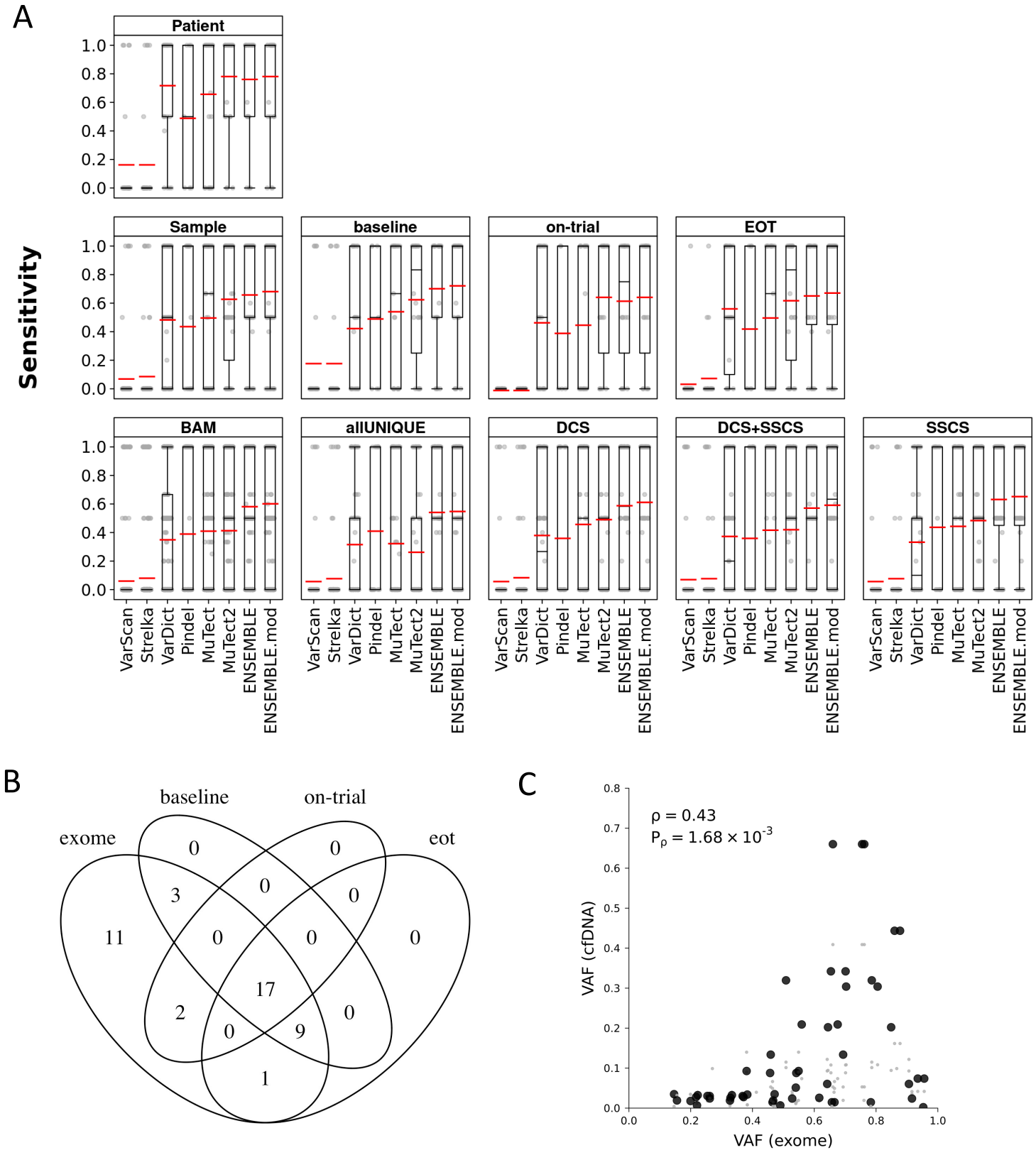

Supplementary Figure 5: A) Sensitivity estimates were obtained for each mutation caller using number of expected mutations (based on whole-exome sequencing of the bulk tumour) positively detected in the ctDNA samples. Estimates were obtained for each BAM (level of evidence provided by ConsensusCruncher), each ctDNA sample (timepoint; based on ANY level of evidence) and each patient (detected in any sample). MuTect2 had the highest individual sensitivity value, and this was further improved using our custom ensemble approach. Boxplot shows median and 1st to 3rd quartiles while red bar indicates mean sensitivity. B) Number of expected mutations (exome) detected in the baseline, cycle 2 (on-trial) and end-of-treatment samples. C) Correlation of VAFs between exome and ctDNA samples for expected mutations; black points are baseline samples.