

Supplementary Table 1

Association data for MM risk variants identified in previous, major genome-wide association studies.
 RAF: risk allele frequency, extracted from Ensembl (1000 genomes Phase 3, EUR). *major alleles underlined

Candidate gene	locus	rsID	Risk allele*	RAF	Discovery study				Present study					
					Ref.	OR	P - value	Sweden freq	Iceland freq	Denmark freq	Norway freq	OR	P - value	P - het
<i>DTNB</i>	2p23.3	rs6746082	<u>A</u>	0.48	Broderik <i>et al.</i>	1.29	1.22x10 ⁻⁷	0.76	0.76	0.77	0.75	1.19	1.62x10 ⁻¹⁰	0.42
<i>SP3</i>	2q31.1	rs4325816	<u>T</u>	0.77	Went <i>et al.</i>	1.12	7.37x10 ⁻⁹	0.78	0.77	0.77	0.76	1.08	5.16x10 ⁻³	0.39
<i>ULK4</i>	3p22.1	rs1052501	C	0.19	Broderik <i>et al.</i>	1.32	7.47x10 ⁻⁹	0.16	0.14	0.15	0.16	1.20	4.34x10 ⁻⁹	0.26
<i>ACTRT3, MYNN, LRRC34</i>	3q26.2	rs10936599	<u>C</u>	0.76	Chubb <i>et al.</i>	1.26	8.7x10 ⁻¹⁴	0.74	0.79	0.74	0.74	1.16	3.14x10 ⁻⁸	0.65
<i>ELL2</i>	5q15	rs56219066	<u>T</u>	0.72	Swaminathan <i>et al.</i>	1.25	9.6x10 ⁻¹⁰	0.74	0.71	0.75	0.74	1.15	3.80x10 ⁻⁸	0.43
<i>CEP120</i>	5q23.2	rs6595443	T	0.45	Went <i>et al.</i>	1.11	1.20x10 ⁻⁸	0.43	0.43	0.42	0.43	1.08	1.37x10 ⁻³	0.85
<i>JARID2</i>	6p22.3	rs34229995	G	0.02	Mitchell <i>et al.</i>	1.37	1.31x10 ⁻⁸	0.03	0.03	0.02	0.03	1.30	2.74x10 ⁻⁵	0.57
<i>PSORS1C2</i>	6p21.3	rs2285803	T	0.26	Chubb <i>et al.</i>	1.19	9.67x10 ⁻¹¹	0.31	0.35	0.30	0.30	1.17	1.37x10 ⁻¹¹	0.13
<i>ATG5</i>	6q21	rs9372120	G	0.19	Mitchell <i>et al.</i>	1.18	9.09x10 ⁻¹⁵	0.22	0.20	0.21	0.22	1.14	1.80x10 ⁻⁶	0.88
<i>CDCA7L</i>	7p15.3	rs4487645	<u>C</u>	0.66	Broderik <i>et al.</i>	1.38	3.33x10 ⁻¹⁵	0.66	1.00	0.67	0.66	1.26	5.20x10 ⁻¹⁵	0.21
<i>AC004917.1, CDC71L</i>	7q22.3	rs17507636	<u>C</u>	0.74	Went <i>et al.</i>	1.12	9.20x10 ⁻⁹	0.76	0.74	0.74	0.75	1.12	2.73x10 ⁻⁵	0.25
<i>POT1, RP11-3B12.1</i>	7q31.33	rs58618031	<u>T</u>	0.73	Went <i>et al.</i>	1.12	2.73x10 ⁻⁸	0.72	0.76	0.72	0.73	1.06	2.02x10 ⁻²	0.68
<i>SMARCD3</i>	7q36.1	rs7781265	A	0.09	Mitchell <i>et al.</i>	1.19	9.79x10 ⁻⁹	0.12	0.15	0.12	0.13	1.22	3.27x10 ⁻¹⁰	0.81
<i>CCAT1</i>	8q24.21	rs1948915	C	0.33	Mitchell <i>et al.</i>	1.13	4.20x10 ⁻¹¹	0.37	0.34	0.36	0.34	1.09	2.20x10 ⁻⁴	0.056
<i>CDKN2A</i>	9p21.3	rs2811710	<u>C</u>	0.64	Mitchell <i>et al.</i>	1.15	1.72x10 ⁻¹³	0.66	0.62	0.65	0.65	1.10	2.19x10 ⁻⁵	0.023
<i>WAC</i>	10p12.1	rs2790457	<u>G</u>	0.74	Mitchell <i>et al.</i>	1.12	1.77x10 ⁻⁸	0.73	0.71	0.73	0.72	1.11	6.64x10 ⁻⁵	0.15
<i>CCND1</i>	11q13.3	rs603965 (rs9344)	<u>G</u>	0.50	Weinhold <i>et al.</i>	1.82	2.92x10 ⁻¹⁰	0.52	0.53	0.54	0.55	1.08	7.30x10 ⁻⁴	0.29
<i>PRR14, SRCAP, RP11-146F11.1</i>	16p11.2	rs13338946	C	0.28	Went <i>et al.</i>	1.15	1.02x10 ⁻¹³	0.27	0.27	0.27	0.25	1.12	6.39x10 ⁻⁶	0.56
<i>RFWD3</i>	16q23.1	rs7193541	<u>T</u>	0.61	Mitchell <i>et al.</i>	1.13	5.00x10 ⁻¹²	0.58	0.58	0.58	0.59	1.06	9.44x10 ⁻³	0.65
<i>TNFRSF13B</i>	17p11.2	rs4273077	G	0.10	Chubb <i>et al.</i>	1.26	7.67x10 ⁻⁹	0.11	0.08	0.10	0.10	1.32	3.33x10 ⁻¹⁴	0.44
<i>KLF2</i>	19p13.11	rs11086029	T	0.23	Went <i>et al.</i>	1.14	6.79x10 ⁻¹¹	0.22	0.25	0.24	0.25	1.05	4.70x10 ⁻²	0.88
<i>PREX1</i>	20q13.13	rs6066835	C	0.09	Mitchell <i>et al.</i>	1.26	1.36x10 ⁻¹³	0.08	0.10	0.08	0.09	1.20	1.55x10 ⁻⁶	0.024
<i>HMGXB4, TOM1</i>	22q13.1	rs138740	C	0.34	Swaminathan <i>et al.</i>	1.18	5.7x10 ⁻⁸	0.37	0.42	0.37	0.38	1.08	6.37x10 ⁻⁴	0.8
<i>CBX7</i>	22q13.1	rs877529	A	0.44	Chubb <i>et al.</i>	1.23	7.63x10 ⁻¹⁶	0.46	0.45	0.44	0.47	1.15	1.12x10 ⁻⁹	0.3

Broderick P *et al.* Common variation at 3p22.1 and 7p15.3 influences multiple myeloma risk. *Nat Genet.* 2012;44(1):58–61.

Chubb D *et al.* Common variation at 3q26.2, 6p21.33, 17p11.2 and 22q13.1 influences multiple myeloma risk. *Nat Genet.* 2013;45(10):1221–5.

Mitchell JS *et al.* Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. *Nat Commun.* 2016;7(May).

Swaminathan B *et al.* Variants in ELL2 influencing immunoglobulin levels associate with multiple myeloma. *Nat Commun.* 2015;6(May):1–8.

Weinhold N *et al.* The CCND1 c.870G>A polymorphism is a risk factor for t(11;14)(q13;q32) multiple myeloma. *Nat Genet.* 2013;45(5):522–5.

Went M *et al.* Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. *Nat Commun.* 2018;9(1):1–10.