GPR183 mediates the capacity of the novel CD47-CD19 bispecific
 antibody TG-1801 to heighten ublituximab-umbralisib (U2) anti-lymphoma
 activity

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Marcelo Lima Ribeiro,^{1,2*} Núria Profitós-Pelejà,^{1*} Juliana Carvalho Santos,^{1*}
Pedro Blecua,³ Diana Reyes Garau,¹ Marc Armengol,^{1;4} Miranda FernándezSerrano,^{1;4} Hari P. Miskin,⁵ Francesc Bosch,^{4;6;7} Manel Esteller,^{3;8;9} Emmanuel
Normant,⁵ and Gael Roué^{1;4;6;7}

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¹Lymphoma Translational Group and ³Cancer Epigenetics Group, Josep 10 Carreras Leukemia Research Institute, Badalona, Spain; ²Laboratory of 11 Immunopharmacology and Molecular Biology, Sao Francisco University Medical 12 School, Braganca Paulista, São Paulo, Brazil; ⁴Autonomous University of 13 Barcelona, Barcelona, Spain; ⁵TG Therapeutics, New York, NY, USA; 14 ⁶Department of Hematology, Vall d'Hebron University Hospital, Barcelona, 15 Spain; ⁷Experimental Hematology, Vall d'Hebron Institute of Oncology, 16 Barcelona, Spain; ⁸Centro de Investigación Biomédica en Red de Cáncer 17 (CIBERONC), Instituto de Salud Carlos III, Barcelona, Spain; ⁹Institució 18 Catalana de Recerca i Estudis Avançats (ICREA), Barcelona, Spain. 19

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* MLR, NPP and JCS contributed equally to this work.

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Corresponding authors: Marcelo L. Ribeiro, PhD. Lymphoma Translational
Group, IJC. Ctra de Can Ruti, Camí de les Escoles s/n, 08916 Badalona
(Barcelona), SPAIN. Tel: (+34) 93 5572800 Ext. 4081. E-mail:

<u>mlima@carrerasresearch.org</u>; Emmanuel Normant, Pharm.D., PhD., Vice
president preclinical sciences, TG Therapeutics, 2 Gansevoort street, New
York, NY, 10014, USA, Tel: 1-781-813-9481. E-mail: <u>enormant@tgtxinc.com</u>.

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30 Abstract

Targeted therapies have considerably improved the survival rate of B-cell non-31 Hodgkin lymphoma (B-NHL) patients in the last decade; however, most 32 subtypes remain incurable. TG-1801, a bispecific antibody that targets CD47 33 selectively on CD19+ B-cells, is under clinical evaluation in relapsed/refractory 34 35 B-NHL patients either as a single-agent or in combination with ublituximab, a CD20 antibody, which is also being combined with the PI3K δ /CK1e inhibitor, 36 umbralisib ("U2"-regimen). In this study, we demonstrated that TG-1801 37 potentiates ublituximab-mediated antibody-dependent cell death (ADCC) and 38 antibody-dependent cell phagocytosis (ADCP), leading to an additive anti-39 tumour effect of the TG-1801/U2 combination in B-NHL co-cultures. 40 Accordingly, in a B-NHL xenotransplant model, the triplet achieved a 93% 41 tumour growth inhibition, with 40% of the animals remaining tumour-free 35 42 43 days after the last dosing. Transcriptomic analysis further uncovered the upregulation of the G protein-coupled receptor, GPR183, as a crucial event 44 associated with TG-1801/U2 synergism, while pharmacological blockade or 45 genetic depletion of this factor impaired ADCP initiation, as well as cytoskeleton 46 remodelling and cell migration, in B-NHL cultures exposed to the drug 47 combination. Thus, our results set the preclinical rationale and support a 48 combination strategy of TG-1801 with PI3Ko- and CD20-targeting agents in 49 patients with B-NHL. 50

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52 Introduction

Cluster of differentiation 47 (CD47), also known as integrin-associated protein 53 (IAP), is a cell surface receptor that is part of the immunoglobulin superfamily 54 and interacts with the macrophage receptor signal regulatory protein-alpha 55 (SIRPa). This interaction sends a "do-not-eat-me" signal to macrophages, which 56 mediates immune evasion in several types of cancers (Barclay and Van den 57 Berg, 2014). High levels of CD47 have been observed in both lymphoid and 58 myeloid neoplasm in which this factor is both an adverse prognostic indicator 59 and a valid anti-cancer target with several therapeutic antibodies currently being 60 tested in clinical trials. In B-cell lymphoma, these trials frequently involve a 61 combination with an anti-CD20 therapy, to ensure a proper engagement of the 62 Fc receptors at the surface of macrophages and natural killer (NK) effector 63 cells. The anti-CD20 mAb rituximab has been the most common IgG1 antibody 64 65 tested in this setting, and has demonstrated combinatorial activity in both 66 indolent and aggressive B-cell lymphomas (Armengol et al., 2021; Matlung et al., 2017). However, as CD47 is widely expressed on the surface of a broad 67 range of cell types, including erythrocytes and platelets, a major limitation of 68 69 CD47 blocking agents is the target-mediated drug disposition and the potential side effects, which include anaemia or thrombocytopenia. 70

TG-1801 is a novel bi-specific antibody that binds to CD47 with sub-micromolar
affinity and to CD19 with a sub-nanomolar affinity. This thousand-fold difference
between its affinity to CD19 and CD47 allows TG-1801 to bind selectively to
CD19-positive B cells but not CD19-negative red blood cells or platelets
(Buatois et al., 2018; Hatterer et al., 2020). TG-1801 is currently being tested

clinically as a single agent and in combination with the glyco-engineered CD20 76 77 antibody ublituximab in patients with relapsed/refractory B-cell lymphoma. Ublituximab, in association with the dual PI3K δ /CK1 ϵ inhibitor umbralisib (a 78 combination named U2), has demonstrated clinical activity in B-cell lymphoma. 79 and a biologic license application for U2 in chronic lymphocytic leukaemia (CLL) 80 81 has been recently accepted for review by the FDA (Lunning et al., 2019). Here 82 we studied the triplet combination of TG-1801 and U2 in in vitro and in vivo models of aggressive B-cell lymphoma. 83

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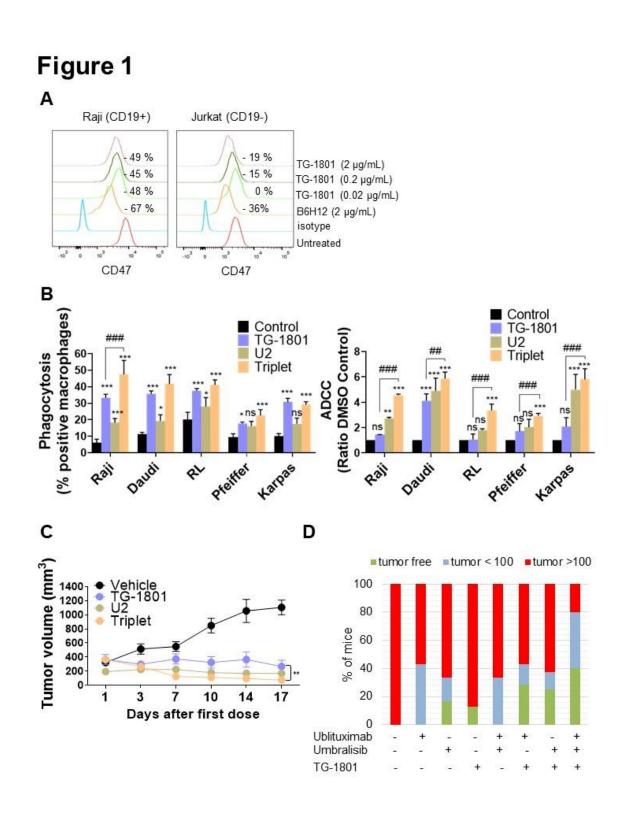
85 Results and Discussion

CD47 blockade in CD19+ cells potentiates the anti-tumour effect of U2 regimen

To determine the working concentrations of TG-1801 in vitro, we first developed 88 89 a CD47 occupancy assay using the Burkitt lymphoma (BL) cell line Raji. In this assay, TG-1801 reached a plateau of 48% CD47 occupancy at a dose as low 90 as 20 ng/mL, slightly lower than the 67% occupancy achieved by the first-in-91 class CD47 blocking mAb, B6H12 (Mateo et al., 1999) (Figure 1A). This 92 difference may potentially be explained by the lower level of expression of 93 CD19 compared to CD47 in the BL cell line (Figure 1 - figure supplement 1). As 94 expected, TG-1801, but not B6H12-mediated target occupancy, was highly 95 dependent on CD19 expression, as shown in the T-ALL-derived, CD19 96 97 negative, Jurkat cells, where no significant CD47 occupancy was detected with TG-1801 at doses as high as 2 µg/mL, contrasting with the sustained binding of 98 B6H12 (Figure 1A). A panel of human B-cell lymphoma cell lines (n=10) with 99 different levels of CD47 and CD19 expression, were cultured in the presence of 100

M1-polarized primary macrophages or primary circulating PBMCs from healthy 101 102 donors as a source of effector cells, to assess the TG-1801 antibody-dependent cell phagocytosis (ADCP) or antibody-dependent cell cytotoxicity (ADCC), 103 respectively. As shown in Figure 1 - figure supplement 2, ADCP and ADCC 104 were both increased 2-6 fold after CD47 ligation in these cells, and both 105 appeared to be related to neither the expression levels of CD47 nor the 106 107 CD47/CD19 ratios, in accordance with previous reports (Buatois et al., 2018). Interestingly, the analysis of the pro-cytotoxic or pro-phagocytic activities of the 108 triplet regimen in five representative B-NHL cell lines, including two DLBCL 109 110 (Pfeiffer and Karpas-422), two BL (Raji and Daudi), and one FL (RL), showed an improvement in these activities when compared to the TG-1801 single-agent 111 treatment (Figure 1B). In line with this observation, in Raji tumour-bearing mice, 112 113 all molecules were active as single agents (88%, 76% and 50% tumour growth inhibition (TGI) with ublituximab, TG-1801 or umbralisib, respectively, Figure 1 -114 115 figure supplement 3), and the activity of the triplet was higher (93% TGI) after a 116 17-day treatment. Furthermore, 40% of the mice remained tumour-free 35 days after the last dose in the triplet arm with no detectable toxicity (Figures 1C and 117 118 1D, and data not shown). These in vitro and in vivo data suggested that the addition of TG-1801 to the U2 combination induced a mechanism that promoted 119 a stronger innate immune response. 120

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Figure 1. U2 regimen cooperates with CD47 blockade in in vitro and in 124 vivo models of B-cell lymphoma. A) FACS-mediated CD47 occupancy assay 125 in the CD19+ Burkitt lymphoma cell line Raji, and in the CD19- T-ALL cells 126 Jurkat. Results showed a CD19-dependent, optimal competition of 20 ng/mL 127 TG-1801 with the PE-labelled anti-CD47 antibody (N=3). B) ADCP (left panel) 128 and ADCC (right panel) activities were assessed in five representative B-cell 129 lymphoma cell lines (N=3). Values are expressed as mean ± SD. C) TG-1801, 130 U2 and the triplet combination were dosed orally in the Raji xenograft model. D) 131 Mice with no tumour or low tumour size were kept alive for another 35 days. At 132 133 day 52 all the mice either tumour-free (green) or bearing a small tumour (blue, < 100 mm³) were alive. The TG-1801-U2 combo group showed an increased 134 number of tumour free or low tumour burden bearing mice (green and blue 135 136 bars). * p<0.05, ** p<0.01, *** p<0.001, when compared to control group. (N= 8-6 mice per group) ### p<0.001 when compared to TG-1801 alone. ns = non-137 138 significant.

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GPR183 is upregulated in response to TG-1801/U2 combination treatment 140 To uncover the mechanisms underlying the superior effect of the triplet, 141 transcriptomic analyses were carried out on a set of six samples that included 142 Raji xenograft tumours (n=2) and CD20+ cells isolated from Raji, Daudi and two 143 BL primary samples co-cultured with the bone marrow-derived stromal cell line 144 (BMSC) stromaNKtert (Dlouhy al., 2020), M2-polarized 145 et primary macrophages, primary circulating PBMCs, and either TG-1801 or the TG-146 1801+U2 triplet. As shown in Figure 2A, a total of 20 genes were significantly 147 up- or down-regulated in the triplet compared to TG-1801 treatment in all six 148

samples. A Gene Set Enrichment Analysis (GSEA) identified inflammatory 149 150 (NES = 2.43, FDR = 0) and TNF α -driven signatures (NES = 2.43, FDR = 0) as predominantly activated upon treatment with the triple combination, when 151 compared to TG-1801 single agent therapy, suggesting that the stronger activity 152 of the triplet was based on the activation of an immune-related anti-tumour 153 effect. In the heatmap showing a set of genes strongly activated in all six 154 samples after the triplet treatment (Figure 2B), the highest up-regulated gene in 155 both signatures was the G protein-coupled receptor 183 (GPR183, also known 156 as Epstein-Barr virus (EBV)-induced G protein-coupled receptor 2, EBI2). 157 158 GPR183 was also one of the 20 upregulated genes previously identified in the volcano plot (Figure 2A). An increase in GPR183 expression after U2 addition 159 to TG-1801 was confirmed in vitro by gPCR analysis in the four cell lines-160 161 derived samples (Figures 2C and 2D), by western blot in the Raji and Daudi cell lines (Figure 2E and source data 1), and by immunohistochemistry (IHC) in 162 163 tumour specimen from the Raji xenograft model (Figure 2F). GPR183 was first 164 identified by sequence similarity as a GPCR induced by EBV infection. This proinflammatory receptor, which upregulation is associated with a better prognosis 165 of DLBCL patients treated with the standard immunochemotherapeutic (R-166 CHOP) regimen according to published gene array database (gse10846; R2: 167 Visualization 168 Genomics Analysis Platform (http://r2.amc.nl and http://r2platform.com), plays an important role in B-cell motility and positioning 169 during the germinal centre reaction (Liu et al., 2011; Pereira et al., 2009), and 170 the gradient of its natural ligand, oxysterol, acts as a chemoattractant of 171 GPR183+ cells. Accordingly, among a panel of eight genes identified besides 172 GPR183 in the two inflammation gene signatures, the transcript of the sole 173

chemoattractant gene *CCL20* was upregulated by the triple combination in the three *in vitro* and *in vivo* models (Figures 2C and 2D). Also, increased tumour infiltration of mouse macrophages (F4/80 IHC staining) together with a reduction in mitotic index (histone H3-pSer10 IHC staining) were observed in triplet-treated tumours when compared to either TG-1801 or U2 arms (Figure 2F).

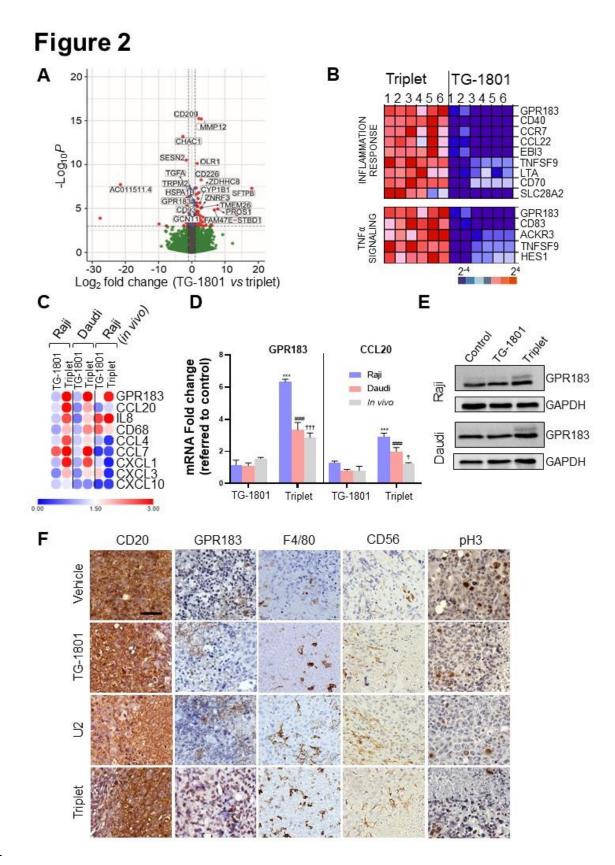




Figure 2. Upregulation of GPR183 is a hallmark of the response to U2 and 183 184 TG-1801 combination in vitro and in vivo. A) Volcano plot showing the most relevant significantly differentially expressed genes between triplet and TG-185 1801 treatments. Genes that underwent the same modulation in the three in 186 vitro and in vivo models (N=20) have been labelled. B) Gene set enrichment 187 analysis was performed using the GSEA software to analyse the enriched gene 188 sets in the triplet samples compared to the samples treated with TG-1801. 189 Samples were sorted from left to right: 1-Raji, 2-Daudi, 3-4- BL primary samples 190 and 5-6 CD20+ cells isolated from 2 representative Raji xenograft specimens. 191 192 C) GPR183 upregulation was confirmed in these samples and compared to the 11 inflammatory genes extracted from GSEA analysis. Data are presented in 193 fold-change related to the control (N=3). Clustering was performed using 194 Morpheus (hierarchical, one minus Pearson correlation) available 195 at https://software.broadinstitute.org/morpheus/. D) GPR183 and CCL20 transcript 196 197 levels followed the same evolution in vitro and in vivo according to the different treatment regimens. E) Immunoblot evaluation of GPR183 (SantaCruz, #sc-198 514342) in both Raji and Daudi showed an increased GPR183 protein 199 expression after the combination treatment (N=3). F) Immunohistochemistry 200 (IHC) labelling of CD20 (Clone L26, Sigma-Aldrich), GPR183 (Clone G-12, 201 Santa Cruz), F4/80 (Clone SP115, Abcam), Histone H3-pSer10 (Clone E173, 202 Abcam) and CD56/NCAM-1 (Clone EPR1827, Abcam) in tissue sections from 203 tumour specimens (N=3). *** p<0.001, ### p<0.001, and † p<0.05 and ^{†††} 204 p<0.001 when compared to control group in Raji (in vitro), Daudi (in vitro) and 205 Raji (*in vivo*) models, respectively. ns = non-significant. 206

Figure 2E — source data 1 - raw unedited blot.

208 GPR183 is required for B-cell trafficking and macrophage-dependent

209 phagocytosis after triple combination treatment

To investigate how the upregulation of GPR183 in target cells could impact their 210 recognition and phagocytosis by M1 macrophages, a single-clone derived Raji-211 GPR183^{KO} cell was generated by CRISPR/Cas9 gene editing (Figure 3A and 212 213 source data 1), using previously described procedures (Ribeiro et al., 2021) and co-cultured for 24h with primary M1 macrophages and BMSCs under 214 Nanoshuttle-driven magnetic levitation (Souza et al., 2010) in a conditioned 215 medium to form functional 3D spheroids. Compared to the Raji-GPR183^{wt}, the 216 Raji-GPR183^{KO} spheroids harboured a complete blockade of M1 cell infiltration 217 within the multicellular aggregates, both at basal levels and upon treatment with 218 the triplet (Figure 3B). Accordingly, ADCP activity was abrogated in the Raji-219 GPR183^{KO} cell cultures (Figure 3C) highlighting the critical role of GPR183 in 220 the recruitment of macrophages. ADCC was also compromised, although to a 221 222 lower extent (Figure 3C). Supporting these results, global inflammatory 223 signature, and especially CCL20 gene overexpression, were not detected anymore in Raji-GPR183^{KO} co-cultures exposed to triplet therapy (Figure 3D). 224 To understand whether a functional GPR183 was required for the TG-1801+U2 225 synergistic interaction, Raji cells were exposed for 1h to the GPR183 inhibitor 226

NIBR189 (Gessier et al., 2014), washed out, and co-cultured for 3h with M1polarized macrophages, in the presence of U2 +/- TG-1801. As shown in Figure
3E, relative ADCP was decreased by 3-fold after GPR183 pharmacological
blockade, when compared to untreated Raji cells.

Since GPR183 is a known antagonist of chemokine-mediated B cell migration
(Barroso et al., 2012), a transwell migration assay using recombinant CXCL12

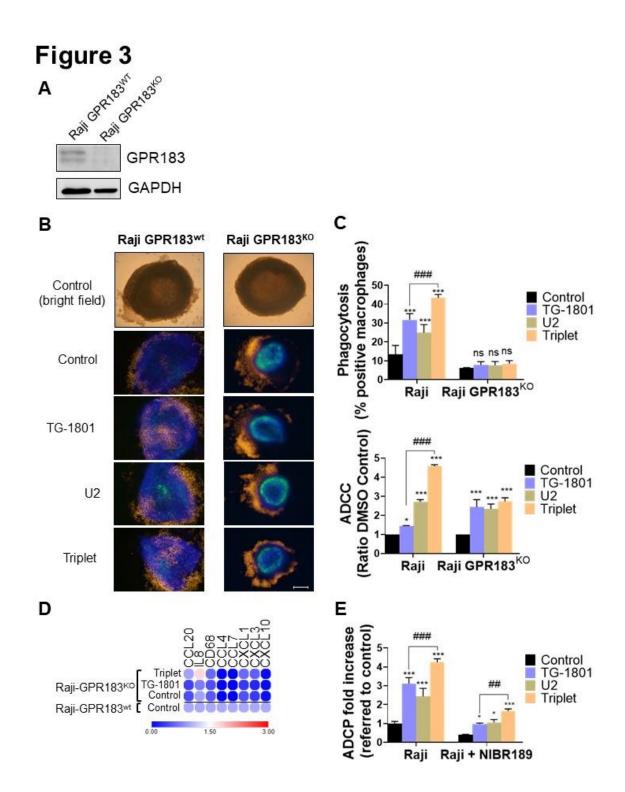
as a chemoattractant was set up, to compare the Raji parental to the Raji-233 GPR183^{KO} cells and to NIBR189-pretreated cells. Figure 3F shows that cell 234 migration was significantly impaired by both U2 and TG-1801 treatments, and 235 that the combination of the two drugs led to an accentuated inhibition. This 236 effect was completely lost either after GPR183 pharmacological inhibition by 237 NIBR189 or after the genetic deletion of the receptor. Accordingly, F-actin 238 polymerization was decreased by 70% in Raji cells exposed to the triplet 239 treatment and this effect was completely lost in the absence of GPR183 or after 240 NIBR189 treatment (Figures 3G and 3H), in agreement with previous studies 241 242 that highlighted the relevance of F-actin disruption in target cells in the antilymphoma effect of anti-CD47 antibodies (Barbier et al., 2009). 243

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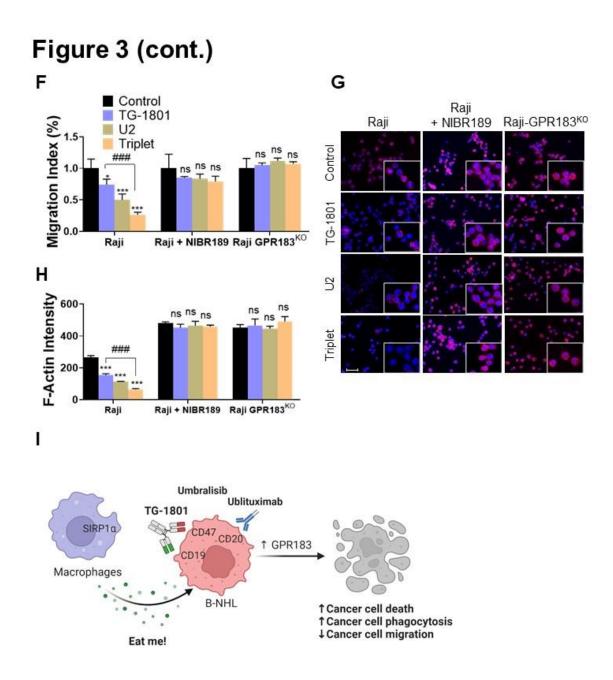
245 While the synergistic anti-tumour effect of CD47-targeting drugs, when combined with IgG1 antibodies, has classically been related to the inhibition of 246 247 the "do-not-eat-me" signal, here we propose a novel and additional mechanism based on the overexpression of the proinflammatory receptor GPR183. Our 248 results support a role for GPR183 in the recognition and elimination in vitro and 249 in vivo of tumour B cells by activated macrophages (Figure 3I). Future studies 250 will be aimed at understanding whether GPR183 could be a biomarker for the 251 activity of therapeutic combinations containing CD47 targeted therapy. Testing 252 253 whether this discovery can be generalized to other drugs from the same families is underway. 254

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Figure 3. GPR183 activity is required to impair B cell trafficking and to
potentiate macrophage-dependent phagocytosis in triplet-treated cells. A)
Immunoblot evaluation of GPR183 in both Raji-GPR183^{WT} and Raji-GPR183^{KO}
cells. B) Raji-GPR183^{WT} or Raji-GPR183^{KO} 3D spheroid in presence or absence
of 10 ng/mL TG-1801 +/- U2 (10 µg/mL ublituximab + 1 µM umbralisib) for one
more day. The infiltration of M1 macrophages was evaluated by live-cell red

fluorescence (N=3). Scale bar: 500 µm. C) The phagocytosis and cytotoxicity 267 rates were assessed in Raji-GPR183^{WT} and Raji-GPR183^{KO} cultures with 268 pHrodo-stained B cells (top graph) and ADCC (bottom graph), as previously 269 described (N=3). D) Raji-GPR183^{WT} and Raji-GPR183^{KO} were co-cultured with 270 BMSCs, M2-polarized primary macrophages and PBMCs (4:1:1:1) and treated 271 with vehicle, TG-1801 or the triplet combination for 24h. Then, purified CD20+ 272 cells were subjected to RNA extraction and qPCR. Data are presented in fold-273 change related to the Raji-GPR183^{WT} control (N=3). E) ADCP activities were 274 assessed in Raji cells with or without the GPR183 inhibitor NIBR189 prior to 275 treatment with 10 ng/mL TG-1801 +/- U2 combo (N=3). F) The cell migration 276 index of Raji-GPR183^{WT}, Raji-GPR183^{KO} cells exposed to the GPR183 inhibitor 277 NIBR189, in presence or absence of 10 ng/mL TG-1801 +/- U2 combination 278 279 (N=3). G) F-actin levels were assessed in the different cultures exposed to TG-1801 +/- U2 as in E), followed by staining with a TRITC-labelled phalloidin and 280 281 direct red fluorescence recording. Nuclei were counterstained with DAPI (blue) (N=3). Scale bar: 50 µm. H) F-actin fluorescence intensity from Raji-GPR183^{WT}, 282 Raji-GPR183^{KO}, and NIBR189-treated Raji cells in presence or absence of TG-283 1801 +/- U2 (N=3). Values are expressed as mean ± SD. * p<0.05, ** p<0.01, 284 *** p<0.001, when compared to control group. ^{##} p<0.01 and ^{##} p<0.001 when 285 compared to TG-1801 alone. ns = non-significant. I) Mechanism of action of the 286 TG-1801/U2 triplet combination therapy in B-NHL. The novel CD47-CD19 287 bispecific antibody potentiates the anti-tumour activity of the ublituximab-288 umbralisib regimen through activation of the pro-inflammatory GPR183, thus 289 promoting macrophage-dependent phagocytosis, B-cell cytoskeleton 290 remodelling and B-cell motility. 291

Figure 3A—source data 1 - raw unedited blot.

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- 295 Materials and Methods
- 296 Cell lines

Five DLBCL (Pfeiffer, TMD-8, HBL-1, SUDHL-5, Karpas-422), three Burkitt lymphoma (Raji, Daudi, Ramos), two Follicular lymphomas (DOHH-2, RL), and one T-cell Acute Lymphoblastic Leukemia (Jurkat) cell lines used in this study were grown in Advanced-RMPI 1640 supplemented with 5% heat-inactivated FBS, 2 mmol/L glutamine, 50 μg/mL penicillin-streptomycin (Thermo Fisher, MA, USA).

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304 Occupancy assay

305 Cytofluorimetric quantification of CD47 and CD19 levels in a panel of 10 B-NHL 306 cell lines. Cells were stained with PE-labelled anti-CD47 or anti-CD19 307 antibodies (Becton Dickinson) and the absolute number of membrane-bound 308 molecules of CD47 or CD19 was estimated using QuantiBRITE PE beads (BD 309 Biosciences) on a FACSCanto II (Becton Dickinson). Data were analysed using 310 FlowJo software package.

For the detection of surface CD47, Raji (CD19+), or Jurkat (CD19-) cells were stained with a phycoerythrin (PE)-labelled anti-CD47 (B6H12 clone) or isotype control antibody (BD Biosciences). The cells were pre-treated for 1 h with TG-1801 or an anti-human CD47 (B6H12 clone) control antibody. For quantification, a total of 10,000 events were acquired on a FACSCanto II (Becton Dickinson). Relative median fluorescence intensity (MFI) was calculated using FlowJo software package as the ratio between CD47 and control signal intensity.
Shown are the percentages of occupancy, defined as the decreases in CD47
MFI ratios evoked by anti-CD47-treatment, using untreated cells as a calibrator.
B6H12 clone was used as a CD19-independent positive control of CD47
occupancy.

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323 Peripheral blood mononuclear cells isolation and macrophage
 324 polarization.

Peripheral blood mononuclear cells (PBMCs) were purified by standard Ficoll-Hypaque (GE Healthcare, UK) gradient centrifugation from buffy coats of human healthy donors and cultured freshly in Advanced-RMPI 1640 supplemented with 5% heat-inactivated FBS, 2 mmol/L glutamine, 50 µg/mL penicillin-streptomycin (Thermo Fisher, MA, USA).

RosetteSep[™] Human Monocyte Enrichment Cocktail (Stemcell Technologies, 330 331 Canada) was used to purify human monocytes from buffy coats following manufacturer specifications. For M1 or M2 macrophage polarization, the 332 selected monocytes were cultured in complete Advanced-RMPI 1640 333 supplemented with either 20 ng/mL human GM-CSF (PeproTech, RockyHill, 334 NJ), for M1 differentiation, or 20 ng/mL human M-CSF (PeproTech), for M2 335 differentiation, and incubated for 6 days. On day 6 M0 macrophages were 336 activated with 100 ng/mL human IFN-y (PeproTech) and 50 ng/mL LPS, for M1 337 macrophage polarization for 24 h. 338

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342 Antibody-dependent cell-mediated cytotoxicity (ADCC) and phagocytosis

343 (ADCP) assays

ADCC activity was assessed in B-cell lymphoma cell lines co-cultured for 4 hours with freshly obtained PBMCs (1:10, target:effector), in the presence of 10 ng/mL TG-1801 +/- U2 dual assets (10 μ g/mL ublituximab + 1 μ M umbralisib), using and a LDH release assay (Roche). The ADCC was calculated using the following formula:

ADCC percentage = [(sample release – spontaneous release)/(maximal release
- spontaneous release)]*100.

Spontaneous release, corresponding to target cells incubated with effector cells without antibody, was defined as 0% cytotoxicity, with maximal release (target cells lysed with 1% Triton X-100) defined as 100% cytotoxicity. The average percentage of ADCC and standard deviations of the triplicates of each experiment were calculated.

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357 ADCP activity was assessed in B-cell lymphoma cell lines co-cultured for 4 hours with M1-polarized macrophages (1:5, target:effector), in the presence of 358 10 ng/mL TG-1801 +/- U2 dual assets (10 µg/mL ublituximab + 1 µM 359 umbralisib), using and the pHrodo-stained B cells (IncuCvte[®] pHrodo[®] Red Cell 360 Labelling Kit for Phagocytosis, Sartorius). Following phagocytosis assay, the 361 non-phagocytosed cells were removed by washing with PBS 2-3 times and 362 phagocytosis was analysed by fluorescent microscopy (EVOS Cell Imaging 363 Systems -Thermo-Fisher) 364

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367 Xenograft mouse model and IHC staining

368 Eight-week-old NOD/SCID IL2Ry-null (NSG) male and female mice (Janvier Labs, France) were subcutaneously injected with Raji cells and tumour-bearing 369 mice were randomized using GraphPad Prism 9.0 software and assigned to one 370 of the following treatment arms (8-6 mice per group): TG-1801 (5 mg/kg, qw), 371 ublituximab (5 mg/kg, gw), umbralisib (150 mg/kg, bid), ublituximab (5 mg/kg, 372 qw) + umbralisib (150 mg/kg, bid), TG-1801+ublituximab combo, TG-373 1801+umbralisib combo or the triplet (U2 + TG-1801), or an equal volume of 374 vehicle for 17 days. Tumour volumes were measured each 2-3 days with 375 376 external callipers. The number of animals used in each of the experimental groups is based on the literature and previous results from the group (Ribeiro et 377 al., 2021). Immunohistochemical staining of representative tumour specimens 378 379 (N=3) was performed using anti-CD20 (Sigma), anti-GPR183 (Santa Cruz), anti-F4/80 (Abcam), anti-Histone H3-pSer10 (Abcam) and anti-CD56/NCAM-1 380 (Abcam). Preparations were evaluated using an Olympus microscope and 381 MicroManager software. 382

IHC signal intensity was quantified in at least 5 pictures of two representative tumour specimens from the Raji xenograft model, using QuPath v.0.2.3 (Queen's University, Belfast, Northern Ireland). Cell detection was conducted as previously described (Bankhead et al., 2017) using QuPath's built-in "Positive cell detection" by calculating the per cent of positively stained cells in each field.

389 **RNA sequencing (RNA-seq) analysis**

390 Two Burkitt lymphoma (BL) cell lines (Daudi and Raji) and two BL primary 391 samples were co-cultured with bone marrow stromal cells (BMSCs), M2-

polarized macrophages and PBMCs (4:1:1:1) in the presence of 10 ng/mL TG-392 393 1801 +/- U2. After 24h incubation, CD20+ target cells were isolated using the EasySep Human Biotin Positive Selection Kit II (StemCell Technologies, 394 Canada) and the biotinylated anti-CD20 antibody (BioLegend, CA, USA). 395 Purified CD20+ cells, together with representative bulk Raji xenografts with > 396 95% tumour B cells were subjected to RNA-seg analysis according to previous 397 procedures (Ribeiro et al., 2021). Sequencing data have been deposited at the 398 Gene Expression Omnibus (GEO) of the National Center for Biotechnology 399 Information (GSE199413). Volcano plot showing the most relevant significantly 400 401 differentially expressed genes between triplet and TG-1801 treatments, with |Log2 fold change| > 1.5 and p-adj value < 0.01 (red dots). Grey, green and blue 402 dots identified genes with insignificant transcriptional and/or statistical variation. 403 404 Briefly, the raw fastq RNAseq files of each condition were quality checked and gene expression was estimated using Salmon software (https://combine-405 406 lab.github.io/salmon/). Differential expression analysis was then carried out using the negative binomial distribution (DESeq2 407 software, https://bioconductor.org/packages/release/bioc/html/DESeg2.html), 408 accounting for and filtering the effects of the respective controls. 409

Purified CD20+ cells, together with representative Raji xenografts were subjected to RNA extraction and qPCR validation. Briefly, total RNA was extracted using TRIZOL (Thermo Fisher) following manufacturer's instructions. One microgram of RNA was retrotranscribed to complementary DNA using moloney murine leukemia virus reverse transcriptase (Thermo Fisher) and random hexamer primers (Roche). mRNA expression was analyzed in duplicate by quantitative real-time PCR and the relative expression of each gene was

quantified by the comparative cycle threshold method $(\Delta\Delta C_t)$ β -actin (Fw: 417 GACGACATGGAGAAAATCTG, Rv: ATGATCTGGGTCATCTTCTC) were used 418 as an endogenous control. The sequences used for the primers are the 419 following **GPR183** (Fw: GACTGGAGAATCGGAGATGC, Rv: 420 CAGCAATGAAGCGGTCAATA), CCL20 (Fw: CCAATGAAGGCTGTGACATCA, 421 Rv: AGTCTGTTTTGGATTTGCGCA), IL8 (Fw: AAGGAAAACTGGGTGCAGAG, 422 GCTTGAAGTTTCACTGGCATC), 423 Rv: CD68 (Fw: CCTCCAGCAGAAGGTTGTCT, Rv: CGAAGGGATGCATTCTGAGC), CCL4 424 (Fw: TTCCTCGCAACTTTGTGGTA, Rv: GCTTGCTTCTTTTGGTTTGG), CCL7 425 (Fw: TGG AGA GCTACAGAAGGACCA, Rv: GGGTCAGCACAGATCTCCTT), 426 CXCL1 CATCCAAAGTGTGAACGTGAA, 427 (Fw: Rv: CTATGGGGGGATGCAGGATT), CXCL3, 428 (Fw: CAAAGTGTGAATGTAAGGTCCCC, Rv: CGGGGTTGAGACAAGCTTTC) and 429 CXCL10 (Fw: CCTGCAAGCCAATTTTGTCCA, Rv: 430 TGGCCTTCGATTCTGGATTCA). 431

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433 Generation of Raji-GPR183^{KO} cells

The generation of a CRISPR-Cas9 gene-editing tool was employed to edit the 434 Raji parental cells line to create GPR183 knockout, 0.5 x 10⁶ cells were 435 electroporated on a Nucleofector II device (program A032, Lonza) with 36 pmol 436 SpCas9 Nuclease V3, 44 pmol CRISPR-Cas9 tracRNA ATTO 550, 44 pmol Alt-437 (GPR183^{KO} R CRISPR-Cas9 crRNA Hs.Cas9.GPR183.1.AA 5'-438 CAATGAAGCGGTCAATACTC AGG -3`) (IDT-Integrated DNA Technologies). 439 GPR183^{KO} cells were resuspended in 96-well plates with a limiting dilution of 440

0.3 cells per well. The GPR183^{KO} biallelic clones were confirmed by Sanger
Sequencing and western blot. Raji-GPR183^{KO} is available upon request.

443

444 Western blot analysis

Total protein extracts were obtained from cell lines and tumour specimens using 445 RIPA (Sigma-Aldrich) buffer and subjected to SDS-PAGE. Membrane-446 transferred proteins were revealed by incubating with primary and secondary 447 antibodies followed by chemiluminescence detection using the ECL system 448 (Pierce) and a Fusion FX imaging system (Vilber Lourmat). Band intensity was 449 450 quantified using Image J software and normalized to housekeeping protein (GAPDH). Values were referred to the indicated control and added below the 451 corresponding band. If not otherwise specified, representative data from N = 2452 453 experiments are shown.

454

455 **3D multicellular spheroid generation**

One hundred thousand Raji-GPR183^{WT} or Raji-GPR183^{KO} cells were then 456 stained with Hoechst 33342 blue dye (Invitrogen) and cultivated in a conditional 457 medium with 25,000 StromaNKtert-GFP cells for 2 days to generate the BL 3D 458 spheroids. Then, 25,000 M1-macrophages were stained with PKH26 459 red-fluorescent dye and added to 3D spheroid in presence or absence of 10 460 ng/mL TG-1801 +/- U2 (10 µg/mL ublituximab + 1 µM umbralisib) for one more 461 day. The M1-macrophages infiltration was evaluated by live-cell red 462 fluorescence at EVOS Cell Imaging Systems (Thermo-Fisher). 463

464

465 **Transwell migration assay and F-actin staining**

Briefly, Raji-GPR183^{WT}, Raji-GPR183^{KO} and Raji parental cells exposed to the 466 467 GPR183 inhibitor NIBR189 (Sigma-Aldrich, Germany) were cultured for 1 h in culture medium not containing foetal bovine serum but supplemented with 0.5% 468 bovine serum albumin (Sigma-Aldrich), in the presence or absence of 10 ng/mL 469 TG-1801 +/- U2 combination, and analysed for CXCL12-dependent chemotaxis, 470 as previously described (Balsas et al., 2017). Values were referred to cells 471 472 cultured without CXCL12. F-actin levels were assessed after exposure to TG-1801 +/- U2, followed by staining with a TRITC-labelled phalloidin and direct red 473 fluorescence recording. 474

475 Ethical issues

Animals were handled following protocols approved by the Animal Ethics
Committee of the University of Barcelona (registry num. 38/18).

Institutional Review Board approvals for the study protocol (ref PI-20-040), amendments, and written informed consent documents from BL patients and healthy donors were obtained prior to study initiation. Study procedures were conducted in accordance with the Declaration of Helsinki. Buffy coats were provided by the Blood and Tissue Bank of Catalonia (agreement NE-A1-IJC).

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485 Statistical analysis

Presented data are the mean ± SD or SEM of 3 independent experiments. All
statistical analyses were done by using GraphPad Prism 9.0 software
(GraphPad Software). Comparison between 2 groups of samples was evaluated
by nonparametric Mann–Whitney test to determine how the response is affected

491 by 2 factors. Pearson test was used to assess the statistical significance of 492 correlation. Results were considered statistically significant when p-value < 493 0.05.

494

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505

506 **Competing Interests**: H. Miskin reports personal fees from TG Therapeutics, 507 Inc. during the conduct of the study. E. Normant reports employment and 508 ownership of stock with TG Therapeutics. G. Roué reports grants from TG 509 Therapeutics and Instituto de Salud Carlos III during the conduct of the study. 510 The remaining authors have no competing financial interests.

511

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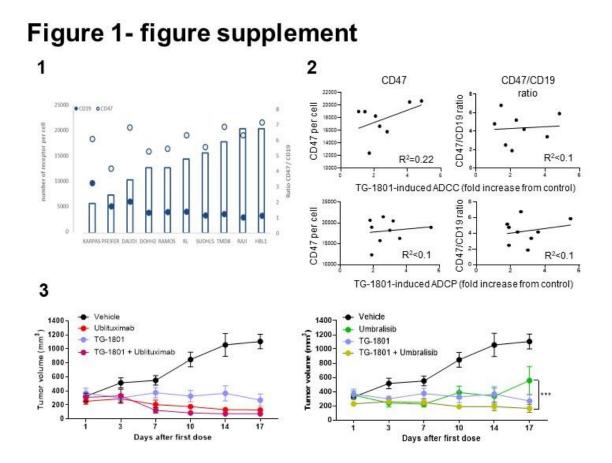


Figure 1- figure supplement legend

1) Cytofluorimetric quantification of CD47 and CD19 levels in a panel of 10 B-NH cell lines. 2) CD47 and CD19 expression levels, as well as their ratios, were plotted against the corresponding phagocytosis and ADCC quantification for each cell line described in 1), and the correlation coefficient was calculated using GraphPad Prism software. 3) NSG mice were subcutaneously injected with Raji cells and tumour-bearing animals were randomly assigned to one of the following treatment arms (8-6 mice per group): TG-1801 (5 mg/kg, qw), ublituximab (5 mg/kg, qw), umbralisib (150 mg/kg, bid), TG-1801+ublituximab combo (left panel) or TG-1801+umbralisib combo (right panel), or an equal volume of vehicle, for 17 days. Tumour volumes were recorded each 2-3 days using external callipers. *** p<0.001.

Figure 1

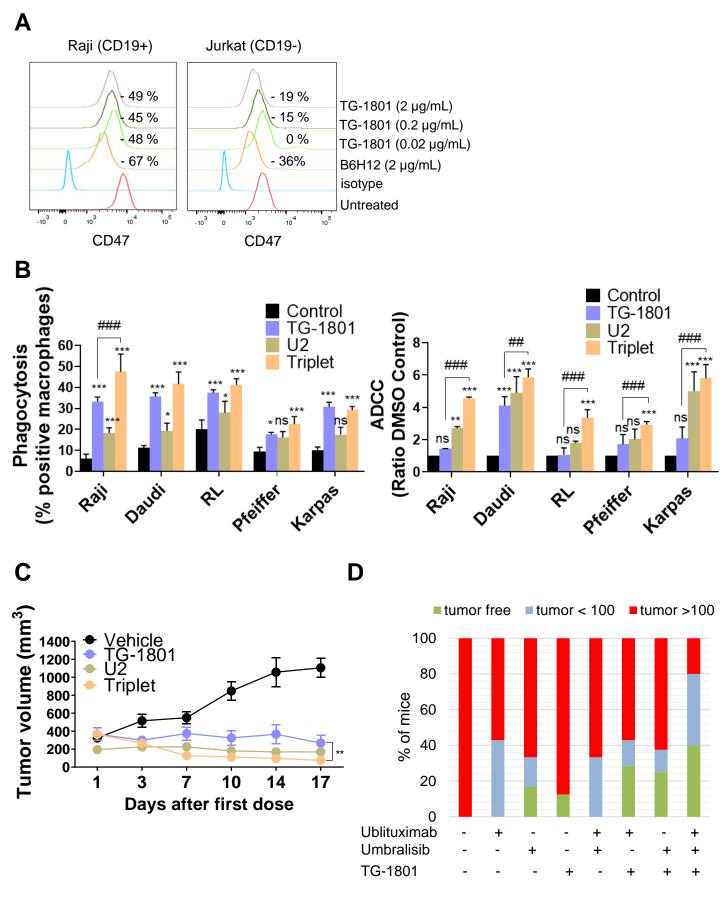
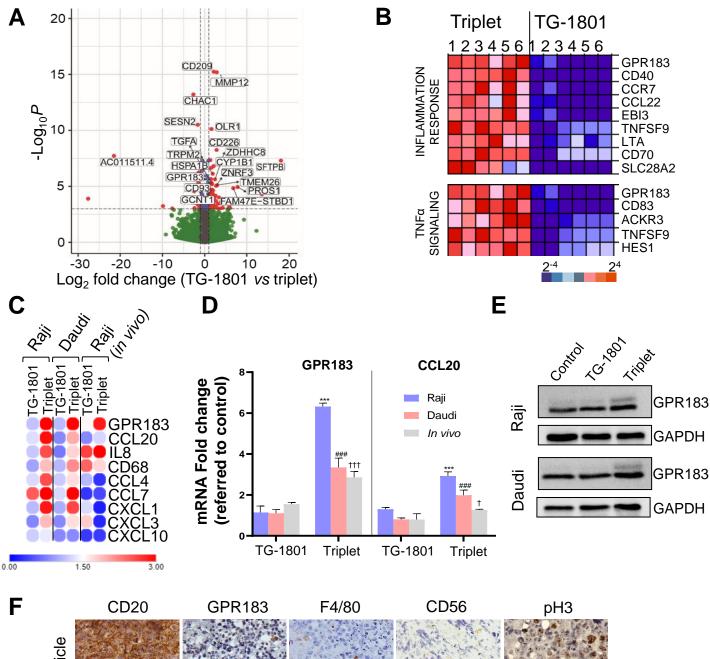
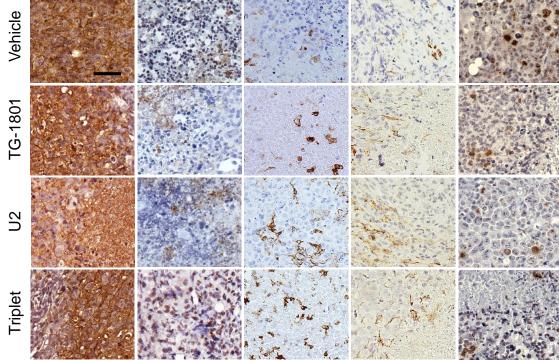


Figure 2





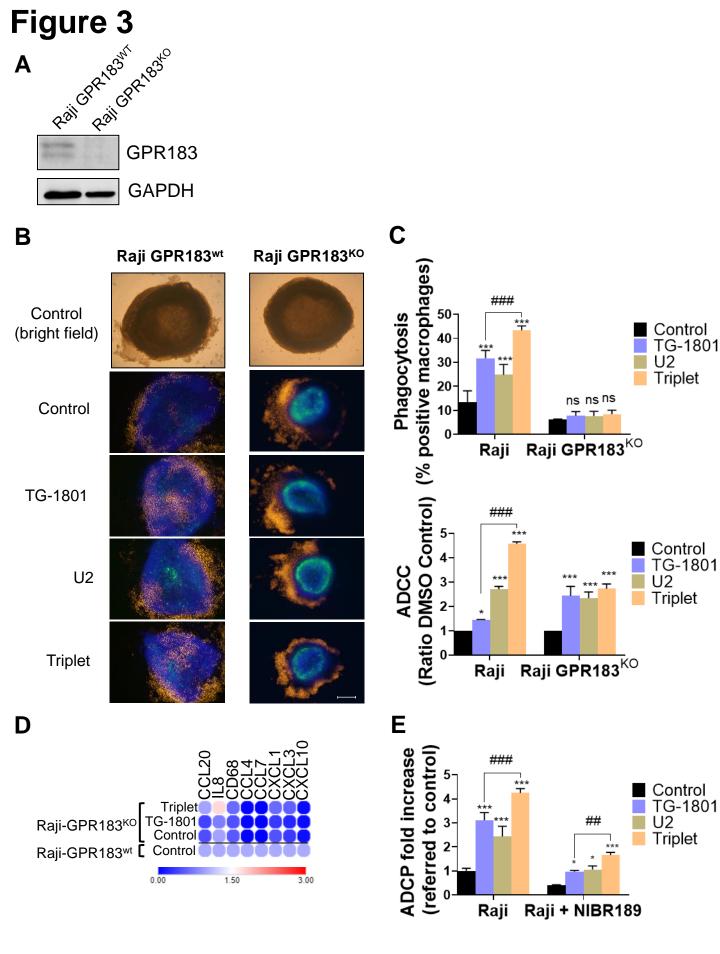
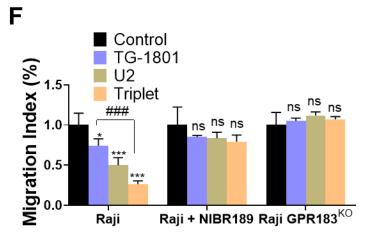
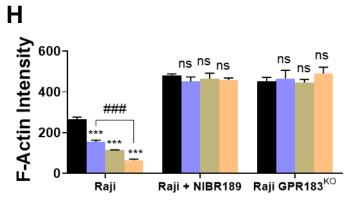
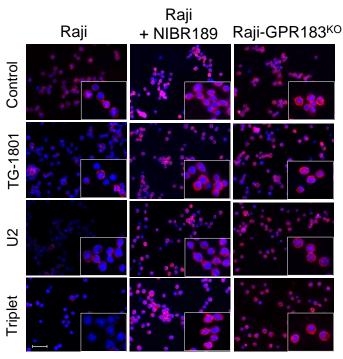


Figure 3 (cont.)







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