Table S1

Table S1. Baseline patient characteristics, 2001-2019

Characteristics	Calendar period				Total	
	2001-2013		2014-2019			
	No.	(%)	No.	(%)	No.	(%)
Total No. of patients	**237**		**110**		**347**	
Sex						
Male	147	(62)	78	(71)	225	(65)
Female	90	(38)	32	(29)	122	(35)
Age at diagnosis, years						
Median (IQR)	71 (63-77)		73 (67-78)		72 (64-95)	
≤65	77	(32)	22	(20)	99	(29)
>65	160	(68)	88	(80)	248	(71)
First-line treatment						
Best supportive care only	66	(28)	33	(30)	99	(29)
Anti-neoplastic therapy without alloSCT	159	(67)	62	(56)	221	(64)
Anti-neoplastic therapy with alloSCT	12	(5)	15	(14)	27	(8)
Death during follow-up	207	(87)	92	(84)	299	(86)
Median follow-up, months (IQR)	15.1 (4.4-36.1)		16.8 (9.4-33.1)		15.8 (5.3-33.9)	

Abbreviations: IQR, interquartile range; and alloSCT, allogeneic stem cell transplantation

Table S2

Table S2. Median overall survival and projected 1-, 5-, and 10-year overall survival according to baseline characteristics

Characteristics	Median OS, months	95% CI		1-year OS	95% CI		5-year OS	95% CI		10-year OS	95% CI	
Overall cohort	15.8	13.8	17.2	61%	56%	66%	18%	14%	22%	14%	10%	18%
Demographics												
Sex												
Male	15.3	12.9	16.7	59%	52%	65%	17%	12%	22%	13%	8%	18%
Female	17.0	12.9	22.3	65%	56%	73%	21%	14%	28%	15%	9%	23%
Age, years												
≤65	25.3	16.1	41.9	71%	61%	79%	38%	28%	47%	35%	26%	45%
>65	14.3	12.2	16.1	57%	51%	63%	10%	7%	14%	5%	2%	8%
Calendar period												
2001-2013	15.1	12.5	17.1	59%	53%	65%	19%	15%	25%	15%	11%	20%
2014-2019	16.7	14.7	19.5	65%	55%	73%	14%	8%	22%		NA	
Cytogenetics (2014-2019 cohort)												
Normal karyotype	17.2	14.7	25.2	64%	53%	73%	17%	9%	27%		NA	
Abnormal karyotype	13.8	4.1	17.5	53%	26%	74%	7%	0%	26%		NA	
Molecular genetics (2014-2019 cohort)												
Epigenetic mutations[a]	15.3	11.2	27.9	65%	44%	80%		NA			NA	
Signaling mutations[b]	18.5	11.2	NR	79%	47%	93%	32%	9%	58%		NA	
Splicing mutations[c]	11.2	9.2	NR	50%	21%	74%		NA			NA	
Number of mutations												
No mutations	15.6	11.3	23.9	60%	45%	71%	13%	5%	23%		NA	
One mutation	19.4	15.5	36.5	86%	63%	95%	8%	1%	27%		NA	
Two mutations	18.5	9.1	NR	82%	45%	95%		NA			NA	
Three or more mutations	12.7	9.4	27.9	56%	30%	76%		NA			NA	

Abbreviations: OS, overall survival; CI, confidence interval; NA, not applicable (due to no observations) and NR, not reached

[a]Includes mutations in *ASXL1, TET2, EZH2*, and *DNMT3A*.

[b]Includes mutations in *JAK2, CALR, KIT, IDH2*, and *KRAS/NRAS*.

[c]Includes mutation in *SRSF2*.

Table S3

Table S3. Cox regression analysis, 2001-2019

Characteristics	Model w/o adjustment for primary therapy			Model w/ adjustment for primary therapy		
	HR	95% CI	*P*	HR	95% CI	*P*
Sex						
Male	1	(ref)		1	(ref)	
Female	0.86	0.67 - 1.12	0.269	0.87	0.67 - 1.13	0.304
Age at diagnosis						
≤65 years	1	(ref)		1	(ref)	
>65 years	2.07	1.53 - 2.81	<0.001	1.85	1.34 - 2.55	<0.001
Calendar period						
2001-2013	1	(ref)		1	(ref)	
2014-2019	0.79	0.60 - 1.03	0.081	0.85	0.64 - 1.11	0.235
Primary therapy						
Best supportive care only				0.83	0.63 - 1.10	0.201
Anti-neoplastic therapy without alloHSCT				1	(ref)	
AlloHSCT				0.51	0.26 - 0.97	0.039

Abbreviations: w/o, without; 'w/, with; HR, hazard ratio; CI, confidence interval; and alloHSCT, allogeneic hematopoietic stem cell transplantation.

Table S4

Table S4. Cox regression, 2014-2019

Characteristics	Univariable				Multivariable (full model)				Multivariable (forward selection)			
	HR	**95% CI**		***P***	**HR**	**95% CI**		***P***	**HR**	**95% CI**		***P***
Demographics												
Female sex	**0.58**	**0.34**	**1.00**	**0.048**	0.58	0.30	1.12	0.102				
Age >65 years	**2.72**	**1.38**	**5.36**	**0.004**	**2.22**	**1.05**	**4.70**	**0.036**	**2.55**	**1.29**	**5.03**	**0.007**
Blood and bone marrow features												
Hemoglobin ≤10 g/dL	**1.85**	**1.14**	**3.01**	**0.013**	**3.18**	**1.61**	**6.26**	**0.001**	**1.68**	**1.03**	**2.74**	**0.037**
Platelets ≤100 x 10^9 L	1.29	0.78	2.15	0.324	0.80	0.41	1.57	0.512				
Circulating blasts in PB	1.38	0.73	2.60	0.318	1.20	0.52	2.76	0.667				
BM blast ≥5%	1.24	0.69	2.20	0.471	0.86	0.39	1.87	0.700				
BM fibrosis present	1.55	0.78	3.09	0.210	1.70	0.76	3.81	0.201				
Cytogenetic abnormalities present	1.78	0.97	3.26	0.061	1.55	0.76	3.16	0.233				
Molecular genetics												
Epigenetic mutations present[a]	0.91	0.53	1.57	0.730	0.71	0.23	2.22	0.559				
Signaling mutations present[b]	0.66	0.31	1.37	0.264	0.90	0.34	2.37	0.836				
Splicing mutations present[c]	1.27	0.63	2.59	0.505	1.80	0.68	4.82	0.238				
Number of mutations												
No mutations	1	(ref)			1	(ref)						
One mutation	0.86	0.49	1.51	0.592	0.60	0.27	1.35	0.215				
Two mutations	0.77	0.34	1.74	0.528	1.02	0.35	2.96	0.967				
Three or more mutations	0.92	0.46	1.86	0.822	0.86	0.18	4.18	0.850				

Abbreviations: HR, hazard ratio; CI, confidence interval; PB, peripheral blood; and BM, bone marrow

Bold estimates indicate those statistically significant with a *P* of < 0.05

[a]Includes mutations in *ASXL1, TET2, EZH2*, and *DNMT3A*

[b]Includes mutations in *JAK2, CALR, KIT, IDH2*, and *KRAS/NRAS*

[c]Includes mutation in *SRSF2*.

Table S5

Table S5. Baseline patient characteristics of recipients of an alloHSCT, 2014-2019

Characteristics	2014-2019 cohort	
	No.	(%)
Total No. of patients	**15**	**(100)**
Demographics		
Sex		
Male	11	(73)
Female	4	(27)
Age, years		
Median (IQR)	58 (54-66)	
≤65	11	(73)
>65	4	(27)
Blood counts, median (IQR)		
Hemoglobin, g/dL	10.6 (8.1-13.9)	
Platelets, x $10/^{9}$ L	160 (85-264)	
Neutrophils, x $10/^{9}$ L	26.5 (23.2-60.0)	
Monocytosis (>1 x $10/^{9}$ L)	4	(27)
Blasts, %[a]	1	(1-7)
Bone marrow features		
Blast data available, n/N (%)	13/15 (87%)	
Median (IQR), %	3	(1-5)
<5%	8	(62)
≥5%	5	(38)
Fibrosis data available, n/N (%)	13/15	(87%)
Fibrosis present	11	(85)
Cytogenetics		
Available	15	(100)
Normal karyotype	14	(14)
Abnormal karyotype[b]	1	(1)
Trisomy[b]	1	(1)
Molecular genetics		
Available	15	(100)
ASXL1 mutation	2	(13)
SETBP1 mutation	3	(20)
SRSF2 mutation	2	(13)
CSFR3 mutation	2	(13)
JAK2 mutation	3	(20)
TET2 mutation	2	(13)
RUNX1 mutation	0	(0)
EZH2 mutation	0	(0)
Other mutations[e]	4	(27)
Number of mutations		
No mutations	6	(40)
One mutation	3	(20)
Two mutations	3	(20)
Three or more mutations	3	(20)
Death during follow-up	92	(613)
Median follow-up, months (IQR)	28.7 (16.1-49.8	

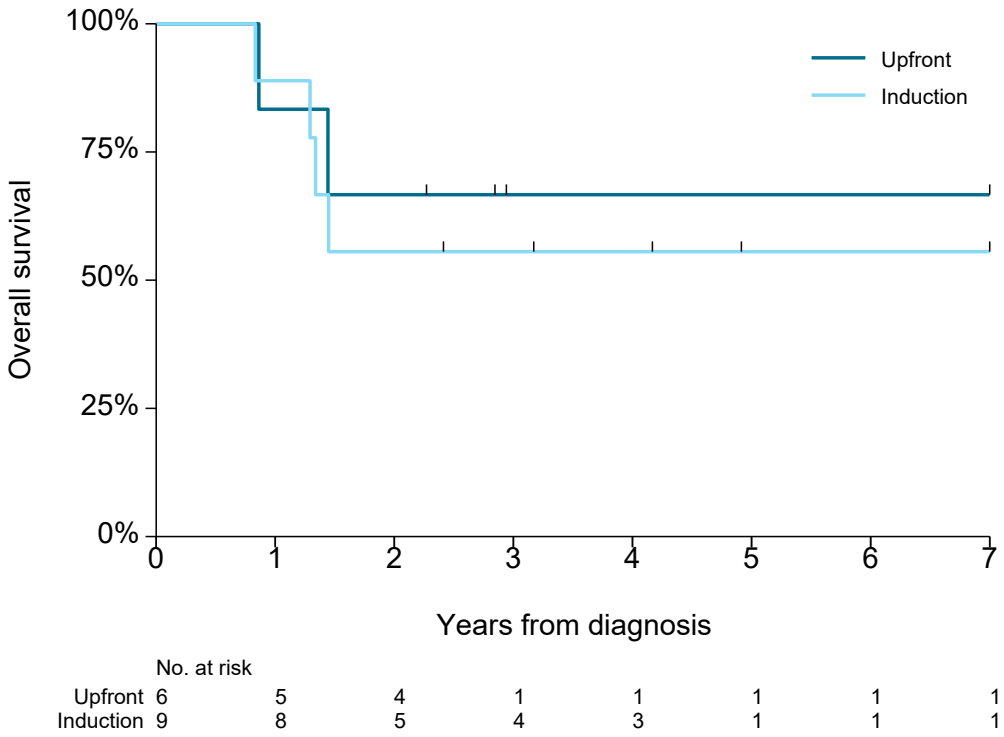
Abbreviations: IQR, interquartile range; and alloSCT, allogeneic stem cell transplantation.

[a]Missing in 1 patient

[b]Abnormal karyotype includes trisomy 13

[c]Includes patients with the following mutations: KIT (n=1), CEPBA (n=1), NPM1 (n=1), and ETNK1 mutation (n=1). Of note, a patient can harbour several mutations.

Figure S1



Overall survival of patients with MDS/MPN with neutrophilia in the Netherlands, after alloHSCT 2001-2019.

The figure shows the overall survival of patients with MDS/MPN with neutrophilia diagnosed during 2001-2019 according to induction regimen (upfront versus induction therapy)