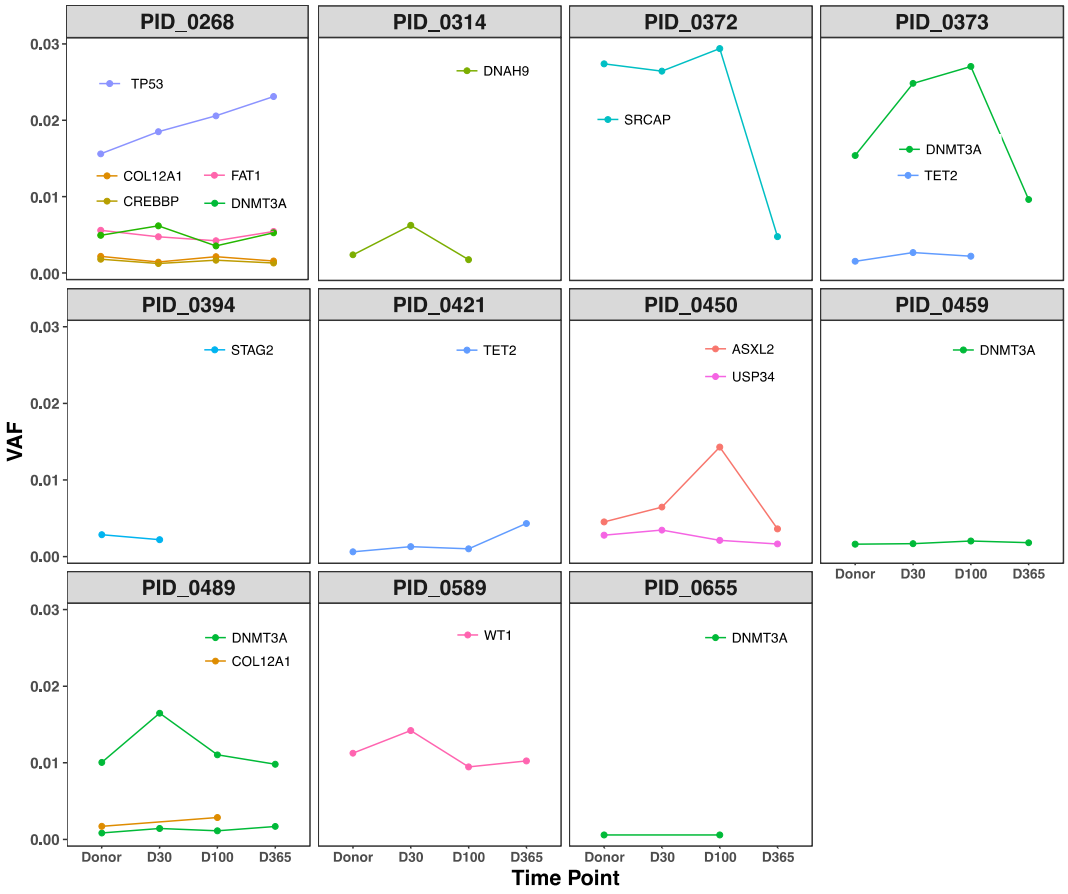

Fig. S1. Engrafted donor mutations in recipients. Dots connected by a line indicate that the same mutation was observed at multiple time points. A total of 19 mutations from 11 donors engrafted in the recipients, with 14 mutations persisting through 360 days (D360) post-HSCT in recipients. Four donors harbored more than one somatic mutation in these genes.

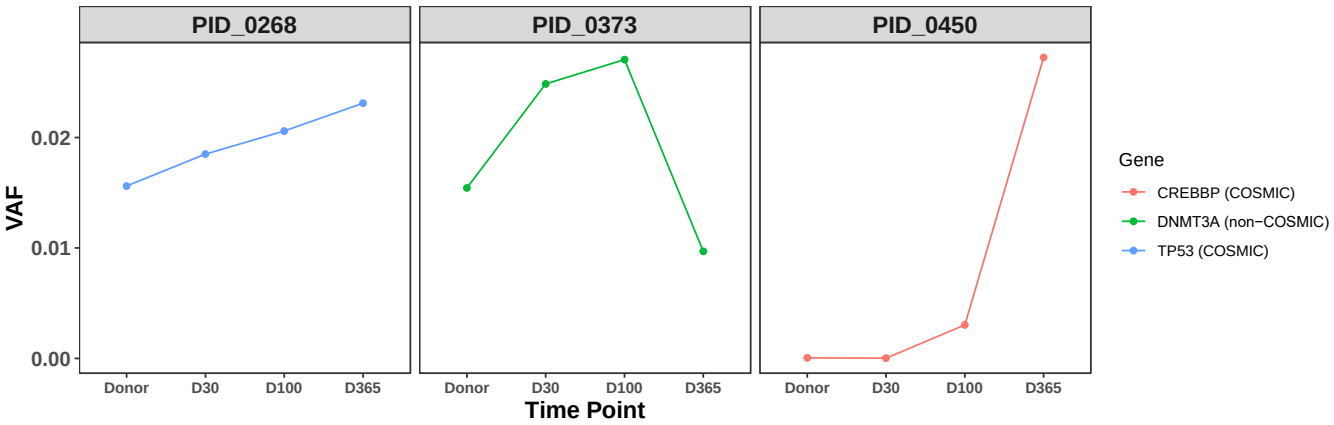

Fig. S2. Clonal expansion of mutations reaching the threshold for CHIP (≥0.02 VAF) in three patients after HSCT. Engraftment of *DNMT3A* (PID_0373) and *TP53* (PID_0268) mutations was identified by ECS, whereas engraftment of the *CREBBP* (PID_0450) mutation was identified by ddPCR.

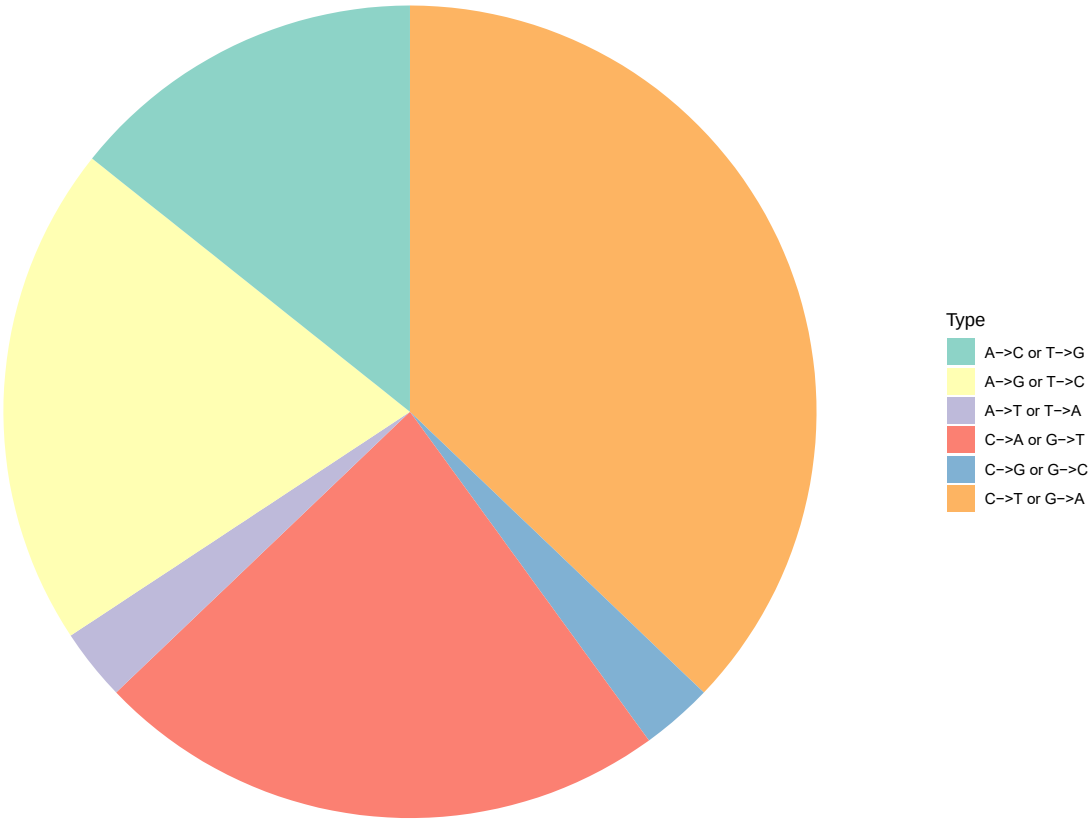

Fig. S3. Types of somatic substitutions in recipients after HSCT. The C→T/G→A transition (orange), consistent with age-related clonal hematopoiesis, was the most prevalent *(14)*.

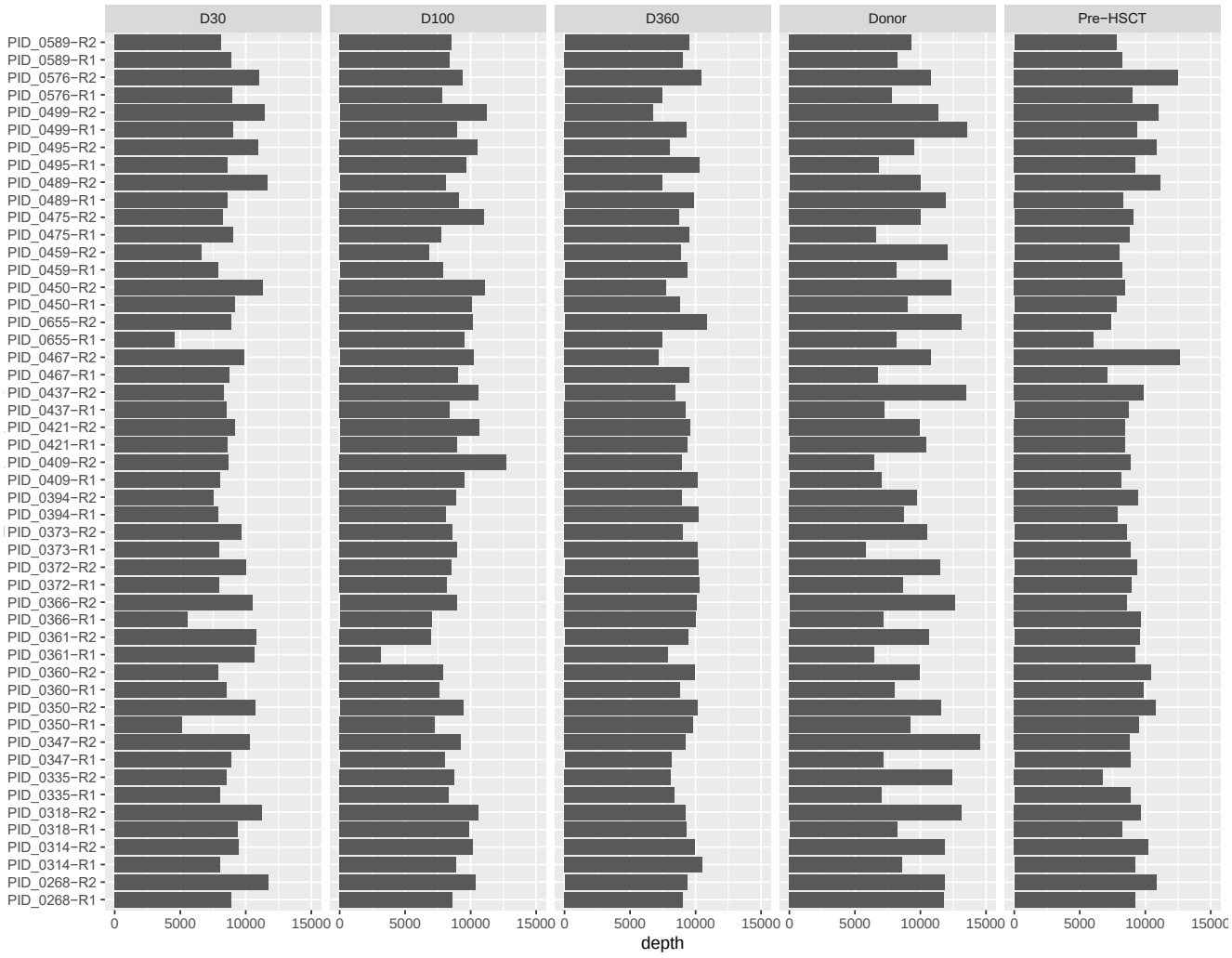

Fig. S4. The sequencing depth of each ECS library at all time points. There were no significant differences in sequencing depth (p-value >0.05, two-sided Wilcoxon rank-sum tests).

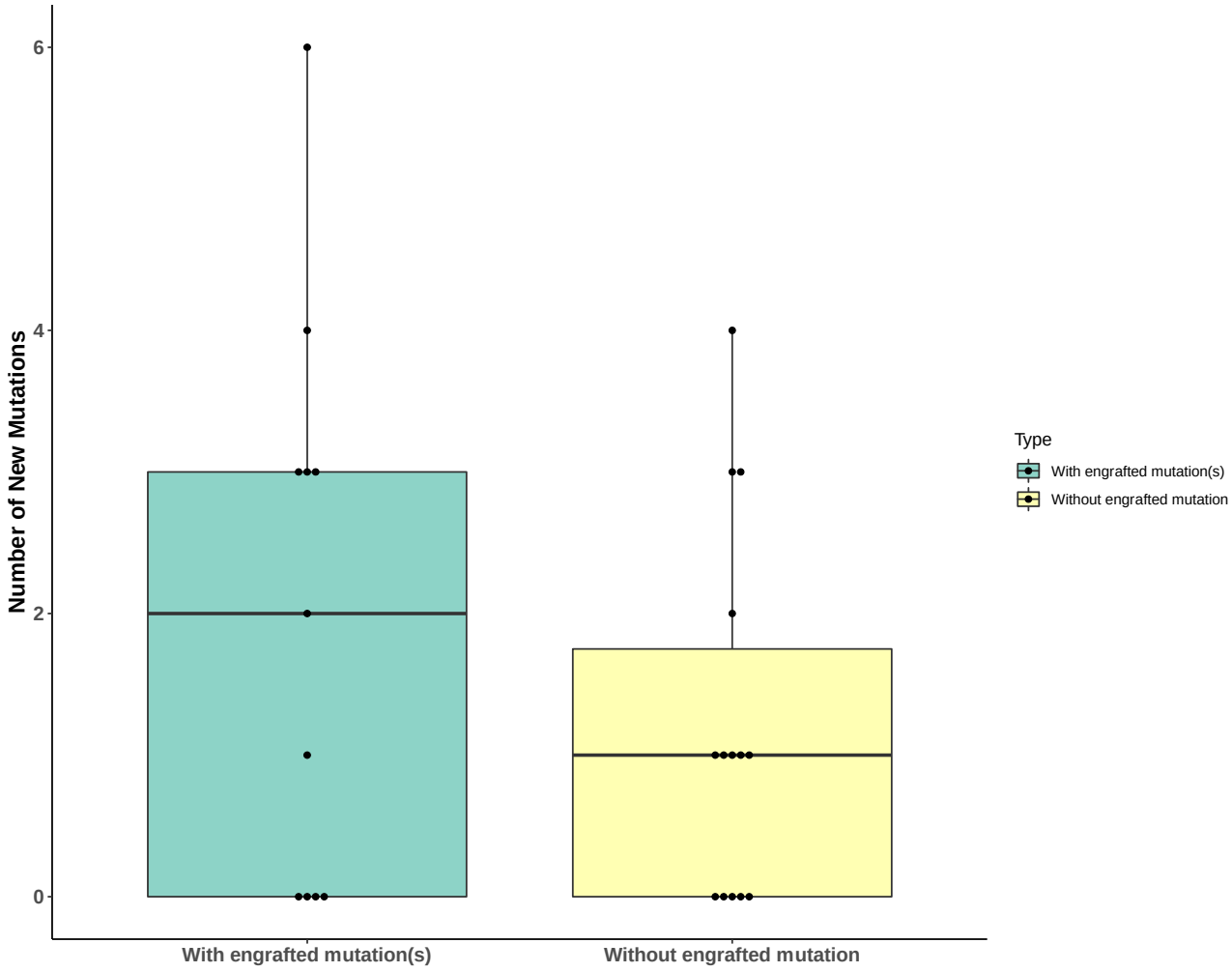

Fig. S5. New mutations detected in recipients after HSCT. There was no significant difference in the number of new mutations between recipients with engrafted donor-derived mutations and recipients without (p-value=0.44, two-sided Wilcoxon rank-sum test).

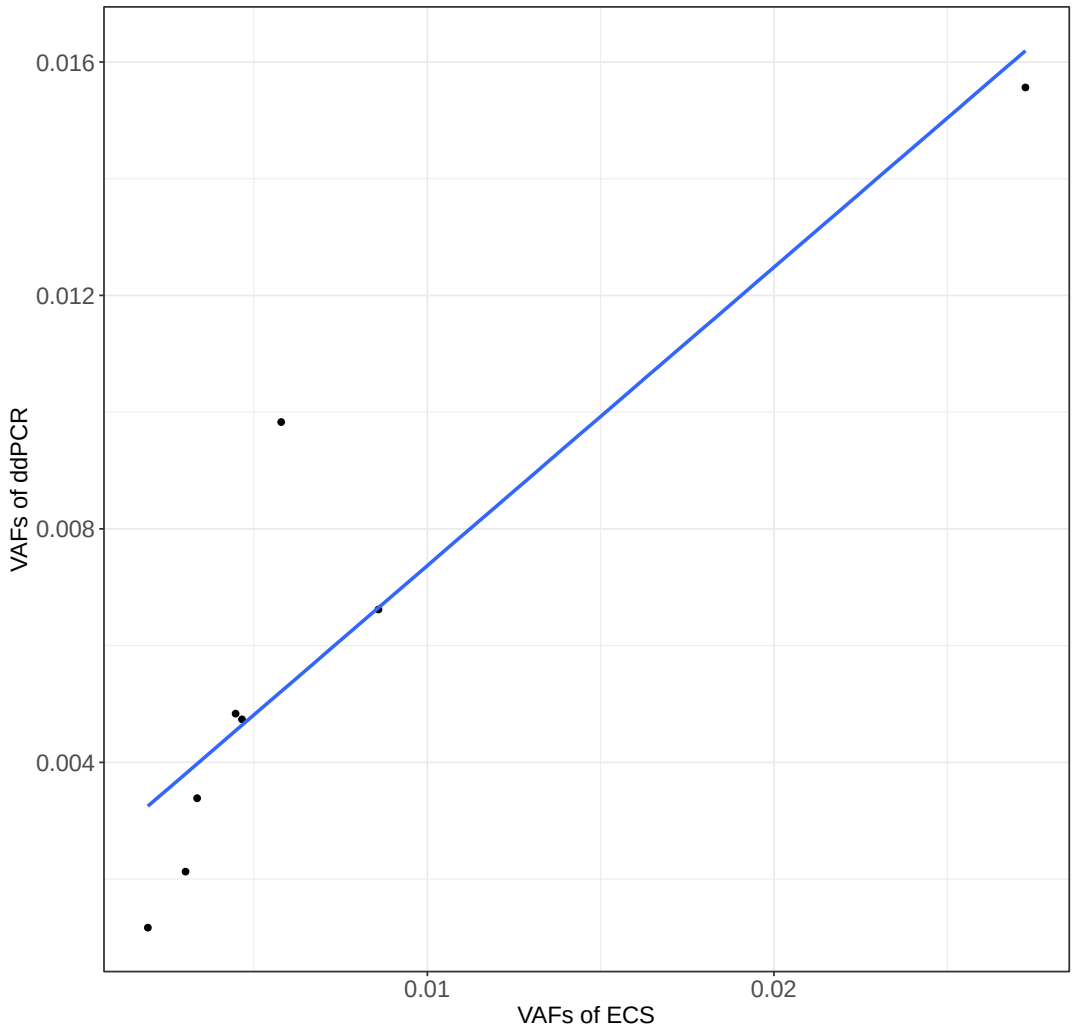

Fig. S6. ECS calls validated by ddPCR. Positive correlation with Pearson correlation coefficient = 0.9003, p-value = 0.002296.

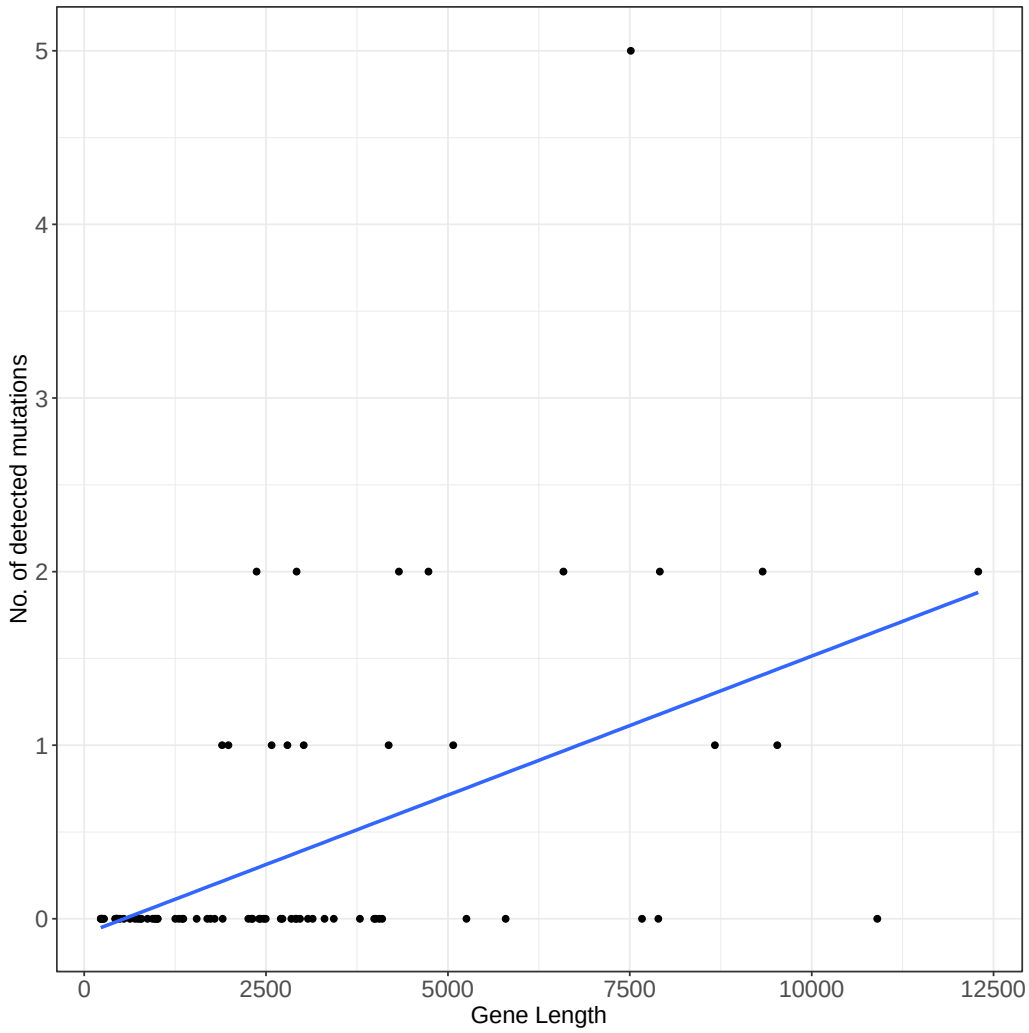

Fig. S7. Number of detected mutations in genes according to gene length. Positive correlation with Pearson correlation coefficient = 0.5131, p-value <0.00001.

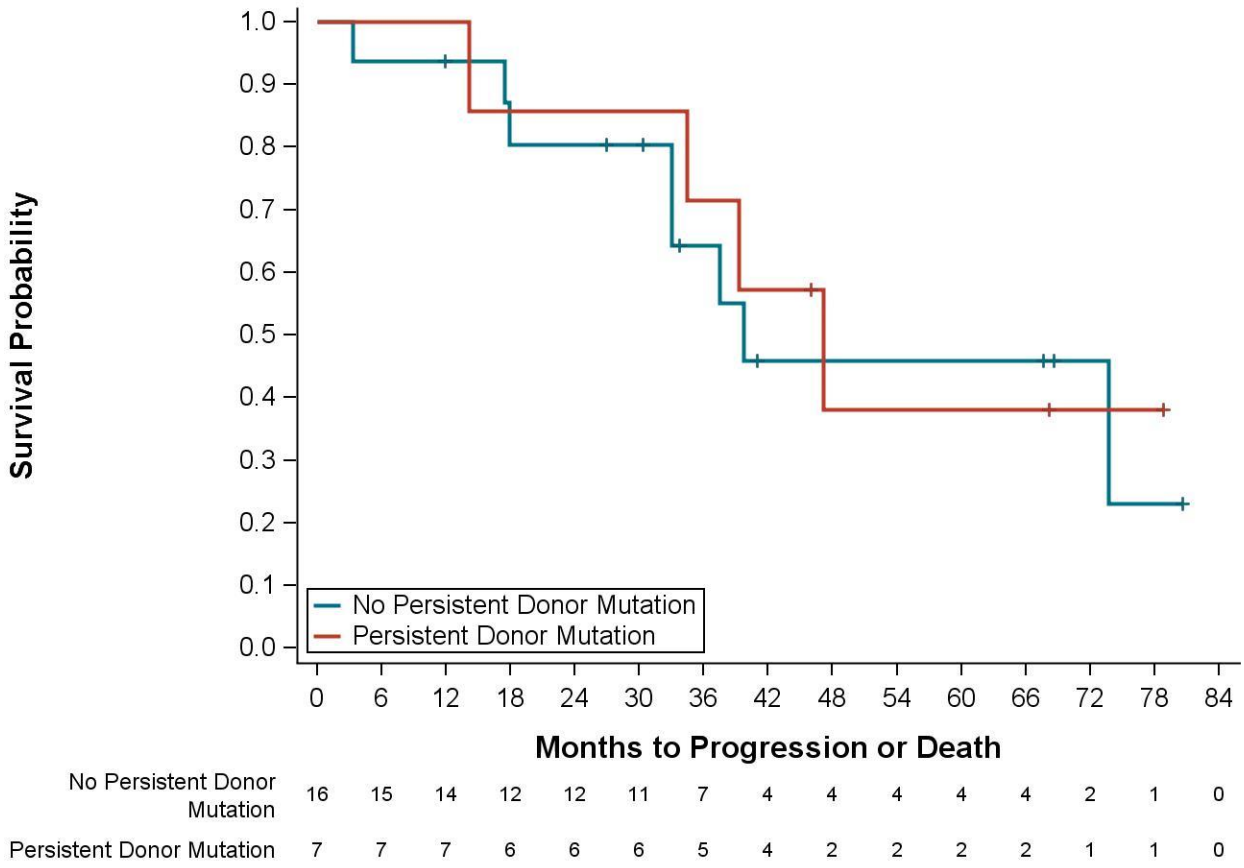

Fig. S8. Leukemia-free survival of recipients with or without persistent engraftment of donor-derived mutations. n.s., p-value = 0.7636.

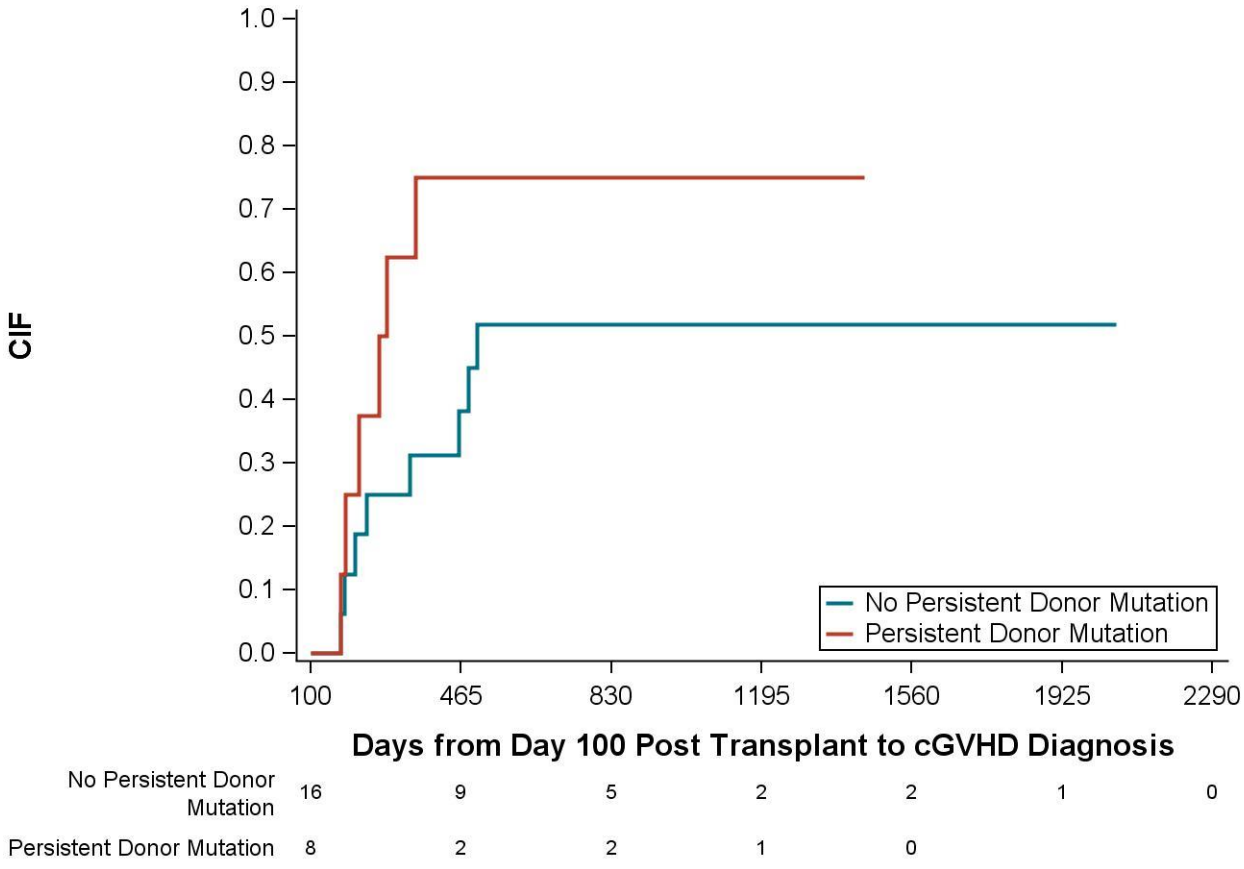

Fig. S9. Cumulative incidence of chronic GvHD in recipients with or without persistent engraftment of donor-derived mutations. n.s., p-value = 0.1755.