Table 33. Classification accuracies obtained by using *k*-NN to predict genetic subtype among the B lineage ALLs

Class	No of samples	No. misclassified	Apparent accuracy	Sensitivity	Specificity
TCF3/PBX1	6	0	100	100	100
Hyperdiploid >50 chromosomes	29	0	100	100	100
ETV6/RUNX1	20	1	95	95	97.1

Apparent accuracy was determined by leave-one-out crossvalidation.
Sensitivity = the number of positive samples predicted/the number of true positives
Specificity = the number of negative samples predicted/the number of true negatives