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Supplementary Materials for

Detection of somatic mutations and HPV in the saliva and plasma of patients with head and neck squamous cell carcinomas

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This PDF file includes:

Other Supplementary Material for this manuscript includes the following:
(available at www.sciencetranslationalmedicine.org/cgi/content/full/7/293/293ra104/DC1)

Supplementary Materials

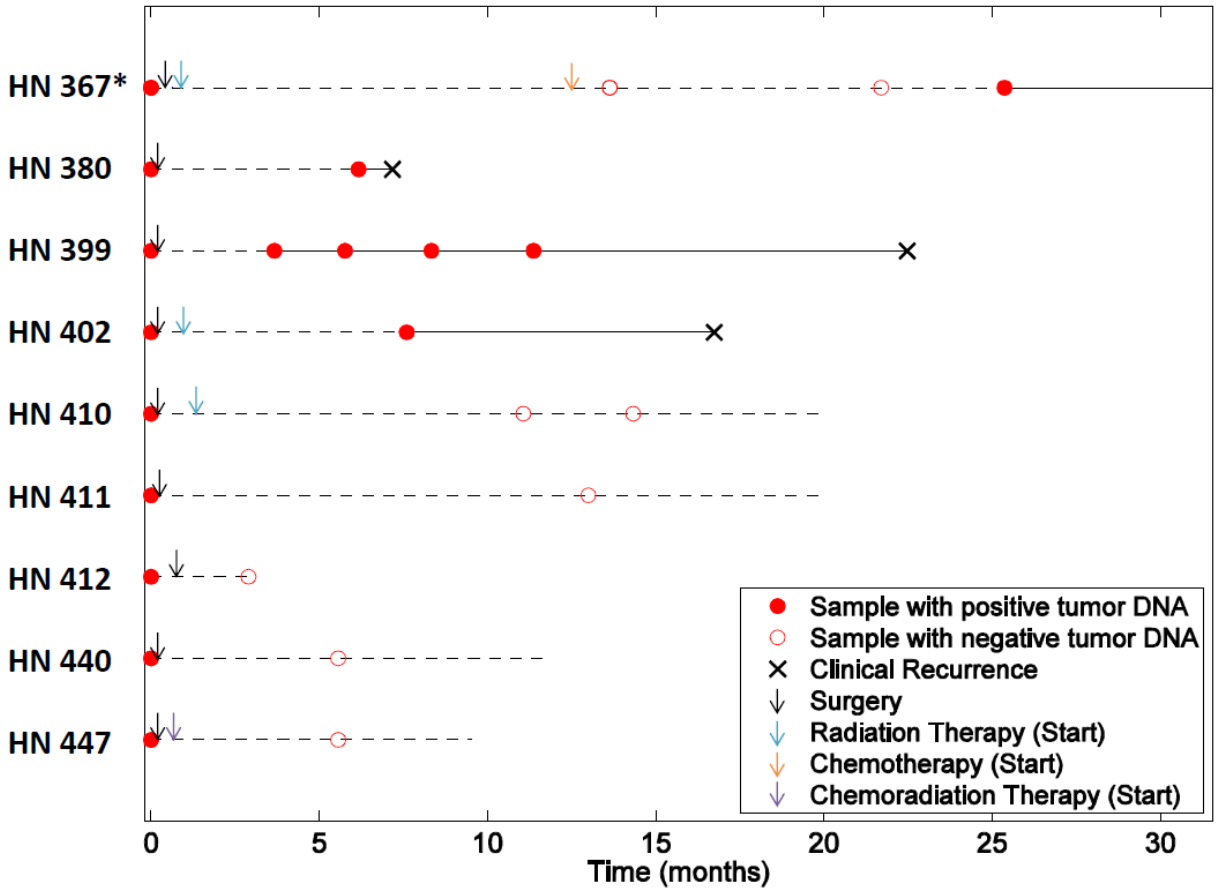

Fig. S1. Tumor DNA is detectable in the saliva of patients before recurrence becomes clinically evident. Nine patients were followed-up for a median of 12 months after surgery. Dashed lines transition to solid lines when tumor DNA was detected after surgery. *Twenty-five months prior to surgery, patient 367 also underwent chemoradiation therapy.

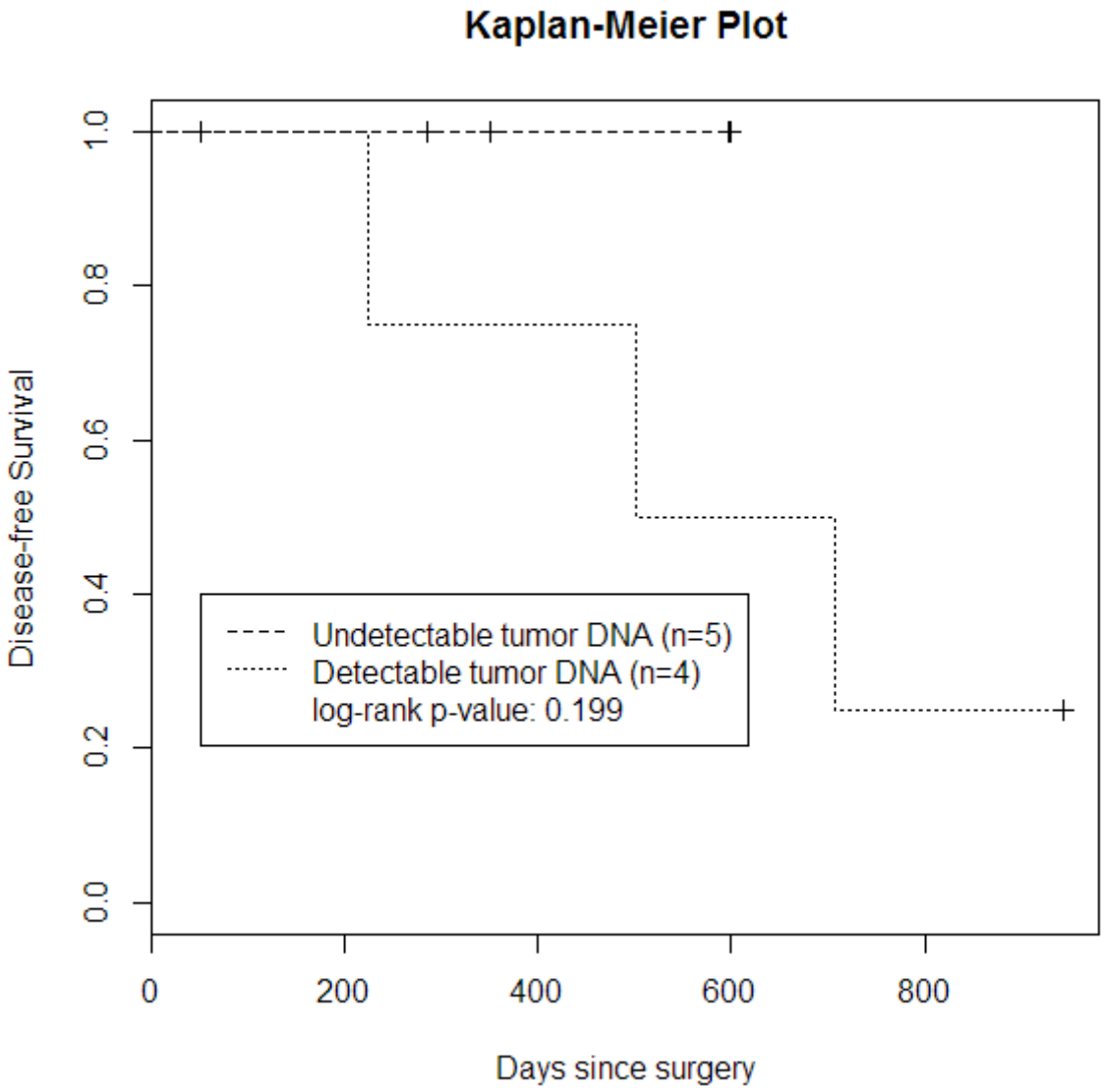

Fig. S2. Patients with undetectable tumor DNA after surgery have better disease-free survival.

Table S1. Patient demographics. The clinical information, tumor characteristics, and presence of tumor DNA in samples collected from 93 patients enrolled in this study are listed (OC = oral cavity, OP = oropharynx, L = larynx, H = hypopharynx, and NA = not available).

Table S2. Primer sequences used in multiplex assay for identification of driver mutations in tumors. Amplicons included commonly mutated gene regions in HNSCC.

Table S3. Amounts of tumor-derived DNA in saliva and plasma. The mutation identified in the tumor of each patient is listed, along with the fractions of mutant allele in saliva and plasma. In addition, the numbers of mutant and wild-type reads in patient samples vs. controls are listed for each mutation assayed. For patients with recurrent disease, treatments received and the interval prior to sample collection are listed. Patients in **BOLD** had both saliva and plasma available (OC = oral cavity, OP = oropharynx, H = hypopharynx, and L = larynx).