This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Assays & screens			
Whole-exome sequencing to identify antigens for adoptively transferred, autologous tumor-infiltrating lymphocytes (TILs)	Whole-exome sequencing could help to identify mutated antigens to express in TILs for adoptive transfer immunotherapy. Whole-exome sequencing identified nonsilent, somatic mutations in the DNA of melanoma cells that were absent from that of matched normal cells. A peptide-major histocompatibility complex (MHC) binding algorithm was then used to select high-affinity candidate T cell epitopes that would be recognized by TILs. Top candidate epitopes were synthesized and screened for their ability to induce interferon- γ (IFNG; IFN- γ) release from TIL cell lines derived from three patients with melanoma. Next steps include evaluating the association between TIL recognition of mutant antigens and long-term tumor regression.	Unpatented; licensing status not applicable	Robbins, P.F. <i>et al. Nat. Med.</i> ; published online May 5, 2013; doi:10.1038/nm.3161 Contact: Paul F. Robbins, National Institutes of Health, Bethesda, Md. e-mail: paulrobbins@mail.nih.gov
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