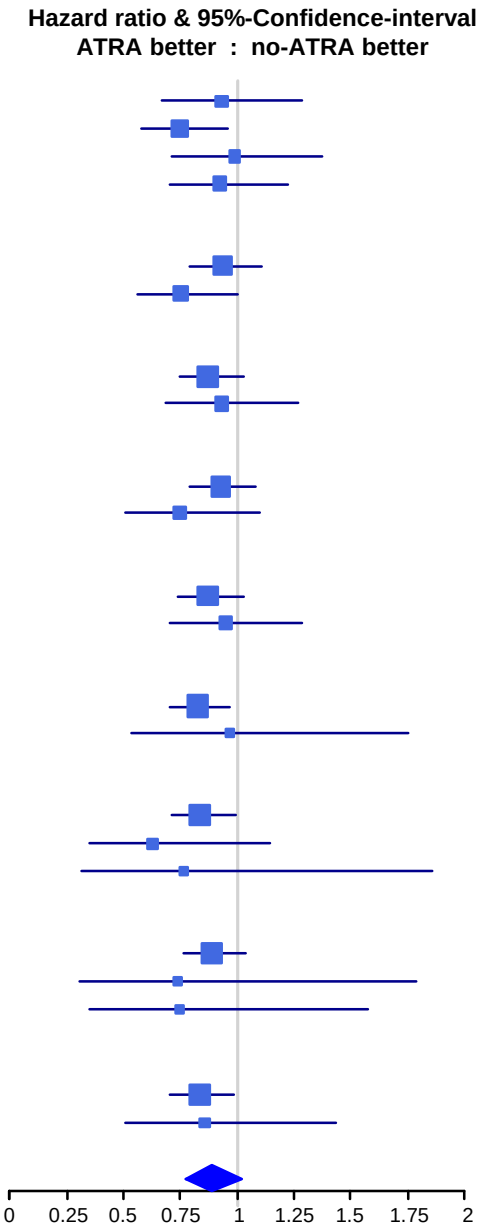
Supplementary Figure 2: Event-free Survival, per-protocol analysis

	Events/Patients ATRA	Events/Patients no ATRA	HR (95% CI)	P-value	P-value for interaction*
ELN risk-group					**0.579**
favorable	71/143	75/148	0.93 (0.67, 1.29)	0.66	
inter-1	113/151	128/153	0.75 (0.58, 0.96)	0.02	
inter-2	72/89	73/91	0.99 (0.71, 1.37)	0.95	
high	98/115	99/109	0.93 (0.70, 1.23)	0.59	
NPM1					**0.261**
wild-type	266/354	284/366	0.94 (0.80, 1.11)	0.47	
mutated	88/143	100/144	0.75 (0.56, 1.00)	0.05	
***FLT3*-ITD**					**0.706**
negative	283/409	310/420	0.87 (0.74, 1.03)	0.10	
positive	79/99	89/110	0.93 (0.69, 1.26)	0.66	
Mutated *NPM1*/*FLT3*-ITD negativ					**0.363**
negative	307/409	329/422	0.93 (0.79, 1.08)	0.35	
positive	49/90	55/89	0.75 (0.51, 1.10)	0.14	
DNMT3A					**0.600**
wild-type	265/374	305/403	0.87 (0.74, 1.03)	0.11	
mutated	91/123	78/105	0.95 (0.70, 1.29)	0.74	
IDH1					**0.608**
wild-type	270/393	308/405	0.83 (0.70, 0.97)	0.02	
mutated	22/28	22/27	0.97 (0.54, 1.76)	0.92	
IDH2					**0.601**
wild-type	259/376	296/390	0.84 (0.71, 0.99)	0.04	
mutated-R140	20/30	24/29	0.63 (0.35, 1.14)	0.13	
mutated-R172	11/13	9/10	0.76 (0.31, 1.86)	0.54	
CEBPA					**0.782**
wild-type	323/443	346/456	0.89 (0.76, 1.03)	0.13	
monoallelic	9/14	11/13	0.74 (0.30, 1.79)	0.50	
biallelic	12/24	16/25	0.74 (0.35, 1.57)	0.44	
RUNX1					**0.984**
wild-type	252/369	285/381	0.84 (0.70, 0.99)	0.04	
mutated	25/32	35/39	0.86 (0.51, 1.44)	0.56	
All	**389/544**	**417/556**	**0.89 (0.77, 1.02)**	**0.09**