

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Table of somatic variants discovered using eWGS, including variant allele frequencies (VAFs) in eWGS, bulk RNA-seq, and scRNA-seq data, as well as Mutant Cell Detection Rate (and related statistics), subclone assignments, and lists of mutation-containing cells.

File Name: Supplementary Data 2

Description: Summary coverage metrics for 200 cancer-relevant genes.

File Name: Supplementary Data 3

Description: Somatic variant false positive rates computed from control AML samples.

File Name: Supplementary Data 4

Description: Normalized expression data used to generate heatmaps for each case (Fig. 2, Supp. Fig. 2-5).

File Name: Supplementary Data 5

Description: Differentially expressed genes for (a) genes whose expression is correlated with the *GATA2*^{R361C} subclone, calculated using all putative AML cells, (b) genes whose expression is correlated with *GATA2*^{R361C} itself, calculated using all putative AML cells (c) genes whose expression is correlated with the *GATA2*^{R361C} subclone, calculated using mutant cells, and (d) 198 genes in the putative *VIM* regulon represented in Fig. 5h.