Gene expression profile and genomic changes in disease progression of early-stage chronic lymphocytic leukemia

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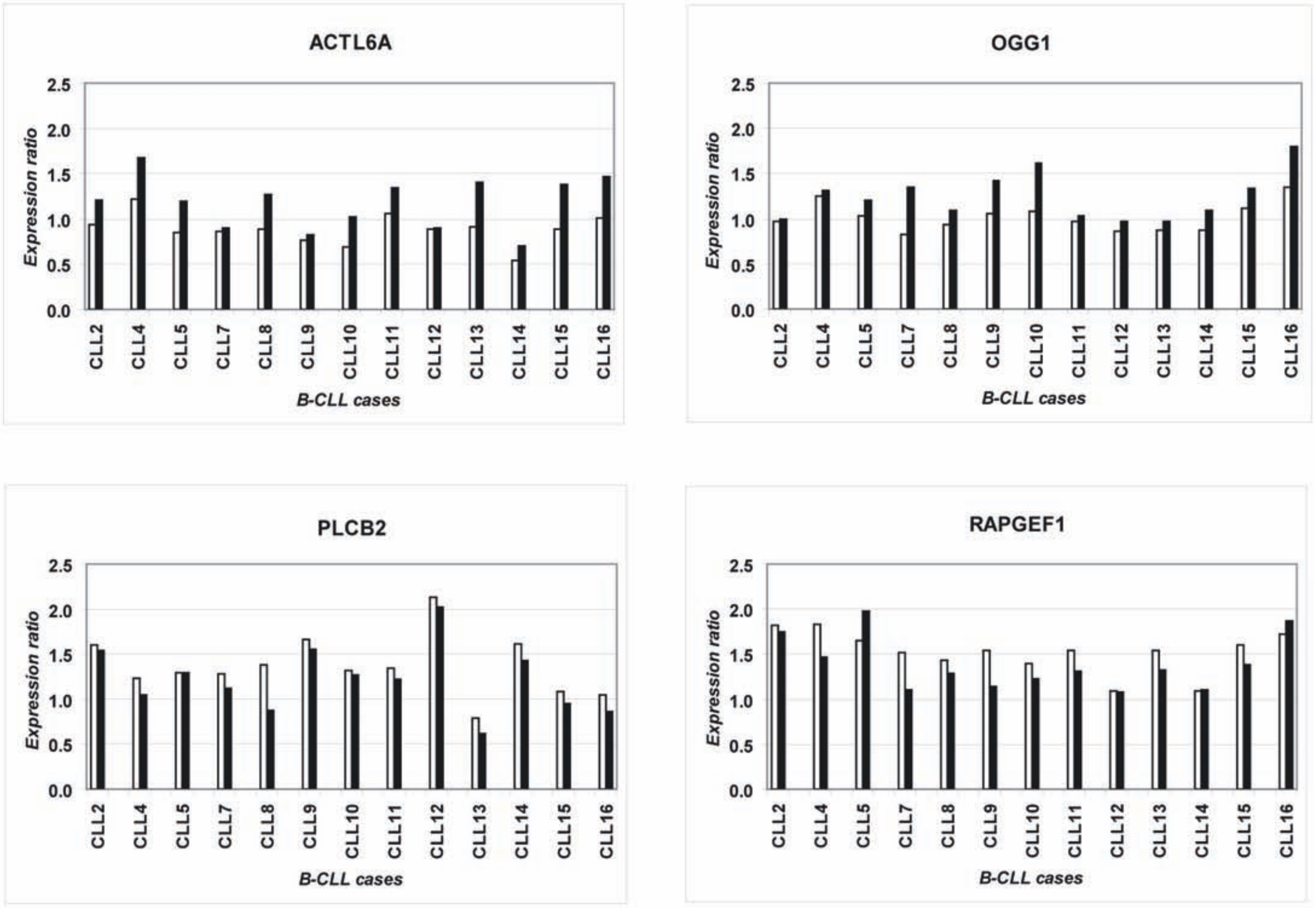
Haematologica. 2008 Jan; 93:(1)132-136. DOI: 10.3324/haematol.11694

Supplementary data



Supplementary Figure 1: qRT-PCR validation of genes ACTL6A, OGG1, PLCB2 and RAPGEF1. 10 patients from the microarray study were used for the validation (CLL2-CLL13) as well as 3 new patients (CLL14-CLL16). White bars correspond to the sample at diagnosis and black bars to the progressed sample. Expression ratios were calculated by the 2 -DDCt method using b-glucoronidase (GUS) as endogenous control.