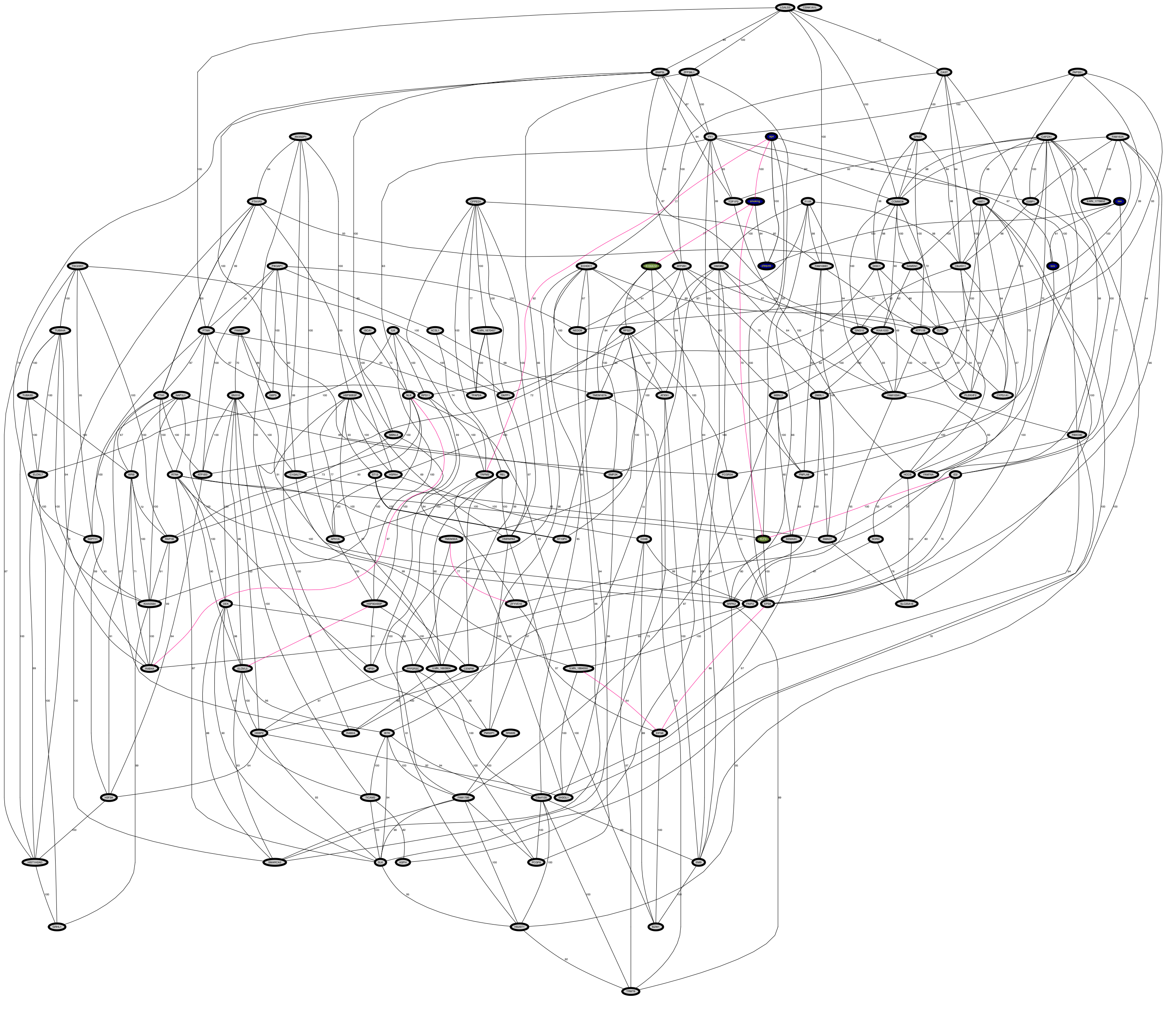
Supplementary Text S2
Network plots for all ICA modules.

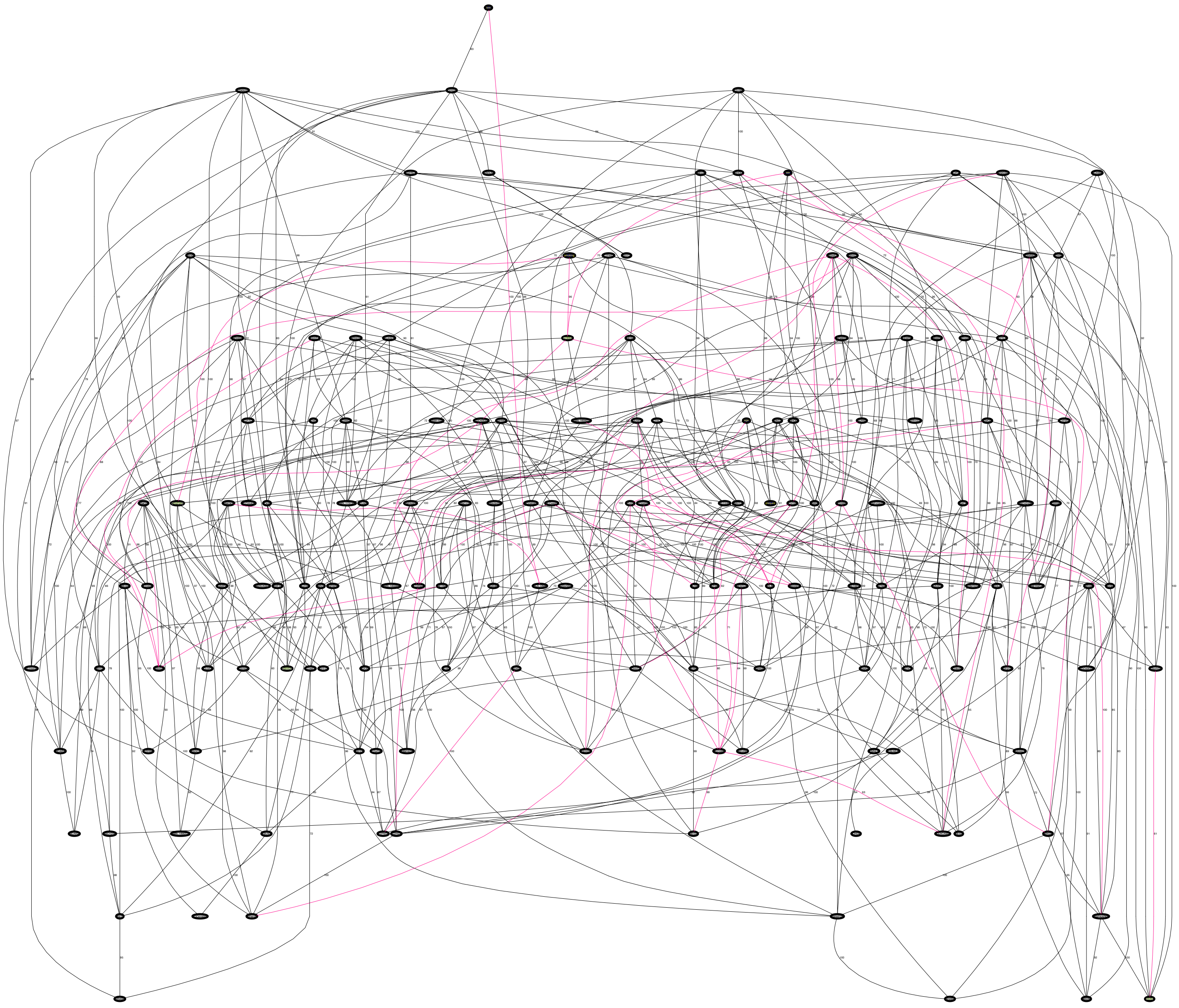
Verdugo *et al.*

The following graphs represent network skeletons for each ICA module estimated by the PC-algorithm applied to 1000 data bootstraps (see Methods in main text). Edges among variables are drawn if detected in at least 60% of data resamples. The recovery percentages are indicated to the right of the medial section of each edge. Line thickness is proportional to the edge's partial correlation. Black edges denote positive and pink edges negative partial correlations. Plaques and risk factors are in blue. Genes directly connected to smoking are in green and those directly connected to plaques are in orange. Other genes are in gray. Only genes that are involved in the shortest paths connecting smoking to plaques are shown. Genes connected to both smoking and plaques are in red.

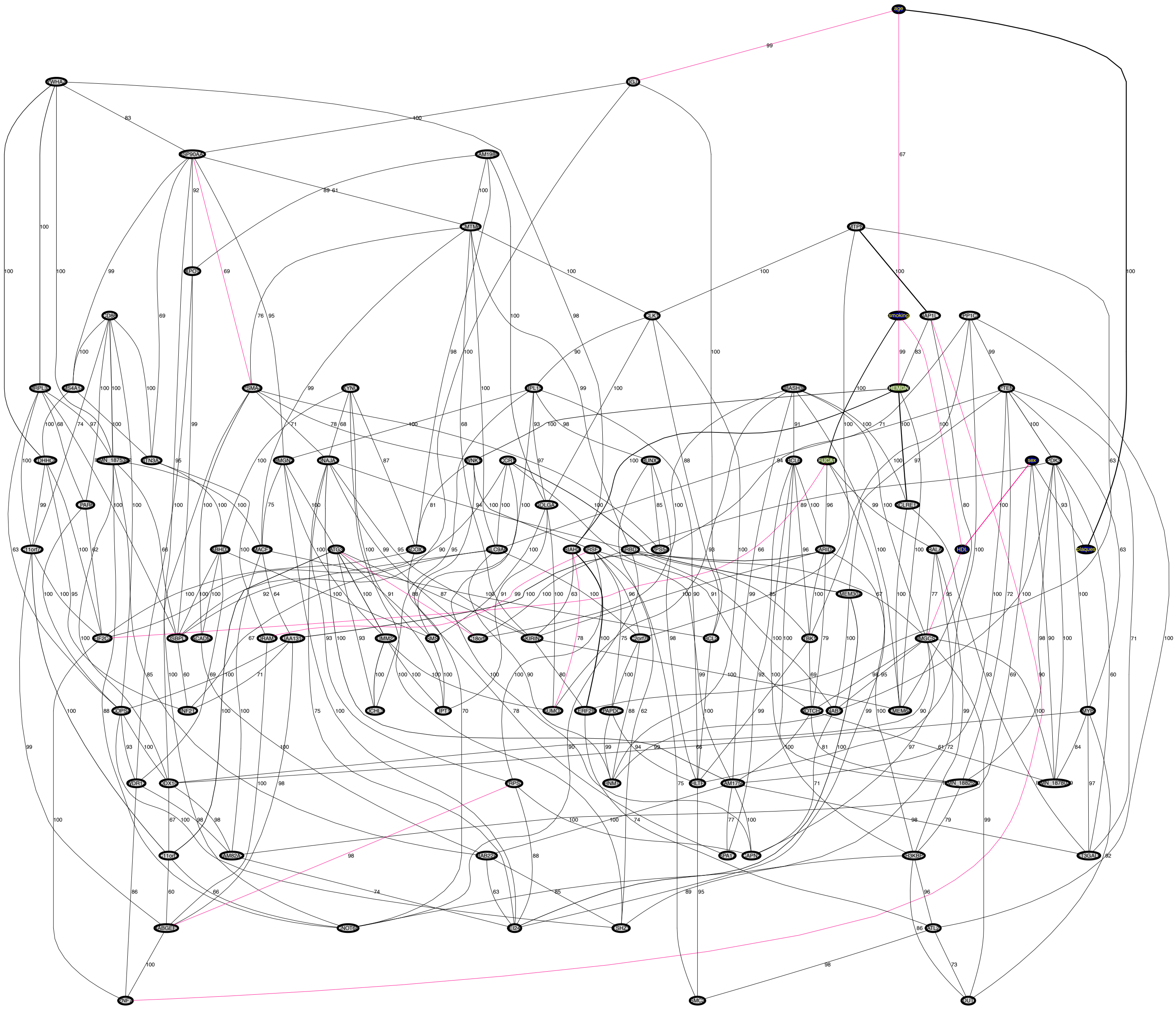
Network Skeleton for Pattern 4



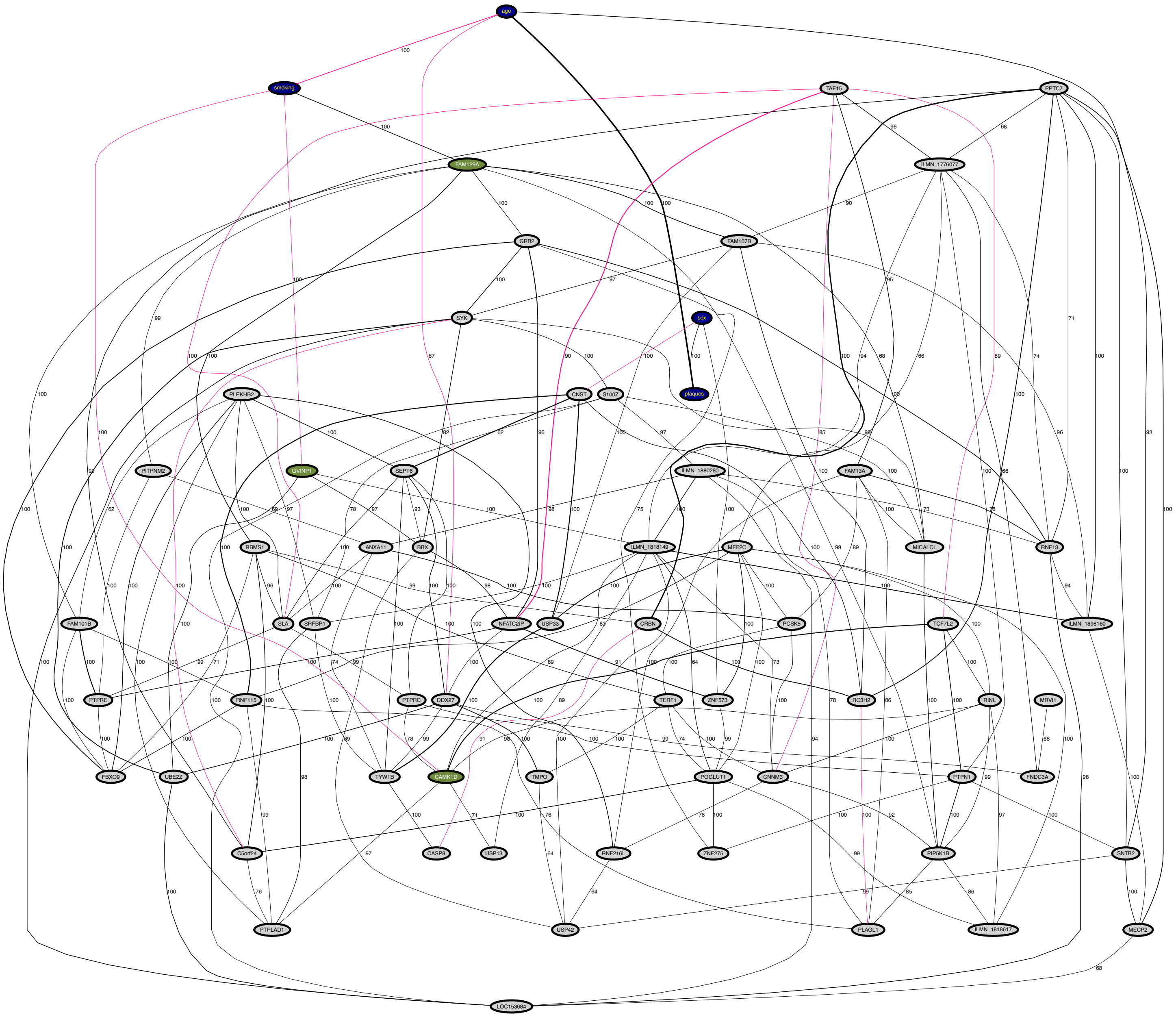
Network Skeleton for Pattern 11



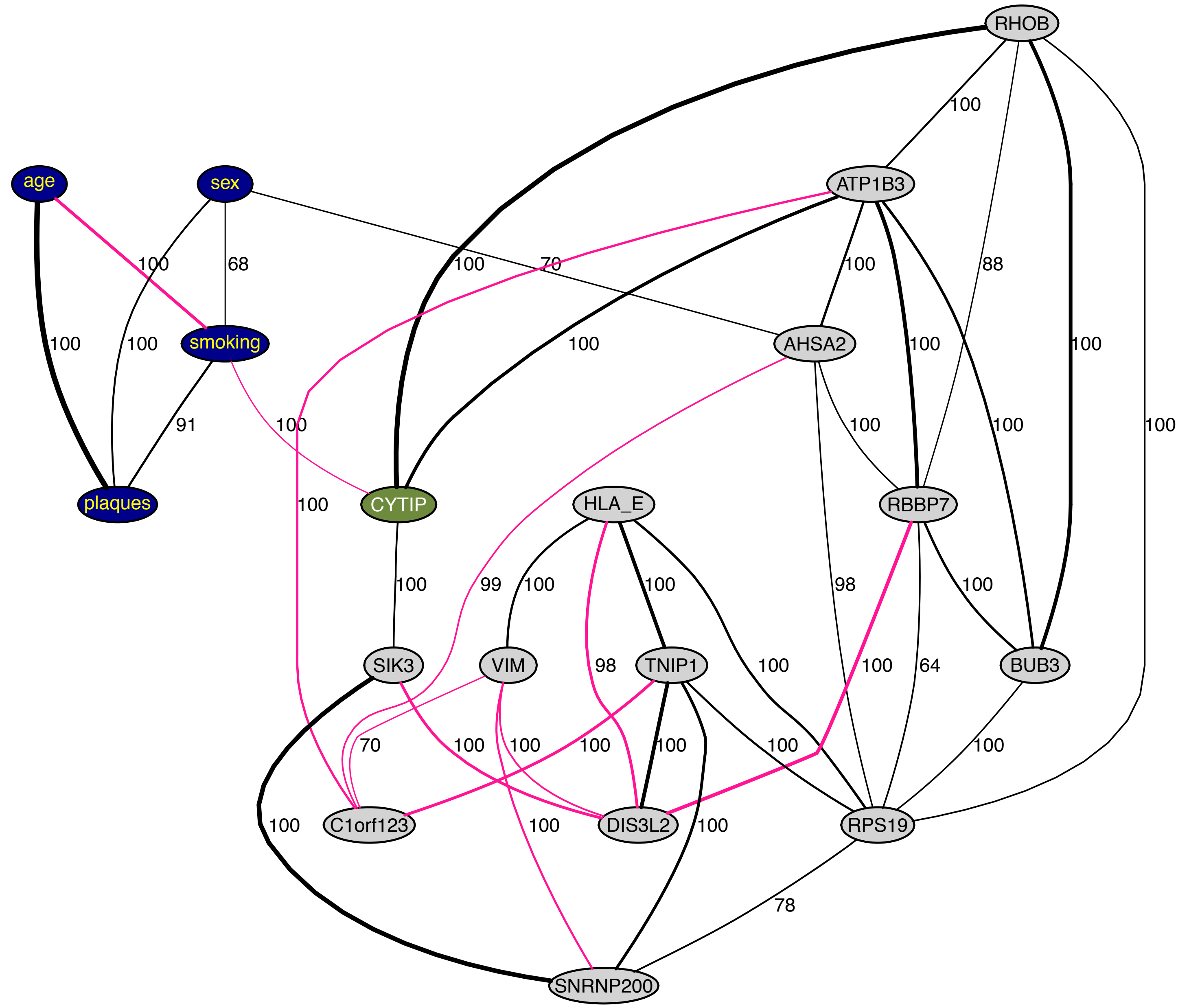
Network Skeleton for Pattern 12



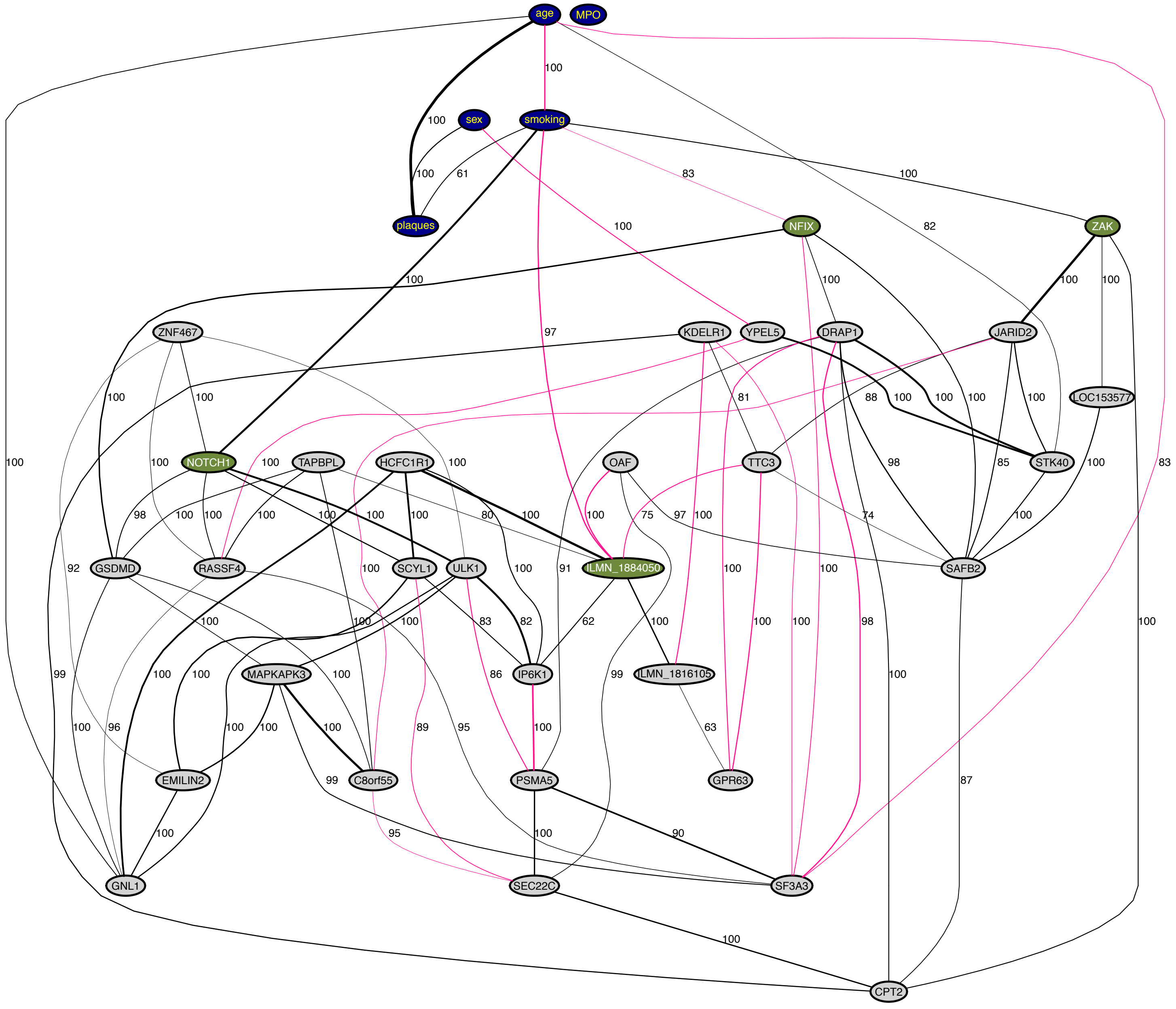
Network Skeleton for Pattern 14



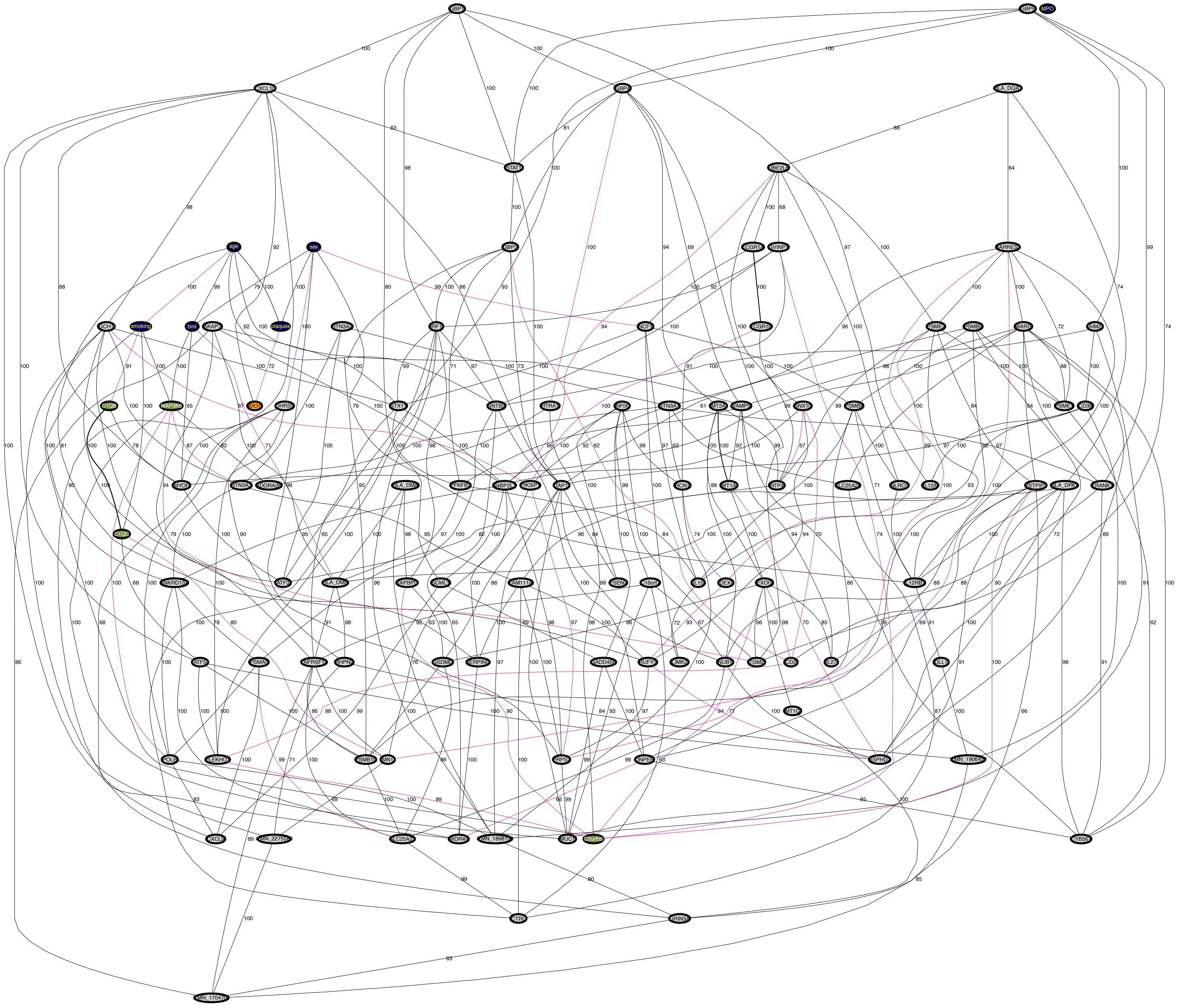
Network Skeleton for Pattern 15



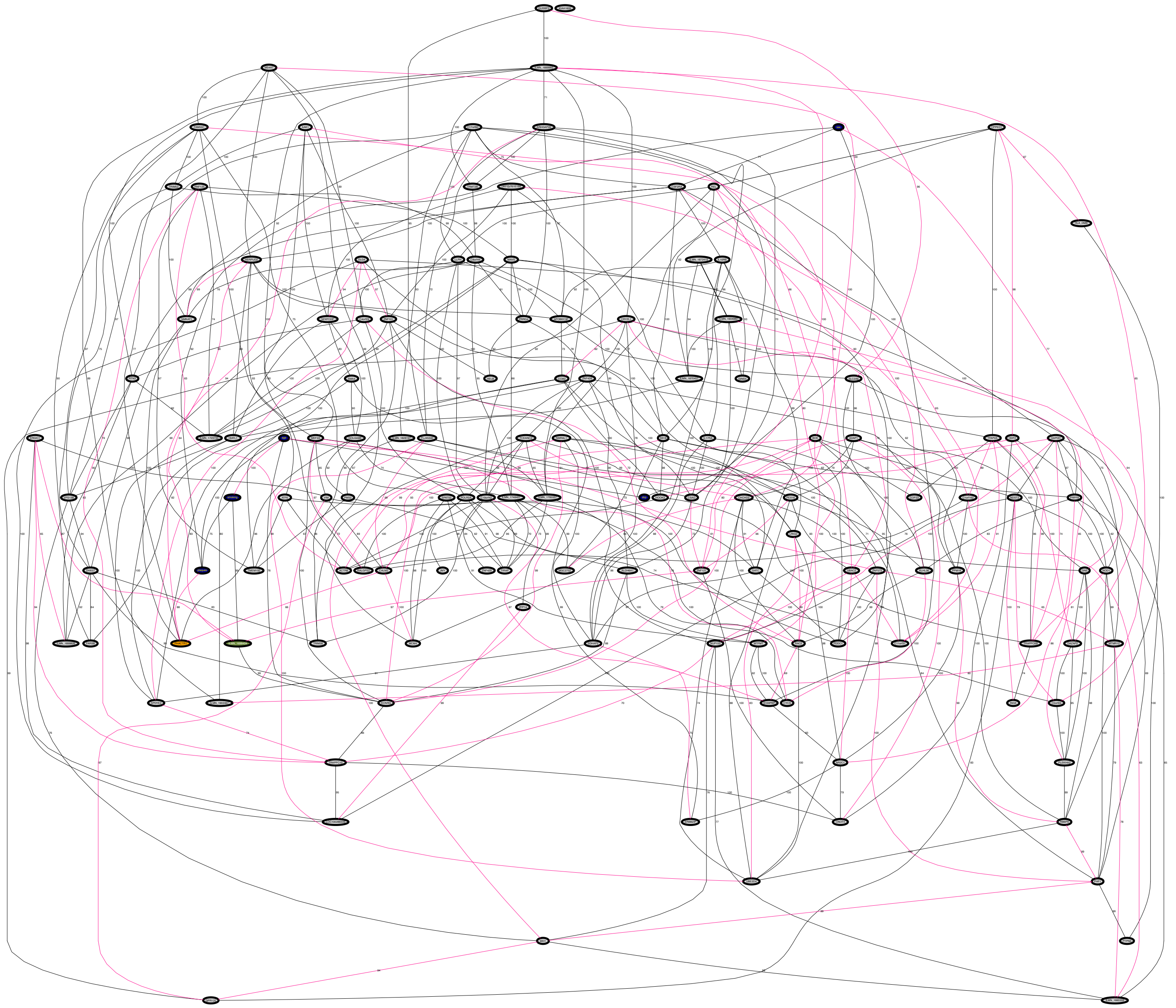
Network Skeleton for Pattern 17



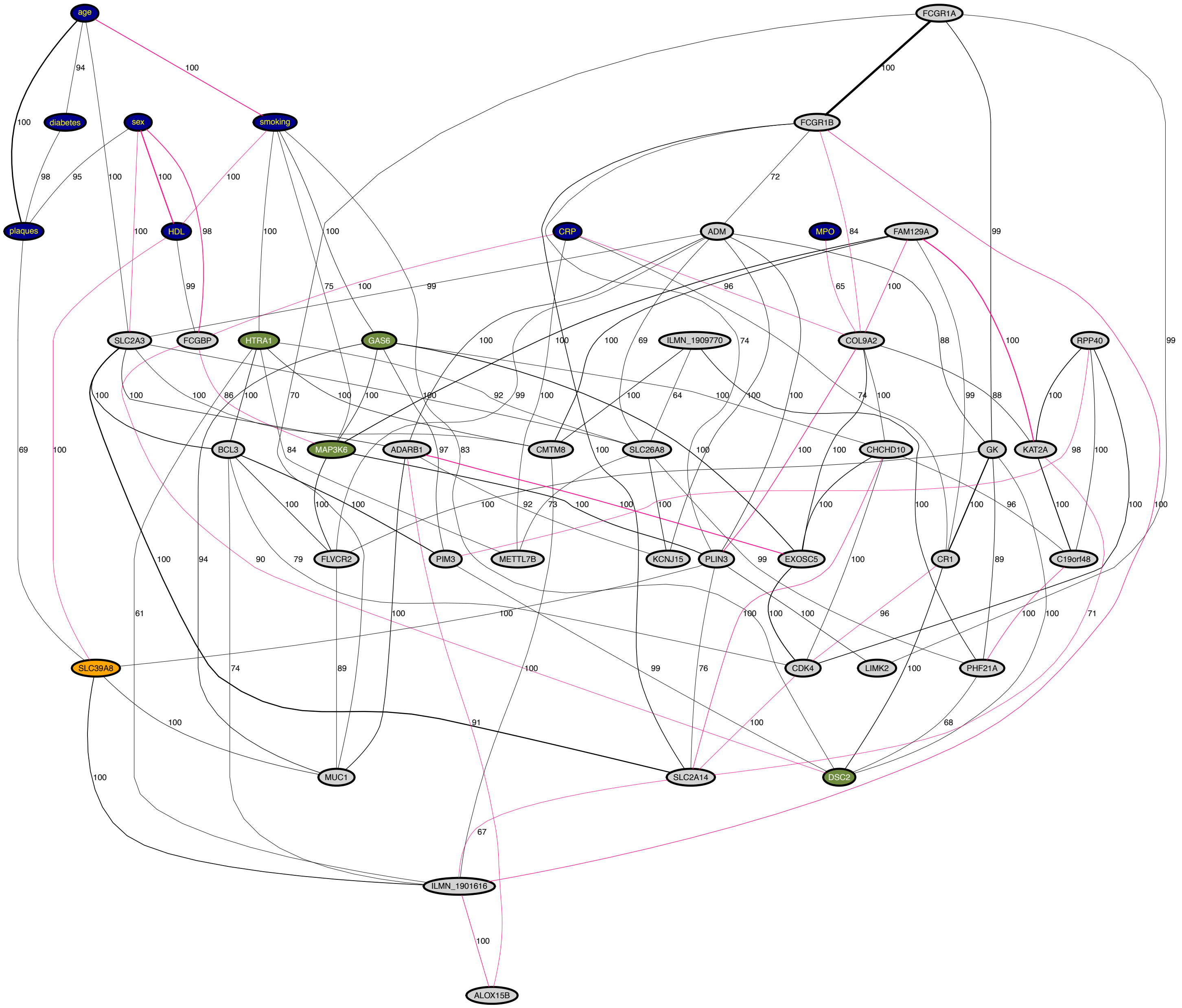
Network Skeleton for Pattern 18



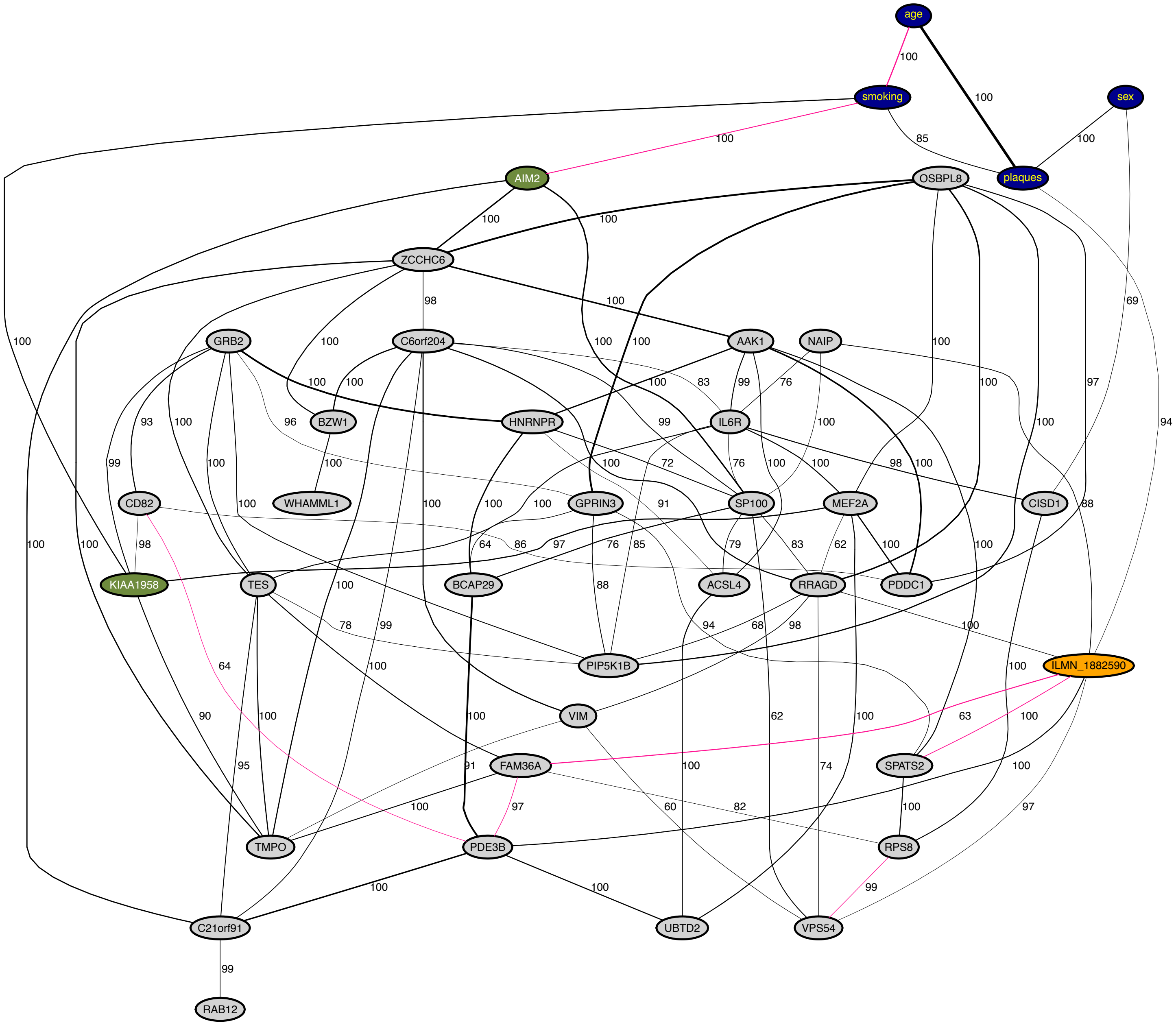
Network Skeleton for Pattern 19



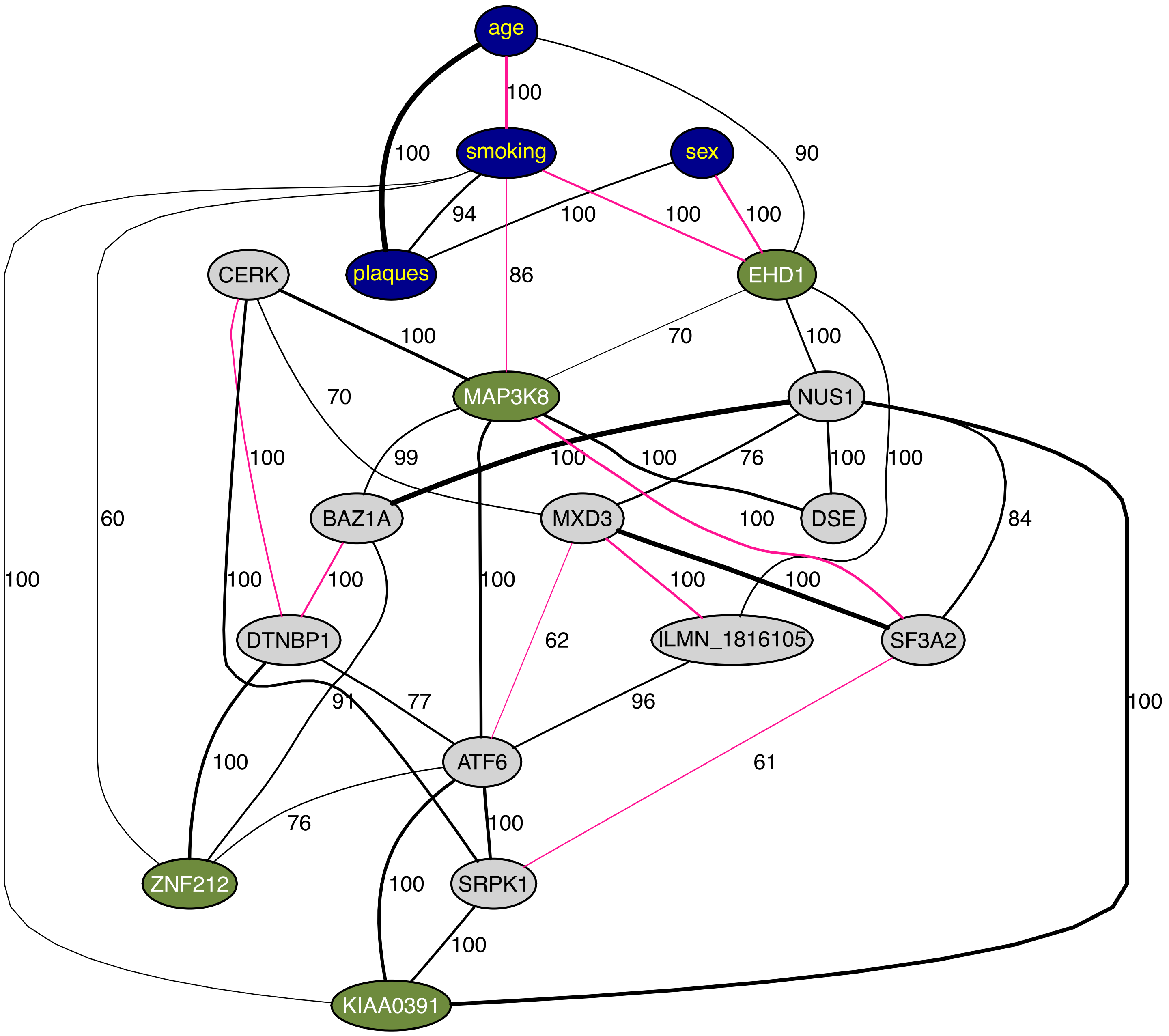
Network Skeleton for Pattern 21



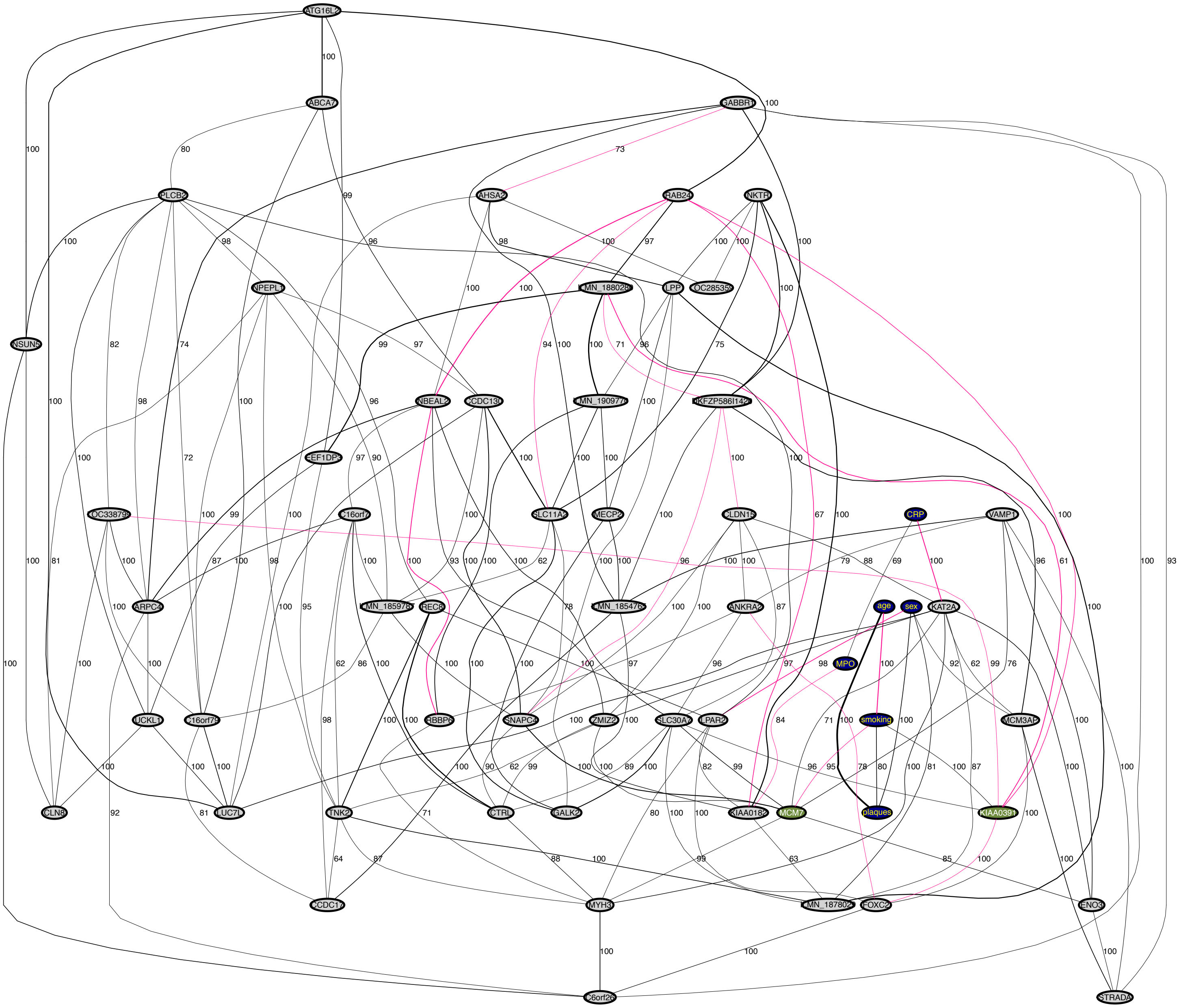
Network Skeleton for Pattern 23



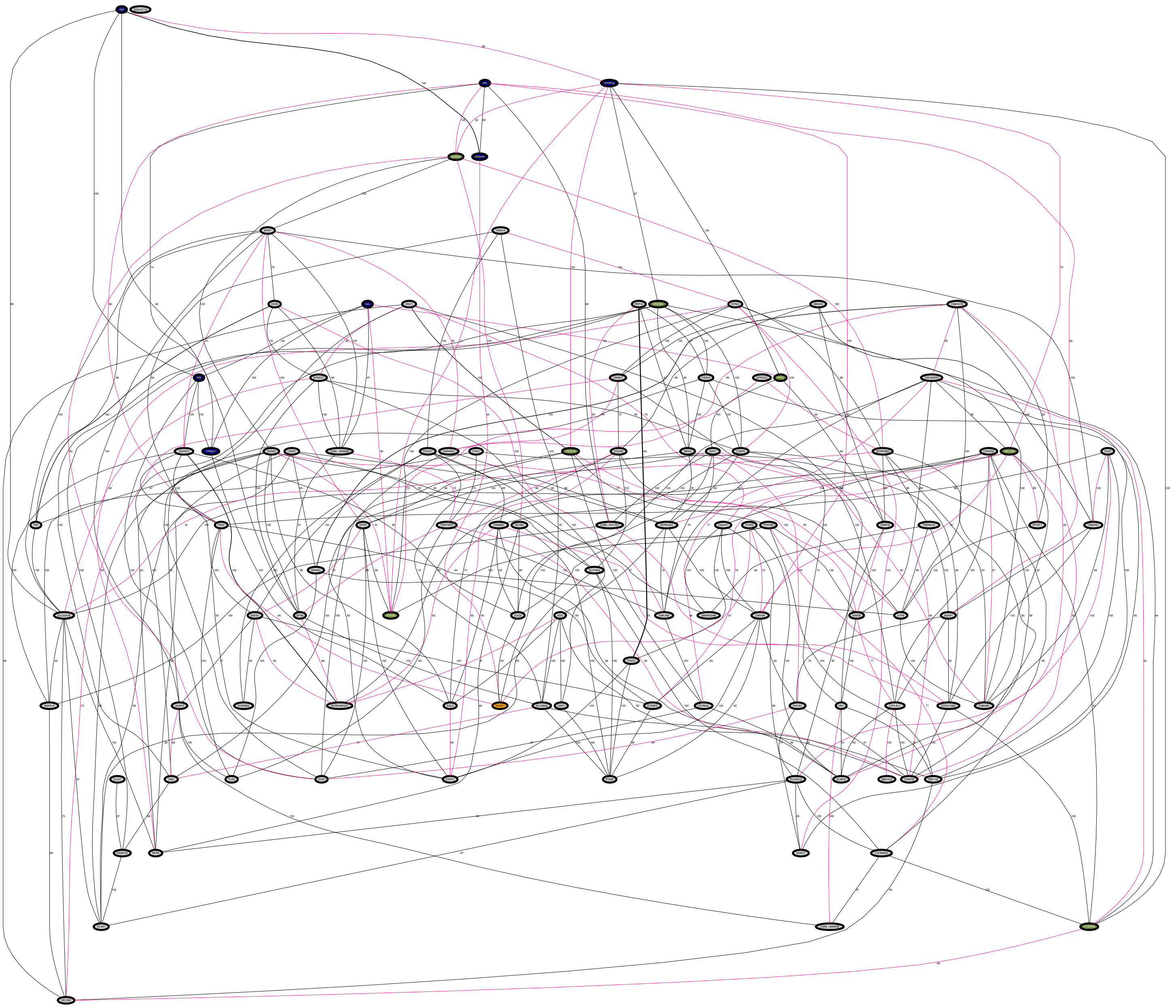
Network Skeleton for Pattern 27



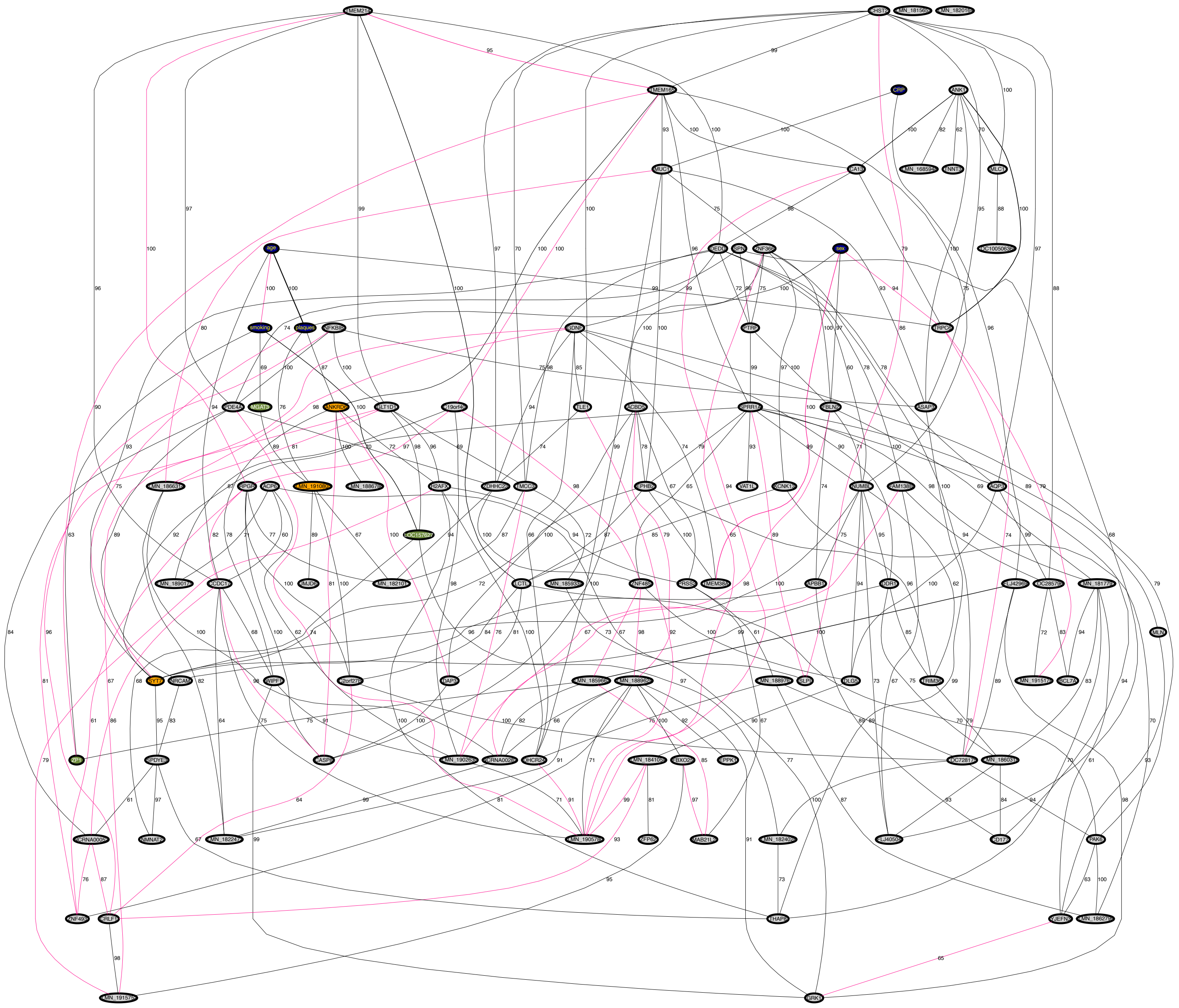
Network Skeleton for Pattern 28



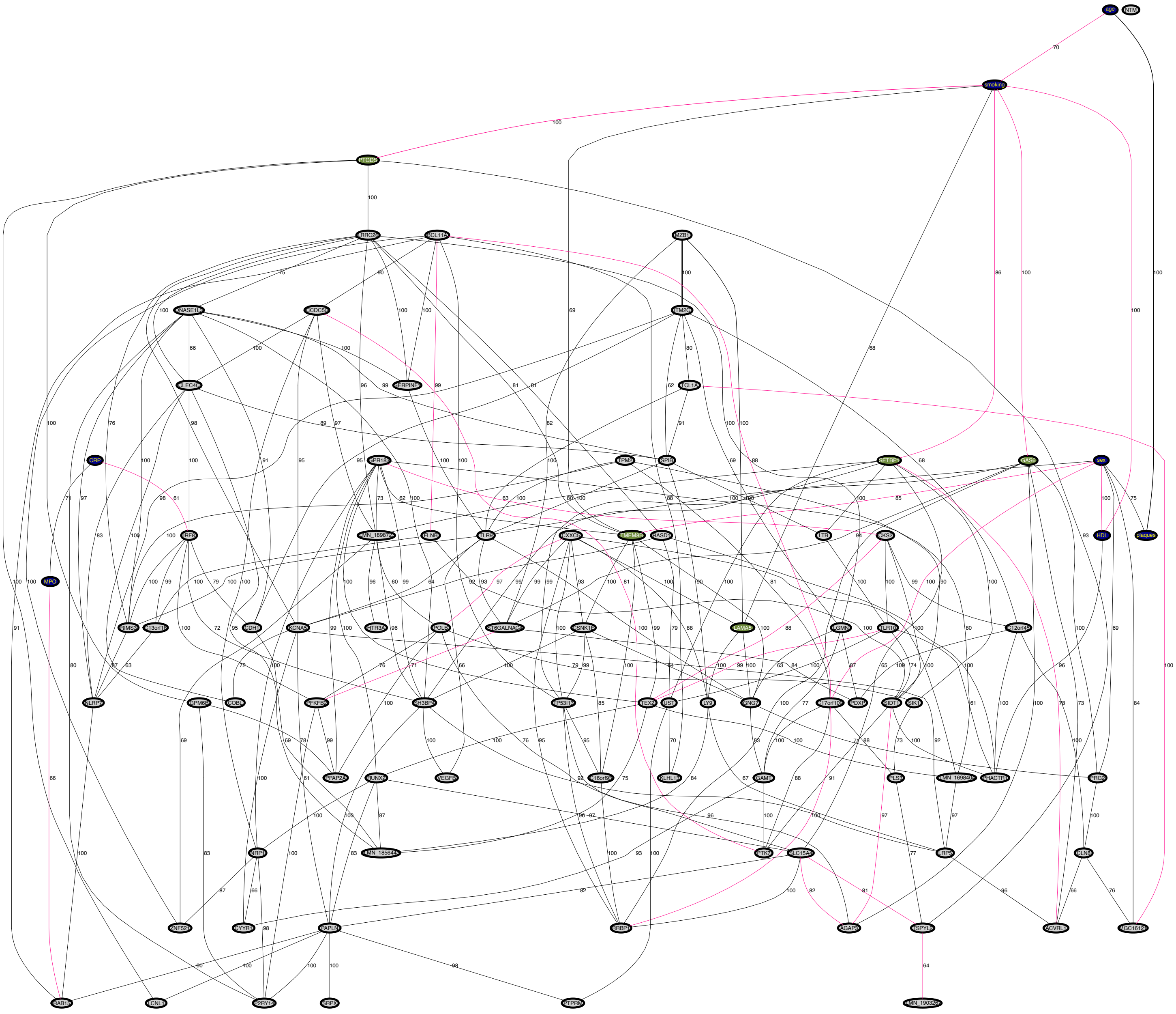
Network Skeleton for Pattern 29



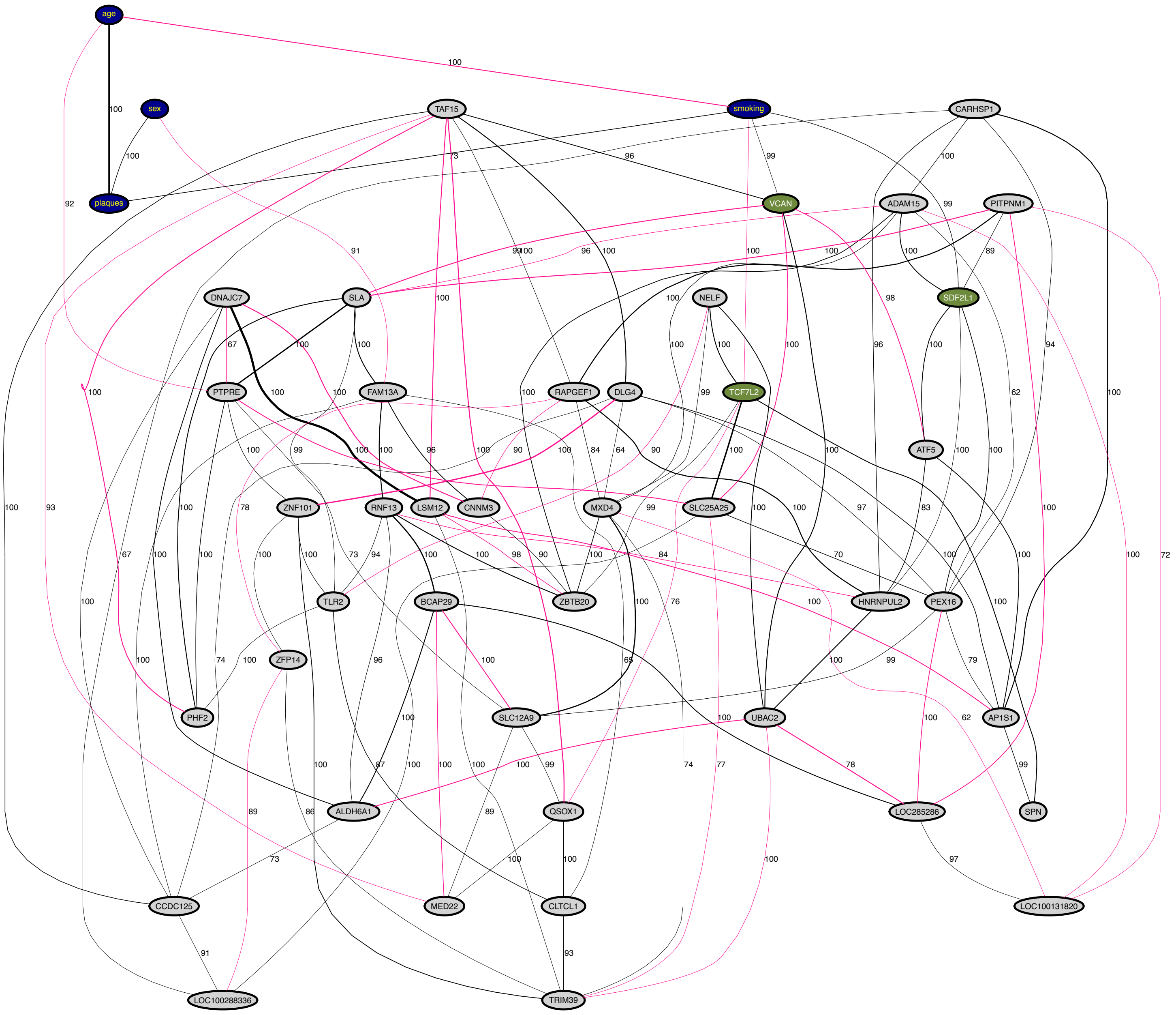
Network Skeleton for Pattern 30



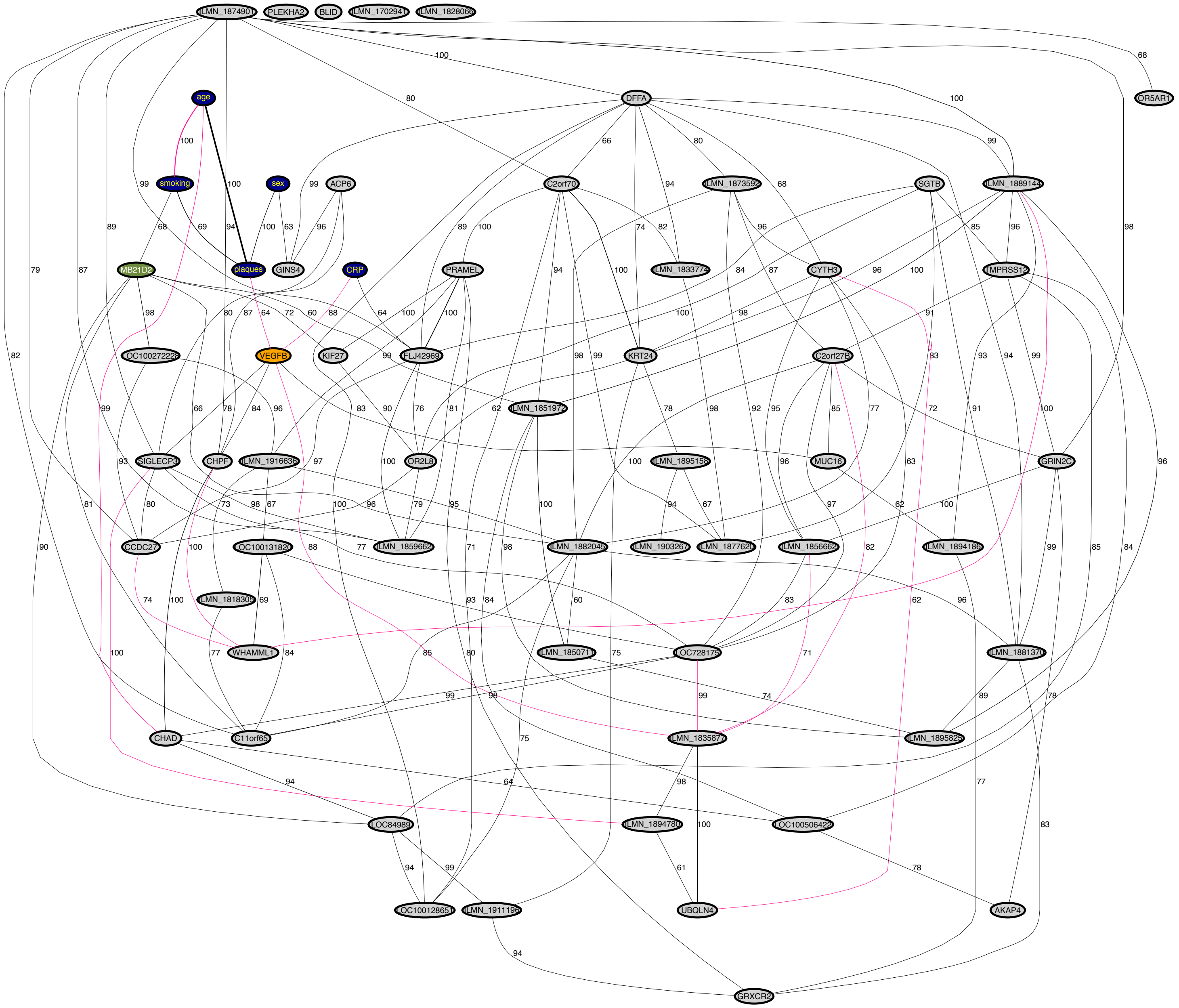
Network Skeleton for Pattern 31



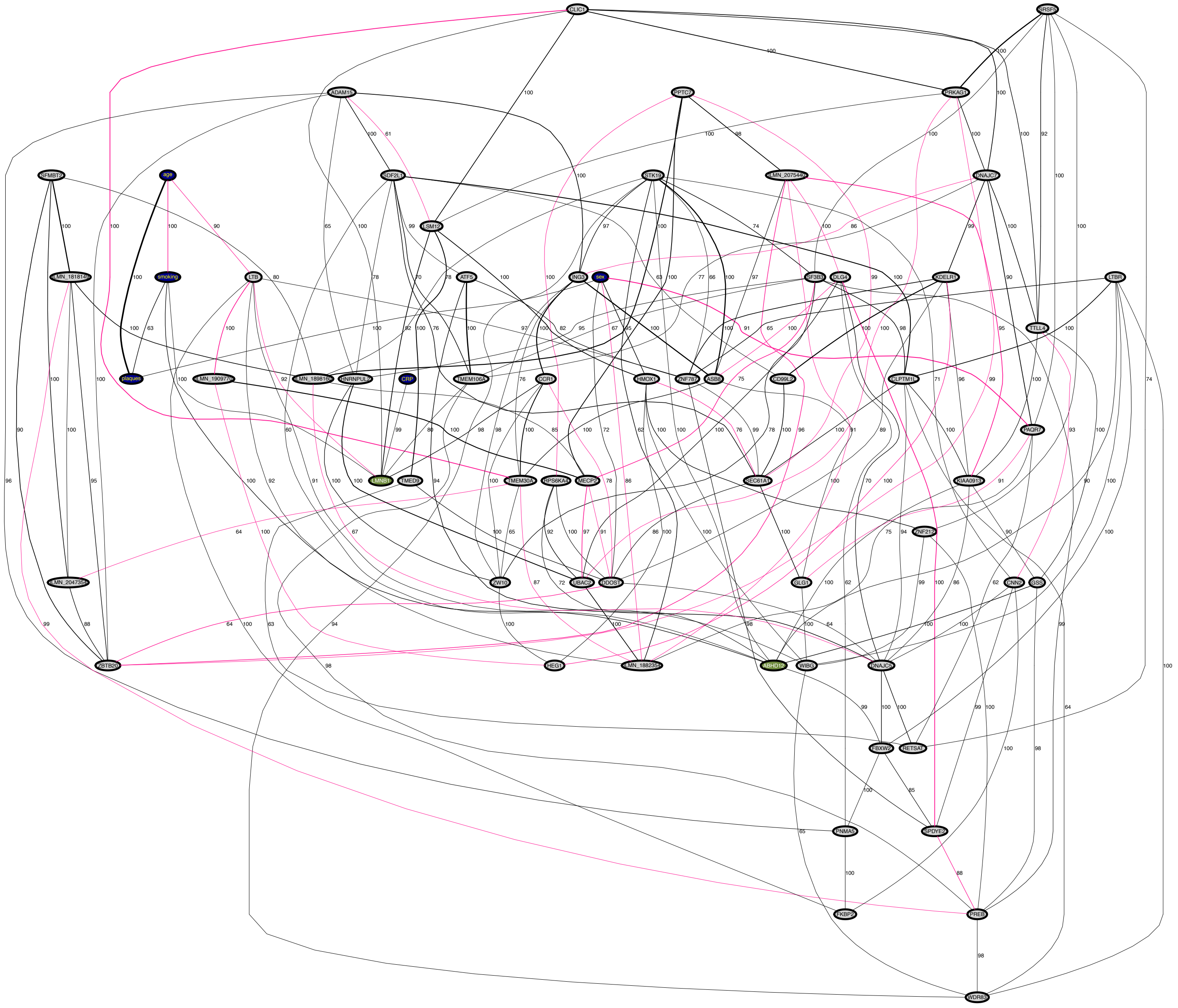
Network Skeleton for Pattern 33



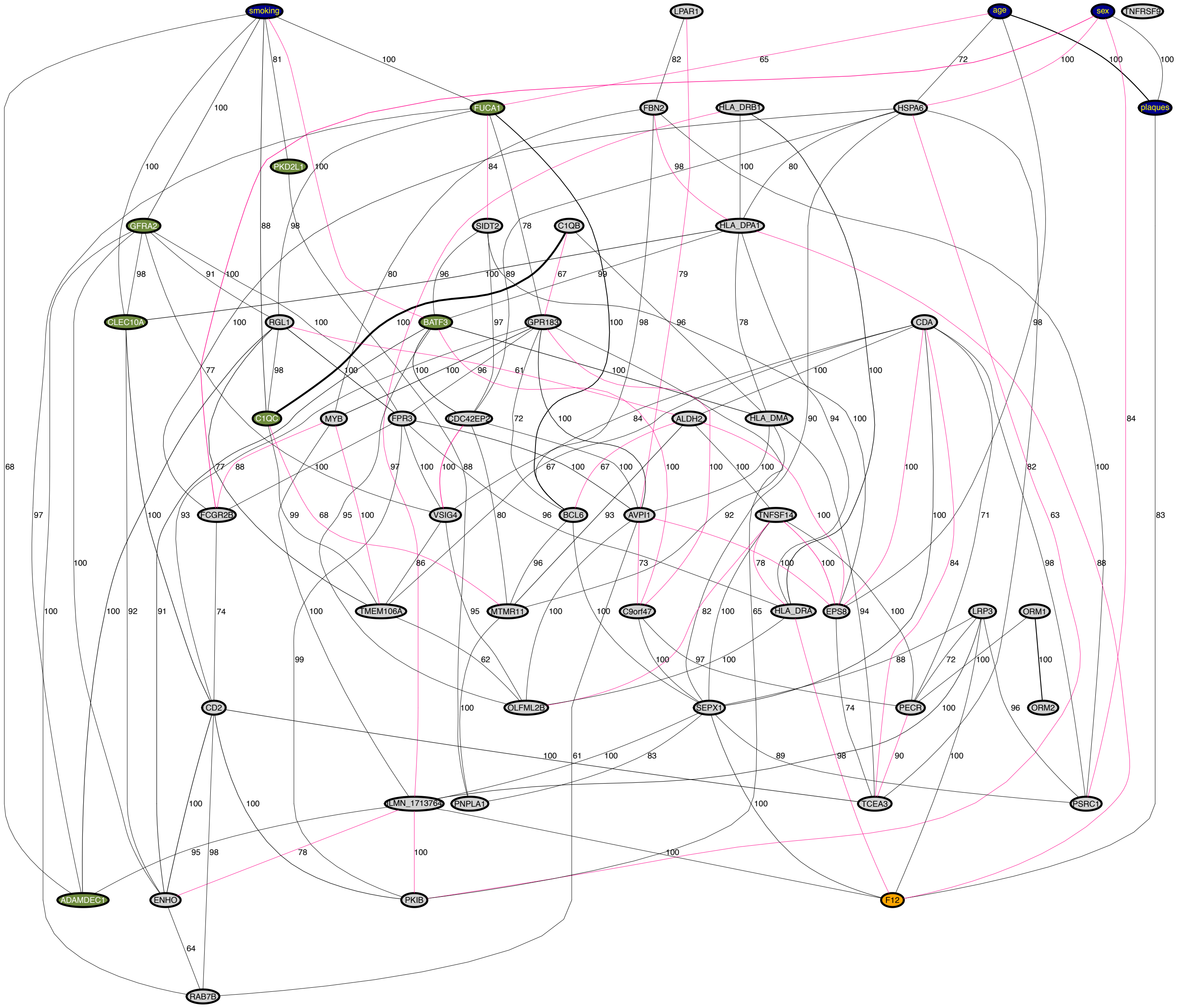
Network Skeleton for Pattern 34



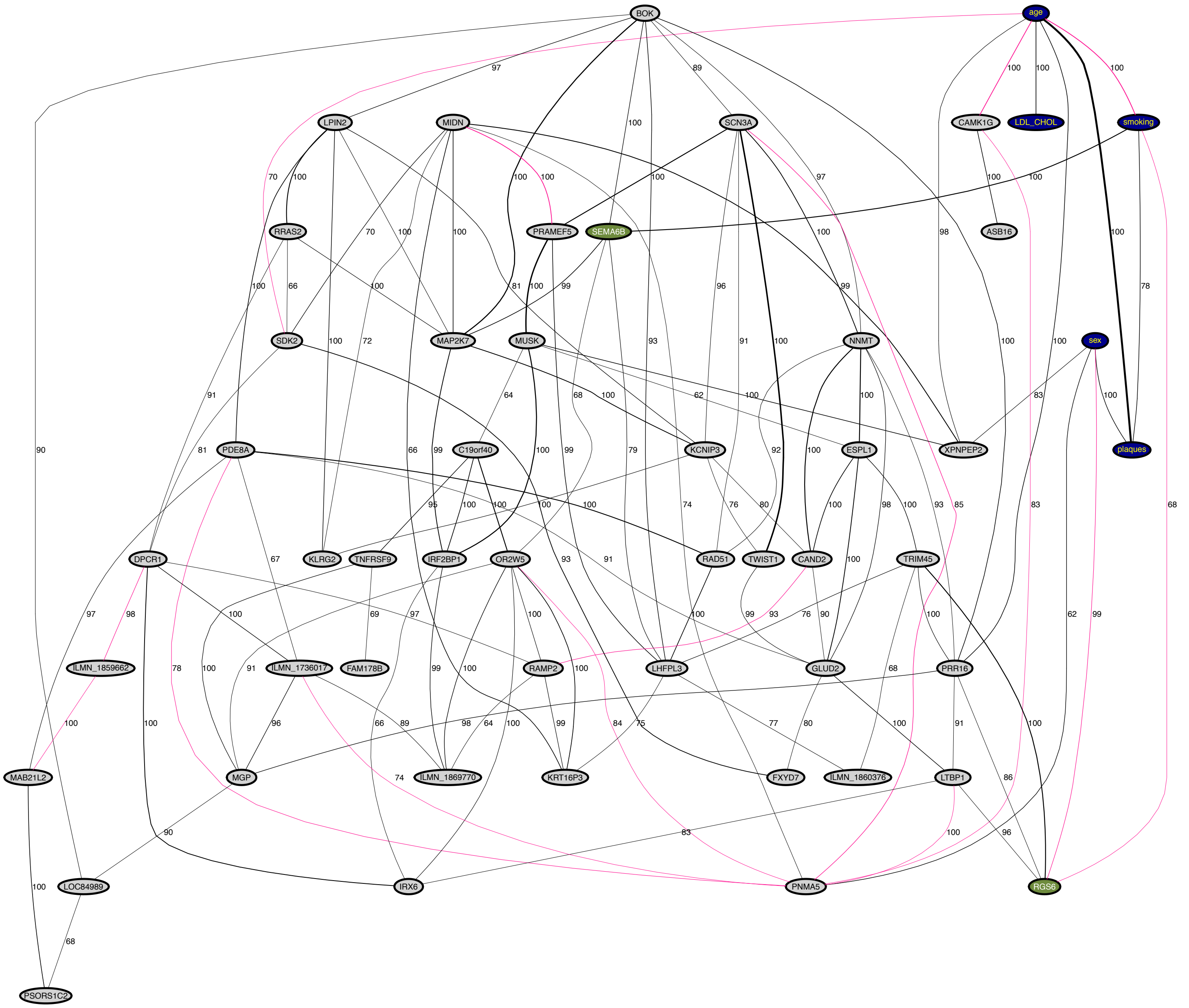
Network Skeleton for Pattern 36



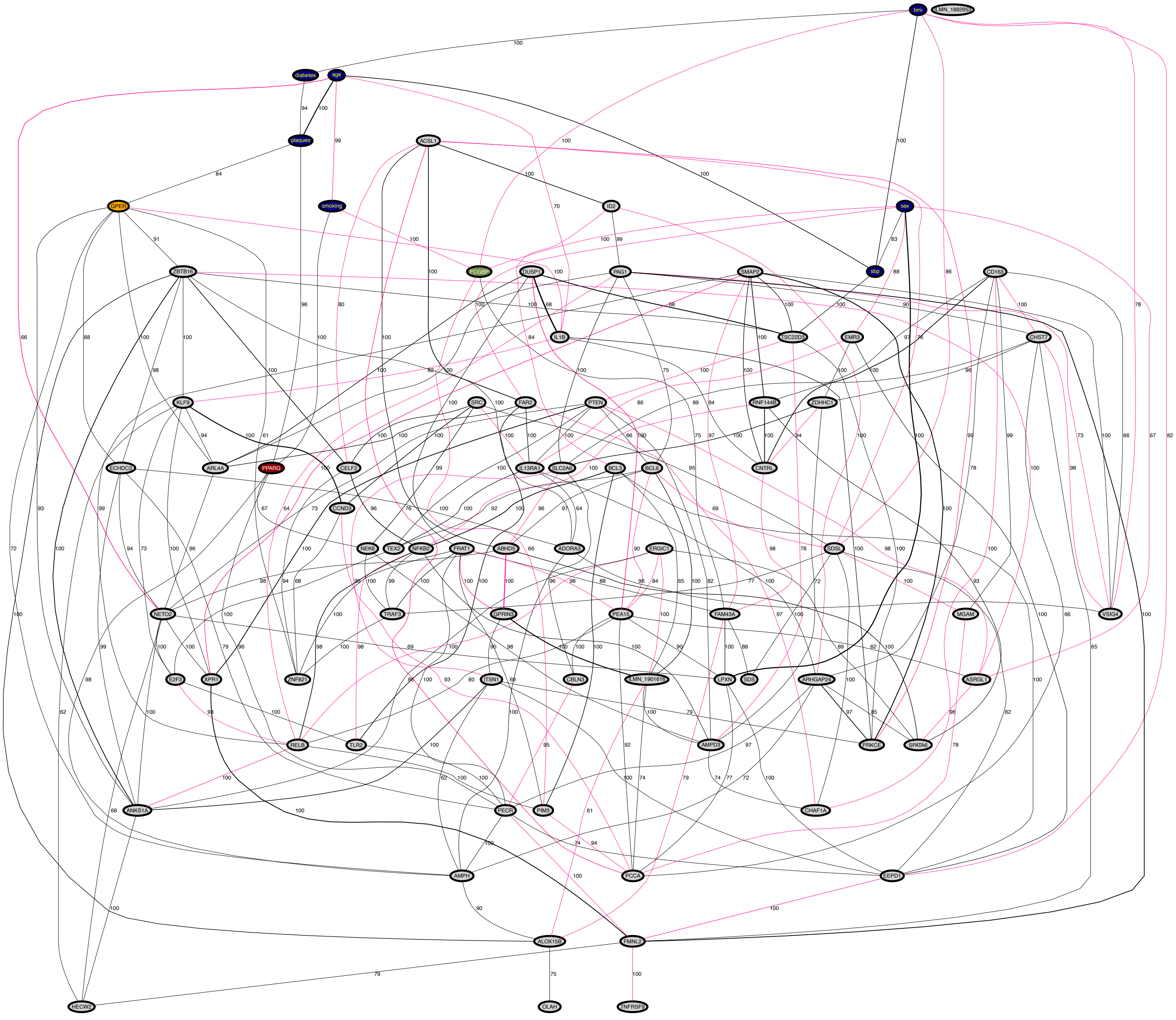
Network Skeleton for Pattern 39



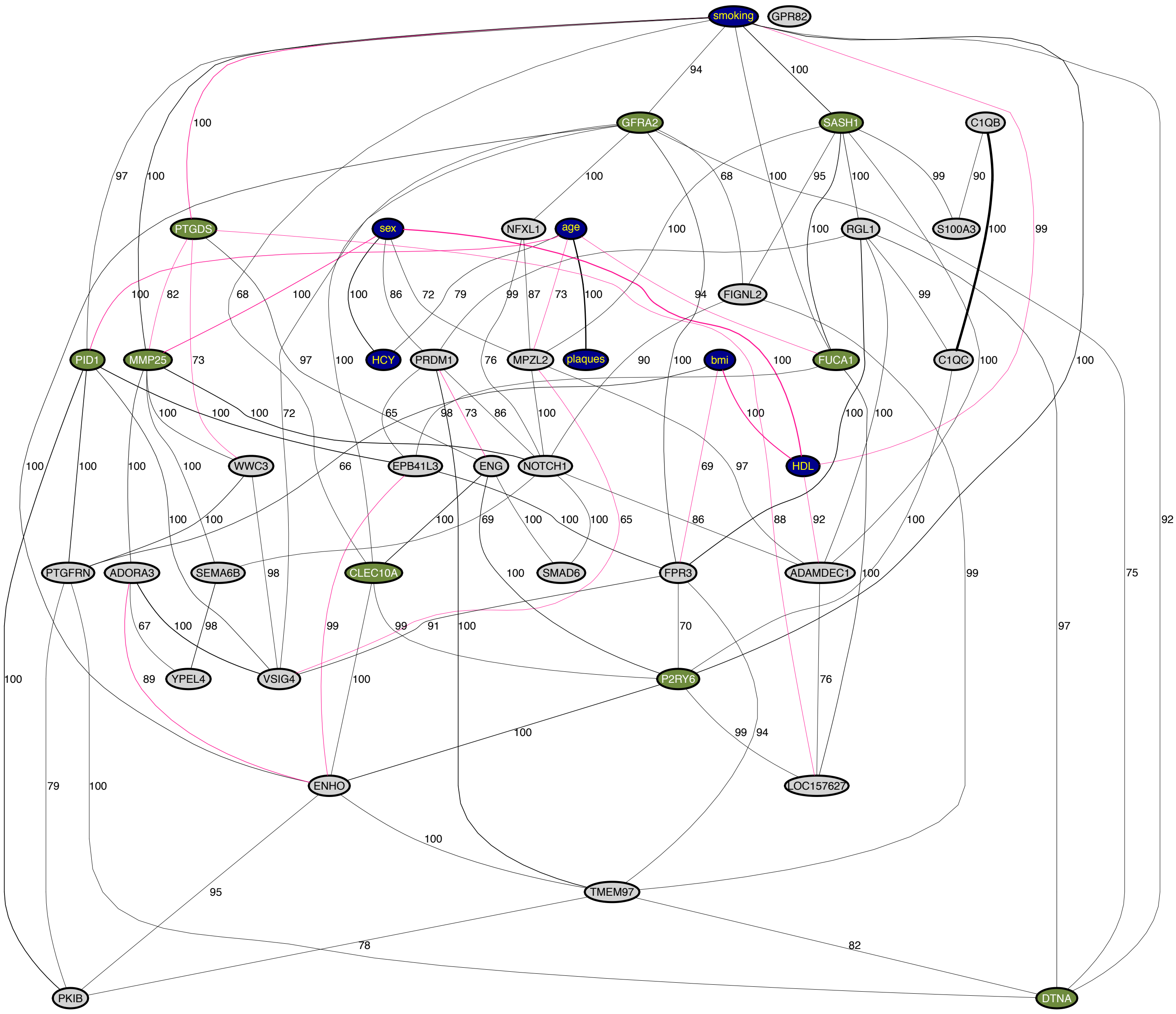
Network Skeleton for Pattern 41



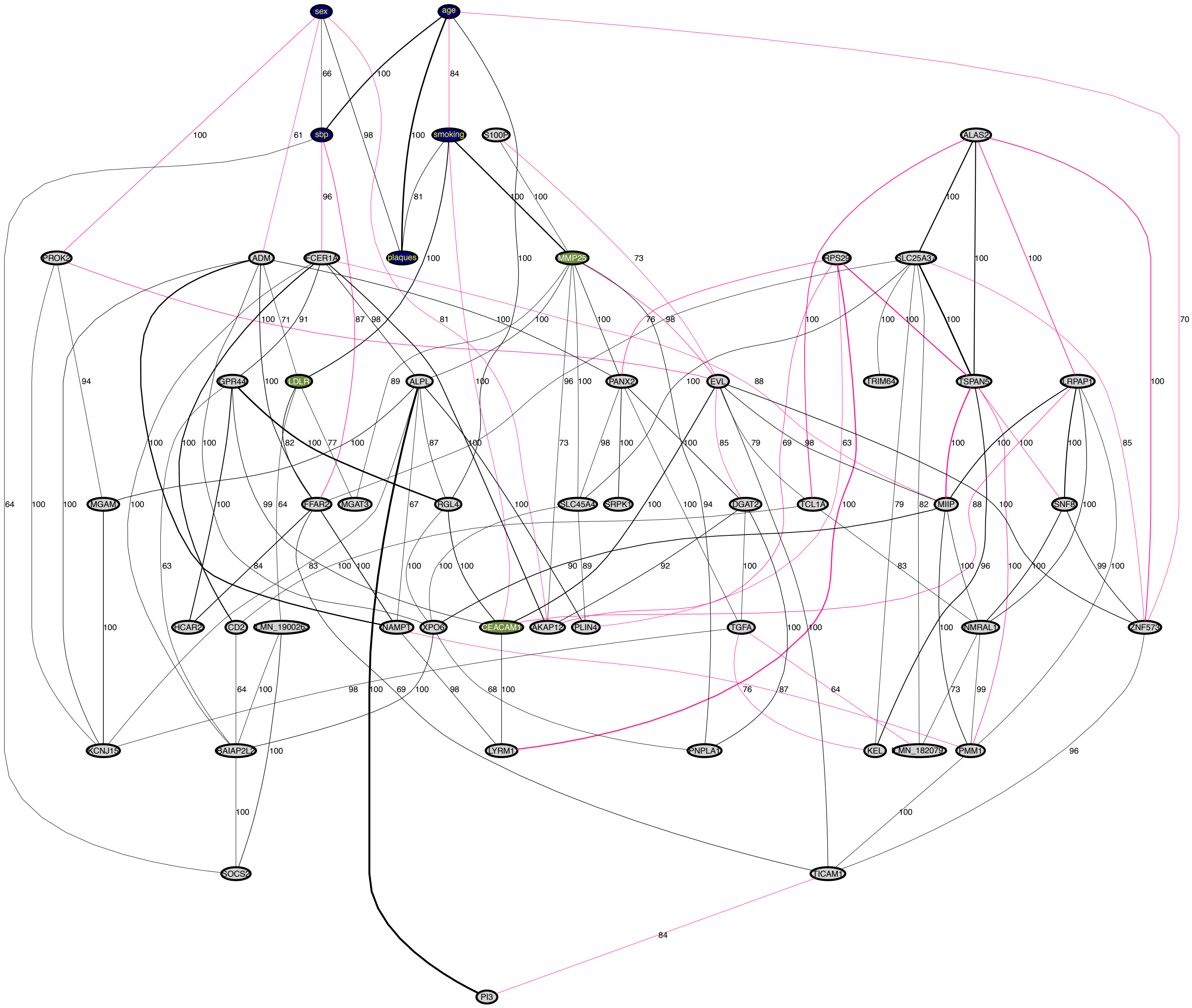
Network Skeleton for Pattern 42



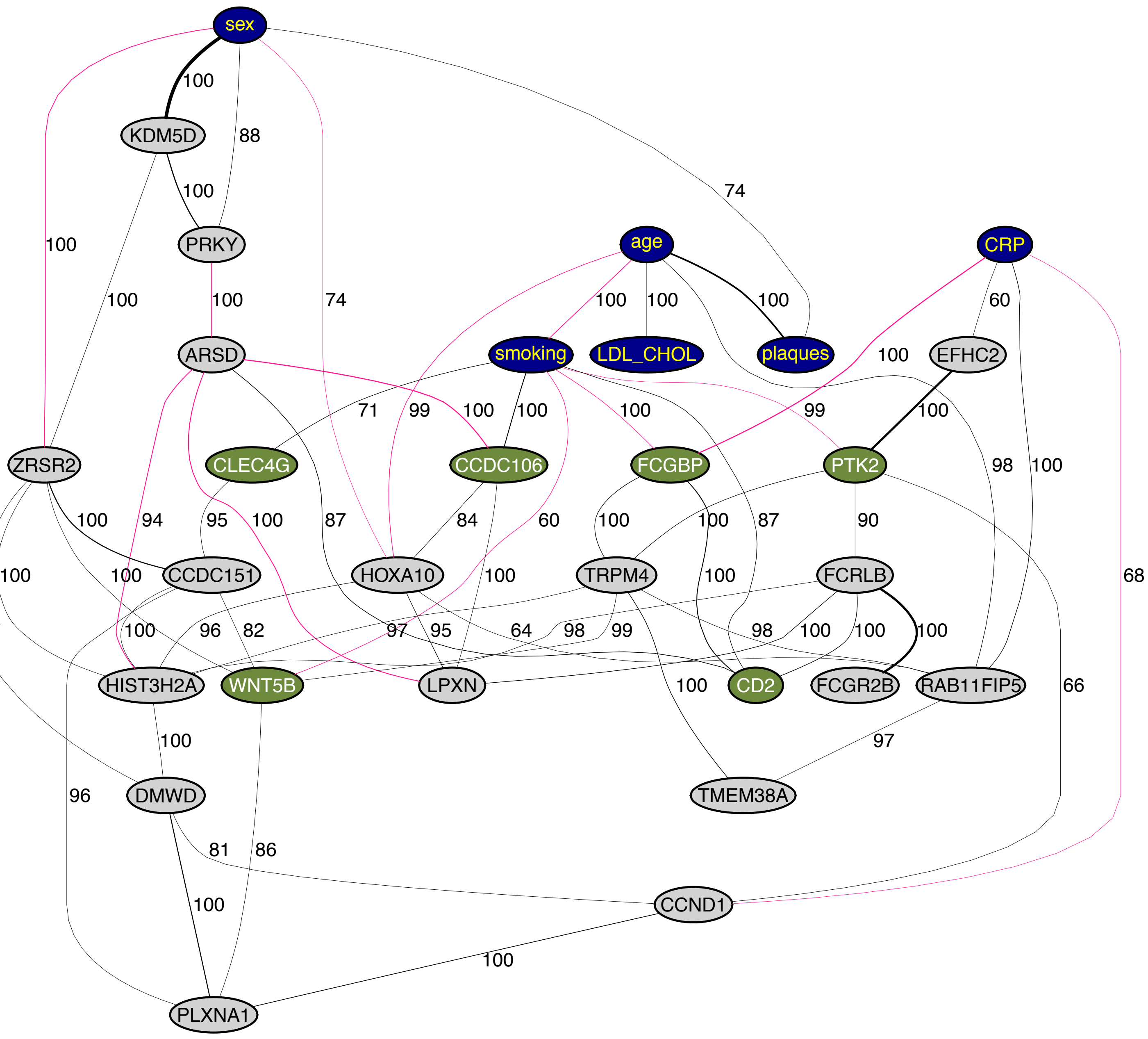
Network Skeleton for Pattern 43



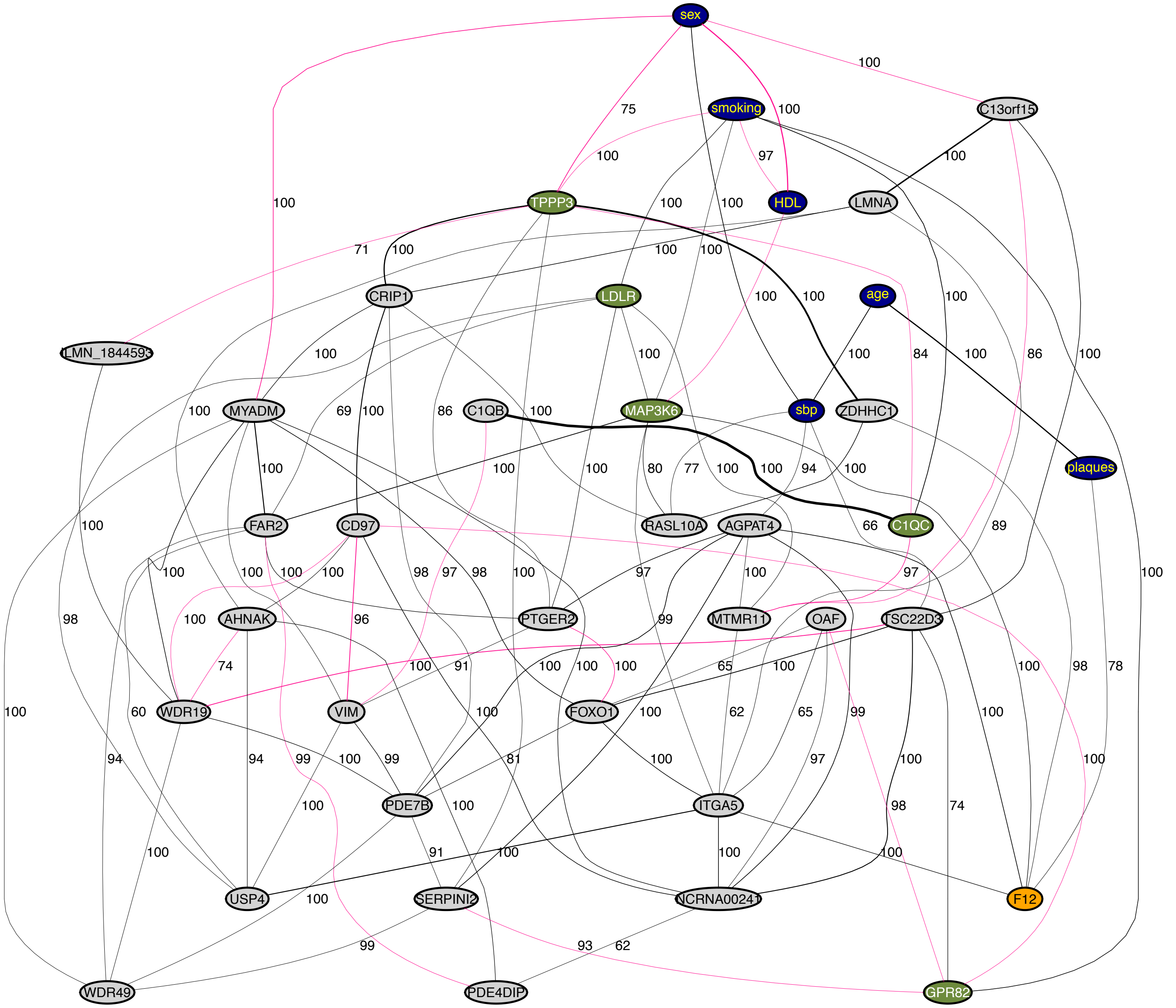
Network Skeleton for Pattern 45



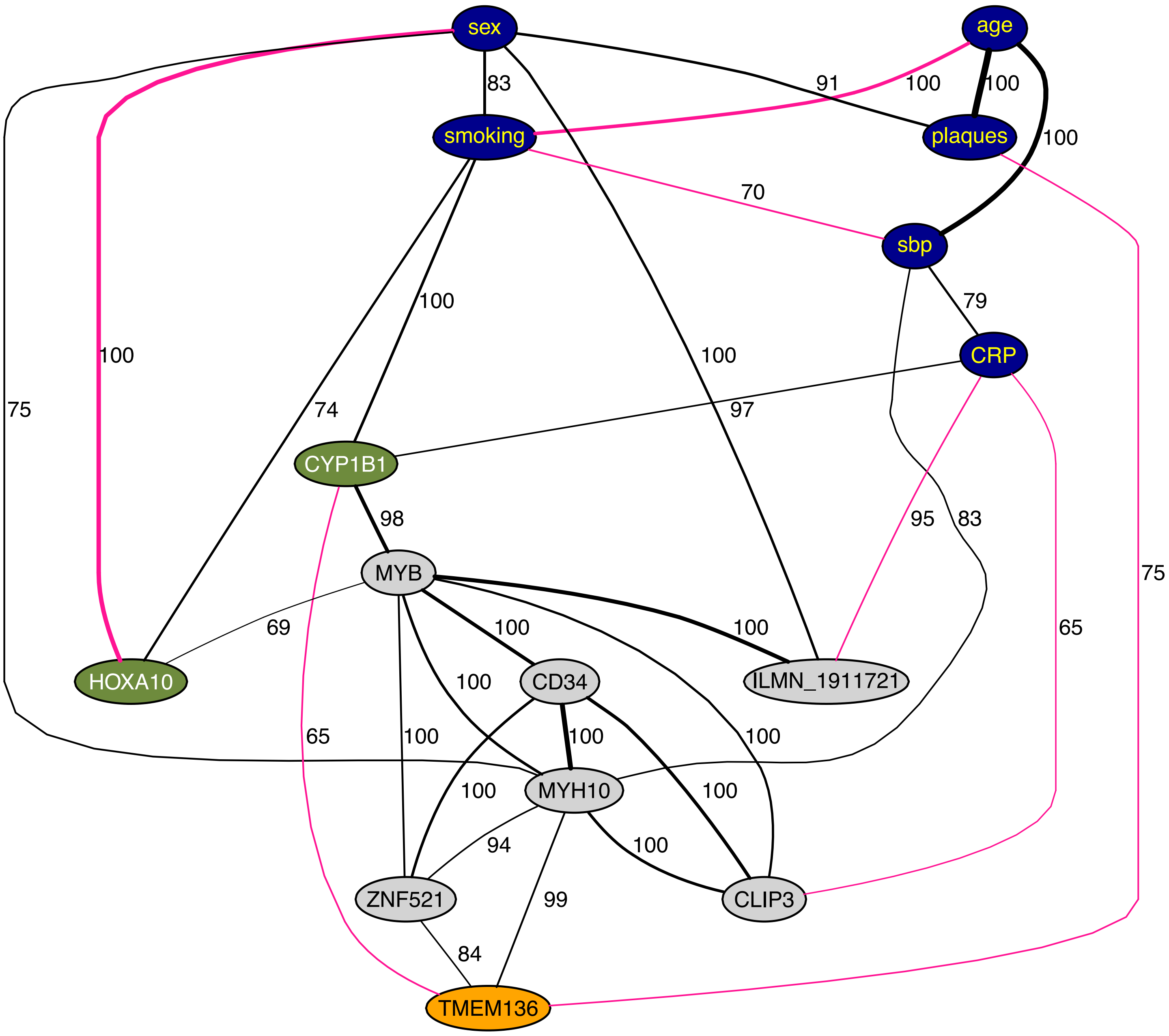
Network Skeleton for Pattern 48



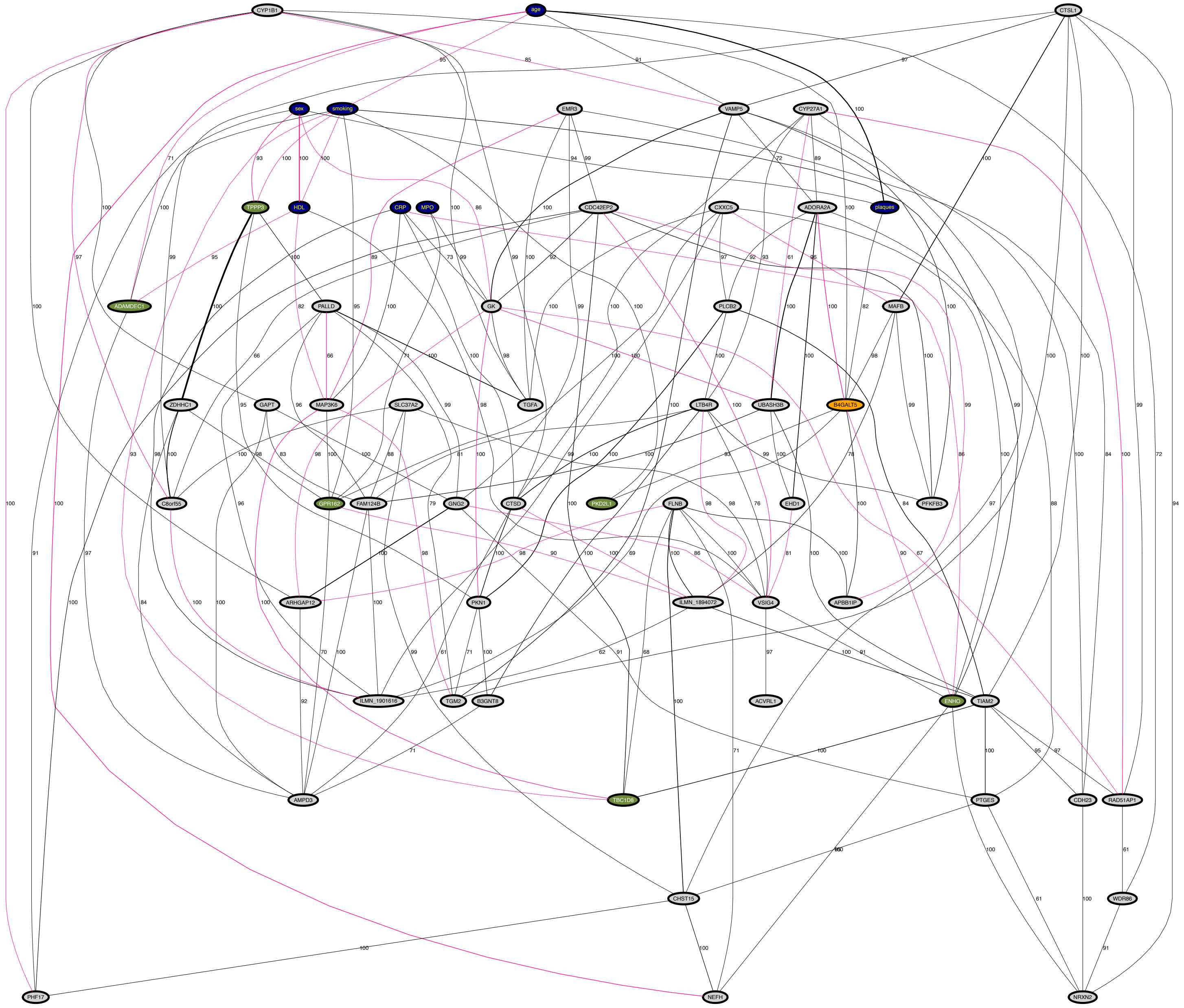
Network Skeleton for Pattern 49



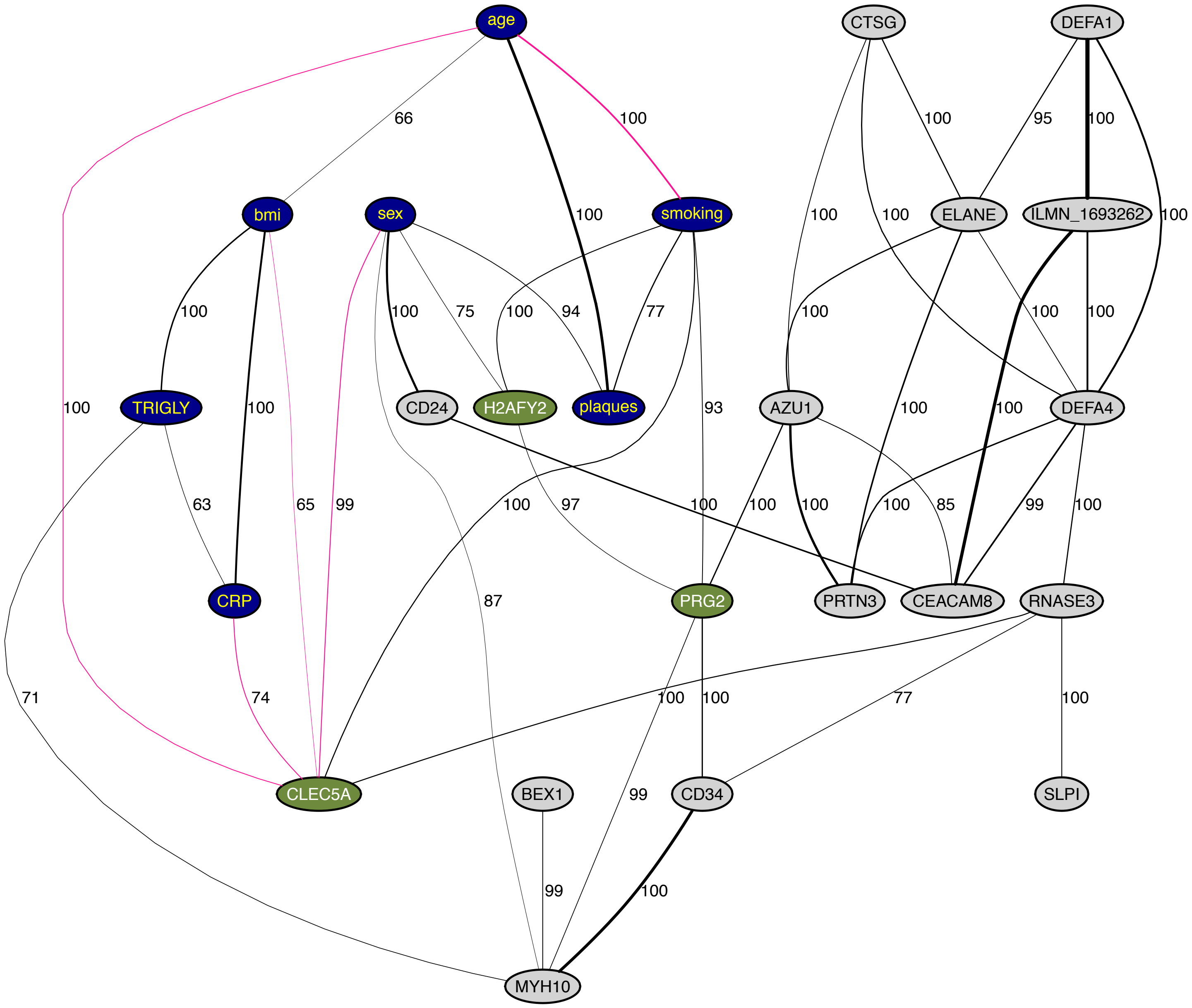
Network Skeleton for Pattern 51



Network Skeleton for Pattern 52



Network Skeleton for Pattern 54



Network Skeleton for Pattern 58