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Concordance Between WHO 2022 and ICC 2022 Classifications of Myeloid Neoplasms: A Single-Center Clinicopathological and Molecular Analysis

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Abstract

The simultaneous publication of the 5th edition World Health Organization (WHO 2022) and International Consensus Classification (ICC 2022) systems for myeloid neoplasms raised concerns about divergent diagnoses in clinical practice. We retrospectively classified 71 consecutive patients with myeloid neoplasms (myelodysplastic syndromes [MDS], n=34; chronic myelomonocytic leukemia [CMML], n=25; non-CMML MDS/myeloproliferative neoplasm [MDS/MPN] overlap, n=12) diagnosed at a single academic center between 2019 and 2023 according to both WHO 2022 and ICC 2022 criteria. Targeted next-generation sequencing (40-gene myeloid panel) was performed on all cases. TP53 biallelic status was determined by multihit detection or presumptive loss of heterozygosity (variant allele frequency [VAF] >50%). ICC classification of MDS with mutated TP53 (MDS-mTP53) was restricted to cases meeting the VAF ≥10% threshold. Overall exact subtype concordance was 66/71 (93.0%; kappa=0.917). At the entity-equivalent level, concordance rose to 69/71 (97.2%; kappa=0.967), and at the umbrella category level it was 71/71 (100%). All 5 discordant cases occurred within the MDS group: 2 resulted from the ICC's distinct TP53-mutated category capturing single-hit TP53 cases with VAF ≥10% that WHO classifies by morphology, and 3 reflected nomenclature differences (MDS-IB1 vs MDS-IB). CMML (25/25) and MDS/MPN (12/12) were fully concordant. SF3B1 mutation was associated with favorable outcome (log-rank p=0.035). WHO 2022 and ICC 2022 show very high concordance when ICC VAF thresholds are strictly applied, with discordance confined to a narrow but conceptually important divergence in TP53-mutated MDS.

Introduction

The classification of myeloid neoplasms underwent a landmark bifurcation in 2022, when the World Health Organization (WHO) released its 5th edition classification [1] simultaneously with the International Consensus Classification (ICC) [2]. For the first time, two authoritative systems emerged from partially overlapping expert panels, creating uncertainty about whether patients would receive different diagnoses depending on which framework their institution adopted [3, 4].

Both classifications represent substantial advances over the revised 4th edition WHO 2016 system [5]. They share a commitment to integrating molecular data into the diagnostic algorithm, recognizing entities such as SF3B1-mutated MDS and refining blast-threshold criteria [1, 2]. However, several areas of divergence have generated active debate [3, 6, 7].

The most consequential divergence concerns TP53-mutated myelodysplastic syndromes. The WHO 2022 system created a specific entity, MDS with biallelic TP53 inactivation (MDS-biTP53), restricted to cases with two or more TP53 hits and a variant allele frequency (VAF) > 10% [1]. Cases with a single TP53 mutation are classified according to standard morphological criteria. The ICC 2022 recognizes MDS with mutated TP53 (MDS-mTP53) as a broader category encompassing both single-hit and multihit cases, provided the VAF exceeds 10% [2]. This distinction carries potential prognostic and therapeutic

implications [8, 9]. Critically, both systems require VAF ≥ 10% for TP53-specific classification, a threshold that has not been consistently applied in prior comparative studies.

Additional differences include nomenclature changes (WHO's retention of MDS-IB1/MDS-IB2 versus ICC's consolidated MDS-IB/MDS-EB), the recognition of CMML with oligomonocytic features (CMML-O) by WHO but not ICC, and differences in MDS/MPN overlap classification [1, 2, 10].

In this study, we systematically applied both WHO 2022 and ICC 2022 criteria to a consecutive cohort of 71 patients with MDS, CMML, and non-CMML MDS/MPN overlap syndromes at a single academic center. We employed a tiered concordance framework, strict application of ICC VAF thresholds, and integrated IPSS-R scoring to quantify agreement and assess the clinical correlates of classification discordance.

Materials and methods

Study design and patient selection

This retrospective, cross-sectional study was conducted at a single academic center. We identified 71 consecutive patients diagnosed with myeloid neoplasms between January 2019 and December 2023 who had adequate bone marrow material and targeted NGS data. The study was approved by the Ankara University Human Research Ethics Committee on 28 February 2023 (Approval No: İ02-87-23). Informed consent was obtained from all individual participants included in the study, in accordance with the Declaration of Helsinki.

Patients were categorized: MDS (n = 34), CMML (n = 25), and non-CMML MDS/MPN overlap (n = 12).

Pathological evaluation

All bone marrow aspirate smears and trephine biopsy sections were reviewed by two experienced hematopathologists blinded to prior diagnoses. Aspirate smears were stained with May–Grünwald–Giemsa and Prussian blue. Trephine biopsies were evaluated for cellularity, reticulin fibrosis grade (MF-0 through MF-3, European Consensus grading [11]), and megakaryocyte morphology. Immunohistochemistry included CD34, CD61, and CD117.

Differential cell counts were performed on 500-cell aspirate smears. Ring sideroblasts were quantified on Prussian blue–stained smears. Peripheral blood monocyte counts were reviewed to distinguish absolute from relative monocytosis.

Molecular analysis

Targeted NGS was performed on all 71 cases using a 40-gene myeloid panel (Supplementary Table S1) on an Illumina MiSeq platform. Only pathogenic and likely pathogenic variants (per ACMG/AMP guidelines [12]) with VAF ≥ 2% were reported. Mutation burden was defined as the number of pathogenic/likely pathogenic mutations per patient across genes represented in the panel.

TP53 biallelic assessment

TP53 biallelic inactivation was defined as the presence of two or more distinct TP53 mutations (multihit), or a single TP53 mutation with VAF > 50% (presumptive loss of heterozygosity [LOH]), consistent with WHO 2022 criteria [1]. Copy-neutral LOH data from SNP arrays were not available; therefore, biallelic status was determined by multihit detection and the VAF > 50% surrogate. Cases with a single TP53 mutation at VAF ≤ 50% were designated as single-hit (Supplementary Table S2).

Application of ICC VAF threshold

A critical methodological consideration is the ICC 2022 requirement of VAF ≥ 10% for the MDS-mTP53 designation [2]. In our cohort, 3 of 5 single-hit TP53 cases had VAF below 10% (0.52%, 4.15%, and 1.15%). These cases did not meet ICC criteria for MDS-mTP53 and were classified by morphology under both systems, rendering them concordant. Only cases meeting both pathogenicity and VAF ≥ 10% criteria were classified as MDS-mTP53 under ICC.

Dual classification

Each case was independently classified according to both WHO 2022 [1] and ICC 2022 [2] criteria by consensus of the two reviewing pathologists. The complete case-by-case WHO–ICC cross-tabulation is provided in Supplementary Table S3.

Concordance assessment

Concordance was assessed using a three-tiered framework:

Level 1 (Exact subtype): Complete agreement on the specific subtype.

Level 2 (Entity-equivalent): Agreement after merging nomenclature variants (e.g., WHO MDS-IB1 mapped to ICC MDS-IB).

Level 3 (Umbrella category): Agreement at the overarching disease category level (MDS, CMML, or MDS/MPN).

Inter-system agreement was quantified using Cohen’s kappa statistic.

IPSS-R scoring

The Revised International Prognostic Scoring System (IPSS-R) was calculated for MDS patients with available hemoglobin, platelet count, absolute neutrophil count, bone marrow blast percentage, and cytogenetic risk category data (n = 27 of 34; 7 cases had missing cytogenetic or blast data). Cytogenetic risk was categorized per IPSS-R criteria [13]. Individual IPSS-R data are provided in Supplementary Table S4.

Statistical analysis

Categorical variables were compared using chi-squared or Fisher's exact test. Continuous variables were compared using Kruskal–Wallis test. Survival analysis was performed using Kaplan–Meier method with log-rank tests. Given the small sample size and limited events, Cox proportional hazards regression was not performed for subgroups with fewer than 20 events; all survival results are exploratory. Overall survival was measured from diagnosis to death or last follow-up. A two-sided $p < 0.05$ was considered significant. Analyses were performed using SPSS version 28.0.

Results

Patient characteristics

A total of 71 patients were included: 34 MDS, 25 CMML, and 12 non-CMML MDS/MPN. The median age was 67 years (IQR 56–74) for MDS, 65 (IQR 54–70) for CMML, and 65 (IQR 62–72) for MDS/MPN. There was a female predominance in MDS (20F:14M), whereas CMML (17M:8F) and MDS/MPN (10M:2F) showed male predominance (Supplementary Table S6).

Bone marrow morphology

Median bone marrow cellularity differed among groups: 83.0% (IQR 70–95) for MDS, 94.8% (IQR 90–100) for CMML, and 95.8% (IQR 92–100) for MDS/MPN (p=0.002). Reticulin fibrosis ≥2 was present in 10/32 (31.2%) MDS, 8/25 (32.0%) CMML, and 9/12 (75.0%) MDS/MPN cases (p=0.015), with significantly higher fibrosis in MDS/MPN (Supplementary Table S5).

Aspirate cytology

Ring sideroblasts were identified in 23/34 (67.6%) MDS, 0/25 (0%) CMML, and 7/12 (58.3%) MDS/MPN cases (p<0.001). Mean bone marrow monocyte percentage was significantly higher in CMML (8.8%) compared with MDS (1.7%) and MDS/MPN (3.1%, p<0.001) (Table 3).

Mutation landscape

The median number of pathogenic/likely pathogenic mutations per patient was 3 (range 0–6) in MDS, 4 (range 2–7) in CMML, and 4 (range 3–9) in MDS/MPN (Supplementary Table S7). In MDS, the most

frequently mutated genes were SF3B1 (13/34, 38.2%), TET2 (11/34, 32.4%), TP53 (10/34, 29.4%), and DNMT3A (10/34, 29.4%). In CMML, TET2 (19/25, 76.0%), SRSF2 (15/25, 60.0%), and ASXL1 (11/25, 44.0%) predominated. In MDS/MPN, ASXL1 (7/12, 58.3%) and JAK2 (7/12, 58.3%) were most prevalent. No TP53, SF3B1, or JAK2 mutations were detected in CMML. The mutational landscape across disease groups is illustrated in Fig. 5.

TP53 mutations and biallelic assessment

TP53 mutations were detected exclusively in MDS (10/34, 29.4%). Individual case details including specific mutations, VAFs, and biallelic assessment methods are provided in Supplementary Table S2. Of the 10 cases, 5 harbored biallelic TP53 inactivation: 2 by multihit (4 and 6 distinct mutations, respectively) and 3 by presumptive LOH (single mutations with VAFs of 78%, 80%, and 99%). The remaining 5 cases had single-hit TP53 mutations with VAFs of 0.52%, 1.15%, 4.15%, 14%, and 35%. The distribution of TP53 VAFs and biallelic status is shown in Fig. 3.

Classification concordance: the central finding

Table 1 and Supplementary Table S3 summarize the WHO–ICC cross-tabulation. The flow of diagnostic categories from WHO 2022 to ICC 2022 is illustrated in Fig. 1. CMML was classified identically (CMML-1, n=18; CMML-2, n=7). MDS/MPN was fully concordant (MDS/MPN-NOS, n=9; MDS/MPN-T-SF3B1, n=3).

With strict application of the ICC VAF ≥10% threshold, tiered concordance was:

Level 1 (exact subtype): 66/71 (93.0%); Cohen’s kappa = 0.917

Level 2 (entity-equivalent): 69/71 (97.2%); Cohen’s kappa = 0.967

Level 3 (umbrella category): 71/71 (100%)

These tiered concordance results are depicted in Fig. 2.

Within MDS, 29/34 cases (85.3%) were concordant at the exact subtype level. Subgroup-level concordance rates are presented in Fig. 4. Five cases were discordant.

Discordance analysis

The 5 discordant cases fell into two categories (Table 2):

TP53-driven reclassifications (n=2): Two single-hit TP53 cases with VAF ≥10% (Case #48: VAF 35%, classified as MDS-LB by WHO and MDS-mTP53 by ICC; Case #57: VAF 14%, classified as MDS-IB1 by WHO and MDS-mTP53 by ICC). These represent genuine conceptual divergence.

Sub-threshold TP53 cases (n=3): Three additional single-hit TP53 cases had VAFs below 10% (0.52%, 4.15%, 1.15%). These did not meet ICC VAF criteria for MDS-mTP53 and were classified by morphology under both systems, rendering them concordant. Notably, 2 of these 3 cases also had VAFs below the

2% reporting threshold, raising the question of whether these represent true somatic mutations or sequencing artifacts at the limit of detection.

Nomenclature-only discordances (n=3): Three MDS-IB1 (WHO) cases mapped to MDS-IB (ICC), reflecting naming convention differences with no biological distinction.

IPSS-R distribution in MDS

IPSS-R scores were calculable for 27/34 MDS patients (Supplementary Table S4). The median score was 3.0 (range 1.0–6.5). The distribution was: Very Low 2 (7.4%), Low 14 (51.9%), Intermediate 8 (29.6%), High 2 (7.4%), Very High 1 (3.7%) (Supplementary Fig. S2).

Among TP53-biallelic cases with calculable IPSS-R (n=3): scores were 3.5 (Intermediate), 4.5 (Intermediate), and 6.0 (High), confirming clustering in adverse categories. Single-hit TP53 cases showed heterogeneous IPSS-R: one scored 2.0 (Low, VAF 0.52%) and another 4.5 (Intermediate, VAF 14%), supporting the concept that single-hit TP53 at low VAF may behave more like its morphological counterpart.

Formal IPSS-M calculation was not possible with our data, as the validated online calculator (https://mds-risk-model.com) requires inputs beyond our panel's coverage. However, the combination of IPSS-R scores and TP53 biallelic status provides a molecular risk approximation consistent with IPSS-M principles.

Exploratory survival analysis

Survival data were available for 47 of 71 patients, with 18 deaths recorded over a median follow-up of 8.8 months (IQR 4.9–21.8). Deaths by group: MDS 5/34, CMML 6/25, MDS/MPN 7/12.

By Kaplan–Meier analysis with log-rank test, SF3B1 mutation was associated with favorable survival (p=0.035; Supplementary Fig. S1). In MDS/MPN, none of the 3 SF3B1-mutated patients died versus 7/8 wild-type (p=0.040), though these numbers are very small.

Importantly, WHO 2022 versus ICC 2022 subgroup-based survival stratification did not differ significantly (p=0.747), suggesting that the 2 genuine classification discordances do not translate into detectably different prognostic stratification.

Discussion

Very high concordance with strict VAF application

This study demonstrates that WHO 2022 and ICC 2022 classifications are highly concordant when ICC VAF thresholds are strictly applied: exact concordance was 93.0% (kappa = 0.917, "almost perfect" agreement) and entity-equivalent concordance was 97.2% (kappa = 0.967). This level of agreement is

higher than reported in some prior studies [14–16], likely because we rigorously applied the ICC's own VAF ≥ 10% requirement for MDS-mTP53 designation.

The importance of strict VAF threshold application cannot be overstated. Three of our TP53-mutated cases had VAFs below 10% (0.52%, 4.15%, 1.15%). Had these been classified as MDS-mTP53 under ICC—as might occur if the VAF threshold is not explicitly enforced—concordance would have appeared lower (88.7%), and the number of TP53-driven discordances would have been inflated from 2 to 5. This finding underscores the need for explicit reporting of TP53 VAF data in classification concordance studies.

The TP53 question: a narrow but important divergence

The 2 genuine TP53-driven discordances illustrate the conceptual tension between the systems. Case #48 (VAF 35%, MDS-LB by WHO, MDS-mTP53 by ICC) and Case #57 (VAF 14%, MDS-IB1 by WHO, MDS-mTP53 by ICC) represent patients where the ICC system prioritizes the presence of a TP53 mutation at actionable VAF, while WHO classifies by morphology unless biallelic inactivation is demonstrated.

The landmark study by Bernard et al. [8] demonstrated that biallelic TP53 inactivation, but not monoallelic mutation, consistently predicts dismal outcomes. Our IPSS-R data support this distinction: biallelic cases clustered in Intermediate-to-High IPSS-R categories (3.5–6.0), while the single-hit case with the lowest VAF (0.52%) scored only 2.0 (Low). The absence of cnLOH data remains an important caveat, as some single-hit cases could harbor biallelic inactivation through mechanisms our assay did not detect [8, 9].

IPSS-R and molecular risk integration

The addition of IPSS-R data to our concordance analysis provides a prognostic framework missing from most prior comparative studies. The finding that the majority of our MDS patients fall in Low-to-Intermediate IPSS-R categories (median 3.0) reflects the predominance of lower-risk disease in our cohort. Formal IPSS-M calculation [17] was not feasible with our current data, but the integration of IPSS-R with molecular profiling suggests that classification discordances are concentrated in cases where prognostic scoring would already identify adverse biology.

Mutation landscape and disease biology

The mutation profiles recapitulate established molecular signatures [18–20]. TET2 (76%) and SRSF2 (60%) predominance in CMML, SF3B1 enrichment (38%) in MDS, and JAK2/ASXL1 co-enrichment (58% each) in MDS/MPN are consistent with larger cohorts [10, 18, 20, 21]. The complete absence of TP53 in CMML confirms the distinct pathobiology of this entity.

Fibrosis, TP53, and multiparametric risk

Among 10 MDS cases with reticulin fibrosis ≥ 2, 3 harbored TP53 mutations. This overlap may identify a particularly high-risk subgroup, though numbers preclude formal analysis. Neither classification explicitly addresses this interaction [22, 23].

SF3B1 and prognosis

The favorable prognostic impact of SF3B1 mutation (log-rank p = 0.035) is consistent with established evidence [24–26]. The striking finding in MDS/MPN (0/3 SF3B1-mutated deaths vs 7/8 wild-type, p = 0.040) is consistent with MDS/MPN-T-SF3B1 as a favorable entity [27], though the very small numbers mandate cautious interpretation.

Classification and clinical practice

The finding that survival stratification did not differ between WHO and ICC assignments (p = 0.747) provides reassurance. The kappa values of 0.917 (exact) and 0.967 (entity-equivalent) support practical interchangeability for the majority of myeloid neoplasm diagnoses [28].

Limitations

This is a single-center, retrospective study with a moderate sample size (n = 71). CnLOH data were unavailable; some single-hit TP53 cases may harbor biallelic inactivation through undetected mechanisms. The median follow-up (8.8 months) is short with only 18 events, precluding multivariable survival modeling. IPSS-R was calculable for only 27/34 MDS patients due to missing cytogenetic data. Formal IPSS-M calculation was not performed. Systematic karyotype data were available for 29/34 MDS patients; the remaining had cytogenetics not performed. Flow cytometric monocyte subsetting was not available.

Conclusions

WHO 2022 and ICC 2022 classifications demonstrate very high concordance (93.0% exact, 97.2% entity-equivalent) when ICC VAF thresholds are strictly applied. Only 2 genuine TP53-driven discordances were identified, both involving single-hit TP53 mutations with VAF ≥ 10%—representing a narrow but conceptually important divergence on the biological significance of monoallelic TP53 mutations. IPSS-R scoring confirms adverse risk clustering in TP53-biallelic cases regardless of classification system. These findings support the practical interchangeability of both systems for the vast majority of myeloid neoplasm diagnoses.

Declarations

Ethics approval: This study was approved by the Ankara University Human Research Ethics Committee on 28 February 2023 (Approval No: İ02-87-23). All procedures performed were in accordance with the ethical standards of the institutional research committee and with the 1964 Declaration of Helsinki and its later amendments.

Human ethics and consent to participate: Informed consent was obtained from all individual participants included in the study. The study was approved by the Ankara University Human Research

Ethics Committee (Approval No: İ02-87-23, dated 28 February 2023) and was performed in accordance with the Declaration of Helsinki.

Consent for publication: Not applicable. This study uses anonymized retrospective data; no individual identifying information is presented.

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Competing interests: The authors declare no competing interests.

Availability of data and materials: The datasets generated and analyzed during the current study are available from the corresponding author on reasonable request. Supplementary data including patient-level TP53 assessment (Table S2), WHO–ICC cross-tabulation (Table S3), IPSS-R scoring (Table S4), bone marrow morphology (Table S5), peripheral blood findings (Table S6), mutation landscape (Table S7), survival curves (Fig. S1), and IPSS-R distribution (Fig. S2) are provided as supplementary materials.

Author contributions: EKÇ: Study conception and design, data acquisition, molecular and morphological analysis, statistical analysis, manuscript drafting. SY: Morphological analysis, data verification, critical manuscript revision. DK: Clinical data collection, patient management, data verification. SKT: Patient management, clinical data interpretation, critical manuscript revision. MÖ: Clinical supervision, patient management, critical manuscript revision. IK: Study supervision, morphological review, data analysis and interpretation, critical manuscript revision. All authors read and approved the final version of the manuscript.

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Tables

Table 1 Concordance between WHO 2022 and ICC 2022 classifications

A. Three-tiered concordance analysis

Concordance level	Concordant/Total	Percentage	Cohen's κ
Exact subtype	66/71	93.0%	0.917
Entity-equivalent	69/71	97.2%	0.967
Umbrella category	71/71	100%	1.000

B. Subgroup concordance analysis

Disease group	Exact concordance	Entity-equivalent
MDS (n=34)	29/34 (85.3%)	32/34 (94.1%)
CMML (n=25)	25/25 (100%)	25/25 (100%)
MDS/MPN (n=12)	12/12 (100%)	12/12 (100%)

Table 2 Characteristics of discordant cases between WHO 2022 and ICC 2022

Case	WHO 2022	ICC 2022	TP53 VAF	Biallelic status	IPSS-R	Discordance type
#48	MDS-LB	MDS-mTP53	35%	Single-hit	2.5	TP53-driven
#57	MDS-IB1	MDS-mTP53	14%	Single-hit	4.5	TP53-driven
#30	MDS-IB1	MDS-IB	N/A	N/A	3.0	Nomenclature
#42	MDS-IB1	MDS-IB	N/A	N/A	N/A	Nomenclature
#55	MDS-IB1	MDS-IB	N/A	N/A	4.0	Nomenclature

MDS-LB MDS with low blasts, MDS-IB1 MDS with increased blasts 1 (WHO), MDS-IB MDS with increased blasts (ICC), MDS-mTP53 MDS with mutated TP53, VAF variant allele frequency, IPSS-R Revised International Prognostic Scoring System, N/A not applicable

Table 3 Baseline demographic and laboratory characteristics

Characteristic	MDS (n=34)	CMML (n=25)	MDS/MPN (n=12)	p value
Age, median (IQR)	67 (56–74)	65 (54–70)	65 (62–72)	0.512
Sex, M/F	14/20	17/8	10/2	0.003
Hemoglobin, g/dL, median (IQR)	9.0 (7.8–10.5)	10.8 (9.0–12.5)	10.2 (8.5–11.8)	0.018
Platelets, ×10⁹/L, median (IQR)	138 (67–245)	87 (52–142)	298 (123–485)	0.002
WBC, ×10⁹/L, median (IQR)	4.8 (3.2–7.1)	12.5 (7.8–22.0)	9.8 (6.2–15.5)	<0.001
ANC, ×10⁹/L, median (IQR)	2.8 (1.5–4.5)	5.2 (3.0–9.8)	6.5 (3.8–10.2)	<0.001

MDS myelodysplastic syndromes, CMML chronic myelomonocytic leukemia, MDS/MPN myelodysplastic/myeloproliferative neoplasms, IQR interquartile range, WBC white blood cell count, ANC absolute neutrophil count

Figures

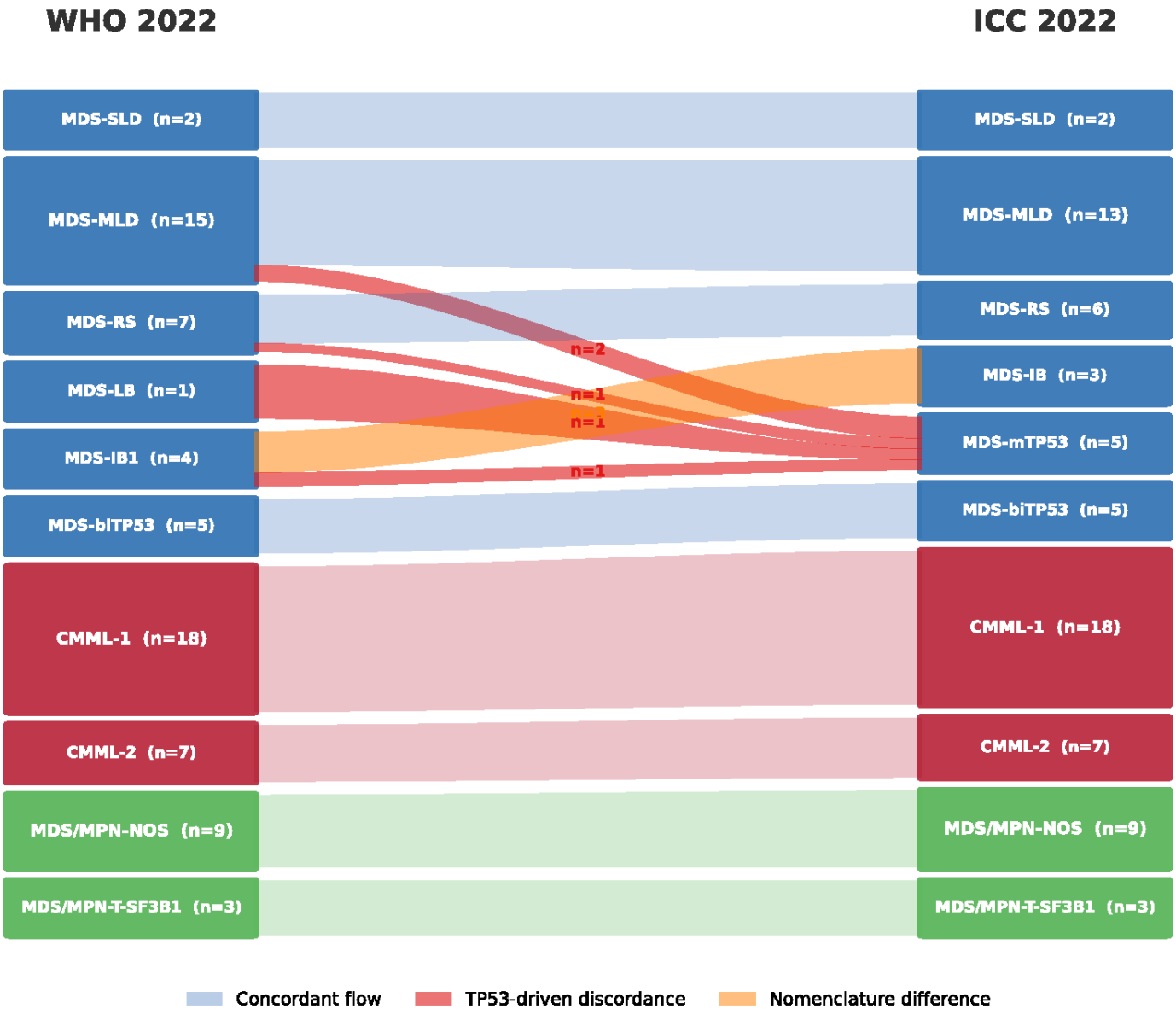


Figure 1

Alluvial diagram showing the flow of diagnostic categories from WHO 2022 to ICC 2022 classification across 71 patients with myeloid neoplasms. The width of each flow band is proportional to the number of cases. Concordant classifications are shown in blue; discordant cases are highlighted in red.

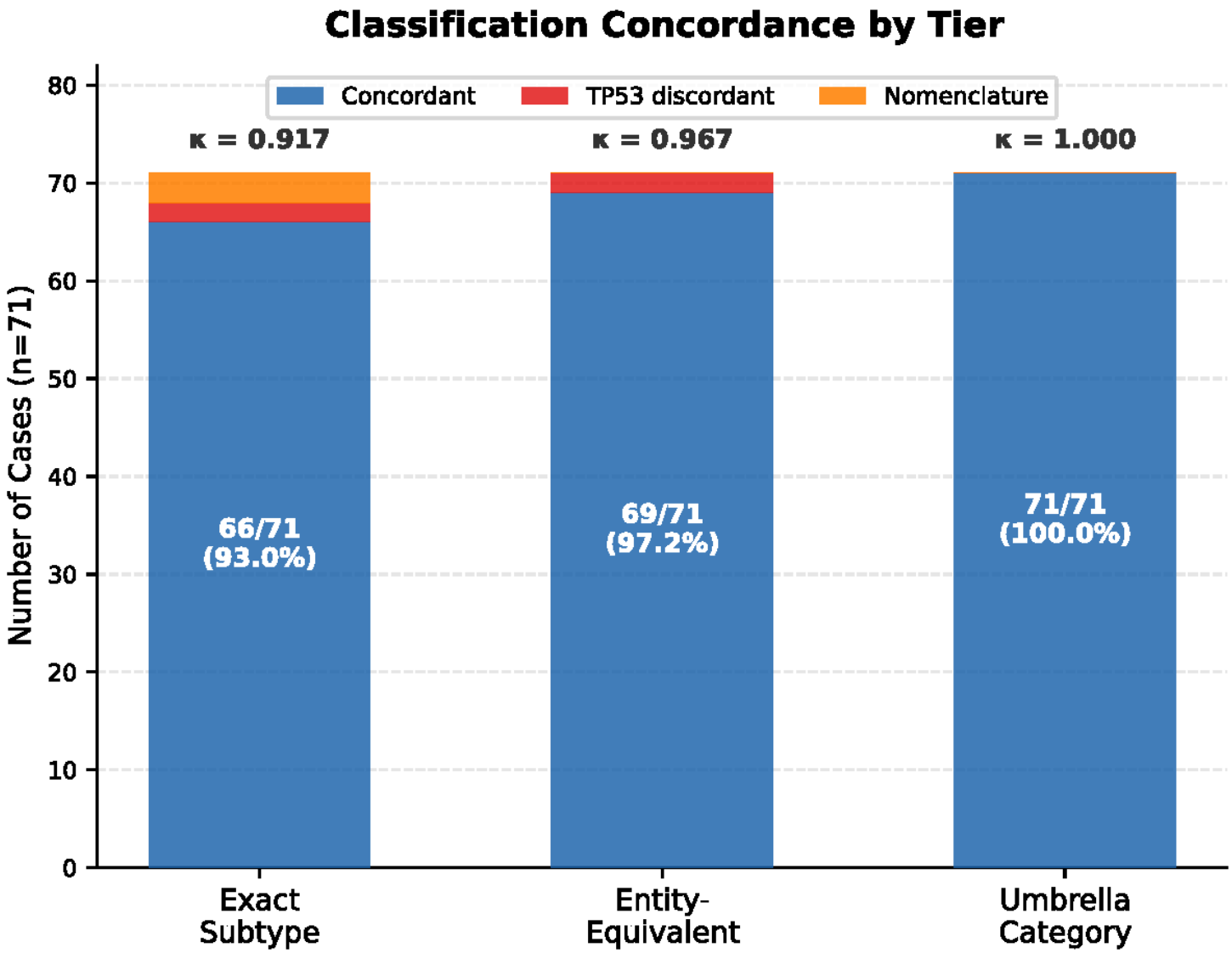


Figure 2

Three-tiered concordance analysis between WHO 2022 and ICC 2022 classifications. Bar chart depicting concordance rates at the exact subtype level (93.0%), entity-equivalent level (97.2%), and umbrella category level (100%).

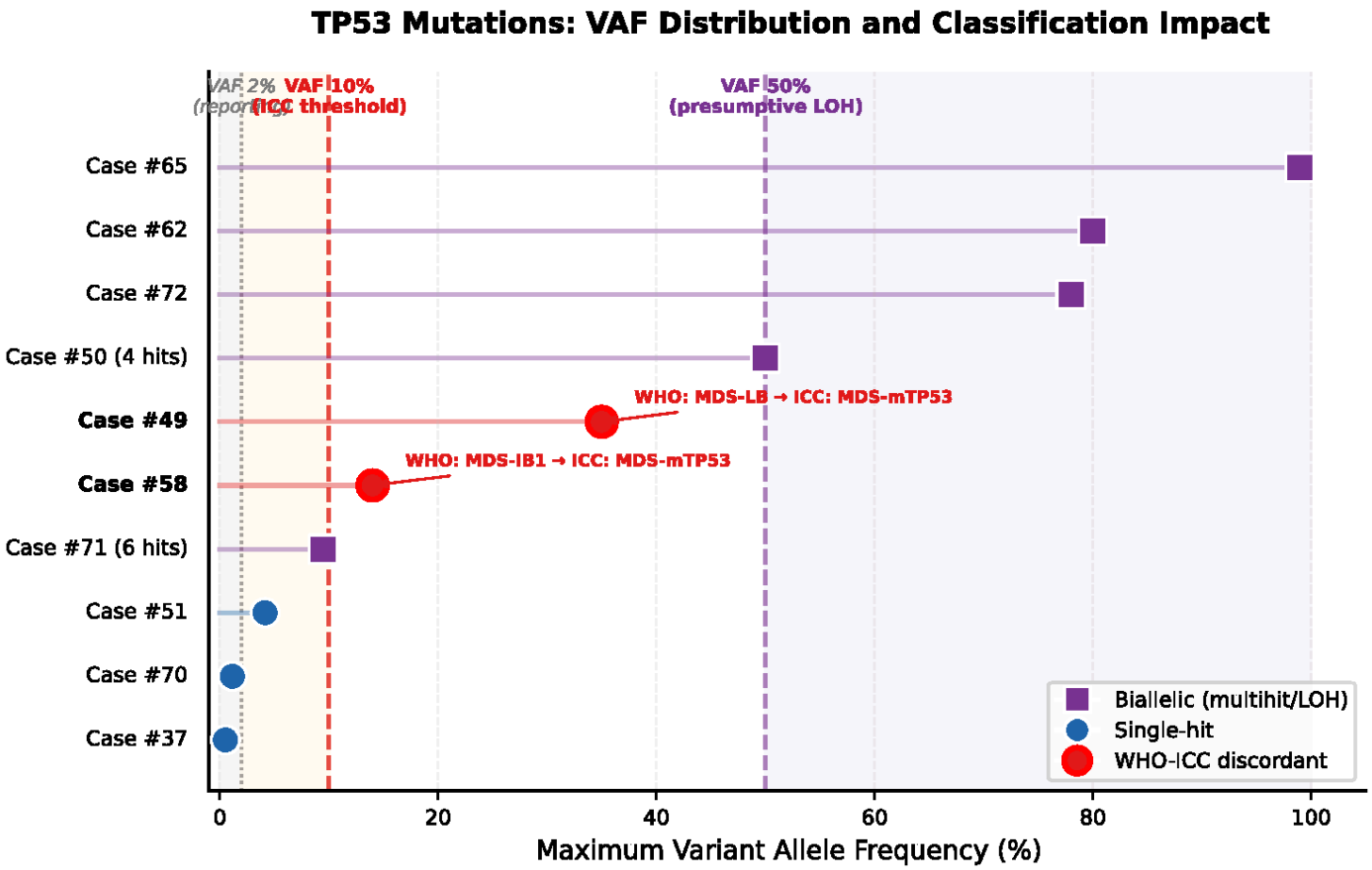


Figure 3

TP53 variant allele frequency (VAF) distribution and biallelic status assessment. Scatter plot showing VAF values for all 10 TP53-mutated MDS cases, stratified by biallelic (multihit or presumptive LOH) versus single-hit status. The horizontal dashed line indicates the ICC VAF ≥10% threshold.

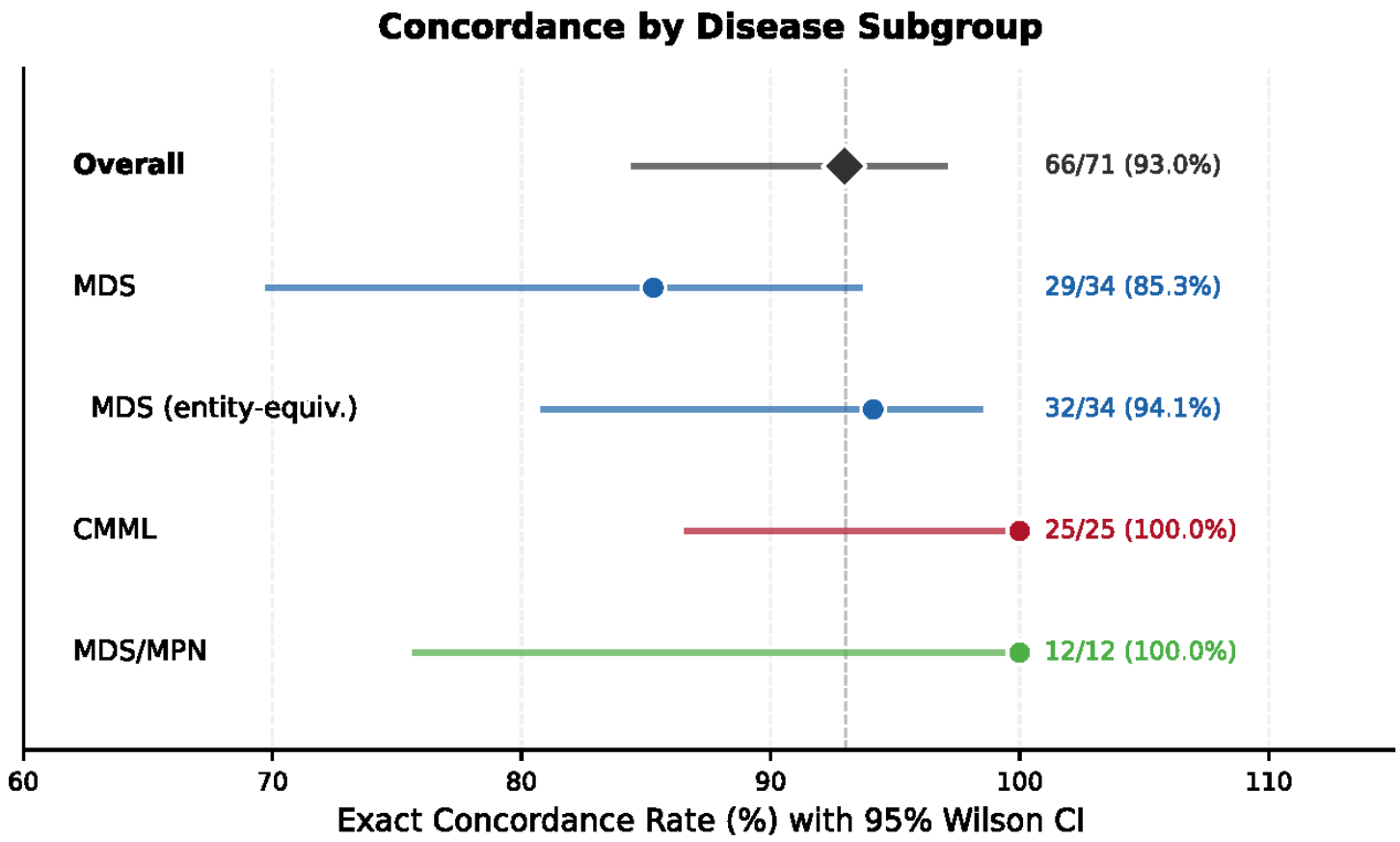


Figure 4

Forest plot of subgroup-level concordance rates between WHO 2022 and ICC 2022 classifications for MDS, CMML, and MDS/MPN groups at exact and entity-equivalent levels.

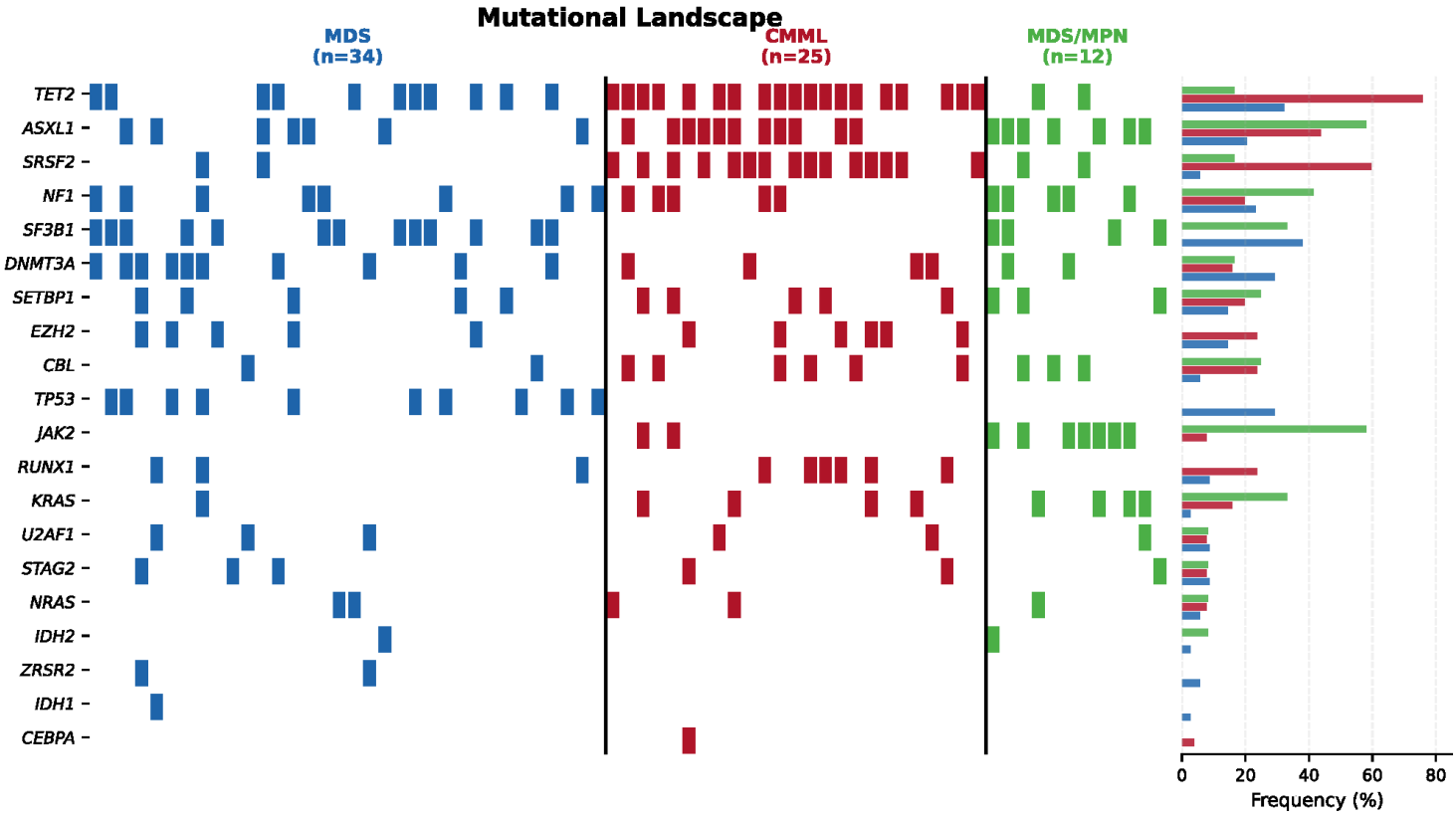


Figure 5

Mutational landscape of myeloid neoplasms across the three disease groups (MDS, CMML, MDS/MPN). Oncoplot showing the frequency and distribution of pathogenic/likely pathogenic mutations detected by the 40-gene NGS panel.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- SupplementaryTableS1.xlsx
- SupplementaryTablesS2S3S4.xlsx
- SupplementaryTablesS5S6S7.xlsx
- SupplementaryFigS1KaplanMeier.pdf
- SupplementaryFigS2IPSSRDistribution.pdf