

HMD22 mAb IGHV-Cy1

Fig. S1A

		FR1															
1	a	ggt	cca	gct	gca	gga	gtc	tgg	atc	tcc	tgc	aag	gct	tct	ggg	tat	46
		Gly	Pro	Ala	Ala	Gly	Val	Trp	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	15
		CDR1						FR2									
47		acc	ttc	aca	act	gct	gga	atg	cac	tgg	gtg	caa	aag	atg	cca	gga	91
16		Thr	Phe	Thr	Thr	Ala	Gly	Met	His	Trp	Val	Gln	Lys	Met	Pro	Gly	30
		CDR2															
92		aag	gct	ttg	aag	tgg	att	ggc	tgg	ata	aac	acc	cac	tct	gga	gtg	136
31		Lys	Ala	Leu	Lys	Trp	Ile	Gly	Trp	Ile	Asn	Thr	His	Ser	Gly	Val	45
		FR3															
137		cca	aaa	tat	gca	gaa	gac	ttc	aag	gga	cgg	ttt	gcc	ttc	tct	ttg	181
46		Pro	Lys	Tyr	Ala	Glu	Asp	Phe	Lys	Gly	Arg	Phe	Ala	Phe	Ser	Leu	60
		D															
227		aat	gag	gac	acg	gct	acg	tat	ttc	tgt	gcg	gta	gag	ggc	ttt	gac	271
76		Asn	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys	Ala	Val	Glu	Gly	Phe	Asp	90
		JH															
272		tac	tgg	ggc	caa	ggc	acc	act	ctc	aca	gtc	tcc	tca	gcc	aaa	acg	316
91		Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser	Ala	Lys	Thr	105
		Cy1															
317		aca	ccc	cca	tct	gtc	tat	cca	ctg	gcc	cct	gga	tct	gct	gcc	caa	361
106		Thr	Pro	Pro	Ser	Val	Tyr	Pro	Leu	Ala	Pro	Gly	Ser	Ala	Ala	Gln	120
		FR1															
362		act	aac	tcc	atg	gtg	acc	ctg	gga	tgc	ctg	gtc	aag	ggc	tat	ttc	406
121		Thr	Asn	Ser	Met	Val	Thr	Leu	Gly	Cys	Leu	Val	Lys	Gly	Tyr	Phe	135
		FR1															
407		cct	gag	cca	gtg	aca	gtg	acc	tgg	aac	tct	gga	tcc	ctg	tcc		451
136		Pro	Glu	Pro	Val	Thr	Val	Thr	Trp	Asn	Ser	Gly	Ser	Leu	Ser		149

HMD22 mAb IGKV-C κ

																	FR1
1	cc	aga	tgt	gtg	atg	acc	cag	act	cca	tcc	tcc	ctg	gct	atg	tca	gta	47
1		Arg	Cys	Val	Met	Thr	Gln	Thr	Pro	Ser	Ser	Leu	Ala	Met	Ser	Val	15
48	gga	cag	aag	gtc	act	atg	agc	tgc	aag	tcc	agt	cag	agc	ctt	tta		92
16	Gly	Gln	Lys	Val	Thr	Met	Ser	Cys	Lys	Ser	Ser	Gln	Ser	Leu	Leu		30
93	aat	agt	agc	aat	caa	aag	aac	tat	ttg	gcc	tgg	tac	cag	cag	aaa		137
31	Asn	Ser	Ser	Asn	Gln	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys		45
138	cca	gga	cag	tct	cct	aaa	ctt	ctg	ata	tac	ttt	gca	tcc	act	agg		182
46	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Phe	Ala	Ser	Thr	Arg		60
183	gaa	tct	ggg	gtc	cct	gat	cgc	ttc	ata	ggc	agt	gga	tct	ggg	aca		227
61	Glu	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ile	Gly	Ser	Gly	Ser	Gly	Thr		75
228	gat	ttc	act	ctt	acc	atc	agc	agt	gtg	cag	gct	gaa	gac	ctg	gca		272
76	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp	Leu	Ala		90
273	gat	tac	ttc	tgt	cag	caa	cat	tat	agc	act	ccg	ctc	acg	ttc	ggt		317
91	Asp	Tyr	Phe	Cys	Gln	Gln	His	Tyr	Ser	Thr	Pro	Leu	Thr	Phe	Gly		105
318	gct	ggg	acc	aag	ctg	gag	ctg	aaa	cgg	gct	gat	gct	gca	cca	ac		362
106	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	Arg	Ala	Asp	Ala	Ala	Pro			120