Supplementary Information

PIK3CA and CCM mutations fuel cavernomas through a cancer-like mechanism

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Supplementary Tables

Table S1 Human CCM bulk tissue mutation data: Mutation data for each human CCM analyzed in this study using targeted sequencing, ddPCR, or SNaPshot. Each sample is notated as either familial (F), sporadic (S), or unknown (blank) as well as the affected gene for familial samples (CCM1/2/3). ddPCR and SNaPshot assay results for *PIK3CA* E542K, E545K, and H1047R for each sample are listed including the detected allele frequency as well as final mutation call. SNaPshot calls are color coded by variant and ddPCR results are colored according to the detected allele frequency for each variant. Sequencing data for *PIK3CA* are reported as the number of alt and ref reads supporting the listed variant, the allele frequency, and the final mutation call. *PIK3CA* variants shown in red text denote samples with insufficient coverage to make a definitive variant call per the thresholds detailed in the methods section; variant calls for these samples rely on a positive result by ddPCR and confirmation by a tertiary assay (SNaPshot). Germline and somatic mutations in the CCM genes are reported in respective columns listing the chromosomal coordinates in hg19, the predicted functional consequence of the variant, the number of reads supporting the alt and ref alleles, and the resulting allele frequency. The functional consequence of missense and in-frame indels are predicted by *in silico* tools SIFT (scale: 0-1, higher is more damaging) and PROVEAN (scale: continuous, <-2.5 predicted damaging) where available.

Table S2 Human CCM snDNA-seq read counts: Number of total, mutant, and wild type supporting reads present in each nucleus for *PIK3CA* and CCM mutations. Each nucleus is denoted by an 18bp oligo barcode which is incorporated into each read to define the nucleus of origin. These data were processed to generate Fig 2e. and Extended Data Figure 7c-f.