Exome sequencing identifies recurrent BCOR alterations and the absence of KLF2, TNFAIP3 and MYD88 mutations in splenic diffuse red pulp small B-cell lymphoma

Discovery

- whole-exome sequencing
- 10 splenic diffuse red pulp lymphoma paired samples
  - normal
  - tumour

selection of 109 somatic mutations

Validation

- 42 splenic diffuse red pulp lymphoma
- 46 splenic marginal zone lymphoma
- 8 hairy-cell leukaemia samples

Genetic landscape

Splenic diffuse red pulp lymphoma
- frequent BCOR mutations
- absence of alterations in genes regulating the NFκB pathway (KLF2, TNFAIP3 and MYD88 triple-negatives)
- absence of BRAF mutations

Jallades et al., Haematologica, 2017