The **IL7R-JAK** pathway is mutated in 27.7% of T-ALL

**IL7R-JAK1/3-STAT5**
- IL7R mut (7.1%, n=11)
- JAK1 mut (2.6%, n=4)
- JAK3 mut (11%, n=17)
- STAT5 mut (1.2%, n=2)
- Combined **IL7R-JAK1/3-STAT5** mut (5.8%, n=9)

**IL7R-JAK1/3-STAT5** wild type (72.3%)

Mutations in **IL7R-JAK** genes and epigenetic modulators are significantly associated

- **IL7R-JAK**
  - wild type (n=112)
  - mutation (n=43)

**PRC2 deletion/mutation**
- 13.4% wild type
- 27.9% mutation

**PRC2 wild type**
- 86.6% wild type
- 72.1% mutation

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**IL7R-JAK**
- wild type (n=112)
- mutation (n=43)

**PHF6 deletion/mutation**
- 13.4% wild type
- 34.9% mutation

**PHF6 wild type**
- 86.6% wild type
- 65.1% mutation

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Vicente et al., Haematologica, 2015