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3 **Cell therapy with IL-10-producing group 2 innate lymphoid cells suppresses**
4 **Graft-versus-Host disease**
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46 **Abstract**

47 IL-10 producing group 2 innate lymphoid cells (ILC2₁₀) have immunoregulatory functions, and limit
48 harmful immune responses across various tissues. Despite their crucial roles in maintaining immune
49 homeostasis, the cell therapy potential of human ILC2₁₀ has not been demonstrated, due to both limited
50 numbers in human peripheral blood and lack of definitive markers for identification. Here, we isolate and
51 expand circulating human ILC2₁₀, and assess their cell therapy potential in a humanized model of Graft-
52 versus-Host Disease (GVHD). Cell therapy with human ILC2₁₀ decreased GVHD severity and prolonged
53 survival of NOD-*scid* IL2R γ ^{null} (NSG) mice. Adoptive transfer of ILC2₁₀ inhibited pathogenic T cell
54 proliferation and intestinal infiltration, and suppressed CD4⁺ Th1 and CD8⁺ Tc1 cells in an IL-4 and IL-
55 10 dependent manner. Critically, increased proportions of ILC2s did not correlate with higher rates of
56 cancer relapse in HSCT recipients, and adoptive transfer of ILC2₁₀ did not compromise graft-versus-
57 leukemic (GVL) effects in a humanized model. Finally, we identify CD49d and CD86 as novel markers
58 that discriminate ILC2₁₀ from conventional ILC2s. Collectively, these findings demonstrate the potential
59 of harnessing ILC2₁₀ in cell therapies for GVHD and other immune-driven pathologies.

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62 **List of Abbreviations**

63 **ADT** – Antibody derived tags
64 **aGVHD** – Acute Graft-Versus-Host Disease
65 **AML** – Acute myeloid leukemia
66 **BMT** – Bone marrow transplant
67 **CBA** – Cytometric Bead Array
68 **CITE-Seq** – Cellular Indexing of Transcriptomes and Epitopes by Sequencing
69 **EOMES** – Eomesodermin
70 **FACS** – Fluorescence Activated Cell Sorting
71 **GVL** – Graft-Versus-Leukemia Effect
72 **HSCT** – Hematopoietic Stem Cell Transplant
73 **IHC** – Immunohistochemistry
74 **IL** – Interleukin
75 **ILCs** – innate lymphoid cells
76 **ILC1** – Group 1 innate lymphoid cells
77 **ILC2** - Group 2 innate lymphoid cells
78 **ILC2₁₀** – IL-10-producing ILC2s
79 **ILC3** - Group 3 innate lymphoid cells
80 **KIR** – Killer Cell Immunoglobulin-like Receptors
81 **LTi** – Lymphoid Tissue Inducer Cells
82 **MDSC** – Myeloid derived suppressor cell
83 **MSC** – Mesenchymal stromal cell
84 **NK Cells** – Natural Killer cells
85 **NSG** – NOD-scid-IL2R g^{null}
86 **PMA** – Phorbol 12-myristate 13-acetate
87 **RT** – Room Temperature
88 **S.I.** – Small Intestine
89 **sLT** – Surface Lymphotoxin
90 **Tc1** – Cytotoxic T cell type 1
91 **TGF- β** – Transforming Growth Factor Beta
92 **Th1** – T helper 1
93 **Th17** – T helper 17
94 **Tc1** – Type 1 CD8+ cytotoxic T cell
95 **Tr1** – Type 1 Regulatory T cell
96 **Treg** – Regulatory T cell
97 **XenoGVHD** – Xenogeneic Graft-versus-Host Disease
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103 **Introduction**

104 Group 2 innate lymphoid cells (ILC2s) have important roles in orchestrating immune responses and
105 controlling tissue homeostasis. Initially described as a homogeneous population defined by expression of
106 CD127, CD161 and CRTh2 in humans, recent findings have made it clear that ILC2s can differ in
107 phenotype and function, both between and within tissues(1–4). For example, environmental signals can
108 promote inflammatory ILC2s such as those that underly harmful immune responses in allergy and
109 asthma, or instead promote immunoregulatory ILC2s that limit harmful inflammation in diverse
110 contexts(5–8). While human ILC2 heterogeneity has been widely described, we are only beginning to
111 appreciate how these distinct ILC2 populations interface with other immune cells, as well as how these
112 different populations can be inhibited or harnessed in immunotherapy approaches.

113 IL-10-producing group 2 innate lymphoid cells (ILC2₁₀) have been shown to inhibit immune responses
114 in mouse models of inflammation and transplantation(9–14). For example, IL-2 administration induced
115 IL-10 production in murine lung-resident ILC2s that have important functions in inhibiting and
116 preventing lung inflammation (10), and intestinal mouse ILC2s were the primary producers of IL-10 at
117 steady state and during disease(12). While there are few studies of human ILC2₁₀, they are significantly
118 reduced in individuals with allergies, but expand in response to allergy immunotherapy and are
119 associated with treatment response(13), supporting human ILC2₁₀ regulatory activity can be promoted
120 with immunotherapy approaches to promote immune tolerance. The authors attempted to define unique
121 ILC2₁₀ markers, reporting that KLRG1 marked ILC2s that produced IL-10 along with other signature
122 ILC2 cytokines(13). However, KLRG1 has also been widely reported on ILC2s with pro-inflammatory
123 functions, limiting the use of KLRG1 as a unique marker for ILC2₁₀(15–18). Therefore, identifying
124 phenotypic features demarcating inflammatory and regulatory ILC2s is needed to enable comprehensive

125 analysis of these functionally distinct ILC2 populations to health and disease, and to perform in depth
126 studies of ILC₂₀ biology.

127 In addition to transplantation and autoimmunity, tolerogenic therapies are being widely pursued for the
128 prevention and treatment of Graft-versus-Host Disease (GVHD) following allogeneic Hematopoietic
129 Stem Cell Transplantation (HSCT). HSCT is a therapy commonly used to treat those with hematological
130 malignancies, wherein transplanted donor stem cells develop into lymphocytes and attack cancerous
131 cells, in what is termed the Graft-Versus-Leukemia(GVL) effect. While HSCT is often curative, up to
132 80% of patients develop acute GVHD characterized by donor T cells attacking healthy recipient
133 tissues(19). Despite prophylactic use of post-transplant cyclophosphamide, acute GVHD remains the
134 major cause of non-relapse associated morbidity and mortality, effecting 30-50% of HSCT recipients(20–
135 24). Further, 30% of patients that develop GVHD fail to respond to corticosteroids or other broad
136 immunosuppressive agents. Several regulatory cell therapy approaches have been explored in clinical
137 trials, including adoptive transfer of regulatory T cells (Tregs). While evidence of Tregs limiting harmful
138 allogeneic T cells have been reported, to date these cell therapies have only achieved limited clinical
139 efficacy, and patients still require immunosuppression(25, 26). Therefore, there is an urgent need to
140 develop more effective therapies for GVHD that do not impair GVL responses.

141 Prior studies reported ILCs are particularly sensitive to pre-HSCT conditioning therapies, where they are
142 depleted from peripheral blood and tissues(27–29). Early Natural Killer (NK) cell reconstitution, in
143 particular expansion of CD56^{bright} NK cells(30, 31), or the presence of activated ILC2s and group 3
144 ILCs(ILC3s) are associated with reduced GVHD incidence(32). Intriguingly, Bruce *et al.* showed that
145 adoptive transfer of mouse ILC2s improved intestinal barrier function via ILC2-derived amphiregulin
146 (AREG), and transferred ILC2s recruited and activated myeloid derived suppressor cells (MDSCs) in an
147 allogeneic bone marrow transplant model (27). Whether ILC₂₀ specifically have protective functions in
148 cell therapies for GVHD, and if ILC₂₀ would have any direct effects on allogeneic T cell responses, has

149 not been explored. However, growing reports support ILC2₁₀ could be harnessed to promote immune
150 tolerance (9–14).

151 Several challenges have prevented assessment of the cell therapy potential of human ILC2₁₀, the first and
152 foremost being the relative paucity of human ILC2s in peripheral blood and lack of effective expansion
153 protocols. To overcome this challenge, we developed methods to robustly expand ILC2₁₀ that display a
154 stable phenotype. We then demonstrate cell therapy with ILC2₁₀ limits GVHD in a preclinical humanized
155 mouse model, and that ILC2₁₀ do not impair GVL responses critical for HSCT therapeutic effectiveness.
156 We define novel markers of expanded ILC2₁₀ that enable discrimination and isolation of ILC2₁₀ from
157 conventional ILC2s. We also identify ILC2₁₀ directly suppress allogeneic T cell responses in a manner
158 distinct from Tregs, as well as display distinct protective mechanism than what has been reported with
159 conventional ILC2s. Findings herein provide proof-of-concept data to support cell therapy applications
160 of human ILC2₁₀ for T cell-driven pathologies such as those that underlie GVHD.

161

162 **Results**

163 **Expansion of human ILC2s with an ILC2₁₀ phenotype**

164 Recent studies reporting protective functions of ILC2s and ILC2₁₀ in multiple contexts supported that
165 targeting or harnessing ILC2s in immunotherapy approaches may have benefits in dampening harmful
166 inflammation. To explore this possibility, we first had to develop methods to isolate and expand large
167 numbers of human ILC2s. ILC2s are present in very low abundance in peripheral blood and tissues, and
168 most expansion protocols from mouse rely on *in vivo* cytokine administration prior to isolating ILC2s
169 from bone marrow or other tissues, which would not be compatible with cell therapy approaches. Here,

170 we isolated human ILC2s, as well as NK cells and ILC3s for comparison, from normal donor peripheral
171 blood mononuclear cells (PBMCs) by flow cytometry sorting using a combination of ILC markers and
172 gating out lineage positive cells (**Supplemental Figure.1A, B**). CD56^{dim} NK cells were sorted as live
173 lineage⁻CD45⁺CD56⁺CD16⁺, ILC2s as live lineage⁻CD45⁺CD94⁻CD16⁻NKG2D⁻CD127⁺CRTh2⁺CCR6⁻
174 and ILC3s as live lineage⁻CD45⁺CD94⁻CD16⁻NKG2D⁻CD127⁺CRTh2⁻CD117⁺CCR6⁺. NK cells were
175 expanded in NK MACS media supplemented with IL-2, IL-15 and IL-18, ILC2s were then expanded in
176 X-VIVO media supplemented with IL-2, IL-7 and IL-33, and ILC3s were expanded in X-VIVO media
177 with IL-1 β , IL-2, IL-7 and IL-23. ILC2s and ILC3s exhibited robust expansion using this protocol,
178 resulting in an average of $2.3 \times 10^4 \pm 7.2 \times 10^3$ and $9.8 \times 10^3 \pm 3.6 \times 10^3$ fold expansion respectively after 34
179 days in culture(**Supplemental Figure.1C**). Post-expansion, ILC2s strongly co-expressed IL-4, IL-13, IL-
180 9 and GM-CSF following PMA-ionsomycin stimulation, with low to no expression of IFN- γ , IL-17A or
181 IL-22(**Figure.1A,B, Supplemental Figure.1D**). In contrast, expanded CD56^{dim} NK cells co-expressed
182 IFN- γ and TNF- α and ILC3s expressed IL-22 and GM-CSF, with low IL-17A expression(**Figure.1A,B**,
183 **Supplemental Figure.1D,2A**). Secreted cytokine production in expanded ILCs was quantified using
184 cytometric bead array(CBA) following stimulation with IL-2. ILC2s secreted high amounts of IL-4, IL-9,
185 IL-5 and IL-13, whereas NK cells and ILC3s did not produce significant amounts of these cytokines and
186 instead produced canonical cytokines including IFN- γ and TNF- α or IL-22, respectively(**Figure.1C**,
187 **Supplemental Figure.2B**). In addition to cytokine expression, we also examined chemokine production.
188 Expanded ILC2s also produced the chemokines CCL2, CCL11, CCL20 and CXCL10 (**Supplemental**
189 **Figure.2D**). To confirm ILC2 stability, we assessed the phenotype of expanded ILC2s when cultured in
190 ILC3 or NK cell medium for 10 days(**Supplemental Figure.3A-J**). Expanded ILC2s maintained
191 expression of signature cytokines and did not upregulate cytokines associated with NK cells or ILC3s,
192 supporting once activated and expanded, human ILC2s from healthy donor blood maintained a stable
193 ILC2 phenotype.

194 To confirm expanded ILC2s maintained an ILC2-associated gene and protein expression profile, as well
195 as enable detailed phenotyping of expanded ILC2s, we preformed Cellular Indexing of Transcriptomes
196 and Epitopes by Sequencing(CITE-seq) on expanded ILCs. Expanded ILCs were stained with a
197 TotalSeq-C antibody cocktail and labelled with hashtag antibodies to enable easy identification after
198 sequencing(**Figure.1D, Supplemental Table 1**). All ILCs examined expressed lineage defining markers
199 that differentiated them from other family members. CD56^{bright} and CD56^{dim} NK cells expressed *GNLY*
200 and CD56, while the CD56^{dim} NK cells expressed CD16. ILC3s strongly expressed CD117 and ILC2s
201 expressed *PTGDR2*, *GATA3*, *IL17RB*, *IL13* and *IL5* (**Figure.1E**). Intriguingly, one of the top genes
202 identified as being uniquely expressed by *ex vivo* expanded ILC2s was *IL-10* (**Figure.1E**), which we
203 validated by flow cytometry and cytometric bead array(**Figure.1F,G**). Expanded ILC2 supernatants had
204 consistently high levels of IL-10 secretion across all donors, and a high proportion of IL-10⁺ cells were
205 noted in the majority of donors examined(**Figure.1F,G**). Therefore, ILC2s isolated and expanded using
206 our approach had a phenotype consistent with being ILC2₁₀.

207 Due to recent studies that identified murine ILC2₁₀ as having immunoregulatory properties, including
208 being able to suppress T cells(10, 13, 33), we assessed expanded ILC2s with ILC2₁₀ phenotype for
209 potential immunoregulatory properties beyond IL-10 production, or expression markers that overlapped
210 with other regulatory populations such as regulatory CD4⁺FOXP3⁺ Tregs and T regulatory 1 (Tr1) cells.
211 Low or background expression of checkpoint molecules such as PD-1, PD-L1, CTLA-4, LAG3 was
212 observed at both the RNA and protein level, and no *FOXP3* gene transcript was observed(**Supplemental**
213 **Figure.4A,B**)(34, 35). Additionally, we did not detect *IL12A* and *EBI3*, which make up the regulatory
214 cytokine IL-35(**Supplemental Figure.4A,B**). Despite ubiquitous transcriptional expression of *TGFBI*
215 across ILC subsets, no protein-level expression of active TGF-β1 was observed in expanded NK cells,
216 ILC2s or ILC3s(**Supplemental Figure.2C, Supplemental Figure.4B**). While these regulatory molecules
217 were absent, expanded ILC2s expressed *ENTPD1*, the gene for CD39(**Supplemental Figure.4C**) and

218 also weakly expressed *NT5E* (CD73). However only ILC2s and CD56^{bright} NK cells exhibited surface
219 CD73 protein expression(**Supplemental Figure.4C**). Flow cytometry analysis verified expanded ILC2s
220 co-expressing high levels of CD73, in line with reports of *ex vivo* ILC2s(36) as well as
221 CD39(**Supplemental Figure.4D,E**), which are known to inhibit the functional activity of T cells(37, 38).
222 IL-10 expression on ILC2s was correlated with co-expression of IL-4, as well as amphiregulin (AREG)
223 but had no significant correlation to expression levels IL-9 or IL-13 cytokines(**Figure1.H-K**). High
224 amphiregulin was also notable, as it is a key tissue reparative effects(27, 39, 40), and was linked to ILC2s
225 protective effects in limiting GVHD, supporting dual regulatory and reparative potential of expanded
226 ILC2₁₀.

227

228 **Adoptive transfer of allogeneic human ILC2₁₀ suppresses xenogeneic GVHD**

229 Pre-clinical models and patient-based studies have linked CD4⁺ T helper 1(Th1) and CD8⁺ cytotoxic T
230 cells (Tc1) to aGVHD pathology(41–44). 30% of aGVHD patients do not respond to first line
231 corticosteroid treatment, with less than one-third of non-responders surviving past one year(45),
232 highlighting the need to identify cells and molecules that limit pathogenic T cell responses post-HSCT.
233 Due to prior mouse studies supporting potential applications of ILC2 transfer for GVHD(27, 46), and
234 increasing appreciation of immunoregulatory functions of ILC2₁₀, we sought to assess the cell therapy
235 potential of human ILC2₁₀ using a preclinical xenogeneic GVHD model(xenoGVHD). In this model, 6–
236 8-week-old female NOD-scid-IL2R γ ^{null} (NSG) mice are irradiated and injected with human PBMCs. T
237 cells from transferred PBMCs engraft into NSG mice and induce tissue pathology similar to acute GVHD
238 (47). NSG mice are monitored for signs of xenoGVHD, using weight-loss and a composite xenoGVHD
239 score, which measures fur loss, skin inflammation, hunch, activity, and pain (**Figure.2A**). T cell

240 engraftment, as well as detailed phenotyping is performed on circulating immune cells and immune cells
241 within tissues at endpoint or indicated times.

242 Using this model, we assessed whether cell therapy with ILC2₁₀ could limit human T cell-mediated
243 pathology. NSG mice that received PBMCs alone or PBMCs and ILC2₁₀ were first compared for signs
244 of GVHD and how this corresponded with T cell engraftment. After 14 days, engraftment of human
245 CD45⁺CD3⁺T cells was observed in the blood, with no significant difference in T cell proportions
246 between NSG mice given human PBMCs alone or mice treated with ILC2₁₀, indicating ILC2₁₀ did not
247 inhibit T cell engraftment(**Figure.2B-D**). This was of note, as cell therapy with Tregs in this xenoGVHD
248 model results in impaired T cell engraftment (48). Despite not impacting T cell engraftment, female NSG
249 mice treated with ILC2₁₀ had significantly delayed onset and reduced GVHD symptoms, including
250 decreased weight-loss across 3 independent experiments (**Figure.2E-H**). These effects were also
251 observed in separate experiments in male NSG mice, although with slight differences in xenoGVHD
252 kinetics(**Supplemental Figure.5A-C**). This single infusion of ILC2₁₀ not only reduced xenoGVHD
253 severity but also significantly improved overall survival(**Figure.2I**). Notably ILC2₁₀-treated mice only
254 reached endpoint due to weight-loss, but other GVHD symptoms were still very low and mice would
255 otherwise not have reached endpoint(**Figure.2E,F**).

256 To assess if ILC2₁₀ could also treat GVHD upon onset, allogeneic ILC2₁₀ were adoptively transferred
257 after T cell engraftment and onset of xenoGVHD symptoms. Here, T cell engraftment was confirmed
258 prior to ILC2₁₀ transfer, and mice had begun displaying early xenoGVHD symptoms. When human
259 ILC2₁₀ were transferred at day 9, this resulted in similar protection from xenoGVHD to when ILC2₁₀
260 were administered prophylactically at day 0(**Supplemental Figure 6**). Taken together, cell therapy with
261 allogeneic expanded human ILC2₁₀ limited pathology and enhanced overall survival in this model of
262 GVHD when administered both prophylactically and upon GVHD onset.

263

264 **ILC2₁₀ inhibit allogeneic T cell responses in xenoGVHD**

265 We next sought to determine how ILC2₁₀ protected from GVHD. Similar to previous reports, T cells
266 made up >96% of engrafted human CD45⁺ cells across all organs analyzed (**Figure 2B-D** and
267 **Supplemental Figure.7A-D**)(47). Despite no differences in engraftment at day 14, we noted at endpoint
268 a moderate increase in CD4⁺ Th cells and reciprocal decrease in cytotoxic CD8⁺ T cells in the blood,
269 bone marrow and spleen of NSG mice receiving ILC2₁₀ cell therapy(**Figure.2J**). We observed CD4⁺ and
270 CD8⁺ T cells had reduced expression of Ki-67 in the blood, bone marrow and spleen of NSG mice
271 treated with ILC2₁₀, indicating reduced T cell proliferation (**Figure.3A-D, Supplemental Figure.8A,B**).
272 This was not accompanied by changes in T cell expression of checkpoint molecules examined including
273 PD-1, CTLA-4 and CD25 (**Supplemental Figure.9A-C**).

274 Previous research has indicated that CXCR3⁺ T cells drive trafficking to target organs including intestines
275 in mouse models of GVHD(49, 50). CXCR3 also marks CD4⁺ Th1 and CD8⁺ Tc1 cells(51–53) which
276 induce intestinal damage in GVHD models and correlate with disease in patients(41, 43). We therefore
277 asked whether ILC2₁₀ influenced T cell phenotypes and intestinal trafficking within the xenoGVHD
278 model. CD3 immunohistochemical(IHC) staining of tissues revealed a stark reduction in T cell
279 infiltration into colons of ILC2₁₀-treated mice, with no change in T cell infiltration noted in the lungs,
280 spleen, or liver(**Figure.3E,F, Supplemental Figure.10A-G**). Across compartments examined, mice
281 receiving ILC2₁₀ cell therapy had reduced CXCR3 expression by CD4⁺ and CD8⁺ T cells(**Figure.3G-J**,
282 **Supplemental Figure.8C,D**), with no increase in CRTh2 or CCR6, markers of CD4⁺ T helper 2 (Th2)
283 and T helper 17 (Th17) cells, respectively(52–54). Adoptive transfer of human ILC2₁₀ therefore did not
284 promote differentiation to other T cell subsets, but inhibited CD4⁺Th1 and CD8⁺Tc1 cells(**Figure.3G-J**,
285 **Supplemental Figure.8C,D**)(52–54).

286

287 **Inverse correlation between ILC2s and pathogenic T cells in HSCT recipients**

288 Due to ILC2₁₀-mediated suppression of CD4⁺ Th1 and CD8⁺ Tc1 cells in the xenoGVHD model, and
289 prior studies reported increased CD56^{bright} NK cells, ILC2s and ILC3s in peripheral blood of HSCT
290 patients that did not develop GVHD compared to those that did(32), we were interested in the
291 relationships between ILCs and T cell subsets in HSCT recipients with differing clinical outcomes. We
292 analyzed the proportion of subsets of ILCs and T cells in the blood of HSCT patients at the time of
293 aGVHD diagnosis and compared proportions of these populations in patients without aGVHD and
294 healthy donors(**Supplemental Figure.11A, Supplemental Table 2**). All HSCT recipients were given
295 prophylactic post-transplant cyclophosphamide, and two were treated with additional
296 immunosuppression at the time of sample acquisition. In line with previous literature, patients without
297 aGVHD had decreased proportions of CD56^{dim} NK cells and increased proportions of CD56^{bright} NK
298 cells(30, 31)(**Supplemental Figure.11B,C**). Similarly, patients that developed aGVHD had a reduced
299 proportion of total helper ILCs (Lin⁻ CD127⁺)(**Figure.4A,B**), with reduced proportions of ILC1s, ILC2s
300 and ILC3s compared to healthy controls(**Figure.4C,D**). HSCT patients without aGVHD, however, had
301 significantly higher proportions of ILC2s, but no significant differences in ILC1s or ILC3s compared to
302 patients with aGVHD with our sample size (**Figure.4C,D**).

303 We next examined the correlation of ILCs with T cell subsets in HSCT recipient peripheral blood.
304 Similar to what we observed with ILC2 therapy in the xenoGVHD model, HSCT recipients with aGVHD
305 had increased CD4⁺ Th1 and CD8⁺ Tc1 cells as a proportion of total CD4⁺ and CD8⁺ T cells
306 respectively(**Figure.4E,F**), with no significant difference in circulating Th17 cells (51–53). Elevated
307 ILC2s, significantly correlated with low proportions of Th1 cells as a percent of CD3⁺ T across all HSCT
308 patients(**Figure.4G–H**). Therefore, ILC2s proportions following HSCT are associated with decreased

309 pathogenic T cell responses, mirroring findings in our xenoGVHD model, and further supporting the
310 therapeutic potential of ILC2s for GVHD. While this paralleled the inverse relationship observed in
311 xenoGVHD model, a caveat was that we were not able to specifically examine whether these ILC2s were
312 specifically ILC2₁₀, as markers of IL10⁺ILC2s had not been established.

313

314 **Expanded IL-10⁺ILC2s regulate CD4⁺ and CD8⁺ T cells via IL-4 and IL-10**

315 We next asked whether ILC2₁₀ could directly regulate allogeneic T cells. *In vitro* co-cultures were
316 performed with ILC2₁₀ and allogeneic naïve CD4⁺ or CD8⁺ T cells. Culture with ILC2₁₀ resulted in a
317 significant reduction in IFN- γ ⁺ and IFN- γ ⁺/TNF- α ⁺ CD4⁺ T cells(**Figure.5A,B**). Decreased IFN- γ was
318 also observed when allogeneic ILC2₁₀ were cultured with CD8⁺ T cells(**Figure.5C,D**). To confirm *in vivo*
319 findings that cell therapy with ILC2₁₀ reduced Th1 and Tc1 cells without increasing proportions of Th2
320 or Th17 cells, we also examined cytokines expressed by other T cell subsets. No increase in IL-17A, IL-
321 22, IL-4, IL-9 or IL-13 was observed with addition of ILC2₁₀ to cultures with CD4⁺ or CD8⁺ T
322 cells(**Supplemental Figure.12A,B**). Thus, decreased IFN- γ does not appear to be due to T cell
323 differentiation into other T cell subsets, but ILC2₁₀-mediated inhibition of CD4⁺ Th1 and CD8⁺Tc1 cells.

324 We next explored whether various molecules associated with ILC2s or ILC2₁₀ identified by CITE-seq
325 controlled ILC2-mediated regulation of T cells interactions. We noted that allogeneic T cells activated in
326 the presence of supernatants from IL-2-stimulated ILC2₁₀ had comparable suppression of T cells to that
327 of adding ILC2s to T cell cultures directly(**Supplemental Figure.12C,D**), indicating one or more
328 secreted factors produced by ILC2₁₀ underlies their ability to inhibit T cells.

329 ILC2₁₀ were therefore cultured with allogeneic T cells in the presence or absence of neutralizing
330 antibodies or inhibitors to secreted molecules of interest(IL-10, CD39, CD73), as well as ILC2 cytokines
331 (IL-4, IL-9, IL-13)(6, 55, 56). The addition of an IL-4-neutralizing antibody strongly reduced ILC2₁₀-
332 mediated suppression of IFN- γ by CD4⁺ T cells *in vitro*, but blocking IL-9, IL-13 or CD39/CD73 had no
333 effect(**Figure.5E,F, Supplemental Figure.12E, Supplemental Figure.13A**). Neutralizing IL-10 also
334 decreased suppression of CD4⁺ T cell-IFN- γ , but to a lesser extent than IL-4(**Figure.5E,F,**
335 **Supplemental Figure.13A**). In contrast, the combination of anti-IL-4 and anti-IL-10 abrogated ILC2₁₀-
336 mediated suppression of IFN- γ by CD8⁺ T cells, which was not observed with anti-IL-4 or anti-IL-10
337 alone(**Figure.5E,G, Supplemental Figure.13B**). ILC2₁₀ suppression of allogeneic CD4⁺ and CD8⁺ T
338 cells cytokine production requires IL-4 and IL-10, with differing contributions of IL-4 and IL-10 to the
339 regulation of CD8⁺ and CD4⁺ T cells.

340

341 **Allogeneic human ILC2₁₀ do not suppress T cell mediated graft-versus-leukemia effects**

342 The GVL effect is critical for success of allogeneic HSCT for treating hematological malignancies.
343 While cell therapy with ILC2₁₀ did not impair T cell engraftment, ILC2₁₀ suppressed xenogeneic T cell
344 responses. A key question therefore was whether cell therapy with ILC2₁₀ would inhibit T cell-mediated
345 GVL effects. Within our clinical cohort, we assessed circulating ILC2 proportions and how they
346 correlated with relapse status. No significant differences in ILC2 proportions was observed in the blood
347 of patients which went on to experience relapse of their malignancy, supporting that increased
348 proportions of ILC2s are not associated with reduced GVL effects(**Figure.6A**).

349 We next assessed whether ILC2₁₀ cell therapy would negatively impact T cell-mediated GVL-effects in a
350 in a humanized mouse model. Briefly, MV4-11 cells, an acute myeloid leukemia cell line, were injected

351 into mice 5 days prior to transfer of PBMCs alone or PBMCs with allogeneic expanded human ILC2₁₀
352 (**Figure.6B**). The ability of T cells to kill MV4-11 cells was then assessed at day 14 following PBMC
353 transfer. As expected, PBMC injection resulted in a reduction in MV4-11 cells in the bone marrow
354 compared to mice receiving MV4-11 cells alone(**Figure.6C,D**). Mice treated allogeneic ILC2₁₀ had
355 comparable reductions in MV4-11 cells within the bone marrow to that observed with mice receiving
356 PBMCs alone(**Figure.6C,D**), supporting ILC2₁₀ were not impeding T cell-mediated GVL responses.
357 Importantly, within the same mice, ILC2₁₀ treatment reduced xenoGVHD symptoms similar to what was
358 observed without MV4-11 transfer(**Figure.6E**), clearly showing simultaneous protection from
359 pathogenic T cell responses that underlie GVHD without impairing T cell-mediated GVL effects.
360 Collectively our findings support ILC2₁₀ do not limit the anti-leukemic effect of allogeneic T cells
361 despite protecting from GVHD, therefore representing a strong candidate for cell-based therapies for
362 GVHD following HSCT.

363

364 ***Ex vivo* expanded ILC2₁₀ highly express CD49d and CD86**

365 Despite consistently high levels of IL-10 in our *ex vivo* expanded ILC2₁₀, we noted heterogeneity in the
366 proportions of IL-10⁺ cells between ILC2 isolations from different donors. In order to improve
367 consistency of ILC2₁₀ in cell expansions, as well as define key molecules that differentiate IL-10⁺ILC2s
368 from IL10⁻ILC2s, we performed differential gene expression analysis of *IL10*⁺ILC2s to *IL10*⁻ILC2s in
369 our CITEseq dataset on expanded human ILCs. Elevated expression of CD86 and *ITGA4* (CD49d) was
370 noted on the *IL10*⁺ILC2s(**Figure.7A**), which was confirmed by flow cytometry to identify IL-10⁺ILC2s
371 (**Figure.7B,C**). We also examined CD117 expression, as *ex vivo* ILC2s had variable expression of
372 CD117 during isolation, and KLRG1, which was previously reported to be expressed by IL-10-producing
373 ILC2(13). Both IL-10⁺ and IL-10⁻ILC2s had very low expression of these molecules, although we noted a

374 small but significant fold increase in CD117 expression(**Figure.7D,E**). Using tSNE clustering following
375 flow cytometry staining, a distinct cluster expressing IL-10 was defined by high expression of CD49d
376 and CD86 (**Figure.7F**). Dividing expanded ILC2s into populations based on expression of CD49d, CD86
377 or co-expression revealed CD49d and CD86 marked IL10-expressing ILC2s with the highest IL-10
378 expression on CD49d⁺CD86⁺ ILC2s(**Figure.7F**). CD49d and CD86 expression therefore identify *ex vivo*
379 expanded ILC2₁₀, and can be used to isolate ILC2₁₀ in expansion cultures.

380 To assess the potential utility of these markers to identify ILC2₁₀ in patient-based studies, we examined
381 the publicly available scRNA-seq dataset of ILCs from patients with grass-pollen allergy treated with
382 either grass-pollen sublingual allergen-specific immunotherapy(GP-SLIT) or placebo (PL-SLIT)(13).
383 Here, the authors reported that patients treated with GP-SLIT had improved outcomes and increased
384 proportions of ILC2₁₀ at 12-month and 24-month follow-ups compared to placebo treated patients.
385 Further, the authors reported KLRG1 expression defined ILC2₁₀, and pathways related to IL-10
386 signalling and regulation were upregulated in at both time points following GP-SLIT. We re-analyzed
387 this scRNA-seq dataset to evaluate whether the increased IL-10 expression by ILC2s was associated with
388 increases in CD49d and CD86. Following clustering of ILC2s from GP-SLIT treated patients, there was
389 increased expression of *IL10* as reported, as well as *IL4* (**Figure.7G**). Further, GP-SLIT treated patients
390 had elevated expression of *IL2RA*, *IL7R* and *IL1RL1*, receptors for the cytokines used for our ILC2₁₀
391 expansion (**Figure.7G**). Notably, ILC2s from GP-SLIT treated patients had elevated expression of
392 *ITGA4* (CD49d) and *CD86*, in addition to elevated *KLRG1* expression as reported (**Figure.7G**). This
393 elevated expression of CD49d and CD86 that correlated with ILC2₁₀ supports the potential broad
394 applications of these markers to differentiate ILC2₁₀ from inflammatory ILC2s in human studies.

395

396

397 **Discussion**

398 This proof-of-concept study demonstrates the cell therapy potential of human ILC2₁₀, and their capacity
399 to directly regulate harmful T cell responses that drive GVHD pathology. ILC2₁₀ were robustly expanded
400 using our approach, and displayed a stable phenotype. Importantly, ILC2₁₀ cell therapy inhibited
401 development of GVHD in humanized mouse models without impairing GVL effects essential for the
402 success of HSCT. These findings mirror HSCT patient-based studies, where high ILC2 proportions are
403 associated with protection from GVHD, without increased risk of cancer relapse. Human CD4⁺ and
404 CD8⁺ T cells had reduced proliferation, tissue trafficking, and intestinal infiltration following ILC2₁₀
405 treatment, and there were decreased proportions of CD4⁺Th1 and CD8⁺Tc1 cells across multiple tissue
406 sites with ILC2₁₀ therapy. Direct regulation of allogeneic T cell responses in this manner is unique to
407 ILC2₁₀ cell therapy, as it was not reported in mouse studies of conventional ILC2s, or in Treg studies
408 using this xenogeneic GVHD model (27). CD86 and CD49d marked *ex vivo* expanded ILC2₁₀, which
409 suppressed IFN- γ in CD4⁺ and CD8⁺ T cells through a combination of IL-10 and IL-4. Altogether, our
410 findings support that human ILC2₁₀ have potential applications in cell therapies aimed at limiting
411 immune-driven pathologies.

412 ILC2s display significant heterogeneity and can adopt proinflammatory or tissue protective functions
413 depending on cytokines and microenvironment factors (2, 9, 10, 12–14, 33). ILC2₁₀ have been shown to
414 inhibit immune responses in diverse contexts, including inflammation in the lungs, intestines, and
415 neurological system(9–14). In humans, individuals with grass-pollen allergies have ILC2s with reduced
416 capacity to produce IL-10 following stimulation, and patients who respond to allergy immunotherapy
417 have increased proportions of IL-10⁺ILC2s(13). In the context of transplantation, Huang *et al.*
418 demonstrated mouse ILC2₁₀ could prolong islet allograft survival by suppressing T cell attack of
419 transplanted islets(33). These growing reports demonstrate important functions for ILC2₁₀ in regulating

420 immunity. However, to date we have lacked markers that accurately identify ILC2₁₀ from conventional
421 ILC2s. In one of the few studies that attempted to identify unique markers of ILC2₁₀, Golebski *et al.*
422 reported KLRG1⁺ILC2s produced IL-10 along with other signature ILC2 cytokines(13). However,
423 KLRG1 has also been associated with inflammatory ILC2s, and may instead mark activated or memory
424 like ILC2 populations, not specifically ILC2₁₀(15–18). In our study, CITE-seq analysis of expanded
425 human ILC2₁₀ revealed limited expression of KLRG1, but instead high levels of CD49d and CD86. Flow
426 cytometry confirmed that ILC2s co-expressing CD49d and CD86 had the greatest expression of IL-10.
427 To assess the potential broad utility of these markers, we reanalyzed the publicly available dataset from
428 Golebski *et al* of ILCs isolated from grass-pollen allergy patients that responded to allergen
429 immunotherapy. We show *ITGA4* (CD49d) and *CD86* increased following allergy immunotherapy, in
430 addition to *KLRG1* previously reported. CD49d and CD86 therefore also enabled tracking expansion of
431 ILC2₁₀ in a completely different context, supporting their broad utility in differentiating conventional
432 ILC2s from ILC2₁₀ in human studies. *Ex vivo* expanded ILC2₁₀ from peripheral blood did not express
433 KLRG1, which may indicate KLRG1 is downregulated in *ex vivo* cultures, or that KLRG1 is
434 differentially expressed by ILC2₁₀ in different tissues or contexts. The combination of CD49d and CD86
435 distinguished IL-10⁺ ILC2s from conventional ILC2s in both studies, however, and our findings support
436 these markers can be used to isolate them or track ILC2₁₀ responses in human studies.

437 A wide range of prophylactic therapeutics have been explored to treat and prevent aGVHD, including
438 post-transplant cyclophosphamide, calcineurin inhibitors like cyclosporine and other
439 immunosuppressants like mycophenolate, anti-thymocyte globulin and sirolimus. While these treatments
440 dramatically reduced incidence of aGVHD, development of aGVHD remains a major clinical challenge,
441 affecting 30-50% of HSCT recipients(19–24). In a recent multicenter review which included a wide
442 range of different treatment modalities, more than half of HSCT patients required a hospital stay within
443 100 days of transplant, with the primary reason being development of aGVHD, with severe GVHD

444 (grades III-IV) occurring in 41.9% of patients(20, 21). Patients diagnosed with severe aGVHD were
445 primarily managed with increased steroid doses (51.3% of patients), however, at follow-up, 52.8% of
446 these patients were deceased(20, 21). Therefore, novel therapies are greatly needed to improve success of
447 HSCT.

448 Here we examined direct effects of ILC2₁₀ on allogeneic T cells that underlie GVHD pathology, which
449 had not previously been explored. Adoptively transferred human ILC2₁₀ suppressed allogeneic CD4⁺ Th1
450 and CD8⁺ Tc1 cells across multiple tissue compartments, and we noted an inverse relationship between
451 ILC2s and CD4⁺Th1 cells in peripheral blood of HSCT recipients protected from GVHD. These findings
452 collectively support ILC2₁₀ have direct suppressive capacity that can be harnessed in cell therapies, and
453 also that ILC2₁₀ immunoregulatory activity extends beyond effects in the intestine. Prior mouse studies of
454 conventional ILC2s reported ILC2-derived amphiregulin promotes intestinal repair and ILC2-mediated
455 recruitment of MDSCs to the gut limits intestinal GVHD pathology locally, an important distinction with
456 what we observed with human ILC2₁₀ (27, 46). In support of ILC2₁₀ having similar reparative functions
457 to conventional ILC2s, however, expanded human ILC2₁₀ expressed very high levels of amphiregulin.
458 While it would have been interesting to explore human ILC2₁₀ effects on MDSCs or other immune
459 populations, this is not possible using the xenogeneic GVHD model, which is almost exclusively
460 engrafted by human T cells, with very limited contribution from myeloid cells, NK cells or B cells.
461 Additional protective mechanism therefore likely exist, and could be explored in humanized models that
462 support engraftment of other immune cells in future studies. However, use of this model enabled
463 identification direct ability of ILC2₁₀ to suppress allogeneic CD4⁺ and CD8⁺ T cells responses across
464 multiple anatomical locations. Whether human ILC2₁₀-mediated T cell regulation has broader cell
465 therapy applications in T cell-driven pathologies, such as transplant rejection or T cell-driven
466 autoimmune disorders will be an important area to explore moving forward.

467 Human ILC₂₁₀ suppress allogeneic xenoGVHD severity to similar levels as previously reported with
468 polyclonal Tregs in this model(57). In clinical trials, evidence of Tregs limiting allo-immune responses
469 was noted. However, use of polyclonal Tregs has not achieved significant response rates, with most
470 patients still developing GVHD and requiring global immunosuppression(25, 26), highlighting the need
471 for more effective therapies. We show that ILC₂₁₀ do not inhibit T cell engraftment, as was reported with
472 Tregs in this model (48), but instead inhibit T cell proliferation, effector functions and tissue trafficking.
473 Therefore, ILC₂₁₀-protective mechanisms are distinct from those observed with Treg cell therapy.

474 From a cell manufacturing perspective, ILC₂₁₀ might also have several advantages over Tregs. Tregs are
475 typically sourced from the transplant donor or recipient, necessitating time sensitive isolation and
476 expansion(58, 59). Our study using allogeneic ILC₂₁₀, and a mouse study that demonstrated 3rd party
477 ILC2s can protect from intestinal damage(27, 46) support the possibility of using 3rd party donors as an
478 ‘off-the-shelf’ source of ILC₂₁₀, which would have advantages over current Treg approaches. Further,
479 Tregs have limited expansion potential, whereas we show ILC₂₁₀ from peripheral blood exhibit robust
480 expansion *ex vivo*. In addition to these cell manufacturing advantages, human ILC₂₁₀ have very high co-
481 expression of amphiregulin, representing another potential benefit over human Tregs, which unlike
482 mouse Tregs do not produce amphiregulin endogenously(27, 46). It will therefore be interesting to
483 compare and contrast ILC₂₁₀ and Treg immunoregulatory mechanism in future studies, and explore
484 whether dual regulatory and tissue-protective functions of human ILC₂₁₀ could offer an additional
485 therapeutic advantage. What is clear however, is that ILC₂₁₀ display regulatory functions, and can limit
486 inflammation in diverse contexts, therefore providing a strong rational to explore ILC₂₁₀-based cell
487 therapies for a wide range of pathologies.

488

489 **Methods**

490

491 **Human PBMC Isolation**

492 Fresh blood was collected in EDTA collection tubes (BD Biosciences). In some instances, frozen PBMC
493 samples were obtained from the Messner Allogeneic Transplant Program Biobank. PBMCs were
494 isolated using Lymphoprep(StemCell Technologies) per manufacturer instructions.

495

496 **Flow Cytometry**

497 Surface marker staining was performed for 30min after 15min blocking with human TruStain
498 FcX(BioLegend). Cells were washed in FACS buffer(PBS+2% FCS) and fixed in 2%paraformaldehyde
499 in PBS(ThermoFisherScientific). For intracellular staining, cells were fixed and permeabilized using
500 FOXP3/Transcription Factor Staining set(eBioscience) and incubated with intracellular antibodies at
501 room temperature(RT) for 30min. Samples were acquired on a LSR Fortessa(BD Biosciences) and data
502 analyzed using FlowJo v10 software. Antibody details listed in **Supplemental Table 3**.

503

504 **Human ILC Sorting**

505 PBMCs were stained with human TruStain FcX(BioLegend) and incubated with a cocktail of lineage
506 antibodies conjugated to the FITC listed in **Supplemental Table 4**. Cells are washed in FACS buffer,
507 resuspended in EasySep Buffer(StemCell Technologies) and enriched using the EasySep FITC Positive
508 Selection Kit II(StemCell Technologies) per manufacturer instructions. Enriched cells were stained with
509 antibody cocktail(**Supplemental Table 5**), and sorted using a FACSaria Fusion(BD Biosciences).

510

511 **Human ILC Expansion**

512 Sorted human ILC2s and ILC3s were cultured in complete X-VIVO 15 media(Lonza) supplemented with
513 5% human AB serum(Sigma), 100U/mL Penicillin-Streptomycin(Gibco) and 1x GlutaMAX(Gibco).
514 ILC2s were expanded using 100 IU/mL IL-2(SteriMax), 20ng/mL IL-7 and 20 ng/mL IL-33(BioLegend).

515 ILC3s were expanded using 100 IU/mL IL-2, 20ng/mL of IL-1 β , IL-7 and IL-23(BioLegend). CD56^{bright}
516 and CD56^{dim} NK cells were expanded in NK MACS media(Miltenyi) supplemented with 5% human AB
517 500 IU/mL of IL-2, and 20ng/mL of IL-15 and IL-18(Biolegend).

518

519 **Cytokine and Chemokine Assays**

520 For intracellular cytokine analysis, 2x10⁵ cells were stimulated with Cell Stimulation
521 Cocktail(eBioscience) for 6hrs, with GolgiStop and GolgiPlug(BD Biosciences) added after 2hrs. Cells
522 were then intracellularly stained with antibodies as detailed in **Supplemental Table 6**. For secreted
523 factor analysis, 1x10⁵ cells were plated in complete X-Vivo media and stimulated with 100 IU/mL of IL-
524 2. After 16hrs, supernatant was collected and stored at -80°C. Analytes were measured using the 12-plex
525 LegendPlex Human Th Cytokine Panel(BioLegend) or the 13-plex LegendPlex Human Proinflammatory
526 Chemokine Panel 1(BioLegend) on thawed supernatant samples per manufacturer's instructions.

527

528 **Xenogeneic GVHD Mouse Model**

529 Six-to-ten-week-old NOD.Cg-*Prkdc*^{scid}*Il2rg*^{tm1Wjl}/SzJ(NSG) mice were given 150cGy irradiation one day
530 prior to intravenous tail vein injection of 1x10⁷ freshly isolated PBMCs with or without 1x10⁷ expanded
531 allogeneic ILC2s in PBS at the same time or with ILC2s administered 9 days later (upon GVHD onset)
532 (47, 60). Control mice were injected with PBS either at Day 0 or Day 9. Mice were monitored daily for
533 symptoms of GVHD including weight loss, fur loss and skin inflammation, hunch, activity, and pain,
534 scored on a scale of 0–3. At endpoint, blood, bone marrow and spleens were harvested as previously
535 described(60, 61). For intestinal immune cells, intestines were flushed, sliced, and rinsed in 1xPBS.
536 Tissue was cut into segments, added to 2mM EDTA in 1xPBS and incubated for 30min at RT. Tissue
537 was strained and the remaining tissue was added to digestion buffer containing 1,650NPA-U BP
538 protease(VitaCyte), 2,500CDA-U CollagenaseMA(VitaCyte), and 100 μ g/mL DNaseI(StemCell
539 Technologies) in Hank's Balanced Salt Solution with calcium(Wisent Bio Products). Tissue was then cut

540 and incubated at 37°C for an additional 30min. Tissue was passed through a 70µm filter and washed in
541 RPMI (Gibco)+5%FCS twice.

542

543 For graft-versus leukemia experiments, six-to-ten-week-old NSG mice were given 250cGy irradiation
544 one day prior to intravenous tail vein injection of 2×10^6 MV4-11 cells per mouse. Five days later, mice
545 were given 5×10^6 PBMCs alone or with 5×10^6 expanded human ILC2s. Mice were sacrificed 14 days
546 after PBMC injection, and the presence of MV4-11 cells in bone marrow was assessed.

547

548 **Histology**

549 Harvested spleen, lung and colon tissue were fixed for 3 days in 10% neutral buffered formalin and
550 stored in 70% ethanol. Paraffin embedding, tissue slicing, H&E and immunohistochemical staining was
551 performed by the UHN Pathology Research Program Laboratory. Quantification of cells expressing IHC
552 markers was performed using the HALO Image Analysis Platform and reported as a percent of all cells.

553

554 **Co-Cultures**

555 Naïve CD4⁺ and total CD8⁺ T cells were isolated from the healthy donor blood using the EasySep Human
556 Naïve CD4⁺ T cell or the EasySep Human CD8⁺ T cell isolation kit(StemCell Technologies). T cells were
557 plated at 5×10^4 per well and stimulated with human CD3/CD28 T-Activator DynaBeads(Gibco) at 1:8
558 beads:T cell ratio. Expanded ILC2s were added 1:1 to the T cells. T cells were assessed for markers after
559 72hrs by flow cytometry. For ILC supernatant experiments, expanded ILC2s were plated 5×10^4 cells/mL
560 in complete X-Vivo media without cytokines. After 16hrs, supernatant was harvested, centrifuged at
561 1500rpm for 10min and stored at -80°C. Supernatant was thawed on day of T cell cultures, and added 1:1
562 with T cells. Fresh supernatant was added every 24hrs for 3days. For inhibitor experiments, UltraLeaf anti-
563 human IL-4, IL-9, IL-10, and IL-13(BioLegend) were added at 10µg/mL. ARL67156(Tocris) and

564 PBS12379(Tocris) were added at 1 μ g/mL to inhibit activity of CD39 and CD73, respectively. Inhibitors
565 were added at day zero and every 24hrs for 72hrs.

566

567 **CITE-seq on expanded ILCs and analysis**

568 1x10⁶ expanded CD56^{bright}, CD56^{dim}, ILC2s and ILC3s were washed twice in 1x Cell Staining
569 Buffer(BioLegend) and incubated in TruStain FcX for 15min. Cells were incubated with a TotalSeq-C
570 antibody cocktail as well as hashtag antibodies to allow for post sequencing differentiation of distinct
571 expanded ILC subsets(BioLegend, **Supplemental Table 1**) for 30min. Antibody concentrations and
572 background signal were determined as previously described(62). Cells were washed 3x in Cell Staining
573 Buffer and resuspended in 1xPBS with 0.04% BSA(Millipore Sigma). Samples were prepared for
574 sequencing using the 10X Genomics Single Cell 5' v2 platform in accordance with manufacturer's
575 instructions for capture of 12,000 cells per samples. Reverse transcription, cDNA amplification and
576 sequencing libraries using the 10X Genomics Single Cell 5' v2 reagents. Samples were sequenced to a
577 depth of 40,000 reads. Read alignment to the reference human genome (GRCh38/hg38) and gene
578 expression matrices were generated using CellRanger v6.1.2. Single cells were filtered to exclude cells
579 that expressed >10% mitochondrial content, <1000 total transcripts and <200 unique genes. Data was log
580 normalized, principal component analysis was preformed, and cells were clustered by the top 20
581 principal components with the Louvain community algorithm using Seurat's FindNeighbors and
582 FindClusters(63). Cell cycle genes were assigned using Seurat's CellCycleScoring and regressed out
583 during scaling. Clusters were visualized using the Uniform Manifold Approximation and
584 Projection(UMAP)(64). Clusters were assigned to ILC subsets based on expression of hashtag antibodies,
585 lack of lineage markers and expression of subset associated markers(**Figure 6a**). Cluster defining
586 markers were identified using FindMarkers in Seurat. Differential expression of genes was visualized
587 using EnhancedVolcano(65).

588

589 **Data availability**

590 CITEseq dataset of expanded human ILCs will be made publicly available via NCBI GEO at the time of
591 publication. Publicly available single-cell RNA-sequencing dataset of ILCs in patients undergoing grass-
592 pollen allergy immunotherapy was originally published as part of studies by Golebski *et al* (13).

593

594 **Statistics**

595 Statistical significance was determined by Kruskal-Wallis test or one-tailed Mann-Whitney test. The log-
596 rank(Mantel-Cox) test was used for Kaplan-Meir curves. Analysis of correlational data was calculated
597 using Spearman correlation. The number of replicates is represented by *n* and is indicated in each figure
598 legend. *p<0.05; **P<0.01; ***P<0.001; ****P<0.0001; ns, not significant. Error bars represent standard
599 deviation unless otherwise stated. Data analysis was preformed using GraphPad Prism v9.

600

501 **Study Approval**

502 Patient study protocols were approved by the Research Ethics Board at University Health Network in
503 accordance with the Helsinki Declaration (UHN REB 19-6351), with all patients provided written,
504 informed consent. Healthy peripheral blood was obtained from donors through the Canadian Blood
505 Services Blood4Research program, with each donor providing written, informed consent(UHN REB 17-
506 6229, CBS Approved Study 2020-047). Animal study protocols were approved by the University Health
507 Network Animal Care Committee(UHN AUP 6203) and all ethical regulations were followed.

508

509 **List of Supplementary Material**

510

511 **Supplemental Figure 1. Flow cytometry gating strategy for ILC sorting**

512

513 **Supplemental Figure 2. Analysis of chemokines and cytokines produced by expanded ILC**
514 **populations**

515

516 **Supplemental Figure 3. Stability of signature cytokines on ILC2s with ILC2₁₀ phenotype upon**
517 **culture in different cytokine conditions**

518

519 **Supplemental Figure 4. Expression of nTreg and Tr1 markers on expanded ILCILC2s with ILC2₁₀**
520 **phenotype.**

521

522

523 **Supplemental Figure 5. Expanded human ILC2s suppress symptoms and improve survival of**
524 **xenogeneic GVHD in male mice**

525

526 **Supplemental Figure 6. Delayed injection of expanded human ILC2s improve weight-loss in**
527 **xenogeneic GVHD mice**

528

529 **Supplemental Figure 7. Engrafted human CD45⁺ cells are primarily T cells in xenogeneic GVHD**
530 **mice**

531

532 **Supplemental Figure 8. Representative flow cytometry analysis of Ki-67 and CXCR3 on CD4⁺ and**
533 **CD8⁺ T cells *in vivo* across tissues**

534

535 **Supplemental Figure 9. Activation and checkpoint molecule expression on CD4⁺ and CD8⁺ T cells**

536

537 **Supplemental Figure 10. H&E Staining and human CD3 immunohistochemical staining tissues of**
538 **xenoGVHD mouse model**

539

540 **Supplemental Figure 11. ILC Gating strategy to analyze ILCs in HSCT recipient peripheral blood**

541

542 **Supplemental Figure 12. Effect of ILC2 supernatant and addition of various inhibitors to ILC2- T**
543 **cell co-cultures**

544

545 **Supplemental Figure 13. Non-normalized IFN- γ expression on CD4⁺ and CD8⁺ T cells cultured**
546 **with ILC2s**

547

548 **Supplemental Table 1: CITE-Seq TotalSeqC antibody details**

549

550 **Supplemental Table 2: Patient and Healthy Donor Characteristics**

551

552 **Supplemental Table 3: Antibodies used for flow cytometry**

553

554 **Supplemental Table 4: Lineage Antibodies for ILC Sort**

555

556 **Supplemental Table 5: Antibodies for ILC sort**

557

558 **Supplemental Table 6: Intracellular Antibodies used for Flow Cytometry**

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560
561

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324 **Author contributions**

325 KTR, ASC, JM and SQC designed patient-based studies. KTR, JBL, LZ and SQC designed and
326 implemented xenogeneic GVHD studies. JM established the Hans Messner biobank and the
327 infrastructure required. ASC, INB, TAM and JM liaised with patient care teams to obtain human samples

328 for study. KTR, JAM, JMM, SJC and SQC developed ILC isolation and expansion methods. KTR, SJC,
329 JAM, JMM, DTB, WC, NS, JA, and YX performed experiments and analysed data. KTR, SJC, JMM and
330 SQC designed and implemented the bioinformatic pipeline for scCITEseq. SQC, JBL, AM, LZ and JM
331 supervised the work. KTR and SQC wrote the manuscript, which all authors reviewed and edited.

332 **Competing interests**

333 Authors declare that they have no competing financial interests. KTR, SJC, JAM, JMM and SQC have
334 filed a provisional patent for human ILC expansion methods (Provisional Patent Application#:
335 63/353,823) and KTR, SJC, WC and SQC have filed a provisional patent for marker combinations for
336 ILC₂₁₀ isolation (Provisional Patent Application#: 63/469,234)

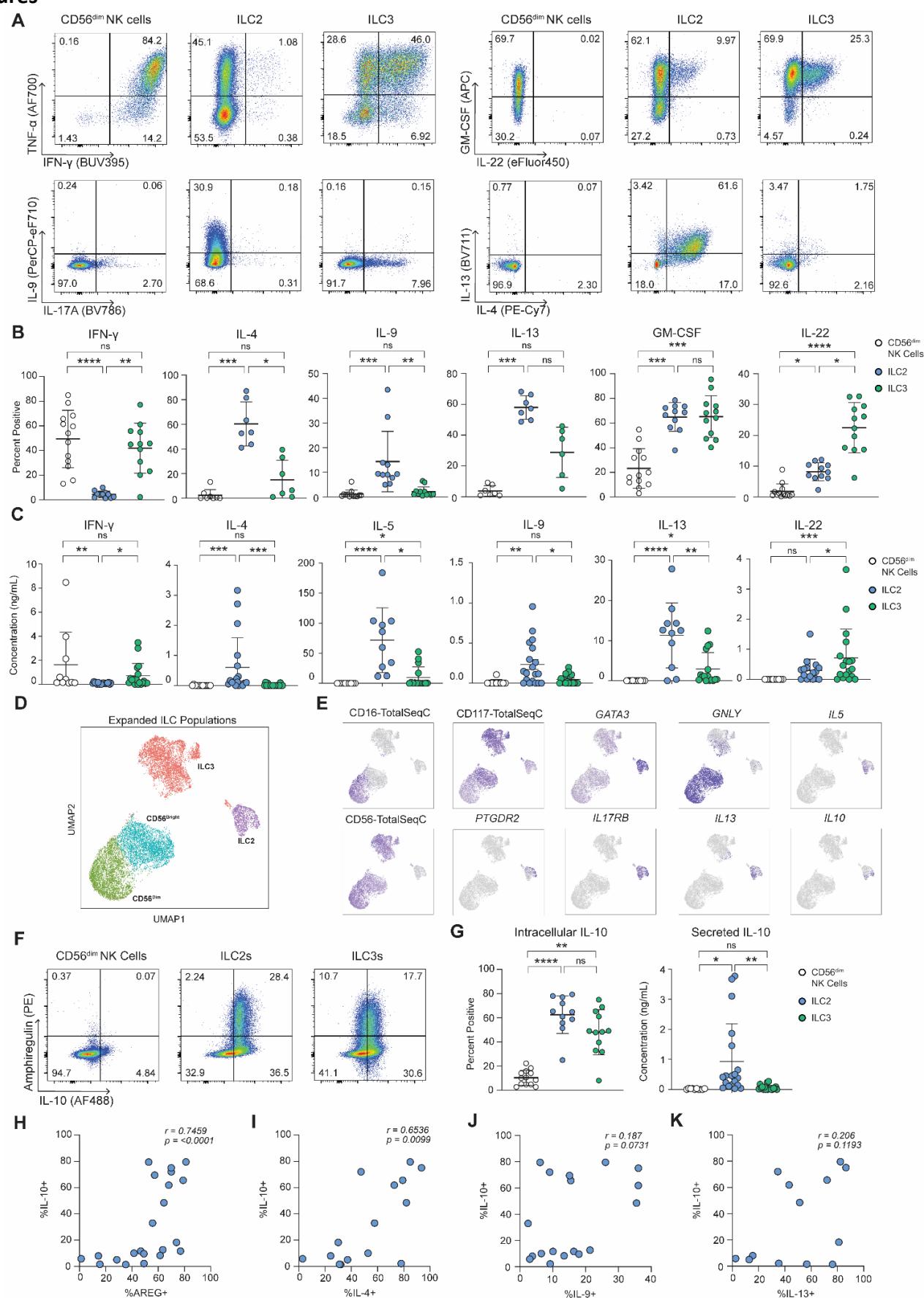
337 **Materials and correspondence**

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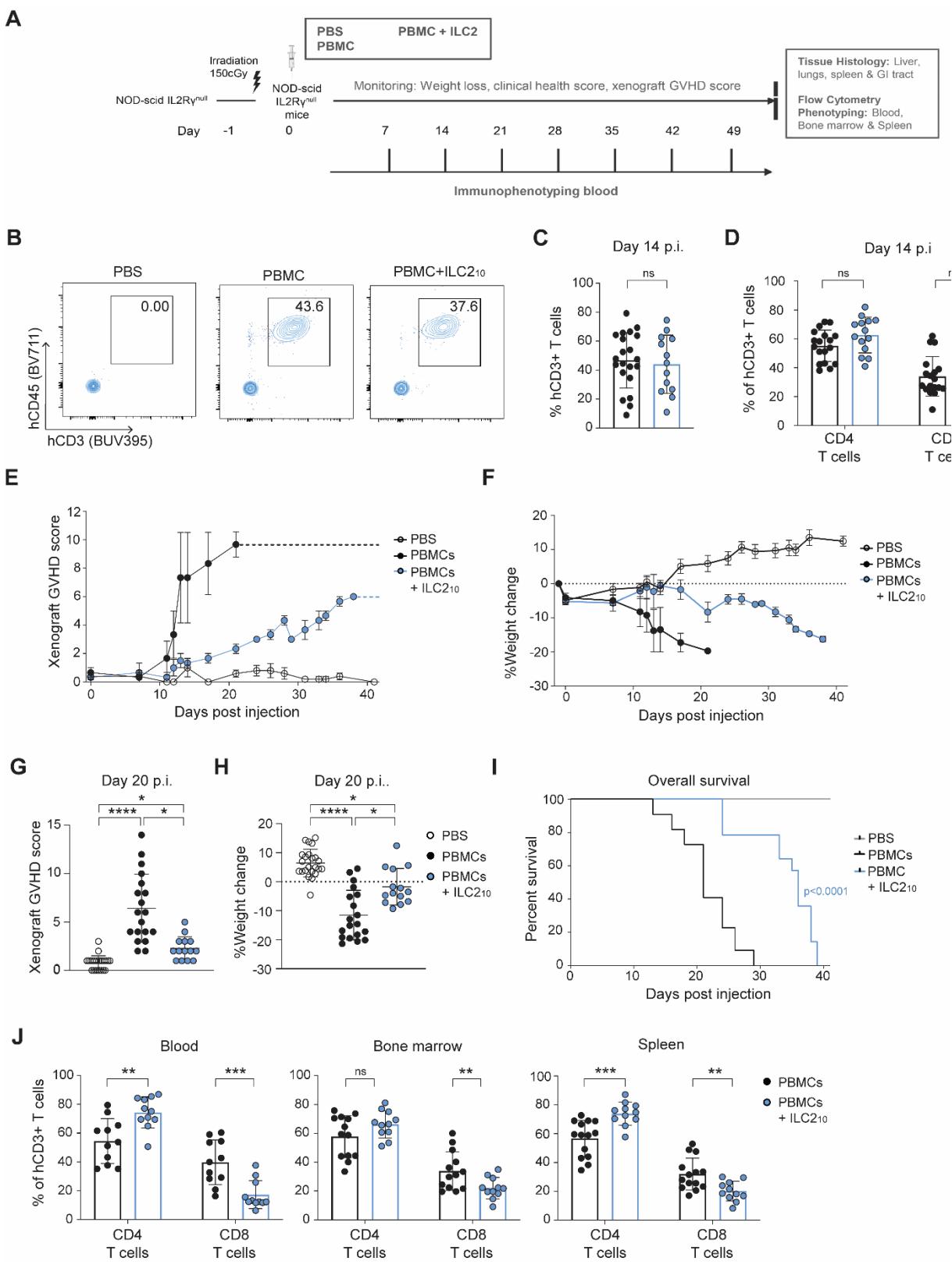
Figures



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343 **Figure 1. Expanded human ILC2₁₀ maintain expression of signature cytokines.** To explore the role of
344 human ILC2s in GVHD, human ILCs were isolated from peripheral blood using flow cytometry and
345 expanded *ex vivo* using ILC subset-specific cytokines, as ILC2s are present in very low abundance in
346 peripheral blood. ILC2s expanded using our approach displayed an ILC2₁₀ phenotype. Representative (A)
347 and average (B) of intracellular cytokine staining for signature cytokines in CD56^{dim} NK cells, ILC2s and
348 ILC3s at day 20 of expansion after stimulation with phorbol 12-myristate 13-acetate(PMA) and ionomycin.
349 (C) Cytometric bead array analysis of secreted cytokines after plating ILCs at a concentration of 2x10⁵
350 cells/mL for 16-hour stimulation with 100U/mL of IL-2. (D) UMAP representation of CITE-seq of
351 expanded ILC subsets. ILC subsets indicated were isolated by flow cytometry, expanded and then stained
352 with CITE-seq antibody cocktail as outlined in **Supplemental Table 2**. Each population was also labeled
353 with a unique hashtag antibody to facilitate post sequencing identification. (E) Feature plots showing
354 protein level expression of CD16, CD56 and CD117 and RNA level expression of *PTGDR2*, *GATA3*,
355 *IL17RB*, *GNLY*, *IL13*, *IL5* and *IL-10* on expanded ILC subsets. (F) Representative intracellular IL-10 and
356 amphiregulin expression by expanded CD56^{dim} NK cells, ILC2s and ILC3s after PMA/Ionomycin
357 stimulation. (G) Average intracellular IL-10 expression assessed by flow cytometry (n=13, 11 and 12 for
358 CD56^{dim} NK cells, ILC2s and ILC3s respectively) and secreted IL-10 by cytometric bead array by
359 expanded ILC subsets (n=12, 19 and 20 for CD56^{dim} NK cells, ILC2s and ILC3s respectively). Correlation
360 of IL-10 expression with amphiregulin (G), IL-4 (H), IL-9 (J) or IL-13 (K)(n=22, 15, 18 and 13
361 respectively) on expanded ILC2s with ILC2₁₀ phenotype.
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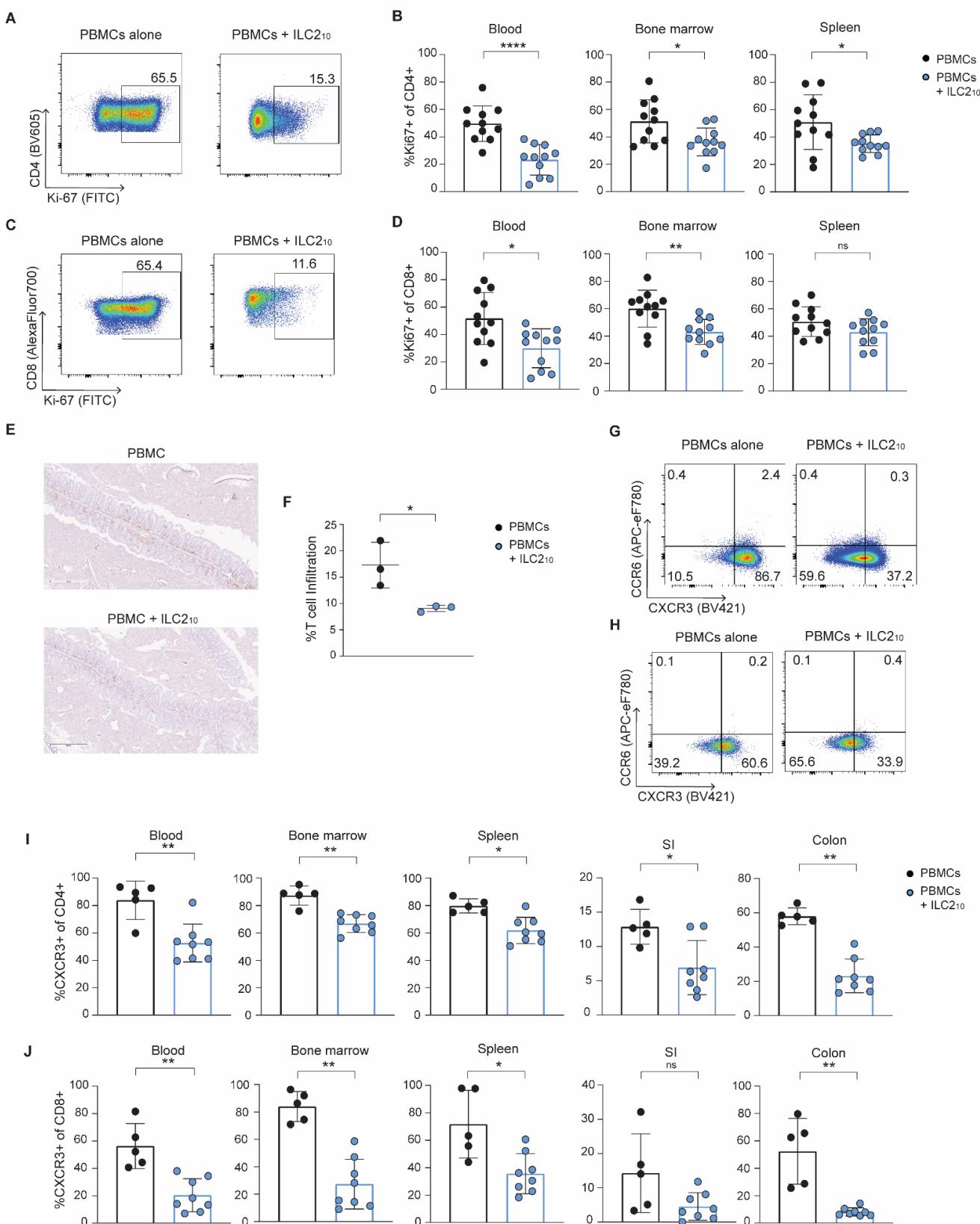
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Figure 2. Cell therapy with human ILC2₁₀ suppresses xenogeneic GVHD. To assess whether human ILC2₁₀ could limit GVHD, we employed an established xenogeneic model of GVHD involving PBMC transfer into NOD-scid-IL2R_g^{null} mice (NSG). (A) Overview of the xenogeneic GVHD model to assess whether ILC2₁₀ would prophylactically limit GVHD. Briefly, NSG mice are irradiated and receive either PBS, human PBMCs, to induce multiorgan tissue pathology, or PBMCs and ILC2₁₀ together. Mice are

370 monitored for symptoms of xenogeneic GVHD including weight loss, survival and a composite xenogeneic
371 GVHD score consisting of hunch, skin inflammation and fur loss, activity, pain and percent weight change.
372 Blood is drawn at 7-day intervals for confirmation of human immune cell engraftment and
373 immunophenotyping. At the humane or experimental endpoint, mice are euthanized, and tissues collected
374 for histology or flow cytometry analysis. **(B)** Representative engraftment human CD3⁺ CD45⁺ T cells at
375 day 14 post injection of human PBMCs alone or with ILC2₁₀. **C,D** Average engraftment of human CD3⁺
376 CD45⁺ (**C**), or CD4⁺ and CD8⁺ T cells (**D**), in the blood 14 days post injection across 3 independent
377 experiments (n=21 for NSG mice receiving human PBMC and n=13 for NSG mice receiving human
378 PBMC plus allogeneic ILC2₁₀ mice from 3 independent experiments). **E,F** (**E**) Representative xenogeneic
379 GVHD score (n=3/group in this experiment), and (**F**) representative weight loss (n=3/group in this
380 experiment) of 3 independent experiments. **G,H** Average of xenogeneic (**G**) GVHD score and (**H**) weight
381 loss of mice at day 20 post injection across three independent experiments (n=23 for PBS treated NSG
382 mice, n=19 for NSG mice receiving human PBMCs alone and n=14 for NSG mice receiving human PBMC
383 plus allogeneic ILC2₁₀ respectively across 3 independent experiments). **I**) Survival of mice treated with
384 ILC2₁₀ across 3 independent experiments (n=23, 19 and 14 for NSG mice receiving PBS, PBMC and
385 PBMC+ ILC2₁₀ respectively). Experimental endpoint was day 40 for any mice not reaching human
386 endpoint. **J**) Average proportion of CD4⁺ and CD8⁺ T cells of total human CD3⁺ T cells in the blood, bone
387 marrow and spleens of NSG mice at endpoint (n=11 and 13 from PBMC and PBMC+ ILC2₁₀ respectively
388 from 3 independent experiments).

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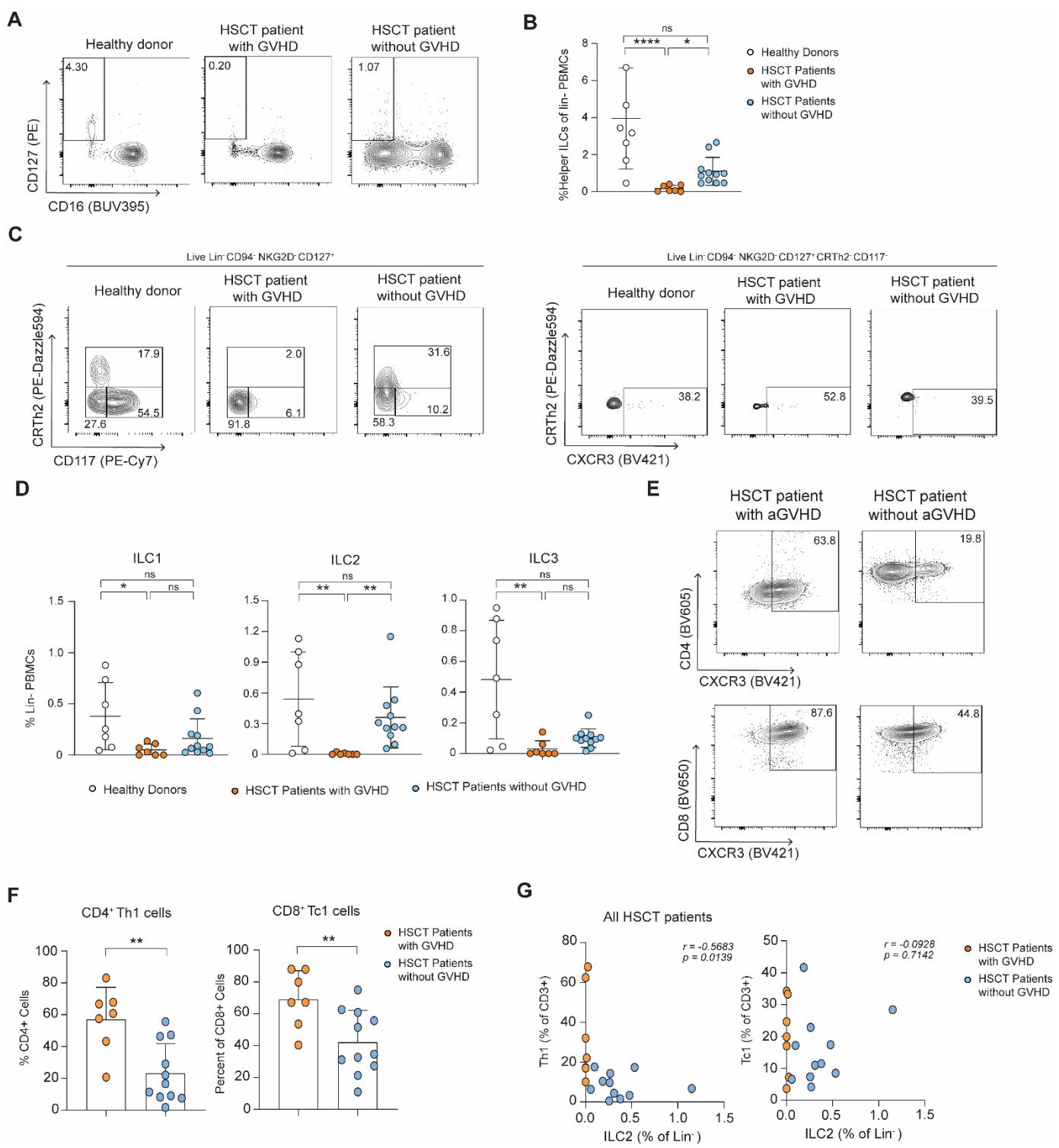
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Figure 3. Cell therapy with ILC₂₁₀ suppresses CD4⁺ and CD8⁺ T cell proliferation, intestinal infiltration and CXCR3 expression. Effect of ILC₂₁₀ transfer on T cell phenotypes and proliferation in xenogeneic GVHD model were assessed by flow cytometry at endpoint. (A) Representative Ki-67

395 expression by circulating human CD4⁺ T cells from the blood at end point **(B)** Average Ki-67 expression
396 in blood, bone marrow or spleen at endpoint by human CD4⁺ T cells from 3 independent experiments(n=11
397 mice per condition from 3 independent experiments). **(C)** Representative Ki-67 expression by circulating
398 human CD8⁺ T cells. **(D)** Average Ki-67 expression in the blood, bone marrow or spleen at endpoint on
399 human CD8⁺ T cells from 3 independent experiments(n=11 mice per condition from 3 independent
400 experiments) **(E)** Representative human CD3 immunohistochemistry of the colon of mice treated with
401 PBMCs or PBMCs plus ILC2₁₀ (10x magnification). **(F)** Average T cell infiltration in the colon of mice
402 treated with PBS, PBMCs or PBMCs + ILC2₁₀. Quantified using CD3 immunohistochemistry and the
403 HALO algorithm and normalized to background in PBS mice. **G,H** Representative CXCR3 expression on
404 circulating human CD4⁺ **(G)** or CD8⁺ **(H)** T cells. Average CXCR3 expression on human CD4⁺ **(I)** or
405 CD8⁺ **(J)** T cells in the blood, bone marrow, spleen, colon, and small intestines at experimental endpoint
406 (n=5 from 2 independent experiments).
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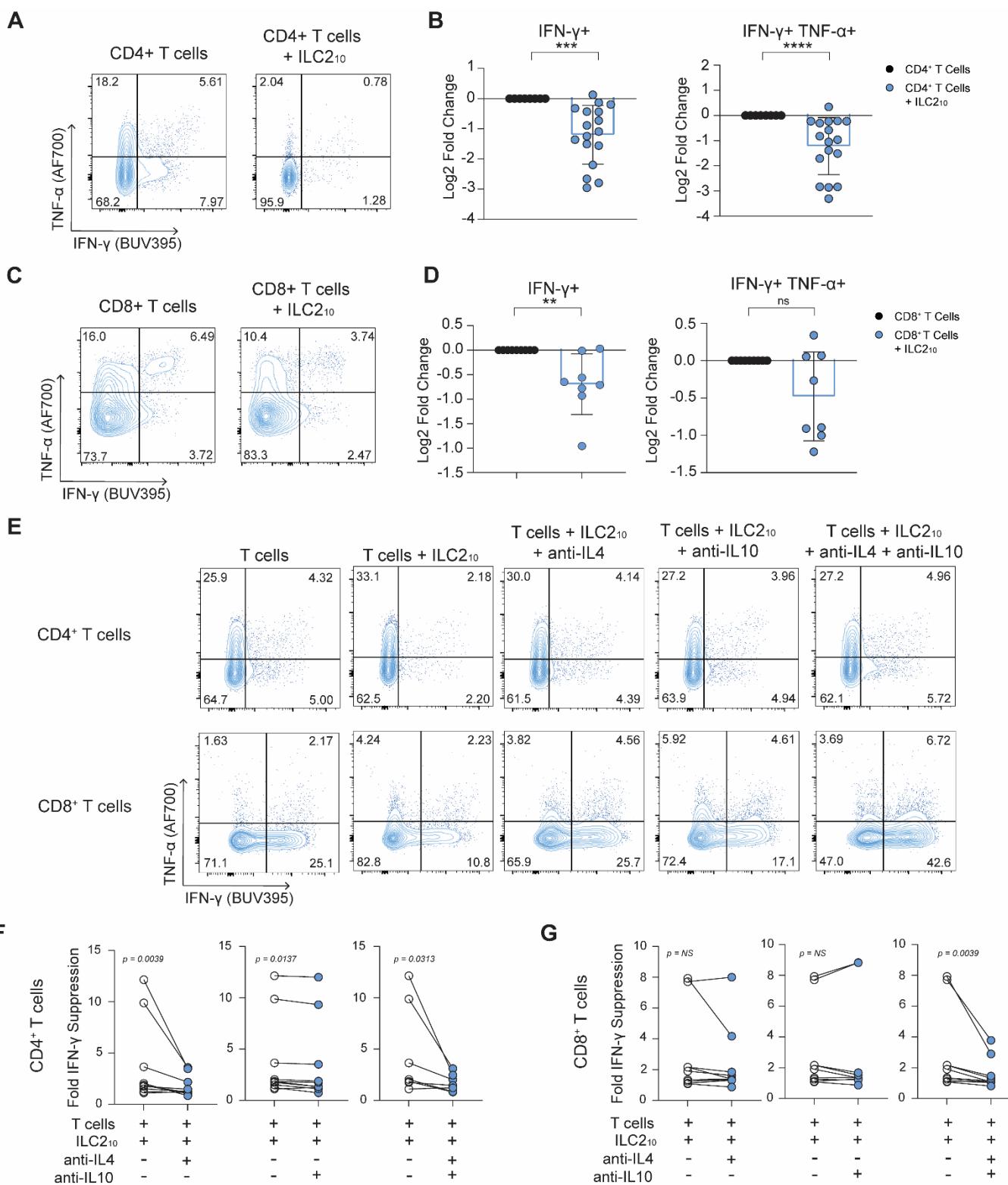


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924 **Figure 4. Increased circulating ILC2s is associated with decreased CD4⁺ Th1 cells in HSCT**
925 **recipients protected from GVHD.** PBMCs from healthy donors, and HSCT patients with or without
926 GVHD were assessed for ILC proportions and phenotypes using flow cytometry. **A,B** Representative flow
927 plots (A) and summary graphs (B) of total CD127⁺ helper ILCs in PBMCs as a proportion of live CD45⁺
928 lineage negative cells. Lineage markers are CD3, CD4, CD8, CD14, CD19, CD20, CD33, CD34, CD123,
929 CD138, CD303, FC ϵ RI and TCR γ δ . **C,D** Representative (C) and average (D) CD117⁻, CRTIh2⁺, CXCR3⁺
930 ILC1s, CRTIh2⁺ ILC2s and CRTIh2⁻ CD117⁺ ILC3s in PBMCs as a proportion of live CD45⁺ lineage
931 negative cells. **(E)** Representative CD4⁺ Th1 and CD8⁺ Tc1 cells in HSCT patients with or without aGVHD

932 development. (F) CD4⁺ Th1 and CD8⁺ Tc1 cells across HSCT patients as a proportion of CD4⁺ and CD8⁺
 933 T cells respectively. (G) Correlation of Th1 and Tc1 cells with ILC2s across all HSCT patients.

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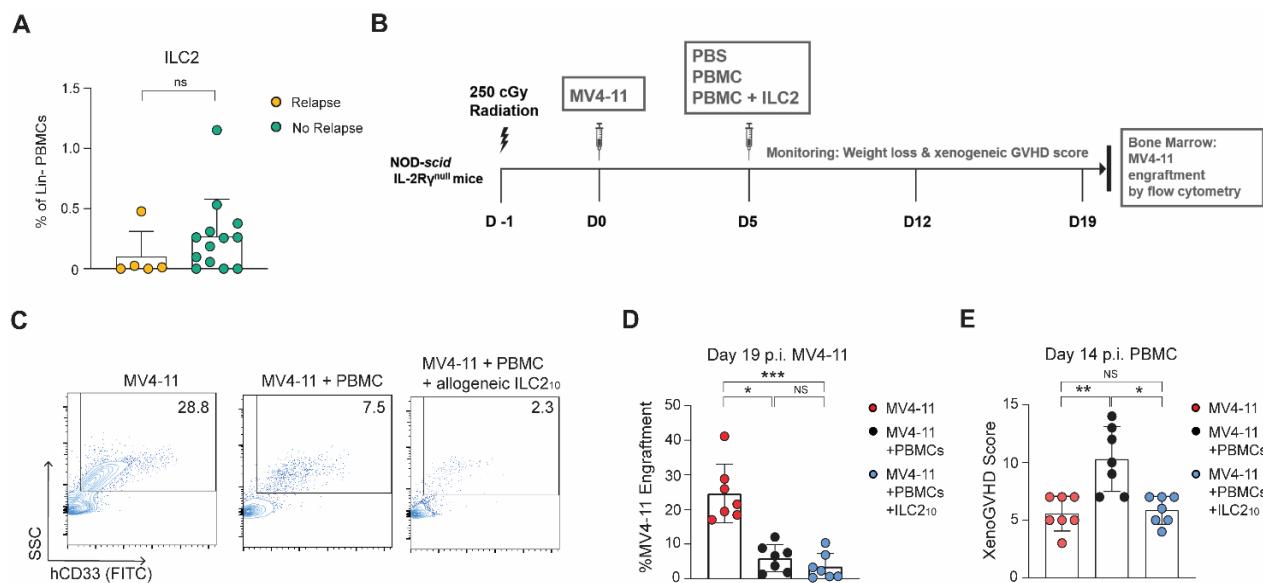
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937 **Figure 5. ILC2₁₀ suppress CD4⁺ and CD8⁺ T cell cytokine production via a combination of IL-4 and**
 938 **IL-10.** To determine whether cell therapy with ILC2₁₀ protective effects were due to direct effects of
 939 **ILC2₁₀ on allogeneic CD4⁺ and CD8⁺ T cells, we performed *in vitro* co-cultures. Expanded ILC2₁₀ were**

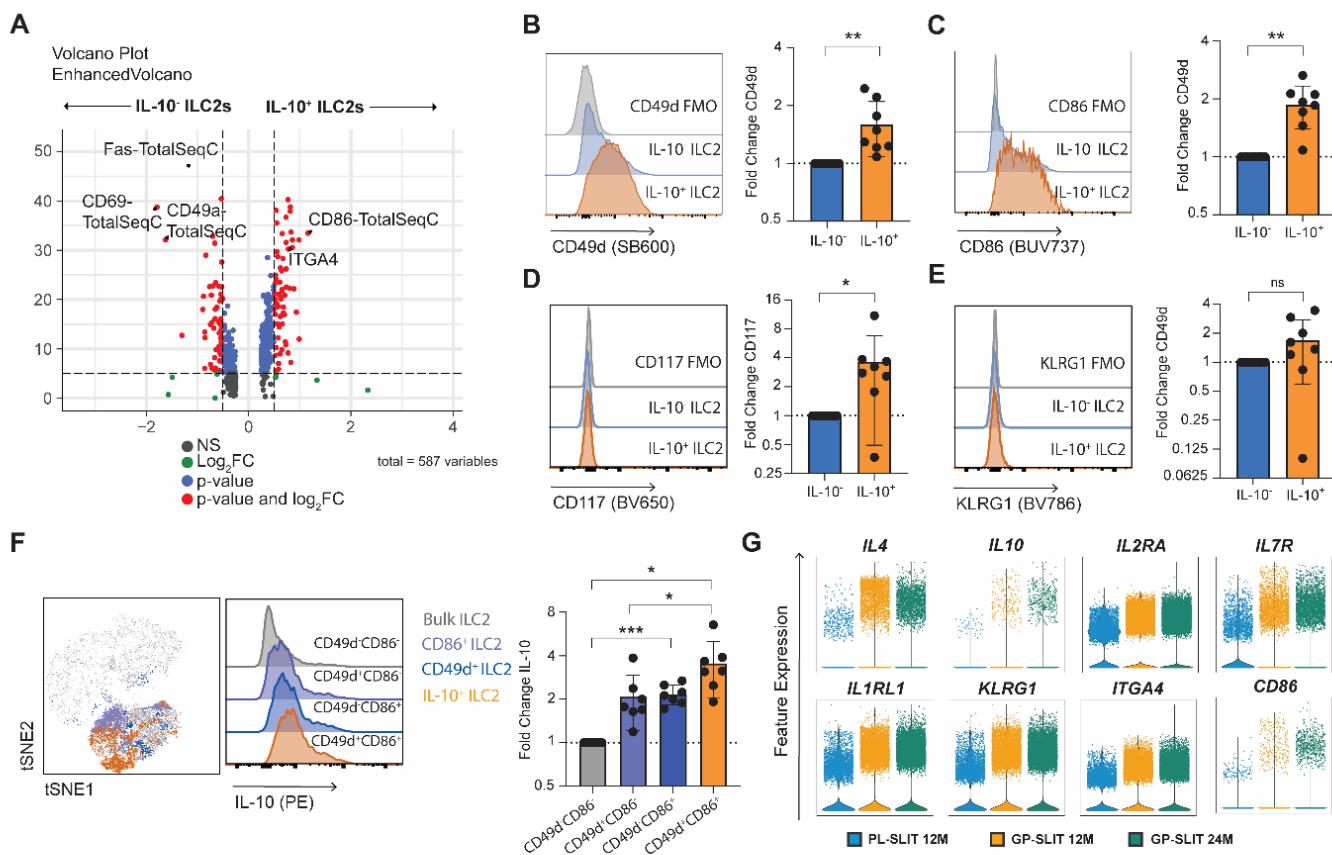
940 cultured with naïve CD4⁺ and CD8⁺ T cells that were activated with anti-CD3/anti-CD28 beads. After 4
941 days in culture, intracellular cytokine staining was assessed by flow cytometry. **(A)** Representative IFN- γ
942 and TNF- α expression by naïve CD4⁺ T cells cultured with or without allogeneic ILC2₁₀ at day 4. **(B)**
943 Average decrease in IFN- γ production or IFN- γ and TNF- α co-expression represented as log₂fold change
944 compared to CD4⁺ T cells alone (n=17). **(C)** Representative IFN- γ and TNF- α expression on CD8⁺ T cells
945 co-cultured with allogeneic ILC2₁₀ and stimulated with anti-CD3/CD28 beads over 4 days by
946 representative flow cytometry plots. **(D)** Average decrease in IFN- γ and co-expression of IFN- γ and TNF-
947 α representative as log₂fold change compared to CD8⁺ T cells alone (n=8). **(E)** Representative CD4⁺ and
948 CD8⁺ T cell IFN- γ expression when cultured with or without ILC2₁₀ in the presence of indicated blocking
949 anti-IL-4 and/or anti-IL-10 antibodies. Effects on fold change in IFN- γ expression by CD4⁺ **(F)** or CD8⁺
950 **(G)** T cells after culture with ILC2₁₀ with the addition of anti-IL-4 (n=10), anti-IL-10 (n = 10) or anti-IL-
951 4 and anti-IL-10 (n=7) blocking antibodies
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Figure 6. Cell therapy with ILC2₁₀ does not impede T cell-mediated graft-versus-leukemia effect. (A) Circulating ILC2s from HSCT patients as a proportion of lineage negative PBMCs. Patients were grouped based on whether they experienced cancer relapse (n=5) or not (n=13). Follow up periods at time of assessment ranged from 30 to 120 days. **(B)** Overview of humanized GVL model, whereby MV4-11 AML cells are transplanted into NSG mice. PBMCs are administered at D5 following MV4-11 transfer, and engrafted T cells reduced MV4-11 cell engraftment. **(C)** Representative MV4-11 cells in bone marrow of NSG mice treated with PBS, PBMCs or PBMCs with ILC2₁₀. **(D)** Average MV4-11 engraftment in NSG mice treated with PBS, PBMCs or PBMCs with ILC2₁₀ from two independent experiments (n=7/group) **(E)** Average xenogeneic GVHD score at day 19 from 2 independent experiments (n = 7/group). Day 19 corresponded to 14 days following injection of PBMCs with or without ILC2₁₀.



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Figure 7. CD49d and CD86 mark human ILC2₁₀. (A) Volcano plot of top differentially expressed transcripts and antibody-derived tags (ADT) between IL-10⁺ and IL-10⁻ expanded human ILC2s. To validate uniquely expressed surface markers of ILC2₁₀, flow cytometry was performed on additional donors for CD49d CD86. (B-E) Representative and average expression of CD49d (B), CD86 (C), as well as CD117 (D), and KLRG1 (E) by IL-10⁺ and IL-10⁻ ILC2s following PMA/ionomycin stimulation (n=7). (F) Average expression of IL-10 following PMA-ionomycin stimulation on ILC2s based on expression of CD49d and CD86 as a representative IL-10 expression, tSNE clustering based on co-expression and average graphs (n=7). (G) Violin plots of gene expression of CD86 and CD49d, as well as other ILC2₁₀-associated molecules, from publicly available scRNAseq dataset of grass-pollen allergy patients treated with placebo (PL-SLIT) or grass-pollen allergen immunotherapy (GP-SLIT) at 12 or 24 month follow-up (n = 2 patients per group).

Supplementary Materials

Cell therapy with IL-10-producing group 2 innate lymphoid cells suppresses Graft-versus-Host disease

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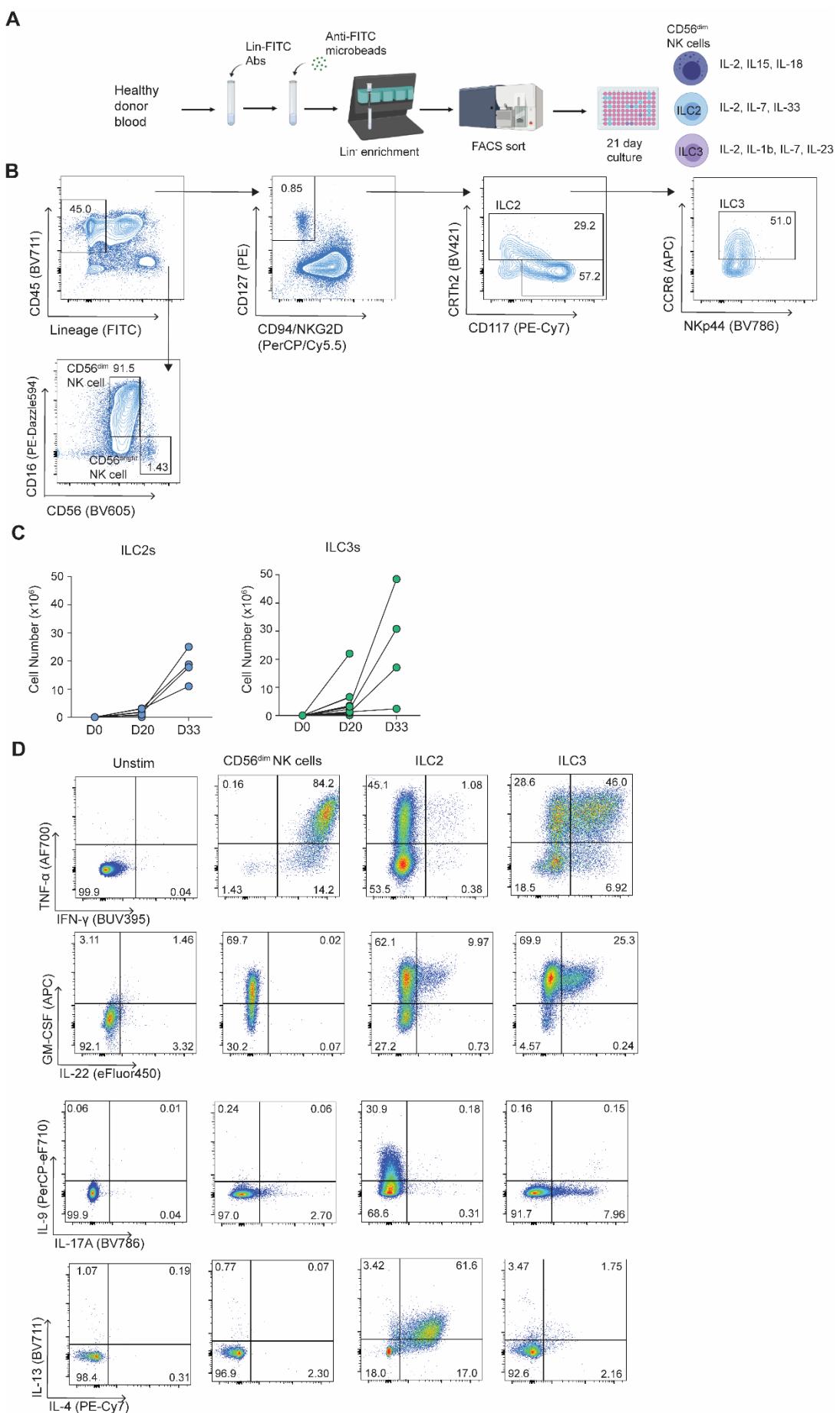
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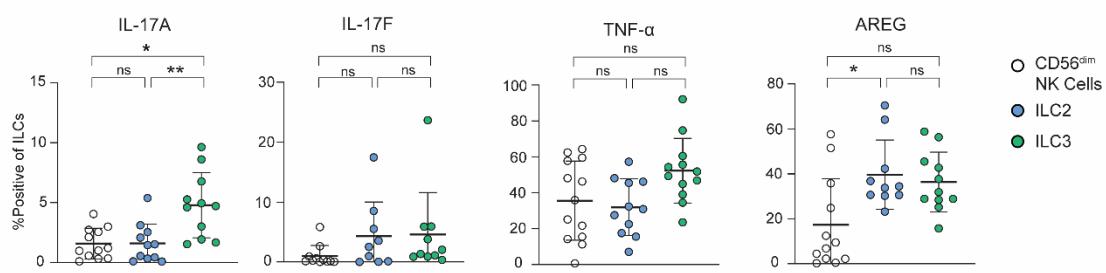
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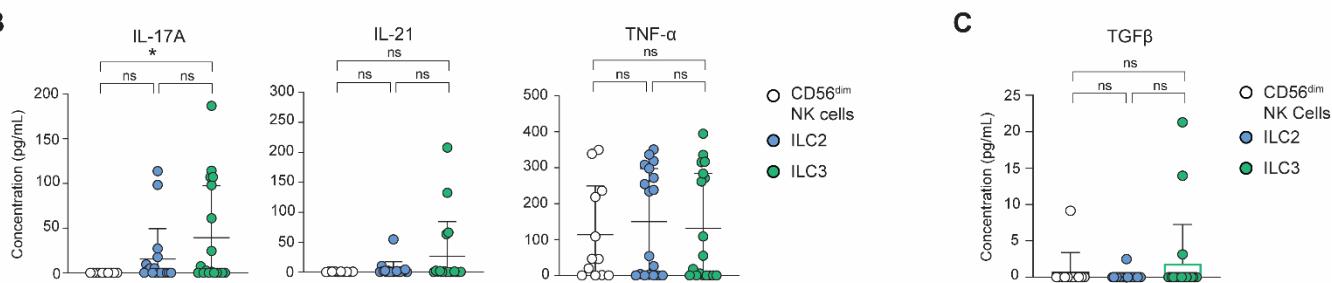


Supplemental Figure 1. Flow cytometry gating strategy for ILC sorting. To explore the role of human ILC2s in GVHD, human ILCs had to be isolated from peripheral blood using flow cytometry and expanded ex vivo using ILC subset-specific cytokines as they are present in very low abundance in peripheral blood. **(A)** Overview of isolation and expansion of human ILC subsets. Briefly, total PBMCs are isolated from healthy donor blood. PBMCs are incubated with FITC-conjugated lineage antibodies. Lineage antibodies added are CD3 (OKT3), CD3 (UCHT1), CD4, CD8a, CD14, CD15, CD19, CD20, TCR $\alpha\beta$, TCR $\gamma\delta$, CD33, CD34, CD203c, FC ϵ RI, CD79a and CD138. Anti-FITC magnetic microbeads are added, and cells are enriched for lineage $^-$ cells using StemCell magnets. Enriched cells are FACS sorted for CD56 $^{\text{dim}}$ NK cells, ILC2s and ILC3s. ILC2s are cultured with 100U/mL IL-2, 10ng/mL IL-7 and 10ng/mL IL-33, ILC3s are cultured with 100U/mL IL-2, 10ng/mL IL-7, 10ng/mL IL-1 β , and 10ng/mL of IL-23 and CD56 $^{\text{dim}}$ NK cells are cultured with 500U/mL IL-2, 10ng/mL IL-15, and 10ng/mL of IL-18. **(B)** Representative gating strategy for ILC subsets. All ILCs are gated as Live, CD45 $^+$ and Lin $^-$. NK cells are then gating as CD56 $^+$ CD16 $^+$ for CD56 $^{\text{dim}}$ NK cells and CD56 $^{\text{bright}}$ CD16 $^+$ for CD56 $^{\text{bright}}$ NK cells. Helper ILCs are then sorted as live, lineage $^-$ CD94 $^-$ NKG2D $^-$ CD127 $^+$ with ILC2s being CRTh2 $^+$ CCR6 $^-$ and ILC3s being CRTh2 $^-$ CD117 $^+$ CCR6 $^+$. **(C)** Cell expansion yields of ILC2s and ILC3s at day 20 and day 33. **(D)** Expanded ILCs intracellular cytokine staining with unstimulated ILCs as the gating control.

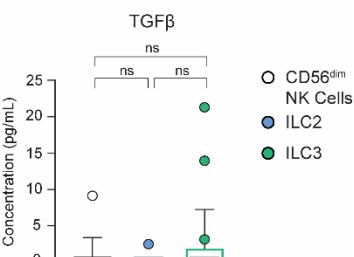
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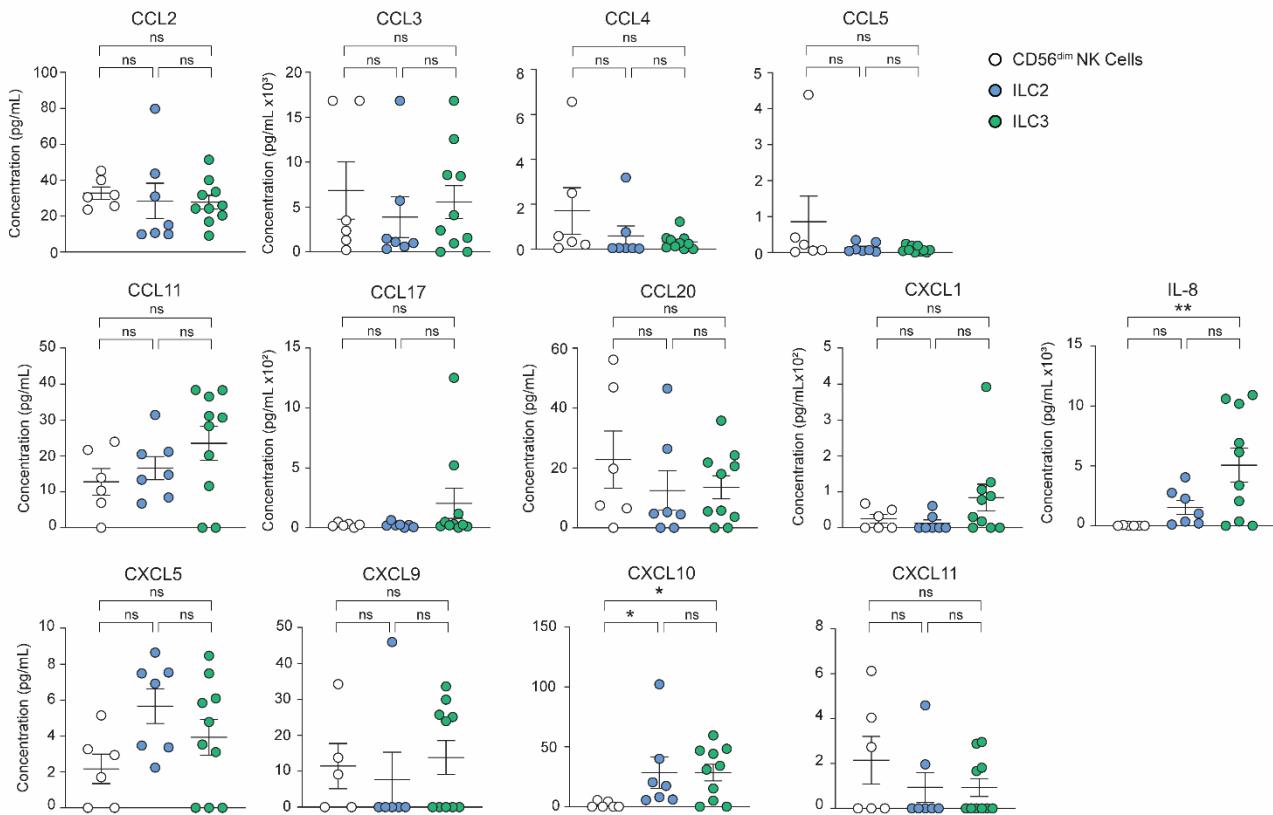
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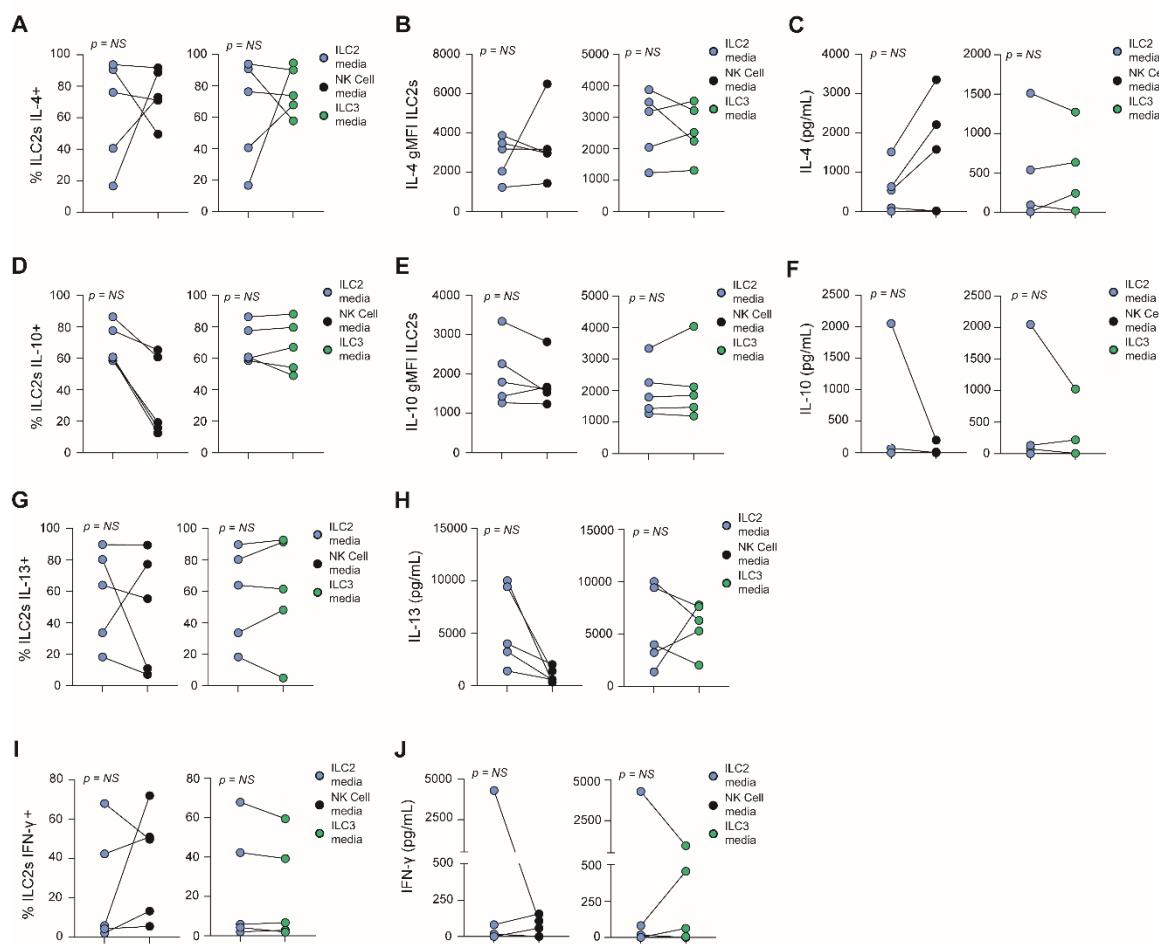


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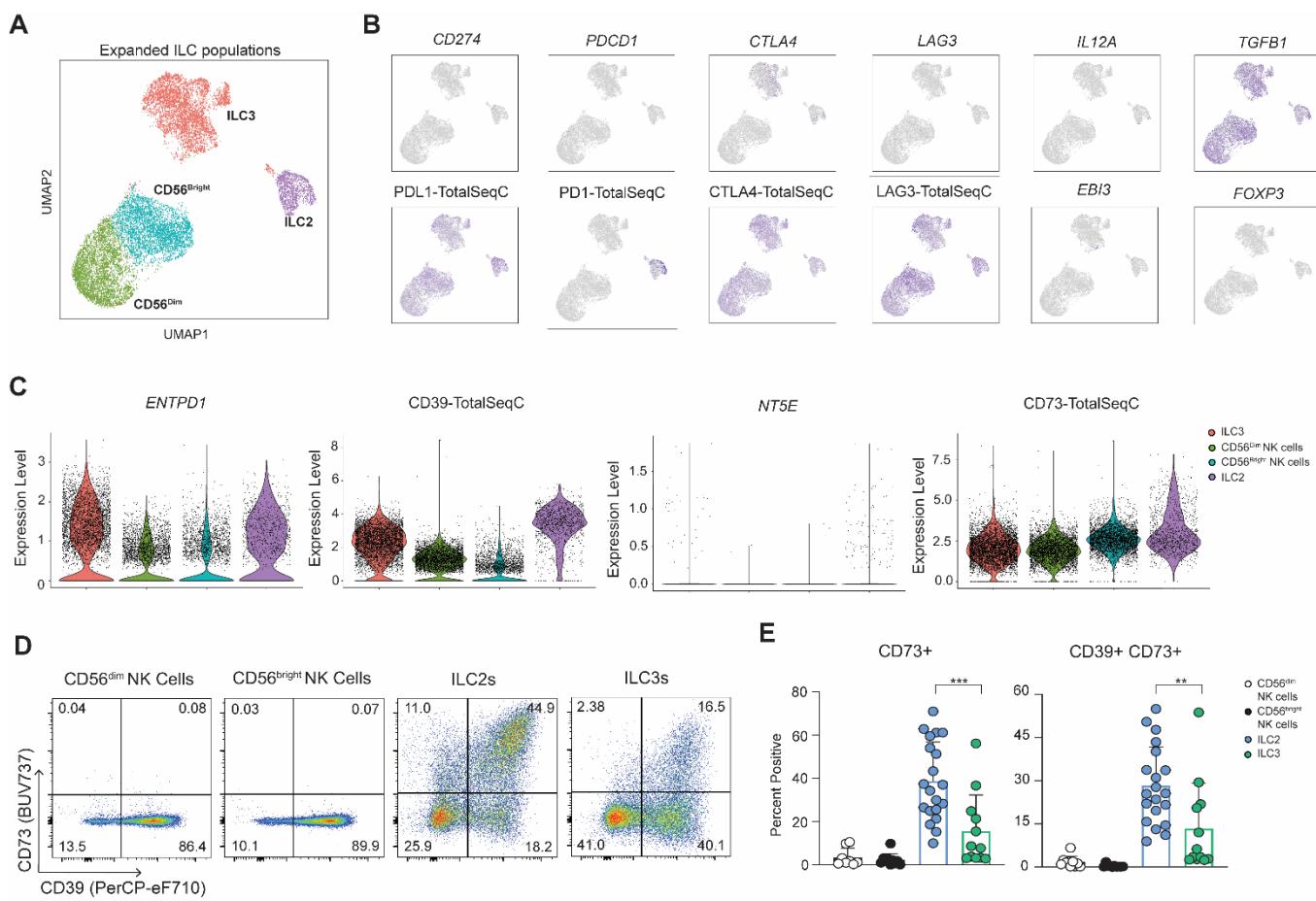


Supplemental Figure 2. Analysis of chemokines and cytokines produced by expanded ILC populations. Further chemokine and cytokine analysis of ILC2s with an ILC2 $_{10}$ phenotype, as compared to NK cells and ILC3s. **(A)** Intracellular cytokine staining for IL-17A, IL-17F, TNF- α and Amphiregulin after 6-hour stimulation with phorbol 12-myristate 13-acetate and ionomycin and blocked with monensin and brefeldin A (n=13, 11 and 12 for CD56 $^{\text{dim}}$ NK cells, ILC2s and ILC3s respectively). **(B)** Cytometric bead array (CBA) analysis of secreted IL-17A, IL-21, and TNF- α after plating ILCs at a concentration of 2×10^5 cells/mL for 16-hour stimulation with 100U/mL of IL-2 (n=13, 18 and 18 for CD56 $^{\text{dim}}$ NK cells,

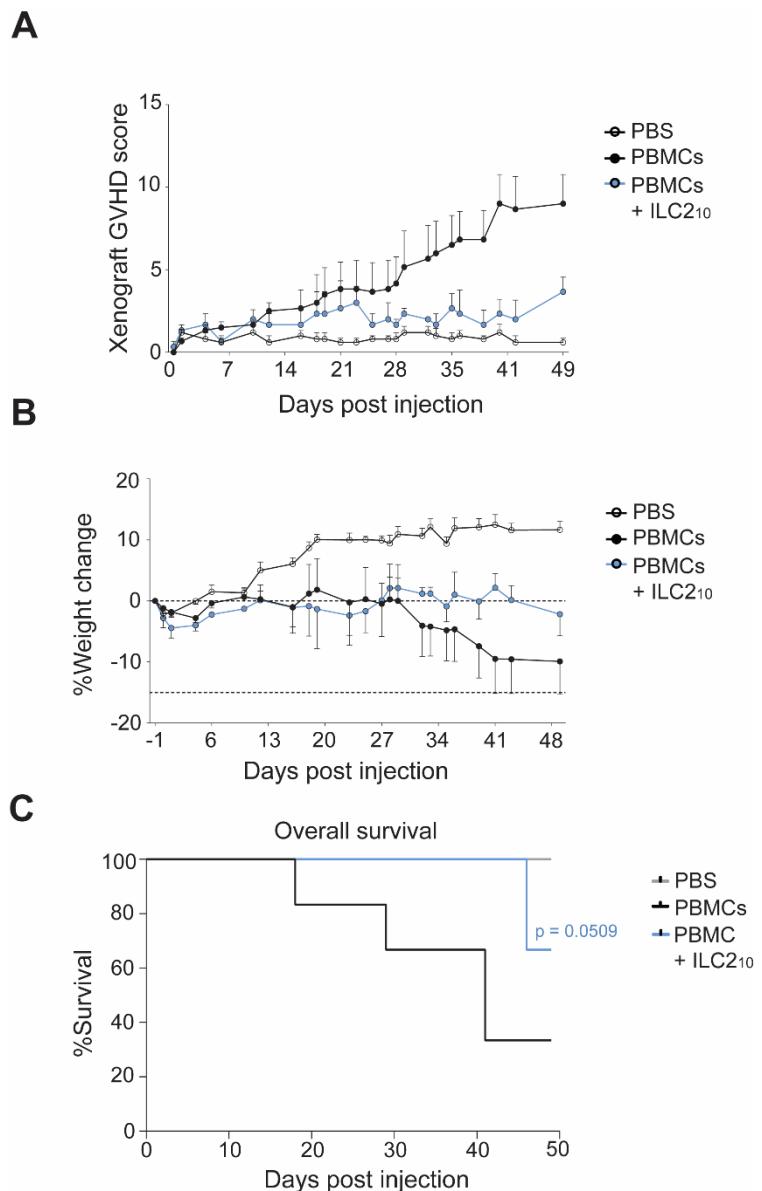
ILC2s and ILC3s respectively). **(C)** CBA analysis of secreted active TGF- β 1 after plating ILCs at a concentration of 2×10^5 cells/mL for 16-hour stimulation with 100U/mL of IL-2 (n=13, 18 and 18 for CD56^{dim} NK cells, ILC2s and ILC3s respectively). **(D)** CBA analysis of secreted chemokines after plating ILCs at a concentration of 2×10^5 cells/mL for 16-hour stimulation with 100U/mL of IL-2. (n=6, 7 and 10 for CD56^{dim} NK cells, ILC2s and ILC3s respectively).



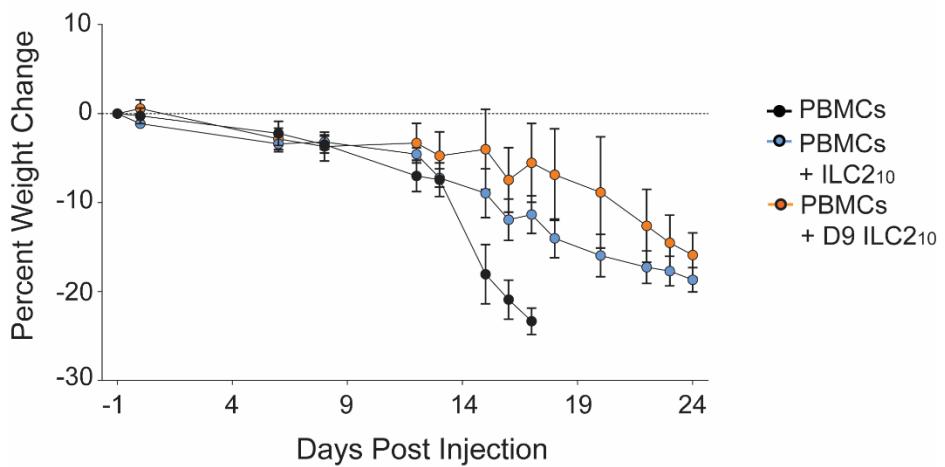
Supplemental Figure 3. Stability of signature cytokines on ILC2s with ILC2₁₀ phenotype upon culture in different cytokine conditions. ILC2₁₀ were expanded in ILC2 medium (X-VIVO15 Complete with IL-2, IL-7, and IL-33). These ILC2₁₀ were then removed from culture, washed, and plated in NK cell media (NK MACS medium with IL-2, IL-15, and IL-18) or ILC3 medium (X-VIVO15 Complete with IL-2, IL-7, IL-1 β and IL-23). Intracellular cytokines were measured after 6-hour stimulation with phorbol 12-myristate 13-acetate and ionomycin and blocked with monensin and brefeldin A. **A, B** Expression of IL-4 on expanded ILC2₁₀ cultured in NK cell medium or ILC3 medium compared to ILC2 medium. This was measured as the percent of ILC2₁₀ positive for IL-4 (A) or the gMFI of IL-4 (B). **(C)** Cytometric bead array (CBA) analysis of changes in secreted IL-4 from ILC2s cultured in NK cell or ILC3 medium. **D, E** Expression of IL-10 on expanded ILC2₁₀ cultured in NK cell or ILC3 medium compared to ILC2 medium measured as the percent of ILC2s positive (D) or gMFI (E) of IL-10. **(F)** CBA analysis of changes in secreted IL-10 on expanded ILC2s subsequently cultured in NK cell or ILC3 medium. **G, H** Expression of IL-13 on expanded ILC2₁₀ cultured in NK cell or ILC3 medium compared to ILC2 medium measured as the percent of ILC2s positive (G) or gMFI (H) of IL-13. **(I)** Expression of IFN- γ on ILC2₁₀ cultured in ILC2 medium by percent positive following stimulation compared to culturing in NK cell or ILC3 medium. **(J)** CBA analysis of changes in secreted IFN- γ from ILC2s cultured in NK cell or ILC3 medium.



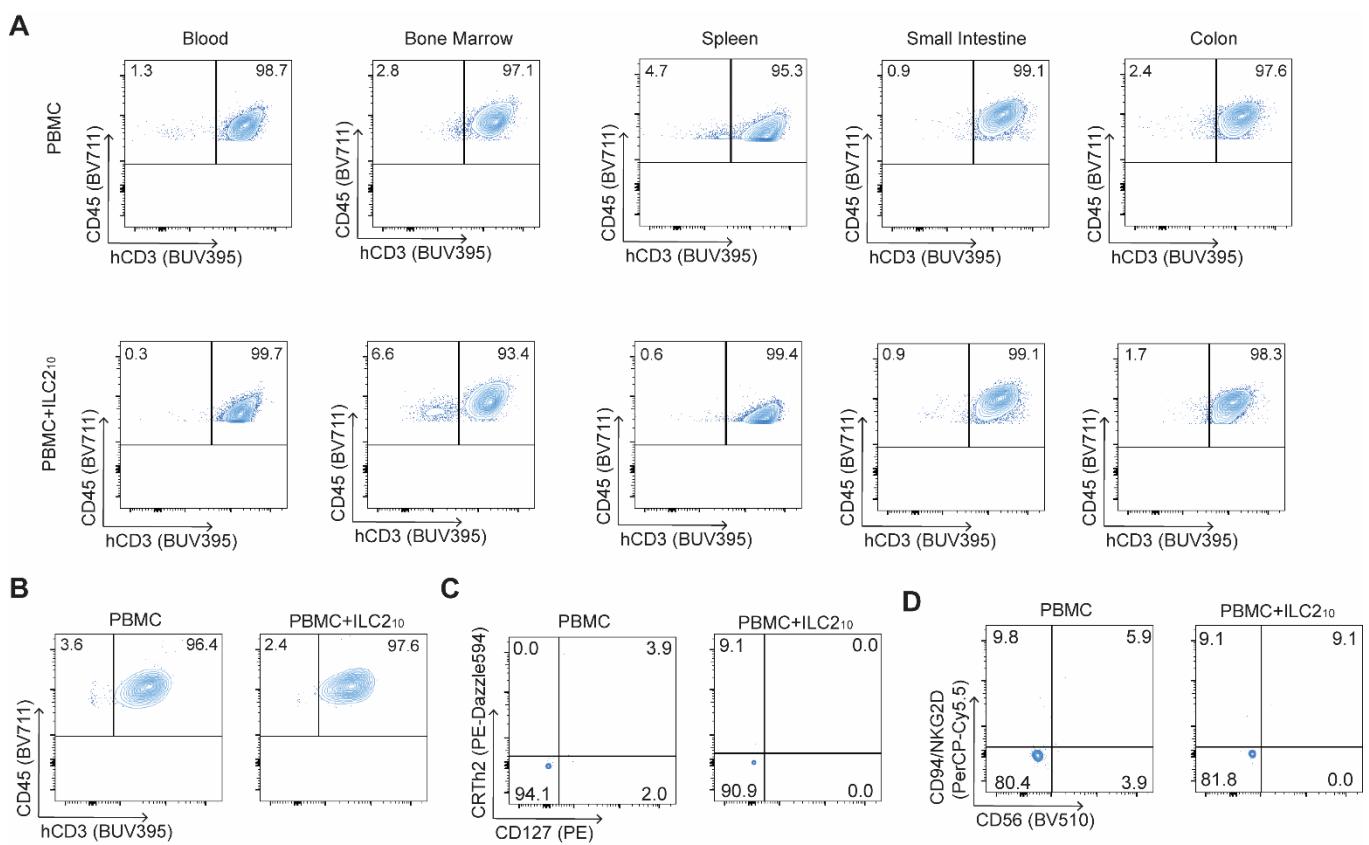
Supplemental Figure 4. Expression of nTreg and Tr1 markers on expanded ILC2s with ILC2₁₀ phenotype. (A) UMAP plots of expanded ILC subsets after CITE-seq. ILC subsets were isolated using FACS, expanded and then separately stained with an antibody cocktail. Each cell population was stained with a unique hashtag antibody to allow identification post sequencing. (B) Feature plots showing expression of markers linked to Treg and Tr1 cell function. Protein level expression is shown of PD-L1, PD-1, CTLA-4 and LAG-3 and RNA level expression of *CD274*, *PDCD1*, *CTLA4*, *LAG3*, *IL12A*, *EBI3*, *FOXP3* and *TGFB1* on expanded ILC subsets. (C) Violin plots of single cell expression of protein level CD39 and CD73 and RNA expression of *ENTPD1* and *NT5E* after expansion. Flow cytometry expression of CD39 and CD73 on expanded ILC subsets shown as representative flow plots (D) and summary graphs (E) (n = 10-20).



Supplemental Figure 5. Expanded human ILC2₁₀ suppress symptoms and improve survival of xenograft GVHD in male mice. (A-C) Xenogeneic GVHD score (A) weight loss (B) and overall survival (C) of male mice given PBS, 1x10⁷ human PBMCs to induce xenograft GVHD or 1x10⁷ PBMCs with an equal number of expanded human ILC2₁₀ over 7 weeks (n=5).

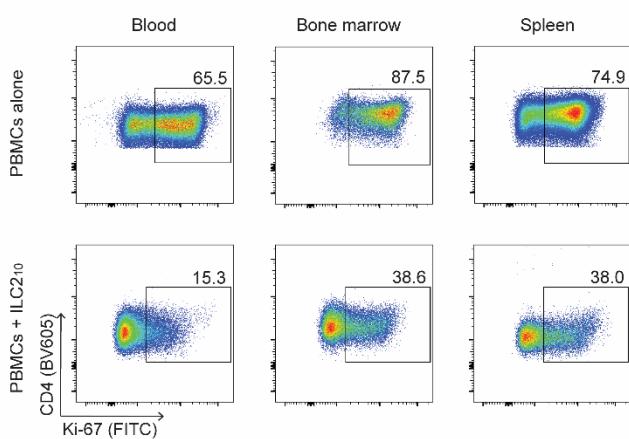


Supplemental Figure 6. Delayed injection of expanded human ILC2₁₀ improve weight-loss in xenoGVHD mice. Weight-loss over time of xenogeneic GVHD mice treated with expanded human allogeneic ILC2₁₀ at day 0 or 9 days following PBMC injection (n=3 for PBMC+ILC2₁₀ groups and n=5 for PBMCs alone).

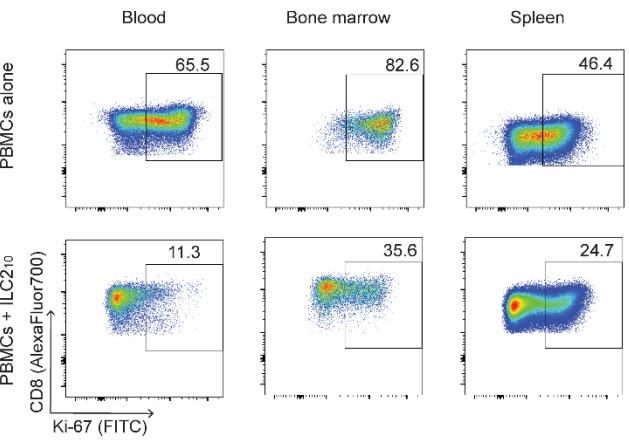


Supplemental Figure 7. Engrafted human CD45⁺ cells are primarily T cells in xenogeneic GVHD mice. Flow cytometry plots of engrafted CD45⁺ human cells in NSG mice given PBMCs alone or with allogeneic expanded ILC2₁₀. **A,B** Engraftment of human CD3⁺ T cells gated on CD45⁺ at endpoint (A) or day 14 post PBMC injection (B). **C,D** Proportion of human helper ILCs and ILC2s gated on CD45⁺CD3⁻ cells (C) and NK cells gated on CD45⁺CD3⁻ cells (D).

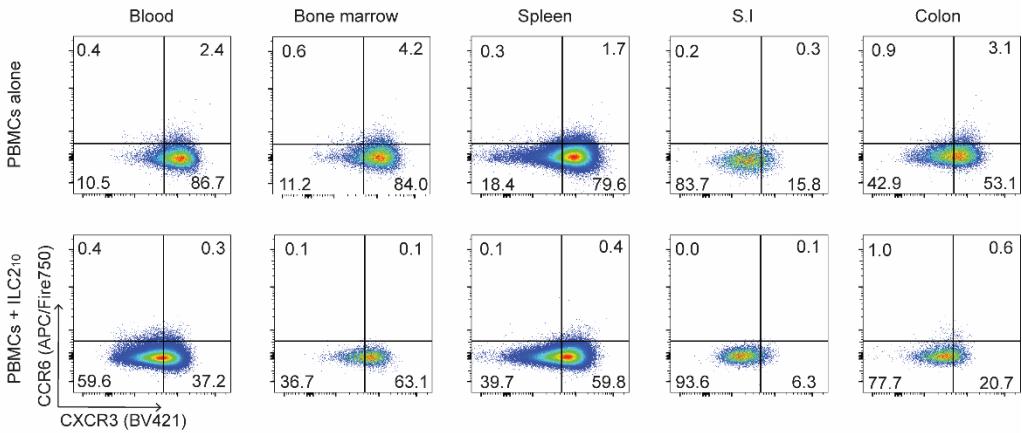
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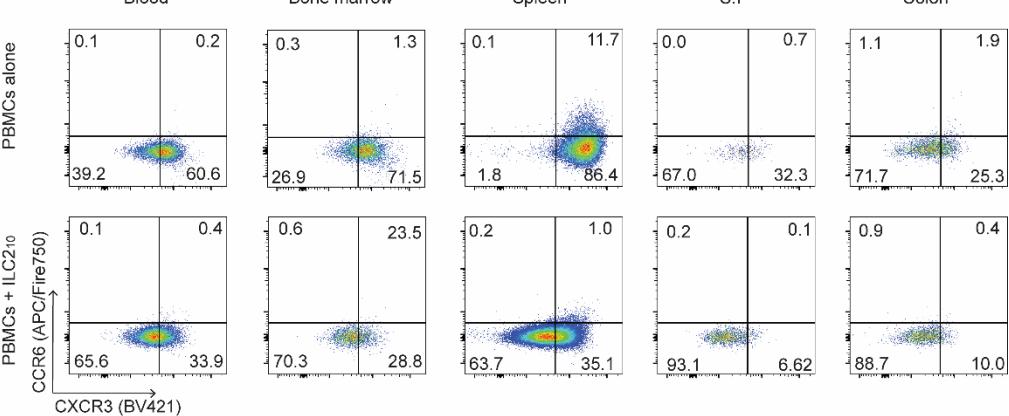
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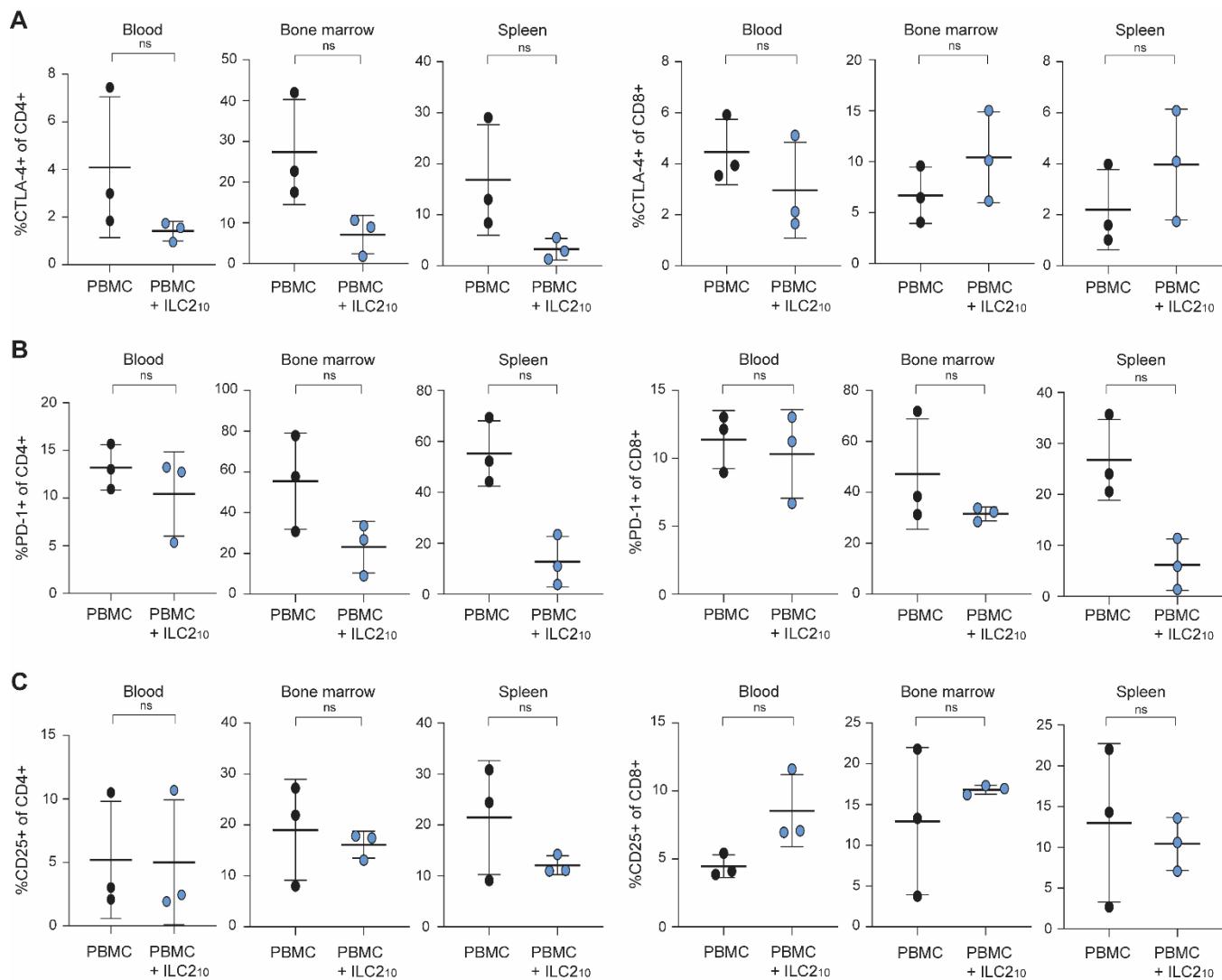
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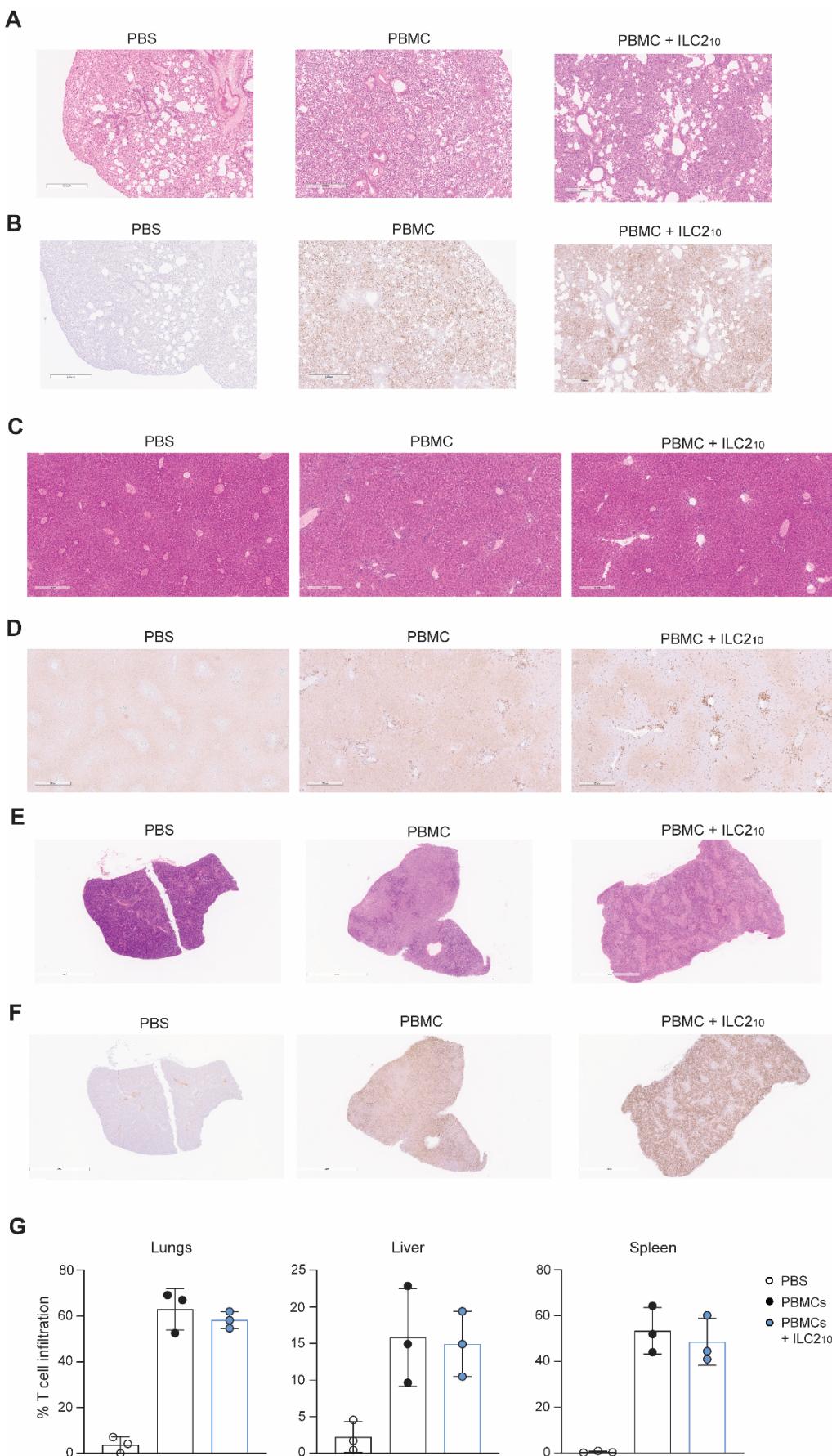


Supplemental Figure 8. Representative flow cytometry analysis of Ki-67 and CXCR3 on CD4⁺ and CD8⁺ T cells *in vivo* across tissues. A,B Representative FACS plots showing Ki-67 expression on CD4⁺ (**A**) and CD8⁺ (**B**) T cells in the blood, bone marrow and spleens of NSG mice given PBMCs or PBMCs with ILC2₁₀ infusion. **C,D** Representative FACS plots showing CXCR3 expression on CD4⁺ (**C**) and CD8⁺ (**D**) T cells in the blood, bone marrow, spleen, small intestines (S.I.) and colon of NSG mice given PBMCs or PBMCs with ILC2₁₀ infusion.

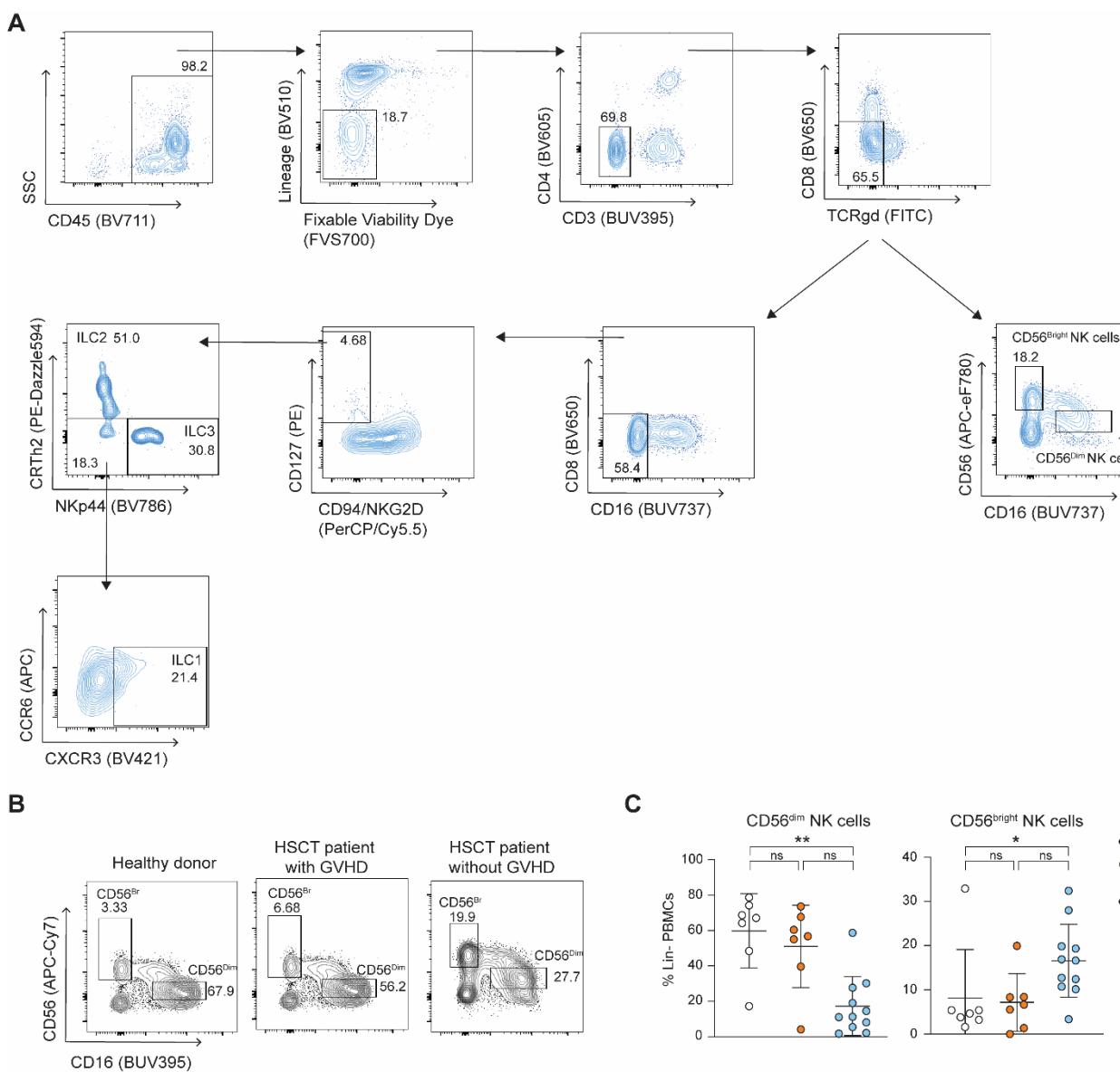


Supplemental Figure 9. Activation and checkpoint molecule expression on CD4⁺ and CD8⁺ T cells.

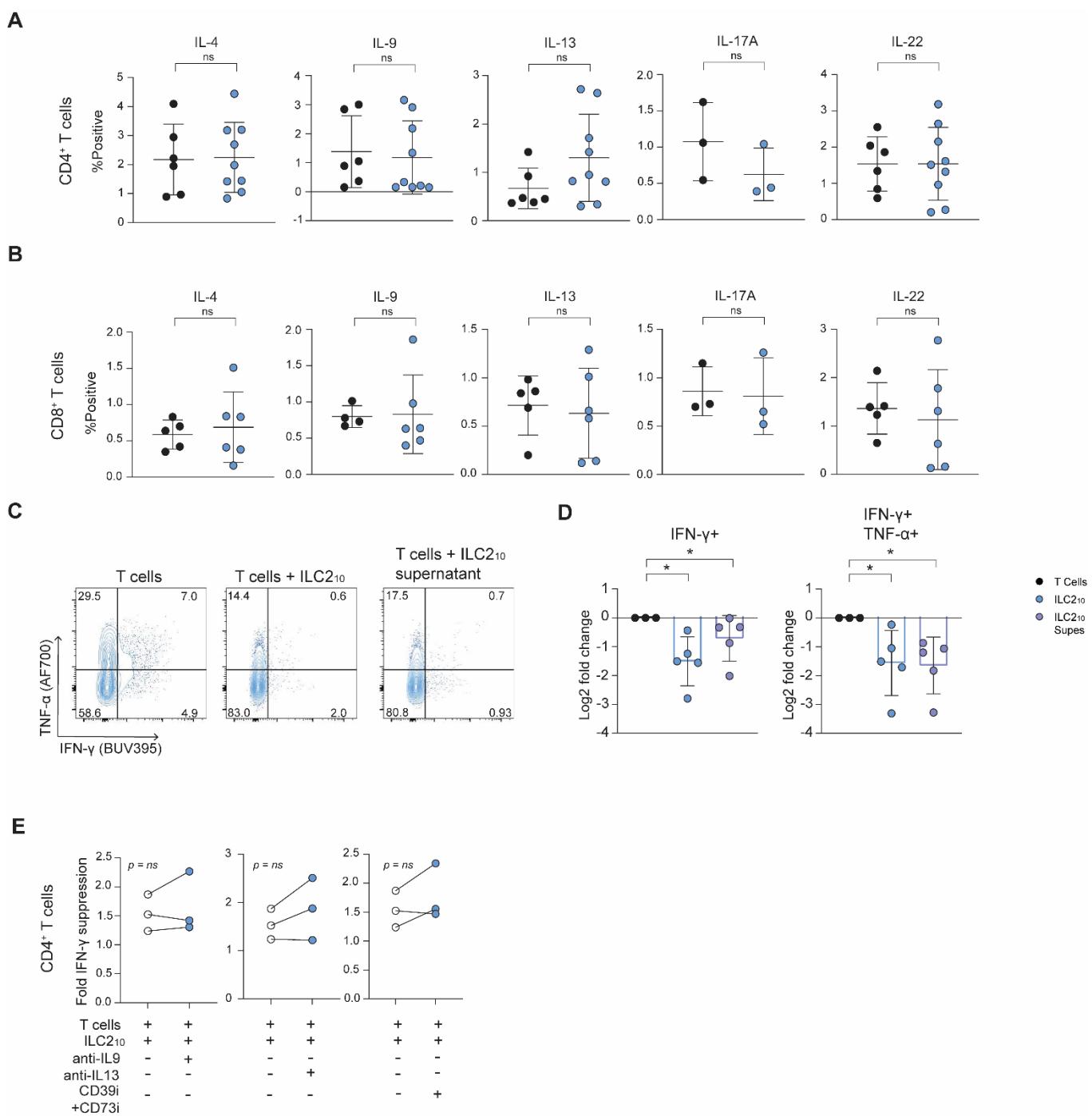
A-C Expression of CTLA-4 (A) PD-1 (B) and CD25 (C) on CD4⁺ and CD8⁺ T cells in the blood, bone marrow and spleens of NSG mice given PBMCs or PBMCs with ILC210 infusion (n = 3).



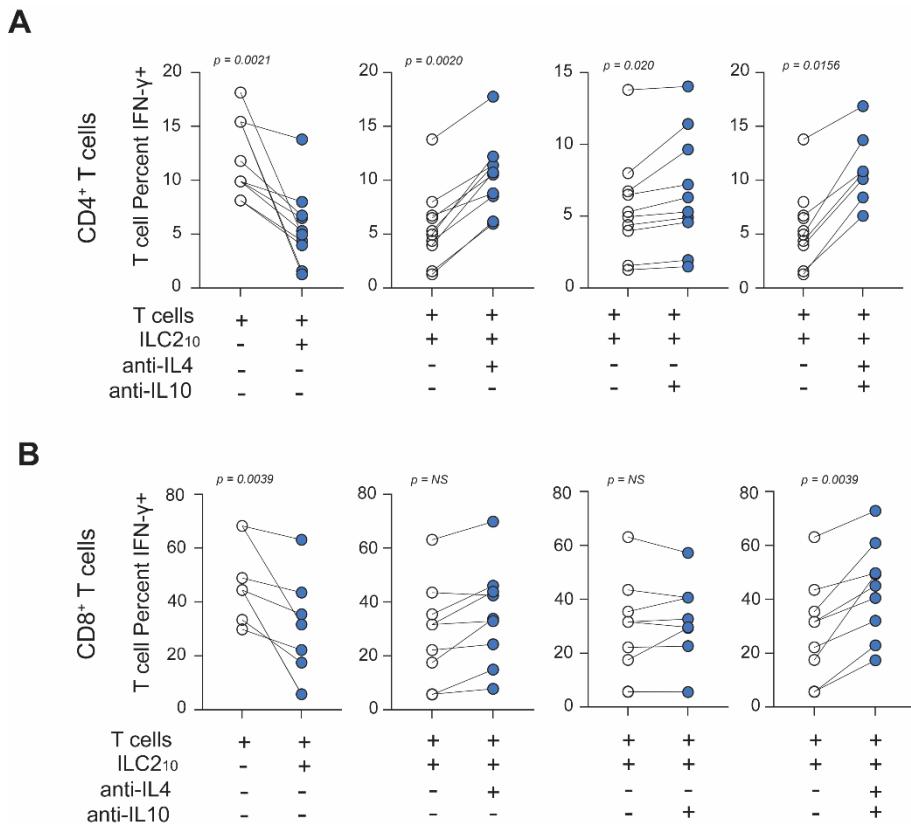
Supplemental Figure 10. H&E Staining and human CD3 immunohistochemical staining tissues of xenoGVHD mouse model. **A,B** Representative H&E (**A**) and human CD3 (**B**) staining on lungs from NSG mice given PBS, PBMCs or PBMCs with ILC2₁₀ taken at endpoint 8x magnification. **C,D** Representative H&E (**C**) and human CD3 (**D**) staining on livers from NSG mice given PBS, PBMCs or PBMCs with ILC2₁₀ taken at endpoint at 8x magnification. **E,F** Representative H&E (**E**) and human CD3 (**F**) staining on spleens from NSG mice given PBS, PBMCs or PBMCs with ILC2₁₀ taken at endpoint 2x magnification. **(G)** Average T cell infiltration in the lungs, liver and spleen of mice treated with PBS, PBMCs or PBMCs + ILC2₁₀. Quantified using CD3 immunohistochemistry and the HALO algorithm (n=3).



Supplemental Figure 11. ILC Gating strategy to analyze ILCs in HSCT recipient peripheral blood. PBMCs from healthy donors, and HSCT patients with or without aGVHD were assessed for ILC proportions and phenotypes using flow cytometry. (A) Lineage markers are CD14, CD19, CD20, CD33, CD34, CD123, CD138, CD303, and FC ϵ RI. Cells are gated as CD45⁺, Lineage⁻, Live, CD4⁻, CD3⁻, CD8⁻, and TCR γ δ ⁻. NK cells are then gating as CD56⁺ CD16⁺ for CD56^{dim} NK cells and CD56^{bright} CD16⁻ for CD56^{bright} NK cells. Helper ILCs are then gated as CD16⁻ CD94⁻ NKG2D⁻ CD127⁺ with ILC1s gated as CD117⁻ CRTTh2⁺ CXCR3⁺, ILC2s as CRTTh2⁺ and ILC3s as CRTTh2⁻ CD117⁺. **B,C** Representative flow plots (B) and summary graphs (C) of CD56^{dim} CD16⁺ and CD56^{bright} CD16⁻ NK cells in PBMCs, as a proportion of live CD45⁺ lineage negative cells.



Supplemental Figure 12. Effect of ILC2₁₀ supernatant and addition of various inhibitors to ILC2₁₀-T cell co-cultures. **A,B** Summary graphs of intracellular IL-4, IL-9, IL-13, IL-17A and IL-22 on CD4⁺ (n=6 T cells, n=9 ILC2₁₀) (A) and CD8⁺ (n=5 T cells, n=6 ILC2₁₀) (B) T cells after co-culture with ILC2₁₀. **C,D** Representative FACS plots (C) and summary graphs (D) of IFN- γ expression by CD4⁺ T cells cultured alone, with ILC2₁₀ or with ILC2₁₀ supernatant (n=5). (E) Changes in fold IFN- γ expression after co-culture of CD4⁺ T cells with ILC2₁₀ with the addition of IL-9 or IL-13 antibodies or with CD39 and CD73 inhibitors on CD4⁺ T cells (n=3).



Supplemental Figure 13. Non-normalized IFN- γ expression on CD4⁺ and CD8⁺ T cells cultured with ILC2₁₀. (A) Percent expression of IFN- γ by CD4⁺ T cells cultured alone or with ILC2₁₀ in the presence or absence of neutralizing antibodies towards IL-4, IL-10 and IL-4 and IL-10 together (n=10 from 5 independent experiments) (B) Percent expression of IFN- γ by CD8⁺ T cells cultured alone or with ILC2₁₀ in the presence or absence of neutralizing antibodies towards IL-4, IL-10 and IL-4 and IL-10 together (n=7 from 5 independent experiments)

Supplemental Table 1: CITE-Seq TotalSeqC antibody details

Marker	Oligotag	Volume (μ L per 1×10^6 cells)
CD56	TCCTTCCTGATAGG	0.625
CD161	GTACGCAGTCCTTCT	1.04
CD117	AGACTAATAGCTGAC	2.5
CD16	AAGTTCACTCTTGCG	0.25
TIGIT	TTGCTTACCGCCAGA	5
CD335	ACAATTGAAACAGCG	1
CD294	TGTTTACGAGAGGCC	6.25
CD127	GTGTGTTGTCCTATG	0.5
CD196	GATCCCTTGTCACT	0.125
CD314	CGTGTGGTTCCTCA	2.66
CD336	GGGCAATTAGCGAGT	12.5
CD94	CTTCCGGTCCTACA	0.5
KLRG1	GTAGTAGGCTAGACC	0.5
CD183	GCGATGGTAGATTAT	0.5
TCR γ δ	CTTCCGATTCAATTCA	1.0625
CD45	TCCCTTGCAGATTAC	0.4
TCRV α 24-J α 18	AACTTCTGTGGTAGC	2.5
TCR α β	CGTAACGTAGAGCGA	0.075
CD8a	GCTGCGCTTCCATT	0.5
CD3	CTCATTGTAACTCCT	0.125
CD4	TGTTCCCGCTCAACT	0.25
CD138	ACTCTTCGTTTACG	8.5
CD14	TCTCAGACCTCCGTA	0.125
CD206	TCAGAACGTCTAACT	1.67
HLADR	AATAGCGAGCAAGTA	2.65
CD45RO	TCAATCCTCCGCTT	2.6
CD45RA	CTCCGAATCATGTTG	3.125
CD25	TTTGTCTGTACGCC	0.5
CD223	CATTGTCTGCCGGT	1.25
CX3CR1	AGTATCGTCTCTGGG	0.625
TLSPR	CAGTCCTCTGTCA	10
CD49b	GCTTTCTTCAGTATG	0.25
CD38	TGTACCCGCTTGTGA	0.5
CD57	AACTCCCTATGGAGG	0.125
CD49a	ACTGATGGACTCAGA	0.125
CD278	CGCGCACCCATTAAA	0.3125
CD357	ACCTTCGACACTCG	5
CD39	TTACCTGGTATCCGT	0.25
CD69	GTCTCTGGCTTAAA	0.625
CD279	ACAGCGCCGTATTTA	2.5

CD152	ATGGTTCACGTAATC	1.25
CD107a	CAGCCCAC TGCAATA	0.15625
CD95	CCAGCTCATTAGAGC	1.25
CD134	AACCCACC GTTGT TA	0.625
CD137L	ATT CGCCTACG CAA	1.25
CD40	CTCAGATGGAGTATG	0.025
CD137	CAGTAAGTT CGGGAC	10.625
CD194	AGCTTACCTGCACGA	2.125
CD27	GC ACTCCTGCATGTA	0.425
CD28	TGAGAACGAC CCTAA	0.03125
GARP	AGGTATGGTAGAGTA	2.5
CD122	TCATTT CCTCCGATT	2.5
CD184	TCAGGT CCTT CAAC	2.5
CD49d	CCATTCAACTCCGG	2.5
CD274	GTT GTCCGACAATAC	0.15625
CD120b	GCGCAACTCCTTGTA	0.255
CD80	ACGAATCAATCTGTG	0.625
CD32	GCTTCCGAATTACCG	0.10625
CD11b	GACAAGTGATCTGCA	0.2
CD64	AAGTATGCC TACGA	0.10625
CD86	GTCTTGTCAGTGCA	0.0425
CD163	GCTTCTCCTCCTTA	0.53125
CD197	AGTT CAGTC AACCGA	0.5
CD73	CAGTT CCTCAGTTCG	10
Integrin β 7	TCCTTGGATGTACCG	10
CD366	TGTCCTACCCAACTT	10
CD103	GACCTCATTGTGAAT	10

Supplemental Table 2: Patient and Healthy Donor Characteristics

	Acute GVHD (n=7)	No Acute GVHD (n=11)	Healthy Donors (n=7)
Sex M/F (%M)	5/2 (71.4)	6/5 (54.5)	4/3 (57.1)
Age			
20-29	1 (14.3)	0 (0)	1 (14.3)
30-39	0 (0)	2 (18.2)	0 (0)
40-49	3 (42.9)	0 (0)	4 (57.1)
50-59	0 (0)	4 (36.4)	1 (14.3)
60-69	3 (42.9)	3 (27.3)	1 (14.3)
70-79	0 (0)	2 (18.2)	0 (0)
Diagnosis			
HL	1 (14.3)	0 (0)	N/A
AML	3 (57.1)	7 (64.4)	N/A
MF	0 (0)	1 (9.1)	N/A
B-ALL	0 (0)	2 (18.2)	N/A
MDS	3 (57.1)	1 (9.1)	N/A
Conditioning			
RIC	5 (71.4)	6 (54.5)	N/A
MAC	2 (28.6)	5 (45.5)	N/A
Donor			
MUD	4 (57.1)	6 (54.5)	N/A
MSD	2 (28.6)	3 (27.3)	N/A
Haplo	1 (14.3)	2 (18.2)	N/A
Grade of aGVHD			
1	1 (14.3)	0 (0)	N/A
2	0 (0)	0 (0)	N/A
3	4 (57.1)	0 (0)	N/A
4	2 (28.6)	0 (0)	N/A
Immunosuppression			
PTC γ	7 (100)	11 (100)	N/A
CSA+Budesonide	2 (28.6)	0 (0)	N/A

Data expressed as n (%). HL, Hodgkin's Lymphoma; AML, acute myeloid leukemia; MF, myelofibrosis; BLL, B-cell acute lymphoblastic leukemia; MDS, myelodysplastic syndrome; RIC, reduced intensity conditioning; MAC, myeloablative conditioning; MUD, matched unrelated donor; MSD, matched sibling donor; Haplo, haploidentical transplant. PTC γ , post-transplant cyclophosphamide. CSA, cyclosporin.

Supplemental Table 3: Antibodies used for flow cytometry

Target	Fluorophore	Clone	Company	Dilution
Amphiregulin	PE	AREG559	eBioscience	1:25
CCR6	APC	G034e3	BioLegend	1:25
CCR6	APC/Fire750	G034e3	BioLegend	1:50
CD117	PE-Cy7	1D11	BioLegend	1:50
CD117	BV650	104D2	BioLegend	1:50
CD123	BV510	6H6	BioLegend	1:100
CD127	PE	HIL-7R-M21	BD	1:50
CD138	FITC	MI15	BioLegend	1:100
CD138	BV510	MI15	BioLegend	1:100
CD14	FITC	M5E2	BioLegend	1:200
CD14	BV510	M5E2	BioLegend	1:200
CD15	FITC	W6D3	BioLegend	1:200
CD16	PE-Dazzle594	3G8	BioLegend	1:100
CD16	BUV737	3G8	BD	1:100
CD19	FITC	HIB19	BioLegend	1:200
CD19	BV510	HIB19	BioLegend	1:200
CD20	FITC	2H7	BioLegend	1:200
CD20	BV510	2H7	BioLegend	1:200
CD203c	FITC	NP4D6	BioLegend	1:100
CD25	APC	BC86	eBioscience	1:25
CD3	FITC	OKT3	BioLegend	1:100
CD3	FITC	UCHT1	BioLegend	1:100
CD3	BUV395	UCHT1	BD	1:100
CD3	BUV496	SK7	BD	1:50
CD3	BV510	OKT3	BioLegend	1:100
CD303	BV510	201A	BioLegend	1:100
CD33	FITC	HIM3-4	BioLegend	1:100
CD33	BV510	P67.6	BioLegend	1:100
CD34	FITC	581	BioLegend	1:100
CD34	BV510	581	BioLegend	1:100
CD39	PerCP-eF710	eBioA1 (A1)	eBioscience	1:100
CD4	FITC	RPA-T4	BioLegend	1:200
CD4	BV605	RPA-T4	BD	1:200
CD45	BUV711	HI30	BioLegend	1:100
CD45	BUV395	HI30	BD	1:100
CD49d	SuperBright600	9F10	eBioscience	1:50
CD56	BV605	HCD56	BioLegend	1:50
CD56	APC-Cy7	HCD56	BioLegend	1:50
CD73	BUV737	AD2	BD	1:50
CD79	FITC	HM47	BioLegend	1:100
CD8a	FITC	RPA-T8	BioLegend	1:200
CD8a	BV650	RPA-T8	BD	1:50
CD8a	AF700	RPA-T8	eBioscience	1:100

CD86	BUV737	2331 (FUN1)	BD	1:100
CD94	PerCP/Cy5.5	DX22	BioLegend	1:100
CRTh2	BV421	BM16	BioLegend	1:25
CRTh2	PE-Dazzle594	BM16	BioLegend	1:25
CTLA-4	PE-Cy7	14D3	eBioscience	1:50
CXCR3	BV421	G025H7	BioLegend	1:50
FC ϵ R1a	FITC	AER-37	BioLegend	1:100
FC ϵ R1a	BV510	AER-37	BioLegend	1:100
Fixable Viability Dye eF450	eF450	--	eBioscience	1:1000
Fixable Viability Dye eF506	eF506	--	eBioscience	1:1000
Fixable Viability Stain 700	FVS700	--	BD	1:1000
GM-CSF	APC	BVD2-21C11	BioLegend	1:50
IFN- γ	BUV395	B27	BD	1:100
IL-10	AF488	JES3-9D7	eBioscience	1:25
IL-10	PE	JES3-9D7	BioLegend	1:25
IL-13	BV711	JES10-5A2	BD	1:50
IL-17A	BV786	N49-653	BD	1:25
IL-17F	PE-CF594	033-782	BD	1:25
IL-22	eF450	22URTI	eBioscience	1:25
IL-4	PE-Cy7	MP4-25D2	BioLegend	1:100
IL-9	PerCP-eF710	MH9D1	eBioscience	1:50
Ki-67	FITC	20Raj1	eBioscience	1:25
KLRG1	BV786	2F1/KLRG1	BioLegend	1:50
NKG2D	PerCP/Cy5.5	1D11	BioLegend	1:100
NKp44	BV786	p44-8	BD	1:50
PD-1	BV785	EH12.2H7	BioLegend	1:100
TCR α β	FITC	IP26	BioLegend	1:200
TCR γ δ	FITC	B1	BioLegend	1:100
TNF- α	AF700	MAb11	eBioscience	1:50
Zombie NIR Fixable Viability Dye	Zombie NIR	--	BioLegend	1:1000

Supplemental Table 4: Lineage Antibodies for ILC Sort

Target	Fluorophore	Clone	Company	Dilution
CD138	FITC	MI15	BioLegend	1:100
CD14	FITC	M5E2	BioLegend	1:200
CD15	FITC	W6D3	BioLegend	1:200
CD19	FITC	HIB19	BioLegend	1:200
CD20	FITC	2H7	BioLegend	1:200
CD203c	FITC	NP4D6	BioLegend	1:100
CD3	FITC	OKT3	BioLegend	1:100
CD3	FITC	UCHT1	BioLegend	1:100
CD33	FITC	HIM3-4	BioLegend	1:100
CD34	FITC	581	BioLegend	1:100
CD4	FITC	RPA-T4	BioLegend	1:200
CD79	FITC	HM47	BioLegend	1:100
CD8a	FITC	RPA-T8	BioLegend	1:200
FC ϵ R1a	FITC	AER-37	BioLegend	1:100
TCR $\alpha\beta$	FITC	IP26	BioLegend	1:200
TCR $\gamma\delta$	FITC	B1	BioLegend	1:100

Supplemental Table 5: Antibodies for ILC sort

Target	Fluorophore	Clone	Company	Dilution
CCR6	APC	G034e3	BioLegend	1:25
CD117	PE-Cy7	1D11	BioLegend	1:50
CD127	PE	HIL-7R-M21	BD	1:50
CD16	PE-Dazzle594	3G8	BioLegend	1:100
CD45	BV711	HI30	BioLegend	1:100
CD56	BV605	HCD56	BioLegend	1:50
CD94	PerCP/Cy5.5	DX22	BioLegend	1:100
CRTh2	BV421	BM16	BioLegend	1:25
Fixable Viability Stain 700	FVS700	--	BD	1:1000
NKG2D	PerCP/Cy5.5	1D11	BioLegend	1:100
NKp44	BV786	p44-8	BD	1:50

Supplemental Table 6: Intracellular Antibodies used for Flow Cytometry

Target	Fluorophore	Clone	Company	Dilution
Amphiregulin	PE	AREG559	eBioscience	1:25
GM-CSF	APC	BVD2-21C11	BioLegend	1:50
IFN- γ	BUV395	B27	BD	1:100
IL-10	AF488	JES3-9D7	eBioscience	1:25
IL-10	AF488	JES3-9D7	BioLegend	1:25
IL-10	PE	JES3-9D7	BioLegend	1:50
IL-13	BV711	JES10-5A2	BD	1:50
IL-17A	BV786	N49-653	BD	1:25
IL-17F	PE-CF594	033-782	BD	1:25
IL-22	eF450	22URTI	eBioscience	1:25
IL-4	PE-Cy7	MP4-25D2	BioLegend	1:100
IL-9	PerCP-eF710	MH9D1	eBioscience	1:50