Cyclophosphamide (CY) is a commonly used chemotherapy agent in the conditioning regimen for hematopoietic cell transplant (HCT). - Variable exposure of CY may affect the HCT outcomes [1,2], but its predictors are not well-studied. - We aimed to explore potential single nucleoside polymorphisms (SNPs) that are associated with pharmacokinetics (PK) of CY.

**Materials**
- **Design**: Observational pharmacogenomic-PK study
- **Patients**: Adults HCT recipients on non-myeloablative regimen with CY
- **Methods**: Conducted stepwise multiple linear regression model selection by non-compartmental analysis.

**Results**
- **Evaluation**: Conducted for 141 SNPs.
- **Statistical analysis**: 1. Excluded SNPs without association with PM AUCs (p > 0.05).
   2. Combined 3 genotypes into 2 groups when %AUC difference was <10%.
   3. Eliminated highly correlated SNPs in linkage disequilibrium (R² > 0.9).
   4. Combined 3 genotypes into 2 groups when %AUC difference was <10%.
   5. Final model included significant SNPs (p < 0.05) and CrCL.

**Conclusion**
- We confirmed a previously reported effect of a CY2B6 variant on PK of CY in a different population.
- We identified novel SNPs that are associated with PM exposure. These variants need to be validated in other populations and their functionality needs to be assessed.

### References