Figure 6A

	Matsuda et al	Tomlinson et al	Protein sequence
IGHV1-2	VH 1-2	DP-75	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMG WINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCAR
IGHV1-3	VH 1-3	DP-25	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLEWMG WSNAGNGNTKYSQEFQGRVTITRDTSASTAYMELSSLRSEDMAVYYCAR
IGHV1-8	VH 1-8	DP-15	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGW MNPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARG
IGHV1-18	VH 1-18	DP-14	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGW ISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
IGHV1-24	VH 1-24	DP-5	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMG GFDPEDGETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCAT
IGHV1-45	VH 1-45	--	QMQLVQSGAEVKKTGSSVKVSCKASGYTFTYRYLHWVRQAPGQALEWMG WITPFNGNTNYAQKFQDRVTITRDRSMSTAYMELSSLRSEDTAMYYCAR
IGHV1-46	VH 1-46	DP-7	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGI INPSGGSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
IGHV1-58	VH 1-58	DP-2	QMQLVQSGPEVKKPGTSVKVSCKASGFTFTSSAMQWVRQARGQRLEWIGW IVVGSGNTNYAQKFQERVTITRDMSTSTAYMELSSLRSEDTAVYYCAA
IGHV1-69*01	VH 1-69	DP-10	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGG IIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAR
IGHV1-69*06, IGHV1-e	VH 1-69	DP-88	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGG IIPIFGTANYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCAR
IGHV1-c	--	--	KSGASVKVSCSFSGFTITSYGIHWVQQSPGQGLEWMGWINPGNGSPSYAKK FQGRFTMTRDMSTTTAYTDLSSLTSEDMAVYYYAR
IGHV1-f	--	DP-3	EVQLVQSGAEVKKPGATVKISCKVSGYTFTDYYMHWVQQAPGKGLEWMGL VDPEDGETIYAEKFQGRVTITADTSTDTAYMELSSLRSEDTAVYYCAT
IGHV2-5	VH 2-5	DP-76	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALI YWNDDKRYSPSLKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCAHR
IGHV2-26	VH 2-26	DP-26	QVTLKESGPVLVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKALEWLAH IFSNDEKSYSTSLKSRLTISKDTSKSQVVLTMTNMDPVDTATYYCARI
IGHV2-70	VH 2-70	DP-27	QVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMCVSWIRQPPGKALEWLALI DWDDDKYYSTSLKTRLTISKDTSKNQVVLTMTNMDPVDTATYYCARI
IGHV3-7	VH 3-7	DP-54	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVA NIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR
IGHV3-9	VH 3-9	DP-31	EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSG ISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKD

Figure 6A

	Matsuda et al	Tomlinson et al	Protein sequence
IGHV1-2	VH 1-2	DP-75	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMG WINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCAR
IGHV1-3	VH 1-3	DP-25	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLEWMG WSNAGNGNTKYSQEFQGRVTITRDTSASTAYMELSSLRSEDMAVYYCAR
IGHV1-8	VH 1-8	DP-15	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGW MNPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARG
IGHV1-18	VH 1-18	DP-14	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGW ISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
IGHV1-24	VH 1-24	DP-5	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMG GFDPEDGETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCAT
IGHV1-45	VH 1-45	--	QMQLVQSGAEVKKTGSSVKVSCKASGYTFTYRYLHWVRQAPGQALEWMG WITPFNGNTNYAQKFQDRVTITRDRSMSTAYMELSSLRSEDTAMYYCAR
IGHV1-46	VH 1-46	DP-7	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGI INPSGGSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
IGHV1-58	VH 1-58	DP-2	QMQLVQSGPEVKKPGTSVKVSCKASGFTFTSSAMQWVRQARGQRLEWIGW IVVGSGNTNYAQKFQERVTITRDMSTSTAYMELSSLRSEDTAVYYCAA
IGHV1-69*01	VH 1-69	DP-10	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGG IIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAR
IGHV1-69*06, IGHV1-e	VH 1-69	DP-88	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGG IIPIFGTANYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCAR
IGHV1-c	--	--	KSGASVKVSCSFSGFTITSYGIHWVQQSPGQGLEWMGWINPGNGSPSYAKK FQGRFTMTRDMSTTTAYTDLSSLTSEDMAVYYYAR
IGHV1-f	--	DP-3	EVQLVQSGAEVKKPGATVKISCKVSGYTFTDYYMHWVQQAPGKGLEWMGL VDPEDGETIYAEKFQGRVTITADTSTDTAYMELSSLRSEDTAVYYCAT
IGHV2-5	VH 2-5	DP-76	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALI YWNDDKRYSPSLKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCAHR
IGHV2-26	VH 2-26	DP-26	QVTLKESGPVLVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKALEWLAH IFSNDEKSYSTSLKSRLTISKDTSKSQVVLTMTNMDPVDTATYYCARI
IGHV2-70	VH 2-70	DP-27	QVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMCVSWIRQPPGKALEWLALI DWDDDKYYSTSLKTRLTISKDTSKNQVVLTMTNMDPVDTATYYCARI
IGHV3-7	VH 3-7	DP-54	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVA NIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR
IGHV3-9	VH 3-9	DP-31	EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSG ISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKD

Figure 6B

IGHV3-11	VH 3-11	DP-35	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYI SSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR
IGHV3-13	VH 3-13	DP-48	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEWVSA IGTAGDTYYPGSVKGRFTISRENAKNSLYLQMNSLRAGDTAVYYCAR
IGHV3-15	VH 3-15	DP-38	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVG RIKSKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTT
IGHV3-16	VH 3-16		EVQLVESGGGLVQPGGSLRLSCAASGFTFSNSDMNWARKAPGKGLEWVSG VSWNGSRTHYVDSVK.RRFIISRDNSRNSLYLQKNRRRAEDMAVYYCVR
IGHV3-20	VH 3-20	DP-32	EVQLVESGGGVVRPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVS GINWNGGSTGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYHCAR
IGHV3-21	VH 3-21	DP-77	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSI SSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR
IGHV3-23	VH 3-23	DP-47	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAI SGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK
IGHV3-30	VH 3-30	DP-49	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
IGHV3-30-3	--	DP-46	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAV ISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
IGHV3-30-5	--	--	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK
IGHV3-33	VH 3-33	DP-50	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVA VIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
IGHV3-35	VH 3-35	DP-59	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNSDMNWVHQAPGKGLEWVSG VSWNGSRTHYADSVKGRFIISRDNSRNTLYLQTNSLRAEDTAVYYCVR
IGHV3-38	VH 3-38P	--	EVQLVESGGGLVQPRGSLRLSCAASGFTVSSNEMSWIRQAPGKGLEWVSSI SGGSTYYADSRKGRFTISRDNSKNTLYLQMNNLRAEGTAAYYCARY
IGHV3-43	VH 3-43	DP-33	EVQLVESGGVVVQPGGSLRLSCAASGFTFDDYTMHWVRQAPGKGLEWVSLI SWDGGSTYYADSVKGRFTISRDNSKNSLYLQMNSLRTEDTALYYCAKD
IGHV3-48	VH 3-48	DP-51	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSY ISSSSSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCAR
IGHV3-49	VH 3-49	3-49RB	EVQLVESGGGLVQPGRSLRLSCTASGFTFGDYAMSWFRQAPGKGLEWVGF IRSKAYGGTTEYAASVKGRFTISRDDSKSIAYLQMNSLKTEDTAVYYCTR
IGHV3-53	VH 3-53	DP-42	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI YSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
IGHV3-64	VH 3-64	DP-61	EVQLVESGEGLVQPGGSLRLSCAASGFTFSSYAMHWVRQAPGKGLEYVSAI SSNGGSTYYADSVKGRFTISRDNSKNTLYLQMGSLRAEDMAVYYCAR
IGHV3-66	VH 3-66	DP-86	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI YSCGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
IGHV3-72	VH 3-72	DP-29	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDHYMDWVRQAPGKGLEWVG RTRNKANSYTTEYAASVKGRFTISRDDSKNSLYLQMNSLKTEDTAVYYCAR
IGHV3-73	VH 3-73	DA-11	EVQLVESGGGLVQPGGSLKLSCAASGFTFSGSAMHWVRQASGKGLEWVGR IRSKANSYATAYAASVKGRFTISRDDSKNTAYLQMNSLKTEDTAVYYCTR
IGHV3-74	VH 3-74	DP-53	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMHWVRQAPGKGLVWVS RINSDGSSTSYADSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCAR

Figure 6B

IGHV3-11	VH 3-11	DP-35	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYI SSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR
IGHV3-13	VH 3-13	DP-48	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEWVSA IGTAGDTYYPGSVKGRFTISRENAKNSLYLQMNSLRAGDTAVYYCAR
IGHV3-15	VH 3-15	DP-38	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVG RIKSKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTT
IGHV3-16	VH 3-16		EVQLVESGGGLVQPGGSLRLSCAASGFTFSNSDMNWARKAPGKGLEWVSG VSWNGSRTHYVDSVK.RRFIISRDNSRNSLYLQKNRRRAEDMAVYYCVR
IGHV3-20	VH 3-20	DP-32	EVQLVESGGGVVRPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVS GINWNGGSTGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYHCAR
IGHV3-21	VH 3-21	DP-77	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSI SSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR
IGHV3-23	VH 3-23	DP-47	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAI SGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK
IGHV3-30	VH 3-30	DP-49	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
IGHV3-30-3	--	DP-46	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAV ISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
IGHV3-30-5	--	--	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK
IGHV3-33	VH 3-33	DP-50	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVA VIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
IGHV3-35	VH 3-35	DP-59	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNSDMNWVHQAPGKGLEWVSG VSWNGSRTHYADSVKGRFIISRDNSRNTLYLQTNSLRAEDTAVYYCVR
IGHV3-38	VH 3-38P	--	EVQLVESGGGLVQPRGSLRLSCAASGFTVSSNEMSWIRQAPGKGLEWVSSI SGGSTYYADSRKGRFTISRDNSKNTLYLQMNNLRAEGTAAYYCARY
IGHV3-43	VH 3-43	DP-33	EVQLVESGGVVVQPGGSLRLSCAASGFTFDDYTMHWVRQAPGKGLEWVSLI SWDGGSTYYADSVKGRFTISRDNSKNSLYLQMNSLRTEDTALYYCAKD
IGHV3-48	VH 3-48	DP-51	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSY ISSSSSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCAR
IGHV3-49	VH 3-49	3-49RB	EVQLVESGGGLVQPGRSLRLSCTASGFTFGDYAMSWFRQAPGKGLEWVGF IRSKAYGGTTEYAASVKGRFTISRDDSKSIAYLQMNSLKTEDTAVYYCTR
IGHV3-53	VH 3-53	DP-42	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI YSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
IGHV3-64	VH 3-64	DP-61	EVQLVESGEGLVQPGGSLRLSCAASGFTFSSYAMHWVRQAPGKGLEYVSAI SSNGGSTYYADSVKGRFTISRDNSKNTLYLQMGSLRAEDMAVYYCAR
IGHV3-66	VH 3-66	DP-86	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI YSCGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
IGHV3-72	VH 3-72	DP-29	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDHYMDWVRQAPGKGLEWVG RTRNKANSYTTEYAASVKGRFTISRDDSKNSLYLQMNSLKTEDTAVYYCAR
IGHV3-73	VH 3-73	DA-11	EVQLVESGGGLVQPGGSLKLSCAASGFTFSGSAMHWVRQASGKGLEWVGR IRSKANSYATAYAASVKGRFTISRDDSKNTAYLQMNSLKTEDTAVYYCTR
IGHV3-74	VH 3-74	DP-53	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMHWVRQAPGKGLVWVS RINSDGSSTSYADSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCAR

Figure 6C

IGHV3-d	--	--	EVQLVESRGVLVQPGGSLRLSCAASGFTVSSNEMSWVRQAPGKGLEWVSSI SGGSTYYADSRKGRFTISRDNSKNTLHLQMNSLRAEDTAVYYCKK
IGHV4-4	VH 4-4	DP-70	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPAGKGLEWIGRIY TSGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-28	VH 4-28	DP-68	QVQLQESGPGLVKPSDTLSLTCAVSGYSISSSNWWGWIRQPPGKGLEWIGYI YYSGSTYYNPSLKSRVTMSVDTSKNQFSLKLSSVTAVDTAVYYCAR
IGHV4-30-1	--	--	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIG YIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-30-2	--	DP-64	QLQLQESGSGLVKPSQTLSLTCAVSGGSISSGGYSWSWIRQPPGKGLEWIG YIYHSGSTYYNPSLKSRVTISVDRSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-30-4	--	DP-78	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYYWSWIRQPPGKGLEWIG YIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-31	VH 4-31	DP-65	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIG YIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-34	VH 4-34	DP-63	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEI NHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARG
IGHV4-39	VH 4-39	DP-79	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGS IYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-59	VH 4-59	DP-71	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIY YSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-61	VH 4-61	DP-66	QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGGYYWSWIRQPPGKGLEWIG YIYYSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-b	--	DP-67	QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGLEWIGSI YHSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV5-51	VH 5-51	DP-73	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII YPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR
IGHV5-a	--	--	EVQLVQSGAEVKKPGESLRISCKGSGYSFTSYWISWVRQMPGKGLEWMGRI DPSDSYTNYSPSFQGHVTISADKSISTAYLQWSSLKASDTAMYYCAR
IGHV6-1	VH 6-1	DP-74	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSAAWNWIRQSPSRGLEWLG RTYYRSKWYNDYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCAR
IGHV7-4-1	--	DP-21	QVQLVQSGSELKKPGASVKVSCKASGYTFTSYAMNWVRQAPGQGLEWMG WINTNTGNPTYAQGFTGRFVFSLDTSVSTAYLQICSLKAEDTAVYYCAR
IGHV7-81	VH 7-81	--	QVQLVQSGHEVKQPGASVKVSCKASGYSFTTYGMNWVPQAPGQGLEWMG WFNTYTGNPTYAQGFTGRFVFSMDTSASTAYLQISSLKAEDMAMYYCAR

51 functional

5 open reading frames

Figure 6C

IGHV3-d	--	--	EVQLVESRGVLVQPGGSLRLSCAASGFTVSSNEMSWVRQAPGKGLEWVSSI SGGSTYYADSRKGRFTISRDNSKNTLHLQMNSLRAEDTAVYYCKK
IGHV4-4	VH 4-4	DP-70	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPAGKGLEWIGRIY TSGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-28	VH 4-28	DP-68	QVQLQESGPGLVKPSDTLSLTCAVSGYSISSSNWWGWIRQPPGKGLEWIGYI YYSGSTYYNPSLKSRVTMSVDTSKNQFSLKLSSVTAVDTAVYYCAR
IGHV4-30-1	--	--	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIG YIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-30-2	--	DP-64	QLQLQESGSGLVKPSQTLSLTCAVSGGSISSGGYSWSWIRQPPGKGLEWIG YIYHSGSTYYNPSLKSRVTISVDRSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-30-4	--	DP-78	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYYWSWIRQPPGKGLEWIG YIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-31	VH 4-31	DP-65	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIG YIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-34	VH 4-34	DP-63	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEI NHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARG
IGHV4-39	VH 4-39	DP-79	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGS IYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-59	VH 4-59	DP-71	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIY YSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-61	VH 4-61	DP-66	QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGGYYWSWIRQPPGKGLEWIG YIYYSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-b	--	DP-67	QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGLEWIGSI YHSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV5-51	VH 5-51	DP-73	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII YPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR
IGHV5-a	--	--	EVQLVQSGAEVKKPGESLRISCKGSGYSFTSYWISWVRQMPGKGLEWMGRI DPSDSYTNYSPSFQGHVTISADKSISTAYLQWSSLKASDTAMYYCAR
IGHV6-1	VH 6-1	DP-74	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSAAWNWIRQSPSRGLEWLG RTYYRSKWYNDYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCAR
IGHV7-4-1	--	DP-21	QVQLVQSGSELKKPGASVKVSCKASGYTFTSYAMNWVRQAPGQGLEWMG WINTNTGNPTYAQGFTGRFVFSLDTSVSTAYLQICSLKAEDTAVYYCAR
IGHV7-81	VH 7-81	--	QVQLVQSGHEVKQPGASVKVSCKASGYSFTTYGMNWVPQAPGQGLEWMG WFNTYTGNPTYAQGFTGRFVFSMDTSASTAYLQISSLKAEDMAMYYCAR

51 functional

5 open reading frames

Figure 7A

	Zachau	Protein sequence
IGKV1-5	L12	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASS LESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYNSYS
IGKV1-6	L11	AIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQDYNYP
IGKV1-8	L9	AIRMTQSPSSFSASTGDRVTITCRASQGISSYLAWYQQKPGKAPKLLIYAASTL QSGVPSRFSGSGSGTDFTLTISCLQSEDFATYYCQQYYSYP
IGKV1-9	L8	DIQLTQSPSFLSASVGDRVTITCRASQGISSYLAWYQQKPGKAPKLLIYAASTL QSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQLNSYP
IGKV1-12	L5	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFP
IGKV1-13	L4/18a	AIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKAPKLLIYDASSL ESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFNSYP
IGKV1-16	L1	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWFQQKPGKAPKSLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSYP
IGKV1-17	A30	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASS LQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP
IGKV1-27	A20	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTL QSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAP
IGKV1-33	O18	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASN LETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYDNLP
IGKV1-37	O14	DIQLTQSPSSLSASVGDRVTITCRVSQGISSYLNWYRQKPGKVPKLLIYSASNL QSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYGQRTYNAPP
IGKV1-39	O12	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTP
IGKV1D-08	L24	VIWMTQSPSLLSASTGDRVTISCRMSQGISSYLAWYQQKPGKAPELLIYAAST LQSGVPSRFSGSGSGTDFTLTISCLQSEDFATYYCQQYYSFP
IGKV1D-12	L19	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFP
IGKV1D-13	L18	AIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKAPKLLIYDASSL ESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFNNYP
IGKV1D-16	L15	DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPEKAPKSLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSYP
IGKV1D-17	L14	NIQMTQSPSAMSASVGDRVTITCRARQGISNYLAWFQQKPGKVPKHLIYAASS LQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP
IGKV1D-33	O8	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASN LETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYDNLP
IGKV1D-37	O4	DIQLTQSPSSLSASVGDRVTITCRVSQGISSYLNWYRQKPGKVPKLLIYSASNL QSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYGQRTYNAPP

Figure 7A

	Zachau	Protein sequence
IGKV1-5	L12	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASS LESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYNSYS
IGKV1-6	L11	AIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQDYNYP
IGKV1-8	L9	AIRMTQSPSSFSASTGDRVTITCRASQGISSYLAWYQQKPGKAPKLLIYAASTL QSGVPSRFSGSGSGTDFTLTISCLQSEDFATYYCQQYYSYP
IGKV1-9	L8	DIQLTQSPSFLSASVGDRVTITCRASQGISSYLAWYQQKPGKAPKLLIYAASTL QSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQLNSYP
IGKV1-12	L5	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFP
IGKV1-13	L4/18a	AIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKAPKLLIYDASSL ESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFNSYP
IGKV1-16	L1	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWFQQKPGKAPKSLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSYP
IGKV1-17	A30	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASS LQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP
IGKV1-27	A20	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTL QSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAP
IGKV1-33	O18	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASN LETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYDNLP
IGKV1-37	O14	DIQLTQSPSSLSASVGDRVTITCRVSQGISSYLNWYRQKPGKVPKLLIYSASNL QSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYGQRTYNAPP
IGKV1-39	O12	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTP
IGKV1D-08	L24	VIWMTQSPSLLSASTGDRVTISCRMSQGISSYLAWYQQKPGKAPELLIYAAST LQSGVPSRFSGSGSGTDFTLTISCLQSEDFATYYCQQYYSFP
IGKV1D-12	L19	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFP
IGKV1D-13	L18	AIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKAPKLLIYDASSL ESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFNNYP
IGKV1D-16	L15	DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPEKAPKSLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSYP
IGKV1D-17	L14	NIQMTQSPSAMSASVGDRVTITCRARQGISNYLAWFQQKPGKVPKHLIYAASS LQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP
IGKV1D-33	O8	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASN LETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYDNLP
IGKV1D-37	O4	DIQLTQSPSSLSASVGDRVTITCRVSQGISSYLNWYRQKPGKVPKLLIYSASNL QSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYGQRTYNAPP

Figure 7B

IGKV1D-39	O2	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTP
IGKV1D-42	L22	DIQMIQSPSFLSASVGDRVSIICWASEGISSNLAWYLQKPGKSPKLFLYDAKDL HPGVSSRFSGRGSGTDFTLTIISLKPEDFAAYYCKQDFSYPP
IGKV1D-43	L23	AIRMTQSPFSLSASVGDRVTITCWASQGISSYLAWYQQKPAKAPKLFIYYASSL QSGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQQYYSTP
IGKV2-24	A23	DIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLI YKISNRFSGVPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQATQFP
IGKV2-28	A19	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLI YLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
IGKV2-29	A18b	DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWYLQKPGQSPQLLI YEVSSRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGIHLP
IGKV2-30	A17	DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQRPGQSPRR LIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWP
IGKV2-40	O11	DIVMTQTPLSLPVTPGEPASISCRSSQSLLDSDDGNTYLDWYLQKPGQSPQLL IYTLSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQRIEFP
IGKV2D-24	A7	DIVMTQTPLSSPVTLGQPASISFRSSQSLVHSDGNTYLSWLQQRPGQPPRLLI YKVSNRFSGVPDRFSGSGAGTDFTLKISRVEAEDVGVYYCTQATQFP
IGKV2D-26	A5	EIVMTQTPLSLSITPGEQASISCRSSQSLLHSDGYTYLYWFLQKARPVSTLLIYE VSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDFGVYYCMQDAQDPP
IGKV2D-28	A3	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLI YLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
IGKV2D-29	A2	DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWYLQKPGQPPQLLI YEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQSIQLP
IGKV2D-30	A1	DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQRPGQSPRR LIYKVSNWDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWP
IGKV2D-40	O1	DIVMTQTPLSLPVTPGEPASISCRSSQSLLDSDDGNTYLDWYLQKPGQSPQLL IYTLSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQRIEFP
IGKV3-7	L10	EIVMTQSPPTLSLSPGERVTLSCRASQSVSSSYLTWYQQKPGQAPRLLIYGAS TRATSIPARFSGSGSGTDFTLTISSLQPEDFAVYYCQQDHNLPP
IGKV3-11	L6	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWP
IGKV3-15	L2	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAS TRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP

Figure 7B

IGKV1D-39	O2	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTP
IGKV1D-42	L22	DIQMIQSPSFLSASVGDRVSIICWASEGISSNLAWYLQKPGKSPKLFLYDAKDL HPGVSSRFSGRGSGTDFTLTIISLKPEDFAAYYCKQDFSYPP
IGKV1D-43	L23	AIRMTQSPFSLSASVGDRVTITCWASQGISSYLAWYQQKPAKAPKLFIYYASSL QSGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQQYYSTP
IGKV2-24	A23	DIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLI YKISNRFSGVPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQATQFP
IGKV2-28	A19	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLI YLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
IGKV2-29	A18b	DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWYLQKPGQSPQLLI YEVSSRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGIHLP
IGKV2-30	A17	DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQRPGQSPRR LIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWP
IGKV2-40	O11	DIVMTQTPLSLPVTPGEPASISCRSSQSLLDSDDGNTYLDWYLQKPGQSPQLL IYTLSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQRIEFP
IGKV2D-24	A7	DIVMTQTPLSSPVTLGQPASISFRSSQSLVHSDGNTYLSWLQQRPGQPPRLLI YKVSNRFSGVPDRFSGSGAGTDFTLKISRVEAEDVGVYYCTQATQFP
IGKV2D-26	A5	EIVMTQTPLSLSITPGEQASISCRSSQSLLHSDGYTYLYWFLQKARPVSTLLIYE VSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDFGVYYCMQDAQDPP
IGKV2D-28	A3	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLI YLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
IGKV2D-29	A2	DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWYLQKPGQPPQLLI YEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQSIQLP
IGKV2D-30	A1	DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQRPGQSPRR LIYKVSNWDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWP
IGKV2D-40	O1	DIVMTQTPLSLPVTPGEPASISCRSSQSLLDSDDGNTYLDWYLQKPGQSPQLL IYTLSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQRIEFP
IGKV3-7	L10	EIVMTQSPPTLSLSPGERVTLSCRASQSVSSSYLTWYQQKPGQAPRLLIYGAS TRATSIPARFSGSGSGTDFTLTISSLQPEDFAVYYCQQDHNLPP
IGKV3-11	L6	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWP
IGKV3-15	L2	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAS TRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP

Figure 7C

IGKV3-20	A27	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGAS SRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP
IGKV3D-07	L25	EIVMTQSPATLSLSPGERATLSCRASQSVSSSYLSWYQQKPGQAPRLLIYGAS TRATGIPARFSGSGSGTDFTLTISSLQPEDFAVYYCQQDYNLP
IGKV3D-11	L20	EIVLTQSPATLSLSPGERATLSCRASQGVSSYLAWYQQKPGQAPRLLIYDASN RATGIPARFSGSGPGTDFTLTISSLEPEDFAVYYCQQRSNWH
IGKV3D-15	L16	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAS TRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP
IGKV3D-20	A11	EIVLTQSPATLSLSPGERATLSCGASQSVSSSYLAWYQQKPGLAPRLLIYDAS SRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP
IGKV4-1	B3	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKL LIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTP
IGKV5-2	B2	ETTLTQSPAFMSATPGDKVNISCKASQDIDDDMNWYQQKPGEAAIFIIQEATTL VPGIPPRFSGSGYGTDFTLTINNIESEDAAYYFCLQHDNFP
IGKV6-21	A26	EIVLTQSPDFQSVTPKEKVTITCRASQSIGSSLHWYQQKPDQSPKLLIKYASQS FSGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCHQSSSLP
IGKV6D-21	A10	EIVLTQSPDFQSVTPKEKVTITCRASQSIGSSLHWYQQKPDQSPKLLIKYASQS FSGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCHQSSSLP
IGKV6D-41	A14	DVVMTQSPAFLSVTPGEKVTITCQASEGIGNYLYWYQQKPDQAPKLLIKYASQ SISGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQQGNKHP

38 functional

8 open reading frames

Figure 7C

IGKV3-20	A27	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGAS SRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP
IGKV3D-07	L25	EIVMTQSPATLSLSPGERATLSCRASQSVSSSYLSWYQQKPGQAPRLLIYGAS TRATGIPARFSGSGSGTDFTLTISSLQPEDFAVYYCQQDYNLP
IGKV3D-11	L20	EIVLTQSPATLSLSPGERATLSCRASQCVSSYLAWYQQKPCQAPRLLIYDASN RATGIPARFSGSGPGTDFTLTISSLEPEDFAVYYCQQRSNWH
IGKV3D-15	L16	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAS TRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP
IGKV3D-20	A11	EIVLTQSPATLSLSPGERATLSCGASQSVSSSYLAWYQQKPGLAPRLLIYDAS SRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP
IGKV4-1	B3	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKL LIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTP
IGKV5-2	B2	ETTLTQSPAFMSATPGDKVNISCKASQDIDDDMNWYQQKPGEAAIFIIQEATTL VPGIPPRFSGSGYGTDFTLTINNIESEDAAYYFCLQHDNFP
IGKV6-21	A26	EIVLTQSPDFQSVTPKEKVTITCRASQSIGSSLHWYQQKPDQSPKLLIKYASQS FSGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCHQSSSLP
IGKV6D-21	A10	EIVLTQSPDFQSVTPKEKVTITCRASQSIGSSLHWYQQKPDQSPKLLIKYASQS FSGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCHQSSSLP
IGKV6D-41	A14	DVVMTQSPAFLSVTPGEKVTITCQASEGIGNYLYWYQQKPDQAPKLLIKYASQ SISGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQQGNKHP

38 functional

8 open reading frames

Figure 8A

	Kawasaki et al	Frippiat et al	Protein sequence
IGLV1-36	VL 1-11	1a	QSVLTQPPSVSEAPRQRVTISCSGSSSNIGNNAVNWYQQLPGKAPKLLIYYDD LLPSGVSDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGP
IGLV1-40	VL 1-13	1e	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAPKLLIYG NSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGS
IGLV1-44	VL 1-16	1c	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNN QRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGP
IGLV1-47	VL 1-17	1g	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVYWYQQLPGTAPKLLIYSNN QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSGP
IGLV1-50	VL 1-18	1f	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYVVHWYQQLPGTAPKLLIYG NSNRPSGVPDQFSGSKSGTSASLAITGLQSEDEADYYCKAWDNSLNA
IGLV1-51	VL 1-19	1b	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNN KRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAG
IGLV2-08	VL 1-2	2c	QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIY EVSKRPSGVPDRFSGSKSGNTASLTVSGLQAEDEADYYCSSYAGSNNF
IGLV2-11	VL 1-3	2e	QSALTQPRSVSGSPGQSVTISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIY DVSKRPSGVPDRFSGSKSGNTASLTISGLQAEDEADYYCCSYAGSYTF
IGLV2-14	VL 1-4	2a2	QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIYE VSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTSSSTL
IGLV2-18	VL 1-5	2d	QSALTQPPSVSGSPGQSVTISCTGTSSDVGSYNRVSWYQQPPGTAPKLMIYE VSNRPSGVPDRFSGSKSGNTASLTISGLQAEDEADYYCSLYTSSSTF
IGLV2-23	VL 1-7	2b2	QSALTQPASVSGSPGQSITISCTGTSSDVGSYNLVSWYQQHPGKAPKLMIYE GSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCCSYAGSSTF
IGLV2-33	VL 1-9	2f	QSALTQPPFVSGAPGQSVTISCTGTSSDVGDYDHVFWYQKRLSTTSRLLIYN VNTRPSGISDLFSGSKSGNMASLTISGLKSEVEANYHCSLYSSSYTF
IGLV3-1	VL 2-1	3r	SYELTQPPSVSVSPGQTASITCSGDKLGDKYACWYQQKPGQSPVLVIYQDSK RPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTA
IGLV3-9	VL 2-6	3j	SYELTQPLSVSVALGQTARITCGGNNIGSKNVHWYQQKPGQAPVLVIYRDSN RPSGIPERFSGSNSGNTATLTISRAQAGDEADYYCQVWDSSTA
IGLV3-10	VL 2-7	3p	SYELTQPPSVSVSPGQTARITCSGDALPKKYAYWYQQKSGQAPVLVIYEDSK RPSGIPERFSGSSSGTMATLTISGAQVEDEADYYCYSTDSSGNH
IGLV3-12	VL 2-8	3i	SYELTQPHSVSVATAQMARITCGGNNIGSKAVHWYQQKPGQDPVLVIYSDSN RPSGIPERFSGSNPGNTATLTISRIEAGDEADYYCQVWDSSSDHP
IGLV3-16	VL 2-11	3a	SYELTQPPSVSVSLGQMARITCSGEALPKKYAYWYQQKPGQFPVLVIYKDSE RPSGIPERFSGSSSGTIVTLTISGVQAEDEADYYCLSADSSGTYP
IGLV3-19	VL 2-13	3l	SSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNN RPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHL
IGLV3-21	VL 2-14	3h	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVVYDDS DRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDHP
IGLV3-22	VL 2-15	3e	SYELTQLPSVSVSPGQTARITCSGDVLGENYADWYQQKPGQAPELVIYEDSE RYPGIPERFSGSTSGNTTTLTISRVLTEDEADYYCLSGDEDNP
IGLV3-25	VL 2-17	3m	SYELTQPPSVSVSPGQTARITCSGDALPKQYAYWYQQKPGQAPVLVIYKDSE RPSGIPERFSGSSSGTTVTLTISGVQAEDEADYYCQSADSSGTYP
IGLV3-27	VL 2-19	--	SYELTQPSSVSVSPGQTARITCSGDVLAKKYARWFQQKPGQAPVLVIYKDSE RPSGIPERFSGSSSGTTVTLTISGAQVEDEADYYCYSAADNNL

Figure 8A

	Kawasaki et al	Frippiat et al	Protein sequence
IGLV1-36	VL 1-11	1a	QSVLTQPPSVSEAPRQRVTISCSGSSSNIGNNAVNWYQQLPGKAPKLLIYYDD LLPSGVSDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGP
IGLV1-40	VL 1-13	1e	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAPKLLIYG NSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGS
IGLV1-44	VL 1-16	1c	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNN QRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGP
IGLV1-47	VL 1-17	1g	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVYWYQQLPGTAPKLLIYSNN QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSGP
IGLV1-50	VL 1-18	1f	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYVVHWYQQLPGTAPKLLIYG NSNRPSGVPDQFSGSKSGTSASLAITGLQSEDEADYYCKAWDNSLNA
IGLV1-51	VL 1-19	1b	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNN KRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAG
IGLV2-08	VL 1-2	2c	QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIY EVSKRPSGVPDRFSGSKSGNTASLTVSGLQAEDEADYYCSSYAGSNNF
IGLV2-11	VL 1-3	2e	QSALTQPRSVSGSPGQSVTISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIY DVSKRPSGVPDRFSGSKSGNTASLTISGLQAEDEADYYCCSYAGSYTF
IGLV2-14	VL 1-4	2a2	QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIYE VSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTSSSTL
IGLV2-18	VL 1-5	2d	QSALTQPPSVSGSPGQSVTISCTGTSSDVGSYNRVSWYQQPPGTAPKLMIYE VSNRPSGVPDRFSGSKSGNTASLTISGLQAEDEADYYCSLYTSSSTF
IGLV2-23	VL 1-7	2b2	QSALTQPASVSGSPGQSITISCTGTSSDVGSYNLVSWYQQHPGKAPKLMIYE GSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCCSYAGSSTF
IGLV2-33	VL 1-9	2f	QSALTQPPFVSGAPGQSVTISCTGTSSDVGDYDHVFWYQKRLSTTSRLLIYN VNTRPSGISDLFSGSKSGNMASLTISGLKSEVEANYHCSLYSSSYTF
IGLV3-1	VL 2-1	3r	SYELTQPPSVSVSPGQTASITCSGDKLGDKYACWYQQKPGQSPVLVIYQDSK RPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTA
IGLV3-9	VL 2-6	3j	SYELTQPLSVSVALGQTARITCGGNNIGSKNVHWYQQKPGQAPVLVIYRDSN RPSGIPERFSGSNSGNTATLTISRAQAGDEADYYCQVWDSSTA
IGLV3-10	VL 2-7	3p	SYELTQPPSVSVSPGQTARITCSGDALPKKYAYWYQQKSGQAPVLVIYEDSK RPSGIPERFSGSSSGTMATLTISGAQVEDEADYYCYSTDSSGNH
IGLV3-12	VL 2-8	3i	SYELTQPHSVSVATAQMARITCGGNNIGSKAVHWYQQKPGQDPVLVIYSDSN RPSGIPERFSGSNPGNTATLTISRIEAGDEADYYCQVWDSSSDHP
IGLV3-16	VL 2-11	3a	SYELTQPPSVSVSLGQMARITCSGEALPKKYAYWYQQKPGQFPVLVIYKDSE RPSGIPERFSGSSSGTIVTLTISGVQAEDEADYYCLSADSSGTYP
IGLV3-19	VL 2-13	3l	SSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNN RPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHL
IGLV3-21	VL 2-14	3h	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVVYDDS DRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDHP
IGLV3-22	VL 2-15	3e	SYELTQLPSVSVSPGQTARITCSGDVLGENYADWYQQKPGQAPELVIYEDSE RYPGIPERFSGSTSGNTITLTISRVLTEDEADYYCLSGDEDNP
IGLV3-25	VL 2-17	3m	SYELTQPPSVSVSPGQTARITCSGDALPKQYAYWYQQKPGQAPVLVIYKDSE RPSGIPERFSGSSSGTTVTLTISGVQAEDEADYYCQSADSSGTYP
IGLV3-27	VL 2-19	--	SYELTQPSSVSVSPGQTARITCSGDVLAKKYARWFQQKPGQAPVLVIYKDSE RPSGIPERFSGSSSGTTVTLTISGAQVEDEADYYCYSAADNNL

Figure 9

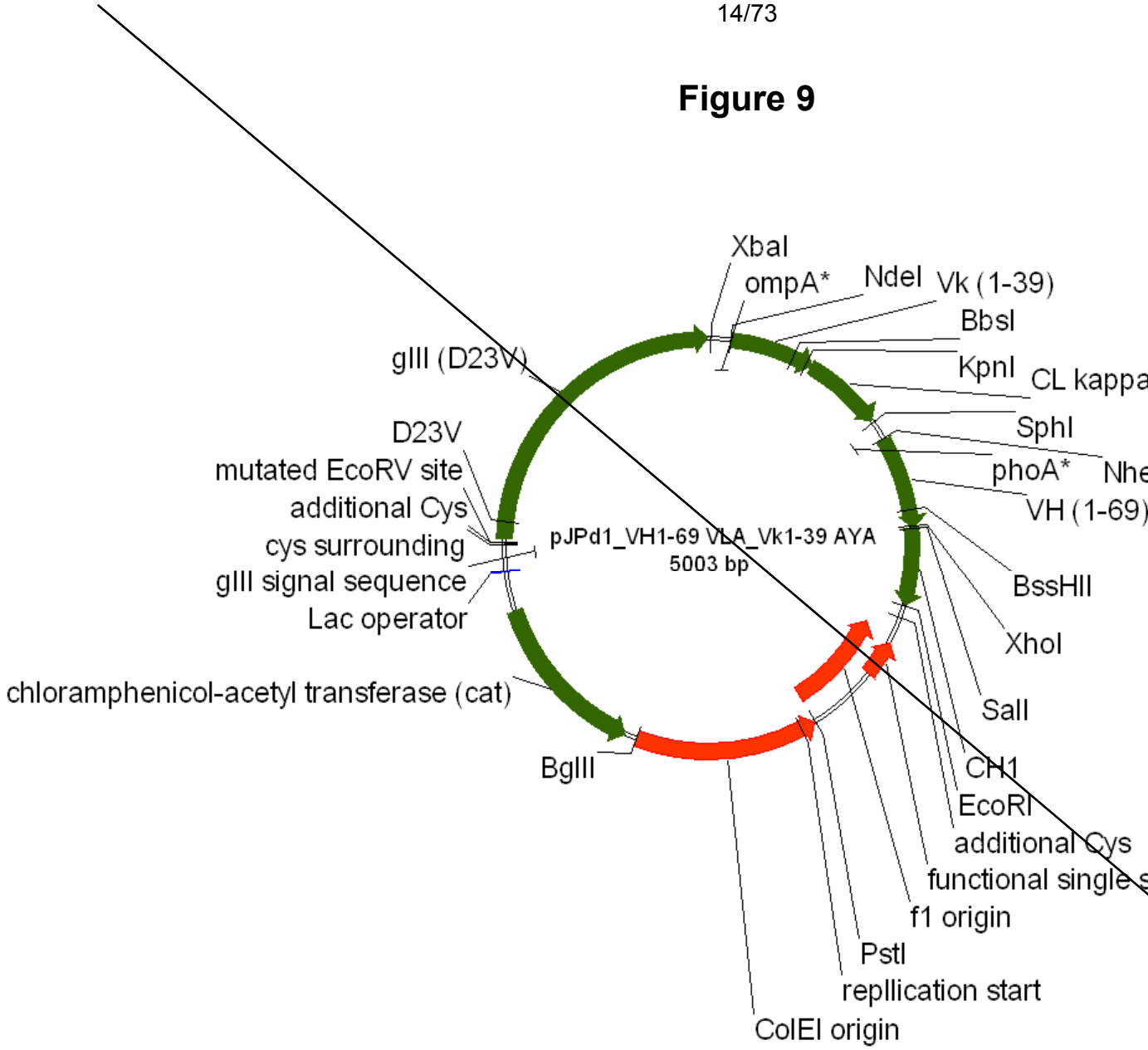

XbaI
ompA*
NdeI
Vk (1-39)
BbsI
KpnI
CL kappa
SphI
phoA*
VH (1-69)
BssHII
XhoI
SalI
CH1
EcoRI
additional Cys
functional single s
f1 origin
PstI
repllication start
ColEI origin
BglII
chloramphenicol-acetyl transferase (cat)
Lac operator
gIII signal sequence
cys surrounding
additional Cys
mutated EcoRV site
D23V
gIII (D23V)
pJPd1_VH1-69 VLA_Vk1-39 AYA
5003 bp

Figure 9

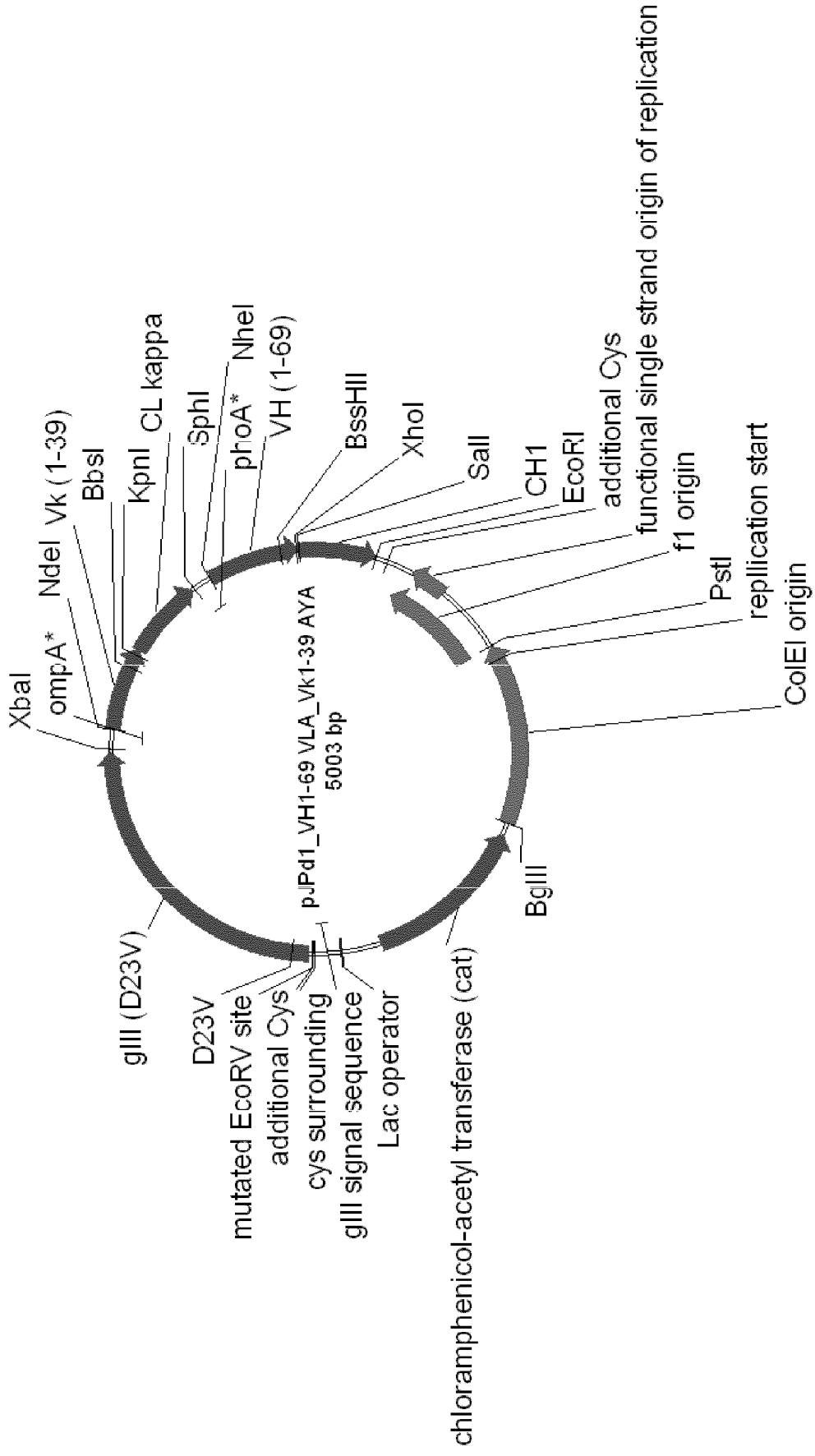

pJPd1_VH1-69 VLA_Vk1-39 AYA
5003 bp
XbaI
ompA*
NdeI
Vk (1-39)
BbsI
KpnI
CL kappa
SphI
phoA*
NheI
VH (1-69)
BssHII
XhoI
SalI
CH1
EcoRI
additional Cys
functional single strand origin of replication
f1 origin
PstI
repllication start
ColEI origin
BglII
chloramphenicol-acetyl transferase (cat)
Lac operator
gIII signal sequence
cys surrounding
additional Cys
mutated EcoRV site
D23V
gIII (D23V)

Figure 10

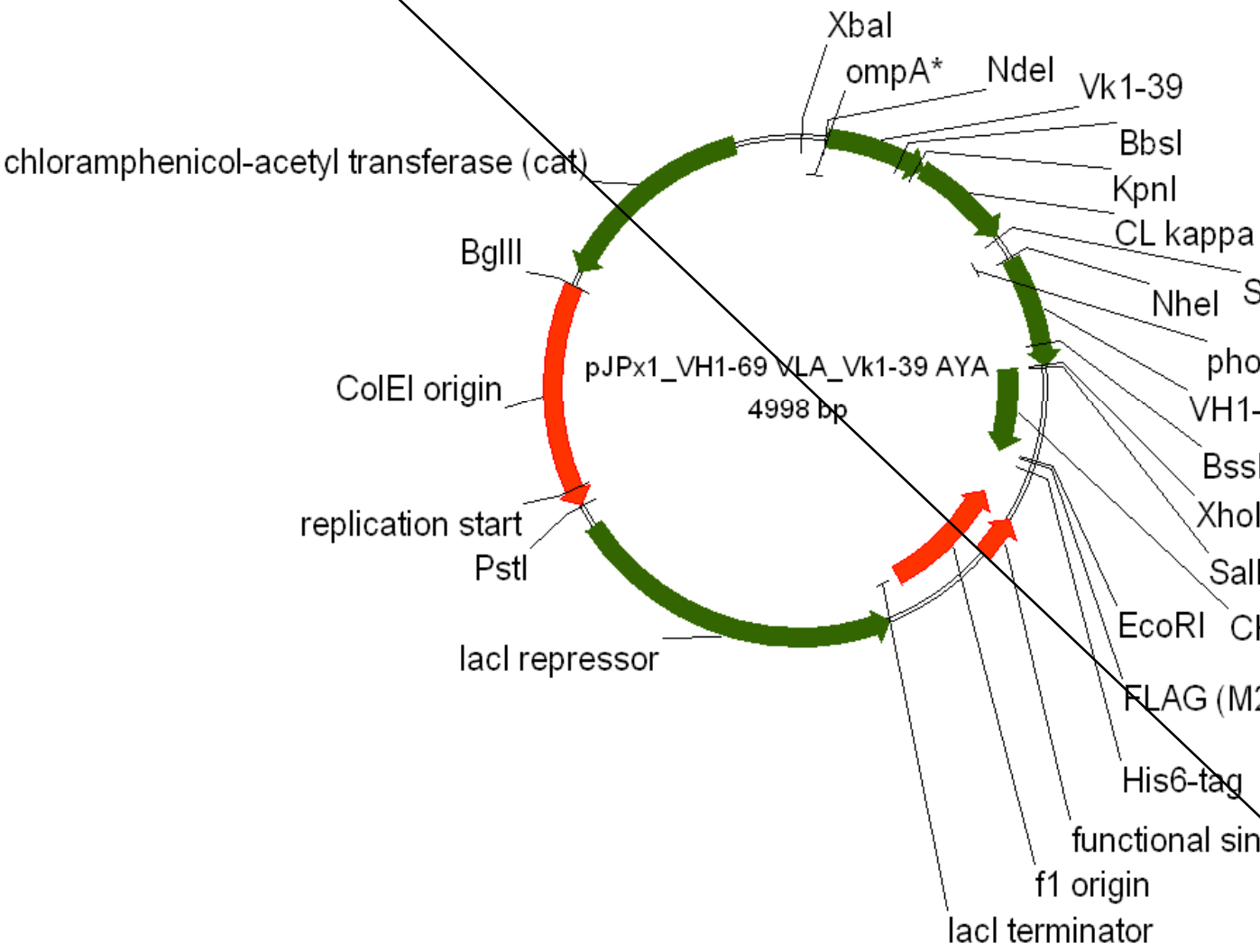

XbaI
ompA*
NdeI
Vk1-39
BbsI
KpnI
CL kappa
NheI
chloramphenicol-acetyl transferase (cat)
BglII
ColEI origin
pJPx1_VH1-69 VLA_Vk1-39 AYA
4998 bp
replication start
PstI
lacI repressor
EcoRI
FLAG (M
His6-tag
functional sin
f1 origin
lacI terminator

Figure 10

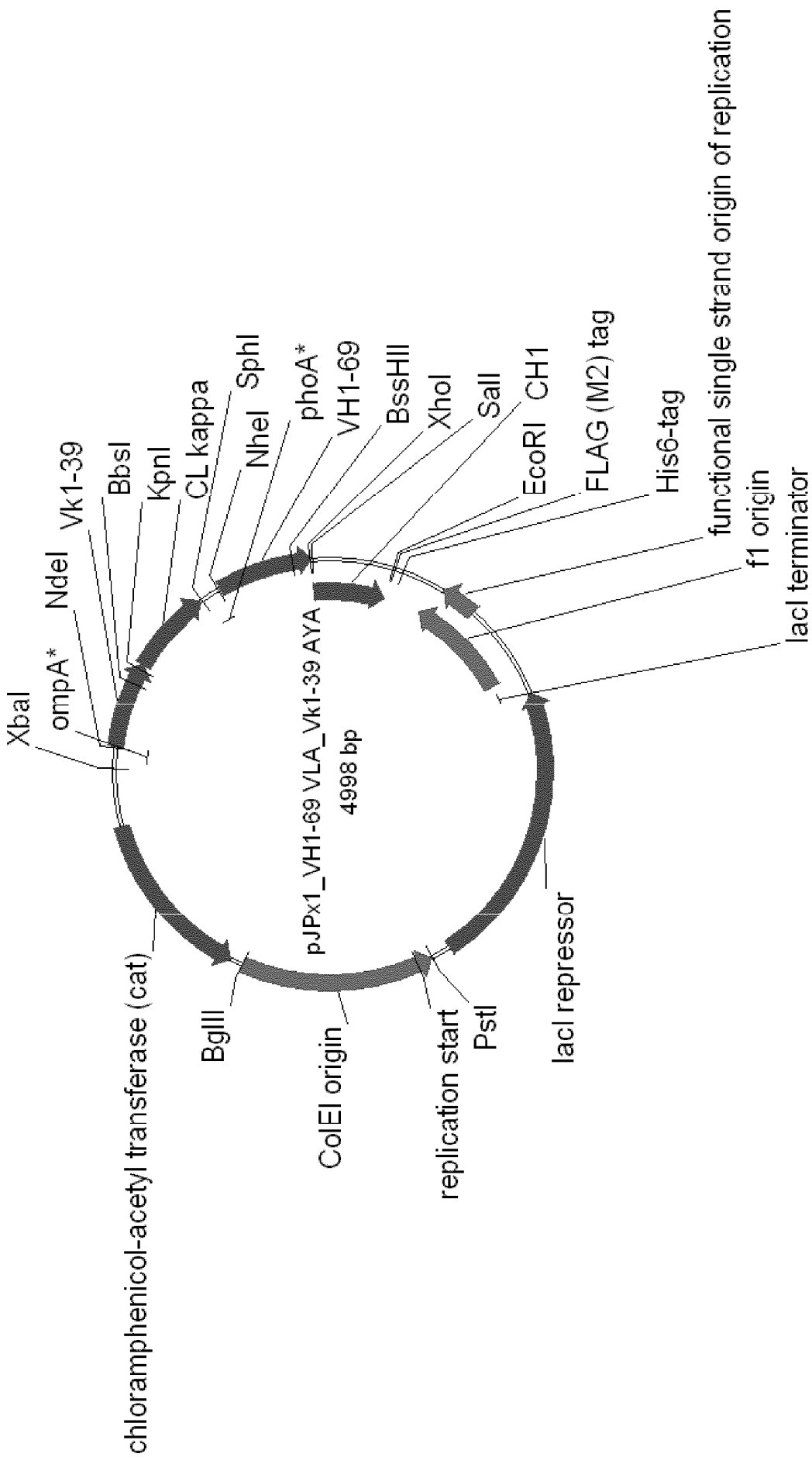

pJPx1_VH1-69 VLA_Vk1-39 AYA
4998 bp
XbaI
ompA*
NdeI
Vk1-39
BbsI
KpnI
CL kappa
NheI
SphI
phoA*
VH1-69
BssHII
XhoI
SalI
EcoRI CH1
FLAG (M2) tag
His6-tag
functional single strand origin of replication
f1 origin
lacI terminator
lacI repressor
PstI
replication start
ColEI origin
BglII
chloramphenicol-acetyl transferase (cat)

Figure 11

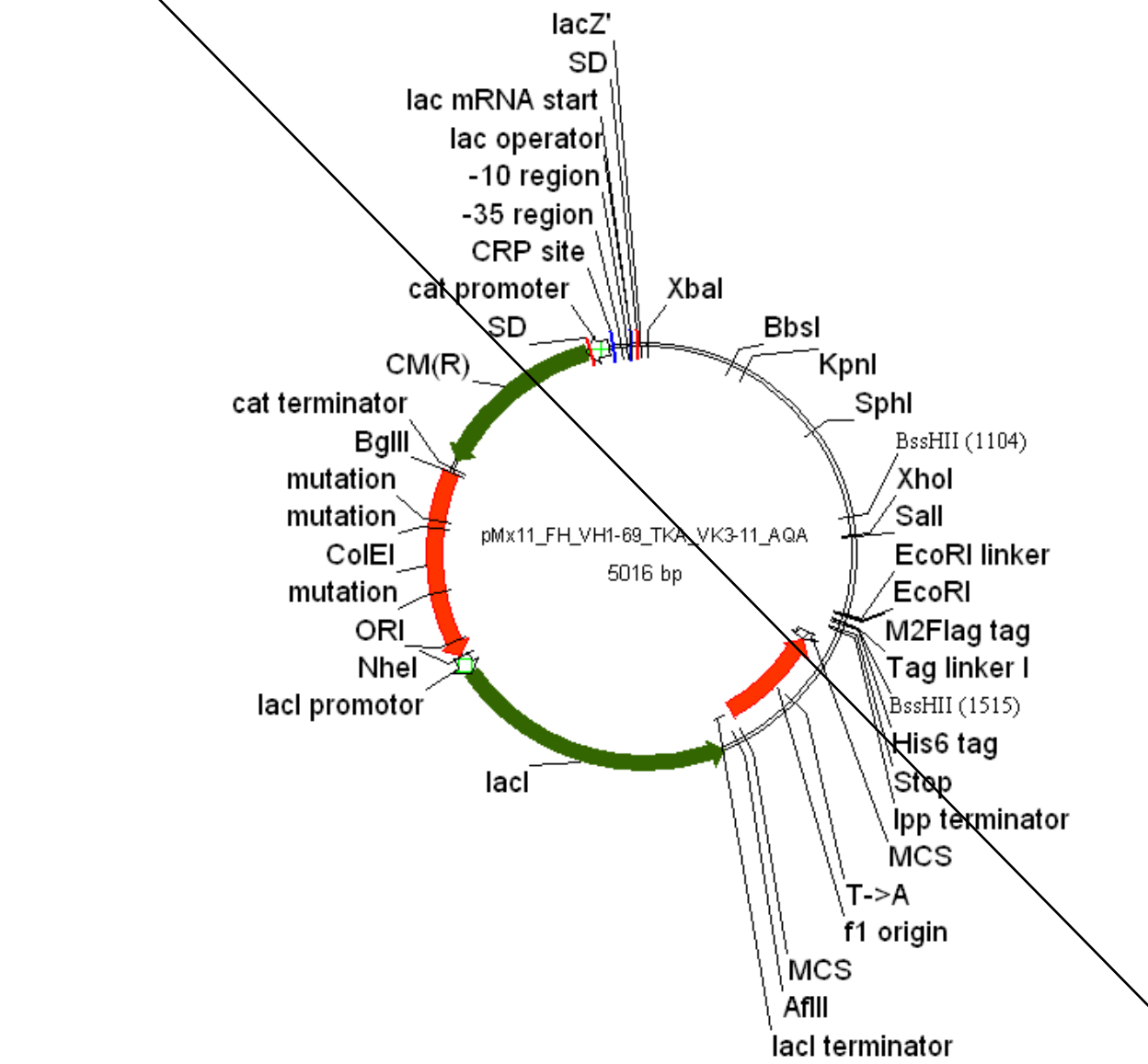

lacZ'
SD
lac mRNA start
lac operator
-10 region
-35 region
CRP site
cat promoter
SD
XbaI
BbsI
KpnI
SphI
BssHII (1104)
XhoI
SalI
EcoRI linker
EcoRI
M2Flag tag
Tag linker I
BssHII (1515)
His6 tag
Stop
lpp terminator
MCS
T->A
f1 origin
MCS
AflII
lacI terminator
lacI
lacI promotor
NheI
ORI
mutation
ColEI
mutation
mutation
BglII
cat terminator
CM(R)
pMx11_FH_VH1-69_TKA_VK3-11_AQA
5016 bp

Figure 11

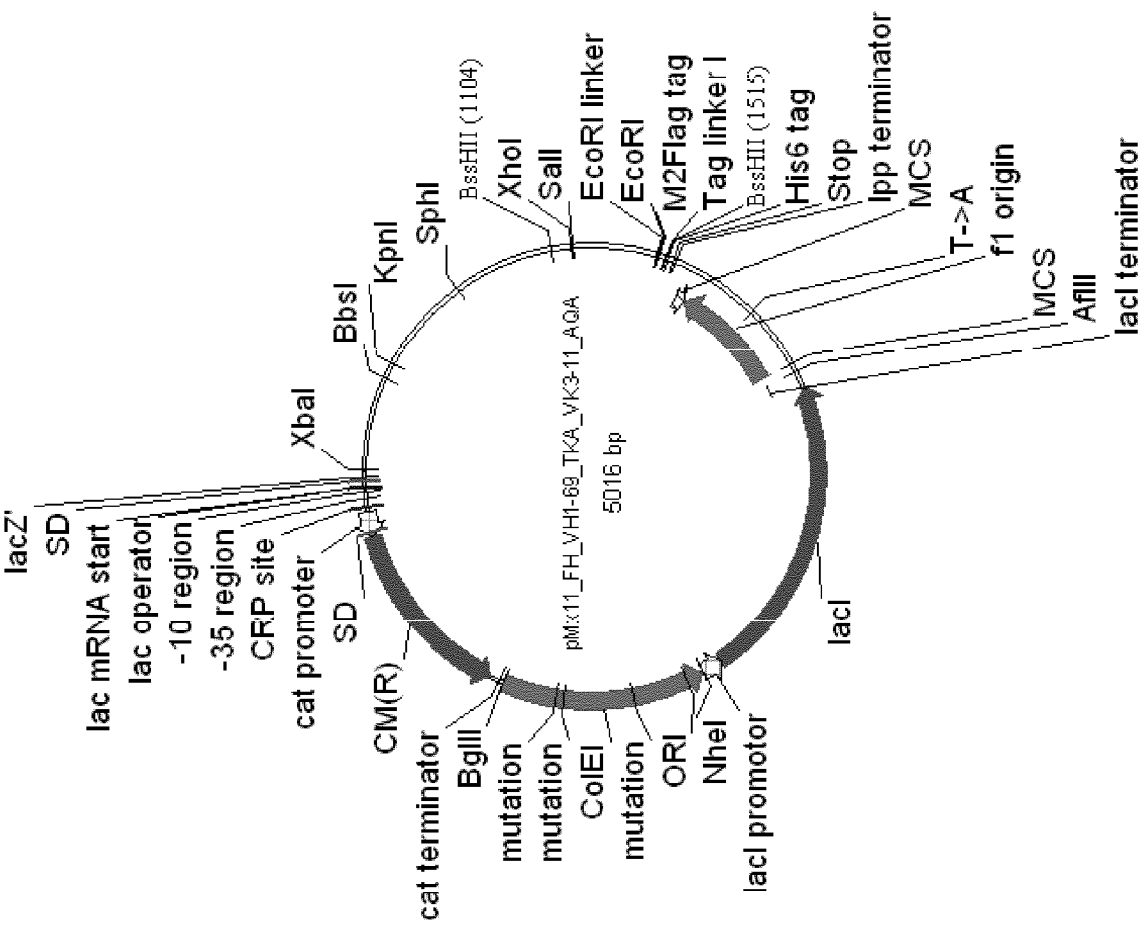

pMx11_FH_VH1-69_TKA_VK3-11_AQA
5016 bp
lacZ'
SD
lac mRNA start
lac operator
-10 region
-35 region
CRP site
cat promoter
SD
CM(R)
cat terminator
BglII
mutation
mutation
ColEI
mutation
ORI
NheI
lacI promotor
lacI
XbaI
BbsI
KpnI
SphI
BssHII (1104)
XhoI
SalI
EcoRI linker
EcoRI
M2Flag tag
Tag linker I
BssHII (1515)
His6 tag
Stop
lpp terminator
MCS
T->A
f1 origin
MCS
AflII
lacI terminator

Figure 12

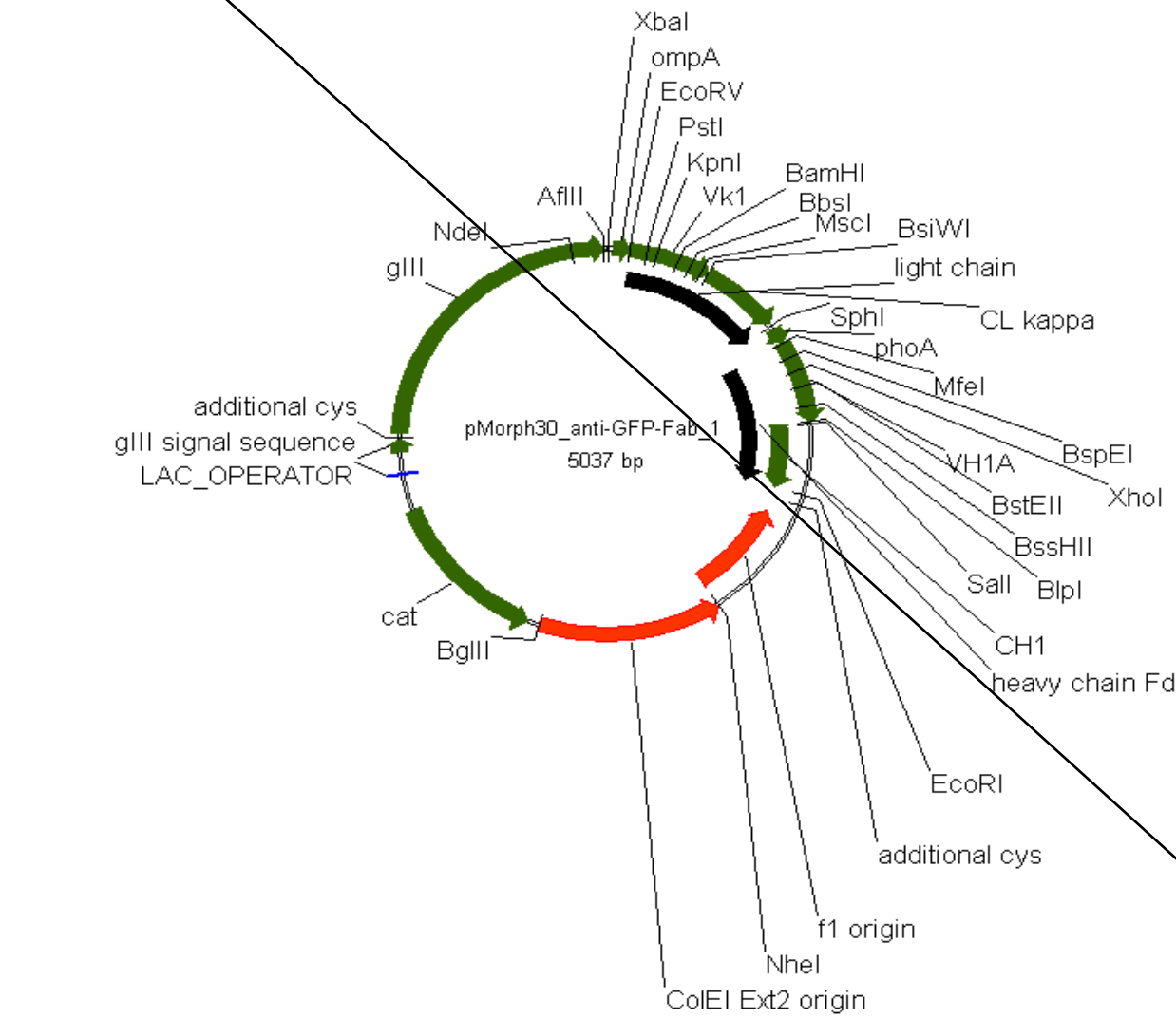

XbaI
ompA
EcoRV
PstI
KpnI
BamHI
AflII
Vk1
BbsI
NdeI
MscI
BsiWI
gIII
light chain
CL kappa
SphI
phoA
MfeI
additional cys
gIII signal sequence
LAC_OPERATOR
pMorph30_anti-GFP-Fab_1
5037 bp
BspEI
VH1A
XhoI
BstEII
BssHII
SalI
BlpI
CH1
heavy chain Fd
cat
BglII
EcoRI
additional cys
f1 origin
NheI
ColEI Ext2 origin

Figure 12

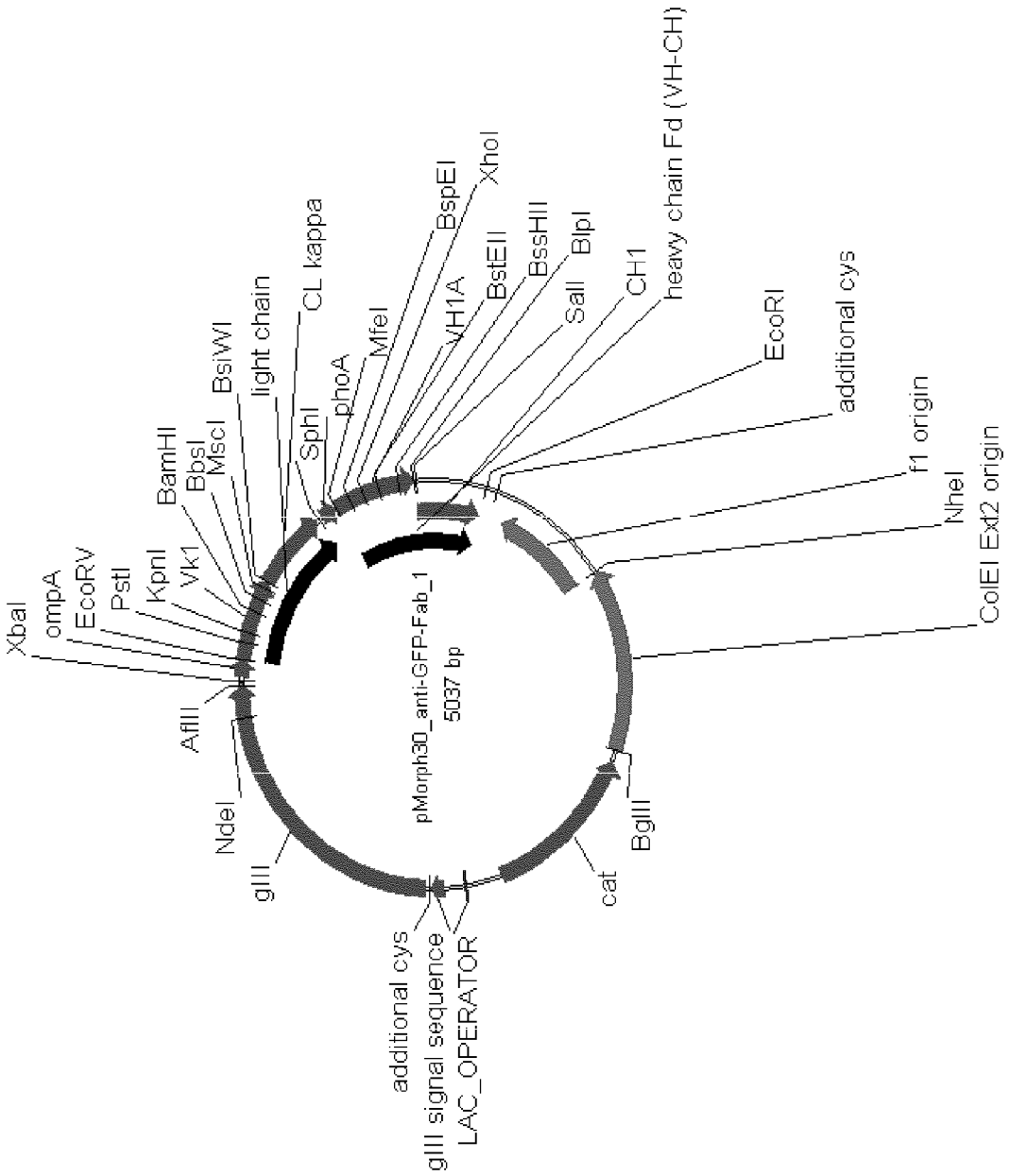

pMorph3D_anti-GFP-Fab_1
5037 bp
XbaI
ompA
EcoRV
PstI
KpnI
VK1
BamHI
BbsI
MscI
BsiWI
light chain
CL kappa
SphI
phoA
MfeI
VH1A
BstEII
BspEI
XhoI
BssHII
SalI
BlpI
CH1
heavy chain Fd (VH-CH)
EcoRI
additional cys
f1 origin
NheI
ColEI Ext2 origin
BglII
cat
gIII
NdeI
AflII
additional cys
gIII signal sequence
LAC_OPERATOR

Figure 13

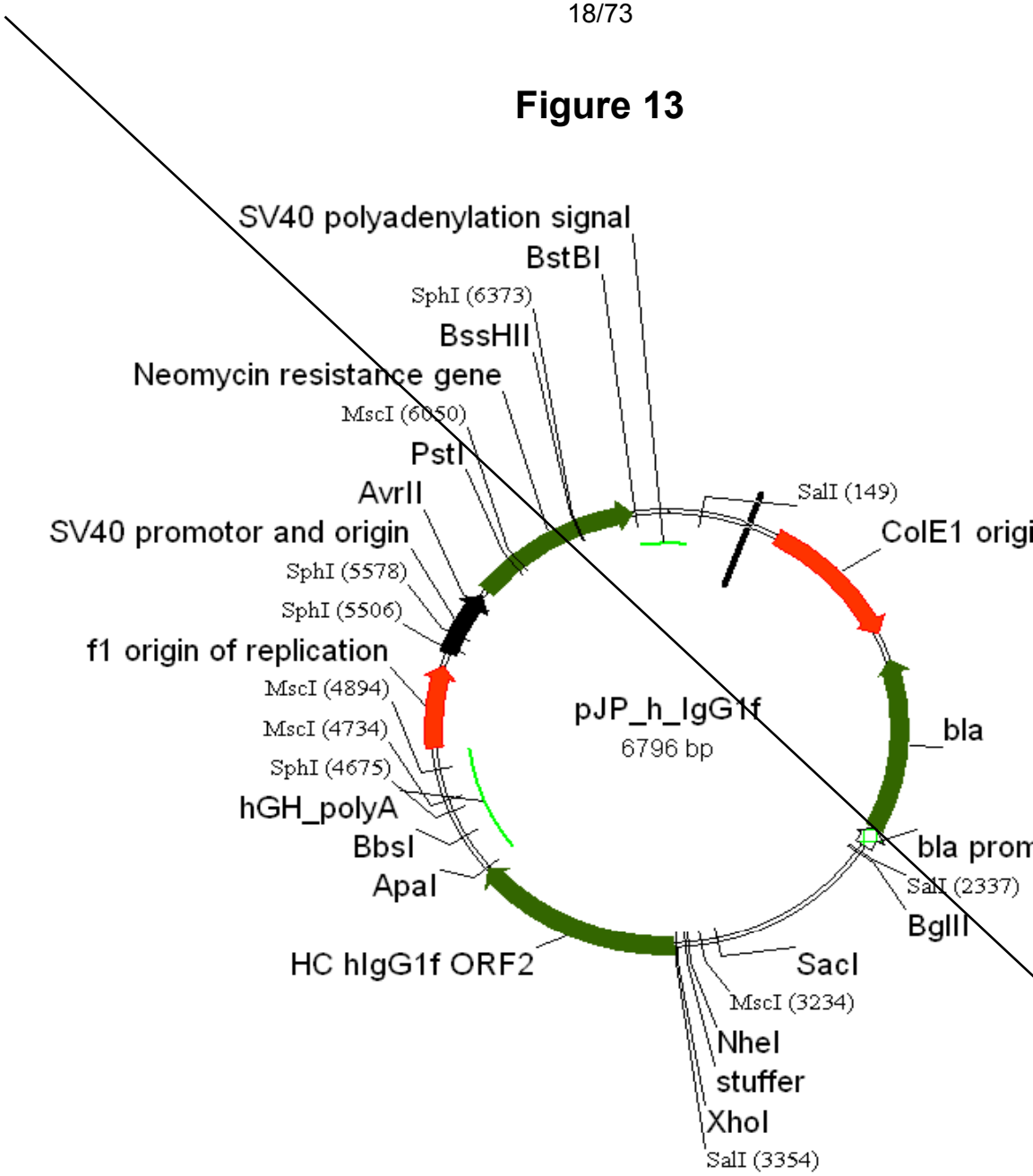

SV40 polyadenylation signal
BstBI
SphI (6373)
BssHII
Neomycin resistance gene
MscI (6050)
PstI
AvrII
SV40 promotor and origin
SphI (5578)
SphI (5506)
f1 origin of replication
MscI (4894)
MscI (4734)
SphI (4675)
hGH_polyA
BbsI
ApaI
HC hIgG1f ORF2
SacI
MscI (3234)
NheI
stuffer
XhoI
SalI (3354)
SalI (149)
ColE1 origi
pJP_h_IgG1f
6796 bp
bla
bla prom
SalI (2337)
BglII

Figure 13

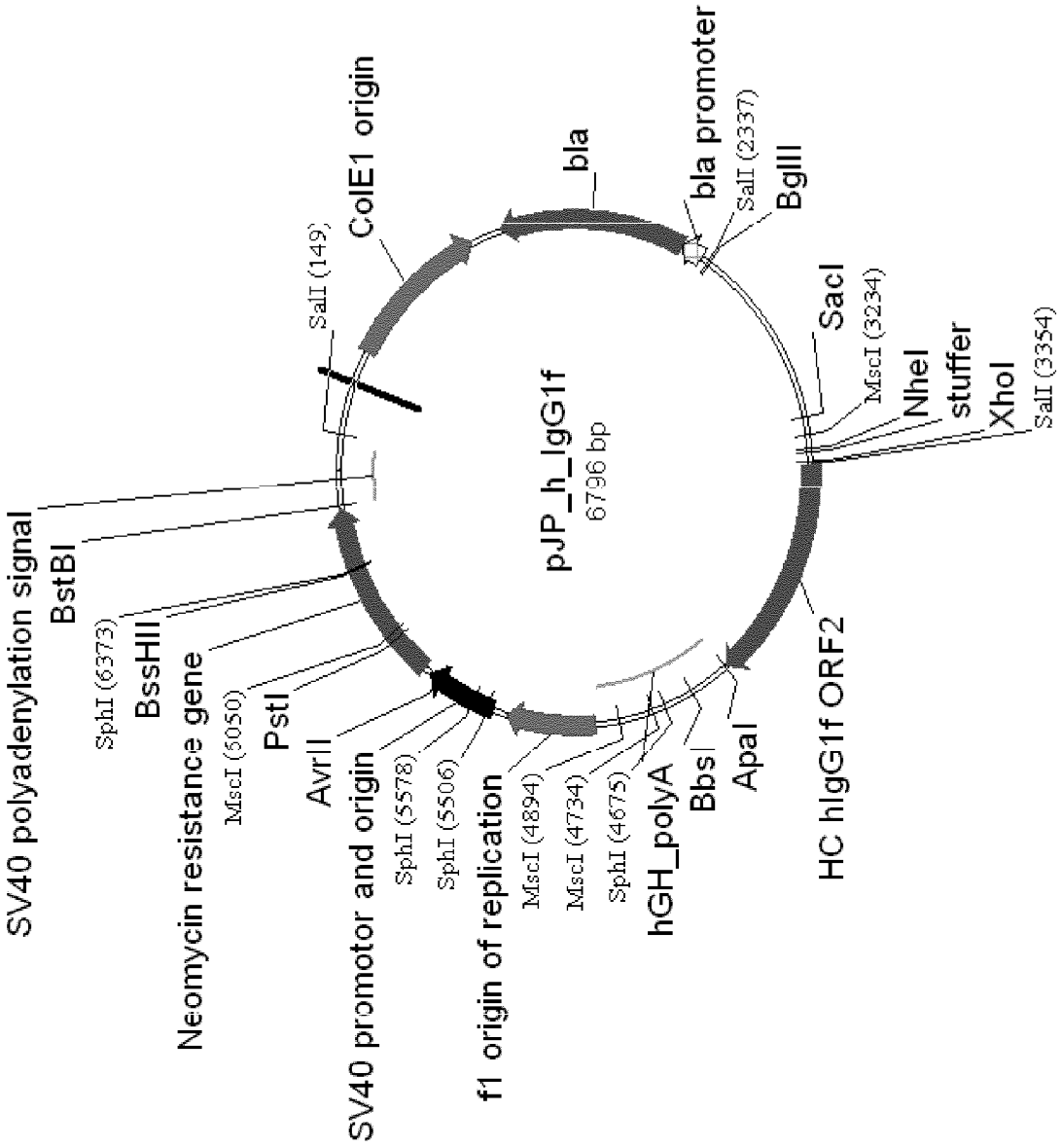

pJP_h_IgG1f
6796 bp
SV40 polyadenylation signal
BstBI
SphI (6373)
BssHII
Neomycin resistance gene
MscI (6050)
PstI
AvrII
SV40 promotor and origin
SphI (5578)
SphI (5506)
f1 origin of replication
MscI (4894)
MscI (4734)
SphI (4675)
hGH_polyA
BbsI
ApaI
HC hIgG1f ORF2
SalI (149)
ColE1 origin
bla
bla promoter
SalI (2337)
BglII
SacI
MscI (3234)
NheI
stuffer
XhoI
SalI (3354)

Figure 14

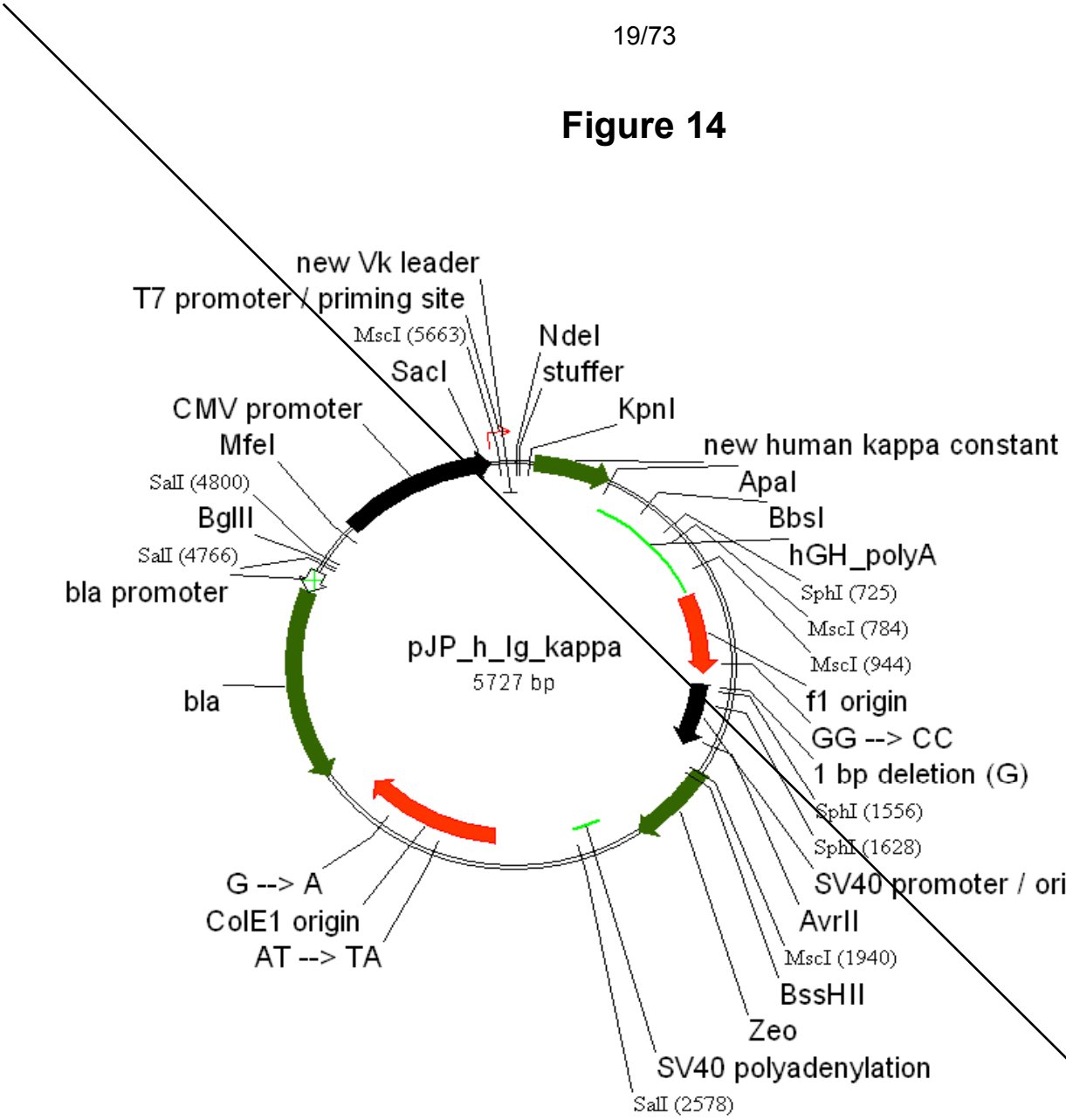

new Vk leader
T7 promoter / priming site
MscI (5663)
NdeI
stuffer
SacI
KpnI
CMV promoter
MfeI
new human kappa constant
ApaI
SalI (4800)
BglII
BbsI
SalI (4766)
hGH_polyA
bla promoter
SphI (725)
MscI (784)
pJP_h_Ig_kappa
5727 bp
MscI (944)
f1 origin
bla
GG --> CC
1 bp deletion (G)
SphI (1556)
SphI (1628)
SV40 promoter / ori
G --> A
AvrII
ColE1 origin
MscI (1940)
AT --> TA
BssHII
Zeo
SV40 polyadenylation
SalI (2578)

Figure 14

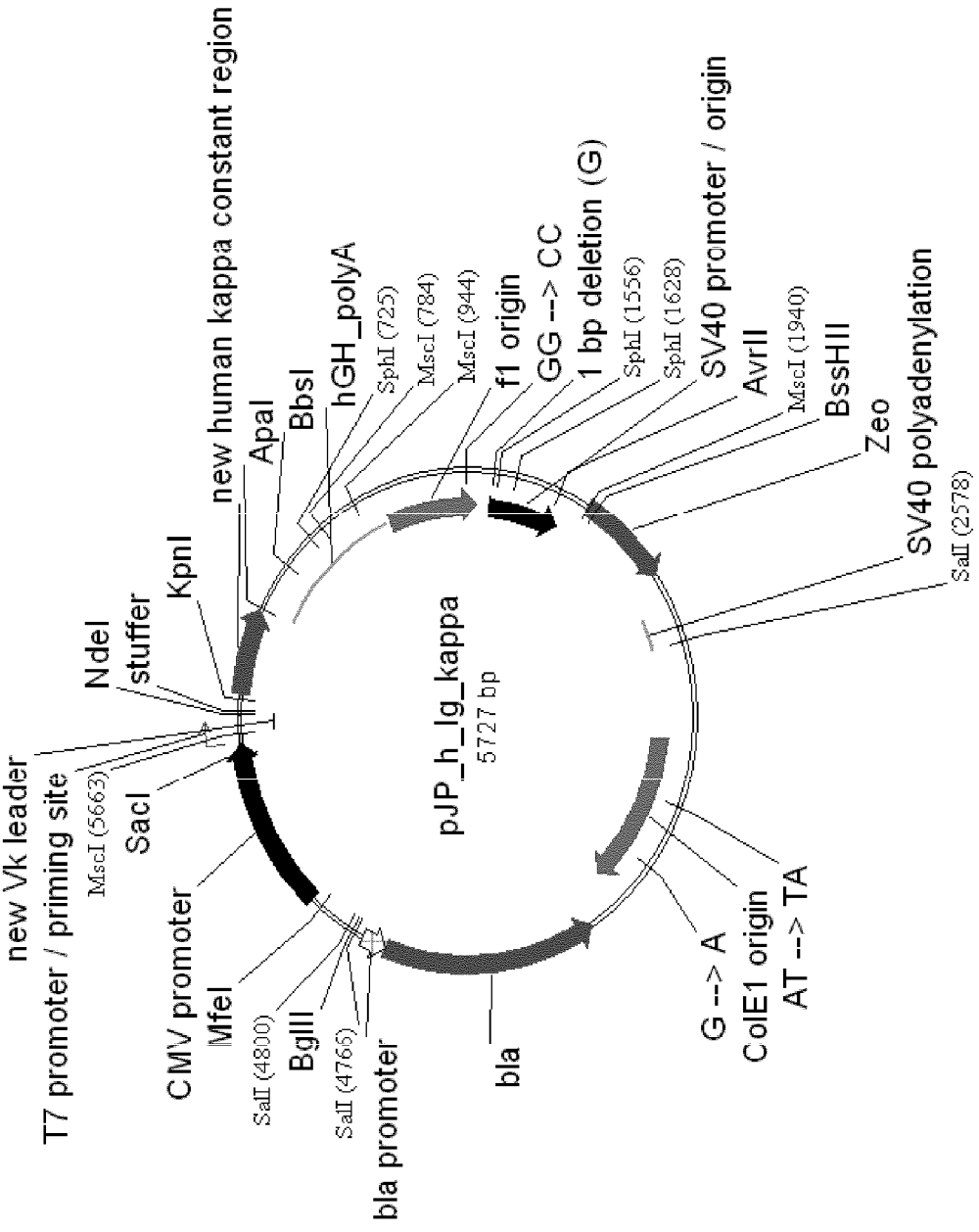

pJP_h_lg_kappa
5727 bp
new Vk leader
T7 promoter / priming site
MscI (5663)
SacI
NdeI
stuffer
KpnI
CMV promoter
MfeI
SalI (4800)
BglII
SalI (4765)
bla promoter
bla
G --> A
ColE1 origin
AT --> TA
new human kappa constant region
ApaI
BbsI
hGH_polyA
SphI (725)
MscI (784)
MscI (944)
f1 origin
GG --> CC
1 bp deletion (G)
SphI (1556)
SphI (1628)
SV40 promoter / origin
AvrII
MscI (1940)
BssHII
Zeo
SV40 polyadenylation
SalI (2578)

Figure 15

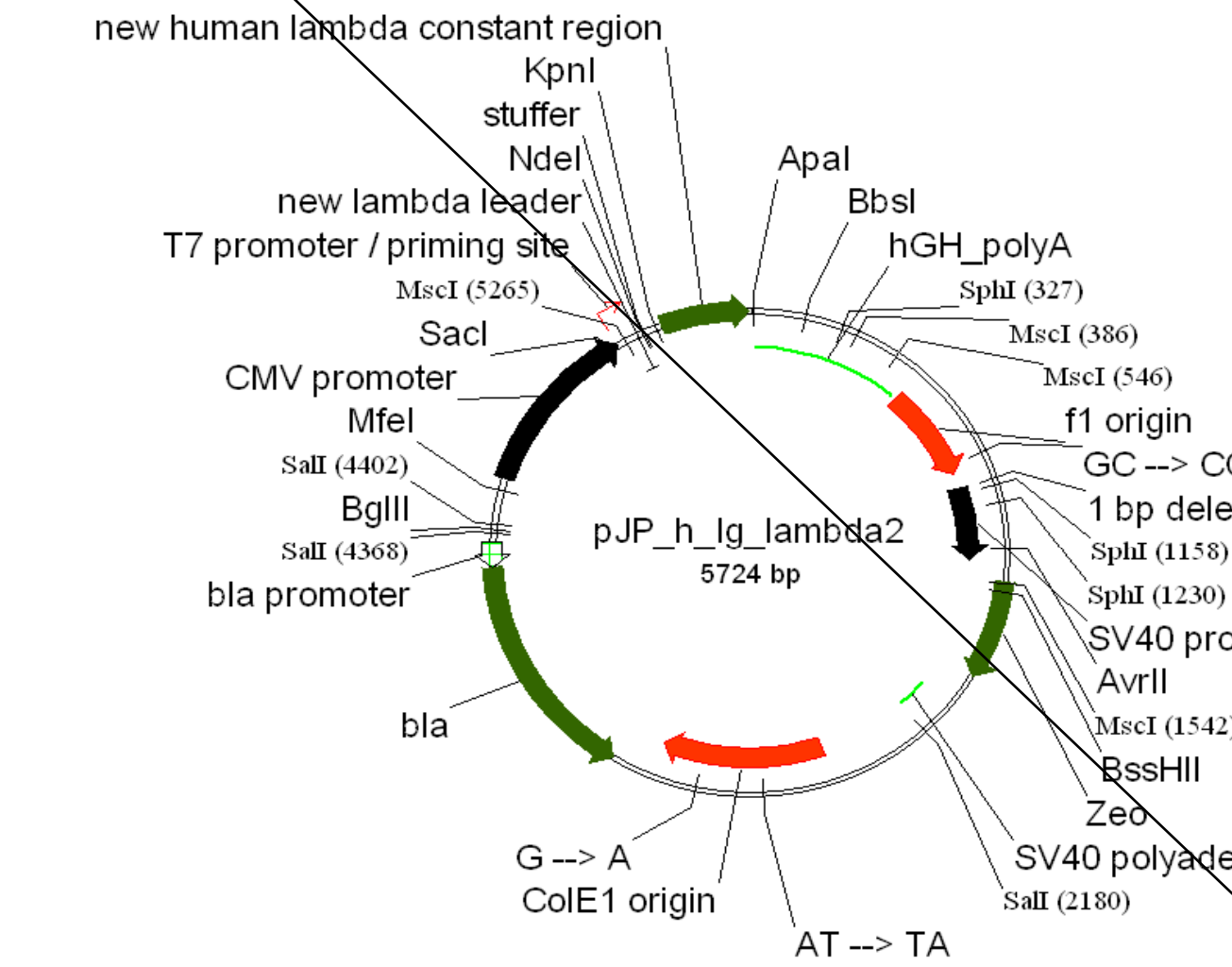

new human lambda constant region
KpnI
stuffer
NdeI
new lambda leader
T7 promoter / priming site
MscI (5265)
SacI
CMV promoter
MfeI
SalI (4402)
BglII
SalI (4368)
bla promoter
bla
G --> A
ColE1 origin
AT --> TA
SalI (2180)
SV40 polyade
Zeo
BssHII
MscI (1542)
AvrII
SV40 pro
SphI (1230)
SphI (1158)
1 bp dele
GC --> C
f1 origin
MscI (546)
MscI (386)
SphI (327)
hGH_polyA
BbsI
ApaI
pJP_h_lg_lambda2
5724 bp

Figure 15

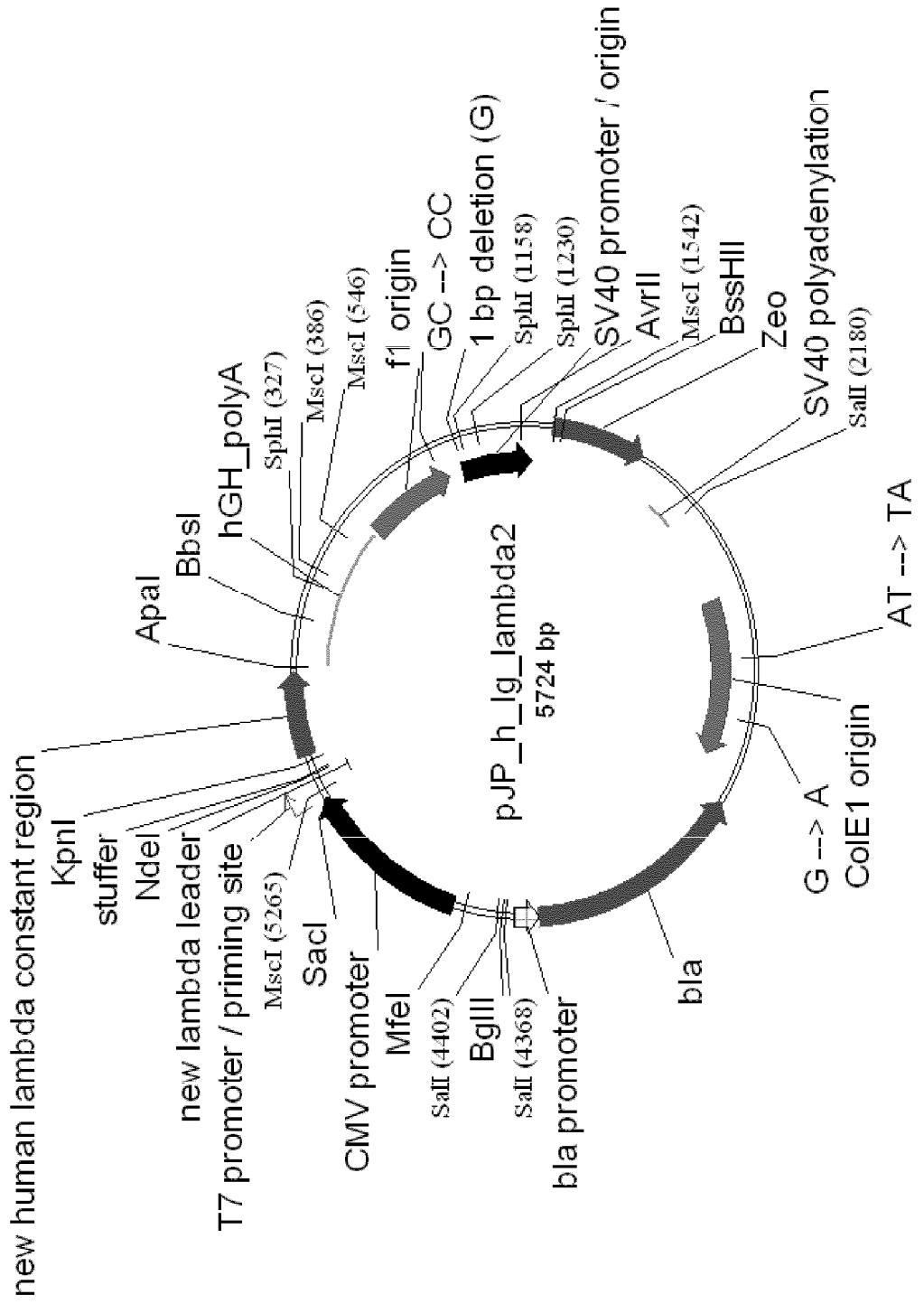
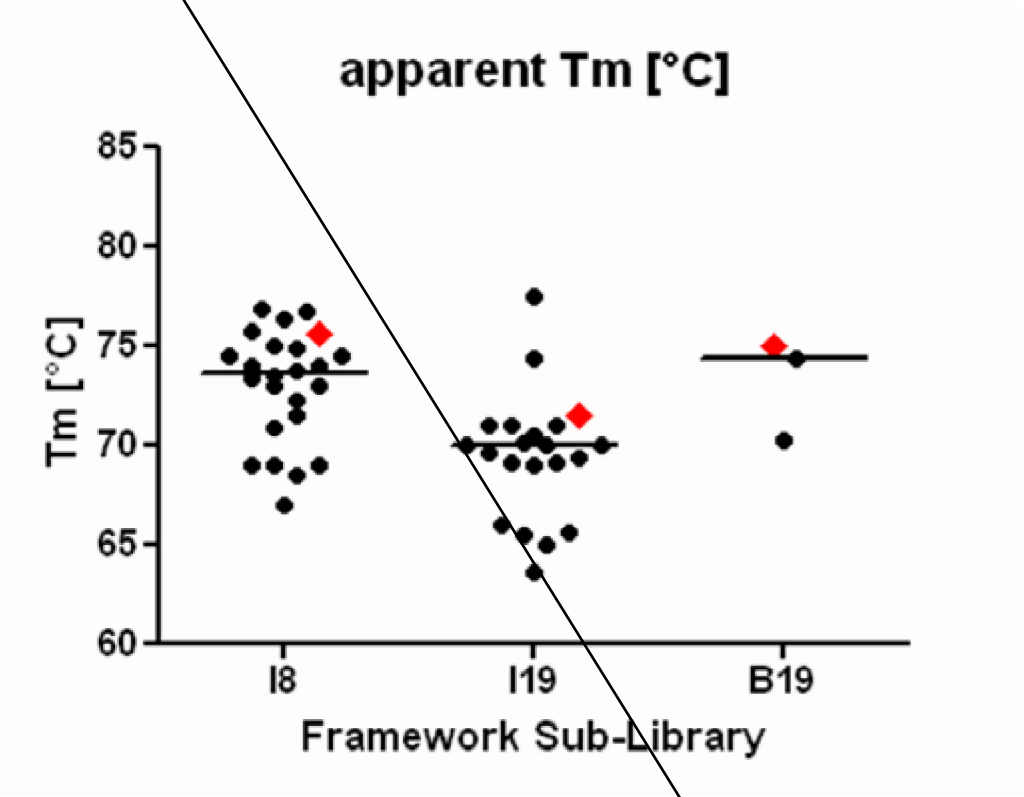

pJP_h_lg_lambda2
5724 bp
new human lambda constant region
KpnI
stuffer
NdeI
new lambda leader
T7 promoter / priming site
MscI (5265)
SacI
CMV promoter
MfeI
SalI (4402)
BglII
SalI (4368)
bla promoter
bla
G --> A
ColE1 origin
AT --> TA
SalI (2180)
Zeo
SV40 polyadenylation
BssHII
MscI (1542)
AvrII
SV40 promoter / origin
SphI (1230)
SphI (1158)
1 bp deletion (G)
GC --> CC
f1 origin
MscI (546)
MscI (386)
SphI (327)
hGH_polyA
BbsI
ApaI

Figure 39



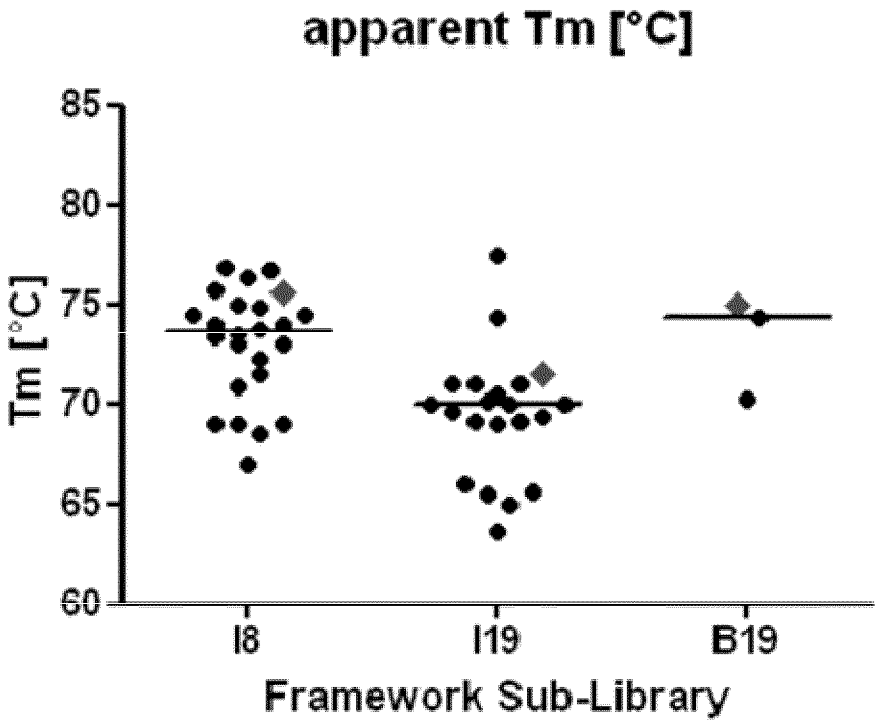
Key: Apparent midpoints of unfolding of selected Fabs as determined by Differential Scanning Fluorimetry (DSF) as described in Example 9.1.2. Each dot represents one unique Fab. Squares indicate the control Fabs as described in Example 9 with the constant CDR3s as described in Ewert S. et al.(2004), J. Mol. Biol. 325, p. 531ff. Bars indicate the Median.

I8 represents VH3-23/VK1-39

I19 represents VH3-23/VL3-1

B19 represents VH1-18/VL3-1

Figure 39



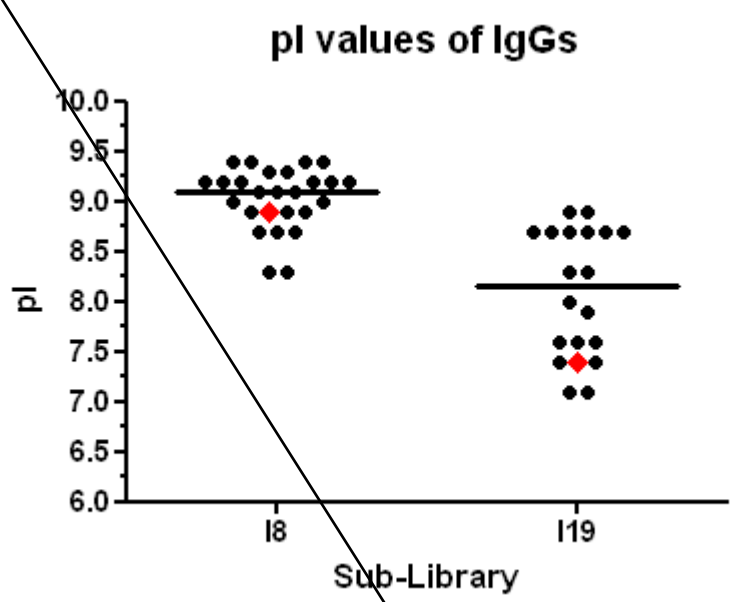
Key: Apparent midpoints of unfolding of selected Fabs as determined by Differential Scanning Fluorimetry (DSF) as described in Example 9.1.2. Each dot represents one unique Fab. Squares indicate the control Fabs as described in Example 9 with the constant CDR3s as described in Ewert S. et al.(2004), J. Mol. Biol. 325, p. 531ff. Bars indicate the Median.

I8 represents VH3-23/VK1-39

I19 represents VH3-23/VL3-1

B19 represents VH1-18/VL3-1

Figure 45

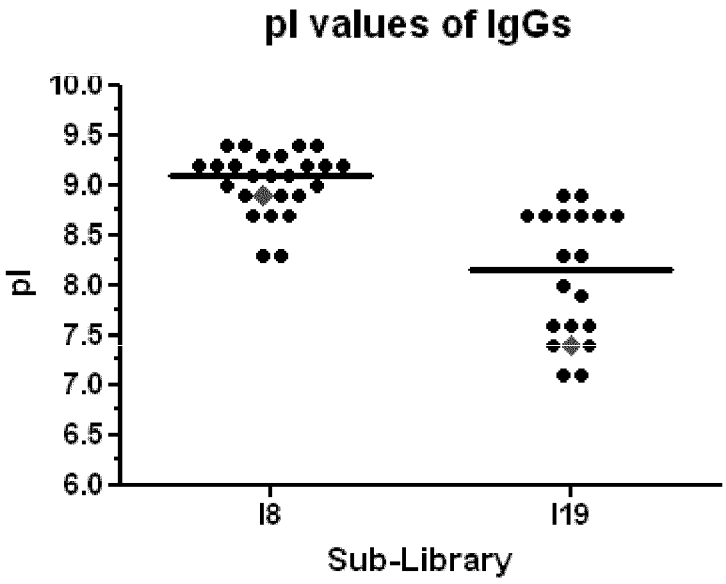


Key: pI values of selected IgGs as described in Example 9.2.4. Each dot represents one unique IgG. Squares indicate the control IgGs as described in Example 9 with the constant CDR3s as described in Ewert S. et al.(2004), J. Mol. Biol. 325, p. 531ff. Bars indicate the Median.

I8 represents VH3-23/VK1-39

I19 represents VH3-23/VL3-1

Figure 45

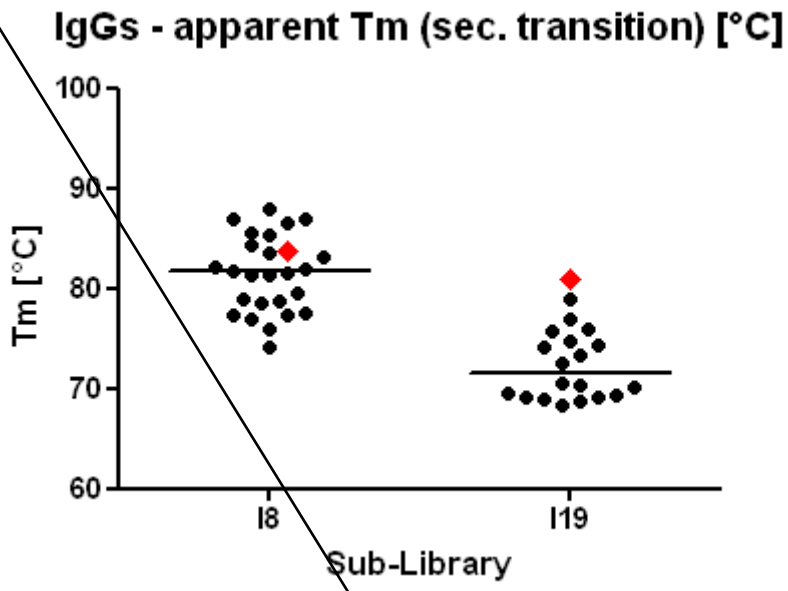


Key: pI values of selected IgGs as described in Example 9.2.4. Each dot represents one unique IgG. Squares indicate the control IgGs as described in Example 9 with the constant CDR3s as described in Ewert S. et al.(2004), J. Mol. Biol. 325, p. 531ff. Bars indicate the Median.

I8 represents VH3-23/VK1-39

I19 represents VH3-23/VL3-1

Figure 46

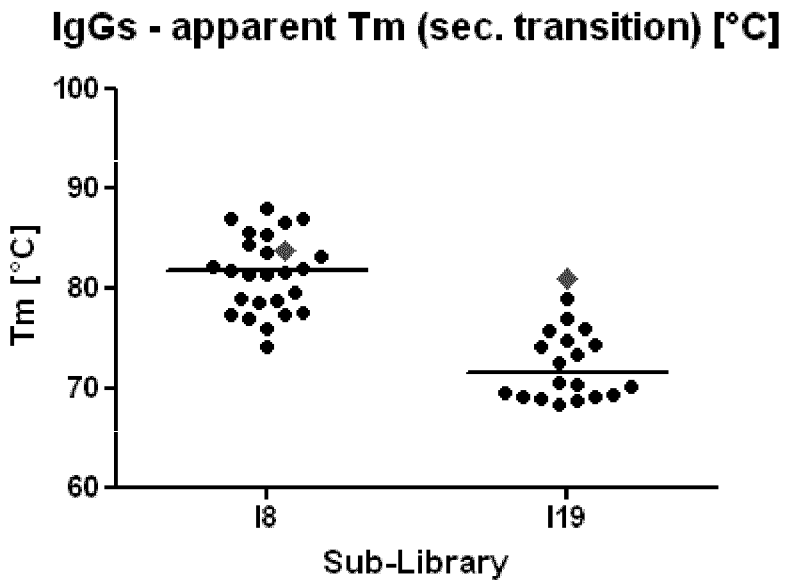


Key: Apparent midpoints of unfolding of selected IgGs as determined by Differential Scanning Fluorimetry (DSF) as described in Example 9.2.2. Each dot represents one unique IgG. Squares indicate the control IgGs as described in Example 9 with the constant CDR3s as described in Ewert S. et al.(2004), J. Mol. Biol. 325, p. 531ff. Bars indicate the Median.

I8 represents VH3-23/VK1-39

I19 represents VH3-23/VL3-1

Figure 46

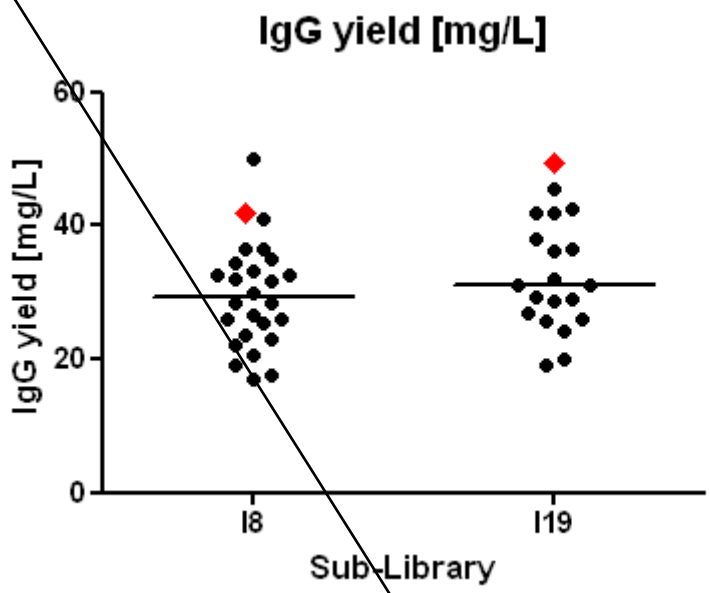


Key: Apparent midpoints of unfolding of selected IgGs as determined by Differential Scanning Fluorimetry (DSF) as described in Example 9.2.2. Each dot represents one unique IgG. Squares indicate the control IgGs as described in Example 9 with the constant CDR3s as described in Ewert S. et al.(2004), J. Mol. Biol. 325, p. 531ff. Bars indicate the Median.

I8 represents VH3-23/VK1-39

I19 represents VH3-23/VL3-1

Figure 47

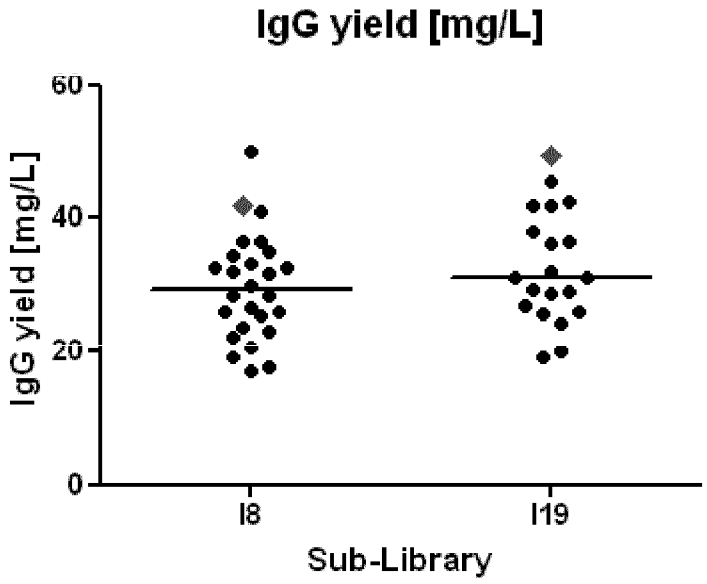


Key: Expression yields of selected IgGs as determined by UV-spectrophotometry as described in Example 9.2.1. Each dot represents one unique IgG. Squares indicate the control IgGs as described in Example 9 with the constant CDR3s as described in Ewert S. et al.(2004), J. Mol. Biol. 325, p. 531ff. Bars indicate the Median.

I8 represents VH3-23/VK1-39

I19 represents VH3-23/VL3-1

Figure 47

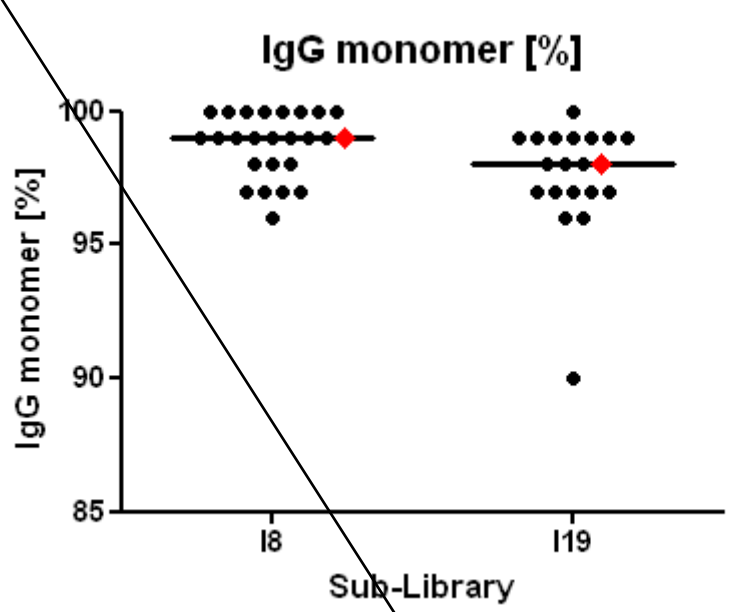


Key: Expression yields of selected IgGs as determined by UV-spectrophotometry as described in Example 9.2.1. Each dot represents one unique IgG. Squares indicate the control IgGs as described in Example 9 with the constant CDR3s as described in Ewert S. et al.(2004), J. Mol. Biol. 325, p. 531ff. Bars indicate the Median.

I8 represents VH3-23/VK1-39

I19 represents VH3-23/VL3-1

Figure 48

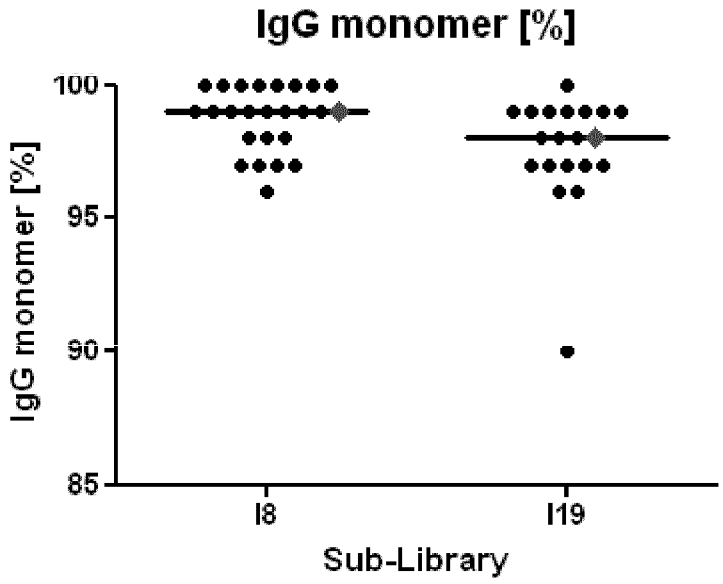


Key: Monomer content of selected IgGs as determined by size exclusion chromatography (SEC) as described in Example 9.2.3. Each dot represents one unique IgG. Squares indicate the control IgGs as described in Example 9 with the constant CDR3s as described in Ewert S. et al.(2004), J. Mol. Biol. 325, p. 531ff. Bars indicate the Median.

I8 represents VH3-23/VK1-39

I19 represents VH3-23/VL3-1

Figure 48



Key: Monomer content of selected IgGs as determined by size exclusion chromatography (SEC) as described in Example 9.2.3. Each dot represents one unique IgG. Squares indicate the control IgGs as described in Example 9 with the constant CDR3s as described in Ewert S. et al.(2004), J. Mol. Biol. 325, p. 531ff. Bars indicate the Median.

I8 represents VH3-23/VK1-39

I19 represents VH3-23/VL3-1