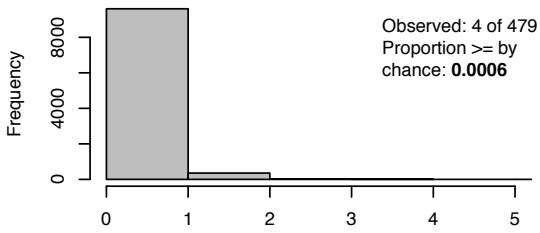
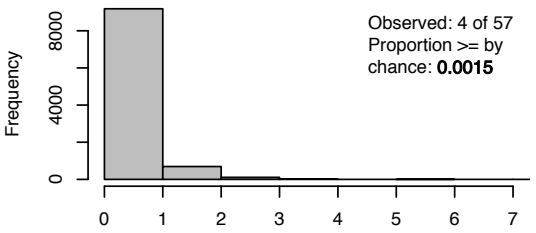
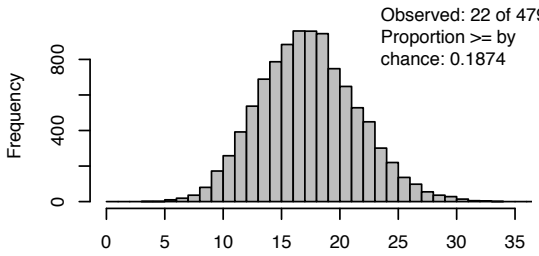


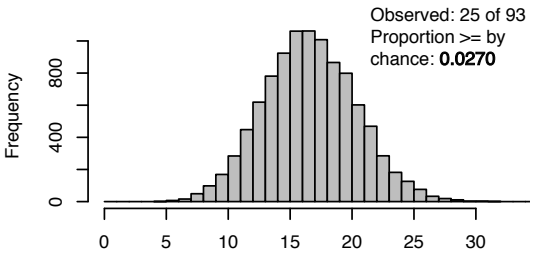
Overlap Random CGH Regions with Observed SeqCNV Regions



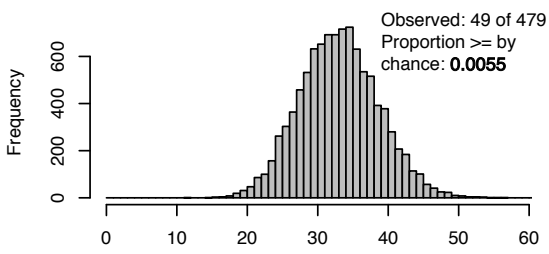
Overlap Random SeqCNV Regions with Observed CGH Regions



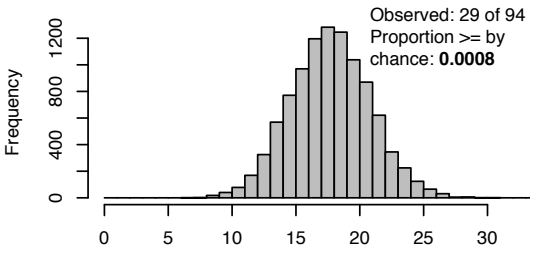
Overlap Random CGH Regions with Observed NAM Regions



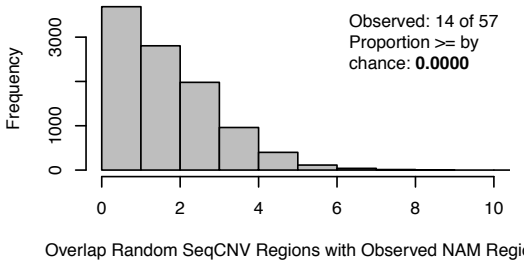
Overlap Random NAM Regions with Observed CGH Regions



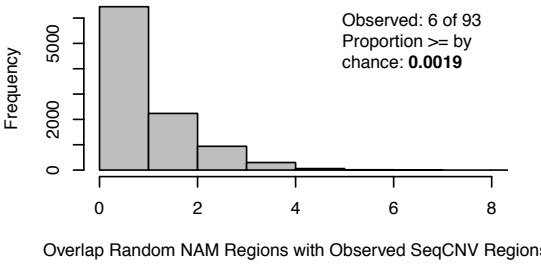
Overlap Random CGH Regions with Observed Sweep Regions



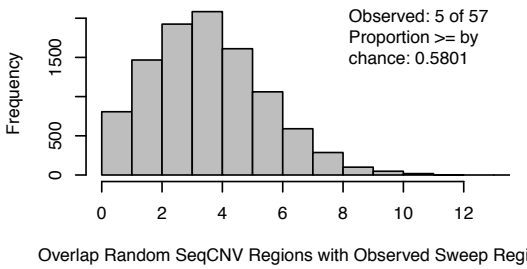
Overlap Random Sweep Regions with Observed CGH Regions



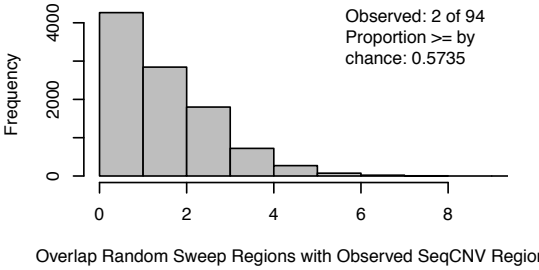
Overlap Random SeqCNV Regions with Observed NAM Regions



Overlap Random NAM Regions with Observed SeqCNV Regions



Overlap Random SeqCNV Regions with Observed Sweep Regions



Overlap Random Sweep Regions with Observed SeqCNV Regions

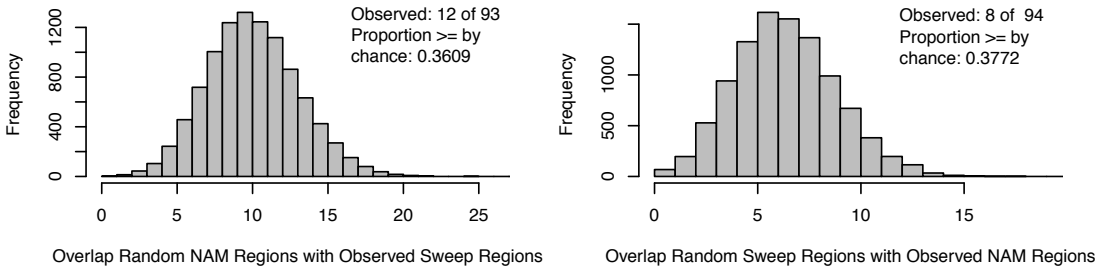


Figure S7 Simulation experiment testing the pair-wise overlap between each source of evidence [comparative genome hybridization (CGH) copy number variation (CNV) regions, sequence depth CNV regions (SeqCNV), regions exceeding the 99.9% outlier threshold (Sweep Regions), and regions identified in the nested association mapping (NAM) population] by chance compared with the empirically observed overlap. Regions with the empirically observed size were randomly placed throughout the genome 10,000 for each source of evidence. Comparisons were then made between the random data and observed data to test the overlap that was observed by chance.