Figure S1. Correlation of DNA copy number aberrations (left) to survival statistics. Brighter green indicates a higher rate of loss. The 6q, 10, and 11q21-ter chromosomal regions are circled. Both figures are taken from Reference 6.

Figure S2. List of the 57 downregulated, candidate tumor suppressor genes identified by expression microarray analysis. Data from three studies are shown: Kabbarah, et al (Ref. 6), Riker, et al (Ref. 16), and Talantov, et al (Ref. 15). The relevant comparisons are shown: MvP is Metastases versus Primary Tumors; MvN is Metastases versus Nevi. The colors represent fold-downregulation as shown in the legend. Nine genes are marked that did not have shRNAs in the pLKO vector at the time of analysis, and were not inlcuded.

Figure S3. A, Representative allograft tumors from the iNRAS-463 cell line primary shRNA screen. These mice were sacrificed on day 56 post-injection and show a comparison between the significantly scoring 6q and 10-3 pools versus the shGFP and parental controls. B, No significant cooperation is seen when simultaneously knocking down Tacc2 and Tcf7l2. Error bars are SEM.

Figure S4. Phenotypes of human melanoma cell lines with knocked down or overexpressed Ablim1. A, RT-PCR quantitation of Ablim1 knockdown efficiency in the WM115 cells depicted in Fig. 6A. B, *in vitro* growth curves of the fast-growing SKMel28 or the slow-growing HMVII melanoma cell lines overexpressing GFP or Ablim1. C, *in vivo* growth curves of 1205Lu xenograft tumors expressing shRNAs against GFP or Ablim1. D, Ablim1 knockdown enhances the tumor take rate in WM115 and 1205Lu cells, n = 10 per cohort. The 1205Lu tumors are the same as in panel C.

Figure S5. A, Microarray data showing gene expression levels of the top four candidate tumor suppressors. Shown are iNRAS allograft tumors exposed to doxycycline withdrawal, which extinguishes mutant NRAS expression, or pharmacological inhibition of MEK by AZD244 (Ref. 16). n = 6 per cohort. B, TCGA data matrix of NRAS/BRAF hotspot mutations ($NRAS^{G12}$, $NRAS^{Q61}$, or $BRAF^{V600}$), NRAS/BRAF non-hotspot mutations (yellow), NF1 mutations, or PTEN mutations, subdivided by Chromosome 10 loss. C, TCGA data subdivided by the presence or absence of BRAF/NRAS hotspot mutations without NF1 mutations. D, TCGA data subdivided by the presence or absence of NF1 mutations.