Supplementary information, Figure S1

Figure S1 Depth and coverage of whole-exome sequencing of target regions for paired tumor (T) and normal (N) DNA from 12 patients with Cushing’s disease. Panel A shows the distribution of fold coverage of target regions. The bold lines in boxes represent the medians and the lines outside the boxes present the max and min fold coverage. Panel B shows the fraction of target bases covered by 30 reads, 20 reads or 10 reads per sample.