

Figure 1. Discriminatory genes (potential disease related genes) and Non-discriminatory genes.

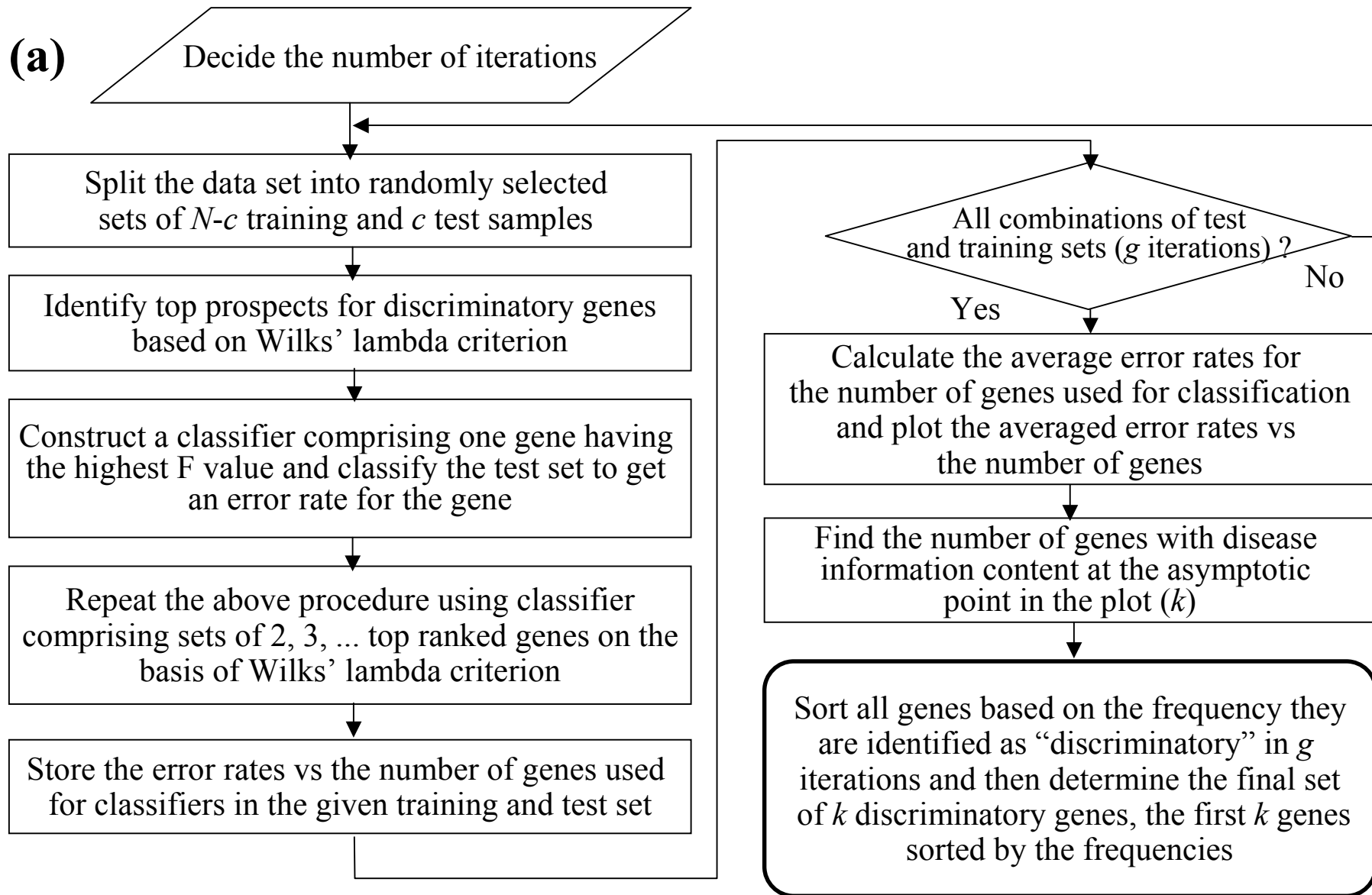


Figure 2. (a) Leave one out cross-validation (LOOCV) algorithm, where N is the total number of samples and c is the number of classes, so that one sample from each class is included in the test.

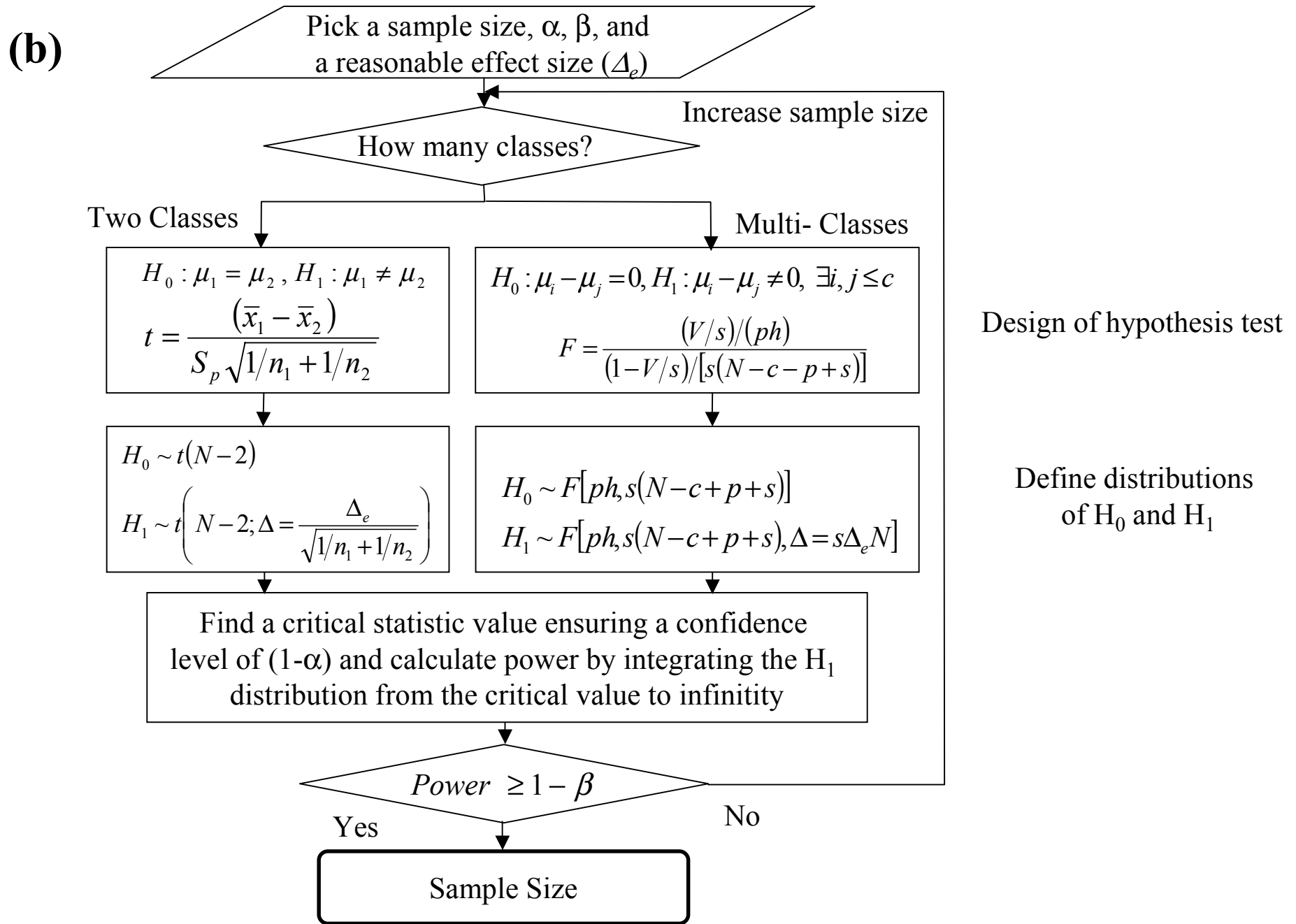


Figure 2. (b) Power analysis algorithm for determination of the minimum sample size.

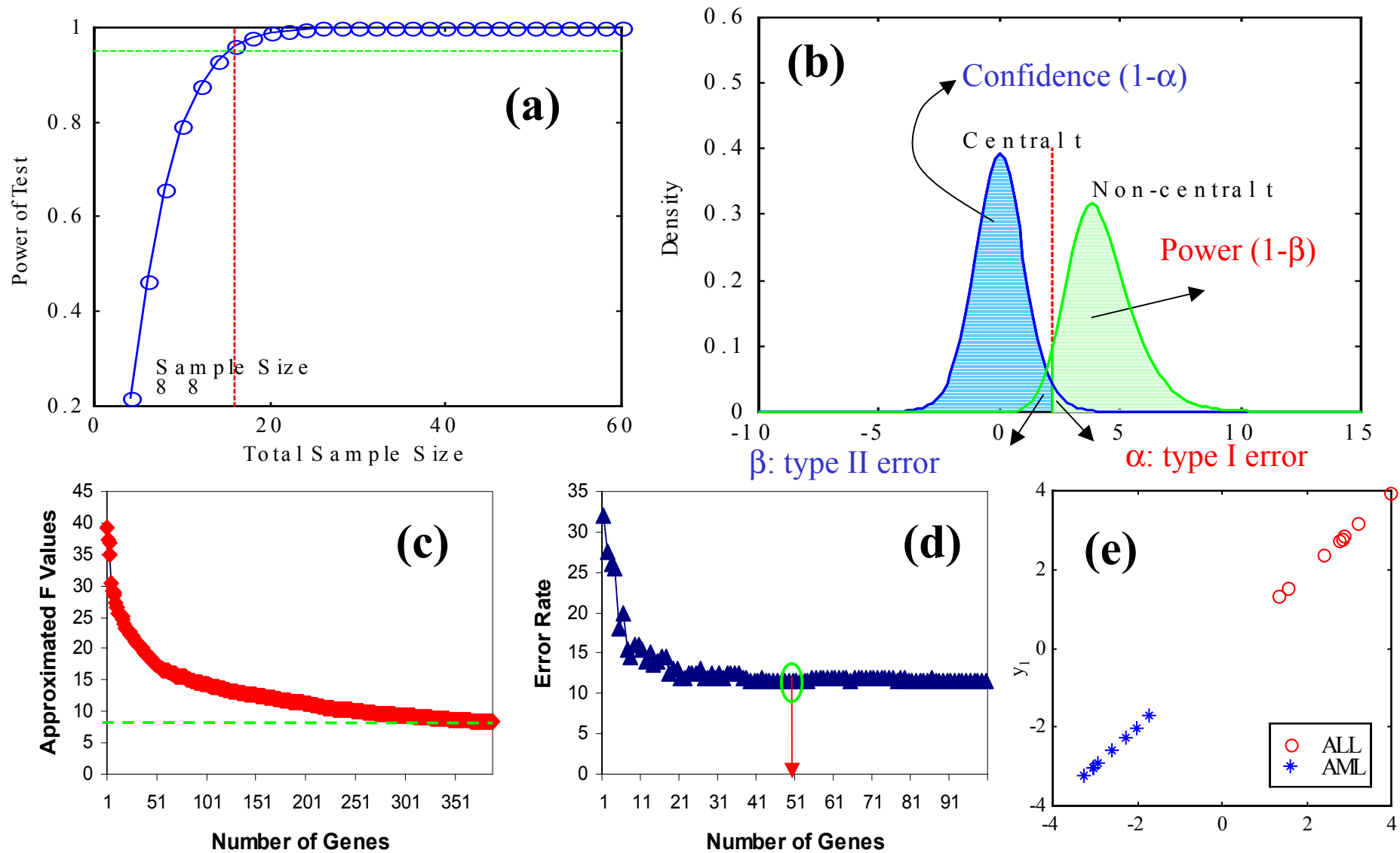


Figure 3. determination of minimum sample size for two-class (ALL, AML) distinction, selection of discriminatory genes with the estimated sample sizes of two classes, and FDA projection. (a) Power plot versus sample size showing how to determine the sample size required for two class distinction (8 from each class). (b) The distributions of H_0 and H_1 for the determined sample size. (c) Univariate F statistic values of the initial 388 discriminatory genes with a threshold ($F_{0.01(1,18)} = 8.2854$) in randomly selected 8 ALL and 8 AML samples out of the entire data set. (d) Leave-one-out cross-validation applied to estimate the classification error rates and then to select the 50 most discriminatory genes with the same samples. (e) Separation of the 8 ALL and 8 AML samples in the two-dimensional FDA projection space defined discriminant axes of the 50 discriminatory genes.

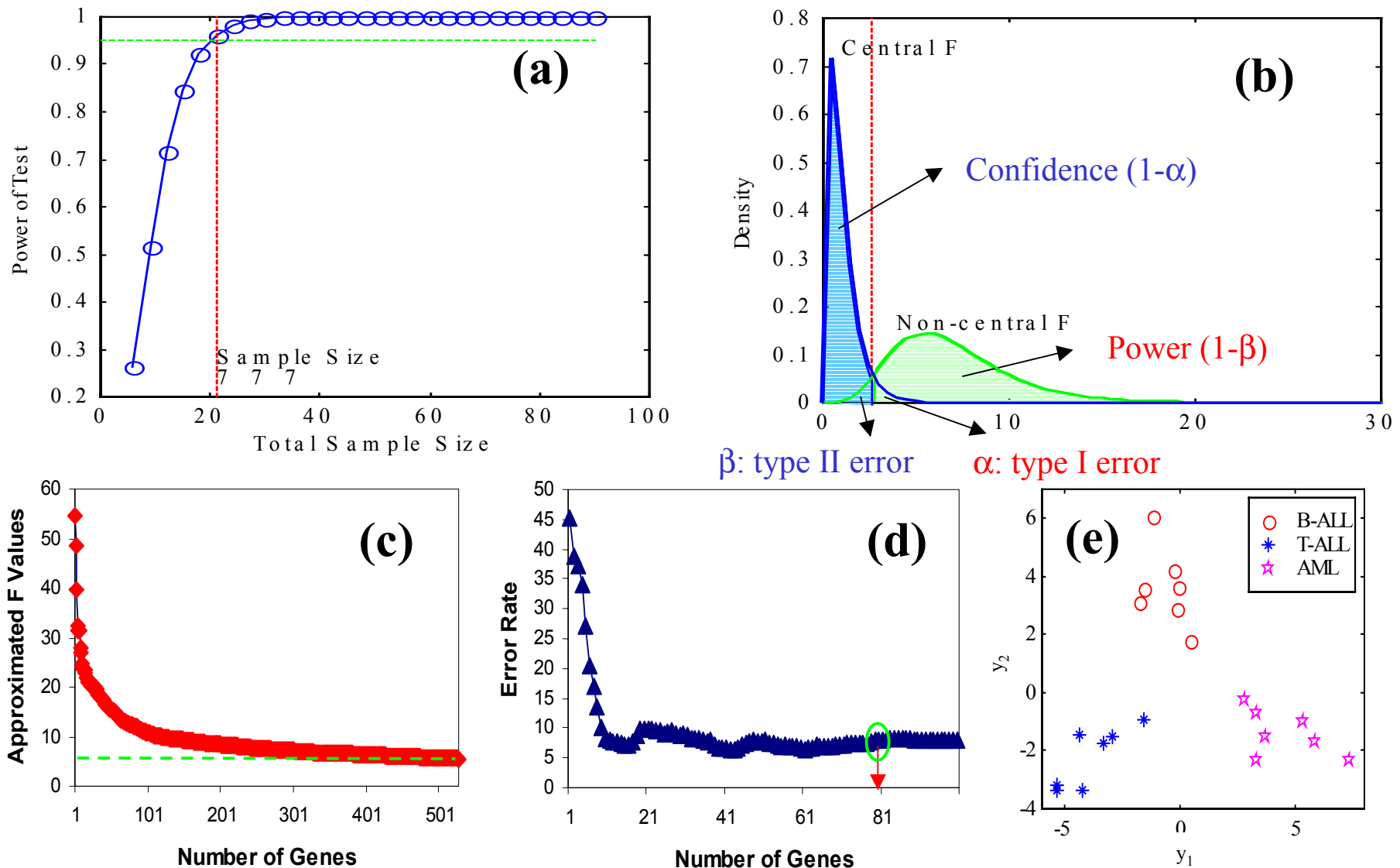


Figure 4. determination of minimum sample size for the three-class (B-ALL, T-ALL, AML) distinction, selection of discriminatory genes with the estimated sample sizes of three classes, and FDA projection. (a) Power plot versus sample size showing how to determine the minimum sample size (7 from each class). (b) The distributions of H_0 and H_1 for the determined sample size. (c) Univariate F statistic values of the initial 527 discriminatory genes with a threshold ($F_{0.01(2,26)} = 5.5263$) in randomly selected 7 B-ALL, 7 T-ALL and 7 AML samples out of the entire data set. (d) Leave-one-out cross-validation applied to estimate the classification error rates and then to select the 80 most discriminatory genes with the same samples. (e) Separation of the 7 B-ALL, 7 T-ALL and 7 AML samples in the two-dimensional FDA projection space defined discriminant axes of the discriminatory 80 genes.