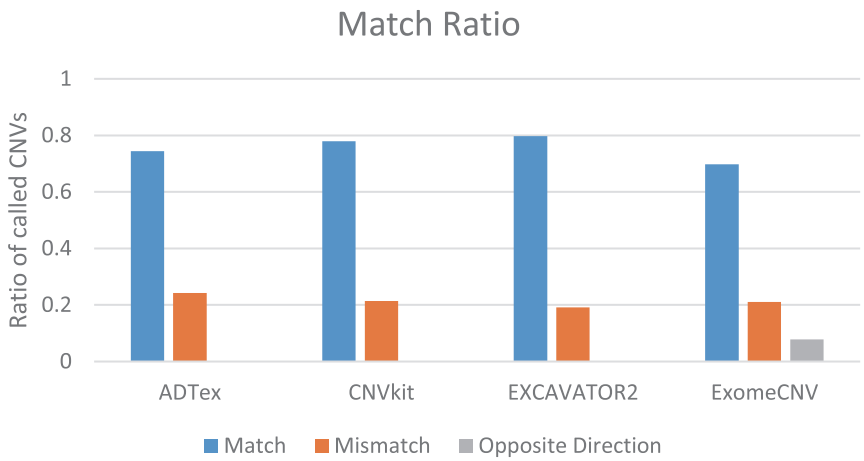
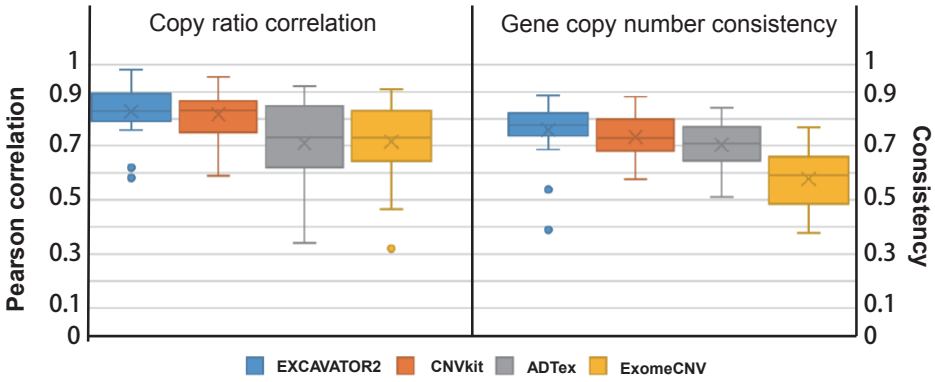
# Figure S6

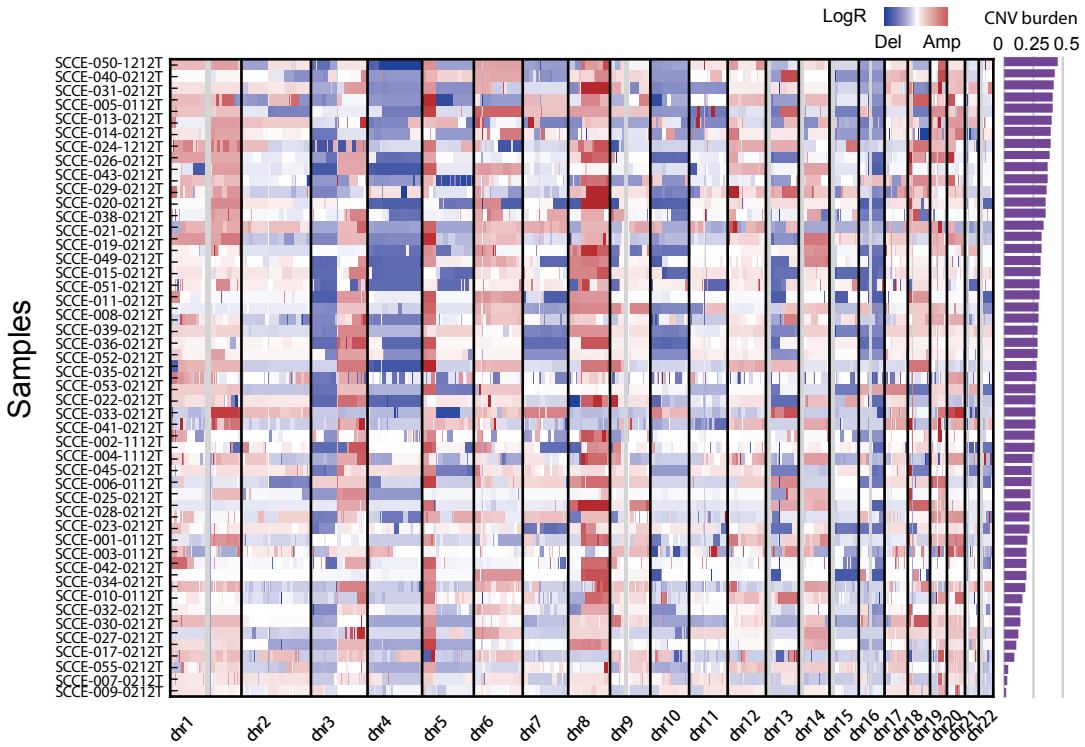
a




b




c



**Supplementary information, Figure S6** Confirmation of exome-based SCNVs with OncoScan CNV assay. **a** The percentages of WES-based CNVs overlapped with the reference CNV set. Match: a CNV region overlaps with the reference at a level of more than 90%. Mismatch: a CNV region overlaps with the reference at a level of less than 90%. Opposite direction: an overlapping gain region was called as a loss, and vice versa. **b** Copy ratio correlation(left) and gene copy number consistency (right) between WES-based CNVs and the reference CNV set. **c** SCNA burden across patients with SCCE. Left: heat map of SCNA of 55 patients with SCCE. Each row depicts a patient. Right panel: SCNA burden for each patient. SCNA burden of each patient is calculated by “length of all copy number segments/whole genome length”.