Genes with a spike expression are clustered in chromosome (sub)bands and spike (sub)bands have a powerful prognostic value in patients with multiple myeloma

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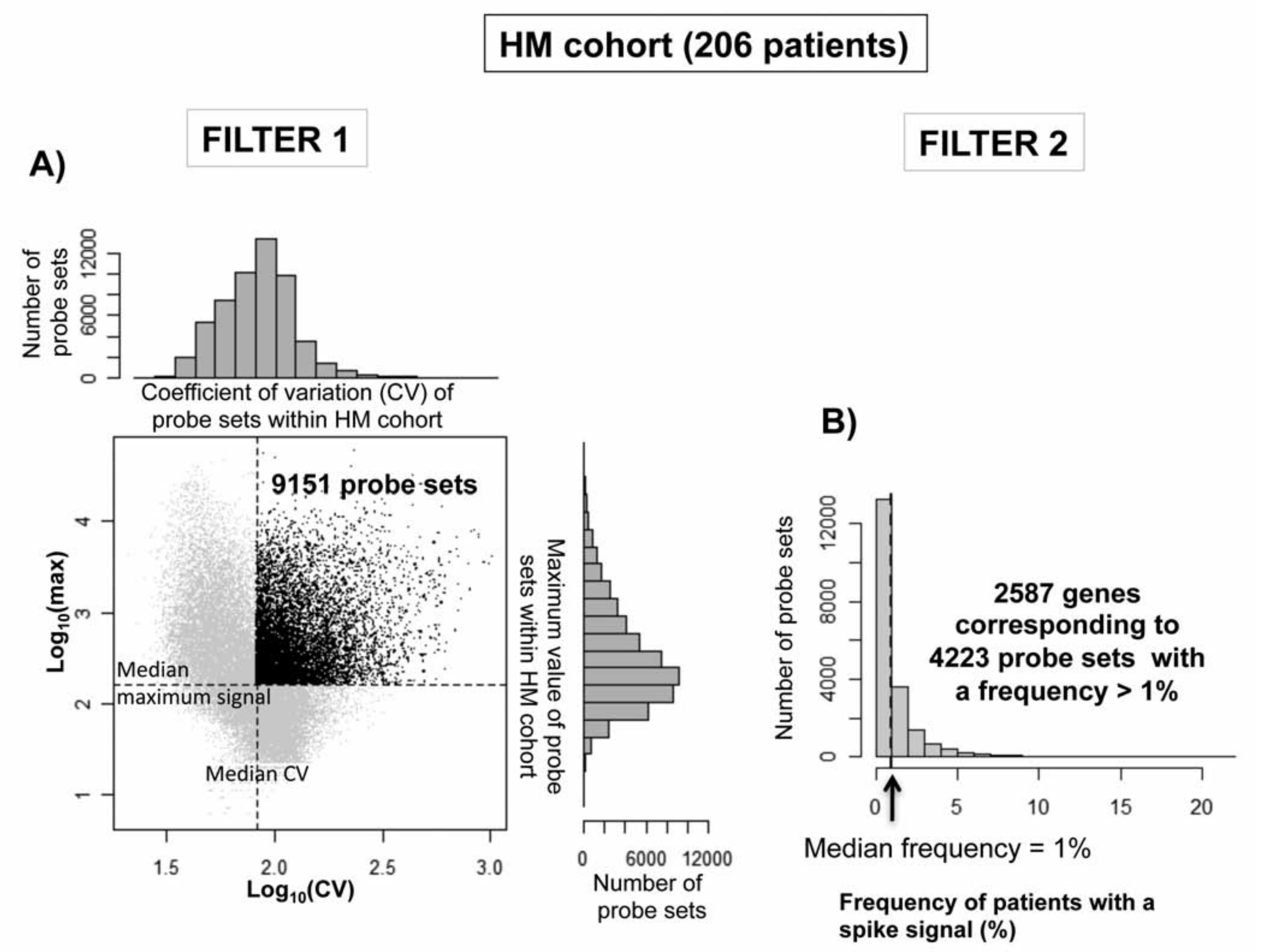
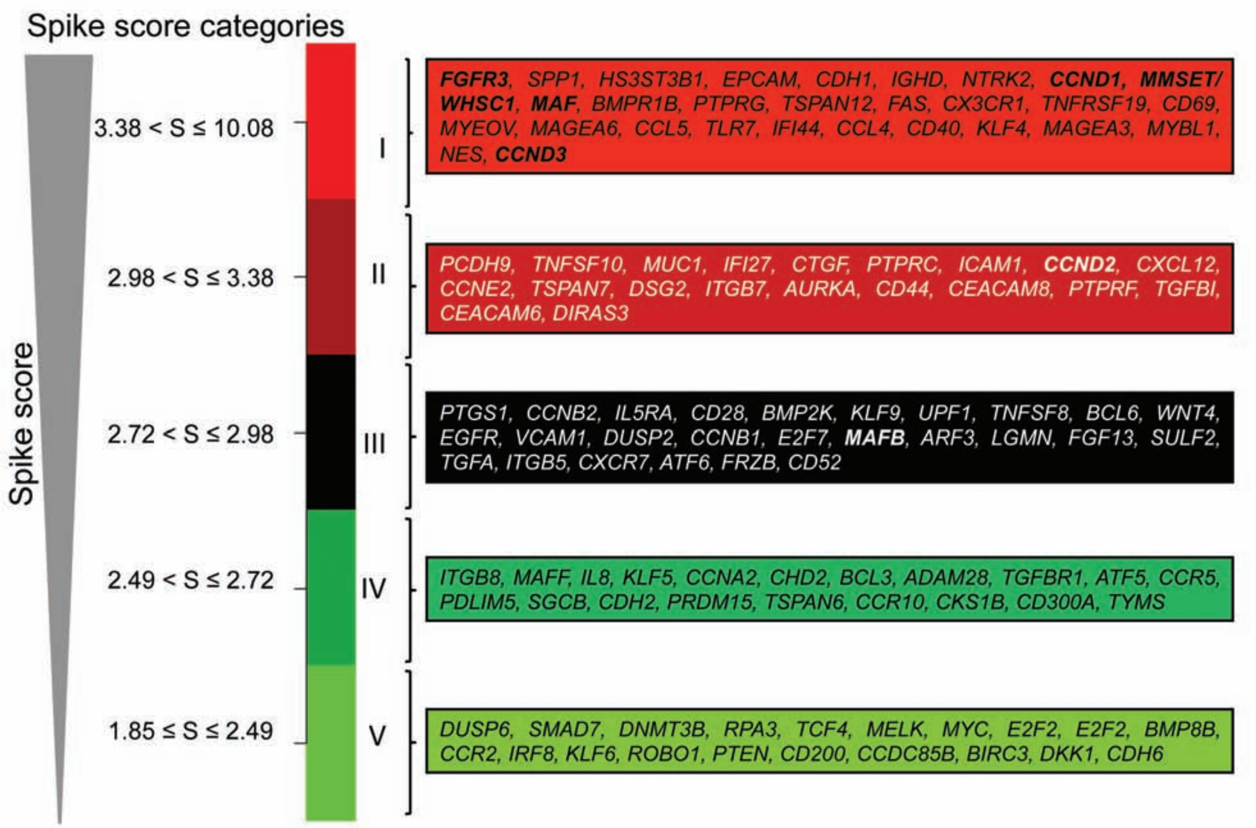
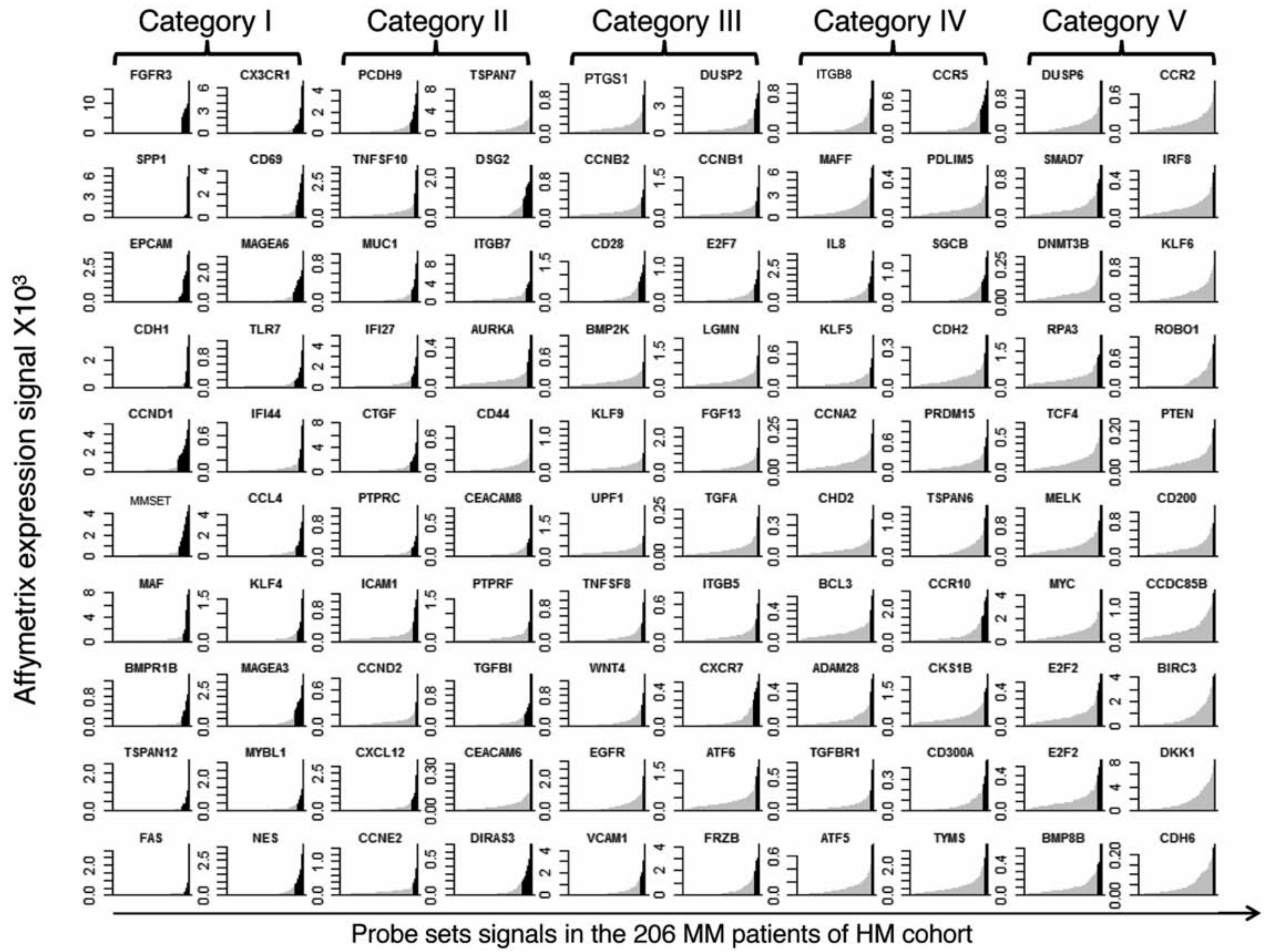


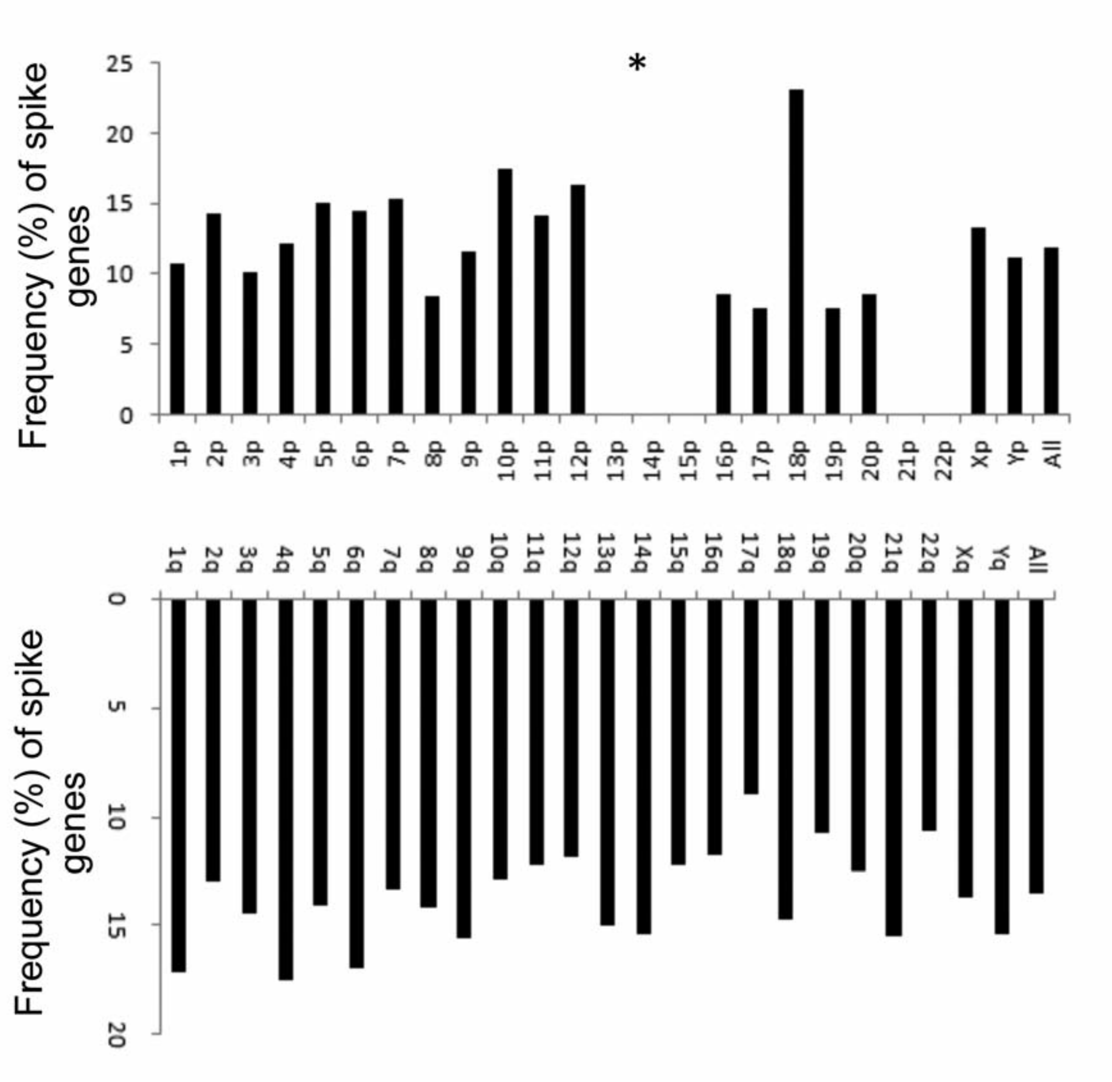
Online Supplementary Figure S1. Two filter selections of spike genes/EST. (A) Filter 1. The 54613 probe sets of the U133 2.0 plus Affymetrix microarray were ranked according to the coefficient of variation (ratio of mean to standard deviation) and to the maximum signal among patients of the HM cohort, selecting the 9151 probe sets with a coefficient of variation and maximum signal equal or above the median value. (B) Filter 2 uses the box plot probe set signal distribution. It selects probe sets whose signal in some patients was Q3+3*IQR, Q3 being quartile 3 of the probe set signals among patients' samples and IQR the interquartile range (Q3-Q1). The histograms show the number of probe sets for which the percentage of patients with a signal Q3+3*IQR was higher or equal to a given percentage for the HM cohort. A percentage > 1% make it possible to select for 4223 probe sets for the HM cohort. These probe sets probed for 2587 unique genes/EST of known chromosomal localization.



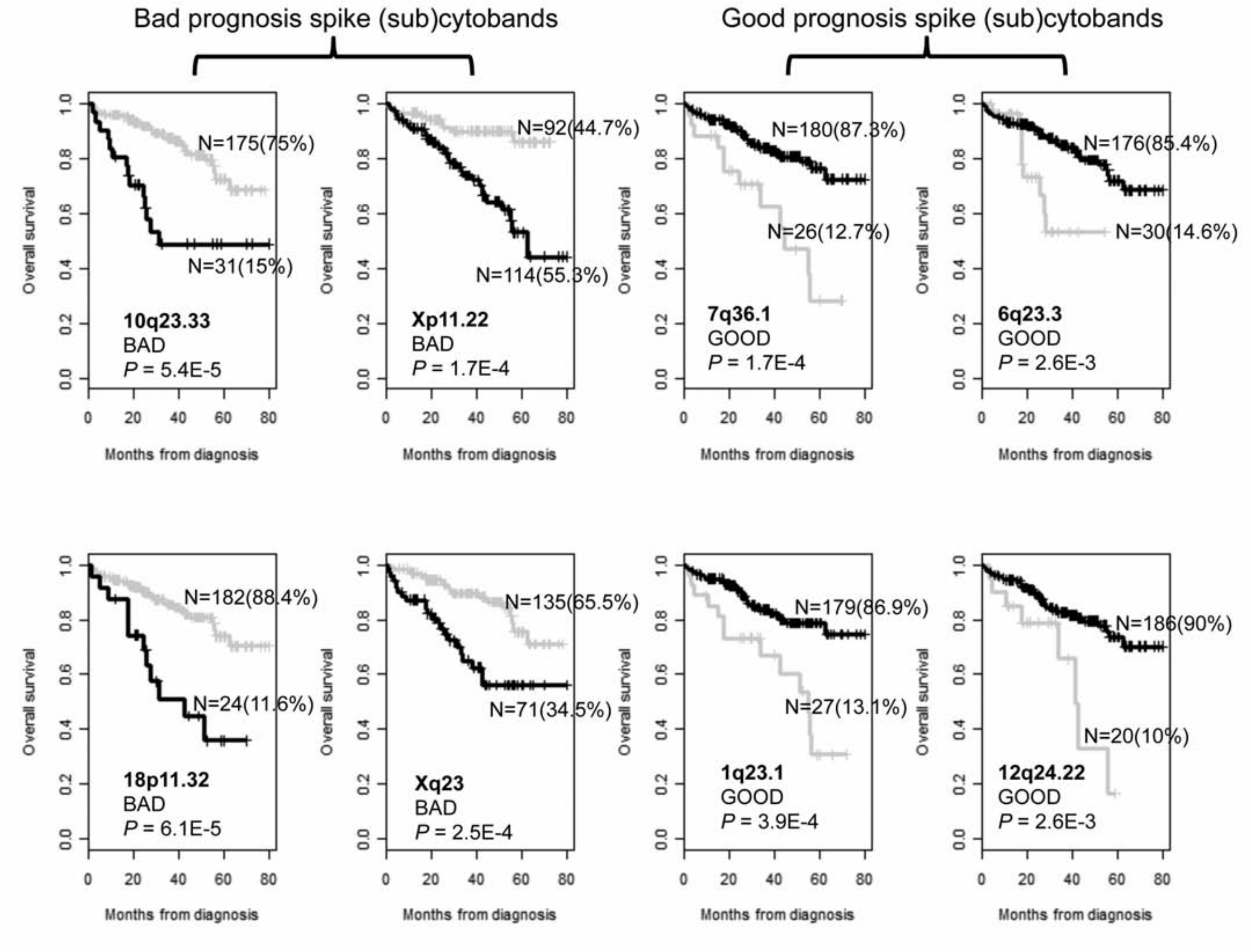
Online Supplementary Figure S2. Distribution of spike genes/EST in five spike categories according to their spike score. Spike probe sets were grouped in five nearly equally sized categories (I to V according to decreasing spike scores). Each category comprises 502-525 probe sets. The most spiked genes are displayed.



Online Supplementary Figure S3. *MAS5* normalized signals of spike genes representative of each five spike categories. For each gene/EST, *MAS5* normalized signals in patients of the HM cohort were ranked. The signals of patients in the spike group are shown as black lines, those in the non-spike group as gray lines. Twenty spiking genes in each category were chosen. Data illustrate the high spike signals of category I genes compared to category V genes.

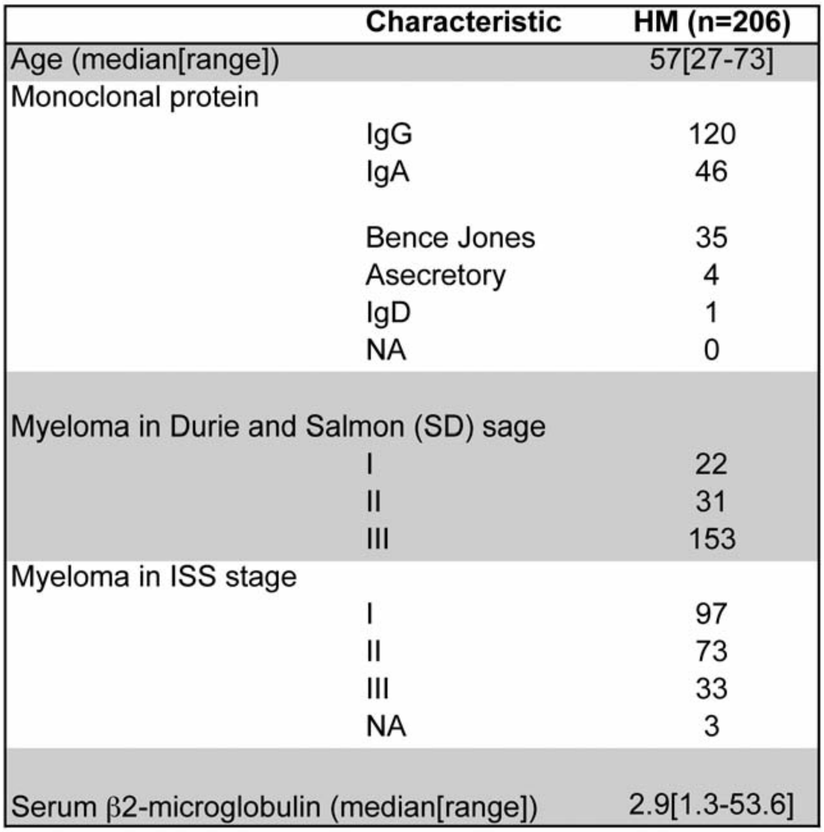


Online Supplementary Figure S4. Chromosomal distribution of spike genes. Data are the frequencies of spike genes among genes located in each short or long chromosome arm. * The frequency of spike genes among genes in chromosome long arms is significantly enriched compared to that in short arms ($P<10^{-4}$).



Online Supplementary Figure S5. Prognostic value of spike (sub)bands using the HM cohort of 206 patients. To look for the prognostic value of a given spike (sub)band, a spike (sub)band signal was defined for each patient as the mean of the signals of the spike genes within this (sub)band. Using this parameter, 55 of the 149 spike (sub)bands had prognostic value using the R package MaxStat function and multiple testing correction in the HM cohort. The Kaplan Meier survival curves are shown for the four spike (sub)bands with the worst prognosis and the four with the best prognosis.

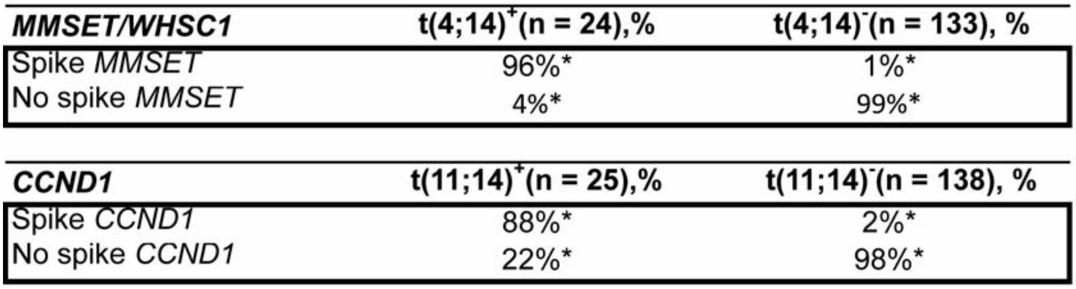
Online Supplementary Table S1. Clinical characteristics of patients in the HM cohort. Data are median values and ranges for age, serum monoclonal protein, serum-β2-microglobulin and the Salmon-Durie and International Staging System (ISS) stages. NA, not available.



	Characteristic	HM (n=206)
Age (median[range])		57[27-73]
Monoclonal protein		
	IgG	120
	IgA	46
	Bence Jones	35
	Asecretory	4
	IgD	1
	NA	0
Myeloma in Durie and Salmon (SD) sage		
	I	22
	II	31
	III	153
Myeloma in ISS stage		
	I	97
	II	73
	III	33
	NA	3
Serum β2-microglobulin (median[range])		2.9[1.3-53.6]

Online Supplementary Table S2. SEE PDF

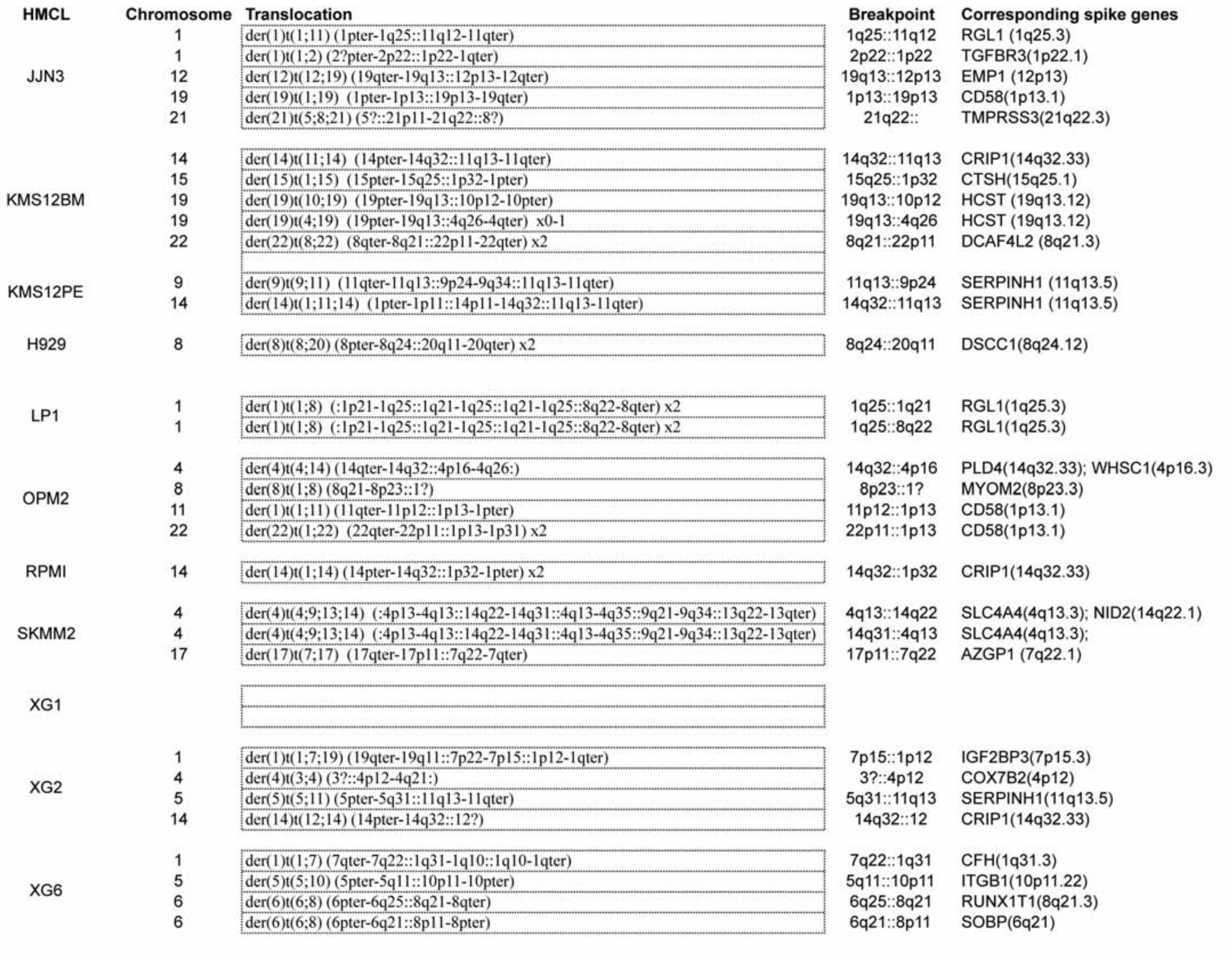
Online Supplementary Table S3. Genetic abnormalities of patients with spike *MMSET* and spike *CCND1.* Interphase FISH analysis was performed on CD138-purified plasma cells for 157 to 163 patients of the HM series. Patients were separated into two groups: patients with spike *MMSET/WHSC1* MM cells and patients without spike *MMSET/WHSC1* MM cells or patients with spike *CCND1* MM cells and without spike *CCND1* MM cells, as assayed with Affymetrix microarrays. Data are the percentages of patients within these two groups with the biological parameters. *The percentages were different with a χ^2 test ($P<0.05$).



MMSET/WHSC1	**t(4;14)$^+$(n = 24),%**	**t(4;14)$^-$(n = 133), %**
Spike *MMSET*	96%*	1%*
No spike *MMSET*	4%*	99%*

CCND1	**t(11;14)$^+$(n = 25),%**	**t(11;14)$^-$(n = 138), %**
Spike *CCND1*	88%*	2%*
No spike *CCND1*	22%*	98%*

Online Supplementary Table S4. Genes with a spike expression in HMCL with a translocation-associated breakpoint involving the gene-containing cytoband.



HMCL	Chromosome	Translocation	Breakpoint	Corresponding spike genes
JJN3	1	der(1)t(1;11) (1pter-1q25::11q12-11qter)	1q25::11q12	RGL1 (1q25.3)
	1	der(1)t(1;2) (2?pter-2p22::1p22-1qter)	2p22::1p22	TGFBR3(1p22.1)
	12	der(12)t(12;19) (19qter-19q13::12p13-12qter)	19q13::12p13	EMP1 (12p13)
	19	der(19)t(1;19) (1pter-1p13::19p13-19qter)	1p13::19p13	CD58(1p13.1)
	21	der(21)t(5;8;21) (5?::21p11-21q22::8?)	21q22::	TMPRSS3(21q22.3)
KMS12BM	14	der(14)t(11;14) (14pter-14q32::11q13-11qter)	14q32::11q13	CRIP1(14q32.33)
	15	der(15)t(1;15) (15pter-15q25::1p32-1pter)	15q25::1p32	CTSH(15q25.1)
	19	der(19)t(10;19) (19pter-19q13::10p12-10pter)	19q13::10p12	HCST (19q13.12)
	19	der(19)t(4;19) (19pter-19q13::4q26-4qter) x0-1	19q13::4q26	HCST (19q13.12)
	22	der(22)t(8;22) (8qter-8q21::22p11-22qter) x2	8q21::22p11	DCAF4L2 (8q21.3)
KMS12PE	9	der(9)t(9;11) (11qter-11q13::9p24-9q34::11q13-11qter)	11q13::9p24	SERPINH1 (11q13.5)
	14	der(14)t(1;11;14) (1pter-1p11::14p11-14q32::11q13-11qter)	14q32::11q13	SERPINH1 (11q13.5)
H929	8	der(8)t(8;20) (8pter-8q24::20q11-20qter) x2	8q24::20q11	DSCC1(8q24.12)
LP1	1	der(1)t(1;8) (:1p21-1q25::1q21-1q25::1q21-1q25::8q22-8qter) x2	1q25::1q21	RGL1(1q25.3)
	1	der(1)t(1;8) (:1p21-1q25::1q21-1q25::1q21-1q25::8q22-8qter) x2	1q25::8q22	RGL1(1q25.3)
OPM2	4	der(4)t(4;14) (14qter-14q32::4p16-4q26:)	14q32::4p16	PLD4(14q32.33); WHSC1(4p16.3)
	8	der(8)t(1;8) (8q21-8p23::1?)	8p23::1?	MYOM2(8p23.3)
	11	der(1)t(1;11) (11qter-11p12::1p13-1pter)	11p12::1p13	CD58(1p13.1)
	22	der(22)t(1;22) (22qter-22p11::1p13-1p31) x2	22p11::1p13	CD58(1p13.1)
RPMI	14	der(14)t(1;14) (14pter-14q32::1p32-1pter) x2	14q32::1p32	CRIP1(14q32.33)
SKMM2	4	der(4)t(4;9;13;14) (:4p13-4q13::14q22-14q31::4q13-4q35::9q21-9q34::13q22-13qter)	4q13::14q22	SLC4A4(4q13.3); NID2(14q22.1)
	4	der(4)t(4;9;13;14) (:4p13-4q13::14q22-14q31::4q13-4q35::9q21-9q34::13q22-13qter)	14q31::4q13	SLC4A4(4q13.3);
	17	der(17)t(7;17) (17qter-17p11::7q22-7qter)	17p11::7q22	AZGP1 (7q22.1)
XG1				
XG2	1	der(1)t(1;7;19) (19qter-19q11::7p22-7p15::1p12-1qter)	7p15::1p12	IGF2BP3(7p15.3)
	4	der(4)t(3;4) (3?::4p12-4q21:)	3?::4p12	COX7B2(4p12)
	5	der(5)t(5;11) (5pter-5q31::11q13-11qter)	5q31::11q13	SERPINH1(11q13.5)
	14	der(14)t(12;14) (14pter-14q32::12?)	14q32::12	CRIP1(14q32.33)
XG6	1	der(1)t(1;7) (7qter-7q22::1q31-1q10::1q10-1qter)	7q22::1q31	CFH(1q31.3)
	5	der(5)t(5;10) (5pter-5q11::10p11-10pter)	5q11::10p11	ITGB1(10p11.22)
	6	der(6)t(6;8) (6pter-6q25::8q21-8qter)	6q25::8q21	RUNX1T1(8q21.3)
	6	der(6)t(6;8) (6pter-6q21::8p11-8pter)	6q21::8p11	SOBP(6q21)

Online Supplementary Table S5. List of cancer census genes identified as spike genes in multiple myeloma.

Probe sets	Gene name	Chromosome band	Spike score	spike categor
204379_s_at	FGFR3	4p16.3	10,08	1
216365_x_at	IGL@	22q11.22	7,25	1
201131_s_at	CDH1	16q22.1	5,81	1
221658_s_at	IL21R	16p12.1	5,40	1
214651_s_at	HOXA9	7p15.2	5,14	1
211635_x_at	IGH@	14q32.33	4,85	1
208711_s_at	CCND1	11q13.3	4,60	1
215025_at	NTRK3	15q25.3	4,59	1
222777_s_at	WHSC1	4p16.3	4,59	1
209348_s_at	MAF	16q23.2	4,59	1
211643_x_at	IGK@	2p11.2	4,44	1
203510_at	MET	7q31.2	3,92	1
209289_at	NFIB	9p22.3	3,88	1
204159_at	CDKN2C	1p32.3	3,80	1
214617_at	PRF1	10q22.1	3,68	1
204798_at	MYB	6q23.3	3,64	1
217143_s_at	TRA@	14q11.2	3,64	1
212148_at	PBX1	1q23.3	3,55	1
244023_at	SYK	9q22.2	3,49	1
210394_x_at	SSX4	Xp11.23	3,46	1
201497_x_at	MYH11	16p13.11	3,44	1
201700_at	CCND3	6p21.1	3,39	1
213693_s_at	MUC1	1q22	3,34	2
205386_s_at	MDM2	12q15	3,32	2
200952_s_at	CCND2	12p13.32	3,28	2
210001_s_at	SOCS1	16p13.13	3,21	2
210497_x_at	SSX2	Xp11.22	3,17	2
204249_s_at	LMO2	11p13	3,14	2
1559078_at	BCL11A	2p16.1	3,11	2
224861_at	GNAQ	9q21.2	3,01	2
231411_at	LHFP	13q14.11	2,97	3
228758_at	BCL6	3q27.3	2,93	3
1569652_at	MLLT3	9p21.3	2,92	3
235925_at	TCF12	15q21.3	2,92	3
1565483_at	EGFR	7p11.2	2,92	3
214157_at	GNAS	20q13.32	2,91	3
205330_at	MN1	22q12.1	2,89	3
1555779_a_at	CD79A	19q13.2	2,89	3
227613_at	ZNF331	19q13.42	2,87	3
202861_at	PER1	17p13.1	2,86	3
222670_s_at	MAFB	20q12	2,84	3
1555763_x_at	MKL1	22q13.2	2,84	3
214815_at	TRIM33	1p13.2	2,83	3
203755_at	BUB1B	15q15.1	2,78	3
204784_s_at	MLF1	3q25.32	2,75	3
206674_at	FLT3	13q12.2	2,73	3
230389_at	FNBP1	9q34.11	2,72	4
208885_at	LCP1	13q14.13	2,70	4
204908_s_at	BCL3	19q13.32	2,69	4
202643_s_at	TNFAIP3	6q23.3	2,68	4
1556499_s_at	COL1A1	17q21.33	2,67	4
203749_s_at	RARA	17q21.2	2,67	4
1559975_at	BTG1	12q21.33	2,63	4
228898_s_at	SMARCB1	22q11.23	2,62	4
215771_x_at	RET	10q11.21	2,60	4
223514_at	CARD11	7p22.2	2,58	4
235461_at	TET2	4q24	2,58	4
224847_at	CDK6	7q21.2	2,57	4
1562731_s_at	MDS2	1p36.11	2,56	4
209383_at	DDIT3	12q13.3	2,54	4
205051_s_at	KIT	4q12	2,54	4
244110_at	MLL	11q23.3	2,50	5
200934_at	DEK	6p22.3	2,50	5
201465_s_at	JUN	1p32.1	2,48	5
209959_at	NR4A3	9q22.33	2,45	5
1552611_a_at	JAK1	1p31.3	2,44	5
1559227_s_at	VHL	3p25.3	2,43	5
225575_at	LIFR	5p13.1	2,43	5
224838_at	FOXP1	3p13	2,39	5
221911_at	ETV1	7p21.2	2,39	5
202431_s_at	MYC	8q24.21	2,37	5
203490_at	ELF4	Xq26.1	2,32	5
209193_at	PIM1	6p21.2	2,31	5
233254_x_at	PTEN	10q23.31	2,30	5
209604_s_at	GATA3	10p14	2,29	5
210538_s_at	BIRC3	11q22.2	2,04	5

Online Supplementary Table S6. Spike (sub)bands significantly enriched in spike genes.

Chromosome bands	chromosome fragile site	chromosome band designations	Pronostic value	Total number of genes	Number of spikgenes	%of spike genes	Median[range] spike score	Spaning region (Mb)	List of spike genes
1p21.2	FRA1E	R-band	Good	18	4	22,22	3.02[2.55-3.95]	1.103738	*CCDC76; GPR88; VCAM1; S1PR1*
1p22.1		R-band	Good	21	4	19,05	2.57[2.28-3.61]	2.204861	*TGFBR3; FNBP1L; BCAR3; GCLM*
1p31.1		G-band		47	10	21,28	2.88[2.14-5.68]	13.659346	*SFRS11; CTH; PTGER3; LRRIQ3; LHX8; SLC44A5; IFI44L; IFI44; LPHN2; TTLL7*
1p35.2		R-band	Good	19	4	21,05	3.12[2.13-3.75]	0.987402	*LAPTM5; SDC3; SERINC2; BAI2*
1p36.12		G-band		42	10	23,81	2.98[2.36-3.62]	3.445977	*PLA2G2D; WNT4; ZBTB40; C1QA; C1QC; C1QB; LUZP1; TCEA3; E2F2; ID3*
1q21.2		G-band	Bad	26	6	23,08	2.66[2.42-5.31]	2.053259	*CKS1B; LOC100292701; HIST2H2AA3; HIST2H2BE; MTMR11; PLEKHO1; CA14*
1q23.1		R-band	Good	37	7	18,92	3.26[2.68-3.7]	2.162552	*NES; FCRL3; FCRL2; FCRL1; CD5L; CD1A; MNDA*
1q23.3		R-band		56	13	23,21	2.92[2.24-3.83]	3.946931	*SLAMF1; PPOX; FCER1G; FCGR2C; HSPA6; FCGR3B; FCRLA; FCRLB; ATF6; UHMK1; DDR2; NUF2; PBX1*
1q25.1	FRA1G	R-band		20	4	20	2.9[2.01-4.71]	0.975675	*TNFSF4; ANKRD45; GAS5; RABGAP1L*
1q25.2		G-band		26	6	23,08	3.25[2.76-4.81]	3.024739	*ASTN1; RASAL2; RALGPS2; FAM20B; TOR3A; TOR1AIP1*
1q25.3		R-band		38	7	18,42	2.88[2.36-3.39]	2.409019	*GLUL; RGS16; DHX9; NCF2; RGL1; C1orf21; FAM129A*
1q31.3		G-band	Bad	16	5	31,25	3.29[2.6-5.34]	1.986793	*CFH; CFHR4; ASPM; DENND1B; PTPRC*
1q32.2		G-band		29	9	31,03	2.5[2.21-5.64]	4.273352	*PFKFB2; CR2; PLXNA2; LAMB3; G0S2; HSD11B1; TRAF3IP3; IRF6; TRAF5*
1q32.3		R-band		26	9	34,62	2.91[2.2-4.67]	1.567742	*C1orf97; NEK2; LPGAT1; DTL; LOC100287039; ATF3; FAM71A; BATF3; VASH2*
1q41		G-band	Bad	34	9	26,47	2.84[2.46-3.73]	8.617623	*CENPF; USH2A; GPATCH2; TGFB2; MARK1; C1orf115; HLX; DUSP10; SUSD4*
1q42.12		G-band		17	4	23,53	2.67[2.32-3.83]	1.230187	*LBR; LEFTY2; ACBD3; ITPKB*
1q42.13		R-band	Bad	33	6	18,18	2.84[2.09-3.9]	3.016171	*CDC42BPA; C1orf69; HIST3H2A; RHOU; C1orf96; GALNT2*
2p11.2	FRA2L	R-band		52	9	17,31	2.9[2.46-4.44]	4.874776	*LOC129293; SFTPB; GNLY; RGPD1; IGKC; IGKV4-1; IGK@; LOC100291464; LOC652493*
2p16.1		G-band		21	6	28,57	2.93[2.55-3.22]	5.473905	*NCRNA00117; CCDC88A; EFEMP1; CCDC85A; BCL11A; PAPOLG*
2p21		R-band		45	8	17,78	2.71[2.28-5.92]	5.47275	*SGK493; ZFP36L2; SIX2; PRKCE; EPAS1; RHOQ; EPCAM; KCNK12*
2p23.1		R-band		11	4	36,36	2.86[2.45-3.56]	1.002806	*LBH; CAPN13; GALNT14; EHD3*
2p25.1		R-band	Bad	29	5	17,24	2.92[2.25-4.87]	2.855267	*ID2; MBOAT2; RRM2; ROCK2; GREB1*
2q13	FRA2B	R-band	Good	42	9	21,43	2.95[2.49-3.57]	3.792062	*ANKRD57; LIMS3; BUB1; BCL2L11; MERTK; CHCHD5; SLC20A1; IL1B; LOC100130100*
2q24.3		G-band	Bad	17	7	41,18	2.51[2.33-4.25]	4.862853	*FIGN; GRB14; COBLL1; SCN3A; GALNT3; STK39; LASS6*
2q32.1	FRA2H	G-band		17	4	23,53	2.93[2.64-3.73]	5.458394	*FRZB; ZNF804A; CALCRL; GULP1*
2q34		G-band		18	4	22,22	3.23[2.6-3.76]	3.109455	*PIKFYVE; MAP2; C2orf67; ERBB4*
3q13.13		G-band		17	5	29,41	3.18[2.45-3.94]	2.520085	*KIAA1524; TRAT1; MORC1; DPPA4; PVRL3*
3q13.2		R-band	Bad	22	7	31,82	2.84[2.18-3.82]	1.478506	*PHLDB2; C3orf52; GCET2; CD200; ATG3; CCDC80; BOC*
3q21.1		R-band		23	5	21,74	3.1[2.52-3.81]	1.713622	*CASR; CSTA; PARP15; MYLK; CCDC14*
3q23		R-band	Bad	24	5	20,83	3.34[2.7-4.8]	3.483412	*RBP1; CLSTN2; XRN1; PCOLCE2; SR140*
3q24		G-band	Bad	18	4	22,22	2.72[2.16-2.81]	2.795816	*PLOD2; PLSCR4; PLSCR1; CPA3*
3q26.33		G-band	Bad	15	4	26,67	2.5[2.2-4.62]	3.394298	*GNB4; MRPL47; SOX2; ATP11B*
3q27.2		G-band		12	4	33,33	2.7[2.51-3.53]	0.837856	*C3orf70; EHHADH; LIPH; TRA2B*
4p13		G-band		10	4	40	3.96[2.27-5.26]	1.141006	*UCHL1; LIMCH1; BEND4; SHISA3*
4q12	FRA4B	R-band		37	6	16,22	3.23[2.54-5.21]	5.010067	*SGCB; KIT; NMU; HOPX; SPINK2; IGFBP7*
4q13.3		G-band		53	13	24,53	3.12[2.2-4.05]	4.718285	*SULT1B1; CSN2; RUFY3; DCK; SLC4A4; RASSF6; IL8; PF4; PPBP; CXCL3; CXCL2; MTHFD2L; AREG*
4q21.21		G-band		13	5	38,46	2.53[2.2-2.95]	2.875546	*ANXA3; BMP2K; ANTXR2; PRKG2; RASGEF1B*
4q22.1		G-band	Good	25	5	20	3.27[2.44-6.99]	1.903881	*SPP1; ABCG2; HERC6; SNCA; MMRN1*
4q24		G-band		25	4	16	2.66[2.55-4.05]	4.104841	*BANK1; TET2; FLJ20184; NPNT*
4q31.3		R-band	Bad	24	4	16,67	3.42[2.64-6.97]	1.244328	*DKFZP434I0714; TMEM154; TLR2; SFRP2*
4q32.1		G-band		22	7	31,82	2.72[2.15-4.36]	3.925188	*MAP9; GUCY1A3; GUCY1B3; TDO2; PDGFC; C4orf18; RAPGEF2*
4q35.1		R-band	Good	30	7	23,33	2.64[2.41-3.16]	2.969863	*WWC2; STOX2; ACSL1; C4orf47; PDLIM3; SORBS2; TLR3*
5p13.1		R-band		18	8	44,44	2.58[2.11-3.81]	2.831983	*LIFR; FYB; DAB2; PTGER4; RPL37; CARD6; C6; PLCXD3*
5p13.2		G-band		28	5	17,86	2.85[2.3-3.1]	3.623063	*LOC100272216; SPEF2; IL7R; NIPBL; LOC100287032*
5q12.1		G-band	Bad	16	5	31,25	2.83[2.51-3.57]	3.543198	*PDE4D; DEPDC1B; LOC728153; IPO11*
5q13.2		G-band	Bad	32	6	18,75	2.81[2.45-3.67]	4.459146	*CCNB1; CCDC125; LOC653188; MAP1B; TMEM171; RGNEF*
5q13.3		R-band		27	5	18,52	2.68[2.48-3.16]	2.191619	*ENC1; FAM169A; SV2C; F2R; F2RL1*
5q23.2		R-band		21	4	19,05	2.78[2.38-3.53]	3.844342	*PPIC; GRAMD3; ALDH7A1; MARCH3*
5q33.1		R-band		22	5	22,73	3.12[2.45-3.15]	1.060015	*SYNPO; MYOZ3; RBM22; GPX3; SPARC*
5q33.3		R-band	Good	30	6	20	2.58[2.03-4.09]	1.776635	*TIMD4; HAVCR2; NIPAL4; THG1L; CLINT1; EBF1*
5q35.1		R-band		27	6	22,22	3.34[2.42-4.49]	3.080576	*LOC133874; LCP2; FGF18; ATP6V0E1; C5orf41; STC2*
5q35.2		G-band		30	5	16,67	2.6[2.15-3.97]	2.992541	*CPEB4; C5orf47; HMP19; SFXN1; HK3*
6p12.1		G-band		18	4	22,22	2.87[2.55-3.13]	3.822632	*ELOVL5; RPS16P5; DST; ZNF451*
6p12.2		R-band		12	4	33,33	3[2.51-3.1]	0.615825	*PAQR8; EFHC1; LOC730101; GSTA4*
6p12.3		G-band		28	5	17,86	3.17[2.55-4.42]	3.506622	*RCAN2; CYP39A1; TDRD6; PLA2G7; CRISP3*
6p21.3		R-band	Good	5	4	80	3.78[3.38-4.43]	1.024947	*LST1; HLA-DRA; HLA-DQA1; HLA-DRB4*
6p21.32		G-band		40	8	20	3.09[2.32-3.41]	0.838823	*HLA-DRB6; HLA-DRB1; HLA-DQB1; HLA-DMB; HLA-DMA; HLA-DPA1; HLA-DPB1; KIFC1*
6p22.2	FRA6C	R-band	Bad	51	10	19,61	2.88[2.25-3.28]	1.420154	*CMAH; SLC17A4; HFE; HIST1H4C; HIST1H2BC; HIST1H2AD; HIST1H2BG; HIST1H2AE; HIST1H4H; BTN1A1*
6p22.3		G-band		37	7	18,92	2.7[2.5-3.8]	8.675157	*MYLIP; DEK; RNF144B; SOX4; GPLD1; C6orf62; FAM65B*
6p25.2		G-band		24	5	20,83	3.12[2.79-5.26]	0.835337	*SERPINB9; TUBB2A; TUBB2B; SLC22A23; C6orf145*
6q14.1		G-band		23	4	17,39	2.68[2.53-2.81]	5.742247	*MYO6; SH3BGRL2; TTK; FAM46A*
6q15	FRA6G	R-band	Bad	25	5	20	3.11[2.16-4.26]	1.786665	*CNR1; RNGTT; GABRR1; MDN1; BACH2*
6q21	FRA6F	R-band		58	10	17,24	3.01[2.19-4.45]	8.633844	*BVES; POPDC3; AIM1; SOBP; FOXO3; SESN1; CDC2L6; SLC16A10; FYN; MARCKS*
6q23.2		G-band		29	8	27,59	3.24[2.38-3.79]	3.3299	*EPB41L2; ENPP1; CTGF; VNN1; VNN2; RP4-662A9.2; SLC2A12; SGK1*
6q23.3		R-band	Good	24	5	20,83	2.64[2.51-3.64]	2.90947	*MYB; MAP7; IFNGR1; TNFAIP3; PERP*
6q24.1		G-band		13	5	38,46	2.66[2.6-4.44]	3.166807	*HECA; TXLNB; CITED2; LOC729070; GPR126*
6q25.3		R-band	Good	32	8	25	2.71[2.21-3.16]	2.083678	*SNX9; SYNJ2; TULP4; SYTL3; EZR; TAGAP; SOD2; MAS1*
7p12.1		G-band	Bad	7	4	57,14	3.07[2.53-3.71]	2.591518	*FIGNL1; GRB10; COBL; POM121L12*
7p15.2		G-band		28	5	17,86	3.2[2.4-5.14]	0.503529	*SKAP2; HOXA1; HOXA7; HOXA9; HOXA10*
7p15.3		R-band	Bad	28	8	28,57	2.88[2.5-4.13]	2.394696	*LOC541472; IL6; FAM126A; GPNMB; IGF2BP3; DFNA5; OSBPL3; CYCS*
7p21.3		G-band		15	4	26,67	2.63[2.31-3.1]	4.934054	*RPA3; THSD7A; VWDE; SCIN*
7q21.11		G-band		13	5	38,46	2.96[2.65-3.03]	5.941266	*MAGI2; GNAI1; CD36; HGF; SEMA3A*
7q21.3		G-band		33	7	21,21	3.18[2.08-4.41]	3.194891	*GNG11; COL1A2; SGCE; PEG10; PPP1R9A; PDK4; ACN9*
7q22.3		R-band		22	4	18,18	2.78[2.55-2.91]	1.078457	*SYPL1; PIK3CG; PRKAR2B; HBP1*
7q31.1		G-band		21	5	23,81	3.28[2.56-3.48]	4.332826	*NRCAM; DOCK4; ZNF277; IFRD1; C7orf53*
7q31.2	FRA7G	R-band		15	5	33,33	2.73[2.31-3.92]	0.737046	*TFEC; LOC100128868; tcag7.929; CAV2; MET*
7q31.31		G-band		9	4	44,44	3.53[2.2-4.42]	0.561529	*TSPAN12; C7orf58; WNT16; FAM3C*
7q36.1		R-band	Good	66	13	19,7	2.99[2.19-4.51]	2.591152	*ATP6V0E2; LOC285972; GIMAP8; GIMAP7; GIMAP4; GIMAP6; GIMAP1; GIMAP5; TMEM176B; TMEM176A; ABP1; ASB10; LOC100128822*
8p21.2		G-band		26	5	19,23	2.98[2.6-4.3]	3.962263	*SLC25A37; ADAM28; CDCA2; DPYSL2; EPHX2*
8q12.1		G-band		24	4	16,67	2.63[2.14-3.72]	2.522446	*FAM110B; TOX; CA8; RAB2A*
8q21.11		G-band		17	4	23,53	2.57[2.39-3.08]	3.261215	*LOC100128126; HNF4G; LOC100192378; ZFHX4*
8q21.3		G-band		25	6	24	2.82[2.24-4.76]	5.860019	*ATP6V0D2; CNGB3; DCAF4L2; MMP16; TMEM64; RUNX1T1*
8q22.1	FRA8B	R-band		32	8	25	2.9[2.67-4.02]	4.044076	*RBM12B; CDH17; GEM; ESRP1; CCNE2; PLEKHF2; UQCRB; LAPTM4B*
8q24.12		G-band	Bad	13	4	30,77	4.01[2.6-5.17]	1.327375	*MAL2; ENPP2; DSCC1; SNTB1*
8q24.13		R-band		25	5	20	3.16[2.44-3.54]	1.368279	*FAM83A; C8orf76; ATAD2; FBXO32; MTSS1*
9p21.1		G-band		14	4	28,57	2.9[2.47-3.09]	5.162559	*LINGO2; DDX58; LOC100129250; B4GALT1*
9q21.13		G-band		20	9	45	3.14[2.79-3.73]	5.884817	*TRPM3; LOC286382; TMEM2; GDA; ZFAND5; ANXA1; PCSK5; RFK; GCNT1*
9q22.33		R-band	Good	29	6	20,69	2.58[2.45-2.92]	3.331614	*CDC14B; KIAA1529; TRIM14; TGFBR1; SEC61B; NR4A3*
9q31.1		G-band		25	4	16	3.21[2.72-4.1]	4.894675	*LOC441461; TMEFF1; ALDOB; ABCA1*
9q34.3		R-band		95	16	16,84	2.63[2.28-3.99]	2.979824	*COL5A1; FCN2; FCN1; SOHLH1; NACC2; SNAPC4; SNHG7; LCN6; PTGDS; NPDC1; DPP7; RNF208; FAM166A; NRARP; MRPL41; EHMT1*
10p14		G-band		22	5	22,73	2.48[2.06-3.15]	4.578154	*PRKCQ; ITIH5; TAF3; GATA3; CUGBP2*
10p15.1		R-band		25	8	32	2.73[2.31-3.93]	2.368655	*KLF6; AKR1C2; AKR1C1; AKR1C3; NET1; ASB13; C10orf18; PFKFB3*
10q11.21		R-band	Good	26	7	26,92	2.98[2.42-4.87]	2.07037	*RET; RASGEF1A; LOC439911; CXCL12; RASSF4; C10orf10; LOC338579*
10q11.23		R-band		27	5	18,52	2.49[2.3-2.54]	2.858197	*WDFY4; C10orf72; C10orf128; LOC100133089; PRKG1*
10q23.31		G-band	Bad	23	6	26,09	3.11[2.3-4.38]	1.529433	*PTEN; ANKRD22; FAS; IFIT2; IFIT3; IFIT1*
10q23.33		G-band	Bad	21	6	28,57	2.67[2.08-2.83]	2.345372	*KIF11; CYP26A1; MYOF; CEP55; HELLS; CYP2C9*
10q24.31		R-band	Bad	22	5	22,73	2.55[2.11-2.83]	0.625409	*SCD; SEC31B; PAX2; FAM178A; SEMA4G*
10q25.2	FRA10B	R-band		18	4	22,22	2.47[2.31-3.47]	2.38256	*SMC3; PDCD4; TECTB; TCF7L2*
10q25.3		G-band		24	4	16,67	3.04[2.79-3.74]	2.839936	*ADRB1; C10orf118; ABLIM1; KIAA1598*
10q26.11		R-band		22	7	31,82	2.75[2.45-3.6]	2.419497	*EMX2OS; NANOS1; SFXN4; RGS10; BAG3; INPP5F; SEC23IP*
11p15.1	FRA11I	R-band		46	8	17,39	2.55[2.24-3.15]	2.936037	*LOC283278; PLEKHA7; LOC441453; PIK3C2A; UEVLD; E2F8; FLJ13439; NAV2*
11p15.3		R-band	Bad	12	4	33,33	3.06[2.93-4.43]	1.403548	*GALNTL4; USP47; MICAL2; TEAD1*
11p15.4		G-band		113	20	17,7	2.77[2.1-5.31]	7.567781	*CDKN1C; PHLDA2; HBB; HBD; HBBP1; HBG1; HBE1; OR51B5; TRIM22; CCKBR; PRKCDBP; HPX; DNHD1; ZNF215; ST5; NRIP3; DENND5A; LOC644656; SWAP70; AMPD3*

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11q12.1		G-band		42	9	21,43	3.24[2.52-3.79]	2.893792	PRG2; SERPING1; LPXN; DTX4; MPEG1; FABP5; MS4A3; MS4A6A; MS4A4A
11q24.3		G-band		20	4	20	3.14[2.36-3.33]	1.701026	ETS1; KCNJ5; RICS; ST14
12p11.22		G-band		8	5	62,5	2.64[2.39-3.2]	1.72057	KLHDC5; PTHLH; CCDC91; FAR2; TMTC1
12p12.3		G-band		23	6	26,09	2.91[2.07-4.63]	4.355299	H2AFJ; PTPRO; EPS8; MGST1; LMO3; PLEKHA5
12p13.31		R-band	Good	90	17	18,89	2.81[2.45-3.93]	3.548962	SCNN1A; CD27; VAMP1; LAG3; CD4; CDCA3; C1R; CD163L1; CD163; SLC2A3; C3AR1; CLEC4A; A2M; CLEC2D; CD69; KLRF1; CLEC2B
12q12		G-band		26	6	23,08	2.65[2.22-2.79]	7.2692	CPNE8; LRRK2; CNTN1; PDZRN4; NELL2; SFRS2IP
12q21.2		R-band		16	6	37,5	3.09[2.15-4.51]	3.38326	GLIPR1; PHLDA1; LOC100289208; E2F7; NAV3; SYT1
12q24.13	FRA12D	R-band		25	5	20	3.32[2.76-3.54]	0.314521	OAS1; OAS3; DTX1; LOC100129447; TPCN1
12q24.22		R-band	Good	9	5	55,56	2.87[2.22-3.13]	0.664887	NCRNA00173; RNFT2; HRK; TESC; NOS1
12q24.23		G-band		18	4	22,22	2.95[2.52-4.42]	2.478568	LOC283454; WSB2; HSPB8; CCDC60
13q12.13		R-band		12	4	33,33	2.98[2.76-3.93]	1.396018	FAM123A; ATP8A2; SHISA2; WASF3
13q13.3		G-band	Bad	21	5	23,81	3.17[2.4-3.5]	2.694317	NBEA; MAB21L1; DCLK1; SOHLH2; TRPC4
14q11.2		R-band		93	18	19,35	2.88[2.19-3.79]	4.414596	FLJ39632; OSGEP; NP; RNASE4; ANG; RNASE6; RNASE1; RNASE3; RNASE2; NDRG2; FLJ10357; SUPT16H; SALL2; C6orf142; TRA@; CDH24; SLC7A8; DHRS2
14q22.1		R-band	Good	22	7	31,82	2.78[2.23-4.37]	1.952049	PYGL; FRMD6; GNG2; NID2; PTGDR; PTGER2; FERMT2
14q23.2		R-band	Bad	13	4	30,77	2.98[1.86-4.24]	2.157564	HIF1A; FLJ43390; SGPP1; SYNE2
14q23.3		G-band		22	5	22,73	2.72[2.27-3.25]	2.837082	C14orf50; GPX2; RAB15; LOC645431; PLEK2
14q32.33		R-band		53	17	32,08	3.7[2.48-6.28]	1.868146	PLD4; PACS2; MTA1; CRIP1; IGHG1; IGHE; IGH@; IGHD; IGHM; FAM30A; KIAA0125; IGHA1; LOC100132941; IGHV3-23; LOC100293211; C12orf32; LOC90925
15q15.1		R-band	Bad	61	11	18,03	2.74[2.25-4.16]	2.099347	GPR176; EIF2AK4; BUB1B; CASC5; SPINT1; CHAC1; OIP5; LTK; MGA; SPTBN5; EHD4
15q21.3		G-band	Bad	28	5	17,86	2.92[2.65-5.53]	3.786625	WDR72; UNC13C; TEX9; TCF12; LOC283663
15q22.2		G-band	Bad	23	6	26,09	2.82[2.31-3.63]	4.048262	CCNB2; GCNT3; RORA; VPS13C; TLN2; RPS27L
15q25.2		R-band		27	5	18,52	3.64[2.46-4.41]	1.110884	CPEB1; HOMER2; TM6SF1; SH3GL3; ADAMTSL3
15q26.3		R-band		25	5	20	3.08[2.38-3.43]	3.669952	ARRDC4; SYNM; ADAMTS17; LASS3; TM2D3
16p13.11	FRA16A	R-band	Bad	14	4	28,57	2.99[2.51-3.44]	1.174589	PDXDC1; NTAN1; MYH11; ABCC6
16p13.13		R-band		25	4	16	2.48[2.16-3.21]	0.990948	CIITA; SOCS1; C16orf75; GSPT1
16q12.2		G-band	Bad	26	9	34,62	2.91[2.04-3.79]	3.60291	CHD9; RBL2; CRNDE; LPCAT2; CAPNS2; GNAO1; AMFR; MT1E; MT1F
16q24.1		R-band		29	6	20,69	2.39[2.27-3.94]	1.707686	ADAD2; COTL1; GINS2; C16orf74; COX4I1; IRF8
18p11.21		R-band		22	6	27,27	2.85[2.39-3.59]	1.529521	GNAL; MPPE1; IMPA2; TUBB6; SPIRE1; C18orf1
18p11.22		G-band		16	5	31,25	2.64[2.4-2.71]	1.964579	KIAA0802; ANKRD12; RAB31; TXNDC2; FAM38B
18p11.32		R-band	Bad	18	5	27,78	2.5[2.37-2.73]	2.189424	TYMS; LOC388456; NDC80; SMCHD1; EMILIN2
18q12.1		G-band		25	7	28	2.79[2.38-3.24]	6.542324	CDH2; DSG2; RNF125; FAM59A; KLHL14; NOL4; DTNA
18q21.2		G-band		15	4	26,67	2.62[2.23-3.78]	4.188642	MEX3C; DCC; RAB27B; TCF4
19q13.42		R-band		96	19	19,79	2.87[2.35-4.15]	2.184194	ZNF415; ZNF331; MYADM; CACNG6; TMC4; LILRA6; LILRB2; LILRA3; LAIR1; LAIR2; LILRA2; LILRB1; LILRA1; LILRB4; KIR3DL2; KIR2DS1; NLRP7; NLRP2; BRSK1
20p11.21		R-band	Bad	34	6	17,65	2.85[2.38-4.64]	2.328337	CD93; CST4; TMEM90B; CST7; PYGB; GINS1
20q11.21		R-band		45	8	17,78	2.61[2.2-3.07]	1.728102	DEFB124; ID1; TPX2; C20orf57; HCK; LOC284805; DNMT3B; RP11-49G10.8
20q13.2		G-band	Bad	17	4	23,53	3.22[2.51-4.37]	4.940951	NFATC2; ATP9A; DOK5; AURKA
20q13.32		G-band	Bad	21	4	19,05	3.18[2.91-4.47]	1.062129	LOC149773; GNAS; TUBB1; PHACTR3
21q21.3		G-band		24	4	16,67	3.83[3.3-5.25]	1.450473	NCRNA00158; MIR155HG; JAM2; ADAMTS1
21q22.11		R-band	Good	44	8	18,18	2.79[2.03-3.24]	2.652846	TIAM1; SFRS15; C21orf119; C21orf63; C21orf62; IFNAR1; GART; ITSN1
22q11.22		G-band		18	6	33,33	4.72[3.2-7.25]	0.697094	IGLV4-60; IGLV1-44; IGL@; IGLV3-19; LOC100293440; IGLV4-3
22q12.1		G-band		24	5	20,83	3.57[2.29-4.92]	1.800063	CRYBB1; CRYBA4; MIAT; MN1; XBP1
Xp11.22		G-band	Bad	29	5	17,24	3.11[2.38-3.97]	1.658694	NUDT11; MAGED4; XAGE1A; SSX2; XAGE3
Xp11.23		R-band	Bad	75	14	18,67	3.31[2.27-5.05]	3.047125	LOC401588; CHST7; TIMP1; CFP; SSX1; SSX3; SSX4; PCSK1N; OTUD5; GAGE12F; GAGE12C; GAGE1; GAGE3; PAGE1
Xq13.2		G-band		15	5	33,33	2.84[2.2-5.13]	1.643805	DMRTC1; CXorf50B; XIST; NCRNA00182; SLC16A2
Xq22.1	FRAXC	R-band	Good	38	7	18,42	2.93[2.31-3.82]	2.433912	TSPAN6; XKRX; ARMCX1; TCEAL2; TMSB15A; GPRASP1; BEX1
Xq22.3		R-band		25	5	20	2.9[2.38-3.8]	1.74605	RNF128; NUP62CL; FRMPD3; COL4A6; COL4A5
Xq23		G-band	Bad	24	4	16,67	4.15[3.02-4.81]	0.976933	HTR2C; IL13RA2; LRCH2; PLS3

Online Supplementary Table S7. Chromosome (sub)bands with more than ten spike genes. The 149 (sub)bands with a significantly increased frequency of spike genes were identified using a χ^2 test and multiple testing corrections. Data are for the 15 chromosome (sub)bands with at least ten spike genes.

Chromosome (sub)bands	Number of spike genes	Total number of genes	%of spike genes
11p15.4	20	113	17.70
19q13.42	19	96	19.79
14q11.2	18	93	19.35
14q32.33	17	53	32.08
12p13.31	17	90	18.89
9q34.3	16	95	16.84
Xp11.23	14	75	18.67
4q13.3	13	53	24.53
1q23.3	13	56	23.21
7q36.1	13	66	19.70
15q15.1	11	61	18.03
1p36.12	10	42	23.81
1p31.1	10	47	21.28
6p22.2	10	51	19.61
6q21	10	58	17.24

Online Supplementary Table S8. The maximally selected rank statistic (MaxStat) and multiple testing correction were used to evaluate the prognostic value of spike (sub)bands in the HM cohort. The proportion of patients with a spike band expression above the cutoff determined by MaxStat algorithm is given as % of patients with high spike (sub)band expression. * indicates the 53 sub(bands) used to build an optimum spike band score (see Figure 6).

Spike (sub) band	Spike genes (n)	% of spike genes among genes located in the cytoband	*p*-value	Pronostic value	% of patients with high spike (sub) band expression	List of spike genes
10q23.33*	6	28.57	5.5E-05	Bad	15.0	*KIF11; CYP26A1; MYOF; CEP55; HELLS; CYP2C9*
18p11.32*	5	27.78	6.1E-05	Bad	11.7	*TYMS; LOC388456; NDC80; SMCHD1; EMILIN2*
Xp11.22*	5	17.24	1.7E-04	Bad	55.3	*NUDT11; MAGED4; XAGE1A; SSX2; XAGE3*
Xq23*	4	16.67	2.5E-04	Bad	34.5	*HTR2C; IL13RA2; LRCH2; PLS3*
15q21.3*	5	17.86	3.1E-04	Bad	48.5	*WDR72; UNC13C; TEX9; TCF12; LOC283663*
1q42.13*	6	18.18	3.9E-04	Bad	24.3	*CDC42BPA; C1orf69; HIST3H2A; RHOU; C1orf96; GALNT2*
3q24*	4	22.22	7.8E-04	Bad	25.7	*PLOD2; PLSCR4; PLSCR1; CPA3*
20q13.2*	4	23.53	9.0E-04	Bad	24.3	*NFATC2; ATP9A; DOK5; AURKA*
1q21.2*	6	23.08	1.2E-03	Bad	10.7	*CKS1B; LOC100292701; HIST2H2AA3; HIST2H2BE; MTMR11; PLEKHO1; CA14*
15q22.2*	6	26.09	1.5E-03	Bad	29.1	*CCNB2; GCNT3; RORA; VPS13C; TLN2; RPS27L*
5q12.1*	5	31.25	1.7E-03	Bad	47.1	*PDE4D; DEPDC1B; LOC728153; IPO11*
10q24.31*	5	22.73	1.9E-03	Bad	11.7	*SCD; SEC31B; PAX2; FAM178A; SEMA4G*
1q41*	9	26.47	2.1E-03	Bad	23.3	*CENPF; USH2A; GPATCH2; TGFB2; MARK1; C1orf115; HLX; DUSP10; SUSD4*
3q23*	5	20.83	2.2E-03	Bad	25.2	*RBP1; CLSTN2; XRN1; PCOLCE2; SR140*
1q31.3*	5	31.25	2.7E-03	Bad	30.1	*CFH; CFHR4; ASPM; DENND1B; PTPRC*
16p13.11*	4	28.57	3.2E-03	Bad	18.4	*PDXDC1; NTAN1; MYH11; ABCC6*
20p11.21*	6	17.65	3.3E-03	Bad	16.5	*CD93; CST4; TMEM90B; CST7; PYGB; GINS1*
2p25.1*	5	17.24	3.4E-03	Bad	21.4	*ID2; MBOAT2; RRM2; ROCK2; GREB1*
7p12.1*	4	57.14	4.0E-03	Bad	40.3	*FIGNL1; GRB10; COBL; POM121L12*
5q13.2*	6	18.75	4.9E-03	Bad	55.8	*CCNB1; CCDC125; LOC653188; MAP1B; TMEM171; RGNEF*
15q15.1*	11	18.03	5.9E-03	Bad	25.7	*GPR176; EIF2AK4; BUB1B; CASC5; SPINT1; CHAC1; OIP5; LTK; MGA; SPTBN5; EHD4*
20q13.32*	4	19.05	6.9E-03	Bad	38.3	*LOC149773; GNAS; TUBB1; PHACTR3*
16q12.2*	9	34.62	8.4E-03	Bad	62.1	*CHD9; RBL2; CRNDE; LPCAT2; CAPNS2; GNAO1; AMFR; MT1E; MT1F*
11p15.3*	4	33.33	8.5E-03	Bad	10.7	*GALNTL4; USP47; MICAL2; TEAD1*
3q26.33*	4	26.67	8.9E-03	Bad	50.0	*GNB4; MRPL47; SOX2; ATP11B*
2q24.3*	7	41.18	9.2E-03	Bad	67.5	*FIGN; GRB14; COBLL1; SCN3A; GALNT3; STK39; LASS6*
3q13.2*	7	31.82	9.4E-03	Bad	18.0	*PHLDB2; C3orf52; GCET2; CD200; ATG3; CCDC80; BOC*
14q23.2*	4	30.77	1.0E-02	Bad	18.0	*HIF1A; FLJ43390; SGPP1; SYNE2*
4q31.3*	4	16.67	1.0E-02	Bad	50.0	*DKFZP434I0714; TMEM154; TLR2; SFRP2*
Xp11.23*	14	18.67	1.3E-02	Bad	25.2	*LOC401588; CHST7; TIMP1; CFP; SSX1; SSX3; SSX4; PCSK1N; OTUD5; GAGE12F; GAGE12C; GAGE1; GAGE3; PAGE1*
13q13.3*	5	23.81	1.3E-02	Bad	34.0	*NBEA; MAB21L1; DCLK1; SOHLH2; TRPC4*
6q15*	5	20	1.3E-02	Bad	64.1	*CNR1; RNGTT; GABRR1; MDN1; BACH2*
8q24.12*	4	30.77	1.4E-02	Bad	75.2	*MAL2; ENPP2; DSCC1; SNTB1*
6p22.2	10	19.61	1.4E-02	Bad	36.4	*CMAH; SLC17A4; HFE; HIST1H4C; HIST1H2BC; HIST1H2AD; HIST1H2BG; HIST1H2AE; HIST1H4H; BTN1A1*
10q23.31*	6	26.09	1.5E-02	Bad	10.2	*PTEN; ANKRD22; FAS; IFIT2; IFIT3; IFIT1*
7p15.3*	8	28.57	1.5E-02	Bad	53.4	*LOC541472; IL6; FAM126A; GPNMB; IGF2BP3; DFNA5; OSBPL3; CYCS*
7q36.1*	13	19.7	1.7E-04	Good	87.4	*ATP6V0E2; LOC285972; GIMAP8; GIMAP7; GIMAP4; GIMAP6; GIMAP1; GIMAP5; TMEM176B; TMEM176A; ABP1; ASB10; LOC100128822*
1q23.1*	7	18.92	3.9E-04	Good	86.9	*NES; FCRL3; FCRL2; FCRL1; CD5L; CD1A; MNDA*
6q23.3*	5	20.83	2.6E-03	Good	85.4	*MYB; MAP7; IFNGR1; TNFAIP3; PERP*
12q24.22*	5	55.56	2.6E-03	Good	90.3	*NCRNA00173; RNFT2; HRK; TESC; NOS1*
21q22.11*	8	18.18	2.9E-03	Good	88.3	*TIAM1; SFRS15; C21orf119; C21orf63; C21orf62; IFNAR1; GART; ITSN1*
14q22.1*	7	31.82	4.1E-03	Good	74.8	*PYGL; FRMD6; GNG2; NID2; PTGDR; PTGER2; FERMT2*
6q25.3*	8	25	5.1E-03	Good	80.1	*SNX9; SYNJ2; TULP4; SYTL3; EZR; TAGAP; SOD2; MAS1*
4q22.1*	5	20	5.2E-03	Good	44.7	*SPP1; ABCG2; HERC6; SNCA; MMRN1*
12p13.31*	17	18.89	5.5E-03	Good	89.3	*SCNN1A; CD27; VAMP1; LAG3; CD4; CDCA3; C1R; CD163L1; CD163; SLC2A3; C3AR1; CLEC4A; A2M; CLEC2D; CD69; KLRF1; CLEC2B*
6p21.3*	4	80	6.0E-03	Good	43.7	*LST1; HLA-DRA; HLA-DQA1; HLA-DRB4*
1p21.2*	4	22.22	6.1E-03	Good	88.8	*CCDC76; GPR88; VCAM1; S1PR1*
1p35.2*	4	21.05	6.2E-03	Good	51.5	*LAPTM5; SDC3; SERINC2; BAI2*
5q33.3*	6	20	6.9E-03	Good	65.0	*TIMD4; HAVCR2; NIPAL4; THG1L; CLINT1; EBF1*
1p22.1*	4	19.05	7.0E-03	Good	72.3	*TGFBR3; FNBP1L; BCAR3; GCLM*
4q35.1*	7	23.33	1.2E-02	Good	83.5	*WWC2; STOX2; ACSL1; C4orf47; PDLIM3; SORBS2; TLR3*
10q11.21*	7	26.92	1.2E-02	Good	33.5	*RET; RASGEF1A; LOC439911; CXCL12; RASSF4; C10orf10; LOC338579*
9q22.33*	6	20.69	1.3E-02	Good	68.0	*CDC14B; KIAA1529; TRIM14; TGFBR1; SEC61B; NR4A3*
2q13*	9	21.43	1.4E-02	Good	12.6	*ANKRD57; LIMS3; BUB1; BCL2L11; MERTK; CHCHD5; SLC20A1; IL1B; LOC100130100*
Xq22.1	7	18.42	1.8E-02	Good	74.8	*TSPAN6; XKRX; ARMCX1; TCEAL2; TMSB15A; GPRASP1; BEX1*

Online Supplementary Table S9. List of the 344 spike genes associated with the 55 prognostic spike (sub)bands.

Probe sets	Gene Name	Entrez Gene Name	Location	Type(s)	Drug(s)
206271_at	TLR3	toll-like receptor 3	Plasma Membrane	transmembrane receptor	ampligen
209909_s_at	TGFB2	transforming growth factor, beta 2	Extracellular Space	growth factor	AP-12009
213326_at	VAMP1	vesicle-associated membrane protein 1 (synaptobrevin 1)	Plasma Membrane	transporter	botulinum toxin type B
206172_at	IL13RA2	interleukin 13 receptor, alpha 2	Plasma Membrane	transmembrane receptor	cintredekin besudotox
204491_at	PDE4D	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	Cytoplasm	enzyme	dyphylline, nitroglycerin, arofylline, tetomilast, L 869298, aminophylline, anagrelide, cilomilast, milrinone, rolipram, dipyridamole, L-826,141, roflumilast, tolbutamide, theophylline, pentoxifylline, caffeine
230690_at	TUBB1	tubulin, beta 1	Cytoplasm	other	epothilone B, ixabepilone, colchicine/probenecid, XRP9881, ABT-751, eribulin, MST-997, AL 108, EC145, NPI-2358, milataxel, TPI 287, TTI-237, BMS-275183, docetaxel, vinflunine, vinorelbine, vincristine, vinblastine, paclitaxel, podophyllotoxin, colchicine
202589_at	TYMS	thymidylate synthetase	Nucleus	enzyme	flucytosine, 5-fluorouracil, plevitrexed, nolatrexed, capecitabine, trifluridine, floxuridine, LY231514
209773_s_at	RRM2	ribonucleotide reductase M2	Nucleus	enzyme	gemcitabine, triapine, hydroxyurea, fludarabine phosphate
207309_at	NOS1	nitric oxide synthase 1 (neuronal)	Cytoplasm	enzyme	GW 273629, omega-N-methylarginine
39402_at	IL1B	interleukin 1, beta	Extracellular Space	cytokine	IL-1 trap, canakinumab
236478_at	IFNAR1	interferon (alpha, beta and omega) receptor 1	Plasma Membrane	transmembrane receptor	interferon alfacon-1, PEG-interferon alfa-2a, IFNB1, IFNA2, interferon alfa-2a/ribavirin, pegintron, interferon beta-1b
242903_at	IFNGR1	interferon gamma receptor 1	Plasma Membrane	transmembrane receptor	interferon gamma-1b
230097_at	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	Cytoplasm	enzyme	LY231514
219464_at	CA14	carbonic anhydrase XIV	Plasma Membrane	enzyme	methazolamide, hydrochlorothiazide, acetazolamide, trichloromethiazide, chlorothiazide, chlorthalidone, benzthiazide, sulfacetamide, topiramate
206631_at	PTGER2	prostaglandin E receptor 2 (subtype EP2), 53kDa	Plasma Membrane	G-protein coupled receptor	misoprostol, prostaglandin E2, prostaglandin E1, CP 533536, diclofenac/misoprostol
208079_s_at	AURKA	aurora kinase A	Nucleus	kinase	MLN8054
207106_s_at	LTK	leukocyte receptor tyrosine kinase	Plasma Membrane	kinase	pazopanib
210432_s_at	SCN3A	sodium channel, voltage-gated, type III, alpha subunit	Plasma Membrane	ion channel	riluzole
207307_at	HTR2C	5-hydroxytryptamine (serotonin) receptor 2C	Plasma Membrane	G-protein coupled receptor	risperidone, buspirone, caffeine/ergotamine, blonanserin, asenapine, vabicaserin, opipramol, fluoxetine/olanzapine, epinastine, fenfluramine, quetiapine, olanzapine, nefazodone, mirtazapine, ziprasidone, aripiprazole, apomorphine, ergotamine
212067_s_at	C1R	complement component 1, r subcomponent	Extracellular Space	peptidase	SERPING1
215771_x_at	RET	ret proto-oncogene	Plasma Membrane	kinase	sunitinib
205207_at	IL6	interleukin 6 (interferon, beta 2)	Extracellular Space	cytokine	tocilizumab
1560225_at	CNR1	cannabinoid receptor 1 (brain)	Plasma Membrane	G-protein coupled receptor	trans-(Â±)-nabilone, SLV 319, rimonabant, BAY 38-7271, delta-8-tetrahydrocannabinol, delta-9-tetrahydrocannabinol
217264_s_at	SCNN1A	sodium channel, nonvoltage-gated 1 alpha	Plasma Membrane	ion channel	triamterene/hydrochlorothiazide, amiloride, amiloride/hydrochlorothiazide, triamterene
217757_at	A2M	alpha-2-macroglobulin	Extracellular Space	transporter	
214033_at	ABCC6	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	Plasma Membrane	transporter	
209735_at	ABCG2	ATP-binding cassette, sub-family G (WHITE), member 2	Plasma Membrane	transporter	
203559_s_at	ABP1	amiloride binding protein 1 (amine oxidase (copper-containing))	Extracellular Space	enzyme	
201963_at	ACSL1	acyl-CoA synthetase long-chain family member 1	Cytoplasm	enzyme	
202203_s_at	AMFR	autocrine motility factor receptor	Plasma Membrane	transmembrane receptor	
239196_at	ANKRD22	ankyrin repeat domain 22	Nucleus	transcription regulator	
227034_at	ANKRD57	ankyrin repeat domain 57	Nucleus	transcription regulator	
218694_at	ARMCX1	armadillo repeat containing, X-linked 1	unknown	other	
1553039_a_at	ASB10	ankyrin repeat and SOCS box-containing 10	Nucleus	transcription regulator	
219918_s_at	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	Nucleus	other	
220237_at	ATG3	ATG3 autophagy related 3 homolog (S. cerevisiae)	Cytoplasm	enzyme	
238811_at	ATP11B	ATPase, class VI, type 11B	Plasma Membrane	transporter	
213587_s_at	ATP6V0E2	ATPase, H+ transporting V0 subunit e2	unknown	enzyme	
212062_at	ATP9A	ATPase, class II, type 9A	Plasma Membrane	transporter	
221234_s_at	BACH2 (includes EG:60468)	BTB and CNC homology 1, basic leucine zipper transcription factor 2	Nucleus	transcription regulator	
204966_at	BAI2	brain-specific angiogenesis inhibitor 2	Plasma Membrane	G-protein coupled receptor	
204032_at	BCAR3	breast cancer anti-estrogen resistance 3	Cytoplasm	other	
222343_at	BCL2L11	BCL2-like 11 (apoptosis facilitator)	Cytoplasm	other	
218332_at	BEX1	brain expressed, X-linked 1	Cytoplasm	other	
225990_at	BOC	Boc homolog (mouse)	unknown	other	
207395_at	BTN1A1	butyrophilin, subfamily 1, member A1	Plasma Membrane	other	
209642_at	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	Nucleus	kinase	
203755_at	BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	Nucleus	kinase	
209182_s_at	C10ORF10	chromosome 10 open reading frame 10	Cytoplasm	other	
218546_at	C1ORF115	chromosome 1 open reading frame 115	unknown	other	
215490_at	C1ORF69	chromosome 1 open reading frame 69	unknown	other	
225904_at	C1ORF96	chromosome 1 open reading frame 96	unknown	other	
227424_x_at	C21ORF119	chromosome 21 open reading frame 119	unknown	other	
220543_at	C21ORF62	chromosome 21 open reading frame 62	unknown	other	
227188_at	C21ORF63	chromosome 21 open reading frame 63	unknown	other	
209906_at	C3AR1	complement component 3a receptor 1	Plasma Membrane	G-protein coupled receptor	
219474_at	C3ORF52	chromosome 3 open reading frame 52	unknown	other	
236915_at	C4ORF47	chromosome 4 open reading frame 47	unknown	other	
223832_s_at	CAPNS2	calpain, small subunit 2	Cytoplasm	other	
228323_at	CASC5	cancer susceptibility candidate 5	Nucleus	other	
229082_at	CCDC125	coiled-coil domain containing 125	unknown	other	
232489_at	CCDC76	coiled-coil domain containing 76	unknown	other	
225242_s_at	CCDC80	coiled-coil domain containing 80	Nucleus	other	
214710_s_at	CCNB1	cyclin B1	Nucleus	other	
202705_at	CCNB2	cyclin B2	Cytoplasm	other	
215049_x_at	CD163	CD163 molecule	Plasma Membrane	transmembrane receptor	
223655_at	CD163L1 (includes EG:283316)	CD163 molecule-like 1	Plasma Membrane	transmembrane receptor	
210325_at	CD1A	CD1a molecule	Plasma Membrane	other	
209582_s_at	CD200	CD200 molecule	Plasma Membrane	other	
206150_at	CD27	CD27 molecule	Plasma Membrane	transmembrane receptor	
203547_at	CD4	CD4 molecule	Plasma Membrane	transmembrane receptor	
206680_at	CD5L	CD5 molecule-like	Plasma Membrane	transmembrane receptor	
209795_at	CD69	CD69 molecule	Plasma Membrane	transmembrane receptor	
202878_s_at	CD93	CD93 molecule	Plasma Membrane	other	
221555_x_at	CDC14B	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	Nucleus	phosphatase	
214464_at	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)	Cytoplasm	kinase	
223307_at	CDCA3	cell division cycle associated 3	Cytoplasm	other	
207828_s_at	CENPF	centromere protein F, 350/400ka (mitosin)	Nucleus	other	
218542_at	CEP55	centrosomal protein 55kDa	unknown	other	
213800_at	CFH	complement factor H	Extracellular Space	other	
207874_s_at	CFHR4	complement factor H-related 4	Extracellular Space	transporter	
206380_s_at	CFP	complement factor properdin	Extracellular Space	other	
219270_at	CHAC1	ChaC, cation transport regulator homolog 1 (E. coli)	unknown	other	
1562892_at	CHCHD5	coiled-coil-helix-coiled-coil-helix domain containing 5	unknown	other	
239654_at	CHD9 (includes EG:80205)	chromodomain helicase DNA binding protein 9	Cytoplasm	other	
206756_at	CHST7	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	Cytoplasm	enzyme	
201897_s_at	CKS1B	CDC28 protein kinase regulatory subunit 1B	Cytoplasm	kinase	
209732_at	CLEC2B	C-type lectin domain family 2, member B	Plasma Membrane	other	
233500_x_at	CLEC2D (includes EG:29121)	C-type lectin domain family 2, member D	Plasma Membrane	transmembrane receptor	
219947_at	CLEC4A	C-type lectin domain family 4, member A	Plasma Membrane	transmembrane receptor	

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230609_at	CLINT1	clathrin interactor 1	Cytoplasm	other	
219414_at	CLSTN2	calsyntenin 2	Plasma Membrane	transporter	
229604_at	CMAH	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase) pseudogene	Cytoplasm	enzyme	
213050_at	COBL	cordon-bleu homolog (mouse)	unknown	other	
211032_at	COBLL1	COBL-like 1	unknown	other	
205624_at	CPA3	carboxypeptidase A3 (mast cell)	Extracellular Space	peptidase	
206994_at	CST4	cystatin S	Extracellular Space	other	
210140_at	CST7	cystatin F (leukocystatin)	Extracellular Space	other	
209687_at	CXCL12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	Extracellular Space	cytokine	
244546_at	CYCS (includes EG:54205)	cytochrome c, somatic	Cytoplasm	enzyme	
206424_at	CYP26A1	cytochrome P450, family 26, subfamily A, polypeptide 1	Cytoplasm	enzyme	
220017_x_at	CYP2C9	cytochrome P450, family 2, subfamily C, polypeptide 9	Cytoplasm	enzyme	
229800_at	DCLK1	doublecortin-like kinase 1	Cytoplasm	kinase	
238787_at	DENND1B	DENN/MADD domain containing 1B	unknown	other	
226980_at	DEPDC1B	DEP domain containing 1B	unknown	other	
203695_s_at	DFNA5	deafness, autosomal dominant 5	unknown	other	
231954_at	DKFZP434I0714	hypothetical protein DKFZP434I0714	unknown	other	
214844_s_at	DOK5	docking protein 5	Plasma Membrane	other	
219000_s_at	DSCC1	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)	unknown	other	
215501_s_at	DUSP10	dual specificity phosphatase 10	Nucleus	phosphatase	
227646_at	EBF1	early B-cell factor 1	Nucleus	transcription regulator	
1556608_a_at	EHD4	EH-domain containing 4	Plasma Membrane	enzyme	
237145_at	EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4	unknown	kinase	
224374_s_at	EMILIN2	elastin microfibril interfacer 2	Extracellular Space	other	
209392_at	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	Plasma Membrane	enzyme	
217234_s_at	EZR	ezrin	Plasma Membrane	other	
223625_at	FAM126A	family with sequence similarity 126, member A	Cytoplasm	other	
235590_at	FAM178A	family with sequence similarity 178, member A	unknown	other	
204780_s_at	FAS	Fas (TNF receptor superfamily, member 6)	Plasma Membrane	transmembrane receptor	
243968_x_at	FCRL1	Fc receptor-like 1	Plasma Membrane	other	
224193_s_at	FCRL2	Fc receptor-like 2	Plasma Membrane	transmembrane receptor	
231093_at	FCRL3	Fc receptor-like 3	Plasma Membrane	other	
209209_s_at	FERMT2	fermitin family homolog 2 (Drosophila)	Cytoplasm	other	
242828_at	FIGN	fidgetin	Nucleus	other	
222843_at	FIGNL1	fidgetin-like 1	unknown	enzyme	
231186_at	FLJ43390	hypothetical LOC646113	unknown	other	
215017_s_at	FNBP1L	formin binding protein 1-like	unknown	other	
225464_at	FRMD6	FERM domain containing 6	unknown	other	
206525_at	GABRR1	gamma-aminobutyric acid (GABA) receptor, rho 1	Plasma Membrane	ion channel	
207739_s_at	GAGE1	G antigen 1	unknown	other	
206640_x_at	GAGE12I	G antigen 12I	unknown	other	
207663_x_at	GAGE3	G antigen 3	unknown	other	
239930_at	GALNT2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)	Cytoplasm	enzyme	
203397_s_at	GALNT3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3)	Cytoplasm	enzyme	
1554079_at	GALNTL4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4	Cytoplasm	enzyme	
235310_at	GCET2	germinal center expressed transcript 2	unknown	other	
236140_at	GCLM	glutamate-cysteine ligase, modifier subunit	Cytoplasm	enzyme	
219508_at	GCNT3	glucosaminyl (N-acetyl) transferase 3, mucin type	Plasma Membrane	enzyme	
1552316_a_at	GIMAP1	GTPase, IMAP family member 1	Cytoplasm	other	
219243_at	GIMAP4	GTPase, IMAP family member 4	unknown	other	
218805_at	GIMAP5	GTPase, IMAP family member 5	Cytoplasm	other	
219777_at	GIMAP6	GTPase, IMAP family member 6	unknown	other	
228071_at	GIMAP7	GTPase, IMAP family member 7	unknown	other	
235306_at	GIMAP8	GTPase, IMAP family member 8	unknown	other	
206102_at	GINS1	GINS complex subunit 1 (Psf1 homolog)	Nucleus	other	
231951_at	GNAO1	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	Plasma Membrane	enzyme	
214157_at	GNAS	GNAS complex locus	Plasma Membrane	enzyme	
225710_at	GNB4	guanine nucleotide binding protein (G protein), beta polypeptide 4	Plasma Membrane	enzyme	
224964_s_at	GNG2	guanine nucleotide binding protein (G protein), gamma 2	Plasma Membrane	enzyme	
236026_at	GPATCH2	G patch domain containing 2	unknown	other	
201141_at	GPNMB	glycoprotein (transmembrane) nmb	Plasma Membrane	enzyme	
227846_at	GPR176	G protein-coupled receptor 176	Plasma Membrane	G-protein coupled receptor	
220313_at	GPR88	G protein-coupled receptor 88	Plasma Membrane	G-protein coupled receptor	
204793_at	GPRASP1	G protein-coupled receptor associated sorting protein 1	Cytoplasm	transporter	
209409_at	GRB10	growth factor receptor-bound protein 10	Cytoplasm	other	
206204_at	GRB14	growth factor receptor-bound protein 14	Plasma Membrane	other	
205862_at	GREB1	growth regulation by estrogen in breast cancer 1	Cytoplasm	other	
235458_at	HAVCR2	hepatitis A virus cellular receptor 2	Plasma Membrane	transmembrane receptor	
238022_at	HCG 1815491	colorectal neoplasia differentially expressed (non-protein coding)	unknown	other	
227350_at	HELLS	helicase, lymphoid-specific	Nucleus	enzyme	
219352_at	HERC6	hect domain and RLD 6	unknown	enzyme	
206086_x_at	HFE	hemochromatosis	Plasma Membrane	transmembrane receptor	
200989_at	HIF1A	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	Nucleus	transcription regulator	
214472_at	HIST1H2AD	histone cluster 1, H2ad	Nucleus	other	
214469_at	HIST1H2AE (includes EG:3012)	histone cluster 1, H2ae	Nucleus	other	
214455_at	HIST1H2BC	histone cluster 1, H2bc	Nucleus	other	
210387_at	HIST1H2BG	histone cluster 1, H2bg	Nucleus	other	
205967_at	HIST1H4C	histone cluster 1, H4c	Nucleus	other	
208180_s_at	HIST1H4H (includes EG:8365)	histone cluster 1, H4h	Nucleus	other	
214290_s_at	HIST2H2AA3	histone cluster 2, H2aa3	Nucleus	other	
202708_s_at	HIST2H2BE	histone cluster 2, H2be	Nucleus	other	
221582_at	HIST3H2A	histone cluster 3, H2a	unknown	other	
213831_at	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	Plasma Membrane	transmembrane receptor	
208894_at	HLA-DRA	major histocompatibility complex, class II, DR alpha	Plasma Membrane	transmembrane receptor	
209728_at	HLA-DRB4	major histocompatibility complex, class II, DR beta 4	Plasma Membrane	transmembrane receptor	
214438_at	HLX	H2.0-like homeobox	Nucleus	transcription regulator	
206864_s_at	HRK	harakiri, BCL2 interacting protein (contains only BH3 domain)	Cytoplasm	other	
201566_x_at	ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	Nucleus	transcription regulator	
203153_at	IFIT1	interferon-induced protein with tetratricopeptide repeats 1	Cytoplasm	other	
226757_at	IFIT2	interferon-induced protein with tetratricopeptide repeats 2	unknown	other	
204747_at	IFIT3	interferon-induced protein with tetratricopeptide repeats 3	Cytoplasm	other	
203820_s_at	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	Cytoplasm	translation regulator	
238488_at	IPO11	importin 11	Nucleus	transporter	

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209298_s_at	ITSN1	intersectin 1 (SH3 domain protein)	Cytoplasm	other	
229628_s_at	KIAA1529	KIAA1529	unknown	other	
204444_at	KIF11	kinesin family member 11	Nucleus	other	
220646_s_at	KLRF1	killer cell lectin-like receptor subfamily F, member 1	Plasma Membrane	transmembrane receptor	
206486_at	LAG3	lymphocyte-activation gene 3	Plasma Membrane	transmembrane receptor	
201720_s_at	LAPTM5	lysosomal protein transmembrane 5	Plasma Membrane	other	
212446_s_at	LASS6	LAG1 homolog, ceramide synthase 6	Nucleus	transcription regulator	
223800_s_at	LIMS3	LIM and senescent cell antigen-like domains 3	unknown	other	
235174_s_at	LOC100128822	hypothetical LOC100128822	unknown	other	
1556900_at	LOC149773	hypothetical protein LOC149773	unknown	other	
230245_s_at	LOC283663	hypothetical LOC283663	unknown	other	
1560762_at	LOC285972	hypothetical protein LOC285972	unknown	other	
1561225_at	LOC338579	hypothetical protein LOC338579	unknown	other	
1563117_at	LOC388456	hypothetical gene supported by BC039671	unknown	other	
241972_at	LOC401588	hypothetical LOC401588	unknown	other	
215599_at	LOC653188	glucuronidase, beta pseudogene 3	unknown	other	
1560199_x_at	LOC728153	similar to FAM133B protein	unknown	other	
227889_at	LPCAT2	lysophosphatidylcholine acyltransferase 2	Cytoplasm	enzyme	
227688_at	LRCH2	leucine-rich repeats and calponin homology (CH) domain containing 2	unknown	other	
215633_x_at	LST1	leukocyte specific transcript 1	Plasma Membrane	other	
206163_at	MAB21L1	mab-21-like 1 (C. elegans)	unknown	other	
223313_s_at	MAGED4B	melanoma antigen family D, 4B	unknown	other	
224650_at	MAL2	mal, T-cell differentiation protein 2	Plasma Membrane	transporter	
226084_at	MAP1B	microtubule-associated protein 1B	Cytoplasm	other	
202890_at	MAP7	microtubule-associated protein 7	Cytoplasm	other	
221047_s_at	MARK1	MAP/microtubule affinity-regulating kinase 1	Cytoplasm	kinase	
208210_at	MAS1	MAS1 oncogene	Plasma Membrane	G-protein coupled receptor	
226726_at	MBOAT2	membrane bound O-acyltransferase domain containing 2	unknown	other	
1569484_s_at	MDN1 (includes EG:23195)	MDN1, midasin homolog (yeast)	Nucleus	other	
211913_s_at	MERTK	c-mer proto-oncogene tyrosine kinase	Plasma Membrane	kinase	
230848_s_at	MGA	MAX gene associated	Nucleus	transcription regulator	
212473_s_at	MICAL2	microtubule associated monoxygenase, calponin and LIM domain containing 2	Cytoplasm	other	
205612_at	MMRN1	multimerin 1	Extracellular Space	other	
204959_at	MNDA	myeloid cell nuclear differentiation antigen	Nucleus	other	
223481_s_at	MRPL47	mitochondrial ribosomal protein L47	Cytoplasm	other	
212859_x_at	MT1E	metallothionein 1E	Cytoplasm	other	
217165_x_at	MT1F	metallothionein 1F	Cytoplasm	other	
205076_s_at	MTMR11	myotubularin related protein 11	unknown	other	
204798_at	MYB (includes EG:4602)	v-myb myeloblastosis viral oncogene homolog (avian)	Nucleus	transcription regulator	
201497_x_at	MYH11	myosin, heavy chain 11, smooth muscle	Cytoplasm	other	
201798_s_at	MYOF	myoferlin	Nucleus	other	
226439_s_at	NBEA (includes EG:26960)	neurobeachin	Cytoplasm	other	
237591_at	NCRNA00173	non-protein coding RNA 173	unknown	other	
204162_at	NDC80	NDC80 homolog, kinetochore complex component (S. cerevisiae)	Nucleus	other	
218678_at	NES	nestin	Cytoplasm	other	
226991_at	NFATC2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	Nucleus	transcription regulator	
204114_at	NID2	nidogen 2 (osteonidogen)	Extracellular Space	other	
230188_at	NIPAL4	NIPA-like domain containing 4	unknown	other	
209959_at	NR4A3	nuclear receptor subfamily 4, group A, member 3	Nucleus	ligand-dependent nuclear receptor	
213061_s_at	NTAN1	N-terminal asparagine amidase	Nucleus	enzyme	
219855_at	NUDT11	nudix (nucleoside diphosphate linked moiety X)-type motif 11	Cytoplasm	phosphatase	
213599_at	OIP5	Opa interacting protein 5	Nucleus	other	
209627_s_at	OSBPL3	oxysterol binding protein-like 3	Cytoplasm	other	
224745_x_at	OTUD5	OTU domain containing 5	unknown	other	
206897_at	PAGE1	P antigen family, member 1 (prostate associated)	unknown	other	
206229_x_at	PAX2	paired box 2	Nucleus	transcription regulator	
219295_s_at	PCOLCE2 (includes EG:26577)	procollagen C-endopeptidase enhancer 2	Extracellular Space	other	
218952_at	PCSK1N	proprotein convertase subtilisin/kexin type 1 inhibitor	Extracellular Space	other	
209621_s_at	PDLIM3	PDZ and LIM domain 3	Cytoplasm	other	
1560014_s_at	PDXDC1	pyridoxal-dependent decarboxylase domain containing 1	unknown	other	
236009_at	PERP	PERP, TP53 apoptosis effector	Plasma Membrane	other	
227949_at	PHACTR3	phosphatase and actin regulator 3	Nucleus	other	
225688_s_at	PHLDB2	pleckstrin homology-like domain, family B, member 2	Cytoplasm	other	
218223_s_at	PLEKHO1	pleckstrin homology domain containing, family O member 1	Plasma Membrane	other	
202619_s_at	PLOD2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	Cytoplasm	enzyme	
201215_at	PLS3	plastin 3	Cytoplasm	other	
202430_s_at	PLSCR1	phospholipid scramblase 1	Plasma Membrane	enzyme	
218901_at	PLSCR4	phospholipid scramblase 4	Plasma Membrane	enzyme	
1556291_at	POM121L12 (includes EG:285877)	POM121 membrane glycoprotein-like 12 (rat)	unknown	other	
233254_x_at	PTEN	phosphatase and tensin homolog	Cytoplasm	phosphatase	
215894_at	PTGDR	prostaglandin D2 receptor (DP)	Plasma Membrane	G-protein coupled receptor	
207238_s_at	PTPRC	protein tyrosine phosphatase, receptor type, C	Plasma Membrane	phosphatase	
201481_s_at	PYGB	phosphorylase, glycogen; brain	unknown	enzyme	
202990_at	PYGL	phosphorylase, glycogen, liver	unknown	enzyme	
230563_at	RASGEF1A	RasGEF domain family, member 1A	unknown	other	
226436_at	RASSF4	Ras association (RalGDS/AF-6) domain family member 4	unknown	other	
212332_at	RBL2	retinoblastoma-like 2 (p130)	Nucleus	other	
203423_at	RBP1	retinol binding protein 1, cellular	Extracellular Space	transporter	
1554003_at	RGNEF	Rho-guanine nucleotide exchange factor	unknown	other	
223169_s_at	RHOU	ras homolog gene family, member U	Cytoplasm	enzyme	
221908_at	RNFT2	ring finger protein, transmembrane 2	unknown	other	
211849_s_at	RNGTT	RNA guanylyltransferase and 5'-phosphatase	Nucleus	phosphatase	
202762_at	ROCK2	Rho-associated, coiled-coil containing protein kinase 2	Cytoplasm	kinase	
210426_x_at	RORA	RAR-related orphan receptor A	Nucleus	ligand-dependent nuclear receptor	
238935_at	RPS27L (includes EG:51065)	ribosomal protein S27-like	unknown	other	
204642_at	S1PR1	sphingosine-1-phosphate receptor 1	Plasma Membrane	G-protein coupled receptor	
200832_s_at	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	Cytoplasm	enzyme	
202898_at	SDC3	syndecan 3	Plasma Membrane	other	

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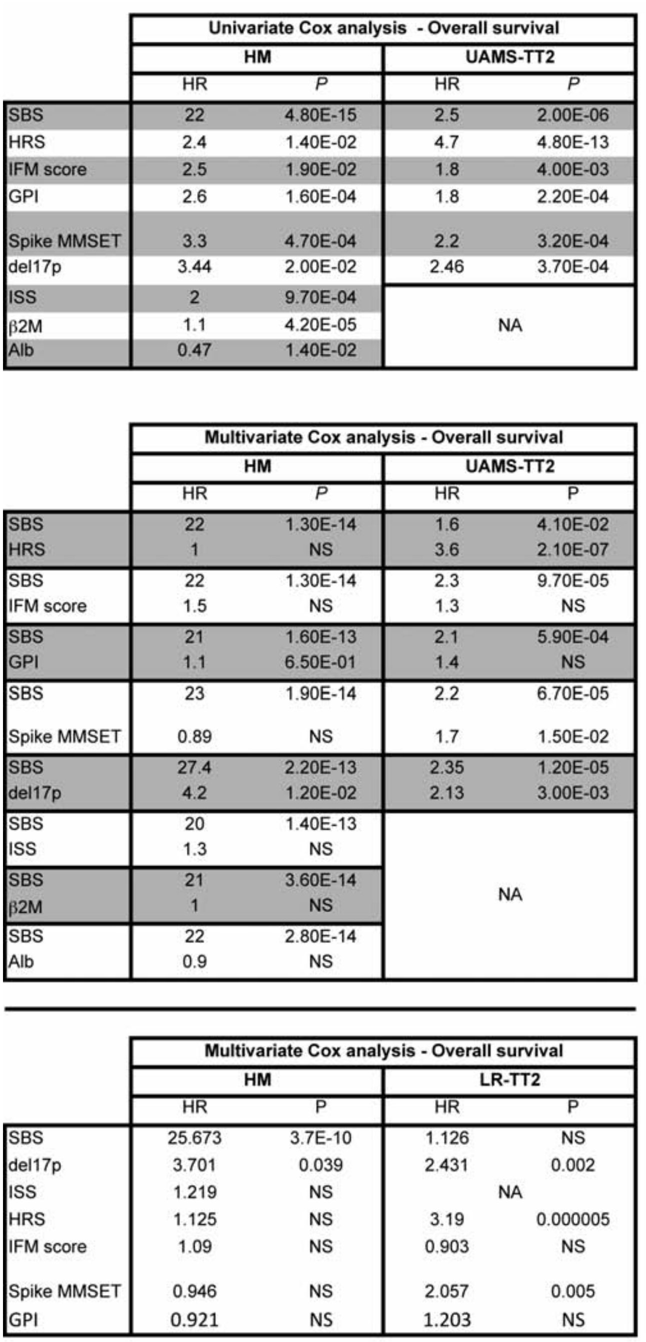
209889_at	SEC31B	SEC31 homolog B (S. cerevisiae)	unknown	other	
244700_at	SEC61B	Sec61 beta subunit	Cytoplasm	transporter	
219194_at	SEMA4G	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G	Plasma Membrane	other	
224762_at	SERINC2	serine incorporator 2	Plasma Membrane	transporter	
223122_s_at	SFRP2	secreted frizzled-related protein 2	Plasma Membrane	transmembrane receptor	
243759_at	SFRS15	splicing factor, arginine/serine-rich 15	Nucleus	other	
223391_at	SGPP1	sphingosine-1-phosphate phosphatase 1	Cytoplasm	phosphatase	
207051_at	SLC17A4	solute carrier family 17 (sodium phosphate), member 4	Plasma Membrane	transporter	
230494_at	SLC20A1	solute carrier family 20 (phosphate transporter), member 1	Plasma Membrane	transporter	
202499_s_at	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	Plasma Membrane	transporter	
1558747_at	SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1	unknown	other	
204466_s_at	SNCA	synuclein, alpha (non A4 component of amyloid precursor)	Cytoplasm	other	
226438_at	SNTB1	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	Plasma Membrane	other	
223027_at	SNX9 (includes EG:51429)	sorting nexin 9	Cytoplasm	transporter	
1566342_at	SOD2	superoxide dismutase 2, mitochondrial	Cytoplasm	enzyme	
220129_at	SOHLH2	spermatogenesis and oogenesis specific basic helix-loop-helix 2	unknown	other	
225728_at	SORBS2	sorbin and SH3 domain containing 2	Nucleus	other	
228038_at	SOX2	SRY (sex determining region Y)-box 2	Nucleus	transcription regulator	
202826_at	SPINT1	serine peptidase inhibitor, Kunitz type 1	Extracellular Space	other	
209875_s_at	SPP1	secreted phosphoprotein 1	Extracellular Space	cytokine	
1556839_s_at	SPTBN5	spectrin, beta, non-erythrocytic 5	Plasma Membrane	other	
236696_at	SR140	U2-associated SR140 protein	Nucleus	other	
206626_x_at	SSX1	synovial sarcoma, X breakpoint 1	Nucleus	transcription regulator	
210497_x_at	SSX2	synovial sarcoma, X breakpoint 2	Nucleus	transcription regulator	
207666_x_at	SSX3	synovial sarcoma, X breakpoint 3	unknown	other	
210394_x_at	SSX4	synovial sarcoma, X breakpoint 4	Nucleus	other	
202786_at	STK39	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	Nucleus	kinase	
231969_at	STOX2	storkhead box 2	unknown	other	
223822_at	SUSD4	sushi domain containing 4	unknown	other	
202761_s_at	SYNE2	spectrin repeat containing, nuclear envelope 2	Nucleus	other	
1555009_a_at	SYNJ2	synaptojanin 2	Cytoplasm	phosphatase	
242109_at	SYTL3	synaptotagmin-like 3	Cytoplasm	other	
1552542_s_at	TAGAP	T-cell activation RhoGTPase activating protein	unknown	other	
211276_at	TCEAL2	transcription elongation factor A (SII)-like 2	unknown	other	
235925_at	TCF12	transcription factor 12	Nucleus	transcription regulator	
224955_at	TEAD1	TEA domain family member 1 (SV40 transcriptional enhancer factor)	Nucleus	transcription regulator	
218872_at	TESC	tescalcin	unknown	other	
243198_at	TEX9	testis expressed 9	unknown	other	
236561_at	TGFBR1	transforming growth factor, beta receptor 1	Plasma Membrane	kinase	
226625_at	TGFBR3	transforming growth factor, beta receptor III	Plasma Membrane	kinase	
219122_s_at	THG1L	tRNA-histidine guanylyltransferase 1-like (S. cerevisiae)	Cytoplasm	enzyme	
213135_at	TIAM1	T-cell lymphoma invasion and metastasis 1	Cytoplasm	other	
1552280_at	TIMD4	T-cell immunoglobulin and mucin domain containing 4	Plasma Membrane	other	
201666_at	TIMP1	TIMP metallopeptidase inhibitor 1	Extracellular Space	other	
212701_at	TLN2	talin 2	Nucleus	other	
204924_at	TLR2	toll-like receptor 2	Plasma Membrane	transmembrane receptor	
238063_at	TMEM154	transmembrane protein 154	unknown	other	
240770_at	TMEM171	transmembrane protein 171	unknown	other	
218345_at	TMEM176A	transmembrane protein 176A	unknown	other	
220532_s_at	TMEM176B	transmembrane protein 176B	unknown	other	
219310_at	TMEM90B	transmembrane protein 90B	unknown	other	
205347_s_at	TMSB15A (includes EG:11013)	thymosin beta 15a	Cytoplasm	other	
202643_s_at	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	Nucleus	other	
203147_s_at	TRIM14	tripartite motif-containing 14	Cytoplasm	other	
220817_at	TRPC4	transient receptor potential cation channel, subfamily C, member 4	Plasma Membrane	ion channel	
209109_s_at	TSPAN6	tetraspanin 6	Plasma Membrane	other	
239742_at	TULP4	tubby like protein 4	Cytoplasm	transcription regulator	
1556096_s_at	UNC13C	unc-13 homolog C (C. elegans)	Cytoplasm	other	
207706_at	USH2A	Usher syndrome 2A (autosomal recessive, mild)	Extracellular Space	other	
223701_s_at	USP47	ubiquitin specific peptidase 47	unknown	peptidase	
203868_s_at	VCAM1	vascular cell adhesion molecule 1	Plasma Membrane	other	
235023_at	VPS13C	vacuolar protein sorting 13 homolog C (S. cerevisiae)	unknown	other	
227174_at	WDR72	WD repeat domain 72	unknown	other	
1554762_a_at	WWC2	WW and C2 domain containing 2	unknown	other	
220057_at	XAGE1D	X antigen family, member 1D	Nucleus	other	
236040_at	XAGE3	X antigen family, member 3	unknown	other	
230349_at	XKRX	XK, Kell blood group complex subunit-related, X-linked	unknown	other	
1555785_a_at	XRN1	5'-3' exoribonuclease 1	Cytoplasm	enzyme	
229264_at	LOC100292701	hypothetical LOC100292701	unknown	unknown	
208235_x_at	GAGE12F	G antigen 12F	unknown	unknown	
243977_at	LOC541472	hypothetical LOC541472	unknown	unknown	
1558345_a_at	LOC439911	hypothetical gene supported by NM_194304	unknown	unknown	
217378_x_at	LOC100130100	similar to hCG26659	unknown	unknown	

Online Supplementary Table S10. Cox univariate and multivariate analysis of overall survival in the HM and UAMS-TT2 patients' cohorts. The prognostic factors were tested as single variables or multiple variables using a Cox-model. *P* values and the hazard ratios (HR) are shown. NS: not significant at a 5% threshold; GPI: gene expression based proliferation index; ISS: International Staging System; HRS: high-risk score; IFM: *Intergroupe Francophone du Myelome*; NA: not available.

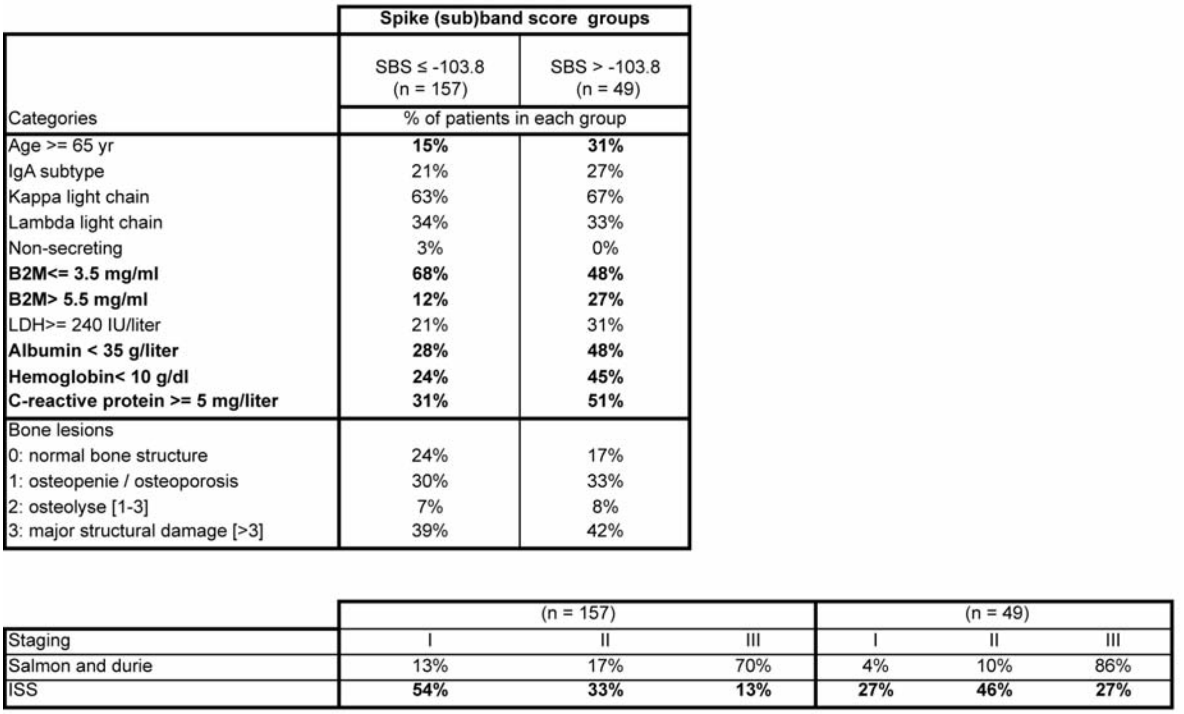


	Univariate Cox analysis - Overall survival			
	HM		UAMS-TT2	
	HR	*P*	HR	*P*
SBS	22	4.80E-15	2.5	2.00E-06
HRS	2.4	1.40E-02	4.7	4.80E-13
IFM score	2.5	1.90E-02	1.8	4.00E-03
GPI	2.6	1.60E-04	1.8	2.20E-04
Spike MMSET	3.3	4.70E-04	2.2	3.20E-04
del17p	3.44	2.00E-02	2.46	3.70E-04
ISS	2	9.70E-04	NA	
β2M	1.1	4.20E-05		
Alb	0.47	1.40E-02		

	Multivariate Cox analysis - Overall survival			
	HM		UAMS-TT2	
	HR	*P*	HR	P
SBS	22	1.30E-14	1.6	4.10E-02
HRS	1	NS	3.6	2.10E-07
SBS	22	1.30E-14	2.3	9.70E-05
IFM score	1.5	NS	1.3	NS
SBS	21	1.60E-13	2.1	5.90E-04
GPI	1.1	6.50E-01	1.4	NS
SBS	23	1.90E-14	2.2	6.70E-05
Spike MMSET	0.89	NS	1.7	1.50E-02
SBS	27.4	2.20E-13	2.35	1.20E-05
del17p	4.2	1.20E-02	2.13	3.00E-03
SBS	20	1.40E-13	NA	
ISS	1.3	NS		
SBS	21	3.60E-14		
β2M	1	NS		
SBS	22	2.80E-14		
Alb	0.9	NS		

	Multivariate Cox analysis - Overall survival			
	HM		LR-TT2	
	HR	P	HR	P
SBS	25.673	3.7E-10	1.126	NS
del17p	3.701	0.039	2.431	0.002
ISS	1.219	NS	NA	
HRS	1.125	NS	3.19	0.000005
IFM score	1.09	NS	0.903	NS
Spike MMSET	0.946	NS	2.057	0.005
GPI	0.921	NS	1.203	NS

Online Supplementary Table S11. Clinical characteristics of patients in the two groups defined by spike (sub)band score. The 206 previously untreated patients of the HM cohort were treated at the university hospitals of Heidelberg and Montpellier. Patients were separated into two groups: low-risk (SBS≤-104.3) and high-risk (SBS>-104.3) SBS groups. Data are the percentages of patients within these two groups with the indicated clinical or biological parameters. When the percentages were different with a χ^2 test ($P \leq 0.05$), data are shown in bold.



	Spike (sub)band score groups	
	SBS ≤ -103.8 (n = 157)	SBS > -103.8 (n = 49)
Categories	% of patients in each group	
Age >= 65 yr	**15%**	**31%**
IgA subtype	21%	27%
Kappa light chain	63%	67%
Lambda light chain	34%	33%
Non-secreting	3%	0%
B2M<= 3.5 mg/ml	**68%**	**48%**
B2M> 5.5 mg/ml	**12%**	**27%**
LDH>= 240 IU/liter	21%	31%
Albumin < 35 g/liter	**28%**	**48%**
Hemoglobin< 10 g/dl	**24%**	**45%**
C-reactive protein >= 5 mg/liter	**31%**	**51%**
Bone lesions		
0: normal bone structure	24%	17%
1: osteopenie / osteoporosis	30%	33%
2: osteolyse [1-3]	7%	8%
3: major structural damage [>3]	39%	42%

	(n = 157)			(n = 49)		
Staging	I	II	III	I	II	III
Salmon and durie	13%	17%	70%	4%	10%	86%
ISS	**54%**	**33%**	**13%**	**27%**	**46%**	**27%**