Genetic factors underlying the risk of bortezomib induced peripheral neuropathy in multiple myeloma patients

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Online Supplementary Table S1. Demographic and clinical characteristics of MM cases and controls restricted to bortezomib treated patients in the IFM 2005-01 trial.

	Discovery set IFM 2005-01 Included in SNP analyses (n=238)		Validation set HOVON-65/GMMG-HD4 Not included in SNP analyses (n=229)		Included in SNP analyses (n=183)		*P* value	Czech Republic dataset Included in SNP analyses (n=48)	
Age									
Median (years)	57		57		57		0.62	nd	
Range (years)	35-68		31-65		32-65			nd	
Sex	n.		n.		n.			n.	
M	132	61%	144	63%	109	60%	0.54	27	56%
F	85	39%	85	37%	74	40%		17	35%
nd								4	8%
ISS			90	39%	82	45%	0.25	22	46%
I	nd		73	32%	46	25%		7	15%
II	nd		48	21%	32	17%		7	15%
III	nd		18	8%	23	13%		12	25%
nd	nd								
M protein heavy chain									
IgA	59	25%	54	24%	35	19%	0.45	12	25%
IgG	129	54%	130	57%	119	65%		29	60%
IgD	6	3%	4	2%	2	1%		0	0%
LCD	0	0%	36	16%	24	13%		3	6%
nd	44	18%	5	2%	3	2%		4	8%
M protein light chain									
Kappa	148	62%	148	65%	122	67%	0.78	27	56%
Lambda	71	30%	76	33%	59	32%		17	35%
nd	19	8%	5	2%	2	1%		4	8%
BiPN grade									
0	139	58%	122	53%	80	44%	0.36	20	42%
1	27	11%	54	24%	52	28%		10	21%
2	57	24%	29	13%	26	14%		13	27%
3	11	5%	16	7%	19	10%		5	10%
4	4	2%	8	3%	6	3%		0	0%

LCD indicates light chain disease; ISS: International Staging System; BiPN: bortezomib induced peripheral neuropathy; nd: not determined.

Online Supplementary Table S2. Power analysis (c2 test) in the discovery set. Indicated are the lowest possible OR to detect (upper;lower) at several levels of *P* and MAF. Number of alleles: 476; number of SNPs: 2,149.

MAF	0.1	0.2	0.3	0.4	0.5
OR (*P*=0.01)	8.57;0.12	3.67;0.27	2.83;0.35	2.54;0.39	2.45;0.41
OR (*P*=0.05)	8.59;0.12	3.23;0.31	2.58;0.39	2.36;0.42	2.28;0.44
OR (*P*=0.10)	7.28;0.14	3.07;0.33	2.48;0.40	2.28;0.44	2.21;0.45
OR (*P*=0.25)	6.00;0.17	2.86;0.35	2.35;0.43	2.18;0.46	2.12;0.47

OR: Odds Ratio; MAF: minor allele frequency.

Online Supplementary Table S3. Power analysis (one-sided test for ORs) in the validation set. Indicated are the lowest possible OR to detect (upper;lower) at several levels of *P* and MAF. Number of alleles: 462; number of SNPs: 51.

MAF	0.1	0.2	0.3	0.4	0.5
OR (*P*=0.01)	3.49;0.29	2.41;0.42	2.12;0.47	2.02;0.50	2.00;0.50
OR (*P*=0.05)	2.93;0.34	2.15;0.47	1.92;0.52	1.85;0.54	1.84;0.55
OR (*P*=0.10)	2.66;0.38	2.03;0.49	1.84;0.54	1.77;0.56	1.75;0.57
OR (*P*=0.25)	2.40;0.42	1.88;0.53	1.73;0.58	1.67;0.60	1.66;0.60

OR: Odds Ratio; MAF: minor allele frequency.

Online Supplementary Table S4. Incidence of peripheral neuropathy shown *per* grade in the HOVON-65/GMMG-HD4 VAD treatment arm.

	HOVON-65/GMMG-HD4 VAD treatment arm	
Peripheral neuropathy grade	n.	
0	254	61.6%
1	115	27.9%
2	31	7.5%
3	11	2.7%
4	1	0.2%

VAD indicates vincristine, adriamycin and dexamethasone.

Online Supplementary Table S5. SNPs associated with BiPN (pointwise $P<0.05$) in the validation set (HOVON-65/GMMG-HD4 and Czech Republic dataset) using a Cochran Mantel-Haenszel stratified association analysis. The genomic inflation factor λ is 1.0

SNP	Chr	Alleles	OR	95% CI	Pointwise *P* value for Cochran Mantel-Haenszel	Permutated *P* for Cochran Mantel-Haenszel	Gene	SNP type
rs13321	9	C > G	1,98	1,28 - 3,04	0,002	0.9191	*TNC*	Coding-nonsynonymous
rs3218634	3	C > G	3,26	1,39 - 7,60	0,003	0.9957	*POLQ*	Coding-nonsynonymous
rs2252784	12	G > A	0,59	0,41 - 0,86	0,003	0.9998	*PTPRB*	Coding-nonsynonymous
rs7071882	10	G > T	0,51	0,32 - 0,79	0,004	0.9659	*MBL2*	Intron
rs2280509	2	C > T	0,53	0,33 - 0,85	0,005	1	*FZD7*	Locus
rs2229113	11	G > A	1,71	1,16 - 2,52	0,006	1	*IL10RA*	Coding-nonsynonymous
rs6131	1	G > A	0,55	0,36 - 0,84	0,006	0.9998	*SELP*	Coding-nonsynonymous
rs11546842	15	C > T	4,33	1,47 - 12,78	0,007	0.9955	*POLG*	Coding-nonsynonymous
rs7096206	10	C > G	1,83	1,14 - 2,92	0,007	1	*MBL2*	Locus
rs1540339	12	G > A	0,61	0,42 - 0,90	0,007	1	*VDR*	Intron
rs11003127	10	G > C	0,53	0,34 - 0,83	0,008	0.9987	*MBL2*	Intron
rs2165810	10	T > A	0,55	0,36 - 0,86	0,009	1	*MBL2*	Intron
rs1024611	17	T > C	1,83	1,17 - 2,87	0,009	1	*CCL2*	Promoter
rs2238476	16	C > T	3,04	1,21 - 7,64	0,009	1	*ABCC1*	Intron,TagSNP:*ABCC1*
rs9954562	18	C > T	0,61	0,42 - 0,89	0,010	1	*NFATC1*	Promoter
rs1799801	16	T > C	1,73	1,15 - 2,61	0,011	1	*ERCC4*	Coding-synonymous
rs3136027	17	A > T	2,27	1,16 - 4,45	0,012	1	*LIG3*	Intron
rs246218	16	C > T	0,50	0,29 - 0,88	0,012	1	*ABCC1*	Intron,TagSNP:*ABCC1*
rs4151060	10	G > T	0,34	0,14 - 0,80	0,014	1	*BTRC*	Coding-nonsynonymous
rs1132054	19	T > C	0,65	0,45 - 0,94	0,014	1	*SULT2B1*	Coding-synonymous
rs799917	17	C > T	0,63	0,43 - 0,92	0,014	1	*BRCA1*	Coding-nonsynonymous
rs2239704	6	G > T	0,63	0,43 - 0,91	0,014	1	*LTA*	Untranslated
rs588701	11	G > A	0,61	0,41 - 0,91	0,015	1	*MRE11A*	Intron,TagSNP:*MRE11A*
rs993568	1	A > G	0,64	0,44 - 0,93	0,016	1	*DPYD*	Intron,TagSNP:*DPYD*
rs3739942	9	A > G	1,75	1,11 - 2,77	0,016	1	*KIAA1984*	Promoter
rs246220	16	C > G	0,49	0,27 - 0,89	0,016	1	*ABCC1*	Intron,TagSNP:*ABCC1*
rs9436299	1	A > C	1,70	1,14 - 2,55	0,017	1	*LEPR*	Intron
rs2976436	8	C > T	0,62	0,43 - 0,92	0,017	1	*NEFL*	Promoter
rs939336	3	G > A	1,60	1,09 - 2,34	0,017	1	*ABCC5*	Coding-synonymous
rs932477	6	G > A	2,15	1,14 - 4,04	0,019	1	*ESR1*	Intron
rs1799799	16	T > C	1,65	1,11 - 2,46	0,019	1	*ERCC4*	Intron
rs246217	16	C > A	0,49	0,27 - 0,89	0,019	1	*ABCC1*	Intron,TagSNP:*ABCC1*
rs1799949	17	C > T	0,62	0,42 - 0,93	0,019	1	*BRCA1*	Coding-synonymous,Untranslated,Intron
rs8058696	16	C > G	1,55	1,06 - 2,26	0,020	1	*ABCC6*	Coding-synonymous
rs2260863	1	C > G	0,61	0,42 - 0,91	0,021	1	*EPHX1*	Intron
rs1800797	7	G > A	0,63	0,43 - 0,92	0,021	1	*IL6*	Locus
rs1399291	1	C > T	0,65	0,45 - 0,95	0,021	1	*DPYD*	Intron,TagSNP:*DPYD*
rs2056048	1	A > C	0,66	0,45 - 0,95	0,021	1	*DPYD*	Intron,TagSNP:*DPYD*
rs310831	12	A > T	2,04	1,08 - 3,84	0,023	1	*E2F7*	Coding-nonsynonymous
rs1799800	16	G > A	1,69	1,10 - 2,60	0,023	1	*ERCC4*	Intron
rs1946519	11	C > A	1,48	1,01 - 2,16	0,024	1	*IL18*	Locus
rs1042713	5	G > A	1,54	1,06 - 2,25	0,025	1	*ADRB2*	Coding-nonsynonymous
rs1501299	3	C > A	1,65	1,08 - 2,52	0,026	1	*ADIPOQ*	Intron
rs1760217	1	T > C	0,62	0,39 - 0,97	0,027	1	*DPYD*	Intron,TagSNP:*DPYD*
rs35620	16	C > G	1,87	1,06 - 3,28	0,028	1	*ABCC1*	Intron,TagSNP:*ABCC1*
rs3778082	6	G > A	1,86	1,09 - 3,20	0,029	1	*ESR1*	Intron
rs11574750	2	C > T	0,39	0,16 - 0,94	0,029	1	*IL8RB*	Coding-synonymous
rs1946518	11	G > T	1,45	0,99 - 2,11	0,029	1	*IL18*	Locus
rs3749442	3	C > T	0,58	0,35 - 0,94	0,029	1	*ABCC5*	Coding-synonymous
rs2976437	8	A > G	0,66	0,45 - 0,96	0,030	1	*NEFL*	Promoter
rs4252596	17	C > A	1,79	1,03 - 3,11	0,030	1	*ERBB2*	Intron
rs2384937	16	T > C	1,79	1,05 - 3,05	0,031	1	*ABCC1*	Intron,TagSNP:*ABCC1*
rs3793345	7	T > C	1,66	1,04 - 2,66	0,032	1	*IGFBP3*	Intron
rs7731453	5	C > A	0,54	0,30 - 0,97	0,032	1	*HMMR*	Coding-nonsynonymous
rs1413228	1	A > G	2,03	1,08 - 3,81	0,032	1	*DPYD*	Intron,TagSNP:*DPYD*
rs529948	6	G > A	1,94	1,03 - 3,67	0,032	1	*NFKBIE*	Promoter
rs1051740	1	T > C	1,59	1,05 - 2,41	0,033	1	*EPHX1*	Coding-nonsynonymous
rs5742714	12	G > C	2,10	1,05 - 4,20	0,034	1	*IGF1*	Untranslated
rs532411	3	C > T	2,13	1,04 - 4,36	0,035	1	*POLQ*	Coding-nonsynonymous
rs7805658	7	G > A	0,66	0,45 - 0,96	0,035	1	*SHFM1*	Intron,TagSNP:*DSS1*
rs2274578	6	G > C	0,66	0,46 - 0,96	0,035	1	*BYSL*	Locus,Untranslated
rs1364283	16	A > C	1,48	1,02 - 2,14	0,036	1	*HSD17B2*	3' UTR
rs7172	1	A > G	0,60	0,38 - 0,97	0,036	1	*PSMB4*	Coding-synonymous
rs16941	17	A > G	0,65	0,44 - 0,96	0,037	1	*BRCA1*	Coding-nonsynonymous
rs1132776	3	C > T	1,52	1,04 - 2,21	0,037	1	*ABCC5*	Coding-synonymous
rs1137101	1	G > A	0,67	0,46 - 0,97	0,038	1	*LEPR*	Coding-nonsynonymous
rs593818	19	G > A	0,69	0,47 - 1,00	0,038	1	*CYP4F12*	Coding-nonsynonymous
rs2214102	7	G > A	0,47	0,23 - 0,97	0,039	1	*ABCB1*	Untranslated
rs4148553	13	G > A	0,67	0,46 - 0,97	0,040	1	*ABCC4*	Untranslated
rs35604	16	A > G	1,77	1,02 - 3,08	0,040	1	*ABCC1*	Intron,TagSNP:*ABCC1*
rs1045105	1	C > A	1,70	0,98 - 2,94	0,042	1	*CNKSR1*	Coding-nonsynonymous
rs730566	3	G > T	1,48	0,97 - 2,26	0,042	1	*TREX1*	Locus
rs523349	2	C > G	0,67	0,45 - 1,00	0,042	1	*SRD5A2*	Intron
rs3131637	6	A > T	0,70	0,48 - 1,02	0,042	1	*LTA*	Locus
rs2274407	13	C > A	2,18	0,99 - 4,80	0,043	1	*ABCC4*	Coding-nonsynonymous
rs1822017	3	C > T	1,68	1,03 - 2,74	0,043	1	*DCBLD2*	Coding-synonymous
rs7242	7	T > G	1,46	1,00 - 2,13	0,044	1	*SERPINE1*	Untranslated
rs3130618	6	C > A	0,56	0,32 - 0,99	0,044	1	*BAT4*	Coding-nonsynonymous
rs6033	1	A > G	0,42	0,20 - 0,91	0,044	1	*F5*	Coding-nonsynonymous
rs8192707	20	A > G	1,73	1,02 - 2,92	0,044	1	*PLCG1*	Coding-nonsynonymous
rs540199	11	A > G	0,67	0,46 - 0,99	0,045	1	*MRE11A*	Intron,TagSNP:*MRE11A*
rs619824	10	G > T	0,70	0,48 - 1,01	0,045	1	*CYP17A1*	3' UTR
rs10079641	5	C > G	0,53	0,29 - 0,98	0,046	1	*MSH3*	Intron
rs2470893	15	G > A	1,54	1,02 - 2,31	0,048	1	*CYP1A1*	Locus
rs1060915	17	T > C	0,68	0,46 - 1,01	0,049	1	*BRCA1*	Coding-synonymous,Untranslated
rs769412	12	A > G	0,45	0,20 - 1,03	0,049	1	*MDM2*	Coding-synonymous
rs2295275	6	T > A	2,40	1,00 - 5,75	0,050	1	*TRERF1*	Coding-nonsynonymous

SNP: single nucleotide polymorphism; Chr: chromosome; OR: odds ratio; CI: confidence interval.

Online Supplementary Table S6. Cross validation of significantly associated SNPs in the IFM 2005-01 discovery set. A Cochran χ^2 test and a Mantel-Haenszel stratified association test were used to analyze SNP associations in the discovery set (IFM 2005-01) and the validation set (HOVON-65/GMMG-HD4 and Czech Republic samples), respectively. A one-sided test for ORs was performed to investigate cross validation of significant SNPs (pointwise $P<0.05$) in the discovery set.

							One-sided test for ORs		IFM 2005-01 discovery set			
SNP	Chr	Alleles			Gene	SNP type	OR	Unadjusted *P* value validation set	Adjusted *P* value validation set	OR	95% CI	Pointwise *P* for χ^2
rs619824	10	G	>	T	*CYP17A1*	3' UTR	0.7	0.03	0.82	0.64	0.44 - 0.93	0.01
rs2857605	6	A	>	G	*TNF*	Intron,TagSNP:TNF	0.69	0.05	0.82	0.57	0.36 - 0.92	0.03
rs6945306	7	G	>	C	*STK31*	Coding-nonsynonymous	1.33	0.08	0.82	1.71	1.17 - 2.52	0.01
rs10759326	9	T	>	G	*IKBKAP*	Coding-synonymous	1.32	0.13	0.82	1.57	0.99 - 2.48	0.05
rs2472299	15	G	>	A	*CYP1A1*	Promoter	0.8	0.13	0.82	0.62	0.42 - 0.92	0.02
rs3136516	11	A	>	G	*F2*	Intron	0.82	0.14	0.82	0.61	0.42 - 0.88	0.01
rs2074351	7	G	>	A	*PON1*	Intron,TagSNP:PON1	1.22	0.18	0.82	1.51	1.01 - 2.26	0.05
rs762551	15	A	>	C	*CYP1A2*	Intron,TagSNP:CYP1A_cluster	0.83	0.18	0.82	0.63	0.42 - 0.93	0.03
rs1149901	10	C	>	T	*GATA3*	Locus,untranslated	1.2	0.2	0.82	1.62	1.07 - 2.45	0.02
rs2124459	21	T	>	C	*CBS*	Intron	0.85	0.21	0.82	0.66	0.45 - 0.96	0.05
rs1052637	2	G	>	C	*DDX18*	Coding-nonsynonymous	0.85	0.21	0.82	0.66	0.45 - 0.97	0.03
rs854556	7	C	>	T	*PON1*	Intron,TagSNP:PON1	0.85	0.21	0.82	0.64	0.44 - 0.95	0.03
rs2227956	6	T	>	C	*HSPA1L*	Coding-nonsynonymous	0.84	0.22	0.82	0.52	0.3 - 0.88	0.02
rs3733890	5	G	>	A	*BHMT*	Coding-nonsynonymous	0.86	0.23	0.82	0.66	0.45 - 0.98	0.04
rs1296028	8	A	>	G	*FDFT1*	3' UTR	0.86	0.24	0.82	0.64	0.42 - 0.99	0.05
rs2228233	14	C	>	T	*NFATC4*	Coding-synonymous	0.9	0.31	0.82	0.65	0.43 - 0.98	0.05
rs3758581	10	G	>	A	*CYP2C19*	Coding-nonsynonymous	1.19	0.31	0.82	2.35	1.12 - 4.97	0.05
rs854555	7	C	>	A	*PON1*	Intron,TagSNP:PON1	1.1	0.31	0.82	1.53	1.05 - 2.24	0.03
rs9640663	7	A	>	G	*PTPN12*	Coding-nonsynonymous	0.91	0.32	0.82	0.67	0.46 - 0.98	0.04
rs121	7	A	>	G	*OSBPL3*	Intron,TAG	1.08	0.34	0.82	1.61	1.11 - 2.32	0.01
rs2239330	16	C	>	T	*ABCC1*	Coding-synonymous	0.92	0.35	0.82	0.59	0.39 - 0.9	0.01
rs878201	1	G	>	A	-	Intergenic	1.07	0.37	0.82	1.54	1.04 - 2.29	0.02
rs2007231	1	T	>	C	*NRAS*	Intron	0.94	0.37	0.82	0.66	0.44 - 0.97	0.04
rs3759217	12	C	>	T	*CDKN1B*	Locus	1.08	0.39	0.83	2.76	1.58 - 4.84	< 0.001
rs440454	6	C	>	T	*RDBP*	Locus,Intron	0.95	0.41	0.83	0.62	0.39 - 0.97	0.03
rs3212254	14	C	>	A	*PARP1*	Intron	1.04	0.46	0.83	2.12	1.04 - 4.31	0.04
rs2686184	8	G	>	A	*BLM*	Intron	1.01	0.48	0.83	1.72	1.19 - 2.49	0.01
rs6768093	3	T	>	A	*ATR*	Locus	0.99	0.49	0.83	0.66	0.45 - 0.96	0.04
rs7169	1	T	>	C	*SLCO1A2*	Untranslated,intron	1	0.5	0.83	1.65	1.14 - 2.39	0.01
rs584589	17	A	>	G	*UGT2B7*	Locus	1	0.51	0.83	2.01	1.16 - 3.47	0.01
rs3776432	5	G	>	A	*PROCR*	Coding-nonsynonymous	0.99	0.51	0.83	1.52	1.04 - 2.24	0.03
rs1641536	17	G	>	A	*SHBG*	3' UTR	1.01	0.52	0.83	0.43	0.22 - 0.86	0.02
rs2033178	12	C	>	T	*IGF1*	Intron	0.93	0.58	0.90	2.42	1.23 - 4.74	0.01
rs4148949	10	C	>	T	*CHST3*	Untranslated	1.05	0.61	0.92	0.6	0.41 - 0.88	0.01
rs1002153	1	T	>	C	*PARP1*	Intron	1.1	0.65	0.94	0.56	0.33 - 0.95	0.03
rs1805405	1	C	>	A	*PARP1*	Intron	1.11	0.66	0.94	0.56	0.33 - 0.95	0.03
rs2231142	4	C	>	A	*ABCG2*	Coding-nonsynonymous	0.83	0.71	0.95	2.12	1.04 - 4.31	0.04
rs11466155	17	C	>	T	*NGFR*	Coding-synonymous	0.89	0.71	0.95	1.87	1.25 - 2.8	0
rs4799055	18	G	>	T	*NFATC1*	Intron	0.87	0.77	0.98	1.61	1.1 - 2.35	0.03
rs228851	20	G	>	T	*NFATC2*	Intron	1.16	0.79	0.98	0.59	0.41 - 0.86	0.01
rs1050152	5	C	>	T	*SLC22A4*	Coding-nonsynonymous	1.18	0.81	0.98	0.68	0.47 - 0.99	0.04
rs9885672	6	T	>	C	*KIAA0274*	Coding-nonsynonymous	0.78	0.82	0.98	1.86	1.08 - 3.21	0.02
rs1801105	2	C	>	T	*HNMT*	Coding-nonsynonymous	0.74	0.85	0.98	1.95	1.06 - 3.6	0.04
rs2228088	6	G	>	T	*TNF*	Coding-synonymous, TagSNP:TNF	1.43	0.87	0.98	0.56	0.36 - 0.87	0.01
rs3817074	19	C	>	T	*BAX*	Intron	0.67	0.9	0.98	1.95	1.06 - 3.6	0.03
rs1405655	19	T	>	C	*NR1H2*	Intron	0.76	0.92	0.98	1.56	1.05 - 2.32	0.04

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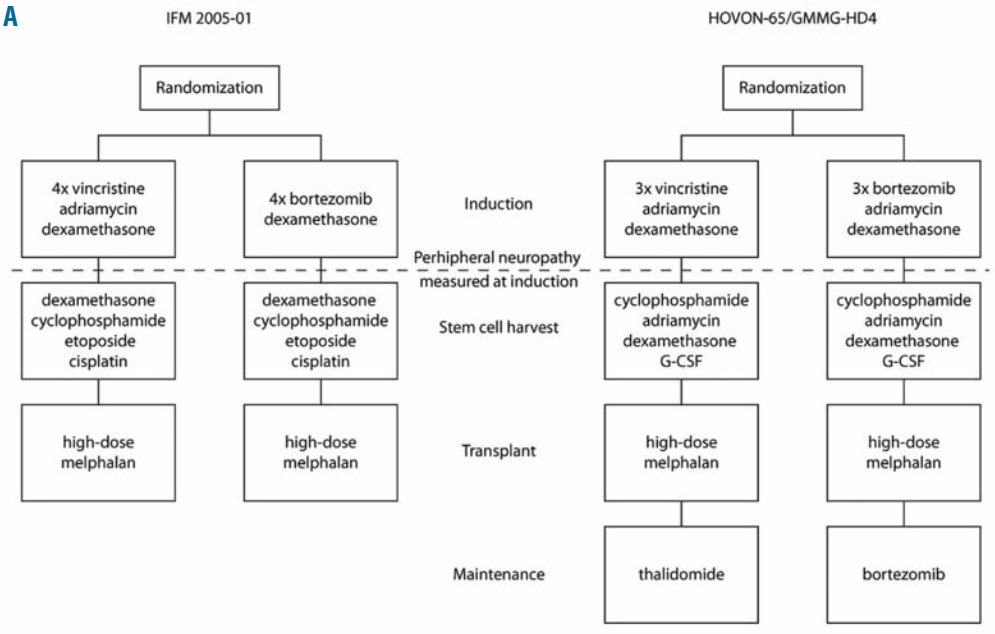
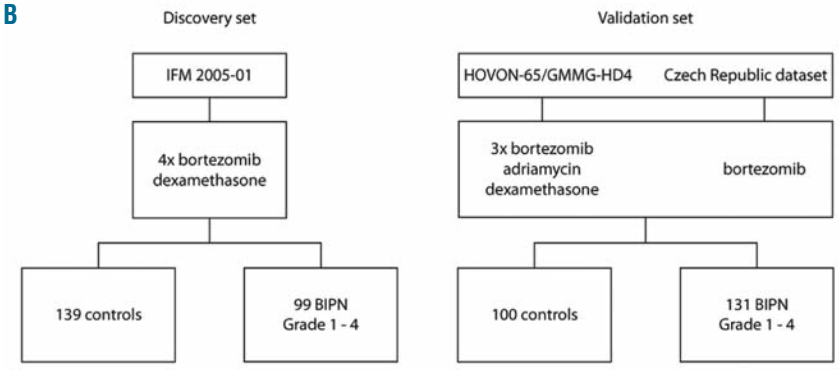
rs2973015	5	A	>	G	*GHR*	Intron	1.34	0.94	0.98	0.63	0.44 - 0.91	0.02
rs504122	13	C	>	T	*HNMT*	Intron,TagSNP:HNMT	1.34	0.94	0.98	0.63	0.43 - 0.93	0.02
rs163078	2	C	>	T	*CYP1B1*	Intron,TagSNP:CYP1B1	1.38	0.94	0.98	0.63	0.43 - 0.92	0.03
rs2976437	8	A	>	G	*NEFL*	Promoter	0.66	0.99	0.99	1.63	1.13 - 2.37	0.01
rs6033	1	A	>	G	*F5*	Coding-nonsynonymous	0.42	0.99	0.99	2.53	1.3 - 4.94	0.01

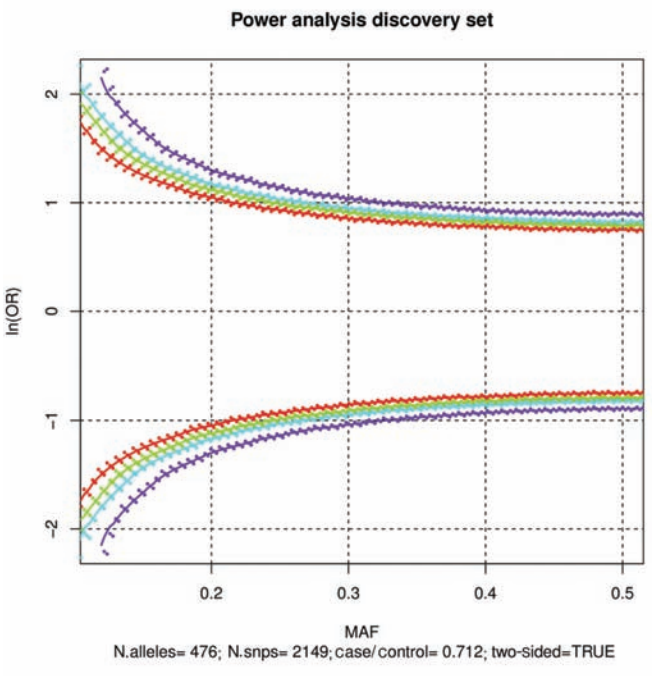
SNP: single nucleotide polymorphism; Chr: chromosome; OR: Odds Ratio; CI: confidence interval; N/A: not applicable.

Online Supplementary Figure S1. Schematic representation of MM patient treatment and numbers. (A) Schematic representation of IFM 2005-01 and HOVON-65/GMMG-HD4 treatment. (B) BiPN case and control comparisons used in SNP analysis for discovery and validation set. GCSF indicates granulocyte colony-stimulating factor.

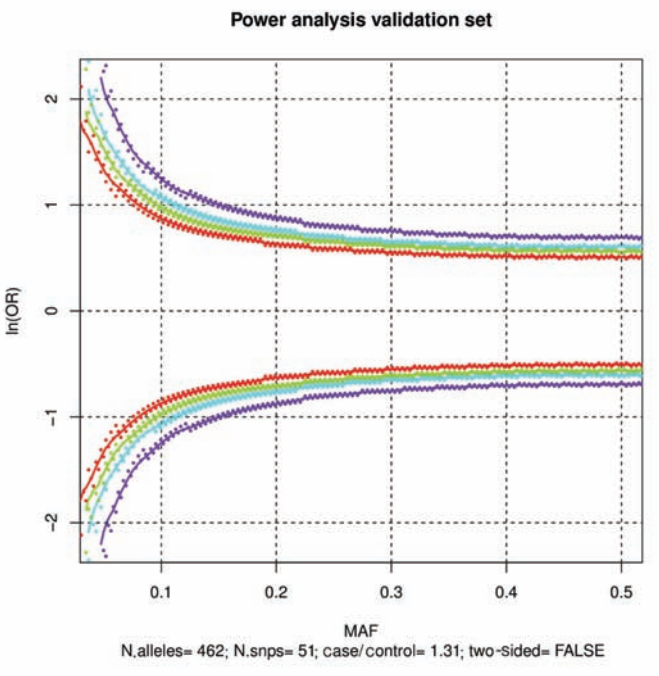




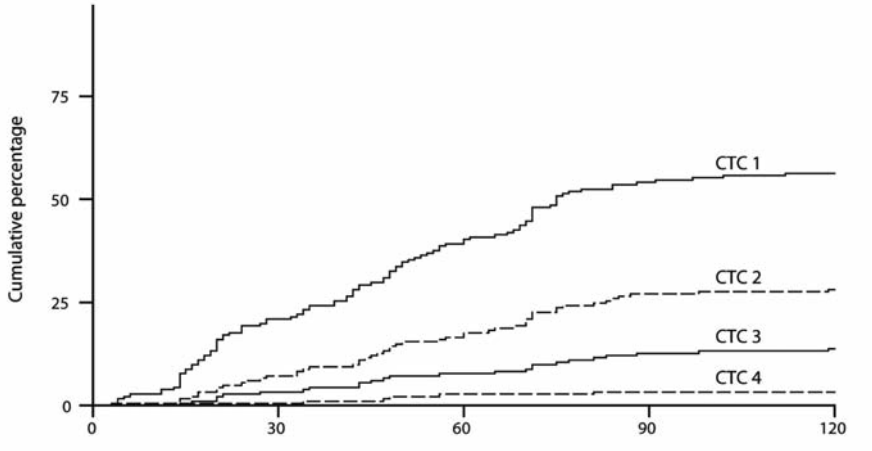
Online Supplementary Figure S2. Power analysis in the discovery set. At several *P* levels; dark blue: *P*=0.01; light blue: *P*=0.05; green: *P*=0.1; red: *P*=0.25.



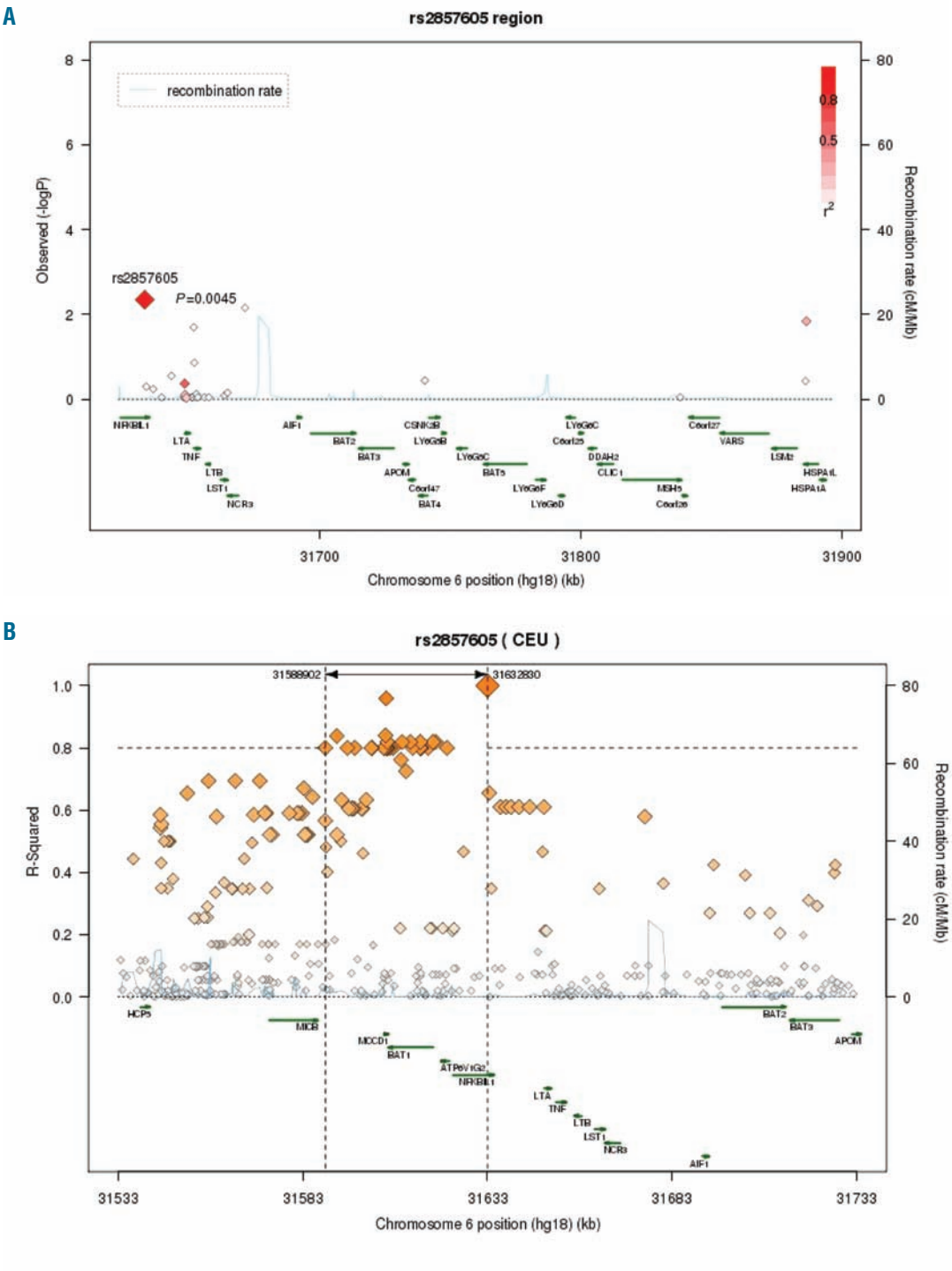
Online Supplementary Figure S3. Power analysis (one-sided test for ORs) in the validation set. At several *P* levels; dark blue: *P*=0.01; light blue: *P*=0.05; green: *P*=0.1; red: *P*=0.25.



Online Supplementary Figure S4. BiPN rates by time to BiPN in the HOVON-65/GMMG-HD4 trial. Cumulative percentage of MM patients from the HOVON-65/GMMG-HD4 (n=412) who developed grade 1 (26%), grade 2 (13%), grade 3 (9%) or grade 4 (3%) BiPN shown in time (days).



Online Supplementary Figure S5. SNP rs2857605 in TNFα region is associated with BIPN. Figures were generated using the web-based tool SNAP.[1] Haploview 4.0 was used to generate the linkage disequilibrium plot. The International HapMap Project was used to calculate recombination rates. (A) Regional linkage disequilibrium plot for SNP rs2857605 in the TNFα gene region at 6p21, which is associated with BIPN. (B) SNPs genotyped across the TNFα gene region.



References

1. Johnson AD, Handsaker RE, Pulit SL, Nizzari MM, O'Donnell CJ, de Bakker PI. SNAP: a web-based tool for identification and annotation of proxy SNPs using HapMap. Bioinformatics. 2008;24(24):2938-9.