

MECHANISTIC MODELLING OF CRS IN T CELL ENGAGERS - AN APPLICATION FOR BLINATUMOMAB

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Background

- Blinatumomab is a CD19/CD3 bispecific T-cell engager (TCE) that redirects cytotoxic T cells against CD19⁺ B-cell malignancies, including B-ALL [1, 2].
- Treatment is associated with transient cytokine elevation within the first 24–48 hours — a clinically significant on-target toxicity whose underlying mechanisms remain poorly understood [1].
- Quantitative Systems Pharmacology (QSP) provides a mechanistic framework linking drug exposure to immune cell kinetics and cytokine dynamics, enabling model-informed dose optimisation [3].

Objective

- Implement a modular QSP T-cell engager platform in QSP Designer [4], integrating physiologically based pharmacokinetic (PBPK) modelling, bispecific TCE avidity [5], cytotoxicity, and cytokine distribution modules [3].
- Calibrate and validate against published blinatumomab pharmacokinetics (PK), T/B-cell kinetics, and cytokine data [1, 2, 6].
- Generate a virtual population to simulate variability in B-cell depletion and cytokine release syndrome (CRS) associated cytokine responses across MT103-104 dose levels [2, 7].
- Identify the optimal dose maximising B-cell complete response (CR) while minimising IL-6-associated CRS risk.

Methods

- PK calibration:** Simulated blinatumomab concentrations were within 2-fold of observed steady-state values [2] (Fig 1a-b).
- T-/B-cell kinetics:** The model reproduced T-cell redistribution and sustained B-cell depletion [1] (Fig 2c-d).
- Cytokine validation:** Simulated cytokine peaks were within 2-fold of observed clinical data [6] (Fig 2e).
- PD validation:** Simulated T-/B-cell timing and count endpoints were consistent with clinical observations [1] (Fig 3).

Fig. 1 Schematic diagram of model description and end-to-end modelling methodology.

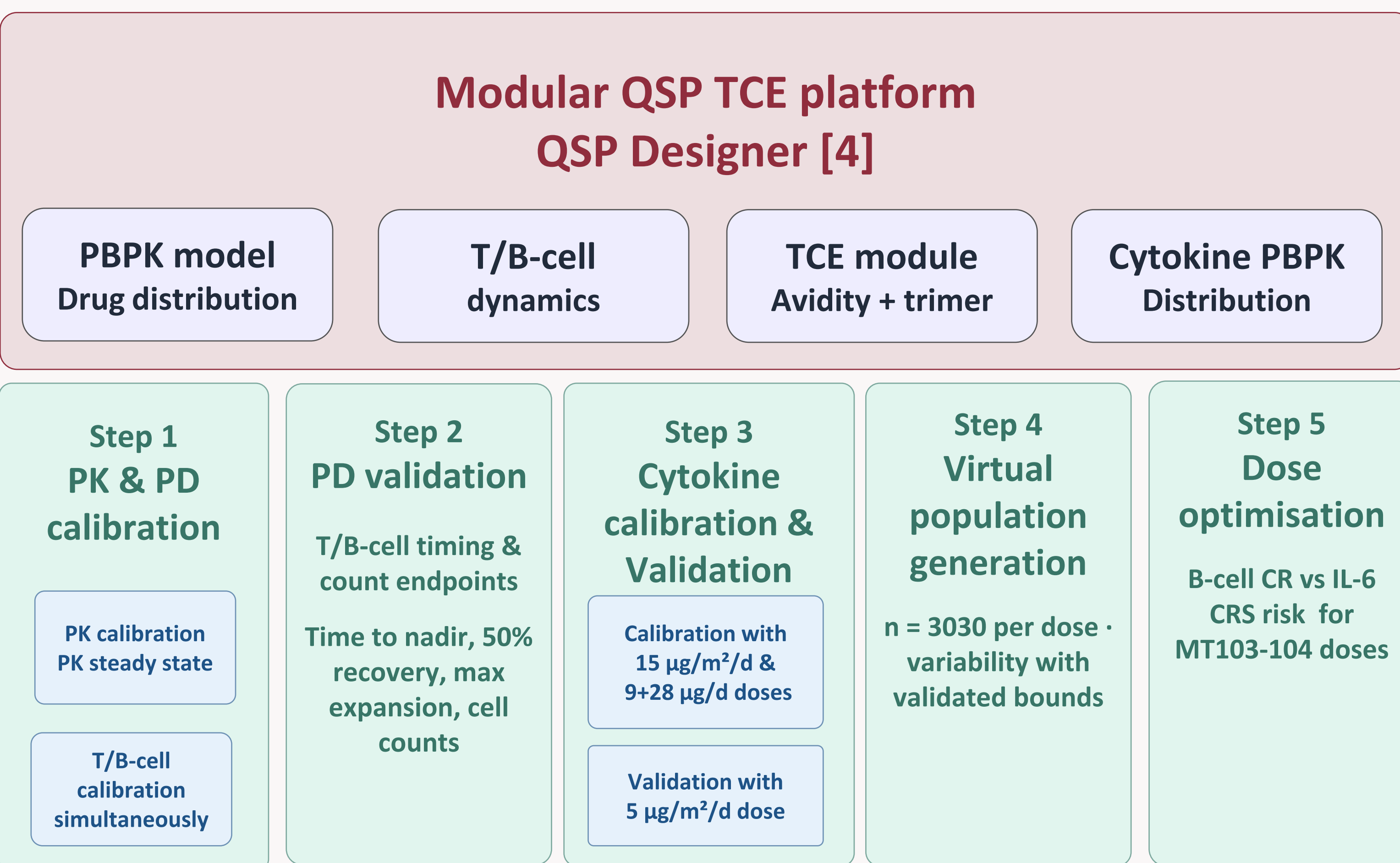


Figure 2. a. b. Simulated vs. observed blinatumomab PK profiles for continuous IV infusion regimens [2], c. Simulated vs. observed T-cell dynamics over 30 days [1], d. Simulated vs. observed B-cell depletion over 30 days [2], e. Cytokine calibration and validation goodness-of-fit analysis[6].

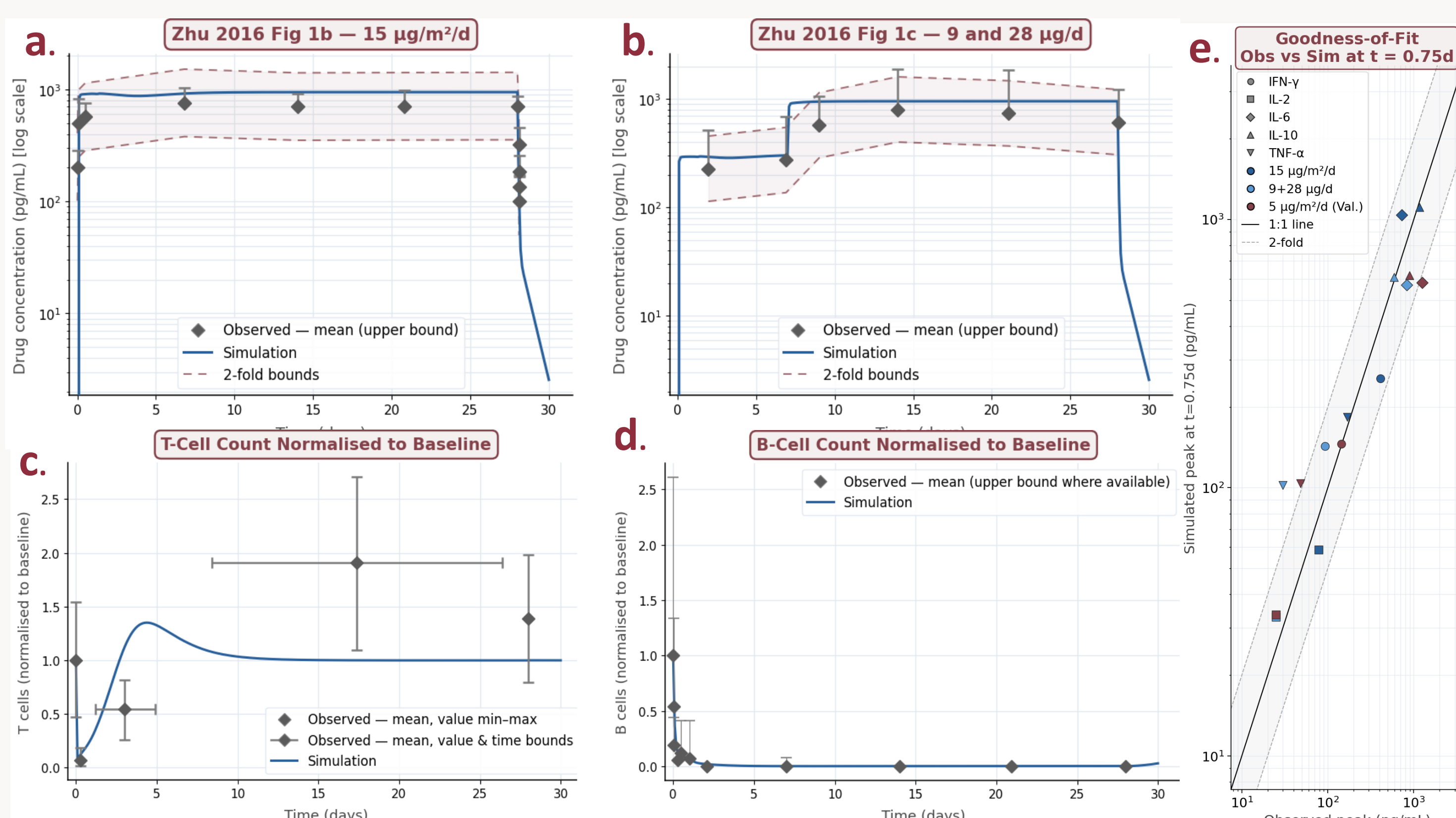
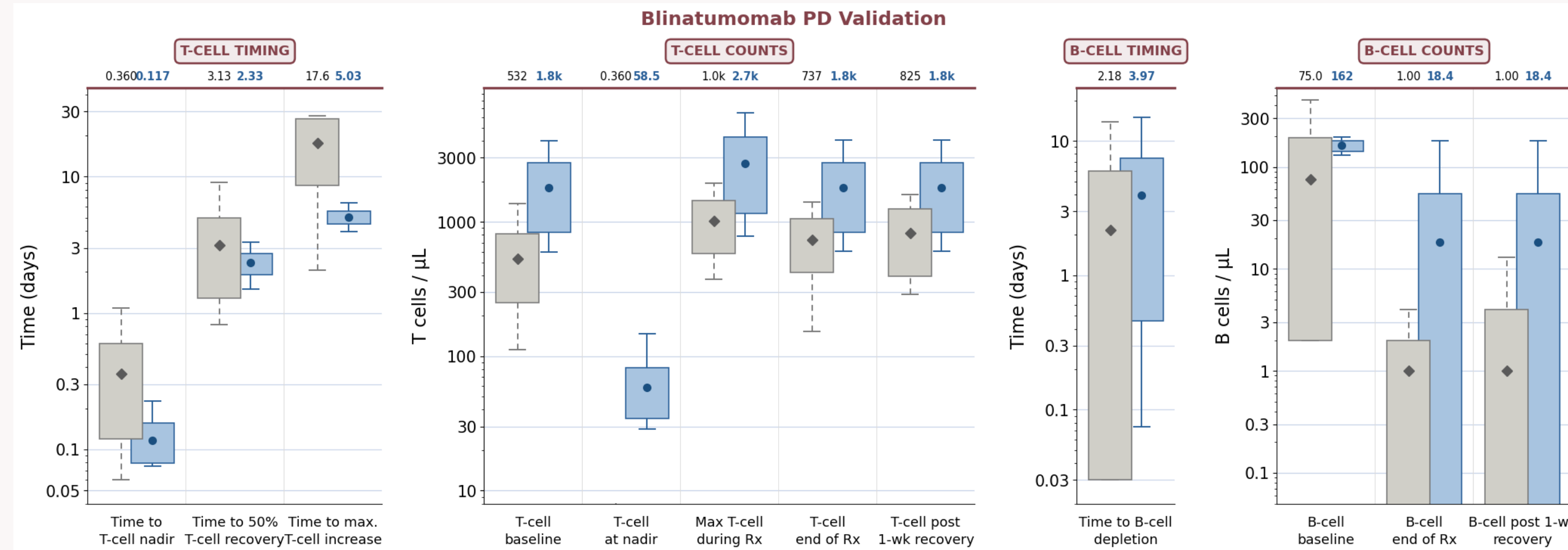


Fig. 3. Blinatumomab PD validation comparing simulated and observed T-/B-cell timing and count endpoints [1].



Results

Virtual Population

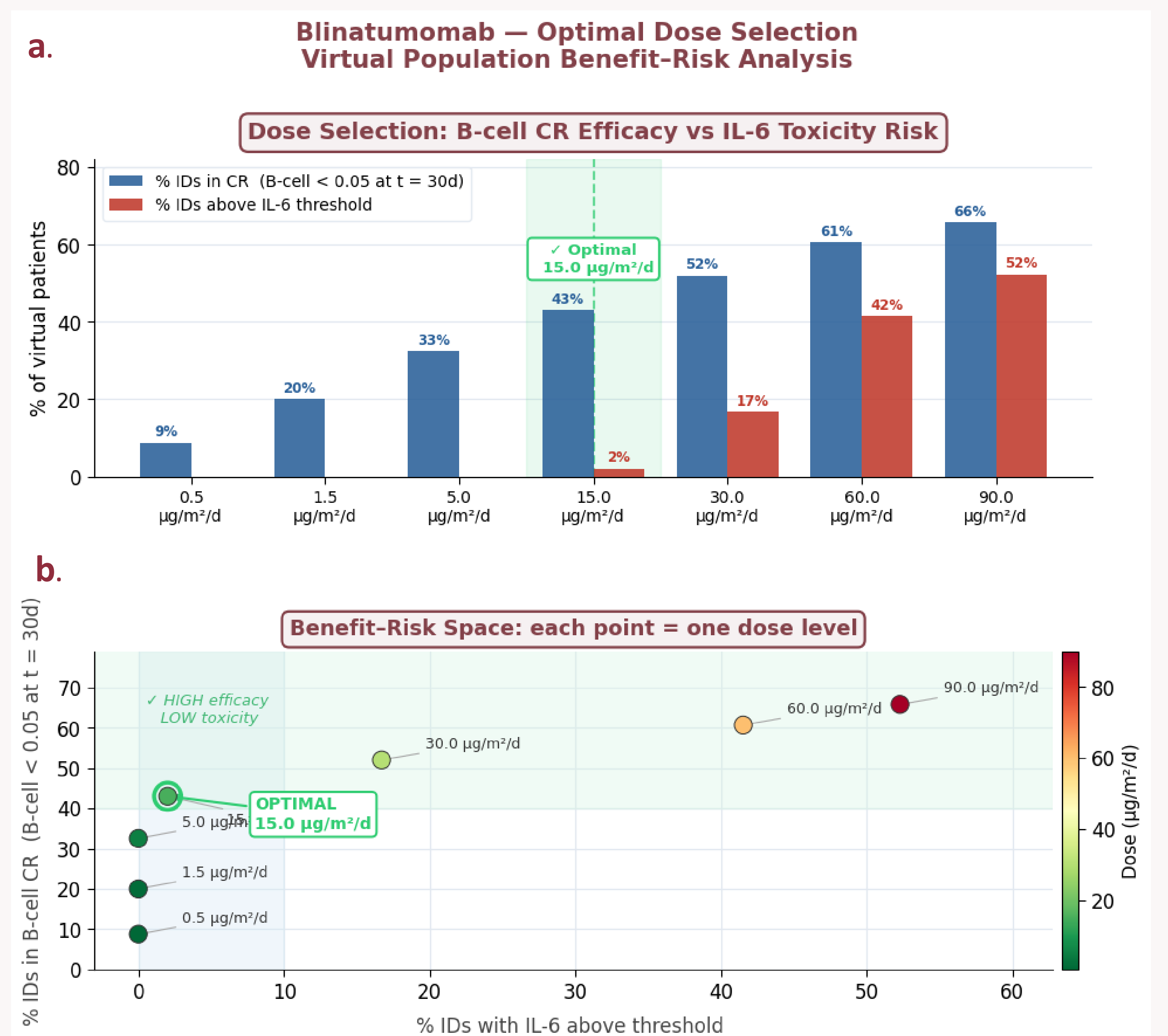
- Virtual population:** A 3030-patient virtual population was generated [8] (Fig. 3), and utilized for probabilistic CR and CRS risk prediction across dose levels [6].
- Dose response:** B-cell CR increased with dose, reaching 66% at 90 µg/m²/day (Fig. 4.a).

Dose Optimisation

- CRS risk:** IL-6-associated CRS risk remained low at 15 µg/m²/day but increased substantially at higher doses (Fig. 4.a).
- Benefit-risk optimisation:** 15 µg/m²/day provided the optimal balance between efficacy and CRS risk (Fig. 4.b).

Fig. 4a. Virtual population benefit-risk analysis identified 15 µg/m²/day as the optimal dose, b. balancing high B-cell CR with low IL-6-associated CRS risk [2, 6].

Note: The conference abstract states 30 µg/m²/day as the optimal dose; full simulation analysis corrects this to 15 µg/m²/day based on the benefit-risk inflection point identified in the virtual population.



Conclusions

- A modular QSP TCE platform model was successfully applied to blinatumomab, linking systemic PK to T-/B-cell dynamics and cytokine-mediated CRS risk.
- Key PD endpoints were reproduced including T-cell redistribution, B-cell depletion, and cytokine dynamics within clinically acceptable limits.
- Virtual population simulations identified **15 µg/m²/day as the optimal target dose**, balancing B-cell CR (43%) with low IL-6-associated CRS risk (2%), consistent with the approved step-dosing regimen [7].
- The modular platform supports rapid adaptation to novel TCE modalities, enabling model-informed dose selection and early benefit-risk optimisation [3, 4, 5].

References

- Klinger M *et al.* Blood 2012;119:6226–33
- Zhu M *et al.* Clin Pharmacokinet 2016;55:1271–88
- Chelliah V *et al.* Clin Pharmacol Ther 2021;109:605–18
- Matthews RJ *et al.* CPT Pharmacometrics Syst Pharmacol 2023;12:889–903
- Flowers D *et al.* J Pharmacokinet Pharmacodyn 2023;50:215–27
- Blincyto (blinatumomab) EPAR. EMA/CHMP/469312/2015
- Xu Y *et al.* CPT Pharmacometrics Syst. Pharmacol. 2015 4, 507–515
- Topp MS *et al.* Lancet Oncol. 2015 16; 57–66



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