

SUPPLEMENTAL MATERIAL

Duan et al., <http://www.jem.org/cgi/content/full/jem.20141308/DC1>

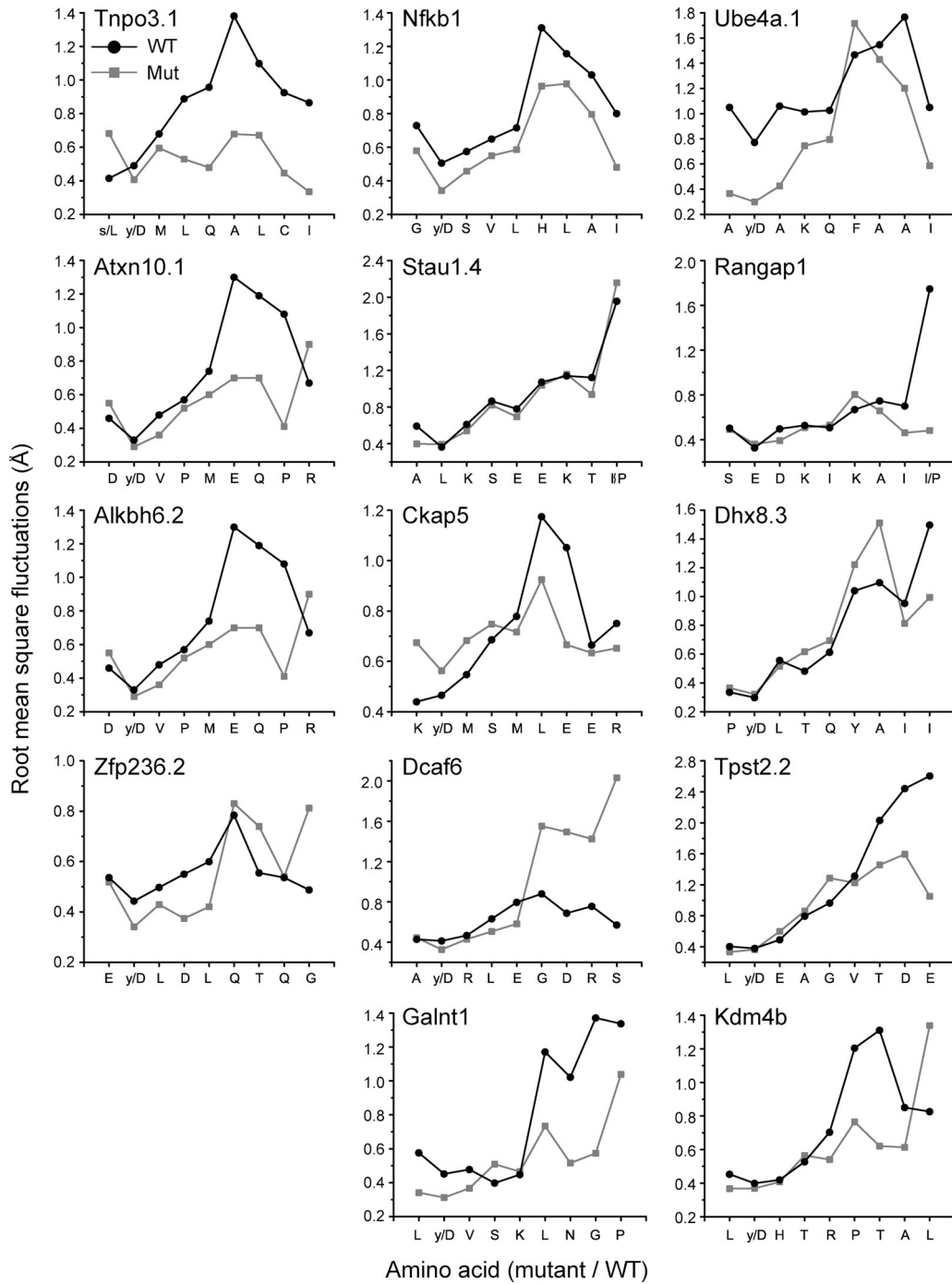
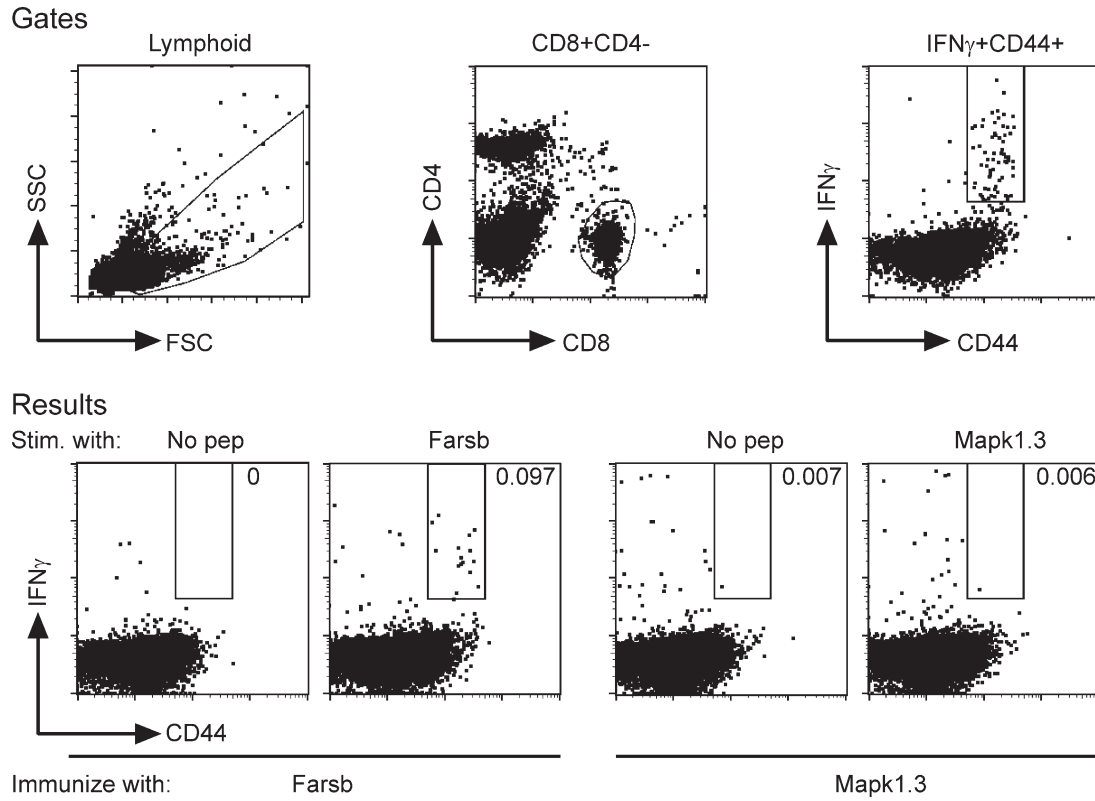
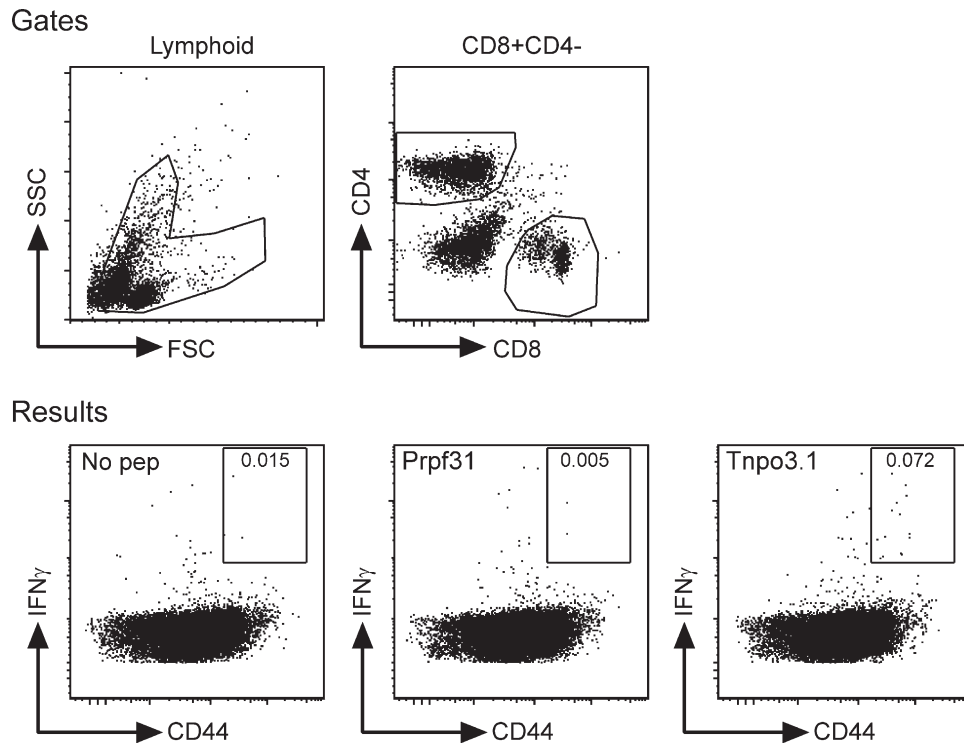


Figure S1. Root mean square fluctuations for the  $\alpha$  carbons of all top DAI ranked nonamers from the structural modeling.



**Figure S2. FACS gating strategy and representative primary data for Fig. 1.** Gating strategy for lymphoid cells, CD8+CD4<sup>-</sup> cells and IFN $\gamma$ +CD44<sup>+</sup> cells stimulated with a cognate peptide, is shown. Also shown are the examples of an immunogenic peptide (Farsb) with a specific response of 0.097% and a nonimmunogenic peptide (Mapk1.3) with a 10-fold less background of 0.007%. In both cases, cells without peptide stimulation were used as a negative control. For each sample, total 95,000–129,000 lymphocytes, or 14,500–17,000 CD8<sup>+</sup>CD4<sup>-</sup> cells, were acquired.



**Figure S3. FACS gating strategy and representative primary data for Fig. 5 C (left panel).** Gating strategy for lymphoid and CD8+CD4- cells (top two panels) and representative FACS plots for responses against *no-pep*, control peptide *Prpf31* and *Tnpo3* peptide (bottom three panels). Note that the response in lack of stimulation, and in response to stimulation by irrelevant peptide control is identical, and that the response to Tnpo3 is 5–7 times higher than background. For each sample, total 150,000 lymphocytes, or a minimum of 19,000 CD8+CD4- cells, were acquired.

Table S1. (Provided as an Excel file file). Predicted neoepitopes of CMS5 and Meth A sarcomas ranked by NetMHC values. The mutations, the genes containing them and their chromosomal locations, the comparisons with the WT allele, and other identifying information, are shown for each tumor in a separate tab.