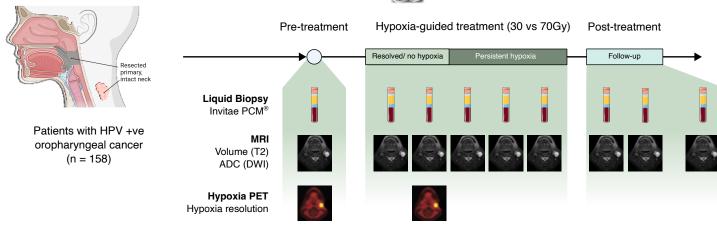


Weekly blood draw and imaging

47 variants per patient)

HPV-35 n = 2

Q3-6 months up to 2 yrs



C b Invitae PCM[®] N = 111 patients n = 980 blood draws Tumor informed MRD assay Tumor naïve HPV assay Tumor/ Normal Whole T/N failed sequening Exome Sequencing N = XX patient HPV-31 HPV-18 (n = 119 pre-treatment n = 2 cfDNA samples T/N pairs; mean target coverage XXX) Somatic variant calling HPV-33 HPV-35 Failed panel design using Invitae pipeline N = XX patient (mean n = XX variants n = 2 cfDNA samples per patient) Number of primers: Selection of target variants HPV-16 n = 17 for MRD tracking and HPV-18 n = 16 Failed library prep HPV-31 n = 2 primer design (mean n = N = XX patient HPV-33 n = 2

n = 1 cfDNA sample

Failed sequencing N = XX patients n = 63 cfDNA samples

N = 111 patients n = 911 cfDNA samples