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# Aim



Describe the health care resource utilisation (HCRU) and associated costs of chronic lymphocytic leukaemia (CLL) by genetic subgrouping in Finland.

### Methods

#### Study design

- This was an observational cohort study using information from the Helsinki University Hospital (HUS) data lake
- The study cohort included all CLL (ICD-10: C91.1; C83.00) patients from January 2012 to August 2023 in the HUS region in Finland
- The analysis cohort included those patients in the study cohort that began first-line (1L) systemic treated between January 2012 and August 2023.
- The index date was defined as the start date of the 1L treatment, from which they were followed-up until end of study, lost to follow-up or death, whichever occurred first.

#### **Data source**

- HUS data lake containing electronic specialised health records of approximately 1.6 million residents, covering roughly 30% of Finland's population
- Pseudonymised data on demographics, diagnoses, outpatient contacts, hospitalisations, medications, procedures, laboratory, genetics, and pathology, and other measurements were collected from electronic medical records

#### **Definitions**

#### **HCRU**:

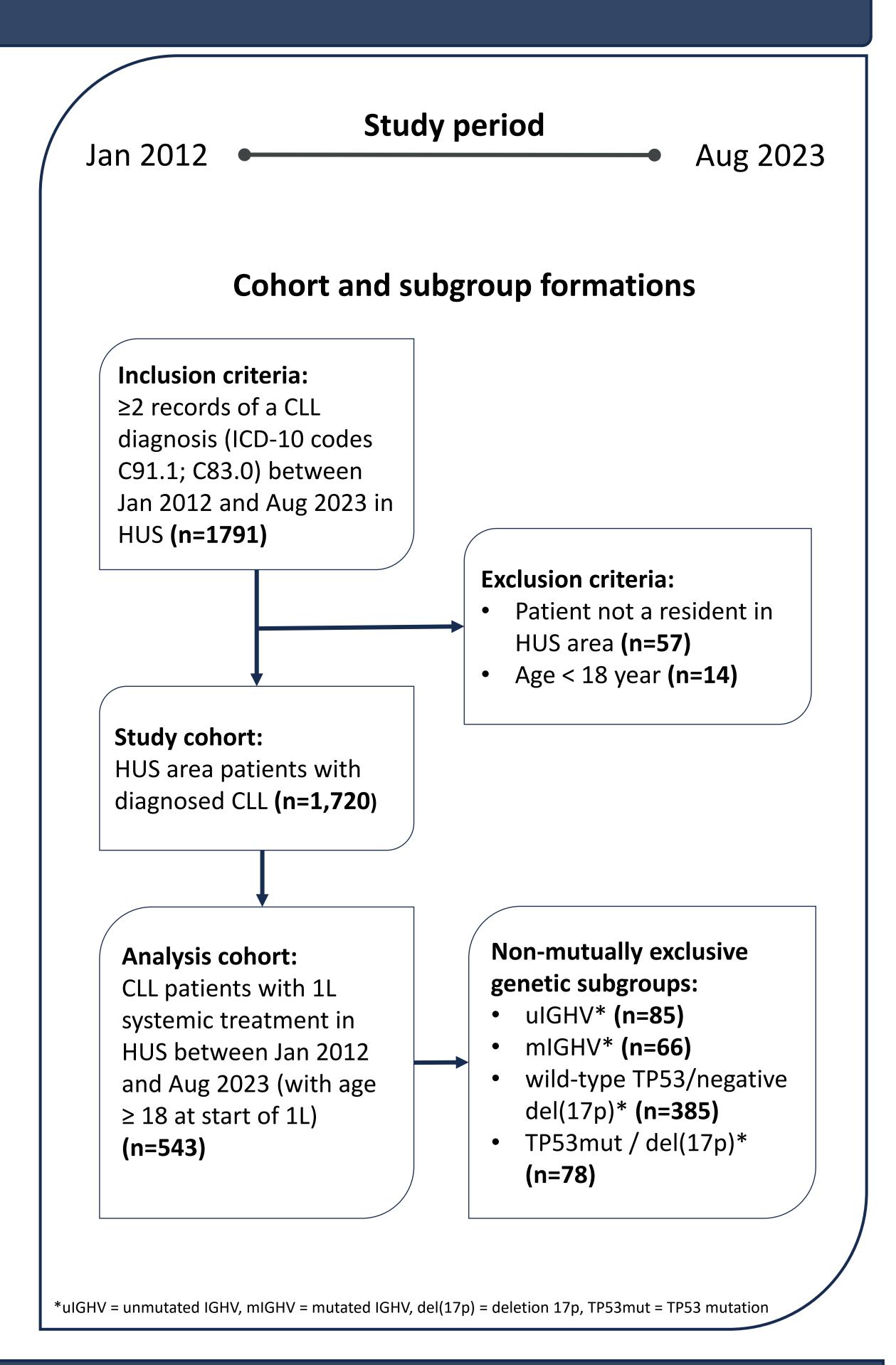
- Recorded all-cause in- and outpatient contacts at HUS specialised healthcare centres
- Calculated from index (1L) until end of follow-up or 3 months before death
- Terminal care HCRU calculated from 3 months before death until death

# HCRU associated costs:

 In- and outpatient contacts at specialised centres priced according to health and social care unit costs in Finland (Mäklin, 2017) inflated to 2022 Euros

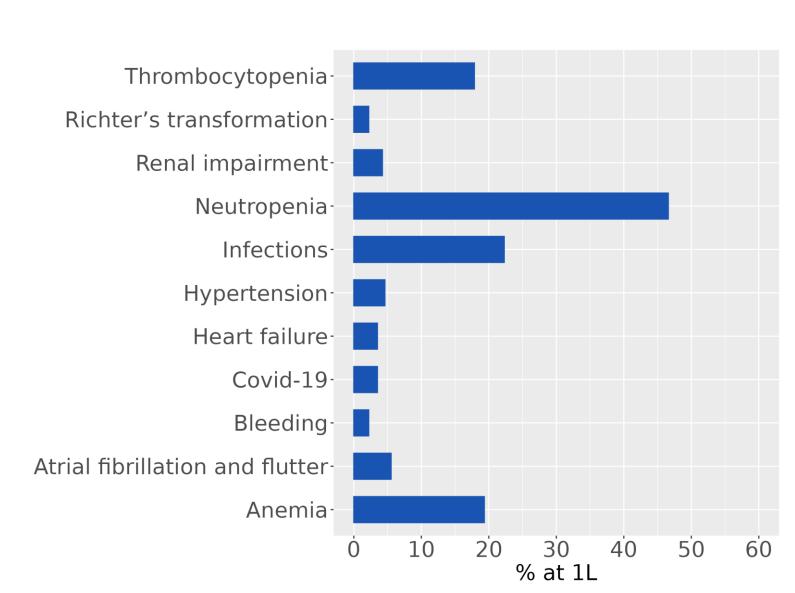
#### **Adverse events:**

- Defined as selected medical conditions identified by test result or ICD-10 code and not present prior to treatment
- Measured over 12 months from 1L treatment initiation or until next treatment initiation
- Included AEs: haematological, cardiovascular, bleeding, renal impairment, infectious, and Richter's transformation.



# **Analysis Cohort Results**

#### **Patient characteristics** n (%) Variable Median (IOR) Mean (SD) Level N = 54371.7(64.8 - 77.4)543 (100%) 70.0 (11.2) Age All < 65 139 (25.6%) 65-74 225 (41.4%) ≥ 75 179 (33.0%) 206 (37.9%) Sex **Female** Male 337 (62.1%) 39.4 (16.6 - 69.5)Follow up (months) 543 (100%) **Genetic testing\*** 480 (88.4%) \*IGHV, TP53, cytogenetics



# In the analysis cohort, neutropenia was the most common AE in 1L with 47% (n=253) patients undergoing at least one neutropenia AE. Infections (excl. Covid-19) follows with 22% (n=121) of the cohort experiencing an infection. Anaemia and thrombocytopenia were also fairly common with 19% (n=105) and 18% (n=97) of the cohort experiencing them, respectively.

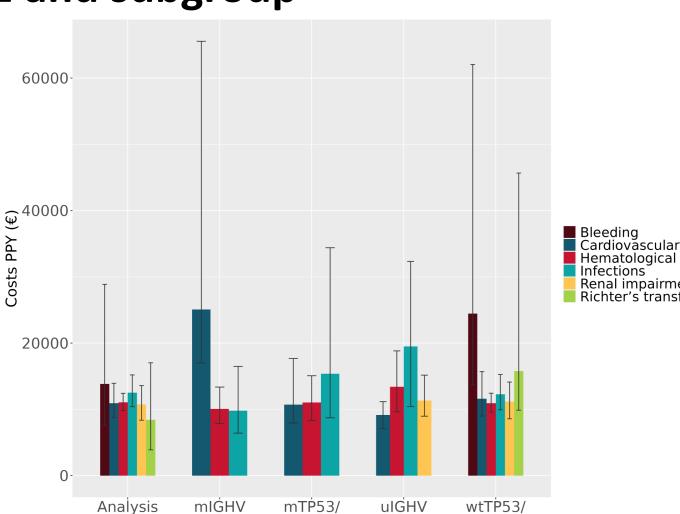
AE in 1L

# **HCRU** costs in 1L by AE and subgroup

The associated HCRU costs for AEs accrued in 1L differ depending on the genetic subgroup. Bleeding was only recorded (for > 5 events\*) in the wild-type TP53/negative del(17p) subgroup, with a cost of approximately € 24K PPY. Richter's transformation AEs were also only recorded (for >5 events\*) in the wild-type TP53 genetic subgroup. This also has a fairly large cost of approximately € 16K PPY. Renal impairment AEs were recorded for the uIGHV and wild-type TP53 subgroups, costing approximately the same at € 11K PPY.

Cardiovascular, haematological, and infections were reported for each genetic subgroup with varying costs.

\*due to confidentiality, only AEs with more than five events are reported



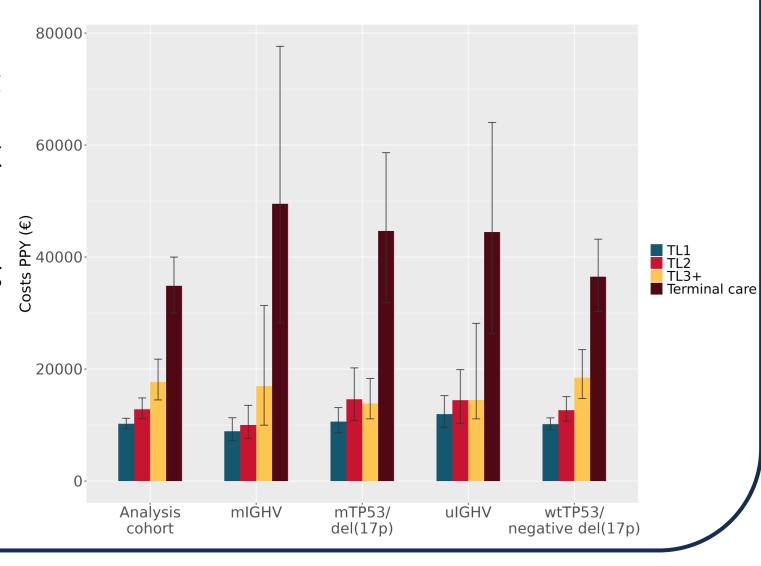
# HCRU costs by treatment line and subgroup

Terminal care has the highest HCRU costs in each genetic subgroup, ranging from € 36.5K to € 49.5K PPY, and for the whole analysis cohort costing € 35K PPY.

Treatment lines 1 to 3 have a substantially lower HCRU costs, ranging between approximately € 10K and € 18K PPY.

The mIGHV genetic subgroup has the

The mIGHV genetic subgroup has the lowest L1 and L2 HCRU costs, approximately € 9K and € 10K PPY, respectfully.



## Conclusions



HCRU and costs vary between genetic subgroups of CLL patients likely reflecting the heterogenous risk profiles of the genetic markers. It is important to identify the patient's genetic prognosis to prevent excessive HCRU to the greatest extent possible.