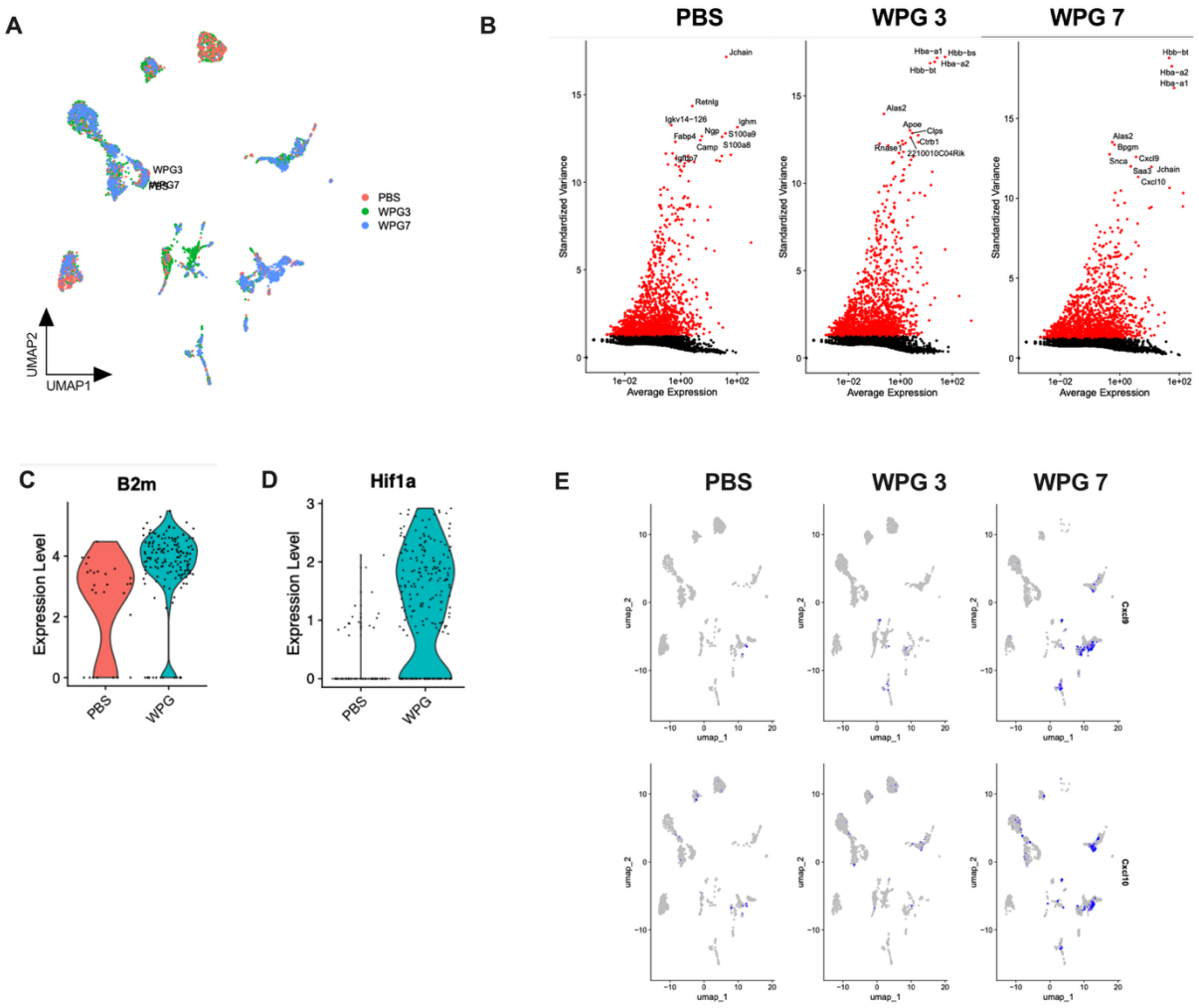
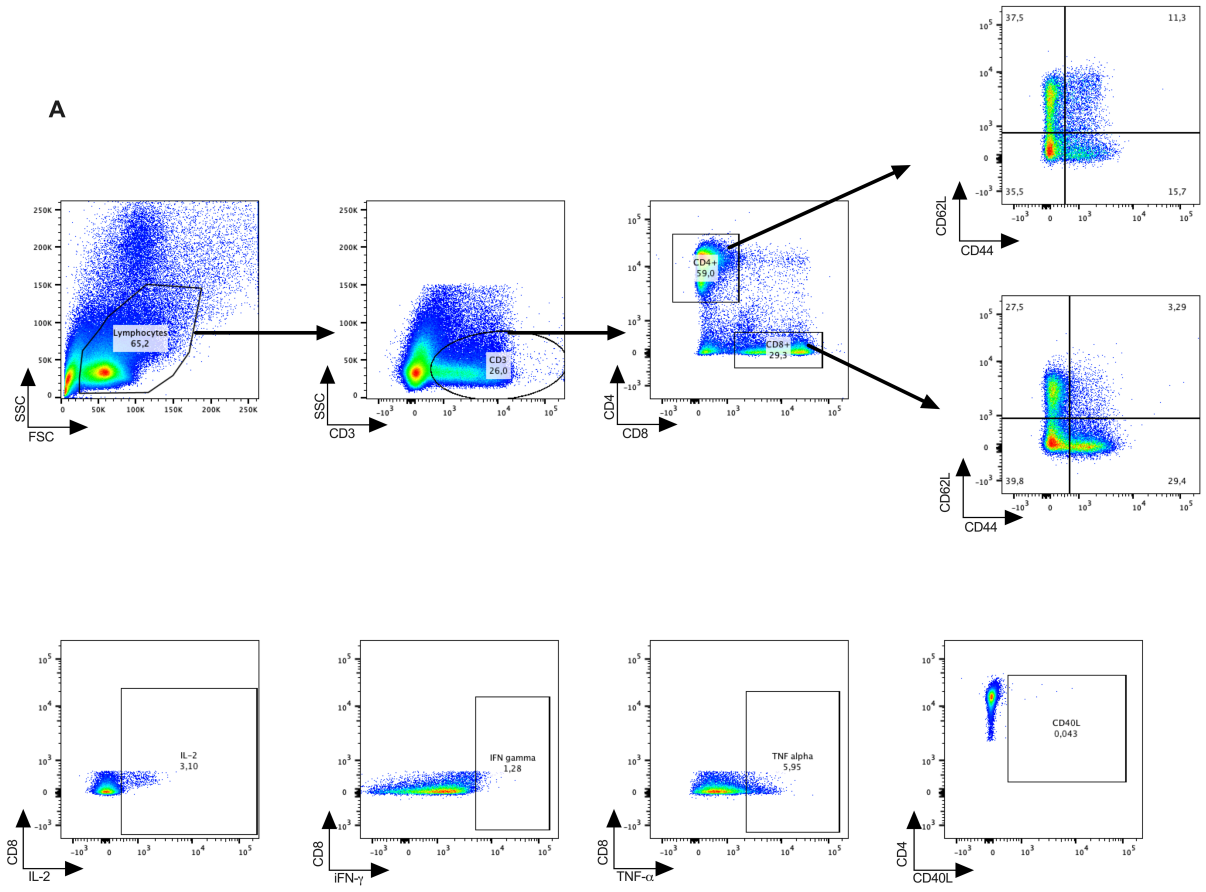
Supplementary Figure Legends

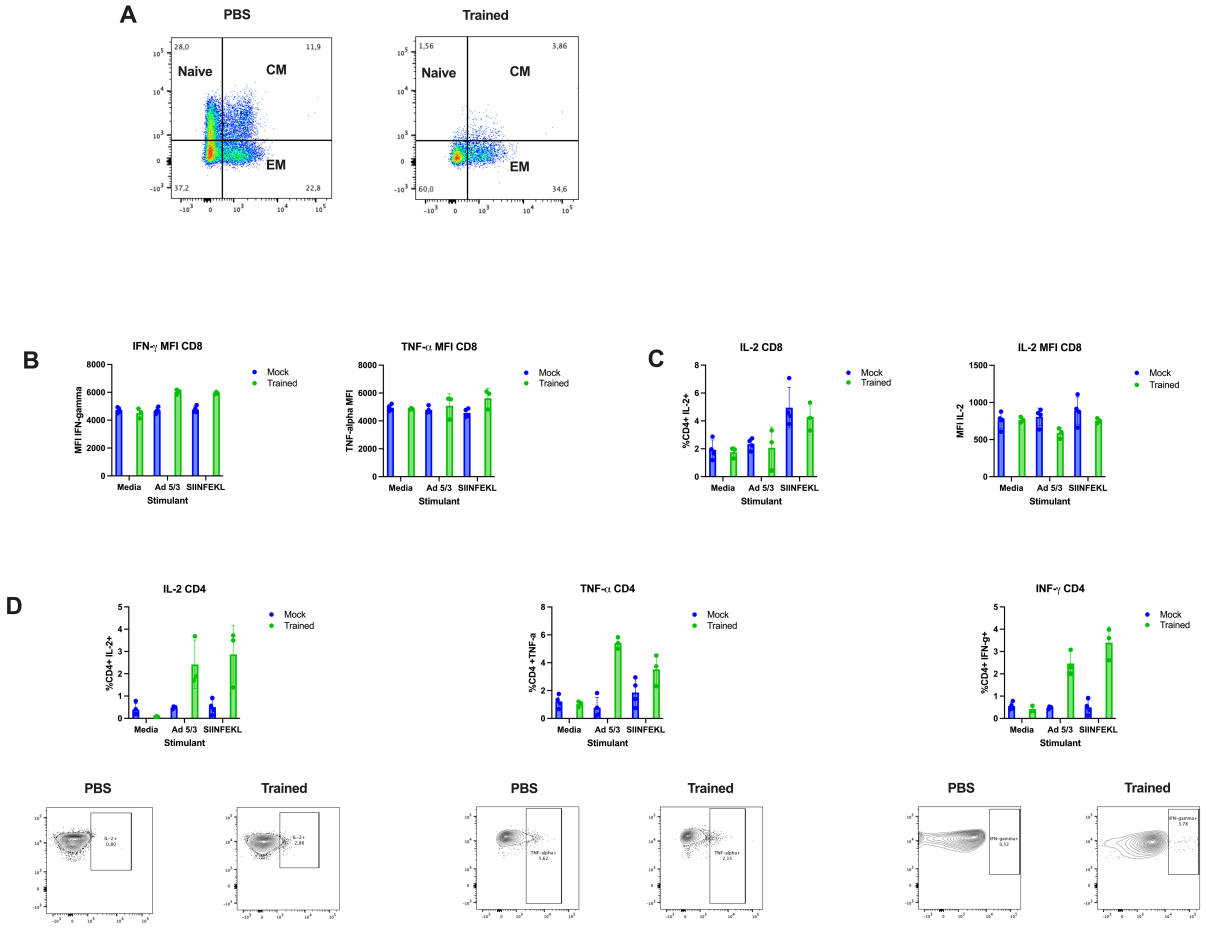
Title: Leveraging glucan-induced trained immunity for the epigenetic and metabolic rewiring of macrophages to enhance colorectal cancer vaccine response



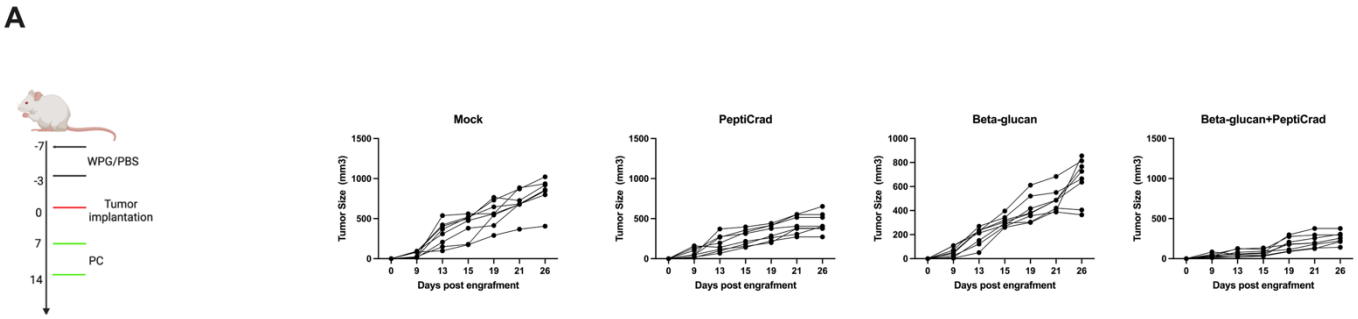
Supplementary Figure ***1 scRNA-sequencing from mice given WPG A*** *UMAP of single cell RNA sequencing of all treatement groups added together, from re-analysed data*[1]*, from mice given PBS (n=3) or WPG (n=3) (sacrificed at day 3 and day 7 post WPG treatment)* ***.B*** *DEG found in the single cell RNA sequencing data for each treatment group.* ***C*** *Violin plot of expression of B2m across samples* ***D*** *Violin plot of expression of Hif1a across samples* ***E*** *UMAP demonstrating the expression Cxlc9 and Cxcl10 across clusters for each treatment group.*



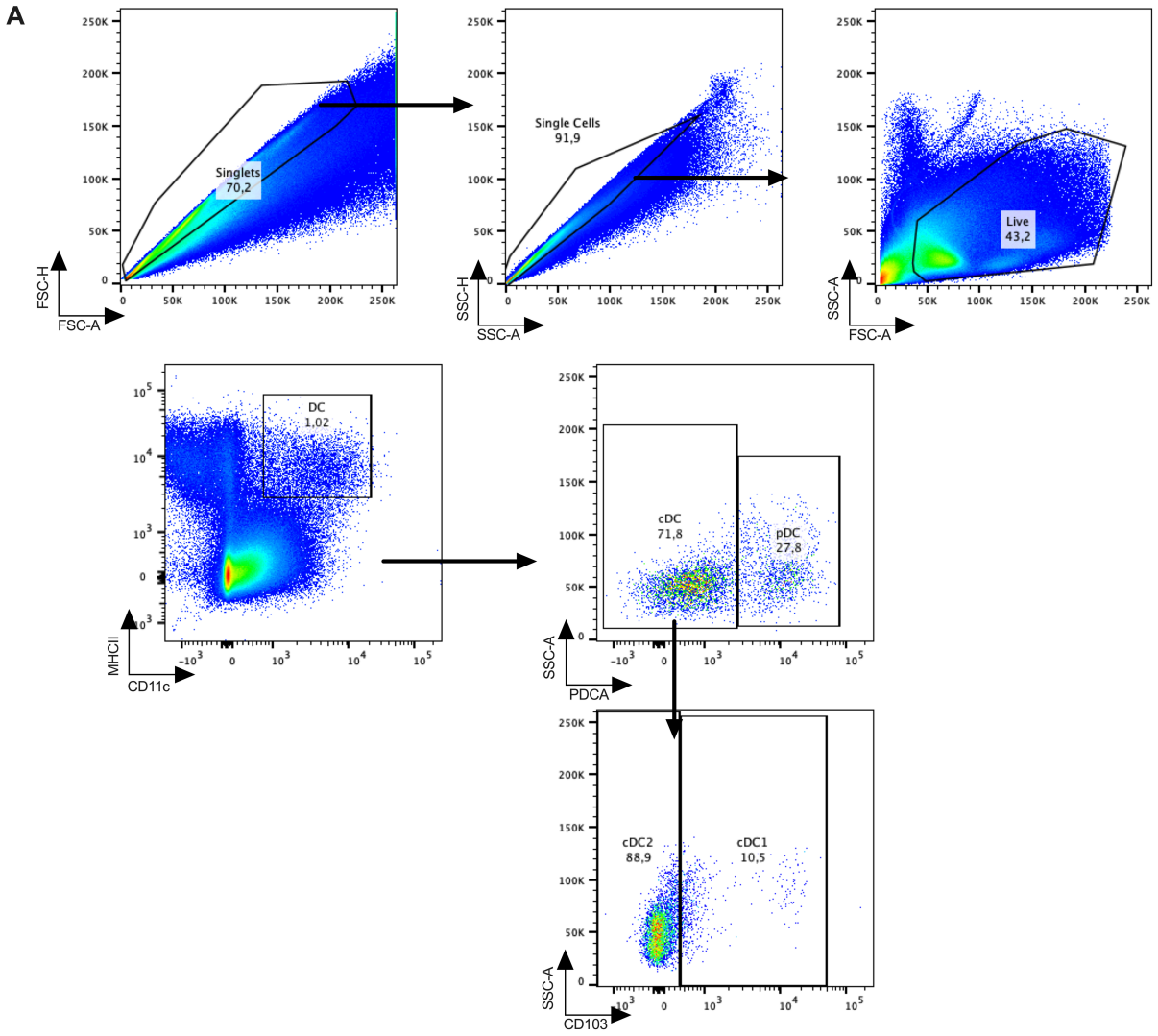
Supplementary Figure 2 Gating strategy for memory and activation of CD3 T cells *A Singlets were added on a SCC vs FSC and the lymphocyte population was gated on. CD3 cells were then gated on and checked fro CD8 and CD4. Both CD4 and CD8 cells were analysed for CD62L and CD44 to determine memory phenotypes. CD44-CD62- were considered CTLs, CD44-CD62L were considered Naïve memory, CD44+CD62L+ were considered central memory and CD44+CD62L- were considered effector memory cells. CD8+ and CD4 T cells were further subjected for IL-2, IFN-γ, TNF-α and CD40L expression. Baseline expression was done based on expression of each cytokine in unstimulated samples.*



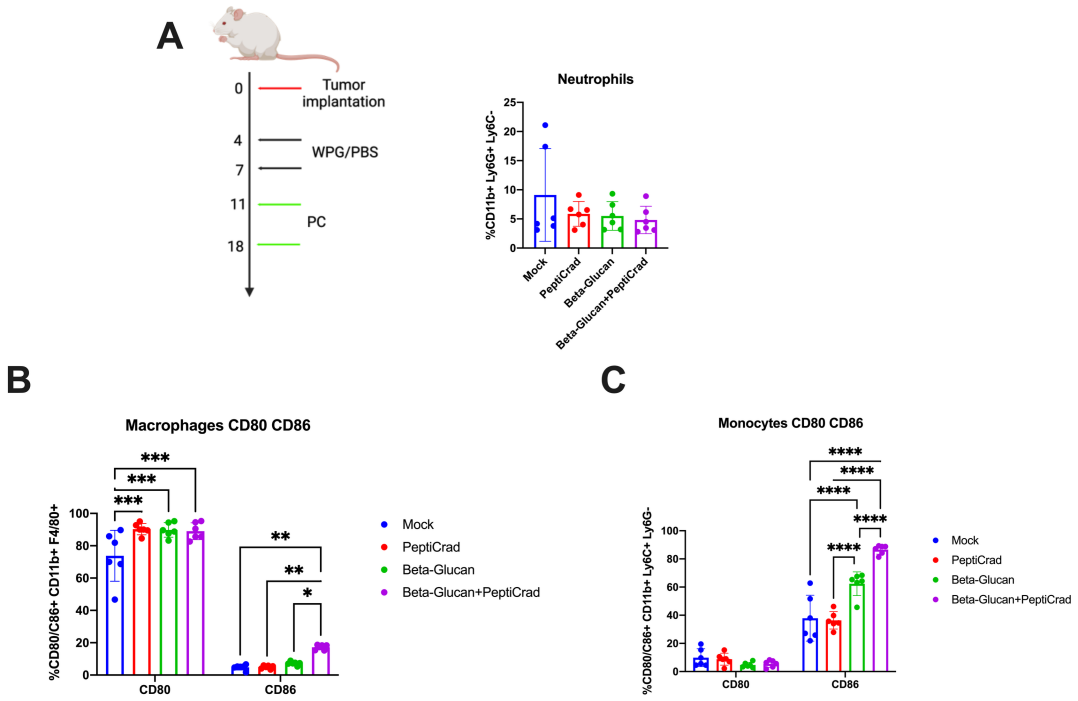
Supplementary Figure 3 WPG immune affects in vaccination ***A*** *Flow cytometry plots demonstrating CD8+ T cell memory substers with splenocytes of mice (n=3), at day 15. Splenocytes were stimulated with SINFEKL peptide.* ***B*** *Mean fluorescence intensity (MFI) IFN-γ and TNF-α for CD8+ T cells when stimulated with media, Ad5/3 or SIINFEKL.* ***C*** *Quantification and MFI of IL-2 expressed from CD8+ T cells across treatment groups (n=3 mice) when stimulated with media, Ad5/3 or SIINFEKL.* ***D*** *Quantification of CD4+ T cells expressing IL-2, TNF-α and IFN-γ when stimulated with media, Ad5/3 or SIINFEKL (n=3 mice). Contour plots demonstrate CD4+ T cells stimulated with SIINFEKL. All data are presented as the mean ± SD.*



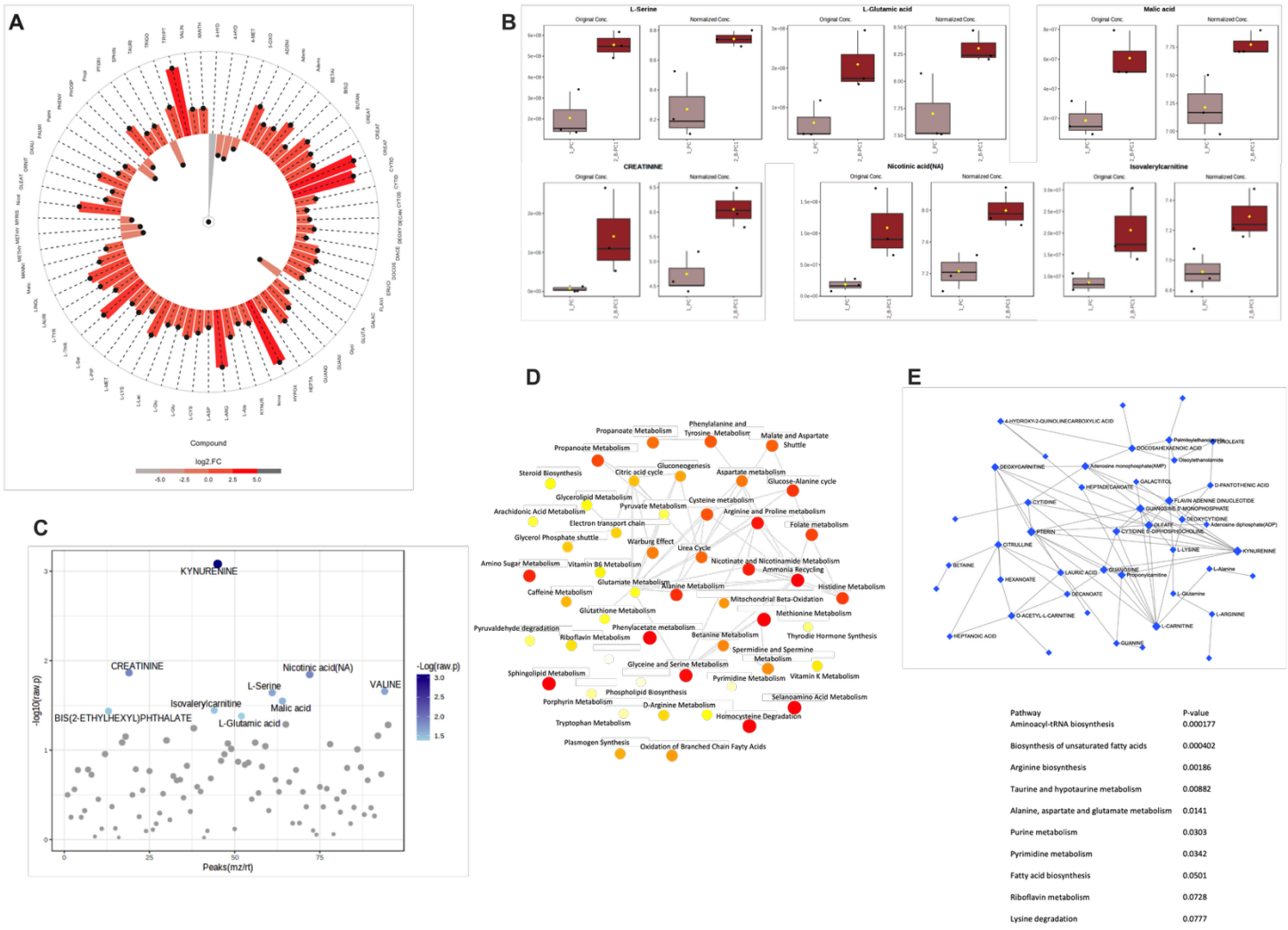
Supplementary Figure 4 **Single mouse tumor volumes from WPG prophylactic strategy** ***A*** *Graphical representation of workflow of animal experiment (Created in BioRender. Hamdan, F. (2026) https://BioRender.com/g9bsknf). Deconvolution for each treatment group for single tumor growth for each mouse (n=8) .*



Supplementary Figure 5 Gating Strategy of DC profiling from lymph nodes ***A*** *Single Cells were gated based on both FSC-H vs FSC-A and SSC-H vs SSC-A. Gated Single cells were then gated for lymphocytes based on FSC-A vs SSC-A. CD11b+ cells were then gated on and analysed for CD11c+ cells. CD11c+ cells were gated and were considered dendritic cells. CD11c+ dendritic cells had PDCA expression analysed. PDCA+ cells were considered pDC. PDCA- cells were then examined for CD103 expression. CD103+ cells were considered cDC1 while CD103- cells were considered cDC2.*



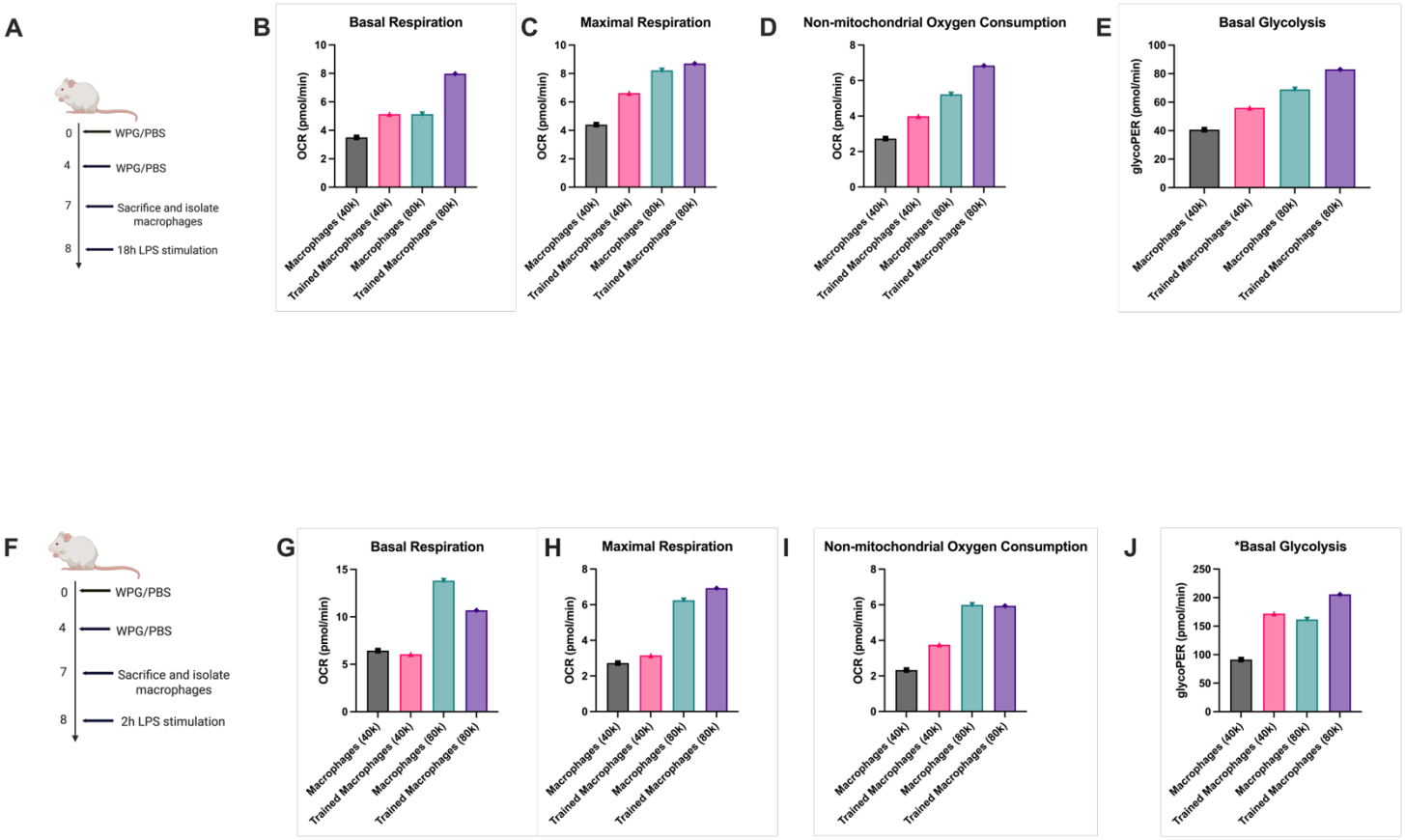
Supplementary Figure 6 Immune infiltration and activation in WPG therapeutic strategy ***A*** *Graphical representation of workflow of animal experiment (Created in BioRender. Hamdan, F. (2026) https://BioRender.com/g9bsknf). Neutrophils were quantified in the tumor microenvironment across treatment groups (n=6 mice).* ***B*** *CD80 (Mock vs PeptiCrad p=0.000; Mock vs Beta-glucan p=0.0005; Mock vs Beta-glucan+PeptiCrad p=0.0009) and CD86 (Mock vs Beta-glucan+PeptiCrad p=0.0084; PeptiCrad vs Beta-glucan+PeptiCrad p=0.0093; Beta-glucan vs Beta-glucan+PeptiCrad p=0.0412) expression was quantified in F4/80+ macrophages in the tumor microenvironment (n=6 mice).* ***C*** *CD80 and CD86 expression was quantified in monocytes in the tumor microenvironment (n=6 mice, "****" $p < 0.0001$). One-way ANOVA was used for all flow cytometry analyses along with a Tukey's multiple comparisons test. All data are presented as the mean ± SD.*



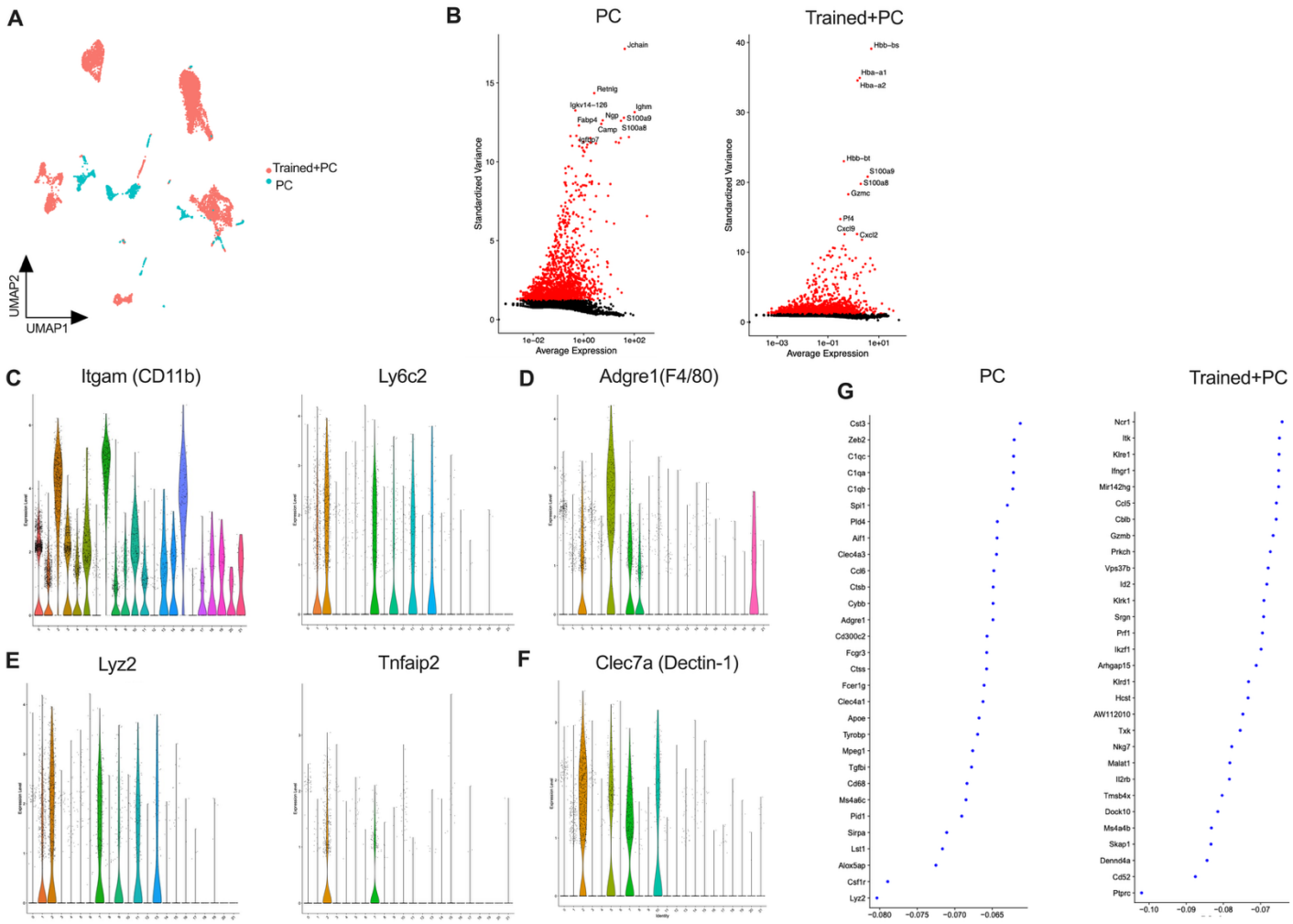
Pathway	P-value
Aminoacyl-tRNA biosynthesis	0.000177
Biosynthesis of unsaturated fatty acids	0.000402
Arginine biosynthesis	0.00186
Taurine and hypotaurine metabolism	0.00882
Alanine, aspartate and glutamate metabolism	0.0141
Purine metabolism	0.0303
Pyrimidine metabolism	0.0342
Fatty acid biosynthesis	0.0501
Riboflavin metabolism	0.0728
Lysine degradation	0.0777

Supplementary Figure 7 Metabolic profiling of mice given PC and PC+ WPG ***A*** *Wheel plot of all metabolites upregulated in Trained+PC group (n=3 mice) compared to PC treatment (n= 3 mice).* ***B*** *Box plots on the quantification of certain metabolites between Trained+PC (n=3 mice) and PC (n=3 mice) treatment groups.* ***C*** *VIP scores (contribution of each metabolite to the separtation of each group) of metabolites among each treatment group.* ***D*** *Differential metabolite analysis on upregulated metabolites from Trained+PC treated mice (n=3) compared to PC treated mice (n=3).* ***E*** *Pathway impact analysis on upregulated metabolites from Trained+PC treated mice (n=3 mice). Pathway*

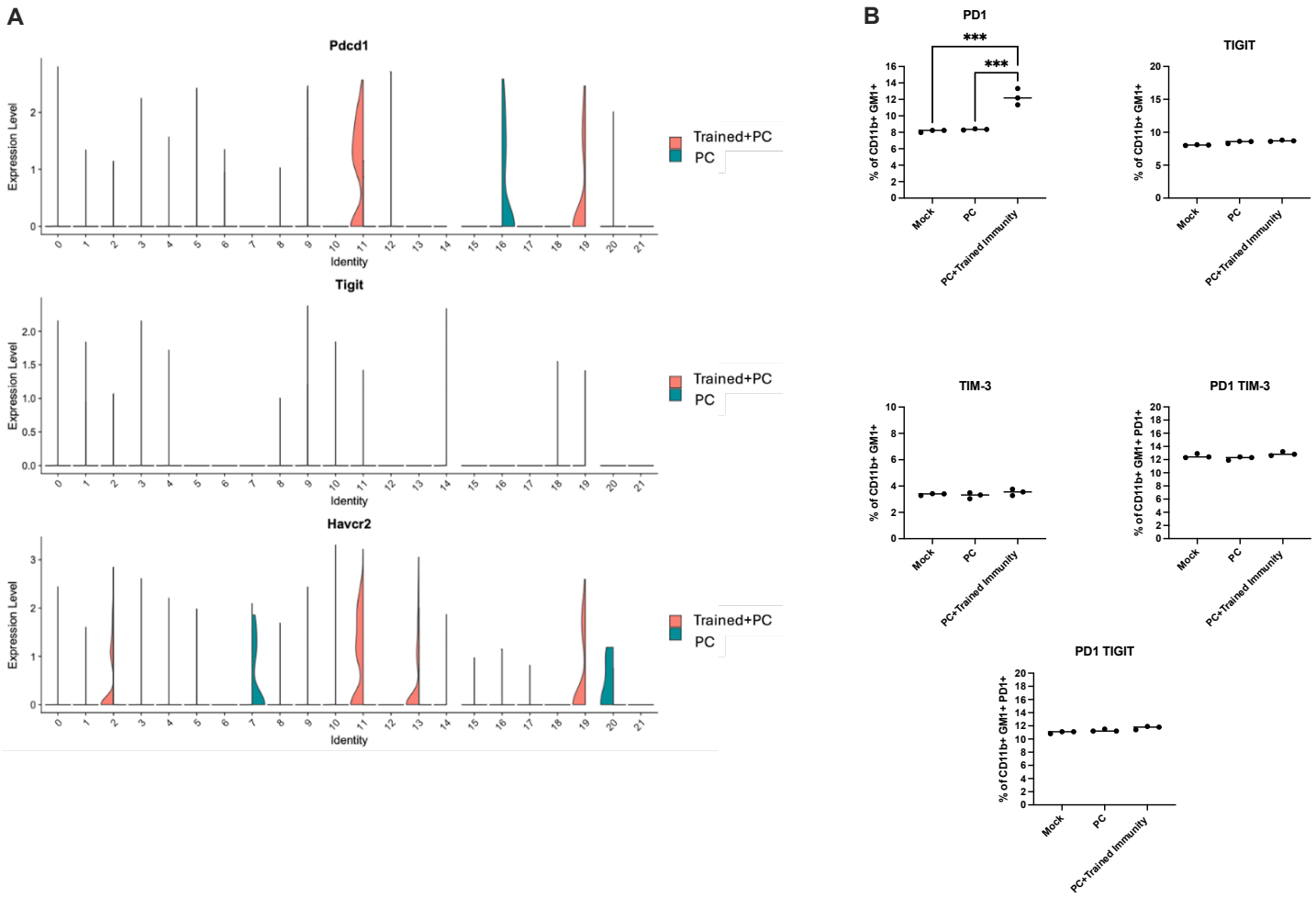
significance was assessed using a two-sided hypergeometric test; topology was based on relative-betweenness centrality



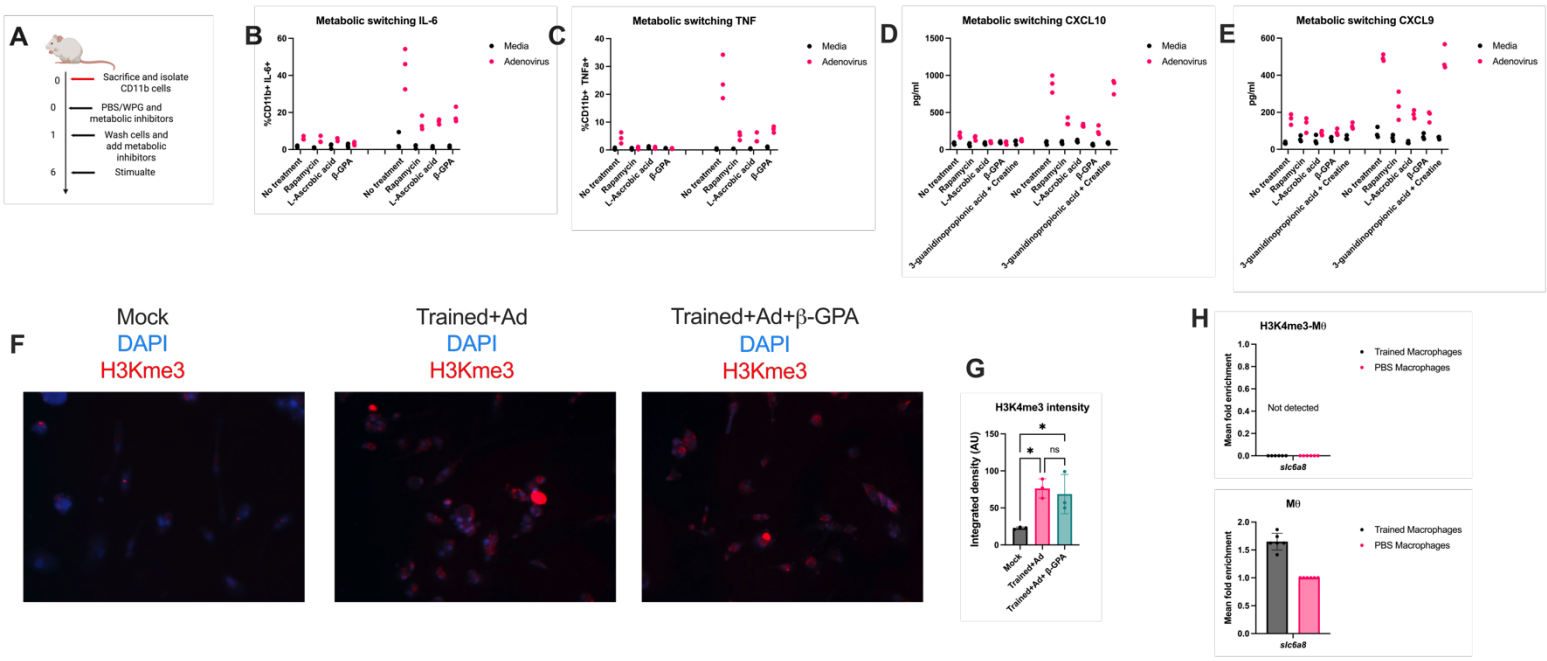
Supplementary Figure 8 Seahorse analysis on macrophages stimulated with WPG ***A*** *Graphical representation of workflow of animal experiment (Created in BioRender. Hamdan, F. (2026) https://BioRender.com/ux8avhz)* ***B*** *Basal respiration (OCAR) of macrophages at two different cell number concentrations (80,000 and 40,000 cells) treated with PBS (n=7 mice) or WPG (n=7 mice) for 18 hours.* ***C*** *Maximal respiration of macrophages treated with PBS or WPG for 18 hours* ***D*** *Non-mitchondrial oxygen consumption from macrophages treated with PBS (n=7 mice) or WPG (n=7 mice) for 18 hours* ***E*** *Basal glycolsysi of macrophages treated with PBS (n=7 mice) or WPG (n=7 mice) for 18hours* ***F*** *Graphical representation of workflow of animal experiment (Created in BioRender. Hamdan, F. (2026) https://BioRender.com/ux8avhzt)* ***G*** *Basal respiration (OCAR) of macrophages at two different cell number concentrations (80,000 and 40,000 cells) treated with PBS (n=7 mice) or WPG (n=7 mice) for 2 hours.* ***H*** *Maximal respiration of macrophages treated with PBS (n=7 mice) or WPG (n=7 mice) for 2 hours* ***I*** *Non-mitchondrial oxygen consumption from macrophages treated with PBS (n=7 mice) or WPG (n=7 mice) for 2 hours* ***J*** *Basal glycolsysi of macrophages treated with PBS (n=7 mice) or WPG (n=7 mice) for 2 hours. All data are presented as the mean.*



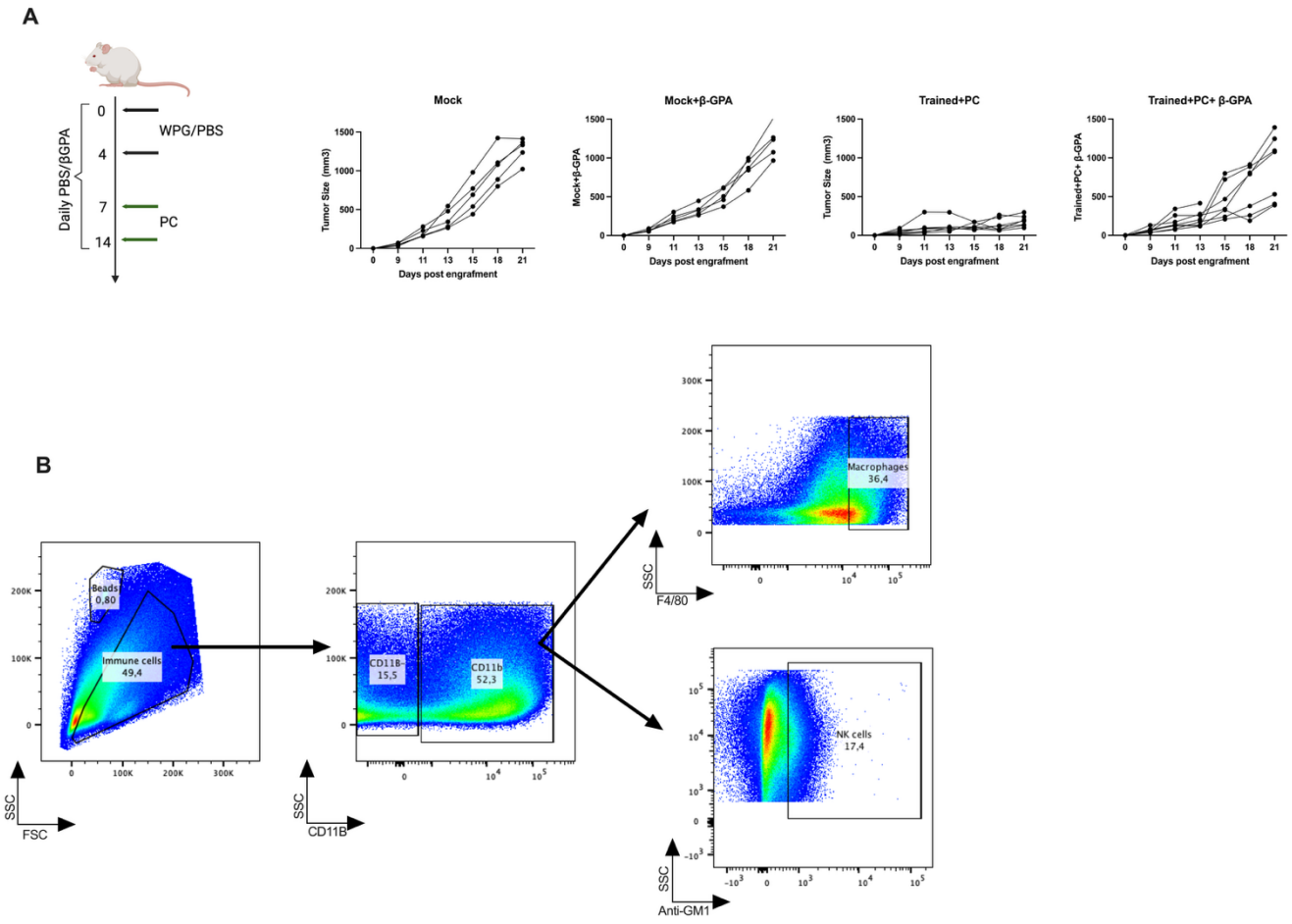
Supplementary Figure 9 scRNA sequencing of mice given PC and PC+ WPG ***A*** *UMAP of single cell RNA sequencing of all treatement groups added together (n=3 mice per treatment group).* ***B*** *DEG found in the single cell RNA sequencing data for each treatment group.* ***C*** *Violin plots on the expression of Itgam and Ly6c2 across all clusters* ***D*** *Violin plots on the expression of Adgre1 across all clusters* ***E*** *Violin plots on the expression of Lyz2 and Tnfaip2 across all clusters* ***F*** *Violin plots on the expression of Clec7a across all clusters* ***G*** *Top 30 associated genes in the priniciple component analysis across treatement groups*



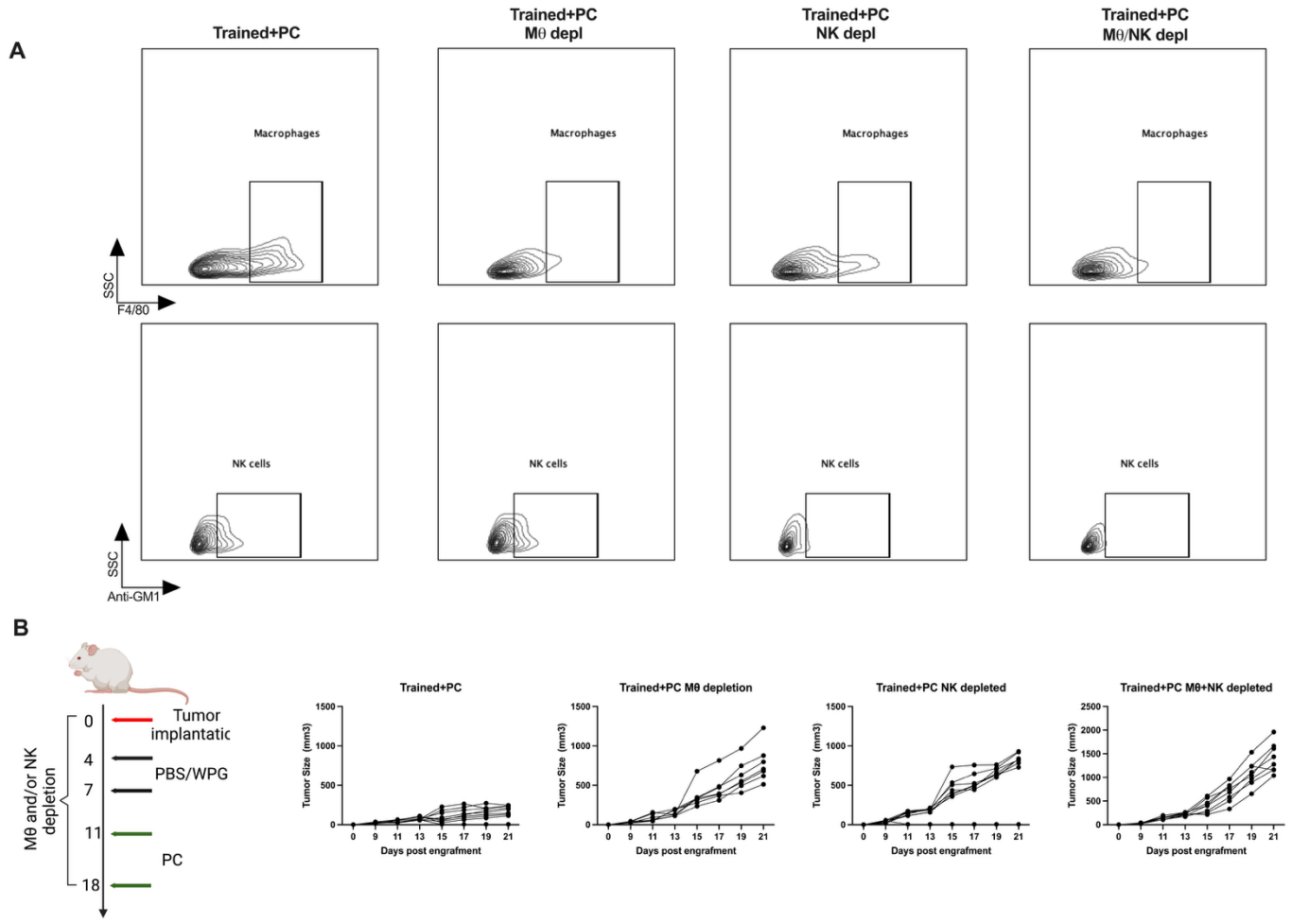
Supplementary Figure 10 NK exhaustion ***A*** *Single-cell RNA sequencing expression levels of pdcd1, Tigit and havcr2 between Trained+PC and PC treated mcie (n=3).* **B** *Flow cytometry expression of exhaustion markers (PD-L1, TIM-3 and TIGIT) from NK cells in the tumor (n=3 mice per treatment group). One-way ANOVA was used for all flow cytometry analyses along with a Tukey's multiple comparisons test (Mock vs PC+Trained Immunity p=0.0003; PC vs PC+Trained Immunity p=0.0004). All data are presented as the mean.*



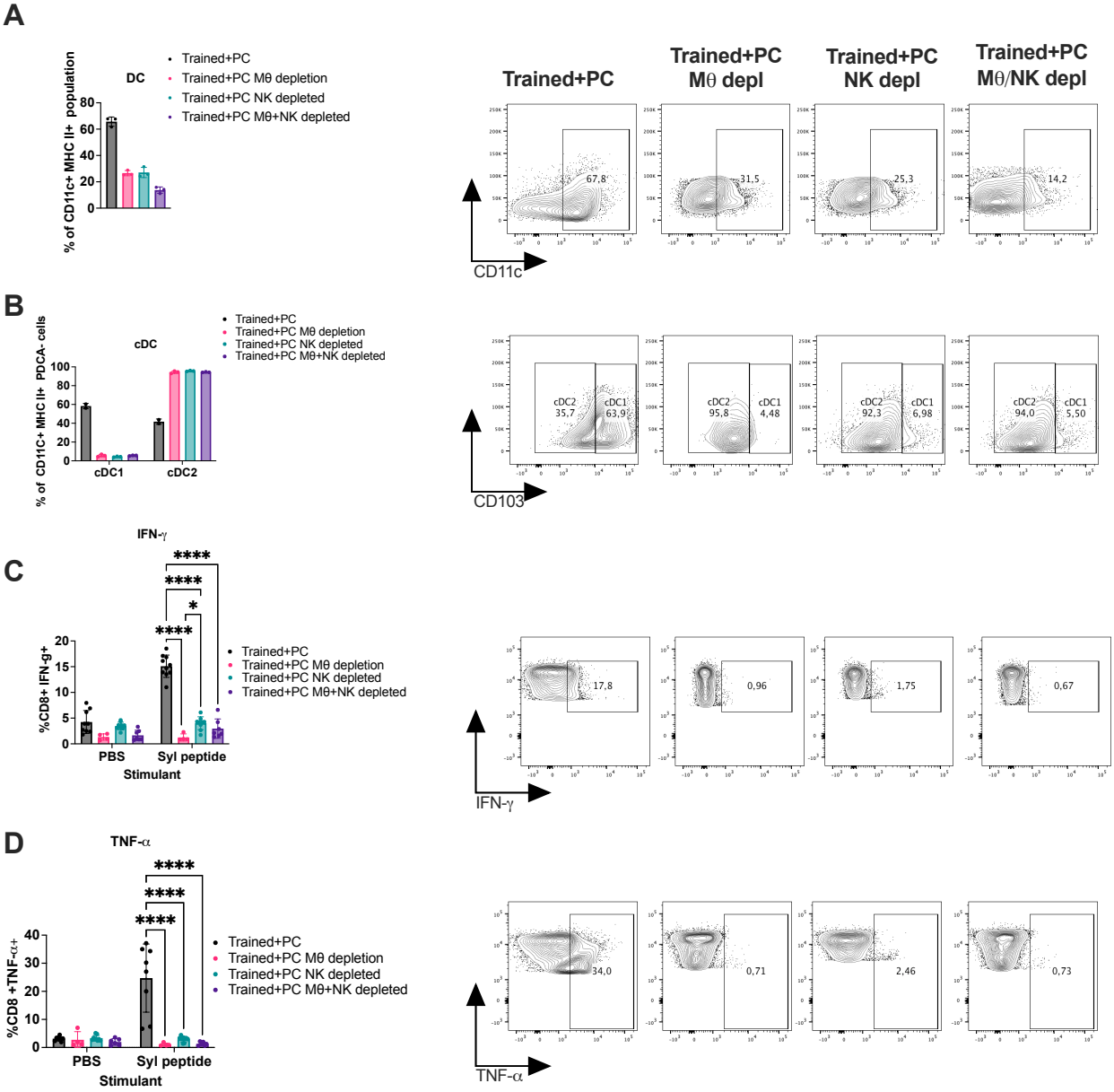
Supplementary Figure 11 Metabolic inhibition of trained immunity ***A*** *Graphical representation of workflow of animal experiment (Created in BioRender. Hamdan, F. (2026) https://BioRender.com/16b56c0t)* ***B*** *Quantification of IL6,* ***C*** *TNF-α ,* ***D*** *CXCL10 and* ***E*** *CXCL9 from non-trained (n=3 mice) and trained (n=3 mice) cells treated with different metabolic inhibitors (during WPG training) and stimulated with media or adenovirus* ***F*** *Immunofluorescence staining of mock or trained CD11b+ F4/80⁺ macrophages cells stimulated with Ad/3 and treated with and without β-GPA for trained immunity marker, H3K4me3, and DAPI.* ***G*** *Image intensity analysis of H3K4me3 signal across each group (Mock vs Trained+Ad p=0.0198; Mock vs Trained+Ad+β-GPA p= 0.0377).* ***H*** *H3K4me3 ChIP-qPCR on slc6a8 loci with PBS or WPG treated macrophages (n=3 mice per treatment group)* ***F*** *RT-qPCR on slc6a8 with PBS (n=3 mice) or WPG treated macrophages(n=3 mice). For H3K4me3 density analysis, a one-way ANOVA test was performed along with a Tukey's multiple comparisons test. All data are presented as the mean ± SD.*



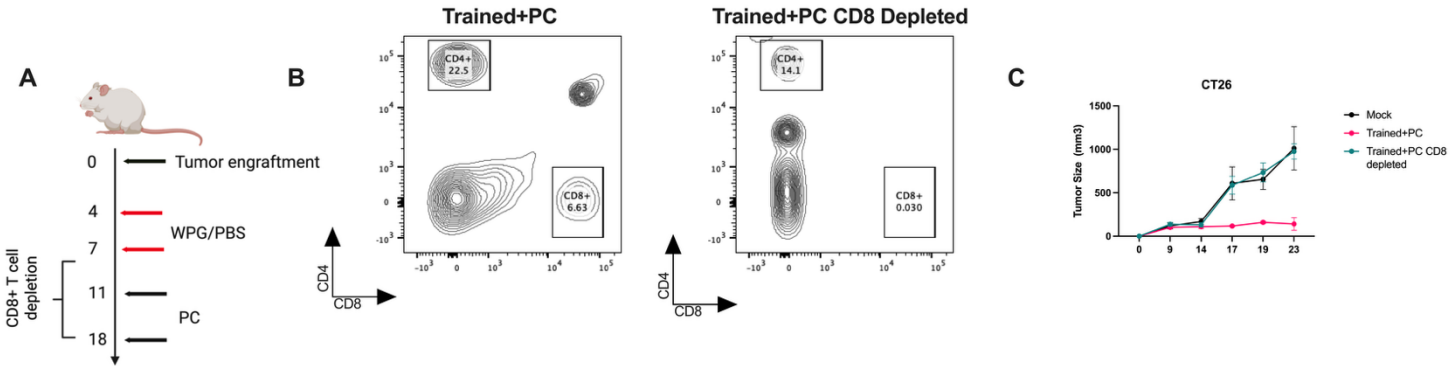
Supplementary Figure 12 Single mouse tumor volumes and gating strategy for NK and Macrophage profiling ***A*** *Graphical representation of workflow of animal experiment (Created in BioRender. Hamdan, F. (2026) https://BioRender.com/0tcj38k). Deconvolution for each treatment group for single tumor growth for each mouse (n=5).* ***B*** *Gating Strategy for macrophage and NK cells gating. Single cells were examinded under FSC-A vs SSC-A. Counting beads were gated and immune cells were also gated. Immune cells were then gated on CD11b+ cells. CD11b+ cells were then gated on macrophages based on F4/80 expression while NK cells were gated on Anti-GM1.*



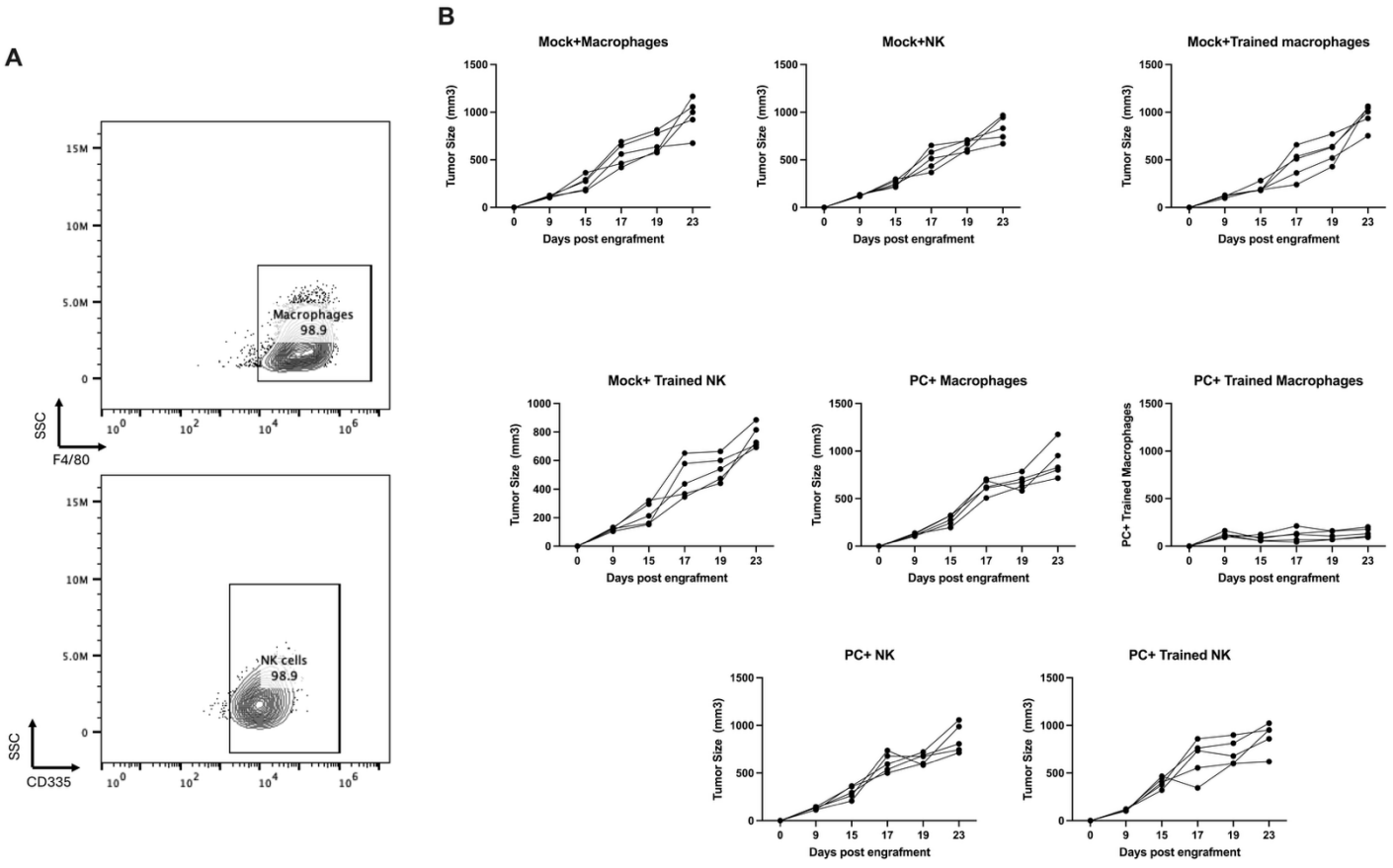
Supplementary Figure 13 NK and macrophage analysis and single mouse tumor volumes A *Flow cytometry plots on macrophage and NK depletion in peripheral blood of mice at day 9.* ***B*** *Graphical representation of workflow of animal experiment (Created in BioRender. Hamdan, F. (2026) https://BioRender.com/sckv9it). Deconvolution for each treatment group for single tumor growth for each mouse (n=8).*



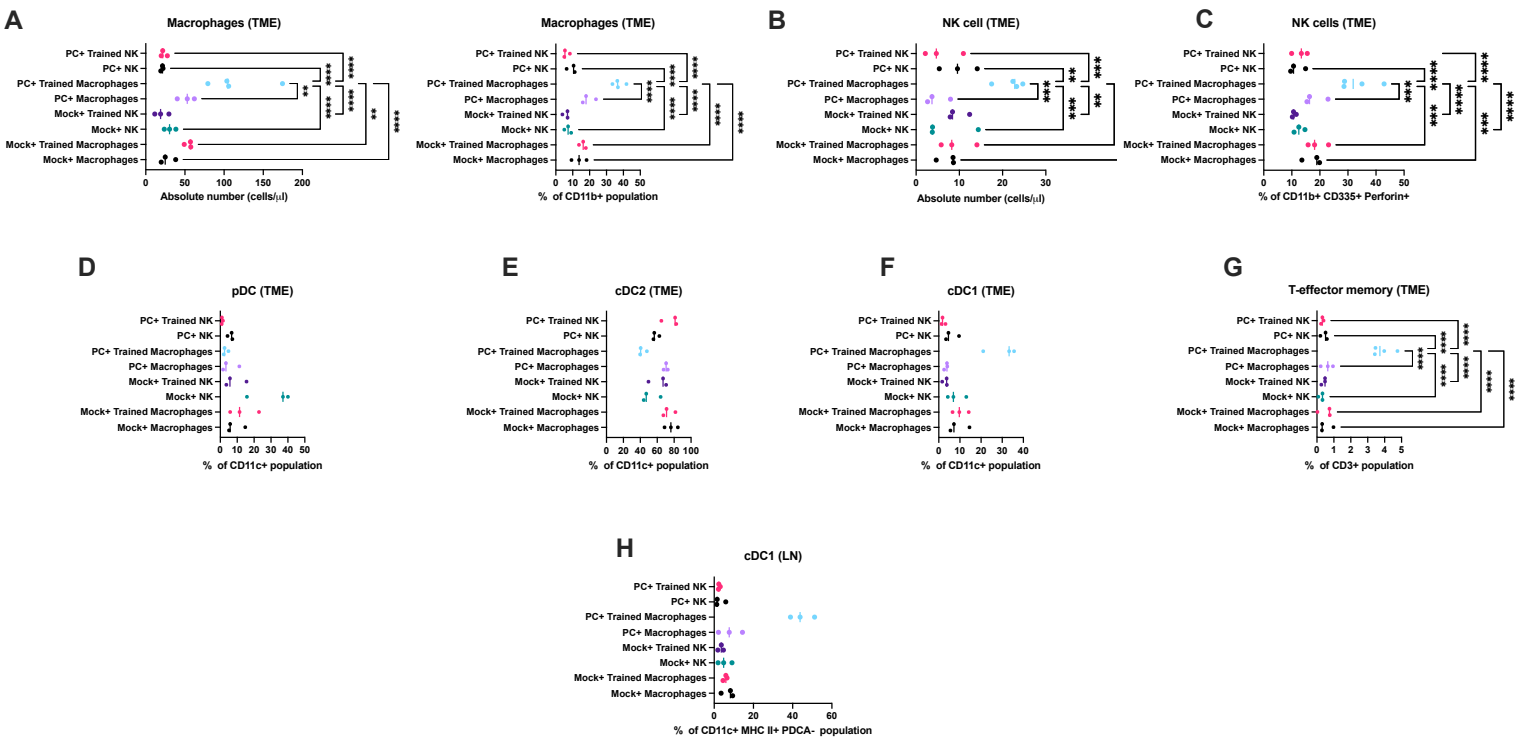
Supplementary Figure 14 CD8+ T cell and DC analysis ***A*** *Quantification of dendritic cells in the draining lymph nodes across different treatment groups (8 mice per group pooled and dots represent technical replicates n=3) at day 23. Contour plots displaying the frequency of dendritic cells across treatment groups* ***B*** *Quantification of dendritic cells populations in the draining lymph nodes across different treatment groups at day 23 (8 mice per group pooled and dots represent technical replicates n=3). Contour plots displaying the frequency of cDC1 and cDC2 across treatment groups* ***C*** *Quantification of CD8+ splenocytes releasing INF-g when stimulated with PBS or Syl peptides across different treatment groups at day 23 (n=8 mice per treatment group; "****" p<0.0001; "*" p=0.0280). Contour plots displaying the frequency of CD8+ splenocytes releasing INF-g when stimulated with Syl peptides across treatment groups* ***D*** *Quantification of CD8+ splenocytes releasing TNF-a when stimulated with PBS or Syl peptides across different treatment groups at day 23 (n=8 mice per treatment group; "****" p<0.0001). Contour plots displaying the frequency of CD8+ splenocytes releasing TNF-a when stimulated with Syl peptides across treatment groups. One-way ANOVA was used for all flow cytometry analyses along with a Tukey's multiple comparisons test. All data are presented as the mean ± SD.*



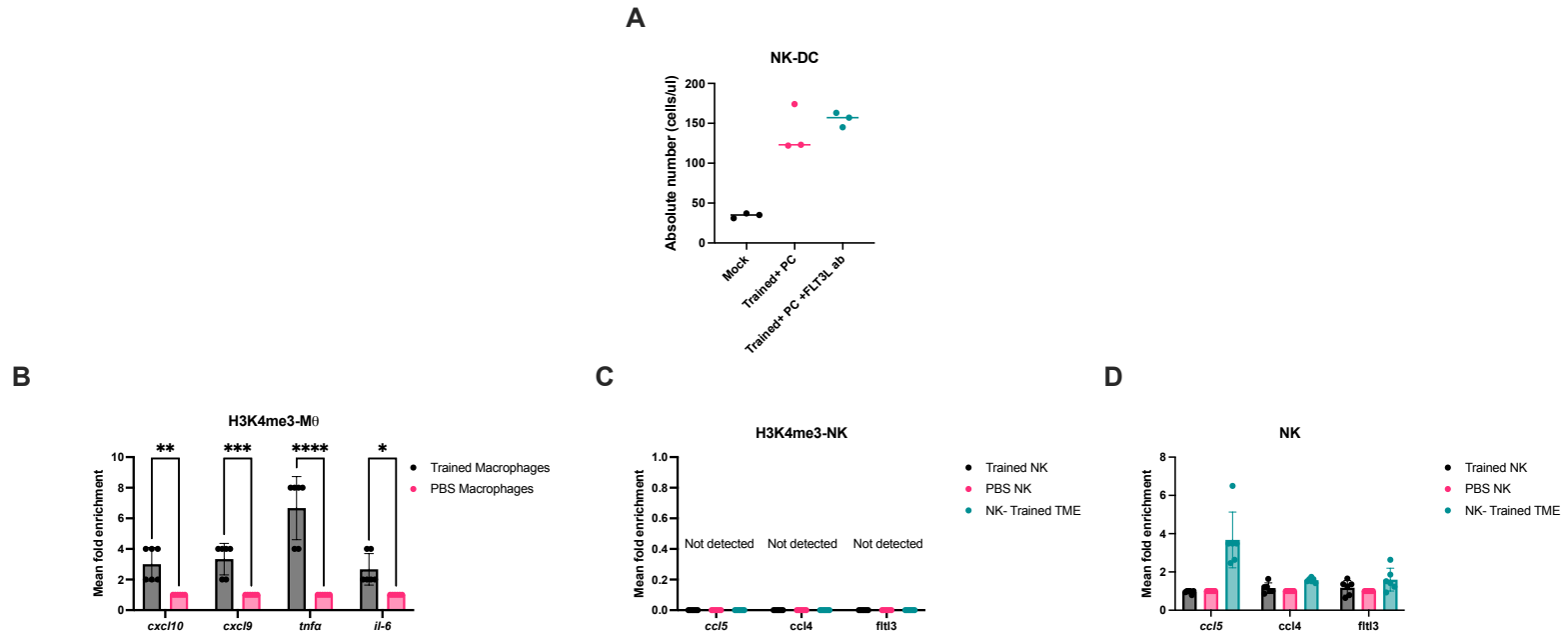
Supplementary Figure 15 CD8+T requirement for WPG enhancement of vaccination ***A*** *Graphical representation of workflow of animal experiment (Created in BioRender. Hamdan, F. (2026) https://BioRender.com/q3k0k3l). Mice were engrafted with CT26 and then stimulated with WPG or PBS at day 4 and 7. At day 6, 500μg of anti-CD8 T cell depleting antibody was given and supplemented every three days with 100μg of anti-CD8 T cell depleting antibody. PC was given at days 11 and 18.* ***B*** *Flow cytometry plots on CD8+ T cell depletion in peripheral blood of mice at day 23* ***C*** *Tumor sizes were measured for each group (n=5 mice per treatment group) every 2-3 days and summarize. All data are presented as the mean ± SD.*



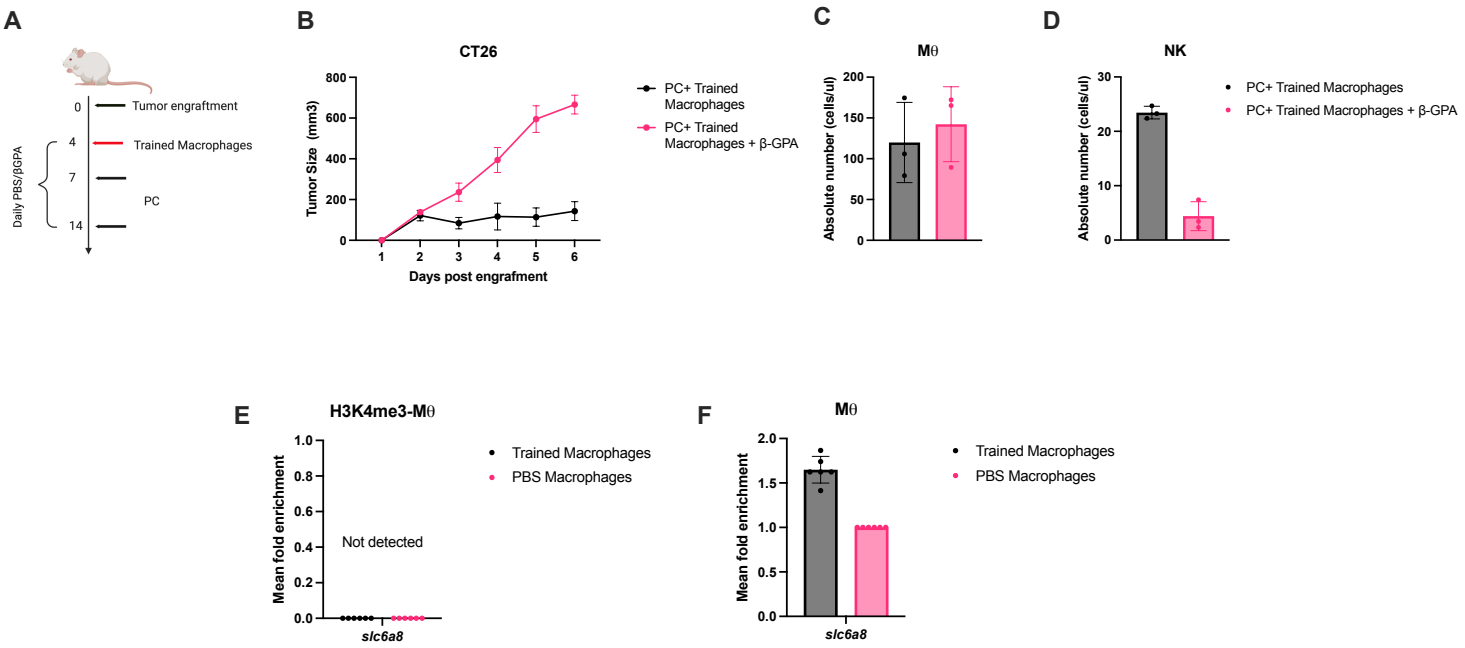
Supplementary Figure 16 Single mouse tumor volumes in adoptive transfer ***A*** *Flow cytometry plots on enriched macrophages and NK cells adoptively transferred to CT26 bearing mice* ***B*** *Deconvolution for each treatment group for single tumor growth for each mouse (n=5).*



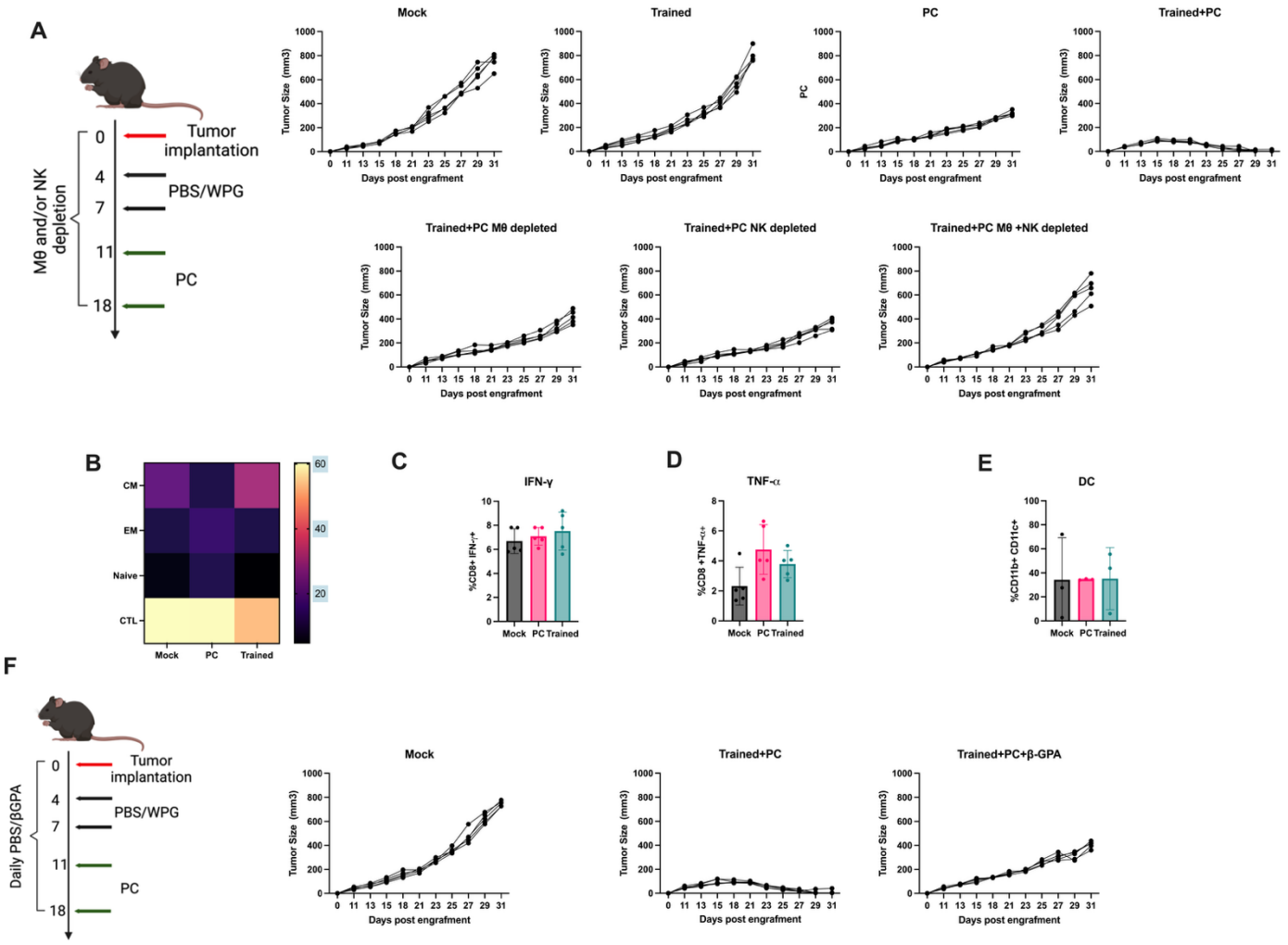
Supplementary Figure 17 Tumor microenvironment immune analysis ***A*** *Absolute numbers and percentages (of CD11b) of macrophages in the tumor microenvironments across each group (n=3-4 mice per treatment group; "****" p<0.0001; PC+Trained macrophages vs Mock+ Trained macrophages p=0.0027; PC+Trained Macrophages vs PC+Macrophages p=0.0018)* ***B*** *Absolute numbers of NK in the tumor microenvironments across each group (PC+ Trained Macrophages vs. Mock+ Macrophages p=0.0008; PC+Trained Macrophages vs Mock+ Trained Macrophages p=0.0034; PC+Trained Macrophages vs NK p= 0.0008; PC+Trained Macrophages vs Mock+ Trained NK p= 0.0039; PC+Trained Macrophages vs PC+Macrophages p=0.001; PC+Trained Macrophages vs PC+NK p=0.0043; PC+Trained Macrophages vs PC+ Trained NK p= 0.0003)* ***C*** *Percentage (of CD11b) of NK cells in the TME expressing Perforin in the tumor microenvironments across each group (n=3-4 mice per treatment group; "****" p <0.0001; PC+Trained Macrophages vs Mock Macrophages p= 0.0003; PC+Trained Macrophages vs Mock +Trained Macrophages p=0.0008; PC+Trained Macrophages vs PC+Macrophages p=0.0004))*. ***D*** *Percentage (of CD11c) of pDC cells in the TME in the tumor microenvironments across each group(5 mice per group pooled and dots represent technical replicates n=3)* ***E*** *Percentage (of CD11c) of cDC2 cells in the TME in the tumor microenvironments across each group (5 mice per group pooled and dots represent technical replicates n=3)* ***F*** *Percentage (of CD11c) of cDC1 cells in the TME in the tumor microenvironments across each group (5 mice per group pooled and dots represent technical replicates n=3)* ***G*** *Percentage (of CD3) of T effector CD8+ memory T cells in the TME in the tumor microenvironments across each group (n=3-4 mice per group; "****" p <0.0001)* ***H*** *Percentage (of CD11c PDCA-) of cDC cells in the TME in the draining lymph nodes across each group (5 mice per group pooled and dots represent technical replicates n=3). One-way ANOVA was used for all flow cytometry analyses along with a Tukey's multiple comparisons test. All data are presented as the mean ± SD.*



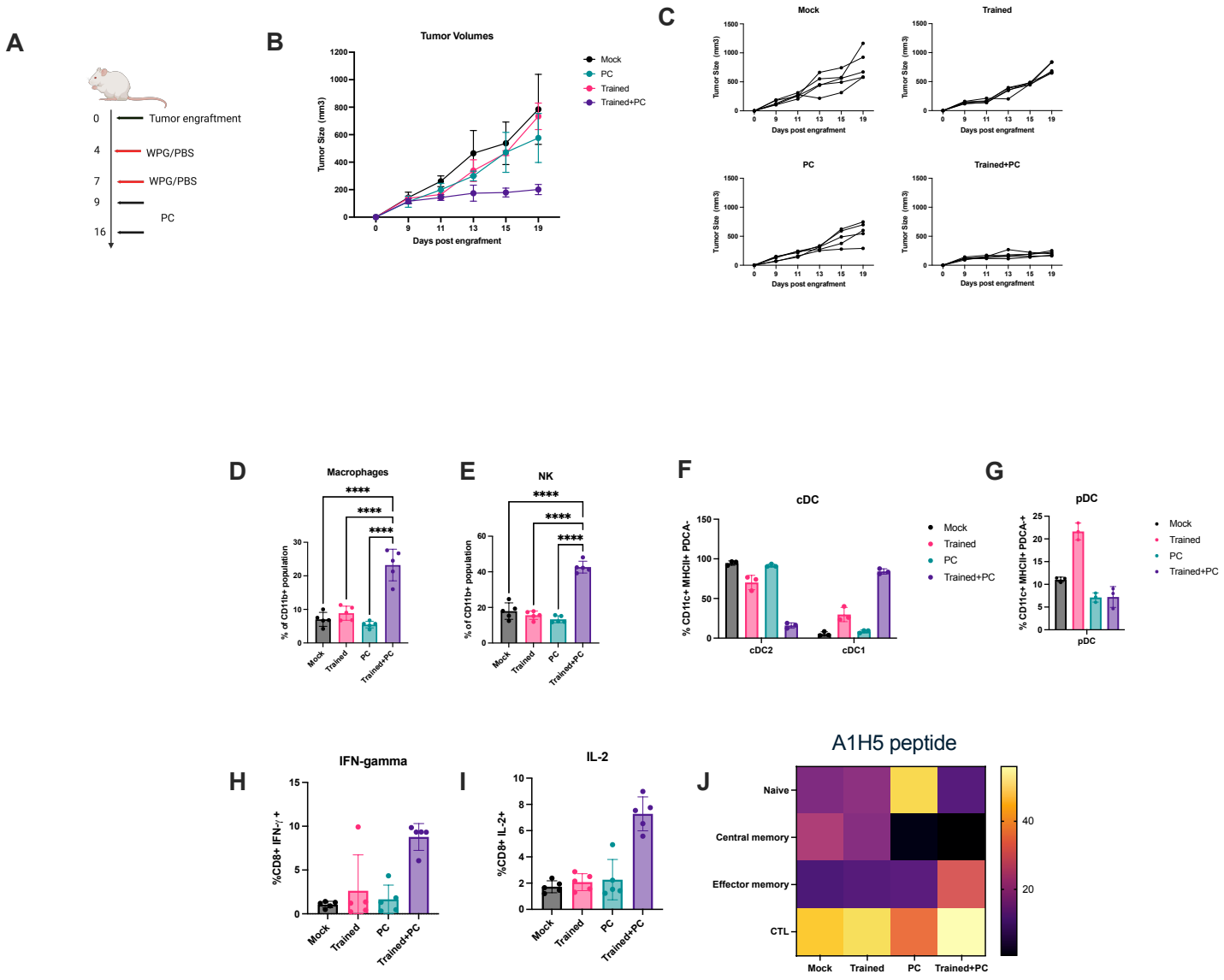
Supplementary Figure 18 ChIP-qpcr and RT-qpcr of Macrophages and NK cells A DC chemotaxis assay in which NK cells stimulated with Ad5/3 were treated with 10 µg/mL anti-FLT3L antibody (n=3) ***B*** *H3K4me3 ChIP-qPCR with macrophages treated with PBS or WPG on cxcl9 (p=0.0007), cxcl10(p=0.0040), tnfa ("****" < 0.0001) and il6 loci (p=0.0204) (n=6).* ***C*** *H3K4me3 ChIP-qPCR with NK cells treated with PBS or WPG on ccl5, ccl4 and ftl3 loci (n=6).* ***D*** *RT-qPCR with NK cells treated with PBS or WPG on ccl5, ccl4 and ftl (n=6). Fold enrichment statistical tests were done with a two-way ANOVA along with a Šídák's multiple comparisons test. All data are presented as the mean ± SD.*



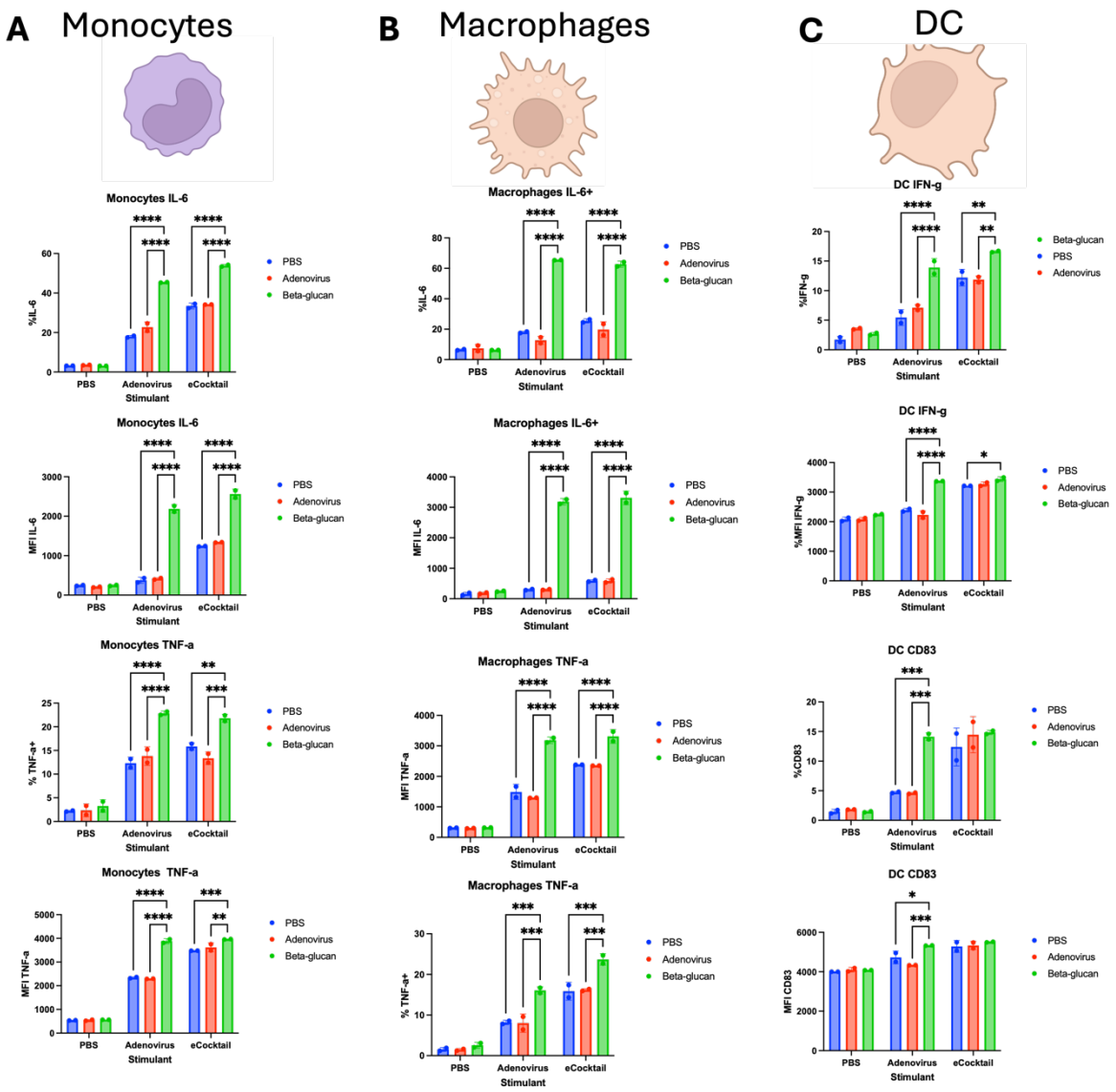
Supplementary Figure 19 β-GPA effects on trained macrophages. ***A*** Graphical *representation of workflow of animal experiment(Created in BioRender. Hamdan, F. (2026) https://BioRender.com/yjkdsok). Mice were engrafted with CT26 were injected with trained macrophages at day 4 and later treated with PC at day 7 and 14. Daily doses of β-GPA or PBS were given starting day 4.* ***B*** *Tumor sizes were measured for each group every 2-3 days and summarized (n=3 mice per treatment group)* ***C*** *Absolute number of macrophages in the tumor microenvironment across treatment groups (n=3 mice per treatment group)* ***D*** *Absolute number of NK cells in the tumor microenvironment across treatment groups* **E** *H3K4me3 ChIP-qPCR with macrophages treated with PBS or WPG on slc6a8 loci (n=6).* **F** *RT-qPCR with macrophages cells treated with PBS or WPG on slc6a8 (n=6). All data are presented as the mean ± SD.*



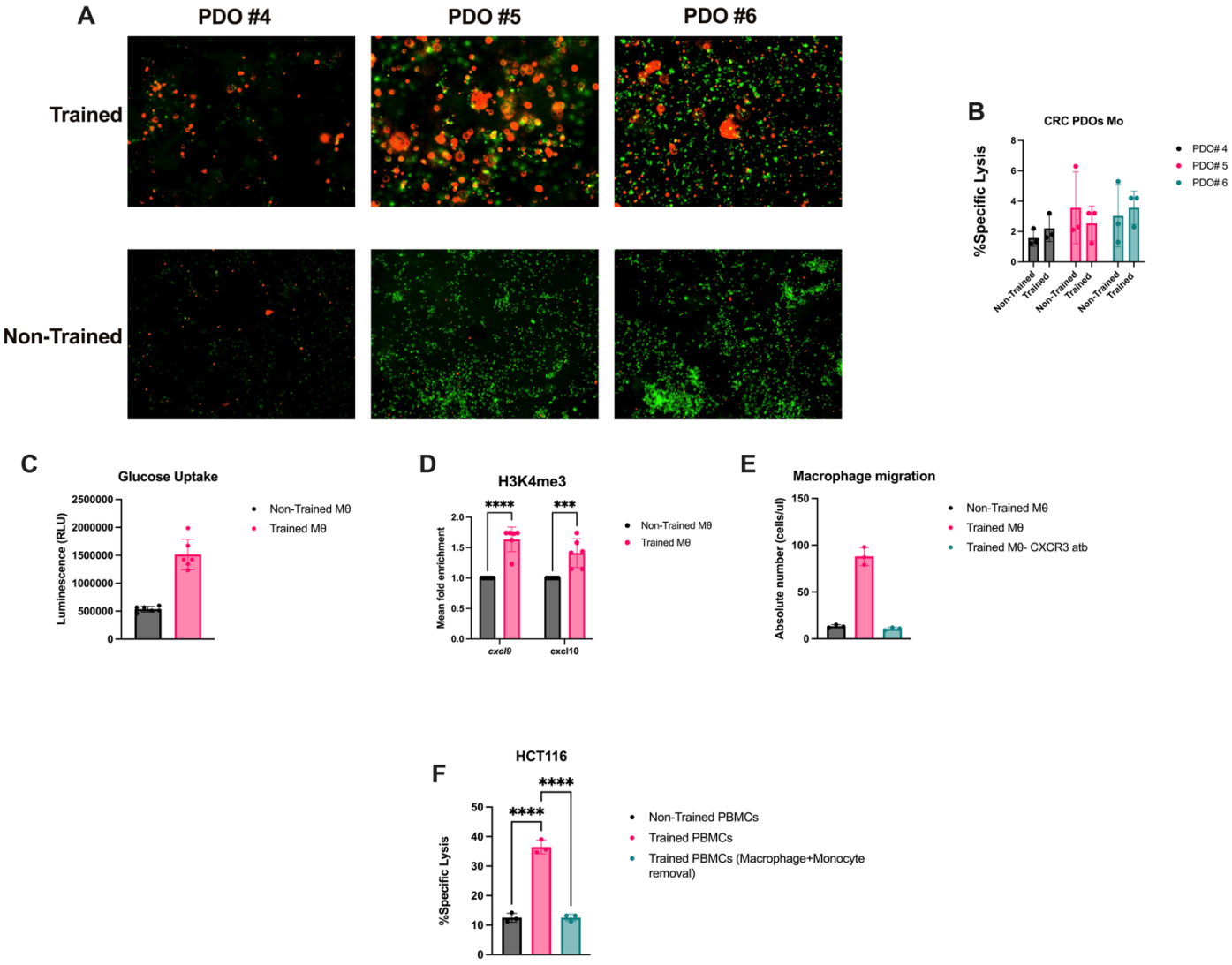
Supplementary Figure 20 WPG-induced training in MC38 models ***A*** *Graphical representation of workflow of animal experiment (Created in BioRender. Hamdan, F. (2026) https://BioRender.com/3c0jk7s). Deconvolution for each treatment group for single tumor growth for each mouse (n=5).* ***B*** *Heat map on the quantification of CD8+ T cell memory subsets across different treatment groups.* ***C*** *Quantification of CD8+ T cells expressing IFN-γ when stimulated with MC38 peptides (n=5 mice per treatment group)* ***D*** *Quantification of CD8+ T cells expressing TNF-α when stimulated with MC38 peptides (n=5 mice per treatment group).* ***E*** *Quantification of dendritic cells in the draining lymphnodes across treatment groups (5 mice per group pooled and dots represent technical replicates n=3).* ***F*** *Graphical representation of workflow of animal experiment (Created in BioRender. Hamdan, F. (2026) https://BioRender.com/3nxhps2). Deconvolution for each treatment group for single tumor growth for each mouse (n=5). All data are presented as the mean ± SD.*



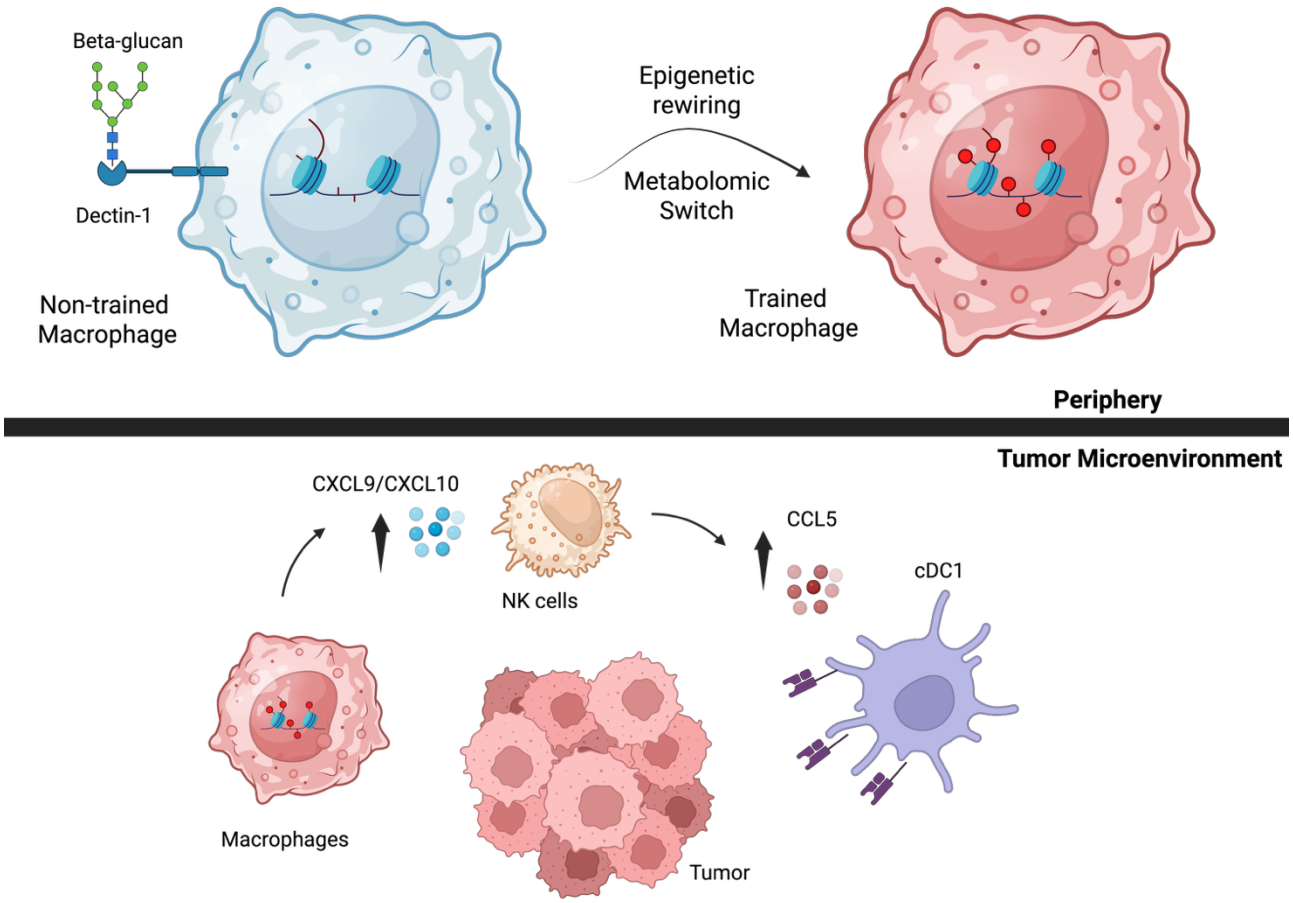
Supplementary Figure 21 WPG-induced training in Colon-26 models ***A*** *Graphical representation of workflow of animal experiment (Created in BioRender. Hamdan, F. (2026) https://BioRender.com/ xc9uxox). Mice were engrafted with Colon-26 and then stimulated with PBS or WPG at day 4 and 7. Mice were then treated with PC at days 9 and 16.* ***B*** *Tumor sizes were measured for each group every 2-3 days and summarize (n=5 mice per treatment group)* ***C*** *Deconvolution for each treatment group for single tumor growth for each mouse (n=5).* ***D*** *Cell percentage (of CD11b) of macrophages in the tumor microenvironment across treatment groups (n=5 mice per treatment group; "****" p <0.0001)* ***E*** *Cell percentage (of CD11b) of NK in the tumor microenvironment across treatment groups (n=5 mice per treatment group; ; "****" p <0.0001)* ***F*** *Cell percentage (of CD11c PDCA-) of cDCs in the draining lymph node across treatment groups* ***G*** *Cell percentage (of CD11c) of pDCs in the draining lymph node across treatment groups* ***H*** *Quantification of CD8+ T cells expressing INF-γ when stimulated with Colon-26 peptides (A1H5) (n=5 mice per treatment group).* ***I*** *Quantification of CD8+ T cells expressing IL.2 when stimulated with Colon-26 peptides (A1H5) (n=5 mice per treatment group)* ***J*** *Heat map on the quantification of CD8+ T cell memory subsets across different treatment groups when stimulated with Colon-26 peptides (A1H5) (n=5 mice per treatment group). One-way ANOVA was used for all flow cytometry analyses along with a Tukey's multiple comparisons test. All data are presented as the mean ± SD.*



Supplementary Figure 22 WPG-training in human PBMCs ***A*** *Isolated monocytes (n=3) were quantified with the secretion of IL-6 ("****" p <0.0001) and TNF-alpha (%; "**" p=0.0030; "***" p =0.0008) (MFI; "****" p<0.0001; "***" p=0.0007; "**" p=.0040) when trained or not traied under different stimulus.* ***B*** *Differentiaed macrophages (n=3) from monocytes were quantified with the secretion of IL-6 ("****" p <0.0001) and TNF-alpha(MFI; "****" p<0.0001) (%; "***" p=.0004) when trained or not traied under different stimulus.* ***C*** *Differentiaed dendritic (n=3) cells from monocytes were quantified with the secretion of INF-γ (%; "****" p<0.0001; "**" p=0.0030) (MFI; "****" p<0.0001; "*" p=0.0204) and CD83 (%; "***" p=0.0003) (MFI; "***" p=0.0003; "*" p=.0300) when trained or not traied under different stimulus. One-way ANOVA was used for all flow cytometry analyses along with a Tukey's multiple comparisons test. All data are presented as the mean ± SD. All schematics were created in BioRender. Hamdan, F. (2026) https://BioRender.com/7qcvyuo*



Supplementary Figure 23 WPG-induced training in patient derived organoids ***A*** *Z-stalks of confocal images for T-cell killing of PDO obtained from patient #4, #5 and #6.* ***B*** *Quantification of specific lysis, from LDH release, from each patient across with trained and non-trained Macrophages/monocytes (n=3)* ***C*** *Glucose uptake from trained and non-trained macrophages (n=6).* ***D*** *H3K4me3 ChIP-qPCR with macrophages treated with PBS or WPG on cxcl9 and cxcl10 (n=6; "****" p <0.0001; "***" p=0.0003).* ***E*** *Aboslute number of NK cells migrated through a transwell system by Ad5/3 treated macrophages (n=3).* ***F*** *Quantification of specific lysis, from LDH release, of HCT116 cells with PBMCs (n=3; "****" p <0.0001). Fold enrichment statistical tests were done with a two-way ANOVA along with a Šídák's multiple comparisons test. One-way ANOVA was used for all specific lysis analyses along with a Tukey's multiple comparisons test. All data are presented as the mean ± SD.*



Supplementary Figure 24 **Mechanism of action of WPG-induced trained immunity in enhancing vaccine effects** Periphary macrophages are trained with WPG and are metabolomically and epigenetically reprogrammed. They migrate to the tumor and express CXCL9 and CXCL10 promoting a NK-cDC1 axis via CCL5. Created in BioRender. Hamdan, F. (2026) https://BioRender.com/i1yry9d

Primer name	Sequence (5' to 3')	Application
mCXCL9 FW	AGCTTTGACTTGTGAGGAAAGG	ChIP-qPCR
mCXCL9 RV	TATTGAGTCACTGTGTTGGAGTTGA	ChIP-qPCR
mCXCL10 FW	GGGAGAGGGAAATTCCA	ChIP-qPCR
mCXCL10 RV	TTTCCCTCCCTGAGTCC	ChIP-qPCR
mSLC6A8 FW	ATCCTGGCACTCATCAACAGCG	ChIP-qPCR
mSLC6A8 RV	GGTAGGCAATGAAGGCTAGACC	ChIP-qPCR
mTNF FW	GGTGCCTATGTCTCAGCCTCTT	ChIP-qPCR
mTNF RV	GCCATAGAACTGATGAGAGGGAG	ChIP-qPCR
mIL-6 FW	TACCACTTCACAAGTCGGAGGC	ChIP-qPCR
mIL-6 RV	CTGCAAGTGCATCATCGTTGTTC	ChIP-qPCR
mCCL5 FW	CACCATTCACACACATG	ChIP-qPCR
mCCL5 RV	GTCAAGGGATCTGATAGG	ChIP-qPCR
mCCL4 FW	ACCCTCCCACTTCCTGCTGTTT	ChIP-qPCR
mCCL4 RV	CTGTCTGCCTCTTTTGGTCAGG	ChIP-qPCR
mFltl2FW	CGCGCATCACTCCCTCATAC	ChIP-qPCR
mFltl2RV	CAAAGCCAAGTTCACCGCTT	ChIP-qPCR
mCCL4 FW	ACCCTCCCACTTCCTGCTGTTT	RT-qPCR
mCCL4 RV	CTGTCTGCCTCTTTTGGTCAGG	RT-qPCR
mCCL5 FW	CCTGCTGCTTTGCCTACCTCTC	RT-qPCR
mCCL5 RV	ACACACTTGGCGGTTCCTTCGA	RT-qPCR
mFltl2FW	CGCGCATCACTCCCTCATAC	RT-qPCR
mFltl2RV	CAAAGCCAAGTTCACCGCTT	RT-qPCR
mSLC6A8 FW	GGTCAAATCCACGGGAAAGAT	RT-qPCR
mSLC6A8 RV	CCACGAAGCCAGCAAAGAAGC	RT-qPCR
mGapdhFW	TGCACCACCAACTGCTTAGC	RT-qPCR
mGapdhRV	GGCATGGACTGTGGTCATGAG	RT-qPCR
hCXCL9 FW	GTGGTGTTCTTTTCCTCTTGGG	ChIP-qPCR
hCXCL9 RV	ACAGCGACCCTTTCTCACTAC	ChIP-qPCR
hCXCL10 FW	CTCCAGTCTCAGCACCATGA	ChIP-qPCR
hCXCL10 RV	GCTCCCCTCTGGTTTTAAGG	ChIP-qPCR

Supplementary Table 1: Primers used for RT-qPCR and ChIP-qPCR experiments.

References

1) Geller, A. E. et al. The induction of peripheral trained immunity in the pancreas incites antitumor activity to control pancreatic cancer progression. Nature Communications 2022 13:1 13,1-20 (2022).