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Antibody-independent mechanisms regulate the establishment of
 chronic *Plasmodium* infection

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27 Supplementary Figures

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Supplementary Figure 1. Principal Components Analysis plot of transcriptomes from *P. chabaudi* AS parasites collected at acute and chronic phases of infection in wild-type and mutant mice. Wild-type C57Bl/6 (blue), B6. μ MT-/- (red) and TCR α -/-(green) mice were infected by mosquito bites. Parasite mRNA were collected during the acute (open circles) and chronic (close circles) of infection. Gene expression does not differ greatly between parasites in wild-type (blue), μ MT-/- (red) or TCRaKO (green) mice. Changes between the acute and chronic phases are consistent between the three genetic backgrounds.



41 genome assembly

Pir genes are shown in the context of the subtelomeric region from the telomeric repeats
to the last *pir* or *fam-a* gene. Those genes co-expressed across mice over the course of
infection are highlighted in orange. Genes are coloured by subfamily.



47 Supplementary Figure 3. Similarity of *pir* genes between different subtelomeres.

48 Protein sequences for all pir genes were BLASTed against each other (blastall 2.2.25; E ≥ 0.01 ; sequence identity $\geq 80\%$). Matches between a node and itself were ignored. 49 50 For any two nodes the greatest match length was taken, rather than summing the match 51 lengths for the two nodes. For each pair of subtelomeres, the total length of the hits was determined and used as the edge weight in the graph. Edges with <300 amino acids were 52 53 excluded. The maximum number of amino acids was 1972. The figure shows two 54 particularly similar arrays of pir genes: L1-rich 3L, 6L, 6R and S7-rich 3R, 13R, 4L and 55 9L. Visual inspection of the subtelomeres suggests that 4R is similarly rich in L1 pirs as 56 the first group, while 12L and 2L are rich in S7s like the latter group. 3L has both L1-rich 57 and S7-rich regions, which explains why it links the two principal subtelomere types.



58 59

60 Supplementary Figure 4. Heatmap of *pir* gene expression at ChAPL and AAPL loci. 61 10 wild-type C57Bl/6 mice, 5 B6.µMT-/- mice and 3 TCRα-/- mice were infected by 62 mosquito bites. Each column represents values obtained from an individual mouse. The 63 first nine columns represent samples collected during the acute phase. The next ten 64 columns represent samples collected during the chronic phase. Pir genes were ordered by 65 their position in the genome. On the side, numbers indicate chromosomes and letters 66 indicate the location on that chromosome: L for left hand end, R for right hand end. 67 ChAPLs and AAPLs are highlighted. For each gene, red represents its maximal 68 expression, green its minimal expression. The maximum and minimum values for each 69 gene are shown in a separate heatmap.



73 intergenic regions of ChAPL genes. (A) Sequence logo of the identified motif. Z-score 74 23.9, robustness 7/10 (B) Motif location in intergenic region (excluding UTRs) upstream 75 of pir genes from ChAPLs and AAPLs. Blue arrows indicate an instance of the 76 TAACCTA motif on the forward strand, red arrows the reverse strand. The motif occurs 77 in 19/27 ChAPL genes tested. Reliable upstream intergenic regions could not be 78 determined for all genes: there are a total of 32 ChAPL and 28 AAPL genes. The motif 79 rarely occurs upstream of AAPL genes (3/22 tested) and only in the reverse orientation. 80 Motifs in the forward orientation tend to occur closer to the transcription start site (TSS) 81 of the gene, whereas those in the reverse orientation are more distal to the TSS.





87 subsequently passaged into naïve recipient mice after one, three, four or six weeks (n=15)

88	mice per group). (B) B6.µMT donor mice were infected by mosquito bites and parasites
89	were passaged into naïve wild type recipient mice after six weeks ($n=5$ mice). For both
90	experiments, we show parasitaemia and changes in temperature, weight, and red blood
91	cell density over the course of infection in recipient mice compared to wild type mice
92	directly infected by mosquito bites (MT; light blue dotted line) or with serially blood
93	passaged parasites (SBP; light red dotted line). Each dot represents the average ±SEM.



97 Supplementary Figure 7. Course of infections initiated with acute clones

98 One donor mouse was infected by mosquito bites. Individual P. chabaudi AS parasites 99 were subsequently cloned during the acute phase of infection. After their expansion, 100 recipient mice were infected with clonal populations of parasites (n= 5 mice per group). 101 For each clonal infection, we show parasitaemia and changes in temperature and weight 102 over the course of infection in recipient mice compared to mice directly infected by 103 mosquito bites (MT; light blue dotted line) or with serially blood passaged parasites 104 (SBP; light red dotted line). Each dot represents the average ±SEM. The red arrow 105 indicates the clone derived from the acute phase that reached relatively high parasitaemia 106 and induced significant temperature loss in naïve mice.



109 Supplementary Figure 8. Heatmap of *pir* gene expression at ChAPLs and AAPLs in

110 three acute and three chronic clones.

One donor mouse was infected by mosquito bites. Individual *P. chabaudi* AS parasites were subsequently cloned during the acute and chronic phase of infection. After their expansion, recipient mice were infected with clonal populations of parasites (n= 3 mice per group). For each clonal infection, parasite RNA were extracted during the late trophozoite stage after completion of seven cycles of schizogony. Each column represents the values obtained from 3 individual mice infected with the same clonal population of parasites. The first three columns represent clones from the acute phase, the next three columns represent clones from the chronic phase. *Pir* genes were ordered by their position in the genome. On the side, chromosomes numbers are indicated as well as the location on that chromosome: L for left hand, R for right hand. ChAPLs and AAPLs are highlighted. For each gene, red represents its maximal expression, green its minimal expression. The maximum and minimum values for each gene are shown in a separate heatmap.



126 127

Days post-infection

27 Supplementary Figure 9. Course of infection in mice infected with chronic clones

One donor mouse was infected by mosquito bites. Individual parasites were subsequentlycloned during the chronic phase of infection. After their expansion, recipient mice were

infected with clonal populations of parasites (n= 5 mice per group). For each clonal
infection, we show parasitaemia and changes in temperature and weight over the course
of infection in recipient mice compared to mice directly infected by mosquito bites (MT;
light blue dotted line) or with serially blood passaged parasites (SBP; light red dotted
line). Each dot represents the average ±SEM.



136 Supplementary Figure 10. Generation of, and competition between mCherry-tagged

137 MT parasites and NeonGreen-tagged SBP parasites.

138 (A) The modified p230p locus of chromosome 3 (illustrated for *Pc*EFp230p mCherry) 139 and the location of PCR primers used to verify integration. (B) PCR verification of 140 integration. Integration of the plasmid was verified with primer set P2/P3 and the loss of 141 the wild type locus shown using primer set P1/P3. Lanes 1-4 contain samples from 142 parasites transfected with PcEFp230p mCherry (1), PcEFp230p mNeonGreen (2), PcAS 143 wild type parasites (3), water control (4). (C) Southern Blot analysis of EcoRV digested 144 genomic DNA to show integration of PcEFp230p mNeonGreen and 145 PcEFp230p mCherry, lane 1, PcEFp230p mNeonGreen; lane 2, PcEFp230p mCherry, 146 lane 3 wild-type DNA. TgDHFR probe hybridises to restriction fragments of 12.3 kb and 147 12.4kb (lane 1) and 9.8 kb and 10.7 kb (lane 2), showing integration (12.3 kb; 9.8 kb) and 148 linearised plasmid (12.4; 10.7) hybrids, respectively. (D) mCherry (Fluo 1) tagged 149 parasites were Mosquito-Transmitted (MT), and neonGreen (Fluo 2) tagged parasites 150 were Serially Blood-Passaged (SBP). Different proportions of the two were used to infect recipient mice by IP injection of 10^5 parasites (n= 10 mice per group). We show the 151 152 percentages of parasites being SBP or MT as defined by flow cytometry at days 0, 5, 8, 153 12 and 28 post-infection (P.I.).



154

155 Supplementary Figure 11. Course of mixed infections performed with transgenic

156 and wild type parasites.

157 (A) mCherry (Fluo 1) tagged parasites were Mosquito-Transmitted (MT), and neonGreen (Fluo 2) tagged parasites were Serially Blood-Passaged (SBP). Different proportions of 158 the two were used to infect recipient mice by IP injection of 10^5 parasites (n= 10 mice per 159 group). As a control, a group of recipient mice was infected by IP injection of 10⁴ SBP 160 161 parasites. We show the parasitaemia and changes in temperature and weight change over 162 the course of infection for each group compared to mice infected with 100% MT 163 parasites (light blue dotted line) or 100% SBP parasites (light red dotted line). Each dot 164 represents the average ±SEM. (B) The same experiment was performed with wild type 165 MT and SBP parasites. We show maximum parasitaemia, temperature change, weight 166 change (upper panel) and time of recrudescence (lower panel) for each group and for 167 mice infected with 100% MT parasites (blue dotted line) or 100% SBP parasites (red 168 dotted line). Each dot represents the average ±SEM. Each group has been compared to 169 mice infected with 10^5 SBP parasites (*P<0.05; **P<0.01; ***P<0.001, two-sided Mann 170 Whitney Test).



173 Supplementary Figure 12: Competition between SBP and MT parasites in mice

174 deficient of T-, B- and phagocytic cells.

175 (A) Flow cytometric analysis was performed on splenocytes from B6.RAG-1-/- mice

- 176 mice 24h after treatment with clodronate liposomes or saline (n=2 per group). The bars
- 177 represent the total number of each cell type. Gating strategies are shown for Neutrophils
- 178 (Neu), Monocytes (Mo); Macrophages (M Φ) and Dendritic cells (DC) on the plots and
- below the chart. (B) mCherry (Fluo 1) tagged parasites were Mosquito-Transmitted
- 180 (MT), and mNeonGreen (Fluo 2) tagged parasites were Serially Blood-Passaged (SBP).
- 181 Different proportions of the two were used to infect recipient mice (B6.RAG-1-/- mice

182 treated with saline or clodronate liposomes) by i.p. injection of 10^5 parasites (n= 5 mice

183 per group). The percentage of parasites being SBP (as determined by flow cytometry) is

184 indicated. Each dot represents the average ± standard error of the mean (SEM).

185



189



192 (A) Course of infection of *P. chabaudi* CB in C57Bl/6 mice. Samples were taken where

A P. chabaudi CB in C57 Bl/6 mice

B P. chabaudi AS in Grammomys sudaster rats

194	surdater. (C) The CB isolate of <i>P. chabaudi</i> has a very similar genome sequence to that of
195	the AS isolate. We observed that the orthologous AAPLs and ChAPLs behave in a very
196	similar way, with 6L and 6R highly expressed during the chronic infection, while AAPL
197	loci were much reduced in expression. (D) Infections of thicket rats with P. chabaudi AS
198	again highlighted lower expression of AAPLs and higher expression of ChAPLs during
199	the chronic stage of infection.



Supplementary Figure 14. Chronic pir gene expression in P. berghei.

(A) Course of infection of *P. berghei* ANKA in Brown Norway rats. Samples were taken

- where indicated with a red arrow. (B) P. berghei has a significantly diverged repertoire of
- pir genes from P. chabaudi and their arrangement in the subtelomeres did not allow
- identification of gene clusters resembling P. chabaudi AAPLs or ChAPLs. However,

209 during chronic infection of brown rats with this species we observed a general reduced

210 expression of *pir* genes. The small number which we could identify as more highly

211 expressed in chronic infections were enriched for L2 *pirs*, rather than L1s as we saw in *P*.

212 chabaudi. (C) The chronicity-associated L2s we observe in P. berghei are from a small

- 213 number of highly similar loci, which is this respect, are reminiscent of *P. chabaudi*
- 214 ChAPLs and AAPLs. Furthermore the *P. berghei* L2s have protein sequence features
- 215 (long variable region, second putative transmembrane domain) more similar to P.
- 216 *chabaudi* ChAPL L1s than *P. chabaudi* L2s. These results suggest that these L2 genes
- 217 may perform the same function in *P. berghei* as the ChAPL L1s in *P. chabaudi*.

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PCHAS_0626400 PCHAS_0601000 PCHAS_0626500 PCHAS_0301700 PCHAS_0626800 PCHAS_0302000 PCHAS_0600800 PCHAS_0301500 PCHAS_0601200 PCHAS_0626300 PCHAS_0318500 PCHAS_0319100

PBANKA_1400061

PCHAS_0301600 PCHAS_0626200 PCHAS_0626600 PCHAS_0301900 PCHAS_0600900 PCHAS_0601100 PCHAS_0301400 PCHAS_0626400 PCHAS_0601000 PCHAS_0626500 PCHAS_0301700 PCHAS_0626800 PCHAS_0302000 PCHAS_0600800 PCHAS_0301500 PCHAS_0601200 PCHAS_0626300 PCHAS_0318500 PCHAS_0319100

PBANKA_1040561 PBANKA_1400061

PBANKA_0500781

PBANKA_1000081

PCHAS_0301600 PCHAS_0626200 PCHAS_0626600 PCHAS_0301900 PCHAS_0600900 PCHAS_0601100 PCHAS_0301400 PCHAS_0626400 PCHAS_0601000 PCHAS_0626500 PCHAS_0301700 PCHAS_0626800 PCHAS 0302000 PCHAS_0600800 PCHAS_0301500 PCHAS_0601200 PCHAS_0626300 PCHAS_0318500 PCHAS_0319100

PBANKA_1000081

PCHAS_0301600 PCHAS 0626200

PCHAS_0626600

PCHAS_0301900

PCHAS_0600900

PCHAS_0601100

PCHAS_0301400

PCHAS_0626400

PCHAS_0601000

PCHAS_0626500

PCHAS_0301700

PCHAS_0626800

PCHAS_0302000 PCHAS 0600800

PCHAS_0301500

PCHAS_0601200

PCHAS_0626300 PCHAS_0318500 PCHAS_0319100

PBANKA_0216000

PBANKA_1040561

PBANKA_1400061

PBANKA_0300100

PBANKA_0623700 PBANKA_1200061

PBANKA_0500781 PBANKA_1000081



Red gene ids = P. chabaudi ChAPL L1s Black gene ids = P. chabaudi L2s Green gene ids = P. berghei L2s



219	Supplementary	Figure 15.	Protein	sequence	alignment	of <i>P</i> .	chabaudi	ChAPL	L1
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- 220 pirs, L2 pirs and P. berghei L2 pirs.
- *P. berghei* L2 *pirs* share several features with *P. chabaudi* ChAPL L1s. They are the
 longest *pirs* in the respective genomes. This is due to a long, variable central domain
 between the highly conserved N and C terminal domains as well as an extended C
 terminal domain which contains a second putative transmembrane domain.
- 225

226 Supplementary Tables

227

228 Supplementary Table 1. Lists of gene differentially expressed between acute and

229 chronic phases for WT, and KO parasites

- 230 See Excel file "Supplementary Table 1"
- 231

Up/Down in DE between acute and Fold change Gene family Genes chronic in wt mice (%) chronic range 118 (56%) 11/107 -8.5 - +3.6 Pir 210 -4.6 - +3.8 Fam-a 145 35 (24%) 7/28 Lysophospholipase 29 6 (21%) 1/5 -4.3 - +2.7 Fam-c 22 3 (14%) 0/3 -3.6 - +1.4 Fam-b 27 3 (11%) 0/3 -3.7 - -1.1 21 0 (0%) 0/0 Fam-d n/a

232 Supplementary Table 2.

233

234 Supplementary Table 3. Comparison of v2 and v3 assemblies of the *Plasmodium*

235 chabaudi AS nuclear genome.

236

	P. chabaudi AS v2 (9)	P. chabaudi AS v3 (this work)			
Assembly size (Mb)	18.83	18.94			
Contigs/chromosomes	37/14	14/14			
N50 (Mb)	1.63	1.63			
Gaps	3	0			
Telomeric sequences/telomeres	14/28	28/28			
Pir genes	198	212			
Fam-a genes	134	145			

237

238

240 Supplementary Table 4. List of genes belonging to AAPL and ChAPL gene clusters.

241 Clusters were defined as those pir genes coexpressed across acute and chronic phases 242 within a particular subtelomere, plus any pir genes not coexpressed, but between 243 coexpressed pirs. These extra genes can be identified by a 'No' in the 'Coexpressed' 244 column.

Locus	Locus	Gene id	Pir	Coexpressed?
type	name		subfamily	
ChAPL	3L	PCHAS_0300900	L4	Yes
		PCHAS_0301100	L4	Yes
		PCHAS_0301200	L4	Yes
		PCHAS_0301400	L1	Yes
		PCHAS_0301500	L1	Yes
		PCHAS_0301600	L1	Yes
		PCHAS_0301700	L1	Yes
		PCHAS_0301800	L4	Yes
		PCHAS_0301900	L1	Yes
		PCHAS_0302000	L1	Yes
		PCHAS_0302100	L4	Yes
ChAPL	6L	PCHAS_0600700	L1	Yes
		PCHAS_0600800	L1	Yes
		PCHAS_0600900	L1	Yes
		PCHAS_0601000	L1	Yes
		PCHAS_0601100	L1	Yes
		PCHAS_0601200	L1	Yes
ChAPL	6R	PCHAS_0626200	L1	Yes
		PCHAS_0626300	L1	Yes
		PCHAS_0626400	L1	Yes
		PCHAS_0626500	L1	Yes
		PCHAS_0626600	L1	Yes
		PCHAS_0626700	L4	Yes
		PCHAS_0626800	L1	Yes
		PCHAS_0626900	L4	Yes
		PCHAS_0627100	L4	Yes
AAPL	2L	PCHAS_0200011	L4	Yes
		PCHAS_0200015	S7	Yes
		PCHAS_0200021	S1	Yes
		PCHAS_0200025	S7	Yes
		PCHAS_0200031	L4	Yes
AAPL	3R	PCHAS_0319600	L4	Yes
		PCHAS_0319700	S7	Yes

		PCHAS_0319800	S7	No
		PCHAS_0319900	S7	No
		PCHAS_0320000	S7	Yes
		PCHAS_0320100	L4	Yes
		PCHAS_0320200	S1	Yes
AAPL	4L	PCHAS_0400111	S1	Yes
		PCHAS_0400121	L4	Yes
		PCHAS_0400200	S7	Yes
		PCHAS_0400300	S7	Yes
		PCHAS_0400400	S7	Yes
		PCHAS_0400500	L4	Yes
AAPL	12L	PCHAS_1200200	S7	Yes
		PCHAS_1200300	L4	Yes
		PCHAS_1200400	S7	Yes
		PCHAS_1200500	S7	Yes
		PCHAS_1200600	S7	Yes
		PCHAS_1200700	S7	Yes
AAPL	13R	PCHAS_1370900	L1	Yes
		PCHAS_1371100	L1	Yes
		PCHAS_1371200	S7	Yes
		PCHAS_1371300	S7	Yes
		PCHAS_1371400	S7	Yes
		PCHAS_1371500	S1	No
		PCHAS_1371600	S7	Yes

- 246 Supplementary Table 5. Expression levels of *pir* genes during chronic and acute
- 247 stages of infections of wild type mice, B6μMT, B6.TCRα-/- mice with P. chabaudi
- 248 AS, wild type mice with P. chabaudi CB, brown rat with P. berghei and
- 249 Grammoymys surdaster with P. chabaudi AS.
- 250 See Excel file "Supplementary Table 5.xlsx".
- 251
- 252 Supplementary Table 6. Expression levels of *pir* genes in cloned parasite lines
- 253 See Excel file "Supplementary Table 6.xlsx".
- 254
- 255 Supplementary Table 7. Genes where expression level during the acute phase was
- 256 correlated with the time at recrudescence.
- 257 See Excel file "Supplementary Table 7.xlsx".
- 258
- 259 Supplementary Table 8. Primer sequences used to verify integration of plasmid
- 260 constructs.

Primer	Sequence
P1	TATCTATAAGGGAAGATACTCAT
P2	
	GTAAAGGGTTAATTCTTATATG
P3	
	CTTCTATGTTGGATACACTTTGC

Supplementary Table 9. Differentially expressed *pir* genes in *P. berghei* chronic infections. We compared both acute and both chronic samples with an FDR < 0.1 and then both acute samples against each of the chronic samples individually with the same cutoff. This allowed for that fact that we have relatively few replicates and therefore low statistical power as well as that we expect *pir* changes not to be consistent between replicates as this is what we observed in *P. chabaudi*. We find that while L2s are always upregulated in chronic infection, they are never downregulated.

270

	Pir subfamily	Acute vs. Chronic	Acute vs. Chronic 1	Acute vs. Chronic 2
Pirs up in	Pseudogenes	1	2	1
chronic	L1			1
	L2	1	1	4
	L3			
	S1		2	
	S2			
	S4			
	S5			
	S8		1	
Pirs down	Pseudogenes	2	2	8
in chronic	L1	4	6	4
	L2			
	L3	1	1	1
	S1	5	5	10
	S2	4	4	6
	S4	2	2	6
	S5			
	S8		1	2

272 Supplementary Table 10. RNA-seq libraries used in the study.

273 All samples are from blood stage parasites isolated at 11:00 (reverse light cycle), when >90% of the parasites were at the late 274 trophozoite stage of development. In the sample names T1 = acute phase and T2 = chronic phase, while numbers such as 21-1 refer to 275 a particular mouse, so T1 21-1 and T2 21-1 refer to acute and chronic phase samples from mouse 21-1. The library type column 276 describes the fragment size of the library e.g. 200-450bp, the number of PCR cycles e.g. 10 and the type of sequencing e.g. 100bp PE 277 = 100bp read lengths from both ends of the fragment. Description includes point of infection (acute = peak parasitaemia, chronic = first recrudescence), host genotype (Mus musculus C57BL/6 B6.wt = wild type, B6.µMT-/-, B6.TCRa-/-; Gs = Grammomys surdaster; 278 Rn = Rattus norvegicus), and parasite isolate/species (AS = P. c. chabaudi AS; CB = P. chabaudi CB; Pb = P. berghei ANKA) and 279 280 clone name for the cloned samples.

Sample	Accession	Library	Description	Days	%	%	%	%	%
name	number	type		post	parasitaemia	rings	trophozoites	schizonts	gametocytes
				infection					
		200-450,	Acute,	9	3.13				
		10,	B6.wt, AS						
T1_20-14	ERS346505	100bp PE				1	98	1	0
		200-450,	Acute,	9	1.3				
		10,	B6.wt, AS						
T1_21-1	ERS346506	100bp PE				0	99	1	0
		200-450,	Acute,	9	1.16				
		10,	B6.wt, AS						
T1_21-2	ERS346508	100bp PE				1	97	2	0
		200-450,	Acute,	9	3.59				
		10,	B6.wt, AS						
T1_21-4	ERS346513	100bp PE				1.6	97.6	0.8	0
T1_21-14	ERS346519	200-450,	Acute,	9	1.95	8	89	3	0

		10,	B6.wt, AS						
		100bp PE							
		200-450,	Chronic,	34	0.17				
		10,	B6.wt, AS						
T2_20-14	ERS346512	100bp PE				1	99	0	0
		200-450,	Chronic,	43	0.2				
		10,	B6.wt, AS						
T2_21-1	ERS346510	100bp PE				4	96	0	0
		200-450,	Chronic,	39	0.22				
		10,	B6.wt, AS						
T2_21-2	ERS346509	100bp PE				0	99	0	1
		200-450,	Chronic,	32	0.62				
		10,	B6.wt, AS						
T2_21-4	ERS346504	100bp PE				1	98	0	1
		200-450,	Chronic,	36	0.33				
		10,	B6.wt, AS						
T2_21-14	ERS346499	100bp PE				0	98	0	2
		200-450,	Acute,	9					
		10,	B6.wt, AS						
T1_42-1	ERS423636	100bp PE			8.8	1	99	0	0
		200-450,	Acute,	9					
		10,	B6.wt, AS						
<u>T1_42-7</u>	ERS423642	100bp PE			9	4.5	95.5	0	0
		200-450,	Acute,	9	7.2				
		10,	B6.µMT, AS						
<u>T1_43-2</u>	ERS423654	100bp PE				1.5	98.5	0	0
		200-450,	Acute,	9	10.5				
		10,	В6.μМТ,						
T1_43-6	ERS423656	100bp PE				1	99	0	0
T1 45-2	ERS423647	200-450,	Acute,	9	2.64	0.5	99.5	0	0

		10,	B6.wt, AS						
		100bp PE							
		200-450,	Acute,	9	3.6				
		10,	B6.wt, AS						
T1_45-6	ERS423649	100bp PE				1.5	98.5	0	0
		200-450,	Acute,	9					
		10,	B6.µMT, AS						
T1_46-4	ERS423657	100bp PE			6.05	25	74.5	0.5	0
		200-450,	Acute,	9					
		10,	B6.µMT, AS						
T1_46-6	ERS423638	100bp PE			11.2	7.5	92.5	0	0
		200-450,	Acute,	9					
		10,	B6.TCRα-/-,						
T1_47-1	ERS423644	100bp PE	AS		8.25	3	97	0	0
		200-450,	Acute,	9					
		10,	B6.TCRα-/-,						
T1_47-2	ERS423650	100bp PE	AS		4.18	5	94.5	0.5	0
		200-450,	Acute,	9					
		10,	B6.TCRα-/-,						
T1_47-4	ERS423655	100bp PE	AS		33.7	4.5	95.5	0	0
		200-450,	Chronic,	31					
		10,	B6.wt, AS						
T2_42-1	ERS423640	100bp PE			0.42	0	100	0	0
		200-450,	Chronic,	30					
		10,	B6.wt, AS						
T2_42-7	ERS423637	100bp PE			0.2	0	98	0	2
		200-450,	Chronic,						
		10,	B6.µMT, AS						
T2_43-2	ERS423645	100bp PE		52	3.2	0	100	0	0
T2_43-3	ERS423639	200-450,	Chronic,	64	1.68	0.5	99	0.5	0

		10,	B6.µMT, AS						
		100bp PE	• •						
		200-450,	Chronic,						
		10,	B6.µMT, AS						
T2_43-6	ERS423648	100bp PE		73	2.05	3	96.5	0	0.5
		200-450,	Chronic,						
		10,	B6.wt, AS						
T2_45-2	ERS423641	100bp PE		33	0.12	0	100	0	0
		200-450,	Chronic,						
		10,	B6.wt, AS						
T2_45-4	ERS423653	100bp PE		30	0.26	4	96	0	0
		200-450,	Chronic,						
		10,	B6.wt, AS						
T2_45-6	ERS423658	100bp PE		34	0.21	2	98	0	0
		200-450,	Chronic,						
		14,	B6.µMT, AS						
T2_46-4	ERS423652	100bp PE		59	1.1	2	97	0	1
		200-450,	Chronic,						
		10,	B6.µMT, AS						
T2_46-6	ERS423646	100bp PE		33	0.26	4	96	0	0
		200-450,	Chronic,						
		10,	B6.TCRα-/-,						
T2_47-1	ERS423659	100bp PE	AS	30	6.26	4.5	95.5	0	0
		200-450,	Chronic,						
		10,	B6.TCRα-/-,						
T2_47-2	ERS423651	100bp PE	AS	30	12.54	0	100	0	0
		200-450,	Chronic,						
		14,	B6.TCRα-/-,						
T2 47-4	ERS423643	100bp PE	AS	30	29	2	96	1.5	0.5
53-1	ERS792706	100-300,	Acute,	7	1.04	3	97	0	0

		10, 75bp	B6.wt, AS,						
		PE	clone f						
		100-300,	Acute,	7	2.7				
		10, 75bp	B6.wt, AS,						
53-2	ERS792707	PE	clone f			3	96	1	0
		100-300,	Acute,	7	3.55				
		10, 75bp	B6.wt, AS,						
53-3	ERS792708	PE	clone f			1	99	0	0
		100-300,	Acute,	7	0.86				
		10, 75bp	B6.wt, AS,						
54-1	ERS792709	PE	clone a			0	90	7	3
		100-300,	Acute,	7	2.3				
		10, 75bp	B6.wt, AS,						
54-2	ERS792710	PE	clone a			3	91	6	0
		100-300,	Acute,	7	1.8				
		10, 75bp	B6.wt, AS,						
54-3	ERS792711	PE	clone a			0	100	0	0
		100-300,	Acute,	7	2.4				
		10, 75bp	B6.wt, AS,						
55-1	ERS792712	PE	clone b	_		0	99	1	0
		100-300,	Acute,	7	7.9				
		10, 75bp	B6.wt, AS,			_			
55-2	ERS792713	PE	clone b	_		5	91	2	2
		100-300,	Acute,	7	0.07				
		10, 75bp	B6.wt, AS,				100		
55-3	ERS792714	PE	clone b	_		0	100	0	0
		100-300,	Chronic,	7	2				
		10, 75bp	B6.wt, AS,						
56-1	ERS/92/15	PE	clone k	_		1	97		1
56-2	ERS792716	100-300,	Chronic,	7	2.2	21	73	5	1

		10, 75bp	B6.wt, AS,						
		PE	clone k						
		100-300,	Chronic,	7	3.3				
		10, 75bp	B6.wt, AS,						
56-3	ERS792717	PE	clone k			29	61	10	0
		100-300,	Chronic,	7					
		10, 75bp	B6.wt, AS,						
57-1	ERS792718	PE	clone n		0.67	4	90	4	2
		100-300,	Chronic,	7					
		10, 75bp	B6.wt, AS,						
57-2	ERS792719	PE	clone n		2.65	33	64	3	0
		100-300,	Chronic,	7					
		10, 75bp	B6.wt, AS,						
57-3	ERS792720	PE	clone n		3.4	5	90	3	2
		100-300,	Chronic,	7					
		10, 75bp	B6.wt, AS,						
58-1	ERS792721	PE	clone p		2.8	11	88	1	0
		100-300,	Chronic,	7					
		10, 75bp	B6.wt, AS,						
58-2	ERS792722	PE	clone p		14.7	1	98	0	1
		100-300,	Chronic,	7					
		10, 75bp	B6.wt, AS,						
58-3	ERS792723	PE	clone p		6.2	3	94	2	1
		100-300,	Acute,	7					
		15, 75bp	B6.wt, CB						
MTCB1	ERS1390889	PE			7.9	17.3	77.8	4.6	0.2
		100-300,	Acute,						
		15, 75bp	B6.wt, CB						
MTCB2	ERS1391216	PE		7	19.3	14.9	83.3	1.4	0.4
MTCB3	ERS1391219	100-300,	Acute,	7	7.4	17.6	81.6	0.6	0.2

		15, 75bp	B6.wt, CB						
		PE							
		100-300,	Acute,						
		15, 75bp	B6.wt, CB						
MTCB4	ERS1391221	PE		7	10.1	8.2	91.3	0.4	0
		100-300,	Acute,						
		15, 75bp	B6.wt, CB						
MTCB5	ERS1391557	PE		7	9.2	8.9	91.1	0	0
		100-300,	Acute,						
		15, 75bp	B6.wt, CB						
MTCB6	ERS1391598	PE		7	11.2	11	88.0	0.88	0
		100-300,	Chronic,						
		10, 75bp	B6.wt, CB						
T2_05_6	ERS1348217	PE		59	0.09	0	100	0	0
		100-300,	Chronic,						
		10, 75bp	B6.wt, CB						
T2_05_10	ERS1348218	PE		28	0.09	3	97	0	0
		100-300,	Acute, Gs,						
		10, 75bp	AS						
681_T1	ERS1348224	PE		9	11	0	100	0	0
		100-300,	Acute, Gs,						
		10, 75bp	AS						
701_T1	ERS1348225	PE		9	21.67	0	100	0	0
		100-300,	Acute, Gs,						
		10, 75bp	AS						
703_T1	ERS1348226	PE		9	31	0	100	0	0
		100-300,	Chronic, Gs,						
		10, 75bp	AS						
681_T2	ERS1348227	PE		27	1.6	0	100	0	0
701_T2	ERS1348228	100-300,	Chronic, Gs,	27	2.5	0	100	0	0

		10 75hm	AC						
		10, 730p	AS						
		PE							
		100-300,	Chronic, Gs,						
		10, 75bp	AS						
703_T2	ERS1348229	PE		27	2.5	0	100	0	0
		100-300,	Acute, Rn,						
		10, 75bp	Pb						
PbBN1_T1	ERS1348206	PE		10	0.69	20	80	0	0
		100-300,	Acute, Rn,						
		10, 75bp	Pb						
PbBN2_T1	ERS1348207	PE		10	1.36	20	79	0	1
		100-300,	Chronic, Rn,						
		10, 75bp	Pb						
PbBN1_T2	ERS1348208	PE		15	0.06	30	70	0	0
		100-300,	Chronic, Rn,						
		10, 75bp	Pb						
PbBN2_T2	ERS1348209	PE		15	0.0.9	30	70	0	0