

The specific transcriptional profile and clonal selection of monoclonal gammopathy of undetermined significance-like behavior predict an exceptionally favorable prognosis in multiple myeloma

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Supplementary data For

The Specific Transcriptional Signature and Clonal Selection of MGUS-like Behavior Predict an Exceptionally Favorable Prognosis in Multiple Myeloma

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Contents:

Table S1: Clinical features and therapeutic options: MGUS-like vs. Classical MM cohort

Table S2: Details and description of MGUS-like 44-gene signature

Figure S1: Validation of the specific MGUS-like gene signature: (A) The baseline features of two subsets of according to MGUS-like gene signature score in MMRF cohort. Statistical significance was determined by Chi-square test. (B-C) PFS and OS of patients according to MGUS-like signature score. (D) Cox regression model of PFS and OS for MGUS-like gene signature. (E-F) PFS and OS of MGUS-like high patients according to achievement of CR. Log rank (Mantel-Cox) test was used for comparison of survival curves.

Table S1 Clinical features and therapeutic options: MGUS-like vs. Classical MM cohort

Clinical features and treatment (%)	All patients (n=632)	MGUS-like (n=35)	Classical MM (n=513)	<i>P</i> value
Age (median; years)	58(29-83)	56(38-70)	58(29-79)	0.093
Sex	M:366, F:266	M:15, F:20	M:306, F:207	0.075
M-component				0.841
IgG	306(48.4)	18 (51.4)	242 (47.2)	
IgA	146(23.1)	8 (22.9)	120 (23.4)	
Light chain	122(19.3)	5 (14.3)	103 (20.1)	
Others	58(9.2)	4 (11.4)	48 (9.3)	
ISS staging				0.050
I	115(18.2)	9 (25.7)	91 (17.7)	
II	232(36.7)	17(48.6)	186 (36.3)	
III	285(45.1)	9 (25.7)	236 (46.0)	
RISS staging				0.229
I	78/592(13.2)	5/33 (15.2)	61/484(12.6)	
II	398/592(67.2)	25/33 (75.8)	318/484(65.7)	
III	116/592(19.6)	3/33 (9.1)	105/484(21.7)	
Anemia	409/631(64.8)	15/35(42.9)	340/513(66.3)	0.009
Thrombocytopenia	69/628(11.0)	1/35(2.9)	60/510 (11.8)	0.161
Renal dysfunction	78/632(12.3)	3/35(8.6)	67/513(13.1)	0.603
Elevated LDH	102/628(16.2)	3/35(8.6)	92/509(18.1)	0.175
Bone disease	533/608(87.7)	23/32(71.9)	445/493(90.3)	0.004
Extramedullary disease (EMD)	114/608(18.7)	4/32(12.5)	100/493(20.3)	0.364
Immunoparesis	505/612(82.5)	25/33(75.8)	416/497(83.7)	0.233
Cytogenetic abnormality				
Del (17p)	61/619(9.9)	3/35(8.6)	56/502(11.2)	0.786
Del (13q)	278/593(46.9)	16/35(45.7)	230/482(47.7)	0.862
t (4;14)	88/540(16.3)	4/33(12.1)	75/439(17.1)	0.630
t (14;16)	14/531(2.6)	0/33	14/431(3.2)	0.613
t (14;20)	3/505(0.6)	0/31	2/409(0.5)	1.000
t (11;14)	89/526(16.9)	10/30(33.3)	65/430(15.1)	0.018
Gain (1q)	277/592(46.8)	11/34(32.4)	240/480(50.0)	0.052
HRCAs	151/540(28.0)	7/34(20.6)	133/437(30.4)	0.250
Therapeutic options				
First-line treatment				0.179
BTZ+Len-based	119(18.8)	1(2.9)	92(17.9)	
BTZ+Tha-based	26(4.1)	1(2.9)	21(4.1)	
BTZ-based	398(63.0)	28(80.0)	330(64.3)	
Len-based	34(5.4)	1(2.9)	25(4.9)	
Tha-based	55(8.7)	4(11.4)	45(8.5)	
ASCT	183(29.0)	6(17.1)	170(33.1)	0.060

Data are presented as n (%) and median (range) unless otherwise indicated. Abbreviations: M=male;

F=female; ISS: international staging system; R-ISS: Revised-ISS; Anemia: hemoglobin<100g/L; Thrombocytopenia: platelets<100×10³/μL; Renal dysfunction: serum creatinine>177μmol/L; Elevated LDH: lactate dehydrogenase>247U/L; Immunoparesis: serum IgM< 0.46g/L; HRCAs: high risk cytogenetic abnormalities, including t(4;14), t(14;16) or del (17p); BTZ: Bortezomib; Len: Lenalidomide; Tha: Thalidomide; ASCT: auto stem cell transplantation.

Table S2 MGUS-like 44-genes signature

Ensembl Gene ID	Weight	Gene Symbol	Chromosome	Description
ENSG00000123130	6.23458902	ACOT9	chrX	Acyl-CoA Thioesterase 9
ENSG00000169877	22.0583512	AHSP	chr16	Alpha Hemoglobin Stabilizing Protein
ENSG00000136872	15.3174976	ALDOB	chr9	Aldolase, Fructose-Bisphosphate B
ENSG00000167772	13.122381	ANGPTL4	chr19	Angiopoietin Like 4
ENSG00000273017	29.7764523		chr21	
ENSG00000128335	6.61929413	APOL2	chr22	Apolipoprotein L2
ENSG00000172232	16.1929677	AZU1	chr19	Azurocidin 1
ENSG00000164047	13.3004335	CAMP	chr3	Cathelicidin Antimicrobial Peptide
ENSG00000105369	20.7505632	CD79A	chr19	CD79a Molecule
ENSG00000111328	7.26833006	CDK2AP1	chr12	Cyclin Dependent Kinase 2 Associated Protein 1
ENSG00000105205	16.2975883	CLC	chr19	Charcot-Leyden Crystal Galectin
ENSG00000182871	44.9499241	COL18A1	chr21	Collagen Type XVIII Alpha 1 Chain
ENSG00000088882	23.9269288	CPXM1	chr20	Carboxypeptidase X, M14 Family Member 1
ENSG00000135144	26.545797	DTX1	chr12	Deltex E3 Ubiquitin Ligase 1
ENSG00000221968	9.69789695	FADS3	chr11	Fatty Acid Desaturase 3
ENSG00000077942	20.6569389	FBLN1	chr22	Fibulin 1
ENSG00000184922	6.96207788	FMNL1	chr17	Formin Like 1
ENSG00000167468	6.15116916	GPX4	chr19	Glutathione Peroxidase 4
ENSG00000231389	21.4965284	HLA-DPA1	chr6	Major Histocompatibility Complex, Class II, DP Alpha 1
ENSG00000196126	12.9948399	HLA-DRB1	chr6	Major Histocompatibility Complex, Class II, DR Beta 1
ENSG00000198502	27.8530267	HLA-DRB5	chr6	Major Histocompatibility Complex, Class II, DR Beta 5
ENSG00000157992	13.0590514	KRTCAP3	chr2	Keratinocyte Associated Protein 3
ENSG00000175445	14.6916764	LPL	chr8	Lipoprotein Lipase
ENSG00000172264	24.7507874	MACROD2	chr20	Mono-ADP Ribosylhydrolase 2
ENSG00000176845	12.9115057	METRNL	chr17	Meteorin Like, Glial Cell Differentiation Regulator

ENSG00000167634	24.6233668	NLRP7	chr19	NLR Family Pyrin Domain Containing 7
ENSG00000254206	11.2973423	NPIP11	chr16	Nuclear Pore Complex Interacting Protein Family Member B11
ENSG00000099250	24.0825169	NRP1	chr10	Neuropilin 1
ENSG00000046651	5.73131948	OFD1	chrX	OFD1 Centriole And Centriolar Satellite Protein
ENSG00000181649	13.3506705	PHLDA2	chr11	Pleckstrin Homology Like Domain Family A Member 2
ENSG00000007541	7.43247919	PIGQ	chr16	Phosphatidylinositol Glycan Anchor Biosynthesis Class Q
ENSG00000090924	13.920942	PLEKHG2	chr19	Pleckstrin Homology And RhoGEF Domain Containing G2
ENSG00000196415	17.3506422	PRTN3	chr19	Proteinase 3
ENSG00000266677	15.2804003		chr17	
ENSG00000170989	12.534374	S1PR1	chr1	Sphingosine-1-Phosphate Receptor 1
ENSG00000145284	19.4549282	SCD5	chr4	Stearoyl-CoA Desaturase 5
ENSG00000170542	18.4258409	SERPINB9	chr6	Serpin Family B Member 9
ENSG00000120057	47.2660388	SFRP5	chr10	Secreted Frizzled Related Protein 5
ENSG00000115616	29.3188604	SLC9A2	chr2	Solute Carrier Family 9 Member A2
ENSG00000073861	19.3868913	TBX21	chr17	T-Box Transcription Factor 21
ENSG00000088992	15.0466978	TESC	chr12	Tescalcin
ENSG00000157873	5.27539437	TNFRSF14	chr1	TNF Receptor Superfamily Member 14
ENSG00000174521	11.7745518	TTC9B	chr19	Tetratricopeptide Repeat Domain 9B
ENSG00000128218	59.6075848	VPREB3	chr22	V-Set Pre-B Cell Surrogate Light Chain 3

Figure S1

