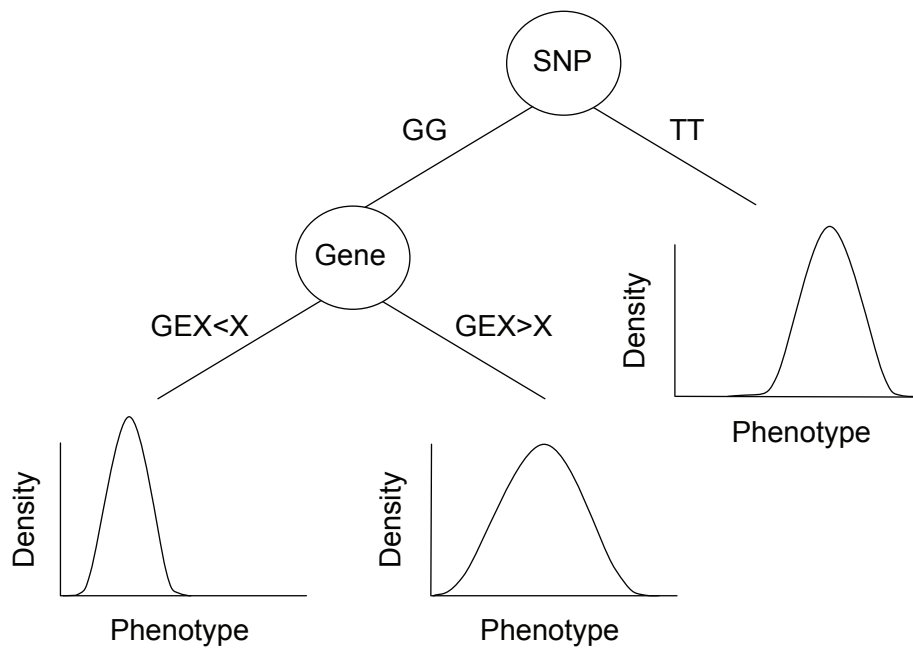# Figure S1

Figure S1. **An illustration of a standard decision tree model**. In this model, the internal nodes store the split functions based on either gene expression or genotyping data, while the leaf nodes provide the most probable phenotype based on a Gaussian model. Such tree has been previously utilized in (Lee *et al.* 2006), (Chen and Zhang 2013).