

CLONE ID	MF1/bkgrd (H929 cell bind)	seq_aa_CDR1	seq_aa_CDR2	seq_aa_CDR3
308607	558.6	GFTFSSYA (SEQ ID NO: 1)	ISGSGGST (SEQ ID NO: 5)	VKDWNNTTMMITE (SEQ ID NO: 19)
308915	284.8	GFTFTNYA (SEQ ID NO: 2)	ISGGGGST (SEQ ID NO: 54)	VKDWNNTTMMITE (SEQ ID NO: 19)
314189	123.5	GFTFSSYA (SEQ ID NO: 1)	ITENGGST (SEQ ID NO: 6)	VKDWNNTTMMITE (SEQ ID NO: 19)
314196	133.6	GFTFSSYA (SEQ ID NO: 1)	ITGDGGST (SEQ ID NO: 7)	VKDWNNTTMMITE (SEQ ID NO: 19)
314201	76.9	GFTFSSYA (SEQ ID NO: 1)	IIGSGGST (SEQ ID NO: 8)	VKDWNNTTMMITE (SEQ ID NO: 19)
314202	193.1	GFTFSSYA (SEQ ID NO: 1)	IIGSGGST (SEQ ID NO: 8)	VKDWNNTTMMITE (SEQ ID NO: 19)
314205	102.8	GFTFSSYA (SEQ ID NO: 1)	ITGSGGTT (SEQ ID NO: 9)	VKDWNNTTMMITE (SEQ ID NO: 19)
314212	125.9	GFTFSSYA (SEQ ID NO: 1)	LTGNGDST (SEQ ID NO: 10)	VKDWNNTTMMITE (SEQ ID NO: 19)
314213	135.2	GFTFSSYA (SEQ ID NO: 1)	ITGSGGST (SEQ ID NO: 11)	VKDWNNTTMMITE (SEQ ID NO: 19)
314219	166.9	GFTFSSYA (SEQ ID NO: 1)	IIGSGGST (SEQ ID NO: 8)	VKDWNNTTMMITE (SEQ ID NO: 19)
314224	175.8	GFTFSSYA (SEQ ID NO: 1)	IIGSGGST (SEQ ID NO: 8)	VKDWNNTTMMITE (SEQ ID NO: 19)
314225	148.9	GFTFSSYA (SEQ ID NO: 1)	ITGSGDST (SEQ ID NO: 12)	VKDWNNTTMMITE (SEQ ID NO: 19)
314228	99.1	GFTFSSYA (SEQ ID NO: 1)	LTGSGDST (SEQ ID NO: 13)	VKDWNNTTMMITE (SEQ ID NO: 19)
314229	124.2	GFTFSNYA (SEQ ID NO: 3)	ITGDGGST (SEQ ID NO: 7)	VKDWNNTTMMITE (SEQ ID NO: 19)
314231	157.3	GFTFSRYA (SEQ ID NO: 4)	IVGSGGNT (SEQ ID NO: 14)	VKDWNNTTMMITE (SEQ ID NO: 19)
314232	79.0	GFTFSSYA (SEQ ID NO: 1)	ITGSGGST (SEQ ID NO: 11)	VKDWNNTTMMITE (SEQ ID NO: 19)
314235	128.3	GFTFSNYA (SEQ ID NO: 3)	LTGSGGST (SEQ ID NO: 15)	VKDWNNTTMMITE (SEQ ID NO: 19)
314501	251.1	GFTFTNYA (SEQ ID NO: 2)	IIGSGGST (SEQ ID NO: 8)	VKDWNNTTMMITE (SEQ ID NO: 19)
314502	169.7	GFTFSSYA (SEQ ID NO: 1)	IIGSGGST (SEQ ID NO: 8)	VKDWNNTTMMITE (SEQ ID NO: 19)
314503	183.3	GFTFSNYA (SEQ ID NO: 3)	IIGSGGST (SEQ ID NO: 8)	VKDWNNTTMMITE (SEQ ID NO: 19)
314504	176.8	GFTFSSYA (SEQ ID NO: 1)	IIGSGGST (SEQ ID NO: 8)	VKDWNNTTMMITE (SEQ ID NO: 19)
314506	243.1	GFTFSNYA (SEQ ID NO: 3)	IIGSGGST (SEQ ID NO: 8)	VKDWNNTTMMITE (SEQ ID NO: 19)
314508	209.0	GFTFSNYA (SEQ ID NO: 3)	IIGSGGST (SEQ ID NO: 8)	VKDWNNTTMMITE (SEQ ID NO: 19)
314509	241.5	GFTFSNYA (SEQ ID NO: 3)	IIGSGATT (SEQ ID NO: 16)	VKDWNNTTMMITE (SEQ ID NO: 19)
314510	171.1	GFTFSNYA (SEQ ID NO: 3)	IIGSGGST (SEQ ID NO: 8)	VKDWNNTTMMITE (SEQ ID NO: 19)
314512	213.8	GFTFSSYA (SEQ ID NO: 1)	IIGSGGST (SEQ ID NO: 8)	VKDWNNTTMMITE (SEQ ID NO: 19)
314518	182.9	GFTFSSYA (SEQ ID NO: 1)	IIGSGGST (SEQ ID NO: 8)	VKDWNNTTMMITE (SEQ ID NO: 19)
314521	234.8	GFTFSNYA (SEQ ID NO: 3)	IVGGGGTS (SEQ ID NO: 17)	VKDWNNTTMMITE (SEQ ID NO: 19)
314523	195.1	GFTFSNYA (SEQ ID NO: 3)	ITGDGGST (SEQ ID NO: 7)	VKDWNNTTMMITE (SEQ ID NO: 19)
314524	82.9	GFTFSSYA (SEQ ID NO: 1)	IVGGGGTS (SEQ ID NO: 17)	VKDWNNTTMMITE (SEQ ID NO: 19)
314527	134.3	GFTFSSYA (SEQ ID NO: 1)	IIGSGGTT (SEQ ID NO: 18)	VKDWNNTTMMITE (SEQ ID NO: 19)
314528	154.8	GFTFSNYA (SEQ ID NO: 3)	ITGSGGST (SEQ ID NO: 11)	VKDWNNTTMMITE (SEQ ID NO: 19)
314530	222.3	GFTFSSYA (SEQ ID NO: 1)	IVGGGGTS (SEQ ID NO: 17)	VKDWNNTTMMITE (SEQ ID NO: 19)
314533	205.3	GFTFSNYA (SEQ ID NO: 3)	IIGSGGST (SEQ ID NO: 8)	VKDWNNTTMMITE (SEQ ID NO: 19)

FIG. 1

FIG. 2

CLONE ID	seq_aa_FRI_FR4
308607	EVQLLESGGGLVQPGGSLRLSAAAGFTFSYAMNWIRQAPGKGLEWVSGISGGGGSTYYADSVKGRFTISRDN SKNTVYLQMNSLRA EDTAVYYCVKDWNTTMITERGGQGLVTVSS (SEQ ID NO: 20)
308915	EVQLLESGGGLVQPGGSLRLSAAAGFTFSYAMNWIRQAPGKGLEWVSGISGGGGSTYYADSVKGRFTISRDN SKNTVYLQMNSLRA EDTAVYYCVKDWNTTMITERGGQGLVTVSS (SEQ ID NO: 21)
314189	EVQLLESGGGLVQPGGSLRLSAAAGFTFSYAMTWVRQAPGKGLEWVSGITENGSGSTYYADSVKGRFTISRDN SKNTLDLQMNSLRA EDTAVYYCVKDWNTTMITERGGQGLVTVSS (SEQ ID NO: 22)
314196	EVQLLESGGGLVQPGGSLRLSAAAGFTFSYAMSWVRQAPGKGLEWVSGITGDSIFVADSVKGRFTISRDN SKNTVYLQMNSLRA EDTAVYYCVKDWNTTMITERGGQGLVTVSS (SEQ ID NO: 23)
314201	EVQLLESGGGLVQPGGSLRLSAAAGFTFSYAMSWVRQAPGKGLEWVSGIHGGGGSTYYADSVKGRFSISRDN SKNTLDLQMNSLRA EDTAVYYCVKDWNTTMITERGGQGLVTVSS (SEQ ID NO: 24)
314202	EVQLLESGGGLVQPGGSLRLSAAAGFTFSYAMNWVRQAPGKGLEWVSGITGSGGTYYADSVKGRFTISRDN SKNTVYLQMNSLRA EDTAVYYCVKDWNTTMITERGGQGLVTVSS (SEQ ID NO: 25)
314205	EVQLLESGGGLVQPGGSLRLSAAAGFTFSYAMNWVRQAPGKGLEWVSGITGSGGTYYADSVKGRFTISRDN SKNTVYLQMNSLRA EDTAVYYCVKDWNTTMITERGGQGLVTVSS (SEQ ID NO: 26)
314212	EVQLLESGGGLVQPGGSLRLSAAAGFTFSYAMNWVRQAPGKGLEWVSGITGNGDSTYYADSVKGRFTISRDN SKNTVYLQMNSLRA EDTAVYYCVKDWNTTMITERGGQGLVTVSS (SEQ ID NO: 27)
314213	EVQLLESGGGLVQPGGSLRLSAAAGFTFSYAMNWVRQAPGKGLEWVSGITGSGGGSTYYADSVKGRFSISRDN SKNTLDLQMNSLRA EDTAVYYCVKDWNTTMITERGGQGLVTVSS (SEQ ID NO: 28)
314219	EVQLLESGGGLVQPGGSLRLSAAAGFTFSYAMNWVRQAPGKGLEWVSGIHGGGGSTYYADSVKGRFTISRDN SKNTVYLQMNSLRA EDTAVYYCVKDWNTTMITERGGQGLVTVSS (SEQ ID NO: 29)
314224	EVQLLESGGGLVQPGGSLRLSAAAGFTFSYAMNWVRQAPGKGLEWVSGIHGGGGSTYYADSVKGRFTISRDN SKNTVYLQMNSLRA EDTAVYYCVKDWNTTMITERGGQGLVTVSS (SEQ ID NO: 30)
314225	EVQLLESGGGLVQPGGSLRLSAAAGFTFSYAMNWVRQAPGKGLEWVSGITGSGDSTYYAASVKGRFSISRDN SQNTLDLQMNSLRA EDTAVYYCVKDWNTTMITERGGQGLVTVSS (SEQ ID NO: 31)
314228	EVQLLESGGGLVQPGGSLRLSAAAGFTFSYAMSWVRQAPGKGLEWVSGITGSGDSTYYADSVKGRFTISRDN SKNTVYLQMNSLRA EDTAVYYCVKDWNTTMITERGGQGLVTVSS (SEQ ID NO: 32)
314229	EVQLLESGGGLVQPGGSLRLSAAAGFTFSYAMTWIRQAPGKGLEWVSGITGDSIFVADSVKGRFSISRDN SKNTLDLQMNSLRA EDTAVYYCVKDWNTTMITERGGQGLVTVSS (SEQ ID NO: 33)
314231	EVQLLESGGGLVQPGGSLRLSAAAGFTFSYAMNWIRQAPGKGLEWVSGIVGSGGNTYYADSVKGRFSISRDN SKNTVYLQMNSLRA EDTAVYYCVKDWNTTMITERGGQGLVTVSS (SEQ ID NO: 34)
314232	EVQLLESGGGLVQPGGSLRLSAAAGFTFSYAMSWVRQAPGKGLEWVSGITGSGGGSTYYADSVKGRFSISRDN SKNTLDLQMNSLRA EDTAVYYCVKDWNTTMITERGGQGLVTVSS (SEQ ID NO: 35)
314235	EVQLLESGGGLVQPGGSLRLSAAAGFTFSYAMNWVRQAPGKGLEWVSGITGSGGGSTYYADSVKGRFTISRDN SKNTVYLQMNSLRA EDTAVYYCVKDWNTTMITERGGQGLVTVSS (SEQ ID NO: 36)

Fig 2 (CONT.)

314501	EVQLLESGGGLVQPGGSLRLSCAASGFTFTNYAMNWVRQAPGKGLEWVSGIIGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCVKDWNTTMITERGQGLVTVSS (SEQ ID NO: 37)
314502	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSGIIGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCVKDWNTTMITERGQGLVTVSS (SEQ ID NO: 38)
314503	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSGIIGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCVKDWNTTMITERGQGLVTVSS (SEQ ID NO: 39)
314504	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSGIIGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCVKDWNTTMITERGQGLVTVSS (SEQ ID NO: 40)
314506	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSGIIGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCVKDWNTTMITERGQGLVTVSS (SEQ ID NO: 41)
314508	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSGIIGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCVKDWNTTMITERGQGLVTVSS (SEQ ID NO: 42)
314509	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSGIIGSGGATYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAIYYCVKDWNTTMITERGQGLVTVSS (SEQ ID NO: 43)
314510	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSGIIGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCVKDWNTTMITERGQGLVTVSS (SEQ ID NO: 44)
314512	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSGIIGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCVKDWNTTMITERGQGLVTVSS (SEQ ID NO: 45)
314518	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSGIIGSGGSTFYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCVKDWNTTMITERGQGLVTVSS (SEQ ID NO: 46)
314521	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSGIVGGGGTYYADSVRGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCVKDWNTTMITERGQGLVTVSS (SEQ ID NO: 47)
314523	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMTWIRQAPGKGLEWVSGITDGGSTFYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCVKDWNTTMITERGQGLVTVSS (SEQ ID NO: 48)
314524	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMTWIRQAPGKGLEWVSGIVGGGGTYYADSVRGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCVKDWNTTMITERGQGLVTVSS (SEQ ID NO: 49)
314527	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSGIIGSGGTYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAIYYCVKDWNTTMITERGQGLVTVSS (SEQ ID NO: 50)
314528	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSGITGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCVKDWNTTMITERGQGLVTVSS (SEQ ID NO: 51)
314530	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSGIVGGGGTYYADSVRGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCVKDWNTTMITERGQGLVTVSS (SEQ ID NO: 52)
314533	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSGIIGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCVKDWNTTMITERGQGLVTVSS (SEQ ID NO: 53)

FIG. 3

CLONE ID	MPi/bkgd (H929 cell bind)	MPi/bkgd (RP18226 cell bind)	% APRIL binding	ELISA hBCMA/bkgd	ELISA (gS1)/bkgd	ELISA BvP score
308607	not measured	not measured	not measured	not measured	not measured	not measured
308815	not measured	not measured	not measured	not measured	not measured	not measured
314189	123.5	not measured	not measured	not measured	not measured	not measured
314196	133.6	not measured	not measured	not measured	not measured	not measured
314201	76.2	not measured	not measured	not measured	not measured	not measured
314202	157.3	not measured	not measured	not measured	not measured	not measured
314205	102.8	not measured	not measured	not measured	not measured	not measured
314212	115.9	not measured	not measured	not measured	not measured	not measured
314213	135.2	not measured	not measured	not measured	not measured	not measured
314219	196.9	not measured	not measured	not measured	not measured	not measured
314224	77.2	not measured	not measured	not measured	not measured	not measured
314223	148.9	not measured	not measured	not measured	not measured	not measured
314228	99.1	not measured	not measured	not measured	not measured	not measured
314229	124.2	not measured	not measured	not measured	not measured	not measured
314231	157.3	not measured	not measured	not measured	not measured	not measured
314232	78.6	not measured	not measured	not measured	not measured	not measured
314235	118.3	not measured	not measured	not measured	not measured	not measured
314501	not measured	not measured	not measured	not measured	not measured	not measured
314502	123.2	not measured	not measured	not measured	not measured	not measured
314503	25.2	not measured	not measured	not measured	not measured	not measured
314504	27.9	not measured	not measured	not measured	not measured	not measured
314506	26.2	not measured	not measured	not measured	not measured	not measured
314508	26.2	not measured	not measured	not measured	not measured	not measured
314509	21.1	not measured	not measured	not measured	not measured	not measured
314510	171.3	not measured	not measured	not measured	not measured	not measured
314512	27.9	not measured	not measured	not measured	not measured	not measured
314518	27.9	not measured	not measured	not measured	not measured	not measured
314521	27.2	not measured	not measured	not measured	not measured	not measured
314523	27.2	not measured	not measured	not measured	not measured	not measured
314524	23.9	not measured	not measured	not measured	not measured	not measured
314527	134.3	not measured	not measured	not measured	not measured	not measured
314528	154.8	not measured	not measured	not measured	not measured	not measured
314530	not measured	not measured	not measured	not measured	not measured	not measured
314533	27.2	not measured	not measured	not measured	not measured	not measured

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FIG. 4

DAY 35 SERUM - ELISA TESTING (testing from 6/12 animals)

Assayed 1:500 dilution of d35 serum

Signal/H.S.A, adjusted for each animal

huBCMA-Fc	CyBCMA	huBCMA e coli frag	huBCMA full wht germ	hu IgG1kappa	H.S.A	Animal
325	296	501	245	188		r12431 (HC27)
281	226	417	247	207		r12455 (HC27)
262	267	418	245	303		r12514 (HC27)
314	306	519	444	24		r12271 (HC28)
260	290	421	413	296		r12276 (HC28)
594	476	978	935	176		r12278 (HC28)
1182	24	1787	1194	11		r12516 (HC27)
62	50	51	40	4		goat anti huBCMA

FIG. 5

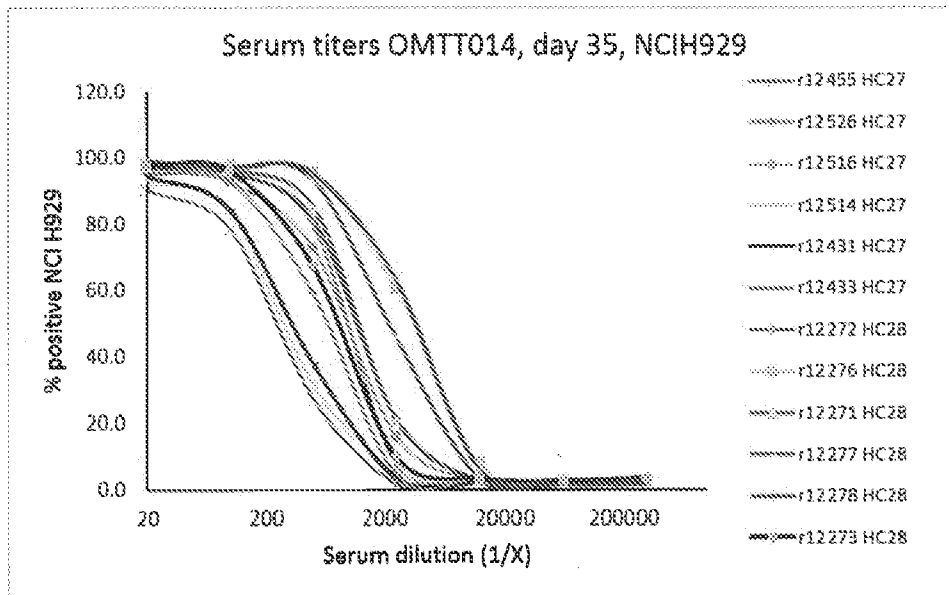


FIG. 6

