Figure S1

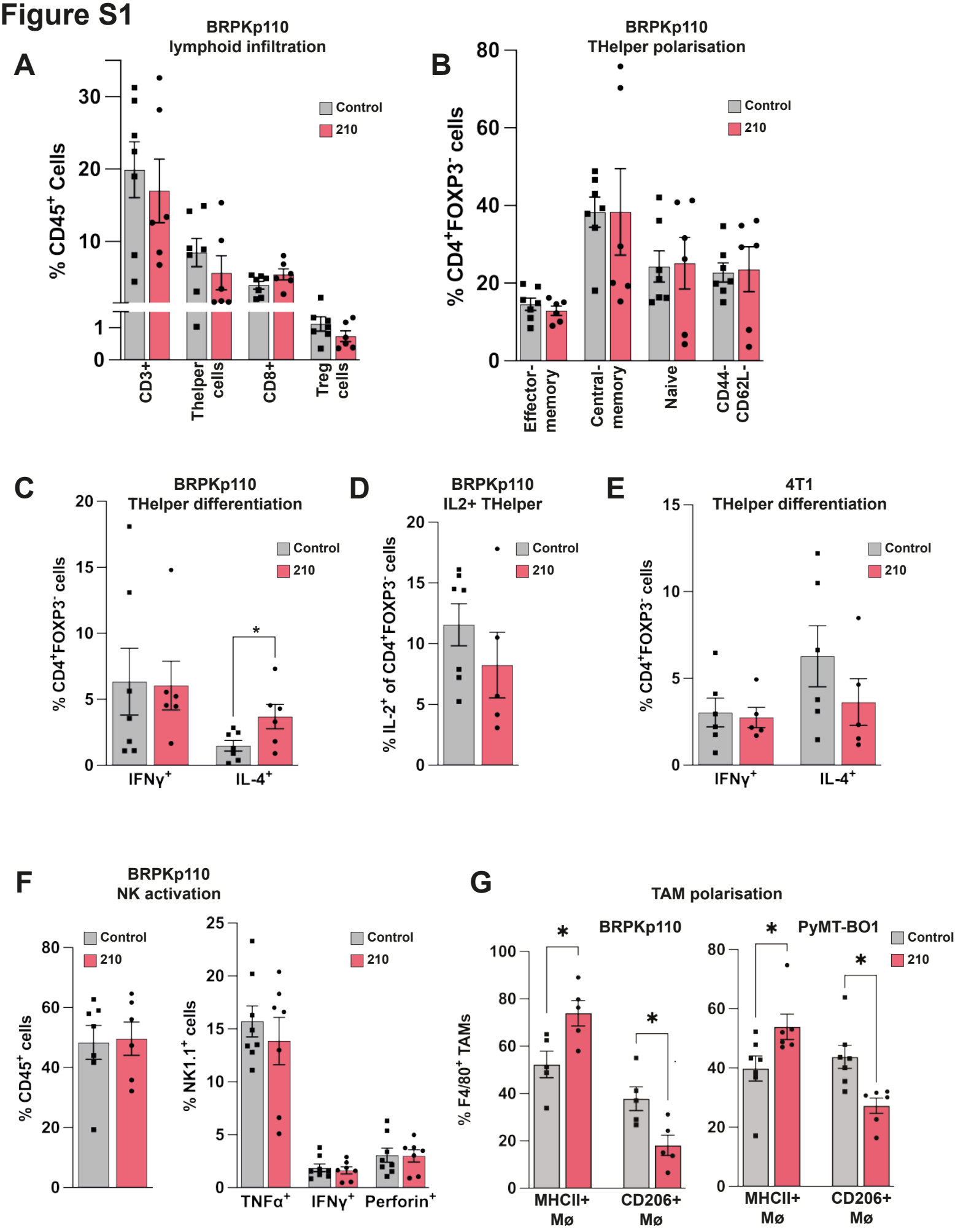

A
BRPKp110
lymphoid infiltration
% CD45+ Cells
Control
210
CD3+
THelper cells
CD8+
Treg cells
B
BRPKp110
THelper polarisation
% CD4+FOXP3- cells
Control
210
Effector-memory
Central-memory
Naive
CD44-CD62L-
C
BRPKp110
THelper differentiation
% CD4+FOXP3- cells
Control
210
IFNγ+
IL-4+
D
BRPKp110
IL2+ THelper
% IL-2+ of CD4+FOXP3- cells
Control
210
E
4T1
THelper differentiation
% CD4+FOXP3- cells
Control
210
IFNγ+
IL-4+
F
BRPKp110
NK activation
% CD45+ cells
Control
210
% NK1.1+ cells
TNFα+
IFNγ+
Perforin+
G
TAM polarisation
BRPKp110
PyMT-BO1
% F4/80+ TAMs
Control
210
MHCII+ Mø
CD206+ Mø

Figure S2

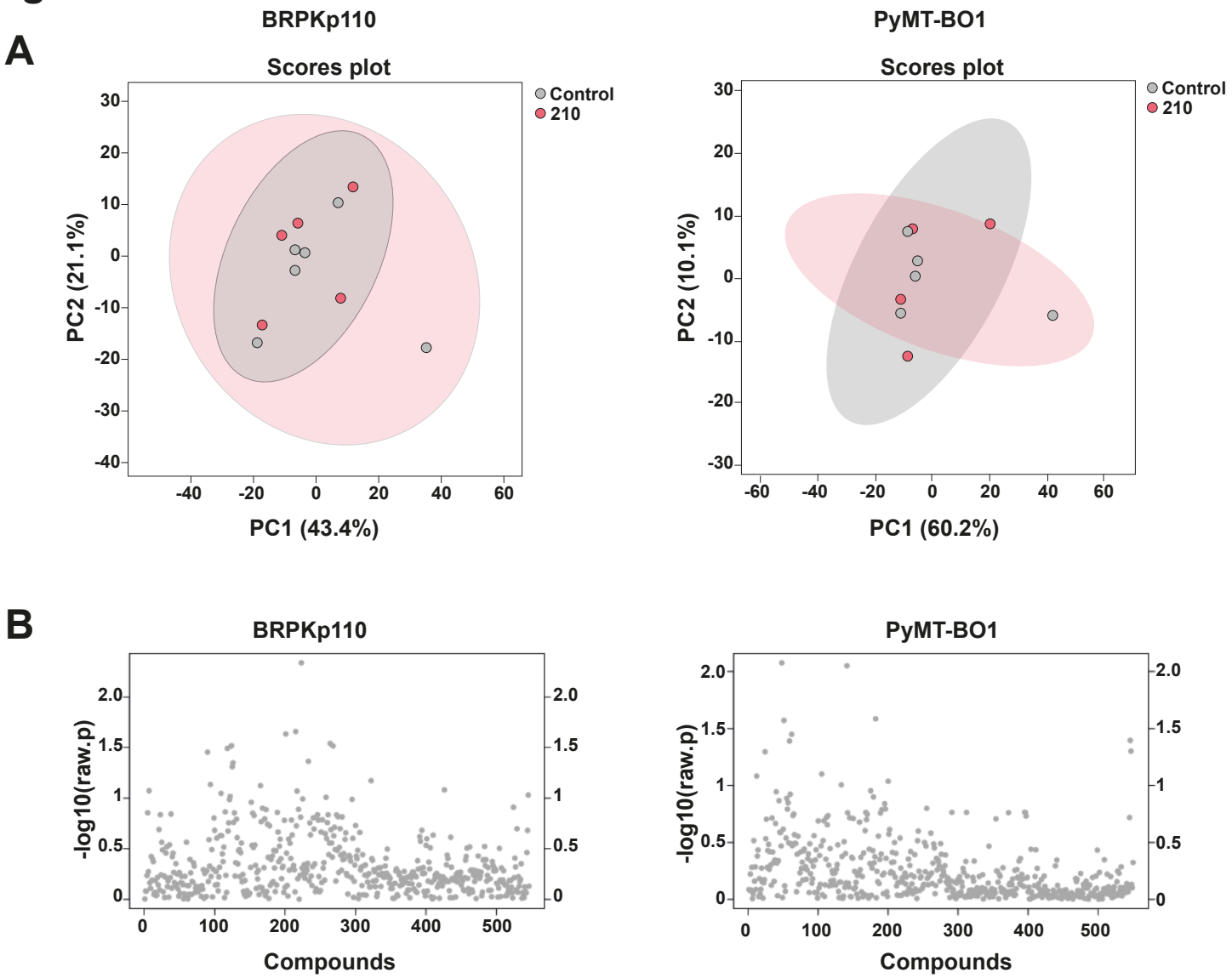

A
BRPKp110
Scores plot
Control
210
PC2 (21.1%)
PC1 (43.4%)
PyMT-BO1
Scores plot
Control
210
PC2 (10.1%)
PC1 (60.2%)
B
BRPKp110
-log10(raw.p)
Compounds
PyMT-BO1
-log10(raw.p)
Compounds
C
BRPKp110
Tetradecanedioic acid
Hexosylceramide (d18:2/23:0)
Phosphatidyl-choline ae C34:2
Lysophosphatidyl-choline a C24:0
Phosphatidyl-choline ae C36:2
Phosphatidyl-choline aa C36:0
Cholesteryl ester 17:1
Cholesteryl ester 17:0
Phosphatidyl-choline aa C30:0
Cholesteryl ester 14:0
Cholesteryl ester 18:1
Cholesteryl ester 18:0
Control
210
PyMT-BO1
Hexosylceramide (d16:1/24:0)
Trihexosylceramide (d18:1/24:1)
Dodecanoyl-carnitine
Diacylglyceride (16:0_20:3)
Ceramide (d18:1/24:0)
Aspartic Acid
Lysine
1-Methylhistidine
Trihexosylceramide
Indoleacetic acid
Alanine
Proline
Control
210

Figure S3

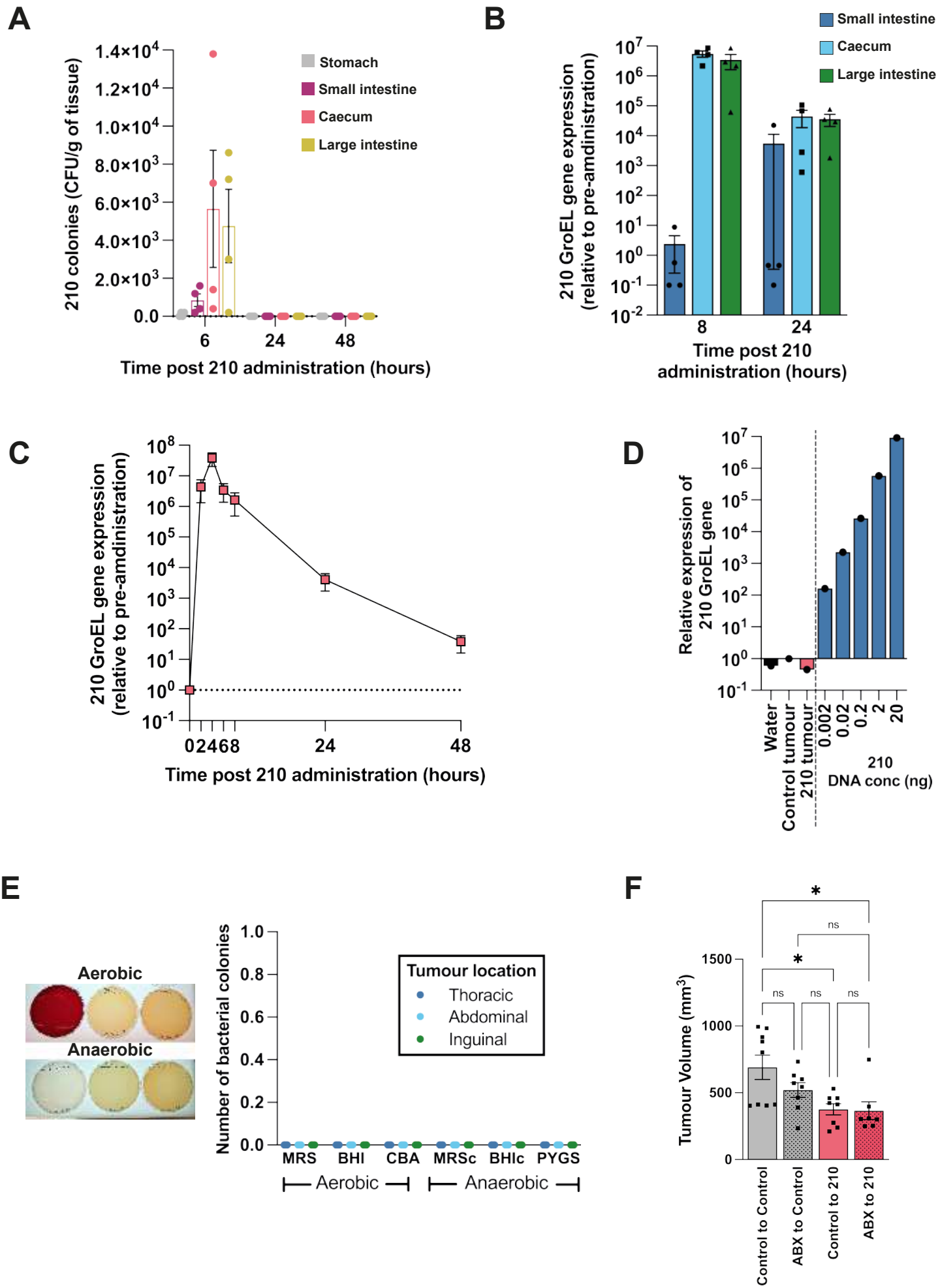

A
210 colonies (CFU/g of tissue)
Stomach
Small intestine
Caecum
Large intestine
Time post 210 administration (hours)
B
210 GroEL gene expression (relative to pre-amdinistration)
Small intestine
Caecum
Large intestine
Time post 210 administration (hours)
C
210 GroEL gene expression (relative to pre-amdinistration)
Time post 210 administration (hours)
D
Relative expression of 210 GroEL gene
Water
Control tumour
210 tumour
210 DNA conc (ng)
E
Aerobic
Anaerobic
Number of bacterial colonies
Tumour location
Thoracic
Abdominal
Inguinal
MRS
BHI
CBA
MRSc
BHIc
PYGS
Aerobic
Anaerobic
F
Tumour Volume (mm3)
ns
Control to Control
ABX to Control
Control to 210
ABX to 210

Figure S4

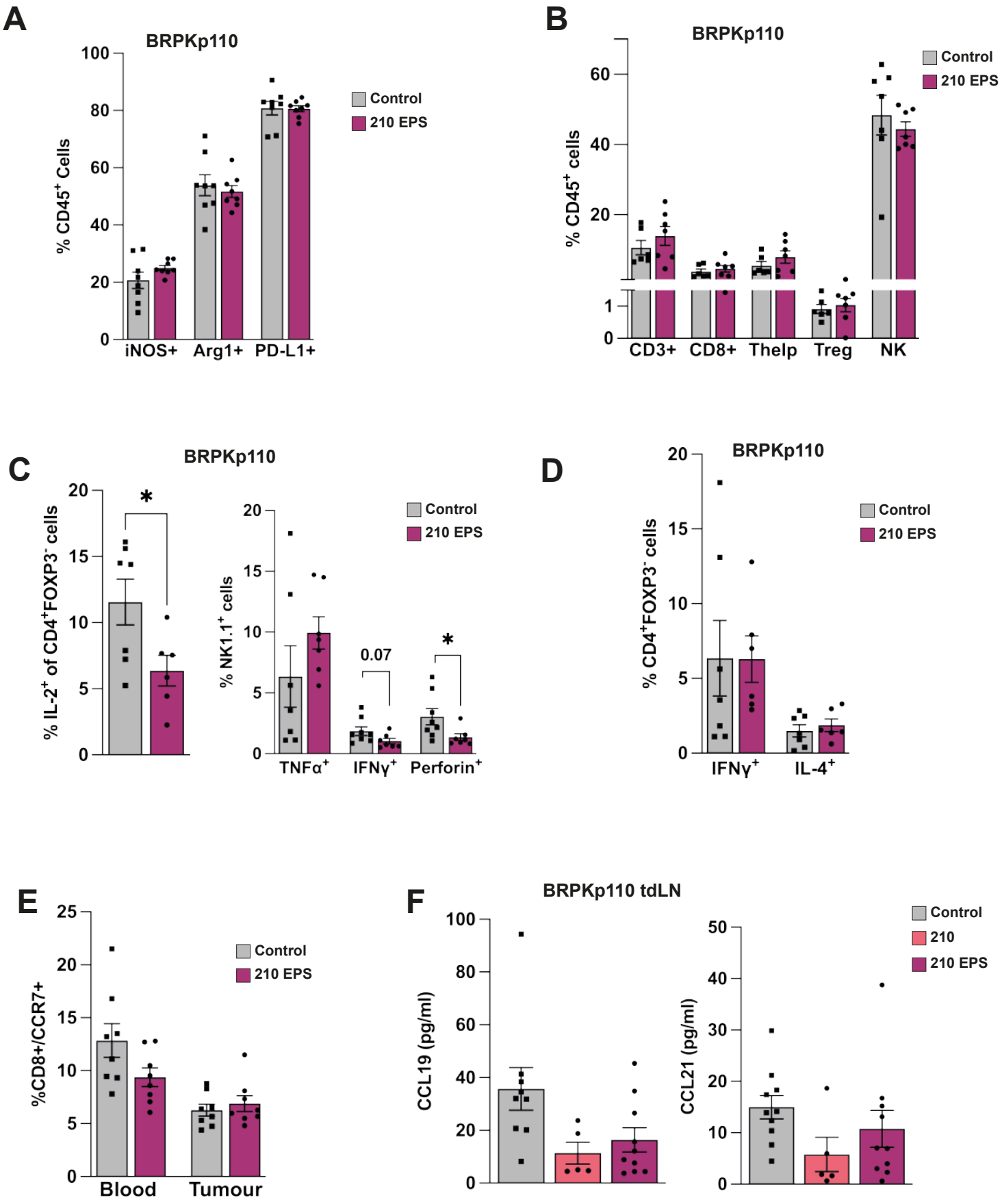
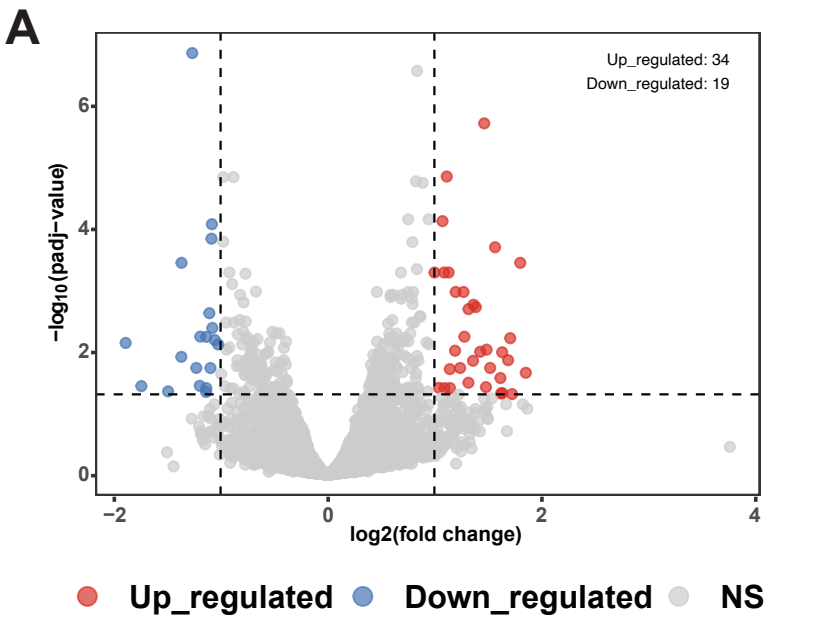

A
BRPKp110
% CD45+ Cells
iNOS+
Arg1+
PD-L1+
Control
210 EPS
B
BRPKp110
% CD45+ cells
CD3+
CD8+
Thelp
Treg
NK
Control
210 EPS
C
BRPKp110
% IL-2+ of CD4+FOXP3- cells
*
% NK1.1+ cells
0.07
*
TNFα+
IFNγ+
Perforin+
Control
210 EPS
D
BRPKp110
% CD4+FOXP3- cells
IFNγ+
IL-4+
Control
210 EPS
E
%CD8+/CCR7+
Blood
Tumour
Control
210 EPS
F
BRPKp110 tdLN
CCL19 (pg/ml)
CCL21 (pg/ml)
Control
210
210 EPS

Figure S5


A
Up_regulated: 34
Down_regulated: 19
−log10(padj−value)
log2(fold change)
Up_regulated
Down_regulated
NS

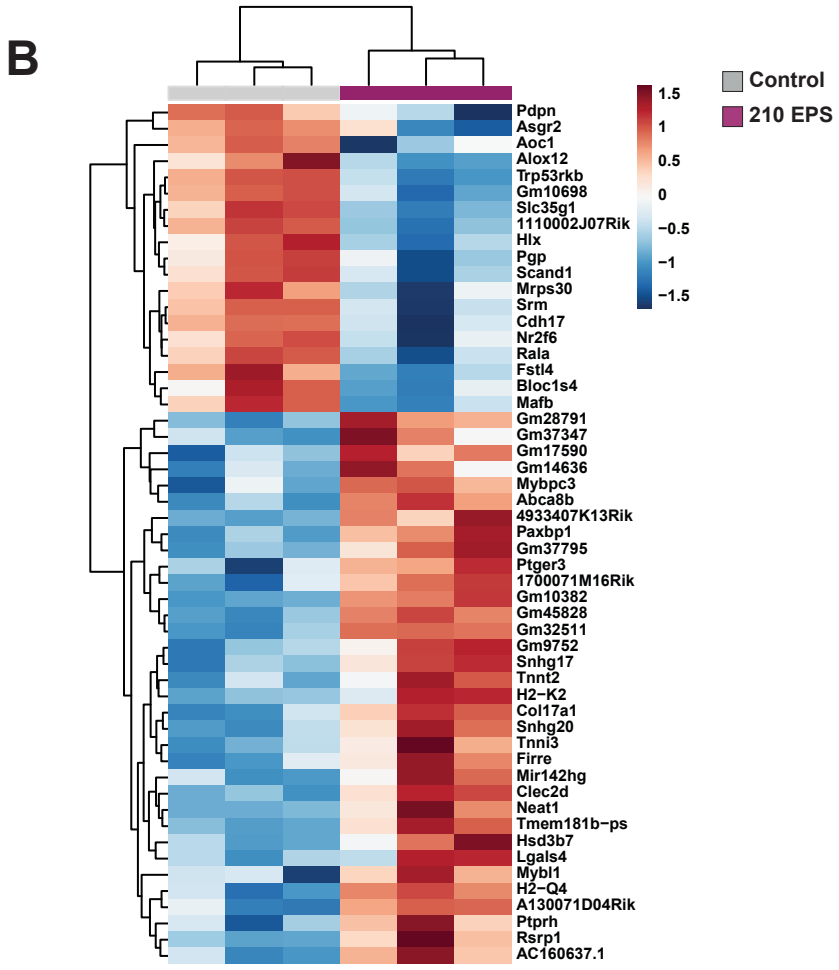

B
Control
210 EPS
1.5
1
0.5
0
−0.5
−1
−1.5
Pdpn
Asgr2
Aoc1
Alox12
Trp53rkb
Gm10698
Slc35g1
1110002J07Rik
Hlx
Pgp
Scand1
Mrps30
Srm
Cdh17
Nr2f6
Rala
Fstl4
Bloc1s4
Mafb
Gm28791
Gm37347
Gm17590
Gm14636
Mybpc3
Abca8b
4933407K13Rik
Paxbp1
Gm37795
Ptger3
1700071M16Rik
Gm10382
Gm45828
Gm32511
Gm9752
Snhg17
Tnnt2
H2−K2
Col17a1
Snhg20
Tnni3
Firre
Mir142hg
Clec2d
Neat1
Tmem181b−ps
Hsd3b7
Lgals4
Mybl1
H2−Q4
A130071D04Rik
Ptprh
Rsrp1
AC160637.1

Figure S6

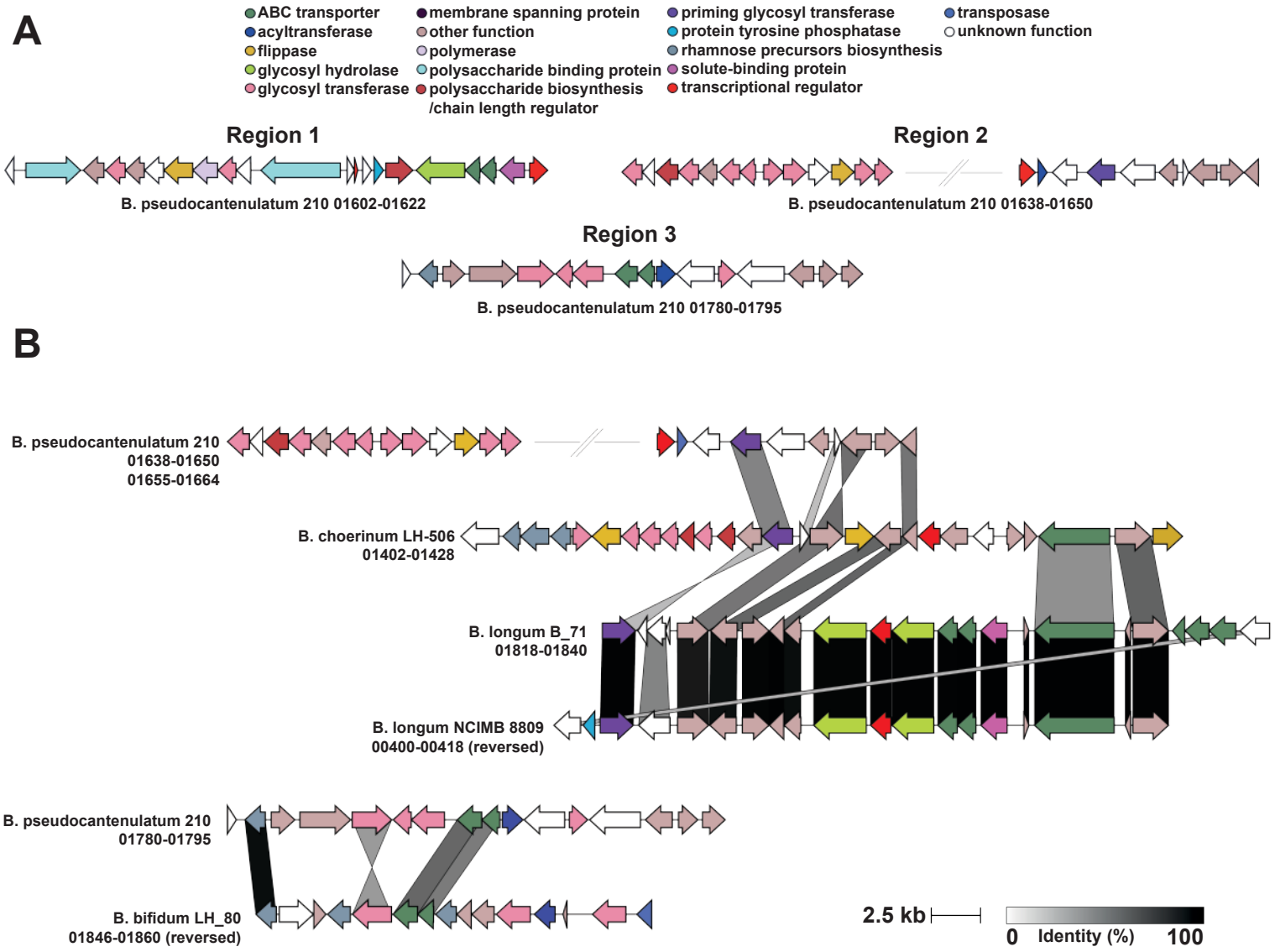

A
ABC transporter
acyltransferase
flippase
glycosyl hydrolase
glycosyl transferase
membrane spanning protein
other function
polymerase
polysaccharide binding protein
polysaccharide biosynthesis /chain length regulator
priming glycosyl transferase
protein tyrosine phosphatase
rhamnose precursors biosynthesis
solute-binding protein
transcriptional regulator
transposase
unknown function
Region 1
B. pseudocantenulatum 210 01602-01622
Region 2
B. pseudocantenulatum 210 01638-01650
Region 3
B. pseudocantenulatum 210 01780-01795
B
B. pseudocantenulatum 210 01638-01650 01655-01664
B. choerinum LH-506 01402-01428
B. longum B_71 01818-01840
B. longum NCIMB 8809 00400-00418 (reversed)
B. pseudocantenulatum 210 01780-01795
B. bifidum LH_80 01846-01860 (reversed)
2.5 kb
0
Identity (%)
100

Figure S7

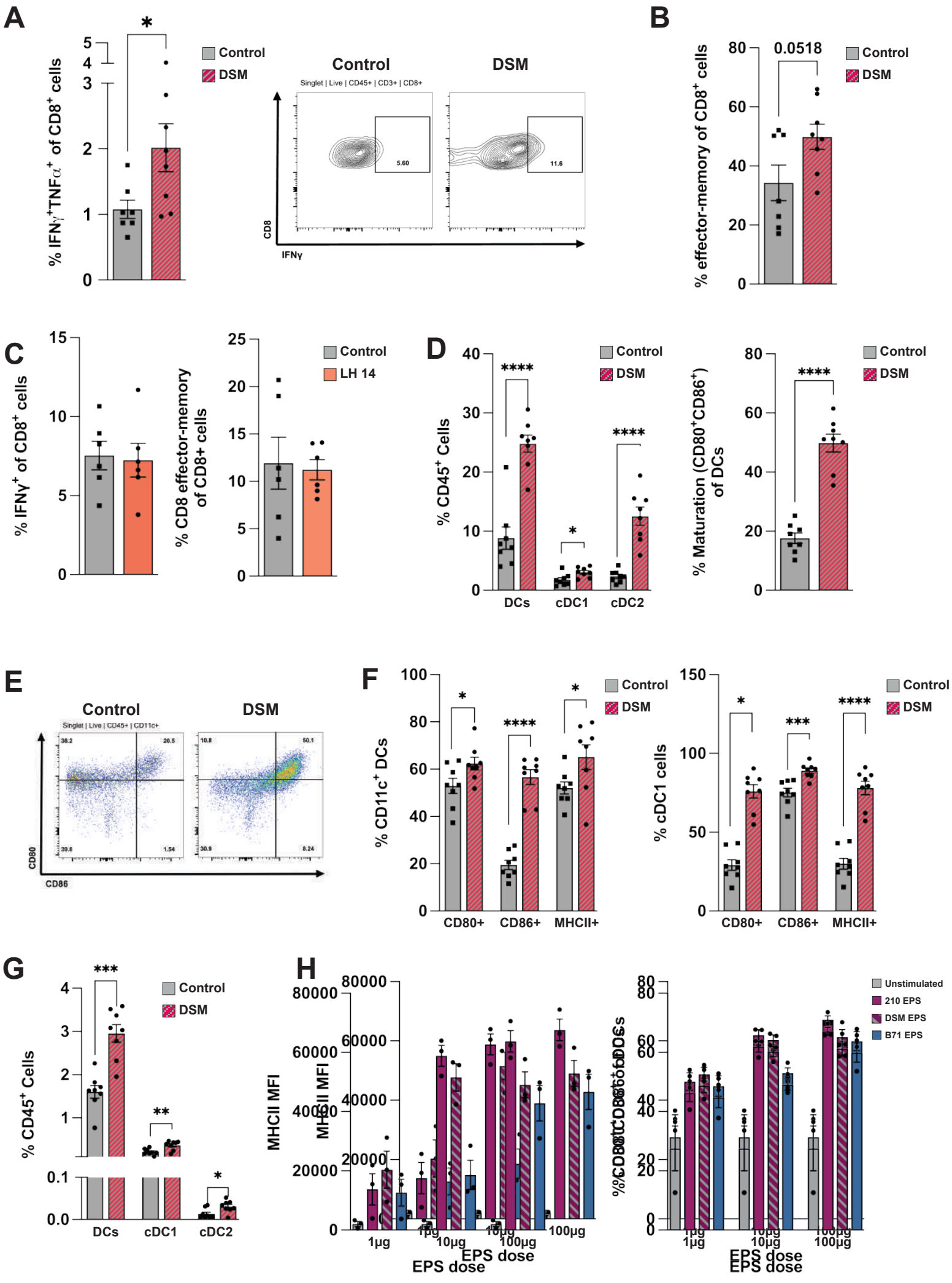
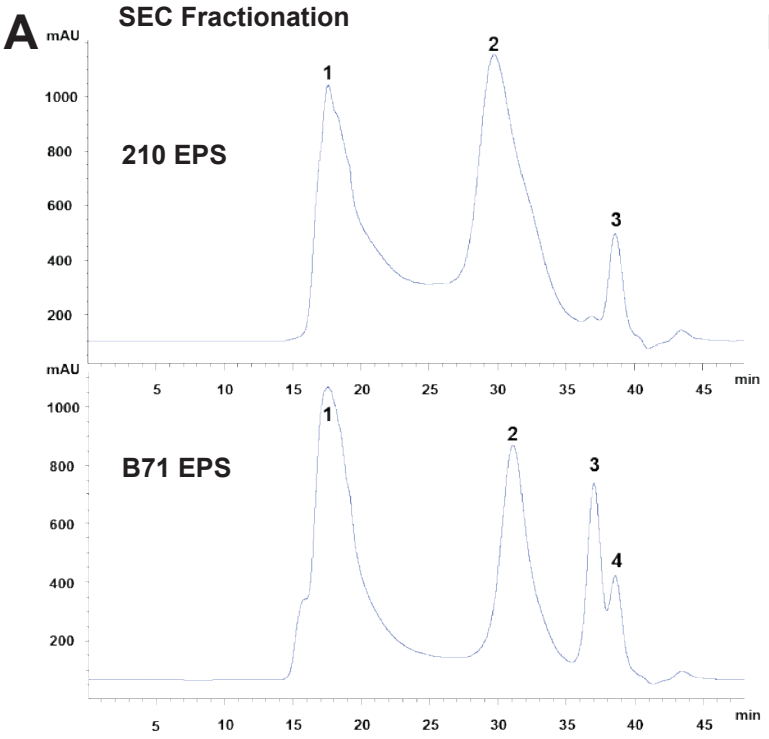
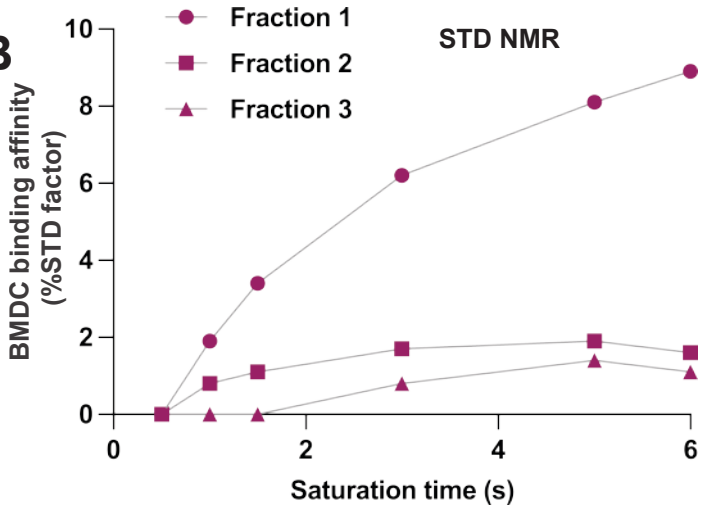

A
% IFNγ+TNFα+ of CD8+ cells
Control
DSM
Control
DSM
Singlet | Live | CD45+ | CD3+ | CD8+
5.60
11.6
CD8
IFNγ
B
% effector-memory of CD8+ cells
0.0518
Control
DSM
C
% IFNγ+ of CD8+ cells
% CD8 effector-memory of CD8+ cells
Control
LH 14
D
% CD45+ Cells
DCs
cDC1
cDC2
Control
DSM
% Maturation (CD80+CD86+) of DCs
E
Control
DSM
Singlet | Live | CD45+ | CD11c+
CD80
CD86
F
% CD11c+ DCs
% cDC1 cells
CD80+
CD86+
MHCII+
Control
DSM
G
% CD45+ Cells
DCs
cDC1
cDC2
Control
DSM
H
MHCII MFI
EPS dose
Unstimulated
210 EPS
DSM EPS
B71 EPS

Figure S8

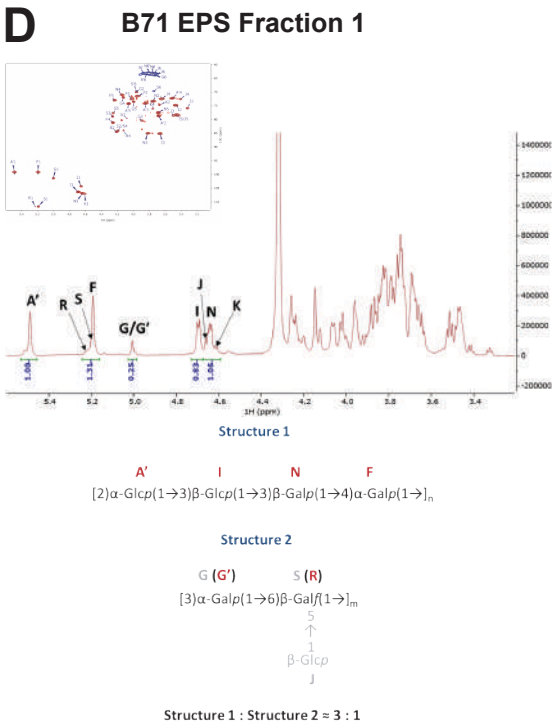


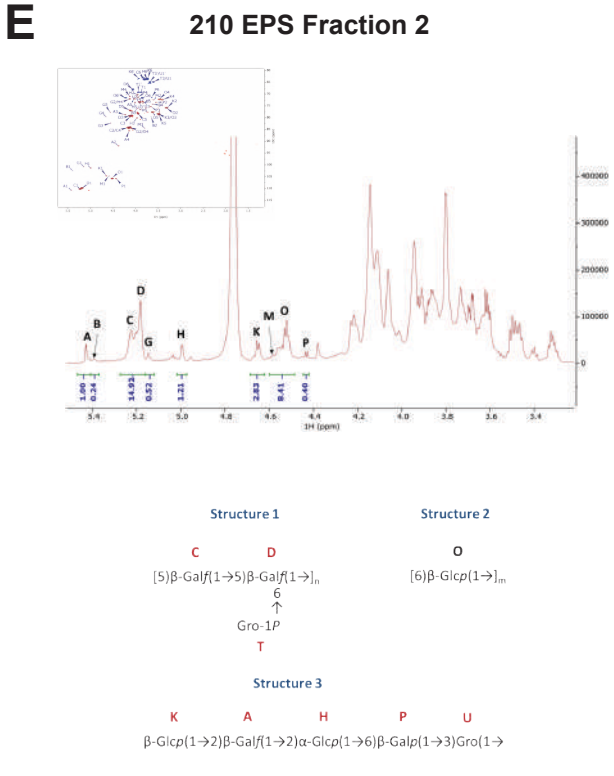


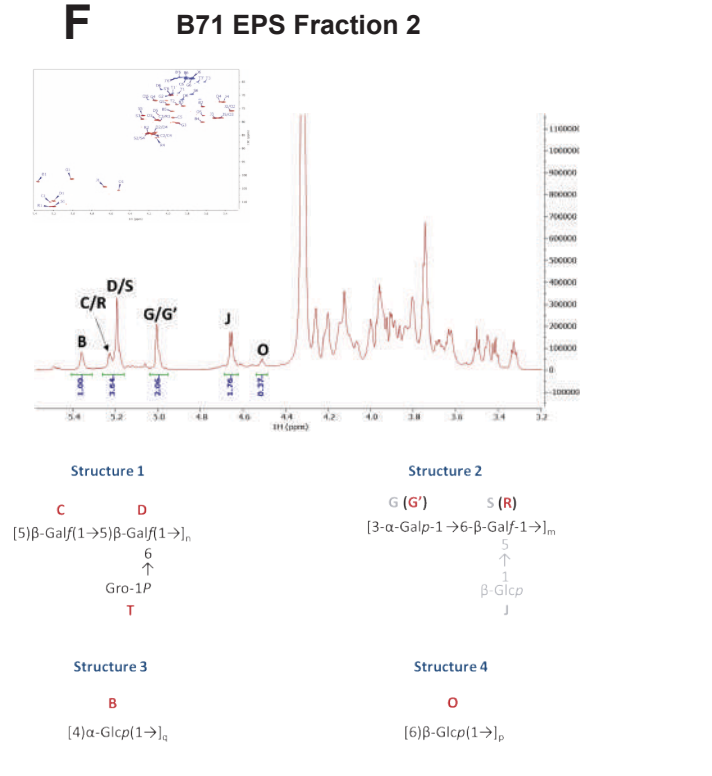
C

Sample Name	Molecular Weight (kDa) of SEC fractions			
	Fraction 1	Fraction 2	Fraction 3	Fraction 4
EPS 210	> 200 (V_0)	29.1	2.2	-
EPS B71	> 200 (0_0)	19.4	3.5	2.2

V_0 = void volume of Superose 12 SEC column







Supplementary Figure Legends

Figure S1. The *B. pseudocatenulatum* 210-induced immune phenotype is not primarily associated with gross changes in lymphoid infiltration but is accompanied by tumour-associated macrophage repolarisation. (A) Quantification of lymphoid cell infiltration in BRPKp110 primary tumours following 210 administration. n = 6–7. (B) Quantification of T helper cell differentiation states in BRPKp110 tumours. n = 6–7. (C) Quantification of IFNγ+ and IL-4+ CD4+FOXP3− T helper cells in BRPKp110 tumours. n = 6–7. (D) Quantification of IL-2+ CD4+FOXP3− T helper cells in BRPKp110 tumours. n = 6–7. (E) Quantification of IFNγ+ and IL-4+ CD4+FOXP3− T helper cells in 4T1 tumours. n = 5–6. (F) Quantification of NK cell abundance and TNFα, IFNγ and perforin expression in BRPKp110 tumours. n = 6–8. (G) Quantification of MHCII+ and CD206+ tumour-associated macrophages in BRPKp110 and PyMT-BO1 tumours. n = 5–7. Statistical significance was assessed by two-tailed unpaired t test. *P < 0.05.

Figure S2. Administration of *B. pseudocatenulatum* 210 does not significantly alter serum metabolite levels in untargeted analyses. (A) PCoA score plots of serum metabolite profiles from BRPKp110- and PyMT-BO1-bearing animals treated with PBS control or 210; shaded ellipses indicate 95% confidence intervals. BRPKp110, n = 5–6; PyMT-BO1, n = 4–5. (B) Differential metabolite significance plots for BRPKp110 and PyMT-BO1 sera following 210 treatment. (C) Heatmaps showing the top differentially abundant serum metabolites in BRPKp110 and PyMT-BO1-bearing animals following 210 treatment. Statistical significance was assessed by two-tailed unpaired t test with FDR correction.

Figure S3. *B. pseudocatenulatum* 210 is transiently detectable after oral administration, does not colonise tumours, and acts independently of secondary commensals.
(A) Quantification of culturable 210 colonies recovered from stomach, small intestine, caecum and large intestine of germ-free monocolonised mice at the indicated timepoints. n = 4. (B) Quantification of *B. pseudocatenulatum* 210 GroEL gene abundance by qPCR in wild-type small intestine, caecum and large intestine following administration. n = 4. (C) Time-course of faecal GroEL gene abundance following 210 administration. (D) Standard curve for GroEL qPCR using serial dilutions of 210 DNA and controls. (E) Representative aerobic and anaerobic culture plates and quantification of bacterial colonies recovered from MMTV-PyMT tumours at different anatomical sites. (F) Endpoint BRPKp110 tumour volumes following antibiotic pre-treatment and subsequent supplementation with vehicle or 210. n = 7–9. Statistical significance was assessed by one-way ANOVA with Tukey's multiple-comparisons test. *P < 0.05.

Figure S4. *B. pseudocatenulatum* 210 EPS-induced anti-tumour immunity is not accompanied by major changes in alternative lymphoid effector populations or tdLN chemokines. (A) Quantification of iNOS+, Arg1+ and PD-L1+ tumour-associated macrophages in BRPKp110 primary tumours following 210 EPS administration. n = 7. (B) Quantification of lymphoid cell infiltration in BRPKp110 primary tumours following 210 EPS administration. n = 7. (C) Quantification of IL-2+ CD4+FOXP3− T helper cells and TNFα, IFNγ and perforin expression by NK1.1+ cells in BRPKp110 tumours following 210 EPS administration. n = 6–7. (D) Quantification of IFNγ+ and IL-4+ CD4+FOXP3− T helper cells in BRPKp110 tumours following 210 EPS administration. n = 6–7. (E) Quantification of CCR7+ CD8+ T cells in blood and tumour following 210 EPS administration. (F) Quantification of CCL19 and CCL21 levels in BRPKp110 tumour-draining lymph nodes following

treatment with control, 210, or 210 EPS.
Statistical significance was assessed by two-tailed unpaired t test. *P < 0.05.

Figure S5. RNASeq identifies differential gene expression in BMDCs following *B. pseudocatenulatum* 210 EPS stimulation. (A) Volcano plot showing differentially expressed genes in BMDCs treated with 210 EPS versus PBS control. Upregulated genes are shown in red, downregulated genes in blue. (B) Heatmap of differentially expressed genes in BMDCs treated with 210 EPS versus PBS control. Genes with adjusted P ≤ 0.05 were considered differentially expressed.

Figure S6. Putative EPS biosynthetic loci are highly variable across *Bifidobacterium* strains used in this study. (A) Predicted architecture of putative EPS biosynthetic loci in *B. pseudocatenulatum* 210. (B) Homology maps comparing 210 loci with those of *B. choerinum* LH506, *B. longum* B71, *B. longum* NCIMB 8809 and *B. bifidum* LH80. Gene functions were predicted from combined blastp, RefSeq protein database and dbCAN3 analyses as described in Methods.

Figure S7. *B. pseudocatenulatum* DSM20438 recapitulates key immune features of 210, whereas LH14 does not. (A) Quantification and representative flow cytometry plots of IFNγ+TNFα+ CD8+ T cells in BRPKp110 tumours following DSM20438 treatment. n = 7–8. (B) Quantification of CD8+ effector-memory differentiation in BRPKp110 tumours following DSM20438 treatment. n = 7–8. (C) Quantification of IFNγ+ CD8+ T cells and CD8+ effector-memory differentiation following LH14 treatment. n = 6. (D) Quantification of circulating DCs, cDC1 and cDC2 subsets, and mature (CD80+CD86+) DCs following DSM20438 treatment. n = 7–8. (E) Representative flow cytometry plots of mature tumour DCs following DSM20438 treatment. (F) Quantification of CD80, CD86 and MHCII expression on tumour DCs and cDC1 cells following DSM20438 treatment. n = 7–8. (G) Quantification of DC, cDC1 and cDC2 frequencies in tdLNs following DSM20438 treatment. n = 7–8. (H) Dose-response analysis of MHCII mean fluorescence intensity and CD80+CD86+ maturation in BMDCs stimulated for 24 h with purified EPS from 210, DSM20438 or B71. Statistical significance was assessed by two-tailed unpaired t test. ****P < 0.0001, ***P < 0.001, **P < 0.01, *P < 0.05.

Figure S8. SEC fractionation and NMR analysis reveal structural heterogeneity of purified 210 EPS and B71 EPS. (A) Size exclusion chromatography traces of purified 210 EPS and B71 EPS showing three and four fractions, respectively. (B) On-cell STD NMR analysis of 210 EPS fractions 1–3, showing highest binding-associated signal for fraction 1. (C) Estimated molecular weights of SEC fractions from 210 EPS and B71 EPS. (D) NMR spectrum and proposed structures identified in B71 EPS fraction 1. (E) NMR spectrum and proposed structures identified in 210 EPS fraction 2. (F) NMR spectrum and proposed structures identified in B71 EPS fraction 2.

Supplementary Tables

Supplementary Table 1

Species	Strain designation	Proven-ience	Host	Host gender	Geographical location	Birth mode	Birth weight (g)	Diet at sampling	Age at sampling (d)
Bifidobacterium bifidum	LH_80	in-house	Human infant	Male	Norfolk, UK	Emergency caesarean	508	Formulae	150
Bifidobacterium pseudocatenulatum	210	in-house	Human infant	Female	Norfolk, UK	Vaginal	3500	Breast milk	159
Bifidobacterium choerinum	LH_506	in-house	Barbary sheep	n/a	Norfolk, UK	n/a	n/a	n/a	n/a
B. longum subsp. longum	NCIMB 8809	public	Human infant	n/a	n/a	n/a	n/a	n/a	n/a
B. longum subsp. longum	B_71	in-house	Human infant	Male	Berkshire, UK	Vaginal	n/a	Formulae	70
Bifidobacterium pseudocatenulatum	DSM204387	public	Human infant	n/a	n/a	n/a	n/a	n/a	n/a
Bifidobacterium pseudocatenulatum	LH14	in-house	Human infant	Male	Norfolk, UK	Vaginal	3500	Breast milk	102

Supplementary Table 2A: ^{1}H and ^{13}C NMR chemical shifts of sugar residues identified from 210 EPS fraction 1 NMR spectra. Values in boldface are glycosylated or substituted positions.

No.	Residue		Chemical shift (ppm)						HMBC	NOESY
			1	2	3	4	5	6		
F	**4-α-Gal*p***	^{1}H	5.18	3.92	4.04	4.11	4.25	3.84	**J3**	**J3**
		^{13}C	98.4	71.2	71.8	**81.5**	73.9	62.9		
I	**4-α-Glc*p***	^{1}H	4.97	3.62	3.87	3.71	4.23		**F4**	**F4**
		^{13}C	102.6	74.3	74.1	**80.6**	73.3			
J	**3,6-β-Gal*p***	^{1}H	4.66	3.74	3.78	4.17	3.80	3.75/3.61	**N3 Lac2**	**N3**
		^{13}C	106.7	72.3	**80.2**	68.0	76.1	**71.5**		
N	**3-β-Gal*p***	^{1}H	4.53	3.73	3.84	4.18	3.74	3.80/3.74	**I4**	**I4**
		^{13}C	105.4	72.9	**84.9**	71.2	77.7	63.8		
Lac	**Lactate**	^{1}H	-	3.91	1.32				**J6**	**J6**
		^{13}C	183.2	**80.5**	21.1					

Supplementary Table 2B. The chemical shifts table for the minor residue identified in EPS 210 SEC fraction 1 NMR spectra whose inter-residue could not be identified. Values in boldface are glycosylated or substituted positions

No.	Residue		Chemical shift (ppm)						HMBC	NOESY
			1	2	3	4	5	6		
		SEC Peak 1								
G	3-Hex	^{1}H	5.14	4.13	4.54	3.95				
		^{13}C	100.6	72.0	**82.3**	**79.2**				
L	3-β-Galp	^{1}H	4.61	3.68	3.77	4.15				
		^{13}C	107.1	74.6	**76.1**	**68.0**				

Supplementary Table 3: Monosaccharide compositions and total carbohydrate content in EPS 210 and EPS 871 samples.

Sugar residue	EPS 210 (400 µg)		EPS 871 (400 µg)	
	Weight (µg)	mol %	Weight (µg)	mol %
Arabinose (Ara)	1.8	0.8	3.8	1.3
Rhamnose (Rha)	0.7	0.3	0.9	0.3
Fucose (Fuc)	0.3	0.1	0.3	0.1
Xylose (Xyl)	2.4	1.1	2.2	0.8
Glucuronic Acid (GlcA)	2.1	0.7	3.9	1.1
Mannose (Man)	3.9	1.5	2.1	0.6
Galactose (Gal)	182.7	67.8	186.8	55.5
Glucose (Glc)	73.8	27.4	134.2	39.9
N-Acetylglucosamine (GlcNAc)	1.2	0.3	1.6	0.4
Lactate-substituted Galactose	Detected	Detected	ND	ND
Total	**268.8**	**100.0**	**335.9**	**100.0**
% CHO	**67.2**		**84.0**	

ND: Not detected

Supplementary Table 4: Relative percentage of each detected linked glycosyl residue in EPS 210 and EPS 871 samples.

Glycosyl residue	Relative % area	
	Sample: EPS 210	**Sample: EPS 871**
t-Ara*f*	0.2	0.2
t-Xyl*p*	0.1	ND
2-Rha*p*	0.1	0.1
t-Man*p*	0.4	0.2
t-Glc*p*	2.6	7.9
t-Hex*f*	0.8	0.2
t-Gal*p*	0.8	0.4
4-Ara*f* or 5-Ara*f*	0.3	0.3
2 Xyl*p* + 4 Xyl*p*	0.2	0.1
2,4-Rha*p*	Tr	ND
3-Glc*p*	ND	12.2
2-Man*p*	0.4	0.7
2-Glc*p*	0.9	13.8
2-Hex*f*	0.1	ND
3-Gal*p*	26.0	26.4
3-Hex*f*	0.8	0.7
6-Man*p*	0.1	0.0
6-Glc*p*	3.9	0.9
4-Gal*p* or 5-Gal*f*	37.5	17.0
4-Glc*p*	19.8	8.5
6-Gal*f*	0.6	1.9
6-Gal*p*	0.5	0.1
3,4-Gal*p*	1.0	0.5
3,4-Glc*p*	0.2	0.1
2,3-Glc*p*	ND	0.2
2,6-Man*p*	0.4	0.1
2,6 Glc*p* + 4,6-Glc*p*	0.5	0.3
4,6-Gal*p* or 5,6-Gal*f*	0.5	7.0
2,6-Hex*f*	1.4	ND
3,6-Gal*p*	ND	0.3
Total	**100**	**100**

Abbreviations: ND: not detected; Tr: traces (<0.01%); t: terminal; Ara*f*: Arabinofuranosyl; Ara*p*: Arabinopyranosyl; Glc*p*: Glucopyranosyl; Hex*f*: Hexofuranosyl; Gal*p*: Galactopyranosyl; Gal*f*: Galactofuranosyl; Man*p*: Mannopyranosyl; Rha*p*: Rhamnopyranosyl; Xyl*p*: Xylopyranosyl.

Supplementary Table 5A: ^{1}H and ^{13}C NMR chemical shifts of sugar residues identified from 210 EPS fraction 2 NMR spectra. Values in boldface are glycosylated or substituted positions.

No.	Residue		Chemical shift (ppm)						HMBC	NOESY
			1	2	3	4	5	6		
A	2-β-Gal*f*	^{1}H	5.43	4.38	4.24	4.15	4.03	3.80	**H2**	**H2**
		^{13}C	110.2	**91.8**	78.7	85.4	72.0	63.9		
C	5-β-Gal*f*	^{1}H	5.22	4.15	4.12	4.15	3.94	3.80	**D5**	**D5**
		^{13}C	110.1	84.5	79.4	84.5	**78.3**	63.9		
D	5-β-Gro1P-6-Gal*f*	^{1}H	5.19	4.14	4.11	4.14	4.09	4.06	**C5**	**C5**
		^{13}C	109.8	84.3	79.3	84.3	**77.2**	**68.0**		
H	3-α-Gal*p*	^{1}H	4.99	3.96	3.96	4.12	3.99	3.74	**P6**	
		^{13}C	101.3	70.2	**80.0**	72.0	73.5	63.8		
K	β-Glc*p*	^{1}H	4.64	3.30	3.50	3.40	3.46	3.92/3.72	**A2**	
		^{13}C	104.5	75.8	78.5	72.4	78.5	63.6		
O	6-β-Glc*p*	^{1}H	4.51	3.33	3.50	3.45	3.62	4.21/3.86	**O6**	**O6**
		^{13}C	105.7	75.8	78.5	72.5	77.7	**71.7**		
P	6-β-Gal*p*	^{1}H	4.42	3.56	3.65	3.95	3.90	3.64		
		^{13}C	105.8	73.5	75.4	71.5	76.6	**71.4**		
T	Gro-1*P*	^{1}H	3.95/3.89	3.90	3.61/3.68				**D6 (*^{31}P HMBC*)**	
		^{13}C	**69.2**	73.5	64.8					
U	3-Gro	^{1}H	3.68/3.61	3.94	3.90/3.78					
		^{13}C	65.1	73.2	**73.7**					

Supplementary Table 5B: The chemical shifts table for the minor residue identified in EPS 210 SEC fraction 2, whose inter-residue could not be identified. Values in boldface are glycosylated or substituted positions.

B	2-Hex	^{1}H	5.36	3.64	3.95	3.62	3.83			
		^{13}C	102.3	**80.0**	76.0	74.3	74.1			
G	3,4-Hex	^{1}H	5.14	4.13	4.54	4.65	4.56		M3	
		^{13}C	100.6	72.0	**82.3**	79.6	**77.7**			
M	3-β-Gal*p*	^{1}H	4.57	3.62	3.78	4.11	3.72		G4	
		^{13}C	104.6	72.4	**84.4**	71.0				

Supplementary Table 6: ^{1}H and ^{13}C NMR chemical shifts of sugar residues identified from B71 EPS fraction 1 NMR spectra. Values in boldface are glycosylated or substituted positions.

No.	**Residue**		**Chemical shift (ppm)**						**HMBC**	**NOESY**
			1	**2**	**3**	**4**	**5**	**6**		
A'	2-α-Glc*p*	^{1}H	5.48	3.69	3.85	3.52	4.07	3.81	**I3**	**I3**
		^{13}C	99.3	**78.6**	74.2	72.2	74.3	63.2		
F	4-α-Gal*p*	^{1}H	5.20	3.96	4.02	4.26	4.23	3.73	**A'2**	**A'2**
		^{13}C	99.1	71.5	72.6	**81.1**	73.0	63.4		
G/G'	3-α-Gal*p*	^{1}H	5.01	3.96	3.90	4.12	4.02	3.74	**S6**	**S6**
		^{13}C	101.4	70.0	**80.4**	72.0	73.5	63.9		
I	3-β-Glc*p*	^{1}H	4.69	3.47	3.67	3.64	3.46	3.74/3.87	**N3**	**N3**
		^{13}C	106.4	74.8	**85.1**	72.6	78.2	63.2		
J	β-Glc*p*	^{1}H	4.66	3.33	3.50	3.41	3.45	3.74	**S5**	**S5**
		^{13}C	104.3	75.9	78.6	72.6	78.5	63.7		
N	3-β-Gal*p*	^{1}H	4.64	3.76	3.82	4.15	3.69	3.76/3.78	**F4**	**F4**
		^{13}C	106.9	73.4	**85.0**	71.0	77.5	63.3		
R	6-β-Gal*f*	^{1}H	5.23	4.21	4.08	4.12			**3.93/80.06 (G'3)**	
		^{13}C	111.7	84.5	79.6	86.0				
S	5,6-β-Gal*f*	^{1}H	5.20	4.20	4.26	4.21	4.26	3.75/3.96	**G3**	**G3**
		^{13}C	111.7	84.1	78.9	84.4	**77.6**	**69.7**		

Supplementary Table 7: ^{1}H and ^{13}C NMR chemical shifts of sugar residues identified from B71 EPS fraction 2 NMR spectra. Values in boldface are glycosylated or substituted positions.

No.	Residue		Chemical shift (ppm)						HMBC	NOESY
			1	**2**	**3**	**4**	**5**	**6**		
B	4-α-Glc*p*	^{1}H	5.37	3.64	3.83	3.63	3.95	3.81/3.88	**B4**	**B4**
		^{13}C	102.3	74.3	74.0	**80.0**	76.0	63.3		
C	5-β-Gal*f*	^{1}H	5.22	4.15	4.12	4.15	3.94	3.80	**D5**	**D5**
		^{13}C	110.1	84.5	79.4	84.5	**78.3**	63.9		
D	5-β-Gro1P-6-Gal*f*	^{1}H	5.19	4.13	4.11	4.13	4.09	4.06	**C5**	**C5**
		^{13}C	109.6	84.1	79.2	84.1	**77.2**	**68.0**		
G/G'	3-α-Glc*p*	^{1}H	5.01	3.96	3.90	4.12	4.02	3.74	**S6**	**S6**
		^{13}C	101.4	70.0	**80.4**	72.0	73.5	63.9		
J	3-β-Glc*p*	^{1}H	4.66	3.33	3.50	3.41	3.45	3.74/3.91	**S5**	
		^{13}C	104.3	75.9	**78.6**	72.6	78.5	63.6		
O	6-β-Glc*p*	^{1}H	4.51	3.33	3.45	3.45	3.63	3.85/4.19	**O6**	**O6**
		^{13}C	105.7	75.9	78.5	72.5	77.7	**71.7**		
R	6-β-Gal*f*	^{1}H	5.23	4.21	4.08	4.12				**G3**
		^{13}C	111.7	84.5	79.6	86.0				
S	5,6-β-Gal*f*	^{1}H	5.20	4.20	4.26	4.21	4.26	3.75/3.96		**G3**
		^{13}C	111.7	84.1	78.9	84.4	**77.7**	**69.7**		
T	Gro-1P	^{1}H	3.94/3.89	3.89	3.61/3.67				**D6 (*^{31}P HMBC*)**	
		^{13}C	69.2	73.5	65.0					