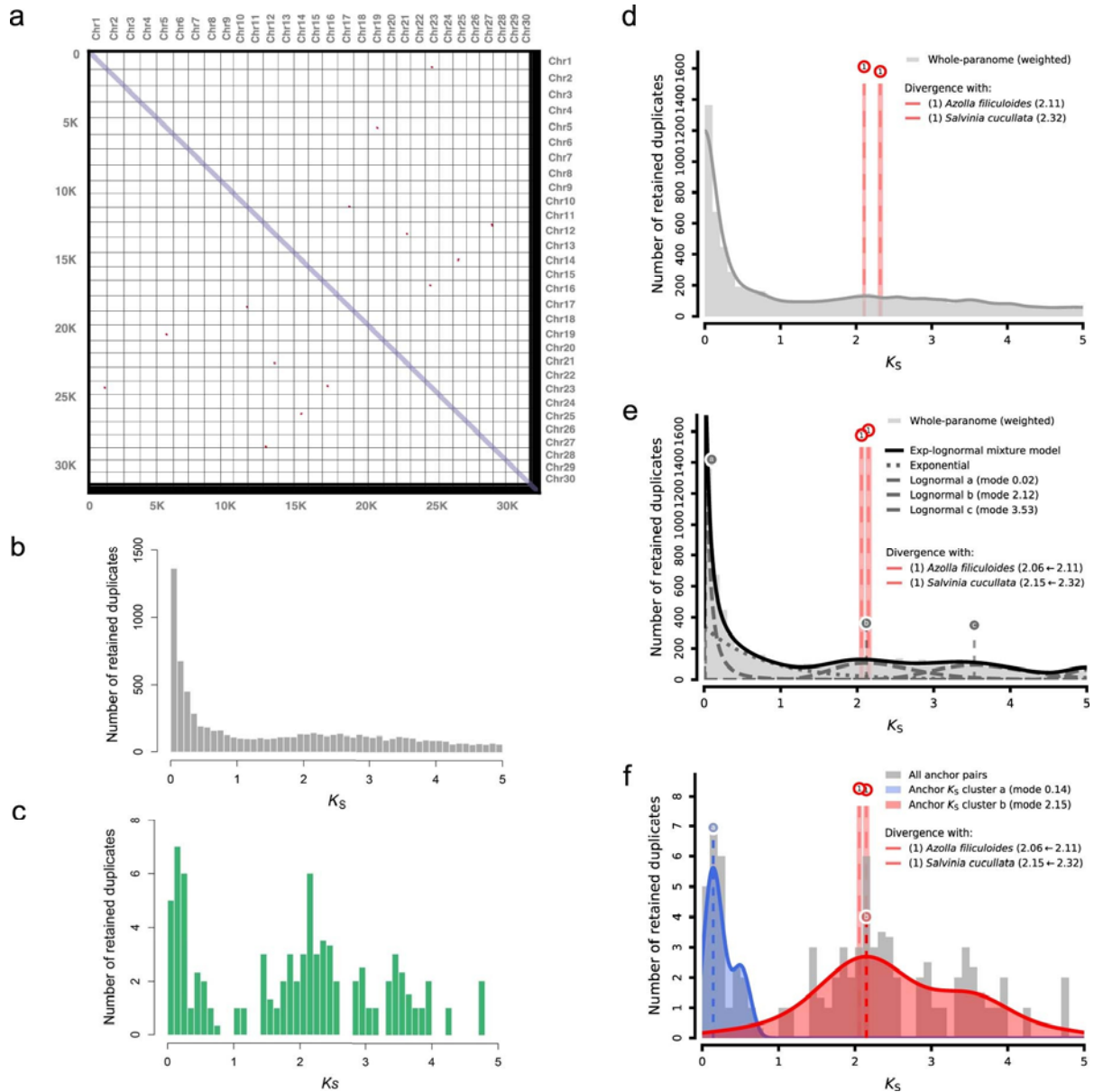


Extended Data Fig. 1: Analyses of whole genome duplication (WGD) events.

From: The genome of homosporous maidenhair fern sheds light on the euphyllophyte evolution and defences



a, Self-alignment dot plot based on paralogous pairs in collinear blocks. **b**, The distribution of K_s of the whole paranome in *A. capillus-veneris*. **c**, The distribution of K_s of the syntenic paralogous pairs in *A. capillus-veneris*. **d**, The analysis of K_s rates for the whole paranome of *A. capillus-veneris* before rate adjustment. Light grey histogram and kernel density estimation (KDE) curve are plotted for the whole paranome K_s distribution. The estimated mean mode and standard deviation from 200 bootstrapped KDEs of each orthologous distribution between *A. capillus-veneris* and other species is shown as dashed red lines and boxes with corresponding K_s values denoted in the legend. **e**, The analysis of K_s rates for the whole paranome of *A. capillus-veneris* after rate adjustment. The whole paranome K_s

distributions are overlaid with rate-adjusted divergence events in coloured vertical lines and boxes. The overall mixture model in the dark solid KDE curve consists of an exponential component in dotted grey curve and optimized log-normal components in dashed grey curves. Each log-normal component is labelled with a letter, shown as vertical dashed grey lines with circular labels. Rate-adjusted mode estimates of orthologous K_S distributions between *A. capillus-veneris* and other species, representing speciation events, are drawn as numbered vertical long-dashed lines and associated coloured boxes showing the mean and the standard deviation. Lines representing the same speciation event in the phylogeny share colour and numbering while here only one speciation event is involved with *A. capillus-veneris*. Horizontal arrows in figure legends 'divergence with' part indicate the K_S shifts resulted from the substitution rate adjustments. **f**, The analysis of *ksrates* for anchor pairs of *A. capillus-veneris* after rate adjustment. The K_S distributions of two anchor pair clusters, namely a and b in filled blue and red KDE curves with associated peak, derived from the lognormal mixture modeling of median K_S values for the collinear segment pairs, are shown as a grey histogram. Rate-adjusted mode estimates of orthologous K_S distributions between *A. capillus-veneris* and other species, representing speciation events, are drawn as numbered vertical long-dashed lines, and associated coloured boxes showing the mean and the standard deviation. Lines representing the same speciation event in the phylogeny share colour and numbering while here only one speciation event is involved with *A. capillus-veneris*. Horizontal arrows in figure legends 'divergence with' part indicate the K_S shifts resulted from the substitution rate adjustments.