

# Appendix 1

## A

### IGHV1-69 SLE1

QVQLVQSGAEVKKPGSSVKVCKASGGTFSSYTI SWVRQAPGQGLEWMGRIIPILGIANYAQKFQGRVTITADKSTSTAYMELSSLRSED TAVYYCAR  
.....  
R..... A..... TP..... SV.T.R VTAA.....  
.....S..... A..... M..... SV.T.K  
..H..... ..Y..TT.D.H....

### IGHV1-69 SLE2

QVQLVQSGAEVKKPGSSVKVCKASGGTFSSYTI SWVRQAPGQGLEWMGRIIPILGIANYAQKFQGRVTITADKSTSTAYMELSSLRSED TAVYYCAR  
.....  
.....Q... T..... R  
.....V..... R  
.....Q..... R  
.....N..... V..... R D.....  
.....NN..... L..... S.....  
.....S.N.VG..... ..N.... ..V.....  
.....SV.T.R  
.....M.E.T.H.....  
.....M.E.T.....

### IGHV1-69 SLE3

QVQLVQSGAEVKKPGSSVKVCKASGGTFSSYTI SWVRQAPGQGLEWMGRIIPILGIANYAQKFQGRVTITADKSTSTAYMELSSLRSED TAVYYCAR  
.....  
..L..... D..... F.T..... R VTAA.....  
.....T..... D..... KSM.DVY...RR.....A..R  
.....FV.A..... ML..... E.N.....  
..N.P..... FET..... E.R  
.....A..... V..... T.....  
.....L.....

### IGHV1-69 SLE4

QVQLVQSGAEVKKPGSSVKVCKASGGTFSSYTI SWVRQAPGQGLEWMGRIIPILGIANYAQKFQGRVTITADKSTSTAYMELSSLRSED TAVYYCAR  
.....  
.....V..  
.....L..

### IGHV1-69 SLE5

QVQLVQSGAEVKKPGSSVKVCKASGGTFSSYTI SWVRQAPGQGLEWMGRIIPILGIANYAQKFQGRVTITADKSTSTAYMELSSLRSED TAVYYCAR  
.....  
.....R..... V.....  
NP.T....QL.AR.....S.....  
.....T.....  
.....EP.T.....  
.....E.....  
.....P.....  
.....SV.T.K D.....P.

### IGHV1-69 SLE6

QVQLVQSGAEVKKPGSSVKVCKASGGTFSSYTI SWVRQAPGQGLEWMGRIIPILGIANYAQKFQGRVTITADKSTSTAYMELSSLRSED TAVYYCAR  
.....  
.....L..

## B

### IGHV3-7 SLE1

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAR  
.....  
..H..... V.SR..... T.....  
.....D..... L.L....K  
.....D.K..... L.L....K  
.....V.L....K

### IGHV3-7 SLE2

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAR  
.....P.R.....  
..H..... N.E.N... F.R..... D...  
..G..... T..... D.....  
..V..... T.F... TS.....  
..P..... TD.....  
.....D..... M.....  
.....S.....  
.....E.....  
.....L.D.....  
.....L.G.....  
.....L.M...R  
.....V.....

### IGHV3-7 SLE3

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAR  
.....DD.A.H....  
.....D..... GF.R..... T.....  
.....H..... D.....  
..P..... R..... DN..

### IGHV3-7 SLE4

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAR  
.....K..... HCPR

### IGHV3-7 SLE5

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAR  
.....V..... GF.R..... D...  
.....V...R SD.....P.

### IGHV3-7 SLE6

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAR  
.....A.... T.....D...  
.....V.SR.....

C

IGKV2-28 SLE1

DIVMTQSP<sup>LS</sup>LPVTPGEPASISCRSSQSL<sup>L</sup>HSNGYNYLDWYLQKPGQSPQLLIYLG<sup>S</sup>NRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP

.....R.....R.....S.....L.....  
 .....S.....A.....  
 .....S.....V.....  
 .....A.....V.....  
 .....A.....  
 .....E.....  
 .....G.....L.....  
 .....L.....H.....  
 .....V.....Y.....  
 .....E.....N.....  
 .....Y.....  
 .....L.....

IGKV2-28 SLE2

DIVMTQSP<sup>LS</sup>LPVTPGEPASISCRSSQSL<sup>L</sup>HSNGYNYLDWYLQKPGQSPQLLIYLG<sup>S</sup>NRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP

.....Y.....R.....A.....E.....  
 .....D..A..S.L..R.....D.....  
 .....H.....E.....  
 .....E.....

IGKV2-28 SLE3

DIVMTQSP<sup>LS</sup>LPVTPGEPASISCRSSQSL<sup>L</sup>HSNGYNYLDWYLQKPGQSPQLLIYLG<sup>S</sup>NRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP

.....D..A..S.L..R.....L.Q.....S.....

IGKV2-28 SLE4

DIVMTQSP<sup>LS</sup>LPVTPGEPASISCRSSQSL<sup>L</sup>HSNGYNYLDWYLQKPGQSPQLLIYLG<sup>S</sup>NRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP

.....W.C.S.M.R.....T.....

IGKV2-28 SLE5

DIVMTQSP<sup>LS</sup>LPVTPGEPASISCRSSQSL<sup>L</sup>HSNGYNYLDWYLQKPGQSPQLLIYLG<sup>S</sup>NRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP

.....T.....A.....I.....  
 .....D..A..S.L..R.....A.....  
 .....S.....A.....R.....  
 .....S.....L.Q.....

IGKV2-28 SLE6

DIVMTQSP<sup>LS</sup>LPVTPGEPASISCRSSQSL<sup>L</sup>HSNGYNYLDWYLQKPGQSPQLLIYLG<sup>S</sup>NRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP

.....D.V.T.....  
 .....D..A..S.L..R.....D.A.....  
 .....S.N.Q.P.....

D

IGKV3-20 SLE1

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS<sup>S</sup>P

.....K.....P.....A.....S.R.....  
 .....V.....K.....T.G.....R.S.N.....  
 .....H.....N.....  
 .....H.....N.....T.....  
 .....M.....A.....V.....S.....A.....  
 .....N.....K.....C.....T.....  
 .....W.....T.....R.....  
 .....V.....W.....A.....  
 .....N.....N.T.A.....  
 .....V.....  
 .....G.....

IGKV3-20 SLE2

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS<sup>S</sup>P

.....V.....G.I..-W.....K.....V.....N.....  
 .....F.....I.N..-N.....K.....D.....H.....  
 .....D.....N.....L.....  
 .....S.....I..-T.W.....K.....L.....  
 .....A.....D.G.....K.....W..T.....  
 .....K.....L.T..K.....T.....  
 .....D.....P.....  
 .....A.....V.....

IGKV3-20 SLE3

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS<sup>S</sup>P

.....K.....I..-W.....K.....V.....  
 .....R.Q.M.....S.S..A.V.D.....I.T=-.....K.....C.....  
 .....A.....H.....F.M.V.....D.K.....  
 .....V.L.....W..T.....R.....  
 .....F.....T.....  
 .....E.....R.....  
 .....S.....  
 .....S.....

IGKV3-20 SLE4

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS<sup>S</sup>P

.....V.....  
 LS...NR  
 LS...DNR

IGKV3-20 SLE5

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS<sup>S</sup>P

.....L.N.....

.....K.....  
 .....S.A.M.....

A...LQS.V.S.

**IGKV3-20 SLE6**

EIVLTQSPGTL<sup>S</sup>LS<sup>S</sup>SPGERATL<sup>S</sup>SCRAS<sup>S</sup>QSVSSSYLAWYQQKPKGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP

.....  
 .....K.....  
 .....T.....  
 .....G.....  
 .....H.....  
 .....W.....  
 A...LQS.V.S.  
 .....T.....

**E**

**Heavy joining peptides**

IGHJ4 ..YFDYWGQGT <sup>S</sup> LVTVSS	IGHJ6 ...YGM <sup>S</sup> DVWGQGT <sup>S</sup> LVTVSS
SLE1 ..... .A.....	SLE1 ..-..... ..... YYY.....K
SLE2 ..... G..... L..... Y.....	SLE2 ..... Y.....
SLE3    AH..... ..... .S..... PET.....	SLE3 ..... .....
SLE4 ..... L..R.....	SLE4 ..-.....K
SLE5    L..R..... ..... R..... D..... L..R..... GT..N..R.....	SLE5        TL..... ..... E..... Y..-..... GRG.....
SLE6 ..... .....	SLE6 ..... .....

**Kappa joining peptides**

IGKJ2 ....YTFGQGT <sup>S</sup> KLEIK	IGKJ4 .....LTFGGG <sup>S</sup> TKVEIK
SLE1    L.....R ..... LPI.....R	SLE1    SYP..... DSSSDPVV.....
SLE2    GSSP..... QTPP..... SFPW.....	SLE2    SNWP..... STWP..... GWV.....
SLE3    CS..... L.....V.	SLE3    P..... QTP.....
SLE4 ..... .....	SLE4 ..... .....
SLE5    FP.....	SLE5    THP.....
SLE6 ..... .....	SLE6 ..... .....

**Supplementary figure 1.** *De novo* sequencing of affinity-purified anti-SmD IgGs from 6 patients with systemic lupus erythematosus (SLE) reveals clonal restriction with common heavy (H)- and light (L)- chain variable (V)- and joining (J)- regions. **A.** IGHV1-69 gene family usage. **B.** IGHV3-7 gene family usage. **C.** IGKV2-28 gene family usage. **D.** IGKV3-20 gene family usage. A number of public V-region mutations were identified which are tabulated by proteomic heat map in Figure 3. A number of privately mutated peptides within each affinity-purified anti-SmD IgG sample were also sequenced. **E.** Sequencing of J-regions reveals an IGHJ4, IGHJ6, IGKJ2, and IGKJ4. Dots indicate homology with the germline sequence derived from the ImMunoGeneTics database; mutations divergent from germline are indicated in text; germline complementary determining regions are underlined; - indicates deletion; spaces indicate areas of incomplete sequence.