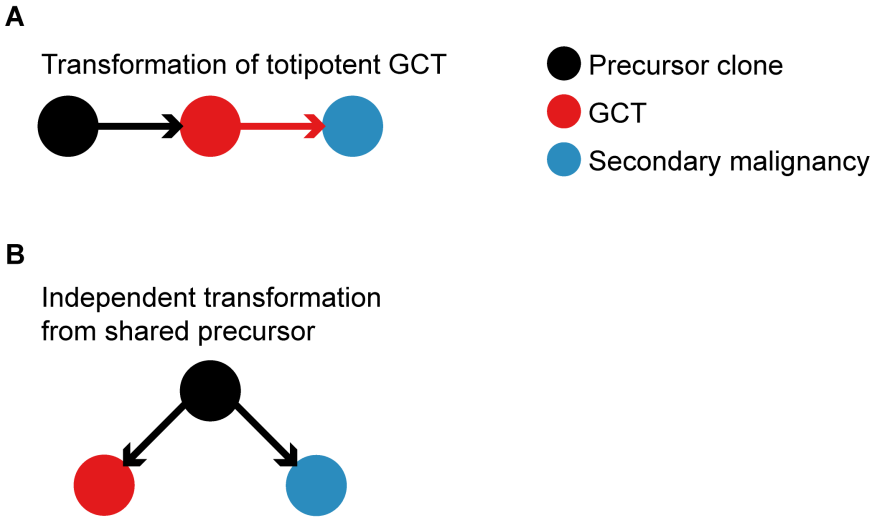
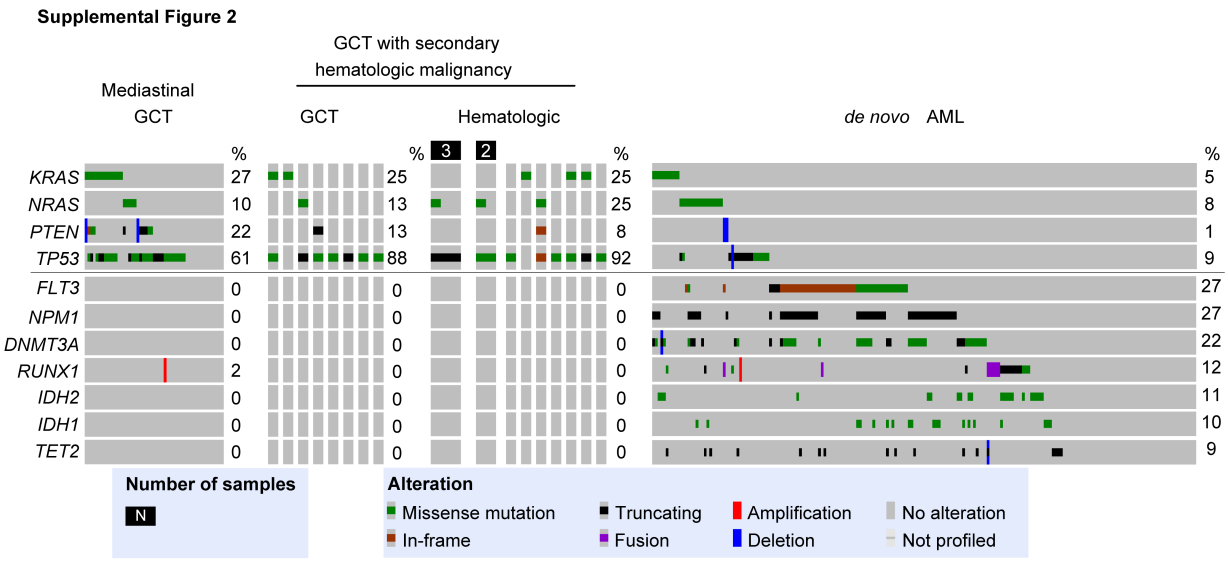
Supplemental Figure 1

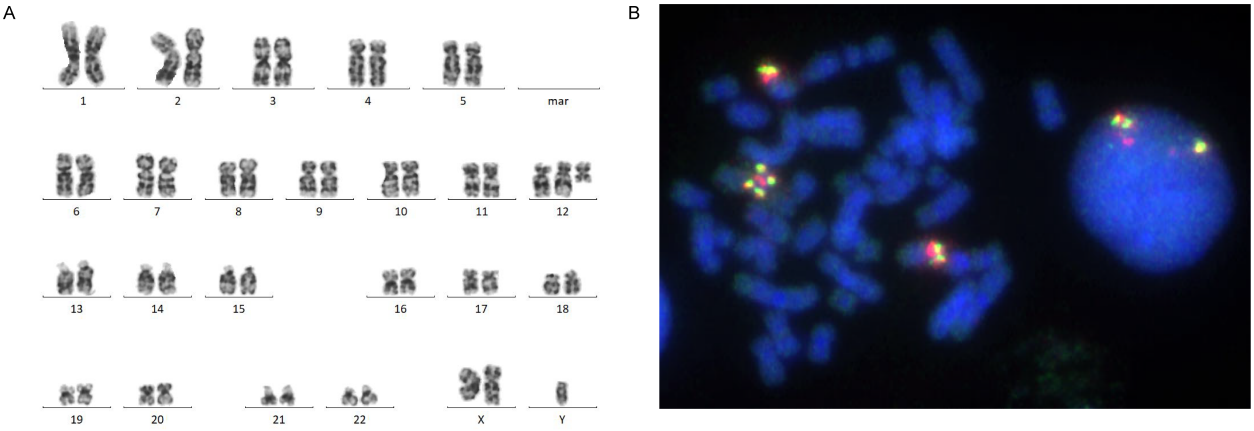


Supplemental Figure 1. Proposed models for development of "secondary malignancies" in the setting of germ cell tumors (GCTs). (A) Transformation from totipotent cells within an established GCT to a secondary malignancy. **(B)** Independent transformations giving rise to GCT and malignancy of another clinical/histologic type of cancer form a single shared precursor clone.



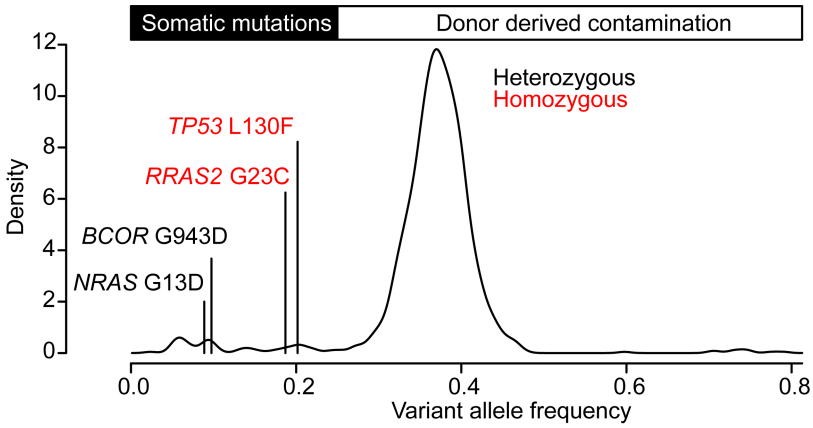
Supplemental Figure 2. Genetic and clinical characteristics of patients with germ cell tumors (GCTs) and concomitant hematologic malignancies. Oncoprint of the most prevalent genetic alterations in patients with mediastinal GCTs and no secondary malignancy diagnosis (left; n=51), mediastinal GCT with hematologic malignancy (middle; n=8 for GCT and n=12 for hematologic malignancy samples), or *de novo* AML (n=200, from the AML TCGA (13)).

Supplemental Figure 3



Supplemental Figure 3. Evidence of Isochromosome 12p (i12p) as an early cytogenetic event in hematologic malignancy developing the setting of germ cell tumor (GCT). (A) Karyogram of chronic myelomonocytic leukemia (CMML) cells in a patient with i(12p) mediastinal nonseminomatous GCT (Patient 15, **Supplemental Tables 1-2**). The karyogram presented has i(12p) and +X, which was present in 14 cells (**Supplemental Table 2**). This was accompanied by multiple additional clones with additional complex cytogenetic abnormalities, thereby identifying i(12p) as an early cytogenetic event in the CMML development for this patient. **(B)** FISH analysis of AMKL (Patient 8, **Supplemental Tables 1-2**) shows +i(12p) in one metaphase (left) and interphase (right) cell. ETV6 break-part probes at 12p13 (orange and green together) along with a centromeric probe CEP12 probe (red) were detected in an i(12p) with paired two fusion signals on each side of the i(12p).

Supplemental Figure 4



Supplemental Figure 4. Post allogenic transplant histiocytic sarcoma sample variant allele frequencies (VAFs) from patient shown in Figure 4. Putative true somatic mutations and donor derived contamination were identified via two complimentary methods: (1) VAFs were clustered using an average silhouette and K-medoid method; (2) Approximate maximum VAF of true somatic mutations was estimated using the VAF of *RRAS2* G23C that is biallelic in both the pre-allogenic GCT and MDS samples. *TP53* L130F is therefore inferred to be homozygous (either LOH or CNLOH). *NRAS* G13D inferred to be clonal heterozygous. *BCOR* G943G appears heterozygous as the donor derived DNA has additional non-mutated copies of chromosome X.