

## Multiple myeloma shows no intra-disease clustering of immunoglobulin heavy chain genes

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[Online Supplementary Table 1S.](#) Final collection of 214 unique *IGHV* multiple myeloma sequences (Literature Series-LS). [SEE PDF FILE](#)

[Online Supplementary Table 2S.](#) Final collection of 131 unique *IGHV* multiple myeloma sequences (Institutional Series, IS). [SEE PDF FILE](#)

[Online Supplementary Table 3S.](#) Final collection of 28,376 unique *IGHV* sequences of non-multiple myeloma cohort.

ENTITY	# <i>IGHV</i> sequences
B-cell lymphoproliferative disorders	4291 (1106 lymphomas; 3185 CLL)
Normal B cells	16288 (including 461 PC from healthy donors)
Immunoderegulation disorders (allergy, asthma, various types of immunodeficiency)	4614
Autoreactive B cells	2695
Phage display libraries	488
<b>TOTAL</b>	<b>28376</b>

*IGHV*: immunoglobulin heavy chain gene; *CLL*: chronic lymphocytic leukemia; *PC*: plasma cells. The complete database is available upon request.

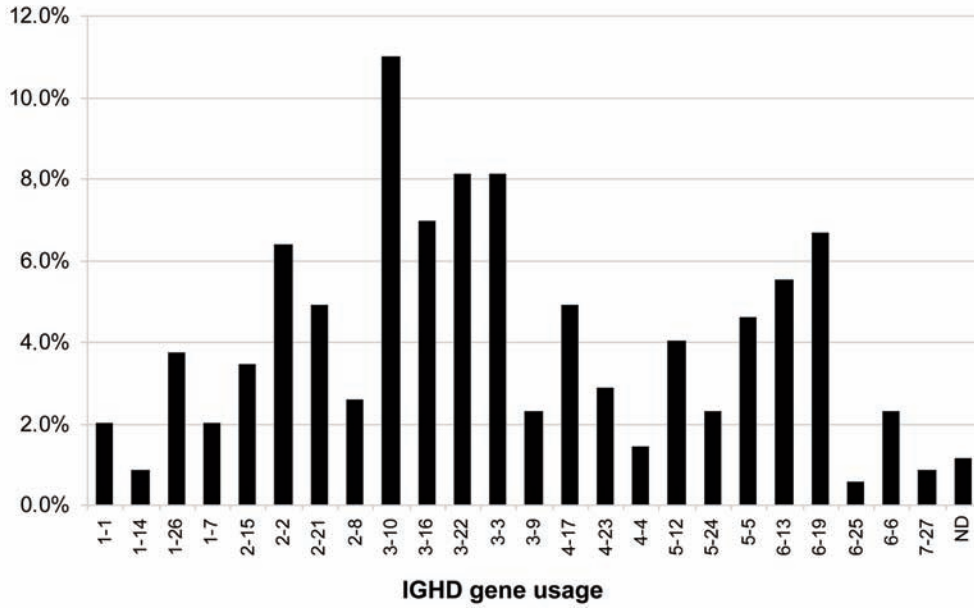
[Online Supplementary Table 4S.](#) Description of *IGHV-D-J* genes usage in multiple myeloma (MM total). [SEE PDF FILE](#)

[Online Supplementary Table 5S.](#) Comparison between multiple myeloma IS and previously published smaller multiple myeloma series in terms of *IGHV-D-J* gene usage. [SEE PDF FILE](#)

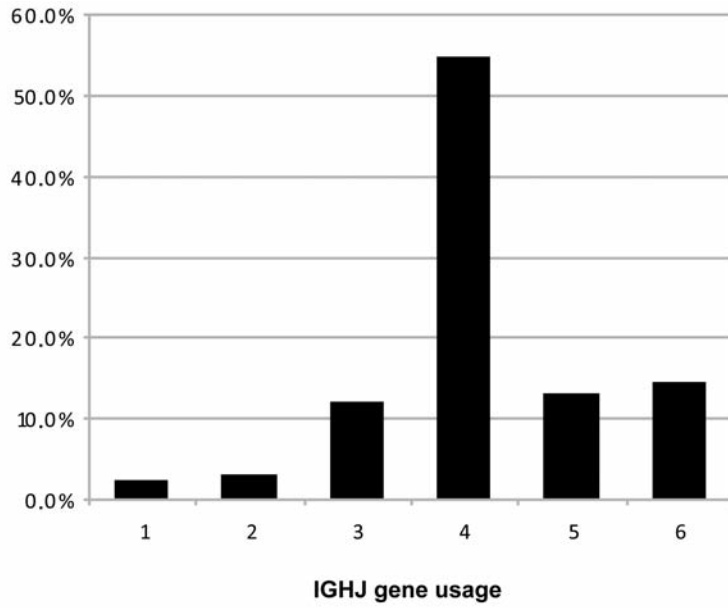
[Online Supplementary Table 6S.](#) Available biological and clinical features of multiple myeloma patients showing unmutated *IGH*. [SEE PDF FILE](#)

[Online Supplementary Table 7S.](#) The three best alignments by HCDR3 driven clustering observed among multiple myeloma sequences. [SEE PDF FILE](#)

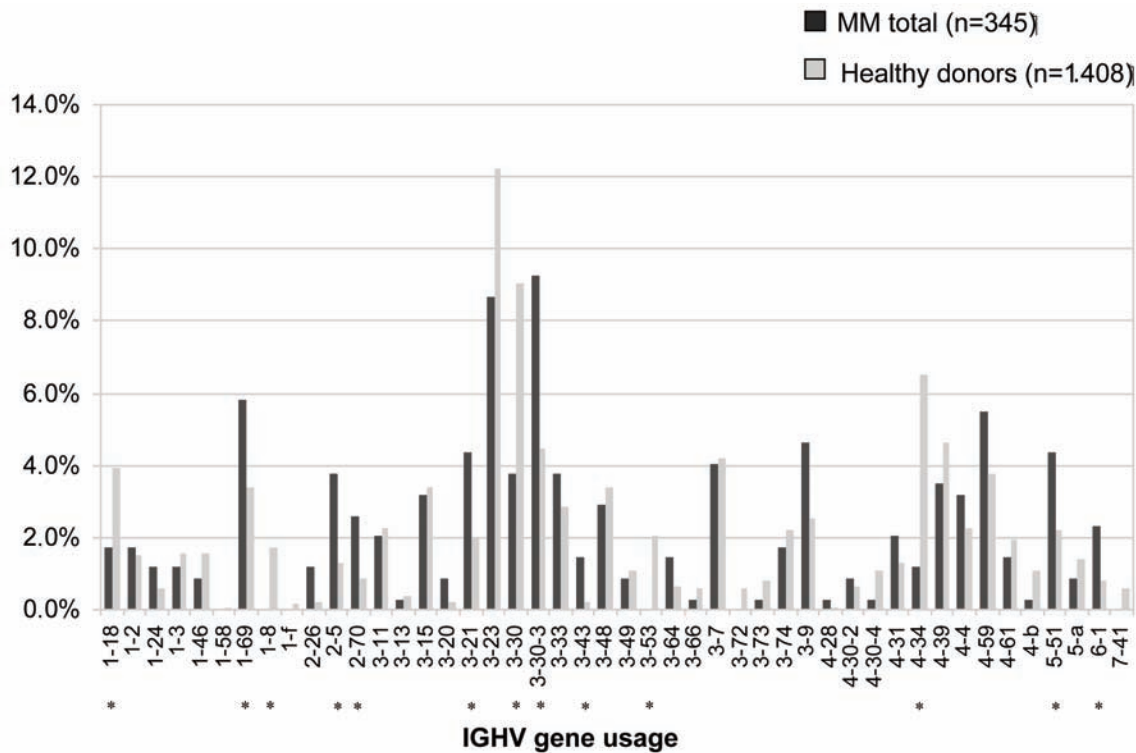
[Online Supplementary Table 8S.](#) HCDR3 driven clustering among multiple myeloma total series and non-multiple myeloma cohort. [SEE PDF FILE](#)



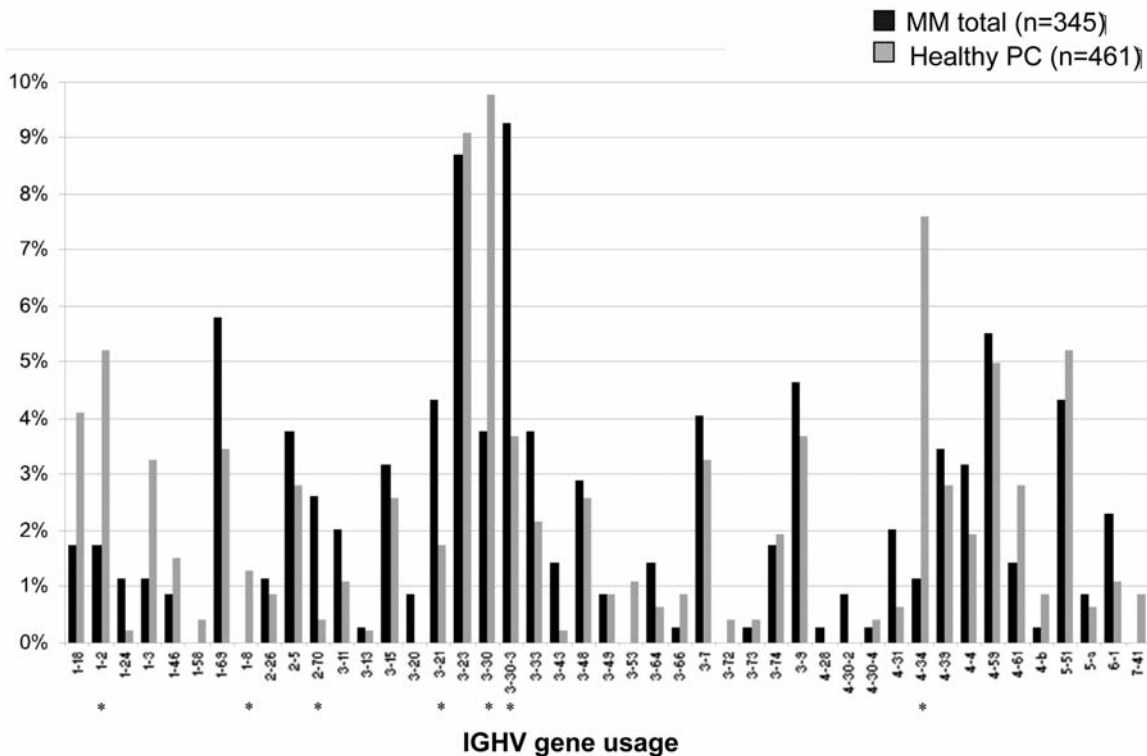
Online Supplementary Figure 1S. *IGHD* gene usage of multiple myeloma total series. MM: multiple myeloma; *IGHD*: immunoglobulin heavy chain diversity region.



Online Supplementary Figure 2S. *IGHJ* gene usage of multiple myeloma total series. MM: multiple myeloma; *IGHJ*: immunoglobulin heavy chain joining region.



Online Supplementary Figure 3S. Comparison between multiple myeloma total series and healthy donors published database in terms of *IGHV* gene usage. \*Statistically significant difference ( $P<0.05$ ) between MM total and healthy donors; <sup>1</sup> MM: multiple myeloma total, black columns; *IGHV*: immunoglobulin heavy chain variable region; gray columns, healthy donors published database.<sup>1</sup>



Online Supplementary Figure 4S. Comparison between multiple myeloma total series and healthy plasma cells published database in terms of *IGHV* gene usage. \*Statistically significant difference ( $P<0.05$ ) between MM total and healthy PC; <sup>2</sup> MM total: multiple myeloma total, black columns; PC: healthy plasma cells, gray columns; *IGHV*: immunoglobulin heavy chain variable region.

## References

- 1 Stamatopoulos K, Belessi C, Moreno C, Boudjoghra M, Guida G, Smilevska T, et al. Over 20% of patients with chronic lymphocytic leukemia carry stereotyped receptors: Pathogenetic implications and clinical correlations. *Blood* 2007;109(1):259-70.