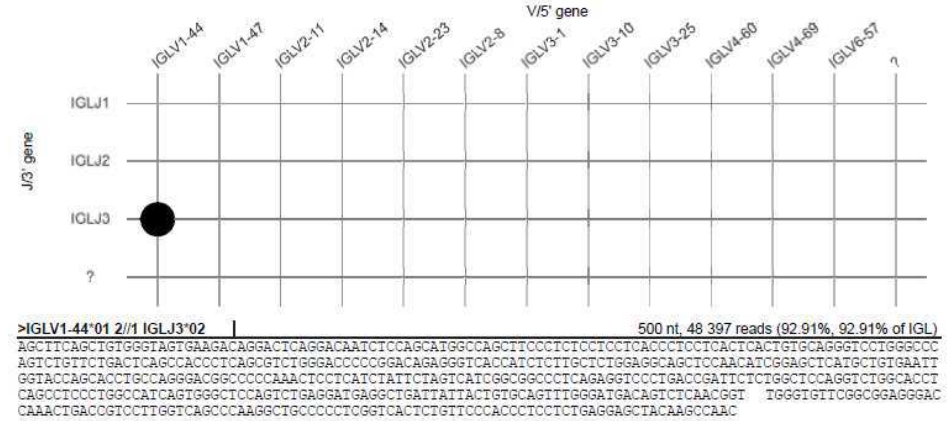


A

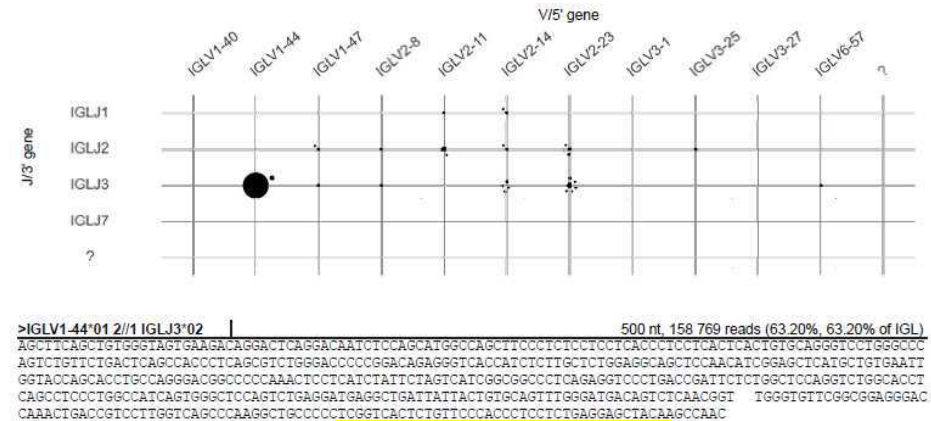
Patient Id	IGLV gene	Clone size from analyzed reads	Total number of reads per sample
p2	IGLV1-44	96.67%	228994
p4	IGLV1-44	18.64%	205251
p5	IGLV1-44	79.77%	301406
p7	IGLV1-44	91.2%*	228890
p8	IGLV1-44	91.3%*	206320
p9	IGLV1-44 and IGLV3-1	3.4% and 27.78%	217839
p10	IGLV1-44	43.62%	17225
p11	IGLV1-44	0.482%	28875
p12	IGLV1-44	4.591%	67492
p13	IGLV1-44	1.545%	36847
p14	IGLV1-44	41.95%	43677
p15	IGLV1-44	63.2%	56035
p16	IGLV1-44	49.77%	57670
p17	IGLV1-44	53.19%	160762
p18	IGLV1-44	84.89%*	291384
p19	IGLV1-40	54.98%	185639
p20	IGLV1-40	8.2%	56931
p22	IGLV1-40	45.7%	238369
p23	IGLV1-40	4.6%	125686
p24	IGLV1-40	71.93%	33789
p25	IGLV1-36	59.16%	46422
p26	IGLV1-36 and IGLV2-14	12.24% and 21.72%	107096
p27	IGLV3-1	89.3%	58365
p28	IGLV3-1	96.08%	558286
p29	IGLV3-1	2.569%	63266
p30	IGLV3-25	6.6%	168466

B

Vidjil analysis - p15 example

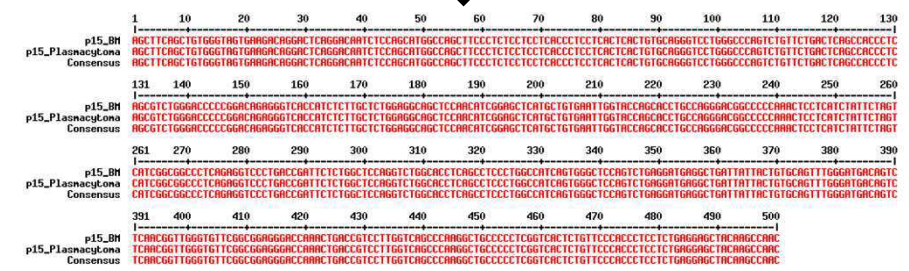


Bone marrow lesion



Bone marrow aspirate

Alignment



Supplemental Figure 1 : Analysis of the λ LC repertoire of patients with POEMS syndrome using Vidjil tool. (A) Percentage of the clonal λ LC sequences in the λ repertoire obtained with RACE-RepSeq and using Vidjil tool for analysis (www.vidjil.org). All sequences were obtained from bone marrow aspirates except for * corresponding to bone marrow lesion biopsies. (B) Example of Vidjil tool analysis for patient 15 (p15). Clonal sequences from bone marrow aspirate and lesion are identical using multalin alignment tool (<http://multalin.toulouse.inra.fr/multalin/>).



Supplemental Figure 2 : (A) Clonal VJ domain sequences obtained for three patients (p23, p9, p30) by Illumina sequencing in two independent experiments and (B) clonal VJ domain sequences obtained for two other patients (p28, p22) by Illumina sequencing in two independent experiments compared to Sanger sequencing, using multalin alignment tool (<http://multalin.toulouse.inra.fr/multalin/>).


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Com4      QSVLTQPPS-ASGTPGQRVSIISCSGS TSNI----GSNT VNWYLHLPGTAPKLLIY SN-----N QRPFGVP-DRFSGSK--SGTSASLAISGLQSEDEADYYC AAWDDSLDG
Com6      QSVLTQPPS-ASGTPGQRVTIISCSGS SSNI----GRNT VHWYQQLPGTAPKFLIF NT-----Y DRPSGVA-DRFAGSK--SDTSASLAISGLQSDDEADYYC ATWDDNLNE
AL1       QSVLTQPPS-ASGTPGQRVTIISCSGG TSNI----GDNS VHWYQQLPGTAPKLLIY SN-----D QRPFGVA-DRFSGSK--SGTSASLAISALQSEDEADYYC SSWDDSLHG
AL2       QSVLTQPPS-ASGTPGQRVTIISCSGS SSNI----ASNS VHWYQHLPGTAPKLLIY SN-----N QRPFGVP-DRFSGSK--SGTSASLAISGLQSEDEADYYC GWDDSVTG
IGLV1-44  QSVLTQPPS-ASGTPGQRVTIISCSGS SSNI----GSNT VNWYQQLPGTAPKLLIY SN-----N QRPFGVP-DRFSGSK--SGTSASLAISGLQSEDEADYYC AAWDDSLNG

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	FR1	CDR1	FR2	CDR2	FR3	CDR3
AF462673	QSVLTHPPS-VSGAPGQRVTIISCTGS	RSNIG---SGYE	IHWYQQLPGEAPQLLIY	GD-----T	NRPSGVP-DRFSGSK--SGTSASLAITGLQAEDEADYHC	QSYDISRSG
AF320834	QSVLTQPPS-VSGAPGQWVTIISCTGS	RSNIG---AGFD	VHWYQQLPGSAPKLLIY	AN-----I	YRPSGVP-DRFSGSK--SGTSASLAITGLQPEDEANYC	QSYDNNPNT
EF589558	QSVLTQPPS-VSGAPGQRVTIISCTGS	SSNIG---AGYY	VHWYQQLPGTAPKLLIY	GN-----I	NRPSGVT-DRFSGSK--SGTSASLAITGLQAEDEADYYC	HSYDNLISA
EF589450	QSVLTQPPS-VSGAPGQRVTIISCTGS	SSNIG---AGYD	VHWYQQLPGTAPKLLIY	AN-----N	NRPSGVP-DRFSASK--SGTSASLAITGLQAEDEADYFC	QSYDSSLGG
EU599322	QSVLTQPPS-VSGAPGQRVTIISCTGS	RSNIG---AGYH	VHWYQQLPGTAPKLLIY	AD-----T	NRPSGVP-DRFSGSK--SGTSASLAITGLQAEDEAEYIC	QSYDTNLV-
EF589512	QSVLTQPPS-VSGAPGQRVTIISCTGS	TSNIG---ARYD	VHWYQQLPGAAPKLLIY	GN-----T	NRPSGVP-DRFSGSK--SGTSASLAITGLQAEDEADYYC	QSYDNLISG
EF589542	QSVLTQPPS-VSGAPGQWVTIISCTGS	NSNIG---TGYD	LHWYQQLPGTAPKLLIY	GN-----T	NRPSGVP-DRFSGSK--SGTSASLAITGLQAEDEADYYC	QTYDSSVSA
AF320844	QSVLTQPPS-VSGAPGQRVTIISCTGS	SSNIG---AGID	VHWYQQLPGTAPKLLIY	DN-----I	NRPSGVP-DRFSGSK--SATSASLAITGLQADDEADYYC	QSYDSSLG
AF490938	-----XPX-VSGAPGQRVTIISCTGS	SSNLG---AGYD	VHWYQQLPGTAPKVIYIY	GN-----N	IRPSGVP-DRISGSK--SGTSASLAITGLQAEDEADYYC	QSYDRSG--
EF589403	QSVLTQPPS-VSGAPGQRVTIISCTGS	SSNIG---AGYE	VHWYQQLPGTAPKLLMY	GN-----T	NRPSGVP-DRFSGSK--SGSSASLAITGLQAEDESYYC	QSYDSSMSG
EF589431	QSVLTQPPS-VSGAPGQRVTIISCTGS	SSNIG---ARYD	VHWYQHLPGTAPKLLIY	AN-----N	NRPSGVP-DRFSGSK--SGTSASLAITGLQAEDEALYYC	QSYDSSLSD
F01703	QSVLTQPPS-VSGAPGQRVTIISCTGS	SSNIG---AGNH	VHWYQQLPGTAPKLLIF	HN-----N	-----ARFSVSK--SGSSATLAITGLQAEDEADYYC	-----
DQ098786	QSVLTQPPS-VSGAPGQRVTIISCTGS	SSNIG---AGYD	VHWYQQLPGTAPKLLIY	GN-----K	NRPSGVP-DRFSASK--SGTSASLAITGLQADDEADYYC	QSYDSSLR-
DQ098812	----TQPPS-VSGAPGQRVTIISCTGS	RSNIG---AGYD	VHWYQQLPGTAPKLLIY	GN-----T	NRPSGVP-NRFSGAK--SGTSASLAITGLQAEDEGDYYC	QSYDNLISG
DQ098814	QSVLTQPPS-VSGAPGQRVTIISCTGN	KSNIG---AGYD	VHWYQLIPGTAPKLLIY	GN-----V	NRLSGVP-DRFSGSK--SGTSASLAITGLQAEDEADYYC	QSYDTSVNG
AY180392	-----QRVTIISCTGS	SSNIV---EGHD	VHWYQQLPGKAPKLLIY	GN-----N	NRPSGVP-DRFSGSK--SGTSASLAITGLQAEDEADYYC	QSYDSSLSF
AL3	QSVLTQPPS-VSGAPGQRVTIISCTGS	SSNIG---AGYD	VHWYQQLIPGTAPKLLIY	LN-----T	NRPSGVP-DRFSGSK--SDTSASLAITGLQAEDEADYYC	QSYDNLISG
AL4	QSVLTQPPS-VSGAPDQRVTIISCTGT	SSNIG---AHYD	VHWYQHLPGTAPKLLIY	GN-----N	NRPSGVP-DRFSGSK--SDISASLAITGLQAEDEGDYFC	QSYDRLSG
IGLV1-40	QSVLTQPPS-VSGAPGQRVTIISCTGS	SSNIG---AGYD	VHWYQQLPGTAPKLLIY	GN-----S	NRPSGVP-DRFSGSK--SGTSASLAITGLQAEDEADYYC	QSYDSSLG

Supplemental Figure 3: Deduced amino-acid sequences of monoclonal IGLV1-44 and IGLV1-40 ð light chain variable domains of AL amyloidosis or other plasma cell disorders patients compared to germline sequences according to IMGT numbering. Per1 to Per14 from Perfetti et al26, com2 to com6 from Comenzo et al27, AL1 to AL4 personal data, all other sequences from the Boston university AL-Base database28. A and P mutations in position 38 for IGHV1-44 and N in position 40 for IGHV1-40 are in red underlined.