LETTER TO THE EDITOR

CSF3R mutations and variants in myeloid neoplasms: associated phenotypes, co-mutations, and survival trends

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Supplementary Material

CSF3R mutations and variants in myeloid neoplasms: associated phenotypes and co-mutations

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Legends

Figure S1: **Distribution of CSF3R Mutations/variants by Position**: This figure illustrates the distribution of CSF3R mutations/variants along the protein, highlighting that mutations/variants in extracellular domain are mostly classified as variants of unknown significance (VUS, Blue color) while pathogenic mutations/variants (red color) are more prevalent in the cytoplasmic domains.

Figure S2: **Chi-Square Analysis of Co-mutations**: This figure presents the results of a chi-square analysis comparing the frequency of co-mutations in each myeloid neoplasm(vs other myeloid neoplasm), excluding pre-malignant conditions.

Table S1: Distribution of all co-mutations across different disease groups: This is an all-inclusive table showing the distribution of all co-mutations in different disease groups.

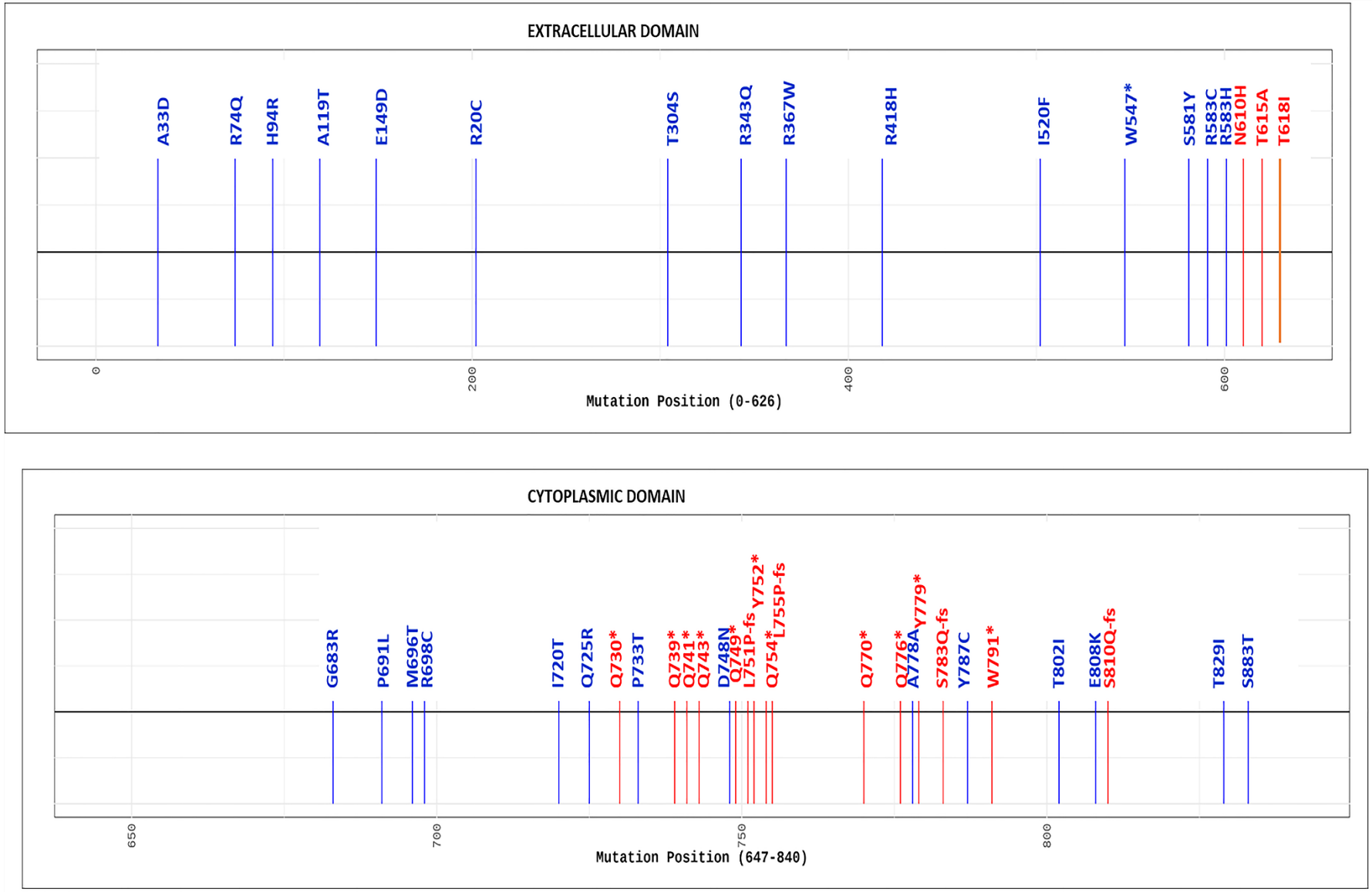
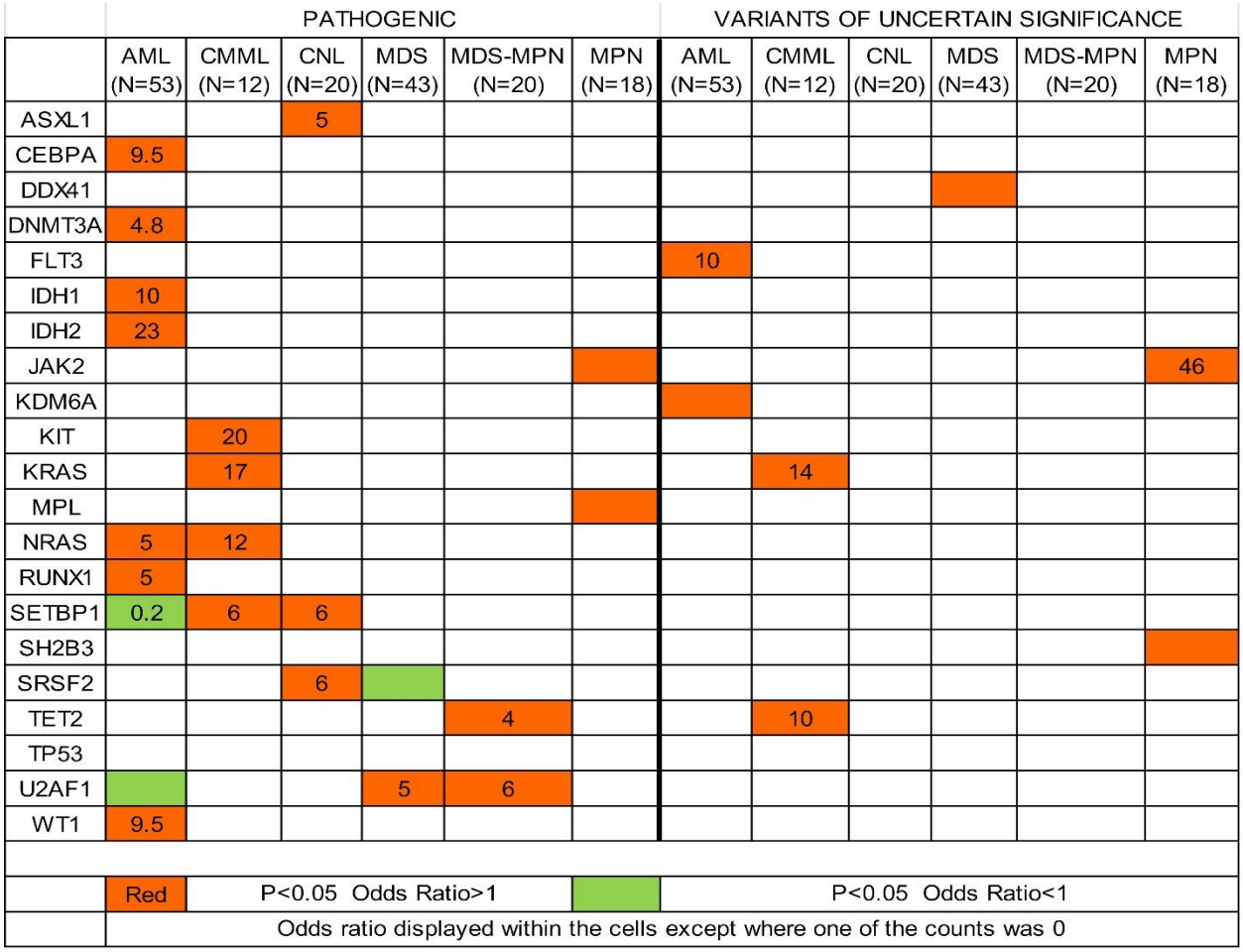


Figure S1: Distribution of CSF3R Mutations/variants by Position: This figure illustrates the distribution of CSF3R mutations/variants along the protein, highlighting that mutations/variants in extracellular domain are mostly classified as **variants of unknown significance (VUS, Blue color)** while **pathogenic mutations/variants (red color)** are more prevalent in the cytoplasmic domains.



	PATHOGENIC						VARIANTS OF UNCERTAIN SIGNIFICANCE					
	AML (N=53)	CMML (N=12)	CNL (N=20)	MDS (N=43)	MDS-MPN (N=20)	MPN (N=18)	AML (N=53)	CMML (N=12)	CNL (N=20)	MDS (N=43)	MDS-MPN (N=20)	MPN (N=18)
ASXL1			5									
CEBPA	9.5											
DDX41												
DNMT3A	4.8											
FLT3							10					
IDH1	10											
IDH2	23											
JAK2												46
KDM6A												
KIT		20										
KRAS		17						14				
MPL												
NRAS	5	12										
RUNX1	5											
SETBP1	0.2	6	6									
SH2B3												
SRSF2			6									
TET2					4			10				
TP53												
U2AF1				5	6							
WT1	9.5											
	Red	P<0.05 Odds Ratio>1					P<0.05 Odds Ratio<1					
	Odds ratio displayed within the cells except where one of the counts was 0											

Figure S2: Chi-Square Analysis of Co-mutations: This figure presents the results of a chi-square analysis comparing the frequency of co-mutations in each myeloid neoplasm(vs other myeloid neoplasm), excluding pre-malignant conditions.

AML: Acute myeloid leukemia, CMML: chronic myelomonocytic leukemia, CNL: chronic neutrophilic leukemia, MDS: myelodysplastic syndrome, MDS-MPN: Myelodysplastic/ Myeloproliferative neoplasm, MPN: Myeloproliferative neoplasms (myelofibrosis, polycythemia vera, chronic myeloid leukemia, and essential thrombocythemia), PM: Premalignant conditions, SM: Systemic Mastocytosis.

Table S1: Distribution of all co-mutations across different disease groups*											
	AML (N=53)	CMML (N=12)	CNL (N=20)	MDS (N=43)	MDS-MPN (N=20)	MPN (N=18)	PM (N=15)	VUS n=91	Pathogenic n=91	Total (N=182)	p value
ASXL1	17(32%)	6(50%)	12(71%)	15(35%)	6 (32%)	5 (28%)	1 (7%)	16(18%)	46(53%)	62(35%)	0.016
TET2	5 (9%)	4 (33%)	0	9 (21%)	6 (32%)	2 (11%)	4 (27%)	15(17%)	15 (17%)	30(17%)	0.073
SRSF2	9 (17%)	2 (17%)	8 (47%)	3 (7%)	2 (11%)	2 (11%)	1 (7%)	9 (10%)	18 (21%)	27(15%)	0.015
DNMT3A	13(25%)	2 (17%)	0	5 (12%)	3 (16%)	1 (6%)	2 (13%)	10 11%)	16 (18%)	26 15%)	0.27
RUNX1	14(26%)	1 (8%)	1 (6%)	6 (14%)	2 (11%)	0	0	8 (9%)	16 (18%)	24(14%)	0.048
SETBP1	4 (8%)	4 (33%)	7 (41%)	4 (9%)	4 (21%)	0	0	4 (4%)	19 (22%)	23(13%)	< 0.001
U2AF1	1 (2%)	2 (17%)	0	8 (19%)	5 (26%)	2 (11%)	2 (13%)	8 (9%)	12 (14%)	20(11%)	0.051
NRAS	10(19%)	4 (33%)	0	1 (2%)	2 (11%)	0	0	5 (6%)	12 (14%)	17(10%)	0.004
EZH2	8 (15%)	0	2 (12%)	2 (5%)	3 (16%)	0	0	4 (4%)	11 (13%)	15 (8%)	0.21
BCOR	6 (11%)	2 (17%)	0	4 (9%)	0	0	1 (7%)	7 (8%)	6 (7%)	13 (7%)	0.39
IDH2	9 (17%)	1 (8%)	1 (6%)	0	0	0	1 (7%)	3 (3%)	9 (10%)	12 (7%)	0.038
TP53	4 (8%)	0	0	7 (16%)	1 (5%)	0	0	10(11%)	2 (2%)	12 (7%)	0.14
CEBPA	8 (15%)	0	0	1 (2%)	2 (11%)	0	0	2 (2%)	9 (10%)	11 (6%)	0.066
SF3B1	3 (6%)	0	1 (6%)	2 (5%)	3 (16%)	1 (6%)	0	6 (7%)	4 (5%)	10 (6%)	0.61
KRAS	2 (4%)	4 (33%)	1 (6%)	0	1 (5%)	1 (6%)	0	4 (4%)	5 (6%)	9 (5%)	0.001
ZRSR2	0	0	1 (6%)	5 (12%)	0	2 (11%)	1 (7%)	5 (6%)	4 (5%)	9 (5%)	0.2
FLT3	7 (13%)	1 (8%)	0	0	1 (5%)	0	0	5 (6%)	4 (5%)	9 (5%)	0.077
JAK2	2 (4%)	0	0	0	0	7 (39%)	0	8 (9%)	1 (1%)	9 (5%)	< 0.001

IDH1	4 (8%)	0	0	2 (5%)	0	2 (11%)	0	3 (3%)	5 (6%)	8 (5%)	0.53
STAG2	1 (2%)	1 (8%)	1 (6%)	2 (5%)	2 (11%)	0	0	2 (2%)	5 (6%)	7 (4%)	0.66
GATA2	3 (6%)	0	0	2 (5%)	0	1 (6%)	0	2 (2%)	4 (5%)	6 (3%)	0.83
WT1	5 (9%)	0	0	0	1 (5%)	0	0	1 (1%)	5 (6%)	6 (3%)	0.2
CBL	2 (4%)	1 (8%)	1 (6%)	0	0	1 (6%)	0	3 (3%)	2 (2%)	5 (3%)	0.68
DDX41	0	0	0	3 (7%)	0	0	0	3 (3%)	0	3 (2%)	0.21
ETNK1	2 (4%)	1 (8%)	0	0	0	0	0	1 (1%)	2 (2%)	3 (2%)	0.48
ETV6	0	0	1 (6%)	1 (2%)	0	0	1 (7%)	2 (2%)	1 (1%)	3 (2%)	0.55
PHF6	2 (4%)	0	0	1 (2%)	0	0	0	1 (1%)	2 (2%)	3 (2%)	0.90
CALR	0	0	0	1 (2%)	0	1 (6%)	0	2 (2%)	0	2 (1%)	0.65
KDM6A	2 (4%)	0	0	0	0	0	0	2 (2%)	0	2 (1%)	0.69
KIT	1 (2%)	1 (8%)	0	0	0	0	0	0 (0.0%)	2 (2%)	2 (1%)	0.41
MPL	1 (2%)	0	0	0	0	1 (6%)	0	1 (1%)	1 (1%)	2 (1%)	0.7
NPM1	2 (4%)	0	0	0	0	0	0	1 (1%)	1 (1%)	2 (1%)	0.68
TERT	1 (2%)	0	0	1 (2%)	0	0	0	2 (2%)	0	2 (1%)	0.97
ANKRD26	1 (2%)	0	0	0	0	0	0	1(1%)	0	1 (0.6%)	0.94
SH2B3	0	0	0	0	0	1 (6%)	0	1 (1%)	0 (0.0%)	1 (0.6%)	0.26
SMC1A	1 (2%)	0	0	0	0	0	0	0 (0%)	1 (1%)	1 (0.6%)	0.94

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