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Supplemental Information

Diverse CD8 T Cell Responses to Viral Infection Revealed by the Collaborative Cross

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Supplemental Figure 1

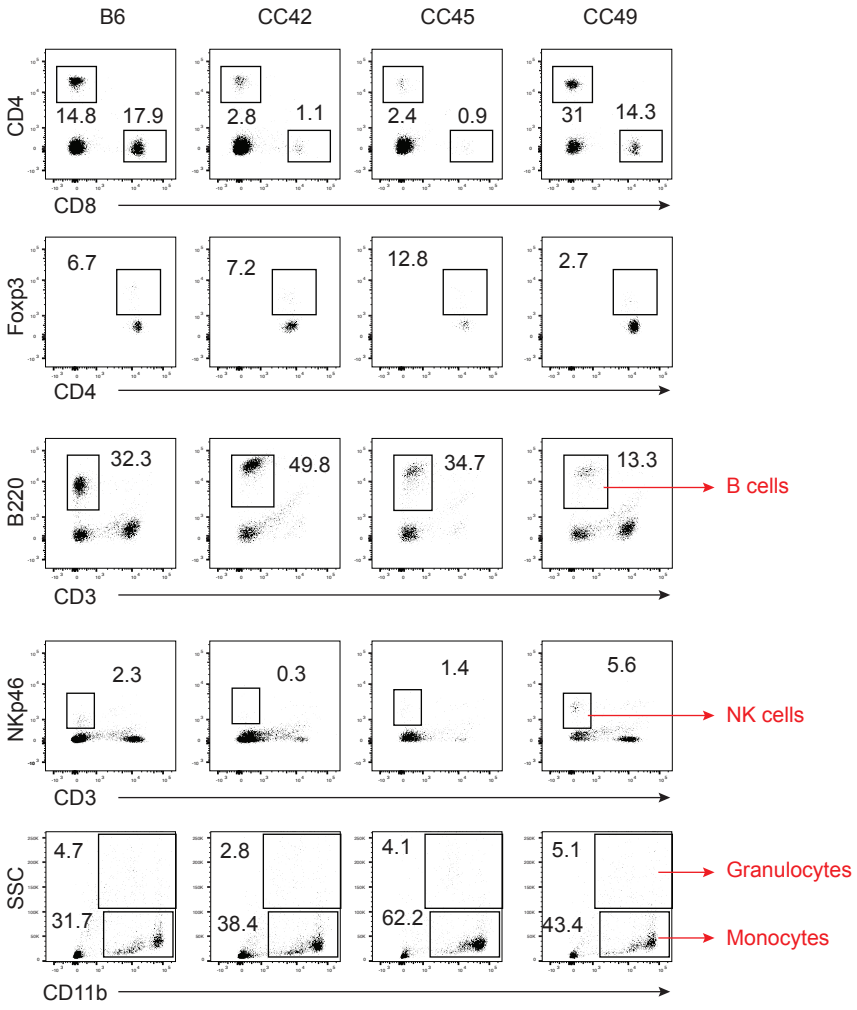

Figure S1: Gating strategy for detection of immune cell subsets prior to infection, related to Fig. 1. Representative dot plots for detection of CD4 and CD8 T cells, Foxp3+ CD4 T cells, B220+/CD3- B cells, NKp46+/CD3- NK cells, and SSChi/CD11bhi granulocytes and SSClo/CD11bhi monocytes for B6 mice and three strains of CC mice prior to infection.

Supplemental Figure 2

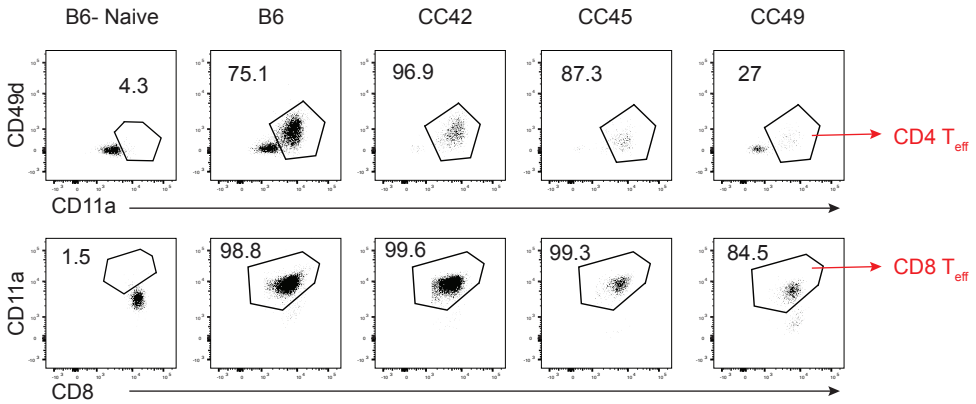

Figure S2: Gating strategy for detection of effector (Teff) CD4 and CD8 T cells, related to Fig. 2. Representative dot plots for detection of CD4 Teff (CD49dhi/CD11ahi) and CD8 Teff (CD11ahi/CD8alo) cells on d8 after LCMV-Armstrong infection for B6 mice and three strains of CC mice.

Supplemental Figure 3

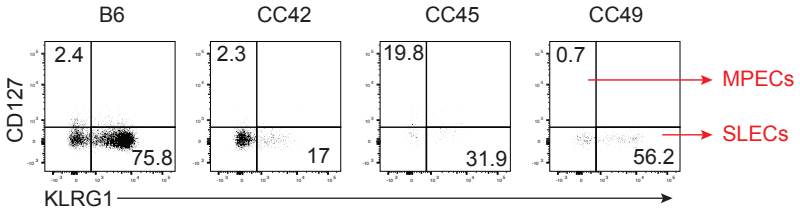

Figure S3: Gating strategy for detection of effector CD8 T cell subsets, related to Fig. 3. Representative dot plots for detection of short lived effector cells (SLECs- KLRG1hi/CD127lo) and memory precursor effector cells (MPECs- KLRG1lo/CD127hi) for gated CD8 Teff cells (CD11ahi/CD8alo) on d8 after LCMV-Armstrong infection for B6 mice and three strains of CC mice.

Supplemental Figure 4

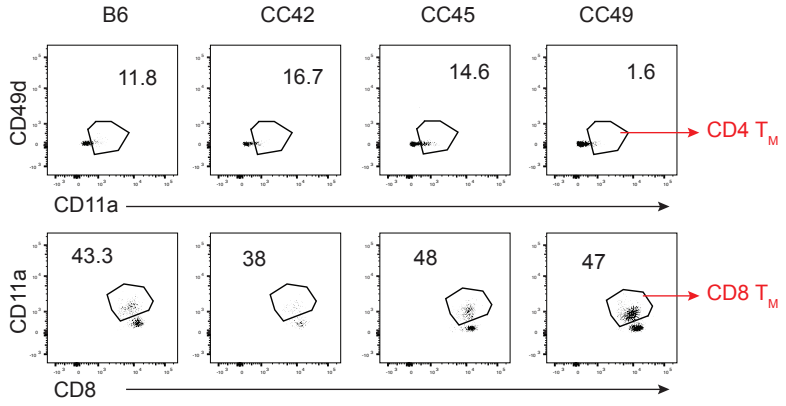

Figure S4: Gating strategy for detection of memory (TM) CD4 and CD8 T cells, related to Fig. 4. Representative dot plots for detection of CD4 TM (CD49dhi/CD11ahi) and CD8 TM (CD11ahi/CD8alo) cells on d75 after LCMV-Armstrong infection for B6 mice and three strains of CC mice.

Supplemental Figure 5

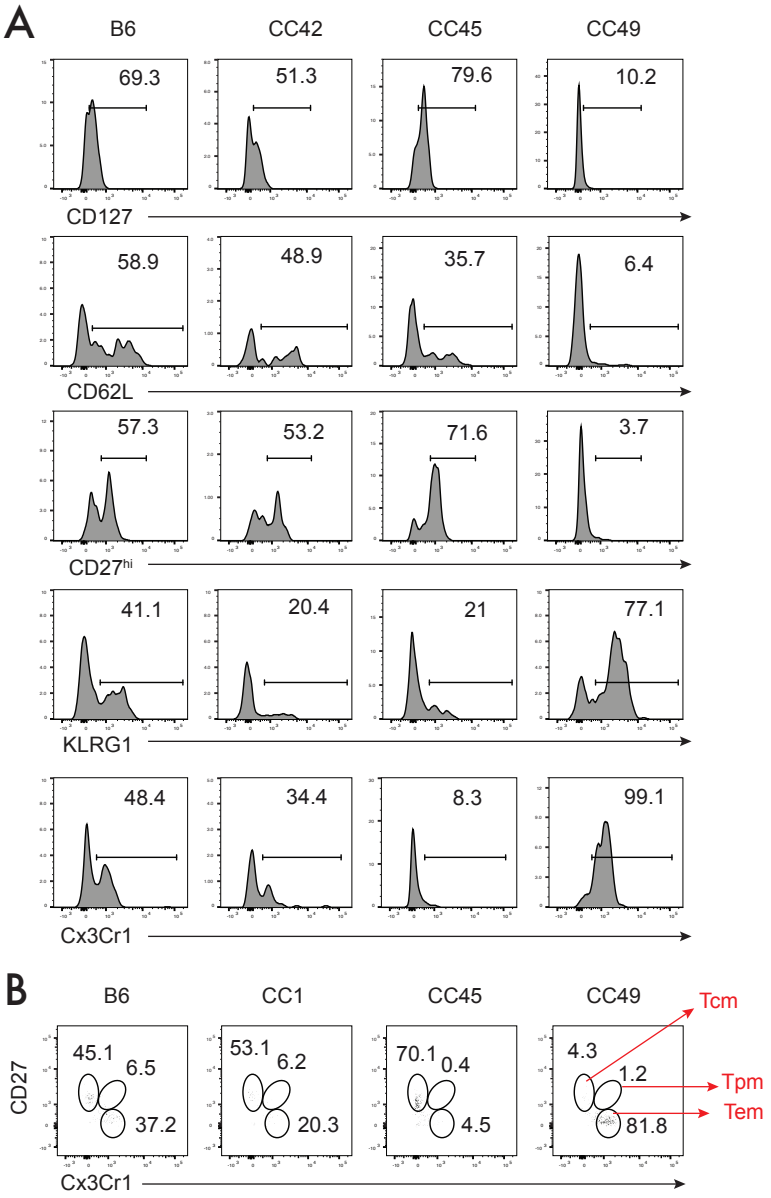

Figure S5: Gating strategy for identification of memory CD8 T cell phenotype and subset representation, related to Fig. 5. (A) Representative histograms for expression of CD127, CD62L, CD27hi, KLRG1, and Cx3Cr1 for gated CD8 TM cells (CD11ahi/CD8alo) on d75 after LCMV-Armstrong infection for B6 mice and three strains of collaborative cross (CC) mice. (B) Representative dot plots for detection of effector memory (Tem- Cx3Cr1hi/CD27lo), peripheral memory (Tpm- Cx3Cr1int/CD27hi), and central memory (Tcm- Cx3Cr1lo/CD27hi) subsets for gated CD8 TM cells (CD11ahi/CD8alo) on d75 after LCMV-Armstrong infection for B6 mice and three strains of CC mice.

Supplemental Figure 6

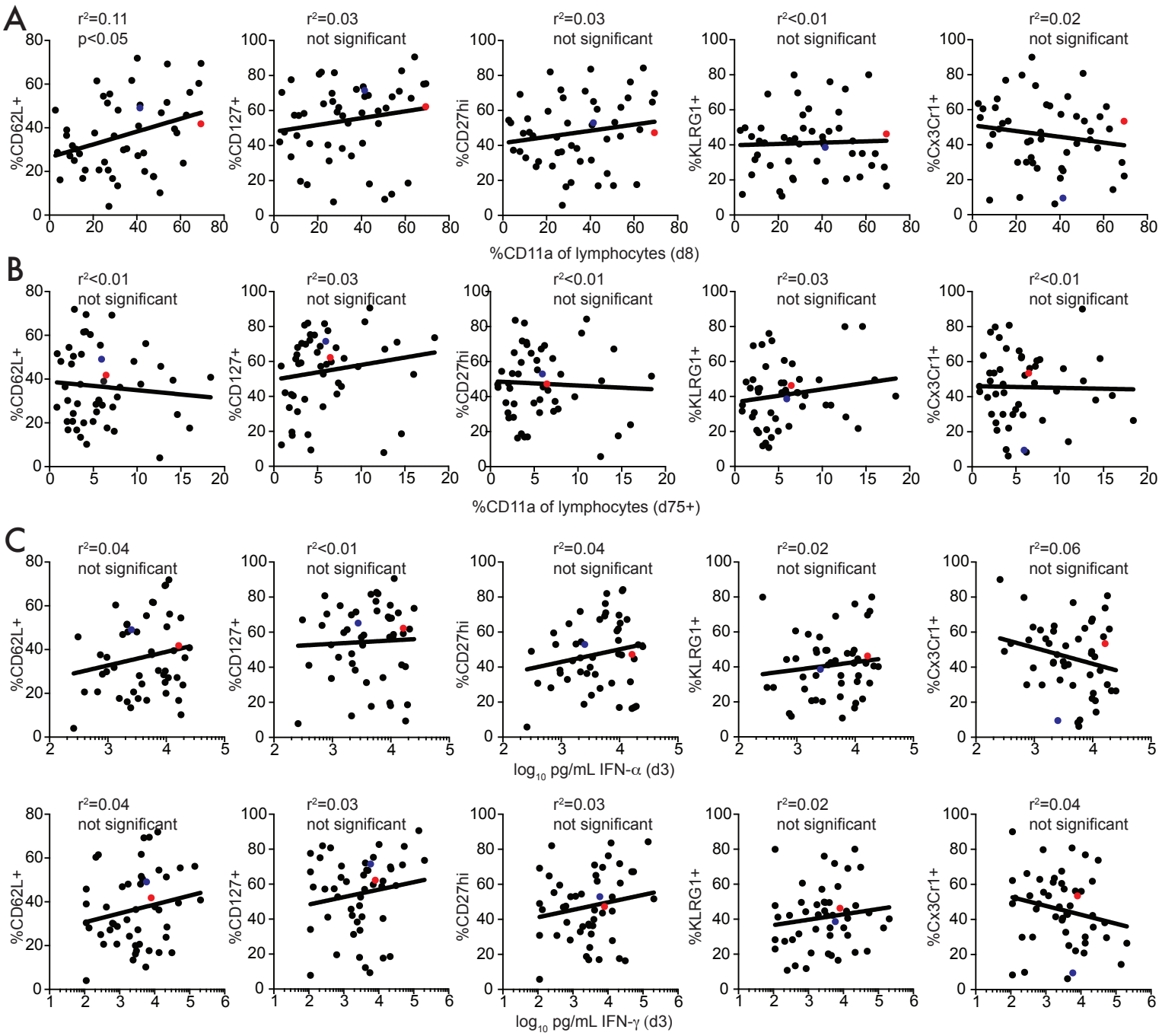

Figure S6: Phenotype of memory CD8 T cells does not correlate with magnitude of systemic cytokine response or adaptive CD8 T cell responses, related to Fig. 5. (A) Percentage of CD8 TM cells (d75) expressing CD127, CD62L, CD27hi, KLRG1, or Cx3Cr1 (y axis) relative to percentage of Tem cells (CD11ahi/CD8alo) (x axis) on d8 post infection. (B) Percentage of CD8 TM cells (d75) expressing CD127, CD62L, CD27hi, KLRG1, or Cx3Cr1 (y axis) relative to percentage of TM cells (CD11ahi/CD8alo) (x axis) on d75 post infection. (C) Percentage of CD8 TM cells (d75) expressing CD127, CD62L, CD27hi, KLRG1, or Cx3Cr1 (y axis) relative to concentration of IFN-g detected in serum (x axis) on d3 post infection. (D) Percentage of CD8 TM cells (d75) expressing CD127, CD62L, CD27hi, KLRG1, or Cx3Cr1 (y axis) relative to concentration of IFN-g detected in serum (x axis) on d3 post infection. n=2 to 20 mice per group. Red dots indicate B6 mice, blue dots indicate BALB/c mice, and black dots indicate CC strains. Statistical significance of R-squared values based on linear regression analysis.

Supplemental Figure 7

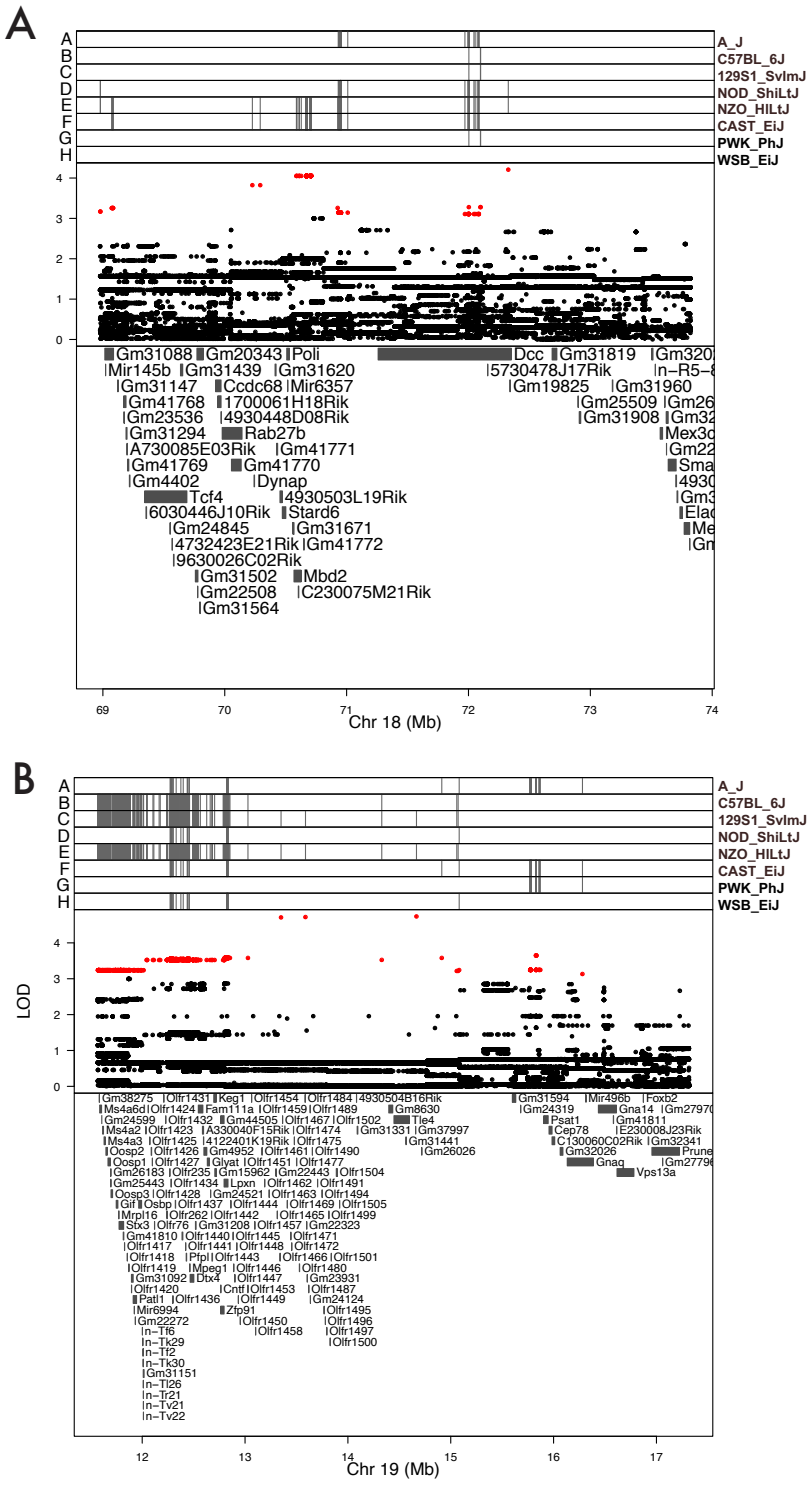

Figure S7: Map of SNPs in chromosome 18 & 19 QTL regions associated CD62L+ CD8 TM cells, related to Fig. 6. (A) The top panel shows the association of each SNP with CD62L+ CD8 TM cells. Chr 18 is on the X-axis and the LOD score is on the Y-axis. The middle panel shows the SNPs in the QTL interval region and SNPs with LOD score >3 are plotted in red. The bottom panel shows the genes in the interval from Mouse Genome Informatics. (B) The top panel shows the association of each SNP with CD62L+ CD8 TM cells. Chr 19 is on the X-axis and the LOD score is on the Y-axis. The middle panel shows the SNPs in the QTL interval region and SNPs with LOD score >3 are plotted in red. The bottom panel shows the genes in the interval from Mouse Genome Informatics.

Supplemental Table 1. CC strains. Related to STAR Methods.			
#	**Strain Name**	**H2-D^{b}**	**# of mice**
1	CC003/UNC	Yes	3
2	CC002/UNC	Yes	3
3	CC019/TAUUNC	No	3
4	CC037/TAUUNC	Yes	2
5	CC001/UNC	Yes	2
6	CC041/TAUUNC	Yes	3
7	CC068/TAUUNC	Yes	3
8	CC055/TAUUNC	No	3
9	CC006/TAUUNC	Yes	3
10	CC071/TAUUNC	No	2
11	CC051/TAUUNC	Yes	3
12	CC041/TAUUNC	Yes	3
14	CC011/UNC	Yes	3
15	CC057/UNC	No	3
16	CC036/UNC	Yes	3
17	CC035/UNC	No	3
18	CC023/GENIUNC	Yes	3
19	CC053/UNC	No	3
20	CC031/GENIUNC	Yes	3
21	CC008/GENIUNC	No	3
22	CC032/GENIUNC	Yes	3
23	CC030/GENIUNC	No	3
24	CC025/GENIUNC	No	1
25	CC012/GENIUNC	No	3
26	CC027/GENIUNC	Yes	3
27	CC079/TAUUNC	No	3
28	CC065/UNC	No	3
29	CC072/TAUUNC	Yes	3
30	CC004/TAUUNC	Yes	3
31	CC005/TAUUNC	No	3
33	CC059/TAUUNC	Yes	3
34	CC013/GENIUNC	No	3
35	CC015/UNC	No	2
36	CC024/GENIUNC	No	3
37	CC017/UNC	No	3
38	CC021/UNC	No	3
39	CC046/UNC	Yes	3
40	CC056/GENIUNC	No	3
41	CC043/GENIUNC	Yes	3
42	CC044/UNC	Yes	3
43	CC050/UNC	No	2
44	CC052/GENIUNC	Yes	3
45	CC058/UNC	No	3
46	CC060/UNC	No	3
47	CC061/GENIUNC	Yes	3
48	CC063/UNC	No	3
49	CC078/TAUUNC	No	3