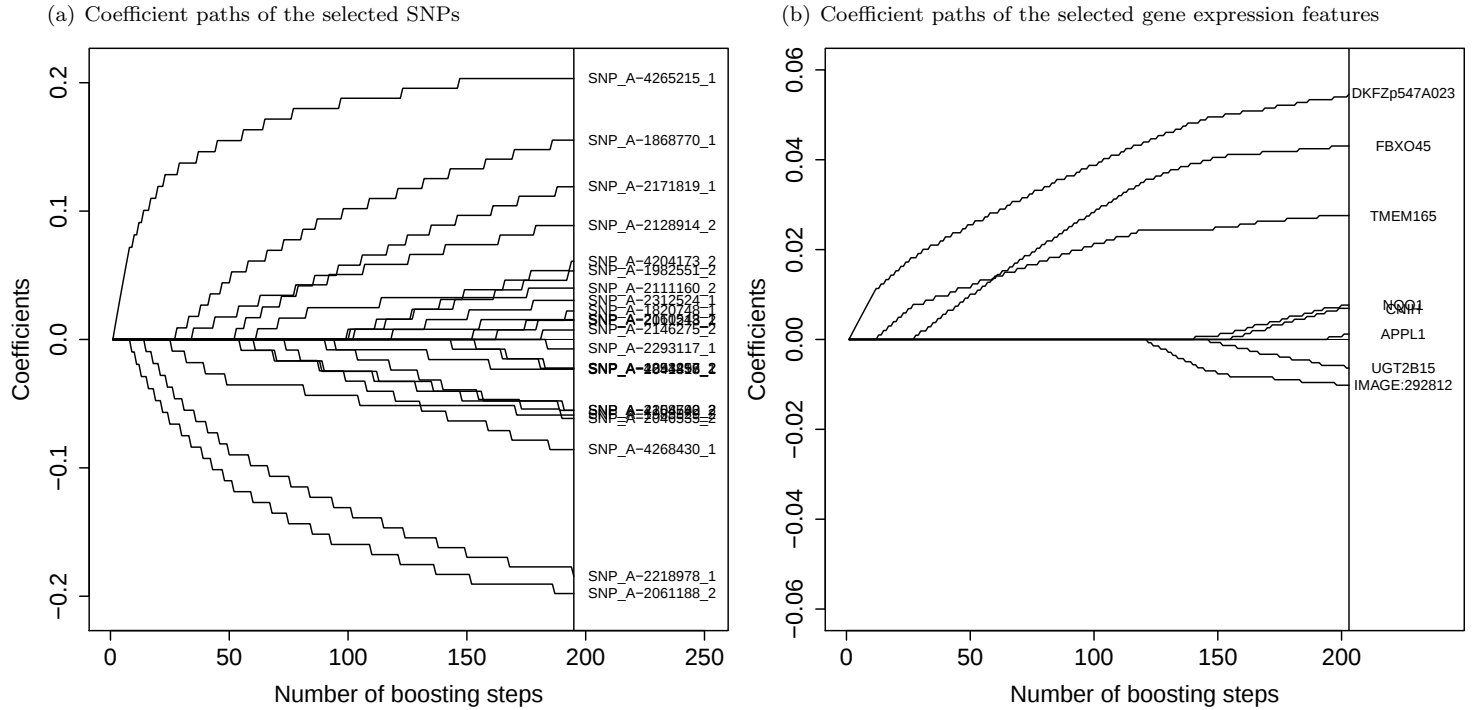


Coefficient paths of SNP and GEP measurements (first AML application example)



Parameter estimates obtained from componentwise likelihood-based boosting for the SNP microarray data (left panel) and parameter estimates obtained from componentwise likelihood-based boosting for the microarray-based GEP data conditioning on the overlap samples (right panel), plotted against the number of boosting steps. The optimal number of boosting steps is 194 for the SNP data and 202 for the GEP data conditioning on the overlap samples.