Supplemental Information

Methods

EORTC/MSG Categorization of IFD: Categorizations of invasive fungal disease (including invasive aspergillosis) were based on independent review of medical records by two infectious diseases physicians according to 2019 revised guidelines of the European Organisation for the Research and Treatment of Cancer (EORTC). The categories are as follows:

- *Proven*- Defined by a positive fungal isolate from a sterile site or biopsy proven tissue invasion.
- *Probable*- Defined by the presence of:
  - Any characteristic host factor including:
    - Recent history of neutropenia
    - History of allogeneic stem cell transplant
    - Prolonged use of corticosteroids
    - Treatment with T-cell immunosuppressants
    - Inherited severe immunodeficiency
  - Any Clinical feature including:
    - CT finding characteristic of lower respiratory tract fungal infection
    - Tracheobronchitis (visualized by bronchoscopy)
    - Sinonasal infection
    - CNS infection
    - Disseminated Candidiasis
  - Mycologic evidence:
    - Cytology or culture from a non-sterile site (such as bronchoalveolar lavage)
    - Detection of fungal antigen or cell wall constituent in blood, BAL, or CSF:
      - Galactomannan
      - 1,3- beta-d-glucan
- *Possible*- Defined by the presence of a host factor and clinical feature above, but lacking mycologic evidence

Given that mycologic evidence may often be lacking despite a high index of clinical concern, patients with possible IFD who were treated with antifungal agents ("possible-treated") were considered separately than those who were not.

Tables (excel file)

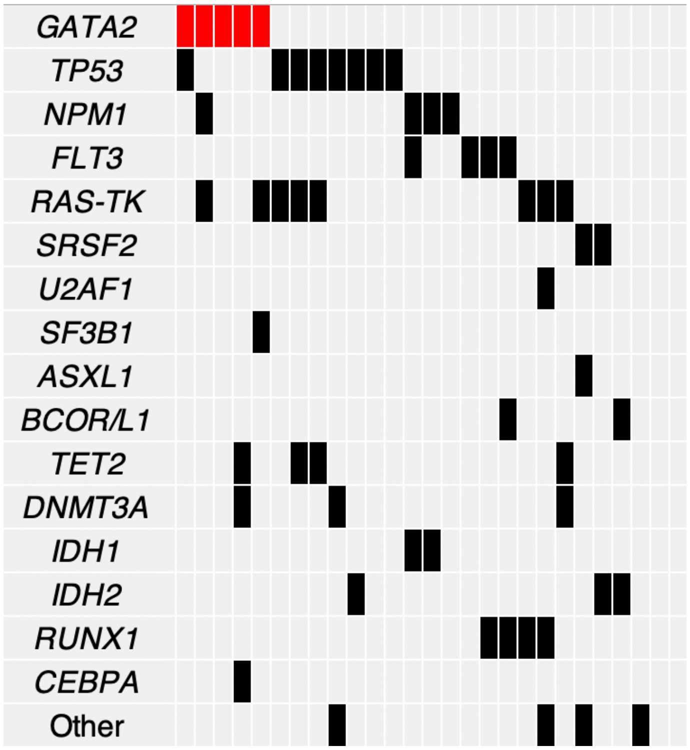
Supplemental Table 1: Patient, Disease, and Mutation Characteristics of IA Cohort

Supplemental Table 2: Mutation Frequency Among Myeloid Malignancy Patients at DFCI

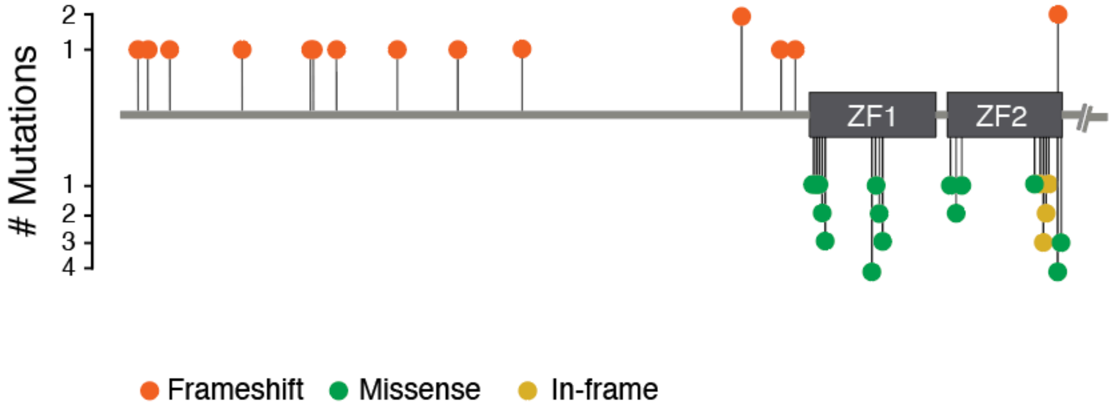
Supplemental Table 3: Summary of 51 Evaluable Patients in *GATA2* Cohort

Supplemental Table 4: Characteristics of 51 evaluable Patients in *GATA2* Cohort

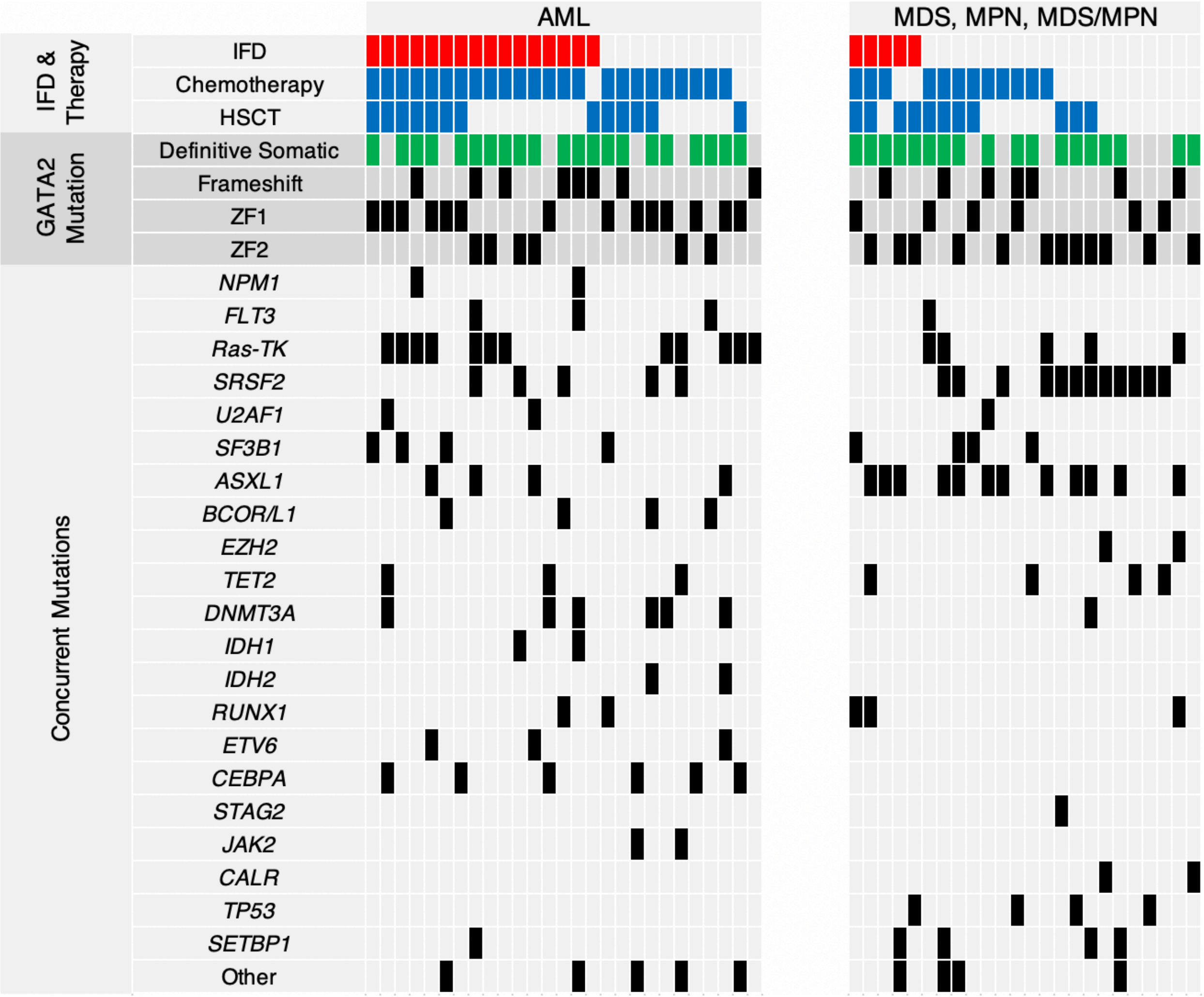
Supplemental Table 5: Statistical enrichment analyses of *GATA2* cohort



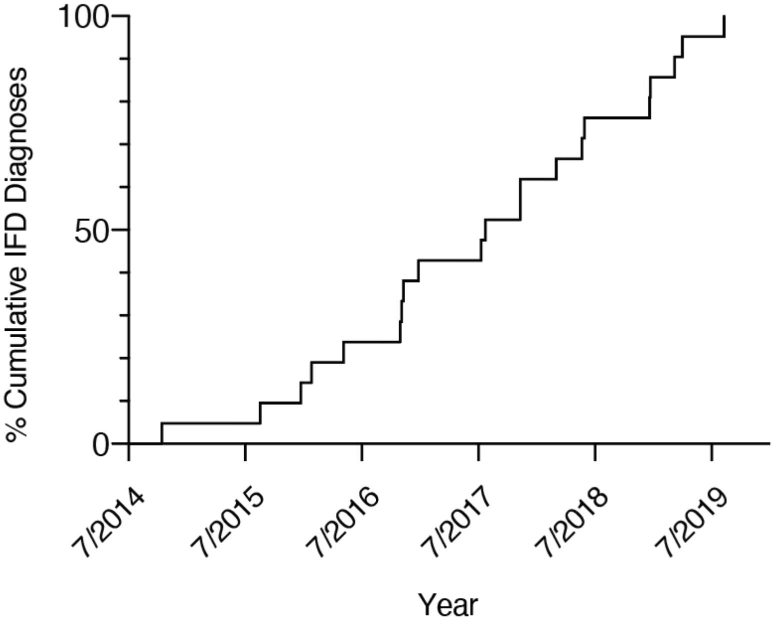
Supplemental Figure 1. Co-mutation distribution of 27 evaluable patients in IA Cohort. Each column represents a patient in the cohort.



Supplemental Figure 2. Distribution of mutations in coding region of *GATA2* gene among 51 evaluable patients in *GATA2* cohort.



Supplemental Figure 3. IFD, treatment, *GATA2* mutation characteristics, and co-mutation distribution of 51 evaluable patients in *GATA2* Cohort. Each column represents a patient in the cohort.



Supplemental Figure 4. Cumulative proven, probable, and possible-treated IFD diagnoses in *GATA2* cohort over the 5 year study period from 7/2014 to 9/2019 (21 total events).