	ThermoFisher Scientific	Cat#C6827
10× HBSS	ThermoFisher Scientific	14065056
TRIzol-LS	Invitrogen	10296028
Mouse CXCL9/MIG DuoSet ELISA	R&D systems	DY492
Mouse CXCL10/IP-10/CRG-2 DuoSet ELISA	R&D systems	DY466
CytoTox96 non-radioactive cytotoxicity assay kit	Promega	G1780
High Capacity RNA-to-cDNA Kit	Appliedbiosystems	4387406
Ribosomal RNA Control Reagents	Appliedbiosystems	4308329
<i>Cxcl9</i> ASSAY ID: Mm01345159_m1	Thermo Fisher	4448892
<i>Cxcl10</i> ASSAY ID: Mm00445235_m1	Thermo Fisher	4453320
Experimental Models: Organisms/Strains		
<i>Cxcr3</i> <sup>-/-</sup>	The Jackson Laboratory	JAX: 005796
BDCA2-DTR	The Jackson Laboratory	JAX: 014176
<i>Clec7a</i> <sup>-/-</sup>	(Saijo et al., 2007)	N/A
<i>Card9</i> <sup>-/-</sup>	(Hsu et al., 2007)	JAX:028652
<i>Ccr2</i> <sup>-/-</sup>	The Jackson Laboratory	JAX: 004999

<i>Ifnar1</i> <sup>-/-</sup>	The Jackson Laboratory	JAX: 32045
<i>Ifnlr</i> <sup>-/-</sup>	(Lin et al., 2016)	N/A
C57BL/6	The Jackson Laboratory	JAX: 000664
C57BL/6.SJL	Charles River Laboratories	Stock No. 564
<i>Rag2</i> <sup>-/-</sup> <i>Il2rg</i> <sup>-/-</sup>	Taconic	JAX: 4111
MRP8-Cre-IRES/GFP	The Jackson Laboratory	JAX: 021614
Oct-4/rtTA	The Jackson Laboratory	Oct-4/rtTA
CCR2-DTR	(Hohl et al., 2009)	N/A
REX3 Tg	(Groom et al., 2012)	N/A
Software and Algorithms		
Prism 8	Prism 8	N/A
Flow Jo 9.9.6	Flow Jo 9.9.6	N/A

552

## 553 RESOURCE AVAILABILITY

554 Further information and requests for resources or reagents should be directed to the Lead

555 Contact, Tobias M. Hohl (hohlt@mskcc.org).

## 556 Materials Availability

557 This study did not generate new unique reagents.

## 558 Data and Code Availability

559 This study did not generate or analyze new datasets or codes.

## 560 EXPERIMENTAL MODEL AND SUBJECT DETAILS

### 561 Mice

562 *Cxcr3*<sup>-/-</sup>, C57BL/6 (CD45.2<sup>+/+</sup>), BDCA2-DTR mice were purchased from Jackson Laboratories

563 (JAX: 014176). *Rag2*<sup>-/-</sup>*Il2rg*<sup>-/-</sup> mice (Stock No. 4111) were purchased from Taconic. *Ccr2*<sup>-/-</sup>

564 (JAX: 004999) (Serbina and Pamer, 2006), *Ifnar1*<sup>-/-</sup> (JAX: 32045) (Jia et al., 2009), and *Ifnlr*<sup>-/-</sup>

565 (Lin et al., 2016) mice were provided by Dr. Eric Pamer (University of Chicago) and Dr. Sergei

566 Kotenko (Rutgers), respectively. Bones from REX3 Tg (CXCL9-Red Red fluorescent



567 protein/CXCL10-Blue fluorescent protein reporter) mice (Groom et al., 2012) were provided by  
568 Dr. Andrew Luster (Massachusetts General Hospital). *Clec7a*<sup>-/-</sup> mice (Saijo et al., 2007) were  
569 provided by Dr. Shinobu Saijo (University of Tokyo). *Card9*<sup>-/-</sup> mice (Hsu et al., 2007b) were  
570 provided by Dr. Xin Lin (Tsinghua University). MRP8-Cre-IRES/GFP and Oct-4/rtTA mice  
571 were crossed to generate ROSA26-iDTR<sup>Mrp8-Cre</sup> mice. C57BL/6 and C57BL/6.SJL mice were  
572 crossed to generate CD45.1<sup>+</sup>CD45.2<sup>+</sup> recipient mice for mixed BM chimeras. CCR2-DTR<sup>+/-</sup>  
573 (Hohl et al., 2009) and non-transgenic littermates on the *Rag2*<sup>-/-</sup>*Il2rg*<sup>-/-</sup> background were  
574 maintained on amoxicillin- and Vitamin E-containing chow. All experiments with CCR2-DTR,  
575 CCR2-DTR *Rag2*<sup>-/-</sup>*Il2rg*<sup>-/-</sup> and BDCA2-DTR mice used co-housed littermate controls. For  
576 experiments in which the breeding strategy did not yield littermate controls, gene-knockout mice  
577 were co-housed with C57BL/6 mice for 14 days prior to infection, whenever possible. All mouse  
578 strains were bred and housed in the MSKCC or Rutgers Research Animal Resource Center under  
579 specific pathogen-free conditions. All animal experiments were conducted with sex- and age-  
580 matched mice and performed with MSKCC or Rutgers Institutional Animal Care and Use  
581 Committee approval. Animal studies complied with all applicable provisions established by the  
582 Animal Welfare Act and the Public Health Services Policy on the Humane Care and Use of  
583 Laboratory Animals.

#### 584 **Generation of Bone Marrow Chimeric Mice**

585 For single BM chimeras, CD45.1<sup>+</sup> C57BL/6.SJL recipients were lethally irradiated (900cG),  
586 reconstituted with either  $2-5 \times 10^6$  CD45.2<sup>+</sup> Rex3-Tg, CD45.2<sup>+</sup> ROSA26-iDTR<sup>Mrp8-Cre</sup>, or  
587 CD45.2<sup>+</sup> non-Cre iDTR littermates BM cells. For mixed BM chimeras, CD45.1<sup>+</sup>CD45.2<sup>+</sup>  
588 recipients were irradiated and reconstituted with a 1:1 mixture of CD45.1<sup>+</sup> C57BL/6.SJL and  
589 CD45.2<sup>+</sup> *Cxcr3*<sup>-/-</sup> or CD45.2<sup>+</sup> *Ccr2*<sup>-/-</sup> BM cells. After BM transplantation, recipient mice received

590 400 µg/ml enrofloxacin in the drinking water for 21 days to prevent bacterial infections and  
591 rested for 6-8 weeks prior to experimental use.

## 592 ***Aspergillus fumigatus* culture and Infection Model**

593 *A. fumigatus* Af293, Af293-dsRed (Jhingran et al., 2012), and CEA10 (Girardin et al., 1993)  
594 strains were cultured on glucose minimal medium slants at 37°C for 4-7 days prior to harvesting  
595 conidia for experimental use. To generate FLARE conidia, briefly,  $7 \times 10^8$  Af293-dsRed conidia  
596 were rotated in 10 µg/ml Biotin XX, SSE in 1 ml of 50 mM carbonate buffer (pH 8.3) for 2 hr at  
597 4 °C, incubated with 20 µg/ml Alexa Fluor 633 succinimidyl ester at 37 °C for 1 h, resuspended  
598 in PBS and 0.025% Tween 20 for use within 24 hr (Heung et al., 2015; Jhingran et al., 2016;  
599 Jhingran et al., 2012). To generate morphologically uniform heat-killed swollen conidia,  
600  $5 \times 10^6$ /ml conidia were incubated at 37° C for 14 hours in RPMI-1640 and 0.5 µg/ml  
601 voriconazole and heat killed at 100 °C for 30 minutes (Hohl et al., 2005). To infect mice with 30-  
602 60 million live or heat-killed *A. fumigatus* cells, conidia were resuspended in PBS, 0.025%  
603 Tween-20 at a concentration of  $0.6-1.2 \times 10^9$  cells and 50 µl of cell suspension was administered  
604 via the intranasal route to mice anesthetized by isoflurane inhalation.

## 605 **EXPERIMENTAL DETAILS**

### 606 **Analysis of *in vivo* and *in vitro* conidial uptake and killing**

607 To analyze of conidia uptake and killing, FLARE conidia were used to infect mice (*in vivo*) or  
608 co-culture with BM leukocyte (*in vitro*). In data analyses for a given leukocyte subset, conidial  
609 uptake refers to the frequency of fungus-engaged leukocytes, i.e. the sum of dsRed<sup>+</sup>AF633<sup>+</sup> and  
610 dsRed<sup>-</sup>AF633<sup>+</sup> leukocytes. Conidial viability within a specific leukocyte subset refers to the  
611 frequency of leukocytes that contain live conidia (dsRed<sup>+</sup>AF633<sup>+</sup>) divided by the frequency of  
612 all fungus-engaged leukocytes (dsRed<sup>+</sup>AF633<sup>+</sup> and dsRed<sup>-</sup>AF633<sup>+</sup>).

613 ***In vivo* Cell Depletion**

614 To ablate specific cells, CCR2-DTR, CCR2-DTR, *Rag2<sup>-/-</sup>Il2rg<sup>-/-</sup>*, ROSA26-iDTR<sup>Mrp8-Cre</sup>,  
615 BDCA2-DTR, and non-transgenic littermate controls were injected i.p. with 10 ng/g body weight  
616 DT on Day -1, Day 0, and Day +2 pi (Espinosa et al., 2017; Swiecki et al., 2010), unless noted  
617 otherwise.

618 **Analysis of Infected Mice**

619 Single cell lung suspensions were prepared for flow cytometry as described in (Hohl et al.,  
620 2009), with minor modifications. Briefly, perfused murine lungs were placed in a gentle  
621 MACS™ C tube and mechanically homogenized in 5 ml RPMI-1640, 10% FBS, and 0.1 mg/ml  
622 DNase using a gentle MACS™ Octo Dissociator (Miltenyi Biotec) in the absence of  
623 collagenase. Lung cell suspensions were lysed of RBCs, enumerated, and stained with  
624 fluorophore-conjugated antibodies prior to flow cytometric analysis on a BD LSR II or flow  
625 cytometric sorting on a BD Aria, flow plot analysis was performed using FlowJo v.9.6.6  
626 software.

627 Neutrophils were identified as CD45<sup>+</sup> CD11b<sup>+</sup> Ly6C<sup>lo</sup> Ly6G<sup>+</sup> cells, inflammatory monocytes  
628 as CD45<sup>+</sup> CD11b<sup>+</sup> CD11c<sup>-</sup> Ly6G<sup>-</sup> Ly6C<sup>hi</sup> cells, Mo-DCs as CD45<sup>+</sup> CD11b<sup>+</sup> CD11c<sup>+</sup> Ly6G<sup>-</sup>  
629 Ly6C<sup>hi</sup> MHC class II<sup>+</sup> cells, and pDCs as CD45<sup>+</sup> CD11c<sup>int</sup> SiglecF<sup>-</sup> CD19<sup>-</sup> NK1.1<sup>-</sup> CD11b<sup>-</sup>  
630 B220<sup>+</sup> SiglecH<sup>+</sup> cells.

631 To analyze the lung fungal burden, perfused murine lungs were homogenized using a PowerGen  
632 125 homogenizer (Fisher) in 2 mL PBS, 0.025% Tween-20, and plated on Sabouraud dextrose  
633 agar. To analyze cytokine levels by ELISA, whole lungs were weighed and mechanically  
634 homogenized in 2 mL PBS containing protease inhibitor. To analyze cytokine levels by qRT-  
635 PCR, total RNA from cells was extracted with TRIzol (Invitrogen). One to two micrograms of

636 total RNA were reverse-transcribed using High-Capacity cDNA Reverse Transcription Kit  
637 (Applied Biosystems). TaqMan Fast Universal Master Mix (2×), TaqMan probes (Applied  
638 Biosystems) for each gene were used and normalized to glyceraldehyde-3-phosphate  
639 dehydrogenase. Gene expression was calculated using the  $\Delta\Delta C_t$  method relative to the naïve  
640 sample. For histology, perfused lungs were fixed in 4% paraformaldehyde, embedded in paraffin,  
641 sectioned in 4  $\mu\text{m}$  slices, stained with hematoxylin and eosin (H&E) or modified Gomori  
642 methenamine silver (GMS), and digitally scanned using a Zeiss Mirax Desk Scanner. Images  
643 were captured from whole slide images, acquired with an Aperio ScanScope (Aperio  
644 Technologies) using 5× and 20× objectives at the Molecular Cytology Core Facility (MSKCC).  
645 BAL LDH and albumin levels were measured with a CytoTox96 non-radioactive cytotoxicity  
646 assay kit and a BCG albumin assay kit, respectively.

#### 647 **Reactive Oxygen Production**

648 Intracellular ROS levels were measured in cells using CM-H2DCFDA [5-(and 6-) chloromethyl-  
649 2,7-dichlorodihydrofluorescein diacetate, acetyl ester] as described in (Espinosa et al., 2017;  
650 Hackstein et al., 2012). Briefly, single cell lung suspensions were incubated with 1  $\mu\text{M}$  CM-  
651 H2DCFDA in Hanks' balanced salt solution at 37° C for 45 min according to manufacturer's  
652 instruction, and analyzed by flow cytometry.

#### 653 **QUANTIFICATION AND STATISTICAL ANALYSIS**

654 Data are representative of at least 2 independent experiments, as indicated. All results are  
655 expressed as mean ( $\pm$  SEM), unless stated otherwise. The Mann-Whitney test was used for  
656 comparisons of two groups, unless noted otherwise. The Kruskal-Wallis test was used for multi-  
657 group comparisons, unless noted otherwise. Survival data was analyzed by long-rank test. All  
658 statistical analyses were performed with GraphPad Prism software, v8.2.0.

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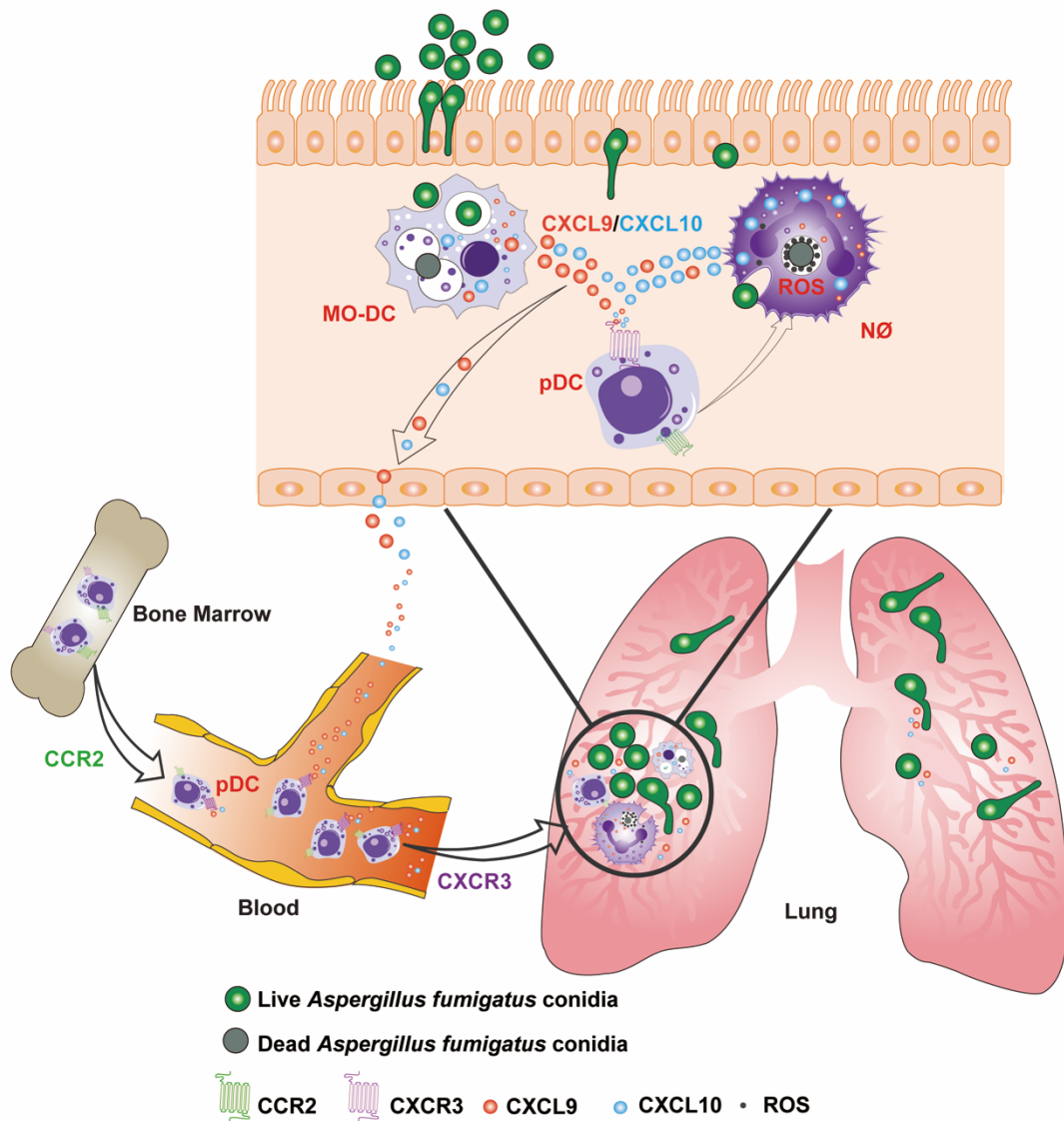
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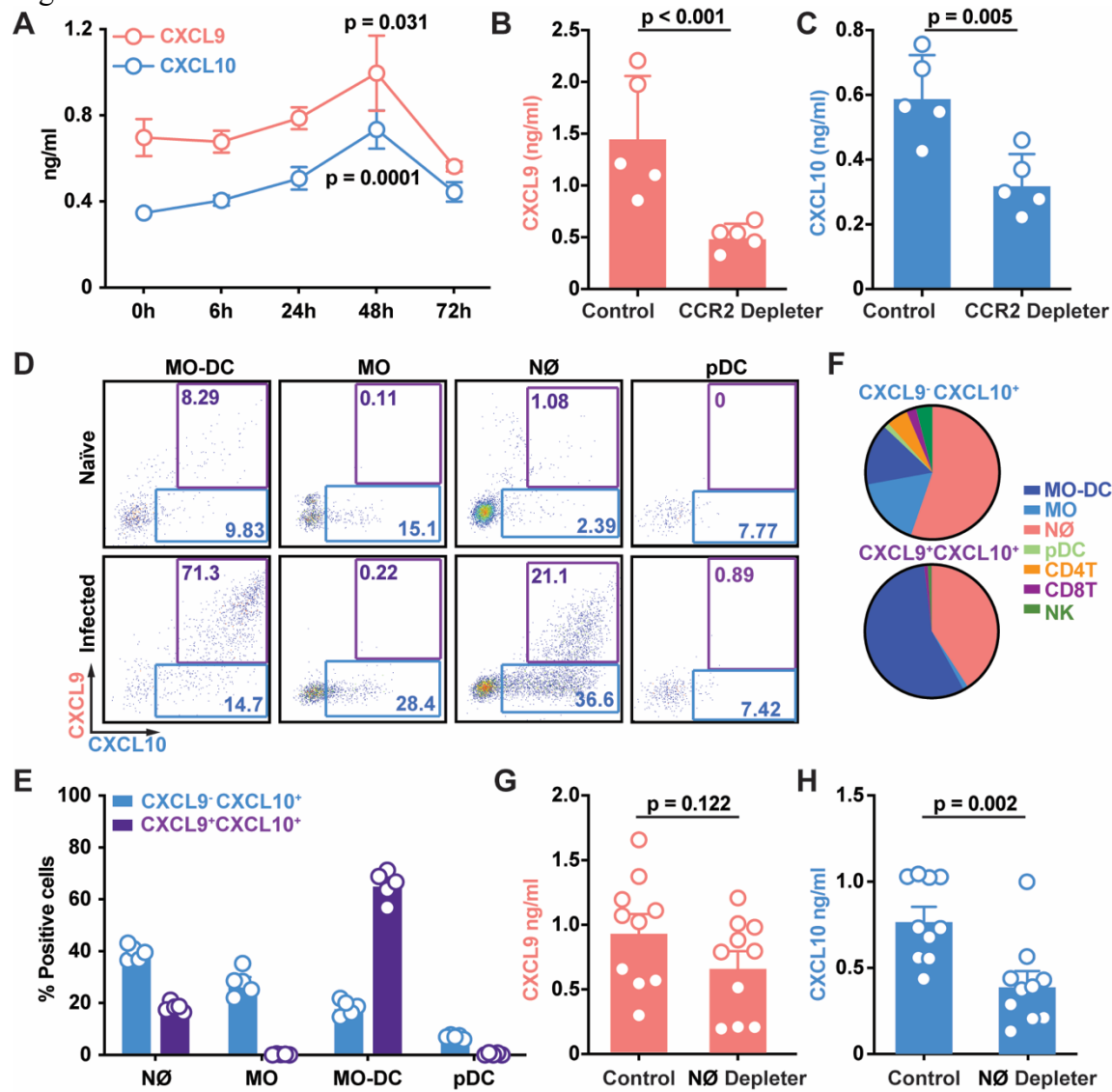
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1016 Graphical Abstract



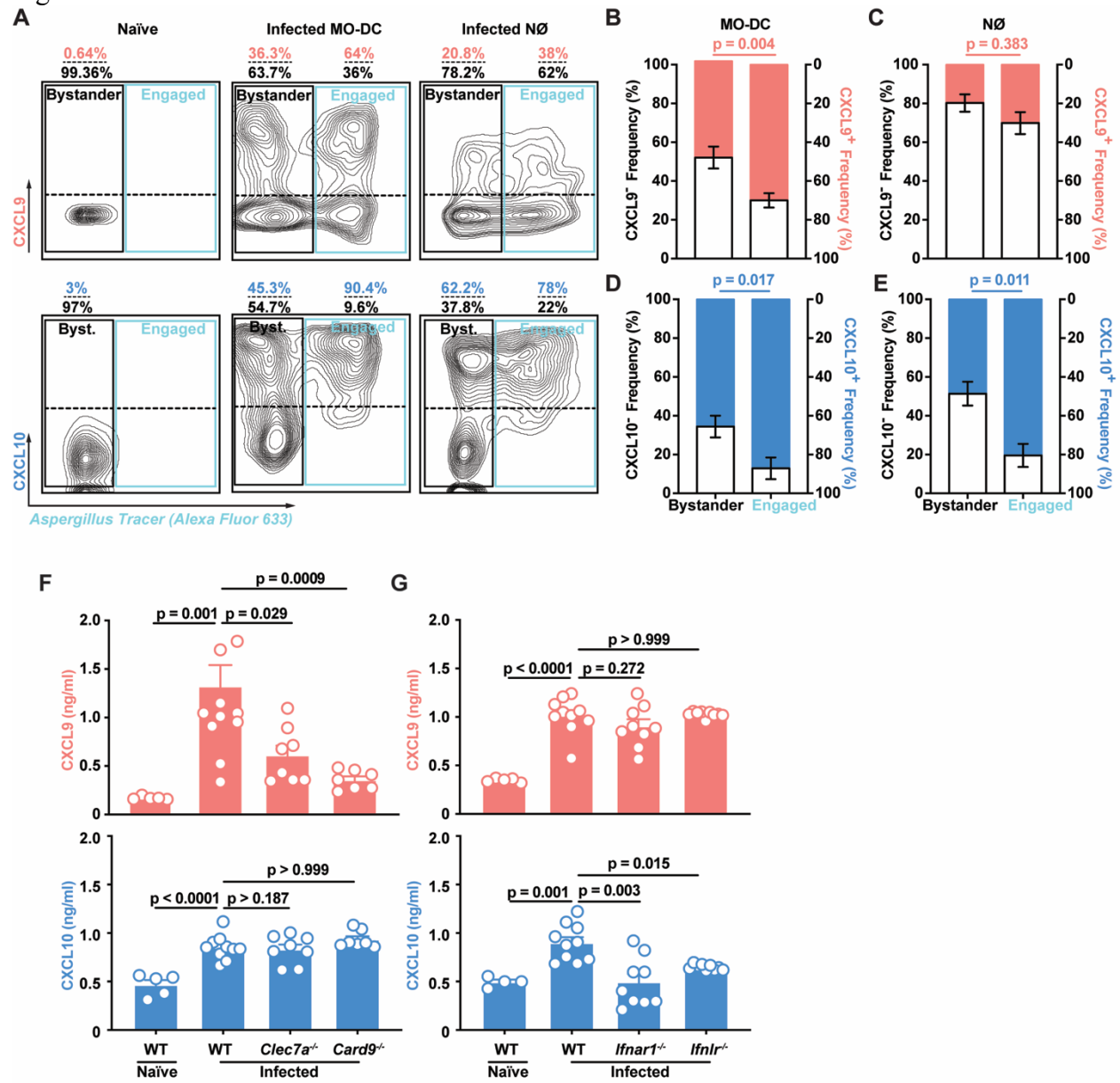
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1018 Figure 1.



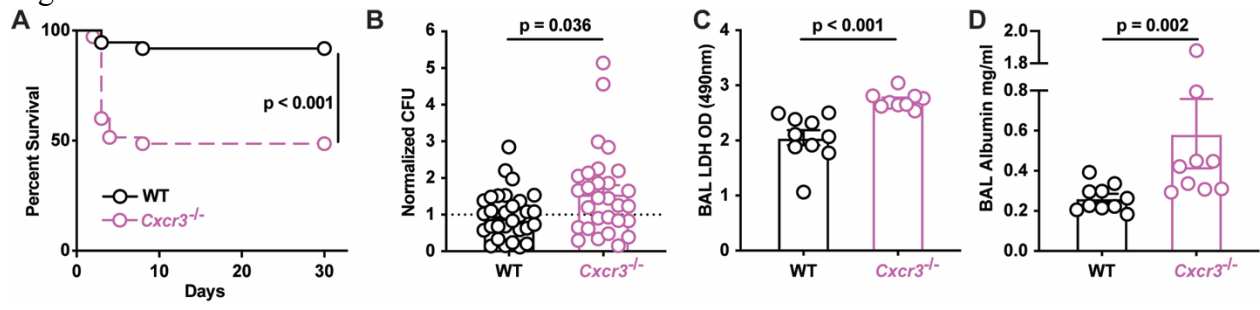
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1020 Figure 2.



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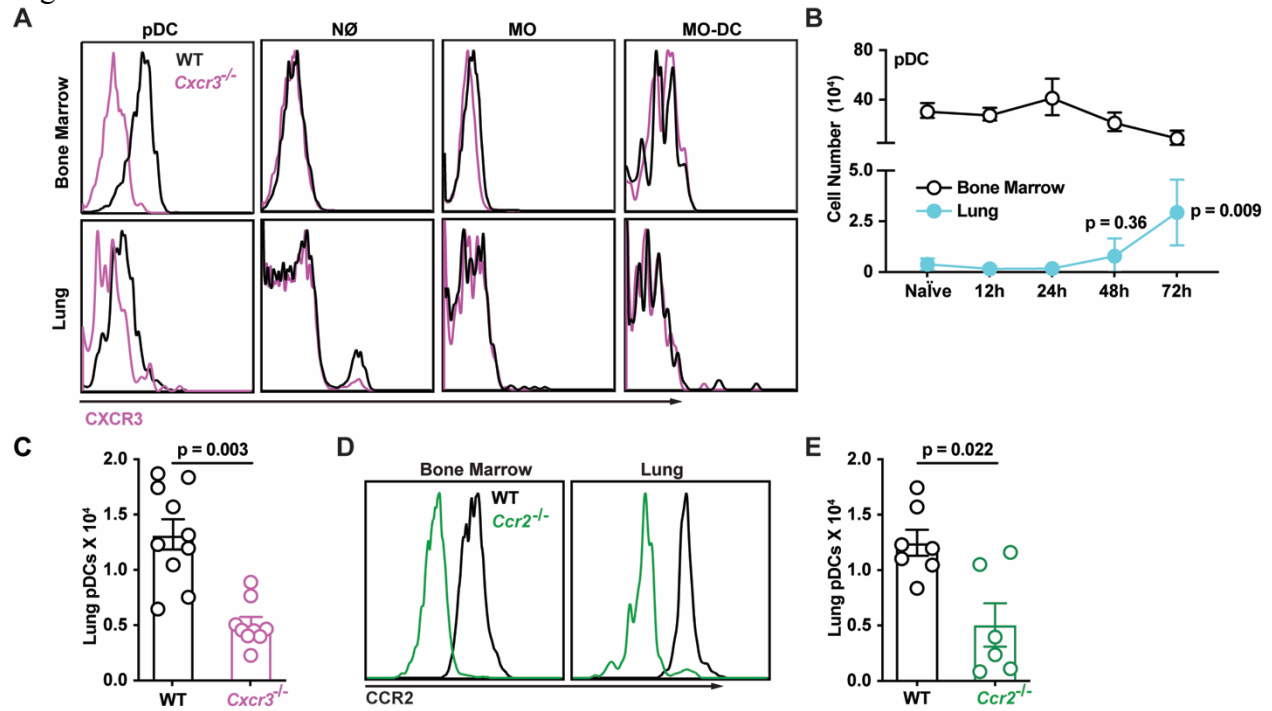
1022 Figure 3.



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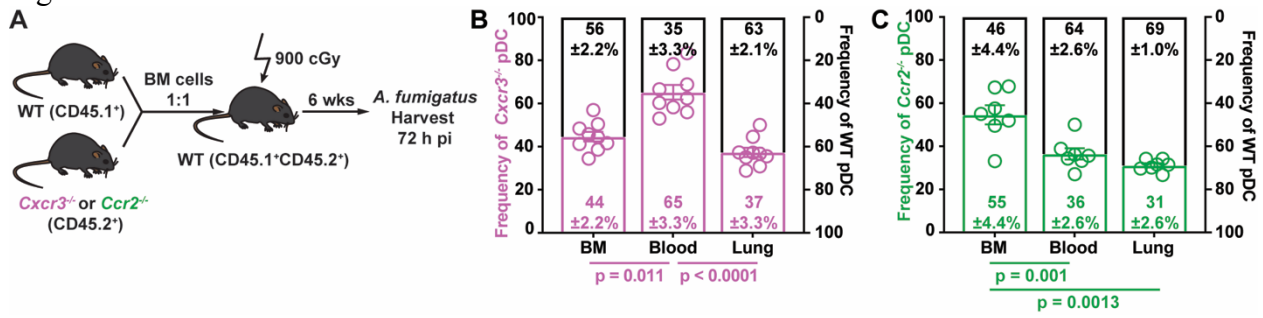


1025 Figure 4.



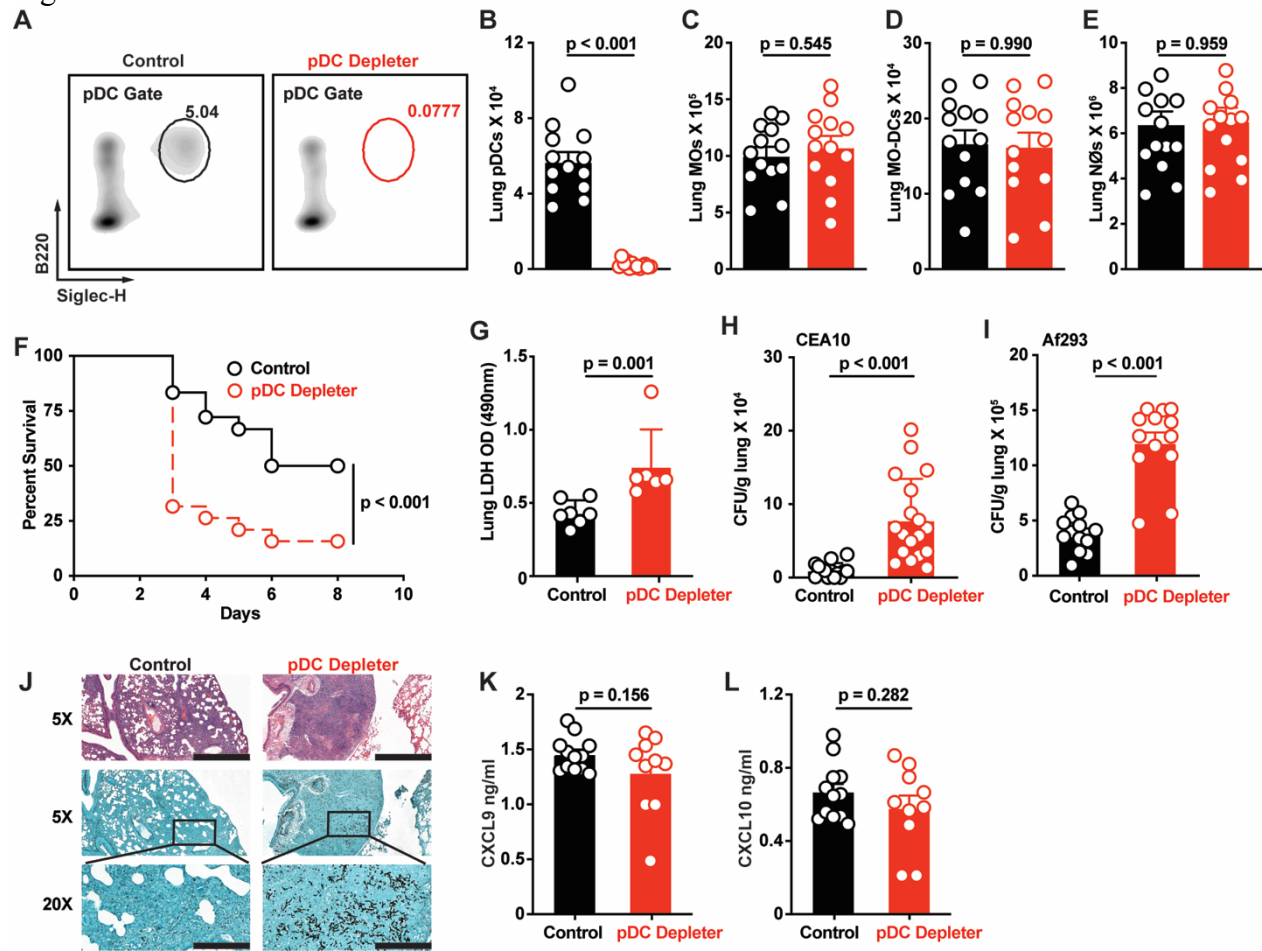
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1028 Figure 5.



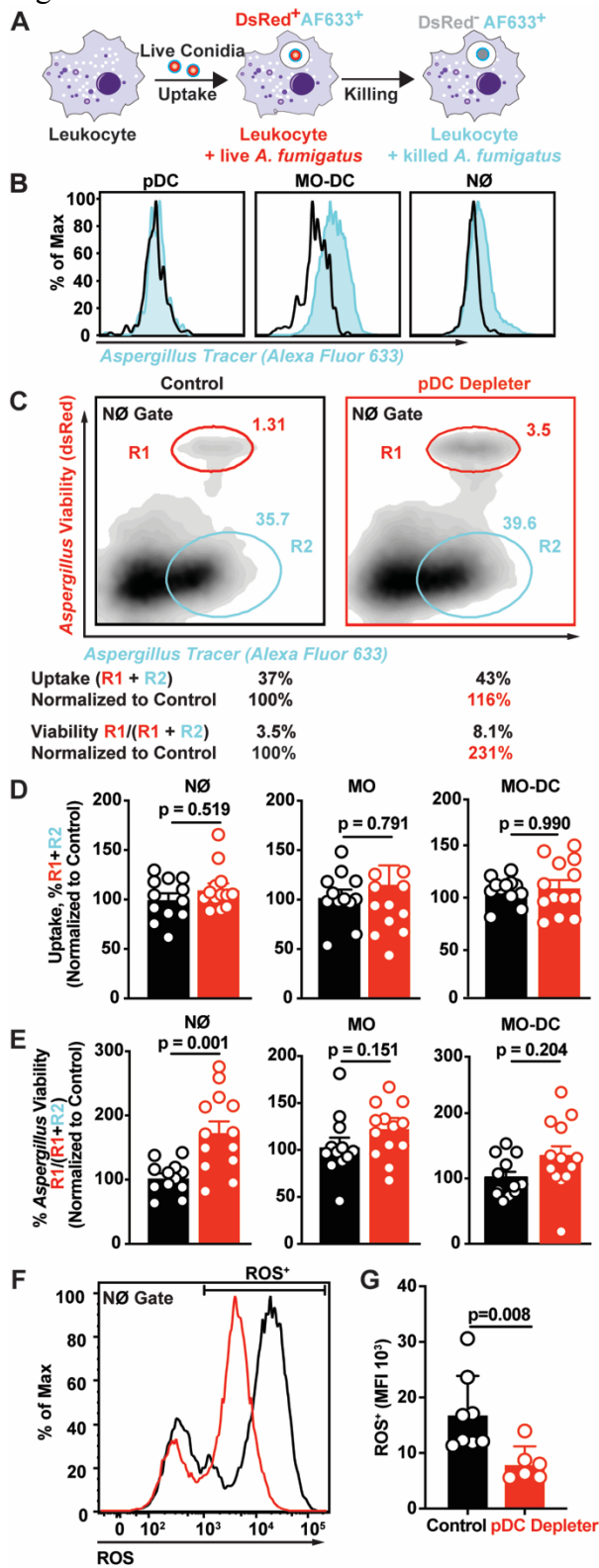
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1030 Figure 6.



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1032 Figure 7.



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1035 **Supplemental Information**

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1037 **CXCR3 links neutrophil, monocyte-derived DC, and plasmacytoid DC crosstalk to enhance**

1038 **innate immune defense during *Aspergillus* infection**

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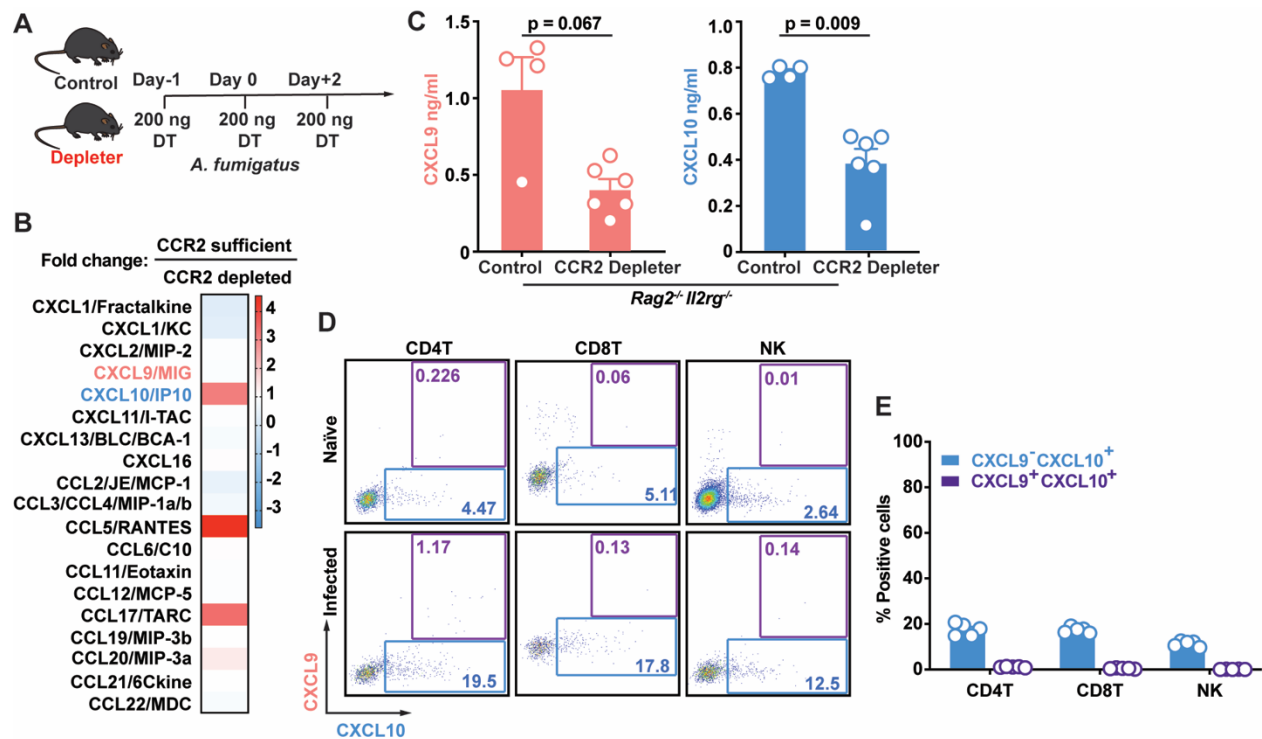
1040 Yahui Guo<sup>1,\*</sup>, Shinji Kasahara<sup>1,\*</sup>, Anupam Jhingran<sup>1</sup>, Nicholas L. Tosini<sup>1</sup>, Bing Zhai<sup>1</sup>, Mariano

1041 A. Aufiero<sup>1,3</sup>, Kathleen A.M. Mills<sup>1,4</sup>, Mergim Gjonbalaj<sup>1</sup>, Vanessa Espinosa<sup>5</sup>, Amariliz

1042 Rivera<sup>5,6</sup>, Andrew D. Luster<sup>7</sup>, Tobias M. Hohl<sup>1,2,3,4,#</sup>

1043 SUPPLEMENTAL INFORMATION

1044



1045

1046 **Figure S1. CCR2<sup>+</sup> myeloid cells regulate CXCL9 and CXCL10 production during *A.***

1047 ***fumigatus* infection. Related to Figure 1.**

1048 (A) Experimental Scheme: Diphtheria toxin (DT) was administered intraperitoneally (i.p.) as  
 1049 indicated to ablate DTR<sup>+</sup> cells in mouse strains that express the CCR2-DTR transgene (Depleter)  
 1050 or non-transgenic littermates that not do express the CCR2-DTR transgene (Control).

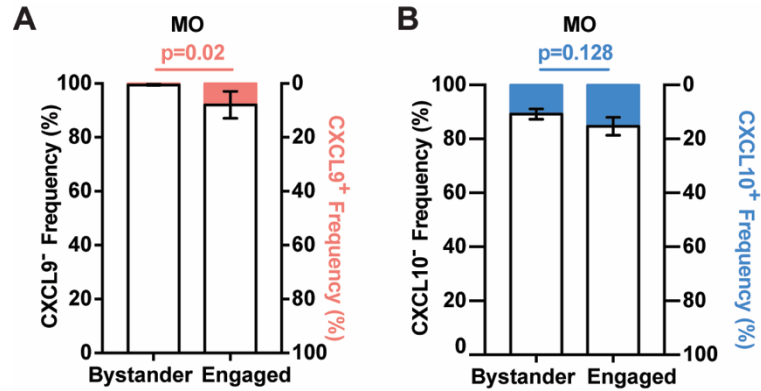
1051 (B) Fold change in lung chemokine levels in CCR2-sufficient (CCR2-DTR<sup>-/-</sup> *Rag2<sup>-/-</sup> Il2rg<sup>-/-</sup>*)  
 1052 versus CCR2-depleted (CCR2-DTR<sup>+/-</sup> *Rag2<sup>-/-</sup> Il2rg<sup>-/-</sup>*) mice that lack lymphoid lineage cells 36 h  
 1053 pi with  $3 \times 10^7$  CEA10 conidia, as measured by proteome profiler array (n = 2 per group, data  
 1054 pooled from 2 experiments).

1055 (C) Lung CXCL9 and CXCL10 levels in CCR2-DTR<sup>+/-</sup> *Rag2<sup>-/-</sup> Il2rg<sup>-/-</sup>* and littermates (CCR2-  
 1056 DTR<sup>-/-</sup> *Rag2<sup>-/-</sup> Il2rg<sup>-/-</sup>*) (n = 4-6) at 48 h pi with  $3 \times 10^7$  CEA10 conidia.

1057 (D) Representative plots of RFP (CXCL9) and BFP (CXCL10) expression in indicated lung  
1058 leukocytes isolated from Rex3 Tg → C57BL/6.SJL BM chimeric mice at baseline (naïve, top  
1059 row) and 48 h pi with  $3 \times 10^7$  CEA10 conidia (infected, bottom row). The blue and purple gates  
1060 indicate the frequency of BFP<sup>+</sup> (CXCL9<sup>+</sup>) and BFP<sup>+</sup>RFP<sup>+</sup> (CXCL9<sup>+</sup> CXCL10<sup>+</sup>) cells,  
1061 respectively.

1062 (E) The graphs indicate the frequency of CXCL9<sup>-</sup> CXCL10<sup>+</sup> and CXCL9<sup>+</sup> CXCL10<sup>+</sup> CD4<sup>+</sup> T  
1063 cells, CD8<sup>+</sup> T cells and NK cells at 48 h pi.

1064 (C, E) Data are representative of two independent experiments. Dots represent individual mice  
1065 and data are presented as mean ± SEM, (C) Statistical analysis: Mann-Whitney test.



1066

1067 **Figure S2. Monocyte CXCL9 and CXCL10 expression during *A. fumigatus* infection.**

1068 **Related to Figure 2.**

1069 (A) Proportion of RFP<sup>+</sup> (CXCL9<sup>+</sup>; pink bar) and RFP<sup>-</sup> (CXCL9<sup>-</sup>; white bar); and (B) BFP<sup>+</sup>

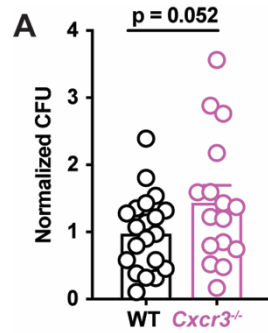
1070 (CXCL10<sup>+</sup>; blue bar) and BFP<sup>-</sup> (CXCL10<sup>-</sup>; white bar) expression in indicated bystander and

1071 fungus-engaged leukocytes isolated infected Rex3 Tg → C57BL/6.SJL BM chimeric mice (n =

1072 7) with  $3 \times 10^7$  AF633-labeled CEA10 conidia.

1073 (A and B) Data are presented as mean ± SEM. Statistical analysis: Mann-Whitney test.





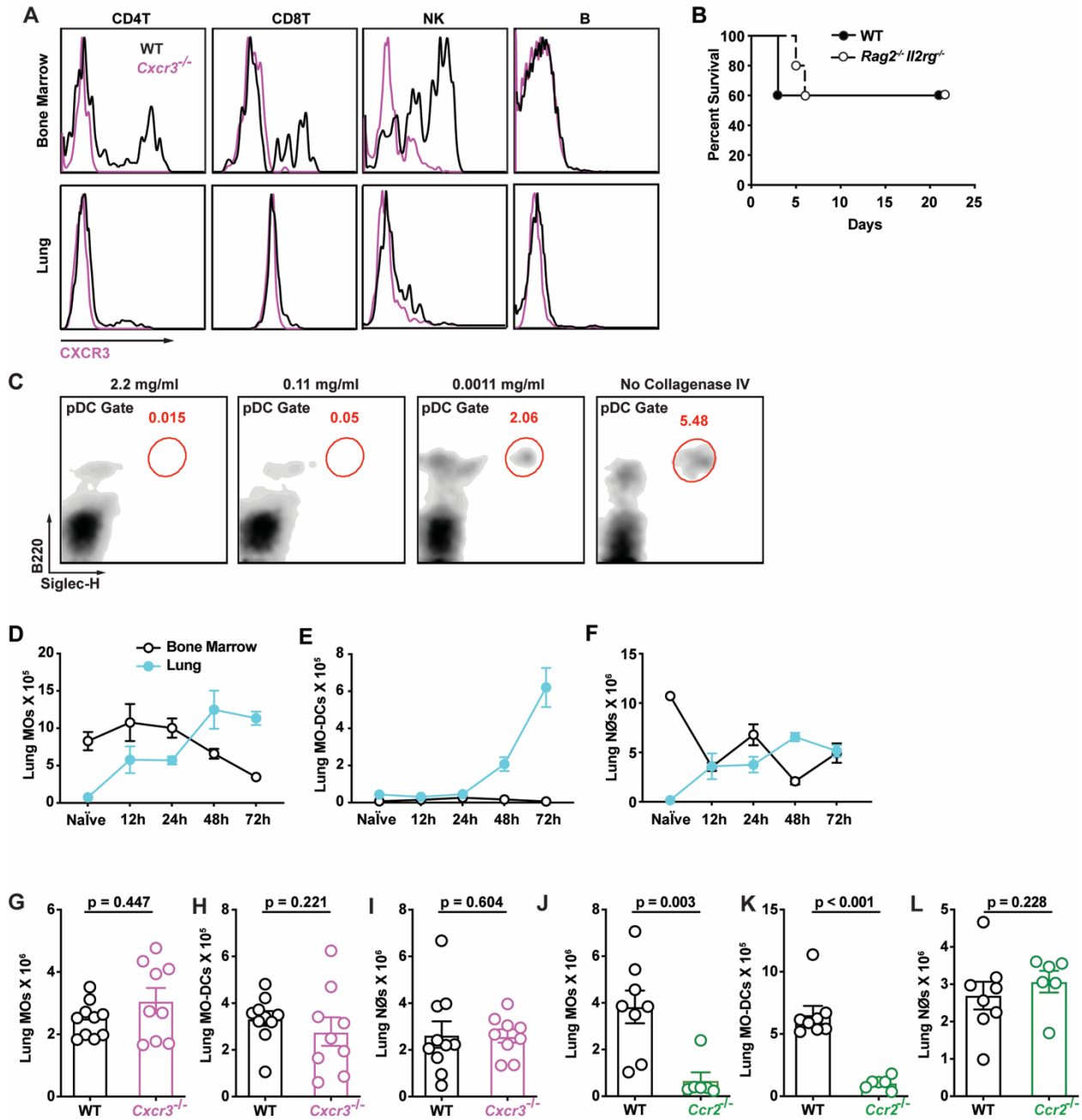
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1075 **Figure S3. CXCR3 is critical for anti-*Aspergillus* defense. Related to Figure 3.**

1076 (A) Normalized Lung CFUs in C57BL/6 (WT) and *Cxcr3*<sup>-/-</sup> mice 72 h pi with  $3 \times 10^7$  CEA10

1077 conidia. Dots represent individual mice and data were pooled from 2 independent experiments.

1078 Data are presented as mean  $\pm$  SEM. Statistical analysis: Mann-Whitney test.



1079

1080 **Figure S4. CXCR3 expression on lung leukocytes and pDC identification in lung digests.**

1081 **Related to Figure 4.**

1082 (A) Representative CXCR3 surface expression in the indicated bone marrow (top row) and lung

1083 (bottom row) leukocytes that were isolated from C57BL/6 (WT, black lines; *Cxcr3*<sup>+/+</sup>) or *Cxcr3*<sup>-/-</sup>

1084 mice (purple lines).

1085 (B) Kaplan-Meier survival of C57BL/6 (n = 5) and *Rag2<sup>-/-</sup>Il2rg<sup>-/-</sup>* (n = 5) mice challenged with 4-  
1086  $8 \times 10^7$  CEA10 conidia.

1087 (C) Representative flow cytometry plots of B220<sup>+</sup>Siglec-H<sup>+</sup> lung pDCs with the indicated  
1088 concentration of type IV collagenase included in lung preparations to obtain single cells for flow  
1089 cytometric analysis.

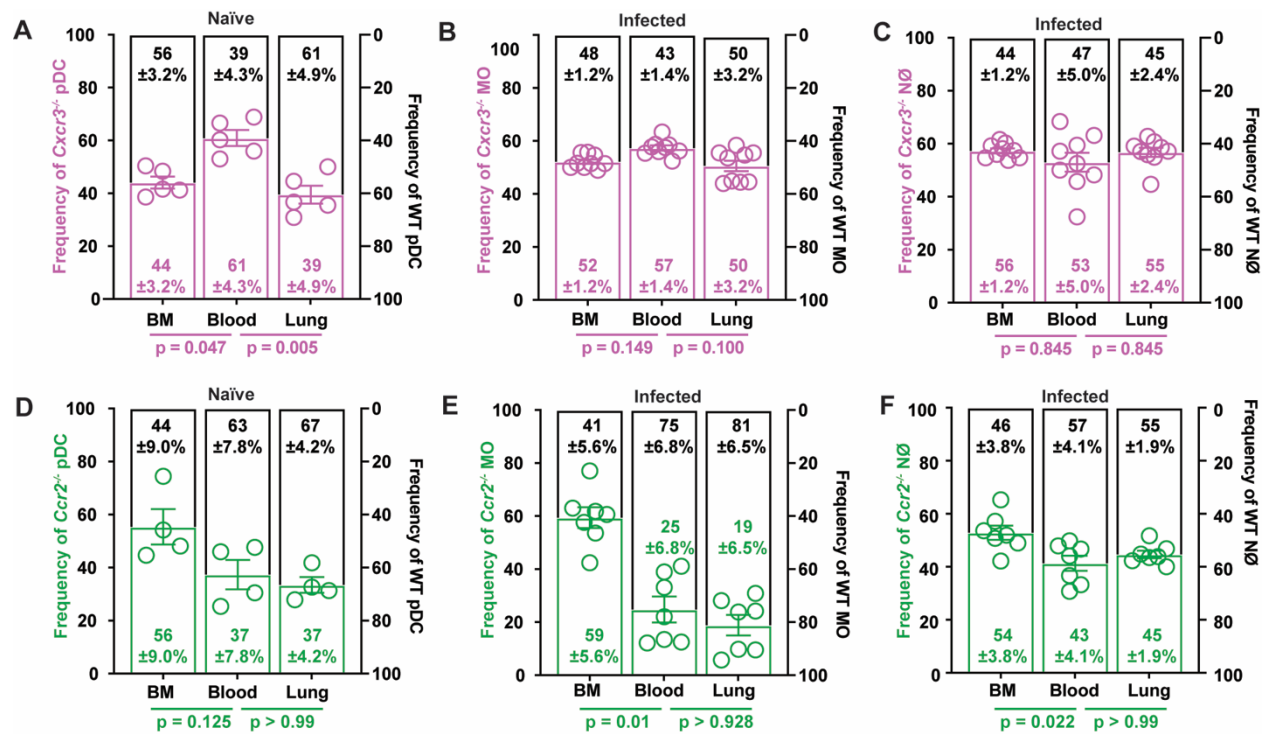
1090 (D-F) Lung (blue filled dots) and bone marrow (open black dots) (D) monocyte, (E) Mo-DC, and  
1091 (F) neutrophil numbers at baseline and indicated times pi with  $3 \times 10^7$  CEA10 conidia (n = 5).

1092 (G-H) Lung (G) monocyte, (H) Mo-DC, and (I) neutrophil numbers in C57BL/6 (WT; open  
1093 black dots) and *Cxcr3<sup>-/-</sup>* mice (open purple dots) at 72 h pi (n = 10).

1094 (J-L) Lung (J) monocyte, (K) Mo-DC, and (L) neutrophil numbers in C57BL/6 (WT; open black  
1095 dots) and *Ccr2<sup>-/-</sup>* mice (open green bars) at 72 h pi (n = 10).

1096 (D-L) Data are representative of two independent experiments. Dots represent individual mice  
1097 and data are presented as mean  $\pm$  SEM. Statistical analysis: Mann-Whitney test.

1098



1099

1100 **Figure S5. CXCR3 does not regulate the trafficking of lung monocytes, Mo-DCs, and**

1101 **neutrophils. Related to Figure 5.**

1102 (A) Relative frequencies of *Cxcr3*<sup>-/-</sup> (open purple bars) and *Cxcr3*<sup>+/+</sup> (open black bars) pDCs in

1103 the BM, blood, and lung of mixed BM chimeric (1:1 mix of CD45.1<sup>+</sup> *Cxcr3*<sup>+/+</sup> and CD45.2<sup>+</sup>

1104 *Cxcr3*<sup>-/-</sup> BM cells → CD45.1<sup>+</sup>CD45.2<sup>+</sup>) mice at baseline.

1105 (B and C) Relative frequencies of *Cxcr3*<sup>-/-</sup> (open purple bars) and *Cxcr3*<sup>+/+</sup> (open black bars) (B)

1106 monocytes and (C) neutrophils in the BM, blood, and lung of mixed BM chimeric (1:1 mix of

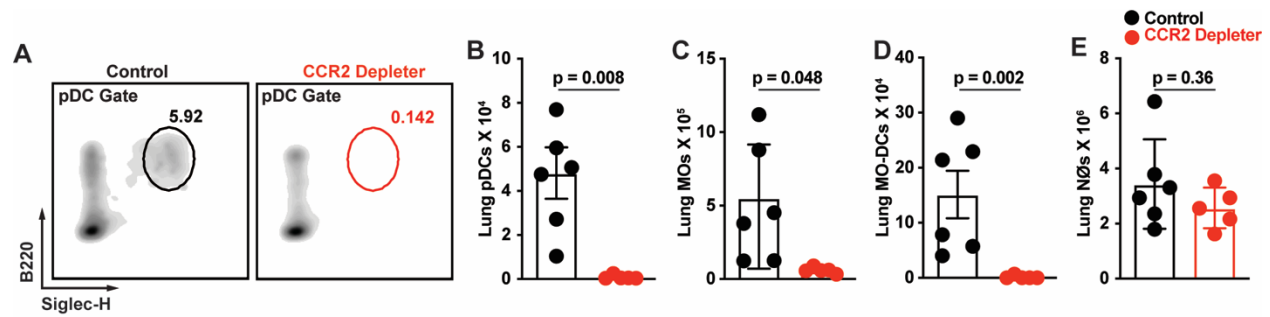
1107 CD45.1<sup>+</sup>*Cxcr3*<sup>+/+</sup> and CD45.2<sup>+</sup>*Cxcr3*<sup>-/-</sup> BM cells → CD45.1<sup>+</sup>CD45.2<sup>+</sup>) mice 72 h pi.(D) Relative

1108 frequencies of *Ccr2*<sup>-/-</sup> (open green bars) and *Ccr2*<sup>+/+</sup> (open black bars) pDCs in the BM, blood,

1109 and lung of mixed BM chimeric (1:1 mix of CD45.1<sup>+</sup>*Cxcr3*<sup>+/+</sup> and CD45.2<sup>+</sup>*Cxcr3*<sup>-/-</sup> BM cells →

1110 CD45.1<sup>+</sup>CD45.2<sup>+</sup>) mice at baseline.

- 1111 (E-F) Relative frequencies of *Ccr2*<sup>-/-</sup> (open green bars) and *Ccr2*<sup>+/+</sup> (open black bars) (E)
- 1112 monocytes and (F) neutrophils in the BM, blood, and lung of mixed BM chimeric (1:1 mix of
- 1113 CD45.1<sup>+</sup>*Ccr2*<sup>+/+</sup> and CD45.2<sup>+</sup>*Ccr2*<sup>-/-</sup> BM cells → CD45.1<sup>+</sup>CD45.2<sup>+</sup>) mice 72 h pi.
- 1114 (A-F) Data were pooled from 2 or 3 independent experiments and presented as mean ± SEM,
- 1115 Statistical analysis: Mann-Whitney test.



1116

1117 **Figure S6. pDCs are depleted in CCR2 Depletor mice. Related to Figure 6.**

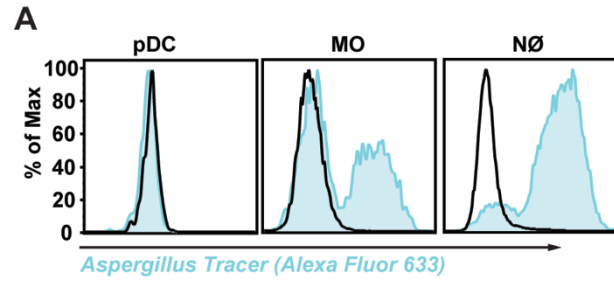
1118 (A) Representative flow cytometry plots of lung B220<sup>+</sup>Siglec-H<sup>+</sup> pDC, (B) lung pDC, (C) lung

1119 monocyte, (D) lung Mo-DC, and (E) lung neutrophil numbers in DT-treated CCR2 Depletor

1120 mice (CCR2-DTR<sup>+/-</sup>; red symbols) and non-Tg littermate controls (CCR2-DTR<sup>-/-</sup>; black symbols)

1121 at 72 h pi with  $3 \times 10^7$  CEA10 conidia.

1122 (B-E) Data were presented as mean  $\pm$  SEM. Statistical analysis: Mann-Whitney test.



1123

1124 **Figure S7. pDCs do not bind to or engulf *A. fumigatus* conidia. Related to Figure 7.**

1125 (A) AF633 fluorescence intensity in indicated BM leukocytes co-cultured for 24 h with FLARE

1126 (blue line) or AF633-unlabeled conidia (MOI = 5).

1127