Online Supplemental Material for

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Supplemental Information.

Following is a more detailed description of the methods used to generate Figs, 4 A, 4 B, 4 C, 7 D, and 7 E. Table S1 shows the genes corresponding to Figs. 4, B and C and Table S2 shows the genes corresponding to Fig. 7 E. In the respective tables, the genes labeled in the figures are shown in bold.

For the analysis in Fig. 4 B, the following samples were used: (A) WT spleen ($n = 5$); (B) TG spleen ($n = 5$); (C) CD8TG or CD8WT splenocytes ($n = 4$; of these 3 were TG and 1 was WT); (D) WT thymus ($n = 3$); (E) TG thymus ($n = 3$); (F) ONCO spleens ($n = 5$); and (G) ONCO thymus ($n = 3$). The goal was to compare the genes that were "present" in all the samples. A gene was selected (from 12,489 transcripts represented on the microarray) if it was present in at least 3 of the 4 or 5 samples within groups A, B, C, F (WT spleen, TG spleen, CD8 splenocytes, and ONCO spleen, respectively) or if it was present in at least 2 of the 3 samples within groups D, E, G (WT thymus, TG thymus, or ONCO thymus, respectively). 4372 genes were "present" in all of the groups. Data were expressed as ratios defined by (absolute expression of each gene)/527, where 527 relative fluorescence units (RFU) corresponds to the average signal for the 4372 genes being analyzed. The data were analyzed using hierarchical clustering.

In Fig. 4, B and C, the goal was to identify genes that were specific for one of the individual groups (A–G, above). Of the 12,489 genes, 7195 were present in at least one of the groups. We selected 1512 genes that were at least twofold induced in either $ONCO^S$ or $ONCO^T$ over any of the other groups. The data group were analyzed using hierarchical clustering and a set of genes are presented in Fig. 4 B. We did this by evaluating the maximum of the median of genes in group F or G divided by the minimum of the median expression of genes in group A, B, C, D, and E (MAX Med [F or G] ÷ MIN Med [A, B, C, D, or E]). Expression data for these genes was converted to ratios by dividing the absolute expression by 406, where 406 RFU was the average signal for the 7195 genes. Fig. 4 C shows 35 genes which median expression was at least 1.4-fold higher in the splenic and thymic tumors (groups F and G) than in any of the other groups.

In Fig. 7 D we used hierarchical clustering to compare the expression profiles of 6251 'expressed' genes at different time points in 5C.C7 single transgenic and Stat5b/5C.C7 double transgenic backgrounds. A gene was considered expressed if it was 'present' in at least three samples in the 5C.C7 single transgenic ([Group 1] n = 4), Stat5b/5C.C7 double transgenic 2–3 wk ([Group 2], n = 5), 6–8 wk ([Group 3] n = 4), or 12–13 wk ([Group 4], n = 5). In addition, genes that were found to be increased in lymphomas in Stat5b transgenic mice (see Fig. 4 C) were examined over time in 5C.C7 and Stat5b/5C.C7 mice and presented as Fig. 7 E.

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