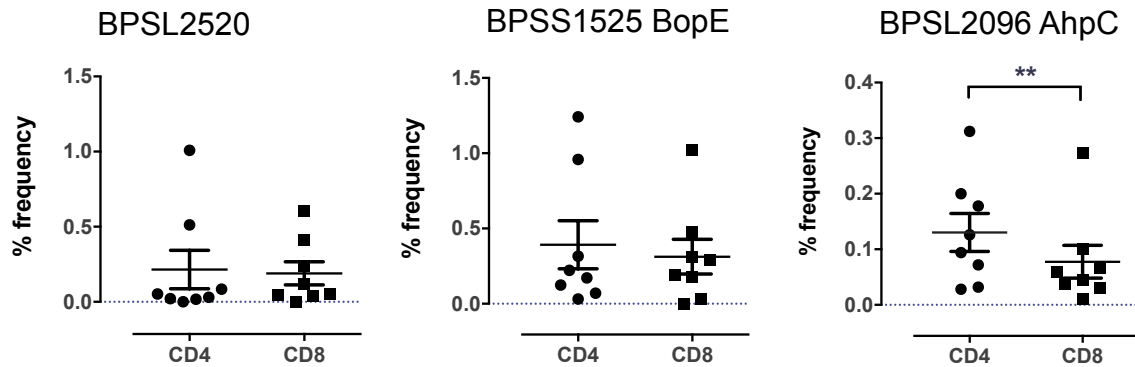


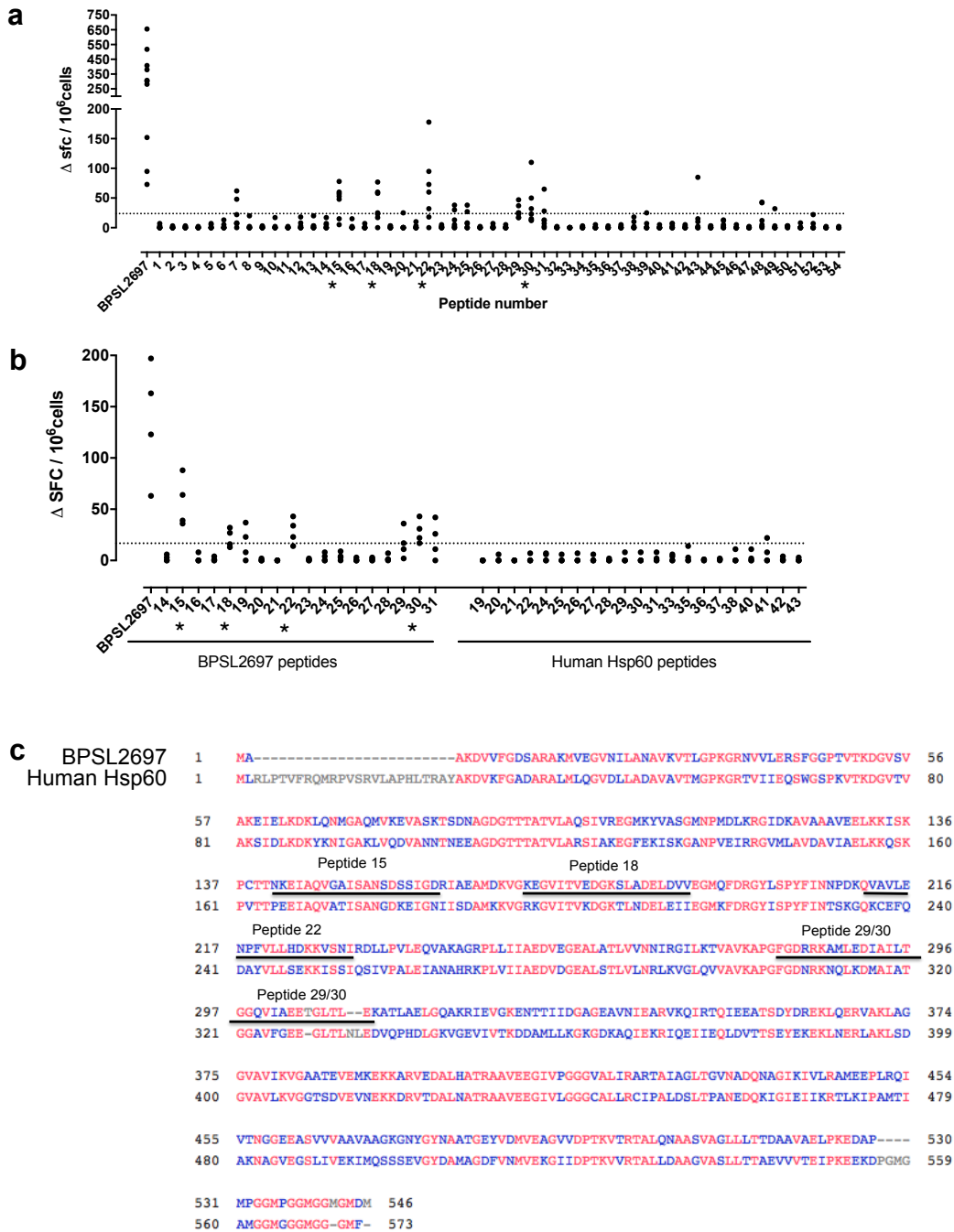
***Supplementary Information***

**Infection with *Burkholderia pseudomallei* – immune correlates of survival in acute melioidosis**

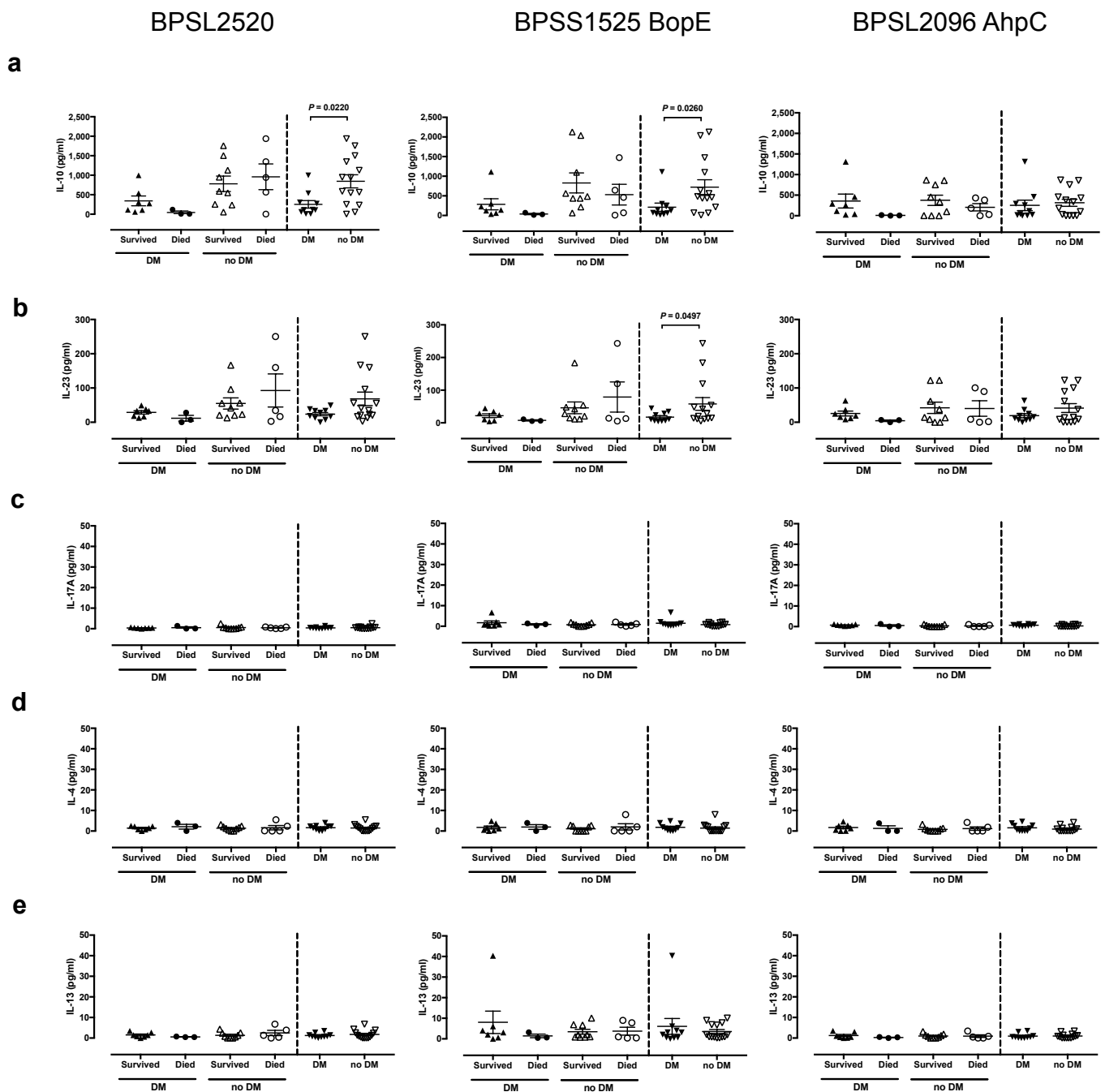
Susanna J Dunachie, Kemajitra Jenjaroen, Catherine J Reynolds, Kathryn J Quigley, Ruhena Sergeant, Manutsanun Sumonwiriya, Panjaporn Chaichana, Suchintana Chumseng, Pitchayanant Ariyaprasert, Patricia Lassaux, Louise Gourlay, Charuporn Promwong, Prapit Teparrukkul, Direk Limmathurotsakul, Nicholas PJ Day, Daniel M Altmann, Rosemary J Boyton



**Supplementary Figure 1. T cell immunity to Bp antigen BPSL2096 is predominantly CD4 T cell mediated.** (A) PBMC from 8 patients with a history of acute melioidosis 12 weeks after recovery from the acute illness were cultured in the presence of 50  $\mu\text{g}/\text{well}$  of BPSL2520, BPSS1525, BPSL2096 or media alone for 18 hours before measurement of  $\text{IFN}\gamma$  production from  $\text{CD4}^+$  (black circles) and  $\text{CD8}^+$  (black squares) T cells by intracellular cytokine staining. Data are presented as % frequency of  $\text{CD4}^+$  or  $\text{CD8}^+$  cell populations. Error bars represent mean  $\pm$  SEM and statistical significance between  $\text{CD4}^+$  and  $\text{CD8}^+$  populations was determined using the Mann Whitney test. \*\* $P = 0.0078$



**Supplementary Figure 2. T cell responses to Bp antigen BPSL2697 do not cross react with the human homolog Hsp60.** Human HLA-DR1 transgenic mice were footpad primed with BPSL2697 as an emulsion with titermax adjuvant. 10 days post immunisation popliteal draining lymph nodes were harvested and IFN $\gamma$  T cell responses to a BPSL2697 20mer peptide panel measured by ELISpot. **(a)** A second cohort of HLA-DR1 mice were footpad primed with BPSL2697 and IFN $\gamma$  T cell responses determined to the epitope rich region of the BPSL2697 peptide panel as well as the corresponding homologous region of the human Hsp60 protein. Responses were defined as positive (\*) if greater than 2SD above the mean of the media only control, which is marked as a dotted line **(b)**. Homology between the Bp protein BPSL2697 and human Hsp60 is shown **(c)**.



**Supplementary Figure 3. Individuals with a diagnosis of diabetes have reduced IL-10 and IL-23 production in response to Bp antigen stimulation than non-diabetics.** Supernatants from IFN $\gamma$  ELISpot cultures using Bp antigens BPSL2520, BPSS1525 and BPSL2096 were assayed for 23 cytokines using a Milliplex MAP Human High sensitivity T cell panel kit. Data for (A) IL-10, (B) IL-23, (C) IL-17A, (D) IL-4 and (E) IL-13 are shown. Data represent 7 diabetic survivors (black triangles), 3 diabetic fatal cases (black circles), 9 non-diabetic survivors (open triangles) and 5 non-diabetic fatal cases (open circles). Error bars represent mean  $\pm$  SEM and statistical significance between groups was determined using the Mann Whitney test.

**S1 Table. Patient cohort demographic data**

Experiment	Cohort	N	Gender		Age Year mean (range)	Diabetes status n (%)	Figure ref
			Male n (%)	Female n (%)			
1. HLA typing	Acute Melioidosis, survived	139	93 (67%)	46 (33%)	54 (19-89)	96 (69%)	S2
	Acute melioidosis, died	44	26 (59%)	18 (41%)	59 (33-84)	27 (61%)	Table
2. T cell responses and survival following acute melioidosis	Acute Melioidosis, survived	31	21 (68%)	4 (31%)	55 (33-78)	6 (46%)	1, 3, 4A, 4B
	Acute melioidosis, died	13	9 (69%)	4 (31%)	54 (30-79)	16 (52%)	
3. T cell responses in survivors 12 weeks post melioidosis versus healthy seronegative controls	Survivors 12 weeks post melioidosis	31	21 (68%)	10 (32%)	54 (32-79)	17 (55%)	1, 3, 4A, 4B
	Healthy seronegative controls	21	11 (52%)	10 (48%)	43 (33-55)	0 (0%)	
4. Antibody levels	Healthy seronegative controls	21	11 (52%)	10 (48%)	43 (33-55)	0 (0%)	5
	Melioidosis (acute & 12 weeks), survived	83	60 (72%)	23 (28%)	53 (32-79)	55 (66%)	
	Acute melioidosis, died	47	28 (60%)	19 (40%)	60 (33-84)	28 (60%)	
5. T cell responses and diabetes status	Diabetic seronegative controls	20	11 (55%)	9 (45%)	56 (23-76)	20 (100%)	6
	Acute Melioidosis, diabetic	22	12 (55%)	10 (45%)	53 (32-79)	22 (100%)	
	Acute melioidosis, non-diabetic	22	18 (82%)	4 (18%)	58 (32-79)	0 (0%)	
6. Transcriptome during acute melioidosis	Diabetic acute melioidosis, survived	8	5 (63%)	3 (37%)	56 (41-67)	8 (100%)	7
	Diabetic acute melioidosis, died	5	3 (60%)	2 (40%)	53 (40-67)	5 (100%)	
7. T cell phenotyping and epitope mapping	Survivors 12 weeks post melioidosis	26	20 (77%)	6 (23%)	54 (33-73)	21 (81%)	4C, S Fig1
8. Cytokine profiling	Diabetic acute melioidosis, survived	7	4 (57%)	3 (43%)	57 (44-79)	7 (100%)	S Fig3
	Diabetic acute melioidosis, died	3	1 (33%)	2 (67%)	51 (49-63)	3 (100%)	
	Non-diabetic acute melioidosis, survived	9	6 (67%)	3 (33%)	58 (32-78)	0 (0%)	
	Non-diabetic acute melioidosis, died	5	4 (80%)	1 (20%)	61 (48-75)	0 (0%)	

**S2 Table. The presence of HLA-B\*46, and HLA-C\*01 is associated with increased mortality following acute melioidosis.**

	Survived (N=139) n (%)	Died (N=44) n (%)	P-value	Odds Ratio	95% CI
<b>HLA-A</b>					
A*1	3 (2)	0 (0)	1	NA	NA
A*2	61 (44)	21 (47)	0.7	1.2	0.6-2.3
A*3	1 (1)	1 (2)	0.4	3.2	0.2-52
A*11	78 (56)	24 (55)	0.9	0.9	0.5-1.9
A*24	41 (29)	11 (25)	0.6	0.8	0.4-1.7
A*26	3 (2)	1 (2)	1	1.1	0.1-10.4
A*29	0 (0)	1 (2)	0.2	NA	NA
A*30	10 (7)	4 (9)	0.7	1.3	0.4-4.3
A*32	2 (1)	0 (0)	1	NA	NA
A*33	31 (22)	9 (20)	0.8	0.9	0.4-2.1
A*34	7 (5)	3 (7)	0.7	1.4	0.3-5.6
A*68	3 (2)	1 (2)	1	1.1	0.1-10.4
A*74	5 (4)	0 (0)	0.3	NA	NA
<b>HLA-B</b>					
B*7	14 (10)	4 (9)	1	0.9	0.3-2.9
B*8	5 (4)	0 (0)	0.3	NA	NA
B*13	34 (24)	13 (30)	0.5	1.3	0.6-2.8
B*15	4 (3)	0 (0)	0.6	NA	NA
B*18	23 (17)	4 (9)	0.3	0.5	0.2-1.5
B*27	12 (9)	2 (5)	0.5	0.5	0.1-2.3
B*35	10 (7)	2 (5)	0.7	0.6	0.1-2.9
B*38	12 (9)	3 (7)	1	0.8	0.2-2.9
B*39	13 (9)	3 (7)	0.8	0.7	0.2-2.6
B*40	1 (1)	0 (0)	1	NA	NA
B*44	9 (6)	4 (9)	0.5	1.4	0.4-4.9
<b>B*46</b>	<b>30 (22)</b>	<b>19 (43)</b>	<b>0.005</b>	<b>2.8</b>	<b>1.3-5.7</b>

B*47	1 (1)	0 (0)	1	NA	NA
B*48	0 (0)	1 (2)	0.2	NA	NA
B*51	15 (11)	3 (7)	0.6	0.6	0.2-2.2
B*52	3 (2)	1 (2)	1	1.1	0.1-10.4
B*54	0 (0)	1 (2)	0.2	NA	NA
B*55	3 (2)	0 (0)	1	NA	NA
B*56	6 (4)	3 (7)	0.5	1.6	0.4-6.8
B*57	0 (0)	1 (2)	0.2	NA	NA
B*58	22 (17)	5 (11)	0.5	0.7	0.2-1.9
B*60	9 (6)	3 (7)	1	1.1	0.3-4.1
B*61	3 (2)	1 (2)	1	1.1	0.1-10.4
B*62	18 (13)	10 (23)	0.1	2.0	0.8-4.7
B*69	1 (1)	0 (0)	1	NA	NA
B*75	14 (10)	1 (2)	0.1	0.2	0.0-1.6
B*76	1 (1)	0 (0)	1	NA	NA
<b>HLA-C</b>					
<b>C*1</b>	<b>32 (23)</b>	<b>21 (48)</b>	<b>0.002</b>	<b>3.1</b>	<b>1.5-6.2</b>
C*3	2 (1)	0 (0)	1	NA	NA
C*4	39 (28)	7 (16)	0.1	0.5	0.2-1.2
C*6	9 (6)	4 (9)	0.5	1.4	0.4-4.9
C*7	68 (49)	25 (57)	0.4	1.4	0.7-2.7
C*8	16 (12)	2 (5)	0.3	0.4	0.1-1.7
C*9	5 (4)	0 (0)	0.3	NA	NA
C*10	48 (35)	15 (34)	1	1.0	0.5-2.0
C*12	8 (6)	2 (5)	1	0.8	0.2-3.8
C*14	9 (6)	1 (2)	0.5	0.3	0.0-2.7
C*15	10 (9)	4 (7)	0.7	1.3	0.4-4.3

The number of individuals (n, %) carrying at least one copy of the allele is shown. Allele and genotype frequency was determined by direct counting. The odds ratio (OR) and 95% confidence interval (CI) were calculated. Allele and genotype frequency comparisons were made by Chi-square or Fisher's exact test (where <5 in a group). P values less than or equal to 0.005 were regarded as significant and are displayed in boldface. NS = not significant; NA = not applicable.

**S3 Table. Protein antigen peptide panels (10aa overlap)  
for *Burkholderia pseudomallei*, BPSL2096 (AhpC)**

<b>Peptide number</b>	<b>Sequence</b>
1	MKTVGDKLEAFTVVAAKPGF
2	FTVVAAKPGFNNHEENGQSA
3	NNHEENGQSAFETVTEASFP
4	FETVTEASFPGKWKIIYFYP
5	GKWKIIYFYPKDFTFVCPT
6	KDFTFVCPTIEVEFAKLAKQ
7	IVEFAKLAKQFEERDAVLLG
8	FEERDAVLLGGSSDNEFVKL
9	GSSDNEFVKLAWRREHKDLD
10	AWRREHKDLDKLNHYSFGDV
11	KLNHYSFGDVKGELIDQLGV
12	KGELIDQLGV RDKEAGVALR
13	RDKEAGVALRATFIVDPDNT
14	ATFIVDPDNTIQHVSVNNLN
15	IQHVSVNNLNVGRSPEEILR
16	VGRSPEEILRILDGLQTDDEL
17	ILDGLQTDDELCPNRAIGGATL



**S4 Table. Protein antigen peptide panels (10aa overlap) for *Burkholderia pseudomallei*, BPSL2697 (GroEL)**

Peptide number	Peptide sequence
1	MAAKDVVFGDSARAKMVEGV
2	SARAKMVEGVNILANAVKVT
3	NILANAVKVTLGPKGRNVVL
4	LGPKGRNVVLERSFGGPTVT
5	ERSFGGPTVTKDGVSVAKEI
6	KDGVSVAKEIELKDKLQNMG
7	ELKDKLQNMGAQMVKEVASK
8	AQMVKEVASKTSDNAGDGTT
9	TSDNAGDGTTTATVLAQSIV
10	TATVLAQSIVREGMKYVASG
11	REGMKYVASGMNPMDLKRG I
12	MNPMDLKRGIDKAVAAVEE
13	DKAVAAVEELKKISKPC TT
14	LKKISKPC TTNKEIAQVGAI
15	NKEIAQVGAI SANS DSSIGD
16	SANS DSSIGDRIAEAMDKVG
17	RIAEAMDKVGKEGVITVEDG
18	KEGVITVEDGKSLADELDVV
19	KSLADELDVVEGMQFDRGYL
20	EGMQFDRGYLSPYFINNPK
21	SPYFINNPKQVAVLENPFV
22	QVAVLENPFVLLHDKKVSNI
23	LLHDKKVSNI RDLLPVLEQV
24	RDLLPVLEQVAKAGRPLLI I
25	AKAGRPLLI IAEDVEGEALA
26	AEDVEGEALATLVVNNIRGI
27	TLVVNNIRGILKTVAVKAPG
28	LKTVAVKAPGFGDRRKAMLE
29	FGDRRKAMLE DIAILTGGQV
30	DIAILTGGQVIAEETGLTLE
31	IAEETGLTLEKATLAELGQA
32	KATLAELGQAKRIEVBKENT
33	KRIEVBKENTTIIDGAGEAV
34	TIIDGAGEAVNIEARVKQIR
35	NIEARVKQIR TQIEEATSDY
36	TQIEEATSDYDREKLQERVA
37	DREKLQERVA KLAGGVAVIK
38	KLAGGVAVIKVGAATEVEMK
39	VGAATEVEMKEKKARVEDAL
40	EKKARVEDALHATRAAVEEG
41	HATRAAVEEGIVPGGGVALI
42	IVPGGGVALIRARTAIAGLT
43	RARTAIAGLTGVNADQNAGI
44	GVNADQNAGIKIVLRAMEEP
45	KIVLRAMEEPLRQIVTNGGE
46	LRQIVTNGGEEASVVVAVA
47	EASVVVAVAAGKGNYGNA
48	AGKGNYGNAATGEYVDMVE
49	ATGEYVDMVEAGVVDPTKVT
50	AGVVDPTKVTRTALQNAASV
51	RTALQNAASVAGLLLTDDAA
52	AGLLLTDDAAVAELPKEDAP
53	VAELPKEDAPMPGGMPGGMG
54	MPGGMPGGMGGMGMDM

**S5 Table. Protein antigen peptide panels (10aa overlap) for HSP60**

Peptide number	Peptide sequence	Peptide number	Peptide sequence
1	MLRLPTVFRQMRPVSR	37	NRLKVGLQVVAVKAPG
2	RQMRPVSRVLAPHLTR	38	VVAVKAPGFGDNRKNQ
3	VLAPHLTRAYAKDVKF	39	FGDNRKNQLKDMAIAT
4	AYAKDVKFGADARALM	40	LKDMAIATGGAVFGEE
5	GADARALMLQGVDLLA	41	GGAVFGEEGLTLNLED
6	LQGVDLLADAVAVTMG	42	GLTLNLEDVQPHDLGK
7	DAVAVTMGPKGRTVII	43	VQPHDLGKVGIVTK
8	PKGRTVIIIEQSWGSPK	44	VGEVIVTKDDAMLLKG
9	EQSWGSPKVTKDGVTV	45	DDAMLLKGKGDKAQIE
10	VTKDGVTVAKSIDLKD	46	KGDKAQIEKRIQEIEE
11	AKSIDLKDKYKNIGAK	47	KRIQEIEEQLDVTTSE
12	KYKNIGAKLVQDVANN	48	QLDVTTSEYEKEKLNE
13	LVQDVANNTNEEAGDG	49	YEKEKLNLERLAKLSDG
14	TNEEAGDGTTTATVLA	50	RLAKLSDGVAVLVKGG
15	TTTATVLARSIAKEGF	51	VAVLVKGGTSDVEVNE
16	RSIAKEGFEEKISKGAN	52	TSDVEVNEKKDRVTD
17	EKISKGANPVEIRRGV	53	KKDRVTDALNATRAAV
18	PVEIRRGVMLAVDAVI	54	LNATRAAVEEGIVLGG
19	MLAVDAVIAELKKQSK	55	EEGIVLGGGCALLRCI
20	AELKKQSKPVTTPEEII	56	GCALLRCIPALDSLTP
21	PVTTPEEIIAQVATISA	57	PALDSLTPANEDQKIG
22	AQVATISANGDKEIGN	58	ANEDQKIGIEI IKRTL
23	NGDKEIGNIISDAMKK	59	IEI IKRTLKIPAMTIA
24	IISDAMKKVGRKGVIT	60	KIPAMTIAKNAGVEGS
25	VGRKGVITVKDGKTLN	61	KNAGVEGSLIVEKIMQ
26	VKDGKTLNDELEIIEG	62	LIVEKIMQSSSEVGYD
27	DELEIIEGMKFDRGYI	63	SSSEVGYDAMAGDFVN
28	MKFDRGYISPYFINTS	64	AMAGDFVNMVEKGIID
29	SPYFINTSKGQKCEFQ	65	MVEKGIIDPTKVVRTA
30	KGQKCEFQDAYVLLSE	66	PTKVVRTALLDAAGVA
31	DAYVLLSEKKISSIQS	67	LLDAAGVASLLTTAEV
32	KKISSIQSIVPALEIA	68	SLLTTAEVVVTEIPKE
33	IVPALEIANAHRKPLV	69	VVTEIPKEEKDPGMGA
34	NAHRKPLVIIAEDVDG	70	EKDPGMGAMGGMGGGM
35	IIAEDVDGEALSTLVL	71	MGGMGGGMGGGMF
36	EALSTLVLNRLKVGLQ		

**S6 Table. Patient cohort comorbidity data**

Presence or absence of diabetes Number of patients (n)	Diabetes 123		No diabetes 60		P value (Fisher)
Mean age (range, SD)	53 (19-89, 12.1)		58 (25-88, 14.4)		<b>0.056*</b>
1 or more non-DM comorbidity	45	37%	32	53%	<b>0.038</b>
2 or more non-DM comorbidity	11	9%	16	27%	<b>0.003</b>
3 or more non-DM comorbidity	1	1%	3	5%	0.1
Age ≥ 65 yrs	19	15%	17	28%	<b>0.048</b>
Renal disease	20	16%	13	22%	0.41
Alcohol excess	3	2%	7	12%	<b>0.015</b>
IHD	14	11%	9	15%	0.64
Lung disease	0	0%	1	2%	-
Liver disease	2	2%	5	8%	<b>0.039</b>

\* Age comparison by Mann-Witney

**S7 Table: Top 100 genes upregulated in human PBMCs upon stimulation with Bp**

Gene name	Fold-Change	P value
PTGS2	17.76	8.58E-15
IL6	16.02	3.58E-13
CSF2	12.50	8.60E-17
CCL20	7.90	7.85E-12
IL1A	7.06	1.87E-10
TNFAIP6	6.21	1.15E-12
IL1F9	6.05	1.01E-10
IDO1	6.00	3.18E-12
EBI3	5.91	3.91E-14
CCL3L1	5.80	3.29E-15
INDO	5.79	5.36E-12
IL24	5.73	5.06E-10
CXCL2	5.64	2.35E-13
CCL3	5.59	8.29E-15
SERPINB7	4.54	2.66E-09
IL1B	4.49	5.12E-06
IL19	4.41	1.64E-07
IL23A	3.66	2.33E-10
CCL3L3	3.59	1.22E-11
F3	3.47	6.40E-10
MIR155HG	3.32	8.54E-17
RIPK2	3.30	2.20E-12
SOD2	3.25	1.30E-12
CXCL1	3.23	1.02E-06
TFPI2	3.09	3.51E-10
NAMPT	2.96	2.11E-08
MMP1	2.92	8.02E-06
GJB2	2.88	9.56E-10
LOC654103	2.80	1.75E-08
OSM	2.78	3.87E-08
MMP10	2.77	1.32E-08
SLC25A37	2.74	3.00E-08
IRAK2	2.72	1.16E-10
C1QTNF1	2.63	1.68E-07
IL2RA	2.60	1.23E-08
TM4SF1	2.57	8.18E-07
ADORA2A	2.46	8.99E-09
IER3	2.46	2.10E-09
PFKFB3	2.43	2.96E-10
LOC387763	2.42	1.84E-09
LOC653778	2.35	8.23E-08
CKB	2.30	4.82E-12

DDIT4	2.30	2.91E-11
MAP1LC3A	2.29	1.02E-06
DUSP5	2.29	5.23E-10
SERPINA1	2.14	5.68E-06
IL8	2.13	3.58E-05
MARCKS	2.12	8.31E-09
BMP6	2.11	2.69E-09
GRAMD1A	2.09	1.47E-06
MAP3K8	2.08	2.95E-10
SERPINB2	2.07	2.58E-06
KIAA1199	2.05	0.000587364
PANX2	2.01	4.44E-10
LAD1	2.01	1.11E-05
LOC143666	2.00	3.16E-10
OSGIN2	1.99	5.22E-10
SYTL3	1.95	3.61E-14
VNN3	1.95	1.94E-06
NFKBIZ	1.95	3.24E-09
ADA	1.94	4.92E-07
MPZL1	1.94	7.19E-10
CCL4L2	1.93	3.12E-07
PDE4B	1.93	1.83E-09
TNFRSF4	1.93	9.29E-10
LAG3	1.89	4.51E-09
CXCL6	1.88	4.10E-05
NFKB2	1.88	1.87E-12
TRAF1	1.87	6.73E-10
RNF144B	1.87	4.94E-08
GBP4	1.87	6.31E-09
BASP1	1.85	1.05E-09
SLC25A24	1.85	4.06E-06
D2HGDH	1.84	2.16E-09
DLL1	1.83	2.22E-06
FAM108C1	1.82	2.92E-06
PALLD	1.81	2.42E-08
GBP5	1.81	1.13E-08
LOC728835	1.79	3.73E-06
CD7	1.79	2.34E-12
PMAIP1	1.78	2.48E-10
SGPP2	1.78	1.93E-07
ZC3H12A	1.76	1.46E-08
NFKBIA	1.74	7.96E-11
SLA2	1.74	3.25E-12
LOC728830	1.73	8.61E-05
CYP4B1	1.73	1.50E-07
EBF1	1.73	2.25E-08

DENND5A	1.72	9.50E-09
SOCS1	1.72	2.04E-08
ITGB8	1.71	1.28E-08
CD83	1.69	6.00E-10
TNFAIP3	1.68	1.36E-10
CXCR4	1.67	2.91E-09
SOCS3	1.66	6.98E-05
USP36	1.65	2.50E-11
IL15RA	1.65	6.16E-12
ITGA1	1.64	1.32E-08
DUSP1	1.64	3.09E-05
IL10	1.64	1.51E-05

**S8 Table: Top 100 genes downregulated in human PBMCs upon stimulation with Bp**

Gene name	Fold-Change	P value
CSF1R	-9.68	5.33E-20
TGFBI	-9.08	8.87E-13
MMP9	-6.73	4.14E-15
FPR3	-6.32	1.54E-14
GPNMB	-6.25	1.65E-12
RNASE1	-5.72	9.57E-10
FUCA1	-5.34	2.84E-11
CYP27A1	-5.29	6.34E-18
SPRED1	-5.22	3.49E-18
FCN1	-4.94	9.70E-14
CYBB	-4.83	8.87E-15
OLR1	-4.57	1.38E-09
FBP1	-4.53	1.00E-11
TIMP2	-4.48	7.45E-16
CCR1	-4.37	2.69E-13
SLAMF8	-4.28	7.31E-18
SLCO2B1	-4.28	4.59E-12
LYZ	-4.27	1.91E-09
AIF1	-4.27	4.18E-15
TNS3	-4.23	6.85E-18
CD9	-4.04	2.19E-12
CD163	-4.01	9.06E-11
CLEC4A	-3.86	3.09E-12
IFI30	-3.81	2.24E-15
SPP1	-3.78	9.68E-12
CTSB	-3.68	4.19E-16
FLJ22662	-3.63	2.36E-12
CCL7	-3.49	2.39E-07
IL18BP	-3.42	5.16E-12
CST3	-3.41	4.54E-15
C4ORF18	-3.40	1.52E-11
EGR2	-3.31	5.18E-12
KCTD12	-3.30	2.51E-12
CD36	-3.26	4.85E-10
GSN	-3.24	9.81E-15
FCGRT	-3.23	9.35E-16
MT1H	-3.20	9.00E-08
CEBPA	-3.15	3.79E-16
ACP5	-3.14	1.69E-12
ANXA2P1	-3.12	4.94E-14
C5AR1	-3.12	2.95E-16
FAM20C	-3.11	8.02E-15

RAB7B	-3.09	5.28E-15
MERTK	-3.01	1.43E-09
CLEC5A	-2.98	3.55E-09
NPL	-2.97	1.46E-13
DAB2	-2.97	1.60E-16
CAMK1	-2.96	3.17E-13
SLC38A6	-2.90	2.84E-17
IGSF6	-2.90	6.86E-13
RGL1	-2.89	1.61E-09
DUSP6	-2.88	1.68E-15
C19ORF59	-2.86	9.36E-05
LHFPL2	-2.84	2.54E-11
SLC11A1	-2.81	6.76E-08
FLVCR2	-2.79	1.10E-14
AADAACL1	-2.76	4.93E-14
RNASE6	-2.75	1.41E-12
SCARB2	-2.74	2.62E-14
ADAP2	-2.74	3.97E-11
GPR162	-2.70	2.11E-15
SIRPA	-2.68	1.20E-17
SGK1	-2.65	1.97E-12
STAB1	-2.64	2.88E-12
CCL2	-2.63	4.57E-06
HK3	-2.62	9.33E-13
ABCC3	-2.62	4.60E-14
FOS	-2.61	7.57E-12
CCL24	-2.61	9.72E-06
SGK	-2.59	2.03E-12
LIPA	-2.59	2.26E-08
PMP22	-2.57	5.15E-07
CXCL16	-2.56	5.53E-07
DPYSL2	-2.55	9.10E-16
PLD3	-2.55	8.47E-12
AVPI1	-2.54	5.87E-13
PLA2G7	-2.50	1.66E-09
MT1G	-2.50	3.50E-06
TMEM51	-2.50	1.31E-11
LMNA	-2.46	6.38E-12
ITGAM	-2.45	3.35E-14
ENG	-2.45	1.90E-19
EMP1	-2.42	2.53E-07
ANXA2	-2.42	7.99E-17
TYROBP	-2.39	4.09E-13
EMR2	-2.38	1.27E-09
PAPSS1	-2.38	5.78E-16
MAFB	-2.37	2.10E-11



CD14	-2.36	3.01E-05
FER1L3	-2.36	3.30E-12
DHRS9	-2.36	1.17E-07
SCG5	-2.36	4.06E-06
CD68	-2.35	3.04E-11
FGL2	-2.34	2.30E-09
LILRB2	-2.32	8.32E-10
PK4	-2.30	9.45E-10
CD276	-2.29	1.96E-17
CLEC12A	-2.27	5.31E-08
SORT1	-2.25	7.85E-13
CX3CR1	-2.23	7.46E-11