

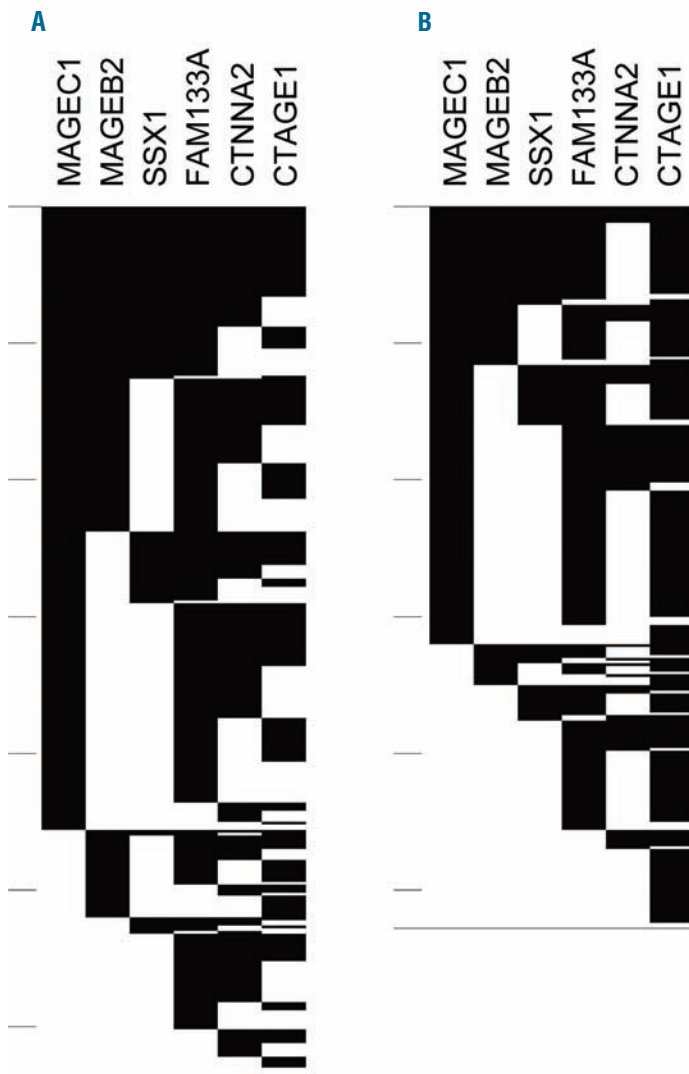
Cancer testis antigens in newly diagnosed and relapse multiple myeloma: prognostic markers and potential targets for immunotherapy

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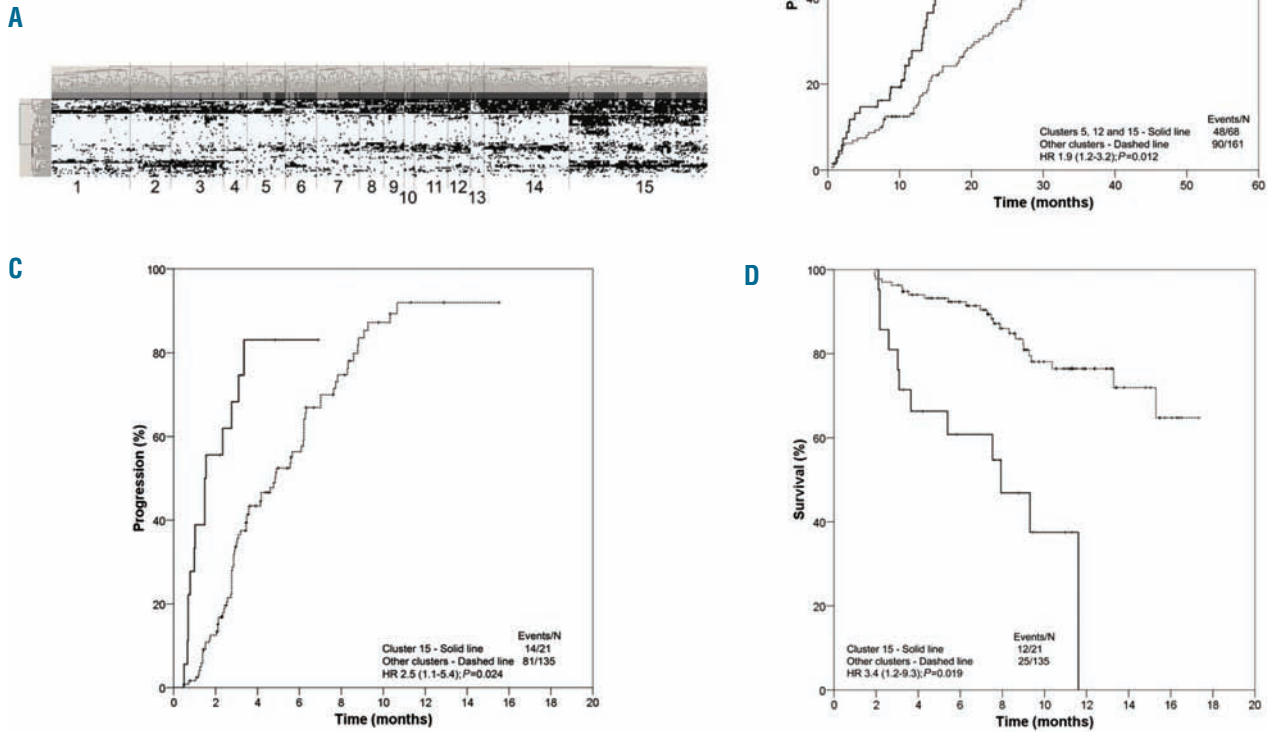
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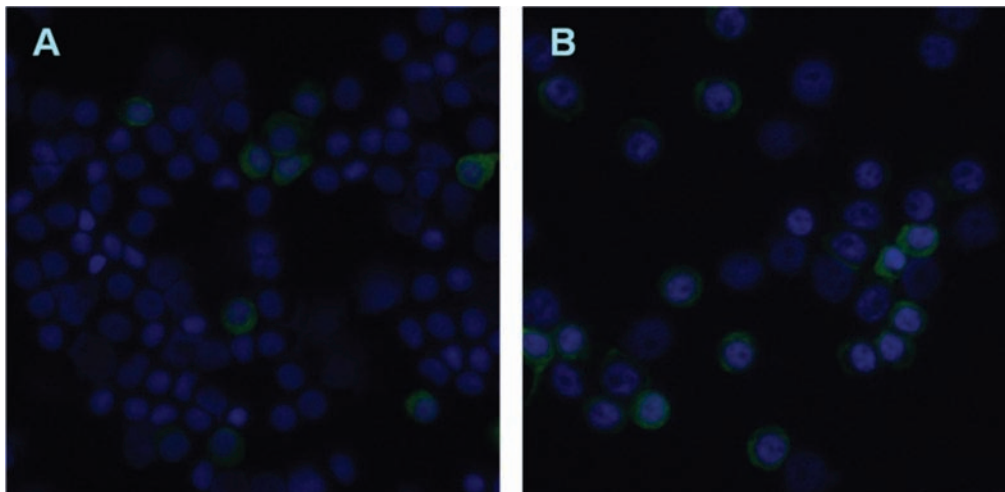
Online Supplementary Figure S1. Co-expression of testis-restricted and testis/brain-restricted CTA genes in newly diagnosed cases (A) and in relapse cases (B). Black indicates presence of expression; white, absence of expression. In the left column in each panel, a bar marks every 50 patients. Genes shown are MAGEC1, MAGEB2, SSX1, FAM133A, CTNNA2 and CTAGE1.



Online Supplementary Figure S2. Cluster analysis of the presence of CTA gene expression. Fifteen clusters are found (A), of which 5, 12 and 15 combined show a correlation to progression free survival in newly diagnosed cases (B). Cluster 15 holds prognostic value for APEX samples (C, D). The bar directly below the sample dendrogram indicates newly diagnosed cases (light gray) and relapse cases (dark gray).



Online Supplementary Figure S3. Expression of MAGEC1 in myeloma specimens of which gene expression microarrays were performed. (A) 10% positive for MAGEC1 and no presence call; (B) 90% positive for MAGEC1 with presence call. Cytospins were fixed in acetone for 5 min and were air-dried for an additional 10 min. Slides were incubated with primary antibody O/N at 4°C, followed by 30 min of incubation with Alexa Fluor-labeled antibodies (Molecular Probes). Sections were embedded in Vectashield (Vector Labs). Antibody for MAGEC1 was CT7-33 (Sigma-Aldrich).



Online Supplementary Table S1. First four columns taken from Ctdatabase.

Gene family	Family member	Chromosomal localization	CT identifier	Status
CTAGE-1	CTAGE1	18p11.2	CT21.1	AB and Plus
CTNNA2	CTNNA2	2p12-p11.1	CT 114	AB and Plus
FAM133A	FAM133A	Xq21.32	CT 115	AB and Plus
GAGE	GAGE4	Xp11.4-p11.2	CT4.4	AB and Plus
GAGE	GAGE8	Xp11.23	CT4.8	AB and Plus
MAGEA	MAGEA1	Xq28	CT1.1	AB and Plus
MAGEA	MAGEA2	Xq28	CT1.2	AB and Plus
MAGEA	MAGEA9	Xq28	CT1.9	AB and Plus
MAGEB	MAGEB1	Xp21.3	CT3.1	AB and Plus
MAGEB	MAGEB2	Xp21.3	CT3.2	AB and Plus
MAGEB	MAGEB4	Xp21.3	CT3.6	AB and Plus
MAGEC1	MAGEC1	Xq26	CT7.1	AB and Plus
MAGEC2	MAGEC2	Xq27	CT10	AB and Plus
PAGE-5	PAGE2	Xp11.21	CT16.4	AB and Plus
SPANX	SPANXC	Xq27.1	CT11.3	AB and Plus
SSX	SSX1	Xp11.23-p11.22	CT5.1	AB and Plus
SSX	SSX2	Xp11.22	CT5.2a	AB and Plus
SSX	SSX3	Xp11.23	CT5.3	AB and Plus
TEX14	TEX14	17q22	CT 113	AB and Plus
TSPY1	TSPY1	Yp11.2	CT78	AB and Plus
ACRBP	ACRBP	12p13.31	CT23	AB and Plus
AF15q14	CASC5	15q14	CT29	AB and Plus
C21orf99	C21orf99	21q11.2	CT85	AB and Plus
CABYR	CABYR	18q11.2	CT88	AB and Plus
CCDC110	CCDC110	4q35.1	CT52	AB and Plus
CEP290	CEP290	12q21.32	CT87	AB and Plus
CTAGE-1	CTAGE5	14q13.3	CT21.3	AB and Plus
FATE	FATE1	Xq28	CT43	AB and Plus
HAGE	DDX43	6q12-q13	CT13	AB and Plus
JARID1B	JARID1B	1q32.1	CT31	AB and Plus
LDHC	LDHC	11p15.5-p15.3	CT32	AB and Plus
LEMD1	LEMD1	1q32.1	CT50	AB and Plus
MAGEA	MAGEA12	Xq28	CT1.12	AB and Plus
MAGEA	MAGEA3	Xq28	CT1.3	AB and Plus
MAGEA	MAGEA4	Xq28	CT1.4	AB and Plus
MAGEA	MAGEA5	Xq28	CT1.5	AB and Plus
MAGEA	MAGEA6	Xq28	CT1.6	AB and Plus
MMA1	DSCR8	21q22.2	CT25.1a	AB and Plus
MORC	MORC1	3q13	CT33	AB and Plus
MPHOSPH1	MPHOSPH1	10q23.31	CT90	AB and Plus
NY-ESO-1	CTAG1B	Xq28	CT6.1	AB and Plus
NY-ESO-1	CTAG2	Xq28	CT6.2a	AB and Plus
OIP5	OIP5	15q15.1	CT86	AB and Plus
PBK	PBK	8p21.2	CT84	AB and Plus
PIWIL2	PIWIL2	8p21.3	CT80	AB and Plus
ROPN1	ROPN1	3q21.1	CT91	AB and Plus
SPA17	SPA17	11q24.2	CT22	AB and Plus
SPACA3	SPACA3	17q11.2	CT54	AB and Plus
SPAG9	SPAG9	17q21.33	CT89	AB and Plus
SPINLW1	SPINLW1	20q12-q13.2	CT71	AB and Plus
SPO11	SPO11	20q13.2-q13.3	CT35	AB and Plus
SSX	SSX4	Xp11.23	CT5.4	AB and Plus
SYCP1	SYCP1	1p13-p12	CT8	AB and Plus
TPTE	TPTE	21p11	CT44	AB and Plus
TPX1	CRISP2	6p21-qter	CT36	AB and Plus
TSGA10	TSGA10	2q11.2	CT79	AB and Plus
XAGE	XAGE1	Xp11.22	CT12.1a	AB and Plus
ZNF165	ZNF165	6p21.3	CT53	AB and Plus
ANKRD45	ANKRD45	1q25.1	CT 117	AB and Plus
ARX	ARX	Xp21	CT 121	AB and Plus
CCDC62	CCDC62	12q24.31	CT 109	AB and Plus
CEP55	CEP55	10q23.33	CT 111	AB and Plus
CT96	TTK	6q13-q21	CT96	AB and Plus
ELOVL4	ELOVL4	6q14	CT 118	AB and Plus
GPAT2	GPAT2	2q11.1	CT 123	AB and Plus
GPATCH2	GPATCH2	1q41	CT 110	AB and Plus
IGSF11	IGSF11	3q13.32	CT 119	AB and Plus
IMP-3	IMP-3	7p11	CT98	AB and Plus
KIAA0100/MLAA-22	KIAA0100	17q11.2	CT 101	AB and Plus
LOC440934	LOC440934	2q36.1	CT75	AB and Plus
LYPD6B	LOC130576	2q23.1-q23.2	CT 116	AB and Plus
MAEL	MAEL	1q24.1	CT128	AB and Plus
NOL4	NOL4	18q12	CT 125	AB and Plus

B1

Gene family	Family member	Chromosomal localization	CT identifier	Status
NUF2/CDCA1	CDCA1	1q23.3	CT106	AB and Plus
ODF1	ODF1	8q22.3	CT133	AB and Plus
ODF2	ODF2	9q34.11	CT134	AB and Plus
PRAME	PRAME	22q11.22	CT130	AB and Plus
PTPN20A	PTPN20A	10q11.22	CT 126	AB and Plus
RHOXF2/PEPP2	PEPP2	Xq24	CT107	AB and Plus
RQCD1	RQCD1	2q35	CT 129	AB and Plus
SPAG4	SPAG4	20q11.21	CT 127	AB and Plus
SPANX	SPANXB2	Xq27.1		AB and Plus
SPEF2	SPEF2	5p13.2	CT 122	AB and Plus
TCC52	TCC52	9p13.3	CT102	AB and Plus
TMEFF	TMEFF1	9q31	CT 120.1	AB and Plus
TMEFF	TMEFF2	2q32.3	CT 120.2	AB and Plus
TMEM108	TMEM108	3q21	CT 124	AB and Plus
BORIS	CTCFL	20q13.31	CT27	only U133Plus2.0
CAGE	DDX53	Xp22.11	CT26	only U133Plus2.0
CCDC33	CCDC33	15q24.1	CT61	only U133Plus2.0 with valid probe set
CCDC36	CCDC36	3p21.31	CT74	only U133Plus2.0
COX6B2	COX6B2	19q13.42	CT59	only U133Plus2.0
CPXCR1	CPXCR1	Xq21.3	CT77	only U133Plus2.0
Cxorf61	Cxorf61	Xq23	CT83	only U133Plus2.0
FAM46D	FAM46D	Xq21.1	CT 112	only U133Plus2.0
MAGEB	MAGEB6	Xp21.3	CT3.4	only U133Plus2.0
NY-SAR-35	FMR1NB	Xq27.3-q28	CT37	only U133Plus2.0
SLCO6A1	SLCO6A1	5q21.1	CT48	only U133Plus2.0
CXorf48	CXorf48	Xq26.3	CT55	AB and Plus
HORMAD1	HORMAD1	1q21.2	CT46	AB and Plus
MAGEB	MAGEB3	Xp21.3	CT3.5	AB and Plus
PASD1	PASD1	Xq28	CT63	AB and Plus
SGY-1	DKKL1	19q13.33	CT34	AB and Plus
SPANX	SPANXA1	Xq27.1	CT11.1	AB and Plus
ADAM2	ADAM2	8p11.2	CT15	AB and Plus
ADAM29	ADAM29	4q34	CT73	AB and Plus
AKAP3	AKAP3	12p13.3	CT82	AB and Plus
ARMC3	ARMC3	10p12.31	CT81	AB and Plus
BRDT	BRDT	1p22.1	CT9	AB and Plus
HSPB9	HSPB9	17q21.2	CT51	AB and Plus
KLKBL4	KLKBL4	16q21	CT67	AB and Plus
MAGEA	MAGEA11	Xq28	CT1.11	AB and Plus
MAGEA	MAGEA8	Xq28	CT1.8	AB and Plus
NLRP4	NLRP4	19q13.42	CT58	AB and Plus
NXF2	NXF2	Xq22.1	CT39	AB and Plus
RBM46	RBM46	4q32.1	CT68	AB and Plus
SYCE1	SYCE1	10q26.3	CT76	AB and Plus
TAF7L	TAF7L	Xq22.1	CT40	AB and Plus
TDRD1	TDRD1	10q25.3	CT41.1	AB and Plus
TDRD1	TDRD6	6p12.3	CT41.2	AB and Plus
TEX15	TEX15	8p12	CT42	AB and Plus
TSP50	TSP50	3p14-p12	CT20	AB and Plus
TSSK6	TSSK6	19p13.11	CT72	AB and Plus
TULP2	TULP2	19q13.1	CT65	AB and Plus
AKAP4	AKAP4	Xp11.2	CT99	AB and Plus
CT45	CT45A5	Xq26.3	CT45.5	AB and Plus
DPPA2	DPPA2	3q13.13	CT100	AB and Plus
IL13RA	IL13RA2	Xq13.1-q28	CT19	AB and Plus
LOC196993	LOC196993	15q23	CT62	AB and Plus
LOC348120	LOC348120	15q11.2	CT60	AB and Plus
LY6K	LY6K	8q24.3	CT97	AB and Plus
PRM	PRM1	16p13.2	CT94.1	AB and Plus
PRM	PRM2	16p13.2	CT94.2	AB and Plus
TEX101	TEX101	19q13.31	CT131	AB and Plus
CAGE1	CAGE1	6p24.3	CT95	only U133Plus2.0
CALR3	CALR3	19p13.11	CT93	only U133Plus2.0
CT45	CT45A1	Xq26.3	CT45.1	only U133Plus2.0
ODF3	ODF3	11p15.5	CT135	only U133Plus2.0 with valid probe set
ODF4	ODF4	17p13.1	CT136	only U133Plus2.0
OTOA	OTOA	16p12.2	CT108	only U133Plus2.0
POTE	POTE15	15q11.2	CT104 .5	only U133Plus2.0
SPATA19	SPATA19	11q25	CT132	only U133Plus2.0

C1				
Gene family	Family member	Chromosomal localization	CT identifier	Status
CT45	CT45A3	Xq26.3	CT45.3	AB and Plus
NY-ESO-1	CTAG1A	Xq28		AB and Plus
GAGE	GAGE12B	Xp11.23		AB and Plus
GAGE	GAGE12C	Xp11.23		AB and Plus
GAGE	GAGE12D	Xp11.23		AB and Plus
GAGE	GAGE12E	Xp11.23		AB and Plus
GAGE	GAGE12F	Xp11.23		AB and Plus
GAGE	GAGE12G	Xp11.23		AB and Plus
GAGE	GAGE12H	Xp11.23		AB and Plus
GAGE	GAGE12I	Xp11.4-p11.2		AB and Plus
GAGE	GAGE12J	Xp11.23		AB and Plus
GAGE	GAGE13	Xp11.23		AB and Plus
GAGE	GAGE2A	Xp11.23	CT4.2	AB and Plus
GAGE	GAGE5	Xp11.4-p11.2	CT4.5	AB and Plus
GAGE	GAGE6	Xp11.4-p11.2	CT4.6	AB and Plus
GAGE	GAGE7	Xp11.4-p11.2	CT4.7	AB and Plus
MAGEA	MAGEA2B	Xq28		AB and Plus
MAGEA	MAGEA9B/LOC728269	Xq28		AB and Plus
NXF2	NXF2B	Xq22.1		AB and Plus
SPANX	SPANXA2	Xq27.1		AB and Plus
SPANX	SPANXB1	Xq27.1	CT11.2	AB and Plus
TSPY1	LOC728137	Yp11.2		AB and Plus
XAGE	XAGE1B	Xp11.22	CT12.1b	AB and Plus
XAGE	XAGE1C	Xp11.22	CT12.1c	AB and Plus
XAGE	XAGE1D	Xp11.22	CT12.1d	AB and Plus
XAGE	XAGE1E	Xp11.22		AB and Plus
CT45	CT45A2	Xq26.3	CT45.2	only U133Plus2.0
CT45	CT45A4	Xq26.3	CT45.4	only U133Plus2.0
CT45	CT45A6	Xq26.3	CT45.6	only U133Plus2.0
CT47	CT47B1	Xq24	CT47.13	Excluded
GAGE	GAGE3	Xp11.23	CT4.3	Excluded
SPANX	SPANXE	Xq27.2		Excluded
BAGE	BAGE2	21p11.1	CT2.2	Excluded
BAGE	BAGE3	21p11.1	CT2.3	Excluded
BAGE	BAGE4	21p11.1	CT2.4	Excluded
BAGE	BAGE5	21p11.1	CT2.5	Excluded
CT64	CT64/BX103208	3q26.1	CT64	genecards negative no hit
FLJ36144/MAD-CT2	MAD-CT2	15q11.2	CT105	genecards negative no hit
TSPY1	TSPY1D	Yp11.2		genecards negative no hit
TSPY1	TSPY1E	Yp11.2		genecards negative no hit
TSPY1	TSPY1F	Yp11.2		genecards negative no hit
TSPY1	TSPY1G	Yp11.2		genecards negative no hit
TSPY1	TSPY1H	Yp11.2		genecards negative no hit
TSPY1	TSPY1I	Yp11.2		genecards negative no hit
CT69	CT69/BC040308	6q23.2	CT69	genecards negative no hit
CT70	CT70/B1818097	Unknown	CT70	genecards negative no hit
CT66	CT66/AA884595	7q11.22	CT66	genecards negative no hit
CT47	CT47A1	Xq24	CT47.1	not on chip according to genecards
CT47	CT47A10	Xq24	CT47.10	not on chip according to genecards
CT47	CT47A11	Xq24	CT47.11	not on chip according to genecards
CT47	CT47A2	Xq24	CT47.2	not on chip according to genecards
CT47	CT47A3	Xq24	CT47.3	not on chip according to genecards
CT47	CT47A4	Xq24	CT47.4	not on chip according to genecards
CT47	CT47A5	Xq24	CT47.5	not on chip according to genecards
CT47	CT47A6	Xq24	CT47.6	not on chip according to genecards
CT47	CT47A7	Xq24	CT47.7	not on chip according to genecards
CT47	CT47A8	Xq24	CT47.8	not on chip according to genecards
CT47	CT47A9	Xq24	CT47.9	not on chip according to genecards
POTE	POTE14	14q11.1	CT104.4	not on chip according to genecards
POTE	POTE18	18p11.21	CT104.6	not on chip according to genecards
POTE	POTE2	2q21.1	CT104.2	not on chip according to genecards
POTE	POTE21	21q11.2	CT104.1	not on chip according to genecards
POTE	POTE22	22q11.1	CT104.7	not on chip according to genecards
POTE	POTE8	8p11.1	CT104.3	not on chip according to genecards
SPANX	SPANXN1	Xq27	CT11.6	not on chip according to genecards
SPANX	SPANXN2	Xq27.3	CT11.7	not on chip according to genecards
SPANX	SPANXN3	Xq27.3	CT11.8	not on chip according to genecards
SPANX	SPANXN4	Xq27.3	CT11.9	not on chip according to genecards
SSX	SSX2b	Xp11.22	CT5.2b	not on chip according to genecards
SSX	SSX4B	Xp11.23		not on chip according to genecards
TAG	TAG	5p15.2	CT49	not on chip according to genecards
TSPY1	TSPY2	Yp11.2		not on chip according to genecards
XAGE	XAGE2B/CTD-2267G17.3	Xp11.22		not on chip according to genecards
XAGE	XAGE-4/RP11-167P23.2	Xp11.21	CT12.4	not on chip according to genecards
CSAGE	CSAG1	Xq28	CT24.1	not on chip according to genecards
SSX	SSX6	Xp11.2		not on chip according to genecards
SSX	SSX7	Xp11.23		not on chip according to genecards
SSX	SSX9	Xp11.23		not on chip according to genecards
PAGE-5	PAGE3	Xp11.21	CT16.6	not on chip according to genecards

D1

Gene family	Family member	Chromosomal localization	CT identifier	Status
MAGEB	MAGEB5	Xp21.3	CT3.3	not on chip according to genecards
PAGE-5	PAGE2B	Xp11.21	CT16.5	not on chip according to genecards
SPANX	SPANXD	Xq27.1	CT11.4	not on chip according to genecards
SPANX	SPANXN5	Xp11.22	CT11.10	not on chip according to genecards
XAGE	XAGE5	Xp11.22	CT12.5	not on chip according to genecards
CTAGE-1	CTAGE-2	18p11.2	CT21.2	splicing/excluded not double reported
NY-ESO-1	LAGE-1b	Xq28	CT6.2b	splicing/excluded not double reported
MMA1	MMA1b	21q22.2	CT25.1b	splicing/excluded not double reported
XAGE	XAGE-3b	Xp11.22	CT12.3b	splicing/excluded not double reported
PAGE-5	CT16.2	X911.21	CT16.2	splicing/excluded not double reported
SEMG1	SEMG1	20q12-q13.2	CT103	no presence call in normal testis
NA88A pseudogene	VENTXP1	Xp21.3	CT18	no presence call in normal testis
SSX	SSX5	Xp11.23		no presence call in normal testis
GAGE	GAGE1	Xp11.4-p11.2	CT4.1	no presence call in normal testis
MAGEC1	MAGEC3	Xq27.2	CT7.2	no presence call in normal testis
CSAGE	CSAG2	Xq28	CT24.2	no presence call in normal testis
CSAGE	CSAG3B	Xq28		represented by CSAG2
FTHL17	FTHL17	Xp21	CT38	no presence call in normal testis
SAGE	SAGE1	Xq26	CT14	no presence call in normal testis
ACTL8	ACTL8	1p36.2-p35	CT57	no presence call in normal testis
BAGE	BAGE	21p11.1	CT2.1	no presence call in normal testis
LIP1	LIP1	21q11.2	CT17	no presence call in normal testis
HOM-TES-85	LUZP4	Xq23	CT28	no presence call in normal testis
MAGEA	MAGEA10	Xq28	CT1.10	no presence call in normal testis
PAGE-5	PAGE4	Xp11.23	CT16.7	no presence call in normal testis
PAGE-5	PAGE5	Xp11.21	CT16.1	no presence call in normal testis
PLAC1	PLAC1	Xq26	CT92	no presence call in normal testis
HCA661	TFDP3	Xq26.2	CT30	no presence call in normal testis
THEG	THEG	19pter-p13	CT56	no presence call in normal testis
XAGE	XAGE2	Xp11.22	CT12.2	no presence call in normal testis
XAGE	XAGE3	Xp11.22-p11.21	CT12.3a	no presence call in normal testis
PAGE-5	PAGE1	Xp11.23	CT16.3	Ctdatabase exclusion
ODF3	ODF3	11p15.5	CT135	no presence call in normal testis (for U133AB)
CCDC33	CCDC33	15q24.1	CT61	no presence call in normal testis (for U133AB)

A2	Tissue restriction in genes on U133Plus2.0 and on U133AB (in parentheses)		
	Testis-restricted n=26 (17)	Genes on chip U133A: 82	Genes on U133Plus2.0: 142
	Testis-selective n=64 (58)	Genes on chip U133B: 41	
	Testis/brain restricted n=12 (9)	Genes represented by others: 26	Genes represented by others: 29
	Not categorized n=69 (39)	Total: 149	Total: 171

Family member	Tissue restriction	Chip U133AB	Chip U133Plus2.0 status	Probe set
CTAGE1	testis/brain-restricted	A	Plus 2.0	220957_at
CTNNA2	testis/brain-restricted	A	Plus 2.0	205373_at
FAM133A	testis/brain-restricted	B	Plus 2.0	239481_at
GAGE4	testis/brain-restricted	A	Plus 2.0	208155_x_at
GAGE8	testis/brain-restricted	A	Plus 2.0	207086_x_at
MAGEA1	testis-restricted	A	Plus 2.0	207325_x_at
MAGEA2	testis-restricted	A	Plus 2.0	214603_at
MAGEA9	testis/brain-restricted	A	Plus 2.0	210437_at
MAGEB1	testis-restricted	A	Plus 2.0	207534_at
MAGEB2	testis-restricted	A	Plus 2.0	206218_at
MAGEB4	testis-restricted	A	Plus 2.0	207580_at
MAGEC1	testis-restricted	A	Plus 2.0	206609_at
MAGEC2	testis/brain-restricted	A	Plus 2.0	220062_s_at
PAGE2	testis-restricted	B	Plus 2.0	231307_at
SPANXC	testis-restricted	A	Plus 2.0	220217_x_at
SSX1	testis-restricted	A	Plus 2.0	206626_x_at
SSX2	testis-restricted	A	Plus 2.0	210497_x_at
SSX3	testis-restricted	A	Plus 2.0	211670_x_at
TEX14	testis-restricted	A	Plus 2.0	221035_s_at
TSPY1	testis-restricted	A	Plus 2.0	207918_s_at
ACRBP	testis-selective	B	Plus 2.0	223717_s_at
CASC5	testis-selective	B	Plus 2.0	228323_at
C21orf99	testis-selective	B	Plus 2.0	237794_at
CABYR	testis-selective	A	Plus 2.0	219928_s_at
CCDC110	testis-selective	B	Plus 2.0	230900_at
CEP290	testis-selective	A	Plus 2.0	205250_s_at
CTAGE5	testis-selective	A	Plus 2.0	215930_s_at
FATE1	testis-selective	B	Plus 2.0	231573_at
DDX43	testis-selective	A	Plus 2.0	220004_at
JARID1B	testis-selective	A	Plus 2.0	211202_s_at
LDHC	testis-selective	A	Plus 2.0	207022_s_at
LEMD1	testis-selective	B	Plus 2.0	229927_at
MAGEA12	testis-selective	A	Plus 2.0	210467_x_at
MAGEA3	testis-selective	A	Plus 2.0	209942_x_at
MAGEA4	testis-selective	A	Plus 2.0	214254_at
MAGEA5	testis-selective	A	Plus 2.0	214642_x_at
MAGEA6	testis-selective	A	Plus 2.0	214612_x_at
DSCR8	testis-selective	B	Plus 2.0	241224_x_at
MORC1	testis-selective	A	Plus 2.0	220850_at
MPHOSPH1	testis-selective	A	Plus 2.0	205235_s_at
CTAG1B	testis-selective	A	Plus 2.0	211674_x_at
CTAG2	testis-selective	A	Plus 2.0	215733_x_at
OIP5	testis-selective	A	Plus 2.0	213599_at
PBK	testis-selective	A	Plus 2.0	219148_at
PIWIL2	testis-selective	A	Plus 2.0	220686_s_at
ROPN1	testis-selective	B	Plus 2.0	233203_at
SPA17	testis-selective	A	Plus 2.0	205406_s_at
SPACA3	testis-selective	B	Plus 2.0	243621_at
SPAG9	testis-selective	A	Plus 2.0	212470_at
SPINLW1	testis-selective	A	Plus 2.0	206318_at
SPO11	testis-selective	A	Plus 2.0	222259_s_at
SSX4	testis-selective	A	Plus 2.0	210394_x_at
SYCP1	testis-selective	A	Plus 2.0	206740_x_at
TPTE	testis-selective	A	Plus 2.0	220205_at
CRISP2	testis-selective	A	Plus 2.0	210262_at
TSGA10	testis-selective	A	Plus 2.0	220623_s_at
XAGE1	testis-selective	A	Plus 2.0	220057_at
ZNF165	testis-selective	A	Plus 2.0	206683_at
ANKRD45	not available	B	Plus 2.0	236421_at
ARX	not available	B	Plus 2.0	238878_at
CCDC62	not available	B	Plus 2.0	231567_s_at
CEP55	not available	A	Plus 2.0	218542_at
TTK	not available	A	Plus 2.0	204822_at
ELOVL4	not available	A	Plus 2.0	219532_at
GPAT2	not available	B	Plus 2.0	235557_at
GPATCH2	not available	B	Plus 2.0	242224_at
IGSF11	not available	B	Plus 2.0	228375_at
IMP-3	not available	A	Plus 2.0	203820_s_at
KIAA0100	not available	A	Plus 2.0	201728_s_at
LOC440934	not available	B	Plus 2.0	230844_at
LOC130576	not available	B	Plus 2.0	228360_at
MAEL	not available	B	Plus 2.0	229475_at
NOL4	not available	A	Plus 2.0	206045_s_at

B2

Family member	Tissue restriction	Chip U133AB	Chip U133Plus2.0 status	Probe set
CDCA1	not available	B	Plus 2.0	223381_at
ODF1	not available	A	Plus 2.0	214485_at
ODF2	not available	B	Plus 2.0	225617_at
PRAME	not available	A	Plus 2.0	204086_at
PTPN20A	not available	A	Plus 2.0	215172_at
PEPP2	not available	A	Plus 2.0	220952_s_at
RQCD1	not available	A	Plus 2.0	213179_at
SPAG4	not available	A	Plus 2.0	219888_at
SPANXB2	not available	A	Plus 2.0	220921_at
SPEF2	not available	B	Plus 2.0	232745_x_at
TCC52	not available	B	Plus 2.0	224789_at
TMEFF1	not available	A	Plus 2.0	205122_at
TMEFF2	not available	B	Plus 2.0	224321_at
TMEM108	not available	B	Plus 2.0	223524_s_at
CTCFL	testis-selective		Plus 2.0	1552368_at
DDX53	testis-restricted		Plus 2.0	1555357_at
CCDC33	testis-selective		Plus 2.0	1563090_at
CCDC36	testis-selective		Plus 2.0	1569690_at
COX6B2	testis-selective		Plus 2.0	1553367_a_at
CPXCR1	testis-restricted		Plus 2.0	1560493_a_at
Cxor61	testis-restricted		Plus 2.0	1559258_a_at
FAM46D	not available		Plus 2.0	1552461_at
MAGEB6	testis-restricted		Plus 2.0	1552858_at
FMR1NB	testis-selective		Plus 2.0	1552906_at
SLCO6A1	testis-selective		Plus 2.0	1552745_at
CXorf48	testis-restricted	A	Plus 2.0	221121_at
HORMAD1	testis/brain-restricted	B	Plus 2.0	223861_at
MAGEB3	testis-restricted	A	Plus 2.0	207579_at
PASD1	testis/brain-restricted	B	Plus 2.0	240687_at
DKKL1	testis-restricted	A	Plus 2.0	220284_at
SPANXA1	testis-restricted	A	Plus 2.0	220922_s_at
ADAM2	testis-selective	A	Plus 2.0	207664_at
ADAM29	testis-selective	A	Plus 2.0	221337_s_at
AKAP3	testis-selective	A	Plus 2.0	207344_at
ARMC3	testis-selective	B	Plus 2.0	240275_at
BRDT	testis-selective	A	Plus 2.0	206787_at
HSPB9	testis-selective	B	Plus 2.0	230510_at
KLKBL4	testis-selective	B	Plus 2.0	231287_s_at
MAGEA11	testis-selective	A	Plus 2.0	210503_at
MAGEA8	testis-selective	A	Plus 2.0	210274_at
NLRP4	testis-selective	B	Plus 2.0	242334_at
NXF2	testis-selective	A	Plus 2.0	220981_x_at
RBM46	testis-selective	B	Plus 2.0	244351_at
SYCE1	testis-selective	B	Plus 2.0	233084_s_at
TAF7L	testis-selective	A	Plus 2.0	220325_at
TDRD1	testis-selective	A	Plus 2.0	221018_s_at
TDRD6	testis-selective	B	Plus 2.0	232692_at
TEX15	testis-selective	A	Plus 2.0	221448_s_at
TSP50	testis-selective	A	Plus 2.0	220126_at
TSSK6	testis-selective	B	Plus 2.0	224409_s_at
TULP2	testis-selective	A	Plus 2.0	206733_at
AKAP4	not available	A	Plus 2.0	207019_s_at
CT45A5	not available	B	Plus 2.0	235700_at
DPPA2	not available	B	Plus 2.0	240301_at
IL13RA2	not available	A	Plus 2.0	206172_at
LOC196993	not available	A	Plus 2.0	214418_at
LOC348120	not available	B	Plus 2.0	231132_at
LY6K	not available	B	Plus 2.0	223687_s_at
PRM1	not available	A	Plus 2.0	206358_at
PRM2	not available	A	Plus 2.0	210122_at
TEX101	not available	B	Plus 2.0	223906_s_at
CAGE1	not available		Plus 2.0	1563787_a_at
CALR3	not available		Plus 2.0	1552421_a_at
CT45A1	not available		Plus 2.0	1567912_s_at
ODF3	not available		Plus 2.0	1553051_s_at
ODF4	not available		Plus 2.0	1552408_at
OTOA	not available		Plus 2.0	1553432_s_at
POTE15	not available		Plus 2.0	1553474_at
SPATA19	not available		Plus 2.0	1559138_a_at

C2		
Family member	Tissue restriction	Corresponding to gene:
CT45A3	not available	CT45A5
CTAG1A	testis-restricted	CTAG1B
GAGE12B	not available	GAGE4, GAGE8
GAGE12C	not available	GAGE4, GAGE8
GAGE12D	not available	GAGE4, GAGE8
GAGE12E	not available	GAGE4, GAGE8
GAGE12F	not available	GAGE4, GAGE8
GAGE12G	not available	GAGE4, GAGE8
GAGE12H	not available	GAGE4, GAGE8
GAGE12I	not available	GAGE4, GAGE8
GAGE12J	not available	GAGE4, GAGE8
GAGE13	not available	GAGE4, GAGE8
GAGE2A	testis/brain-restricted	GAGE4, GAGE8
GAGE5	testis/brain-restricted	GAGE4, GAGE8
GAGE6	testis-restricted	GAGE4, GAGE8
GAGE7	testis/brain-restricted	GAGE4, GAGE8
MAGEA2B	testis-restricted	MAGEA2
MAGEA9B/LOC728269	not available	MAGEA9
NXF2B	not available	NXF2
SPANXA2	testis-restricted	SPANXA1
SPANXB1	testis-restricted	SPANXB2
LOC728137	not available	TSPY1
XAGE1B	not available	XAGE1
XAGE1C	not available	XAGE1
XAGE1D	not available	XAGE1
XAGE1E	not available	XAGE1
CT45A2	not available	CT45A1
CT45A4	not available	CT45A1
CT45A6	not available	CT45A1
CT47B1	not available	
GAGE3	not available	
SPANXE	testis-restricted	
BAGE2	testis-selective	
BAGE3	testis-selective	
BAGE4	testis-selective	
BAGE5	testis-selective	
CT64/BX103208	not available	
MAD-CT2	not available	
TSPY1D	not available	
TSPY1E	not available	
TSPY1F	not available	
TSPY1G	not available	
TSPY1H	not available	
TSPY1I	not available	
CT69/BC040308	testis-restricted	
CT70/BI818097	testis-restricted	
CT66/AA884595	testis-selective	
CT47A1	not available	
CT47A10	not available	
CT47A11	not available	
CT47A2	not available	
CT47A3	not available	
CT47A4	not available	
CT47A5	not available	
CT47A6	not available	
CT47A7	not available	
CT47A8	not available	
CT47A9	not available	
POTE14	not available	
POTE18	not available	
POTE2	not available	
POTE21	not available	
POTE22	not available	
POTE8	not available	
SPANXN1	not available	
SPANXN2	not available	
SPANXN3	not available	
SPANXN4	not available	
SSX2b	not available	
SSX4B	not available	
TAG	not available	
TSPY2	not available	
XAGE2B/CTD-2267G17.3	not available	
XAGE-4/RP11-167P23.2	not available	
CSAG1	not found in testis	
SSX6	not found in testis	
SSX7	not found in testis	
SSX9	not found in testis	
PAGE3	testis/brain-restricted	

D2

Family member	Tissue restriction
MAGEB5	testis-restricted
PAGE2B	testis-restricted
SPANXD	testis-restricted
SPANXN5	testis-restricted
XAGE5	testis-restricted
CTAGE-2	not available
LAGE-1b	not available
MMA1b	not available
XAGE-3b	not available
CT16.2	testis-restricted
SEMG1	not available
VENTXP1	not available
SSX5	not found in testis
GAGE1	testis/brain-restricted
MAGEC3	testis/brain-restricted
CSAG2	testis-restricted
CSAG3B	not available
FTHL17	testis-restricted
SAGE1	testis-restricted
ACTL8	testis-selective
BAGE	testis-selective
LIP1	testis-selective
LUZP4	testis-selective
MAGEA10	testis-selective
PAGE4	testis-selective
PAGE5	testis-selective
PLAC1	testis-selective
TFDP3	testis-selective
THEG	testis-selective
XAGE2	testis-selective
XAGE3	testis-selective
PAGE1	not found in testis
ODF3	not available
CCDC33	testis-selective

A3	Number of genes evaluated (with presence frequency of >5% and <95%, in H65 and in APEX set, respectively)				
	H65 80	APEX 57	y, yes		
Family member	Evaluated KM H65	Evaluated KM APEX	Table 1	Table S4	Table S5
CTAGE1	220957_at		y		
CTNNA2	205373_at	205373_at	y		
FAM133A	239481_at	239481_at	y		
GAGE4	208155_x_at	208155_x_at	y		
GAGE8	207086_x_at	207086_x_at	y		
MAGEA1	207325_x_at	207325_x_at	y		
MAGEA2	214603_at	214603_at	y		
MAGEA9	210437_at		y		
MAGEB1	207534_at		y		
MAGEB2	206218_at	206218_at	y		
MAGEB4	207580_at		y		
MAGEC1	206609_at	206609_at	y		
MAGEC2	220062_s_at	220062_s_at	y		
PAGE2	231307_at		y		
SPANXC			y		
SSX1	206626_x_at	206626_x_at	y		
SSX2	210497_x_at	210497_x_at	y		
SSX3			y		
TEX14	221035_s_at		y		
TSPY1			y		
ACRBP	223717_s_at	223717_s_at		y	
CASC5	228323_at	228323_at		y	
C21orf99	237794_at	237794_at		y	
CABYR	219928_s_at			y	
CCDC110	230900_at	230900_at		y	
CEP290	205250_s_at	205250_s_at		y	
CTAGE5		215930_s_at	y		
FATE1	231573_at	231573_at		y	
DDX43	220004_at	220004_at		y	
JARID1B	211202_s_at	211202_s_at	y		
LDHC	207022_s_at			y	
LEMD1	229927_at	229927_at		y	
MAGEA12	210467_x_at	210467_x_at		y	
MAGEA3	209942_x_at	209942_x_at		y	
MAGEA4				y	
MAGEA5	214642_x_at	214642_x_at		y	
MAGEA6	214612_x_at	214612_x_at		y	
DSCR8	241224_x_at	241224_x_at		y	
MORC1	220850_at	220850_at		y	
MPHOSPH1	205235_s_at	205235_s_at		y	
CTAG1B	211674_x_at	211674_x_at		y	
CTAG2	215733_x_at	215733_x_at		y	
OIP5	213599_at	213599_at		y	
PBK	219148_at	219148_at	y		
PIWIL2		220686_s_at		y	
ROPN1	233203_at	233203_at		y	
SPA17	205406_s_at	205406_s_at		y	
SPACA3	243621_at	243621_at		y	
SPAG9			y		
SPINLW1		206318_at		y	
SPO11	222259_s_at			y	
SSX4	210394_x_at	210394_x_at		y	
SYCP1	206740_x_at	206740_x_at		y	
TPTE	220205_at	220205_at		y	
CRISP2	210262_at			y	
TSGA10	220623_s_at	220623_s_at		y	
XAGE1	220057_at	220057_at		y	
ZNF165	206683_at	206683_at	y		
ANKRD45	236421_at			y	
ARX	238878_at			y	
CCDC62	231567_s_at	231567_s_at		y	
CEP55	218542_at	218542_at		y	
TTK	204822_at	204822_at		y	
ELOVL4	219532_at			y	
GPAT2	235557_at	235557_at		y	
GPATCH2	242224_at	242224_at		y	
IGSF11	228375_at	228375_at		y	
IIMP-3	203820_s_at	203820_s_at		y	
KIAA0100	201728_s_at			y	
LOC440934	230844_at			y	
LOC130576	228360_at	228360_at		y	
MAEL	229475_at	229475_at		y	
NOL4	206045_s_at	206045_s_at		y	

B3					
Family member	Evaluated KM H65	Evaluated KM APEX	Table 1	Table S4	Table S5
CDCA1	223381_at	223381_at		y	
ODF1	214485_at	214485_at		y	
ODF2	225617_at	225617_at		y	
PRAME	204086_at	204086_at		y	
PTPN20A	215172_at			y	
PEPP2	220952_s_at	220952_s_at		y	
RQCD1				y	
SPAG4				y	
SPANXB2	220921_at			y	
SPEF2	232745_x_at	232745_x_at		y	
TCC52				y	
TMEFF1	205122_at	205122_at		y	
TMEFF2	224321_at	224321_at		y	
TMEM108	223524_s_at			y	
CTCFL	1552368_at			y	
DDX53				y	
CCDC33	1563090_at			y	
CCDC36	1569690_at			y	
COX6B2				y	
CPXCR1	1560493_a_at			y	
Cxorf61	1559258_a_at			y	
FAM46D	1552461_at			y	
MAGEB6	1552858_at			y	
FMR1NB	1552906_at			y	
SLCO6A1				y	
CXorf48					y
HORMAD1					y
MAGEB3					y
PASD1					y
DKKL1					y
SPANXA1					y
ADAM2					y
ADAM29					y
AKAP3					y
ARMC3					y
BRDT					y
HSPB9					y
KLKBL4					y
MAGEA11					y
MAGEA8					y
NLRP4					y
NXF2					y
RBM46					y
SYCE1					y
TAF7L					y
TDRD1					y
TDRD6					y
TEX15					y
TSP50					y
TSSK6					y
TULP2					y
AKAP4					y
CT45A5					y
DPPA2					y
IL13RA2					y
LOC196993					y
LOC348120					y
LY6K					y
PRM1					y
PRM2					y
TEX101					y
CAGE1					y
CALR3					y
CT45A1					y
ODF3					y
ODF4					y
OTOA					y
POTE15					y
SPATA19					y

Online Supplementary Table S2. Positive difference in presence frequency between two or more probe sets in relapse data set (AB) and negative difference in newly diagnosed data set (Plus 2) or vice versa.

Probe set	Symbol	Chip	Probe set used	Frequency of presence_plus2	%	Frequency of presence_AB	%
206045_s_at	NOL4	A	Y	174	54%	112	42%
238605_at	NOL4	B	N	222	69%	112	42%
			difference	-48		0	
244351_at	RBM46	B	Y	4	1%	1	0%
242516_x_at	RBM46	B	N	18	6%	0	0%
			difference	-14		1	
233203_at	ROPN1	B	Y	28	9%	44	17%
231535_x_at	ROPN1	B	N	82	26%	6	2%
			difference	-54		38	
206318_at	SPINLW1	A	Y	5	2%	53	20%
206319_s_at	SPINLW1	A	N	13	4%	1	0%
			difference	-8		52	
211670_x_at	SSX3	A	Y	9	3%	15	6%
207666_x_at	SSX3	A	N	29	9%	10	4%
			difference	-20		5	
211731_x_at	SSX3	A	N	31	10%	1	0%
			difference	-2		9	

Online Supplementary Table S3. Patients' characteristics of the newly diagnosed and the relapsed MM patients evaluated for CTA expression.

	HOVON-65/GMMG-HD4	APEX/SUMMIT/CREST	
Age			
median (years)	56	61	<i>P</i> <0.0001*
range (years)	27-65	27-86	
Sex			
F	137 (43)	105 (40)	NS
M	183 (57)	159 (60)	
ISS			
I	122 (38)	69 (26)	NS
II	88 (28)	65 (25)	
III	83 (26)	63 (24)	
nd	27 (8)	67 (25)	
Corrected calcium [mmol/l]			
< 2.75	255 (73)	141 (53)	NS
≥ 2.75	38 (11)	14 (5)	
nd	57 (16)	109 (41)	
Platelets [x10⁹/L]			
≥ 100	272 (85)	128 (48)	<i>P</i> <0.001
< 100	12 (4)	28 (11)	
nd	36 (11)	108 (41)	
Creatinine [μmol/l]			
≤ 173	249 (78)	193 (73)	NS
> 173	34 (11)	20 (8)	
nd	37 (12)	51 (19)	
Mprotein heavy chain			
IgA	60 (19)	55 (21)	<i>P</i> =0.04
IgG	178 (56)	150 (57)	
IgD	3 (1)		
LCD	43 (13)	51 (19)	
non-secretory		4 (2)	
nd	36 (11)	4 (2)	

*. Age <65 was an enrolment criterion for the HOVON65/GMMG-HD4 study, which explains the significant difference shown here.

nd: not determined; NS: not significant.

Online Supplementary Table S4. CTA genes with presence of more than 5% in newly diagnosed or relapse population. The testis-restricted, testis-brain restricted and top 5 testis selective genes are given in Table 1. Here the remaining testis-selective genes, genes with no known tissue restriction and genes only present on platform U133Plus2.0 are given.

Gene symbol	Probe set	Tissue restriction	Newly diagnosed		Relapse		P value Bold, significant
			n	%	n	%	
CASC5	228323_at	testis-selective	238	74.4	236	89.4	<0.0001
CEP290	205250_s_at	testis-selective	218	68.1	135	51.1	<0.0001
OIP5	213599_at	testis-selective	218	68.1	98	37.1	<0.0001
CCDC110	230900_at	testis-selective	207	64.7	48	18.2	<0.0001
MPHOSPH1	205235_s_at	testis-selective	196	61.3	20	7.6	<0.0001
MORC1	220850_at	testis-selective	184	57.5	86	32.6	<0.0001
ACRBP	223717_s_at	testis-selective	144	45	20	7.6	<0.0001
MAGEA6	214612_x_at	testis-selective	144	45	130	49.2	0.3
FATE1	231573_at	testis-selective	126	39.4	93	35.2	0.3
SPA17	205406_s_at	testis-selective	122	38.1	24	9.1	<0.0001
MAGEA3	209942_x_at	testis-selective	121	37.8	125	47.3	0.02
SSX4	210394_x_at	testis-selective	110	34.4	78	29.5	0.2
TSGA10	220623_s_at	testis-selective	109	34.1	13	4.9	<0.0001
SPO11	222259_s_at	testis-selective	89	27.8	3	1.1	<0.0001
MAGEA5	214642_x_at	testis-selective	82	25.6	37	14	0.001
DDX43	220004_at	testis-selective	77	24.1	42	15.9	0.02
TPTE	220205_at	testis-selective	77	24.1	90	34.1	0.01
XAGE1	220057_at	testis-selective	65	20.3	66	25	0.2
SPACA3	243621_at	testis-selective	61	19.1	67	25.4	0.07
CTAG1B	211674_x_at	testis-selective	60	18.8	43	16.3	0.4
CTAG2	215733_x_at	testis-selective	54	16.9	38	14.4	0.4
MAGEA12	210467_x_at	testis-selective	49	15.3	89	33.7	<0.0001
C21orf99	237794_at	testis-selective	47	14.7	103	39	<0.0001
CABYR	219928_s_at	testis-selective	41	12.8	2	0.8	<0.0001
LDHC	207022_s_at	testis-selective	36	11.3	0	0	<0.0001
DSCR8	241224_x_at	testis-selective	33	10.3	24	9.1	0.7
LEMD1	229927_at	testis-selective	28	8.8	27	10.2	0.6
ROPN1	233203_at	testis-selective	28	8.8	44	16.7	0.01
CRISP2	210262_at	testis-selective	20	6.3	7	2.7	0.05
SYCP1	206740_x_at	testis-selective	18	5.6	11	4.2	0.5
MAGEA4	214254_at	testis-selective	10	3.1	15	5.7	0.2
SPINLW1	206318_at	testis-selective	5	1.6	53	20.1	<0.0001
PIWIL2	220686_s_at	testis-selective	2	0.6	61	23.1	<0.0001
SPAG4	219888_at	NA	320	100	257	97.3	0.004
TCC52	224789_at	NA	319	99.7	264	100	1
RQCD1	213179_at	NA	318	99.4	264	100	0.5
TMEFF1	205122_at	NA	296	92.5	94	35.6	<0.0001
TMEFF2	224321_at	NA	288	90	251	95.1	0.03
GPATCH2	242224_at	NA	272	85	180	68.2	<0.0001
KIAA0100	201728_s_at	NA	258	80.6	246	93.2	<0.0001
CEP55	218542_at	NA	247	77.2	48	18.2	<0.0001
TTK	204822_at	NA	220	68.8	134	50.8	<0.0001
LOC130576	228360_at	NA	216	67.5	71	26.9	<0.0001
IGSF11	228375_at	NA	195	60.9	33	12.5	<0.0001
CDCA1	223381_at	NA	187	58.4	148	56.1	0.6
SPEF2	232745_x_at	NA	184	57.5	64	24.2	<0.0001
NOL4	206045_s_at	NA	174	54.4	112	42.4	0.005
TMEM108	223524_s_at	NA	154	48.1	11	4.2	<0.0001
ELOVL4	219532_at	NA	147	45.9	10	3.8	<0.0001
PEPP2	220952_s_at	NA	146	45.6	115	43.6	0.7
PTPN20A	215172_at	NA	106	33.1	17	6.4	<0.0001

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Gene symbol	Probe set	Tissue restriction	Newly diagnosed		Relapse		P value Bold, significant
			n	%	n	%	
PRAME	204086_at	NA	102	31.9	100	37.9	0.1
ODF1	214485_at	NA	91	28.4	12	4.5	<0.0001
GPAT2	235557_at	NA	85	26.6	43	16.3	0.003
ARX	238878_at	NA	80	25	14	5.3	<0.0001
ANKRD45	236421_at	NA	69	21.6	7	2.7	<0.0001
CCDC62	231567_s_at	NA	65	20.3	41	15.5	0.2
IMP-3	203820_s_at	NA	64	20	19	7.2	<0.0001
LOC440934	230844_at	NA	61	19.1	0	0	<0.0001
ODF2	225617_at	NA	47	14.7	69	26.1	0.001
MAEL	229475_at	NA	36	11.3	14	5.3	0.01
SPANXB2	220921_at	NA	27	8.4	5	1.9	0.0004
CPXCR1	1560493_a_at	testis-restricted	165	51.6			
MAGEB6	1552858_at	testis-restricted	24	7.5			
Cxorf61	1559258_a_at	testis-restricted	23	7.2			
DDX53	1555357_at	testis-restricted	13	4.1			
CCDC36	1569690_at	testis-selective	180	56.3			
CCDC33	1563090_at	testis-selective	61	19.1			
CTCF1	1552368_at	testis-selective	27	8.4			
FMR1NB	1552906_at	testis-selective	24	7.5			
SLCO6A1	1552745_at	testis-selective	5	1.6			
COX6B2	1553367_a_at	testis-selective	1	0.3			
FAM46D	1552461_at	NA	26	8.1			

Online Supplementary Table S5.

Table S5A

Gene symbol	Probe set	Tissue restriction	Newly diagnosed		Relapse		P value Bold, significant
			n	%	n	%	
MAGEB3	207579_at	testis-restricted	9	2.8	8	3	1
CXorf48	221121_at	testis-restricted	8	2.5	6	2.3	1
DKKL1	220284_at	testis-restricted	0	0	0	0	NA
SPANXA1	220922_s_at	testis-restricted	0	0	0	0	NA
PASD1	240687_at	testis/brain-restricted	11	3.4	6	2.3	0.5
HORMAD1	223861_at	testis/brain-restricted	7	2.2	0	0	0.02

Table S5B

Gene symbol	Probe set	Tissue restriction	Newly diagnosed		Relapse		P value Bold, significant
			n	%	n	%	
NLRP4	242334_at	testis-selective	12	3.8	3	1.1	0.06
TDRD1	221018_s_at	testis-selective	11	3.4	8	3	0.8
TULP2	206733_at	testis-selective	9	2.8	11	4.2	0.5
SYCE1	233084_s_at	testis-selective	7	2.2	0	0	0.02
ADAM2	207664_at	testis-selective	5	1.6	0	0	0.07
TDRD6	232692_at	testis-selective	5	1.6	0	0	0.07
RBM46	244351_at	testis-selective	4	1.3	1	0.4	0.4
BRDT	206787_at	testis-selective	3	0.9	3	1.1	1
HSPB9	230510_at	testis-selective	3	0.9	0	0	0.3
MAGEA8	210274_at	testis-selective	3	0.9	5	1.9	0.5
ADAM29	221337_s_at	testis-selective	2	0.6	0	0	0.5
MAGEA11	210503_at	testis-selective	2	0.6	0	0	0.5
NXF2	220981_x_at	testis-selective	2	0.6	0	0	0.5
TSP50	220126_at	testis-selective	2	0.6	0	0	0.5
AKAP3	207344_at	testis-selective	0	0	0	0	NA
ARMC3	240275_at	testis-selective	0	0	2	0.8	0.2
KLKBL4	231287_s_at	testis-selective	0	0	0	0	NA
TAF7L	220325_at	testis-selective	0	0	0	0	NA
TEX15	221448_s_at	testis-selective	0	0	0	0	NA
TSSK6	224409_s_at	testis-selective	0	0	0	0	NA

Table S5C

Gene symbol	Probe set	Tissue restriction	Newly diagnosed		Relapse		P value Bold, significant
			n	%	n	%	
LY6K	223687_s_at	NA	11	3.4	6	2.3	0.5
TEX101	223906_s_at	NA	9	2.8	6	2.3	0.8
IL13RA2	206172_at	NA	8	2.5	1	0.4	0.05
CT45A5	235700_at	NA	4	1.3	4	1.5	1
DPPA2	240301_at	NA	3	0.9	3	1.1	1
PRM1	206358_at	NA	3	0.9	0	0	0.3
AKAP4	207019_s_at	NA	2	0.6	1	0.4	1
LOC348120	231132_at	NA	2	0.6	0	0	0.5
LOC196993	214418_at	NA	0	0	0	0	NA
PRM2	210122_at	NA	0	0	0	0	NA

Table S5D

Gene symbol	Probe set	Tissue restriction	Newly diagnosed	
			n	%
ODF4	1552408_at	NA	14	4.4
CT45A1	1567912_s_at	NA	10	3.1
CALR3	1552421_a_at	NA	3	0.9
POTE15	1553474_at	NA	3	0.9
OTOA	1553432_s_at	NA	1	0.3
SPATA19	1559138_a_at	NA	1	0.3
CAGE1	1563787_a_at	NA	0	0
ODF3	1553051_s_at	NA	0	0

Online Supplementary Table S6. Level of expression in gene presence calls. For each gene, cases with a present call were split into those with expression for that gene higher than study specific cut off of expression within that gene or lower than the cut off. Significance of difference in high expression frequency is given with an asterisk. Fisher's Exact test with Benjamini-Hochberg correction (5%). The 80th percentile *per* gene within the cases with present calls was calculated. The median of this value was used as a cut off for determining high expression. All data sets were median centered and standard deviation was set to 1.

Symbol	Probe set	Newly diagnosed	High expression	Relapsed	High expression	Significance
			%		%	
MAGEC1	206609_at	228 (71.3%)	17%	160 (60.6%)	11%	
MAGEB2	206218_at	151 (47.2%)	9%	73 (27.7%)	21%	
SSX1	206626_x_at	97 (30.3%)	19%	78 (29.5%)	14%	
MAGEA1	207325_x_at	70 (21.9%)	23%	42 (15.9%)	31%	
TSPY1	207918_s_at	34 (10.6%)	21%	36 (13.6%)	19%	
MAGEA2	214603_at	30 (9.4%)	57%	22 (8.3%)	32%	
TEX14	221035_s_at	23 (7.2%)	30%	8 (3%)	100% *	
SSX2	210497_x_at	21 (6.6%)	76%	17 (6.4%)	59%	
PAGE2	231307_at	19 (5.9%)	58%	6 (2.3%)	100%	
MAGEB1	207534_at	17 (5.3%)	53%	10 (3.8%)	70%	
MAGEB4	207580_at	17 (5.3%)	53%	3 (1.1%)	0%	
SPANXC	220217_x_at	16 (5%)	19%	8 (3%)	0%	
SSX3	211670_x_at	9 (2.8%)	67%	15 (5.7%)	53%	
FAM133A	239481_at	276 (86.3%)	12%	209 (79.2%)	8%	
CTNNA2	205373_at	194 (60.6%)	12%	70 (26.5%)	21%	
CTAGE1	220957_at	180 (56.3%)	11%	242 (91.7%)	4%	
MAGEC2	220062_s_at	93 (29.1%)	12%	25 (9.5%)	44% *	
GAGE4	208155_x_at	53 (16.6%)	15%	188 (71.2%)	4% *	
GAGE8	207086_x_at	48 (15%)	21%	162 (61.4%)	4% *	
MAGEA9	210437_at	35 (10.9%)	17%	15 (5.7%)	53%	
SPAG9	212470_at	320 (100%)	4%	263 (99.6%)	7%	
CTAGES	215930_s_at	306 (95.6%)	8%	128 (48.5%)	6%	
PBK	219148_at	301 (94.1%)	5%	228 (86.4%)	5%	
ZNF165	206683_at	266 (83.1%)	11%	36 (13.6%)	39% *	
JARID1B	211202_s_at	264 (82.5%)	8%	89 (33.7%)	11%	
CASC5	228323_at	238 (74.4%)	7%	236 (89.4%)	6%	
CEP290	205250_s_at	218 (68.1%)	14%	135 (51.1%)	13%	
OIP5	213599_at	218 (68.1%)	10%	98 (37.1%)	12%	
CCDC110	230900_at	207 (64.7%)	14%	48 (18.2%)	10%	
MPHOSPH1	205235_s_at	196 (61.3%)	17%	20 (7.6%)	25%	
MORC1	220850_at	184 (57.5%)	16%	86 (32.6%)	10%	
ACRBP	223717_s_at	144 (45%)	14%	20 (7.6%)	15%	
MAGEA6	214612_x_at	144 (45%)	15%	130 (49.2%)	16%	
FATE1	231573_at	126 (39.4%)	16%	93 (35.2%)	5%	
SPA17	205406_s_at	122 (38.1%)	16%	24 (9.1%)	29%	
MAGEA3	209942_x_at	121 (37.8%)	21%	125 (47.3%)	15%	
SSX4	210394_x_at	110 (34.4%)	18%	78 (29.5%)	17%	
TSGA10	220623_s_at	109 (34.1%)	16%	13 (4.9%)	0%	
SPO11	222259_s_at	89 (27.8%)	12%	3 (1.1%)	33%	
MAGEA5	214642_x_at	82 (25.6%)	22%	37 (14%)	41%	
DDX43	220004_at	77 (24.1%)	40%	42 (15.9%)	45%	
TPTE	220205_at	77 (24.1%)	10%	90 (34.1%)	17%	
XAGE1	220057_at	65 (20.3%)	29%	66 (25%)	23%	
SPACA3	243621_at	61 (19.1%)	10%	67 (25.4%)	10%	
CTAG1B	211674_x_at	60 (18.8%)	32%	43 (16.3%)	26%	
CTAG2	215733_x_at	54 (16.9%)	31%	38 (14.4%)	34%	
MAGEA12	210467_x_at	49 (15.3%)	31%	89 (33.7%)	11%	
C21orf99	237794_at	47 (14.7%)	23%	103 (39%)	12%	
CABYR	219928_s_at	41 (12.8%)	27%	2 (0.8%)	50%	
LDHC	207022_s_at	36 (11.3%)	61%	0 (0%)	0%	
DSCR8	241224_x_at	33 (10.3%)	48%	24 (9.1%)	88% *	
LEMD1	229927_at	28 (8.8%)	14%	27 (10.2%)	15%	
ROPN1	233203_at	28 (8.8%)	11%	44 (16.7%)	9%	
CRISP2	210262_at	20 (6.3%)	15%	7 (2.7%)	100% *	
SYCP1	206740_x_at	18 (5.6%)	17%	11 (4.2%)	9%	
MAGEA4	214254_at	10 (3.1%)	70%	15 (5.7%)	67%	
SPINLW1	206318_at	5 (1.6%)	100%	53 (20.1%)	13% *	
PIWIL2	220686_s_at	2 (0.6%)	0%	61 (23.1%)	13%	
SPAG4	219888_at	320 (100%)	8%	257 (97.3%)	6%	
TCCS2	224789_at	319 (99.7%)	7%	264 (100%)	4%	
RQCD1	213179_at	318 (99.4%)	8%	264 (100%)	6%	
TMEFF1	205122_at	296 (92.5%)	7%	94 (35.6%)	15%	
TMEFF2	224321_at	288 (90%)	3%	251 (95.1%)	6%	
GPATC2	242224_at	272 (85%)	8%	180 (68.2%)	6%	
KIAA100	201728_s_at	258 (80.6%)	10%	246 (93.2%)	6%	
CEP55	218542_at	247 (77.2%)	8%	48 (18.2%)	35% *	
TTK	204822_at	220 (68.8%)	12%	134 (50.8%)	9%	
LOC130576	228360_at	216 (67.5%)	16%	71 (26.9%)	25%	
IGSF11	228375_at	195 (60.9%)	12%	33 (12.5%)	21%	
CDCA1	223381_at	187 (58.4%)	13%	148 (56.1%)	9%	
SPEF2	232745_x_at	184 (57.5%)	13%	64 (24.2%)	33% *	
NOL4	206045_s_at	174 (54.4%)	11%	112 (42.4%)	15%	
TMEM108	223524_s_at	154 (48.1%)	18%	11 (4.2%)	64% *	
ELOVL4	219532_at	147 (45.9%)	17%	10 (3.8%)	70% *	
PEPP2	220952_s_at	146 (45.6%)	20%	115 (43.6%)	13%	
PTPN20A	215172_at	106 (33.1%)	24%	17 (6.4%)	41%	
PRAME	204086_at	102 (31.9%)	23%	100 (37.9%)	9%	
ODF1	214485_at	91 (28.4%)	8%	12 (4.5%)	17%	
GPAT2	235557_at	85 (26.6%)	31%	43 (16.3%)	35%	
ARX	238878_at	80 (25%)	13%	14 (5.3%)	43%	
ANKRD45	236421_at	69 (21.6%)	19%	7 (2.7%)	71% *	
CCDC62	231567_s_at	65 (20.3%)	22%	41 (15.5%)	20%	
IMP-3	203820_s_at	64 (20%)	9%	19 (7.2%)	16%	
LOC440934	230844_at	61 (19.1%)	20%	0 (0%)	0%	
ODF2	225617_at	47 (14.7%)	17%	69 (26.1%)	10%	
MAEL	229475_at	36 (11.3%)	28%	14 (5.3%)	29%	
SPANXB2	220921_at	27 (8.4%)	26%	5 (1.9%)	60%	

Online Supplementary Table S7. Evaluation of presence of gene expression in normal plasma cells (GSE6477). Order of genes corresponds to Table 1; 84 genes, present on this platform were considered.

Probe set	Symbol	Tissue restriction	
		Normal n	%
206609_at	MAGEC1	1	7% testis-restricted
206218_at	MAGEB2	4	27% testis-restricted
206626_x_at	SSX1	0	0% testis-restricted
207325_x_at	MAGEA1	0	0% testis-restricted
207918_s_at	TSPY1	0	0% testis-restricted
214603_at	MAGEA2	0	0% testis-restricted
221035_s_at	TEX14	0	0% testis-restricted
210497_x_at	SSX2	0	0% testis-restricted
207534_at	MAGEB1	0	0% testis-restricted
207580_at	MAGEB4	0	0% testis-restricted
220217_x_at	SPANXC	1	7% testis-restricted
211670_x_at	SSX3	0	0% testis-restricted
205373_at	CTNNA2	0	0% testis/brain-restricted
220957_at	CTAGE1	14	93% testis/brain-restricted
220062_s_at	MAGEC2	0	0% testis/brain-restricted
208155_x_at	GAGE4	5	33% testis/brain-restricted
207086_x_at	GAGE8	2	13% testis/brain-restricted
210437_at	MAGEA9	0	0% testis/brain-restricted
212470_at	SPAG9	15	100% testis-selective
215930_s_at	CTAGE5	7	47% testis-selective
219148_at	PBK	9	60% testis-selective
206683_at	ZNF165	4	27% testis-selective
211202_s_at	JARID1B	6	40% testis-selective
205250_s_at	CEP290	5	33% testis-selective
213599_at	OIP5	0	0% testis-selective
205235_s_at	MPHOSPH1	0	0% testis-selective
220850_at	MORC1	0	0% testis-selective
214612_x_at	MAGEA6	0	0% testis-selective
205406_s_at	SPA17	0	0% testis-selective
209942_x_at	MAGEA3	0	0% testis-selective
210394_x_at	SSX4	0	0% testis-selective
220623_s_at	TSGA10	0	0% testis-selective
222259_s_at	SPO11	0	0% testis-selective
214642_x_at	MAGEA5	0	0% testis-selective
220004_at	DDX43	2	13% testis-selective
220205_at	TPTE	2	13% testis-selective
220057_at	XAGE1	0	0% testis-selective
211674_x_at	CTAG1B	0	0% testis-selective
215733_x_at	CTAG2	0	0% testis-selective
210467_x_at	MAGEA12	0	0% testis-selective
219928_s_at	CABYR	0	0% testis-selective
207022_s_at	LDHC	0	0% testis-selective
210262_at	CRISP2	0	0% testis-selective
206740_x_at	SYCP1	0	0% testis-selective
214254_at	MAGEA4	0	0% testis-selective
206318_at	SPINLW1	2	13% testis-selective
220686_s_at	PIWIL2	5	33% testis-selective
219888_at	SPAG4	15	100% NA
213179_at	RQCD1	14	93% NA
205122_at	TMEFF1	2	13% NA
201728_s_at	KIAA0100	9	60% NA
218542_at	CEP55	0	0% NA
204822_at	TTK	0	0% NA
206045_s_at	NOL4	0	0% NA
219532_at	ELOVL4	0	0% NA
220952_s_at	PEPP2	10	67% NA
215172_at	PTPN20A	0	0% NA
204086_at	PRAME	4	27% NA
214485_at	ODF1	4	27% NA
203820_s_at	IMP-3	1	7% NA
220921_at	SPANXB2	1	7% NA
207579_at	MAGEB3	0	0% testis-restricted
221121_at	CXorf48	0	0% testis-restricted
220284_at	DKKL1	0	0% testis-restricted
220922_s_at	SPANXA1	0	0% testis-restricted
221018_s_at	TDRD1	0	0% testis-selective
206733_at	TULP2	0	0% testis-selective
207664_at	ADAM2	0	0% testis-selective
206787_at	BRDT	0	0% testis-selective
210274_at	MAGEA8	0	0% testis-selective
221337_s_at	ADAM29	0	0% testis-selective
210503_at	MAGEA11	0	0% testis-selective
220981_x_at	NXF2	0	0% testis-selective
220126_at	TSP50	0	0% testis-selective
207344_at	AKAP3	0	0% testis-selective
220325_at	TAF7L	0	0% testis-selective
221448_s_at	TEX15	0	0% testis-selective
206172_at	IL13RA2	0	0% NA
206358_at	PRM1	0	0% NA
207019_s_at	AKAP4	0	0% NA
214418_at	LOC196993	0	0% NA
210122_at	PRM2	0	0% NA

Online Supplementary Table S8. Significant genes in univariate Kaplan-Meier analysis.

Gene family	Family member	Probe set	<i>P</i> values			
			Kaplan-Meier APEX OS	Kaplan-Meier APEX PFS	Kaplan-Meier H65 OS	Kaplan-Meier H65 PFS
SSX	SSX1	206626_x_at	1.1E-04	3.8E-03	1.7E-03	2.0E-04
MAGEA	MAGEA2	214603_at	1.1E-04	2.8E-03	1.1E-03	
MAGEA	MAGEA1	207325_x_at	2.2E-03		1.5E-03	3.3E-05
MAGEA	MAGEA3	209942_x_at	1.8E-04		2.2E-03	6.1E-05
MAGEA	MAGEA6	214612_x_at	4.9E-04		2.5E-03	5.0E-05
SSX	SSX4	210394_x_at	1.9E-06	7.9E-05	1.9E-03	
CEP55	CEP55	218542_at	1.4E-03			2.7E-03
MAGEA	MAGEA5	214642_x_at			5.7E-03	2.0E-03
MAGEA	MAGEA12	210467_x_at	1.5E-02			1.6E-03
MAGEB	MAGEB2	206218_at	1.4E-02	7.7E-05		
NUF2/CDCA1	CDCA1	223381_at			4.5E-04	6.2E-04
NY-ESO-1	CTAG2	215733_x_at	6.3E-06	9.0E-12		
NY-ESO-1	CTAG1B	211674_x_at	4.1E-05	8.0E-06		
OIP5	OIP5	213599_at	2.4E-03			3.5E-03
SSX	SSX2	210497_x_at	6.2E-06	8.8E-07		
XAGE	XAGE1	220057_at	7.6E-06	3.9E-03		
AF15q14	CASC5	228323_at			4.2E-03	
CEP290	CEP290	205250_s_at	1.1E-02			
CT96	TTK	204822_at			6.1E-03	
GAGE	GAGE8	207086_x_at	9.0E-03			
IMP-3	IMP-3	203820_s_at	4.7E-03			
JARID1B	JARID1B	211202_s_at	3.3E-03			
MAEL	MAEL	229475_at	1.5E-03			
MAGEA	MAGEA9	210437_at			2.9E-03	
MAGEC2	MAGEC2	220062_s_at	2.7E-03			
MMA1	DSCR8	241224_x_at	3.3E-04			
ODF2	ODF2	225617_at	4.2E-03			
SPA17	SPA17	205406_s_at		1.1E-03		