Design and Methods

Patients and Sample Preparation

Two hundred twenty-four patients with plasma cell neoplasms were analyzed, including 211 MM, 10 smoldering MM and 3 with plasma cell leukemia. A total of 114 samples correspond to untreated cases and the remaining 110 to previously treated patients. Data was obtained from the Multiple Myeloma Research Consortium genomics initiative (data available at http://www.broadinstitute.org/mmgp/home). All patients provided written informed consent approving the use of their samples under Institutional Review Board approval. To perform aCGH and GEP, tumor cells were enriched with anti-CD138^{+} immunomagnetic beads (Robosep - StemCell Technologies; Vancouver; Canada) and stored in TRIzol® reagent (Invitrogen, Carlsbad, CA), as previously published by us (13). Nucleic acids were isolated from TRIzol following the protocol supplied by the manufacturer. RNA used for GEP was cleaned up using the QIAGEN RNeasy kit, while the DNA used for aCGH was cleaned up using Puregene DNA isolation kit and using the manufacturer's suggested protocol.

Calculation of total number of chromosomes and copy-number abnormalites using aCGH

All genome-based data reported is based on NCBI build 36 (hg18) of the human genome. High-resolution aCGH was performed with the human genome 244A microarray (Agilent Technologies). Digestion, labeling and hybridization were done as previously published by us (14). Microarrays were scanned with an Agilent DNA Microarray scanner and Feature extraction was performed with

Feature Extraction Software version 9.5. Extracted data was then read into Nexus Copy Number Software version 5.1 (BioDiscovery Inc., El Segundo, CA) as follows: data was smoothed by quadratic correction to minimize any wave-like pattern commonly seen in aCGH studies. Copy number abnormalities were defined by using the Rank segmentation algorithm with a Significant Threshold set at 2.4E-5 with a minimum number of probes per segment set at 3. Maximum contiguous probe spacing was set at 1000 Kb. Genomic regions of gain were set at +0.25 for single copy gain. Values higher than +1.2 were used for defining high copy gains. Genomic regions of loss were set at -0.25 for single copy loss and -1.2 for bialleic loss. Gender correction was applied by using the normal diploid reference used in the hybridization (female, Y chromosome ignored). Next, visual estimation of total chromosome number was performed for each of the 224 samples by using the individual sample drill down menu provided by Nexus software. By using the generated ideograms in the overview and chromosome view, deviation from a normal diploid count of 46 was estimated by accessing the gain or loss of regions bordering the centromere (no probes for centromeres) in metacentric and submetacentric chromosomes 1-12, 16-20 and X, and telomeric of the centromere on the q-arm in the acrocentric chromosomes 13-15, 21 and 22 (**Supplementary Figure S1**). Metacentric or submetacentric chromosomes with loss or gain of both borders would be counted as a loss or gain of that chromosome while a continuous segment of loss or gain on the q-arm of acrocentric chromosomes would be counted as loss or gain of that chromosome. Samples estimated to have ≤44 chromosomes were considered to be hypodiploid, 45-46 chromosomes NH-MM and ≥47 chromosomes H-MM. Samples that are near triploid, near tetraploid, tetraploid and Y chromosome abnormalities were unable to discern since a normal diploid female reference was used in the hybridization. The aCGH approach allows the detection of CNA that are present in at least 30-40% of tumor.

Next, using Nexus software, segmented regions shared by 20% or more of the hypodiploid samples were considered abnormal and listed as an aggregate while the minimal regions of aberrations listed in the aggregate are listed as peaks only (**Supplementary Table S1**). The most frequent minimal regions found in hypodiploid were subsequently compared to the same regions in the NH-MM and H-MM groups.

GEP

GEP was performed on the U133A Plus 2.0 array (Affymetrix) following the manufacture's suggested protocol. In order to simultaneously reduce the batch effect and obtain presence/absence calls we transformed the GEP data using a combination of algorithms as follows. First array data was pre-processed by using the Robust multiarray analysis (RMA) algorithm. Independently, detection calls (Present/Marginal/Absent) were obtained using the MAS5 algorithm. Finally, we merged the raw intensity values obtained from RMA with the detection calls obtained from MAS5, thus reducing the batch effect but maintaining the detection calls. Next, data was filtered on flags, only including cases with Present or Marginal calls in at least 5% of cases. The cutoff of 5% did not exclude any of the genes that are overexpressed as consequence of translocations (the less frequent was MAF translocations found in 6.5% of cases). After filtering on flags, we focused the search on differentially expressed genes (>2-fold change). The analysis was performed in the comparison between ploidy groups, either including all cases or only the untreated MM cases.

Finally, the main gene indices and signatures associated with outcome in MM, including the translocation/cyclin D (TC) classification, UAMS 70-gene index, proliferation index, centrosome signature and NF-kB indices, were calculated as previously described (8, 9, 15-17).

Statistical analysis

Contingency tables using X^2 statistic was used for determining p-values for comparison between groups. Yates' correction was used in cases with at least one group has an expected count smaller than 5.

Supplementary Table S1A. Segmented regions shared by 20% or more of the hypodiploid patients are listed as an aggregate.
Aggregate % cut off = 20.0
Display peaks only = false

Region	Region Length (bp)	Cytoband Location	Event	Frequency %	Count of Gene Symbols	Count of miRNAs	Count of CancerGene Census-Sanger.txt	CancerGeneCensus-Sanger.txt
chr1:812,456-1,565,953	753497	p36.33	CN Loss	20.4081633	47	3	0	
chr1:1,581,019-1,625,318	44299	p36.33	CN Loss	20.4081633	4	0	0	
chr1:1,773,413-3,017,584	1244171	p36.33 - p36.32	CN Loss	20.4081633	24	0	2	TNFRSF14, PRDM16
chr1:3,263,310-9,240,628	5977318	p36.32 - p36.22	CN Loss	20.4081633	58	2	2	PRDM16, RPL22
chr1:9,329,627-11,410,789	2081162	p36.22	CN Loss	20.4081633	28	0	0	
chr1:11,586,998-12,723,109	1136111	p36.22 - p36.21	CN Loss	20.4081633	24	0	0	
chr1:12,769,656-16,662,920	3893264	p36.21 - p36.13	CN Loss	20.4081633	60	0	0	
chr1:16,759,562-29,509,941	12750379	p36.13 - p35.3	CN Loss	20.4081633	213	3	4	SDHB, PAX7, MDS2, ARID1A
chr1:29,719,549-120,367,263	90647714	p35.3 - p12	CN Loss	20.4081633	755	12	19	LCK, SFPQ, THRAP3, MYCL1, MPL, MUTYH, TAL1, STIL, CDKN2C, EPS15, JUN, JAK1, FUBP1, BCL10, BCAR3, RBM15, TRIM33, NRAS, NOTCH2
chr1:150,817,845-150,854,987	37142	q21.3	CN Loss	24.4897959	3	0	0	
chr1:142,721,264-247,249,719	104528455	q21.1 - q44	CN Gain	36.7346939	1125	28	21	PDE4DIP, BCL9, ARNT, MLLT11, TPM3, MUC1, PRCC, NTRK1, FCRL4, SDHC, FCGR2B, FCGR2B, PBX1, PRRX1, ABL2, TPR, CDC73, MDM4, ELK4, SLC45A3, FH
chr1:194,991,898-195,079,790	87892	q31.3	CN Loss	22.4489796	2	0	0	
chr1:246,794,902-246,877,950	83048	q44	CN Loss	20.4081633	4	0	0	
chr2:88,917,839-89,393,871	476032	p11.2	CN Loss	30.6122449	0	0	0	
chr2:91,123,642-91,511,347	387705	p11.1	CN Gain	38.7755102	3	0	0	
chr3:90,303,758-90,391,757	87999	p11.1	CN Gain	24.4897959	0	0	0	
chr3:163,992,372-164,107,354	114982	q26.1	CN Loss	22.4489796	0	0	0	
chr3:163,992,372-164,118,369	125997	q26.1	CN Gain	22.4489796	0	0	0	
chr3:196,826,229-196,942,795	116566	q29	CN Loss	20.4081633	3	1	0	
chr3:196,867,332-196,954,310	86978	q29	CN Gain	20.4081633	3	1	0	

Region	Region Length (bp)	Cytoband Location	Event	Frequency %	Count of Gene Symbols	Count of miRNAs	Count of CancerGene Census-Sanger.txt	CancerGeneCensus-Sanger.txt
chr4:0-3,480,340	3480340	p16.3 - p16.2	CN Loss	20.4081633	64	2	1	FGFR3
chr4:3,611,900-17,401,574	13789674	p16.2 - p15.32	CN Loss	20.4081633	108	3	0	
chr4:20,609,861-26,371,347	5761486	p15.31 - p15.2	CN Loss	20.4081633	22	1	0	
chr4:36,685,307-36,858,065	172758	p14	CN Loss	20.4081633	0	0	0	
chr4:37,199,299-39,273,531	2074232	p14	CN Loss	20.4081633	23	1	0	
chr4:40,618,579-41,827,568	1208989	p14 - p13	CN Loss	20.4081633	8	0	1	PHOX2B
chr4:54,396,571-58,353,803	3957232	q12	CN Loss	20.4081633	29	0	4	PDGFRA, CHIC2, KIT, KDR
chr4:60,749,626-61,316,294	566668	q13.1	CN Loss	20.4081633	0	0	0	
chr4:64,149,701-64,929,191	779490	q13.1	CN Loss	20.4081633	1	0	0	
chr4:65,213,065-67,606,779	2393714	q13.1 - q13.2	CN Loss	20.4081633	4	1	0	
chr4:68,855,793-68,888,732	32939	q13.2	CN Loss	20.4081633	1	0	0	
chr4:68,901,022-69,404,572	503550	q13.2	CN Gain	20.4081633	3	0	0	
chr4:68,981,732-69,404,572	422840	q13.2	CN Loss	53.0612245	3	0	0	
chr4:70,122,045-70,383,115	261070	q13.2	CN Loss	20.4081633	2	0	0	
chr4:70,452,716-71,155,961	703245	q13.3	CN Loss	20.4081633	15	0	0	
chr4:72,125,675-73,118,311	992636	q13.3	CN Loss	20.4081633	3	0	0	
chr4:75,864,664-80,369,676	4505012	q13.3 - q21.21	CN Loss	20.4081633	37	0	0	
chr4:82,220,469-86,154,686	3934217	q21.21 - q21.23	CN Loss	20.4081633	25	1	0	
chr4:86,905,852-90,456,651	3550799	q21.23 - q22.1	CN Loss	20.4081633	32	0	1	AFF1
chr4:91,087,831-93,462,798	2374967	q22.1	CN Loss	20.4081633	3	0	0	
chr4:97,938,611-98,178,234	239623	q22.3	CN Loss	20.4081633	0	0	0	
chr4:98,443,446-98,909,783	466337	q22.3	CN Loss	20.4081633	1	0	0	
chr4:100,175,143-100,417,745	242602	q23	CN Loss	20.4081633	7	0	0	
chr4:105,088,730-105,149,087	60357	q24	CN Loss	20.4081633	0	0	0	
chr4:106,101,902-106,522,471	420569	q24	CN Loss	20.4081633	2	0	1	TET2
chr4:108,582,398-109,062,034	479636	q25	CN Loss	20.4081633	2	0	0	
chr4:109,619,537-109,959,685	340148	q25	CN Loss	20.4081633	5	0	0	
chr4:110,381,958-111,553,216	1171258	q25	CN Loss	20.4081633	12	1	0	
chr4:113,670,978-119,529,301	5858323	q25 - q26	CN Loss	20.4081633	20	8	0	
chr4:119,890,463-120,436,321	545858	q26	CN Loss	20.4081633	4	0	0	
chr4:120,632,674-129,378,390	8745716	q27 - q28.2	CN Loss	20.4081633	34	1	1	IL2
chr4:129,647,039-130,136,598	489559	q28.2	CN Loss	20.4081633	2	0	0	
chr4:137,387,253-145,155,178	7767925	q28.3 - q31.22	CN Loss	20.4081633	32	0	0	
chr4:169,711,967-170,871,890	1159923	q32.3 - q33	CN Loss	20.4081633	5	0	0	
chr4:170,985,726-171,941,195	955469	q33	CN Loss	20.4081633	4	0	0	
chr4:172,653,608-182,749,338	10095730	q34.1 - q35.1	CN Loss	20.4081633	24	0	0	

Region	Region Length (bp)	Cytoband Location	Event	Frequency %	Count of Gene Symbols	Count of miRNAs	Count of CancerGene Census-Sanger.txt	CancerGeneCensus-Sanger.txt
chr4:183,310,039-186,383,157	3073118	q35.1	CN Loss	20.4081633	30	1	0	
chr4:186,872,899-190,384,445	3511546	q35.1 - q35.2	CN Loss	20.4081633	15	0	0	
chr4:190,434,568-190,626,649	192081	q35.2	CN Loss	20.4081633	0	0	0	
chr4:190,734,388-191,131,168	396780	q35.2	CN Loss	20.4081633	2	0	0	
chr5:732,646-831,678	99032	p15.33	CN Loss	22.4489796	1	0	0	
chr5:754,698-900,231	145533	p15.33	CN Gain	24.4897959	1	0	0	
chr6:166,752-189,701	22949	p25.3	CN Gain	20.4081633	0	0	0	
chr6:7,550,799-9,517,469	1966670	p24.3	CN Gain	20.4081633	12	0	0	
chr6:32,513,687-32,563,052	49365	p21.32	CN Gain	22.4489796	1	0	0	
chr6:32,539,335-32,741,769	202434	p21.32	CN Loss	24.4897959	5	0	0	
chr6:80,155,947-80,329,047	173100	q14.1	CN Loss	20.4081633	1	0	0	
chr6:101,077,176-101,941,867	864691	q16.3	CN Loss	20.4081633	1	0	0	
chr6:102,296,584-102,553,844	257260	q16.3	CN Loss	20.4081633	1	0	0	
chr6:102,753,608-108,000,292	5246684	q16.3 - q21	CN Loss	20.4081633	17	1	1	PRDM1
chr6:108,101,289-119,670,546	11569257	q21 - q22.31	CN Loss	20.4081633	79	1	3	FOXO3, ROS1, GOPC
chr6:121,439,539-170,899,992	49460453	q22.31 - q27	CN Loss	20.4081633	278	4	4	MYB, TNFAIP3, FGFR1OP, MLLT4
chr7:38,256,608-38,388,017	131409	p14.1	CN Gain	24.4897959	2	0	0	
chr7:141,790,424-142,209,777	419353	q34	CN Gain	22.4489796	4	0	0	
chr8:0-39,319,045	39319045	p23.3 - p11.23	CN Loss	20.4081633	291	9	4	PCM1, WRN, WHSC1L1, FGFR1
chr8:39,349,089-39,508,473	159384	p11.23 - p11.22	CN Loss	20.4081633	2	0	0	
chr8:39,328,692-39,609,863	281171	p11.23 - p11.22	CN Gain	20.4081633	4	0	0	
chr8:39,679,887-40,796,760	1116873	p11.22 - p11.21	CN Loss	20.4081633	6	0	0	
chr8:41,430,572-42,372,362	941790	p11.21	CN Loss	20.4081633	13	1	1	MYST3
chr8:128,833,813-128,850,729	16916	q24.21	CN Gain	20.4081633	0	0	0	
chr9:10,729,843-11,288,300	558457	p23	CN Gain	26.5306122	0	0	0	
chr9:39,152,128-41,756,778	2604650	p13.1 - p12	CN Gain	20.4081633	12	0	0	
chr9:65,372,337-66,256,518	884181	q12	CN Gain	28.5714286	1	0	0	
chr9:74,979,021-76,626,249	1647228	q21.13	CN Gain	20.4081633	2	0	0	
chr9:107,125,298-107,419,813	294515	q31.1 - q31.2	CN Gain	20.4081633	3	0	0	
chr9:115,683,806-116,076,063	392257	q32	CN Gain	20.4081633	5	1	0	
chr9:128,875,471-128,972,397	96926	q33.3	CN Gain	20.4081633	2	0	0	
chr9:131,976,949-132,361,958	385009	q34.11	CN Gain	20.4081633	2	0	0	
chr9:132,748,133-133,446,626	698493	q34.12 - q34.13	CN Gain	20.4081633	14	0	2	ABL1, NUP214
chr9:136,650,656-137,701,638	1050982	q34.3	CN Gain	20.4081633	23	0	0	
chr9:138,235,564-138,307,416	71852	q34.3	CN Gain	20.4081633	2	0	0	

Region	Region Length (bp)	Cytoband Location	Event	Frequency %	Count of Gene Symbols	Count of miRNAs	Count of CancerGene Census-Sanger.txt	CancerGeneCensus-Sanger.txt
chr10:0-4,369,438	4369438	p15.3 - p15.1	CN Loss	20.4081633	20	0	1	KLF6
chr10:5,120,667-11,085,284	5964617	p15.1 - p14	CN Loss	20.4081633	33	0	1	GATA3
chr10:11,621,707-12,103,633	481926	p14	CN Loss	20.4081633	5	0	0	
chr10:45,963,009-47,043,499	1080490	q11.21 - q11.22	CN Loss	20.4081633	21	0	0	
chr11:55,115,301-55,216,250	100949	q11	CN Gain	20.4081633	4	0	0	
chr11:55,121,501-55,216,250	94749	q11	CN Loss	20.4081633	4	0	0	
chr11:125,929,546-128,048,091	2118545	q24.2 - q24.3	CN Gain	20.4081633	5	0	0	
chr12:0-257,931	257931	p13.33	CN Loss	20.4081633	5	0	0	
chr12:6,706,246-6,943,278	237032	p13.31	CN Loss	20.4081633	20	1	0	
chr12:9,252,652-10,826,157	1573505	p13.31 - p13.2	CN Loss	20.4081633	36	1	0	
chr12:11,547,615-15,458,254	3910639	p13.2 - p12.3	CN Loss	20.4081633	44	3	1	ETV6
chr12:19,279,827-19,696,569	416742	p12.3	CN Loss	20.4081633	2	0	0	
chr12:29,536,323-29,632,916	96593	p11.22	CN Loss	20.4081633	2	0	0	
chr12:37,595,392-39,067,454	1472062	q12	CN Loss	20.4081633	5	0	0	
chr12:39,645,564-43,074,047	3428483	q12	CN Loss	20.4081633	12	0	0	
chr12:43,749,773-46,624,838	2875065	q12 - q13.11	CN Loss	20.4081633	18	0	1	ARID2
chr12:46,734,489-48,880,261	2145772	q13.11 - q13.13	CN Loss	20.4081633	64	1	1	MLL2
chr12:51,505,506-52,603,472	1097966	q13.13	CN Loss	20.4081633	31	0	0	
chr12:52,802,213-53,204,798	402585	q13.13 - q13.2	CN Loss	20.4081633	15	1	0	
chr12:53,762,211-54,493,530	731319	q13.2	CN Loss	20.4081633	23	0	0	
chr12:57,399,278-63,570,619	6171341	q14.1 - q14.3	CN Loss	20.4081633	20	2	0	
chr12:64,223,524-67,240,977	3017453	q14.3 - q15	CN Loss	20.4081633	13	0	1	HMGA2
chr12:74,188,779-76,767,868	2579089	q21.2	CN Loss	20.4081633	9	0	0	
chr12:78,439,974-79,473,077	1033103	q21.2 - q21.31	CN Loss	20.4081633	4	0	0	
chr12:79,684,067-80,120,049	435982	q21.31	CN Loss	20.4081633	5	2	0	
chr12:81,659,258-81,876,615	217357	q21.31	CN Loss	20.4081633	1	0	0	
chr12:88,728,210-89,804,168	1075958	q21.33	CN Loss	20.4081633	0	0	0	
chr12:90,066,902-90,383,947	317045	q21.33	CN Loss	20.4081633	1	0	0	
chr12:91,654,728-95,851,876	4197148	q22 - q23.1	CN Loss	20.4081633	34	2	0	
chr12:97,334,228-97,917,095	582867	q23.1	CN Loss	20.4081633	9	0	0	
chr12:98,776,194-99,627,391	851197	q23.1	CN Loss	20.4081633	10	1	0	
chr12:99,824,137-100,935,534	1111397	q23.1 - q23.2	CN Loss	20.4081633	11	0	0	
chr12:102,297,070-106,876,626	4579556	q23.2 - q23.3	CN Loss	20.4081633	37	0	0	
chr12:107,247,415-108,365,790	1118375	q23.3 - q24.11	CN Loss	20.4081633	17	1	0	
chr12:115,960,178-119,043,920	3083742	q24.22 - q24.23	CN Loss	20.4081633	20	1	0	
chr12:124,090,984-132,349,534	8258550	q24.31 - q24.33	CN Loss	20.4081633	49	0	0	

Region	Region Length (bp)	Cytoband Location	Event	Frequency %	Count of Gene Symbols	Count of miRNAs	Count of CancerGene Census-Sanger.txt	CancerGeneCensus-Sanger.txt
chr13:18,065,953-114,142,980	96077027	q11 - q34	CN Loss	81.6326531	462	14	10	ZMYM2, CDX2, FLT3, BRCA2, LHFP, TTL, FOXO1, LCP1, RB1, ERCC5
chr14:19,242,596-19,493,856	251260	q11.2	CN Gain	20.4081633	7	0	0	
chr14:21,425,337-22,049,477	624140	q11.2	CN Gain	24.4897959	0	0	0	
chr14:18,187,154-106,368,585	88181431	q11.1 - q32.33	CN Loss	28.5714286	779	62	15	CCNB1IP1, NKX2-1, NIN, KTN1, GPHN, RAD51B, TSHR, TRIP11, GOLGA5, DICER1, TCL6, TCL1A, BCL11B, HSP90AA1, AKT1
chr15:18,436,483-20,326,469	1889986	q11.2	CN Gain	20.4081633	20	1	0	
chr15:32,493,970-32,616,911	122941	q14	CN Gain	20.4081633	4	1	0	
chr16:0-8,853,846	8853846	p13.3 - p13.2	CN Loss	20.4081633	229	3	2	TSC2, CREBBP
chr16:9,693,721-10,062,409	368688	p13.2	CN Loss	20.4081633	1	0	0	
chr16:10,245,699-10,411,248	165549	p13.2 - p13.13	CN Loss	20.4081633	1	0	0	
chr16:14,916,289-15,028,645	112356	p13.11	CN Loss	28.5714286	4	1	0	
chr16:21,240,241-21,504,160	263919	p12.2	CN Loss	22.4489796	5	0	0	
chr16:32,054,867-33,530,475	1475608	p11.2	CN Gain	20.4081633	8	0	0	
chr16:33,384,087-35,005,009	1620922	p11.2 - p11.1	CN Loss	20.4081633	8	1	0	
chr16:45,058,242-88,827,254	43769012	q11.2 - q24.3	CN Loss	28.5714286	420	6	8	CYLD, HERPUD1, CDH11, CBFB, CDH1, MAF, CBFA2T3, FANCA
chr16:69,403,327-69,758,575	355248	q22.2	CN Gain	24.4897959	2	0	0	
chr17:641,632-3,262,661	2621029	p13.3	CN Loss	20.4081633	54	4	0	
chr17:3,654,667-4,039,101	384434	p13.2	CN Loss	20.4081633	7	0	0	
chr17:4,471,262-12,817,050	8345788	p13.2 - p12	CN Loss	20.4081633	190	4	6	USP6, RABEP1, TP53, PER1, GAS7, MAP2K4
chr17:41,572,059-41,672,900	100841	q21.31	CN Loss	20.4081633	2	0	0	
chr17:41,518,612-41,774,058	255446	q21.31	CN Gain	30.6122449	4	0	0	
chr19:1,533,909-7,818,392	6284483	p13.3 - p13.2	CN Gain	20.4081633	186	5	4	TCF3, GNA11, SH3GL1, MLLT1
chr19:7,912,626-11,400,284	3487658	p13.2	CN Gain	20.4081633	110	4	1	SMARCA4
chr19:12,771,907-15,304,636	2532729	p13.13 - p13.12	CN Gain	20.4081633	72	6	2	LYL1, BRD4
chr19:15,636,339-15,694,800	58461	p13.12	CN Gain	20.4081633	1	0	0	

Region	Region Length (bp)	Cytoband Location	Event	Frequency %	Count of Gene Symbols	Count of miRNAs	Count of CancerGene Census-Sanger.txt	CancerGeneCensus-Sanger.txt
chr22:22,674,690-22,728,274	53584	q11.23	CN Gain	34.6938776	4	0	0	
chr22:14,797,008-49,691,432	34894424	q11.1 - q13.33	CN Loss	22.4489796	545	16	16	CLTCL1, SEPT5, BCR, BCR, BCR, BCR, SMARCB1, MN1, CHEK2, EWSR1, NF2, PATZ1, MYH9, PDGFB, MKL1, EP300
chrX:2,710,316-58,314,722	55604406	p22.33 - p11.1	CN Loss	44.8979592	375	14	8	KDM6A, SSX1, SSX4, WAS, GATA1, TFE3, SSX2, KDM5C
chrX:61,848,414-154,913,754	93065340	q11.1 - q28	CN Loss	30.6122449	619	63	10	FAM123B, MSN, FOXO4, MED12, NONO, ATRX, SEPT6, ELF4, GPC3, MTCP1
chrX:152,149,307-153,833,933	1684626	q28	CN Gain	20.4081633	71	1	0	

Supplementary Table S1B. Frequent minimal regions of abberation within the aggregate shared by 20% or more of the the hypodiploid patients are listed as peaks only.
Aggregate % cut off = 20.0
Display peaks only = true

Region	Region Length (bp)	Cytoband Location	Event	Frequency %	Count of Gene Symbols	Count of miRNAs	Count of CancerGene Census-Sanger.txt	CancerGene Census-Sanger.txt
chr1:839,662-1,024,498	184836	p36.33	CN Loss	26.5306122	11	0	0	
chr1:1,531,271-1,553,726	22455	p36.33	CN Loss	22.4489796	1	0	0	
chr1:1,581,019-1,625,318	44299	p36.33	CN Loss	20.4081633	4	0	0	
chr1:2,351,622-2,454,845	103223	p36.32	CN Loss	26.5306122	3	0	0	
chr1:3,369,642-3,472,263	102621	p36.32	CN Loss	26.5306122	3	1	0	
chr1:3,966,006-5,956,564	1990558	p36.32 - p36.31	CN Loss	22.4489796	5	0	0	
chr1:10,019,913-10,113,625	93712	p36.22	CN Loss	22.4489796	1	0	0	
chr1:11,586,998-12,723,109	1136111	p36.22 - p36.21	CN Loss	20.4081633	24	0	0	
chr1:12,953,267-13,083,117	129850	p36.21	CN Loss	24.4897959	2	0	0	
chr1:16,194,999-16,283,221	88222	p36.13	CN Loss	24.4897959	5	0	0	
chr1:16,646,534-16,656,936	10402	p36.13	CN Loss	22.4489796	1	0	0	
chr1:16,916,637-17,084,436	167799	p36.13	CN Loss	38.7755102	4	0	0	
chr1:17,119,475-17,139,588	20113	p36.13	CN Loss	38.7755102	1	0	0	
chr1:17,161,121-17,167,451	6330	p36.13	CN Loss	22.4489796	1	0	0	
chr1:17,186,783-17,840,486	653703	p36.13	CN Loss	22.4489796	9	0	1	SDHB
chr1:18,139,524-18,369,605	230081	p36.13	CN Loss	22.4489796	1	0	0	
chr1:19,368,326-19,439,430	71104	p36.13	CN Loss	24.4897959	2	0	0	
chr1:23,820,681-25,023,681	1203000	p36.11	CN Loss	22.4489796	25	0	1	MDS2
chr1:25,469,999-25,539,067	69068	p36.11	CN Loss	28.5714286	2	0	0	
chr1:29,052,291-29,433,242	380951	p35.3	CN Loss	24.4897959	5	0	0	
chr1:30,995,208-31,260,259	265051	p35.2	CN Loss	28.5714286	6	0	0	
chr1:32,043,218-32,055,979	12761	p35.2	CN Loss	26.5306122	1	0	0	
chr1:33,211,291-33,460,611	249320	p35.1	CN Loss	28.5714286	3	0	0	
chr1:33,533,106-33,806,989	273883	p35.1	CN Loss	26.5306122	5	0	0	
chr1:34,462,318-34,750,597	288279	p34.3	CN Loss	28.5714286	0	0	0	
chr1:35,086,134-35,131,465	45331	p34.3	CN Loss	26.5306122	2	0	0	
chr1:37,031,950-37,174,468	142518	p34.3	CN Loss	24.4897959	1	0	0	
chr1:37,692,408-39,108,206	1415798	p34.3	CN Loss	26.5306122	25	0	0	
chr1:41,351,175-41,690,653	339478	p34.2	CN Loss	30.6122449	2	0	0	
chr1:42,429,456-42,628,870	199414	p34.2	CN Loss	28.5714286	2	0	0	
chr1:44,229,064-44,444,639	215575	p34.1	CN Loss	26.5306122	4	0	0	

Region	Region Length (bp)	Cytoband Location	Event	Frequency %	Count of Gene Symbols	Count of miRNAs	Count of CancerGene Census-Sanger.txt	CancerGene Census-Sanger.txt
chr1:44,596,331-44,977,554	381223	p34.1	CN Loss	26.5306122	4	0	0	
chr1:47,432,403-47,677,999	245596	p33	CN Loss	30.6122449	6	0	2	TAL1, STIL
chr1:49,348,985-49,418,970	69985	p33	CN Loss	26.5306122	1	0	0	
chr1:50,828,773-50,944,358	115585	p33	CN Loss	32.6530612	1	0	0	
chr1:51,035,130-51,239,008	203878	p33	CN Loss	34.6938776	2	0	1	CDKN2C
chr1:51,573,727-51,806,123	232396	p32.3	CN Loss	30.6122449	2	0	1	EPS15
chr1:53,450,344-53,771,732	321388	p32.3	CN Loss	28.5714286	8	0	0	
chr1:56,947,051-61,958,233	5011182	p32.2 - p31.3	CN Loss	30.6122449	19	0	1	JUN
chr1:63,743,631-63,830,824	87193	p31.3	CN Loss	30.6122449	3	0	0	
chr1:68,142,810-68,466,173	323363	p31.3	CN Loss	30.6122449	4	1	0	
chr1:69,107,460-71,637,724	2530264	p31.2 - p31.1	CN Loss	30.6122449	12	1	0	
chr1:71,797,450-72,199,233	401783	p31.1	CN Loss	32.6530612	2	0	0	
chr1:74,870,804-75,384,916	514112	p31.1	CN Loss	34.6938776	4	0	0	
chr1:76,299,561-78,467,530	2167969	p31.1	CN Loss	34.6938776	11	0	1	FUBP1
chr1:81,571,019-82,044,915	473896	p31.1	CN Loss	34.6938776	1	0	0	
chr1:84,341,682-85,961,961	1620279	p31.1 - p22.3	CN Loss	38.7755102	21	0	1	BCL10
chr1:93,163,320-93,602,274	438954	p22.1	CN Loss	44.8979592	6	0	0	
chr1:93,753,493-94,796,785	1043292	p22.1 - p21.3	CN Loss	46.9387755	10	1	1	BCAR3
chr1:100,079,142-100,570,592	491450	p21.2	CN Loss	46.9387755	9	1	0	
chr1:101,920,480-103,333,973	1413493	p21.2 - p21.1	CN Loss	40.8163265	4	0	0	
chr1:107,420,029-107,509,343	89314	p13.3	CN Loss	42.8571429	1	0	0	
chr1:109,526,340-109,779,079	252739	p13.3	CN Loss	48.9795918	7	0	0	
chr1:110,268,467-110,376,445	107978	p13.3	CN Loss	48.9795918	3	0	0	
chr1:110,620,520-111,079,319	458799	p13.3	CN Loss	48.9795918	9	0	1	RBM15
chr1:111,292,307-111,441,885	149578	p13.3	CN Loss	48.9795918	1	0	0	
chr1:112,904,019-113,019,968	115949	p13.2	CN Loss	48.9795918	3	0	0	
chr1:113,088,884-113,142,713	53829	p13.2	CN Loss	48.9795918	0	0	0	
chr1:114,161,325-114,305,566	144241	p13.2	CN Loss	48.9795918	6	0	0	
chr1:115,697,276-116,917,322	1220046	p13.2 - p13.1	CN Loss	44.8979592	8	0	0	
chr1:117,011,706-117,947,769	936063	p13.1 - p12	CN Loss	44.8979592	10	2	0	
chr1:118,158,751-118,239,930	81179	p12	CN Loss	42.8571429	1	0	0	
chr1:142,721,264-142,769,684	48420	q21.1	CN Gain	46.9387755	1	0	0	
chr1:144,116,698-144,637,865	521167	q21.1	CN Gain	46.9387755	19	0	0	
chr1:146,263,276-146,726,048	462772	q21.1	CN Gain	46.9387755	8	0	0	

Region	Region Length (bp)	Cytoband Location	Event	Frequency %	Count of Gene Symbols	Count of miRNAs	Count of CancerGene Census-Sanger.txt	CancerGene Census-Sanger.txt
chr1:148,085,050-148,264,859	179809	q21.2	CN Gain	44.8979592	15	0	0	
chr1:149,625,377-149,996,670	371293	q21.3	CN Gain	46.9387755	8	1	0	
chr1:150,043,181-150,113,007	69826	q21.3	CN Gain	46.9387755	6	0	0	
chr1:150,801,762-150,817,845	16083	q21.3	CN Gain	48.9795918	1	0	0	
chr1:150,821,284-150,854,987	33703	q21.3	CN Loss	36.7346939	2	0	0	
chr1:150,854,987-150,859,426	4439	q21.3	CN Gain	55.1020408	0	0	0	
chr1:152,968,261-153,083,996	115735	q21.3	CN Gain	48.9795918	1	0	0	
chr1:153,449,174-153,475,561	26387	q22	CN Gain	46.9387755	3	0	0	
chr1:154,869,530-154,897,489	27959	q23.1	CN Gain	48.9795918	1	0	0	
chr1:158,448,780-158,462,278	13498	q23.2	CN Gain	46.9387755	2	0	0	
chr1:158,572,040-159,181,485	609445	q23.2 - q23.3	CN Gain	46.9387755	13	0	0	
chr1:159,750,003-159,881,152	131149	q23.3	CN Gain	55.1020408	6	0	1	FCGR2B
chr1:161,639,495-163,787,518	2148023	q23.3	CN Gain	51.0204082	6	0	1	PBX1
chr1:166,201,101-166,453,517	252416	q24.2	CN Gain	46.9387755	3	1	0	
chr1:166,550,291-169,498,682	2948391	q24.2 - q24.3	CN Gain	46.9387755	32	2	1	PRRX1
chr1:170,023,150-170,178,182	155032	q24.3	CN Gain	46.9387755	2	0	0	
chr1:170,365,292-170,454,045	88753	q24.3	CN Gain	46.9387755	5	2	0	
chr1:170,898,567-171,919,592	1021025	q24.3 - q25.1	CN Gain	46.9387755	8	0	0	
chr1:172,503,912-172,691,451	187539	q25.1	CN Gain	48.9795918	2	0	0	
chr1:173,369,880-174,166,552	796672	q25.1	CN Gain	48.9795918	3	0	0	
chr1:174,628,090-176,490,317	1862227	q25.2	CN Gain	48.9795918	8	1	0	
chr1:179,838,549-180,022,751	184202	q25.3	CN Gain	48.9795918	1	0	0	
chr1:195,055,145-195,079,790	24645	q31.3	CN Loss	24.4897959	1	0	0	
chr1:195,079,790-195,119,706	39916	q31.3	CN Gain	51.0204082	0	0	0	
chr1:195,209,074-195,334,333	125259	q31.3	CN Gain	46.9387755	3	0	0	
chr1:195,441,549-196,212,307	770758	q31.3	CN Gain	46.9387755	4	0	0	
chr1:199,292,253-199,643,529	351276	q32.1	CN Gain	44.8979592	8	0	0	
chr1:199,935,962-200,027,825	91863	q32.1	CN Gain	46.9387755	3	0	0	
chr1:200,607,154-200,805,490	198336	q32.1	CN Gain	48.9795918	1	0	0	
chr1:201,248,303-201,424,180	175877	q32.1	CN Gain	51.0204082	7	0	0	
chr1:202,378,941-202,647,770	268829	q32.1	CN Gain	48.9795918	7	0	0	
chr1:203,162,093-203,232,561	70468	q32.1	CN Gain	53.0612245	1	0	0	
chr1:206,040,589-207,929,991	1889402	q32.2	CN Gain	48.9795918	12	3	0	
chr1:210,705,519-210,945,960	240441	q32.3	CN Gain	46.9387755	3	0	0	

Region	Region Length (bp)	Cytoband Location	Event	Frequency %	Count of Gene Symbols	Count of miRNAs	Count of CancerGene Census-Sanger.txt	CancerGene Census-Sanger.txt
chr1:211,325,860-212,497,587	1171727	q32.3 - q41	CN Gain	46.9387755	3	0	0	
chr1:212,925,737-215,077,266	2151529	q41	CN Gain	46.9387755	5	0	0	
chr1:218,416,806-222,125,695	3708889	q41 - q42.11	CN Gain	42.8571429	24	1	0	
chr1:222,707,913-223,782,012	1074099	q42.12	CN Gain	42.8571429	4	0	0	
chr1:224,697,506-225,807,058	1109552	q42.12 - q42.13	CN Gain	42.8571429	5	0	0	
chr1:226,941,814-228,151,848	1210034	q42.13	CN Gain	42.8571429	9	0	0	
chr1:229,219,330-232,520,064	3300734	q42.2	CN Gain	42.8571429	24	1	0	
chr1:235,806,343-235,983,279	176936	q43	CN Gain	44.8979592	1	0	0	
chr1:238,452,318-238,551,748	99430	q43	CN Gain	46.9387755	1	0	0	
chr1:239,103,872-240,059,042	955170	q43	CN Gain	44.8979592	7	0	1	FH
chr1:242,267,363-242,306,653	39290	q44	CN Gain	42.8571429	2	0	0	
chr1:243,862,436-244,027,954	165518	q44	CN Gain	42.8571429	2	0	0	
chr1:244,476,716-244,564,342	87626	q44	CN Gain	42.8571429	1	0	0	
chr1:246,800,401-246,817,710	17309	q44	CN Loss	28.5714286	1	0	0	
chr1:246,877,950-246,885,806	7856	q44	CN Gain	73.4693878	1	0	0	
chr2:88,938,716-89,033,006	94290	p11.2	CN Loss	93.877551	0	0	0	
chr2:91,123,642-91,511,347	387705	p11.1	CN Gain	38.7755102	3	0	0	
chr3:90,303,758-90,391,757	87999	p11.1	CN Gain	24.4897959	0	0	0	
chr3:164,031,239-164,094,370	63131	q26.1	CN Gain	48.9795918	0	0	0	
chr3:164,031,239-164,107,354	76115	q26.1	CN Loss	32.6530612	0	0	0	
chr3:196,867,332-196,937,765	70433	q29	CN Gain	30.6122449	3	1	0	
chr3:196,907,731-196,942,795	35064	q29	CN Loss	24.4897959	2	1	0	
chr4:947,911-956,748	8837	p16.3	CN Loss	44.8979592	1	0	0	
chr4:3,290,672-3,386,017	95345	p16.2	CN Loss	22.4489796	1	0	0	
chr4:3,611,900-7,316,519	3704619	p16.2 - p16.1	CN Loss	22.4489796	36	0	0	
chr4:9,213,266-9,683,867	470601	p16.1	CN Loss	24.4897959	2	0	0	
chr4:9,712,266-15,355,377	5643111	p16.1 - p15.32	CN Loss	24.4897959	20	1	0	
chr4:23,005,701-23,772,783	767082	p15.31 - p15.2	CN Loss	24.4897959	1	0	0	
chr4:36,685,307-36,858,065	172758	p14	CN Loss	20.4081633	0	0	0	
chr4:37,199,299-39,273,531	2074232	p14	CN Loss	20.4081633	23	1	0	
chr4:40,618,579-41,827,568	1208989	p14 - p13	CN Loss	20.4081633	8	0	1	PHOX2B
chr4:54,624,289-57,526,926	2902637	q12	CN Loss	22.4489796	25	0	4	PDGFRA, CHIC2, KIT, KDR

Region	Region Length (bp)	Cytoband Location	Event	Frequency %	Count of Gene Symbols	Count of miRNAs	Count of CancerGene Census-Sanger.txt	CancerGene Census-Sanger.txt
chr4:60,749,626-61,316,294	566668	q13.1	CN Loss	20.4081633	0	0	0	
chr4:64,149,701-64,929,191	779490	q13.1	CN Loss	20.4081633	1	0	0	
chr4:65,213,065-67,606,779	2393714	q13.1 - q13.2	CN Loss	20.4081633	4	1	0	
chr4:68,855,793-68,888,732	32939	q13.2	CN Loss	20.4081633	1	0	0	
chr4:68,981,732-69,404,572	422840	q13.2	CN Loss	53.0612245	3	0	0	
chr4:69,063,678-69,404,572	340894	q13.2	CN Gain	28.5714286	2	0	0	
chr4:70,145,362-70,280,460	135098	q13.2	CN Loss	46.9387755	1	0	0	
chr4:70,452,716-71,155,961	703245	q13.3	CN Loss	20.4081633	15	0	0	
chr4:72,125,675-73,118,311	992636	q13.3	CN Loss	20.4081633	3	0	0	
chr4:76,701,945-78,337,115	1635170	q21.1	CN Loss	22.4489796	23	0	0	
chr4:79,320,866-79,668,282	347416	q21.21	CN Loss	24.4897959	1	0	0	
chr4:83,947,247-84,083,273	136026	q21.22	CN Loss	24.4897959	4	0	0	
chr4:87,469,496-89,420,200	1950704	q21.3 - q22.1	CN Loss	22.4489796	21	0	1	AFF1
chr4:91,360,979-91,454,052	93073	q22.1	CN Loss	24.4897959	1	0	0	
chr4:92,140,872-92,276,967	136095	q22.1	CN Loss	24.4897959	1	0	0	
chr4:97,938,611-98,178,234	239623	q22.3	CN Loss	20.4081633	0	0	0	
chr4:98,443,446-98,909,783	466337	q22.3	CN Loss	20.4081633	1	0	0	
chr4:100,175,143-100,417,745	242602	q23	CN Loss	20.4081633	7	0	0	
chr4:105,088,730-105,149,087	60357	q24	CN Loss	20.4081633	0	0	0	
chr4:106,101,902-106,522,471	420569	q24	CN Loss	20.4081633	2	0	1	TET2
chr4:108,582,398-109,062,034	479636	q25	CN Loss	20.4081633	2	0	0	
chr4:109,619,537-109,959,685	340148	q25	CN Loss	20.4081633	5	0	0	
chr4:110,381,958-111,553,216	1171258	q25	CN Loss	20.4081633	12	1	0	
chr4:114,606,904-118,454,059	3847155	q26	CN Loss	22.4489796	7	2	0	
chr4:119,890,463-120,436,321	545858	q26	CN Loss	20.4081633	4	0	0	
chr4:123,586,764-124,681,596	1094832	q27 - q28.1	CN Loss	22.4489796	8	0	1	IL2
chr4:129,094,577-129,268,855	174278	q28.1 - q28.2	CN Loss	22.4489796	3	0	0	
chr4:129,647,039-130,136,598	489559	q28.2	CN Loss	20.4081633	2	0	0	
chr4:138,522,356-141,765,435	3243079	q28.3 - q31.21	CN Loss	22.4489796	20	0	0	
chr4:169,711,967-170,871,890	1159923	q32.3 - q33	CN Loss	20.4081633	5	0	0	
chr4:170,985,726-171,941,195	955469	q33	CN Loss	20.4081633	4	0	0	
chr4:173,241,866-175,950,087	2708221	q34.1	CN Loss	22.4489796	12	0	0	
chr4:181,985,896-182,379,825	393929	q34.3	CN Loss	22.4489796	1	0	0	
chr4:184,070,723-185,304,108	1233385	q35.1	CN Loss	22.4489796	13	0	0	

Region	Region Length (bp)	Cytoband Location	Event	Frequency %	Count of Gene Symbols	Count of miRNAs	Count of CancerGene Census-Sanger.txt	CancerGene Census-Sanger.txt
chr4:187,988,294-188,303,351	315057	q35.2	CN Loss	22.4489796	0	0	0	
chr4:188,897,991-189,862,521	964530	q35.2	CN Loss	24.4897959	4	0	0	
chr4:190,434,568-190,626,649	192081	q35.2	CN Loss	20.4081633	0	0	0	
chr4:190,734,388-191,114,743	380355	q35.2	CN Loss	22.4489796	2	0	0	
chr5:794,513-831,678	37165	p15.33	CN Gain	28.5714286	0	0	0	
chr5:807,365-831,678	24313	p15.33	CN Loss	26.5306122	0	0	0	
chr5:853,989-875,882	21893	p15.33	CN Gain	34.6938776	1	0	0	
chr6:166,752-189,701	22949	p25.3	CN Gain	20.4081633	0	0	0	
chr6:7,550,799-9,517,469	1966670	p24.3	CN Gain	20.4081633	12	0	0	
chr6:32,513,687-32,539,335	25648	p21.32	CN Gain	26.5306122	1	0	0	
chr6:32,576,786-32,631,975	55189	p21.32	CN Loss	55.1020408	2	0	0	
chr6:80,155,947-80,329,047	173100	q14.1	CN Loss	20.4081633	1	0	0	
chr6:101,077,176-101,941,867	864691	q16.3	CN Loss	20.4081633	1	0	0	
chr6:102,296,584-102,553,844	257260	q16.3	CN Loss	20.4081633	1	0	0	
chr6:107,178,840-107,268,905	90065	q21	CN Loss	22.4489796	2	0	0	
chr6:107,562,656-107,983,125	420469	q21	CN Loss	22.4489796	2	0	0	
chr6:113,253,399-117,210,778	3957379	q21 - q22.2	CN Loss	24.4897959	21	0	0	
chr6:119,101,774-119,249,818	148044	q22.31	CN Loss	24.4897959	3	0	0	
chr6:121,610,556-121,961,932	351376	q22.31	CN Loss	24.4897959	2	0	0	
chr6:123,591,435-123,911,535	320100	q22.31	CN Loss	28.5714286	1	0	0	
chr6:126,410,321-126,832,293	421972	q22.32	CN Loss	30.6122449	1	0	0	
chr6:127,487,532-127,566,691	79159	q22.33	CN Loss	30.6122449	1	0	0	
chr6:133,092,150-133,302,912	210762	q23.2	CN Loss	30.6122449	7	0	0	
chr6:134,471,226-134,671,415	200189	q23.2	CN Loss	30.6122449	2	0	0	
chr6:137,009,635-137,150,681	141046	q23.3	CN Loss	32.6530612	1	0	0	
chr6:137,239,149-137,334,100	94951	q23.3	CN Loss	32.6530612	2	0	0	
chr6:138,321,752-140,062,749	1740997	q23.3 - q24.1	CN Loss	30.6122449	16	0	0	
chr6:149,874,192-150,194,741	320549	q25.1	CN Loss	32.6530612	7	0	0	
chr6:152,077,759-152,260,349	182590	q25.1	CN Loss	32.6530612	1	0	0	
chr6:157,258,168-159,357,899	2099731	q25.3	CN Loss	30.6122449	17	0	0	
chr6:159,923,495-160,261,170	337675	q25.3	CN Loss	30.6122449	10	0	0	
chr6:161,478,405-162,227,720	749315	q26	CN Loss	30.6122449	3	0	0	
chr6:165,982,031-166,785,847	803816	q27	CN Loss	32.6530612	9	0	0	
chr6:167,241,274-167,417,116	175842	q27	CN Loss	32.6530612	3	0	1	FGFR1OP

Region	Region Length (bp)	Cytoband Location	Event	Frequency %	Count of Gene Symbols	Count of miRNAs	Count of CancerGene Census-Sanger.txt	CancerGene Census-Sanger.txt
chr6:168,403,104-170,755,838	2352734	q27	CN Loss	30.6122449	17	0	0	
chr7:38,277,012-38,293,363	16351	p14.1	CN Gain	42.8571429	1	0	0	
chr7:142,155,707-142,189,593	33886	q34	CN Gain	26.5306122	2	0	0	
chr8:0-183,103	183103	p23.3	CN Loss	28.5714286	3	0	0	
chr8:1,749,008-1,867,760	118752	p23.3	CN Loss	32.6530612	2	1	0	
chr8:3,542,424-3,862,833	320409	p23.2	CN Loss	30.6122449	1	0	0	
chr8:6,766,533-6,875,791	109258	p23.1	CN Loss	30.6122449	11	0	0	
chr8:7,148,442-7,953,633	805191	p23.1	CN Loss	40.8163265	25	0	0	
chr8:9,926,784-10,319,816	393032	p23.1	CN Loss	30.6122449	1	0	0	
chr8:10,665,554-10,818,524	152970	p23.1	CN Loss	32.6530612	3	1	0	
chr8:14,418,300-14,760,210	341910	p22	CN Loss	24.4897959	2	1	0	
chr8:17,020,938-17,591,778	570840	p22	CN Loss	26.5306122	8	0	0	
chr8:19,332,677-19,707,389	374712	p21.3	CN Loss	28.5714286	1	0	0	
chr8:21,636,828-22,101,084	464256	p21.3	CN Loss	26.5306122	13	0	0	
chr8:22,431,274-24,334,970	1903696	p21.3 - p21.2	CN Loss	26.5306122	28	0	0	
chr8:26,600,923-27,160,101	559178	p21.2	CN Loss	26.5306122	2	1	0	
chr8:36,872,554-37,787,891	915337	p12	CN Loss	22.4489796	6	0	0	
chr8:39,349,089-39,508,473	159384	p11.23 - p11.22	CN Loss	20.4081633	2	0	0	
chr8:39,365,809-39,508,473	142664	p11.23 - p11.22	CN Gain	53.0612245	2	0	0	
chr8:39,679,887-40,796,760	1116873	p11.22 - p11.21	CN Loss	20.4081633	6	0	0	
chr8:41,430,572-42,372,362	941790	p11.21	CN Loss	20.4081633	13	1	1	MYST3
chr8:128,833,813-128,850,729	16916	q24.21	CN Gain	20.4081633	0	0	0	
chr9:10,795,434-11,288,300	492866	p23	CN Gain	28.5714286	0	0	0	
chr9:39,152,128-41,756,778	2604650	p13.1 - p12	CN Gain	20.4081633	12	0	0	
chr9:65,372,337-66,256,518	884181	q12	CN Gain	28.5714286	1	0	0	
chr9:74,979,021-76,626,249	1647228	q21.13	CN Gain	20.4081633	2	0	0	
chr9:107,125,298-107,419,813	294515	q31.1 - q31.2	CN Gain	20.4081633	3	0	0	
chr9:115,918,415-116,076,063	157648	q32	CN Gain	24.4897959	2	1	0	
chr9:128,875,471-128,972,397	96926	q33.3	CN Gain	20.4081633	2	0	0	
chr9:131,976,949-132,361,958	385009	q34.11	CN Gain	20.4081633	2	0	0	
chr9:132,748,133-133,446,626	698493	q34.12 - q34.13	CN Gain	20.4081633	14	0	2	ABL1, NUP214
chr9:136,739,919-137,392,584	652665	q34.3	CN Gain	22.4489796	13	0	0	
chr9:138,235,564-138,307,416	71852	q34.3	CN Gain	20.4081633	2	0	0	

Region	Region Length (bp)	Cytoband Location	Event	Frequency %	Count of Gene Symbols	Count of miRNAs	Count of CancerGene Census-Sanger.txt	CancerGene Census-Sanger.txt
chr10:264,334-446,347	182013	p15.3	CN Loss	26.5306122	2	0	0	
chr10:1,485,684-1,609,377	123693	p15.3	CN Loss	24.4897959	2	0	0	
chr10:1,787,847-2,739,776	951929	p15.3	CN Loss	24.4897959	2	0	0	
chr10:7,332,420-7,381,782	49362	p14	CN Loss	24.4897959	1	0	0	
chr10:11,657,561-11,823,227	165666	p14	CN Loss	22.4489796	1	0	0	
chr10:45,963,009-46,563,413	600404	q11.21 - q11.22	CN Loss	34.6938776	12	0	0	
chr11:55,121,501-55,197,896	76395	q11	CN Gain	57.1428571	4	0	0	
chr11:55,121,501-55,197,896	76395	q11	CN Loss	32.6530612	4	0	0	
chr11:125,929,546-128,048,091	2118545	q24.2 - q24.3	CN Gain	20.4081633	5	0	0	
chr12:0-257,931	257931	p13.33	CN Loss	20.4081633	5	0	0	
chr12:6,706,246-6,943,278	237032	p13.31	CN Loss	20.4081633	20	1	0	
chr12:9,439,842-9,630,339	190497	p13.31	CN Loss	24.4897959	1	0	0	
chr12:14,517,827-14,792,096	274269	p13.1	CN Loss	22.4489796	3	0	0	
chr12:19,279,827-19,696,569	416742	p12.3	CN Loss	20.4081633	2	0	0	
chr12:29,536,323-29,632,916	96593	p11.22	CN Loss	20.4081633	2	0	0	
chr12:37,595,392-39,067,454	1472062	q12	CN Loss	20.4081633	5	0	0	
chr12:39,645,564-43,074,047	3428483	q12	CN Loss	20.4081633	12	0	0	
chr12:45,425,282-45,876,417	451135	q13.11	CN Loss	22.4489796	3	0	0	
chr12:46,734,489-48,880,261	2145772	q13.11 - q13.13	CN Loss	20.4081633	64	1	1	MLL2
chr12:51,505,506-52,603,472	1097966	q13.13	CN Loss	20.4081633	31	0	0	
chr12:52,802,213-53,204,798	402585	q13.13 - q13.2	CN Loss	20.4081633	15	1	0	
chr12:53,762,211-54,493,530	731319	q13.2	CN Loss	20.4081633	23	0	0	
chr12:57,399,278-63,570,619	6171341	q14.1 - q14.3	CN Loss	20.4081633	20	2	0	
chr12:64,223,524-67,240,977	3017453	q14.3 - q15	CN Loss	20.4081633	13	0	1	HMGA2
chr12:75,895,652-76,222,212	326560	q21.2	CN Loss	22.4489796	1	0	0	
chr12:78,439,974-79,473,077	1033103	q21.2 - q21.31	CN Loss	20.4081633	4	0	0	
chr12:79,684,067-80,120,049	435982	q21.31	CN Loss	20.4081633	5	2	0	
chr12:81,696,015-81,744,412	48397	q21.31	CN Loss	22.4489796	1	0	0	
chr12:88,728,210-89,804,168	1075958	q21.33	CN Loss	20.4081633	0	0	0	
chr12:90,066,902-90,383,947	317045	q21.33	CN Loss	20.4081633	1	0	0	
chr12:91,654,728-95,851,876	4197148	q22 - q23.1	CN Loss	20.4081633	34	2	0	
chr12:97,334,228-97,917,095	582867	q23.1	CN Loss	20.4081633	9	0	0	
chr12:98,776,194-99,627,391	851197	q23.1	CN Loss	20.4081633	10	1	0	
chr12:99,824,137-100,935,534	1111397	q23.1 - q23.2	CN Loss	20.4081633	11	0	0	

Region	Region Length (bp)	Cytoband Location	Event	Frequency %	Count of Gene Symbols	Count of miRNAs	Count of CancerGene Census-Sanger.txt	CancerGene Census-Sanger.txt
chr12:102,345,853-104,650,531	2304678	q23.2 - q23.3	CN Loss	22.4489796	21	0	0	
chr12:105,069,862-106,338,072	1268210	q23.3	CN Loss	22.4489796	11	0	0	
chr12:107,247,415-108,365,790	1118375	q23.3 - q24.11	CN Loss	20.4081633	17	1	0	
chr12:117,105,353-117,724,975	619622	q24.23	CN Loss	22.4489796	2	0	0	
chr12:124,294,832-124,427,420	132588	q24.31	CN Loss	26.5306122	1	0	0	
chr12:126,126,532-128,367,962	2241430	q24.32	CN Loss	22.4489796	7	0	0	
chr12:129,056,250-130,013,612	957362	q24.33	CN Loss	22.4489796	8	0	0	
chr12:130,761,856-130,907,311	145455	q24.33	CN Loss	22.4489796	2	0	0	
chr12:131,239,627-131,346,912	107285	q24.33	CN Loss	30.6122449	1	0	0	
chr13:18,065,953-18,233,776	167823	q11	CN Loss	89.7959184	0	0	0	
chr13:18,528,717-24,622,942	6094225	q12.11 - q12.13	CN Loss	93.877551	47	0	1	ZMYM2
chr13:24,660,513-25,815,556	1155043	q12.13	CN Loss	93.877551	6	0	0	
chr13:25,951,098-27,030,239	1079141	q12.13 - q12.2	CN Loss	93.877551	11	0	0	
chr13:27,305,511-28,942,407	1636896	q12.2 - q12.3	CN Loss	93.877551	11	0	2	CDX2, FLT3
chr13:29,067,786-29,917,692	849906	q12.3	CN Loss	93.877551	6	0	0	
chr13:34,811,374-36,771,307	1959933	q13.3	CN Loss	93.877551	17	0	0	
chr13:38,584,783-39,199,635	614852	q13.3	CN Loss	93.877551	3	0	1	LHFP
chr13:41,336,278-42,518,018	1181740	q14.11	CN Loss	93.877551	8	0	0	
chr13:42,837,647-44,133,447	1295800	q14.11	CN Loss	93.877551	8	0	0	
chr13:48,629,311-51,636,043	3006732	q14.2 - q14.3	CN Loss	93.877551	39	2	0	
chr13:52,172,556-53,217,774	1045218	q14.3 - q21.1	CN Loss	91.8367347	4	0	0	
chr13:59,714,650-60,310,579	595929	q21.2	CN Loss	91.8367347	1	0	0	
chr13:64,302,012-66,088,067	1786055	q21.32	CN Loss	91.8367347	3	0	0	
chr13:69,350,745-69,664,857	314112	q21.33	CN Loss	89.7959184	2	0	0	
chr13:71,107,670-75,218,743	4111073	q21.33 - q22.2	CN Loss	89.7959184	15	0	0	
chr13:75,334,858-77,017,476	1682618	q22.2 - q22.3	CN Loss	87.755102	9	0	0	
chr13:77,221,462-77,654,037	432575	q22.3	CN Loss	87.755102	5	0	0	
chr13:79,800,075-80,025,658	225583	q31.1	CN Loss	89.7959184	1	0	0	
chr13:91,857,145-93,261,436	1404291	q31.3	CN Loss	87.755102	3	0	0	
chr13:93,688,805-94,850,267	1161462	q31.3 - q32.1	CN Loss	87.755102	6	0	0	
chr13:94,992,803-95,892,137	899334	q32.1	CN Loss	87.755102	5	0	0	
chr13:98,598,791-98,649,232	50441	q32.3	CN Loss	89.7959184	1	0	0	
chr13:100,300,755-100,883,043	582288	q32.3 - q33.1	CN Loss	87.755102	2	0	0	
chr13:107,675,030-109,716,306	2041276	q33.3 - q34	CN Loss	87.755102	6	0	0	

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chr13:109,918,791-110,642,628	723837	q34	CN Loss	87.755102	9	0	0	
chr13:113,547,076-113,923,428	376352	q34	CN Loss	89.7959184	4	0	0	
chr14:18,753,436-18,977,592	224156	q11.1	CN Loss	40.8163265	0	0	0	
chr14:19,242,596-19,493,856	251260	q11.2	CN Gain	20.4081633	7	0	0	
chr14:19,271,062-19,493,856	222794	q11.2	CN Loss	55.1020408	6	0	0	
chr14:19,996,801-20,400,520	403719	q11.2	CN Loss	51.0204082	13	0	0	
chr14:20,412,281-20,497,996	85715	q11.2	CN Loss	53.0612245	3	0	0	
chr14:20,532,798-20,556,956	24158	q11.2	CN Loss	55.1020408	3	0	0	
chr14:20,639,736-21,211,055	571319	q11.2	CN Loss	48.9795918	17	0	0	
chr14:21,556,736-21,997,018	440282	q11.2	CN Gain	36.7346939	0	0	0	
chr14:22,116,277-22,542,251	425974	q11.2	CN Loss	48.9795918	14	0	0	
chr14:29,359,648-30,281,245	921597	q12	CN Loss	55.1020408	3	0	0	
chr14:31,100,236-31,467,560	367324	q12	CN Loss	53.0612245	1	0	0	
chr14:32,102,347-32,233,613	131266	q13.1	CN Loss	53.0612245	1	0	0	
chr14:32,803,541-32,889,143	85602	q13.1	CN Loss	48.9795918	1	0	0	
chr14:33,342,145-33,722,933	380788	q13.1	CN Loss	53.0612245	2	0	0	
chr14:34,652,184-34,669,127	16943	q13.2	CN Loss	53.0612245	2	0	0	
chr14:36,016,361-36,292,469	276108	q13.3	CN Loss	55.1020408	5	0	1	NKX2-1
chr14:36,573,662-36,860,411	286749	q13.3	CN Loss	55.1020408	3	0	0	
chr14:36,990,392-39,063,548	2073156	q21.1	CN Loss	55.1020408	13	0	0	
chr14:45,041,316-45,410,227	368911	q21.3	CN Loss	59.1836735	0	0	0	
chr14:49,685,636-49,969,583	283947	q22.1	CN Loss	59.1836735	5	0	0	
chr14:50,245,353-50,507,742	262389	q22.1	CN Loss	63.2653061	3	0	1	NIN
chr14:52,481,225-54,215,547	1734322	q22.2	CN Loss	63.2653061	9	0	0	
chr14:54,348,755-55,133,738	784983	q22.2 - q22.3	CN Loss	63.2653061	12	0	1	KTN1
chr14:55,926,421-58,805,073	2878652	q23.1	CN Loss	63.2653061	18	0	0	
chr14:59,060,781-59,786,408	725627	q23.1	CN Loss	65.3061224	5	0	0	
chr14:59,837,861-61,049,076	1211215	q23.1	CN Loss	65.3061224	9	0	0	
chr14:62,311,560-62,702,202	390642	q23.2	CN Loss	65.3061224	1	0	0	
chr14:64,007,865-64,140,209	132344	q23.3	CN Loss	65.3061224	5	0	0	
chr14:64,343,071-65,019,794	676723	q23.3	CN Loss	67.3469388	12	1	0	
chr14:65,109,981-67,046,157	1936176	q23.3 - q24.1	CN Loss	67.3469388	9	0	1	GPHN
chr14:68,712,658-68,789,383	76725	q24.1	CN Loss	71.4285714	1	0	0	
chr14:69,725,906-71,954,630	2228724	q24.2	CN Loss	69.3877551	15	0	0	

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chr14:72,249,958-73,527,907	1277949	q24.2 - q24.3	CN Loss	69.3877551	22	0	0	
chr14:74,137,657-74,736,201	598544	q24.3	CN Loss	67.3469388	14	0	0	
chr14:75,272,721-75,407,692	134971	q24.3	CN Loss	67.3469388	2	0	0	
chr14:78,596,551-79,088,675	492124	q31.1	CN Loss	65.3061224	1	0	0	
chr14:79,271,926-80,550,881	1278955	q31.1	CN Loss	65.3061224	5	0	1	TSHR
chr14:83,701,469-84,044,485	343016	q31.2 - q31.3	CN Loss	63.2653061	0	0	0	
chr14:87,696,172-90,246,939	2550767	q31.3 - q32.11	CN Loss	65.3061224	17	0	0	
chr14:90,491,157-91,037,974	546817	q32.11 - q32.12	CN Loss	65.3061224	6	0	0	
chr14:92,192,974-92,277,942	84968	q32.12	CN Loss	57.1428571	2	0	0	
chr14:96,458,843-98,194,316	1735473	q32.2	CN Loss	57.1428571	2	0	0	
chr14:100,395,344-100,439,066	43722	q32.2 - q32.31	CN Loss	51.0204082	12	8	0	
chr14:101,077,208-102,336,353	1259145	q32.31 - q32.32	CN Loss	53.0612245	16	1	1	HSP90AA1
chr14:103,613,314-103,731,581	118267	q32.33	CN Loss	53.0612245	4	1	0	
chr14:104,969,153-105,037,342	68189	q32.33	CN Loss	55.1020408	4	0	0	
chr14:105,283,523-105,297,284	13761	q32.33	CN Loss	85.7142857	0	0	0	
chr14:105,326,581-105,458,627	132046	q32.33	CN Loss	100	1	0	0	
chr14:105,716,187-105,796,740	80553	q32.33	CN Loss	81.6326531	0	0	0	
chr14:105,836,435-105,851,455	15020	q32.33	CN Loss	77.5510204	0	0	0	
chr15:18,800,326-18,996,809	196483	q11.2	CN Gain	57.1428571	1	0	0	
chr15:19,796,337-19,812,990	16653	q11.2	CN Gain	69.3877551	1	0	0	
chr15:32,493,970-32,584,592	90622	q14	CN Gain	22.4489796	1	0	0	
chr16:181,086-267,830	86744	p13.3	CN Loss	32.6530612	3	0	0	
chr16:338,547-392,104	53557	p13.3	CN Loss	32.6530612	6	0	0	
chr16:527,118-565,423	38305	p13.3	CN Loss	36.7346939	5	0	0	
chr16:681,064-799,650	118586	p13.3	CN Loss	36.7346939	12	1	0	
chr16:1,014,509-1,232,996	218487	p13.3	CN Loss	38.7755102	7	0	0	
chr16:2,008,867-2,151,895	143028	p13.3	CN Loss	30.6122449	11	1	1	TSC2
chr16:2,159,232-2,179,089	19857	p13.3	CN Loss	30.6122449	2	0	0	
chr16:2,532,787-2,642,093	109306	p13.3	CN Loss	36.7346939	3	0	0	
chr16:2,922,054-3,028,649	106595	p13.3	CN Loss	32.6530612	12	0	0	
chr16:7,254,372-7,582,351	327979	p13.2	CN Loss	22.4489796	1	0	0	
chr16:9,693,721-10,062,409	368688	p13.2	CN Loss	20.4081633	1	0	0	
chr16:10,245,699-10,411,248	165549	p13.2 - p13.13	CN Loss	20.4081633	1	0	0	
chr16:14,916,289-15,028,645	112356	p13.11	CN Loss	28.5714286	4	1	0	

Region	Region Length (bp)	Cytoband Location	Event	Frequency %	Count of Gene Symbols	Count of miRNAs	Count of CancerGene Census-Sanger.txt	CancerGene Census-Sanger.txt
chr16:21,320,319-21,504,160	183841	p12.2	CN Loss	24.4897959	4	0	0	
chr16:32,156,702-32,539,907	383205	p11.2	CN Gain	26.5306122	2	0	0	
chr16:33,816,727-33,967,480	150753	p11.2	CN Loss	28.5714286	1	1	0	
chr16:34,279,675-34,318,531	38856	p11.2	CN Loss	28.5714286	0	0	0	
chr16:45,762,177-47,996,838	2234661	q12.1	CN Loss	40.8163265	11	0	0	
chr16:48,615,160-48,875,308	260148	q12.1	CN Loss	42.8571429	3	0	0	
chr16:51,684,773-52,289,133	604360	q12.2	CN Loss	40.8163265	5	0	0	
chr16:54,349,083-54,395,267	46184	q12.2	CN Loss	46.9387755	2	0	0	
chr16:61,370,897-66,143,620	4772723	q21 - q22.1	CN Loss	42.8571429	48	1	2	CDH11, CBFB
chr16:68,608,016-68,657,578	49562	q22.1	CN Loss	55.1020408	3	1	0	
chr16:68,692,838-68,774,678	81840	q22.1	CN Loss	55.1020408	2	0	0	
chr16:68,871,385-69,370,419	499034	q22.1	CN Loss	46.9387755	14	0	0	
chr16:69,427,598-69,758,575	330977	q22.2	CN Gain	28.5714286	2	0	0	
chr16:69,758,575-74,293,697	4535122	q22.2 - q23.1	CN Loss	46.9387755	48	0	0	
chr16:75,667,479-77,212,064	1544585	q23.1	CN Loss	46.9387755	7	0	0	
chr16:79,340,453-81,824,470	2484017	q23.2 - q23.3	CN Loss	44.8979592	17	0	0	
chr16:84,169,279-84,253,444	84165	q24.1	CN Loss	46.9387755	1	0	0	
chr16:86,991,660-87,025,966	34306	q24.2	CN Loss	57.1428571	1	0	0	
chr16:87,297,077-87,366,197	69120	q24.3	CN Loss	55.1020408	4	0	0	
chr16:88,149,232-88,625,378	476146	q24.3	CN Loss	42.8571429	23	0	1	FANCA
chr17:1,866,806-1,915,856	49050	p13.3	CN Loss	22.4489796	7	2	0	
chr17:3,654,667-4,039,101	384434	p13.2	CN Loss	20.4081633	7	0	0	
chr17:6,943,547-7,019,078	75531	p13.1	CN Loss	24.4897959	2	0	0	
chr17:7,044,798-7,310,344	265546	p13.1	CN Loss	24.4897959	28	1	0	
chr17:7,701,260-7,771,326	70066	p13.1	CN Loss	24.4897959	6	0	0	
chr17:41,518,612-41,640,287	121675	q21.31	CN Gain	40.8163265	2	0	0	
chr17:41,572,059-41,672,900	100841	q21.31	CN Loss	20.4081633	2	0	0	
chr19:1,533,909-2,374,544	840635	p13.3	CN Gain	22.4489796	32	2	1	TCF3
chr19:3,630,939-4,586,647	955708	p13.3	CN Gain	22.4489796	35	1	1	SH3GL1
chr19:7,009,957-7,791,919	781962	p13.2	CN Gain	22.4489796	22	0	0	
chr19:8,837,662-8,958,619	120957	p13.2	CN Gain	26.5306122	1	0	0	
chr19:9,347,917-9,464,161	116244	p13.2	CN Gain	26.5306122	4	0	0	
chr19:9,525,368-10,417,257	891889	p13.2	CN Gain	26.5306122	36	1	0	

Region	Region Length (bp)	Cytoband Location	Event	Frequency %	Count of Gene Symbols	Count of miRNAs	Count of CancerGene Census-Sanger.txt	CancerGene Census-Sanger.txt
chr19:14,170,325-14,387,450	217125	p13.12	CN Gain	22.4489796	3	0	0	
chr19:15,636,339-15,694,800	58461	p13.12	CN Gain	20.4081633	1	0	0	
chr22:16,160,916-17,830,686	1669770	q11.1 - q11.21	CN Loss	32.6530612	28	1	1	CLTCL1
chr22:18,204,586-18,452,253	247667	q11.21	CN Loss	32.6530612	9	1	0	
chr22:18,494,729-18,691,852	197123	q11.21	CN Loss	32.6530612	7	1	0	
chr22:20,883,195-20,908,581	25386	q11.22	CN Loss	40.8163265	0	0	0	
chr22:21,027,883-21,046,353	18470	q11.22	CN Loss	38.7755102	0	0	0	
chr22:21,152,680-21,210,353	57673	q11.22	CN Loss	42.8571429	2	0	0	
chr22:21,486,947-21,563,865	76918	q11.22	CN Loss	51.0204082	2	1	0	
chr22:21,969,094-22,188,699	219605	q11.23	CN Loss	30.6122449	3	0	1	BCR
chr22:22,389,893-22,641,999	252106	q11.23	CN Loss	30.6122449	13	0	1	SMARCB1
chr22:22,674,690-22,728,274	53584	q11.23	CN Gain	34.6938776	4	0	0	
chr22:22,728,274-22,742,555	14281	q11.23	CN Loss	36.7346939	2	0	0	
chr22:22,891,885-23,021,604	129719	q11.23	CN Loss	32.6530612	5	0	0	
chr22:23,415,514-23,526,524	111010	q11.23	CN Loss	32.6530612	2	0	0	
chr22:23,978,584-24,243,784	265200	q11.23	CN Loss	36.7346939	3	0	0	
chr22:24,998,642-25,256,796	258154	q12.1	CN Loss	34.6938776	7	0	0	
chr22:26,182,818-26,983,707	800889	q12.1	CN Loss	34.6938776	7	0	1	MN1
chr22:28,359,548-28,492,322	132774	q12.2	CN Loss	32.6530612	3	0	1	NF2
chr22:30,795,064-31,364,273	569209	q12.3	CN Loss	32.6530612	12	0	0	
chr22:37,686,316-37,717,050	30734	q13.1	CN Loss	42.8571429	3	0	0	
chr22:39,216,313-39,284,374	68061	q13.1	CN Loss	28.5714286	1	0	1	MKL1
chr22:41,245,002-41,297,374	52372	q13.2	CN Loss	53.0612245	2	0	0	
chr22:41,519,958-41,591,896	71938	q13.2	CN Loss	32.6530612	1	0	0	
chr22:43,494,775-43,592,300	97525	q13.31	CN Loss	32.6530612	3	0	0	
chr22:45,741,934-46,026,126	284192	q13.31	CN Loss	32.6530612	1	0	0	
chr22:48,709,111-48,800,810	91699	q13.33	CN Loss	42.8571429	2	0	0	
chr22:49,066,894-49,130,579	63685	q13.33	CN Loss	40.8163265	3	0	0	
chrX:2,710,316-2,730,409	20093	p22.33	CN Loss	51.0204082	1	0	0	
chrX:9,023,758-10,213,669	1189911	p22.31 - p22.2	CN Loss	53.0612245	6	0	0	
chrX:12,452,711-14,146,232	1693521	p22.2	CN Loss	51.0204082	17	0	0	
chrX:16,965,800-17,471,557	505757	p22.2 - p22.13	CN Loss	53.0612245	3	0	0	
chrX:17,809,784-19,147,173	1337389	p22.13	CN Loss	53.0612245	8	0	0	
chrX:21,647,135-26,557,004	4909869	p22.12 - p21.3	CN Loss	51.0204082	29	1	0	

Region	Region Length (bp)	Cytoband Location	Event	Frequency %	Count of Gene Symbols	Count of miRNAs	Count of CancerGene Census-Sanger.txt	CancerGene Census-Sanger.txt
chrX:30,236,177-31,450,467	1214290	p21.2	CN Loss	51.0204082	6	0	0	
chrX:32,221,569-32,416,280	194711	p21.1	CN Loss	51.0204082	1	0	0	
chrX:37,219,752-37,685,954	466202	p21.1 - p11.4	CN Loss	48.9795918	4	0	0	
chrX:38,337,382-40,205,880	1868498	p11.4	CN Loss	51.0204082	4	0	0	
chrX:40,244,629-40,656,969	412340	p11.4	CN Loss	51.0204082	5	0	0	
chrX:44,207,398-44,375,059	167661	p11.3	CN Loss	53.0612245	1	0	0	
chrX:46,321,847-49,377,102	3055255	p11.3 - p11.23	CN Loss	51.0204082	93	0	5	SSX1, SSX4, WAS, GATA1, TFE3
chrX:53,119,096-56,695,241	3576145	p11.22 - p11.1	CN Loss	51.0204082	37	2	1	KDM5C
chrX:63,121,207-64,369,761	1248554	q11.1	CN Loss	48.9795918	4	0	1	FAM123B
chrX:66,065,030-67,730,576	1665546	q12 - q13.1	CN Loss	46.9387755	3	0	0	
chrX:68,278,023-68,547,792	269769	q13.1	CN Loss	46.9387755	1	0	0	
chrX:68,946,598-70,231,223	1284625	q13.1	CN Loss	46.9387755	17	0	0	
chrX:70,314,290-70,417,475	103185	q13.1	CN Loss	46.9387755	2	0	0	
chrX:72,133,357-77,789,311	5655954	q13.1 - q21.1	CN Loss	48.9795918	36	6	1	ATRX
chrX:96,122,233-96,290,954	168721	q21.33	CN Loss	51.0204082	1	0	0	
chrX:102,841,134-103,148,041	306907	q22.2	CN Loss	44.8979592	6	0	0	
chrX:103,207,093-106,317,625	3110532	q22.2 - q22.3	CN Loss	44.8979592	18	0	0	
chrX:110,208,043-117,351,322	7143279	q22.3 - q24	CN Loss	38.7755102	29	5	0	
chrX:117,874,062-118,934,791	1060729	q24	CN Loss	40.8163265	18	1	1	SEPT6
chrX:119,236,112-121,879,942	2643830	q24 - q25	CN Loss	38.7755102	22	0	0	
chrX:122,721,996-122,991,816	269820	q25	CN Loss	40.8163265	2	0	0	
chrX:125,110,412-126,326,935	1216523	q25	CN Loss	38.7755102	3	0	0	
chrX:126,487,364-126,595,837	108473	q25	CN Loss	38.7755102	0	0	0	
chrX:127,527,591-129,590,057	2062466	q25	CN Loss	36.7346939	16	0	1	ELF4
chrX:134,496,056-134,861,140	365084	q26.3	CN Loss	40.8163265	8	0	0	
chrX:140,453,205-140,625,483	172278	q27.2	CN Loss	40.8163265	5	0	0	
chrX:146,793,653-147,385,167	591514	q27.3 - q28	CN Loss	36.7346939	3	0	0	
chrX:148,061,383-148,158,515	97132	q28	CN Loss	34.6938776	0	0	0	
chrX:148,945,507-150,636,654	1691147	q28	CN Loss	36.7346939	12	0	0	
chrX:151,723,016-152,267,363	544347	q28	CN Loss	34.6938776	10	0	0	
chrX:152,490,319-152,587,993	97674	q28	CN Loss	34.6938776	3	0	0	

Region	Region Length (bp)	Cytoband Location	Event	Frequency %	Count of Gene Symbols	Count of miRNAs	Count of CancerGene Census-Sanger.txt	CancerGene Census-Sanger.txt
chrX:152,149,307-153,833,933	1684626	q28	CN Gain	20.4081633	71	1	0	
chrX:153,530,795-153,644,109	113314	q28	CN Loss	36.7346939	2	0	0	

Supplementary Table S2. Clinical, demographic and genetic characteristics of the 224 cohort. Demographics can be found at http://www.broadinstitute.org/mmgp/home. Genomic subtype:(H-MM; hyperdiploid multiple myeloma, Hypo; hypodiploid multiple myeloma, NH-MM; non-hyperdiploid multiple myeloma), estimated chromosome number, TC classification (Bergsagel et al. Blood. 2005;106:296-303) and UAMS classification (Shaughnessy et al. Blood 2007 109: 2276-2284) have been added.

Array	Age at Diagnosis	Gender	Race	Diagnosis	Initial Diagnosis Date	Current Status	Heavy chain class	Light chain class	M-spike (g/dL)	Hemoglobin (g/dL)	Platelets (10^9/L)	Beta2-microglobulin (ug/dL)	CRP (mg/dL)	Serum free light chain kappa (mg/dL)	Serum free light chain lambda (mg/dL)	Serum free light chain ratio (kappa:lambda)	Serum creatinine (mg/dL)	Serum calcium (mg/dL)	Serum LDH (U/L)	Serum albumin (g/dL)	Lytic lesions (any time)	Evidence for presence of lytic lesions	Evidence for absence of lytic lesions	Est. Ploidy	Est. Chr #	TC_Class	UAMS
MMRC0001	74	Male	Caucasian	Multiple Myeloma	2003	Treated	IgA	Lambda	5.6	6.8	100	Not available	Not available	0.211	3.73	0.05656836	1.5	10	189	3.1	Yes	Skeletal survey	Not applicable	H-MM	53	D1	PR
MMRC0002	52	Male	Caucasian	Multiple Myeloma	1996	Treated	IgG	Lambda	3.39	11.5	187	3	2.6	Not available	179	0.00659218	1	8.9	Not available	3.6	No	Not applicable	Skeletal survey	H-MM	54	D1	HY
MMRC0003	47	Male	African American	Multiple Myeloma	2005	Untreated	IgG	Lambda	0.31	14.7	44	0.16	0.3	Not available	Not available	Not available	0.95	9.32	205	4.1	Not available	Not applicable	Not applicable	H-MM	51	D2	MY
MMRC0006	55	Male	Caucasian	Multiple Myeloma	2003	Treated	Not available	Kappa	0.15	30.3	286	Not available	Not available	4050	3.17	1277.60252	2.1	9.1	Not available	3.9	No	Not applicable	Skeletal survey/MRI	H-MM	47	D2	PR
MMRC0009	64	Female	Unknown	Multiple Myeloma	2006	Untreated	IgG	Lambda	6.45	8.8	153	0.43	0.3	0.59	116	0.005086	2.45	8.2	285	2.8	Not available	Not applicable	Not applicable	NH-MM	45	4p16	PR
MMRC0010	23	Female	Caucasian	Multiple Myeloma	1988	Treated	IgG	Kappa	1.7	12.9	265	Not available	Not available	Not available	Not available	Not available	1	9.4	158	Not available	No	Not applicable	Skeletal survey	NH-MM	46	Maf	MF
MMRC0011	63	Male	Caucasian	Multiple Myeloma	2006	Untreated	IgG	Lambda	1.6	13.4	327	2.32	0.29	0.732	0.969	0.75541796	1.2	9.4	205	4	Yes	Skeletal survey	Not applicable	H-MM	52	D1	HY
MMRC0012	56	Male	Caucasian	Multiple Myeloma	2002	Treated	IgG	Kappa	1.1	13.6	264	1.61	Not available	3.87	0.856	4.52102804	1	9.1	140	4.2	Yes	Skeletal survey/MRI	Not applicable	H-MM	52	6p21	MY
MMRC0013	62	Female	Asian	Multiple Myeloma	2005	Treated	IgG	Kappa	2.48	7.9	61	1.1	0.7	732	0.76	963.157895	1.03	9.92	686	3.5	Yes	MRI	Not applicable	H-MM	48	D2	PR
MMRC0014	54	Male	Caucasian	Multiple Myeloma	2003	Treated	IgG	Kappa	2.29	12.2	122	Not available	Not available	579	Not available	357.407407	0.9	9	Not available	3.9	Yes	MRI	Not applicable	H-MM	55	D1	MY
MMRC0015	56	Male	Caucasian	Multiple Myeloma	2005	Treated	IgG	Lambda	0.91	13.4	371	2.4	10	Not available	Not available	Not available	1.1	9.3	Not available	3.38	Yes	Skeletal survey/MRI	Not applicable	H-MM	51	D1	MY
MMRC0016	71	Male	Caucasian	Multiple Myeloma	2005	Untreated	IgG	Kappa	2.89	13.4	116	2.5	Not available	69.3	2.74	25.2919708	1.2	9.1	307	3.9	No	Not applicable	Skeletal survey	H-MM	47	Maf	MF
MMRC0018	70	Male	Caucasian	Multiple Myeloma	2006	Untreated	IgG	Kappa	3.53	12.4	143	Not available	Not available	8	6.3	1.269841	0.9	9.1	329	4.4	Yes	MRI	Not applicable	Hypo	40	D1	MY
MMRC0019	72	Male	Caucasian	Multiple Myeloma	2006	Untreated	IgG	Kappa	1.84	12.1	209	1.8	Not available	264	9.75	27.0769231	1.1	9.9	Not available	4	Yes	Skeletal survey	Not applicable	H-MM	50	D1	MY
MMRC0020	63	Male	Caucasian	Multiple Myeloma	2006	Untreated	IgG	Kappa	2.48	14.1	256	0.31	0.3	12.5	0.81	15.4321	1.02	11	180	3.9	Yes	Skeletal survey	Not applicable	H-MM	50	D1	HY
MMRC0021	64	Male	Caucasian	Multiple Myeloma	2006	Untreated	Not available	Kappa	Not available	11.2	267	0.24	0.3	137	0.81	169.1358	0.79	10.2	145	Not available	Yes	Skeletal survey	Not applicable	H-MM	48	11q13	CD1
MMRC0027	44	Female	African American	Multiple Myeloma	2002	Treated	IgG	Kappa	1.67	9.3	11	Not available	Not available	Not available	Not available	Not available	0.97	9.4	Not available	4	Yes	MRI	Not applicable	Hypo	41	Maf	MF
MMRC0028	44	Male	Caucasian	Multiple Myeloma	2004	Untreated	IgG	Not available	2.67	14	286	3.8	2.11	0.71	20.3	0.03497537	1	9.8	389	4	No	Not applicable	Skeletal survey	Hypo	44	4p16	MS
MMRC0029	53	Female	Hispanic	Multiple Myeloma	2006	Untreated	Not available	Kappa	Not available	11.6	315	Not available	3.3	Not available	Not available	Not available	0.7	12.1	Not available	5.4	Not available	Not applicable	Not applicable	Hypo	42	D1+D2	PR
MMRC0030	68	Male	Unknown	Multiple Myeloma	2006	Untreated	IgA	Kappa	0.5	13	228	3.1	Not available	943	269	3.50557621	1	9.8	Not available	4.1	Yes	Skeletal survey/MRI	Not applicable	H-MM	51	D1	PR
MMRC0031	76	Male	Caucasian	Multiple Myeloma	2003	Treated	IgA	Kappa	1.5	11.3	159	Not available	Not available	9.8	1.64	5.97560976	1.3	9.4	131	3.6	Yes	Skeletal survey	Not applicable	H-MM	51	D1	MY
MMRC0032	76	Male	Caucasian	Multiple Myeloma	2006	Treated	IgG	Kappa	1.1	10.7	205	0.0598	0.44	2.97	2.11	1.40758294	1.5	9.2	160	3.9	Yes	Skeletal survey/MRI	Not applicable	H-MM	50	D1	MY
MMRC0034	79	Male	Caucasian	Multiple Myeloma	2002	Treated	Not available	Kappa	0	9.2	106	10.8	Not available	766	4.8	159.583333	1.9	9.2	631	3.9	Yes	Skeletal survey/MRI	Not applicable	H-MM	51	D1	HY
MMRC0035	66	Male	Caucasian	Multiple Myeloma	2001	Treated	IgA	Lambda	2.2	10	111	Not available	Not available	0.684	104	0.00657692	1	9.2	186	Not available	No	Not applicable	Skeletal survey	H-MM	55	D2	LB
MMRC0036	32	Male	Caucasian	Multiple Myeloma	2006	Treated	IgG	Lambda	1.4	12.5	117	5.21	6.12	47	4.71	9.97876858	1.3	8.2	264	3.4	Yes	Skeletal survey	Not applicable	Hypo	44	D1+D2	PR
MMRC0037	66	Male	Caucasian	Multiple Myeloma	2006	Untreated	IgA	Lambda	3.5	11.4	288	3.17	1.7	0.188	1.14	0.16491228	0.9	9.7	131	4.1	No	Not applicable	Skeletal survey	Hypo	41	D2	LB
MMRC0038	67	Male	Caucasian	Multiple Myeloma	2002	Treated	IgG	Kappa	2.4	12.3	169	0.379	9.6	5.46	0.329	16.5957447	1	9.1	171	3.7	Yes	Skeletal survey	Not applicable	H-MM	54	D1	HY
MMRC0039	57	Male	Caucasian	Multiple Myeloma	2003	Treated	Not available	Lambda	0.26	8.1	60	Not available	Not available	837	0.83	1008.434	1.33	9.4	301	3.8	Yes	Skeletal survey	Not applicable	Hypo	40	D1	PR
MMRC0042	62	Male	Caucasian	Multiple Myeloma	2007	Untreated	IgD	Kappa	Not available	12.2	179	4.25	Not available	8660	3	2886.66667	1.3	11.5	194	5.3	Yes	Skeletal survey	Not applicable	Hypo	44	D2	MY
MMRC0043	69	Male	Caucasian	Multiple Myeloma	2007	Untreated	IgG	Lambda	0.74	8.1	330	8.49	Not available	34.6	1190	0.02907563	1.8	9.1	153	2.7	Yes	Skeletal survey/MRI	Not applicable	H-MM	49	D2	PR
MMRC0044	57	Male	Caucasian	Multiple Myeloma	2006	Untreated	IgG	Lambda	3.5	12.6	137	2.8	Not available	0.56	38.1	0.01469816	1.2	9.6	Not available	4.2	No	Not applicable	Skeletal survey	NH-MM	46	11q13	CD1
MMRC0045	40	Female	Caucasian	Multiple Myeloma	2007	Untreated	IgG	Lambda	4.33	10.1	691	0.19	0.3	1.13	54.8	0.02062	0.77	9	168	3.5	Not available	Not applicable	Not applicable	NH-MM	45	D1	CD2
MMRC0046	75	Male	Caucasian	Multiple Myeloma	2005	Treated	Not available	Kappa	0	12.1	439	3.2	Not available	2190	3.73	587.131367	1.3	9.8	187	4.7	Yes	Skeletal survey	Not applicable	NH-MM	46	11q13	CD1
MMRC0048	68	Female	Unknown	Multiple Myeloma	2007	Untreated	IgG	Lambda	6.9	9.9	129	6.45	Not available	1.92	94.1	0.02040383	0.7	8.8	113	2.3	No	Not applicable	Skeletal survey	NH-MM	45	Maf	MF
MMRC0049	64	Male	Caucasian	Multiple Myeloma	2005	Treated	IgA	Lambda	1.61	11.7	208	Not available	Not available	6.57	10.7	0.61401869	1.5	9.2	287	3.9	Yes	Skeletal survey/MRI	Not applicable	H-MM	48	D2	PR
MMRC0050	74	Female	Unknown	Multiple Myeloma	2004	Untreated	IgA	Kappa	2.9	11.3	232	6.37	Not available	15.9	0.057	278.947368	1	9.6	182	3.9	Yes	Skeletal survey	Not applicable	H-MM	51	D2	PR
MMRC0051	38	Male	Caucasian	Smoldering Myeloma	2004	Untreated	IgG	Kappa	3.9	12.1	313	2.68	Not available	35.8	0.248	144.354839	1.1	9.1	177	3.8	No	Not applicable	Skeletal survey	H-MM	55	D1	HY
MMRC0052	48	Female	Caucasian	Smoldering Myeloma	2004	Untreated	IgG	Lambda	2.5	12	286	1.92	Not available	Not available	0.297	0.11986532	1	9	117	3.5	No	Not applicable	Skeletal survey	H-MM	55	D1	HY
MMRC0053	63	Male	Caucasian	Multiple Myeloma	2004	Untreated	IgG	Kappa	3.6	9.2	269	Not available	1	5.22	0.235	22.212766	1.5	10.4	130	3	No	Not applicable	Skeletal survey/MRI	NH-MM	46	11q13	CD2
MMRC0055	57	Male	Caucasian	Smoldering Myeloma	2006	Untreated	IgG	Kappa	3.3	15	227	2.24	Not available	2.41	0.279	8.63799283	0.8	9.3	146	4.1	Yes	Skeletal survey	Not applicable	H-MM	54	D1	HY
MMRC0056	77	Male	Caucasian	Multiple Myeloma	2006	Treated	IgA	Lambda	1.8	15.1	151	1.74	Not available	Not available	15.8	0.00202532	0.8	9.8	178	3.6	Yes	Skeletal survey	Not applicable	Hypo	44	4p16	MS
MMRC0059	56	Female	Caucasian	Multiple Myeloma	2005	Untreated	IgG	Kappa	3.8	12.3	232	1.87	Not available	0.219	Not available	4.65957447	1	9.5	184	3.9	Yes	Skeletal survey	Not applicable	H-MM	55	D1	HY
MMRC0061	62	Male	Caucasian	Multiple Myeloma	2003	Untreated	Not available	Kappa	Not available	14.1	194	3.21	0.1	191	0.24	795.833333	1.2	9.5	175	4.5	Yes	Skeletal survey	Not applicable	Hypo	44	Maf	MF
MMRC0062	40	Male	Caucasian	Multiple Myeloma	2004	Untreated	IgA	Kappa	2.3	11.4	363	2.44	1.06	1.58	1.05	1.5047619	1.2	10.3	105	3.5	Yes	Skeletal survey	Not applicable	H-MM	48	D1+D2	PR
MMRC0063	70	Male	Caucasian	Multiple Myeloma	2006	Treated	IgA	Not available	4.7	9.9	21	Not available	Not available	330	0.265	1245.28302	2	9.2	378	3.3	Not available	Not applicable	Not applicable	H-MM	51	D1	PR
MMRC0065	83	Female	Unknown	Multiple Myeloma	2005	Untreated	IgG	Lambda	3.6	10.1	372	1	Not available	0.132	21	0.00628571	0.8	9.6	Not available	4	No	Not applicable	Skeletal survey	NH-MM	46	11q13	CD2
MMRC0069	56	Female	African American	Multiple Myeloma	2004	Treated	Not available	Lambda	0.11	10.7	180	Not available	Not available	0.56	214	0.00261438	0.5	9.5	530	4.3	Yes	MRI	Not applicable	NH-MM	46	Maf	MF

Array	Age at Diagnosis	Gender	Race	Diagnosis	Initial Diagnosis Date	Current Status	Heavy chain class	Light chain class	M-spike (g/dL)	Hemoglobin (g/dL)	Platelets (10^9/L)	Beta2-microglobulin (ug/dL)	CRP (mg/dL)	Serum free light chain kappa (mg/dL)	Serum free light chain lambda (mg/dL)	Serum free light chain ratio (kappa:lambda)	Serum creatinine (mg/dL)	Serum calcium (mg/dL)	Serum LDH (U/L)	Serum albumin (g/dL)	Lytic lesions (any time)	Evidence for presence of lytic lesions	Evidence for absence of lytic lesions	Est. Ploidy	Est. Chr #	TC_Class	UAMS
MMRC0071	89	Male	Caucasian	Multiple Myeloma	2005	Untreated	IgG	Lambda	4.54	11.2	268	8.8	Not available	12.4	758	0.01635884	2.2	9.1	834	4.1	Yes	Skeletal survey	Not applicable	NH-MM	45	D2	PR
MMRC0072	66	Male	Caucasian	Multiple Myeloma	2006	Untreated	IgG	Kappa	3	11.1	320	3.61	Not available	3.37	0.189	17.8306878	1.1	9.6	140	3.7	Yes	Skeletal survey	Not applicable	H-MM	51	D1	HY
MMRC0073	78	Male	Caucasian	Multiple Myeloma	2004	Treated	IgA	Kappa	1.4	12.4	207	Not available	Not available	1.93	0.894	2.15883669	1.5	9.3	176	Not available	Yes	Skeletal survey	Not applicable	H-MM	47	D2	LB
MMRC0078	73	Male	Caucasian	Multiple Myeloma	2005	Untreated	IgG	Kappa	3	8.3	189	0.0473	15.3	85.4	0.187	456.684492	1.2	11.7	177	2.7	Yes	Skeletal survey	Not applicable	H-MM	50	11q13	CD1
MMRC0079	76	Male	Caucasian	Multiple Myeloma	2005	Untreated	IgA	Kappa	2.4	9.9	187	0.0348	0.24	17.6	1.59	11.0691824	1.1	9.4	106	3.8	No	Not applicable	MRI	NH-MM	46	11q13	CD2
MMRC0080	68	Female	Caucasian	Multiple Myeloma	2005	Untreated	IgG	Kappa	3.1	12.7	190	Not available	2.93	1.03	1.18	0.87288136	0.6	9.3	171	4	No	Not applicable	Skeletal survey/MRI	H-MM	54	D2	PR
MMRC0081	73	Female	Asian	Primary Plasma Cell	2005	Untreated	IgG	Kappa	5.2	9.4	378	0.0851	0.8	246	0.923	266.52221	1.4	10.3	141	3.5	No	Not applicable	Skeletal survey	Hypo	42	D1+D2	PR
MMRC0083	70	Male	Caucasian	Multiple Myeloma	2005	Treated	IgA	Kappa	Not available	12.2	148	0.0189	0.29	3.48	0.949	3.66701791	1.1	9.4	188	2.9	Yes	Skeletal survey	Not applicable	H-MM	52	D1	MY
MMRC0089	60	Male	Caucasian	Multiple Myeloma	2003	Treated	IgG	Lambda	2.39	11.8	54	Not available	Not available	Not available	Not available	Not available	1.6	9.1	2284	3.3	Yes	Skeletal survey	Not applicable	H-MM	50	D2	PR
MMRC0090	50	Male	Unknown	Multiple Myeloma	2005	Untreated	IgG	Kappa	4.4	13.7	203	2.39	Not available	2.2	0.383	5.74412533	1.1	9.2	172	Not available	Yes	Skeletal survey	Not applicable	H-MM	48	D2	MS
MMRC0091	44	Male	Caucasian	Smoldering Myeloma	2004	Treated	IgG	Kappa	2.6	14.5	325	1.81	Not available	3.6	0.27	13.3333333	1.1	9.7	172	4.5	Not available	Not applicable	Not applicable	Hypo	44	4p16	MY
MMRC0092	58	Male	Caucasian	Multiple Myeloma	2004	Untreated	IgG	Kappa	4.1	9.9	200	3.6	Not available	Not available	Not available	Not available	1.3	8.4	427	3.7	Yes	Skeletal survey	Not applicable	H-MM	49	4p16	MY
MMRC0093	66	Male	Caucasian	Multiple Myeloma	2002	Treated	IgA	Kappa	4.19	9.8	76	Not available	Not available	49.1	Not available	30.308642	0.9	9.5	662	3.4	Yes	Skeletal survey	Not applicable	Hypo	44	4p16	MS
MMRC0094	59	Female	Caucasian	Multiple Myeloma	2005	Treated	Not available	Not available	0	13.2	352	2.8	6.5	Not available	Not available	Not available	0.7	8.8	543	4.4	Yes	Skeletal survey/MRI	Not applicable	NH-MM	45	11q13	CD1
MMRC0104	66	Male	Hispanic	Multiple Myeloma	2006	Untreated	IgA	Lambda	5.6	11.3	496	5.01	5.7	0.752	16.5	0.04557576	1.1	11.6	91	Not available	Yes	Skeletal survey	Not applicable	H-MM	51	D1+D2	MY
MMRC0122	70	Male	Caucasian	Multiple Myeloma	2003	Treated	IgG	Kappa	2.4	10.4	147	2.73	Not available	1.33	1.54	0.86363636	1.1	9.7	292	3.4	Yes	Skeletal survey	Not applicable	H-MM	54	D1	PR
MMRC0124	53	Male	Caucasian	Multiple Myeloma	2002	Treated	IgA	Kappa	3.3	7.6	52	Not available	Not available	3.34	0.21	15.9047619	1.3	9.4	128	Not available	No	Not applicable	Skeletal survey	H-MM	53	D1	PR
MMRC0125	57	Male	Caucasian	Multiple Myeloma	2000	Treated	IgG	Kappa	1.7	13.7	123	2.8	Not available	13.3	0.882	15.0793651	1.3	9.8	148	4.4	Yes	Skeletal survey	Not applicable	H-MM	48	D1	HY
MMRC0128	64	Male	Caucasian	Multiple Myeloma	2005	Untreated	IgG	Lambda	2.8	11.3	272	Not available	Not available	Not available	Not available	Not available	1	Not available	Not available	3.8	Yes	Skeletal survey	Not applicable	NH-MM	45	11q13	CD2
MMRC0131	75	Male	Asian	Multiple Myeloma	2004	Treated	Not available	Kappa	Not available	11.8	111	Not available	Not available	118	Not available	Not available	1.42	10.7	195	4.4	Yes	Skeletal survey	Not applicable	Hypo	44	11q13	CD1
MMRC0133	62	Male	Caucasian	Multiple Myeloma	2005	Untreated	IgG	Kappa	4	11.5	170	3	Not available	56.1	0.46	121.956522	0.9	9.1	Not available	4.1	No	Not applicable	Skeletal survey	H-MM	52	None	PR
MMRC0134	71	Male	Caucasian	Multiple Myeloma	2006	Untreated	IgG	Kappa	2.33	11.3	303	4.46	Not available	Not available	Not available	Not available	1	9.5	Not available	3.7	No	Not applicable	Skeletal survey	H-MM	53	11q13	CD2
MMRC0135	86	Male	Caucasian	Multiple Myeloma	2006	Untreated	IgG	Kappa	1.91	10.8	129	7.85	Not available	3380	6.1	554.098361	2.3	9.5	186	4	No	Not applicable	Skeletal survey	H-MM	50	None	LB
MMRC0137	65	Female	Hispanic	Multiple Myeloma	2006	Untreated	Not available	Kappa	Not available	12.9	280	2.19	Not available	751	1.8	417.222222	0.8	10.2	146	4.9	Yes	Skeletal survey	Not applicable	NH-MM	45	11q13	CD1
MMRC0138	59	Female	Caucasian	Multiple Myeloma	2006	Untreated	IgA	Kappa	0.23	12.3	371	5.34	Not available	3640	3.4	1070.58824	1.4	10.7	190	4.5	No	Not applicable	Skeletal survey	Hypo	44	D2	MY
MMRC0139	66	Female	Caucasian	Multiple Myeloma	1998	Treated	IgG	Kappa	2.99	12.5	281	3.13	Not available	395	5.2	75.9615385	0.8	8.7	150	3.8	Yes	MRI	Not applicable	H-MM	51	D1	HY
MMRC0140	53	Male	Caucasian	Multiple Myeloma	2006	Untreated	IgG	Lambda	2.37	11.8	237	6.18	Not available	0.1	182	0.00054945	0.8	9.3	414	3.4	No	Not applicable	MRI	NH-MM	45	None	PR
MMRC0141	76	Male	Caucasian	Multiple Myeloma	2006	Untreated	IgA	Kappa	1.7	10.5	114	6	Not available	3140	2	1570	1.3	9.7	163	3.7	No	Not applicable	Skeletal survey/MRI	H-MM	50	D2	LB
MMRC0144	58	Male	Caucasian	Multiple Myeloma	2007	Untreated	IgG	Kappa	4.57	12.6	279	3.7	Not available	1060	2.8	378.571429	2.5	8.9	159	3.6	No	Not applicable	Skeletal survey/MRI	Hypo	44	D2	PR
MMRC0145	82	Female	Caucasian	Multiple Myeloma	2007	Untreated	IgG	Kappa	0.2	13.1	200	2	Not available	743	4.61	161.171367	0.7	9.6	163	3.8	No	Not applicable	Skeletal survey/MRI	Hypo	43	11q13	CD1
MMRC0147	59	Male	Caucasian	Multiple Myeloma	2007	Untreated	IgA	Lambda	1.5	9.7	135	3.5	Not available	18.4	1090	0.01688073	1.2	8.1	Not available	3.9	Not available	Not applicable	Not applicable	H-MM	53	D1	PR
MMRC0149	73	Male	Hispanic	Multiple Myeloma	2007	Untreated	IgG	Lambda	0.98	7.4	110	9.22	Not available	3.7	141	0.02624113	1.7	8.8	138	4	Yes	Skeletal survey/MRI	Not applicable	NH-MM	45	Maf	MF
MMRC0150	83	Male	Caucasian	Multiple Myeloma	2007	Untreated	IgA	Kappa	Not available	12.1	169	3	Not available	3.82	1.67	2.28742515	1.2	9.6	164	4.3	Yes	Skeletal survey	Not applicable	H-MM	50	D1	MY
MMRC0153	55	Male	Unknown	Multiple Myeloma	2007	Untreated	IgG	Kappa	0.39	11.9	244	Not available	0.3	11.8	1.47	8.027211	0.77	9.5	113	4.3	Yes	MRI	Not applicable	H-MM	47	D1	MY
MMRC0154	54	Male	Caucasian	Multiple Myeloma	2002	Untreated	IgA	Lambda	2.43	10.5	182	Not available	Not available	Not available	Not available	Not available	0.8	9.3	Not available	3.9	No	Not applicable	Skeletal survey/MRI	H-MM	49	D2	PR
MMRC0155	68	Female	African American	Multiple Myeloma	2006	Untreated	Not available	Kappa	Not available	8.1	299	Not available	Not available	Not available	Not available	Not available	2.6	10.9	Not available	3.9	Yes	Skeletal survey	Not applicable	Hypo	44	11q13	CD1
MMRC0156	74	Male	Caucasian	Multiple Myeloma	2007	Untreated	IgG	Kappa	3.2	14.9	250	3.3	Not available	77.5	0.298	260.067114	1.6	9.8	133	4.3	No	Not applicable	Skeletal survey	H-MM	53	None	HY
MMRC0158	70	Female	Unknown	Multiple Myeloma	2006	Untreated	IgG	Kappa	6.35	9.6	246	0.28	0.3	4.6	0.81	5.679012	0.84	9	Not available	3.5	No	Not applicable	Skeletal survey	H-MM	49	D2	MY
MMRC0159	66	Female	Unknown	Multiple Myeloma	2007	Untreated	IgG	Kappa	1.66	9.5	181	Not available	Not available	449	1.26	356.349206	2.04	10.1	181	4.3	Yes	Skeletal survey	Not applicable	H-MM	51	D1	MY
MMRC0160	50	Female	Caucasian	Multiple Myeloma	2007	Untreated	Not available	Lambda	0.53	12	185	Not available	Not available	0.56	6210	9.0177E-05	0.86	10.6	135	4.8	Not available	Not applicable	Not applicable	Hypo	41	6p21	CD1
MMRC0161	68	Male	Caucasian	Multiple Myeloma	2007	Treated	IgG	Kappa	3.6	12	236	3.6	Not available	42.4	Not available	260.122699	1.2	9	Not available	3.5	Yes	Skeletal survey	Not applicable	H-MM	53	D1	HY
MMRC0163	69	Male	Caucasian	Multiple Myeloma	2007	Treated	IgG	Kappa	2.37	10.8	359	2.8	Not available	28.2	4.2	6.71428571	0.8	9.3	131	3.8	Yes	Skeletal survey/MRI	Not applicable	H-MM	49	D1	MY
MMRC0164	52	Female	Caucasian	Multiple Myeloma	2004	Treated	IgA	Not available	0	11	291	1.8	0.39	52.9	1.1	48.0909091	1	10.7	566	5.1	Yes	Skeletal survey	Not applicable	NH-MM	46	11q13	CD1
MMRC0165	76	Female	African American	Multiple Myeloma	2004	Treated	IgG	Kappa	3.1	9	292	Not available	Not available	Not available	Not available	Not available	1.3	9	181	4	No	Not applicable	Skeletal survey	H-MM	50	D1	MY
MMRC0167	56	Male	Caucasian	Multiple Myeloma	2006	Treated	IgG	Kappa	3.9	9.9	248	2.9	Not available	48.2	0.29	166.206897	1.1	8.7	163	3	No	Not applicable	Skeletal survey	H-MM	52	D2	PR
MMRC0168	66	Female	Caucasian	Multiple Myeloma	2007	Untreated	IgA	Kappa	0	11.4	284	2.7	Not available	28.8	0.35	82.2857143	2.8	10.1	124	3.8	Yes	Skeletal survey	Not applicable	H-MM	53	4p16	MS
MMRC0170	70	Female	Caucasian	Multiple Myeloma	2007	Untreated	IgD	Kappa	6.57	14.9	218	2	Not available	8.6	6.5	1.32307692	0.8	8.9	497	4.3	No	Not applicable	Skeletal survey/MRI	H-MM	47	D2	MY
MMRC0171	59	Female	Caucasian	Multiple Myeloma	2007	Untreated	IgG	Kappa	5.55	11.9	227	2.39	Not available	36.7	1.17	31.3675214	1.1	9.2	Not available	3	No	Not applicable	Skeletal survey	Hypo	44	4p16	MS
MMRC0172	66	Female	Caucasian	Multiple Myeloma	2007	Untreated	IgG	Kappa	3.69	9.7	249	Not available	Not available	5290	1.68	3148.80952	1	9.7	182	2.9	Yes	Skeletal survey	Not applicable	Hypo	39	D1	PR
MMRC0173	41	Female	Asian	Multiple Myeloma	2002	Treated	Not available	Not available	Not available	12.3	411	2.2	Not available	684	9.74	70.2258727	0.7	10.2	175	3.8	No	Not applicable	MRI	H-MM	48	D1	MY

Array	Age at Diagnosis	Gender	Race	Diagnosis	Initial Diagnosis Date	Current Status	Heavy chain class	Light chain class	M-spike (g/dL)	Hemoglobin (g/dL)	Platelets (10^9/L)	Beta2-microglobulin (ug/dL)	CRP (mg/dL)	Serum free light chain kappa (mg/dL)	Serum free light chain lambda (mg/dL)	Serum free light chain ratio (kappa:lambda)	Serum creatinine (mg/dL)	Serum calcium (mg/dL)	Serum LDH (U/L)	Serum albumin (g/dL)	Lytic lesions (any time)	Evidence for presence of lytic lesions	Evidence for absence of lytic lesions	Est. Ploidy	Est. Chr #	TC_Class	UAMS
MMRC0174	60	Male	Caucasian	Multiple Myeloma	2006	Treated	IgA	Kappa	4.59	10.7	183	3.5	Not available	Not available	Not available	Not available	0.9	10.1	Not available	4	No	Not applicable	Skeletal survey/MRI	NH-MM	46	11q13	CD2
MMRC0175	64	Female	Caucasian	Multiple Myeloma	2005	Treated	IgG	Lambda	4.4	9.8	227	Not available	Not available	1.68	17.6	0.095455	1	9.4	177	3.7	No	Not applicable	Skeletal survey/MRI	NH-MM	45	11q13	CD2
MMRC0179	68	Female	Caucasian	Multiple Myeloma	2008	Untreated	IgG	Kappa	1.2	12.8	317	2.9	4	Not available	Not available	Not available	0.7	9.5	Not available	4.1	No	Not applicable	Skeletal survey	H-MM	52	D1	MY
MMRC0180	49	Male	Caucasian	Multiple Myeloma	2006	Treated	IgA	Kappa	0	12.7	143	2.91	Not available	1210	1.9	636.842105	0.83	9.2	344	4.5	Yes	MRI	Not applicable	Hypo	44	4p16	PR
MMRC0181	72	Female	Unknown	Multiple Myeloma	2008	Untreated	IgG	Lambda	2.8	12.4	387	3.34	Not available	0.871	51.5	0.01691262	1.1	10.5	185	3.8	Yes	Skeletal survey	Not applicable	H-MM	54	D1	PR
MMRC0182	56	Male	Caucasian	Multiple Myeloma	2007	Untreated	IgG	Kappa	4.04	12.2	312	2.26	Not available	60	8.88	6.75675676	1	8.9	Not available	3.3	Yes	Skeletal survey	Not applicable	H-MM	55	D1+D2	MY
MMRC0183	63	Male	African American	Multiple Myeloma	2007	Untreated	IgG	Kappa	3.94	12.7	239	2.04	0.2	87.5	9.69	9.02992776	1	9.4	227	4	Yes	Skeletal survey	Not applicable	H-MM	52	D1	HY
MMRC0185	59	Male	Caucasian	Multiple Myeloma	2007	Untreated	IgG	Kappa	6.3	9.2	345	9.19	Not available	9.42	1.21	7.78512397	1.2	8.2	141	2.7	No	Not applicable	MRI	H-MM	50	D2	MY
MMRC0186	78	Male	Caucasian	Multiple Myeloma	2007	Untreated	IgA	Kappa	3.47	11	167	0.42	0.3	2.57	0.81	3.17283951	1.12	9.3	140	3.5	Yes	Skeletal survey	Not applicable	NH-MM	46	D2	LB
MMRC0189	65	Male	African American	Multiple Myeloma	2003	Treated	IgA	Kappa	2.58	12.2	244	Not available	Not available	Not available	Not available	Not available	1.3	9	Not available	3.7	No	Not applicable	Skeletal survey	NH-MM	45	4p16	MS
MMRC0191	56	Female	African American	Multiple Myeloma	2004	Treated	IgG	Lambda	6.06	10.9	289	3.9	Not available	Not available	Not available	Not available	0.7	10	364	3.7	Yes	Skeletal survey	Not applicable	H-MM	49	D2	PR
MMRC0192	48	Male	Caucasian	Multiple Myeloma	1998	Treated	IgG	Kappa	2.6	11.4	188	Not available	Not available	49.9	Not available	1229.06404	0.9	9.6	251	3.7	Yes	Skeletal survey	Not applicable	H-MM	54	D1	PR
MMRC0194	60	Female	African American	Multiple Myeloma	2007	Untreated	Not available	Not available		14.5	215	2.7	11	0.166	308	0.00053896	0.8	10.5	Not available	4.7	Yes	Skeletal survey	Not applicable	Hypo	44	11q13	CD2
MMRC0195	58	Female	African American	Multiple Myeloma	2007	Untreated	IgG	Kappa	5.33	12	280	1.5	Not available	Not available	Not available	Not available	1.1	8.9	Not available	3.7	No	Not applicable	Skeletal survey	NH-MM	46	D1	MY
MMRC0196	60	Male	Caucasian	Multiple Myeloma	2006	Treated	IgG	Lambda	1.55	9.4	300	3.9	Not available	0.619	12.7	0.04874016	1	9.5	554	3.8	No	Not applicable	Skeletal survey	H-MM	52	None	PR
MMRC0198	58	Male	Caucasian	Multiple Myeloma	2001	Treated	IgG	Not available	Not available	9.8	168	Not available	Not available	Not available	Not available	Not available	1.3	8.5	Not available	Not available	Yes	Skeletal survey/MRI	Not applicable	Hypo	42	D1	HY
MMRC0200	63	Male	Caucasian	Multiple Myeloma	2007	Untreated	IgA	Kappa	Not available	Not available	199	4.3	253	Not available	278	0.241	10	3.7	13.5	Not available	Yes	Skeletal survey	Not applicable	H-MM	47	11q13	CD2
MMRC0201	62	Male	Caucasian	Multiple Myeloma	2002	Treated	IgG	Kappa	1.1	13.9	288	1.76	Not available	1.94	1.28	1.515625	1.3	9.8	197	Not available	Yes	Skeletal survey	Not applicable	NH-MM	46	D2	PR
MMRC0203	67	Male	Caucasian	Multiple Myeloma	2005	Untreated	IgA	Kappa	0.6	15.4	234	1.95	Not available	2.76	1.03	2.67961165	0.9	9.8	Not available	3.5	No	Not applicable	Skeletal survey	H-MM	51	D1	HY
MMRC0204	65	Male	African American	Multiple Myeloma	2005	Treated	IgG	Kappa	4.1	11.6	279	Not available	Not available	107	0.361	296.398892	1.6	10.2	338	4.3	Yes	Skeletal survey/MRI	Not applicable	H-MM	54	D1	HY
MMRC0206	56	Male	Caucasian	Multiple Myeloma	2003	Treated	IgG	Lambda	2.12	9	129	Not available	Not available	Not available	1360	0.000787	0.8	8.9	156	3.4	No	Not applicable	Skeletal survey	NH-MM	45	4p16	MS
MMRC0207	51	Male	Asian	Multiple Myeloma	2002	Treated	IgG	Lambda	0.14	9.6	76	6.61	2.7	0.12	656	0.00018293	0.8	9.4	Not available	3.9	Yes	MRI	Not applicable	H-MM	47	4p16	MS
MMRC0208	69	Male	Unknown	Smoldering Myeloma	2003	Untreated	IgG	Kappa	3.84	10.6	225	Not available	Not available	Not available	Not available	Not available	1.44	10	Not available	3.4	Not available	Not applicable	Not applicable	H-MM	51	4p16	MS
MMRC0224	62	Female	Caucasian	Multiple Myeloma	2005	Treated	IgG	Kappa	5.7	10.6	190	Not available	70.9	14	0.0798	175.438596	0.8	9	415	3.2	Yes	Skeletal survey	Not applicable	Hypo	43	4p16	PR
MMRC0226	57	Male	Caucasian	Multiple Myeloma	2007	Untreated	IgG	Kappa	Not available	14.2	237	0.0229	0.00186	613	0.35	1751.42857	1	10	142	5	Yes	Skeletal survey	Not applicable	NH-MM	46	11q13	CD1
MMRC0227	35	Female	Caucasian	Multiple Myeloma	2007	Treated	IgG	Lambda	Not available	11.3	236	0.0154	0.00086	0.028	4.07	0.00687961	0.7	9.6	132	3.9	Yes	Skeletal survey	Not applicable	Hypo	43	11q13	CD1
MMRC0228	56	Male	Caucasian	Multiple Myeloma	2005	Treated	IgG	Kappa	Not available	11.8	371	Not available	Not available	1.65	0.311	5.30546624	0.8	9.6	123	4.6	Yes	Skeletal survey	Not applicable	H-MM	54	D1	HY
MMRC0233	72	Female	Caucasian	Multiple Myeloma	1999	Treated	IgG	Kappa	2.3	8	163	0.359	Not available	1310	0.8	1637.5	2	10.8	406	3.3	No	Not applicable	Skeletal survey	H-MM	51	D1	PR
MMRC0239	66	Male	Caucasian	Multiple Myeloma	2003	Treated	IgG	Kappa	2.31	14.7	283	Not available	Not available	88.5	7.02	12.6068376	1.1	8.7	143	3.7	No	Not applicable	Skeletal survey/MRI	Hypo	39	None	MY
MMRC0240	42	Male	Caucasian	Multiple Myeloma	2000	Treated	Not available	Kappa	0	13.8	277	2	Not available	2.82	3.11	0.90675241	0.8	9.9	Not available	4.4	Yes	Skeletal survey	Not applicable	NH-MM	46	6p21	MF
MMRC0243	46	Male	Caucasian	Multiple Myeloma	2008	Untreated	Not available	Kappa	0.17	10.5	258	5.99	3.45	8550	0.83	10301.2048	1.3	10.5	186	4.9	Yes	Skeletal survey	Not applicable	H-MM	48	11q13	CD2
MMRC0244	56	Female	Caucasian	Multiple Myeloma	2008	Untreated	IgG	Kappa	5.3	10.8	373	5.4	Not available	126	0.919	137.10555	0.9	10.6	190	2.6	Yes	Skeletal survey	Not applicable	H-MM	50	D1	MY
MMRC0245	53	Male	Caucasian	Multiple Myeloma	2002	Treated	IgG	Kappa	1.5	9.4	87	3.31	Not available	Not available	Not available	Not available	1.26	9.2	Not available	4.2	Yes	Skeletal survey	Not applicable	H-MM	51	None	PR
MMRC0246	49	Female	Caucasian	Multiple Myeloma	2002	Treated	IgG	Lambda	1.1	9.2	176	7.45	Not available	1.28	502	0.0025498	1.8	9.5	195	4.3	No	Not applicable	Skeletal survey	H-MM	55	None	MY
MMRC0247	Unknown	Male	Caucasian	Multiple Myeloma	unknown	Treated	IgA	Kappa	3.09	8.6	55	Not available	Not available	1270.3	0.8	1587.875	1.2	11.1	378	3.5	Yes	Skeletal survey	Not applicable	NH-MM	46	11q13	CD2
MMRC0248	58	Male	Caucasian	Multiple Myeloma	2003	Treated	IgG	Kappa	5.1	7.9	62	Not available	7.73	1438	9.83	146.286877	2.1	8.5	Not available	Not available	Yes	Skeletal survey	Not applicable	H-MM	54	D1	MY
MMRC0249	56	Male	African American	Multiple Myeloma	2006	Untreated	IgG	Kappa	3.97	9.8	255	9.7	Not available	590	11.4	51.754386	2.06	9.5	125	3.4	No	Not applicable	Skeletal survey/MRI	H-MM	52	D1	MY
MMRC0252	51	Male	Caucasian	Primary Plasma Cell	2008	Untreated	IgG	Lambda	2.35	8.7	111	5.54	31.64	4.45	7500	0.00059333	1.5	6.6	610	2.6	No	Not applicable	Skeletal survey	Hypo	44	4p16	PR
MMRC0256	56	Female	Caucasian	Multiple Myeloma	2008	Untreated	IgG	Kappa	1.76	10.4	227	2.07	1.47	436	5.52	78.9855072	0.9	9.1	Not available	3.8	Yes	Skeletal survey	Not applicable	H-MM	50	D1	MY
MMRC0258	67	Female	Caucasian	Smoldering Myeloma	2006	Untreated	IgA	Kappa	2.9	9.7	526	Not available	2.61	74.3	0.309	240.453074	0.9	9.1	88	3.7	No	Not applicable	Skeletal survey	Hypo	41	D2	CD2
MMRC0259	62	Male	Caucasian	Multiple Myeloma	1996	Treated	IgG	Lambda	1.6	13.3	228	4.12	1.18	0.696	71.7	0.00970711	1.1	9.8	157	4.1	No	Not applicable	Skeletal survey	NH-MM	45	Maf	MF
MMRC0260	53	Male	Caucasian	Multiple Myeloma	2006	Treated	IgG	Kappa	1.9	14.2	324	3.38	Not available	89.2	1.34	66.5671642	1.2	9.4	152	3.6	Yes	Skeletal survey	Not applicable	H-MM	52	D1	MY
MMRC0264	48	Female	Caucasian	Smoldering Myeloma	2005	Untreated	IgG	Lambda	2	14.7	149	2.2	Not available	0.84	18.4	0.04565217	0.8	9.5	Not available	4.6	No	Not applicable	Skeletal survey	Hypo	44	4p16	MS
MMRC0268	62	Female	Caucasian	Multiple Myeloma	2007	Treated	IgG	Kappa	2.7	8.9	163	6.45	14.3	414	2.38	173.94958	0.6	10.6	251	3.3	Yes	Skeletal survey/MRI	Not applicable	H-MM	52	D1	PR
MMRC0272	64	Male	Caucasian	Multiple Myeloma	2006	Treated	IgG	Lambda	2.19	10.1	92	6.2	1.24	0.6	74.8	0.00802139	1.1	9.4	181	4	No	Not applicable	Skeletal survey	H-MM	54	D2	MF
MMRC0277	67	Male	Caucasian	Multiple Myeloma	2008	Untreated	IgG	Kappa	4.7	10.5	151	6.01	Not available	96.7	0.053	1824.5283	0.8	9.5	153	3.9	No	Not applicable	Skeletal survey	Hypo	41	Maf	MF
MMRC0280	45	Female	Caucasian	Multiple Myeloma	2008	Untreated	IgA	Kappa	7.3	7.2	128	9.63	Not available	14.9	0.274	54.379562	0.9	9.6	84	2.7	No	Not applicable	Skeletal survey/MRI	NH-MM	45	11q13	CD2
MMRC0281	71	Female	Caucasian	Smoldering Myeloma	2006	Untreated	IgG	Kappa	2	12.2	233	5.42	Not available	0.786	0.35	2.24571429	1.3	9.4	138	3.7	No	Not applicable	Skeletal survey	Hypo	44	11q13	CD1
MMRC0282	60	Male	Caucasian	Multiple Myeloma	2007	Treated	Not available	Kappa	Not available	12.8	197	0.31	1.5	300	0.8	375	0.62	9.8	185	3.9	No	Not applicable	Skeletal survey/MRI	H-MM	50	D1	MY
MMRC0284	41	Male	Caucasian	Multiple Myeloma	2001	Untreated	Not available	Kappa	Not available	12.8	284	2.6	0.9	689.9	1	689.9	0.7	9.2	347	4.5	No	Not applicable	Skeletal survey	NH-MM	46	11q13	CD2

Array	Age at Diagnosis	Gender	Race	Diagnosis	Initial Diagnosis Date	Current Status	Heavy chain class	Light chain class	M-spike (g/dL)	Hemoglobin (g/dL)	Platelets (10^9/L)	Beta2-microglobulin (ug/dL)	CRP (mg/dL)	Serum free light chain kappa (mg/dL)	Serum free light chain lambda (mg/dL)	Serum free light chain ratio (kappa:lambda)	Serum creatinine (mg/dL)	Serum calcium (mg/dL)	Serum LDH (U/L)	Serum albumin (g/dL)	Lytic lesions (any time)	Evidence for presence of lytic lesions	Evidence for absence of lytic lesions	Est. Ploidy	Est. Chr #	TC_Class	UAMS
MMRC0285	46	Male	Caucasian	Multiple Myeloma	2007	Treated	IgM	Kappa	4.94	12.6	174	Not available	Not available	34.8	0.43	80.81395	0.76	8.3	Not available	Not available	Yes	Skeletal survey	Not applicable	Hypo	44	4p16	MS
MMRC0286	50	Female	Caucasian	Multiple Myeloma	2008	Untreated	IgA	Kappa	1.71	11.7	149	3.27	Not available	446	2.4	185.833333	0.86	9.8	166	4.3	No	Not applicable	Skeletal survey	Hypo	44	Maf	MF
MMRC0287	55	Male	African American	Multiple Myeloma	2004	Treated	IgG	Kappa	4.53	10.7	294	16.7	Not available	1330	3.7	359.459459	1.94	8.9	121	3.3	Yes	MRI	Not applicable	NH-MM	46	11q13	CD2
MMRC0291	51	Male	Caucasian	Multiple Myeloma	2006	Treated	IgA	Lambda	3.4	9.4	120	25.9	Not available	0.149	410	0.00036341	2.5	9.5	181	3.3	Yes	Skeletal survey	Not applicable	NH-MM	45	11q13	CD2
MMRC0298	55	Female	Caucasian	Multiple Myeloma	2007	Untreated	IgG	Lambda	4.46	9.9	235	2	Not available	1.12	1410	0.00079433	0.8	8.9	108	3.2	Yes	Skeletal survey	Not applicable	Hypo	44	11q13	CD2
MMRC0299	68	Male	Caucasian	Multiple Myeloma	2001	Treated	Not available	Kappa	Not available	14.2	145	Not available	Not available	Not available	Not available	Not available	0.8	10.5	Not available	Not available	Yes	Skeletal survey	Not applicable	NH-MM	46	11q13	CD2
MMRC0302	70	Male	Caucasian	Multiple Myeloma	2006	Untreated	IgG	Kappa	4.6	8.9	134	11.3	Not available	1490	0.461	3232.10412	2.4	9.5	110	3	No	Not applicable	Skeletal survey	H-MM	53	D1	MY
MMRC0303	63	Female	Caucasian	Multiple Myeloma	2005	Treated	IgA	Kappa	6.7	9.9	28	Not available	Not available	318	Not available	7832.51232	0.9	9	192	3	Yes	Skeletal survey/MRI	Not applicable	Hypo	41	D2	CD1
MMRC0307	62	Male	Caucasian	Multiple Myeloma	2006	Treated	IgA	Kappa	0.85	10.6	222	Not available	Not available	353	8.33	42.3769508	1.3	9.5	122	3.5	No	Not applicable	Skeletal survey	Hypo	44	D2	MY
MMRC0308	55	Female	Caucasian	Multiple Myeloma	2007	Treated	IgG	Lambda	1.98	10.3	260	8.33	Not available	12.7	1300	0.00976923	1.95	9.3	147	4.31	No	Not applicable	Skeletal survey	Hypo	44	4p16	MF
MMRC0309	Unknown	Male	Caucasian	Multiple Myeloma	unknown	Untreated	IgA	Lambda	1.3	9.7	207	0.43	0.16	12.8	2130	0.00600939	1.5	10.8	104	4.1	Yes	Skeletal survey	Not applicable	NH-MM	45	D2	MY
MMRC0312	69	Female	Caucasian	Multiple Myeloma	2008	Untreated	IgG	Lambda	3.8	10.1	105	7.05	Not available	0.936	1.43	0.65454545	1.1	9.7	124	3.5	No	Not applicable	Skeletal survey	NH-MM	46	11q13	CD2
MMRC0318	24	Male	Caucasian	Multiple Myeloma	2008	Treated	IgG	Lambda	4.7	9.9	391	0.049	0.026	0.027	9.21	0.0029316	0.9	8.6	130	3.4	No	Not applicable	Skeletal survey	NH-MM	46	Maf	MF
MMRC0324	75	Male	Caucasian	Multiple Myeloma	2008	Untreated	IgA	Lambda	0.3	13.6	225	3.7	Not available	0.893	14.3	0.06244755	1.4	10	121	3.8	Yes	Skeletal survey	Not applicable	NH-MM	46	D2	PR
MMRC0329	37	Female	Caucasian	Multiple Myeloma	2005	Treated	IgG	Kappa	4.5	9.5	22	8.2	Not available	317	0.07	4528.57143	0.8	13.6	152	3	Yes	Skeletal survey	Not applicable	H-MM	54	None	PR
MMRC0330	67	Female	African American	Multiple Myeloma	2008	Untreated	IgG	Kappa	3	9.7	233	Not available	50	77	0.639	120.500782	0.7	10	166	4	Yes	Skeletal survey	Not applicable	H-MM	51	D1	HY
MMRC0331	48	Male	Caucasian	Multiple Myeloma	1996	Treated	IgG	Kappa	1.9	8.1	56	7.9	6.1	203	0.26	780.769231	1.2	8.3	198	3	No	Not applicable	Skeletal survey	NH-MM	45	D2	LB
MMRC0332	66	Male	Caucasian	Multiple Myeloma	2008	Treated	IgG	Lambda	Not available	7.9	199	3.45	Not available	6.7	900	0.00744444	0.8	7.7	247	3.1	Yes	MRI	Not applicable	H-MM	52	4p16	MS
MMRC0334	63	Male	Caucasian	Multiple Myeloma	2006	Untreated	IgG	Lambda	2.8	12.7	319	6	0.1	1.82	101	0.0180198	2.3	9.1	133	4	No	Not applicable	Skeletal survey/MRI	Hypo	40	D1+D2	LB
MMRC0340	67	Female	African American	Multiple Myeloma	2008	Untreated	IgA	Kappa	3	10.3	258	Not available	Not available	1390	0.549	2531.87614	10.9	11.7	176	3.7	Yes	Skeletal survey	Not applicable	Hypo	44	Maf	MF
MMRC0343	62	Male	Caucasian	Multiple Myeloma	2008	Treated	Not available	Kappa	Not available	10.3	281	6.96	Not available	763	13.2	57.8030303	1.25	8.6	152	3.8	Yes	Skeletal survey	Not applicable	Hypo	44	11q13	CD1
MMRC0351	67	Male	Caucasian	Smoldering Myeloma	2008	Untreated	IgA	Kappa	2.09	12.6	227	Not available	Not available	28.7	3.73	7.69436997	1.2	9.7	140	4.3	Yes	Skeletal survey	Not applicable	H-MM	53	D1	MY
MMRC0352	62	Male	African American	Multiple Myeloma	2008	Untreated	IgG	Kappa	4.98	8.5	150	Not available	9.6	1290	17.6	73.2954545	1.3	8.6	153	3	Not available	Not applicable	Not applicable	H-MM	50	D2	MY
MMRC0353	46	Male	Caucasian	Multiple Myeloma	2007	Treated	IgA	Kappa	1.81	11.2	144	4.89	10.82	144	8.39	17.1632896	1.3	9.5	180	3.9	Yes	Skeletal survey	Not applicable	H-MM	53	D2	PR
MMRC0355	71	Male	Caucasian	Multiple Myeloma	2008	Untreated	IgA	Kappa	2.77	12.8	164	2.64	0.2	12.6	4.2	3	1.24	9.8	69	3.9	Yes	MRI	Not applicable	H-MM	52	D1	MY
MMRC0356	52	Male	Hispanic	Multiple Myeloma	2008	Untreated	IgG	Kappa	1.3	10.4	248	2.5	7.2	595	2.32	256.465517	1.39	8.2	228	3.7	Yes	MRI	Not applicable	H-MM	50	D2	PR
MMRC0359	63	Male	Caucasian	Multiple Myeloma	2008	Untreated	IgG	Kappa	Not available	12.4	242	0.15	Not available	2.8	0.22	12.7272727	1	8.1	Not available	Not available	Yes	Skeletal survey	Not applicable	NH-MM	45	11q13	CD1
MMRC0360	63	Female	Caucasian	Multiple Myeloma	2005	Treated	IgG	Lambda	1.1	14	234	2.7	Not available	0.87	17.2	0.0505814	0.72	9.4	211	4.2	Yes	Skeletal survey	Not applicable	H-MM	53	D1	PR
MMRC0364	59	Male	Caucasian	Multiple Myeloma	2004	Treated	IgG	Lambda	1.2	13.2	155	3.6	1.7	Not available	3.95	0.00759494	1.2	9.6	178	4.2	No	Not applicable	Skeletal survey/MRI	Hypo	44	4p16	MS
MMRC0365	57	Male	Caucasian	Multiple Myeloma	1996	Untreated	IgA	Kappa	4.3	16.1	173	5.2	Not available	4.03	0.08	50.375	1	8.8	119	3	No	Not applicable	Skeletal survey	H-MM	54	D1	LB
MMRC0372	40	Female	Caucasian	Multiple Myeloma	2008	Untreated	IgG	Lambda	4.85	12	285	Not available	Not available	15.1	32.8	0.46036585	0.8	8.2	117	3.6	Not available	Not applicable	Not applicable	NH-MM	45	11q13	CD2
MMRC0379	56	Female	Caucasian	Multiple Myeloma	2008	Treated	IgA	Kappa	2.2	8.7	204	0.267	1.2	2.7	0.278	9.71223022	0.7	8.7	119	3.6	Yes	Skeletal survey	Not applicable	H-MM	48	D1	MY
MMRC0381	72	Male	Caucasian	Multiple Myeloma	2008	Untreated	IgG	Kappa	4.9	11	271	0.0423	0.0179	2.24	0.251	8.92430279	1.7	9.6	209	4.1	No	Not applicable	Skeletal survey	H-MM	55	D1	HY
MMRC0382	70	Male	Caucasian	Smoldering Myeloma	2008	Untreated	IgG	Lambda	1.7	12.2	327	0.049	0.31	1.72	22.6	0.07610619	1	9.7	157	3.5	No	Not applicable	Skeletal survey	NH-MM	46	11q13	CD2
MMRC0384	50	Male	Caucasian	Multiple Myeloma	2001	Treated	IgG	Kappa	Not available	11.8	208	Not available	Not available	Not available	Not available	Not available	1.2	8.7	Not available	3.9	Yes	Skeletal survey	Not applicable	Hypo	43	4p16	PR
MMRC0386	48	Female	Asian	Multiple Myeloma	1998	Treated	IgG	Kappa	0.17	11.7	20	Not available	Not available	Not available	Not available	Not available	0.7	8.5	760	3.7	Yes	MRI	Not applicable	H-MM	53	Maf	MY
MMRC0387	60	Female	Caucasian	Multiple Myeloma	2009	Untreated	IgG	Kappa	2.7	12	366	0.0225	0.015	16.1	0.41	39.2682927	0.8	9.9	144	4.5	Yes	Skeletal survey	Not applicable	H-MM	52	None	HY
MMRC0389	37	Male	Caucasian	Multiple Myeloma	2002	Treated	IgE	Kappa	6	Not available	69	2.8	0.01	6	25	137	13.4	Not available	4.7	Not available	No	Not applicable	MRI	NH-MM	45	Maf	MF
MMRC0390	71	Female	Caucasian	Multiple Myeloma	1999	Treated	IgG	Lambda	3.7	12.9	271	3.19	Not available	0.125	2.98	0.04194631	1	9.4	106	3.4	No	Not applicable	Skeletal survey	NH-MM	45	11q13	CD1
MMRC0391	51	Male	Caucasian	Multiple Myeloma	2005	Treated	IgG	Kappa	1.3	13.9	293	4.77	Not available	54.5	0.177	307.909605	1.2	10	150	4.3	Yes	Skeletal survey	Not applicable	H-MM	53	D1	HY
MMRC0392	59	Male	Caucasian	Multiple Myeloma	2005	Treated	IgG	Lambda	3	11.8	234	1.61	Not available	Not available	1.29	0.02069767	0.9	7.9	231	3.4	Yes	Skeletal survey	Not applicable	H-MM	52	D1	MY
MMRC0393	79	Male	Caucasian	Multiple Myeloma	2006	Untreated	IgA	Kappa	0.13	12.2	174	3.49	Not available	68.9	28	2.46071429	0.8	9.3	183	3.3	Yes	Skeletal survey/MRI	Not applicable	H-MM	53	D2	MY
MMRC0394	55	Female	Asian	Multiple Myeloma	2006	Treated	IgG	Lambda	Not available	9.6	371	3.1	Not available	0.1	1710	5.848E-05	0.8	10.6	244	3.3	Not available	Not applicable	Not applicable	Hypo	44	11q13	CD1
MMRC0395	59	Male	Caucasian	Multiple Myeloma	2006	Treated	IgA	Kappa	4.47	15.6	166	1.7	Not available	7.73	1.75	4.41714286	0.9	8.8	193	3.9	Yes	MRI	Not applicable	H-MM	52	D1+D2	MY
MMRC0396	40	Male	Asian	Multiple Myeloma	2006	Treated	IgG	Lambda	1.9	12.8	188	2	Not available	6.26	41.9	0.14940334	1	8.9	Not available	4.2	Not available	Not applicable	Not applicable	H-MM	54	D1	HY
MMRC0399	58	Male	Caucasian	Multiple Myeloma	unknown	Treated	IgG	Lambda	2.35	10.3	62	3.26	9.16	10.2	257	0.03968872	1.6	9.2	115	3.7	No	Not applicable	Skeletal survey	NH-MM	45	Maf	MF
MMRC0400	60	Male	Caucasian	Multiple Myeloma	2004	Treated	IgG	Lambda	2.3	9.8	<4	3.85	28.86	Not available	214	0.00252336	1	9.2	175	2.3	Not available	Not applicable	Not applicable	NH-MM	46	11q13	CD1
MMRC0401	59	Female	Caucasian	Multiple Myeloma	2001	Treated	IgG	Kappa	4.2	9.4	205	6.82	Not available	11.5	0.0593	193.929174	1	9.8	133	3.2	Yes	Skeletal survey	Not applicable	H-MM	48	D1	PR
MMRC0402	60	Female	Caucasian	Multiple Myeloma	2007	Treated	IgG	Kappa	3.8	9.3	452	8.76	Not available	3.82	7.79	0.49037227	1	9.2	Not available	3.5	Yes	Skeletal survey	Not applicable	H-MM	52	4p16	PR
MMRC0403	64	Female	Caucasian	Multiple Myeloma	2004	Treated	IgG	Lambda	2.3	12.7	218	2.74	Not available	0.132	49.5	0.00266667	0.8	10	205	Not available	No	Not applicable	Skeletal survey	H-MM	50	D1+D2	PR

Array	Age at Diagnosis	Gender	Race	Diagnosis	Initial Diagnosis Date	Current Status	Heavy chain class	Light chain class	M-spike (g/dL)	Hemoglobin (g/dL)	Platelets (10^9/L)	Beta2-microglobulin (ug/dL)	CRP (mg/dL)	Serum free light chain kappa (mg/dL)	Serum free light chain lambda (mg/dL)	Serum free light chain ratio (kappa:lambda)	Serum creatinine (mg/dL)	Serum calcium (mg/dL)	Serum LDH (U/L)	Serum albumin (g/dL)	Lytic lesions (any time)	Evidence for presence of lytic lesions	Evidence for absence of lytic lesions	Est. Ploidy	Est. Chr #	TC_Class	UAMS
MMRC0406	59	Female	Caucasian	Multiple Myeloma	2009	Untreated	IgA	Kappa	2.94	9.6	238	1.1	Not available	Not available	Not available	Not available	1.31	10	Not available	3.8	Yes	Skeletal survey	Not applicable	H-MM	54	D1	PR
MMRC0408	58	Male	Caucasian	Multiple Myeloma	2009	Untreated	IgA	Lambda	0.4	13.2	249	2.8	Not available	0.03	21.8	0.00137615	1	9.8	152	4.7	No	Not applicable	Skeletal survey/MRI	H-MM	53	D1	HY
MMRC0409	65	Male	Caucasian	Multiple Myeloma	2008	Treated	Not available	Not available	Not available	12.2	238	Not available	Not available	0.66	2.38	0.27731092	1.02	9.4	208	4.1	Yes	Skeletal survey	Not applicable	NH-MM	46	11q13	CD1
MMRC0410	33	Female	African American	Multiple Myeloma	2002	Treated	IgA	Kappa	1.27	9.8	153	2.03	3.95	92.5	Not available	128.472222	0.87	9	234	3.6	Yes	Skeletal survey	Not applicable	Hypo	44	11q13	CD1
MMRC0411	73	Male	Caucasian	Multiple Myeloma	2009	Untreated	Not available	Lambda	0	13	187	1.9	4.44	16.9	121	0.13966942	1.6	9.3	147	4	Yes	MRI	Not applicable	NH-MM	46	11q13	CD1
MMRC0412	49	Male	Caucasian	Multiple Myeloma	2004	Treated	IgG	Kappa	4.49	9	109	5.7	Not available	2100	3.62	580.110497	0.8	8.6	321	3.2	Yes	Skeletal survey	Not applicable	H-MM	52	D2	PR
MMRC0413	78	Male	Caucasian	Multiple Myeloma	2005	Treated	IgG	Lambda	0.19	11	216	9	Not available	15.9	2528	0.00628956	1.2	10.7	408	4.4	Yes	Skeletal survey	Not applicable	H-MM	51	None	MY
MMRC0414	66	Male	Caucasian	Multiple Myeloma	2004	Treated	IgA	Kappa	1.5	11.2	153	2	Not available	2.16	Not available	53.2019704	1	10.4	Not available	Not available	No	Not applicable	Skeletal survey	Hypo	44	11q13	CD1
MMRC0417	78	Male	Caucasian	Multiple Myeloma	2007	Treated	IgG	Kappa	6.04	9.4	5	5.91	2.63	1007.57	0.6	1679.28333	4	8.4	1013	2.1	Not available	Not applicable	Not applicable	H-MM	52	D1	PR
MMRC0418	62	Male	Caucasian	Multiple Myeloma	2009	Untreated	IgG	Lambda	4.32	13.1	209	7.47	Not available	6.1	90.6	0.06732892	1.2	8.9	719	4.6	Yes	Skeletal survey/MRI	Not applicable	H-MM	50	11q13	PR
MMRC0419	65	Female	Caucasian	Primary Plasma Cell	2009	Untreated	IgG	Lambda	0.33	8.9	32	9.97	6.56	Not available	4550	0.00011868	1	10	329	3.3	Yes	Skeletal survey	Not applicable	Hypo	43	11q13	CD1
MMRC0420	46	Male	Caucasian	Multiple Myeloma	2000	Treated	IgG	Kappa	2.67	11.3	428	4.77	Not available	345	3.36	102.678571	1.16	9.7	191	3.94	Yes	Skeletal survey	Not applicable	H-MM	52	D1	MY
MMRC0421	45	Male	Caucasian	Multiple Myeloma	2004	Treated	IgA	Not available	2.12	8	149	0.41	Not available	Not available	Not available	Not available	0.82	9.2	191	3.3	Yes	Skeletal survey	Not applicable	NH-MM	45	4p16	PR
MMRC0422	72	Male	Caucasian	Multiple Myeloma	2007	Treated	IgA	Lambda	2.86	11.9	131	3.4	3	3.23	130	0.02484615	1	9.9	179	3.5	No	Not applicable	Skeletal survey	H-MM	51	None	PR
MMRC0430	61	Female	Caucasian	Multiple Myeloma	2009	Untreated	IgA	Lambda	0.49	11.5	227	1.71	10.35	33.1	20.4	1.62254902	0.7	8.3	157	3.3	Yes	Skeletal survey	Not applicable	H-MM	52	D1+D2	MY
MMRC0431	60	Male	African American	Multiple Myeloma	2004	Treated	IgG	Kappa	1.13	10.5	139	1.59	1.85	845	1.55	545.16129	1.02	8.6	137	3.7	Yes	Skeletal survey	Not applicable	H-MM	52	D1	MY
MMRC0432	59	Female	Caucasian	Multiple Myeloma	1999	Treated	IgA	Kappa	0.64	9.3	108	2.75	2.66	176	0.08	2315.78947	0.76	8.8	Not available	3.8	Yes	Skeletal survey	Not applicable	H-MM	50	D1	MY
MMRC0433	65	Female	Hispanic	Multiple Myeloma	2008	Untreated	IgG	Kappa	Not available	12.2	309	1.9	Not available	377	2.9	130	0.74	8	Not available	3.7	No	Not applicable	Skeletal survey	H-MM	50	4p16	MS
MMRC0434	Unknown	Female	Caucasian	Multiple Myeloma	unknown	Untreated	IgA	Kappa	0.25	13.6	226	Not available	Not available	1200.8	1.5	800.533333	0.9	10	533	4.4	No	Not applicable	Skeletal survey	Hypo	37	D1	MY
MMRC0435	51	Female	Caucasian	Multiple Myeloma	2009	Untreated	IgG	Kappa	4.62	11.5	320	0.33	0.5	197	0.52	378.846154	0.79	10.8	174	4.2	Yes	MRI	Not applicable	H-MM	54	D1	HY
MMRC0436	49	Female	Caucasian	Multiple Myeloma	1998	Treated	IgG	Not available	Not available	10	127	Not available	Not available	Not available	Not available	Not available	0.9	8.4	Not available	3.7	No	Not applicable	Skeletal survey	Hypo	44	11q13	CD2
MMRC0438	54	Female	Caucasian	Multiple Myeloma	2009	Untreated	IgA	Lambda	4.6	7.2	283	6.1	0.1	0.84	2.46	0.34146341	1.2	9.6	111	3.4	No	Not applicable	Skeletal survey	H-MM	52	D1	LB
MMRC0439	71	Male	Caucasian	Multiple Myeloma	2009	Untreated	IgG	Lambda	3.1	13.8	184	3.8	0.3	0.22	27.3	0.00805861	1.1	8.8	125	3.5	No	Not applicable	Skeletal survey	H-MM	52	D2	MY
MMRC0440	42	Female	Caucasian	Multiple Myeloma	2006	Treated	IgG	Kappa	5.39	9.3	179	5.1	Not available	1725	3.6	479.166667	1.03	9.2	Not available	2.4	Yes	Skeletal survey	Not applicable	H-MM	52	D1+D2	PR
MMRC0441	48	Male	Caucasian	Multiple Myeloma	1999	Treated	IgG	Lambda	0.19	9.8	33	Not available	Not available	0.12	46.8	0.0025641	1.52	10.3	778	3.2	Yes	Skeletal survey/MRI	Not applicable	NH-MM	45	None	PR
MMRC0444	58	Male	Caucasian	Multiple Myeloma	2008	Untreated	Not available	Kappa	4.22	11.8	106	2.7	Not available	618.3	1.3	475.615385	0.9	9.3	395	4.1	No	Not applicable	Skeletal survey	NH-MM	46	11q13	CD2
MMRC0445	60	Male	Caucasian	Multiple Myeloma	2006	Treated	IgG	Kappa	4.8	8.5	43	17.1	Not available	73.6	0.22	334.545455	1.19	9.6	1368	3	Not available	Not applicable	Not applicable	H-MM	53	D1+D2	PR

Supplementary Table S3. Cytoband information for the most frequent regions (>20%) of loss and gain in hypodiploid MM. CN: copy-number.

Region	Region Length (bp)	Cytoband Location	Event	Genes	miRNAs	Frequency (%)	Count of Gene Symbols	Gene Symbols	Count of miRNAs	miRNAs
chr1:109,526,340-109,779,079	252739	p13.3	CN Loss	7	0	48.98	7	CELSR2, KIAA1324, MYBPHL, PSMA5, PSRC1, SARS, SORT1	0	
chr1:203,162,093-203,232,561	70468	q32.1	CN Gain	1	0	53.06	1	NFASC	0	
chr4:9,213,266-9,683,867	470601	p16.1	CN Loss	2	0	24.49	2	DRD5, SLC2A9	0	
chr4:83,947,247-84,083,273	136026	q21.22	CN Loss	4	0	24.49	4	LIN54, SEC31A, THAP9, THAP9-AS1	0	
chr6:7,550,799-9,517,469	1966670	p24.3	CN Gain	12	0	20.41	12	BLOC1S5, BLOC1S5-TXNDC5, BMP6, EEF1E1, EEF1E1-MUTED, HULC, LOC100506207, PIP5K1P1, SCARNA27, SLC35B3, SNRNP48, TXNDC5	0	
chr6:137,239,149-137,334,100	94951	q23.3	CN Loss	2	0	32.65	2	PEX7, SLC35D3	0	
chr8:10,665,554-10,818,524	152970	p23.1	CN Loss	3	1	32.65	3	MIR1322, PINX1, XKR6	1	hsa-mir-1322
chr9:115,918,415-116,076,063	157648	q32	CN Gain	2	1	24.49	2	COL27A1, MIR455	1	hsa-mir-455
chr10:7,332,420-7,381,782	49362	p14	CN Loss	1	0	24.49	1	SFMBT2	0	
chr11:125,929,546-128,048,091	2118545	q24.2 - q24.3	CN Gain	5	0	20.41	5	ETS1, KIRREL3, KIRREL3-AS2, KIRREL3-AS3, MIR3167	0	
chr12:29,536,323-29,632,916	96593	p11.22	CN Loss	2	0	20.41	2	OVCH1, TMTC1	0	
chr12:124,294,832-124,427,420	132588	q24.31	CN Loss	1	0	26.53	1	TMEM132B	0	
chr14:68,712,658-68,789,383	76725	q24.1	CN Loss	1	0	71.43	1	EXD2	0	
chr16:2,159,232-2,179,089	19857	p13.3	CN Loss	2	0	30.61	2	CASKIN1, TRAF7	0	

chr16:84,169,279-84,253,444	84165	q24.1	CN Loss	1	0	46.94	1	GSE1	0
chr17:7,701,260-7,771,326	70066	p13.1	CN Loss	6	0	24.49	6	CHD3, CYB5D1, KCNAB3, LOC284023, LSMD1, SCARNA21	0
chr19:9,347,917-9,464,161	116244	p13.2	CN Gain	4	0	26.53	4	ZNF177, ZNF266, ZNF559-ZNF177, ZNF560	0

Supplementary Table S4A. List of differentially expressed genes (>2 fold) comparing ploidy groups. All patients (untreated and treated) are included in the analysis. H-MM: hyperdiploid multiple myeloma; hypodiploid MM; NH-MM: non-hyperdiploid multiple myeloma excluding hypodiploid MM.

Absolute Fold Change H-MM vs Hypodiploid	Regulation	Gene Symbol List #1	Absolute Fold Change H-MM vs NH-MM	Regulation	Gene Symbol List #2	Regulation	Genes from List #1 found in List #2	Absolute Fold change NH-MM vs Hypodiploid	Regulation	Gene Symbol
4.2865275	up	SULF2	10.7169998	up	SULF2	up	SULF2	3.15603415	up	RGS13
3.97504457	up	EDNRB	8.051198	up	C20orf103	up	C20orf103	2.6685157	up	CCND1
3.7402577	up	ELOVL7	5.28408	up	ELOVL7	up	ELOVL7	2.64855373	up	MS4A1
3.4331036	up	KIT	4.4209347	up	BTBD3	up	BTBD3	2.5786445	up	PHLDA1
3.2841845	up	C20orf103	3.6657887	up	KCNS3	up	KCNS3	2.4852283	up	SLC8A1
3.21566957	up	TNFSF10	3.4966884	up	MEIS2	up	MEIS2	2.48468435	up	KCNMB2
2.985325	up	CHSY3	3.4613233	up	COL4A5	up	COL4A5	2.3301468	up	FERMT2
2.951478	up	FRZB	3.14880565	up	NCAM1	up	NCAM1	2.2214367	up	LPAR6
2.9354453	up	DKK1	3.0892851	up	EFEMP1	up	EFEMP1	2.1598148	up	ALOX5AP
2.7945702	up	ATP10B	3.0554025	up	ISL2	up	ISL2	2.09729295	up	LAPTM5
2.7159085	up	ISL2	2.9406377	up	SLAMF1	up	SLAMF1	2.0743825	up	FGD4
2.699904	up	IFI27	2.8735113	up	DKK1	up	DKK1	2.0606165	up	VPREB3
2.5723937	up	SLAMF1	2.83540313	up	EDNRB	up	EDNRB	2.0164328	up	ANK3
2.5227783	up	EFEMP1	2.7482245	up	HIST1H2AC	up	PIK3R3	2.0074186	up	CCL3
2.43937085	up	NCAM1	2.7065172	up	PIK3R3	up	GBA3	2.0032709	up	CXCL12
2.4331262	up	HOMER1	2.70479325	up	GBA3	up	TNFSF10	2.9961271	down	UCHL1
2.3607042	up	DUSP4	2.6813169	up	BTLA	up	KIT	2.6886256	down	CCND2
2.32338373	up	LSAMP	2.66179975	up	DLC1	up	AREG	2.4796239	down	SULF2
2.30034	up	HGF	2.65909187	up	TNFSF10	up	ATP10B	2.451506	down	C20orf103
2.2998998	up	C11orf96	2.5514932	up	RPL35A	up	DUSP4	2.3298788	down	KLHL14
2.2803265	up	RSAD2	2.522679	up	KIT	up	SCYL2	2.18547685	down	XIST
2.272142	up	CMPK2	2.5008726	up	MATR3	up	HOMER1	2.1746008	down	TEAD1
2.25565075	up	GBA3	2.4962819	up	CSF2RB	up	CHSY3	2.1108446	down	BTBD3
2.2362578	up	CD1D	2.4943717	up	TMEM45A	up	LSAMP	2.098341	down	APP

Absolute Fold Change H-MM vs Hypodiploid	Regulation	Gene Symbol List #1	Absolute Fold Change H-MM vs NH-MM	Regulation	Gene Symbol List #2	Regulation	Genes from List #1 found in List #2	Absolute Fold change NH-MM vs Hypodiploid	Regulation	Gene Symbol
2.2070494	up	KCNS3	2.4895275	up	RAPGEF4	up	HGF	2.0363476	down	FGFR3
2.181435	up	PCDH9	2.4675333	up	AREG	up	HIST1H2AE			
2.163352	up	PIK3R3	2.459613	up	RELN	down	MS4A1			
2.151591	up	MFAP3L	2.459447	up	TEAD1	down	CTHRC1			
2.1403291	up	SCYL2	2.4018996	up	ATP10B	down	SLC40A1			
2.1358198	up	TCF4	2.3830395	up	CCDC85A	down	CD99			
2.09727225	up	HIST1H2AE	2.3778881	up	DUSP4	down	MYADM			
2.0943916	up	BTBD3	2.3774562	up	SERPINI1	down	DEK			
2.0911427	up	MEIS2	2.3555975	up	CTGF	down	CYBB			
2.0900524	up	COL4A5	2.3530335	up	COL4A6	down	GSTA4			
2.0713713	up	AREG	2.3207145	up	PTCH1	down	MARCKS			
2.0176997	up	FUT8	2.3191419	up	SLC47A1	down	ADAM28			
2.0086248	up	EPHB1	2.2961385	up	CYP2J2	down	FAM59A			
3.104516	down	S100A4	2.2731627	up	FAM101B	down	PARM1			
3.0635245	down	CTHRC1	2.2629728	up	CDK6	down	CHPT1			
2.8513031	down	CCND2	2.2241602	up	CKS2	down	S100A4			
2.6030746	down	CD99	2.2187657	up	CD200	down	CD81			
2.5456152	down	MYADM	2.21285903	up	SCYL2	down	MIR21			
2.495072	down	WHSC1	2.193868	up	HOMER1	down	TMX4			
2.3559666	down	FGFR3	2.1794877	up	DMRT2	down	PMAIP1			
2.3511474	down	CSDA	2.1649413	up	ID3	down	ZBTB8A			
2.3440972	down	XIST	2.1624149	up	RPL37	down	FAM129A			
2.3168335	down	FAM171B	2.1621146	up	MAGEA3	down	CDKN1C			
2.3100643	down	CRIP1	2.1608565	up	TRAT1	down	TUBA1A			
2.2661436	down	TUBA1A	2.1594791	up	SORD	down	DOCK11			
2.2645333	down	PMAIP1	2.1456108	up	CHSY3					
2.254607	down	C16orf54	2.1373813	up	MAGEC1					
2.2365017	down	MS4A1	2.1308532	up	LSAMP					

Absolute Fold Change H-MM vs Hypodiploid	Regulation	Gene Symbol List #1	Absolute Fold Change H-MM vs NH-MM	Regulation	Gene Symbol List #2	Regulation	Genes from List #1 found in List #2	Absolute Fold change NH-MM vs Hypodiploid	Regulation	Gene Symbol
2.23515595	down	FAM129A	2.1276348	up	MAGEA6					
2.2133589	down	CYBB	2.1224856	up	HK2					
2.2065272	down	MIR21	2.116767	up	TMEM108					
2.194763	down	ZBTB8A	2.1090975	up	RUNX2					
2.1905901	down	S100A6	2.0920303	up	HGF					
2.1725798	down	FAM59A	2.0840614	up	UCHL1					
2.1384022	down	MARCKS	2.0712981	up	AMIGO2					
2.1326687	down	DOCK11	2.0586164	up	CD300A					
2.1263876	down	CD81	2.0494547	up	HIST1H2AE					
2.1235615	down	TMX4	2.04525	up	XRCC4					
2.1222627	down	DEK	2.0408263	up	RAPGEF5					
2.1058807	down	NANOS1	2.0388792	up	KLHL14					
2.0911481	down	CHPT1	2.038801	up	KIAA1217					
2.0831177	down	ARL4C	2.029928	up	CMAH					
2.081713	down	NFIC	2.0036814	up	TSPAN7					
2.05691	down	S100A10	4.71756623	down	MS4A1					
2.0538456	down	SLC40A1	3.6166723	down	CTHRC1					
2.0520182	down	PARM1	3.4650433	down	LAPTM5					
2.0375338	down	CDKN1C	3.3572392	down	SLC40A1					
2.0370557	down	MIR155HG	3.25071334	down	SLC8A1					
2.019967	down	TCEA3	3.23588995	down	CCND1					
2.0057983	down	CST3	3.033253	down	CD99					
2.0041583	down	GSTA4	2.8885415	down	CD28					
2.0002267	down	ADAM28	2.829579	down	MYADM					
			2.8155222	down	DEK					
			2.8084178	down	TMSB4X					
			2.6659551	down	CYBB					
			2.6394722	down	VPREB3					

Absolute Fold Change H-MM vs Hypodiploid	Regulation	Gene Symbol List #1	Absolute Fold Change H-MM vs NH-MM	Regulation	Gene Symbol List #2	Regulation	Genes from List #1 found in List #2	Absolute Fold change NH-MM vs Hypodiploid	Regulation	Gene Symbol
			2.6120038	down	SNX9					
			2.5825458	down	GSTA4					
			2.5326904	down	FGD4					
			2.52322928	down	MARCKS					
			2.5205529	down	ALOX5AP					
			2.5181847	down	CCL3					
			2.489814	down	ADAM28					
			2.48289	down	DEPDC6					
			2.4780946	down	LPAR6					
			2.465891	down	FAM107B					
			2.463702	down	KCNMB2					
			2.4494624	down	RND3					
			2.4433997	down	FAM59A					
			2.4410737	down	NACC2					
			2.43732425	down	RAPH1					
			2.4277265	down	PARM1					
			2.4052553	down	RGS13					
			2.403402	down	CHPT1					
			2.4017472	down	S100A4					
			2.396284	down	CD81					
			2.3960552	down	DPYSL2					
			2.3523478	down	RNASE4					
			2.342687	down	MIR21					
			2.3402903	down	SYNE2					
			2.34002425	down	TMX4					
			2.3280041	down	CNN3					
			2.3249385	down	C20orf112					
			2.3019059	down	IRS2					

Absolute Fold Change H-MM vs Hypodiploid	Regulation	Gene Symbol List #1	Absolute Fold Change H-MM vs NH-MM	Regulation	Gene Symbol List #2	Regulation	Genes from List #1 found in List #2	Absolute Fold change NH-MM vs Hypodiploid	Regulation	Gene Symbol
			2.299664	down	.OC100506966					
			2.28989375	down	FCRL2					
			2.26937685	down	PHLDA1					
			2.267298	down	ACSL1					
			2.2641594	down	MAGED4					
			2.2641363	down	CX3CR1					
			2.26273925	down	FCER2					
			2.2622437	down	MTSS1					
			2.2547321	down	LCP1					
			2.2545323	down	ANG					
			2.252353	down	LRRK2					
			2.2513556	down	CLEC7A					
			2.24427075	down	PMAIP1					
			2.23186945	down	CLEC2D					
			2.224255	down	FHL1					
			2.2145998	down	FAS					
			2.1680305	down	ZBTB8A					
			2.1648962	down	HSPA1A					
			2.1619651	down	CSGALNACT1					
			2.1547794	down	FAM129A					
			2.13943465	down	RRAS2					
			2.1300855	down	HGSNAT					
			2.1268094	down	TMC6					
			2.1178384	down	LGMN					
			2.1170747	down	TIAM1					
			2.1139648	down	GPR126					
			2.111033	down	P2RX1					
			2.1101463	down	FERMT2					

Absolute Fold Change H-MM vs Hypodiploid	Regulation	Gene Symbol List #1	Absolute Fold Change H-MM vs NH-MM	Regulation	Gene Symbol List #2	Regulation	Genes from List #1 found in List #2	Absolute Fold change NH-MM vs Hypodiploid	Regulation	Gene Symbol
			2.1035142	down	ARHGEF40					
			2.097595	down	CDKN1C					
			2.0895984	down	LRP11					
			2.086538	down	PDGFC					
			2.0829113	down	TUBA1A					
			2.0749907	down	OC100507192					
			2.0721712	down	TMEM220					
			2.0649478	down	DOCK11					
			2.0618219	down	COCH					
			2.0569305	down	APLP2					
			2.0541823	down	LPHN2					
			2.0466795	down	ITPKB					
			2.0432904	down	EHD3					
			2.0394733	down	ARAP2					
			2.0301065	down	XK					
			2.021484	down	MED31					
			2.0200353	down	KIAA0495					
			2.0123444	down	C1orf106					
			2.0055432	down	NT5DC2					

Supplementary Table S4B. List of differentially expressed genes (>2 fold) comparing ploidy groups. Only untreated patients are included in the analysis. H-MM: hyperdiploid multiple myeloma; hypodiploid MM; NH-MM: non-hyperdiploid multiple myeloma excluding hypodiploid MM.

Absolute fold change 63 Untreated H-MM vs 26 Untreated Hypodiploid	Regulation	Gene Symbol	Absolute fold change 63 Untreated H-MM vs 25 Untreated NH-MM	Regulation	Gene Symbol	Absolute fold change 25 Untreated NH-MM vs 26 Untreated Hypodiploid	Regulation	Gene Symbol
7.8374878	up	SULF2	10.169378	up	SULF2	4.3595878	up	CCND1
4.319835667	up	EDNRB	8.720821	up	C20orf103	3.62019585	up	KCNMB2
4.1136312	up	ELOVL7	5.8745008	up	ELOVL7	3.55405775	up	RGS13
3.511954	up	DKK1	4.212494	up	BTBD3	3.4184744	up	CCL3
3.337248	up	IFI27	3.79249235	up	NCAM1	3.1157353	up	ANK3
3.265120033	up	TNFSF10	3.68516	up	KCNS3	2.7731922	up	NLGN4X
3.18909465	up	DUSP4	3.6339543	up	AREG	2.7333944	up	IFIT3
3.1107252	up	HOMER1	3.450377033	up	SLAMF1	2.677898933	up	PHLDA1
3.08385	up	CHSY3	3.366394	up	MEIS2	2.6300112	up	RGS1
2.9923103	up	C20orf103	3.1654723	up	UCHL1	2.5123901	up	VPREB3
2.991168	up	AREG	3.1097639	up	EFEMP1	2.5120332	up	DLEU2
2.92650335	up	NCAM1	3.0135958	up	CDK6	2.4933512	up	LOC643733
2.9220684	up	EFEMP1	3.0061573	up	DLC1	2.4544547	up	CD1D
2.6993253	up	RGS13	2.9261923	up	CSF2RB	2.4474936	up	LPHN2
2.6929908	up	PCDH9	2.9135982	up	DUSP4	2.4316318	up	CCL4
2.6434198	up	LSAMP	2.852075867	up	TNFSF10	2.4018512	up	ETV1
2.62810575	up	GBA3	2.8266475	up	FAM101B	2.400507967	up	MS4A1
2.596066	up	CD1D	2.824747	up	MIAT	2.3265703	up	EDNRB
2.5443738	up	SLC47A1	2.777952533	up	HGF	2.3194156	up	HLA-DRA
2.5185776	up	CMPK2	2.7564039	up	GBA3	2.3087444	up	ALOX5AP
2.495253	up	MC4R	2.7443905	up	CTGF	2.2828162	up	SHISA2
2.4933388	up	ISL2	2.7259564	up	PIK3R3	2.2731876	up	LPAR6
2.4616082	up	RSAD2	2.6953673	up	KLHL14	2.1979084	up	PDZRN4
2.3982959	up	SCYL2	2.6471875	up	ISL2	2.193014	up	SORL1
2.3688924	up	ATP10B	2.624508	up	HIST1H2AC	2.1906009	up	DKK1
2.366648	up	IFIT3	2.6023364	up	SERPINI1	2.1604753	up	FCER2
2.3578149	up	FAM13A	2.580625	up	DMRT2	2.158585	up	STAP1
2.3496132	up	KIAA1217	2.578158	up	MAGEC1	2.156401	up	CTHRC1
2.31016205	up	SLAMF1	2.5769286	up	TMEM45A	2.155798	up	BASP1
2.3091137	up	KIT	2.562296	up	MFAP3L	2.1389075	up	LAPTM5
2.3040578	up	PTPRK	2.5323083	up	ITM2C	2.1072114	up	FAM116B
2.2885419	up	CD200	2.5121212	up	CKS2	2.106928167	up	SLC8A1
2.2838604	up	BTLA	2.4977279	up	RBM33	2.088709	up	GAS2
2.2700882	up	C11orf96	2.4814517	up	RELN	2.0726035	up	PTPRK
2.2541695	up	HIST1H2BC	2.457900167	up	SCYL2	2.0702202	up	PAX5
2.2468798	up	HIST1H2AE	2.4259858	up	RPL35A	2.0672903	up	HIST1H2BG
2.2409897	up	HIST1H2AC	2.403167	up	C6orf105	2.055593	up	SNX9
2.2280016	up	RELN	2.3867426	up	MAGI2	2.0541904	up	CD28
2.2221119	up	FRZB	2.3842654	up	C11orf96	2.0512025	up	CMPK2
2.2126427	up	DLC1	2.3841023	up	SLC47A1	2.0507348	up	BANK1
2.2052112	up	MORC1	2.38156165	up	COL4A6	2.050068	up	HEY2
2.1906226	up	PIK3R3	2.326133	up	C10orf10	2.0444646	up	CPVL
2.172171	up	OC10050697	2.3236282	up	CYP2J2	2.0421417	up	CLLU1
2.1453335	up	CTGF	2.3068001	up	RAPGEF4	2.0324483	up	CD69
2.1350782	up	KCNS3	2.2892406	up	PTCH1	2.0171297	up	CHSY3
2.1337342	up	NEB	2.238236	up	KIT	4.46258985	down	CCND2
2.115767	up	SHISA2	2.203504	up	TRAT1	3.2689817	down	BEX5
2.1129681	up	SOX4	2.1962926	up	CCDC85A	3.180017	down	C10orf10

Absolute fold change 63 Untreated H-MM vs 26 Untreated Hypodiploid	Regulation	Gene Symbol	Absolute fold change 63 Untreated H-MM vs 25 Untreated NH-MM	Regulation	Gene Symbol	Absolute fold change 25 Untreated NH-MM vs 26 Untreated Hypodiploid	Regulation	Gene Symbol
2.0788448	up	EPHB1	2.1955392	up	GNG11	2.922838917	down	XIST
2.070251	up	HIST1H2AD	2.18150915	up	IL6R	2.9144108	down	C20orf103
2.0333822	up	XAF1	2.1556356	up	ADM	2.8938076	down	UCHL1
2.029337	up	CCDC85A	2.1470397	up	CD300A	2.87586425	down	IL6R
2.0283742	up	TRAT1	2.13583735	up	XRCC4	2.6815517	down	CDK6
2.0206056	up	DMRT2	2.1356504	up	BTLA	2.6671499	down	ARL4C
2.0049467	up	PIP5K1B	2.1295364	up	IFNGR1	2.58426535	down	RHOB
2.0003886	up	HIST2H2AA3	2.1190097	up	RNF130	2.5425503	down	C6orf105
3.47302	down	RND3	2.1171181	up	ACVR1C	2.4731164	down	PLA2G16
3.1863086	down	CRIP1	2.1114328	up	EDNRB	2.4672585	down	KLHL14
3.175294	down	CSDA	2.103572	up	CDH2	2.4649584	down	ITM2C
3.113781933	down	CCND2	2.099623	up	TMEM108	2.424963	down	RASGRP1
3.1028583	down	C16orf54	2.0887098	up	FAM133A	2.422723	down	MIAT
2.987118867	down	MS4A1	2.082119	up	RPL37	2.4116187	down	BIRC3
2.8545027	down	S100A4	2.0753639	up	CCRL2	2.3917778	down	MEIS2
2.85285365	down	CYBB	2.0750518	up	AMIGO2	2.3809107	down	ITGB1
2.7499437	down	MIR21	2.0707386	up	TEAD1	2.2911768	down	CRNDE
2.7238517	down	TUBA1A	2.0680594	up	MGAT4C	2.277061	down	AHNAK
2.6465838	down	XIST	2.0653343	up	GADD45A	2.25978705	down	C4A
2.6446881	down	MIR155HG	2.0643747	up	MCC	2.2426887	down	RGS10
2.5726948	down	FAM171B	2.0589092	up	IQGAP2	2.2373645	down	CST6
2.5556912	down	DOCK11	2.0560253	up	IL5RA	2.2022467	down	RARRES3
2.5493739	down	CD99	2.0533595	up	INSIG1	2.193525	down	MGAT4A
2.5446892	down	ADAM28	2.052968	up	ZNF91	2.1598351	down	FAM101B
2.4862995	down	NFIC	2.0494304	up	MATR3	2.1479645	down	RRAGD
2.439416	down	FAM59A	2.037319	up	GATM	2.1420588	down	BTBD3
2.36767445	down	CDKN1C	2.0280468	up	GLRX	2.1355603	down	HGF
2.3584964	down	OC10050719	2.022483	up	SVIL	2.1088612	down	NFIA
2.3547568	down	CD81	2.0033107	up	CHST2	2.0783567	down	SRD5A3
2.3528686	down	CD86	6.095937375	down	MS4A1	2.075455	down	CSF2RB
2.298506867	down	RRAS2	5.1189055	down	CCL3	2.059146	down	RPL35A
2.27729975	down	AHNAK	4.16168715	down	CCND1	2.0546982	down	GNAL
2.2658095	down	BEX5	3.7082303	down	SLC40A1	2.0429704	down	RNF130
2.2556746	down	TMX4	3.6133518	down	CTHRC1	2.009547	down	CLIC2
2.2501767	down	ITGB1	3.6002066	down	LAPTM5			
2.2413096	down	CD52	3.4831972	down	CD99			
2.23916825	down	COCH	3.456961475	down	SLC8A1			
2.2242734	down	FMNL2	3.3217118	down	TMSB4X			
2.2178838	down	PARM1	3.08442355	down	KCNMB2			
2.1795208	down	XK	2.99745985	down	CYBB			
2.1777618	down	GALNT1	2.9667659	down	CD28			
2.1597404	down	C1orf106	2.92058135	down	FCRL2			
2.1400235	down	PKP2	2.8319125	down	XK			
2.139887	down	MYADM	2.808313	down	FGD4			
2.0770884	down	RNASE6	2.7689133	down	VPREB3			
2.0765324	down	WHSC1	2.7599619	down	PMAIP1			
2.0649862	down	PMAIP1	2.7258373	down	TMX4			
2.057488	down	CST6	2.6669958	down	ALOX5AP			
2.0542943	down	HSPB1	2.6493802	down	FHL1			
2.053293	down	SLC40A1	2.63879455	down	PHLDA1			
2.0511706	down	S100A10	2.6020594	down	LPAR6			

Absolute fold change 63 Untreated H-MM vs 26 Untreated Hypodiploid	Regulation	Gene Symbol	Absolute fold change 63 Untreated H-MM vs 25 Untreated NH-MM	Regulation	Gene Symbol	Absolute fold change 25 Untreated NH-MM vs 26 Untreated Hypodiploid	Regulation	Gene Symbol
2.0425573	down	FCRL2	2.577518	down	ADAM28			
2.0419686	down	TMEM49	2.5771157	down	SNX9			
2.0408747	down	ZBTB8A	2.5308566	down	MAGED4			
2.033971	down	GSTA4	2.52829	down	PARM1			
2.031488	down	MOCOS	2.4748096	down	PDGFC			
2.027112	down	SLC25A37	2.4575987	down	MAN1C1			
2.0160239	down	SSR1	2.4562442	down	CD81			
2.0113816	down	HOOK1	2.4467309	down	TMC6			
2.0034297	down	TAGLN2	2.4297626	down	SORL1			
2.003061	down	TUBB6	2.41874385	down	RGS1			
2.0020885	down	RHOB	2.4147203	down	LPHN2			
			2.37562565	down	HOOK1			
			2.3666925	down	NT5DC2			
			2.35556	down	CCL4			
			2.3475441	down	SORT1			
			2.3471334	down	LRRK2			
			2.3291678	down	RAPH1			
			2.315784	down	ATP11A			
			2.3098924	down	MXRA7			
			2.3039975	down	ZBTB8A			
			2.28896045	down	FCER2			
			2.2825193	down	DEK			
			2.2311313	down	S100A4			
			2.2272058	down	ITPKB			
			2.2174	down	FAM59A			
			2.2169998	down	MARCKS			
			2.2016704	down	DLEU2			
			2.1953537	down	PTPRC			
			2.191500567	down	RRAS2			
			2.18622	down	CSDA			
			2.177615	down	IRS2			
			2.1756883	down	OC100506130			
			2.1459987	down	CSGALNACT1			
			2.1416297	down	COL24A1			
			2.1275525	down	MIR155HG			
			2.1237047	down	MYADM			
			2.1233642	down	LGMN			
			2.10005	down	ARHGEF40			
			2.0994406	down	BTG1			
			2.0990825	down	GSTA4			
			2.0976927	down	P2RX1			
			2.0948036	down	C20orf112			
			2.093207	down	CHPT1			
			2.089211	down	TIAM1			
			2.0853436	down	DDAH1			
			2.0835571	down	RND3			
			2.0741131	down	C4orf31			
			2.066177	down	SYNE2			
			2.06118625	down	FAIM3			
			2.0494506	down	TRAF5			
			2.0396674	down	SPP1			

Absolute fold change 63 Untreated H-MM vs 26 Untreated Hypodiploid	Regulation	Gene Symbol	Absolute fold change 63 Untreated H-MM vs 25 Untreated NH-MM	Regulation	Gene Symbol	Absolute fold change 25 Untreated NH-MM vs 26 Untreated Hypodiploid	Regulation	Gene Symbol
			2.03624275	down	CAMK2D			
			2.0180802	down	CLLU1			
			2.0165777	down	ACSL1			
			2.0118504	down	C1orf106			
			2.0113883	down	CD27			
			2.0030227	down	FAS			

Supplementary Table S4C. List of differentially expressed genes (>2 fold) comparing ploidy groups. Only treated patients are included in the analysis. H-MM: hyperdiploid multiple myeloma; hypodiploid MM; NH-MM: non-hyperdiploid multiple myeloma excluding hypodiploid MM.

Absolute fold change 62 Treated H-MM vs 23 Treated Hypodiploid	Regulation	Gene Symbol	Absolute fold change 62 Treated H-MM vs 25 Treated NH-MM	Regulation	Gene Symbol	Absolute fold change 25 Treated NH-MM vs 23 Treated Hypodiploid	Regulation	Gene Symbol
5.301402	up	KIT	11.29930525	up	SULF2	4.011272	up	RND3
3.5642896	up	EDNRB	7.4587674	up	C20orf103	3.1951556	up	NACC2
3.5600693	up	C20orf103	5.1578207	up	DKK1	3.0418031	up	MS4A1
3.3880166	up	FRZB	4.7554827	up	ELOVL7	3.0239866	up	NIPAL2
3.3647866	up	COL4A5	4.645975	up	BTBD3	3.016783	up	DEPDC6
3.346345	up	ELOVL7	4.529856	up	COL4A5	2.974732	up	BAMBI
3.3240874	up	ATP10B	4.316355633	up	EDNRB	2.8412814	up	MFAP3L
3.188113	up	MEIS2	3.6454213	up	KCNS3	2.8014125	up	FERMT2
3.1768283	up	TNFSF10	3.6452816	up	MEIS2	2.7564628	up	CXCL12
2.9755263	up	ISL2	3.5292444	up	ISL2	2.7269101	up	ABCA1
2.9249209	up	HGF	3.369561	up	BTLA	2.7164248	up	RGS13
2.8632004	up	CHSY3	3.3048418	up	ATP10B	2.6707659	up	TJP1
2.6558576	up	SLAMF1	3.136067	up	SCN3A	2.6624204	up	SLC8A1
2.6316085	up	COL4A6	3.0617917	up	EFEMP1	2.5945458	up	PPBP
2.5284045	up	LSAMP	3.0615022	up	MATR3	2.5670047	up	SLC7A7
2.5173643	up	SCN3A	3.0514393	up	RUNX2	2.536858	up	SEPP1
2.471796	up	MFAP3L	3.0369947	up	GTSF1	2.4682298	up	HGF
2.4633446	up	C6orf142	3.013368	up	CHSY3	2.4588985	up	NCKAP1
2.4601066	up	RAPGEF4	2.926221	up	TEAD1	2.4523723	up	CX3CR1
2.4451149	up	MAGEA3	2.9025283	up	HIST1H2AE	2.4456306	up	LOC100506966
2.3965703	up	TCF4	2.8777332	up	HIST1H2AC	2.388867	up	PLEKHF2
2.3724144	up	DKK1	2.8714776	up	HOMER1	2.373372	up	CD52
2.3707275	up	MAGEC1	2.853284	up	HK2	2.3618218	up	NTRK2
2.362053	up	C11orf96	2.8488228	up	KIT	2.360655	up	MTSS1
2.3000724	up	TMEM45A	2.779974	up	SORD	2.3555095	up	SAMSN1
2.2962873	up	KCNS3	2.7522752	up	DUSP2	2.3356607	up	LGMN
2.2951112	up	FUT8	2.6930299	up	PIK3R3	2.3183486	up	WNT5A
2.287156	up	TRIM22	2.690662	up	RAPGEF4	2.281848	up	DPYSL2
2.2355707	up	MAGEA6	2.6862051	up	RPL35A	2.2790003	up	FGD4
2.2347808	up	PARP9	2.6791449	up	KIAA1217	2.252793	up	CDH1
2.2278028	up	ADM	2.64715315	up	GBA3	2.250361	up	RCBTB2
2.2274272	up	BTBD3	2.6285737	up	COL4A6	2.2246708	up	FAM107B
2.2073274	up	NCAM1	2.619446	up	ID3	2.206767	up	STS
2.2068546	up	HBD	2.61806825	up	NCAM1	2.1978157	up	FAR2
2.1724	up	ABCA1	2.616146	up	CCR10	2.173313	up	EHD3
2.1723456	up	EFEMP1	2.580133	up	CCDC85A	2.159612	up	RNASE4
2.1650082	up	SULF2	2.5632535	up	CD200	2.157658	up	GPR126
2.161543	up	DDX58	2.484786867	up	TNFSF10	2.147939	up	CD52
2.126363	up	AMIGO2	2.4609212	up	LSAMP	2.1281412	up	CCR1
2.11804	up	CCRL2	2.437368	up	RELN	2.124255	up	LPAR6
2.1021373	up	RPL35A	2.436027	up	MAGEA3	2.1092539	up	MAF
2.100463	up	PIK3R3	2.4232612	up	CD1D	2.1040134	up	CNN3
2.0998201	up	ADAMTS15	2.4212365	up	MAGEA6	2.1035845	up	CSGALNACT1

Absolute fold change 62 Treated H-MM vs 23 Treated Hypodiploid	Regulation	Gene Symbol	Absolute fold change 62 Treated H-MM vs 25 Treated NH-MM	Regulation	Gene Symbol	Absolute fold change 25 Treated NH-MM vs 23 Treated Hypodiploid	Regulation	Gene Symbol
2.0886497	up	STAP1	2.415139	up	TMEM45A	2.0979695	up	SSTR1
2.0858717	up	OSBPL10	2.4027755	up	CD48	2.0867125	up	COBLL1
2.0788004	up	IFI27	2.39555	up	TSPAN7	2.0850272	up	SPINT2
2.077558	up	TSC22D1	2.3950987	up	RAPGEF5	2.0845132	up	C4orf31
2.0717688	up	BBOX1	2.37407315	up	PTPRG	2.0805333	up	PHLDA1
2.0594294	up	RSAD2	2.364712	up	FRZB	2.0782427	up	HBB
2.055078	up	DTX3L	2.3640365	up	DLC1	2.0741217	up	FRMD4B
2.0511374	up	MCC	2.3572571	up	PTCH1	2.0598001	up	HBA1
2.0370967	up	TBCEL	2.3526473	up	FSTL5	2.0593243	up	ADAM28
2.0221114	up	KIAA0125	2.3498769	up	GAS5	2.0589683	up	GCH1
2.0203788	up	MAB21L1	2.3475134	up	STAP1	2.0564282	up	FAM70A
2.0171857	up	C11orf93	2.3444376	up	MOXD1	2.054275	up	GPM6B
2.0141098	up	RPL13A	2.3276613	up	KIAA0125	2.0484784	up	CNTN1
2.0095868	up	GBA3	2.317981029	up	CD44	2.0441153	up	ANG
2.008963	up	CMPK2	2.2802936	up	RSAD2	2.0368006	up	SYNE2
2.002053	up	DAPK1	2.265536	up	CYP2J2	2.025979	up	VLDLR
5.927557	down	CTHRC1	2.2640495	up	HMGA1	2.0232077	up	LAPTM5
3.573488	down	FGFR3	2.2532317	up	CMAH	2.0173497	up	FAS
3.440337	down	S100A4	2.2467791	up	RPL37	2.0136998	up	C14orf106
3.047586	down	MYADM	2.2460074	up	SLC47A1	2.0136273	up	NFIA
2.9937644	down	SERPINE2	2.22407995	up	HIST1H2AD	2.0122812	up	MANSC1
2.9806788	down	WHSC1	2.2218914	up	ADAMTS15	2.0037231	up	ALOX5AP
2.8595383	down	FAM129A	2.218128	up	HIST2H2AA3	5.1896332	down	SULF2
2.8342693	down	S100A6	2.18318605	up	SLAMF1	3.738415	down	APP
2.7794838	down	PMAIP1	2.182227	up	DAPK1	3.608263	down	SERPINE2
2.6763744	down	CD99	2.1729898	up	SERPINI1	3.207351	down	UCHL1
2.6313505	down	PEG10	2.1684679	up	GLIS3	3.1382437	down	TEAD1
2.5627016	down	CCND2	2.162482	up	SCYL2	2.7091646	down	CCR10
2.522483	down	NANOS1	2.15153606	up	TCF4	2.6309031	down	PTPRG
2.4620805	down	MARCKS	2.150691	up	LAG3	2.5839572	down	FGFR3
2.4004479	down	MAP1B	2.144843	up	CMPK2	2.4800947	down	CD48
2.3943129	down	ZBTB8A	2.1361594	up	MORC1	2.473907	down	HIST1H2AM
2.3857043	down	ARMCX1	2.132704	up	IGJ	2.459012	down	NANOS1
2.3789	down	DEFA1	2.1294355	up	BBOX1	2.4010203	down	SLC47A1
2.366166	down	DEK	2.1288912	up	TMEM108	2.3000091	down	MGST1
2.3449962	down	UCHL1	2.1277585	up	CSF2RB	2.2972445	down	GTSF1
2.3098948	down	CHPT1	2.1165745	up	TRAT1	2.2866995	down	CRIM1
2.2982767	down	TCEA3	2.10944285	up	RORA	2.2584882	down	DUSP2
2.2938523	down	NT5DC2	2.104921	up	LYSMD2	2.2500182	down	WHSC1
2.2663374	down	APP	2.10092895	up	HIST1H2BG	2.23344	down	BTLA
2.2636416	down	TMX4	2.0975347	up	HIST1H4B	2.2073114	down	RUNX2
2.2516952	down	TRAF5	2.0809584	up	WDR72	2.183483	down	PPOX
2.2275267	down	CLGN	2.080695	up	RASA4	2.1758645	down	KLHL14
2.2076995	down	LGALS1	2.0723479	up	SLC16A14	2.174081	down	DKK1
2.2021933	down	DSEL	2.0648448	up	AMIGO2	2.158257	down	HIST1H4B
2.1991308	down	PTGER4	2.0574079	up	SNORA68	2.1004102	down	HIST1H2AL

Absolute fold change 62 Treated H-MM vs 23 Treated Hypodiploid	Regulation	Gene Symbol	Absolute fold change 62 Treated H-MM vs 25 Treated NH-MM	Regulation	Gene Symbol	Absolute fold change 25 Treated NH-MM vs 23 Treated Hypodiploid	Regulation	Gene Symbol
2.172375	down	MAGED4	2.0534132	up	GYG1	2.0951185	down	C20orf103
2.1616116	down	TIMP1	2.0473816	up	ID1	2.0900123	down	PEG10
2.1599452	down	C12orf75	2.0462594	up	NDN	2.0858033	down	BTBD3
2.1588404	down	CST3	2.0408182	up	HIST1H2BC	2.0789387	down	HIST2H2AA3
2.1460783	down	NRIP1	2.0403945	up	HBE1	2.0424	down	HIST2H4A
2.141075	down	SGCE	2.0393047	up	ELOVL4	2.0423903	down	HK2
2.1373303	down	ARL4C	2.0361302	up	PTPRK	2.0224657	down	SGCE
2.12624	down	ZNF238	2.035053	up	NCRNA00219	2.0180266	down	CD200
2.1153507	down	NGFRAP1	2.0313098	up	DUSP4			
2.0776472	down	CA2	2.0279284	up	SNHG7			
2.0759559	down	FAM171B	2.0148103	up	CTGF			
2.0738416	down	SLC40A1	2.0104558	up	RALYL			
2.0583532	down	IL8	2.0096865	up	C6orf48			
2.0530481	down	C10orf58	2.0054152	up	C1orf43			
2.0523412	down	CRIM1	2.0000515	up	NPM1			
2.0461214	down	LOC730101	3.7787614	down	MYADM			
2.0410542	down	S100A10	3.6910343	down	MS4A1			
2.0383844	down	SCCPDH	3.6312506	down	CTHRC1			
2.0257137	down	PHACTR1	3.5162913	down	RNASE4			
2.0112958	down	ADAMTS1	3.4619765	down	DEK			
			3.4471743	down	NACC2			
			3.3844101	down	DEPDC6			
			3.33960045	down	FAM107B			
			3.32413695	down	LAPTM5			
			3.29491256	down	SLC8A1			
			3.2696764	down	CX3CR1			
			3.24297	down	DPYSL2			
			3.1091967	down	CCND1			
			3.0810492	down	OC100506966			
			3.0739899	down	MIR21			
			3.0354424	down	SLC40A1			
			3.0283484	down	ANG			
			2.99981904	down	MARCKS			
			2.876248	down	RND3			
			2.8394358	down	HSPA1A			
			2.8367782	down	BAMBI			
			2.8213649	down	CLEC2D			
			2.8086526	down	CD28			
			2.8080237	down	CNN3			
			2.7940528	down	RAPH1			
			2.77867115	down	FGD4			
			2.7738608	down	ADAM28			
			2.7606962	down	CHPT1			
			2.75373115	down	RGS13			
			2.7441237	down	MTSS1			
			2.73921535	down	FAM129A			

Absolute fold change 62 Treated H-MM vs 23 Treated Hypodiploid	Regulation	Gene Symbol	Absolute fold change 62 Treated H-MM vs 25 Treated NH-MM	Regulation	Gene Symbol	Absolute fold change 25 Treated NH-MM vs 23 Treated Hypodiploid	Regulation	Gene Symbol
			2.713625	down	LCP1			
			2.69045875	down	GSTA4			
			2.6821961	down	DOCK11			
			2.6482934	down	SNX9			
			2.6398623	down	CD99			
			2.6186185	down	SYNM			
			2.6089585	down	FERMT2			
			2.60588505	down	COCH			
			2.5934167	down	LY96			
			2.584062633	down	CCND2			
			2.5825603	down	S100A4			
			2.5808342	down	C20orf112			
			2.568051	down	OC100507192			
			2.55778395	down	CD52			
			2.5237489	down	EHD3			
			2.5212796	down	VPREB3			
			2.49298375	down	SYNE2			
			2.47875235	down	CLEC7A			
			2.458626	down	GPR126			
			2.4532785	down	TMEM220			
			2.4353266	down	C12orf55			
			2.42273545	down	FAM59A			
			2.4013884	down	MED31			
			2.38165375	down	FGL2			
			2.3800797	down	ALOX5AP			
			2.3766227	down	SLC7A7			
			2.3682935	down	TMSB4X			
			2.36764565	down	CYBB			
			2.3565981	down	PPBP			
			2.3536572	down	BNIP3			
			2.3527334	down	LPAR6			
			2.34889245	down	ACSL1			
			2.3487878	down	CDKN1C			
			2.3366568	down	CD81			
			2.3331246	down	PARM1			
			2.3126616	down	WEE1			
			2.3028078	down	FAM171B			
			2.301776	down	VAV2			
			2.290693	down	ASS1			
			2.2828422	down	HGSNAT			
			2.2788514	down	CDC14B			
			2.273884	down	SDCBP			
			2.273875	down	WSB2			
			2.272564	down	TUBA1A			
			2.2712004	down	EIF2C4			
			2.2507463	down	ITGB7			

Absolute fold change 62 Treated H-MM vs 23 Treated Hypodiploid	Regulation	Gene Symbol	Absolute fold change 62 Treated H-MM vs 25 Treated NH-MM	Regulation	Gene Symbol	Absolute fold change 25 Treated NH-MM vs 23 Treated Hypodiploid	Regulation	Gene Symbol
			2.2469869	down	LRP11			
			2.2468204	down	S100A12			
			2.24220955	down	FCER2			
			2.2396903	down	FAS			
			2.235869233	down	APLP2			
			2.23559765	down	IRS2			
			2.2353092	down	MAF			
			2.2347581	down	KLF6			
			2.2307065	down	B4GALT1			
			2.229399	down	ZCCHC2			
			2.2195969	down	PHLDA1			
			2.2179942	down	COTL1			
			2.2156124	down	RAB39B			
			2.2091053	down	KIAA0495			
			2.2076192	down	APOBEC3B			
			2.2068613	down	ARAP2			
			2.200987	down	NIPAL2			
			2.1980538	down	SLC16A3			
			2.1957707	down	HBA1			
			2.1891677	down	DEFA1			
			2.1870294	down	NES			
			2.1856816	down	RNASE6			
			2.1813436	down	CSGALNACT1			
			2.1652455	down	LAT2			
			2.163164	down	LRRK2			
			2.1612258	down	ST3GAL1			
			2.1553862	down	CDH1			
			2.1529882	down	C8orf44			
			2.1474257	down	TIAM1			
			2.147295	down	ITGB8			
			2.1472461	down	SV2C			
			2.142878	down	TMX4			
			2.1376185	down	KCNN3			
			2.1345208	down	IL10RA			
			2.128381	down	CRYZ			
			2.1270013	down	P2RX1			
			2.1247206	down	CXCL12			
			2.1135316	down	GBP5			
			2.1107154	down	C16orf54			
			2.1086934	down	LGMN			
			2.1083915	down	ARHGEF40			
			2.1063281	down	BLVRA			
			2.1007984	down	S100A6			
			2.0971184	down	STOX2			
			2.0914404	down	S100A8			
			2.0805807	down	ABLIM1			

Absolute fold change 62 Treated H-MM vs 23 Treated Hypodiploid	Regulation	Gene Symbol	Absolute fold change 62 Treated H-MM vs 25 Treated NH-MM	Regulation	Gene Symbol	Absolute fold change 25 Treated NH-MM vs 23 Treated Hypodiploid	Regulation	Gene Symbol
			2.0798485	down	SSTR1			
			2.071248	down	TTC7B			
			2.0666275	down	RASSF4			
			2.0650864	down	CD86			
			2.0633337	down	TIMP1			
			2.0631785	down	MAP4K4			
			2.0605042	down	PTGER4			
			2.05880535	down	WARS			
			2.0574975	down	ERO1LB			
			2.057218	down	VLDLR			
			2.0527108	down	SLA			
			2.0491462	down	MAP1B			
			2.048676	down	NTRK2			
			2.0386884	down	ZBTB8A			
			2.0327048	down	NUAK1			
			2.0279813	down	MAGED4			
			2.0258296	down	LOC338758			
			2.02484	down	DGKQ			
			2.02358525	down	RRAS2			
			2.0234473	down	E2F7			
			2.011418	down	TLR4			
			2.009416	down	C1orf106			
			2.0090568	down	ZMAT1			
			2.0039794	down	INHBE			
			2.0034828	down	SLC7A11			
			2.0003722	down	CCNE2			

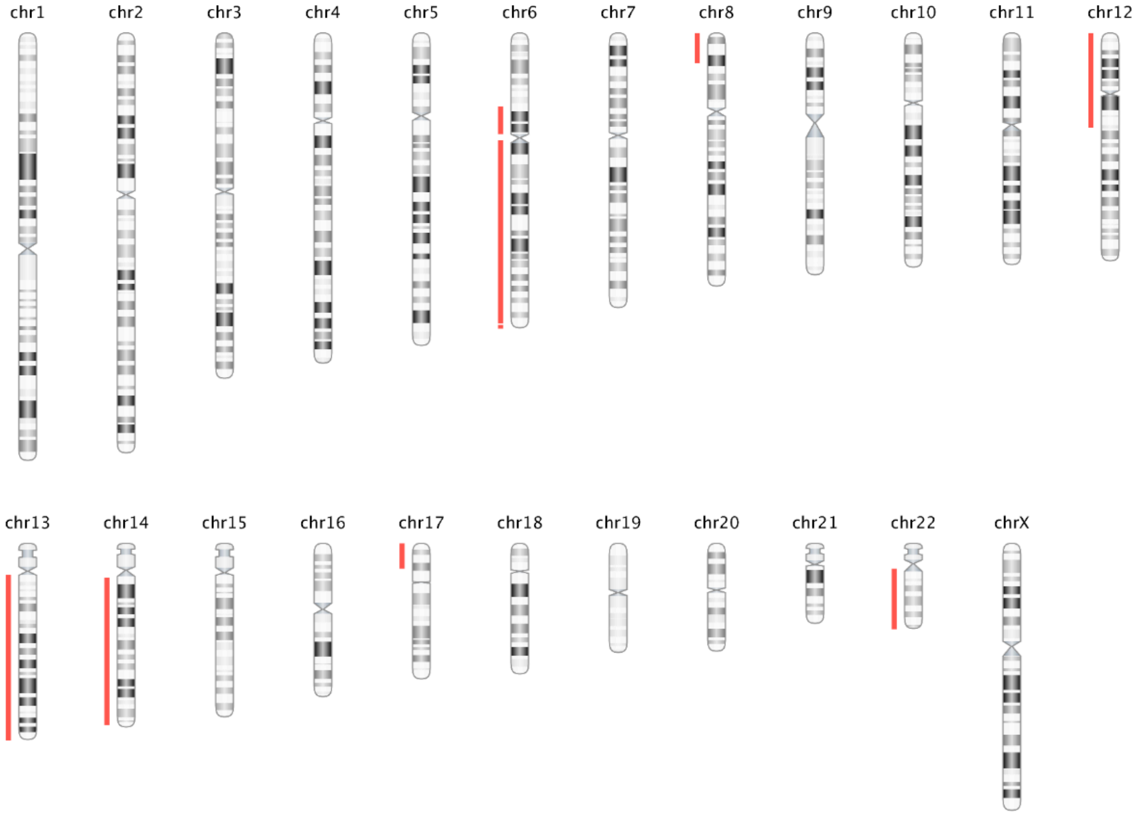
Supplementary Table S5. Ploidy categories broken down into the UAMS classification (Shaughnessy et al. Blood 2007 109: 2276-2284)

	Hypodiploid (n=49)	NH-MM (n=50)	Hypodiploid vs NH-MM	H-MM Treated (n=125)	All groups
UAMS classification	no.(%)	no.(%)	*p* value	no.(%)	*p* value
MS	7 (9)	2 (4)	0.15	6(5)	0.13
MF	6(12)	9 (18)	0.42	2 (2)	0.002
CD1	12 (24)	11 (22)	0.77	2 (2)	<0.001
CD2	4 (8)	17 (34)	0.004	3 (2)	<0.001
HY	1 (2)	0 (0)	0.99	25 (20)	<0.001
LB	2 (4)	2 (4)	0.62	6 (5)	0.96
PR	10 (20)	7 (14)	0.40	38 (30)	0.06
MY	7 (14)	2 (4)	0.15	43 (34)	<0.001

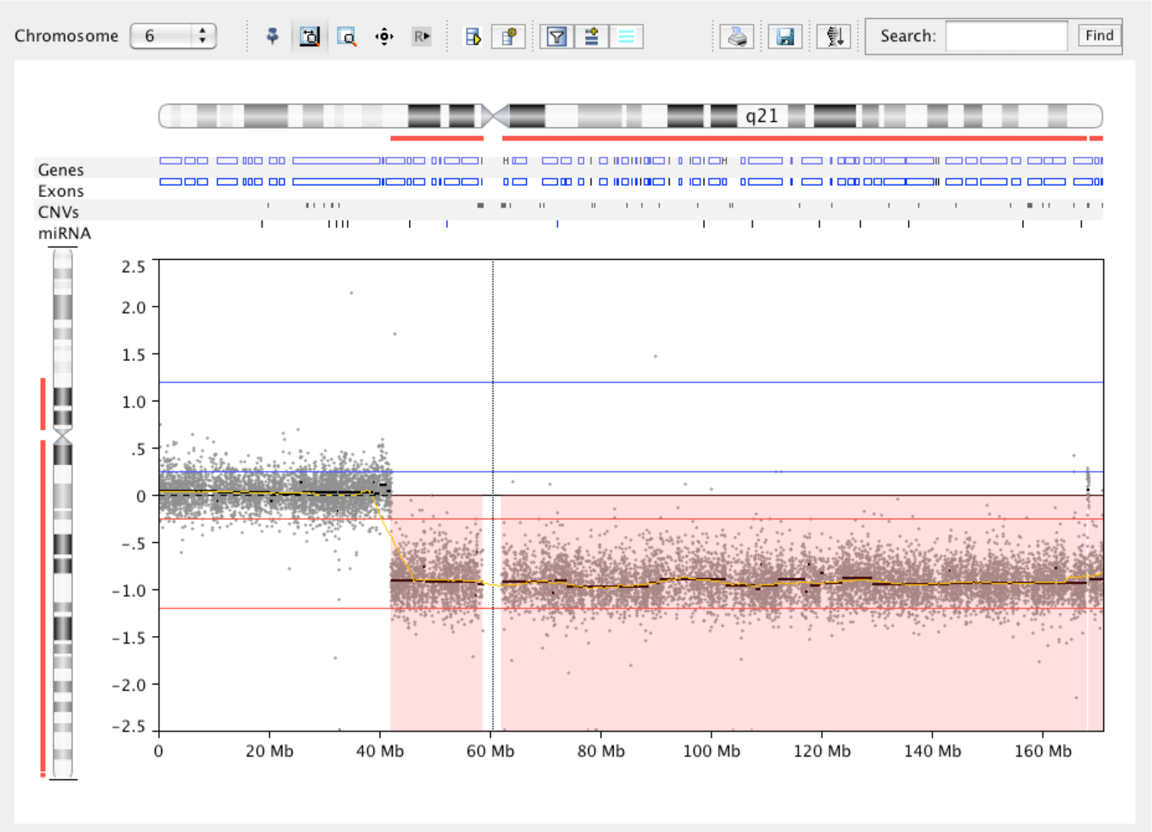
Supplementary Table S6. Concordance between the translocation/cylin D (TC) classification (Bergsagel et al. Blood. 2005;106:296-303) and the UAMS (University of Arkansas for Medical Sciences) clssification (Shaughnessy et al. Blood 2007 109: 2276-2284)

Subtypes	4p16	MAF	6p21	11q13	D1	D1+D2	D2	None	All cases
MS	14						1		15
MF	1	15	1						17
CD1			1	23			1		25
CD2		1		22	1				24
HY					24			2	26
LB					2	1	6	1	10
PR	7	3		1	16	6	15	7	55
MY	2	2	1		30	4	10	3	52
All cases	24	21	3	46	73	11	33	13	224

Supplementary figure S1. S1A. Overview of a female sample categorized as hypodiploid. Visually this sample has an estimated chromosome count of 41 due to the centromeric loss of chromosomes 6 and12 and calls of monosomy for chromosomes 13,14 and 22. Vertical lines to the left indicate loss. **S1B.** Chromosome view of chr6 from S1A. No probes are localized in the centromere and the distance from adjacent probes exceeds the maximum spacing of 1000 Kb resulting in the software to cause a break in the segment. Chr12 in S1A does not exceed the maximum spacing thus a continuous segment.



S1A


Chromosome
6
Search:
Find
q21
Genes
Exons
CNVs
miRNA
2.5
2.0
1.5
1.0
.5
0
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-1.0
-1.5
-2.0
-2.5
0
20 Mb
40 Mb
60 Mb
80 Mb
100 Mb
120 Mb
140 Mb
160 Mb

S1B

Supplementary figure S2. Distribution of total estimated chromosome number from all 224 samples. The Y axis is number of patients and the X axis is the estimated chromosome number. Light gray bars represent hypodiploid cases (39 to 44 chromosomes); dark gray bars correspond to NH-MM (45-46) and black bars to H-MM (47-55). Cases that are near triploid, near tetraploid and tetraploid are not discernable.