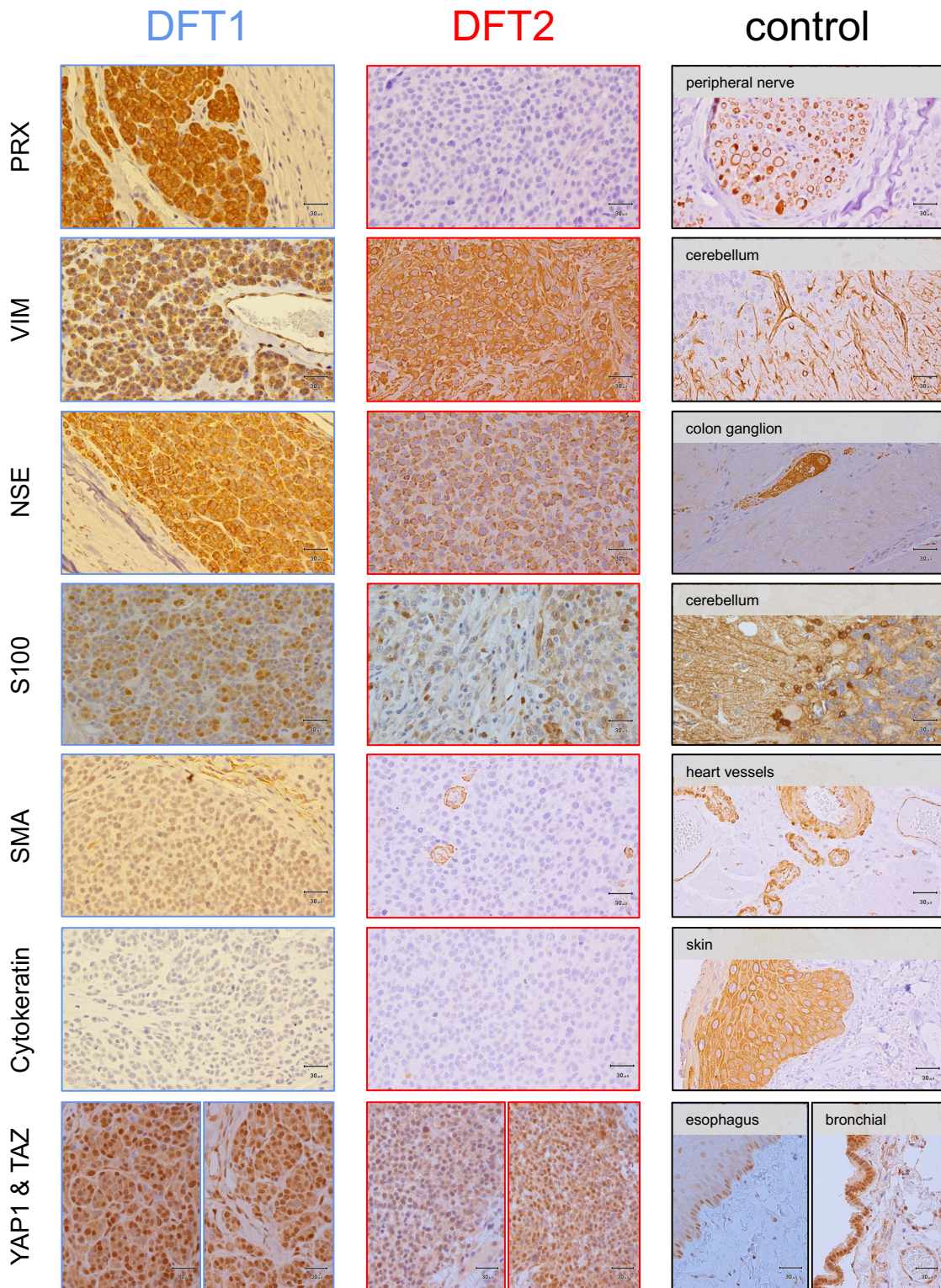


## Supplemental Information

### The Origins and Vulnerabilities of Two

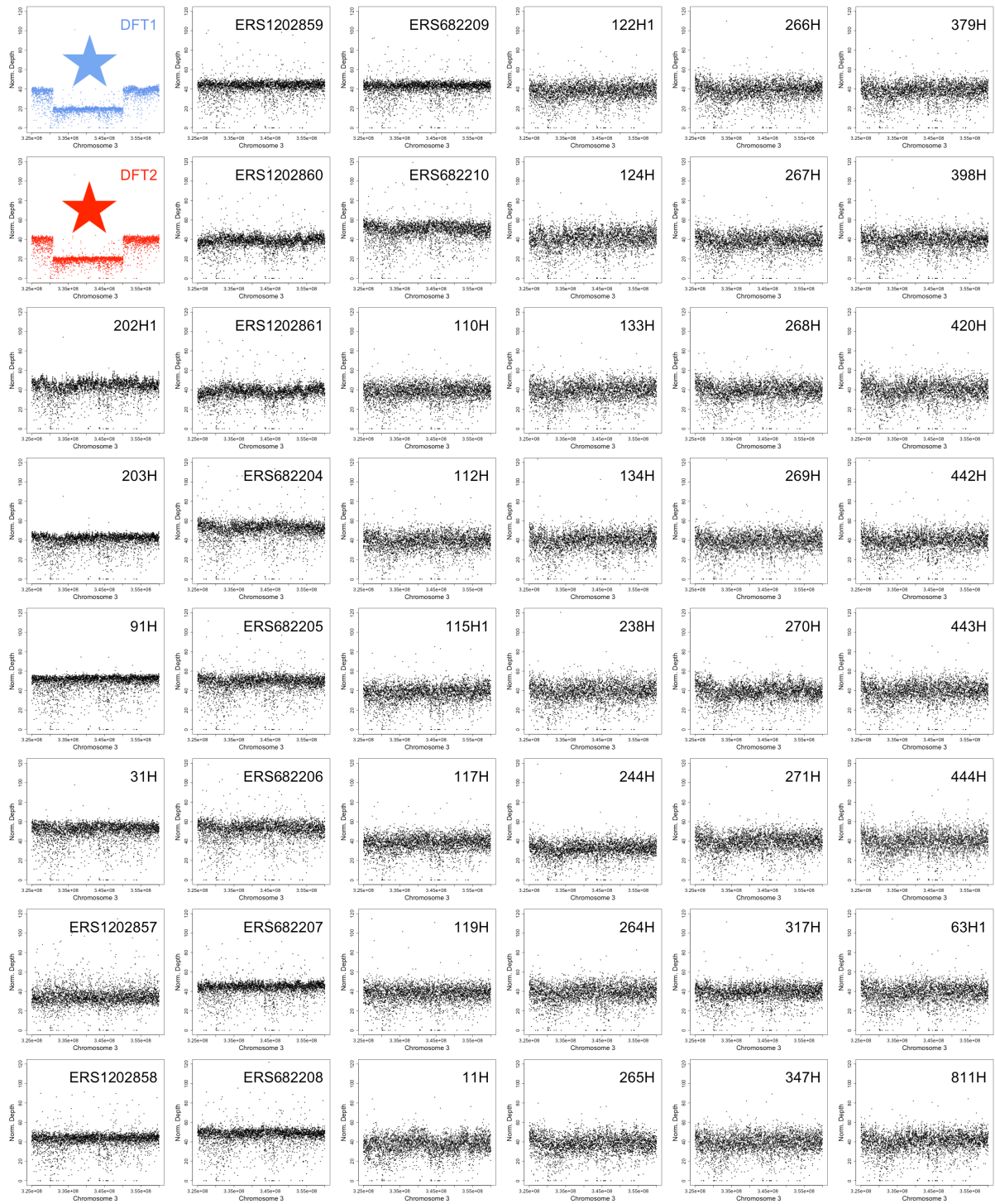
### Transmissible Cancers in Tasmanian Devils

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**Figure S1, related to Figure 1: Immunohistochemistry.**

DFT1 (left), DFT2 (center) and control (right) tissues stained with tissue lineage markers (Loh et al., 2006). PRX is included as a control (Pye et al., 2016b). Scale bar, 30  $\mu$ m. PRX, periaxin; VIM, vimentin; NSE, neural specific enolase; SMA, smooth muscle actin; YAP1 (bottom left panels), yes-associated protein 1; TAZ/WWTR1 (bottom right panels), transcriptional coactivator with PDZ-binding motif/WW domain-containing transcription regulator 1. Nuclear localization of YAP1 and TAZ/WWTR1 indicates dephosphorylated, active states of the proteins (Moroishi et al., 2015; Wu et al., 2018).



**Figure S2, related to Figure 4: Genomic copy number at chromosome 3 locus in DFT1, DFT2 and 46 normal Tasmanian devil genomes.**

Copy numbers of DFT1, DFT2 and 46 normal Tasmanian devil genomes at the chromosome 3 locus that has undergone hemizygous deletion in both DFT1 and DFT2 (Chr3\_SC\_000000273 position 360,001 to Chr3\_SC\_000000312 position 30,000). Dots represent number of sequence reads mapping in 10,000 base pair non-overlapping bins normalized to average sequencing depth. The region that has undergone hemizygous deletion in DFT1 and DFT2 is marked with a blue and red star, respectively.