

## 1 Immunometabolic cues recompose and reprogram the microenvironment around biomaterials

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## 24 Abstract.

25 Circulating monocytes infiltrate and coordinate immune responses in various inflamed tissues, such as  
26 those surrounding implanted biomaterials, affecting therapeutic, diagnostic, tissue engineering and  
27 regenerative applications. Here, we show that immunometabolic cues in the biomaterial microenvironment  
28 govern CCR2- and CX3CR1-dependent trafficking of immune cells, including neutrophils and monocytes;  
29 ultimately, this affects the composition and activation states of macrophage and dendritic cell populations.  
30 Furthermore, immunometabolic cues around implants orchestrate the relative composition of  
31 proinflammatory, transitory and anti-inflammatory CCR2<sup>+</sup>, CX3CR1<sup>+</sup> and CCR2<sup>+</sup>CX3CR1<sup>+</sup> immune cell  
32 populations. Consequently, modifying immunometabolism by glycolytic inhibition drives a pro-regenerative  
33 microenvironment in part by myeloid cells around amorphous polylactide implants. In addition to, Arginase  
34 1-expressing myeloid cells, T helper 2 cells and  $\gamma\delta^+$  T-cells producing IL-4 significantly contribute to shaping  
35 the metabolically reprogramed, pro-regenerative microenvironment around crystalline polylactide  
36 biomaterials. Taken together, we find that local metabolic states regulate inflammatory processes in the  
37 biomaterial microenvironment, with implications for translational medicine.

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40 **Keywords:** monocyte trafficking, immunometabolism, chemokine receptor 2 (CCR2), regenerative  
41 medicine, C-X3-C motif chemokine receptor 1 (CX3CR1)

## 42 Introduction.

43 Control over the immune response to implanted biomaterials is required for medical devices to  
44 effectively function in therapeutic, diagnostic, tissue engineering and regenerative applications<sup>1-4</sup>.  
45 Trafficking of monocytes from the bloodstream into tissues is mediated by CCR2 signaling<sup>5</sup>, and is crucial  
46 to the foreign body response because extravasated monocytes develop into macrophages and dendritic  
47 cells, mediating the inflammatory response around implanted biomaterials. Recent advances in  
48 understanding metabolic adaptation in the biomaterial microenvironment reveal that changes in immune  
49 cell metabolism orchestrate immunological events in complex ways that could be leveraged to enhance  
50 regenerative medicine<sup>6-13</sup>. However, how local immunometabolic cues in the biomaterial microenvironment  
51 regulate the trafficking of immune cells and organize the relative composition of proinflammatory, transitory  
52 and anti-inflammatory or pro-regenerative phenotypes has not been elucidated. Despite a developing  
53 understanding of the changing phenotype(s) of recruited CCR2<sup>+</sup> and CX3CR1<sup>+</sup> cells in response to sterile  
54 injury and in several disease models<sup>14-19</sup>, the immunophenotypic composition of these cells in the  
55 biomaterial microenvironment has not been studied.

58 By fabricating amorphous polylactide (aPLA) implants, with and without embedded metabolic  
59 modulators, and locally implanting these biomaterial formulations in fluorescent reporter and wild-type mice,  
60 we demonstrate that the trafficking of immune cells to biomaterials is dependent on local metabolic cues.  
61 Additionally, prevailing immunometabolic cues in the biomaterial microenvironment regulate the relative  
62 composition of polarized CCR2<sup>+</sup> and CX3CR1<sup>+</sup> populations, with metabolic changes able to create a pro-  
63 regenerative phenotype with the help of myeloid cells in the aPLA biomaterial microenvironment. In addition  
64 to Arginase 1-expressing myeloid cells, T helper 2 cells and  $\gamma\delta^+$  T-cells producing IL-4 contribute to shaping  
65 the pro-regenerative microenvironment surrounding crystalline polylactide (cPLA).  
66

67 **Rewiring metabolism in the amorphous polylactide biomaterial microenvironment controls CCR2-  
68 and CX3CR1-dependent trafficking.**

69 To understand the role of local metabolic cues in the trafficking of immune cells to sites of  
70 biomaterial implantation, we crossed *Ccr2*<sup>RFP/RFP</sup>*Cx3cr1*<sup>GFP/GFP</sup> (CCR2- and CX3CR1-deficient) mice to B6  
71 albino mice (Fig. 1a). The resulting F1 generation, *Ccr2*<sup>RFP/+</sup>*Cx3cr1*<sup>GFP/+</sup> (CCR2- and CX3CR1-expressing)  
72 mice, were surgically incised (without biomaterial implantation) as sham controls; implanted with 7.5mm  
73 long reprocessed amorphous polylactide (hereafter, referred to as aPLA); or implanted with aPLA  
74 incorporating either 2-deoxyglucose (2DG) or aminoxyacetic acid (a.a.) at previously optimized  
75 concentrations<sup>20</sup>. In these dual reporter mice, RFP (CCR2) is expressed in  $\approx$  90% of Ly6C<sup>+</sup> cells, allowing  
76 RFP to predominantly track classical monocytes, the analogue of CD14<sup>+</sup> monocytes in humans<sup>17,18</sup>. GFP  
77 (CX3CR1) is mostly expressed by Ly6C<sup>-</sup> alternative or resident monocytes, the analogue of CD16<sup>+</sup>  
78 monocytes in humans<sup>17</sup>, as well as a subset of natural killer and dendritic cells<sup>17,19</sup>. Thus, intravital  
79 microscopic imaging of tissues adjacent to the implants allowed for visual monitoring of immune cells in the  
80 biomaterial microenvironment (Supplementary Fig. 1a). We used two inhibitors that act at different  
81 metabolic steps; 2DG inhibits hexokinase in the glycolytic pathway<sup>21</sup>, a.a. reduces both mitochondrial  
82 uptake of glycolytic substrates<sup>22</sup> and glutamine metabolism<sup>23</sup>. Lastly, we included sham and aPLA groups  
83 among *Ccr2*<sup>RFP/RFP</sup>*Cx3cr1*<sup>GFP/GFP</sup> mice (effectively knockout mice for these receptors; Supplementary Fig.  
84 2a) to understand the contribution of CCR2- and CX3CR1-expression in the recruitment of immune cells to  
85 the biomaterial microenvironment.

86 We observed an initial increase in CCR2- and CX3CR1-expression that declined over time in all  
87 groups of *Ccr2*<sup>RFP/+</sup>*Cx3cr1*<sup>GFP/+</sup> mice by intravital microscopy (Fig. 1b). CCR2<sup>+</sup> and CX3CR1<sup>+</sup> cells were  
88 observed in tissues of *Ccr2*<sup>RFP/+</sup>*Cx3cr1*<sup>GFP/+</sup> mice, including sham (Supplementary Video 1), aPLA  
89 (Supplementary Video 2), aPLA + a.a. (Supplementary Video 3) and aPLA + 2DG (Supplementary Video  
90 4) groups 10 weeks after surgeries. Notably, CCR2- and CX3CR1-expression appeared elevated in the  
91 aPLA group of *Ccr2*<sup>RFP/+</sup>*Cx3cr1*<sup>GFP/+</sup> mice (Fig. 1b; Supplementary Video 2). Flow cytometric (quantitative)  
92 analyses of tissues around the implants corroborated increased CCR2<sup>+</sup>, CX3CR1<sup>+</sup> and CCR2<sup>+</sup>CX3CR1<sup>+</sup>  
93 cell populations in the aPLA group compared to sham controls; elevated levels were decreased by  
94 incorporation of 2DG but not by a.a. in *Ccr2*<sup>RFP/+</sup>*Cx3cr1*<sup>GFP/+</sup> mice. (Fig. 1c-f; Supplementary Fig. 1b). Among  
95 *Ccr2*<sup>RFP/RFP</sup>*Cx3cr1*<sup>GFP/GFP</sup> mice (Supplementary Fig. 2b), there were no notable differences in CCR2- or  
96 CX3CR1-expression between sham (Supplementary Video 5) and aPLA groups (Supplementary Video 6),  
97 and flow cytometry data corroborated our visual observations (Supplementary Fig. 2c-d). Interestingly,  
98 CCR2<sup>+</sup>CX3CR1<sup>+</sup> cells were decreased with aPLA implantation relative to sham controls in  
99 *Ccr2*<sup>RFP/RFP</sup>*Cx3cr1*<sup>GFP/GFP</sup> mice (Supplementary Fig. 2e).

100 Next, we sought to elucidate the composition of the different CCR2<sup>+</sup>, CX3CR1<sup>+</sup> and  
101 CCR2<sup>+</sup>CX3CR1<sup>+</sup> populations in the implant microenvironment based on CD86 and CD206 expression. We  
102 classified proinflammatory populations<sup>24</sup> as CD86<sup>+</sup>CD206<sup>-</sup>, anti-inflammatory populations<sup>25</sup> as CD206<sup>+</sup>, and  
103 transition populations moving from proinflammatory to anti-inflammatory states<sup>26,27</sup> as CD86<sup>+</sup>CD206<sup>+</sup>.  
104 Among CCR2<sup>+</sup>, CX3CR1<sup>+</sup> and CCR2<sup>+</sup>CX3CR1<sup>+</sup> populations, the proportion of proinflammatory cells were  
105 higher in the aPLA group compared to sham controls in *Ccr2*<sup>RFP/+</sup>*Cx3cr1*<sup>GFP/+</sup> mice (Fig. 1g-i), whereas there  
106 were no differences with *Ccr2*<sup>RFP/RFP</sup>*Cx3cr1*<sup>GFP/GFP</sup> mice (Supplementary Fig. 2f-h). Incorporating a.a.  
107 decreased proinflammatory levels among CX3CR1<sup>+</sup> and CCR2<sup>+</sup>CX3CR1<sup>+</sup> populations in  
108 *Ccr2*<sup>RFP/+</sup>*Cx3cr1*<sup>GFP/+</sup> mice (Fig. 1h-i). The proportion of anti-inflammatory cells among CCR2<sup>+</sup> cells was  
109 decreased with aPLA implantation compared to sham controls in *Ccr2*<sup>RFP/+</sup>*Cx3cr1*<sup>GFP/+</sup> mice, while  
110 incorporating a.a. restored the proportion of these cells to a similar level as the sham controls (Fig. 1j).

111 However, no difference was observed in the proportion of anti-inflammatory CCR2<sup>+</sup> cells in  
112 *Ccr2*<sup>RFP/RFP</sup>*Cx3cr1*<sup>GFP/GFP</sup> mice (Supplementary Fig. 2i). Proportions of anti-inflammatory cells among  
113 CX3CR1<sup>+</sup> and CCR2<sup>+</sup>CX3CR1<sup>+</sup> populations were similar across all groups in *Ccr2*<sup>RFP/+</sup>*Cx3cr1*<sup>GFP/+</sup> mice  
114 (Fig. 1k-l) and *Ccr2*<sup>RFP/RFP</sup>*Cx3cr1*<sup>GFP/GFP</sup> mice (Supplementary Fig. 2j-k). Among, CCR2<sup>+</sup> populations, the  
115 proportion of transition cells was reduced by the implantation of aPLA compared to sham controls in  
116 *Ccr2*<sup>RFP/+</sup>*Cx3cr1*<sup>GFP/+</sup> mice (Fig. 1m), but not *Ccr2*<sup>RFP/RFP</sup>*Cx3cr1*<sup>GFP/GFP</sup> mice (Supplementary Fig. 2l).  
117 Incorporation of either a.a. or 2DG increased proportions of transition cells (Fig. 1m). Similar to  
118 *Ccr2*<sup>RFP/+</sup>*Cx3cr1*<sup>GFP/+</sup> mice (Fig. 1n-o), *Ccr2*<sup>RFP/RFP</sup>*Cx3cr1*<sup>GFP/GFP</sup> mice (Supplementary Fig. 2m-n) showed  
119 no notable differences in proportions of transition cells among CX3CR1<sup>+</sup> and CCR2<sup>+</sup>CX3CR1<sup>+</sup> populations.  
120

121 In comparison to sham controls, the proportion of CD45<sup>+</sup> cells was increased by implantation of  
122 aPLA in *Ccr2*<sup>RFP/+</sup>*Cx3cr1*<sup>GFP/+</sup> mice, while incorporating either a.a. or 2DG significantly diminished this effect  
123 (Fig. 1p). In contrast, the proportion of CD45<sup>+</sup> cells decreased with aPLA implantation in  
124 *Ccr2*<sup>RFP/RFP</sup>*Cx3cr1*<sup>GFP/GFP</sup> mice compared to their sham controls (Supplementary Fig. 2o). In both  
125 *Ccr2*<sup>RFP/+</sup>*Cx3cr1*<sup>GFP/+</sup> mice and *Ccr2*<sup>RFP/RFP</sup>*Cx3cr1*<sup>GFP/GFP</sup> mice, we observed increased fold change of  
126 proinflammatory CD45<sup>+</sup> cells with respect to transition cells or anti-inflammatory cells in the aPLA group  
127 when compared to sham controls (Fig. 1q-r; Supplementary Fig. 2p-q). Also, the fold change of transition  
128 or anti-inflammatory CD45<sup>+</sup> cells with respect to proinflammatory cells was decreased in the aPLA group  
129 when compared to sham controls (Fig. 1s-t; Supplementary Fig. 2r-s). Interestingly, incorporating a.a. had  
130 the dual effect of decreasing proinflammatory and increasing anti-inflammatory proportions of cells (Fig.  
131 1q-t). In comparison to sham controls, Ly6G<sup>+</sup> neutrophils<sup>15</sup> were increased following aPLA implantation in  
132 *Ccr2*<sup>RFP/+</sup>*Cx3cr1*<sup>GFP/+</sup> mice (Fig. 1u), whereas there were no changes in *Ccr2*<sup>RFP/RFP</sup>*Cx3cr1*<sup>GFP/GFP</sup> mice  
133 (Supplementary Fig. 2t). Incorporating either a.a. or 2DG decreased elevated neutrophil levels (Fig. 1u).  
134

### 135 The composition of myeloid cells is reorganized toward pro-regenerative states by 136 immunometabolic cues in the aPLA microenvironment.

137 Having observed that CD45<sup>+</sup> populations were strikingly different among groups in our study (Fig.  
138 1p), we sought to uncover the relative contribution of myeloid cells, including CD11b<sup>+</sup> monocytes<sup>28-30</sup>  
139 (CD11b could also be expressed on subsets of B-cells, neutrophils and macrophages<sup>31</sup>), F4/80<sup>+</sup>  
140 macrophages<sup>31</sup> and CD11c<sup>+</sup> dendritic cells<sup>32,33</sup> to the constitution and polarization of the biomaterial  
141 microenvironment. In comparison to sham controls, we observed elevated monocyte populations following  
142 aPLA implantation in *Ccr2*<sup>RFP/+</sup>*Cx3cr1*<sup>GFP/+</sup> mice, but not in *Ccr2*<sup>RFP/RFP</sup>*Cx3cr1*<sup>GFP/GFP</sup> mice (Fig. 2a-b;  
143 Supplementary Fig. 2u). Incorporating either a.a. or 2DG reduced the frequency of monocytes compared  
144 to aPLA alone (Fig. 2a-b). Interestingly, there was increased fold change of proinflammatory cells with  
145 respect to transition cells or anti-inflammatory monocytes in the aPLA group when compared to sham  
146 controls, with either a.a. or 2DG incorporation modulating proinflammatory monocyte levels (Fig. 2c-d).  
147 Furthermore, the fold change of transition or anti-inflammatory monocytes with respect to proinflammatory  
148 cells was decreased in the aPLA group when compared to sham controls, with either a.a. or 2DG increasing  
149 anti-inflammatory monocyte levels (Fig. 2e-f).

150 We observed decreased macrophage expression in the aPLA group compared to sham controls of  
151 *Ccr2*<sup>RFP/+</sup>*Cx3cr1*<sup>GFP/+</sup> or *Ccr2*<sup>RFP/RFP</sup>*Cx3cr1*<sup>GFP/GFP</sup> mice, whereby incorporating either a.a. or 2DG increased  
152 macrophage expression (Fig. 2a, 2g; Supplementary Fig. 2v). Yet, exploring polarization states revealed  
153 increased fold change of proinflammatory macrophages with respect to transition or anti-inflammatory  
154 macrophages in the aPLA group when compared to sham controls, with either a.a. or 2DG incorporation  
155 reducing proinflammatory macrophage expression (Fig. 2h-i). Moreover, the fold change of transition or  
156 anti-inflammatory macrophages with respect to proinflammatory macrophages was decreased in the aPLA  
157 group when compared to sham controls, with a.a. increasing anti-inflammatory levels (Fig. 2j-k).

158 Dendritic cell populations were decreased in the aPLA group compared to sham controls of  
159 *Ccr2*<sup>RFP/+</sup>*Cx3cr1*<sup>GFP/+</sup> mice, but increased in *Ccr2*<sup>RFP/RFP</sup>*Cx3cr1*<sup>GFP/GFP</sup> mice (Fig. 2l; Supplementary Fig.  
160 2w). Incorporating either a.a. or 2DG increased dendritic cell expression (Fig. 2l). Furthermore, we observed  
161 increased fold change of proinflammatory dendritic cells with respect to transition or anti-inflammatory  
162 dendritic cells in the aPLA group when compared to sham controls, with a.a. reducing proinflammatory  
163 expression (Fig. 2m-n). There were no differences in the fold change of transition or anti-inflammatory  
164 dendritic cells with respect to proinflammatory dendritic cells between groups (Fig. 2o-p). Observed trends

164 in dendritic cells were similar to results of dendritic cells expressing class II major histocompatibility complex  
165 (MHCII) molecules (Fig. 2q-u; Supplementary Fig. 2x).

166

167 **Leveraging immunometabolism with aPLA favorably compares with currently used techniques.**

168 To determine how inhibiting the metabolism of immune cells using 2DG or a.a. compares to  
169 clinically used neutralization strategies<sup>34</sup>, we fabricated aPLA incorporating hydroxyapatite (HA)<sup>20</sup>. Wild-  
170 type B6 mice were surgically incised as sham controls or implanted with 1mm long aPLA formulations (Fig.  
171 3a). Flow cytometric analyses demonstrated elevated neutrophils with aPLA compared to sham controls  
172 among CD45<sup>+</sup> cells; elevated levels were decreased by either a.a. or 2DG, but not by HA (Fig. 3b). There  
173 was increased fold change of proinflammatory CD45<sup>+</sup> cells with respect to transition cells or anti-  
174 inflammatory cells in the aPLA group when compared to sham controls (Fig. 3c-d). Incorporating a.a., 2DG  
175 or HA each decreased the fold change of proinflammatory CD45<sup>+</sup> cells with respect to transition cells (Fig.  
176 3c), but only a.a. or 2DG decreased the fold change of proinflammatory cells with respect to anti-  
177 inflammatory cells (Fig. 3d). The fold change of transition or anti-inflammatory CD45<sup>+</sup> cells with respect to  
178 proinflammatory cells was decreased in the aPLA group when compared to sham controls (Fig. 3e-f). Whereas,  
179 incorporating a.a. or 2DG increased transition and anti-inflammatory expression, HA did not (Fig.  
180 3e-f). Importantly, a.a. had greater effects than HA at decreasing proinflammatory and increasing transition  
181 or anti-inflammatory CD45<sup>+</sup> proportions (Fig. 3c-f).

182 The fold change of proinflammatory monocytes with respect to transition or anti-inflammatory  
183 monocytes was increased in the aPLA group when compared to sham controls (Fig. 3g-h). Elevated  
184 proinflammatory monocytes proportions were consistently decreased by incorporating a.a. or 2DG, with HA  
185 only decreasing elevated proportions with respect to transition cells (Fig. 3g-h). On the other hand, the fold  
186 change of transition or anti-inflammatory monocytes with respect to proinflammatory monocytes was  
187 decreased in the aPLA group when compared to sham controls (Fig. 3i-j). Whereas incorporating a.a. or  
188 2DG increased the proportion of transition monocytes, only a.a. increased the proportion of anti-  
189 inflammatory monocytes (Fig. 3i-j). Notably, a.a. was more effective than HA at consistently reducing  
190 proinflammatory and increasing transition or anti-inflammatory monocyte proportions (Fig. 3g-i).

191 With macrophages, the fold change of proinflammatory cells with respect to transition or anti-  
192 inflammatory cells was increased in the aPLA group when compared to sham controls (Fig. 3k-l). Increased  
193 proinflammatory macrophage proportions were reduced by incorporating a.a. or 2DG, with HA only  
194 decreasing elevated proportions with respect to transition cells (Fig. 3k-l). We observed that a.a. was more  
195 effective than HA at reducing proinflammatory macrophage proportions (Fig. 3k-l). Additionally, the fold  
196 change of transition or anti-inflammatory macrophages with respect to proinflammatory macrophages was  
197 decreased in the aPLA group when compared to sham controls (Fig. 3m-n). As with monocytes,  
198 incorporating a.a. or 2DG increased the proportion of transition macrophages, with only a.a. increasing the  
199 proportion of anti-inflammatory macrophages (Fig. 3m-n).

200 While aPLA implantation did not reduce dendritic cell populations when compared to sham controls,  
201 incorporating a.a., 2DG or HA increased dendritic cell populations (Fig. 3o). Interestingly, the fold change  
202 of proinflammatory dendritic cells with respect to transition or anti-inflammatory dendritic cells was  
203 increased in the aPLA group when compared to sham controls, and incorporating a.a., 2DG or HA  
204 decreased elevated proinflammatory proportions (Fig. 3p-q). We also observed that the fold change of  
205 transition or anti-inflammatory dendritic cells with respect to proinflammatory dendritic cells was decreased  
206 in the aPLA group when compared to sham controls (Fig. 3r-s). Incorporating a.a. or HA increased the  
207 proportion of transition dendritic cells, with a.a., 2DG or HA increasing the proportion of anti-inflammatory  
208 dendritic cells (Fig. 3r-s). When compared with HA, a.a. decreased proinflammatory, and increased  
209 transition or anti-inflammatory proportions (Fig. 3q-s).

210 The expression of MHCII<sup>+</sup> dendritic cells was decreased with aPLA implantation when compared  
211 to sham controls, with incorporating a.a., 2DG or HA increasing MHCII<sup>+</sup> dendritic cell expression (Fig. 3t).  
212 The fold change of proinflammatory MHCII<sup>+</sup> dendritic cells with respect to transition or anti-inflammatory  
213 MHCII<sup>+</sup> dendritic cells was increased in the aPLA group when compared to sham controls, and incorporating  
214 a.a., 2DG or HA decreased elevated proinflammatory proportions (Fig. 3u-v). Also, the fold change of  
215 transition or anti-inflammatory MHCII<sup>+</sup> dendritic cells with respect to proinflammatory MHCII<sup>+</sup> dendritic cells  
216 was decreased in the aPLA group when compared to sham controls (Fig. 3w-x). Incorporating a.a. or HA

217 increased the proportion of transition MHCII<sup>+</sup> dendritic cells, with a.a., 2DG or HA increasing the proportion  
218 of anti-inflammatory MHCII<sup>+</sup> dendritic cells (Fig. 3w-x). In comparison to HA, a.a. decreased  
219 proinflammatory, and increased transition or anti-inflammatory proportions (Fig. 3v-x).

220

## 221 **Immunometabolic cues from crystalline polylactide create a pro-regenerative microenvironment 222 with the help of T-cells.**

223 In comparison to aPLA, we have observed by electrospray ionization-mass spectrometry that  
224 (semi-) crystalline polylactide (cPLA) formulations degrade more slowly<sup>20</sup>. Furthermore, the different  
225 stereochemical compositions of aPLA and cPLA could elicit differential immune cellular responses by  
226 triggering varied bioenergetic signatures<sup>7</sup>. As such, we sought to uncover the composition and phenotypes  
227 of immune cells in the cPLA microenvironment. Wild-type B6 mice were surgically incised as sham controls;  
228 implanted with 1mm long cPLA formulations with and without incorporating a.a. and 3-(3-pyridinyl)-1-(4-  
229 pyridinyl)-2-propen-1-one (3PO; Fig 4a), with 3PO being a small molecule inhibitor of 6- phosphofructo-2-  
230 kinase<sup>35</sup>, the rate limiting enzyme in glycolysis. Flow cytometric analyses demonstrated that there was  
231 increased CD45 expression with cPLA implantation in comparison to sham controls, and elevated levels  
232 were decreased by incorporating a.a. (Fig. 4b). There was increased fold change of proinflammatory CD45<sup>+</sup>  
233 cells with respect to transition cells or anti-inflammatory cells in the cPLA group when compared to sham  
234 controls (Supplementary Fig. 3a-b). Also, the fold change of transition or anti-inflammatory CD45<sup>+</sup> cells with  
235 respect to proinflammatory cells was decreased in the cPLA group when compared to sham controls  
236 (Supplementary Fig. 3c-d). Interestingly, incorporation of a.a. or 3PO did not decrease proinflammatory nor  
237 increase transition or anti-inflammatory CD45<sup>+</sup> proportions (Supplementary Fig. 3a-d).

238 There was no difference in neutrophil expression in the cPLA group when compared with sham  
239 controls (Fig. 4c). We observed increased monocyte expression in the cPLA group when compared to sham  
240 controls; elevated monocyte expression was decreased by incorporating a.a. (Fig. 4d). While there was  
241 increased fold change of proinflammatory monocytes with respect to transition or anti-inflammatory  
242 monocytes, incorporation of a.a. or 3PO did not reduce elevated proinflammatory levels (Supplementary  
243 Fig. 3e-f). The fold change of transition or anti-inflammatory monocytes with respect to proinflammatory  
244 monocytes was decreased in the cPLA group when compared to sham controls, and incorporation of a.a.  
245 or 3PO did not have significant effects (Supplementary Fig. 3g-h).

246 Macrophage expression was increased by cPLA implantation in comparison to sham controls, with  
247 incorporation of a.a. or 3PO reducing elevated expression (Fig. 3e). Furthermore, there was increased fold  
248 change of proinflammatory macrophages with respect to transition or anti-inflammatory macrophages in  
249 the cPLA group when compared to sham controls (Supplementary Fig. 3i-j). The fold change of transition  
250 or anti-inflammatory macrophages with respect to proinflammatory macrophages was decreased in the  
251 cPLA group when compared to sham controls (Supplementary Fig. 3k-l). Incorporation of a.a. or 3PO  
252 neither decreased proinflammatory nor increased anti-inflammatory proportions (Supplementary Fig. 3i-l).

253 Dendritic cell levels were increased in the cPLA group in comparison to sham controls, with a.a. or  
254 3PO further increasing dendritic cell expression (Fig. 4f). Whereas there were no changes in the fold change  
255 of proinflammatory dendritic cells with respect to transition cells, the fold change of proinflammatory  
256 dendritic cells with respect to anti-inflammatory cells was increased in the cPLA group when compared to  
257 sham controls, with incorporation of 3PO reducing elevated levels (Supplementary Fig. 3m-n). The fold  
258 change of transition or anti-inflammatory dendritic cells with respect to proinflammatory cells was decreased  
259 in the cPLA group when compared to sham controls (Supplementary Fig. 3o-p).

260 The expression of MHCII<sup>+</sup> dendritic cells with cPLA implantation was similar to sham controls, and  
261 MHCII<sup>+</sup> expression was increased by incorporation of a.a. (Fig. 4g). In addition, the fold change of  
262 proinflammatory MHCII<sup>+</sup> dendritic cells with respect to transition or anti-inflammatory MHCII<sup>+</sup> dendritic cells  
263 was increased in the cPLA group when compared to sham controls (Supplementary Fig. 3q-r). Also, the  
264 fold change of transition or anti-inflammatory MHCII<sup>+</sup> dendritic cells with respect to proinflammatory MHCII<sup>+</sup>  
265 dendritic cells was decreased in the cPLA group when compared to sham controls (Supplementary Fig. 3s-  
266 t). Incorporation of a.a. or 3PO neither decreased proinflammatory nor increased anti-inflammatory levels  
267 (Supplementary Fig. q-t). While Arginase 1 (Arg1) levels were increased in the cPLA group when compared  
268 to sham controls, incorporation of a.a. further increased Arg 1 levels among CD45<sup>+</sup>, CD11b<sup>+</sup>, F4/80<sup>+</sup>,  
269 CD11c<sup>+</sup> and CD11c<sup>+</sup>MHCII<sup>+</sup> populations (Fig. 4h-l).

270 Given the distinct observation made with cPLA implants, we sought to elucidate the role of the  
271 adaptive immune response, including CD19 B cell activity<sup>36</sup>, CD4 T helper and CD8 cytotoxic T cells<sup>25,37</sup>.  
272 With cPLA implantation, CD8 expression was increased when compared to sham controls, and  
273 incorporation of a.a. decreased elevated levels (Fig. 4m). Similarly, CD4 expression was higher in the cPLA  
274 group compared to sham controls, with 3PO reducing elevated levels (Fig. 4n). CD4<sup>+</sup> cells expressing IFN-  
275  $\gamma$  were reduced in the cPLA group when compared to sham controls; incorporation of a.a. or 3PO tended  
276 to increase IFN- $\gamma$  expression only to levels similar to the sham group (Fig. 4o). In contrast, CD4<sup>+</sup> cells  
277 expressing IL-4 were similar between the cPLA group and sham controls, with incorporation of a.a. or 3PO  
278 increasing IL-4 levels (Fig. 4p). Assessing CD4<sup>+</sup> cells expressing IL-17 revealed reduced expression in the  
279 cPLA group when compared to sham controls; incorporation of a.a. or 3PO tended to increase IL-17  
280 expression only to levels similar to the sham group (Fig. 4q). While the  $\gamma\delta$ -repertoires was decreased in the  
281 cPLA group when compared to sham controls, incorporation of 3PO but not a.a. tended to increase the T  
282 cell receptor repertoires (Fig. 4r). Additionally, while there were no changes in IFN- $\gamma$  and IL-17 expression  
283 from  $\gamma\delta$ <sup>+</sup> T-cells, incorporation of a.a. or 3PO increased IL-4 expression from  $\gamma\delta$ <sup>+</sup> T-cells (Fig. 4s-u). There  
284 were no changes in IL-17 expression from innate lymphoid cells (Fig. 4v). We did not observe changes in  
285 CD19 expression between the cPLA group and sham controls; however, incorporation of 3PO tended to  
286 increase CD19 expression (Fig. 4w).

287

## 288 Discussion.

289 Although polylactide-based medical devices are FDA-approved for applications in adult  
290 reconstructive surgery, drug delivery and nanotechnology, their clinical utility is significantly limited by long-  
291 term, sterile inflammation, which is poorly understood<sup>3,38</sup>. Our findings suggest that the activation states  
292 and trafficking of immune cells to the amorphous polylactide (aPLA) biomaterial microenvironment is  
293 dependent on CCR2 and CX3CR1 expression, with CCR2<sup>5</sup> likely to play a greater role over CX3CR1<sup>18,19</sup>  
294 expression. We reveal that both CCR2 and CX3CR1 signaling could be regulated by locally controlling  
295 glycolytic flux through targeting hexokinase in the biomaterial microenvironment. In liver models of sterile  
296 injury as well as in the heart following myocardial infarction, CCR2<sup>+</sup> monocytes dominate the  
297 proinflammatory phase, with CCR2<sup>+</sup>CX3CR1<sup>+</sup> and CX3CR1<sup>+</sup> monocytes and macrophages playing a  
298 greater role during the anti-inflammatory or reparative phase of healing<sup>14,39</sup>. In our study, however, sterile  
299 aPLA implants increase proinflammatory (CD86<sup>+</sup>CD206<sup>-</sup>) proportions of CCR2<sup>+</sup>, CX3CR1<sup>+</sup> and  
300 CCR2<sup>+</sup>CX3CR1<sup>+</sup> cell populations, while decreasing transition (CD86<sup>+</sup>CD206<sup>+</sup>) and anti-inflammatory  
301 proportions (CD206<sup>+</sup>) of CCR2<sup>+</sup> populations, an effect that required CCR2- and CX3CR1-competency.  
302 Against our hypothesis, incorporation of a.a did not reduce monocyte recruitment around biomaterials;  
303 however, it reshaped the composition of recruited CCR2<sup>+</sup>, CX3CR1<sup>+</sup> and CCR2<sup>+</sup>CX3CR1<sup>+</sup> cell populations  
304 to comprise reduced proinflammatory, and elevated transition and anti-inflammatory proportions. These  
305 transition immune cell populations suggest a reversal of proinflammatory biomaterial responses, playing a  
306 crucial role in angiogenesis and tissue regeneration<sup>26,27</sup>. Consistent with our findings, an increase in  
307 CX3CR1<sup>+</sup> populations is observed around polylactide copolymers<sup>40</sup>.

308 Myeloid cell recruitment to aPLA-based implants appears to be regulated by immunometabolism  
309 in the biomaterial microenvironment. We observed a two-pronged effect of aPLA in constituting a  
310 proinflammatory biomaterial microenvironment—aPLA elevated the relative levels of proinflammatory  
311 monocytes while concurrently decreasing the relative proportions of transition and anti-inflammatory  
312 monocytes. This trend is observable in-vitro with polyethylene wear particles<sup>6,10</sup> and other types of  
313 polylactide materials<sup>7</sup>, whose implantation result in chronic inflammatory responses. Consequently, it is  
314 likely that this two-pronged effect occurs with other classes of biomaterials, providing new insight into  
315 complex ways that biomaterials modify their immune microenvironment.

316 During the inflammatory response to implants, the biomaterial microenvironment is glycolytically  
317 reprogrammed, showing enhanced radiolabeled glucose uptake in mice<sup>20</sup>, an observation made in  
318 implanted human patients<sup>41,42</sup>. Our findings reveal that disrupting elevated glycolytic flux using 2DG or a.a.  
319 decreased proinflammatory monocytes, increased transition and anti-inflammatory monocytes, and  
320 decreased neutrophil recruitment to the biomaterial microenvironment. Paradoxically, aPLA implantation  
321 decreased macrophage and dendritic cell recruitment, while lowering MHCII expression on dendritic cells,  
322 an observation that is thought to imply an immunomodulatory role of polylactide implants<sup>32</sup>. We reproduce

323 these findings, but also uncover that the relative proportion of proinflammatory macrophages, dendritic cells  
324 or dendritic cells expressing MHCII is increased by aPLA implantation. With macrophages and, to lesser  
325 extent, dendritic cells and dendritic cells expressing MHCII, inhibiting glycolysis reduced proinflammatory  
326 and increased transition and anti-inflammatory proportions, providing new insight on how biomaterials could  
327 result in chronic inflammation all the while orchestrating seemingly conflicting immunological events. Of  
328 note, CCR2- and CX3CR1-deficiency prevents the recruitment of neutrophils, monocytes, macrophages,  
329 dendritic cells and MHCII expression on dendritic cells in the aPLA microenvironment, which may be due  
330 to the role of CCR2 in promoting the local activation and maturation of immune cells<sup>43,44</sup>.

331 Historically, chronic inflammation by aPLA is thought to be due to acidic degradation products<sup>34</sup>.  
332 As such, neutralizing aPLA products with alkaline salts, like hydroxyapatite (HA), is currently the mainstay  
333 in clinics. Contrary to HA's effects, a.a. further makes the biomaterial microenvironment acidic<sup>20</sup>; therefore,  
334 in principle, a.a. should worsen aPLA-induced inflammation. We show that, while incorporating a.a. reduced  
335 neutrophil levels, HA increased neutrophil recruitment, accentuating inflammation. To extents greater than  
336 HA's, incorporating a.a. in aPLA implants reduced the relative proportion of proinflammatory immune cells,  
337 including overall nucleated hematopoietic cell populations, monocytes, macrophages, dendritic cells and  
338 dendritic cells expressing MHCII. Furthermore, a.a. largely increased transition and anti-inflammatory  
339 cellular proportions more than HA could. This suggests that, while pH may exert some role in the process,  
340 it is not the sole regulator of immunological events in the polylactide microenvironment.

341 Crystalline polylactide (cPLA) degrades at significantly slower rates than aPLA<sup>20</sup>. In contrast to  
342 observations made with aPLA, cPLA increased macrophage and dendritic cell recruitment, did not elevate  
343 neutrophil levels nor reduce MHCII expression on recruited dendritic cells. Also, unlike with aPLA, glycolytic  
344 inhibition did not reduce myeloid proinflammatory nor increase myeloid transition and anti-inflammatory  
345 proportions. However, glycolytic inhibition in the cPLA microenvironment reduced macrophage recruitment,  
346 specifically increased IL-4-expressing  $\gamma\delta^+$  T-cells and T helper 2 cells, while keeping IFN- $\gamma$  at homeostatic  
347 levels, necessary for tissue physiology<sup>45</sup>. Importantly, a.a. reduced monocyte recruitment and increased  
348 Arg1 expression among overall myeloid populations, including monocytes, macrophages, dendritic cells  
349 and dendritic cells expressing MHCII. This observation is consistent with a.a. inhibiting aspartate  
350 aminotransferase, a key transaminase in the aspartate-arginosuccinate shunt in proinflammatory  
351 macrophages during metabolic reprogramming<sup>46</sup>. Antigen presenting cells are able to activate both class I  
352 and II MHC, following exposure to biomaterials<sup>47</sup>. While a.a. reduced cytotoxic T lymphocytes, 3PO reduced  
353 overall T helper cell recruitment to the cPLA biomaterial microenvironment, consistent with the crucial role  
354 of metabolism on T-cell function<sup>48</sup>.

355 In summary, our findings provide new insight on the role of immunometabolic cues on immune  
356 cellular trafficking to the biomaterial microenvironment, and how this affects the composition and activation  
357 states of immune cell populations. As orally-delivered small molecules, both a.a. and 3PO, as well as their  
358 derivatives, have been well tolerated when administered during clinical trials in cancer and Huntington's  
359 disease<sup>23,49</sup>. Therefore, temporally-regulated, local release of these metabolic modulators from implants to  
360 program the trafficking and polarization of immune cells in the biomaterial microenvironment offers a highly  
361 translatable opportunity that could advance regenerative engineering toward improved human and animal  
362 health.

## 363 **Methods.**

364 **Biomaterial formulation and metabolic modulators.** Amorphous polylactide (aPLA; PLA 4060D) and  
365 semi-crystalline polylactide (cPLA; PLA 3100HP) biomaterials from NatureWorks LLC were used. As  
366 metabolic modulators and for neutralization studies, 3-(3-pyridinyl)-1-(4-pyridinyl)-2-propen-1-one (3PO;  
367 MilliporeSigma), 2-deoxyglucose (2DG; MilliporeSigma), aminoxyacetic acid (a.a.; Sigma-Aldrich) and  
368 hydroxyapatite (HA; 2.5  $\mu\text{m}^2$  particle sizes<sup>50</sup>; Sigma-Aldrich) were incorporated into biomaterials by melt-  
369 blending at 190 °C for 3 mins in a DSM 15 cc mini-extruder (DSM Xplore), then made into pellets using a  
370 pelletizer (Leistritz Extrusion Technology). Afterwards, pellets were made into 1.75 mm (diameter) filaments  
371 using an extruder (Filabot EX2) at 170 °C with air set at 93. Filaments were cut into 1 mm-long or 7.5 mm-  
372 long sizes, then sterilized by ultraviolet radiation for 30 minutes<sup>51</sup>. Based on prior studies<sup>20</sup>, we estimated  
373 that 189 mg of 2DG, 4.86 mg of 3PO, 90 mg of a.a. or 200 mg of HA in 10 g of aPLA or cPLA will  
374 approximate concentrations that were effective when applied in-vitro. To control for melt-blending as a  
375

376 confounder, biomaterials not incorporating metabolic modulators or HA, were processed under similar  
377 conditions to make “reprocessed” formulations.

378  
379 **Mice.** Animal studies were approved by the Institutional Animal Care and Use Committee at Michigan State  
380 University (PROTO202100327). *Ccr2<sup>RFP/RFP</sup>Cx3cr1<sup>GFP/GFP</sup>* mice, B6(Cg)-Tyr<sup>c-2J</sup>/J (B6 albino) mice and  
381 C57BL/6J (wild-type B6) mice were obtained from the Jackson Laboratory. To generate  
382 *Ccr2<sup>RFP/+</sup>Cx3cr1<sup>GFP/+</sup>* mice, we crossed female *Ccr2<sup>RFP/RFP</sup>Cx3cr1<sup>GFP/GFP</sup>* (8-week old) mice to male B6(Cg)-  
383 Tyr<sup>c-2J</sup>/J (B6 albino; 8-week old) mice, as previously described<sup>18,19</sup>. At 4-week old, generated  
384 *Ccr2<sup>RFP/+</sup>Cx3cr1<sup>GFP/+</sup>* mice were assigned n = 3 (two females, one male) per group. Only female mice (n =  
385 3 per group) were used for studies involving *Ccr2<sup>RFP/RFP</sup>Cx3cr1<sup>GFP/GFP</sup>* mice (14-week old) and C57BL/6J  
386 mice (9-week old).

387  
388 **Subcutaneous surgical model.** Anesthesia was accomplished using isoflurane (2-3 %). Using aseptic  
389 technique, the skin of each mouse was shaved and disinfected using iodine and alcohol swabs. Surgical  
390 incision was made through the skin into the subcutis, with or without biomaterial implantation after a pouch  
391 had been made with forceps. Surgical glue (3M Vetbond) was used to close the skin, and each mouse  
392 received intraperitoneal or subcutaneous pre- and post-operative meloxicam (5 mg/ kg) injections as well  
393 as postoperative saline. In *Ccr2<sup>RFP/+</sup>Cx3cr1<sup>GFP/+</sup>* mice and *Ccr2<sup>RFP/RFP</sup>Cx3cr1<sup>GFP/GFP</sup>* mice, the neck (just  
394 caudal to the ear; Supplementary Fig. 1a) was surgically incised (sham) and implanted using 7.5 mm long  
395 filaments to allow for imaging of the biomaterial microenvironment. In C57BL/6J mice, the dorsum (back)  
396 of mice incised (sham) and implanted using 1 mm long filaments.

397  
398 **Intravital microscopic imaging and processing.** Mice were anesthetized using a isoflurane (2-3 %), and  
399 image stacks were acquired using a Leica SP8 DIVE laser multiphoton microscope equipped with Spectra-  
400 Physics Insight X3 dual beam (630 to 1300 nm tunable and 1040 nm fixed) and 4Tune, tunable, super  
401 sensitive hybrid detectors (HyDs). To acquire serial optical sections, a laser beam (940 nm for GFP; 1040  
402 nm for RFP) was focused through a 25x water-immersion lens (NA 1.00 HC PL IRAPO, Leica) and scanned  
403 with a field of view of 0.59 × 0.59 mm<sup>2</sup> at 600 Hz. To visualize a larger area, 3 tiles of optical fields were  
404 imaged using a motorized stage to automatically acquire sequential fields of view. Z-stacks were acquired  
405 in 3 μm steps to image a total depth of 117 μm of tissue. To avoid fluorophore bleed-through, images were  
406 acquired using sequential scanning in between frames. Visualization of collagen was achieved via the  
407 second harmonic signal using the blue channel at 940 nm. Raw image stacks were imported into Fiji  
408 software (v1.53t; National Institute of Health) for tile merging. The tiled images were stitched by a  
409 grid/collection stitching plugin in Fiji. The merged image stacks were then imported into Imaris software  
410 (v10.0.0; Bitplane/Oxford Instruments) for further processing. Melanin autofluorescence from mouse skin  
411 was subtracted from the green and red channels. Also, GFP-expressing cells in the epidermis were  
412 excluded from images, as these are likely dendritic epidermal T cells<sup>52,53</sup>. The filtered red, green, and blue  
413 channels were then z-projected and shown as a single 2D image, with videos created in Imaris to show the  
414 individual slices from processed z-stacks.

415  
416 **Tissue harvesting and dissociation.** After 11 weeks post-operatively, mice were shaved around incision  
417 sites (sham) or biomaterials, then euthanized to obtain biopsies. As some implants had migrated and were  
418 unidentifiable, biopsies were obtained from only visible implants. In *Ccr2<sup>RFP/+</sup>Cx3cr1<sup>GFP/+</sup>* mice and  
419 *Ccr2<sup>RFP/RFP</sup>Cx3cr1<sup>GFP/GFP</sup>* mice, rectangular biopsies (9.5 mm long and 3.75 mm wide) around incision sites  
420 (sham) or biomaterials were collected. In C57BL/6J mice, circular biopsies (8 mm diameter) were collected.  
421 Tissues from different mice belonging to the same group in each study were collected together for  
422 dissociation. Tissues were placed into 10 mL of an enzyme cocktail containing 0.5 mg/ mL Liberase (Sigma-  
423 Aldrich), 0.5 mg/ mL Collagenase Type IV (Stem Cell Technologies), 250 U/ mL Deoxyribonuclease I  
424 (Worthington Biochemical Corporation) in 25mM HEPES buffer (Sigma-Aldrich) on a serrated Petri dish.  
425 Next, tissues were cut with surgical scissors for ~1 minute and moved to an incubator at 37°C with 5% CO<sub>2</sub>  
426 on top of an orbital shaker, shaking at 70 rpm for 1 hour. After the incubation period, the petri dish was  
427 removed and 5 mL of the enzyme cocktail and dissociated cells were put through a 70 μm filter into a 50mL  
428 conical tube. In another 5 mL of enzyme cocktail, undigested (residual) tissues were mechanically

429 dissociated by being pressed against the serrated portion of the petri dish. Afterwards, using a 25 mL  
430 pipette, the 5mL of enzyme cocktail was filtered into a 50mL conical. Any undigested tissue on top of the  
431 70 $\mu$ m filter was further mechanically digested with the thumb press of a syringe plunger for optimal  
432 extraction of cells. Using the same 25mL pipette, 30mL of cold Hanks' Balanced Salt Solution without  
433 calcium, magnesium and phenol red (ThermoFisher Scientific) was used to wash the digestion petri dish  
434 and filtered into the 50mL conical. The cells in the 50mL conical were centrifuged at 350 x g for 10 minutes  
435 and the supernatant was discarded. Sedimented cells were counted then used for flow cytometry.  
436

437 **Flow cytometry.** Following tissue digestion, for experiments involving *Ccr2*<sup>RFP/+</sup>*Cx3cr1*<sup>GFP/+</sup> mice and  
438 *Ccr2*<sup>RFP/RFP</sup>*Cx3cr1*<sup>GFP/GFP</sup> mice, 1.5x10<sup>6</sup> cells /well (n = 3 wells) were used for staining in a polypropylene  
439 96-well round bottom plate. All staining steps were performed in 100  $\mu$ L volume in the dark at 4 °C. Samples  
440 were first incubated with LIVE/DEAD Fixable Blue Dead Cell Stain Kit (1:500, ThermoFisher, L23105) for  
441 30 min. Cells were washed once with flow buffer (1X phosphate buffered saline (PBS), 0.5% bovine serum  
442 albumin), followed by incubation with TruStain FcX PLUS (anti-mouse CD16/32) Antibody (BioLegend,  
443 156603; 0.25  $\mu$ g/sample) for 10 minutes. The following antibodies were mixed and added directly to the cell  
444 suspension: BV421 CD86 (1:200, Biolegend, 105031), PacBlue Ly6G (1:150, Biolegend, 127611), BV605  
445 CD45 (1:300, Biolegend, 103139), BV785 F4/80 (1:300, Biolegend, 123141), PerCP MHCII (1:200,  
446 Biolegend, 107623), PE-Dazzle 594 CD11c (1:500, Biolegend, 117347), APC CD206 (1:200, Biolegend,  
447 141707) and AF700 CD11b (1:400, Biolegend, 101222). Cells and antibody mixture were incubated for 30  
448 minutes. Cells were washed twice with flow staining buffer and fixed with 4% PFA for 10 minutes and  
449 resuspended in a final volume of 100  $\mu$ L for flow cytometry analysis.  
450

451 For experiments involving C57BL/6J mice, 1x10<sup>6</sup> cells were used for staining in a polypropylene 96-well  
452 round bottom plate (n = 3). All staining steps were performed in 100  $\mu$ L volume in the dark at 4°C. Samples  
453 were first incubated with LIVE/DEAD Fixable Blue Dead Cell Stain Kit (1:500, ThermoFisher, cat#L23105)  
454 for 20 minutes. Cells were washed once with flow buffer, followed by incubation with TruStain FcX (anti-  
455 mouse CD16/32) Antibody (BioLegend, 101319; 1  $\mu$ g/sample) in 50  $\mu$ L volume for 10 minutes. The  
456 following antibodies were mixed together and added directly to the cell suspension: BV605 CD45 (1:500,  
457 Biolegend, 103139), AF700 CD11b (1:300, Biolegend, 101222), BV785 F4/80 (1:300, Biolegend, 123141),  
458 BV421 CD86 (1:200, Biolegend, 105031), APC CD206 (1:200, Biolegend, 141707), PerCP MHCII (1:200,  
459 Biolegend, 107623), SparkBlue 550 CD3 (1:100, Biolegend, 100259), APC-Fire 810 CD4 (1:100,  
460 Biolegend, 100479), BB700 CD8a (1:100, Biolegend, 566410), BV711  $\gamma$  $\delta$  TCR (1:200, BD Bioscience,  
461 563994), BV480 Thy 1.2 (CD90.2; 1:40, BD Bioscience, 746840), BUV615 CD19 (1:80, BD Bioscience,  
462 751213), PacBlue Ly6G (1:250, BD Bioscience, 127611) and PE-Dazzle 594 CD11c (1:500, Biolegend,  
463 117347). Cells and antibody mixture were incubated for 30 minutes. Cells were washed once prior to  
464 fixation and permeabilization (BD Cytofix/Cytoperm kit, BDB554714) as per manufacturer's instructions.  
465 Cells were then resuspended in BD Perm/wash buffer with the following antibodies: BV650 IL4 (1:50, BD  
466 Bioscience, cat#564004), APC-Fire750 IFN $\gamma$  (1:80, Biolegend, 505859), AF647 IL-17a (1:200, Biolegend,  
467 506911) and PE-Cy7 Arg1 (1:100, ThermoFisher, 25-3697-80). Cells were incubated with antibody mixture  
468 for 30 minutes. Cells were washed twice with BD Perm/wash buffer followed by resuspension in a final  
469 volume of 100  $\mu$ L for flow cytometry analysis.  
470

471 All samples were analyzed using the Cytek Aurora spectral flow cytometer (Cytek Biosciences, CA, USA).  
472 Fluorescence minus one (FMO) samples were used to guide gating strategies shown in Supplementary  
473 Fig. 1b. Flow cytometry data was analyzed with the software FCSExpress (DeNovo Software, CA, USA).  
474

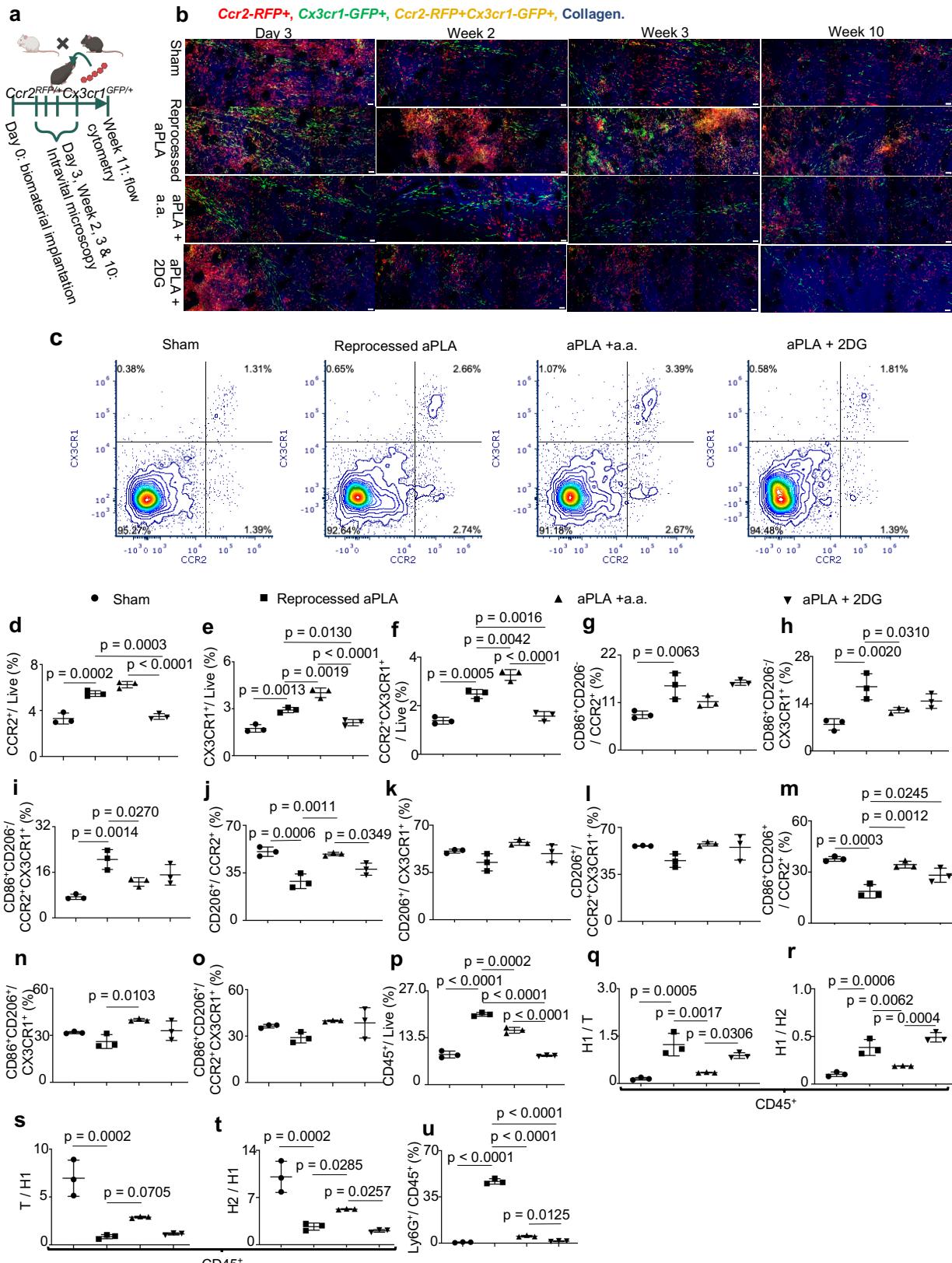
475 **Statistics and reproducibility.** Statistical software (GraphPad Prism Version 9.5.1 (528)) was used to  
476 analyse data presented as mean with standard deviation (SD). Exact statistical test, p-values and sample  
477 sizes are provided in figure legends.  
478

479 **Data availability.** The data supporting the findings of this study are available within the paper and its  
480 Supplementary Information.  
481

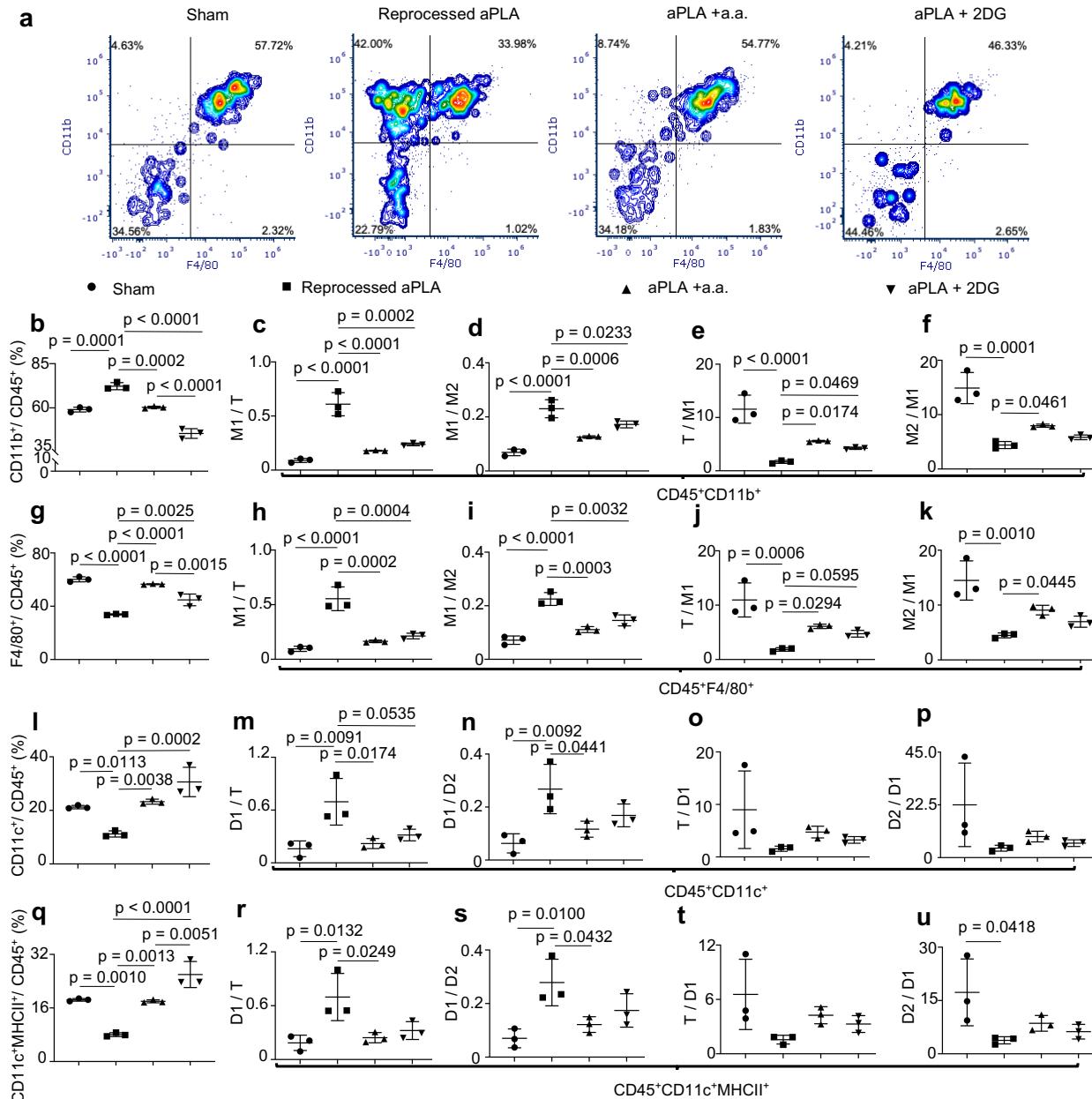
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485  
486 **Author contributions.** Conceptualization, C.V.M. and C.H.C.; Methodology, C.V.M., A.S., A.V.M., E.U.,  
487 K.B.S., H.P., M.M.K., O.M.B., A.T., M.A., A.S., S.C., A.J.O., K.D.H., R.N., S.P., J.H.E., and C.H.C.;  
488 Investigation, C.V.M., A.S., A.V.M., E.U., H.P., M.M.K., O.M.B., A.T., M.A., S.C.; Writing – Original Draft,  
489 C.V.M.; Writing – Review & Editing, C.V.M., A.S., A.V.M., E.U., K.B.S., H.P., M.M.K., O.M.H., A.T., M.A.,  
490 A.K., S.C., A.J.O., K.D.H., R.N., S.P., J.H.E., and C.H.C.; Funding Acquisition, C.H.C.; Resources, R.N.  
491 and C.H.C.; Supervision, A.J.O., K.D.H., R.N., S.P., J.H.E., and C.H.C.

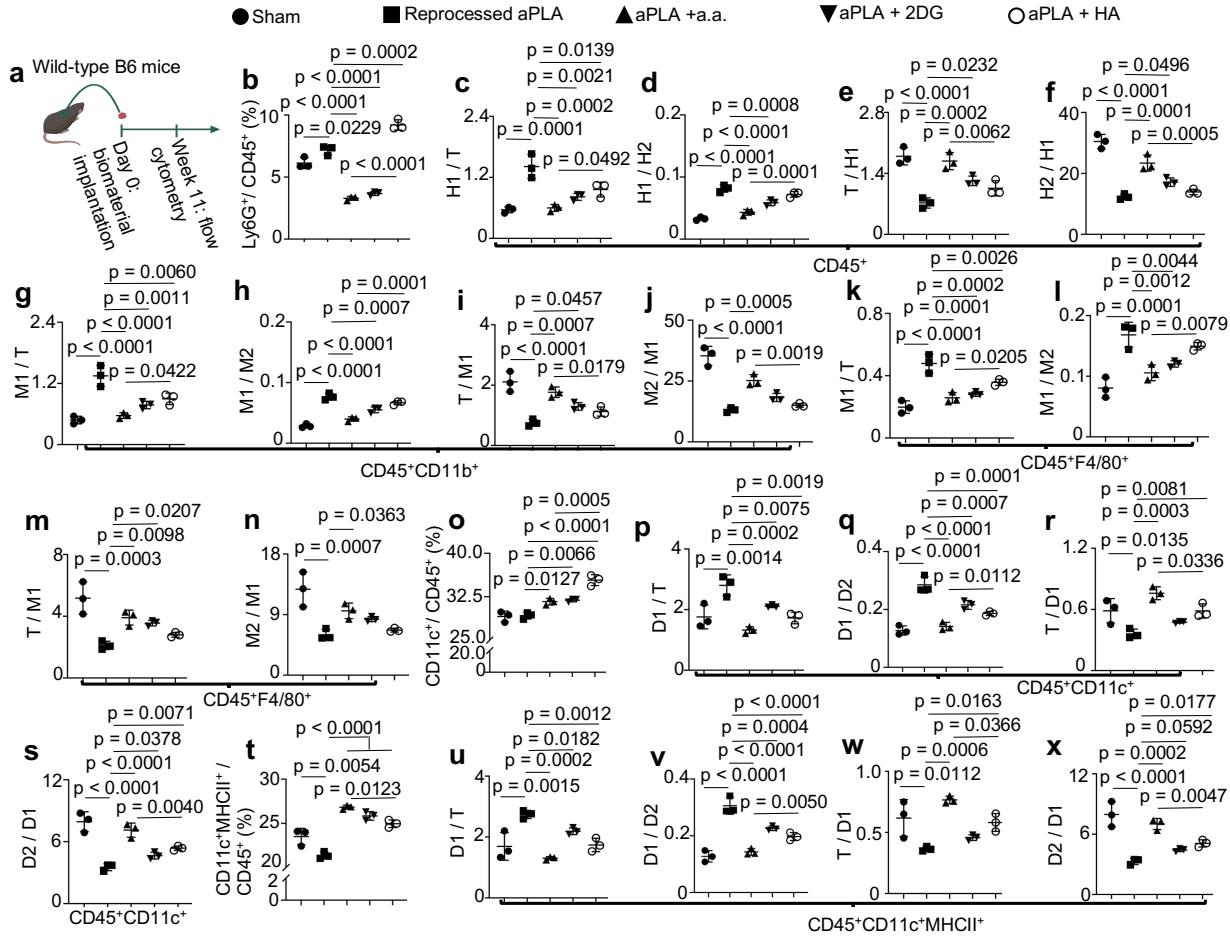
492  
493 **Competing interests.** C.V.M and C.H.C are inventors on a pending patent application filed by Michigan  
494 State University on metabolic reprogramming to biodegradable polymers.



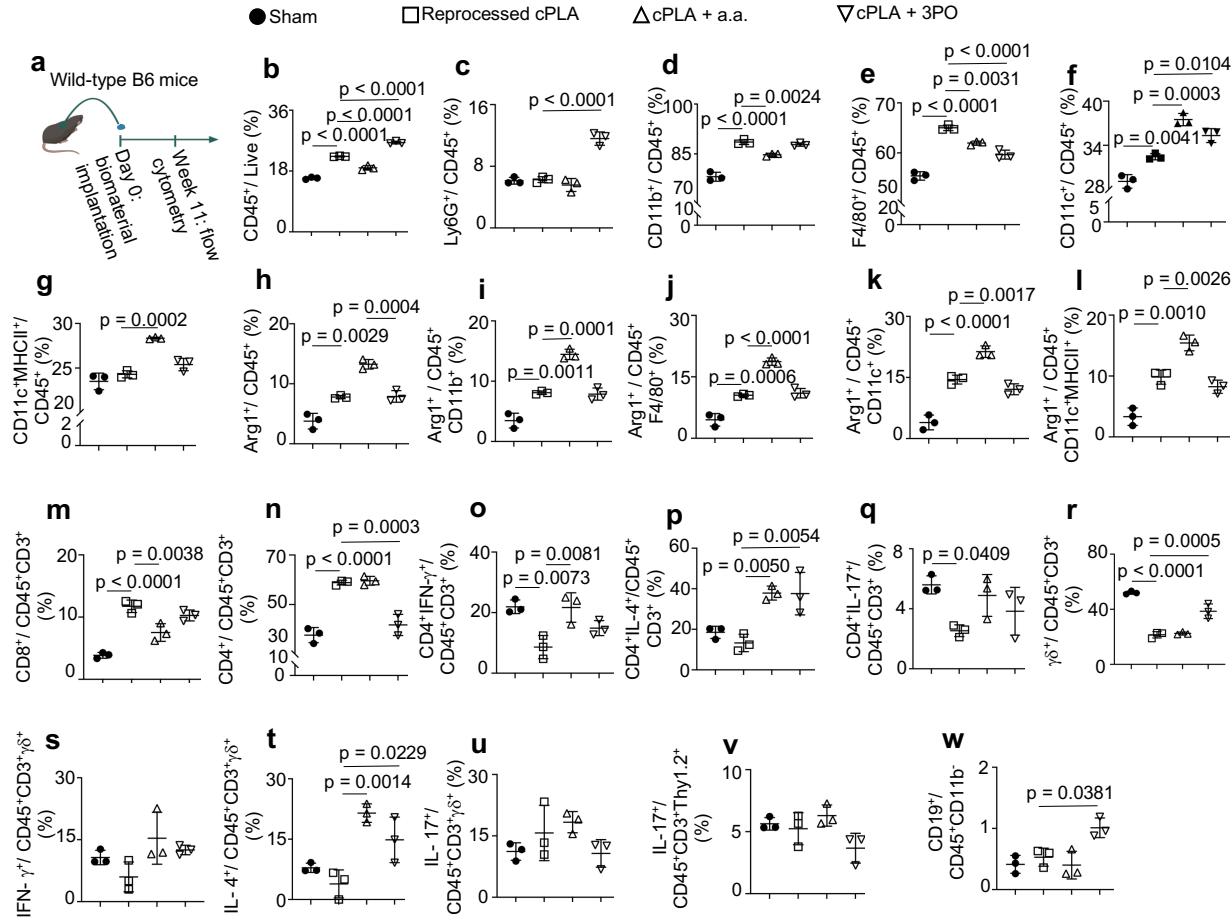
498  
499 **Figure 1 | Locally rewiring immune cell metabolism in the amorphous polylactide biomaterial environment affects CCR2- and**  
500 **CX3CR1-dependent trafficking.** **a**, B6 albino mice were crossed to  $Ccr2^{RFP/RFP} Cx3cr1^{GFP/GFP}$  mice to generate  $Ccr2^{RFP/+} Cx3cr1^{GFP/+}$  mice,  
501 which were surgically incised (sham group) or implanted with biomaterials. Intravital microscopy preceded flow cytometric analysis of  
502 tissues around incision sites (sham group) or biomaterials. **b**, Representative intravital microscopy images around incision sites (sham  
503 group), reprocessed amorphous polylactide (aPLA), aPLA incorporating aminoxyacetic acid (a.a.) or 2-deoxyglucose (2DG); scale bars  
are 50  $\mu$ m. **c**, Representative CCR2 and CX3CR1 flow cytometry plots gated on live cells. **c-e**, Flow cytometry quantification of CCR2<sup>+</sup>(c),  
CX3CR1<sup>+</sup>(d) and CCR2<sup>+</sup>CX3CR1<sup>+</sup>(e) cells. **f-h**, Quantification of proinflammatory (CD86<sup>+</sup>CD206<sup>+</sup>) cells among CCR2<sup>+</sup>(f), CX3CR1<sup>+</sup>(g)  
and CCR2<sup>+</sup>CX3CR1<sup>+</sup>(h) populations. **i-k**, Quantification of anti-inflammatory (CD206<sup>+</sup>) cells among CCR2<sup>+</sup>(i), CX3CR1<sup>+</sup>(j) and  
CCR2<sup>+</sup>CX3CR1<sup>+</sup>(k) populations. **l-n**, Quantification of transition (CD86<sup>+</sup>CD206<sup>+</sup>) cells among CCR2<sup>+</sup>(l), CX3CR1<sup>+</sup>(m) and  
CCR2<sup>+</sup>CX3CR1<sup>+</sup>(n) populations. **o**, Nucleated hematopoietic (CD45<sup>+</sup>) cells. **p-q**, Fold change of proinflammatory (H1; CD86<sup>+</sup>CD206<sup>+</sup>)  
cells with respect to transition (T; CD86<sup>+</sup>CD206<sup>+</sup>) cells (p) or anti-inflammatory (H2; CD206<sup>+</sup>) cells (q). **r-s**, Fold change of T (r) or H2 (s)  
cells with respect to H1 cells. **t**, Neutrophils (CD45<sup>+</sup>Ly6G<sup>+</sup> cells). One-way ANOVA followed by Tukey's or Newman-Keul's multiple  
comparison test, n = 3 mice per group.



**Figure 2 | Polarization states of myeloid cells are regulated by targeting immunometabolism in the amorphous polylactide biomaterial microenvironment.** **a**, Representative flow cytometry plots gated on CD45. **b-f**, Monocytes (CD45<sup>+</sup>CD11b<sup>+</sup> cells). **c-d**, Fold change of proinflammatory (M1; CD86<sup>+</sup>CD206<sup>-</sup>) monocytes with respect to transition (T; CD86<sup>+</sup>CD206<sup>+</sup>) monocytes (c) or anti-inflammatory (M2; CD206<sup>+</sup>) monocytes (d). **e-f**, Fold change of T (e) or M2 (f) monocytes with respect to M1 monocytes. **g**, Macrophages (CD45<sup>+</sup>F4/80<sup>+</sup> cells). **h-i**, Fold change of proinflammatory (M1; CD86<sup>+</sup>CD206<sup>-</sup>) macrophages with respect to transition (T; CD86<sup>+</sup>CD206<sup>+</sup>) macrophages (h) or anti-inflammatory (M2; CD206<sup>+</sup>) macrophages (i). **j-k**, Fold change of T (j) or M2 (k) macrophages with respect to M1 macrophages. **l**, Dendritic (CD45<sup>+</sup>CD11c<sup>+</sup>) cells. **m-n**, Fold change of proinflammatory (D1; CD86<sup>+</sup>CD206<sup>-</sup>) dendritic cells with respect to transition (T; CD86<sup>+</sup>CD206<sup>+</sup>) dendritic cells (m) or anti-inflammatory (D2; CD206<sup>+</sup>) dendritic cells (n). **o-p**, Fold change of T (o) or D2 (p) dendritic cells with respect to D1 dendritic cells. **q**, Dendritic cells expressing class II major histocompatibility complex (MHC II) molecules (CD45<sup>+</sup>CD11c<sup>+</sup>MHCII<sup>+</sup> cells). **r-s**, Fold change of proinflammatory (D1; CD86<sup>+</sup>CD206<sup>-</sup>) MHCII<sup>+</sup> dendritic cells with respect to transition (T; CD86<sup>+</sup>CD206<sup>+</sup>) MHCII<sup>+</sup> dendritic cells (r) or anti-inflammatory (D2; CD206<sup>+</sup>) MHCII<sup>+</sup> dendritic cells (s). **t-u**, Fold change of T (t) or D2 (u) MHCII<sup>+</sup> dendritic cells with respect to D1 MHCII<sup>+</sup> dendritic cells. One-way ANOVA followed by Tukey's or Newman-Keul's multiple comparison test, n = 3 mice per group; amorphous polylactide, aPLA; aminoxyacetic acid, a.a.; 2-deoxyglucose, 2DG.



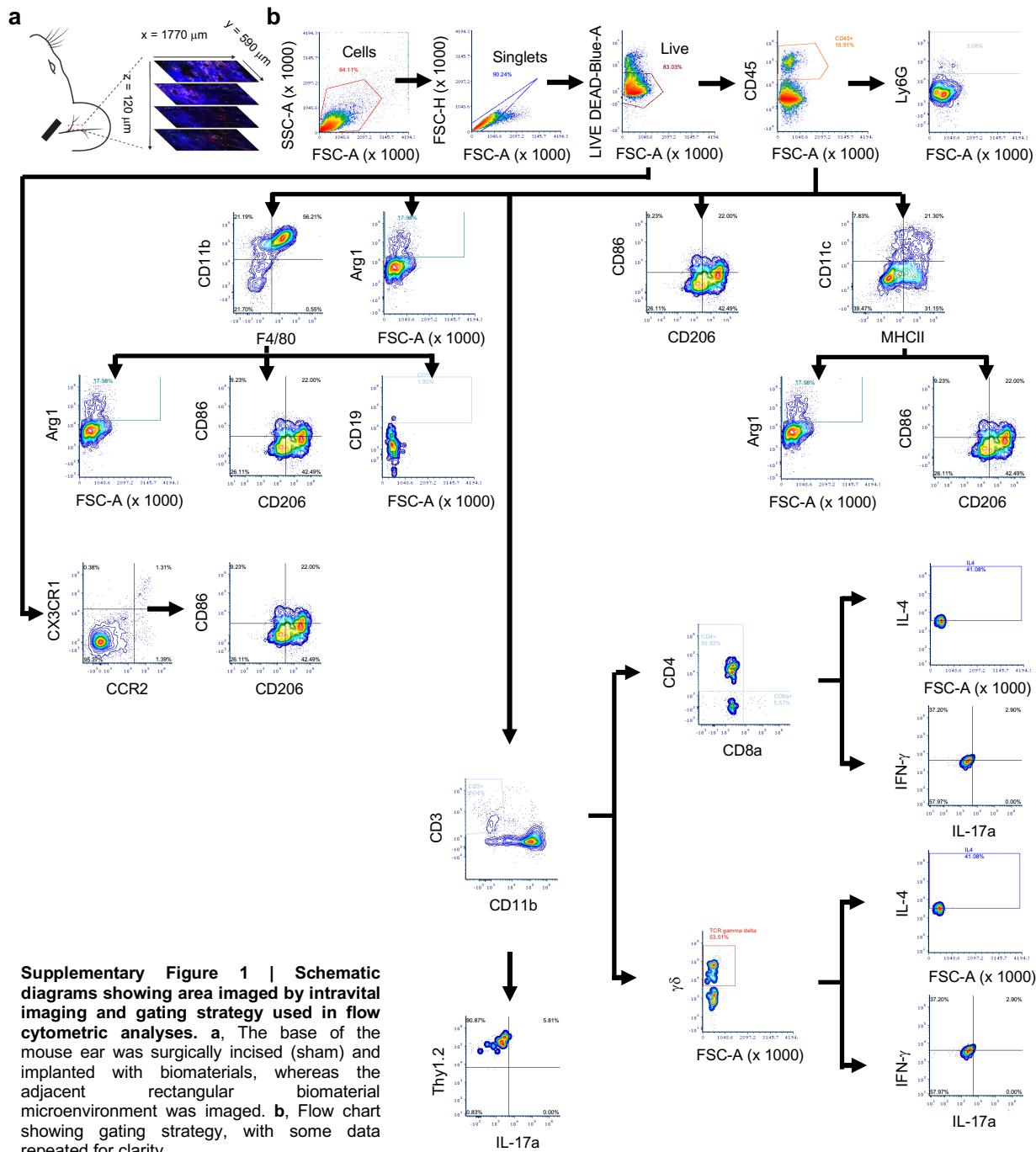
**Figure 3 | Using an acid more favorably modulates activation states of immune cells around amorphous polylactide biomaterials compared to traditional neutralization techniques.** **a**, Wild-type B6 mice were surgically incised (sham group) or implanted with reprocessed amorphous polylactide (aPLA), aPLA incorporating aminoxyacetic acid (a.a.), 2-deoxyglucose (2DG) or hydroxyapatite (HA). Afterwards, flow cytometric analysis of tissues around incision sites (sham group) or biomaterials was undertaken. **b**, Neutrophils (CD45<sup>+</sup>Ly6G<sup>+</sup> cells). **c-d**, Fold change of proinflammatory (H1; CD86<sup>+</sup>CD206<sup>+</sup>) cells with respect to transition (T; CD86<sup>+</sup>CD206<sup>+</sup>) cells (c) or anti-inflammatory (H2; CD206<sup>+</sup>) cells (d), gated for nucleated hematopoietic (CD45<sup>+</sup>) populations. **e-f**, Fold change of T (e) or H2 (f) cells with respect to H1 cells. **g-h**, Fold change of proinflammatory (M1; CD86<sup>+</sup>CD206<sup>+</sup>) monocytes (CD45<sup>+</sup>CD11b<sup>+</sup>) with respect to transition (T; CD86<sup>+</sup>CD206<sup>+</sup>) monocytes (g) or anti-inflammatory (M2; CD206<sup>+</sup>) monocytes (h). **i-j**, Fold change of T (i) or M2 (j) monocytes with respect to M1 monocytes. **k-l**, Fold change of proinflammatory (M1; CD86<sup>+</sup>CD206<sup>+</sup>) macrophages (CD45<sup>+</sup>F4/80<sup>+</sup>) with respect to transition (T; CD86<sup>+</sup>CD206<sup>+</sup>) macrophages (k) or anti-inflammatory (M2; CD206<sup>+</sup>) macrophages (l). **m-n**, Fold change of T (m) or M2 (n) macrophages with respect to M1 macrophages. **o**, Dendritic (CD45<sup>+</sup>CD11c<sup>+</sup>) cells. **p-q**, Fold change of proinflammatory (D1; CD86<sup>+</sup>CD206<sup>+</sup>) dendritic cells with respect to transition (T; CD86<sup>+</sup>CD206<sup>+</sup>) dendritic cells (p) or anti-inflammatory (D2; CD206<sup>+</sup>) dendritic cells (q). **r-s**, Fold change of T (r) or D2 (s) dendritic cells with respect to D1 dendritic cells. **t**, Dendritic cells expressing class II major histocompatibility complex (MHC II) molecules (CD45<sup>+</sup>CD11c<sup>+</sup>MHCII<sup>+</sup> cells). **u-v**, Fold change of proinflammatory (D1; CD86<sup>+</sup>CD206<sup>+</sup>) MHCII<sup>+</sup> dendritic cells with respect to transition (T; CD86<sup>+</sup>CD206<sup>+</sup>) MHCII<sup>+</sup> dendritic cells (u) or anti-inflammatory (D2; CD206<sup>+</sup>) MHCII<sup>+</sup> dendritic cells (v). **w-x**, Fold change of T (w) or D2 (x) MHCII<sup>+</sup> dendritic cells with respect to D1 MHCII<sup>+</sup> dendritic cells. One-way ANOVA followed by Tukey's multiple comparison test, n = 3 mice per group.



**Figure 4 | Locally targeting immunometabolism in the crystalline polylactide environment elevates interleukin-4 (IL-4)-expressing T cell subsets with differential effects on myeloid populations.** **a**, Wild-type B6 mice were surgically incised (sham group) or implanted with reprocessed crystalline polylactide (cPLA), cPLA incorporating aminoxyacetic acid (a.a.) or 3-(3-pyridinyl)-1-(4-pyridinyl)-2-propen-1-one (3PO). Afterwards, flow cytometric analysis of tissues around incision sites (sham group) or biomaterials was undertaken. **b**, Nucleated hematopoietic (CD45<sup>+</sup>) cells. **c**, Neutrophils (CD45<sup>+</sup>Ly6G<sup>+</sup> cells). **d**, Monocytes (CD45<sup>+</sup>CD11b<sup>+</sup> cells). **e**, Macrophages (CD45<sup>+</sup>F4/80<sup>+</sup> cells). **f**, Dendritic (CD45<sup>+</sup>CD11c<sup>+</sup>) cells. **g**, Dendritic cells expressing class II major histocompatibility complex (MHC II) molecules (CD45<sup>+</sup>CD11c<sup>+</sup>MHCII<sup>+</sup> cells). **h-l**, Nucleated hematopoietic cells (h), monocytes (i), macrophages (j), dendritic cells (k), MHCII<sup>+</sup> dendritic cells (l) expressing Arginase 1 (Arg1<sup>+</sup>). **m**, Cytotoxic T lymphocytes (CD45<sup>+</sup>CD3<sup>+</sup>CD8<sup>+</sup> cells). **n**, T helper lymphocytes (CD45<sup>+</sup>CD3<sup>+</sup>CD4<sup>+</sup> cells). **o**, T helper 1 cells expressing interferon-gamma (IFN- $\gamma$ ). **p**, T helper 2 cells expressing interleukin-4. **q**, T helper 17 cells expressing interleukin-17A. **r**, gamma delta ( $\gamma\delta$ ) T (CD45<sup>+</sup>CD3<sup>+</sup> $\gamma\delta$ <sup>+</sup>) cells. **s-u**,  $\gamma\delta$ <sup>+</sup> T cells producing IFN- $\gamma$  (s), IL-4 (t) and IL-17A (u). **v**, Innate lymphoid cells (CD45<sup>+</sup>CD3<sup>+</sup>Thy1.2<sup>+</sup>) producing IL-17A. **w**, B cells (CD45<sup>+</sup>CD11b<sup>+</sup>CD19<sup>+</sup>). One-way ANOVA followed by Tukey's multiple comparison test, n = 3 mice per group.

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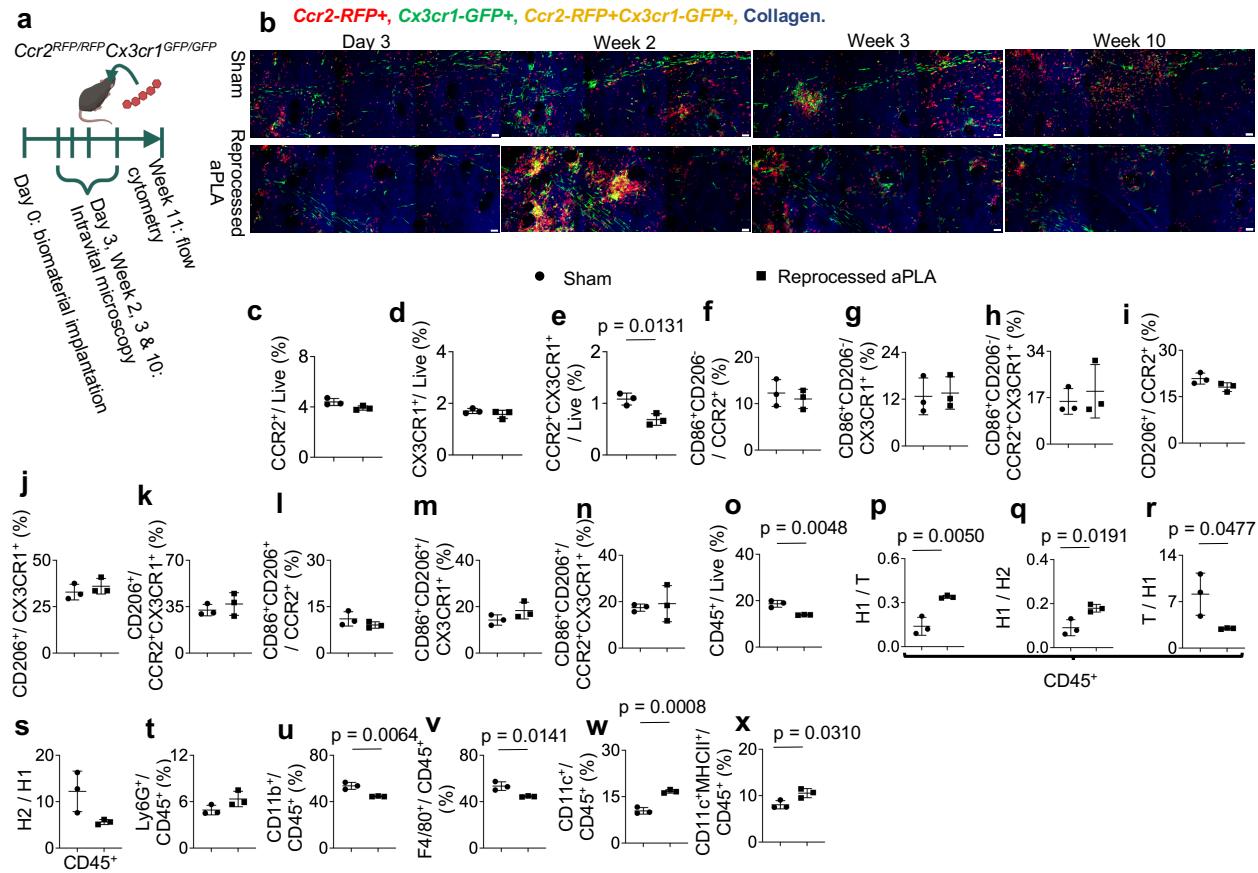


**Supplementary Figure 1 | Schematic diagrams showing area imaged by intravital imaging and gating strategy used in flow cytometric analyses.** **a**, The base of the mouse ear was surgically incised (sham) and implanted with biomaterials, whereas the adjacent rectangular biomaterial microenvironment was imaged. **b**, Flow chart showing gating strategy, with some data repeated for clarity.

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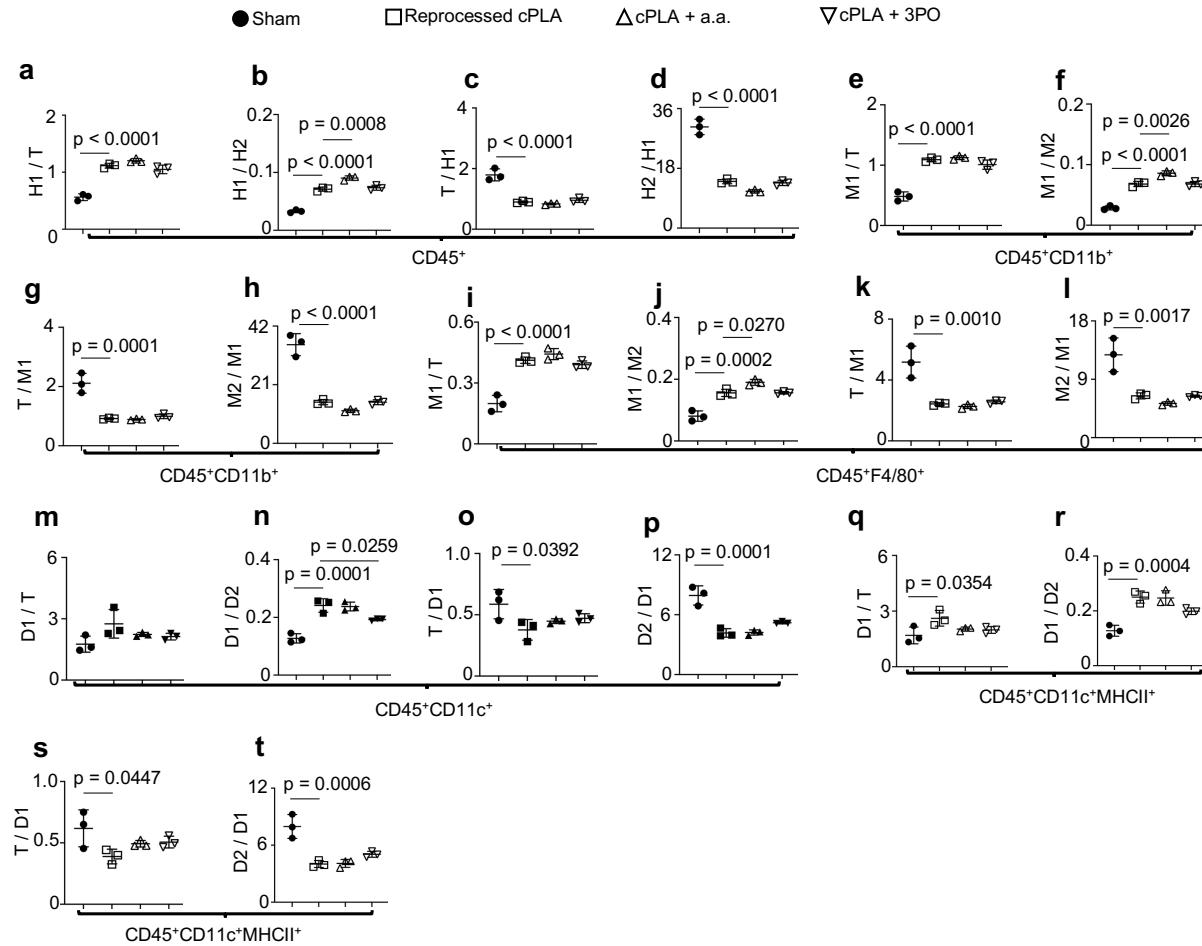
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**Supplementary Figure 2 | Deficiency of CCR2 and CX3CR1 differentially affects the proportion and activation states of cells in the amorphous polylactide biomaterial microenvironment.** **a**, *Ccr2<sup>RF/RF</sup>Cx3cr1<sup>GFP/GFP</sup>* (CCR2- and CX3CR1-deficient) mice were surgically incised (sham group) or implanted with reprocessed amorphous polylactide (aPLA). Afterwards, intravital microscopy and flow cytometric analysis of tissues around incision sites (sham group) or implants were undertaken. **b**, Representative intravital microscopy images at different time points around incision (sham group) or implants (scale bars, 50  $\mu$ m). **c-e**, Flow cytometry quantification of CCR2<sup>+</sup>(c), CX3CR1<sup>+</sup>(d) and CCR2<sup>+</sup>CX3CR1<sup>+</sup>(e) cells. **f-h**, Quantification of proinflammatory (CD86<sup>+</sup>CD206<sup>+</sup>) cells among CCR2<sup>+</sup>(f), CX3CR1<sup>+</sup>(g) and CCR2<sup>+</sup>CX3CR1<sup>+</sup>(h) populations. **i-k**, Quantification of anti-inflammatory (CD206<sup>+</sup>) cells among CCR2<sup>+</sup>(i), CX3CR1<sup>+</sup>(j) and CCR2<sup>+</sup>CX3CR1<sup>+</sup>(k) populations. **l-n**, Quantification of transition (CD86<sup>+</sup>CD206<sup>+</sup>) cells among CCR2<sup>+</sup>(l), CX3CR1<sup>+</sup>(m) and CCR2<sup>+</sup>CX3CR1<sup>+</sup>(n) populations. **o**, Nucleated hematopoietic (CD45<sup>+</sup>) cells. **p-q**, Fold change of proinflammatory (H1; CD86<sup>+</sup>CD206<sup>+</sup>) cells with respect to transition (T; CD86<sup>+</sup>CD206<sup>+</sup>) cells (p) or anti-inflammatory (H2; CD206<sup>+</sup>) cells (q). **r-s**, Fold change of T (r) or H2 (s) cells with respect to H1 cells. **t**, Neutrophils (CD45<sup>+</sup>Ly6G<sup>+</sup> cells). **u**, Monocytes (CD45<sup>+</sup>CD11b<sup>+</sup> cells). **v**, Macrophages (CD45<sup>+</sup>F4/80<sup>+</sup> cells). **w**, Dendritic cells (CD45<sup>+</sup>CD11c<sup>+</sup> cells). **x**, Dendritic cells expressing MHCII (CD45<sup>+</sup>CD11c<sup>+</sup>MHCII<sup>+</sup> cells). Unpaired t-test (two-tailed),  $n = 3$  mice per group.

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**Supplementary Figure 3 | CD86 and CD206 proportions in myeloid populations are not modulated by locally targeting immunometabolism at 11 weeks post-implantation of crystalline polylactide biomaterials.** **a-b**, Fold change of proinflammatory (H1; CD86<sup>+</sup>CD206<sup>-</sup>) cells with respect to transition (T; CD86<sup>+</sup>CD206<sup>+</sup>) cells (a) or anti-inflammatory (H2; CD206<sup>+</sup>) cells (b), gated for nucleated hematopoietic (CD45<sup>+</sup>) populations. **c-d**, Fold change of T (c) or H2 (d) cells with respect to H1 cells. **e-f**, Fold change of proinflammatory (M1; CD86<sup>+</sup>CD206<sup>-</sup>) monocytes (CD45<sup>+</sup>CD11b<sup>+</sup>) with respect to transition (T; CD86<sup>+</sup>CD206<sup>+</sup>) monocytes (e) or anti-inflammatory (M2; CD206<sup>+</sup>) monocytes (f). **g-h**, Fold change of T (g) or M2 (h) monocytes with respect to M1 monocytes. **i-j**, Fold change of proinflammatory (M1; CD86<sup>+</sup>CD206<sup>-</sup>) macrophages (CD45<sup>+</sup>F4/80<sup>+</sup>) with respect to transition (T; CD86<sup>+</sup>CD206<sup>+</sup>) macrophages (i) or anti-inflammatory (M2; CD206<sup>+</sup>) macrophages (j). **k-l**, Fold change of T (k) or M2 (l) macrophages with respect to M1 macrophages. **m-n**, Fold change of proinflammatory (D1; CD86<sup>+</sup>CD206<sup>-</sup>) dendritic (CD45<sup>+</sup>CD11c<sup>+</sup>) cells with respect to transition (T; CD86<sup>+</sup>CD206<sup>+</sup>) dendritic cells (m) or anti-inflammatory (D2; CD206<sup>+</sup>) dendritic cells (n). **o-p**, Fold change of T (o) or D2 (p) dendritic cells with respect to D1 dendritic cells. **q-r**, Fold change of proinflammatory (D1; CD86<sup>+</sup>CD206<sup>-</sup>) MHCII<sup>+</sup> dendritic cells with respect to transition (T; CD86<sup>+</sup>CD206<sup>+</sup>) MHCII<sup>+</sup> dendritic cells (q) or anti-inflammatory (D2; CD206<sup>+</sup>) MHCII<sup>+</sup> dendritic cells (r). **s-t**, Fold change of T (s) or D2 (t) MHCII<sup>+</sup> dendritic cells with respect to D1 MHCII<sup>+</sup> dendritic cells. One-way ANOVA followed by Tukey's multiple comparison test, n = 3 mice per group; crystalline polylactide, cPLA; aminoxyacetic acid, a.a.; 3-(3-pyridinyl)-1-(4-pyridinyl)-2-propen-1-one, 3PO.

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