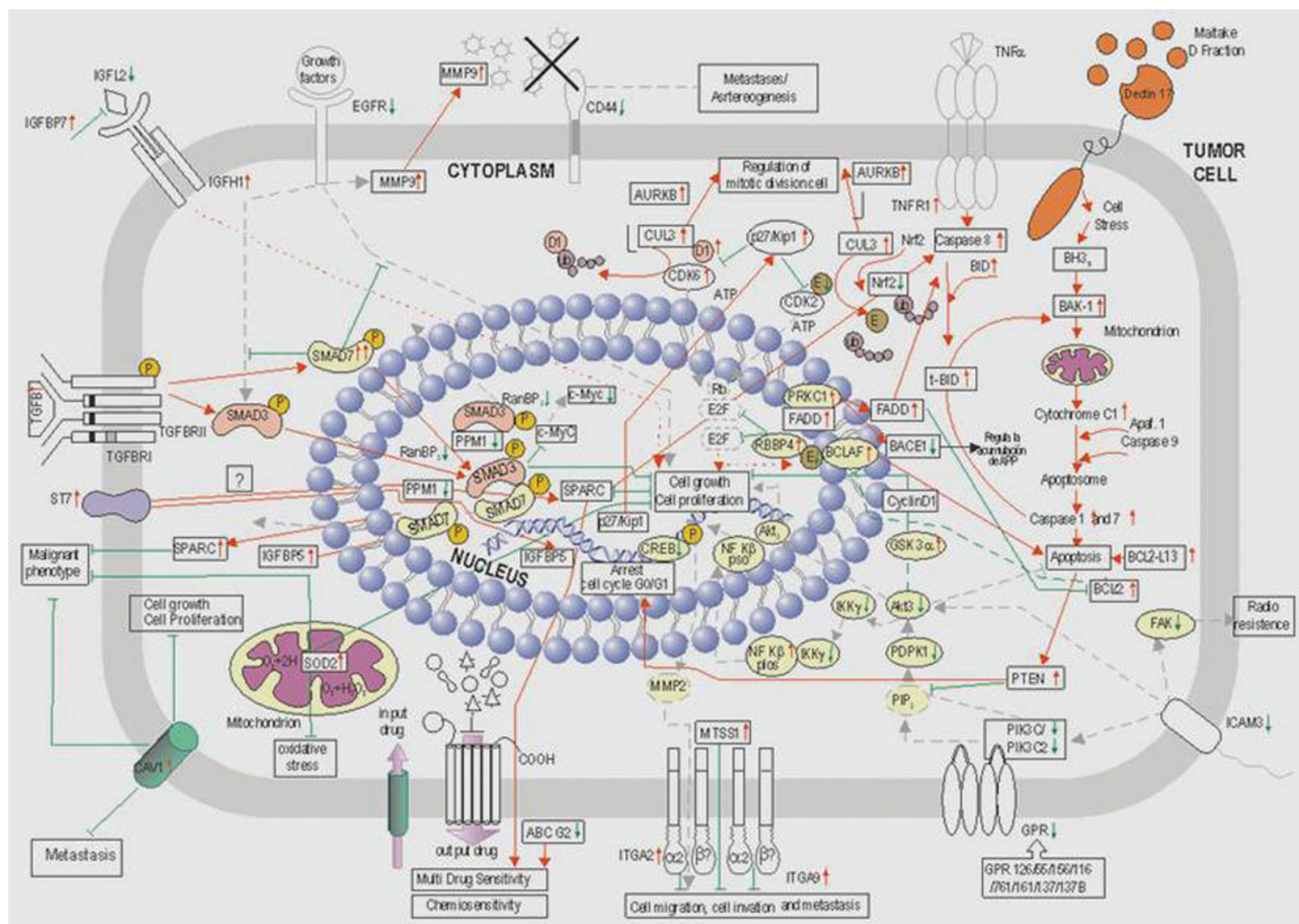


Supplementary Data



SUPPLEMENTARY FIG. S1. Anti-tumoral molecular mechanisms induced by Maitake D-Fraction in MCF-7 cells. cDNA microarray analysis revealed that Maitake D-Fraction modified the expression of 4068 genes (2420 were upmodulated and 1648 were downmodulated) in MCF-7 breast cancer cells in a dose-dependent manner during 24 h of treatment. Maitake D-Fraction suppresses the breast tumoral phenotype through a putative molecular mechanism modifying the expression of certain important genes (such as *IGFBP-7*, *ITGA2*, *ICAM3*, *SOD2*, *CAV-1*, *Cul-3*, *NRF2*, *Cycline E*, *ST7*, and *SPARC*, among others) that are involved in apoptosis stimulation, inhibition of cell growth and proliferation, cell cycle arrest, blocking migration and metastasis of tumoral cells, and inducing multidrug sensitivity. Stimulated (red) and inhibitory (green) pathways are indicated. Discontinuous gray lines represent the genes whose expression has not been changed after Maitake treatment.