Table 8S. HCDR3-driven clustering among multiple myeloma total series and non-multiple myeloma cohort

Sequence accession number	ENTITY	HCDR3 AA sequence (IMGT)	HCDR3 AA identity	HCDR3 AA lenght	IGHV gene	IGHD gene	IGHD reading frame	IGHJ gene	% IDENTITY TO GERMLINE
TO35	MM	C ARENKHEWLVLNYNWFDP W	78,00%	18	IGHV3-21*01	IGHD6-19*01	3	IGHJ5*02	98.92%
AF301524	NHL MALT	C ARANKEQWLVLEYNWFDP W		18	IGHV3-48*02	IGHD6-19*01	3	IGHJ5*01	99.15%
	Subset N1	** **.:****:******							
TO109	MM	C ARPHYCSATTCTGPMHY W	82,00%	17	IGHV4-34*01	IGHD2-2*01	2	IGHJ4*02	90.73%
Z46320	EBV infected B-cell	C ARPHYCSATTCSGPVEY W		17	IGHV4-34*01	IGHD2-2*02	2	IGHJ4*02	95.65%
	Subset N2	***********:**:.*							
TO57	MM	C AKDPGDDFWRGYP-DY W	80,00%	15	IGHV3-30*03	IGHD3-3*01	2	IGHJ4*02	92.44%
AM077130	Healthy B-cell	C AKDLG-DFWSGYPEDY W		15	IGHV3-23*01	IGHD3-3*01	2	IGHJ4*02	99.31%
	Subset N3	*** * *** *** **							
TO48	MM	C AKD-RRGYSYGFLDI W	86,00%	14	IGHV3-23*01	IGHD5-5*01	3	IGHJ4*02	90.77%
AF103111	Healthy B-cell	C AKDSRRGYSYG-LDY W		14	IGHV3-33*01	IGHD5-5*01	3	IGHJ4*02	97.29%
	Subset N4	*** ******* **							

Table legend

* = identical AA residues in both sequences

: = different but highly conserved (very similar) AA

. = different but similar AA

(blank) = dissimilar AA or gaps

Abbreviations

HCDR3, complementarity determining region 3 on heavy chain gene; MM, multiple myeloma; NHL MALT, non Hodgkin Lymphoma involving the mucosa-associated lymphoid tissue; EBV, Epstein-Barr Virus; AA, aminoacids; IMGT, identified by ImMunoGeneTics V-QUEST tools (http://imgt.cines.fr/), see in text reference 20; IGHV, immunoglobulin heavy chain variable gene; IGHD, immunoglobulin heavy chain diversity gene; IGHJ, immunoglobulin heavy chain junction gene.

All MM sequences belong to Institutional Series. Non-MM sequences could be retrieved from NCBI public databases (http://www.ncbi.nlm.nih.gov/)