

Concurrent *DDX41* and *TP53* Alterations in Myeloid Neoplasms: Single-Institution Real-World Clonal Dynamics and Outcomes

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INTRODUCTION

- Germline *DDX41* mutations define a distinct clinicogenomic subtype of MDS/AML — older age, male predominance, normal karyotype and generally favorable outcomes¹.
- DDX41*-mutated disease has been reported to attenuate the adverse prognostic impact of *TP53* alterations².
- Whether that holds in real-world patients with concurrent *DDX41* and *TP53* alterations — and how the two clones behave over time — remains unknown.

AIM

- To characterize baseline features, clonal dynamics, AML transformation and survival in patients with concurrent *DDX41* and *TP53* alterations.
- Specifically: (1) *TP53* and *DDX41* VAF trajectories from diagnosis to progression/transformation; (2) emergence of multi-hit *TP53*, del(17p) and complex karyotype; (3) overall survival from initial diagnosis and from AML transformation.

METHODS

- Single-center retrospective review of 13 patients with concurrent *DDX41* and *TP53* alterations; diagnoses assigned by WHO 2022 classification³.
- NGS and cytogenetics/FISH reviewed at initial diagnosis and at progression or AML transformation.
- Multi-hit *TP53* defined as ≥2 *TP53* mutations, a *TP53* mutation with del(17p)/17p loss, or *TP53* VAF >50%. Complex karyotype defined as ≥3 abnormalities⁴.
- Overall survival estimated by Kaplan–Meier from initial diagnosis and from AML transformation; remaining endpoints summarized descriptively.

CONCLUSIONS

- AML transformation was frequent (8/10, 80%) and outcome after transformation was dismal: median OS 5.1 months from AML transformation.
- TP53* detectable at MDS diagnosis marked aggressive disease: median time to AML 9.4 vs 45.2 months when *TP53* was undetectable at baseline.
- The germline-range *DDX41* VAF stayed fixed near 50% while *TP53* clones expanded or newly emerged, with accrual of multi-hit *TP53*, complex karyotype and del(17p); a second *DDX41* variant was documented in 5/8 at transformation, newly in 3/8.
- These real-world data do not support near-complete mitigation of *TP53*-associated risk by *DDX41* mutation — *TP53* clonal evolution remains clinically relevant and supports serial molecular monitoring.

RESULTS

80%

MDS → AML transformation (8/10)

62.5%

multi-hit *TP53* at transformation (5/8)

9.4 vs 45.2 mo

months to AML by baseline *TP53* status

5.1 mo

median OS from AML transformation

Table 1. Cohort characteristics

Characteristic	n = 13
Age at diagnosis, median (range), y	68.5 (55.9–85.8)
Male	11 (84.6%)
Initial diagnosis: MDS	10 (76.9%)
Initial diagnosis: de novo AML	3 (23.1%)
<i>DDX41</i> variant 1 VAF, median (range)	49.0% (21.0–51.8)
Second <i>DDX41</i> variant at baseline	4 (30.8%)
<i>TP53</i> mutation at baseline	8 (61.5%)
<i>TP53</i> VAF at baseline, range	2.0–57.4%
Multi-hit <i>TP53</i> at baseline	3 (23.1%)
del(17p) at baseline	1 (7.7%)
Complex karyotype at baseline	6 (46.2%)
MDS → AML transformation	8/10 (80.0%)
Time to AML, median (range), mo	17.7 (1.6–92.2)
Allogeneic HCT	6 (46.2%)
CR/CRi to AML-directed therapy	4/9 (44.4%)
Alive at last follow-up	3 (23.1%)
Alive: allo-HCT vs no allo-HCT	3/6 vs 0/7

Figure 1. Overall survival (Kaplan–Meier)

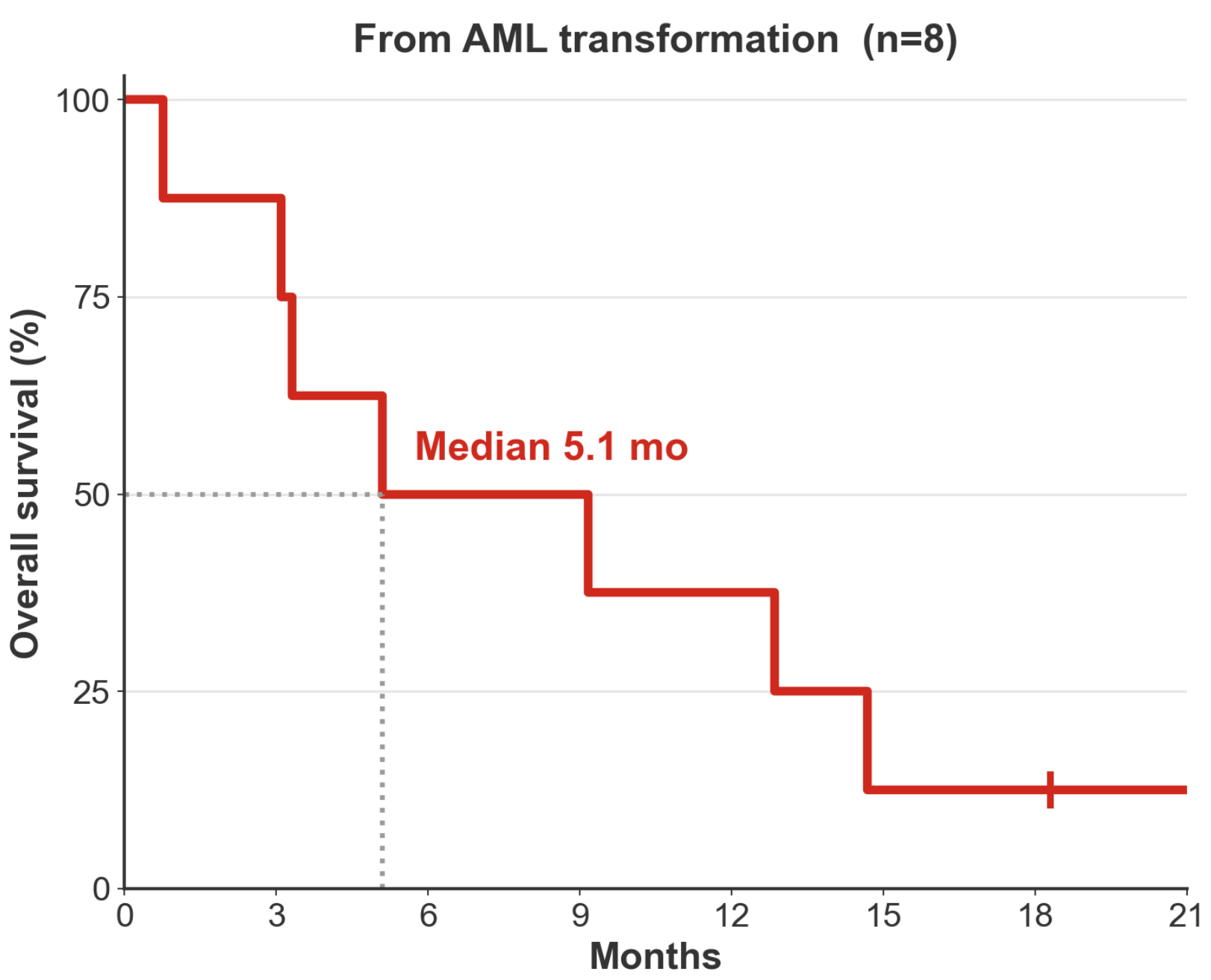
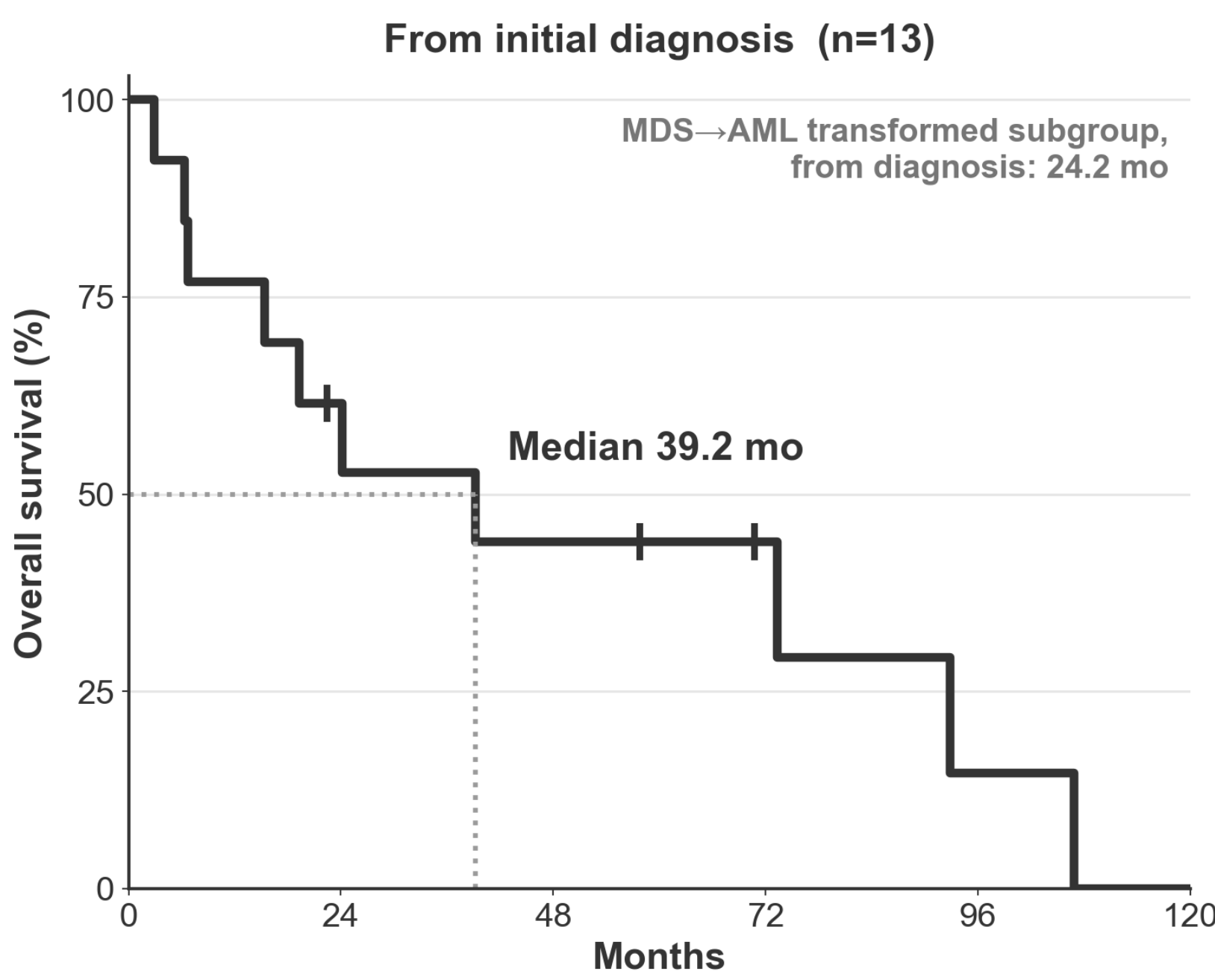
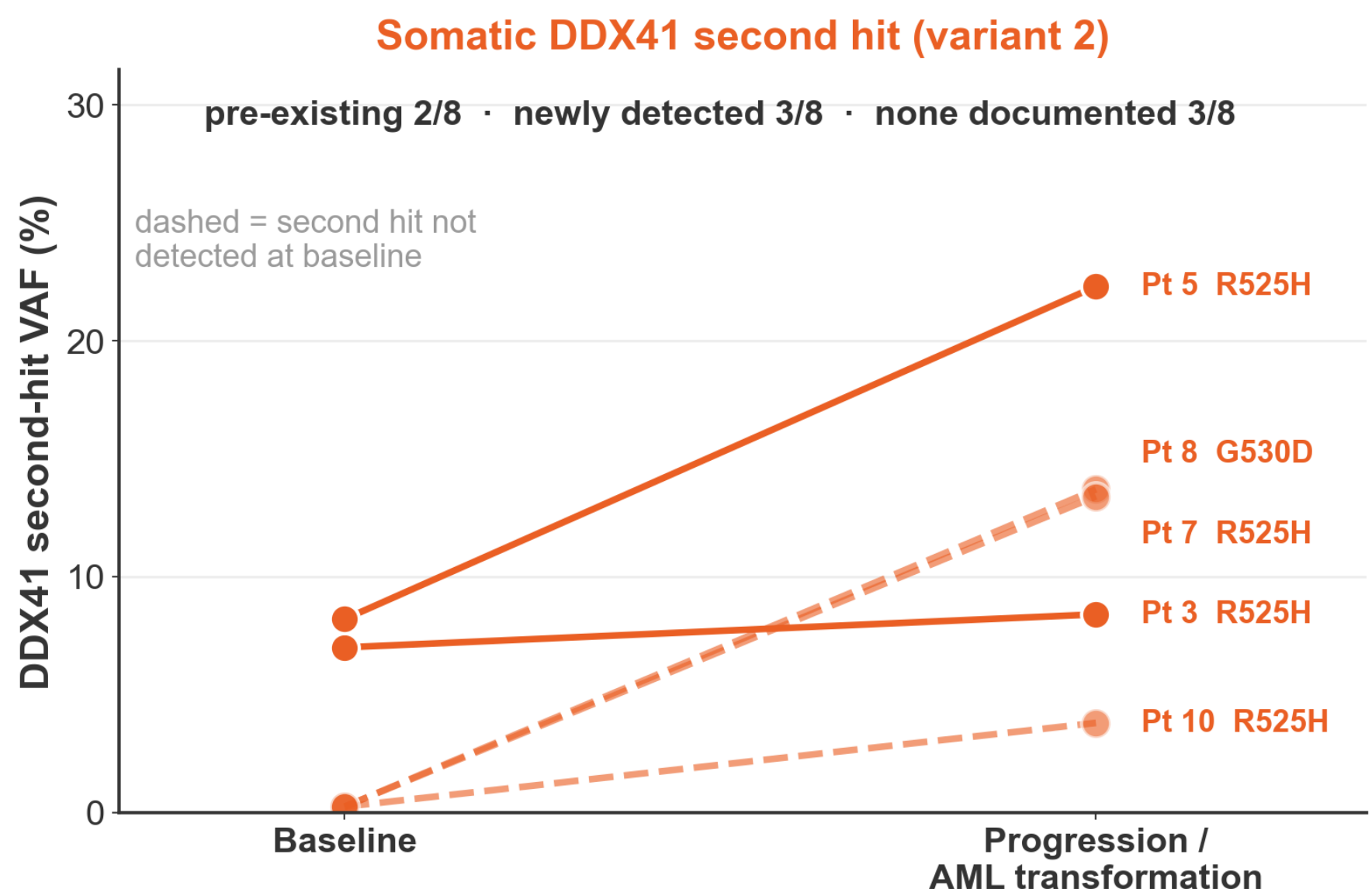


Figure 2. *DDX41* second-hit and *TP53* clonal dynamics



Both panels show the 8 patients who transformed from MDS to AML. R525H — the canonical *DDX41* somatic second hit — accounted for 4 of the 5 second-hit variants. All second hits remained subclonal (3.8–22.3%), whereas the germline-range *DDX41* variant 1 stayed near 50% throughout (median |Δ| 0.9 percentage points).

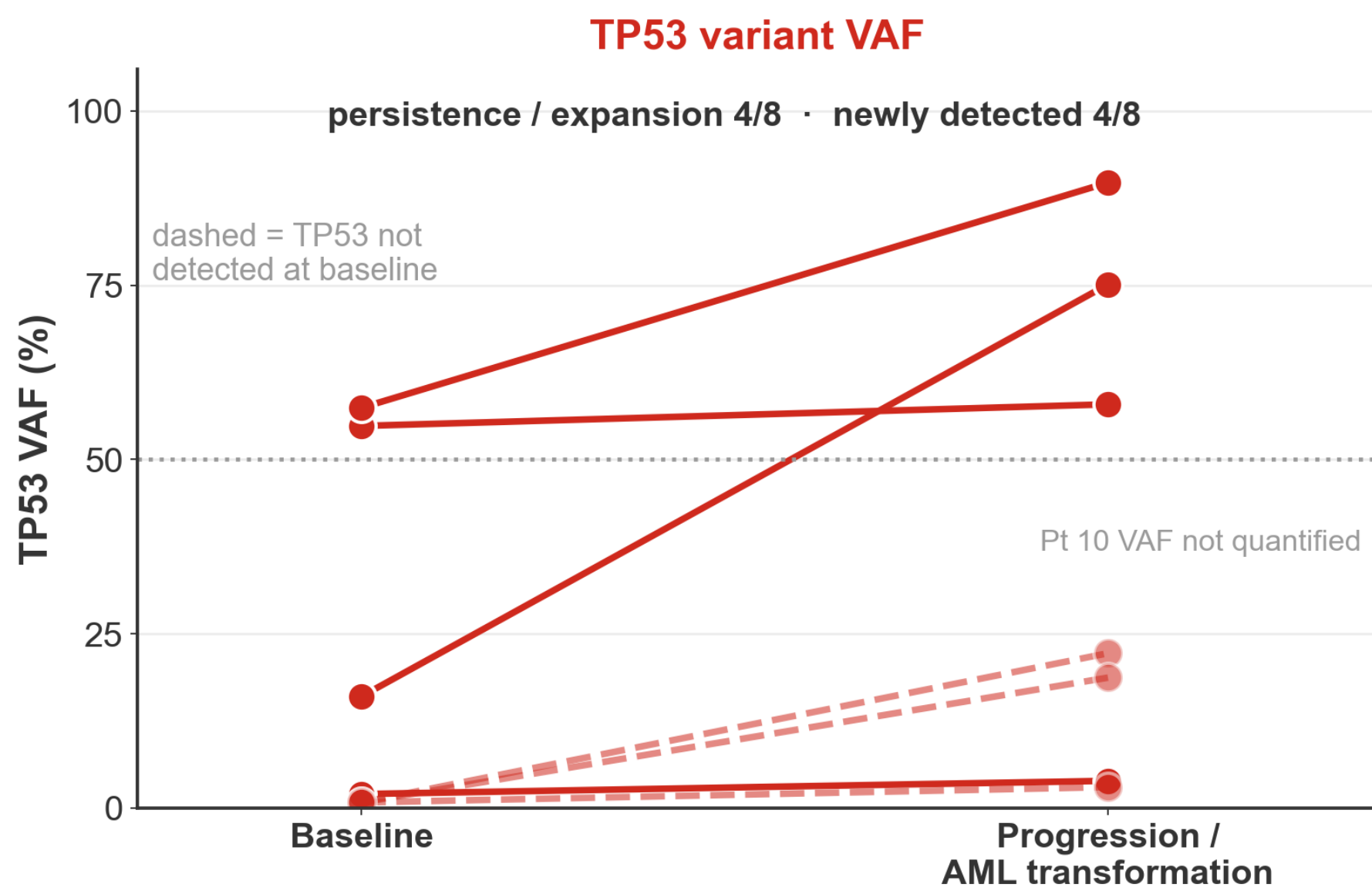
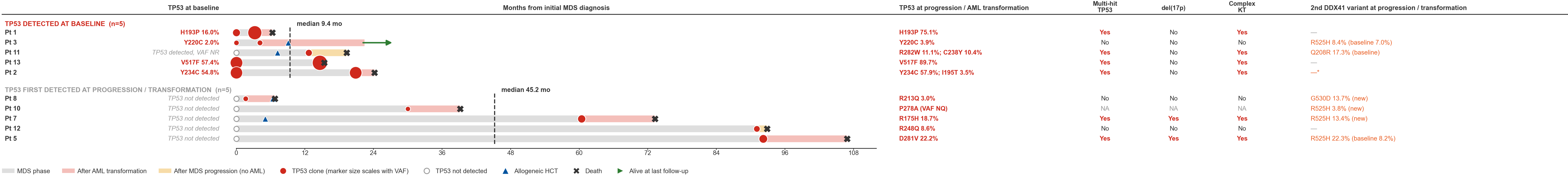


Figure 3. Clonal evolution, disease course and high-risk *TP53* features in the 10 patients with an initial MDS diagnosis



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