Table S1. Detailed results of antibody gene repertoire sequence analysis experiments for bone marrow aspirate specimens from seven patients with AL amyloidosis

Patient	Light chain					Heavy chain				
	Sequences obtained		Genetic features of the dominant sequence			Sequences obtained		Genetic features of the dominant sequence		
	Sequence reads for each of 1-3 technical replicates	Unique clonotypes for each of 1-3 technical replicates	$V_{K\ or\ L}$ gene*	$J_{K\ or\ L}$ gene*	LCDR3 (amino acids)*	Sequence reads for each of 3 technical replicates	Unique clonotypes for each of 3 technical replicates	V_H gene*	J_H gene*	HCDR3 (amino acids)*
AM1	1,963 2,296 1,953	1,006 1,139 1,029	*IGLV3-21* – –	*IGLJ3* – –	QVWDRSSDRPV ----------- -----------	351 391 357	340 366 334	*IGHV4-39* – –	*IGHJ6* – –	VRHGVPSAPYYYYMDI ---------------- ----------------
AM2 *Time-point 1*	5,754 4,755	3,575 2,946	***IGLV3-25*** –	***IGLJ2*** –	**QSADSSGTYEVI** ------------	1,225 1,372 1,260	1,071 1,185 1,082	***IGHV5-51*** – –	***IGHJ4*** – –	**ARRRDGYNFDY** ----------- -----------
Time-point 2	1,590 843 1,018	857 476 591	– – –	– – –	------------ ------------ ------------	470 601 640	288 322 344	– – –	– – –	----------- ----------- -----------
Time-point 3	82 958 977	176 309 299	– – –	– – –	------------ ------------ ------------	353 456 497	185 241 240	– – –	– – –	----------- ----------- -----------
AM3	2,020 2,457 2,250	1,489 1,727 1,647	*IGLV1-47* – –	*IGLJ1* – –	AAWDGSLSGYV ----------- -----------	288 1,060 1,069	226 931 979	*IGHV3-23* – –	*IGHJ3* – –	AKDISYDDILPGYPADAFDI -------------------- --------------------
AM4	994 788 989	817 659 807	*IGLV2-14* – –	*IGLJ1* – –	SSFTSSSSYV ---------- ----------	614 837 819	269 300 291	*IGHV3-23* – –	*IGHJ6* – –	AKRPPYSIYGMDV ------------- -------------
AM5	577	266	*IGLV2-14*	*IGLJ1*	SSYTITNTLV	154 191 113	151 187 110	*IGHV6-1* – –	*IGHJ3* – –	ARTHDDFWSGAFDI -------------- --------------
AM6	1,316	919	*IGKV3-20*	*IGKJ4*	QQYGTSPLT	2,491 2,609 2,770	1,960 2,072 2,199	*IGHV3-23* – –	*IGHJ4* – –	TRKGGYFDF --------- ---------
AM7	475	223	*IGLV6-57*	*IGLJ3*	QSYQGSSGV	828 791 843	735 702 755	*IGHV4-59* – –	*IGHJ4* – –	ARDKYSRGGEYVN ------------- -------------

* The – symbol indicates the genetic feature is identical to that of the sequence above.

Bolded features show consistency of the dominant clone within one individual over a time of 3 years.