

IgE MAb	Light	Heavy chain							Light chain					
		V gene	V gene % identity	J gene	J gene % identity	D gene	Junction	HCDR length	V gene	V gene % identity	J gene	J gene % identity	Junction	LCDR length
4E1	κ	V1-46*01 F, or V1-46*03 F	96.18	J4*02 F	93.75	D3-22*01 F	CATLYYYDDSGYTYDYW	8.8.15	V3-20*01 F	92.2	J1*01 F	100	CQQYGNSPWTF	7.3.9
12D4	λ	V1-45*02 F	97.57	J4*02 F	93.75	D3-22*01 F	CAVAYHYDSSGYPFDHW	8.8.15	V1-40*01 F	96.18	J2*01 F, or J3*01 F	94.74	CQSYDSSLGPPVVF	9.3.12
5H1	κ	V3-30*03 F, or V3-30*18 F or V3-30-5*01 F	90.28	J4*02 F	85.11	D3-16*01 F	CAKDGPIYAYRWGGFLDDW	8.8.16	V3-15*01 F	92.47	J4*01 F	100	CQQYHSWPPLTF	6.3.10
9C1	κ	V3-23*01 F, or V3-23D*01 F	92.01	J6*02 F	79.03	D6-19*01 F	CAKQKRECSGWCKWGGLD VW	8.8.18	V2-28*01 F, or V2D-28*01 F	97.62	J2*01 F	97.3	CMQALQTPYTF	11.3.9
14C10	λ	V3-21*01 F	93.06	J3*02 F	96	D4-17*01 F	CARDTYGDTDDAFDIW	8.8.14	V3-25*03 F	89.25	J3*02 F	89.47	CHVVDRITETYSVVF	6.3.12
7G12	κ	V1-18*01 F	89.24	J4*02 F	82.98	D5-12*01 F	CARGRDSPDHW	8.8.9	V1-5*03 F	92.83	J2*01 F	86.84	CQQYDHPHTF	6.3.9
1A5	λ	V3-30*03 F, or V3-30*18 F or V3-30-5*01 F	96.88	J4*02 F	56	D3-22*01 F	CAKAMDSSGYYCPIYD	8.8.15	V3-19*01 F	97.13	J1*01 F	100	CNSRDSSGNHLVVF	6.3.12
10H9	λ	V3-11*06 F	89.93	J1*01 F	66.67	D2-8*02 F	CAKDYCGSGACYTADPGFF HQW	8.8.20	V3-21*01 F	93.91	J1*01 F	94.74	CQVVDNTNDHPSY VF	6.3.13
11G1	λ	V5-51*03 F	88.89	J6*02 F, or J6*04 F	58.14	ND	CAREVYVASTDSYGMVDV	8.8.18	V2-23*01 F, or V2-23*02 F or V2-23*03 F	88.19	J1*01 F	86.11	CCSYAGGNTYVF	9.3.10
14B2	κ	V3-53*02 F	87.37	J4*02 F	74.07	D5-24*01 F	CVRHGDGWNVYDSW	8.7.12	V3-15*01 F	94.62	J4*01 F	71.05	CQQYNNWPLTF	6.3.9
10D5	κ	V3-21*01 F	90.97	J6*03 F	83.87	D3-22*01 F	CARVMVGLYYYMDIW	8.8.15	V3-20*01 F	94.68	J1*01 F	97.37	CQLYGTSPWTF	7.3.10
18D4	κ	V4-34*02 F, or V4-34*08 F	91.23	J4*02 F	77.08	D1-1*01 F	CGRGRGYTWNW	8.7.10	V1-39*01 F, or V1D-39*01 F	93.55	J2*01 F, or J2*02 (F)	88.57	CQQSYSGPPTF	6.3.9
30A10	κ	V3-21*01 F	97.92	J6*03 F	87.1	D6-13*01 F	CARDGPPIVAAGLIYYMG VW	8.8.20	V1-9*01 F	98.57	J2*02 (F)	97.22	CQHLNSYRTF	6.3.8
4E9	λ	V4-34*02 F	92.28	J6*02 F	93.55	D6-13*01 F	CASSGESSRRGYFYMGMD VW	8.7.19	V1-47*01 F, or V1-47*02 F	92.6	J3*02 F	89.47	CAAWDDLILGPRVF	8.3.12
2E6	λ	V1-69*01 F	91.32	J4*02 F	100	D5-18*01 F	CASYPYGKYFDYW	8.8.12	V1-51*01 F	94.39	J3*02 F	97.14	CGAWDLGLNAGVF	8.3.11
11H12	λ	V3-11*01 F	89.24	J4*02 F	85.11	ND	CARDWGTTLVTFDLW	8.8.13	V4-60*03 F	86.74	J3*02 F	75.68	CFTWDSDSRVF	7.7.9

Supplemental Data Figure 9. Sequence features of filaria-reactive human IgE mAbs.

Antibody germline gene segment usages and their percent identity are shown for variable (V), diverse (D), and joining (J) regions of both light and heavy chains based on the ImMunoGeneTics (IMGT) database. The number of amino acids that make up the CDRs (HCDR & LCDR length) and the amino acids making up the junction is shown.