Twitter Thread by Rebecca Fitzgerald Lab

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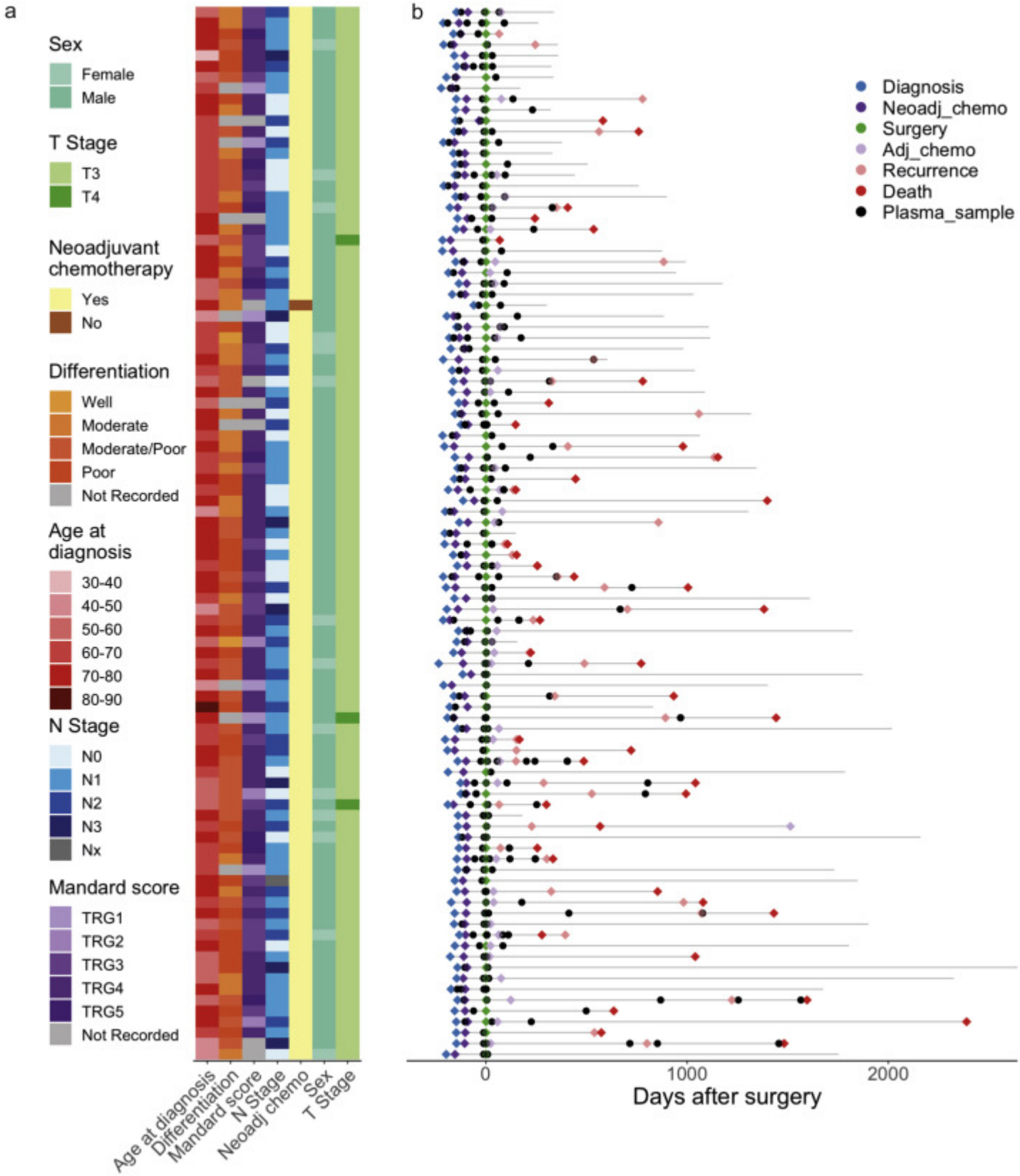
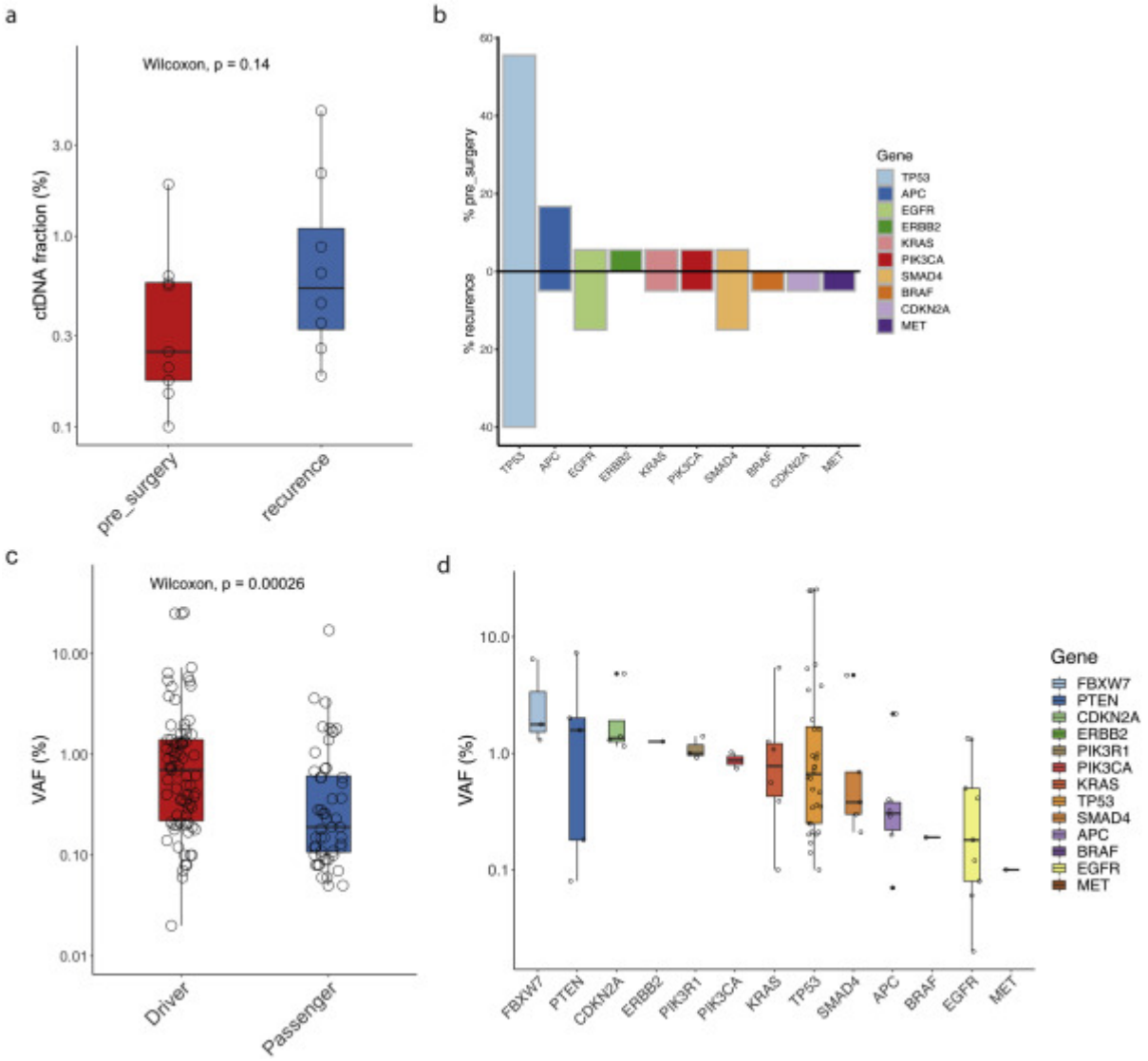
Here is a tweetorial from our latest publication in @Annals_Oncology about longitudinal tracking of esophageal adenocarcinoma. #OesophagealCancer #EsophagealCancer https://t.co/QWvrzBXmK7 1/8

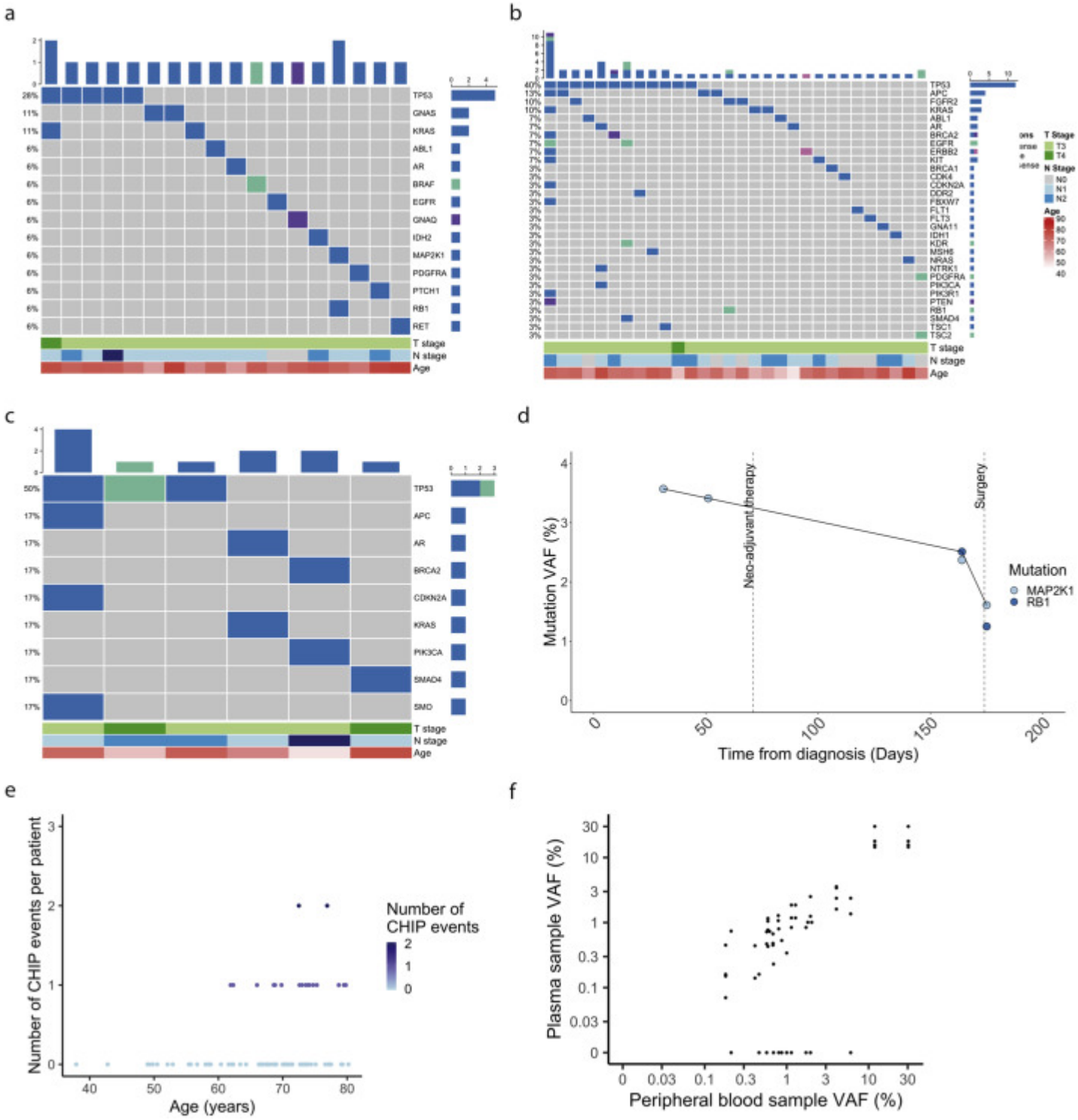
We sequenced 245 plasma samples from 97 patients with oesophageal adenocarcinoma using a 77 gene pan-cancer ctDNA panel. 2/8



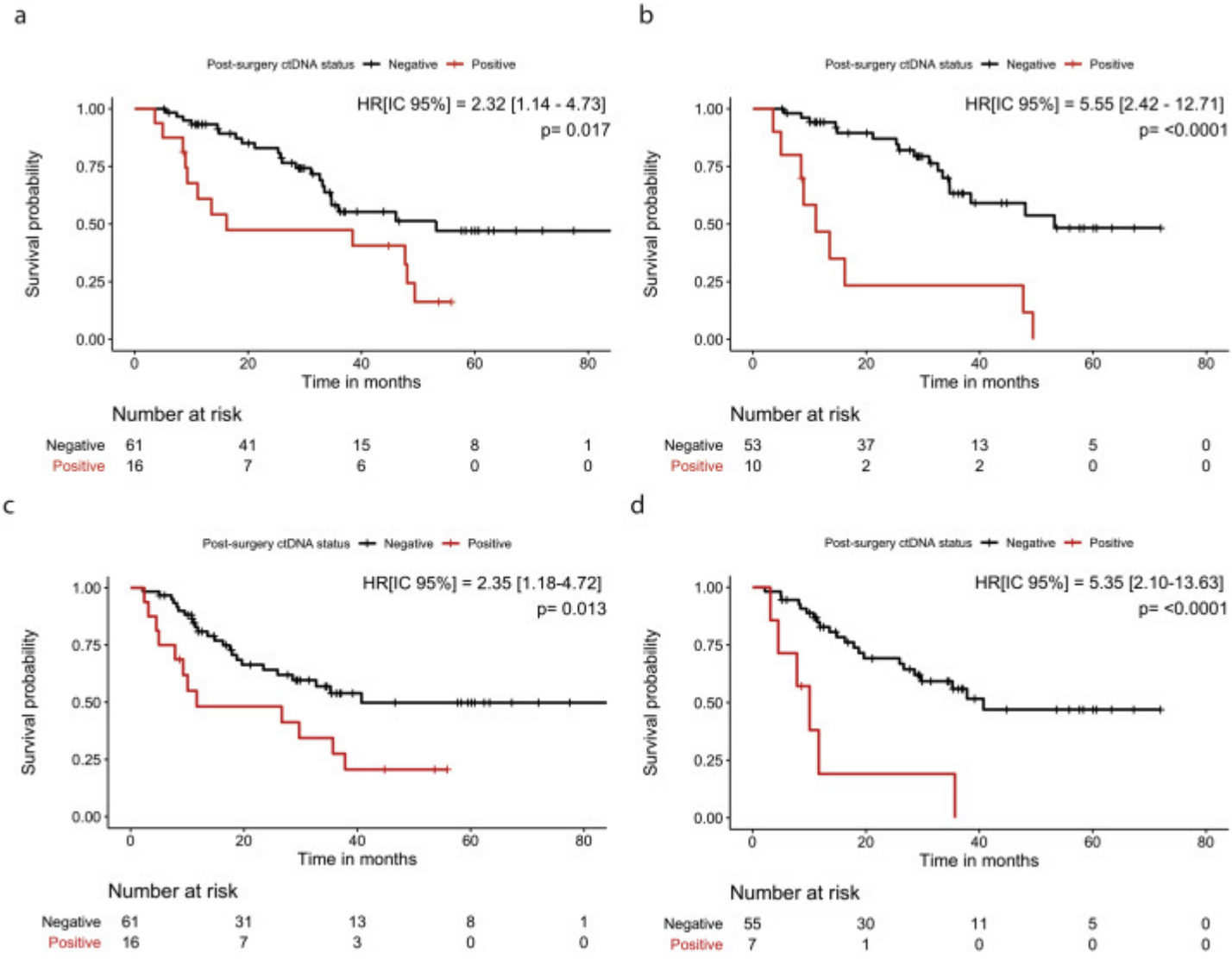
Variants derived from previously characterised driver oesophageal adenocarcinoma genes had a significantly higher VAF than variants from other genes, indicating selection. 3/8



Peripheral blood cell samples were also sequenced for 78/97 patients. CHIP mutations were identified in 23% of cases, longitudinal tracking of CHIP variants suggested these variants were dynamic over time. 4/8



We found patients that were ctDNA positive post-surgery had a significantly poorer survival than ctDNA negative patients, and the elimination of CHIP variants improved the positive predictive value. 5/8



In summary, we demonstrate in a large, national, prospectively-collected dataset that ctDNA in plasma following surgery for EAC is prognostic for relapse. Inclusion of peripheral blood cell samples can reduce or eliminate false positives from CHIP. 6/8

In the future, post-operative ctDNA could be used to risk stratify patients into high- and low-risk groups for intensification or de-escalation of adjuvant chemotherapy. 7/8

Many thanks to our founders and all patients who participated within the OCCAMS consortium framework. The study was carried out by our brilliant PhD student Emma Ococks, medical oncologist @LizzySmyth1, postdoc @AFrankell, and postdoc @neus_snows among others @MRC_CU. 8/8

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