

Figure S1. Trial profile.

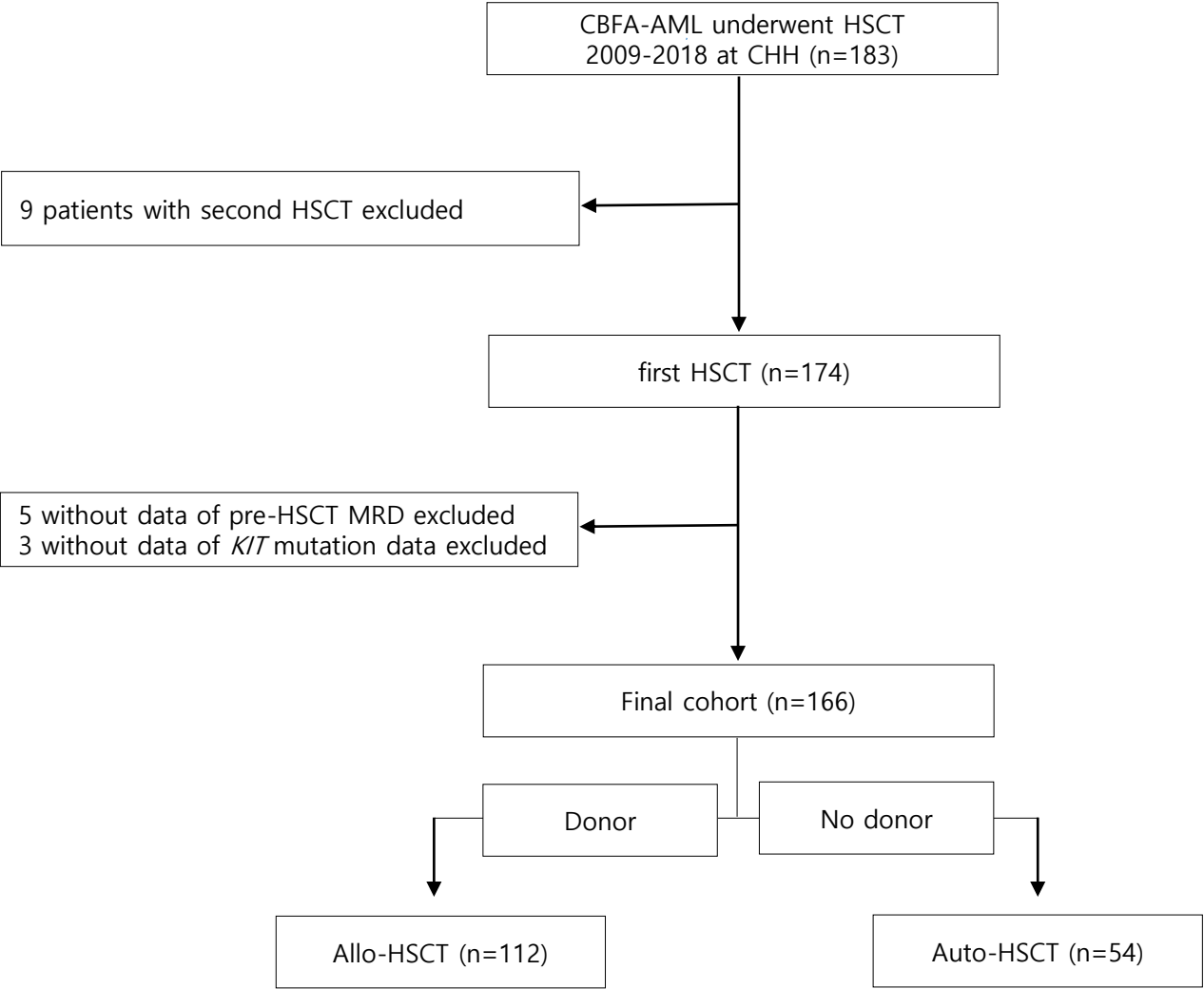


Figure S2. Cumulative incidence of relapse (CIR) according to types of *KIT* mutations. (A) CIR according to D816V *KIT* mutation, (B) D816Y *KIT* mutation, (C) D816H *KIT* mutation, (D) N822K *KIT* mutation, and (E) exon 8 *KIT* mutations.

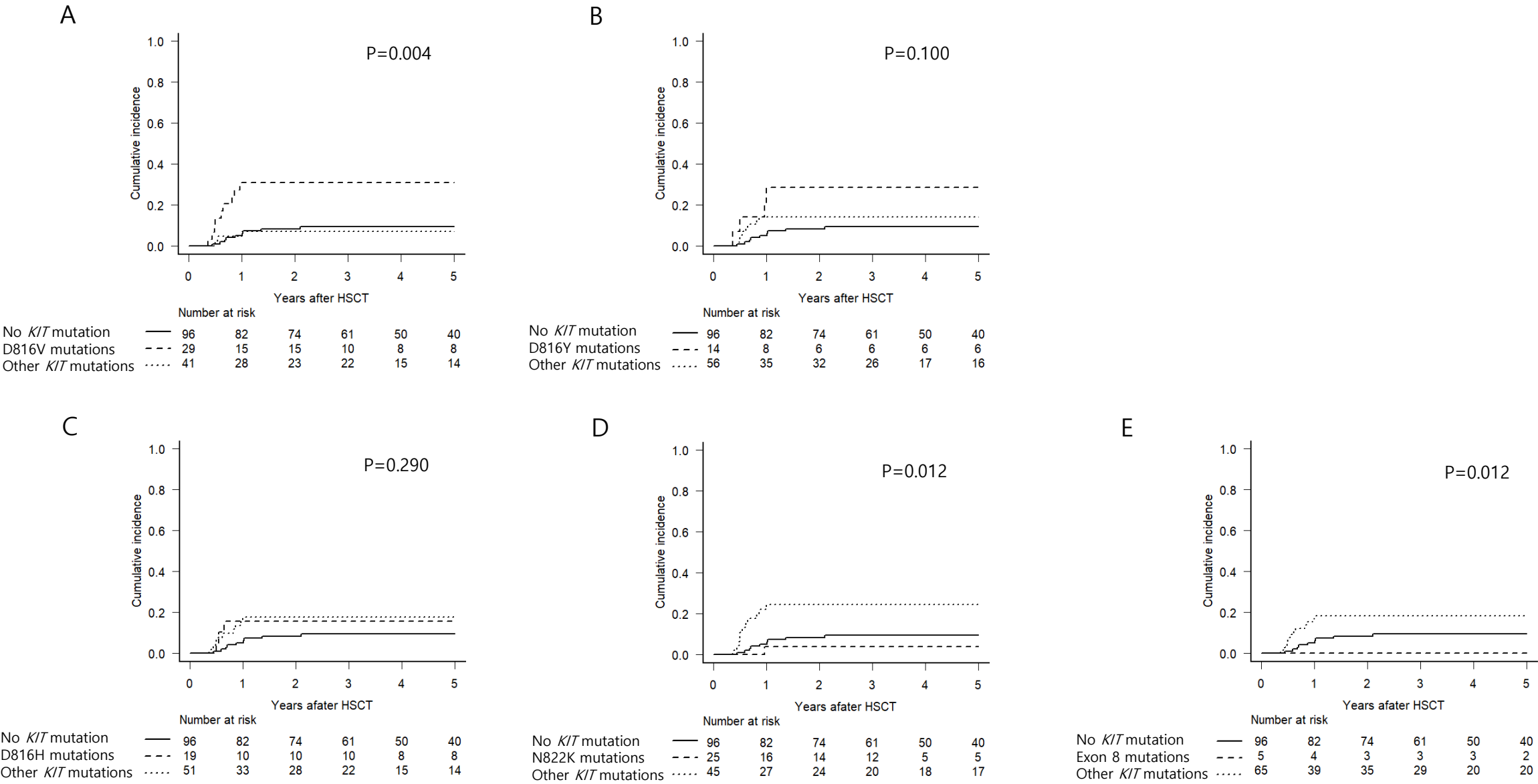


Figure S3. Survival outcomes according to D816V *KIT* mutation. (A) Non-relapse mortality, (B) disease-free survival, and (C) overall survival.

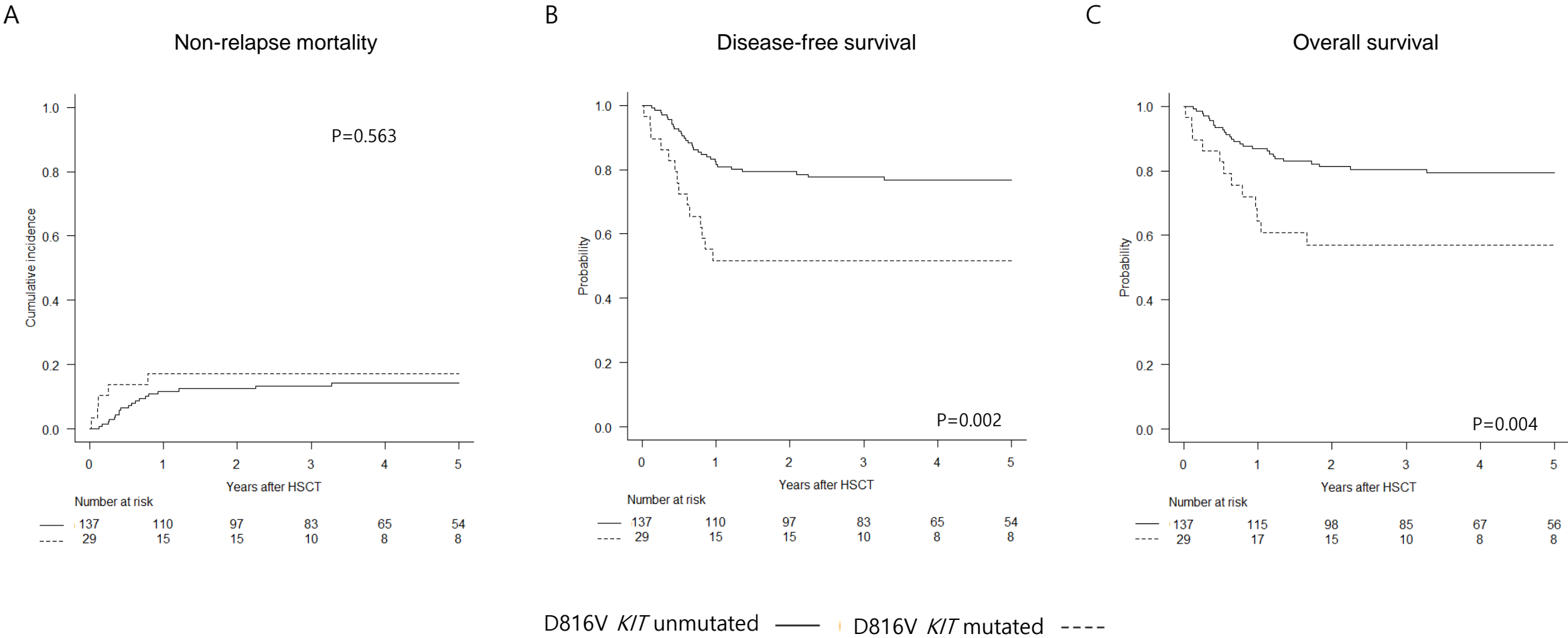


Figure S4. Cumulative incidence of relapse according to various cutoffs of *RUNX1-RUNX1T1* transcript levels at pre-HSCT (A) and at 1 month (B) or 3 months (C) after HSCT.

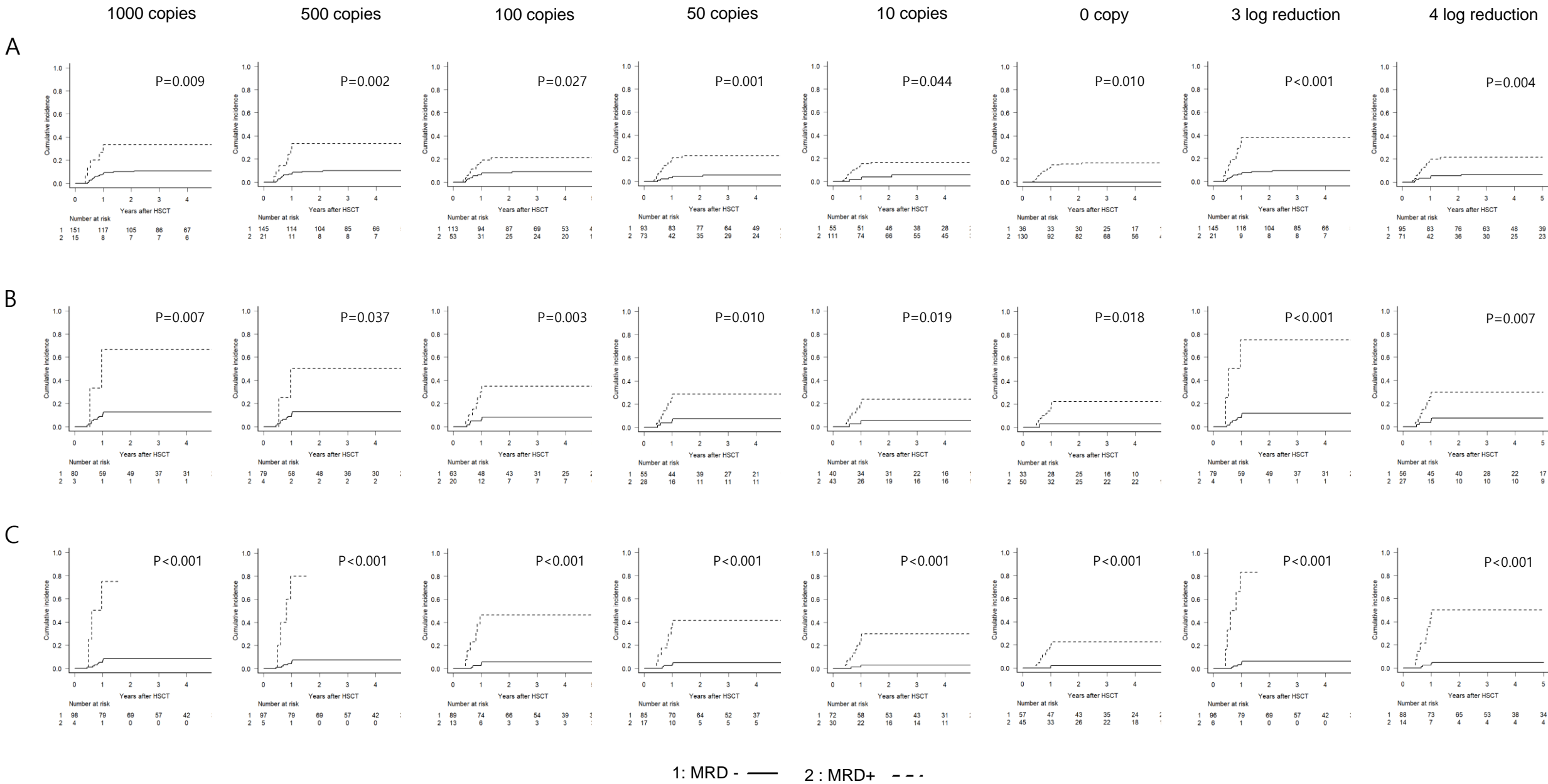


Figure S5. Survival outcomes according to MRD positivity defined by 3 log reduction of *RUNX1-RUNX1T1* levels at each time point. (A) Pre-HSCT and (B) at 1 month or (C) 3 months after HSCT.

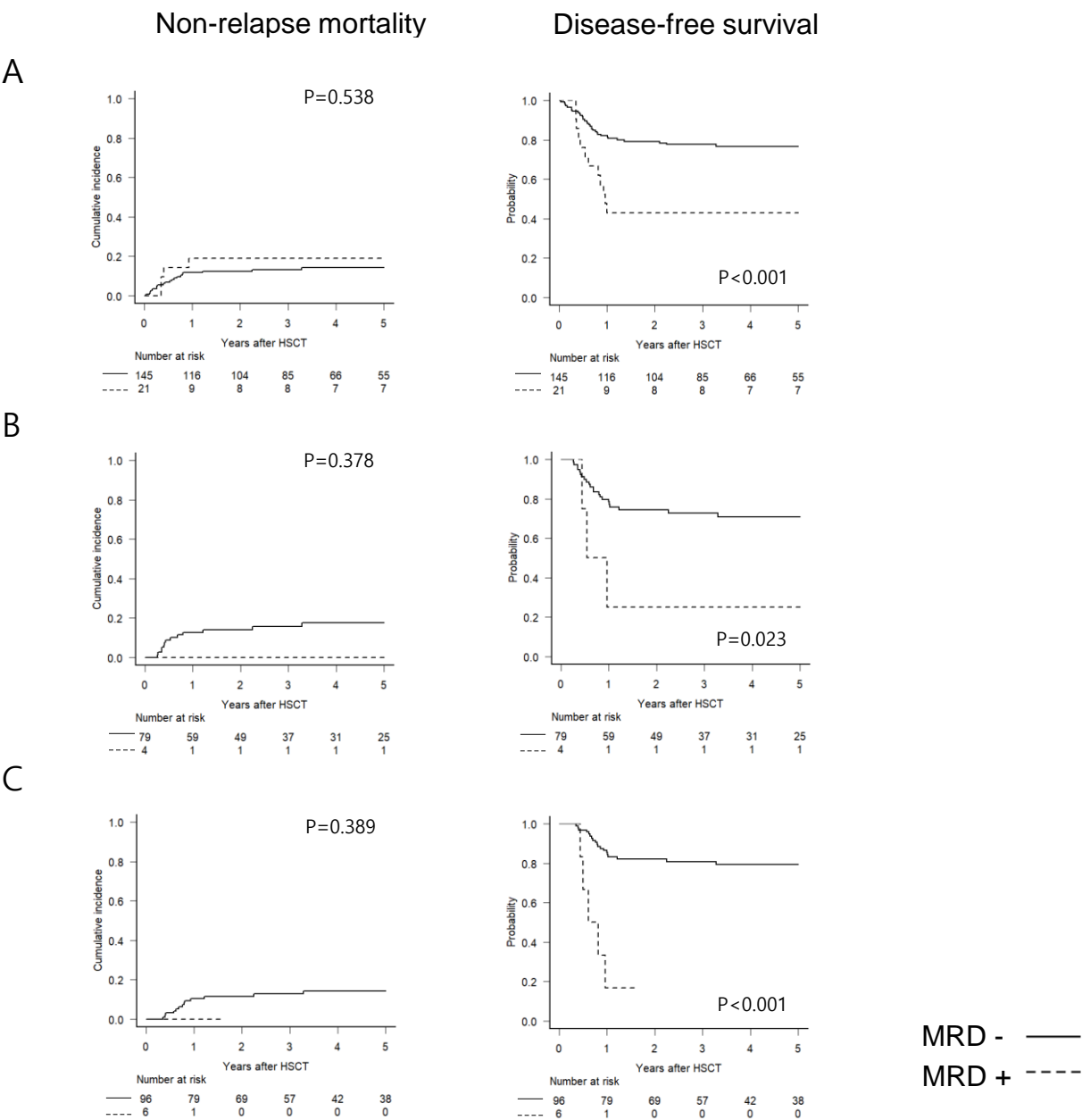


Figure S6. Survival outcomes according to transplant type. (A) Relapse, (B) non-relapse mortality, (C) disease-free survival and (D) overall survival.

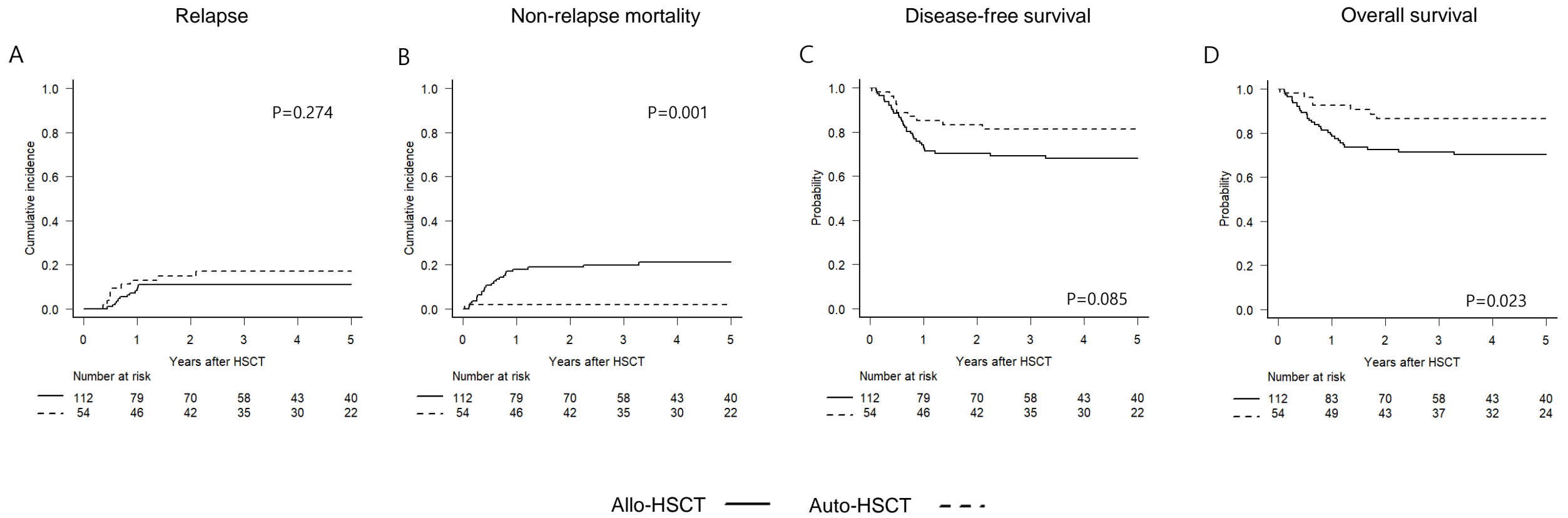


Figure S7. Survival outcomes in each group stratified by both D816V *KIT* mutations and the MRD positivity defined by 3 log reduction of *RUNX1-RUNX1T1* levels at pre-HSCT. (A) Non-relapse mortality, (B) disease-free survival, and (C) overall survival.

