

Table 7S. The three best alignments by HCDR3-driven clustering observed among multiple myeloma sequences

| Sequence accession number | HCDR3 AA sequence (IMGT) | HCDR3 AA identity | HCDR3 AA length | IGHV gene | IGHD gene | IGHD reading frame | IGHJ gene | % IDENTITY TO GERMLINE |
|---------------------------|---|-------------------|-----------------|--------------------|--------------------|--------------------|-----------------|------------------------|
| DQ100929 | C ARG- DS YYYYGMDV W | 78,6% | 13 | IGHV1-46 | IGHD5-24*01 | 3 | IGHJ6*02 | 92,36% |
| X79171 | C ARG NNA YYYYGMDV W | | 14 | IGHV3-30 | IGHD5-12*01 | 3 | IGHJ6*02 | 94,10% |
| | *** : :***** | | | | | | | |
| DQ100976 | C AR- RGEVT VFGADAFDV W | 64,7% | 16 | IGHV3-23*01 | IGHD3-3*01 | 3 | IGHJ3*01 | 93,40% |
| AF442765 | C AR SWG VVT IFGQ DAFDI W | | 17 | IGHV2-5*10 | IGHD3-3*01 | 3 | IGHJ3*02 | 93,81% |
| | ** * ** : ** ***** : | | | | | | | |
| X79174 | C ARGGG SGNYKEKIDF W | 60,0% | 15 | IGHV4-59*01 | IGHD2-15 | 2 | IGHJ4*02 | 91,23% |
| DQ100980 | C ARGG-SGNY- DAFDI W | | 13 | IGHV4-4*02 | IGHD3-10*01 | 2 | IGHJ3*02 | 92,36% |
| | **** ***** : :* : | | | | | | | |

Table legend

* = identical AA residues in both sequences

: = different but highly conserved (very similar) AA

(blank) = dissimilar AA or gaps

(bold) = critical features hampering an effective intra-MM clustering (different IGHV-D-J usage and differences in HCDR3 sequences AA lengths).

Abbreviations

HCDR3, complementarity determining region 3 on heavy chain gene; MM, multiple myeloma; 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.

For sequences references please see Table 1S