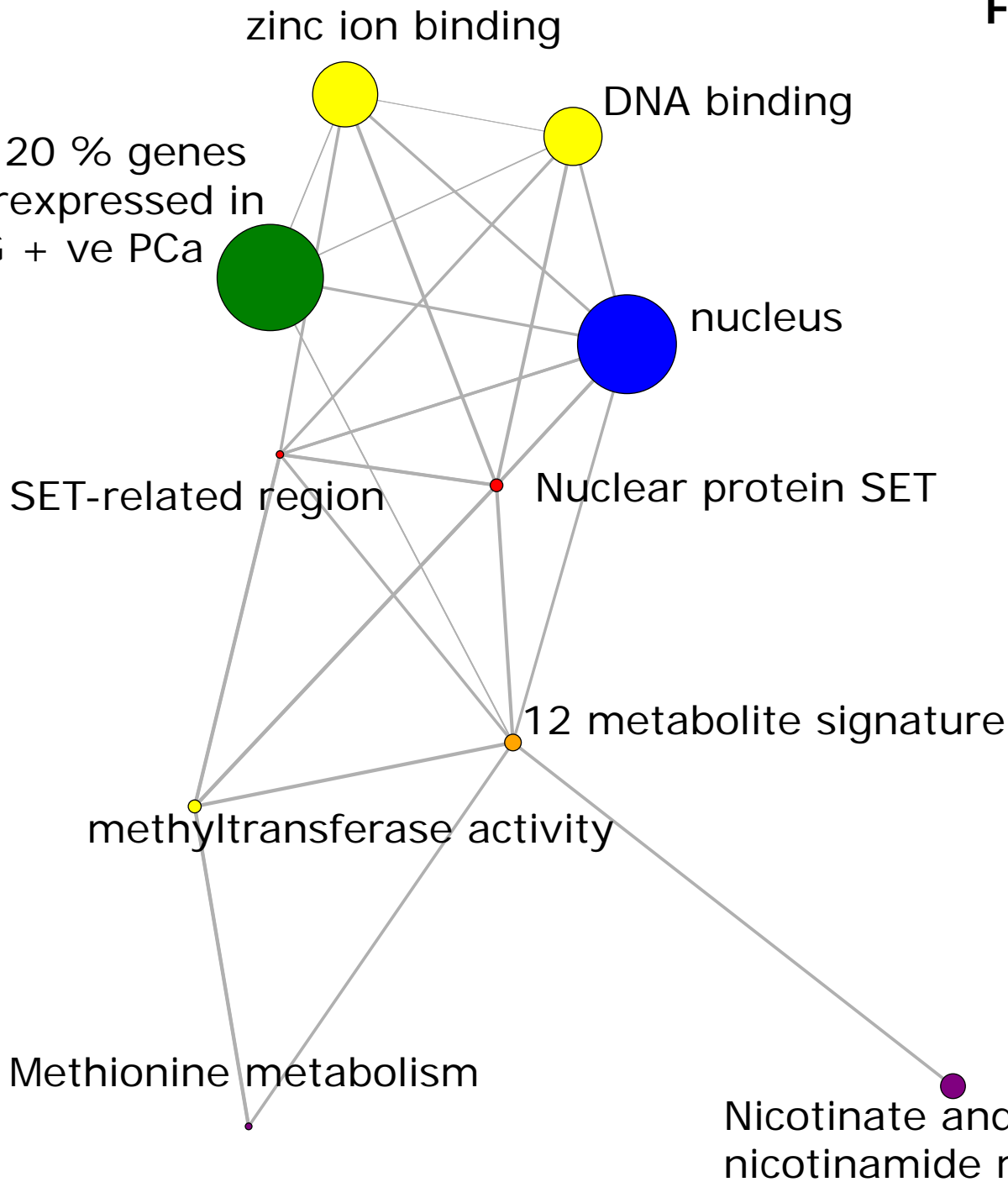


Figure S4

Top 20 % genes
overexpressed in
ERG + ve PCa



GO Cellular component



Oncomine gene expression signature



GO Molecular function



KEGG pathway



InterPro



12 metabolite signature concordant between PCa cell lines
and tissues (organ confined and metastatic)