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 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- β 2-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		
	lgG	120
	IgA	46
	Bence Jones	35
	Asecretory	4
	lgD	1
	NA	0
Myeloma in Durie and Salr	non (SD) sage	
-	1	22
	Ш	31
	Ш	153
Myeloma in ISS stage		
	1	97
	Ш	73
	Ш	33
	NA	3
Serum β2-microglobulin (m	nedian[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.

1 der(1)(1)(1)(per-1q2::1q12-1qer) 1q25::1fq12 RGL1 (1q25.3) JJN3 12 der(1)(1)(2)(2)(per-2q2::1q2-1qer) 1q25::1fq12 RGL1 (1q25.3) JJN3 12 der(1)(1)(2)(2)(per-1q2::1q12-1qer) 1pq13::12p13 EMP1 (12p13) J der(1)(1)(2)(1)(per-1q2::1q22::87) 21q22:: TMPRSS3(21q22.3) KMS12BM 14 der(1)(1)(1)(1)(1)(1)(1)(1)(1)(1)(1)(1)(1)(HMCL	Chromosome	Translocation	Breakpoint	Corresponding spike genes
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1 [der(1)t(1;8) (:1p21-1q25::1q21-1q25::1q21-1q25::Rq22-sqter) x2 1q25::8q22 RGL1(1q25.3) 0PM2 4 [der(4)t(4;14) (14qter-14q32::4p16-4q26:) der(8)t(18) (8q21-8p23::17) 14q32::4p16 8p23::17 PLD4(14q32.33); WHSC1(4p16.3) 8p23::17 0PM2 1 [der(4)t(4;14) (14qter-14q32::4p16-4q26:) der(1)t(1;11) (11qter-1p12::1p13-1pter) 14q32::4p16 8p23::17 PLD4(14q32.33); WHSC1(4p16.3) 8p23::17 RPMI 14 [der(4)t(4;2)(1;2) (22qter-22p11::1p13-1pter) x2 14q32::1p32 CRIP1(14q32.33) SKMM2 4 [der(4)t(4;9;13;14) (:4p13-4q13::1q22-14q31::4q13-4q35::9q21-9q34::13q22-13qter) 14q31::4q122 4q13::14q22 SLC4A4(4q13.3); NID2(14q22.1) 14q31::4q13-4q35::9q21-9q34::13q22-13qter) 14q31::4q13 SLC4A4(4q13.3); NID2(14q22.1) 14q31::4q13 XG1	LP1	1	der(1)t(1;8) (:1p21-1q25::1q21-1q25::1q21-1q25::8q22-8qter) x2	1q25::1q21	RGL1(1q25.3)
OPM2 4 der(4)!(4:14) (14qter-14q32:::4p16-4q26:) der(8)!(1:8) (8q21-8p23::1?) 14q32::4p16 sp23::1? der(1)!(1:11) (11qter-11p12::1p13-1pter) 14q32::4p16 sp23::1? MYOM2(8p23.3) 11p12::1p13 CD58(1p13.1) RPMI 14 der(1)!(1:14) (14pter-14q32::1p32-1pter) x2 14q32::1p32 22p11::1p13 CD58(1p13.1) CD58(1p13.1) CD58(1p13.1) SKMM2 4 der(4)!(4;9;13;14) (:4p13-4q13::14q22-14q31::4q13-4q35::9q21-9q34::13q22-13qter) der(4)!(4;9;13;14) (:4p13-4q13::14q22-14q31::4q13-4q35::9q21-9q34::13q22-13qter) 17 4q13::14q22 der(4)!(4;9;13;14) (:4p13-4q13::14q22-14q31::4q13-4q35::9q21-9q34::13q22-13qter) der(1)!(1;7;17) (17qter-17p11::7q22-7qter) 4q13::14q22 14q31::4q13 SLC4A4(4q13.3); AZGP1 (7q22.1) XG1		1	der(1)t(1;8) (:1p21-1q25::1q21-1q25::1q21-1q25::8q22-8qter) x2	1q25::8q22	RGL1(1q25.3)
OPM2 8 11 22 der(8)(1;8) (8q21-8p23:1?) der(1)(1;11) (11qter-11p12:1p13-1pter) der(22)(1;22) (22qter-22p11:1p13-1pter) 8p23:1? 11p12:1p13 22p11:1p13 22p11:1p13 22p11:1p13 22p11:1p13 22p11:1p13 22p11:1p13 22p11:1p13 22p11:1p13 22p11:1p13 22p11:1p13 2D58(1p13.1) RPMI 14 der(4)((1;14) (14pter-14q32::1p32-1pter) x2 14q32::1p32 4q13::14q22 CRIP1(14q32.3) SKMM2 4 der(4)((4;9;13;14) (:4p13-4q13::14q22-14q31::4q13-4q35::9q21-9q34::13q22-13qter) der(4)(4;9;13;14) (:4p13-4q13::14q22-14q31::4q13-4q35::9q21-9q34::13q22-13qter) 17 4q13::14q22 14q31::4q13 17p11::7q22 SLC4A4(4q13.3); NID2(14q22.1) 14q31::4q13 17p11::7q22 XG1		4	der(4)t(4;14) (14qter-14q32::4p16-4q26:)	14q32::4p16	PLD4(14q32.33); WHSC1(4p16.3)
NL2 11 der(1)t(1;11) (11qter-11p12::1p13-1pter) 11p12::1p13 CD58(1p13.1) 22 der(2)t(1;22) (22qter-22p11::1p13-1p31) x2 22p11::1p13 CD58(1p13.1) RPMI 14 der(4)t(4;9;13;14) (14pter-14q32::1p32-1pter) x2 14q32::1p32 CRIP1(14q32.33) SKMM2 4 der(4)t(4;9;13;14) (14p13-4q13::14q22-14q31::4q13-4q35::9q21-9q34::13q22-13qter) 4q13::14q22 SLC4A4(4q13.3); NID2(14q22.1) 17 der(4)t(4;9;13;14) (14p13-4q13::14q22-14q31::4q13-4q35::9q21-9q34::13q22-13qter) 4q13::4q13 SLC4A4(4q13.3); 17 der(1)t(1;7;17) (17qter-17p11::7q22-7qter) 7p15::1p12 IGF2BP3(7p15.3) XG1	OPM2	8	der(8)t(1;8) (8q21-8p23::1?)	8p23::1?	MYOM2(8p23.3)
22 der(22)t(1;22) (22qter-22p11::1p13-1p3) 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) 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) SKMM2 4 der(4)t(4;9;13;14) (:4p13-4q13::14q22-14q31::4q13-4q35::9q21-9q34::13q22-13qter) 14q31::4q13 SLC4A4(4q13.3); XG1	OT MIZ	11	der(1)t(1;11) (11qter-11p12::1p13-1pter)	11p12::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) (14pter-14q32::1q12-4q13::4q13-4q35::9q21-9q34::13q22-13qter) der(4)t(4;9;13;14) (14pt3-4q13::14q22-14q31::4q13-4q35::9q21-9q34::13q22-13qter) der(17)t(7;17) (17qter-17p11::7q22-7qter) 4q13::14q22 14q31::4q13 SLC4A4(4q13.3); NID2(14q22.1) 14q31::4q13 XG1		22	der(22)t(1;22) (22qter-22p11::1p13-1p31) x2	22p11::1p13	CD58(1p13.1)
SKMM2 4 4 4 4 17 der(4)t(4;9;13;14) (:4p13-4q13::14q22-14q31::4q13-4q35::9q21-9q34::13q22-13qter) der(17)t(7;17) (17qter-17p11::7q22-7qter) 4q13::14q22 14q31::4q13 SLC4A4(4q13.3); 17p11::7q22 SLC4A4(4q13.3); AZGP1 (7q22.1) XG1	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) 14q31::4q13 SLC4A4(4q13.3); XG1 17 der(1)t(1;7;17) (17qter-17p11::7q22-7qter) 17p11::7q22 AZGP1 (7q22.1) XG1 1 der(1)t(1;7;19) (19qter-19q11::7p22-7p15::1p12-1qter) 7p15::1p12 IGF2BP3(7p15.3) XG2 4 der(1)t(1;7;19) (19qter-19q11::7p22-7p15::1p12-1qter) 3?::4p12 COX7B2(4p12) 5 der(5)t(5;11) (5pter-5q31::11q13-11qter) 3?::4p12 COX7B2(4p12) 5 der(1)t(1;7;19) (19qter-1q32::12?) 14q32::12 CRIP1(14q32.33) XG6 1 der(1)t(1;7) (7qter-7q22::1q31-1q10::1q10-1qter) 7q22::1q31 CFH(1q31.3) XG6 5 der(1)t(1;7) (7qter-7q22::1q31-1q10::1q10-1qter) 6q25::8q21 RUNX1T1(8q21.3) XG6 5 der(6)t(6)t(6)t(6)ter-6q21::8p11-8pter) 6q25::8q21 RUNX1T1(8q21.3)		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)
17 der(17)t(7;17) (17qter-17p11::7q22-7qter) 17p11::7q22 AZGP1 (7q22.1) XG1	SKMM2	4	der(4)t(4;9;13;14) (:4p13-4q13::14q22-14q31::4q13-4q35::9q21-9q34::13q22-13qter)	14q31::4q13	SLC4A4(4q13.3);
XG1 1 der(1)t(1;7;19) (19qter-19q11::7p22-7p15::1p12-1qter) 7p15::1p12 IGF2BP3(7p15.3) XG2 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(1)t(1;7) (7qter-7q22::1q31-1q10::1q10-1qter) 7q22::1q31 CFH(1q31.3) XG6 5 der(5)t(5;11) (5pter-5q11::10p11-10pter) 5q11::10p11 ITGB1(10p11.22) 6 der(6)t(6;8) (6pter-6q21::8p11-8pter) 6q21::8p11 SOBP(6q21)		17	der(17)t(7;17) (17qter-17p11::7q22-7qter)	17p11::7q22	AZGP1 (7q22.1)
XG2 1 der(1)t(1;7;19) (19qter-19q11::7p22-7p15::1p12-1qter) 7p15::1p12 IGF2BP3(7p15.3) XG2 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(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) 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-6q21::8p11-8pter) 6q21::8p11 SOBP(6q21)	XG1				
XG2 4 der(4)(1;4)(2):4p12-4p21) 7p22:1p12 GOLZH 5(p12) 5 der(4)(1;4)(2):4p12-4p21) 5q31::11q13 SERPINH1(11q13.5) 14 der(1)t(1;7)(7qter-7q22::1q31-1q10::1q10-1qter) 5q31::11q13 SERPINH1(11q13.5) 14 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-6q21::8q11-8pter) 6q25::8q21 RUNX1T1(8q21.3) 6 der(6)t(6;8)(6pter-6q21::8p11-8pter) 6q25::8q21 SOBP(6q21)		1	[der(1)t(1:7:19)(19ater,19a11:7p22.7p15:1p12.1ater)	7n151n12	IGE28P3(7n15-3)
XG2 1 der(5)((5)(1)(5)ter-5q31::1]q13-1]qter) 5q31::11q13 SERPINH1(11q13.5) 14 der(1)t(1;7)(7qter-7q22::1q31-1q10::1q10-1qter) 5q31::11q13 CRIP1(14q32.33) XG6 5 der(5)t(5;10) (5pter-5q11::10p11-10pter) 5q11::10p11 ITGB1(10p11.22) 6 der(6)t(6;8) (6pter-6q21::8q21-8qter) 6q25::8q21 RUNX1T1(8q21.3) 6 der(6)t(6;8) (6pter-6q21::8p11-8pter) 6q21::8p11 SOBP(6q21)		4	der(4)t(3;4) (3?::4n12-4o21:)	32.4n12	COX7B2(4n12)
XG6 5 der(1)t(1;7) (7qter-7q2::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)	XG2	5	der(5)((5)1) (5nter-5a31::11a13-11ater)	5031.11013	SERPINH1(11g13 5)
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)		14	der(14)t(12;14) (14pter-14q32::12?)	14q32::12	CRIP1(14q32.33)
XG6 5 der(5)!(5:10) (5pter-5q11::10p11-10pter) 5q11::10p11 ITGB1(10p11.22) 6 der(6)!(6:8) (6pter-6q25::8q21-8qter) 6q25::8q21 RUNX1T1(8q21.3) 6 der(6)!(6:8) (6pter-6q21::8p11-8pter) 6q21::8p11 SOBP(6q21)		1	der(1)t(1:7) (7ater-7a22::1a31-1a10::1a10-1ater)	7a22::1a31	CFH(1a31.3)
XG6 6 der(6)t(6;8) (6pter-6q23::8q21-8qter) 6q25::8q21 RUNX1T1(8q21.3) 6 der(6)t(6;8) (6pter-6q21::8p11-8pter) 6q25::8q21 SOBP(6q21)		5	der(5)t(5:10) (5pter-5a11::10p11-10pter)	5g11::10p11	ITGB1(10p11.22)
6 der(6)t(6;8) (6pter-6q21::8p11-8pter) 6q21::8p11 SOBP(6q21)	XG6	6	der(6)t(6:8) (6pter-6q25::8q21-8qter)	6g25::8g21	RUNX1T1(8g21.3)
		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
208/11_s_at	CCND1	11q13.3 15g25 2	4,60	1
215025_at	WHSC1	15q25.5 An16.3	4,59	1
209348 s at	MAF	16023.2	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
21/143_S_dt 212148_at	PRV1	14011.2	3,04	1
244023 at	SYK	9g22 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	55X2	Xp11.22	3,17	2
204249_S_at	BCI 11A	2n16.1	3,14	2
224861 at	GNAO	9a21.2	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
1555//9_a_at	CD79A 7NE331	19013.2	2,89	3
202861 at	PFR1	17013.1	2,87	3
222670 s at	MAFB	20a12	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	RCI2	13q14.13	2,70	4
204908_s_at	TNFAIP3	6g23 3	2,09	4
1556499 s at	COL1A1	17021.33	2,67	4
203749 s at	RARA	17g21.2	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		/q21.2	2,57	4
209383 at	DDIT3	12013 3	2,50	4
205051 s at	KIT	4012	2,54	4
244110 at	MLL	11q23.3	2,50	5
200934 at	DEK	6n22.3	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	FLEA	8q24.21	2,3/	5
203490_at	PIM1	6p21 2	2,52	5
233254 x at	PTEN	10023.31	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	chromosome	chromosome band	Pronostic	Total number of	Number of	%of spike	Median[range]	Spaning	
bands	fragile site	designations	value	genes	spikgenes	genes	spike score	region (Mb)	List of spike genes
1022.1	FRAIE	R-band R-band	Good	21	4	19.05	2.57[2.28-3.61]	2.204861	TGFBR3: FNBP1L: BCAR3: GCLM
1p31.1		G-band	0000	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
1023.1		G-band R-band	Good	37	7	23,08	3.26[2.68-3.7]	2.053259	NES: ECRL3: ECRL2: ECRL1: 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 R band		26	6	23,08	3.25[2.76-4.81]	3.024739	ASTN1; RASAL2; RALGPS2; FAM20B; TOR3A; TOR1AIP1
1q23.3		G-band	Bad	16	5	31.25	3.29[2.6-5.34]	1.986793	CFH: CFHR4: ASPM: DENND18: PTPRC
1q32.2		G-band		29	9	31,03	2.5[2.21-5.64]	4.273352	PFKFB2; CR2; PLXNA2; LAMB3; G052; 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 1c43 12	-	G-band 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		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 2p23 1		R-band R-band		45	8	36.36	2.71[2.28-5.92]	5.47275	SGK493; ZFP36L2; SIX2; PRKCE; EPAS1; RHOQ; EPCAM; KCNK12 JRH: CAPN13: GAINT14: FHD3
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	CRACH	G-band	Bad	17	7	41,18	2.51[2.33-4.25]	4.862853	FIGN; GRB14; COBLL1; SCN3A; GALNT3; STK39; LASS6
2034	FRAZE	G-band G-band		17	4	23,53	3.23[2.64-3.73]	3.109455	PIKEYVE: 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 R-band	Bad	23	5	21,74	3.1[2.52-3.81]	3.483412	CASR; CSTA; PARP15; MYLK; CCDC14 RBP1- CLSTA2: XPN1- PCOLCE2: SP140
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
4012	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 G-band	Good	25	5	20	3.27[2.44-6.99]	1.903881	SPP1; ABCG2; HERC6; SNCA; MMRN1 BANK1: TET2: ELIZO184: MPNT
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 5p13.2		R-band G-band		18	5	44,44	2.58[2.11-3.81]	2.831983	LIFK; FYB; DABZ; PTGEK4; RPL37; CARD6; C6; PLCXD3
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
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 G-band		30	5	16,67	2.6[2.15-3.97]	2.992541	CPEB4; C5orf47; HMP19; SFXN1; HK3
6p12.2	1	R-band		18	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
6p22.2	FRAGC	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	1.11.11.1	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 6q15	FRAGG	G-band R-band	Bad	25	4	20	3.11(2.16-4.26)	1.786665	INTOB; SH3BGRL2; TTK; FAM46A CNR1: RNGTT: GABRR1: MDN1: BACH2
6q21	FRAGE	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
6q25.3		R-band	Good	32	8	25	2.71[2.21-3.16]	2.083678	SNX9; SYNI2; 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	Bad	28	5	17,86	3.2[2.4-5.14]	0.503529	SKAP2; HOXA1; HOXA7; HOXA9; HOXA10
7021.3		G-band	Bao	15	4	26,57	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
7022.3		K-band G-band		22	4	23.81	3.28[2.55-2.91]	4.332826	STPLI; PIK3CG; PIKAR28; HBP1 NRCAM: DOCK4: ZNE277: JERD1: CZorf53
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	6	G-band		9	4	44,44	3.53[2.2-4.42]	0.561529	TSPAN12; C7orf58; WNT16; FAM3C
7036 1		Rehand	Good	66	12	10.7	2 99[2 10 4 51]	2 501152	ATP6VUE2; LOC285972; GIMAP8; GIMAP7; GIMAP4; GIMAP6; GIMAP1; GIMAP5; TMEM176B; TMEM176A; ARP1- ASR10- LOC100128822
8p21.2	5	G-band	6000	26	5	19,7	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
8022.1	FRASB	G-band R-band		32	8	24	2.9[2.67-4.02]	4.044076	AIP6VUU2; CNGB3; UCAF4L2; MMP16; TMEM64; RUNX111 RBM12B: CDH17: GEM: ESRP1: CCNE2: PLEKHE2: UOCRB: 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 G-band		14	4	28,57	2.9[2.47-3.09]	5.162559	LINGO2; DDX58; LOC100129250; B4GALT1 TRPM3: LOC286382: TMEM2: GDA: ZEANDS: ANYA1: PCSK5: REK: 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
9034 3		Rehard		05	16	16.94	2 63/2 28 2 001	2 070934	COL5A1; FCN2; FCN1; SOHLH1; NACC2; SNAPC4; SNHG7; LCN6; PTGDS; NPDC1; DPP7; RNF208; FAM166A; NRARP: MRPI 41: FHMT1
10p14	5	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	12	R-band	Good	26	7	26,92	2.98[2.42-4.87]	2.07037	RET; RASGEF1A; LOC439911; CXCL12; RASSF4; C10orf10; LOC338579
10011.23		R-band G-band	Bad	27	5	18,52	2.49[2.3-2.54]	2.858197	WDF14; C1007/12; C1007/128; LOC100133089; PRKG1 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; TECT8; TCF7L2 ADRB1: C10orf118: ABUM1: KIAA1598
10q26.11		R-band		22	7	31,82	2.75[2.45-3.6]	2.839936	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
11015.4		G-band		113	20	17.7	2.77[2 1-5 31]	7.567781	CUKNIC; PMLUAZ; HBB; HBD; HBBPI; HBGI; HBEI; OR51B5; TRIM22; CCKBR; PRKCDBP; HPX; DNHD1; ZNF215: ST5: NRIP3: DENNDSA: LOC644656: SWAP70: AMPD3
	1	U-Veriu		44.5		A/1/	F11.1[E17.0.01]	1 7.307701	en erel erel inn al ennnern overstude, anner rel enne ea

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11012.1		G-band		42	9	21.43	3.24[2.52-3.79]	2.893792	PRG2: SERPING1: LPXN: DTX4: MPEG1: FABP5: MS4A3: MS4A6A: MS4A4A
11024.3		G-band		20	4	20	3.14[2.36-3.33]	1.701026	ETS1: KCNJ5: RICS: ST14
12011.22		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
									SCNN1A: CD27: VAMP1: LAG3: CD4: CDCA3: C1R: CD163L1: CD163: SLC2A3: C3AR1: CLEC4A: A2M:
12p13.31		R-band	Good	90	17	18,89	2.81[2.45-3.93]	3.548962	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
				2	Q				FLJ39632; OSGEP; NP; RNASE4; ANG; RNASE6; RNASE1; RNASE3; RNASE2; NDRG2; FLJ10357; SUPT16H;
14q11.2		R-band		93	18	19,35	2.88[2.19-3.79]	4.414596	SALL2; C6orf142; TRA@; CDH24; SLC7A8; DHR52
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
					1	-			PLD4; PACS2; MTA1; CRIP1; IGHG1; IGHE; IGH@; IGHD; IGHM; FAM30A; KIAA0125; IGHA1; LOC100132941;
14q32.33		R-band		53	17	32,08	3.7[2.48-6.28]	1.868146	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; GIN52; 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
227222		82.5			0357	100000	200320233000	157355355	ZNF415; ZNF331; MYADM; CACNG6; TMC4; LILRA6; LILRB2; LILRA3; LAIR1; LAIR2; LILRA2; LILRB1; LILRA1;
19q13.42		R-band		96	19	19,79	2.87[2.35-4.15]	2.184194	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; GAR1; 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	0.1	24	5	20,83	3.5/[2.29-4.92]	1.800063	CKTBB1; CKTBA4; MIAI; MN1; XBP1
Xp11.22	-	G-band	Bad	29	5	17,24	3.11[2.38-3.97]	1.658694	NUDIII; MAGED4; XAGEIA; SSX2; XAGE3
Xp11.23		R-band	Bad	75	14	18,67	3.31[2.27-5.05]	3.047125	LOC401588; CH517; HMP1; CFP; S5X1; S5X3; S5X4; PCSKIN; OTOD5; 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.

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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).

		% of spike				
Spike (sub)	Spike	genes among genes located		Pronostic	% of patients with high spike (sub)	
band	genes (n)	in the cytoband	p-value	value	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; AUKKA CKS1B: LOC100292701: HIST2H2AA3; HIST2H2BE: MTMR11;
1q21.2*	6	23.08	1.2E-03	Bad	10.7	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
1041*	9	26.47	2 1E-03	Bad	23.3	CENPF; USH2A; GPATCH2; TGFB2; MARK1; C1orf115; HLX; DUSP10; SUSD4
3023*	5	20.83	2.2E-03	Bad	25.2	RBP1: CLSTN2: XRN1: PCOLCE2: SR140
1031.3*	5	31.25	27E-03	Bad	30.1	CEH: CEHRA: ASPM: DENND18: PTPRC
16n13 11*	4	28.57	3.2E-03	Bad	18.4	PDXDC1: NTAN1: MYH11: ABCC6
20011.21*	6	17.65	3.3E-03	Bad	16.5	CD93: CST4: TMEM90B: CST7: PYGB: GINS1
2025 1*	5	17.24	3.4E-03	Bad	21.4	ID2: MBOAT2: RRM2: ROCK2: GREB1
7012.1*	4	57.14	4.0E-03	Bad	40.3	FIGNL1: GRB10: COBL: POM121L12
5013.2*	6	18.75	4.9E-03	Bad	55.8	CCNB1: CCDC125: LOC653188: MAP1B: TMEM171: RGNEF
	, i i i i i i i i i i i i i i i i i i i					GPR176; EIF2AK4; BUB1B; CASC5; SPINT1; CHAC1; OIP5;
15q15.1*	11	18.03	5.9E-03	Bad	25.7	LTK; MGA; SPTBN5; EHD4
20q13.32*	4	19.05	6.9E-03	Bad	38.3	LOC149773; GNAS; TUBB1; PHACTR3 CHD9; RBL2; CRNDE; LPCAT2; CAPNS2; GNAO1; AMFR;
16q12.2*	9	34.62	8.4E-03	Bad	62.1	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	OTUD5; GAGE12F; GAGE12C; GAGE1; GAGE3; PAGE1
13g13.3*	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 CMAH: SLC17A4: HEF: HIST1H4C: HIST1H2BC: HIST1H2AD:
6p22.2	10	19.61	1.4E-02	Bad	36.4	HIST1H2BG; HIST1H2AE; HIST1H4H; BTN1A1
10q23.31*	6	26.09	1.5E-02	Bad	10.2	PTEN; ANKRD22; FAS; IFIT2; IFIT3; IFIT1 LOC541472; IL6; FAM126A; GPNMB; IGE2RD3; DENA5; OSBPL3;
7p15.3*	8	28.57	1.5E-02	Bad	53.4	CYCS
						ATP6V0E2; LOC285972; GIMAP8; GIMAP7; GIMAP4; GIMAP6; GIMAP1; GIMAP5; TMEM176B; TMEM176A; ABP1; ASB10;
7q36.1*	13	19.7	1.7E-04	Good	87.4	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	TIAM1; SFRS15; C21orf119; C21orf63; C21orf62; IFNAR1; GART;
21q22.11*	8	18.18	2.9E-03	Good	88.3	ITSN1
14q22.1*	7	31.82	4.1E-03	Good	74.8	PYGL; FRMD6; GNG2; NID2; PTGDR; PTGER2; FERMT2
6q25.3* 4q22.1*	8	25	5.1E-03	Good	80.1	SNX9; SYNJ2; TULP4; SYTL3; EZK; TAGAP; SOD2; MAST SPD1: ABCG2: HERC6: SNCA: MMRN1
10-10 045	47	10.00	5.22-00	Good		SCNN1A: CD27; VAMP1; LAG3; CD4; CDCA3; C1R; CD163L1; CD163;
12p13.31*	17	18.89	5.5E-03	Good	89.3	SLC2A3; C3AR1; CLEC4A; A2M; CLEC2D; CD69; KLRF1; CLEC2B
1021.2*	4	22.22	6.1E-03	Good	43.7	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
10011 21*	7	26.02	1.25.00	Good	33 E	RET; RASGEF1A; LOC439911; CXCL12; RASSF4; C10orf10;
9022.33*	6	20.92	1.3E-02	Good	68.0	CDC14B: KIAA1529: TRIM14: TGFBR1: SEC61B: NR4A3
				14 14 14 14	1000	ANKRD57; LIMS3; BUB1; BCL2L11; MERTK; CHCHD5; SLC20A1;
2q13*	9	21.43	1.4E-02	Good	12.6	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.

			1		
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
· · · · · · · · · · · · · · · · · · ·		phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3			dyphylline, nitroglycerin, arofylline, tetomilast, L 869298, aminophylline, anagrelide, cilomilast, milrinone,
204491_at	PDE4D	dunce homolog, Drosophila)	Cytoplasm	enzyme	rolipram, dipyridamole, L-826,141, roflumilast, tolbutamide, theophylline, pentoxifylline, caffeine
					epothilone B, ixabepilone, colchicine/probenecid, XRP9881, ABT-751, eribulin, MST-997, AL 108, EC145, NPI-
			11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	11 - 11 - 11 - 11 - 11 - 11 - 11 - 11	2358, milataxel, TPI 287, TTI-237, BMS-275183, docetaxel, vinflunine, vinorelbine, vincristine, vinblastine,
230690_at	TUBB1	tubulin, beta 1	Cytoplasm	other	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
and the second	100000	NAME AND ADDRESS OF A DECK OF A	NY 3858 N.	A. 1232 A.	interferon alfacon-1, PEG-interferon alfa-2a, IFNB1, IFNA2, interferon alfa-2a/ribavirin, pegintron, interferon
236478_at	IFNAR1	interferon (alpha, beta and omega) receptor 1	Plasma Membrane	transmembrane receptor	beta-1b
242903_at	IFNGR1	interferon gamma receptor 1	Plasma Membrane	transmembrane receptor	interferon gamma-1b
		phosphoribosylglycinamide formyltransferase,			The ACTIVE ACTIVE CAME CONTRACT A
		phosphoribosylglycinamide synthetase,	2.7		
230097_at	GART	phosphoribosylaminoimidazole synthetase	Cytoplasm	enzyme	LY231514
					methazolamide, hydrochlorothiazide, acetazolamide, trichloromethiazide, chlorothiazide, chlorthalidone,
219464_at	CA14	carbonic anhydrase XIV	Plasma Membrane	enzyme	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, diclotenac/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
					risperidone, buspirone, caffeine/ergotamine, bionanserin, asenapine, vabicaserin, opipramol,
202202	UTDAC	e 1. d		e and a second second	fluoxetine/olanzapine, epinastine, fenfluramine, quetiapine, olanzapine, nefazodone, mirtazapine, ziprasidone,
207307_at	C10	5-nydroxytryptamine (serotonin) receptor 2C	Fiasma Memorane	G-protein coupled receptor	anpiprazole, apomorphine, ergotamine
212007_5_81	CIN	complement component 1, r subcomponent	Extracellular space	peptidase	SCHINGT
215771	PET	ret proto oprogene	Plasma Membrana	kinasa	queltelh
205207 at	11.6	interleukin 6 linterferon, heta 2)	Extracellular Space	outokine	tocilinumah
203207_at	1.0	interested o (interestor), occa z)	excidential space	et roland.	trans-(Åt)-nabilone SIV 319 rimonabant RAV 38-7071 delta-8-tetrah-decompahinet delta-9-
1560225 at	CNR1	cannabinoid receptor 1 (brain)	Plasma Membrane	G-protein coupled recentor	tetrahydrocannabinol
217264 + 2*	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	in the second seco
214033 **	ABCC6	ATP-binding cassette, sub-family C (CETR/MPD) member 5	Plasma Membrane	transporter	
209726 -*	ABCCO	ATP, binding cassette, sub-family C (UF IT/ MRP), member 6	Plasma Membrane	transporter	
209735_at	A0002	amiloride binding protein 3 (aming of (WHITE), member 2	Extracellular Conce	converse	
203559_s_at	ACSI *	amilonide binding protein 1 (amilie oxidase (copper-containing))	Extracentiar space	enzyme	
201963_at	ACSLI	acyr-coa synthetase long-chain family member 1	Cytoplasm	enzyme	
202203_s_at	AMER	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_a					
t	ASB10	ankyrin repeat and SOCS box-containing 10	Nucleus	transcription regulator	
		asp (abnormal spindle) homolog, microcephaly associated			
219918_s_at	ASPM	(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	
and the second s	BACH2				
	(includes	BTB and CNC homology 1, basic leucine zipper transcription			
221234 s at	EG:60468)	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	Cytoolasm	other	
222343 at	BCL2111	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	
207305 at	BTN1A1	huturonhilin subfamily 1 member A1	Plasma Membrane	other	
200642 at	DUDI	budding uninhibited by benzimidataler 1 hamolog (upart)	Nucleur	kiesza	
203042_at	811919	budding uninhibited by benzimidatoles 1 homolog (yeast)	Nucleus	kinase	
203755_at	60616	abiamosome 10 energianding frame 10	Cutoplace	ethes	
209102_5_at	C100RF10	chromosome 10 open reading frame 10	cytopiasm	other	
215400 at	CLOREGO	chromosome 1 open reading frame 115	unknown	other	
225904 at	CIOPEOF	chromosome 1 open reading frame 65	unknown	other	
223904_at	CTOUL20	envinosome z open reduing name so	MINING WIT	outer .	
227424	C21085110	chromosome 21 open reading frame 110	unknown	other	
220542 -+	C2108F119	chromosome 21 open reading frame 115	unknown	other	
220345_at	C210RF62	chromosome 21 open reading frame 62	unknown	other	
22/168_at	CRAPT	complement company 3 consister 1	Discos Mambras	G protoin counted records	
209906_at	CIOPEET	complement component sa receptor 1	unknown	orbor	
2154/4_at	CAOREAT	chromosome a open reading frame 52	unknown	other	
230915_at	CADNIC?	cologie constructional construction of the second s	Ortoplarm	other	
223032 5 at	CASCS	concer suscentibility medidate \$	Nucleur	other	
226323_at	COCOCINE	called call demain containing 125	wallow	other	
229082_at	CCDC125	colled-coll domain containing 125	unkriown	other	
232489_01	CCDC76	colled-coll domain containing 76	Nucleur	other	
225242_s_at	CONPI	concursion domain containing ou	Nucleus	other	
202705 -+	CONPO	cyclin B2	Otoolarm	other	
202705_at	CCND2	cyclin be	exception	ound:	
215049	C0163	CD163 molecule	Plasma Membrane	transmembrane recentor	
a south a dt	CD163F1		- sector menneralite	contraction and receptor	
	lincluder				
223655 -	EG-282216	CD163 molecule-like 1	Plasma Membrane	transmembrane recentor	
210325 -+	CD14	CD1a melecula	Plasma Membrane	other	
209583	CD200	CD200 molecule	Plasma Membrane	other	
205302_3_at	CD22	CD27 molecula	Plasma Membrane	transmomhrane measter	
200150_at	CD4	CD4 malagula	Discos Marchane	transmemorane receptor	
20354/_at	004	CDE malanda like	niasma memorane	transmemorane receptor	
200080_at	COSL	COS molecule-like	niasma Memorane	transmembrane receptor	
209795_at	C069	CD09 molecule	Plasma Membrane	transmembrane receptor	
202878_s_at	CD93	CD93 molecule	Plasma Membrane	other	
and the second	101111-0			120102000	
221555_x_at	CDC148	CDC14 cell division cycle 14 homolog B (5. 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	CHCHDS	coiled-coil-helix-coiled-coil-helix domain containing 5	unknown	other	
	CHD9				
	(includes				
239654 at	EG:802051	chromodomain helicase DNA binding protein 9	Cytoplasm	other	
206756 at	CHST7	carbohydrate (N-acetylglucosamine 6-0) sulfotransferase 7	Cytoplasm	enzyme	
201897 5 2*	CKS18	CDC28 protein kinase regulatory subunit 18	Cytoplasm	kinase	
209732 at	CLEC2B	C-type lectin domain family 2 member 8	Plasma Membrane	other	
2007.34_dt	CLEC2D	s size is call domain raining as memory o	s wante mennendhe	ernel	
	lincluder				
223500	EG-201241	C-type Jectin domain family 3 member P	Plasma Membrane	transmembrane measter	
219947 -*	CIECAA	C-type lectin domain family 2, member 0	Plasma Membrane	transmembrane receptor	
s133#_91	PLECHA	percype recon domain raminy 4, member A	preasing memorane	Liansmemorane receptor	

222522	C1.19.177.1			1.4	
230609_at	CLINT1	clathrin interactor 1	Cytoplasm	other	
219414_at	CLSTN2	calsyntenin 2	Plasma Membrane	transporter	
		cytidine monophosphate-N-acetylneuraminic acid hydroxylase			
229604_at	CMAH	(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 E (leukocystatin)	Extracellular Space	other	
200697 at	CYCI 12	chamoking (C.V.C motif) ligand 13 (stromal call darked factor 1)	Extracellular Space	ortokioa	
203007_01	CYCS	chemokine (c-x-c motil) ligand 12 (stromal cell-derived factor 1)	Extracential space	Cytokine	
	Crcs				
100000	(includes	5.2 6	12.22		
244546_at	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	DENND18	DENN/MADD domain containing 1B	unknown	other	
226980 at	DEPDC1B	DEP domain containing 1B	unknown	other	
203695 s at	DENAS	deafness autosomal dominant 5	unknown	other	
205055 3 01	DVE70434107	acantes, autosoniai doniniaite s		ounci	
221054	14	humath stillar installe DVC704340714	under some	ath se	
231934_81	14	nypotnetical protein DKr2P434i0/14	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	E8F1	early B-cell factor 1	Nucleus	transcription regulator	
1556608_a_a	1.50	1817 - 5 - 5 AD - 5 - 5	979 C292 N		
t	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 5 24	EZR	lezrin	Plasma Membrane	other	
223625 at	FAM126A	family with sequence similarity 126 member A	Cytoplasm	other	
235500 at	FAM1794	family with sequence similarity 120, member A	unknown	other	
204790	EAS	Ex (TNE recentor superfamily member 6)	Playma Mambrano	transmomhrono socosto-	
204700_5_at	145	res (ner receptor superianny, member o)	r iaarna mernarane	o ansmeniorane receptor	
242050	ECO11	Fo recorded like 1	Discos Marchan	ather	
243968_X_at	FURL1	rc receptor-like 1	riasma membrane	omer	
224193_s_at	FCRL2	Pc 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	GABRP1	gamma-aminobutyric acid (GABA) recentor, rho 1	Plasma Membrane	ion channel	
207720	GAGE1	G antigen 1	unknown	other	
207739_5_at	GAGET	G anogen 1	unknown	other	
206640_x_at	GAGE12I	G antigen 12	unknown	other	
207663_x_at	GAGE3	G antigen 3	unknown	other	
		UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-			
239930_at	GALNT2	acetylgalactosaminyltransferase 2 (GalNAc-T2)	Cytoplasm	enzyme	
10		UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-			
203397 s at	GALNT3	acetylgalactosaminyltransferase 3 (GalNAc-T3)	Cytoplasm	enzyme	
		UDP-N-acetyl-alpha-D-galactosamine:polypeotide N-			
1554079 at	GAINTIA	acetylealactosaminultransferase like 4	Cutoplasm	000000	
x001010_0t	07 007 110 1	dect Budetosaria fro ansierase nae 4	e topioni	Concerna and Conce	
235310 at	GCET2	germinal center expressed transcript 2	unknown	other	
235310_at	GCET2	germinal center expressed transcript 2	unknown	other	
235310_at 236140_at	GCET2 GCLM	germinal center expressed transcript 2 glutamate-cysteine ligase, modifier subunit	unknown Cytoplasm	other enzyme	
235310_at 236140_at 219508_at	GCET2 GCLM GCNT3	germinal center expressed transcript 2 glutamate-cysteine ligase, modifier subunit glucosaminyl (N-acetyl) transferase 3, mucin type	unknown Cytoplasm Plasma Membrane	other enzyme enzyme	
235310_at 236140_at 219508_at 1552316_a_a	GCET2 GCLM GCNT3	germinal center expressed transcript 2 glutamate-cysteine ligase, modifier subunit glucosaminyl (N-acetyl) transferase 3, mucin type	unknown Cytoplasm Plasma Membrane	other enzyme enzyme	
235310_at 236140_at 219508_at 1552316_a_a t	GCET2 GCLM GCNT3 GIMAP1	germinal center expressed transcript 2 glutamate-cysteine ligase, modifier subunit glucosaminy (N-acety) transferse 3, mucin type GTPase, IMAP family member 1	unknown Cytoplasm Plasma Membrane Cytoplasm	other enzyme enzyme other	
235310_at 236140_at 219508_at 1552316_a_a t 219243_at	GCET2 GCLM GCNT3 GIMAP1 GIMAP4	germinal center expressed transcript 2 glutamate-cysteine ligase, modifier subunit glucosaminyi (N-acetyi) transferase 3, mucin type GTPase, IMAP family member 1 GTPase, IMAP family member 4	unknown Cytoplasm Plasma Membrane Cytoplasm unknown	other enzyme enzyme other other	
235310_at 236140_at 219508_at 1552316_a_a t 219243_at 218805_at	GCET2 GCLM GCNT3 GIMAP1 GIMAP4 GIMAP5	germinal center expressed transcript 2 glutamate-cysteine ligase, modifier subunit glucosaminy (N-acetyl) transferase 3, mucin type GTPase, IMAP family member 1 GTPase, IMAP family member 4 GTPase, IMAP family member 5	unknown Cytoplasm Plasma Membrane Cytoplasm unknown Cytoplasm	other enzyme enzyme other other other	
235310_at 236140_at 219508_at 1552316_a_a t 219243_at 218805_at 219777_at	GCET2 GCLM GCNT3 GIMAP1 GIMAP4 GIMAP5 GIMAP6	germinal center expressed transcript 2 glutamate-cysteine ligase, modifier subunit glucosaminyi (N-acetyl) transferase 3, mucin type GTPase, IMAP family member 1 GTPase, IMAP family member 4 GTPase, IMAP family member 5 GTPase, IMAP family member 5	unknown Cytoplasm Plasma Membrane Cytoplasm unknown Cytoplasm unknown	other enzyme enzyme other other other other	
235310_at 236140_at 219508_at 1552316_a_a t 219243_at 219243_at 218805_at 21977_at 228071_at	GCET2 GCLM GCNT3 GIMAP1 GIMAP4 GIMAP5 GIMAP5 GIMAP7	germinal center expressed transcript 2 glutamate-cysteine ligase, modifier subunit glucosaminyl (N-acetyl) transferase 3, mucin type GTPase, IMAP family member 1 GTPase, IMAP family member 4 GTPase, IMAP family member 5 GTPase, IMAP family member 5 GTPase, IMAP family member 7	unknown Cytoplasm Plasma Membrane Cytoplasm unknown Cytoplasm unknown unknown	other enzyme enzyme other other other other other	
235310_at 236140_at 219508_at 1552316_a_a t 219243_at 219243_at 218805_at 219777_at 228071_at 235306_at	GCET2 GCLM GCNT3 GIMAP1 GIMAP4 GIMAP5 GIMAP5 GIMAP7 GIMAP8	germinal center expressed transcript 2 glutamate-cysteine ligase, modifier subunit glucosaminyi (N-acetyl) transferae 3, mucin type GTPase, IMAP family member 1 GTPase, IMAP family member 4 GTPase, IMAP family member 5 GTPase, IMAP family member 6 GTPase, IMAP family member 7 GTPase, IMAP family member 7 GTPase IMAP family member 8	unknown Cytoplasm Plasma Membrane Cytoplasm unknown Unknown unknown unknown	other enzyme enzyme other other other other other other	
235310_at 236140_at 219508_at 1552316_a_a t 219243_at 219243_at 219777_at 228071_at 235306_at 206102_at	GCET2 GCLM GCNT3 GIMAP1 GIMAP4 GIMAP5 GIMAP5 GIMAP6 GIMAP7 GIMAP8 GIMAP8 GIMS1	germinal center expressed transcript 2 glutamate-cysteine ligase, modifier subunit glucosaminyi (N-acetyl) transferase 3, mucin type GTPase, IMAP family member 1 GTPase, IMAP family member 4 GTPase, IMAP family member 5 GTPase, IMAP family member 6 GTPase, IMAP family member 7 GTPase, IMAP family member 7 GTPase, IMAP family member 7 GTPase, IMAP family member 8	unknown Cytoplasm Plasma Membrane Cytoplasm unknown Cytoplasm unknown	other enzyme enzyme other other other other other other other	
235310_at 236140_at 219508_at 1552316_a_a t 219243_at 219243_at 218805_at 219777_at 228071_at 235306_at 206102_at	GCET2 GCLM GCNT3 GIMAP1 GIMAP4 GIMAP5 GIMAP5 GIMAP6 GIMAP7 GIMAP8 GINS1	germinal center expressed transcript 2 glutamate-cysteine ligase, modifier subunit glucosaminy (IV-acety) transferae 3, mucin type GTPase, IMAP family member 1 GTPase, IMAP family member 4 GTPase, IMAP family member 5 GTPase, IMAP family member 6 GTPase, IMAP family member 7 GTPase, IMAP family member 7 GTPase, IMAP family member 8 GINS complex subunit 1 (Pdf homolog) musine nucleonite bigities necesing 6 notebia. Jabba activation	unknown Cytoplasm Plasma Membrane Cytoplasm unknown Cytoplasm unknown unknown unknown Nucleus	other enzyme enzyme other othe	
235310_at 236140_at 219508_at 1552316_a_a t 219243_at 219243_at 219277_at 228071_at 235306_at 206102_at	GCET2 GCLM GCNT3 GIMAP1 GIMAP5 GIMAP5 GIMAP5 GIMAP6 GIMAP7 GIMAP8 GINS1	germinal center expressed transcript 2 glutamate-cysteine ligase, modifier subunit glucosaminyi (N-acetyl) transferase 3, mucin type GTPase, IMAP family member 1 GTPase, IMAP family member 4 GTPase, IMAP family member 5 GTPase, IMAP family member 6 GTPase, IMAP family member 7 GTPase, IMAP family member 7 GTPase, IMAP family member 8 GTIS complex subunit 1 (Pft homolog) guaraine nucleotide binding protein (G protein), alpha activating	unknown Cytoplasm Plasma Membrane Cytoplasm unknown Unknown unknown Unknown Nucleus Nucleus	other enzyme enzyme other other other other other other other	
235310_at 236140_at 219508_at 1552316_a_a t 219243_at 219243_at 219277_at 22805_at 235306_at 206102_at 231951_at 234515_at	GCET2 GCLM GCNT3 GIMAP1 GIMAP4 GIMAP5 GIMAP6 GIMAP7 GIMAP7 GIMAP8 GINS1 GNA01	germinal center expressed transcript 2 glutamate-cysteine ligase, modifier subunit glucosaminy (In acetty) transferse 3, much type GTPase, IMAP family member 1 GTPase, IMAP family member 5 GTPase, IMAP family member 5 GTPase, IMAP family member 6 GTPase, IMAP family member 7 GTPase, IMAP family member 7 GTPase, IMAP family member 8 GINS complex subunit 1 (Pf1 homolog) guarine nucleotide binding protein (G protein), alpha activating activity polypeptide O	unknown Cytoplasm Plasma Membrane Cytoplasm unknown Cytoplasm unknown unknown unknown Nucleus Plasma Membrane Plasma Membrane	other enzyme enzyme other other other other other other other enzyme enz	
235310_at 236140_at 219500_at 1552316_a_a t 219243_at 218005_at 219777_at 228071_at 235306_at 206100_at 231951_at 214157_at	GCET2 GCLM GCNT3 GIMAP1 GIMAP4 GIMAP5 GIMAP5 GIMAP6 GIMAP7 GIMAP8 GIN51 GNA01 GNAS	germinal center expressed transcript 2 glutamate-cysteine ligase, modifier subunit glucosaminyi (N-acetyl) transferase 3, mucin type GTPase, IMAP family member 1 GTPase, IMAP family member 4 GTPase, IMAP family member 5 GTPase, IMAP family member 6 GTPase, IMAP family member 7 GTPase, IMAP family member 7 GTPase, IMAP family member 8 GINS complex subunit 1 (P4T homolog) guanine nucleotide binding protein (G protein), alpha activating activity polypeptide 0 GNAS complex locus	unknown Cytoplasm Plasma Membrane Cytoplasm unknown Cytoplasm unknown unknown Plasma Membrane Plasma Membrane Plasma Membrane	other enzyme enzyme other other other other other other other enzyme enzyme	
235310_at 236140_at 219508_at 1552316_a_a t 219243_at 218805_at 219777_at 228071_at 235306_at 206102_at 231951_at 2114157_at	GCET2 GCLM GCNT3 GIMAP1 GIMAP4 GIMAP5 GIMAP5 GIMAP7 GIMAP8 GINS1 GNA01 GNA01 GNA5	germinal center expressed transcript 2 glutamate-cysteine ligase, modifier subunit glucosaminy (N-acetyl) transferase 3, mucin type GTPase, IMAP family member 1 GTPase, IMAP family member 4 GTPase, IMAP family member 5 GTPase, IMAP family member 5 GTPase, IMAP family member 7 GTPase, IMAP family member 7 GTPase, IMAP family member 7 GTPase, IMAP family member 8 GINS complex subunit 1 (Pf1 homolog) guanine nucleotide binding protein (G protein), alpha activating activity polypeptide 0 GNAS complex locus guanine nucleotide binding protein (G protein), beta polypeptide	unknown Cytoplasm Plasma Membrane Cytoplasm unknown Cytoplasm unknown unknown unknown Plasma Membrane Plasma M	other enzyme enzyme other other other other other other enzyme en	
235310_at 236140_at 219508_at 1552316_a a t 219243_at 218805_at 219777_at 228071_at 23806_at 206102_at 231951_at 214157_at 225710_at	GCET2 GCLM GCNT3 GIMAP1 GIMAP4 GIMAP5 GIMAP5 GIMAP5 GIMAP6 GIMAP7 GIMAP8 GINS1 GNA01 GNA01 GNA5	germinal center expressed transcript 2 glutamate-cysteine ligase, modifier subunit glucosaminyi (N-acetyl) transferae 3, mucin type GTPase, IMAP family member 1 GTPase, IMAP family member 4 GTPase, IMAP family member 5 GTPase, IMAP family member 6 GTPase, IMAP family member 7 GTPase, IMAP family member 7 GTPase, IMAP family member 8 GINS complex subunit 1 (Psf1 homolog) guanine nucleotide binding protein (G protein), alpha activating activity polypeptide 0 GNAS complex locus guanine nucleotide binding protein (G protein), beta polypeptide 4	unknown Cytoplasm Plasma Membrane Cytoplasm unknown Cytoplasm unknown unknown unknown Plasma Membrane Plasma Membrane Plasma Membrane Plasma Membrane Plasma Plasma Membrane Plasma Plas	other enzyme enzyme other other other other other other other enzyme enzyme enzyme	
235310_at 236140_at 219508_at 1552316_a_a t 219243_at 219243_at 218805_at 219277_at 228071_at 235306_at 206102_at 231951_at 214157_at 225710_at 225710_at 225710_at	GCET2 GCLM GCNT3 GIMAP1 GIMAP2 GIMAP5 GIMAS GNB4 GIMA5	germinal center expressed transcript 2 glutamate-cysteine ligase, modifier subunit glucosaminy (N-acetv)) transferase 3, mucin type GTPase, IMAP family member 1 GTPase, IMAP family member 4 GTPase, IMAP family member 5 GTPase, IMAP family member 5 GTPase, IMAP family member 7 GTPase, IMAP family member 7 GTPase, IMAP family member 7 GTPase, IMAP family member 8 GINS complex subunit 1 (Pd1 homolog) guanine nucleotide binding protein (G protein), alpha activating activity polyapetide Jocus guanien nucleotide binding protein (G protein), beta polyapetide 4 amenie nucleotide binding protein (G protein), gamma 2	unknown Cytoplasm Plasma Membrane Cytoplasm unknown Cytoplasm unknown unknown Unknown Plasma Membrane	other enzyme enzyme other other other other other other other enzyme enz	
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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	LAPTMS	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	
	LOC1001288	 Statistics = 0.0000 (0.000000000000000000000000000			
235174_s_at	22	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_a					
t	LOC728153	similar to FAM133B protein	unknown	other	
227889_at	LPCAT2	lysophosphatidylcholine acyltransferase 2	Cytoplasm	enzyme	
		leucine-rich repeats and calponin homology (CH) domain	- 1 mm 1 1 2 mm		
227688_at	LRCH2	containing 2	unknown	other	
	10000			0.2257.0	
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 18	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	
	MDN1				
1569484_s_a	(includes		100 M 100 M	1001000	
t	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	
		microtubule associated monoxygenase, calponin and LIM domain			
212473_s_at	MICAL2	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	
	1000 000 000 000		10000000000000000000000000000000000000	171.00 IL	
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	
	MYR				
	lincludes				
204798 at	EG:4602)	wmyh myelohlastosis viral oncogene homolog (avian)	Nucleus	transcription regulator	
LOTI DO M	20,4002)	The injection of the offension of the interest of the injection of the inj	The cost	Conseription (Chanton	
201497 x at	MYH11	myosin, beaux chain 11, smooth muscle	Outoplasm	other	
201798 4 at	MYOE	myofarlin	Nuclear	other	
201790_3_80	NREA	niyoteinii	Nucleus	other	
	lincluder				
226430 4 14	EG-26960)	neuroheachin	Cutoplasm	other	
220455_5_01	20.205007		cycopiani	o trici	
227601 .*	NCRNA00173	non-protein coding RNA 173		ath as	
23/331 01		THORE DIGUERT COURSE NIGHT 17.3	lunknown	lother	
237331_81	Trenitrio 175	I I I I I I I I I I I I I I I I I I I	unknown	other	
204162 at	NDCRO	NOC20 homeles linetechers simpley component (C. servician)	Nuclear	other	
204162_at	NDC80	NDC80 homolog, kinetochore complex component (S. cerevisiae)	Nucleus	other	
204162_at 218678_at	NDC80 NES	NDC80 homolog, kinetochore complex component (S. cerevisiae) nestin nuclear factor of activated Tcells, actemizeric, calcineuric-	Nucleus Cytoplasm	other other	
204162_at 218678_at	NDC80 NES	NDC80 homolog, kinet 213 NDC80 homolog, kinetochore complex component (S. cerevisiae) nestin nuclear factor of activated T-cells, cytoplasmic, calcineurin- denondent 2	Nucleus Cytoplasm	other other transcription regulator	
204162_at 218678_at 226991_at	NDC80 NES NFATC2	NDCB0 homolog, kinetochore complex component (S. cerevisiae) nestin nuclear factor of activated T-cells, cytoplasmic, calcineurin- dependent 2. Internantional	Nucleus Cytoplasm Nucleus	other other transcription regulator	
204162_at 218678_at 226991_at 204114_at	NDC80 NES NFATC2 NID2	NDC80 homolog, kinetochore complex component (S. cerevisiae) nestin nuclear factor of activated T-cells, cytoplasmic, calcineurin- dependent 2 nidogen 2 (osteonidogen) NDB-Bib domen constituing 4	Nucleus Cytoplasm Nucleus Extracellular Space	other other transcription regulator other	
204162_at 218678_at 226991_at 204114_at 200188_at	NDC80 NES NFATC2 NID2 NIPAL4 NIPAA3	NDC80 homolog, kinetochre complex component (S. cerevisiae) nestin nuckar factor of activated T-cells, cytoplasmic, calcineurin- dependent 2 nidogen 2 (osteonidogen) NIPA-like domain containing 4 nuckars recoercis cubanili, d. arcsun 4. member 3	unknown Nucleus Cytoplasm Nucleus Extracellular Space unknown	other other transcription regulator other other	
204162_at 218678_at 226991_at 204114_at 230188_at 209959_at 213061_s_at	NDC80 NES NFATC2 NID2 NIPAL4 NR4A3 NTAN1	NDCB0 homolog, kinetochore complex component (S. cerevisiae) nestin nuclear factor of activated T-cells, cytoplasmic, calcineurin- dependent Z nidogen 2 (osteonidogen) NiPA-like domain containing 4 nuclear receptor subfamily 4, group A, member 3 Nacrenia Honoraine amidue	Nucleus Cytoplasm Nucleus Extracellular Space unknown Nucleus Nucleus	other other transcription regulator other other ligand-dependent nuclear receptor	
204162_at 218678_at 226991_at 204114_at 230188_at 203061_s_at 213061_s_at	NDC80 NES NFATC2 NID2 NIPAL4 NR4A3 NTAN1 NTAN1	NDC80 homolog, kinetochore complex component (S. cerevisiae) nestin nuclear factor of activated T-cells, cytoplasmic, calcineurin- dependent 2 nidogen 2 (osteonidogen) NIPA-like domain containing 4 nuclear receptor subfamily 4, group A, member 3 N-terminal asparagine amidase nutrif / ouclearing disbenshare linked malent XL hune motif 11	unknown Nucleus Cytoplasm Nucleus Extracellular Space unknown Nucleus Nucleus Cutronasm	other other other transcription regulator other other iligand-dependent nuclear receptor enzyme obserbatase	
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200000 at					
202002 41	SEC31B	SEC31 homolog B (S. cerevisiae)	unknown	other	
244700 at	SEC618	Sec61 heta subunit	Cytoplasm	transnorter	
244700_dt	366010	Secondera suburn	Cytopiasiii	cransporter.	
		sema domain, immunoglobulin domain (lg), transmembrane			
219194_at	SEMA4G	domain (TM) and short cytoplasmic domain, (semaphorin) 4G	Plasma Membrane	other	
224762 at	SERINC2	serine incorporator 2	Plasma Membrane	transporter	
222122 4 24	CCOD2	recreted fristlad related protein 3	Plarma Membrane	transmembrane meanter	
223122_5_81	SFRFZ	secreted mazed-related protein z	Fiasma memorane	transmemorane receptor	
243759_at	SFR515	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	
220404 at	SLC20A1	solute corrier family 20 (observate transmerted) member 1	Diagona Magnhana	transporter	
230494_at	SUCZUAL	solute carrier family 20 (phosphate transporter), member 1	Plasma Memorane	transporter	
				1.	
202499 s at	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	Plasma Membrane	transporter	
		structural maintenance of chromosomes flexible binge domain			
and the second s		structural maintenance of chromosomes flexible ninge domain	100200000000000000000000000000000000000	012535	
1558747_at	SMCHD1	containing 1	unknown	other	
204466 s at	SNCA	synuclein, alpha (non A4 component of amyloid precursor)	Cytoplasm	other	
-		syntrophin heta 1 (dystrophin-associated protein A1 59kDa			
225420	CAUTER A	syndopian, acta 1 (ayaropian asactated protein A1, 55656,		and the second se	
226438_at	SNIB1	basic component 1)	Plasma Membrane	other	
	SNX9	·			
	lincludes				
222027 18	EG-51420)	sorting payin 9	Outonlasm	transporter	
223027_dt	20.31423	sorting rickins	Cytopiasin	cransporter	
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	
220020	5023	COV (you determining sector V) how 2	Modere	teneralistica considetas	
220030_41	3042	Ski (sex determining region 1)-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 a					
1	SPTRNS	spectrip heta non-enthropytic 5	Plasma Membrane	other	
*	SF 10N3	aperating deta, non-erythocytic 5	r isana memorane	out of	
236696_at	SR140	U2-associated SR140 protein	Nucleus	other	
206626 x at	SSX1	synovial sarcoma. X breakpoint 1	Nucleus	transcription regulator	
at				and a second sec	
Contractor and		The second se	20002000	and the property of the second	
210497_x_at	SSX2	synovial sarcoma, X breakpoint 2	Nucleus	transcription regulator	
207665 * **	SSX3	synovial sarcoma X breakooint ?	unknown	other	
-01000_A_at	-30.3	all and a second of the second points a	and a determined and a de		
Sec. January	10000		13.45.457	11.02007	
210394_x_at	SSX4	synovial sarcoma, X breakpoint 4	Nucleus	other	
202786 at	STK39	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	Nucleus	kinase	
231000 at	CTOV2	statistic theorem in the so (street of statistics), years		ath co	
231969_at	STOX2	storknead 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	
10000		sheer we have a second s		e bitel	
122200a_a_a	100000			2 0225	
t	SYNJ2	synaptojanin 2	Cytoplasm	phosphatase	
242109_at	SYTL3	synaptotagmin-like 3	Cytoplasm	other	
1552542 s a				0.89086	
	TACAD	T will a short a Dha CTD and a short a short a law	the second s	246.00	
t	TAGAP	1-cell activation KnoGTPase 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	
		TEA domain family member 1 (SV40 transcriptional enhancer	reconsected and a second se		
		revolution ranny memoer a provideration provider enhancer		10.000 x x x x x x x x x x x x x x x x x	
224900_at	TEADI	ractor)	Nucleus	transcription regulator	
218872_at	TESC	tescalcin	unknown	other	
and the second se		tactic avaranced 0			
243198 at	TEX9	resus expressed 5	unknown	other	
243198_at	TEX9	transforming growth factor, beta recentor 1	unknown Plarma Membrane	other	
243198_at 236561_at	TEX9 TGFBR1	transforming growth factor, beta receptor 1	unknown Plasma Membrane	other kinase	
243198_at 236561_at 226625_at	TEX9 TGFBR1 TGFBR3	transforming growth factor, beta receptor 1 transforming growth factor, beta receptor III	unknown Plasma Membrane Plasma Membrane	other kinase kinase	
243198_at 236561_at 226625_at 219122_s_at	TEX9 TGFBR1 TGFBR3 THG1L	transforming growth factor, beta receptor 1 transforming growth factor, beta receptor 1 tRNA-histidine guanylyltransferase 1-like (S. cerevisiae)	unknown Plasma Membrane Plasma Membrane Cytoplasm	other kinase kinase enzyme	
243198_at 236561_at 226625_at 219122_s_at 213135 at	TEX9 TGFBR1 TGFBR3 THG1L TIAM1	transforming growth factor, beta receptor 1 transforming growth factor, beta receptor 1 tRNA-histidine guanylyltransferase 1-like (S. cerevisiae) T-cell iymphoma invasion and metastasis 1	unknown Plasma Membrane Plasma Membrane Cytoplasm Cytoplasm	other kinase kinase enzyme other	
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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.

Г	Univariate Cox analysis - Overall survival			
F	HM		UAMS-TT2	
	HR	Р	HR	Р
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		
β 2 Μ	1.1	4.20E-05		NA
Alb	0.47	1.40E-02		

Г	Multivariate Cox analysis - Overall survival			
	HM		UAMS-TT2	
	HR	Р	HR	Р
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		
ISS	1.3	NS		
SBS	21	3.60E-14		
β2M	1	NS		NA
SBS	22	2.80E-14		
Alb	0.9	NS		

Г	Multivariate Cox analysis - Overall survival				
F	HM		LR-TT2		
T	HR	P	HR	Р	
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 ($P \le 0.05$), 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	1	11		L	Ш	III
Salmon and durie	13%	17%	70%	4%	10%	86%
ISS	54%	33%	13%	27%	46%	27%