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Genomic profiling reveals heterogeneous populations of ductal carcinoma in situ of the breast

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Whole-genome sequencing reveals progressive versus stable myeloma precursor conditions as two distinct entities

Persistent repression of tau in the brain using engineered zinc finger protein transcription factors

Fig. 1: Selection of clinicopathological and genomic risk factors for relapse. Fig. 3: Spatial transcriptome analysis of a patient with GATA3 mutation-positive ductal carcinoma in situ (DCIS ...

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