



*Supplement of*

**Modeling demographic-driven vegetation dynamics and ecosystem biogeochemical cycling in NASA GISS's Earth system model (ModelE-BiomeE v.1.0)**

**Ensheng Weng et al.**

*Correspondence to:* Ensheng Weng (wengensheng@gmail.com)

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## 1. Simulated plant cohort structure

The data are the from mean of the simulated years 500 ~600. These panels show each cohort's density (a), height (b), crown area (c), and biomass (d). If there are more than 20 cohorts in a grid, we only show the 20 tallest cohorts. If the total cohorts are less than 20 cohorts, we use zero to make up the cohorts to 20 for convenience.

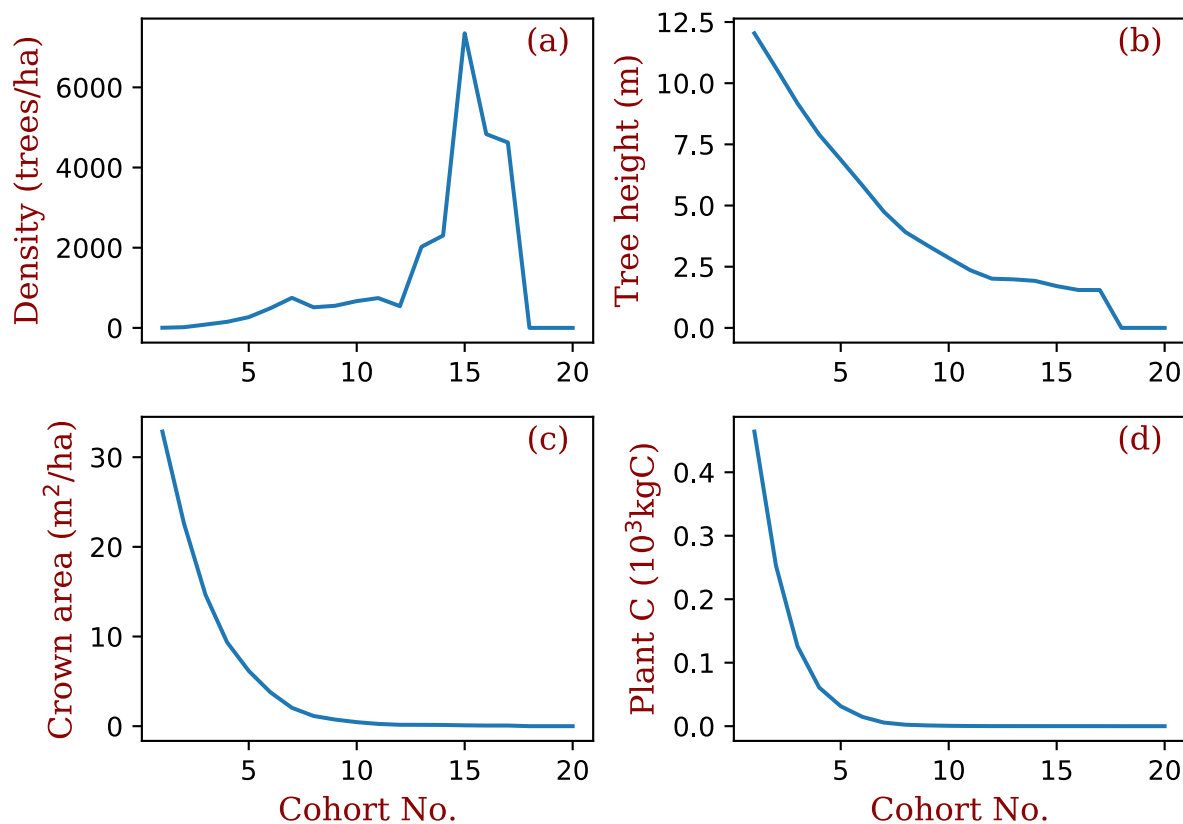
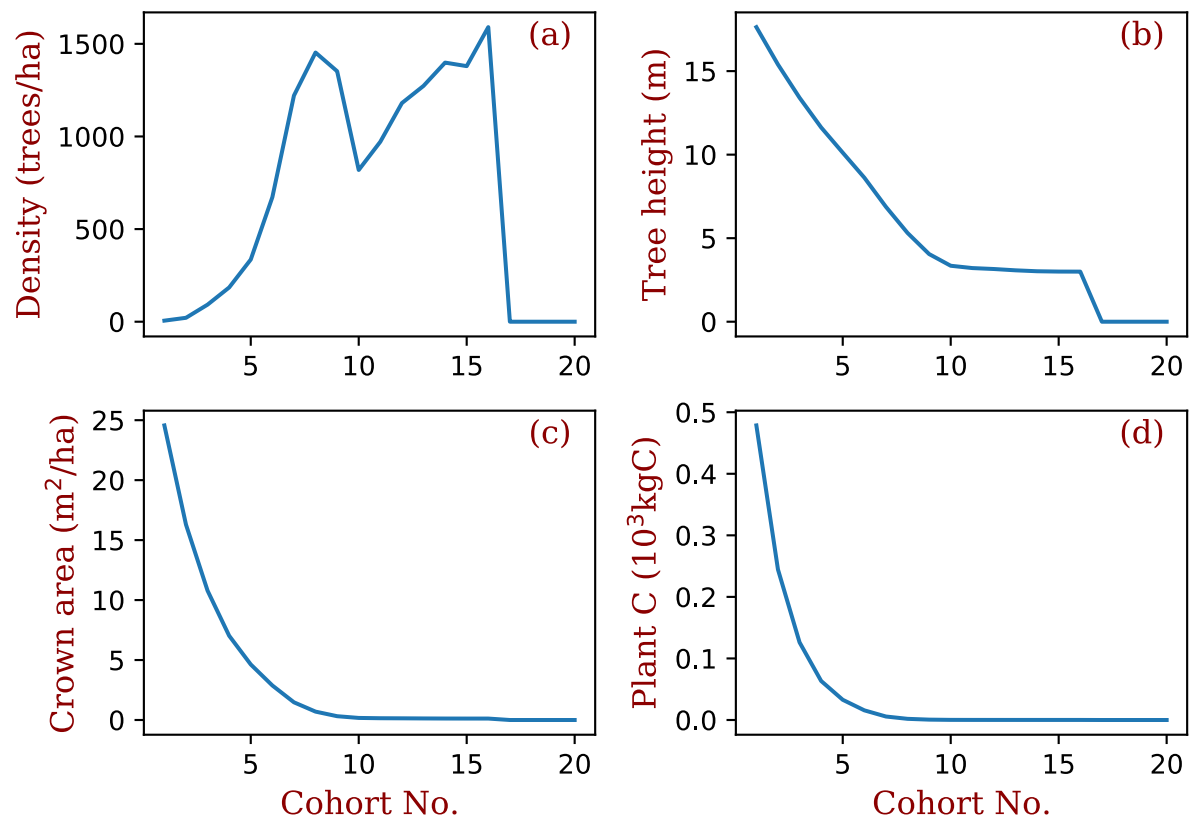
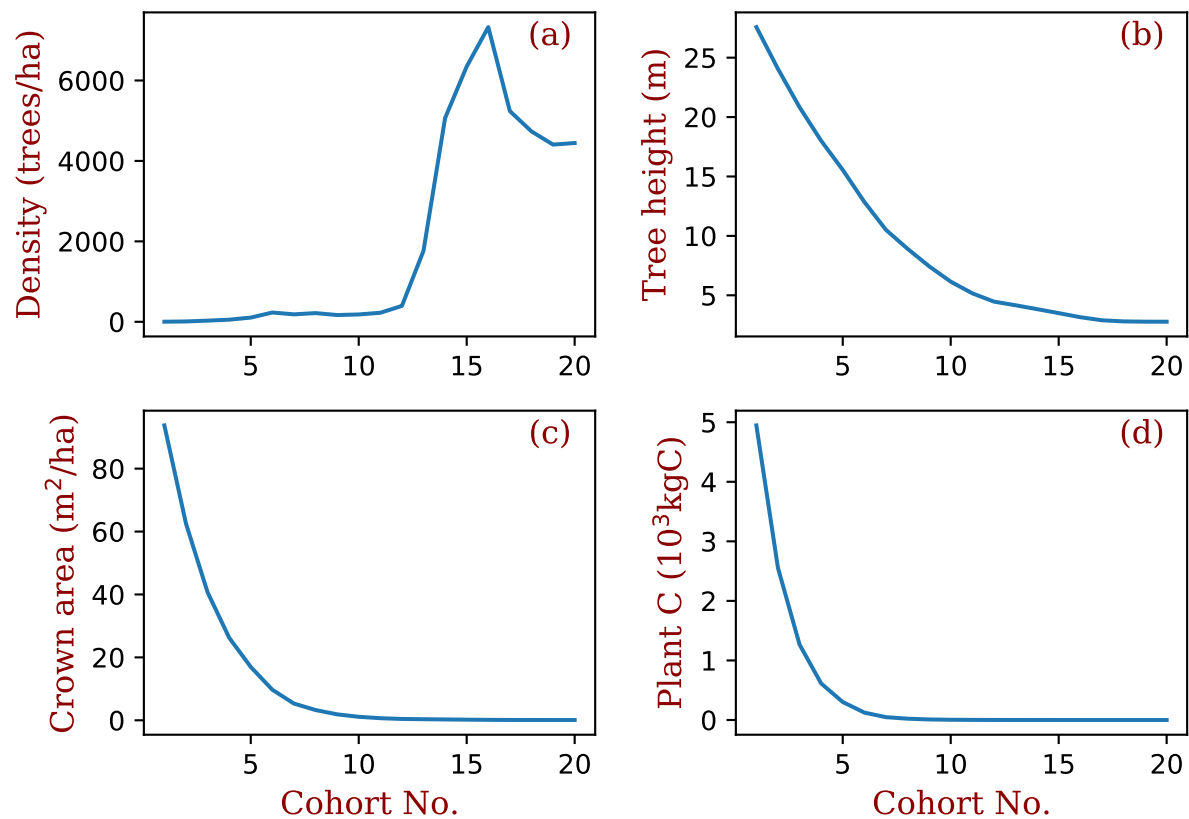


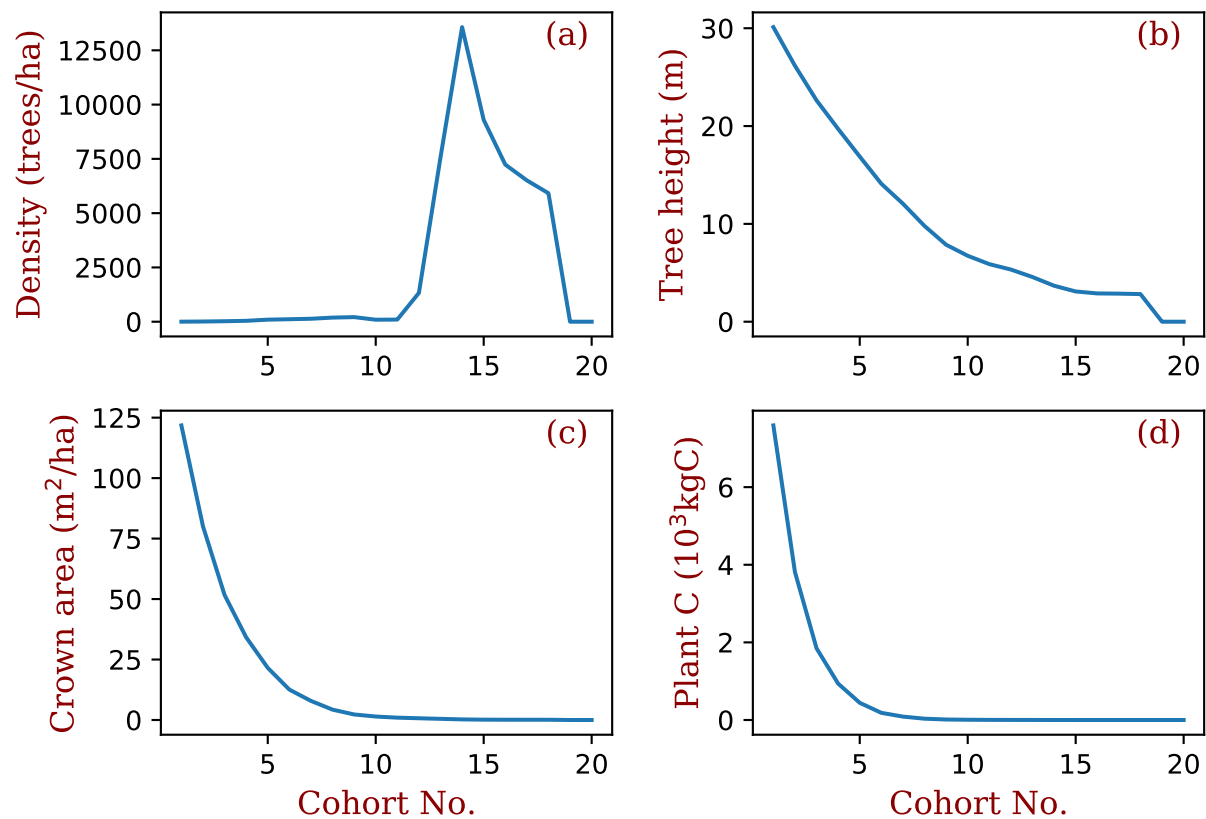
Figure S1. Bonanza Creek (BNC).



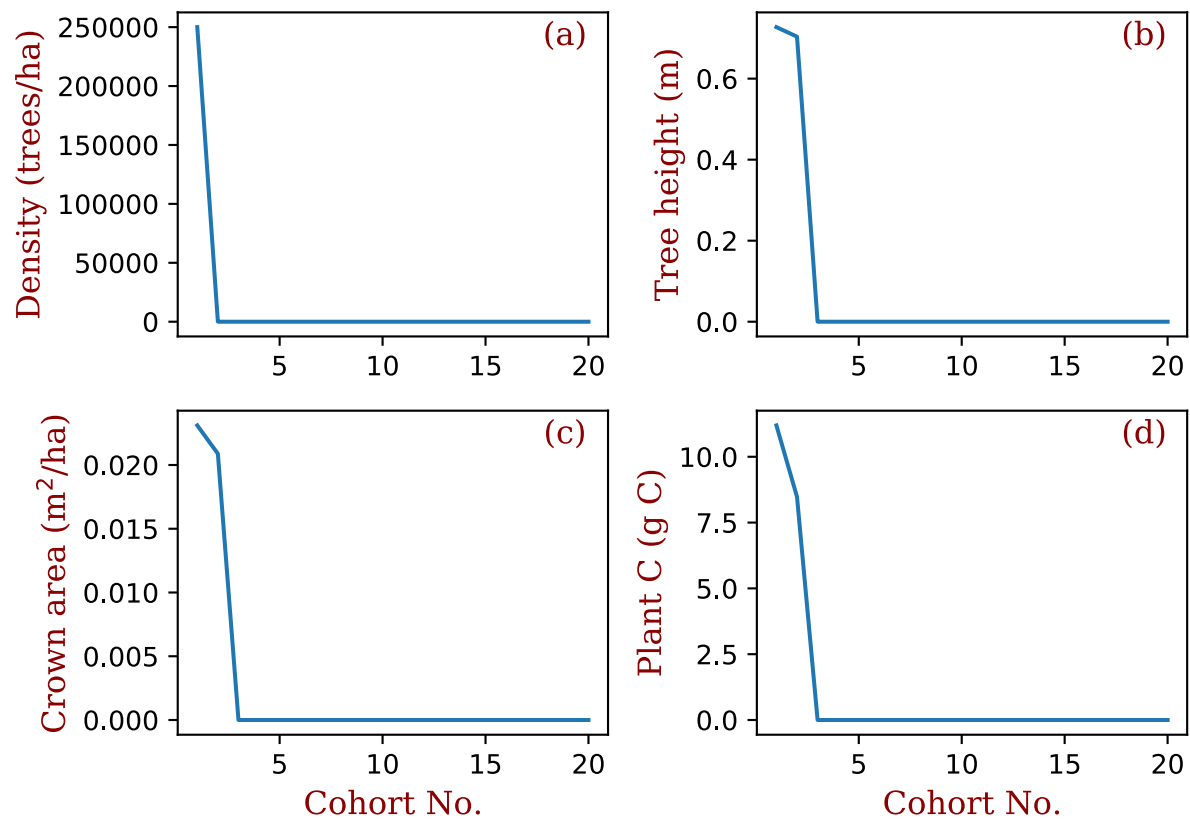
**Figure S2. Manitoba old black spruce site (MNT)**



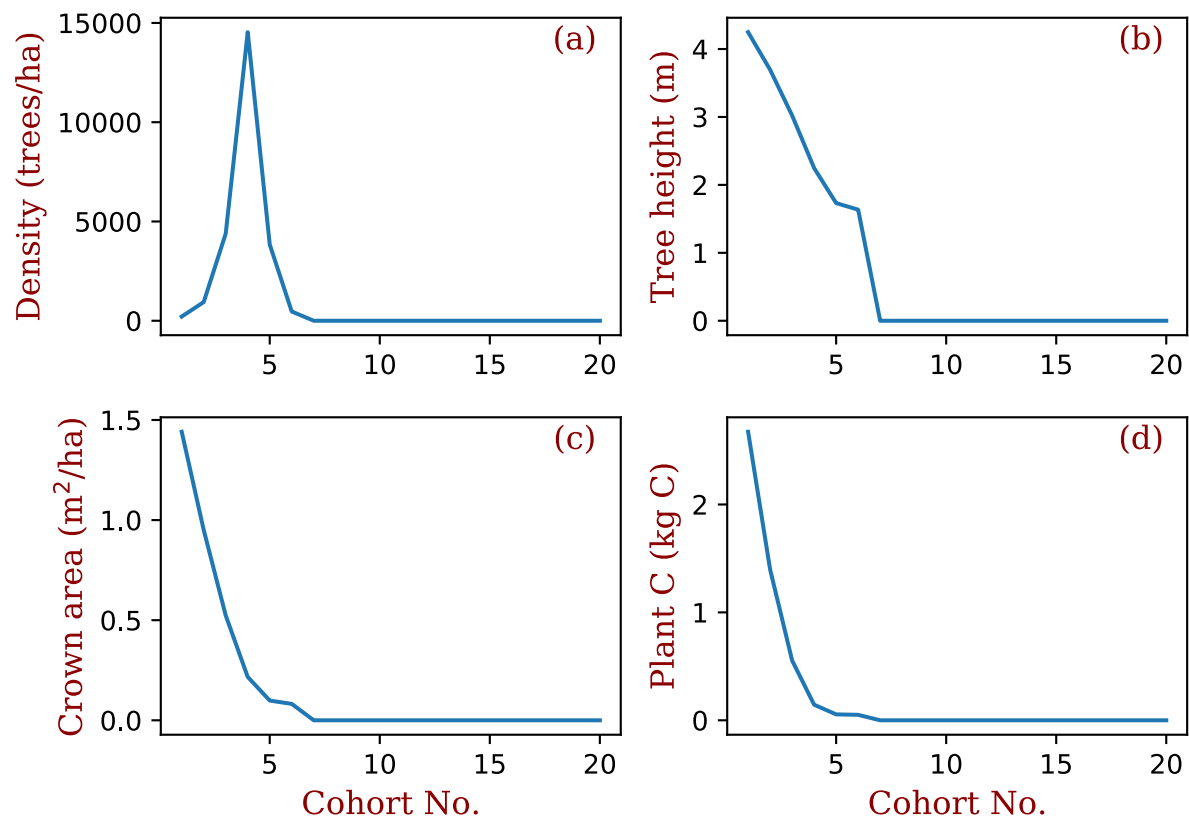
**Figure S3. Harvard Forest (HF)**



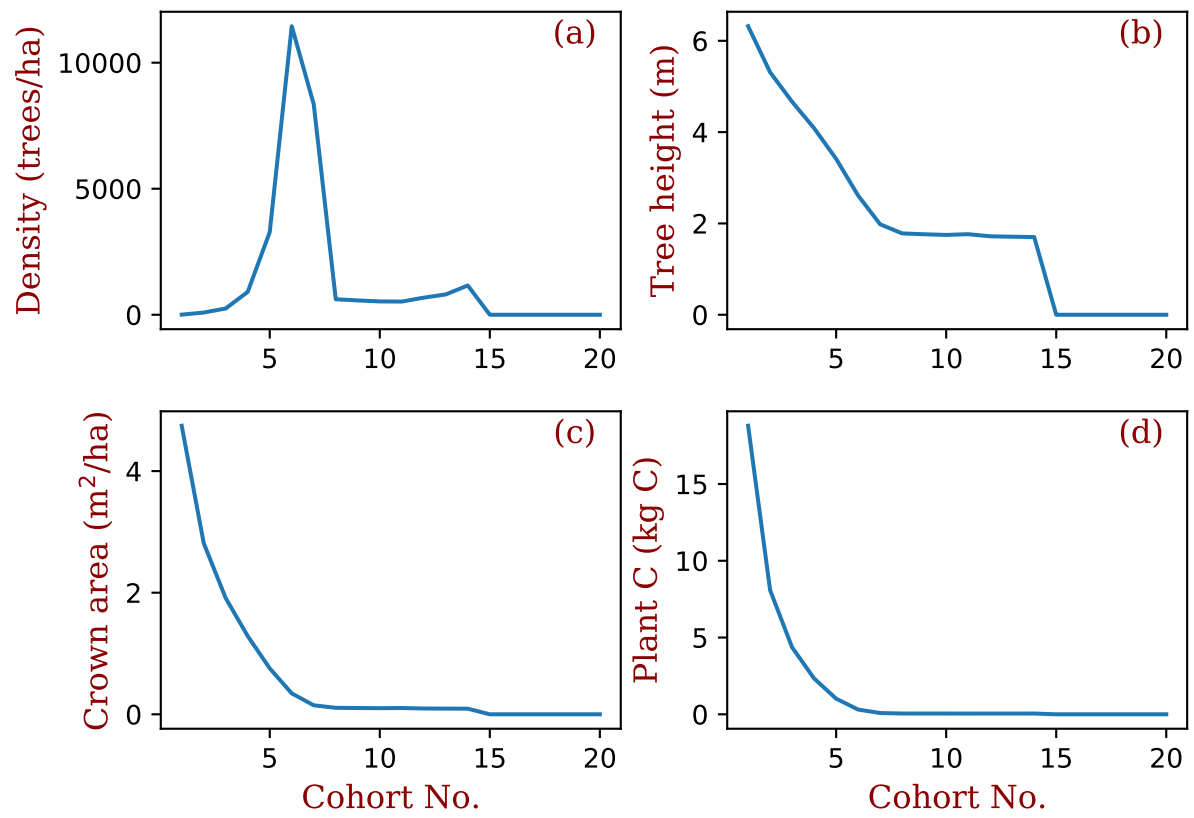
**Figure S4. Oak Ridge (OKR)**



**Figure S5. Konza LTER (KZ)**

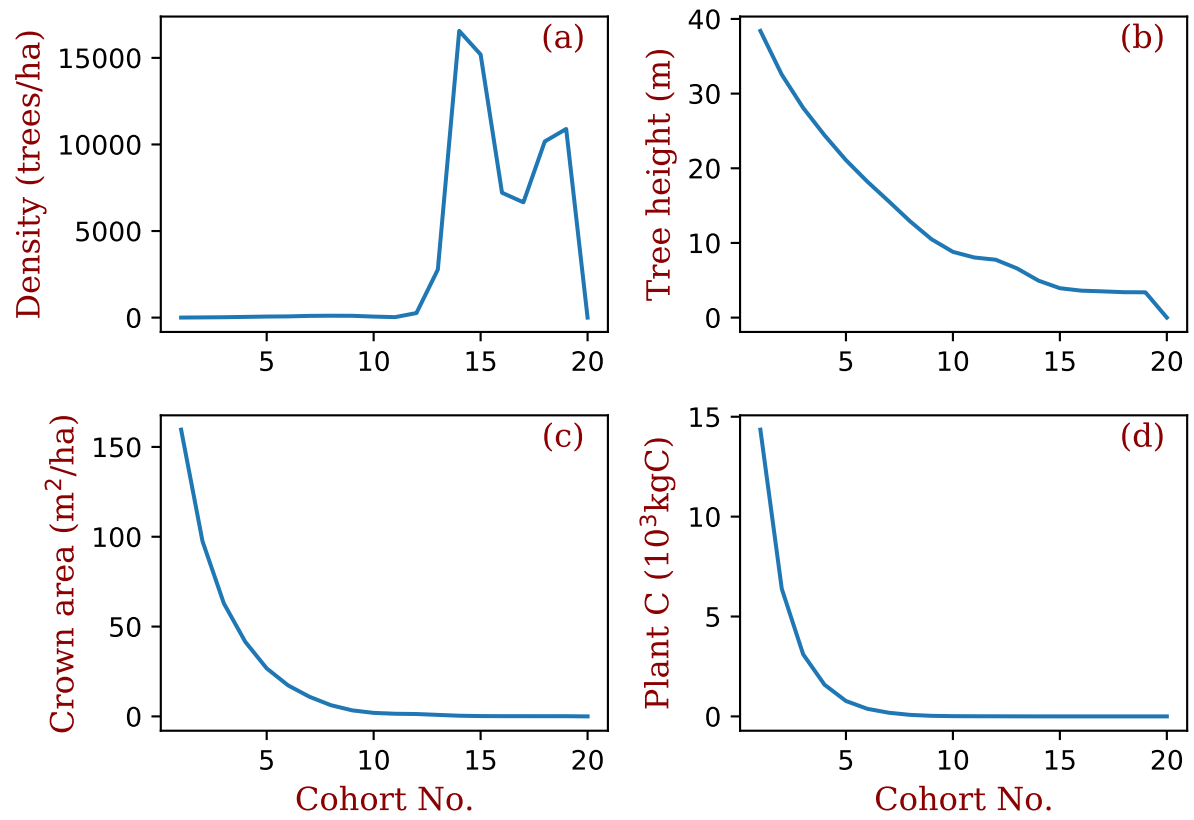


**Figure S6 Sevilleta LTER (SV)**



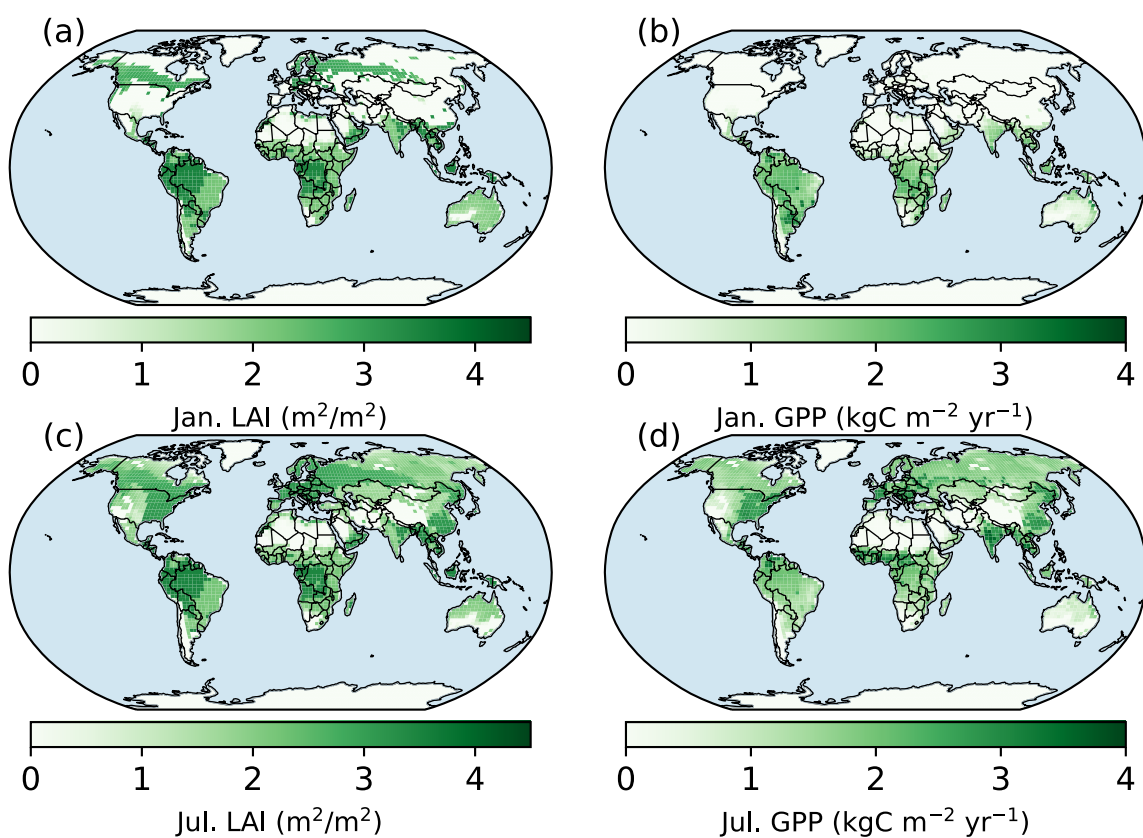
**Figure S7. Walnut Gulch Kendall (WGK)**



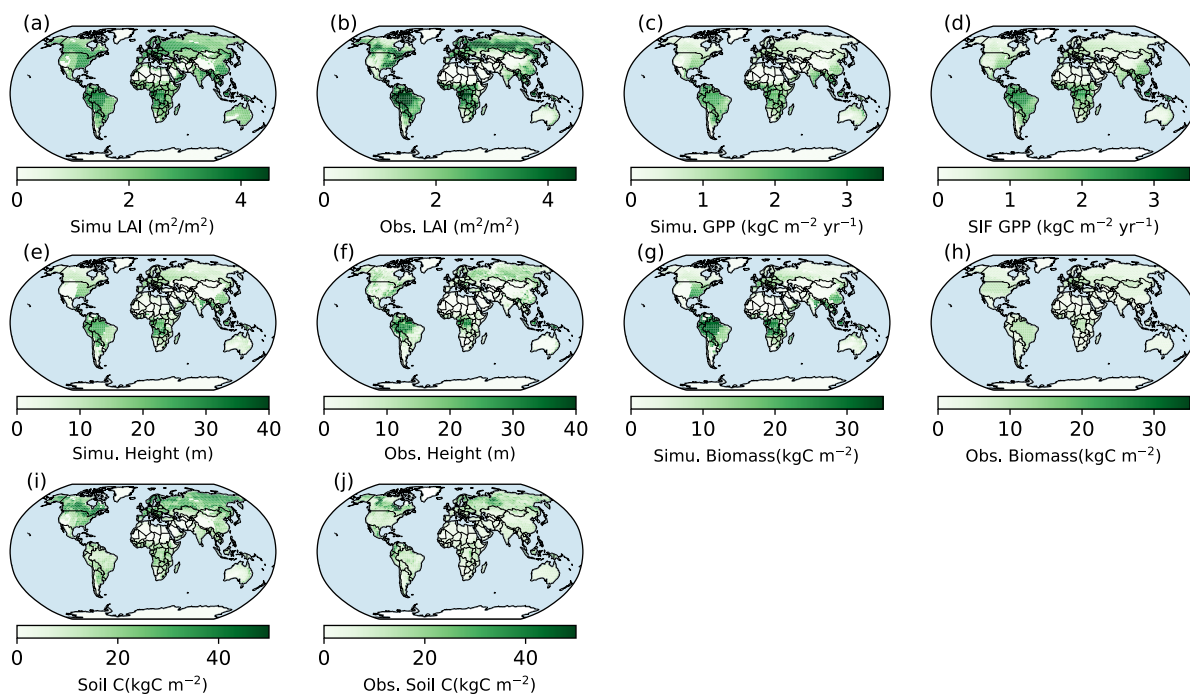


**Figure S8. Brazil Tapajos forest site (TPJ)**

## 2. The simulations of BiomeE at the single cohort setting

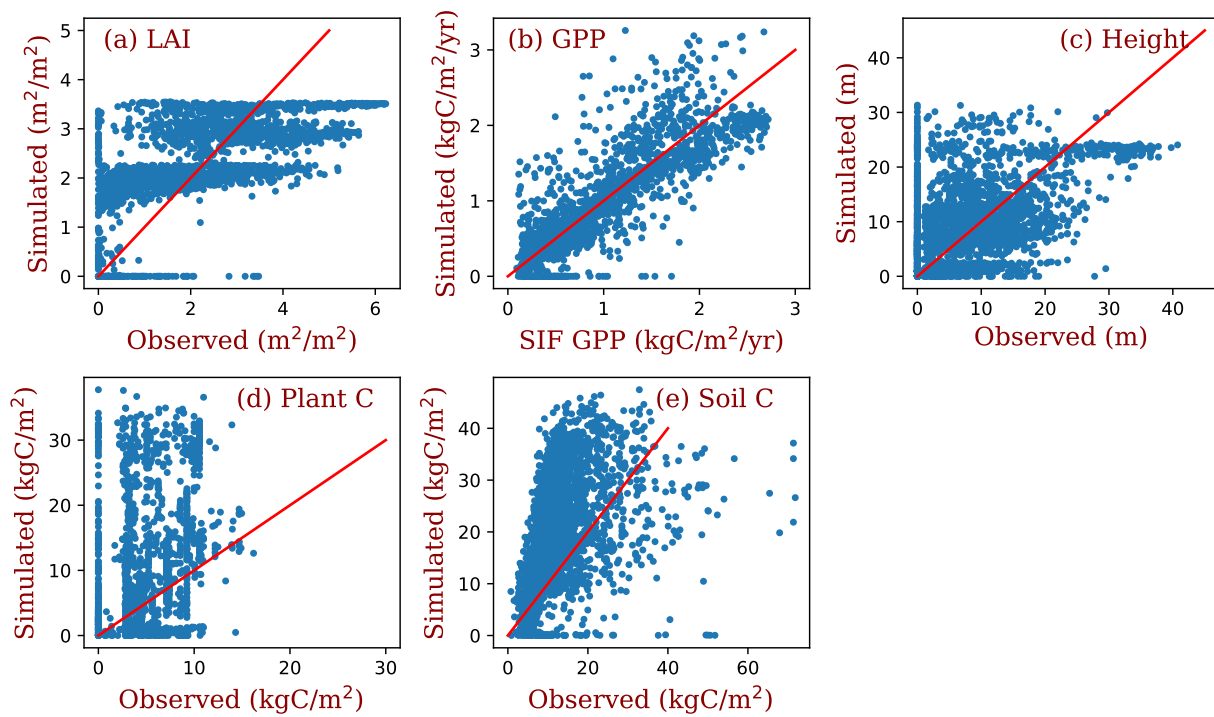


**Figure S9.** Spatial patterns of LAI and GPP in January and July simulated with single cohort setting. Panels a and b are the LAI and photosynthesis of January in the year of 600 (the last year of model run). Panels c and d are July's in the same year.

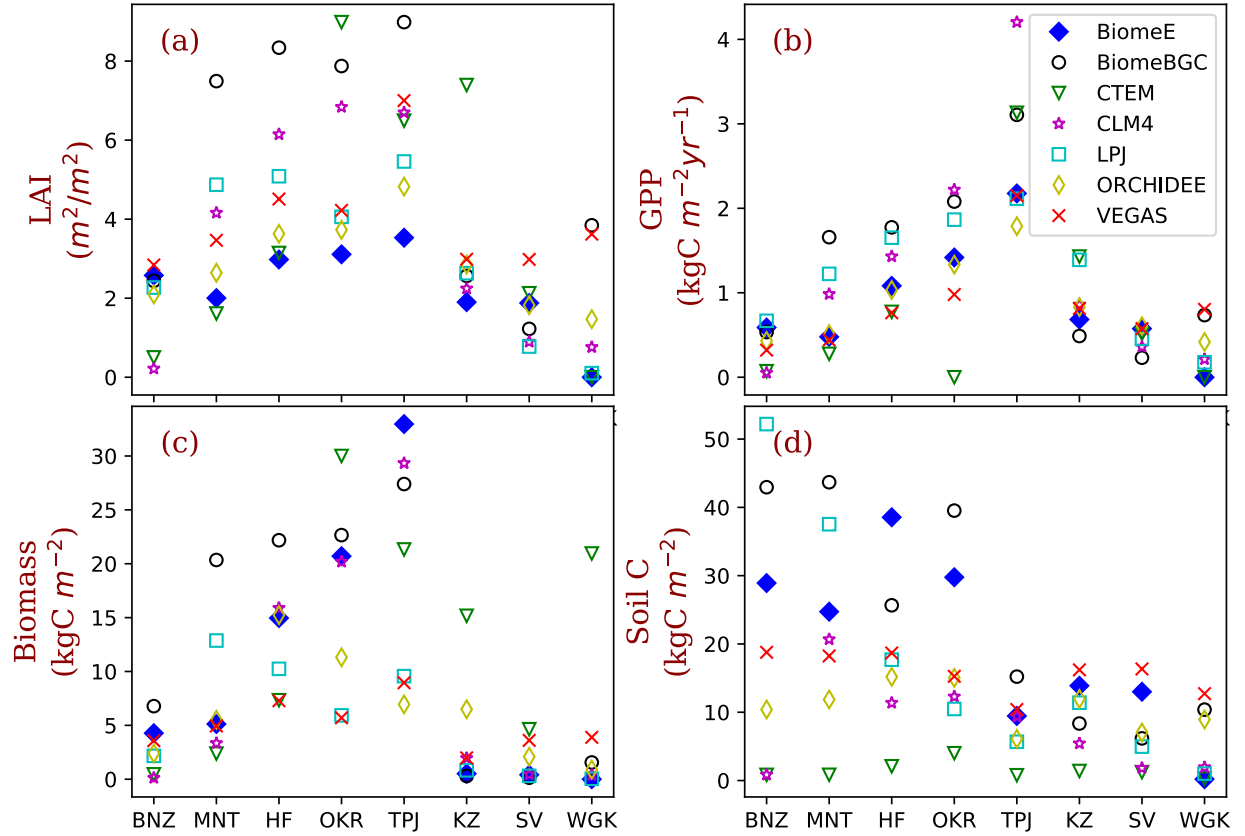


**Figure S10. Spatial patterns of BiomeE (single cohort) simulations and those from data.**

“Obs.” means different way retrieved from observations.

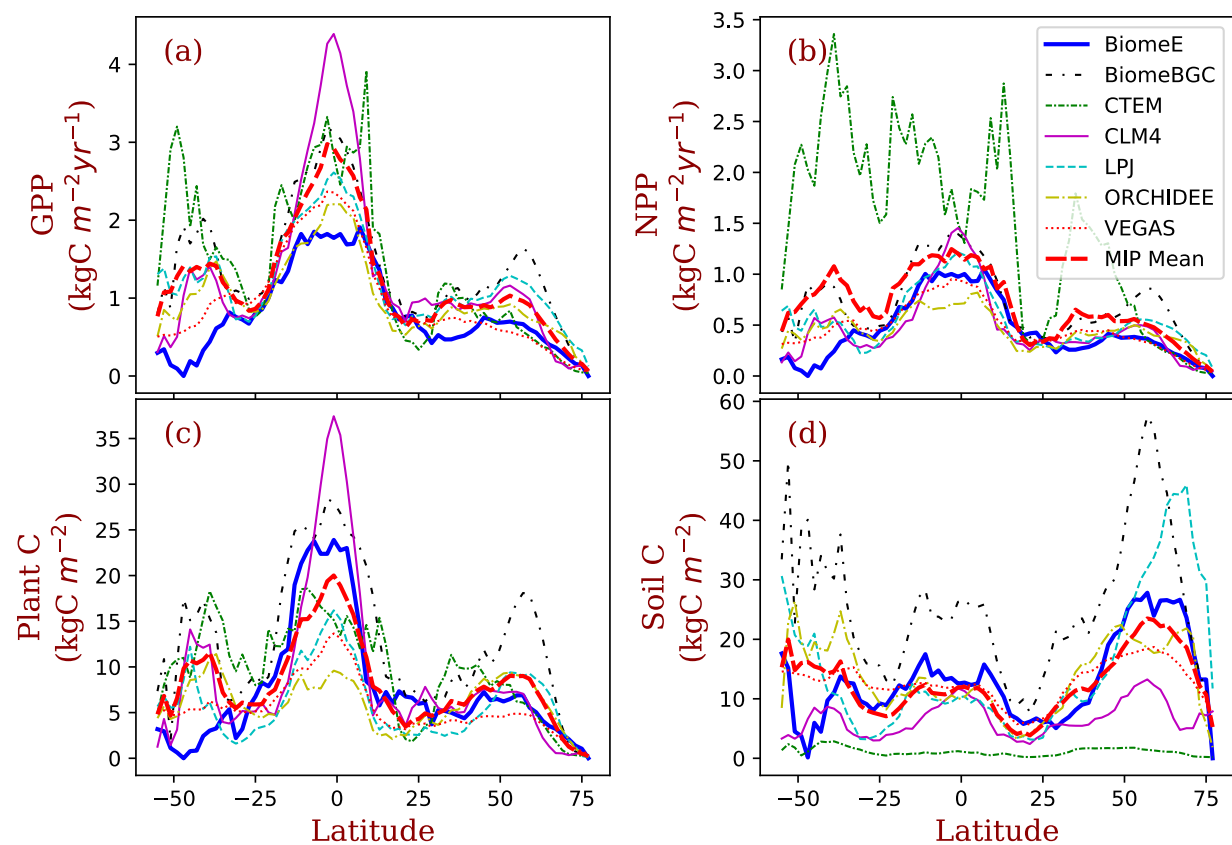


**Figure S11. Grid comparison of the single cohort BiomeE simulations with observations estimates.** The red line in each panel is the 1:1 line.



**Figure S12. Site-level comparison of the single cohort BiomeE with MsTMIP models.**

The abbreviations of the 8 sites (corresponding to model grid cells) and their coordination, dominant PFTs, and climatic conditions are in Table 2 in the main text.



**Figure S13. Latitudinal patterns of GPP, NPP, Biomass, and soil carbon as simulated by BiomeE (with single cohort setting) and MsTMIP models**