Supplementary Appendix to "Novel risk factors for disease progression following detection of monoclonal gammopathy of uncertain significance"

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Table S1. Exclusion Criteria For Study Sample

Description		Number
Initial number of Malmo patients with free light chain assay		797
Exclusions		
Smoldering Multiple Myeloma		18
Missing birthdate or date of MGUS diagnosis.		35
Unknown M-protein subtype.		8
Hematologic event before M-component detection		8
Myeloma	3	
AML	2	
MPD	3	
Study Sample		728

Table S2. Distribution and event totals by each risk category for Mayo 3 and immunoparesis[a] count totals

	Number (Percent)	Number of Events	
		Lymphoid	Myeloid
Mayo 3 count			
0	255 (35.0)	17	5
1	310 (42.6)	32	4
2	142 (19.5)	27	1
3	21 (2.9)	8	0
Immunoparesis and Mayo 3 count			
0	224 (30.8)	12	4
1	273 (37.5)	27	4
2	147 (20.2)	21	2
3	74 (10.2)	18	0
4	10 (1.4)	6	0

a Subtype IgG: IgA <0.88 g/L or IgM<0.27 g/L; Subtype IgA: IgM<0.27 g/L or IgG <6.7 g/L; Subtype IgM: IgA <0.88 g/L or IgG <6.7 g/L
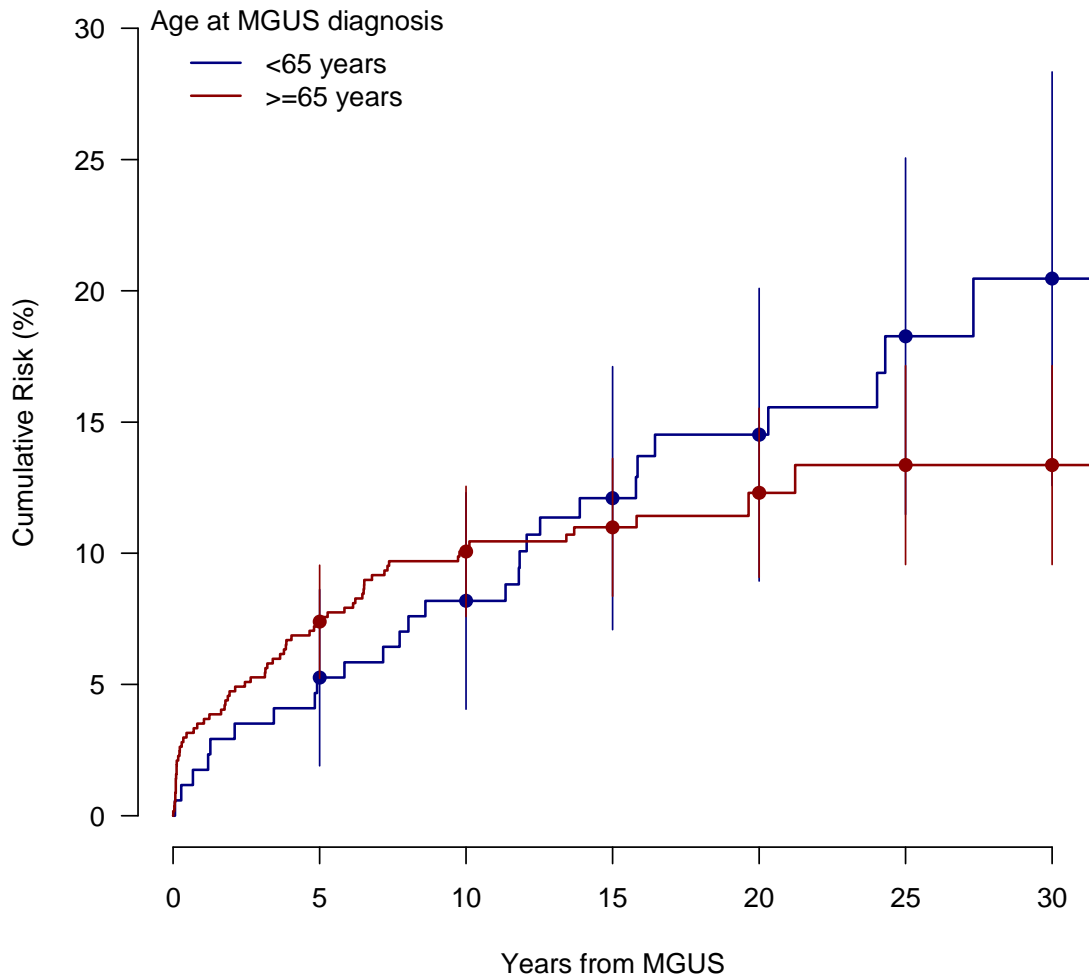
Age		0	5	10	15	20	25	30
<65	N at risk		142	116	77	51	28	10
	Risk %		4.8	7.7	11.7	14.1	18.0	20.3
	(95% CI)		(1.5, 8.0)	(3.7, 11.8)	(6.7, 16.7)	(8.6, 19.7)	(11.1, 24.8)	(12.3, 28.3)
>=65	N at risk		353	256	115	30	12	6
	Risk %		6.5	9.2	10.2	11.5	12.6	12.6
	(95% CI)		(4.4, 8.5)	(6.8, 11.6)	(7.6, 12.7)	(8.3, 14.7)	(8.8, 16.3)	(8.8, 16.3

Figure S1. Cumulative risk of a lymphoid event in years from MGUS diagnosis stratified by age at diagnosis. Bars denote the 95% confidence interval.
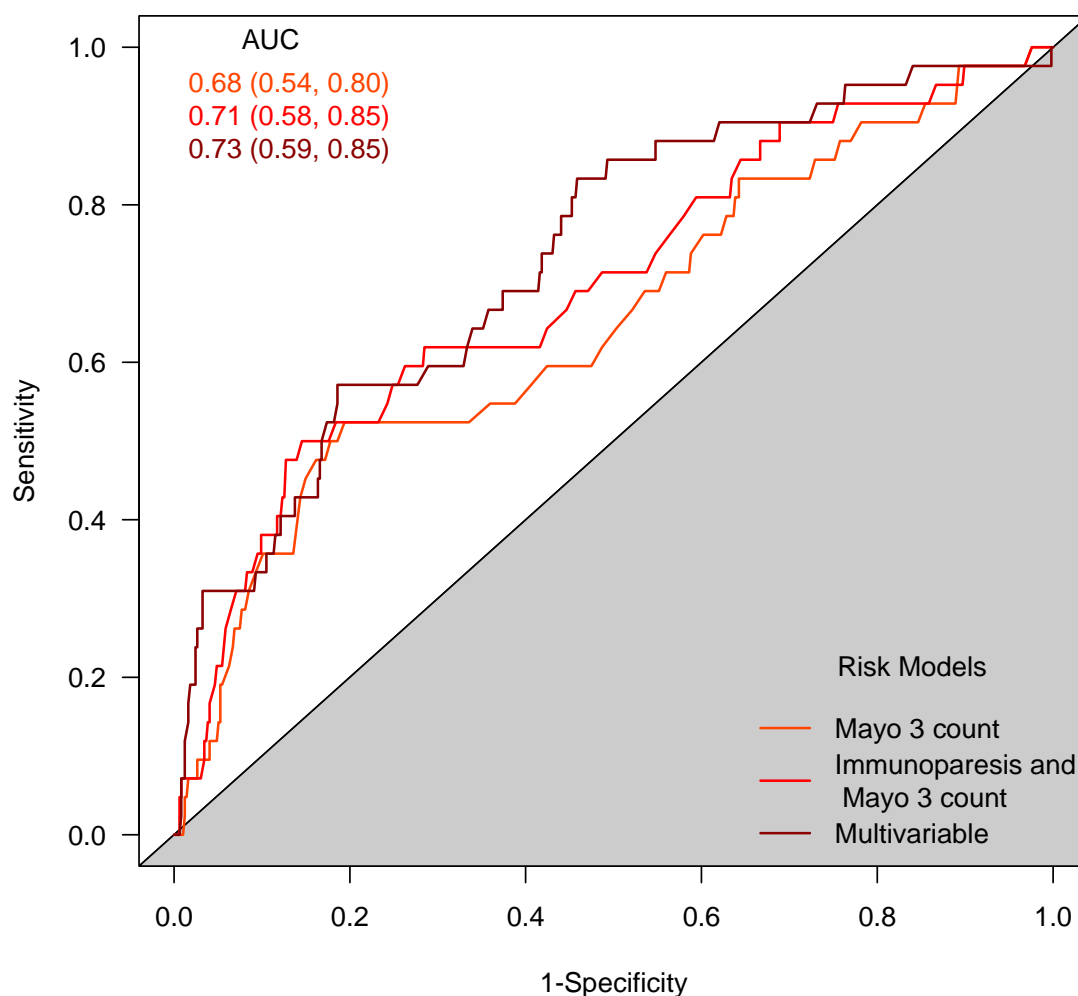
Figure S2 A

Figure S2. Receiver operating characteristic curve for three progression risk models for progression to a lymphoproliferative event following MGUS diagnosis. Curves correspond to the sensitivity and specificity of the models when fit to the full study cohort. The area under the curve (AUC) statistics were determined from a three-fold cross-validation with 150 Monte Carlo samples. **Figure S2 A** shows the comparative discriminatory ability for risk models of progression to any lymphoid event. **Figure S2 B** shows the comparative discriminatory ability for risk models of progression to multiple myeloma.

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Figure S2 B