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Lower residual mutation load following treatment with pevonedistat + azacitidine versus azacitidine alone: Comparative analysis of study arms in P-2001, a randomized phase 2 trial

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Novel targets in MDS

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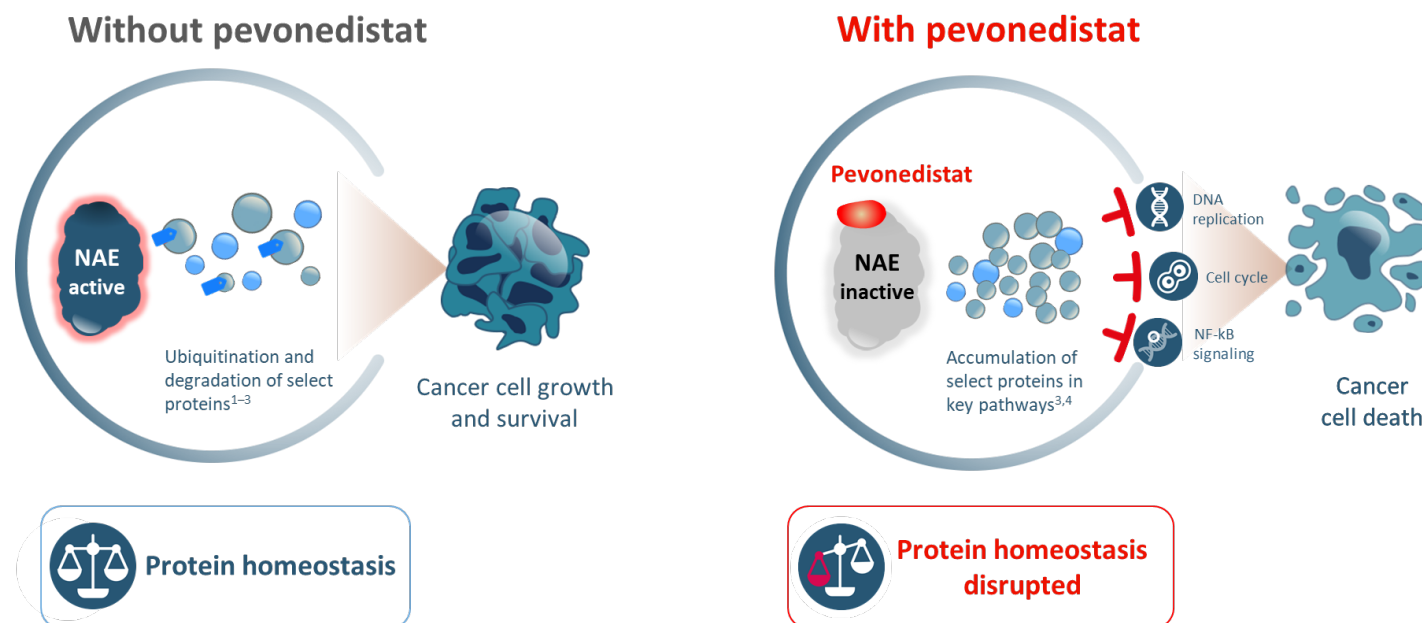
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Introduction

- MDS and AML share foundational biology, molecular mutations that drive disease, and clinical features^{1–4}
- Lower intensity therapy for MDS and AML with 20–30% blasts includes a backbone of HMAs⁵
- Novel, effective therapies that do not worsen myelosuppression are needed

Pevonedistat is a selective NEDD8-activating enzyme (NAE) inhibitor that leads to cancer cell death by disrupting protein homeostasis^{6–9}

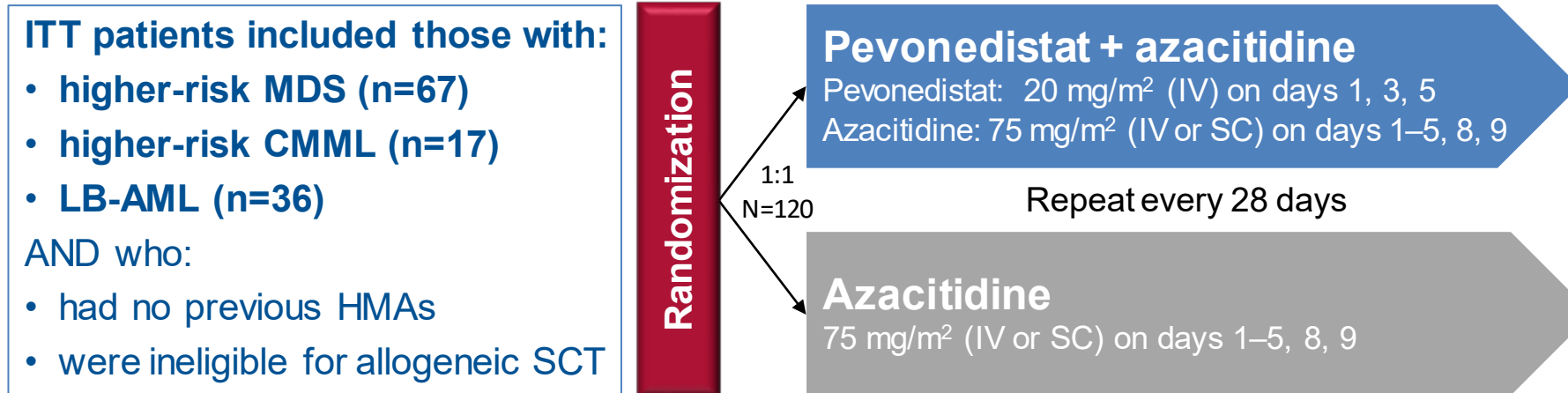


AML, acute myeloid leukemia; CMML, chronic myelomonocytic leukemia; HMA, hypomethylating agent; MDS, myelodysplastic syndromes; NF-κB, nuclear factor kappa-light-chain-enhancer of activated B cells; NEDD8, neural-precursor-cell-expressed developmentally down-regulated protein 8.

1. DiNardo CD, et al. *Am J Hematol* 2016;91:227–32; 2. Solary E. *Blood* 2017;130:126–36; 3. Catenacci DV, Schiller GJ. *Blood Rev* 2005;19:301–19; 4. Cheson BD. *Oncologist* 1997;2:28–39; 5. Bewersdorf JP, et al. *Ther Adv Hematol* 2020;11:1–228; 6. Soucy TA, et al. *Genes Cancer* 2010;1:708–16; 7. Soucy TA, et al. *Nature* 2009;458:732–6; 8. Brownell JE, et al. *Mol Cell* 2010;37:102–111; 9. Swords RT, et al. *Blood* 2010;115:3796–800;

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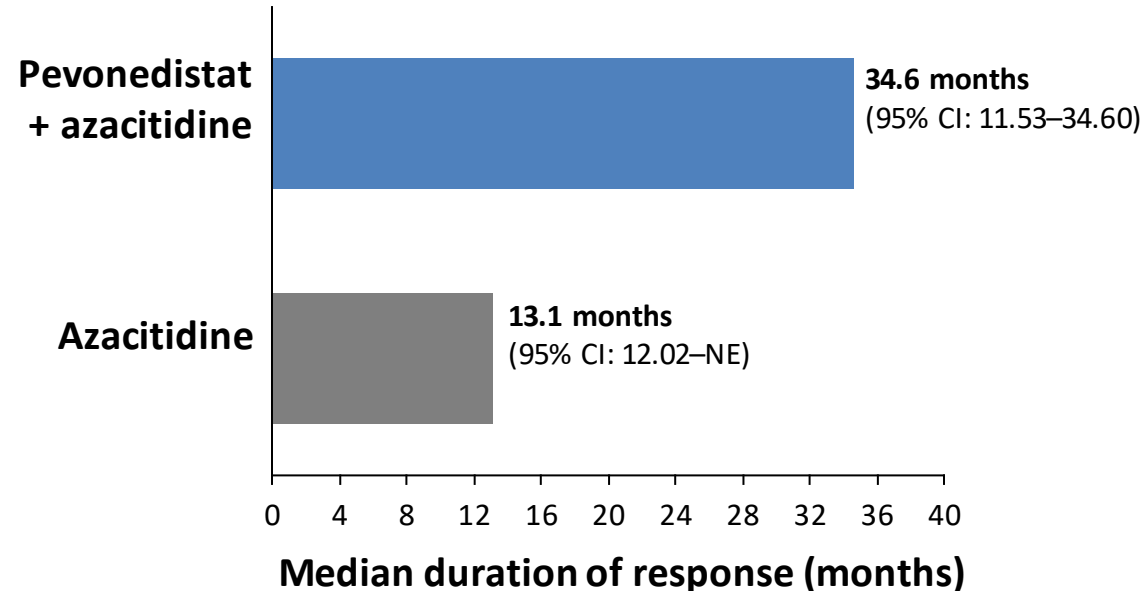
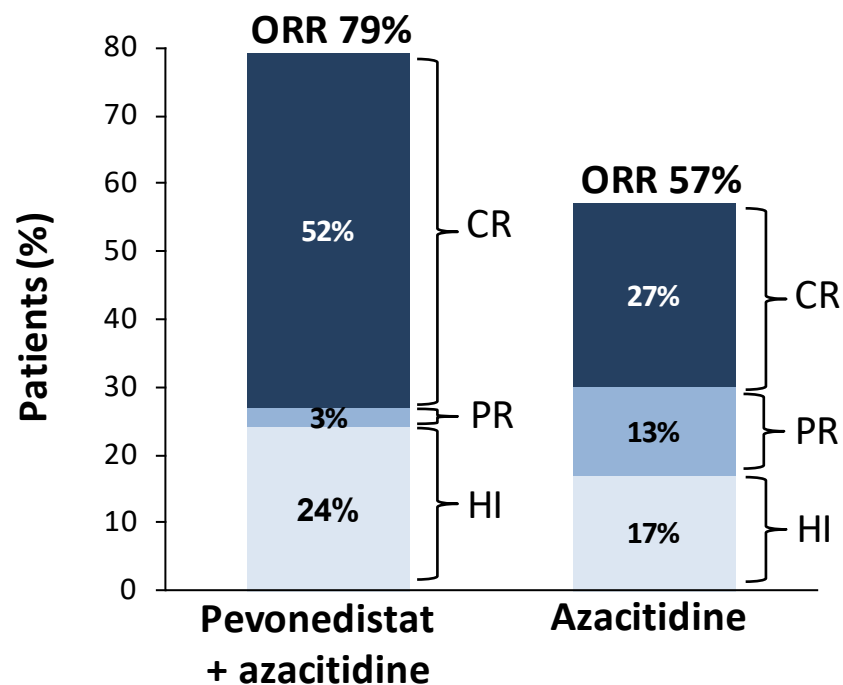
Study P-2001 (NCT02610777): Phase 2, randomized, open-label, global, multicenter study¹



- **Endpoints:**
 - OS
 - EFS (defined as time to death or transformation to AML)

Encouraging clinical efficacy with pevonedistat + azacitidine in patients with higher-risk MDS: Results from study P-2001

Response-evaluable patients with higher-risk MDS (n=59)^{1,2}



Treatment with pevonedistat + azacitidine was associated with nearly triple the median DOR and nearly double the CR in patients with higher-risk MDS (n=67)

CI, confidence interval; CR, complete response; DOR, duration of response; HI, hematological improvement; NE, not evaluable; ORR, overall response rate; PR, partial response.
1. Sekeres MA, *et al. Leukemia* 2021; doi: 10.1038/s41375-021-01125-4; 2. Sekeres MA, *et al.* Presented at the 62nd Annual Meeting and Exposition of the American Society of Hematology, Dec 5–8, 2020 [abstract 653]

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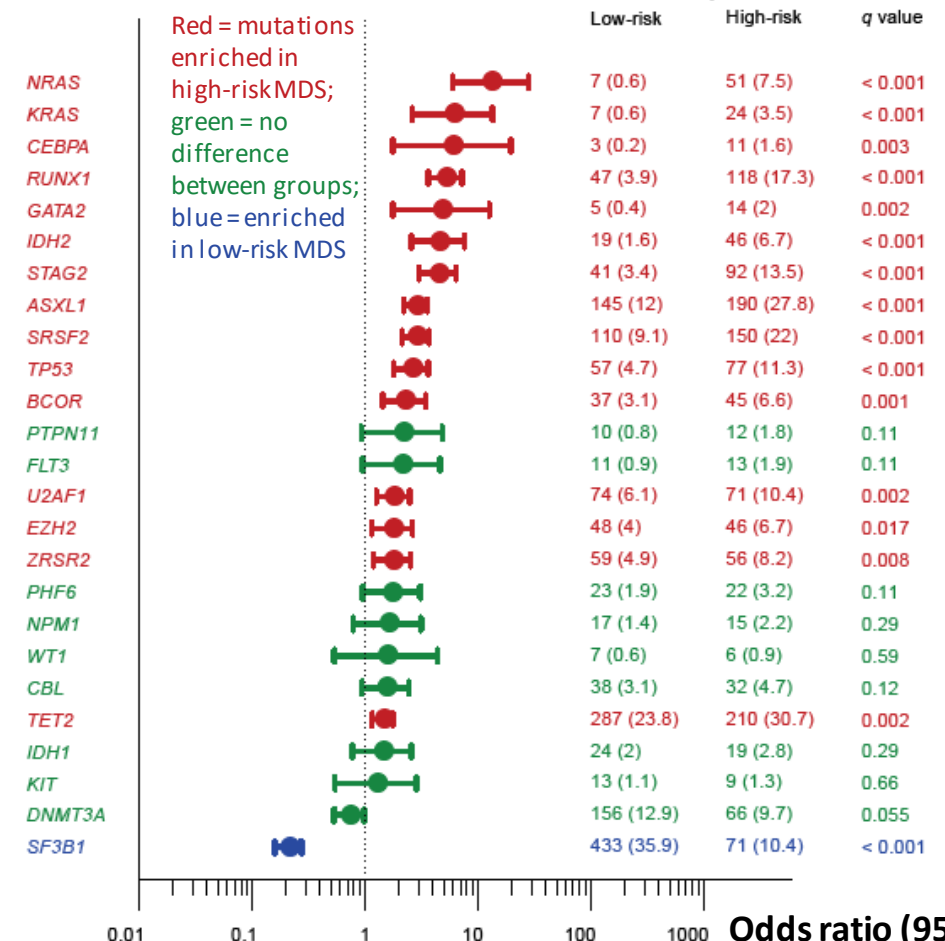


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Mutations associated with leukemic transformation and disease progression are enriched in high-risk vs low-risk MDS

- MDS and secondary AML involve cells that harbor mutations in many of the same genes and functional categories; hence, they are perceived to be a disease continuum¹⁻³
 - Mutations in MAP kinase signaling and myeloid transcription factor genes are associated with disease progression and leukemic transformation⁴
- Based on the clinical findings in P-2001, we hypothesized that treatment with pevonedistat + azacitidine would induce a deeper and more persistent molecular response than azacitidine alone; having an impact on mutation profiles

Univariate analysis of frequency of mutations (odds ratio) between low- vs high-risk MDS⁵

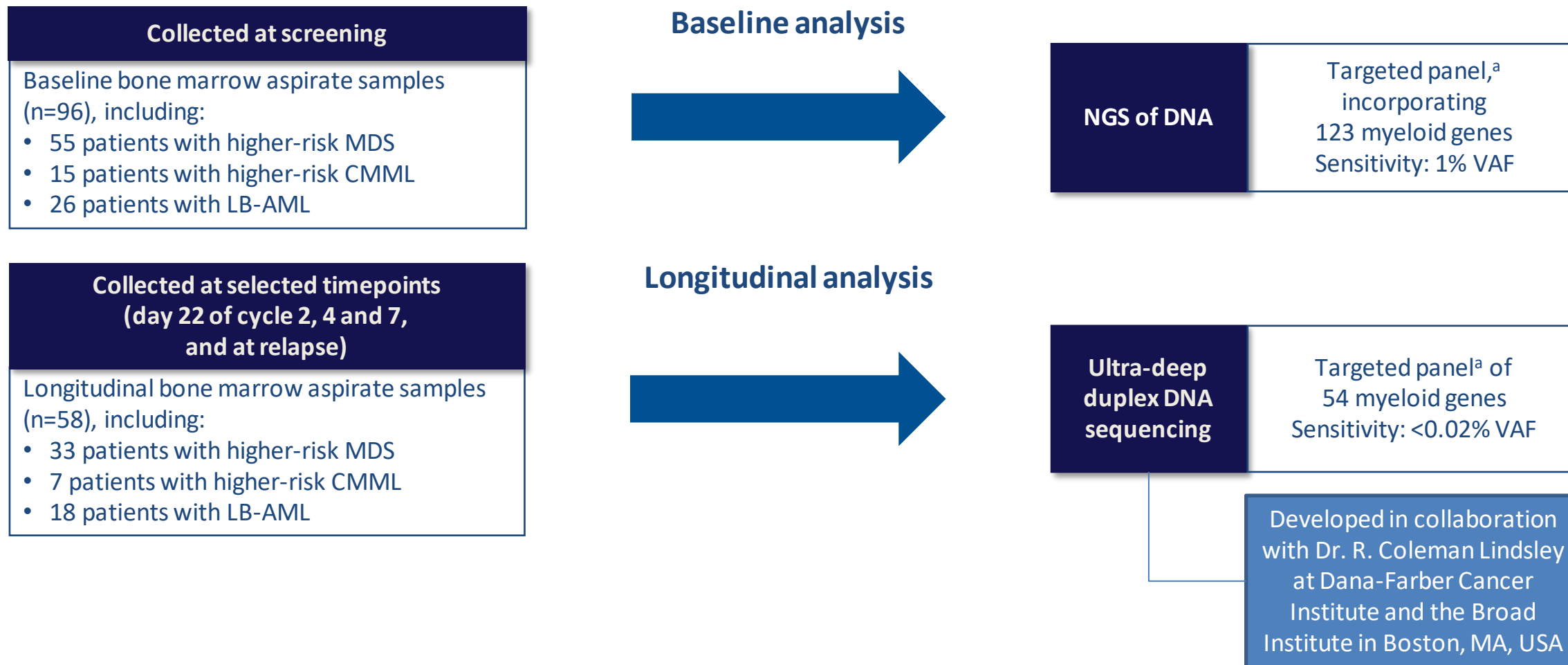


MAP, mitogen-activated protein.

1. DiNardo CD, et al. *Hematology Am Soc Hematol Educ Program* 2016;1:348–55; 2. Murati A, et al. *BMC Cancer* 2012;12:304; 3. Caponetti GC, et al. *Int J Lab Hematol* 2020;42:671–84; 4. Higgins A, et al. *Genes* 2020;11:749; 5. Makishima H, et al. *Nat Genet* 2017;49:204–12. Figure reproduced with permission from the author.

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Residual mutation load: Prespecified comparative analysis of study arms in P-2001



^aSamples were sequenced with a mean target coverage of 9500x using a TruSeq Hybrid Capture Panel incorporating 123 myeloid genes. Single-nucleotide variants and insertions and deletions (indels) were identified with MuTect.

NGS, next-generation sequencing; VAF, variant allele frequency.

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The duplex sequencing cohort was representative of the general study population

Treatment arm	DUPLEX SEQUENCING COHORT (n=45)		STUDY POPULATION (n=120)	
	Pevonedistat + azacitidine (n=22)	Azacitidine (n=23)	Pevonedistat + azacitidine (n=58)	Azacitidine (n=62)
Higher-risk MDS, n (%)	11 (50)	16 (70)	32 (55)	35 (56)
CMML, n (%)	4 (18)	3 (13)	9 (16)	8 (13)
LB-AML, n (%)	7 (32)	4 (17)	17 (29)	19 (31)
Male/female, n (%)	34 (76)/11 (24)		83 (69)/37 (31)	
Age, years, median (range)	73 (44–91)		72 (34–91)	
IPSS-R risk score for patients with MDS+CMML, n (%)	Intermediate: 20 (59) High: 6 (18) Very high: 8 (23)		Intermediate: 29 (35) High: 27 (32) Very high: 28 (33)	
ELN category for patients with AML, n (%)	Adverse: 7 (64) Intermediate: 1 (9) Indeterminate: 3 (27)		Adverse: 15 (62) Intermediate: 3 (13) Indeterminate: 6 (25)	

Results in the ITT population¹

Pevonedistat + azacitidine versus azacitidine

- **Median EFS:** 21.0 versus 16.6 months
(HR: 0.67; 95% CI: 0.42–1.05; P=0.076)

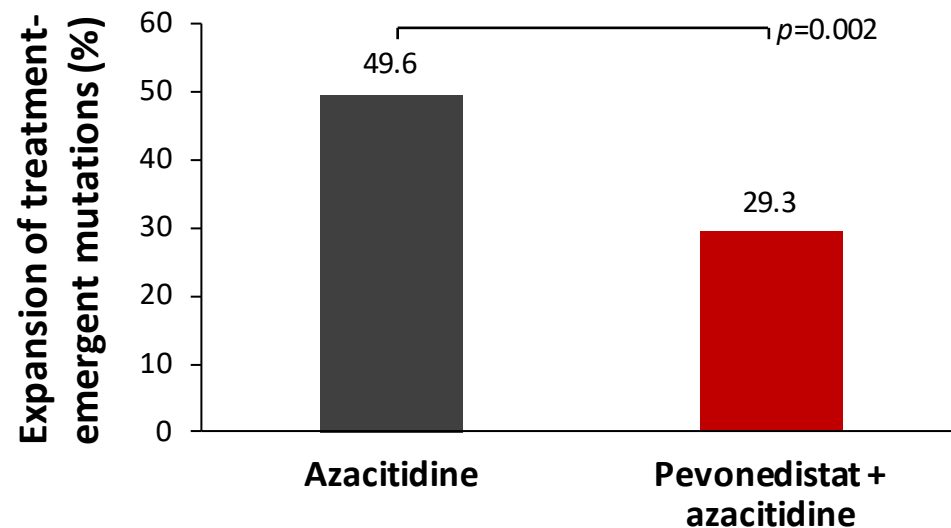
Results in duplex sequencing population

Pevonedistat + azacitidine versus azacitidine

- **Median EFS:** 20.3 versus 16.9 months
(HR: 0.12; 95% CI: 0.024–0.6; P=0.01)

Addition of pevonedistat to azacitidine improved control of clonal expansion, even in patients who did not achieve CR

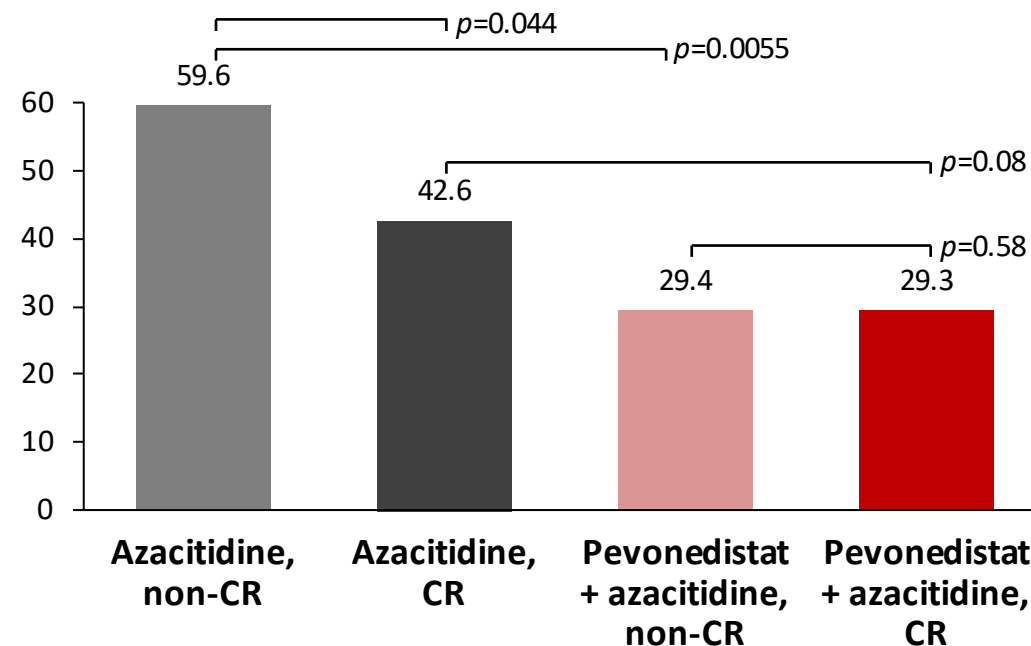
Pevonedistat + azacitidine was associated with significantly less expansion of treatment-emergent mutations than azacitidine alone^a



	Azacitidine	Pevonedistat + azacitidine
Expanding, n	63	27
Non-expanding, n (data not shown)	64	65
P=0.002	0.496	0.293

Pevonedistat controlled clonal expansion in patients who did and did not achieve CR, mCR or CRi

Expansion of treatment-emergent mutations by arm in patients who did and did not achieve CR (%)



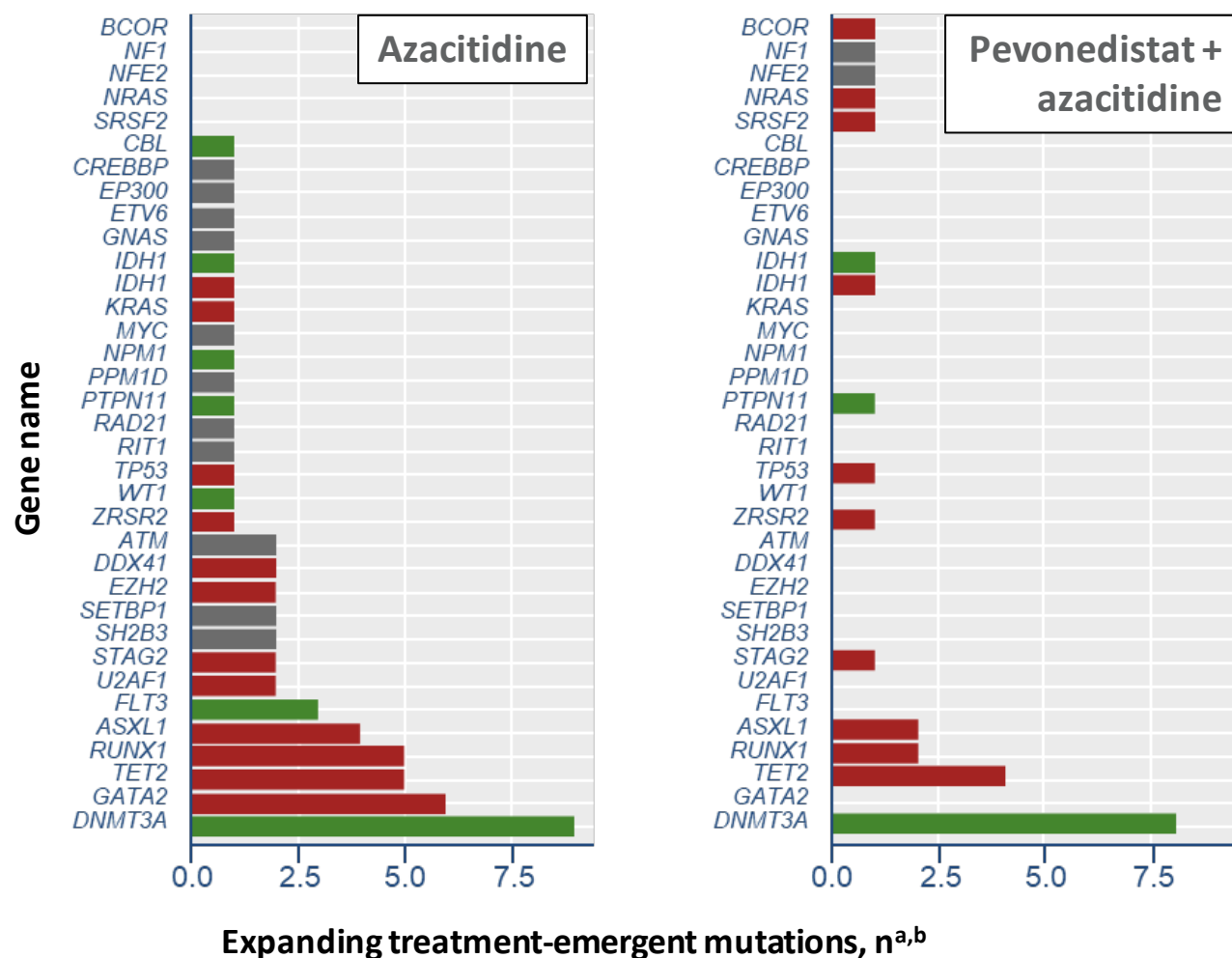
Trend p -value=0.0008

^aExpansion of treatment-emergent mutations was defined as either newly detected or numerically increased VAF after treatment.

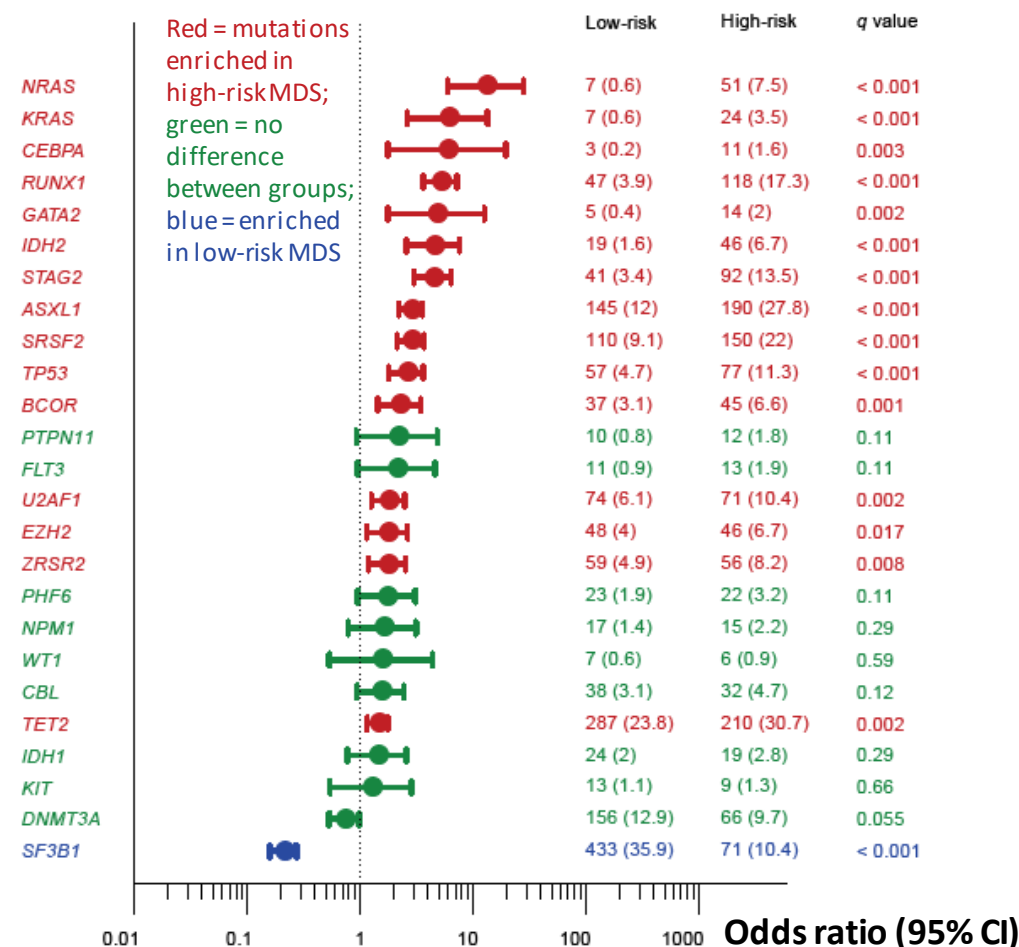
CRi, CR with incomplete blood-count recovery; mCR, marrow CR.

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Treatment effect was seen across genes associated with both lower- and higher-risk MDS



Univariate analysis of frequency of mutations (odds ratio) between low- vs high-risk MDS¹



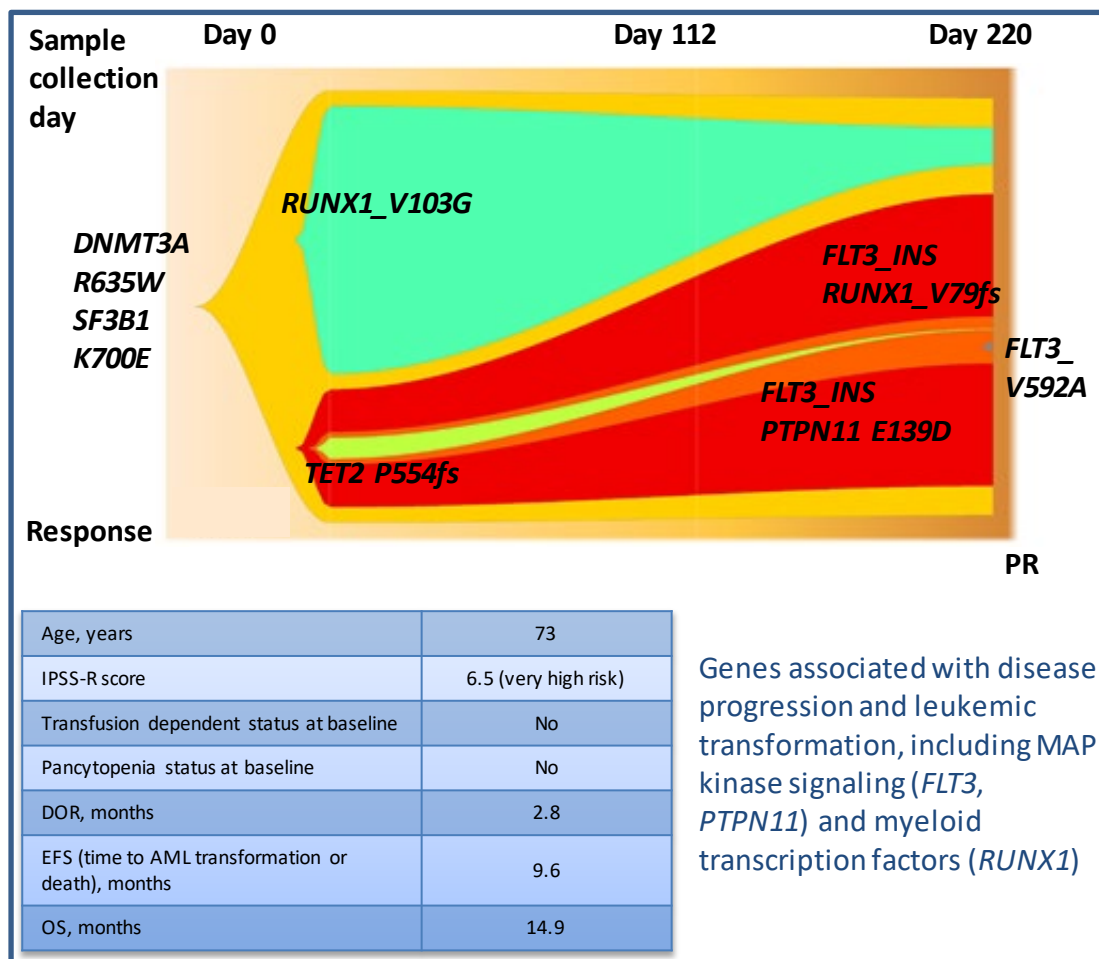
^aExpansion of treatment-emergent mutations was defined as either newly detected or increasing VAF after treatment. ^bNon-expanding data not shown.

1. Makishima H, et al. *Nat Genet* 2017;49:204–12. Figure reproduced with permission from the author.

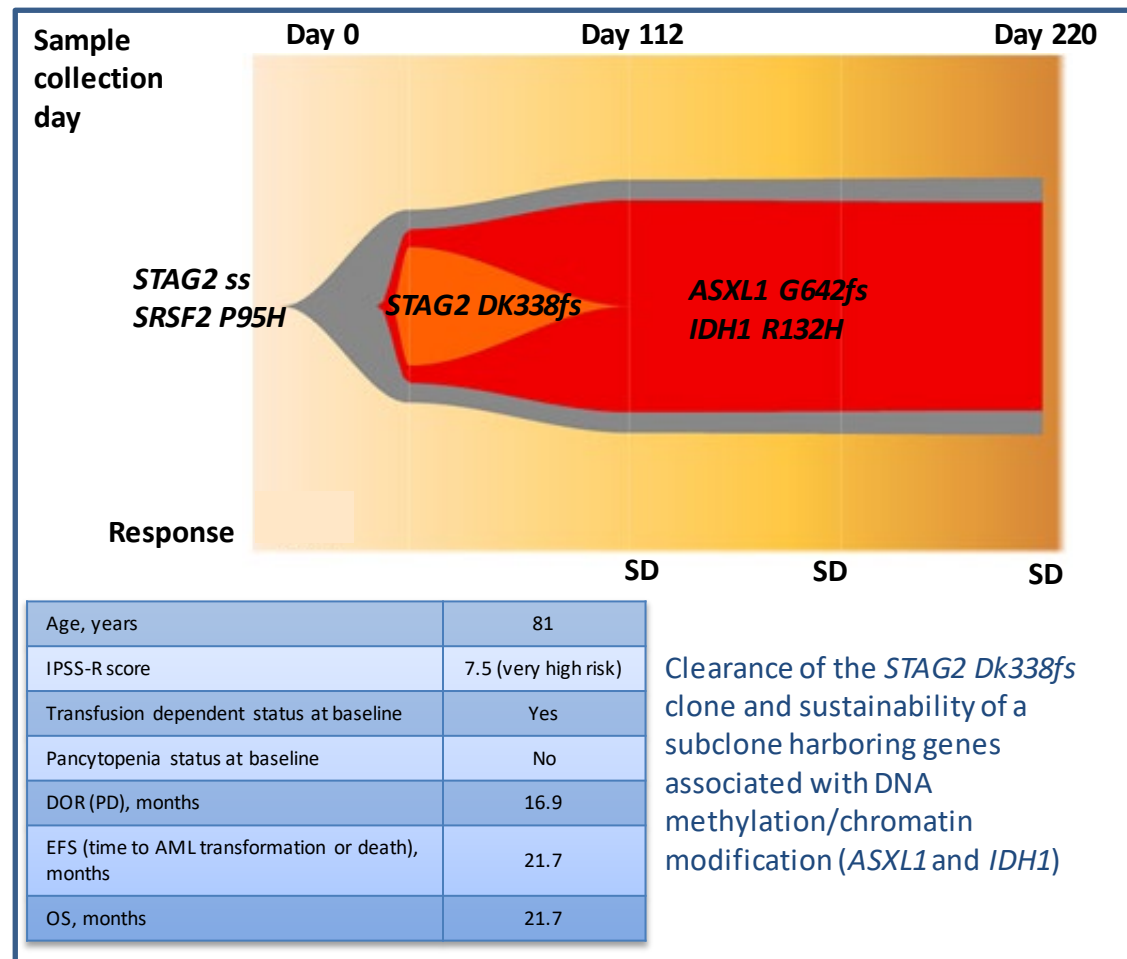
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Higher-risk MDS: Expansion of genes associated with disease progression and leukemic transformation in the azacitidine arm

Patient with higher-risk MDS treated with azacitidine



Patient with higher-risk MDS treated with pevonedistat + azacitidine



Conclusions

- Consistent with clinical findings in P-2001, these data suggest that pevonedistat + azacitidine reduces mutation burden compared with azacitidine alone, with the following potential clinical benefits
 - Lesser likelihood of treatment-emergent resistance
 - Controlled expansion of mutations associated with higher-risk MDS and AML transformation
 - Increased durability of treatment response
- These findings will be further assessed in the following clinical trials:

Trial	Phase	NCT number	Patients	Treatment
PANTHER	3	NCT03268954	Patients with higher-risk MDS, AML (20–30% blasts) or CMML	Pevonedistat + azacitidine versus azacitidine alone
PEVOLAM	3	NCT04090736	Patients with newly diagnosed AML who are unfit for intensive chemotherapy	Pevonedistat + azacitidine versus azacitidine alone
PEVENAZA	2	NCT04266795	Patients with newly diagnosed AML who are unfit for intensive chemotherapy	Pevonedistat + venetoclax + azacitidine versus venetoclax + azacitidine

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