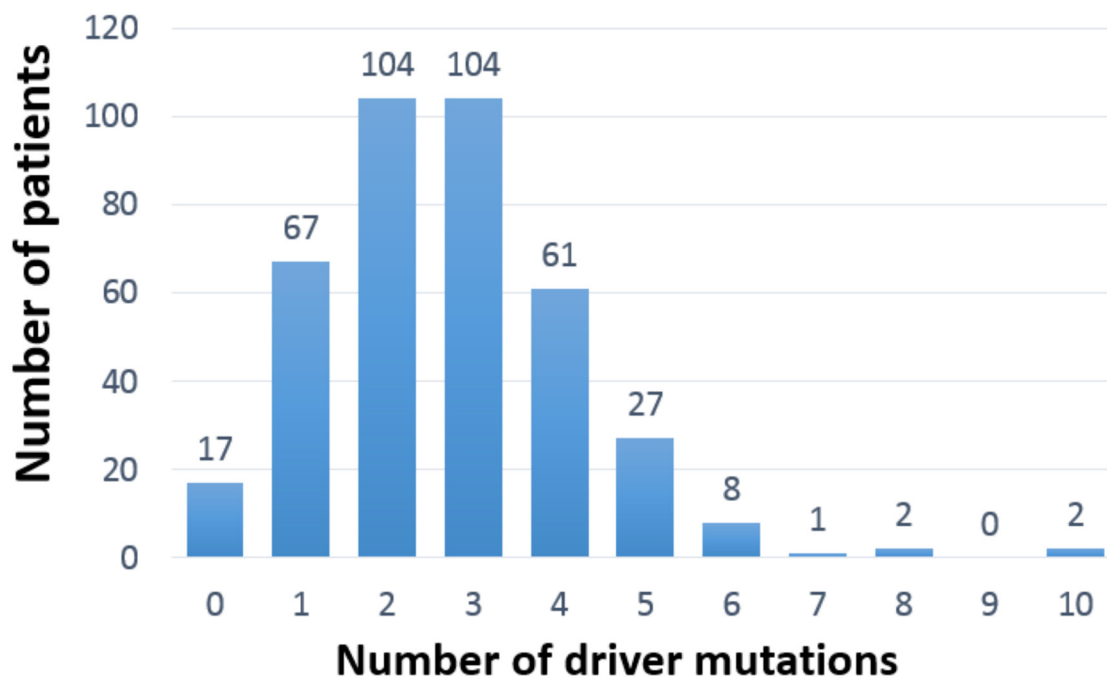
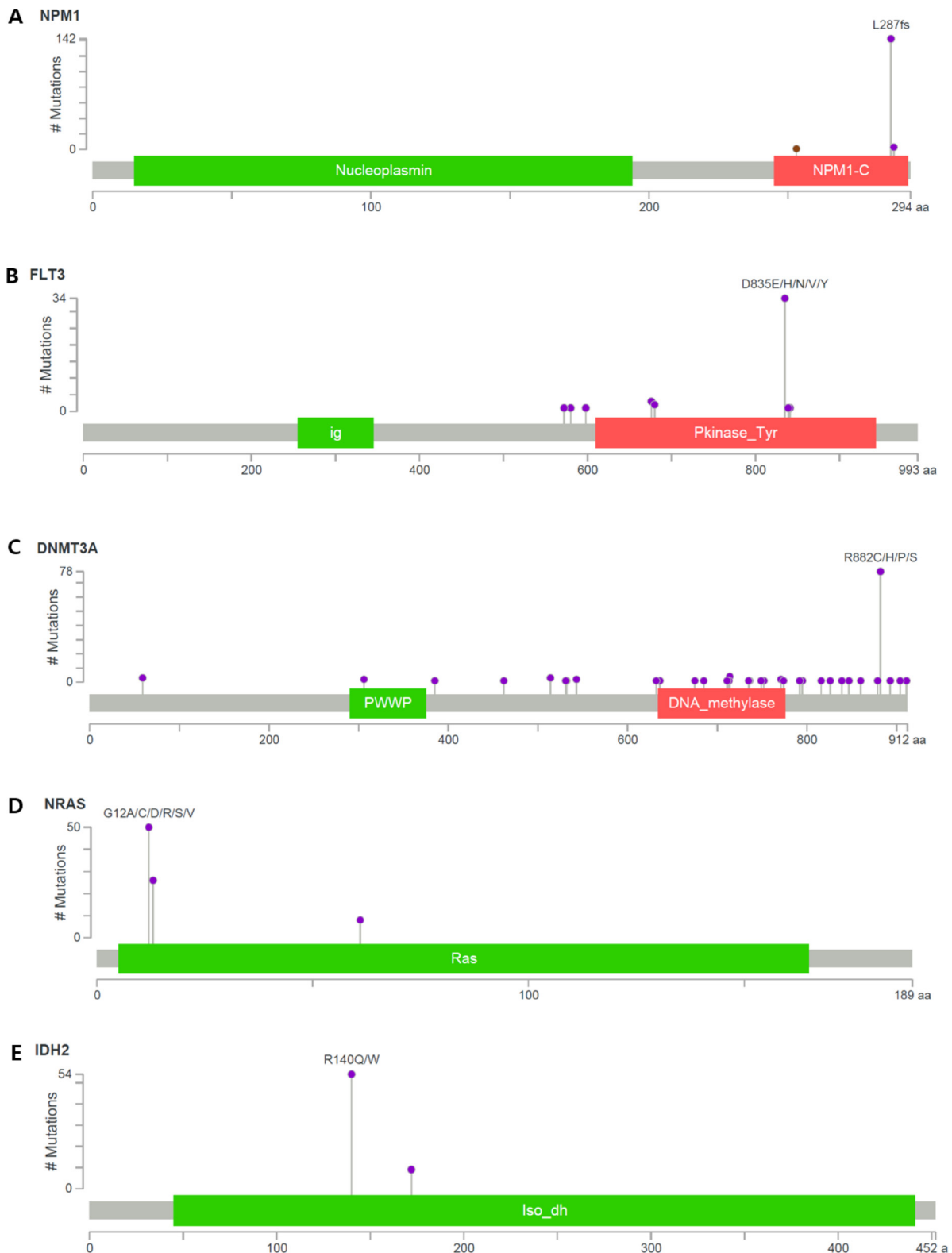


Assessment of a new genomic classification system in acute myeloid leukemia with a normal karyotype

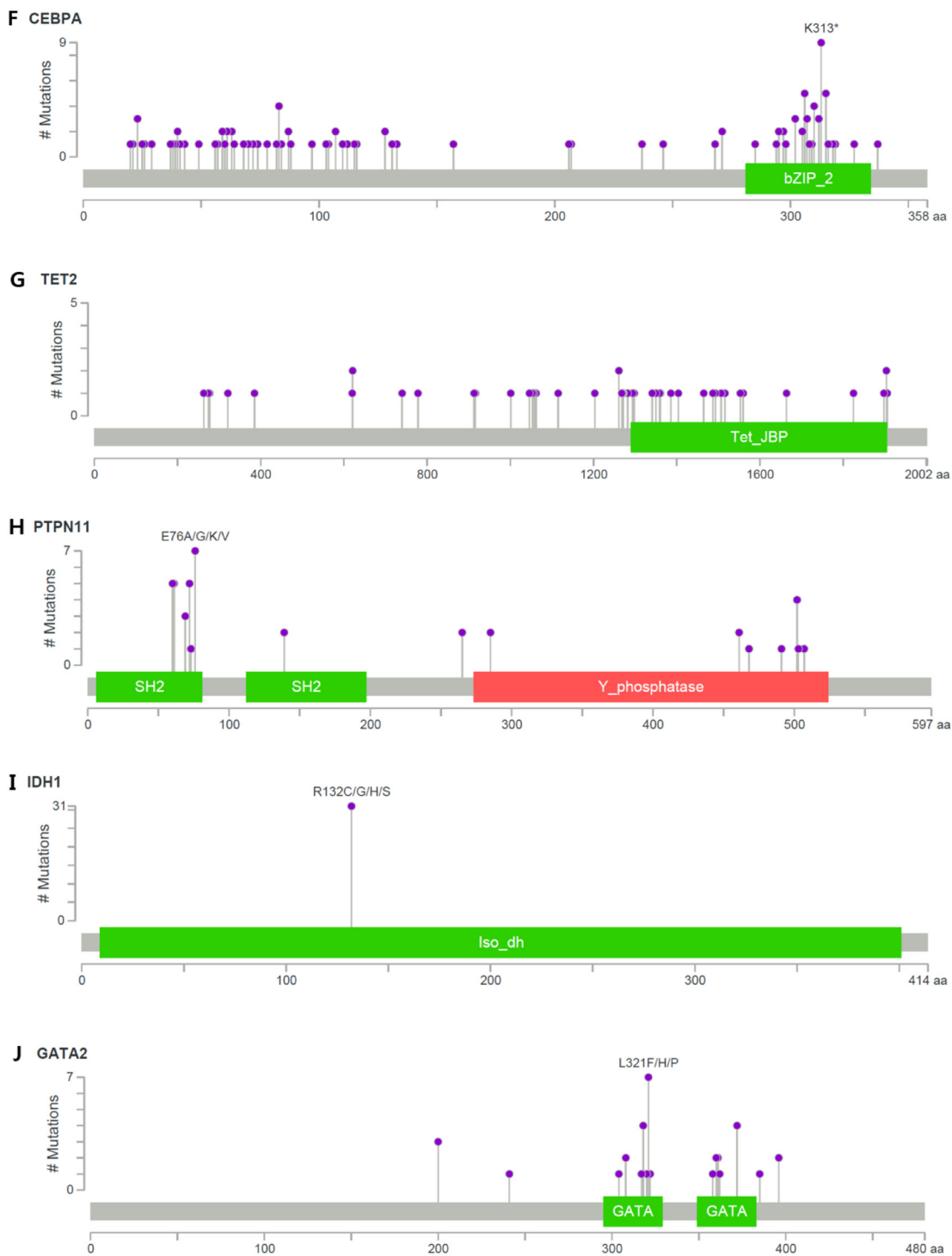
SUPPLEMENTARY MATERIALS



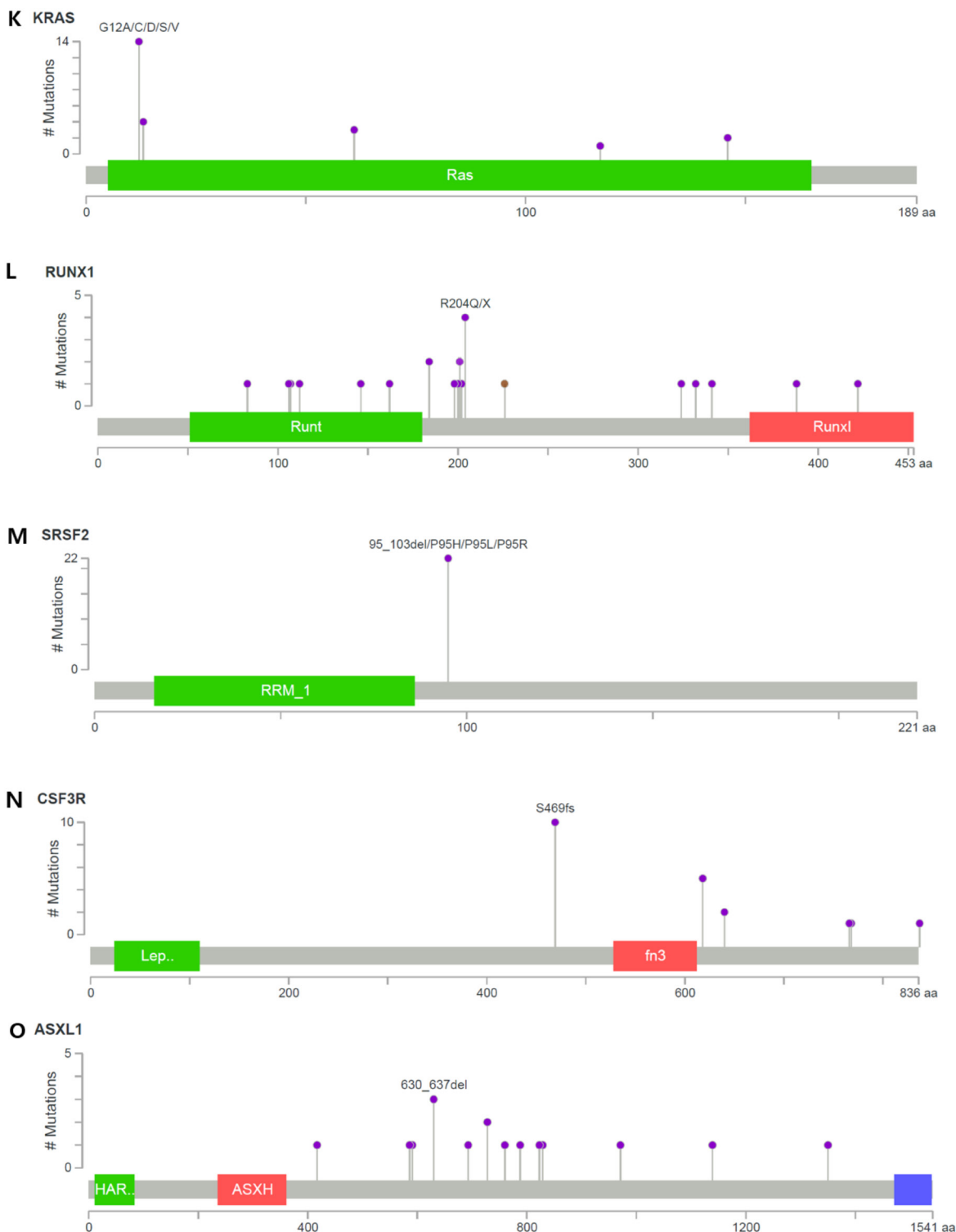
Supplementary Figure 1: Bar plot indicating number of driver events by patient for all patients.



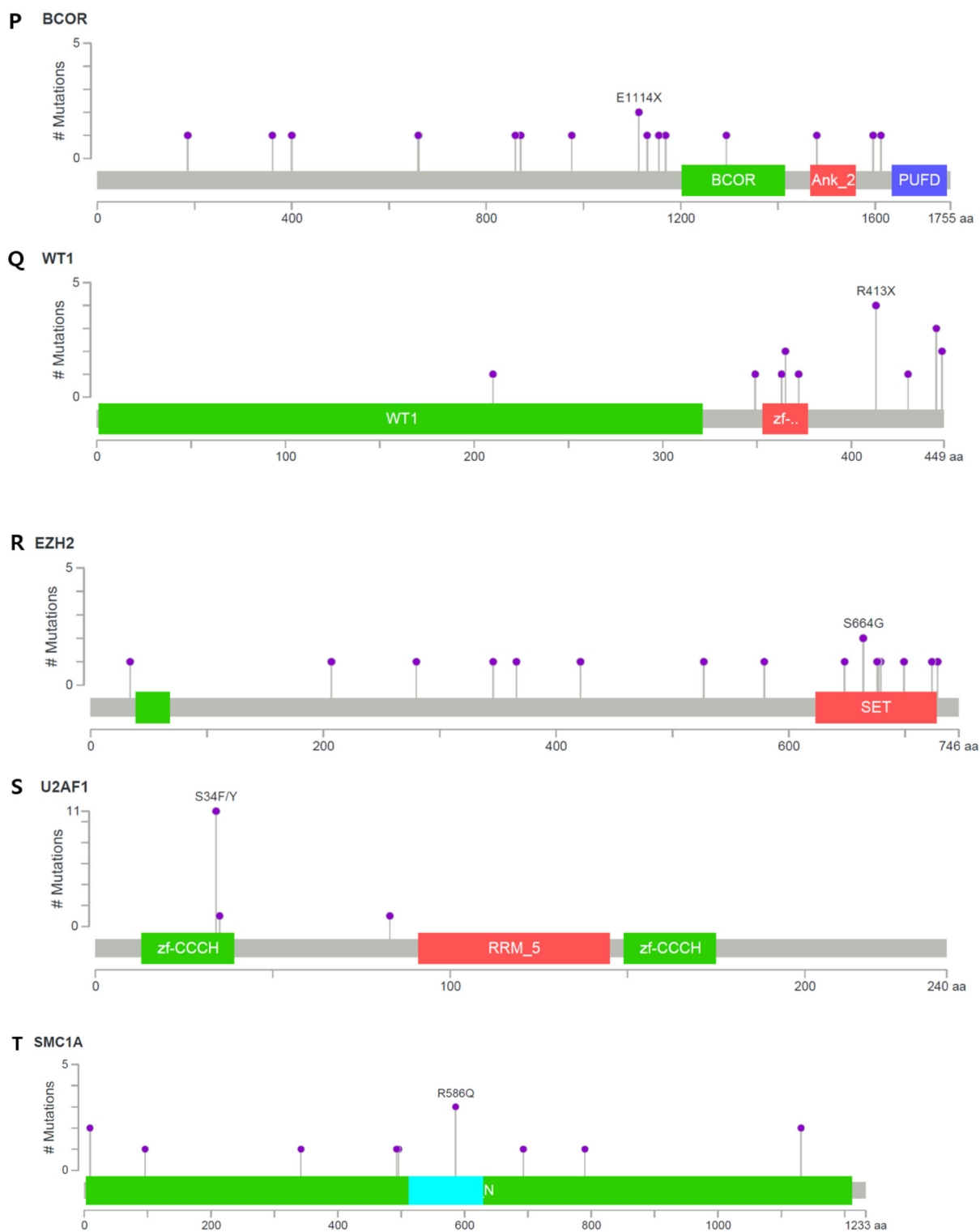
Supplementary Figure 2 (Continued): Lollipop plot of the most frequently detected mutations (A-V) including TP53 (W). We described the location of TP53 mutation in W(a); out cohort, W(b); Metzeler’s [Blood 2016] and, W(c); Papaemanuil’s data [NEJM 2016].



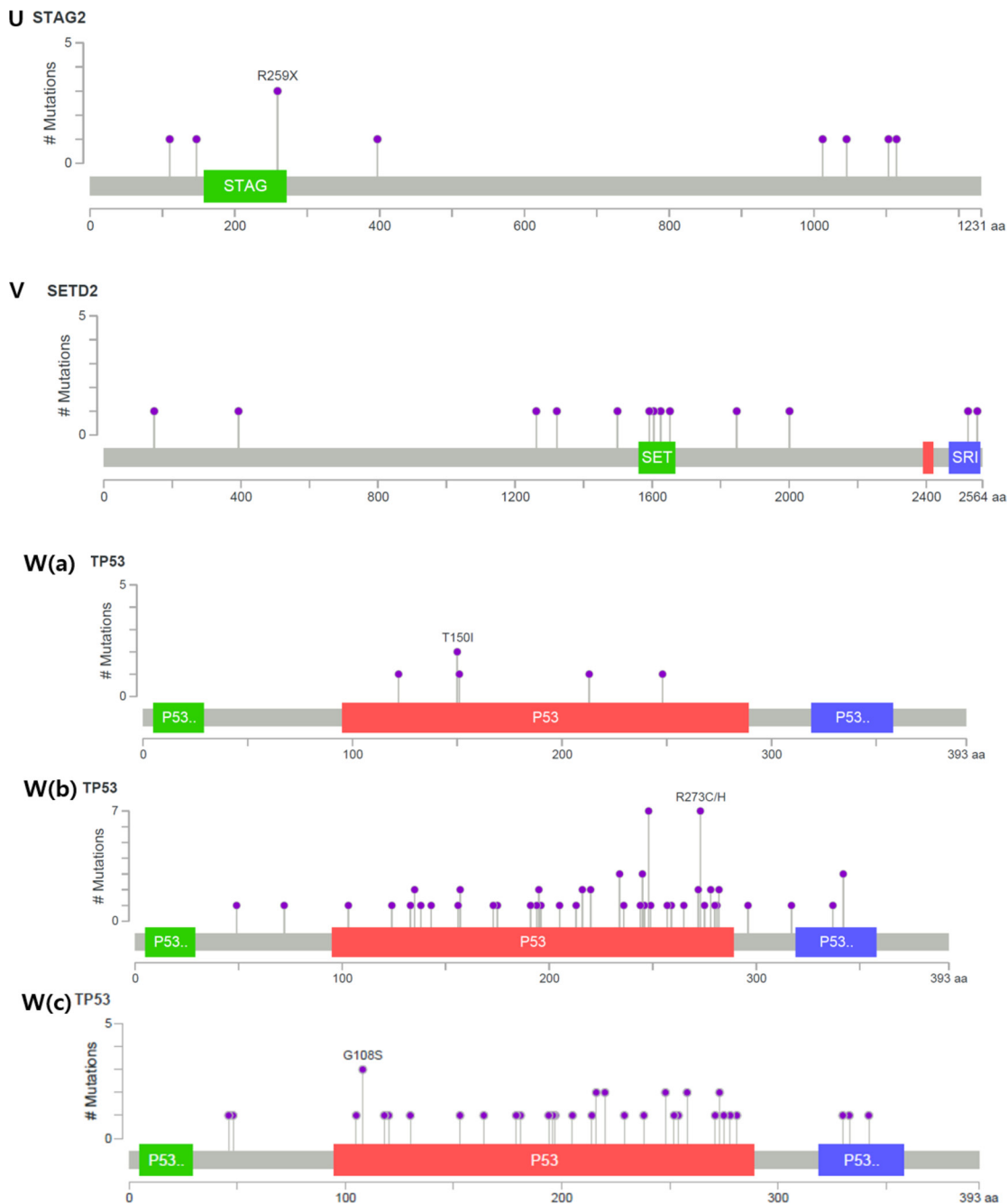
Supplementary Figure 2: Lollipop plot of the most frequently detected mutations (A-V) including TP53 (W). We described the location of TP53 mutation in W(a); out cohort, W(b); Metzeler’s [Blood 2016] and, W(c); Papaemanuil’s data [NEJM 2016]. (Continued)



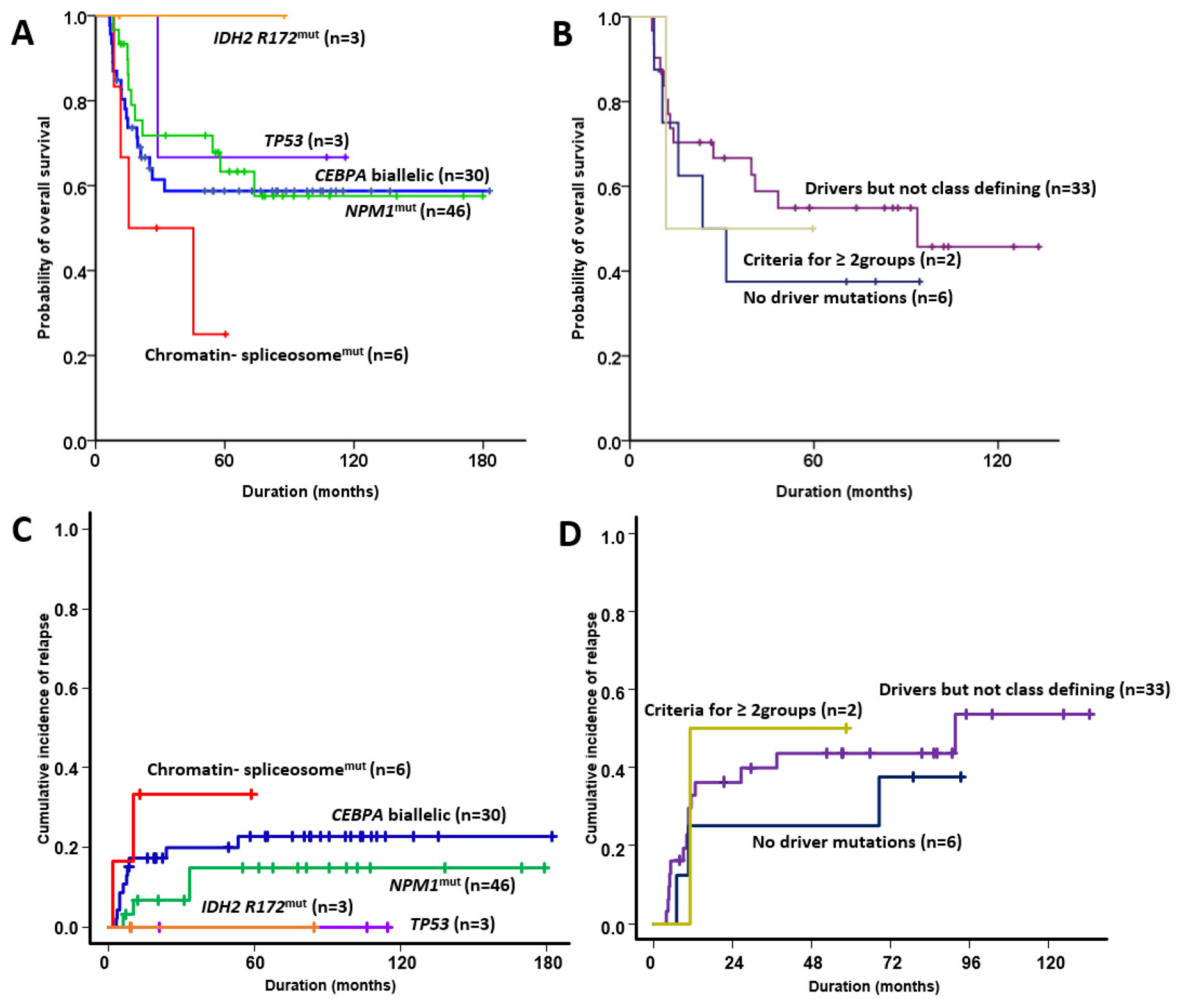
Supplementary Figure 2: Lollipop plot of the most frequently detected mutations (A-V) including TP53 (W). We described the location of TP53 mutation in W(a); out cohort, W(b); Metzeler’s [Blood 2016] and, W(c); Papaemanuil’s data [NEJM 2016]. (Continued)



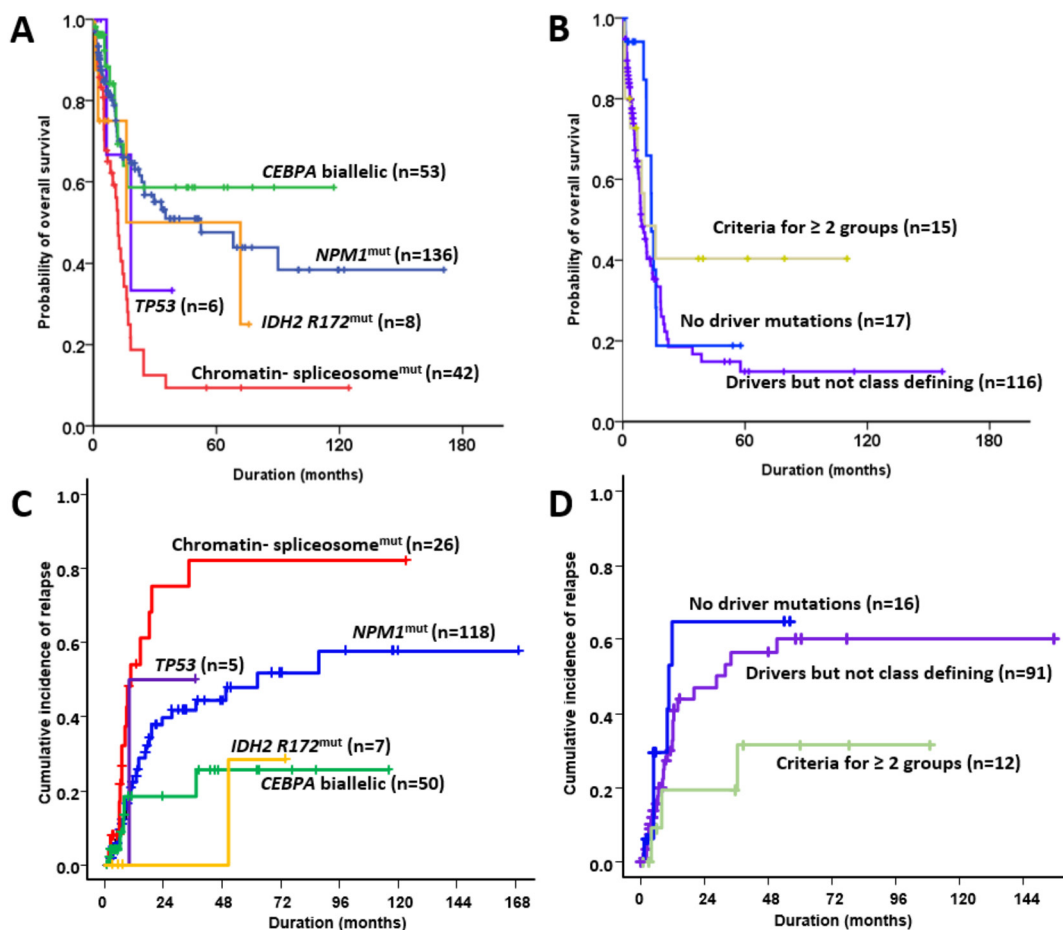
Supplementary Figure 2: Lollipop plot of the most frequently detected mutations (A-V) including TP53 (W). We described the location of TP53 mutation in W(a); out cohort, W(b); Metzeler’s [Blood 2016] and, W(c); Papaemanuil’s data [NEJM 2016]. (Continued)



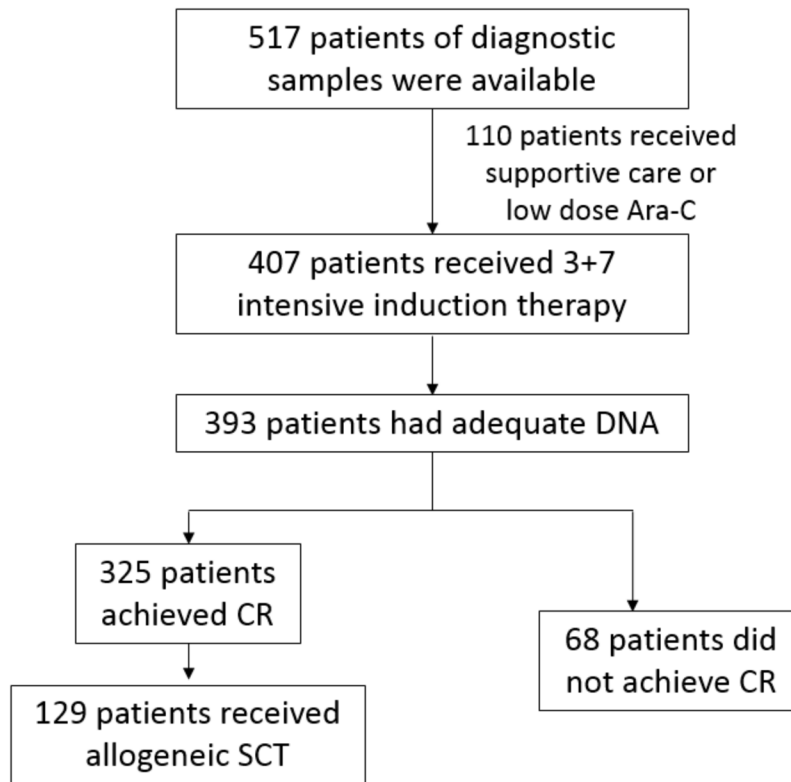
Supplementary Figure 2: Lollipop plot of the most frequently detected mutations (A-V) including *TP53* (W). We described the location of *TP53* mutation in W(a); out cohort, W(b); Metzeler’s [Blood 2016] and, W(c); Papaemanuil’s data [NEJM 2016].



Supplementary Figure 3: Prognostic impact according to genomic classification in patients with normal-karyotype acute myeloid leukemia who underwent allogeneic stem cell transplantation. (A, B) overall survival, and (C, D) relapse incidence.



Supplementary Figure 4: Prognostic impact according to genomic classification in patients with normal-karyotype acute myeloid leukemia (patients undergoing allogeneic SCT were censored at the time of transplantation). (A, B) overall survival, and (C, D) relapse incidence.



Supplementary Figure 5: Flowchart on patients' selection. Abbreviation: CR, complete remission; SCT, stem cell transplantation.

Supplementary Table 1: Gene panels of targeted deep sequencing and gene coverage.

See Supplementary File 1

Supplementary Table 2: Clinical characteristics of 129 patients with normal-karyotype acute myeloid leukaemia who received allogeneic stem cell transplantation

	No. of patients	%
Gender, male	64	49.6
Age, Median (range, years)	49 (15-64)	
WBC, Median value ($\times 10^9/L$), range	25.7 (0.9-397.2)	
< 30.0 $\times 10^9/L$	69	53.5
$\geq 30.0\times 10^9/L$	60	46.5
Donor type		
Matched related	78	60.5
Others	51	39.5
Source		
Bone marrow	26	20.2
PBSC	99	79.8
Conditioning		
Myeloablative	109	84.5
Reduced intensity	20	15.5
GVHD prophylaxis		
CsA \pm MTX	85	65.9
FK506 \pm MTX	44	34.1
Use of T cell depletion		
Yes	33 (23/10) [†]	25.6
No	96	74.4

[†] 23 patients received anti-thymocyte globulin and 10 patients received alemtuzumab for T cell depletion.

Abbreviations: WBC, white blood cells; PBSC, peripheral blood stem cell; GVHD, graft-versus-host disease; CsA, cyclosporine A; MTX, methotrexate.