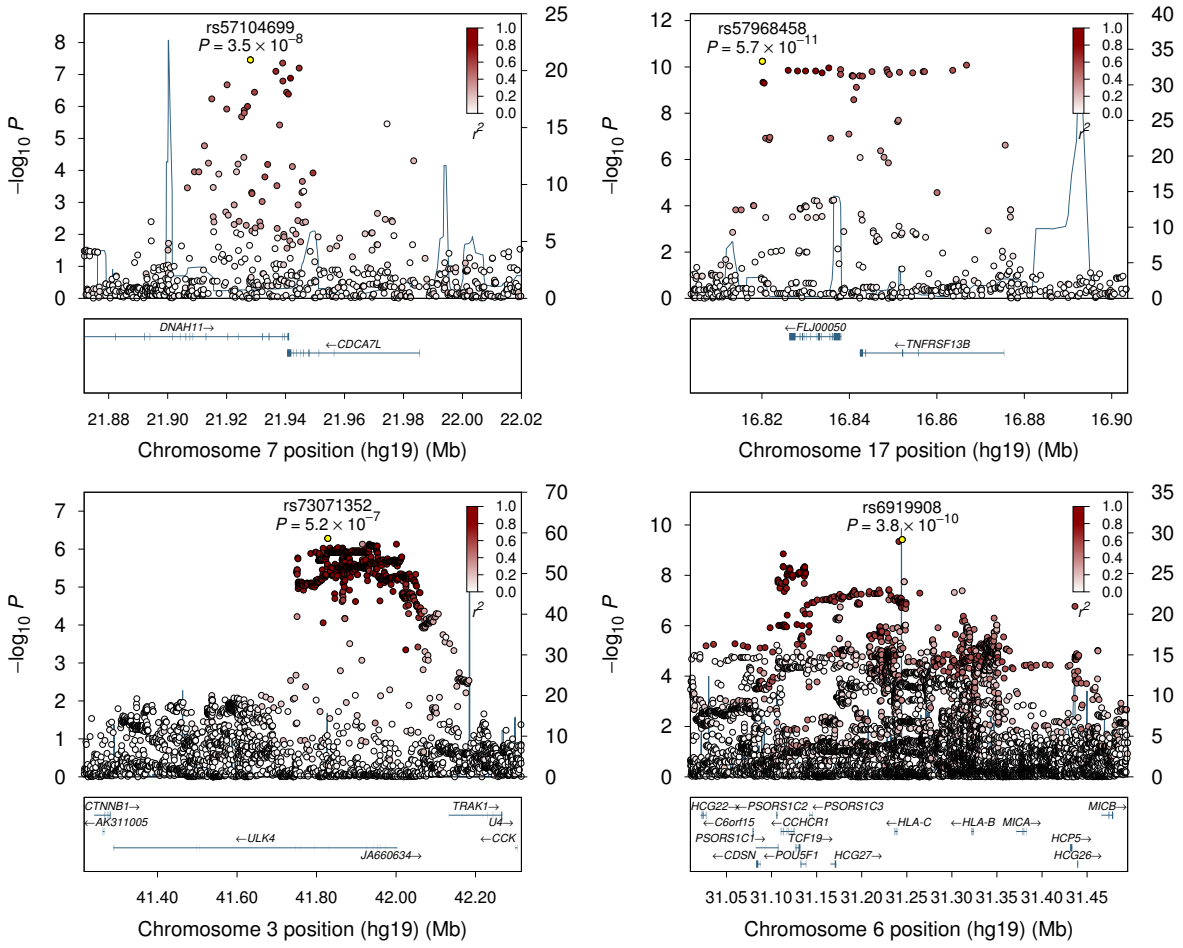
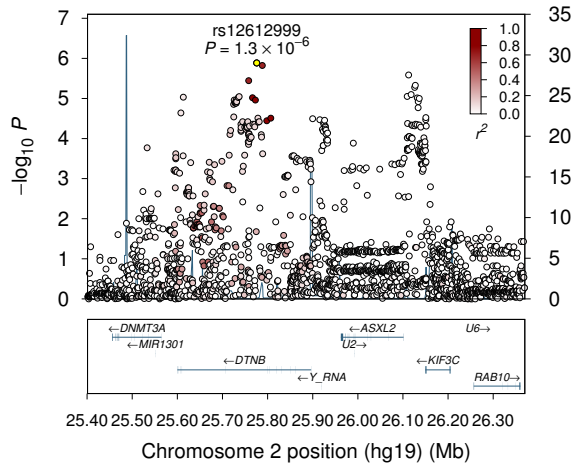
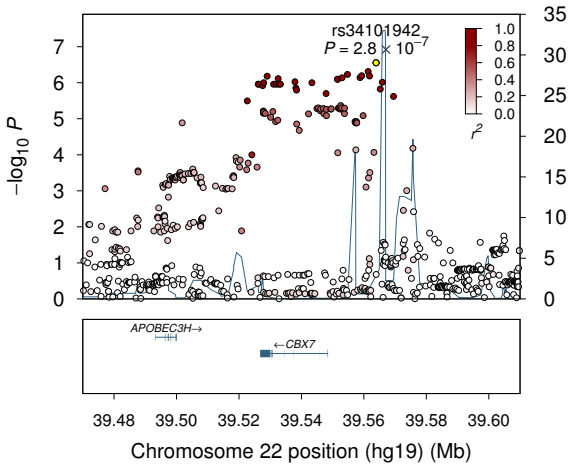
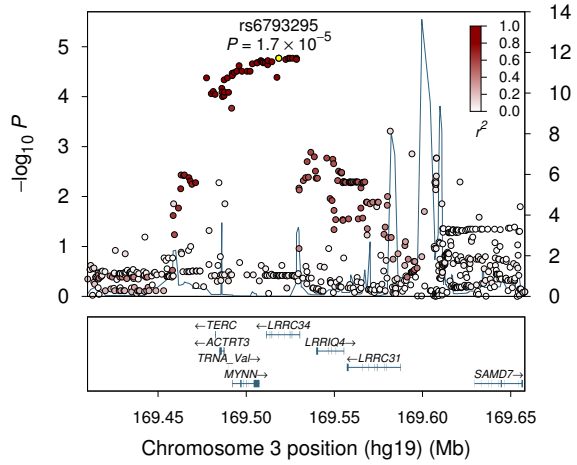
Supplementary Figure 1

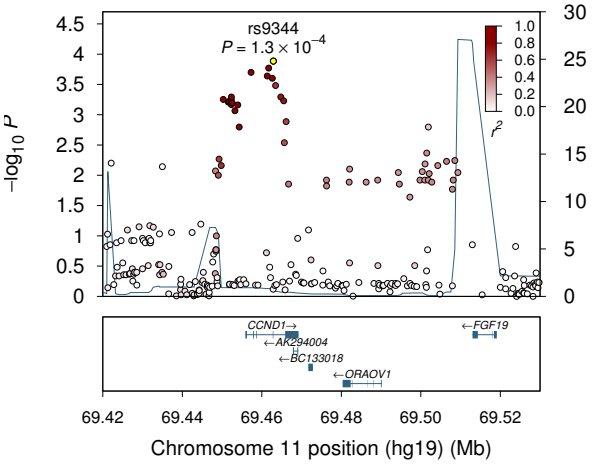
a



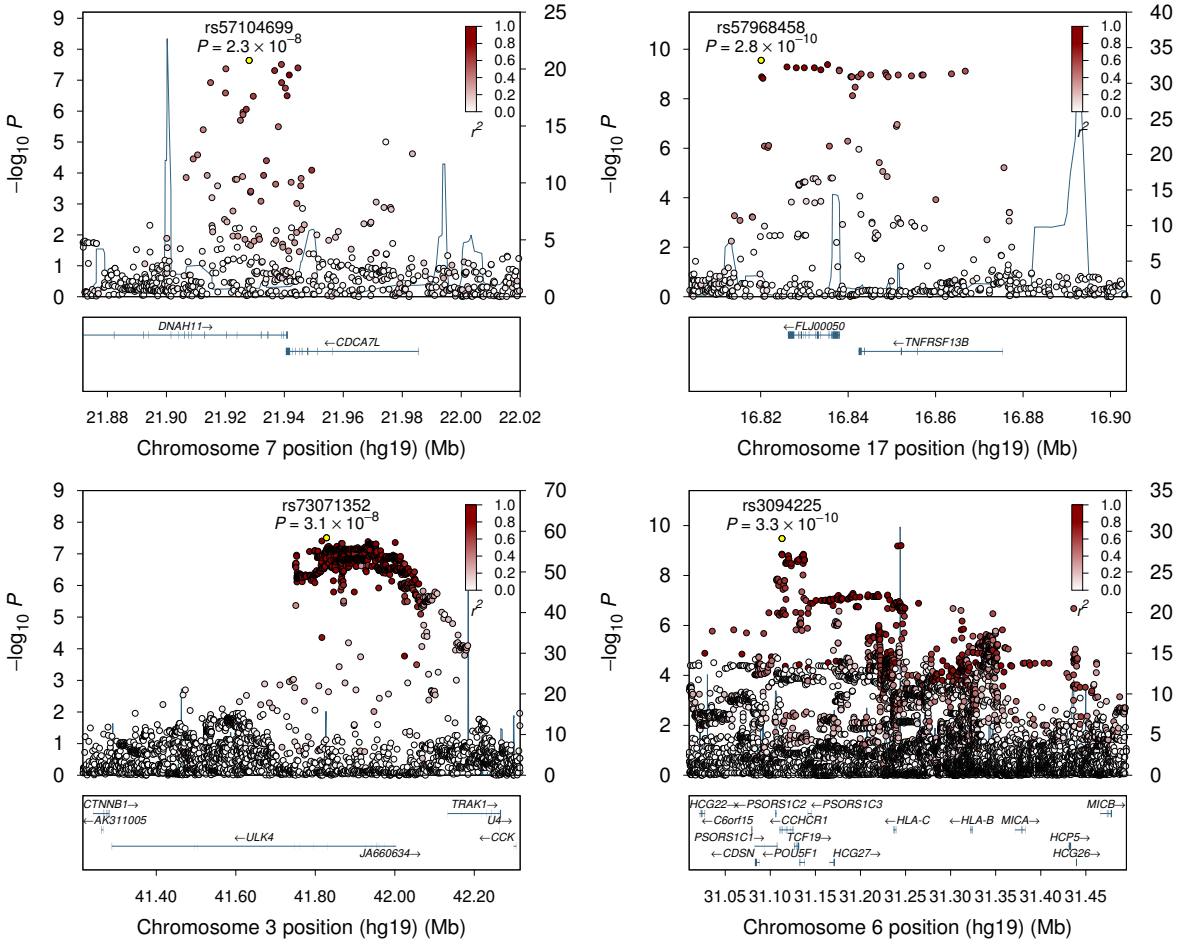

rs12612999
P = 1.3 × 10−6
−log10 P
r2
←DNMT3A
←MIR1301
←DTNB
←Y_RNA
←ASXL2
U2→
U6→
←KIF3C
RAB10→
25.40 25.50 25.60 25.70 25.80 25.90 26.00 26.10 26.20 26.30
Chromosome 2 position (hg19) (Mb)

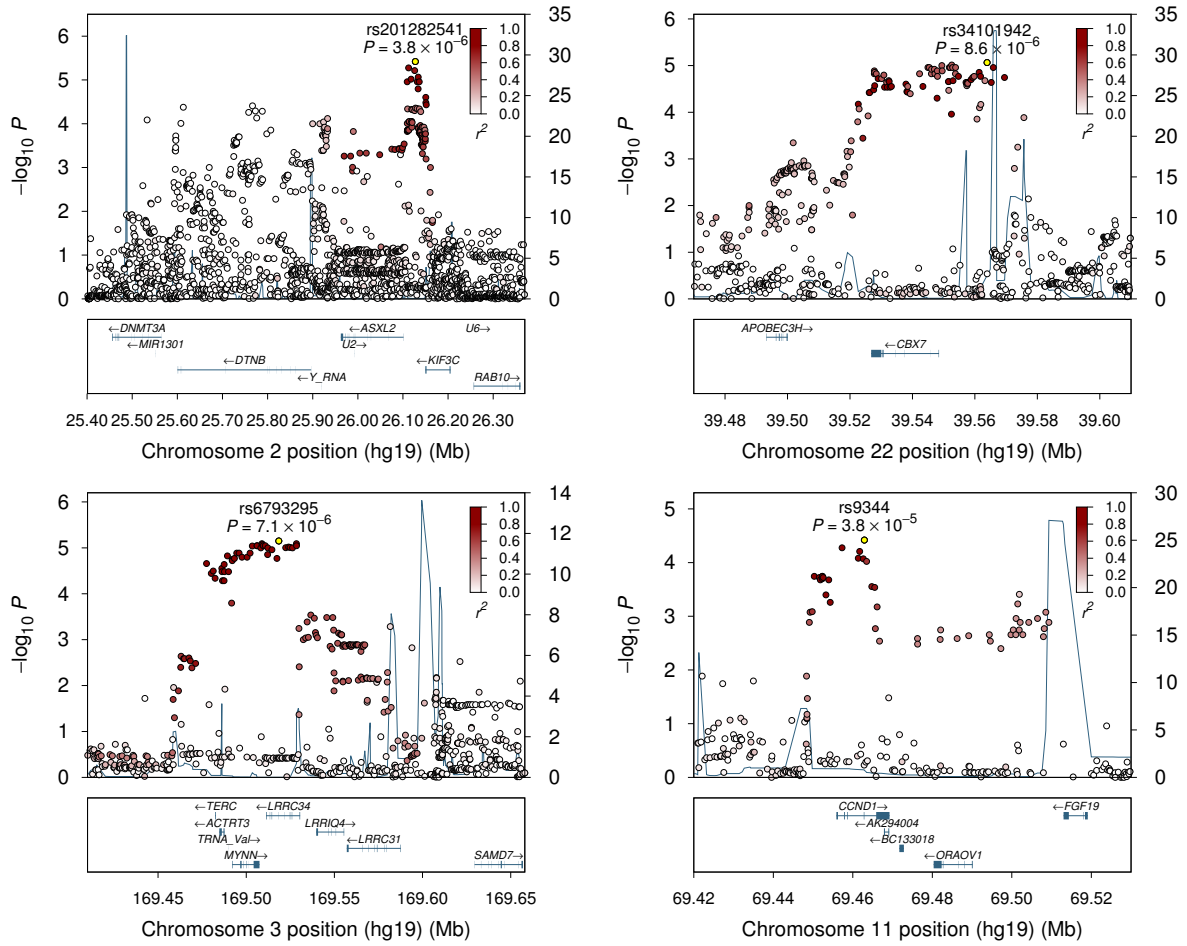

rs34101942
P = 2.8 × 10−7
−log10 P
r2
APOBEC3H→
←CBX7
39.48 39.50 39.52 39.54 39.56 39.58 39.60
Chromosome 22 position (hg19) (Mb)


rs6793295
P = 1.7 × 10−5
−log10 P
r2
←TERC
←ACTRT3
TRNA_Val→
MYNN→
←LRRC34
LRRIQ4→
←LRRC31
SAMD7→
169.45 169.50 169.55 169.60 169.65
Chromosome 3 position (hg19) (Mb)


rs9344
P = 1.3 × 10−4
−log10 P
r2
CCND1→
←AK294004
←BC133018
←ORAOV1
←FGF19
69.42 69.44 69.46 69.48 69.50 69.52
Chromosome 11 position (hg19) (Mb)

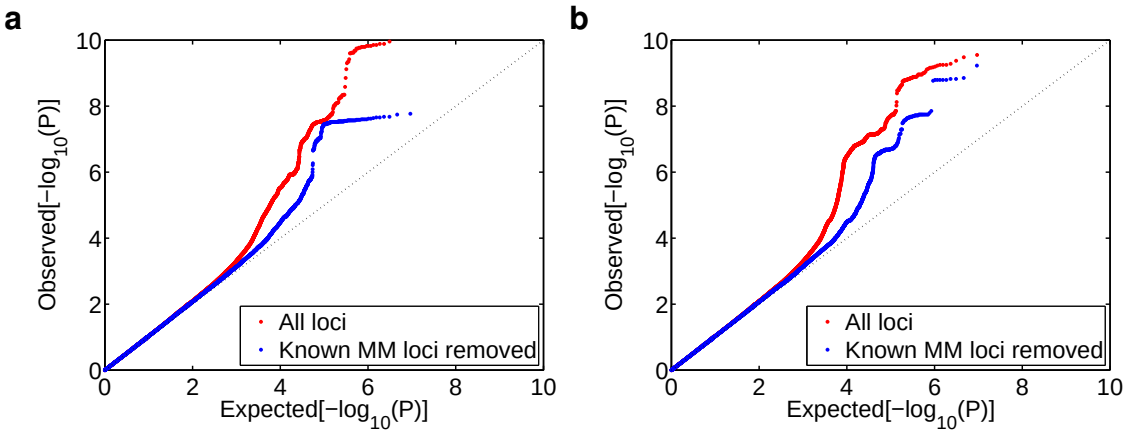
b


rs57104699
P = 2.3 × 10−8
−log10 P
r2
DNAH11→
←CDCA7L
21.88 21.90 21.92 21.94 21.96 21.98 22.00 22.02
Chromosome 7 position (hg19) (Mb)
rs57968458
P = 2.8 × 10−10
←FLJ00050
←TNFRSF13B
16.82 16.84 16.86 16.88 16.90
Chromosome 17 position (hg19) (Mb)
rs73071352
P = 3.1 × 10−8
CTNNB1→
←AK311005
←ULK4
TRAK1→
U4→
←CCK
JA660634→
41.40 41.60 41.80 42.00 42.20
Chromosome 3 position (hg19) (Mb)
rs3094225
P = 3.3 × 10−10
HCG22→ ←PSORS1C2 ←PSORS1C3
MICB→
←C6orf15
←CCHCR1
←HLA-C
←HLA-B
MICA→
PSORS1C1→
TCF19→
HCP5→
←CDSN
←POU5F1
HCG27→
HCG26→
31.05 31.10 31.15 31.20 31.25 31.30 31.35 31.40 31.45
Chromosome 6 position (hg19) (Mb)



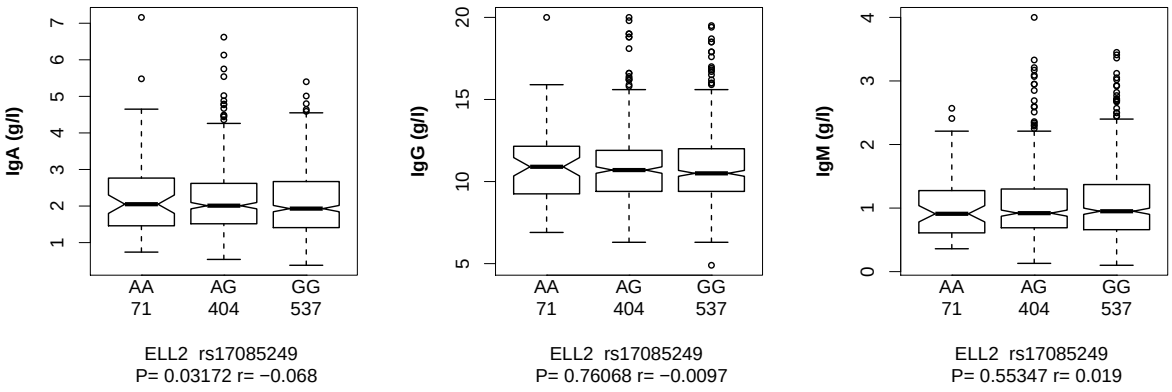
Association plots for MM risk loci identified in previous studies. **(a)** (pages 1 and 2): meta-analysis P values for the Swedish-Norwegian samples and the Icelandic MM samples. **(b)** (pages 3 and 4): meta-analysis P values for the Swedish-Norwegian samples and the Icelandic MM+MGUS samples.

Supplementary Figure 2



Quantile-quantile plots for the meta-analyses of the discovery sets: **(a)** Results obtained with the Swedish-Norwegian data and the Icelandic MM data; **(b)** Results obtained with the Swedish-Norwegian data and the Icelandic MM+MGUS data. A total of 12.1 million SNPs were used in the meta-analyses. Red: results for all SNPs. Blue: results after removing SNPs belonging to MM risk loci discovered in previous association studies (**Supplementary Fig. 1** and **Supplementary Table 1**). We observed minimal inflation of meta-analysis P values (genomic inflation factor λ=1.005 and 1.020 for the two meta-analyses, respectively).

Supplementary Figure 3



Blood concentrations of IgA, IgG and IgM values per genotype in 1,012 Swedish blood donors. These donors were genotyped previously for rs17085249, which is in tight linkage disequilibrium with the *ELL2* sentinel SNP rs56219066 (r^2=0.95). Boxes indicate medians and the first and third quartiles. Whiskers indicate first and third quartiles $\pm$ 1.5 times the interquartile range or the minimum/maximum values. Notches indicate confidence intervals around the median. Pearson correlation P values indicated.

Supplementary Table 1: Association results for known MM risk loci

Chr; Sentinel SNP	Candidate gene(s)	A1/A2[1]	Population	MM + MGUS			MM only			Prev. reported loci; LD values[2]
				RAF	Beta	*P*	RAF	Beta	*P*	
2p23.3 rs12986445	*DTNB, ASXL2*	A/T	Sweden/Norway	0.74	0.16	2.9×10^{-4}	0.74	0.16	2.9×10^{-4}	rs6746082; 0.08/0.005
			Iceland	0.75	0.199	5.1×10^{-3}	0.75	0.299	9.6×10^{-4}	
			Combined	**0.74**	**0.17**	$\mathbf{5.3 \times 10^{-6}}$	**0.74**	**0.18**	$\mathbf{2.6 \times 10^{-6}}$	
3p22.1 rs73071352	*ULK4*	A/G	Sweden/Norway	0.14	0.23	1.9×10^{-5}	0.14	0.23	1.9×10^{-5}	rs1052501; 1/0.81
			Iceland	0.12	0.30	3.4×10^{-4}	0.12	0.28	7.6×10^{-3}	
			Combined	**0.13**	**0.25**	$\mathbf{3.1 \times 10^{-8}}$	**0.14**	**0.24**	$\mathbf{5.2 \times 10^{-7}}$	
3q26.2 rs6793295	*MYNN, LRRC34*	T/C	Sweden/Norway	0.72	0.16	1.5×10^{-4}	0.72	0.16	1.5×10^{-4}	rs10936599; 1/0.92
			Iceland	0.78	0.18	1.6×10^{-2}	0.78	0.19	4.0×10^{-2}	
			Combined	**0.74**	**0.16**	$\mathbf{7.1 \times 10^{-6}}$	**0.73**	**0.165**	$\mathbf{1.7 \times 10^{-5}}$	
6p21.3 rs6919908	*PSORS1C2, HLA*	T/C	Sweden/Norway	0.21	0.26	1.2×10^{-8}	0.21	0.26	1.2×10^{-8}	rs2285803; 0.94/0.57
			Iceland	0.26	0.17	8.3×10^{-3}	0.26	0.22	8.2×10^{-3}	
			Combined	**0.23**	**0.23**	$\mathbf{6.3 \times 10^{-10}}$	**0.23**	**0.25**	$\mathbf{3.8 \times 10^{-10}}$	
7p15.3 rs57104699	*DNAH11, CDCA7L*	A/C	Sweden/Norway	0.66	0.19	1.4×10^{-6}	0.66	0.19	1.4×10^{-6}	rs4487645; 0.96/0.92
			Iceland	0.66	0.18	4.7×10^{-3}	0.66	0.22	7.3×10^{-3}	
			Combined	**0.66**	**0.19**	$\mathbf{2.3 \times 10^{-8}}$	**0.66**	**0.20**	$\mathbf{3.5 \times 10^{-8}}$	
11q13 rs9344	*CCND1*	A/G	Sweden/Norway	0.53	0.147	1.7×10^{-4}	0.53	0.147	1.7×10^{-4}	rs603965; N/A
			Iceland	0.53	0.105	7.8×10^{-2}	0.53	0.078	3.0×10^{-1}	
			Combined	**0.53**	**0.135**	$\mathbf{3.8 \times 10^{-5}}$	**0.53**	0.132	$\mathbf{1.3} \times 10^{-4}$	
17p11.2 rs57968458	*TNFRSF13B*	A/G	Sweden/Norway	0.10	0.35	1.2×10^{-8}	0.10	0.35	1.2×10^{-8}	rs4273077; 0.85/0.39
			Iceland	0.08	0.28	5.6×10^{-3}	0.08	0.40	1.2×10^{-3}	
			Combined	**0.098**	**0.33**	$\mathbf{2.8 \times 10^{-10}}$	**0.098**	**0.36**	$\mathbf{5.7 \times 10^{-11}}$	
22q13.1 rs34101942	*CBX7*	G–/GA	Sweden/Norway	0.62	0.17	2.2×10^{-5}	0.62	0.17	2.2×10^{-5}	rs877529; N/A
			Iceland	0.62	0.10	1.0×10^{-1}	0.62	0.23	2.7×10^{-3}	
			Combined	**0.62**	**0.15**	$\mathbf{8.6 \times 10^{-6}}$	**0.62**	**0.18**	$\mathbf{2.8 \times 10^{-7}}$	

[1]Risk alleles underlined; [2]LD values are represented as D'/r^2 values between sentinel SNPs from this study and the previously reported loci. Abbreviations: RAF, risk allele frequency. Logistic regression and meta-analysis *P* values indicated.

Supplementary Table 2. Novel loci associating with MM or MM+MGUS at $P<5\times10^{-8}$

Populations	EAF	MM		MM+MGUS	
		OR (95%CI)	P value	OR (95%CI)	P value
ELL2 - rs56219066-T					
Sweden/Norway	0.732	1.20 (1.11-1.32)	3.8×10^{-5}	1.20 (1.11-1.32)	3.8×10^{-5}
Iceland	0.711	1.39 (1.17-1.64)	1.1×10^{-4}	1.32 (1.15-1.51)	3.9×10^{-5}
Combined		**1.23 (1.14-1.33)**	**6.5×10^{-8}**	**1.23 (1.15-1.33)**	**1.4×10^{-8}**
TOM1 – rs138740-C					
Sweden/Norway	0.364	1.20 (1.11–1.30)	2.4×10^{-6}	1.20 (1.11–1.30)	2.4×10^{-6}
Iceland	0.415	1.26 (1.09-1.46)	0.0017	1.15 (1.03-1.30)	0.015
Combined		**1.22 (1.13-1.30)**	**1.7×10^{-8}**	**1.19 (1.11-1.27)**	**1.3×10^{-7}**
ARHGAP26 – rs74735889-T					
Sweden/Norway	0.003	4.41 (2.53-7.67)	1.6×10^{-7}	4.41 (2.53-7.67)	1.6×10^{-7}
Iceland	0.002	2.33 (0.79-6.87)	0.12	3.51 (0.79-6.87)	8.4×10^{-4}
Combined		**3.85 (2.35-6.30)†**	**8.2×10^{-8}†**	**4.06 (2.61-6.33)†**	**5.9×10^{-10}†**

Association results for *ELL2* rs56219066, *TOM1* rs138740, and ARHGAP rs74735889 in the meta-analyses of the Swedish-Norwegian and Icelandic discovery samples. †By direct genotyping of the Swedish case and control samples the signal at 5q31 was no longer significant (OR=1.69; *P*=0.014). Abbreviations: EAF, effect allele frequency; OR, odds ratio. Logistic regression and meta-analysis P values indicated.