

## SUPPORTING INFORMATION

S1 Fig.

1	Met	Gly	Asn	Gly	Leu	Trp	Phe	Val	Gly	Val	Ile	Ile	Leu	Gly	Val	Ala	Trp	Gly	Gln	Val	20
21	His	Asp	Trp	His	Ser	Ser	Gly	Gly	Gly	Ser	Gly	Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	40
41	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asp	60
61	Val	Asn	Thr	Ala	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	80
81	Tyr	Ser	Ala	Ser	Phe	Leu	Tyr	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	100
101	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	120
121	Gln	Gln	His	Tyr	Thr	Thr	Pro	Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Ser	140
141	Asp	Met	Pro	Met	Ala	Asp	Pro	Asn	Arg	Phe	Arg	Gly	Lys	Asn	Leu	Val	Phe	His	Ser	Glu	160
161	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	180
181	Cys	Ala	Ala	Ser	Gly	Phe	Asn	Ile	Lys	Asp	Thr	Tyr	Ile	His	Trp	Val	Arg	Gln	Ala	Pro	200
201	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Arg	Ile	Tyr	Pro	Thr	Asn	Gly	Tyr	Thr	Arg	Tyr	Ala	220
221	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Lys	Asn	Thr	Ala	Tyr	Leu	240
241	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ser	Arg	Trp	Gly	Gly	260
261	Asp	Gly	Phe	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ser	280
281	Gly	Gly	Gly	Ser	Gly	Ser	Gly	Gly	Ser	Gly	Thr	Glu	Gln	Thr	Asp	Pro	Trp	Phe	Leu	Asp	300
301	Gly	Leu	Gly	Met	Asp	Arg	Met	Tyr	Trp	Arg	Asp	Thr	Asn	Thr	Gly	Arg	Leu	Trp	Leu	Pro	320
321	Asn	Thr	Pro	Asp	Pro	Gln	Lys	Pro	Pro	Arg	Gly	Phe	Leu	Ala	Pro	Pro	Asp	Glu	Leu	Asn	340
341	Leu	Thr	Thr	Ala	Ser	Leu	Pro	Leu	Leu	Arg	Trp	Tyr	Glu	Glu	Arg	Phe	Cys	Phe	Val	Leu	360
361	Val	Thr	Thr	Ala	Glu	Phe	Pro	Arg	Asp	Pro	Gly	Gln	Leu	Leu	Tyr	Ile	Pro	Lys	Thr	Tyr	380
381	Leu	Leu	Gly	Arg	Pro	Pro	Asn	Ala	Ser	Leu	Pro	Ala	Pro	Thr	Thr	Val	Glu	Pro	Thr	Ala	400
401	Gln	Pro	Pro	Pro	Ser	Val	Ala	Pro	Leu	Lys	Gly	Leu	Leu	Tyr	Asn	Pro	Val	Ala	Ser	Val	420
421	Leu	Leu	Arg	Ser	Arg	Ala	Trp	Val	Thr	Phe	Ser	Ala	Val	Pro	Asp	Pro	Glu	Ala	Leu	Thr	440
441	Phe	Pro	Arg	Gly	Asp	Asn	Val	Ala	Thr	Ala	Ser	His	Pro	Ser	Gly	Pro	Arg	Asp	Thr	Pro	460
461	Pro	Pro	Arg	Pro	Pro	Val	Gly	Ala	Arg	Arg	His	Pro	Thr	Thr	Glu	Leu	Asp	Ile	Thr	His	480
481	Leu	His	Asn	Ala	Ser	Thr	Thr	Trp	Leu	Ala	Thr	Arg	Gly	Leu	Leu	Arg	Ser	Pro	Gly	Arg	500
501	Tyr	Val	Tyr	Phe	Ser	Pro	Ser	Ala	Ser	Thr	Trp	Pro	Val	Gly	Ile	Trp	Thr	Thr	Gly	Glu	520
521	Leu	Val	Leu	Gly	Cys	Asp	Ala	Ala	Leu	Val	Arg	Ala	Arg	Tyr	Gly	Arg	Glu	Phe	Met	Gly	540
541	Leu	Val	Ile	Ser	Met	His	Asp	Ser	Pro	Pro	Val	Glu	Val	Met	Val	Val	Pro	Ala	Gly	Gln	560
561	Thr	Leu	Asp	Arg	Val	Gly	Asp	Pro	Ala	Asp	Glu	Asn	Pro	Pro	Gly	Ala	Leu	Pro	Gly	Pro	580
581	Pro	Gly	Gly	Pro	Arg	Tyr	Arg	Val	Phe	Val	Leu	Gly	Ser	Leu	Thr	Arg	Ala	Asp	Asn	Gly	600
601	Ser	Ala	Leu	Asp	Ala	Leu	Arg	Arg	Val	Gly	Gly	Tyr	Pro	Glu	Glu	Gly	Thr	Asn	Tyr	Ala	620
621	Gln	Phe	Leu	Ser	Arg	Ala	Tyr	Ala	Glu	Phe	Phe	Ser	Gly	Asp	Ala	Gly	Ala	Glu	Gln	Gly	640
641	Pro	Arg	Pro	Pro	Leu	Phe	Trp	Arg	Leu	Thr	Gly	Leu	Leu	Ala	Thr	Ser	Gly	Phe	Ala	Phe	660
661	Val	Asn	Ala	Ala	His	Ala	Asn	Gly	Ala	Val	Cys	Leu	Ser	Asp	Leu	Leu	Gly	Phe	Leu	Ala	680
681	His	Ser	Arg	Ala	Leu	Ala	Gly	Leu	Ala	Ala	Arg	Gly	Ala	Ala	Gly	Cys	Ala	Ala	Asp	Ser	700
701	Val	Phe	Phe	Asn	Val	Ser	Val	Leu	Asp	Pro	Thr	Ala	Arg	Leu	Gln	Leu	Glu	Ala	Arg	Leu	720
721	Gln	His	Leu	Val	Ala	Glu	Ile	Leu	Glu	Arg	Glu	Gln	Ser	Leu	Ala	Leu	His	Ala	Leu	Gly	740
741	Tyr	Gln	Leu	Ala	Phe	Val	Leu	Asp	Ser	Pro	Ser	Ala	Tyr	Asp	Ala	Val	Ala	Pro	Ser	Ala	760
761	Ala	His	Leu	Ile	Asp	Ala	Leu	Tyr	Ala	Glu	Phe	Leu	Gly	Gly	Arg	Val	Leu	Thr	Thr	Pro	780
781	Val	Val	His	Arg	Ala	Leu	Phe	Tyr	Ala	Ser	Ala	Val	Leu	Arg	Gln	Pro	Phe	Leu	Ala	Gly	800
801	Val	Pro	Ser	Ala	Val	Gln	Arg	Glu	Arg	Ala	Arg	Arg	Ser	Leu	Leu	Ile	Ala	Ser	Ala	Leu	820
821	Cys	Thr	Ser	Asp	Val	Ala	Ala	Ala	Thr	Asn	Ala	Asp	Leu	Arg	Thr	Ala	Leu	Ala	Arg	Ala	840
841	Asp	His	Gln	Lys	Thr	Leu	Phe	Trp	Leu	Pro	Asp	His	Phe	Ser	Pro	Cys	Ala	Ala	Ser	Leu	860
861	Arg	Phe	Asp	Leu	Asp	Glu	Ser	Val	Phe	Ile	Leu	Asp	Ala	Leu	Ala	Gln	Ala	Thr	Arg	Ser	880
881	Glu	Thr	Pro	Val	Glu	Val	Leu	Ala	Gln	Gln	Thr	His	Gly	Leu	Ala	Ser	Thr	Leu	Thr	Arg	900
901	Trp	Ala	His	Tyr	Asn	Ala	Leu	Ile	Arg	Ala	Phe	Val	Pro	Glu	Ala	Ser	His	Arg	Cys	Gly	920
921	Gly	Gln	Ser	Ala	Asn	Val	Glu	Pro	Arg	Ile	Leu	Val	Pro	Ile	Thr	His	Asn	Ala	Ser	Tyr	940
941	Val	Val	Thr	His	Ser	Pro	Leu	Pro	Arg	Gly	Ile	Gly	Tyr	Lys	Leu	Thr	Gly	Val	Asp	Val	960
961	Arg	Arg	Pro	Leu	Phe	Leu	Thr	Tyr	Leu	Thr	Ala	Thr	Cys	Glu	Gly	Ser	Thr	Arg	Asp	Ile	980
981	Glu	Ser	Lys	Arg	Leu	Val	Arg	Thr	Gln	Asn	Gln	Arg	Asp	Leu	Gly	Leu	Val	Gly	Ala	Val	1000
1001	Phe	Met	Arg	Tyr	Thr	Pro	Ala	Gly	Glu	Val	Met	Ser	Val	Leu	Leu	Val	Asp	Thr	Asp	Asn	1020
1021	Thr	Gln	Gln	Gln	Ile	Ala	Ala	Gly	Pro	Thr	Glu	Gly	Ala	Pro	Ser	Val	Phe	Ser	Ser	Asp	1040
1041	Val	Pro	Ser	Thr	Ala	Leu	Leu	Leu	Phe	Pro	Asn	Gly	Thr	Val	Ile	His	Leu	Leu	Ala	Phe	1060
1061	Asp	Thr	Gln	Pro	Val	Ala	Ala	Ile	Ala	Pro	Gly	Phe	Leu	Ala	Ala	Ser	Ala	Leu	Gly	Val	1080
1081	Val	Met	Ile	Thr	Ala	Ala	Leu	Ala	Gly	Ile	Leu	Lys	Val	Leu	Arg	Thr	Ser	Val	Pro	Phe	1100
1101	Phe	Trp	Arg	Arg	Glu	End	1106														

**Annotated sequence of gH-scFv chimera in R-VG803 and R-VG809.** Regions of interest are highlighted as follows. Signal sequence, yellow. scFv to HER2, blue. Upstream and downstream Ser-Gly linkers, green. scFv intermediate linker, red. Two residues implicated in MAb 52S epitope, S536 and A537 in wt-gH, fuchsia.