Figure S1. Method-dependent variation in type I error using the ABRF data set. (a) Number of DE genes reported by each method; (b) Points show the absolute log fold change (FC, y-axis) distribution of false positives against the expression level (logCPM, x-axis). DE calling uses data for the same sample generated by different laboratories. Only ABSSeq reports less than 5% DE genes (35766 in total) under p < 0.05. DESeq2 also reduces type I error at low expression level but not low fold-change.