

scFvs (with 5' leader sequence and linker between VH and VL chains)	
CD19 (FMC63.3)	MLLLVTSLLLCELPHPAFLIPDIQMTQTSSLSASLGDRVTISCRAS QDISKYLNWYQQKPDGTVKLLIYHTSRLHSGVPSRFSGSGSGTDYS LTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEITGSTSGSGKPGSG EGSTKGEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQP PRKGLEWLGVIWGSETTYNSALKSRLTIKDNSKSQVFLKMNSLQ TDDTAIYYCAKHYYYGGSYAMDYWGQGTSVTVSS
CD19 (FMC63.3) with 2xHA Tag	MLLLVTSLLLCELPHPAFLIPYDPDYAYPYDVPDYADIQMTQ TTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIYHTSR LHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGG GTKLEITGSTSGSGKPGSGEGSTKGEVKLQESGPGLVAPSQSLSVTC TVSGVSLPDYGVSWIRQPPRKGLEWLGVIWGSETTYNSALKSRL TIKDNSKSQVFLKMNSLQTDDTAIYYCAKHYYYGGSYAMDYWG QGTSVTVSS
CD19 (FMC63.3) with VSV-g Tag	MARSVTLVFLVSLTGLYAAAYTDIEMNRLGKDIQMTQTSSLSAS LGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIYHTSRLHSGVPS RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEIT GSTSGSGKPGSGEGSTKGEVKLQESGPGLVAPSQSLSVTCTVSGVS LPDYGVSWIRQPPRKGLEWLGVIWGSETTYNSALKSRLTIKDNS KSQVFLKMNSLQTDDTAIYYCAKHYYYGGSYAMDYWGQGTSVT VSS
HER2 (4D5)	MARSVTLVFLVSLTGLYAAADIQMTQSPSSLSASVGDRTITCRA SQDVNTAVAWYQQKPGKAPKLLIYSASFLESGVPSRFSGSRSGTDF TLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGSTSGSGKPGS GEGSGEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQA PGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNS LRAEDTAVYYCSRWGGDGFYAMDVWGQGLTVTVSS
B7-H3 (MGA271)	MVATLLVTSLLLCELPHPAFLIPDTEVQLVESGGGLVQPGGSLRLS CAASGFTFSSFGMHVVRQAPGKGLEWVAYISSDSSAIYYADTVKG RFTISRDNKNSLYLQMNSLRDEDTAVYYCGRGRENIIYYGSRDY WGQGTTVTVSSGGGGSGGGGSGGGGSDIQLTQSPSFLSASVGDRT TITCKASQNVDTNVAWYQQKPGKAPKALISASRYSGVPSRFSG SGSGTDFTLTISSLQPEDFATYYCQQYNNYPFTFGQGTKLEIK
GD2 (1A7)	MLLLVTSLLLCELPHPAFLIPDILLTQTPLSLPVSLGDQASISCRSSQ SLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRFSGVPDRFSGSGS GTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELKGSTSGS GKPGSGEGSTKGEVKLQQSGPSLVEPGASVMISCKASGSSFTGYNM NWVRQNIGKSLEWIGAIDPYYGGTSYNQKFKGRATLTVDKSSSTA YMHLKSLTSEDSAVYYCVSGMEYWGQGTSVTVSS
ROR1 (humanized F) with VSV-g Tag	MARSVTLVFLVSLTGLYAAAYTDIEMNRLGKDTQVQLVESGGG WQPGRSLRLSCAASGFIFSEHNMAWVRQAPGKGLEWVATISDDGR NTYYRDSMRGRFTISRDNKNTLYLQMNSLRAEDTAVYYCTSHRY NLFDSWGQGTMTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSAS VGDRTITCKASQNIIDRYLNWYQQKPGKAPKRLIYNTNKLQTVGP SRFSGSGSGTEFTLTISSLQPEDFATYYCLQYNSLPLTFGQGTKLEIK

<b>Hinge-Transmembrane Domains</b>	
CD28 H/TM	AAAIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFPGPSKPFWVLV VVGGVLACYSLLVTVAFIIFWV
CD28 H/TM 2 Cysteine- >Alanine mutation (2CA)	AAAIEVMYPPPYLDNEKSNGTIIHVKGKHLAPSPFPGPSKPFWVL VVVGGVLAAYSLLVTVAFIIFWV
CD8 H/TM	AAATTPAPRPPTPAPTASQPLSLRPEACRPAAGGAVHTRGLDFAC DIYIWAPLAGTCGVLLLSLVITLYCK
<b>Costimulatory Domains</b>	
CD28	RSKRSRLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRS
4-1BB	KRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL
<b>Signaling Domains</b>	
CD3 $\zeta$	RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGH GLYQGLSTATKDTYDALHMQALPPR
CD3 $\zeta$ (1XX)	RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLFNELQKDKMAEAFSEIGMKGERRRGKGH DLFQGLSTATKDTFDALHMQALPPR
Lck	GSGGGGSGCGCSSHPEDDWMENIDVCENCHYPIVPLDGKGTLLIR NGSEVRDPLVTYEGSNPPASPLQDNLVIALHSYEP SHDGD LGFEKG EQLRILEQSGEWWKAQSLTTGQEGFIPNFVAKANSLEPEPWFFKN LSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNQGEV VKHYKIRNLDNGGFYISPRITFPGLHELVRHYTNASDGLCTRLSRPC QTQKPQKPWWEDWEVPRETLKLVERLGAGQFGEVWMGYYNH TKVAVKSLKQGSMPDAFLAEANLMKQLQHQRVRLYAVVTQEP IYIITEYMENGLVDFLKTPSGIKLTINKLLDMAAQIAEGMAFIEERN YIHRDLRAANILVSDTLCKIADFLARLIEDNEYTAREGAKFPIKW TAPEAINYGFTTIKSDVWSFGILLTEIVTHGRIPYPGMTNPEVIQNL RGYRMVRPDNCPEELYQLMRLCWKERPEDRPTFDYLRVLEDDFT ATEGQYQPQP
Fyn	GSGGGGSGCVQCKDKEATKLTEERDGS LNQSSGYRYGTDPTPQHY PSFGVTSIPNYNNFHAAGGQGLTVFGGVNSSSHTGTLRTRGGTGVT LFVALYDYEARTEDDL SFHKGEKFQILNSSEG DWWEARSLTTGET GYIPSNYVAPVDSIQAEWYFGKLGRKDAERQLLSFGNPRGTFILIR ESETTKGAYSLSIRDWDDMKGDHVKHYKIRKLDNGGYIITRAQF ETLQQLVQHYSERAAGLCCRLVVPCHKGMPRLTDLSVKTKDVWEI PRESLQLIKRLGNGQFGEVWMGTWNGNTKVAIKTLKPGTMSPEF LEEAQIMKKLKHDKLVQLYAVVSEEPYIVTEYMNKGSLLDFLKD GEGRALKLPNLVDMAAQVAAGMAYIERMNYIHRDLRSANILVGN GLICKIADFLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKS DVWSFGILLTELVTKGRVPYPGMNNREVLEQVERGYRMPCPQDCP ISLHELMIHCWKKDPEERPTFEYLQSFLEDYFTATEPQYQPGENL NS

<p>PLC<math>\gamma</math>1</p>	<p>GGGGSAGAASPCANGCGPGAPSDAEVLHLCRSLEVGTVMTLFYSK  KSQRPERKTFQVKLETRQITWSRGADKIEGAIDIREIKEIRPGKTSRD  FDRYQEDPAFRPDQSHCFVILYGMFRLKTLSLQATSEDEVNMWIK  GLTWLMEDTLQAPTPLQIERWLRKQFYSDRNREDRISAKDLKNM  LSQVNYRVPNMRFLRERLTDLEQRSGDITYGQFAQLYRSLMYSQAQ  KTMDLPFLEASTLRAGERPELCRVSLPEFQQFLLDYQGELWAVDR  LQVQEFMLSFLRDPLREIEEPYFFLDEFVTFLFSKENS VVNSQLDAV  CPDTMNNPLSHYWISSHNTYLTDGQFSSSESSLEAYARCLRMGCRC  IELDCWDGPDGMPVIYHGHTLTTKIKFSDVLHTIKEHAFVASEYPVI  LSIEDHCSIAQQRNMAQYFKKVLGDTLLTKPVEISADGLPSPNQLK  RKILIKHKKLAEGSAYEEVPTSMMYSENDISNSIKNGILYLEDPVNH  EWYPHYFVLTSSKIYYSEETSSDQGNEDDEEPEVSSSTELHSNEK  WFHGKLGAGRDRHIAERLLTEYCIETGAPDGSFLVRESETFVGDY  TLFWRNGKVQHCRHSRQDAGTPKFFLTDNLVFDSDLYDLITHYQQ  VPLRCNEFEMRLSEVPQTNAHESKEWYHASLTRAQAEHMLMRV  PRDGAFLVRKRNEPNSY AISFRAEGKIKHCRVQQEGQTVMLGNSEF  DSLVDLISYYEKHPLYRKMKLRYPINEEALEKIGTAEPDYGALYEG  RNPFGFYVEANPMPTFKCAVKALFDYKAQREDELTFIKSAIIQNVEK  QEGGWWRGDYGGKKQLWFPSNYVEEMVNPVALEPEREHL DENS  PLGDLLRGVLDVPACQIAIRPEGKNNRLFVFSISMASVAHWSLDVA  ADSQEELQDWVKKIREVAQTADARLTEGKIMERRKKIALELSELV  VYCRPVPFDEEKIGTERACYRDMSSFPETKAEKYVNKAKGKKFLQ  YNRLQLSRIYPKGQRLDSSNYDPLPMWICGSQLVALNFQTPDKPM  QMNQALFMTGRHCGYVLQPSTMRDEAFDPFDKSSRLGLEPCAISIE  VLGARHLPKNGRGIVCPFVEIEVAGAEYDSTKQKTEFVVDNGLNP  VWPAKPFHFQISNPEFAFLRFVVEEDMFSDQNFLAQAATFPVKGLK  TGYRAVPLKNNYSEDLELASLLIKIDIFPAKENGDLSPFSGTSLRER  GSDASGQLFHGRAREGSFESRYQQPFEDFRISQEHLADHFDSRERR  APRRTRVNGDNRL</p>
<p>ZAP-70</p>	<p>GSPDPA AHL PFFYGSISRAEAEHLKLAGMADGLFLLRQCLRSLGG  YVLSLVHDVRFHHFPIERQLNGTYAIAGGKAHCGPAELCEFYSRDP  DGLPCNLRKPCNRPSGLEPQPGVFDCLRDAMVRDYVRQTWKLEG  EALEQAIISQAPQVEKLIATTAHERMPWYHSSLTREEAERKLYSGA  QTDGKFLLRPRKEQGTYALS LIYGKTVYHYLISQDKAGKYCIPEGT  KFDTLWQLVEYLK LKADGLIYCLKEACPNSSASNASGAAAPTLP  HPSTLTHPQRRIDTLNSDGYTPEPARITSPDKPRPMPMDTSVYESPY  SDPEELKDKKLF LKRDNLLIADIELGCGNFGSVRQGVYRMRKKQID  VAIKVLKQGTEKADTEEMMREAQIMHQLDNPYIVRLIGVCQAEAL  MLVMEMAGGGPLHKFLVGKREEIPVSNVAELLHQVSMGMKYLEE  KNFVHRDLAARNVLLVNRHYAKISDFGLSKALGADDSYYTARSA  GKWPLKWYAPECINFRKFSSRSVWSYGVTMWEALS YGQKPYKK  MKGPEVMAFIEQGKRMECPPECPPELYALMSDCWIYKWEDRPDFL  TVEQRM RACYYSLASKVEGPPGSTQKAEACAGNS</p>

ZAP-70 Kinase only	GSLIADIELGCGNFGSVRQGVYRMRKKQIDVAIKVLKQGTEKADT EEMMREAQIMHQLDNPYIVRLIGVCQAEALMLVMEMAGGGPLHK FLVGKREEIPVSNVAELLHQVSMGMKYLEEKNFVHRDLAARNVLL VNRHYAKISDFGLSKALGADDSYYTARSAGKWPLKWYAPECINFR KFSSRSVDVWSYGVTMWEALSYGQKPYKKMKGPEVMAFIEQGKR MECPPECPPELYALMSDCWIYKWEDRPDFTVEQRMRACYYSLG NS
ZAP-70 Interdomain B + Kinase (KIDB)	GSPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTLNSDGYTPEPARI TSPDKPRPMPMDTSVYESPYSDPEELKDKKLFLKRDNLLIADIELGC GNFGSVRQGVYRMRKKQIDVAIKVLKQGTEKADTEEMMREAQIM HQLDNPYIVRLIGVCQAEALMLVMEMAGGGPLHKFLVGKREEIPV SNVAELLHQVSMGMKYLEEKNFVHRDLAARNVLLVNRHYAKISD FGLSKALGADDSYYTARSAGKWPLKWYAPECINFRKFSSRSVDVWS YGVTMWEALSYGQKPYKKMKGPEVMAFIEQGKRMECPPECPPEL YALMSDCWIYKWEDRPDFTVEQRMRACYYSLGNS
ZAP-70 KIDB D461N	GSPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTLNSDGYTPEPARI TSPDKPRPMPMDTSVYESPYSDPEELKDKKLFLKRDNLLIADIELGC GNFGSVRQGVYRMRKKQIDVAIKVLKQGTEKADTEEMMREAQIM HQLDNPYIVRLIGVCQAEALMLVMEMAGGGPLHKFLVGKREEIPV SNVAELLHQVSMGMKYLEEKNFVHRNLAARNVLLVNRHYAKISD FGLSKALGADDSYYTARSAGKWPLKWYAPECINFRKFSSRSVDVWS YGVTMWEALSYGQKPYKKMKGPEVMAFIEQGKRMECPPECPPEL YALMSDCWIYKWEDRPDFTVEQRMRACYYSLGNS
LAT	GSHCHRLPGSYDSTSSDSLYPRGIQFKRPHTVAPWPPAYPPVTSYPP LSQPDLLPIRSPQPLGGSHRTPSSRRSDSGANSVASYENEGASGIR GAQAGWGWGPSWTRLTPVSLPPEPACEDADEDEDDYHNPGYLV VLPDSTPATSTAAPSAPALSTPGIRDSAFSMESIDYVNVPEGESA EASLDGSREYVNVSQELHPGAAKTEPAALSSQEAEEVEEEGAPDYE NLQELNGNS
LAT Y132F	GSHCHRLPGSYDSTSSDSLYPRGIQFKRPHTVAPWPPAYPPVTSYPP LSQPDLLPIRSPQPLGGSHRTPSSRRSDSGANSVASYENEGASGIR GAQAGWGWGPSWTRLTPVSLPPEPACEDADEDEDDYHNPGFLV VLPDSTPATSTAAPSAPALSTPGIRDSAFSMESIDYVNVPEGESA EASLDGSREYVNVSQELHPGAAKTEPAALSSQEAEEVEEEGAPDYE NLQELNGNS
LAT 171-233 deletion ( $\Delta$ GADS)	GSHCHRLPGSYDSTSSDSLYPRGIQFKRPHTVAPWPPAYPPVTSYPP LSQPDLLPIRSPQPLGGSHRTPSSRRSDSGANSVASYENEGASGIR GAQAGWGWGPSWTRLTPVSLPPEPACEDADEDEDDYHNPGYLV VLPDSTPATSTAAPSAPALSTPGIRDSAFSMESIDD

LAT Y171F Y191F (2YF)	GSHCHRLPGSYDSTSSDSLYPRGIQFKRPHTVAPWPPAYPPVTSYPP LSQPDLLPIPRSPQPLGGSHRTPSSRRDSDGANSVASYENEGASGIR GAQAGWGVWGPSWTRLTPVSLPPEPACEDADEDEDDYHNPGYLV VLPDSTPATSTAAPSAPALSTPGIRDSAFSMESIDDFVNVPESGESAE ASLDGSREFVNVSQELHPGAAKTEPAALSSQEAEVEVEEGAPDYEN LQELNGNS
SLP-76	GSGGGGSALRNVPRSEVLGWDPDSLADYFKKLNKYDCEKAVKK YHIDGARFLNLTENDIQKFKLRVPILSKLSQEINKNEERRSIFTRKP QVPRFPEETESHEEDNGGWSSFEEDDYESPNDQDGEDDGDYESP NEEEEAPVEDDADYEPPPSNDEEALQNSILPAKPPFNSNSMYIDRPP SGKTPQQPPVPPQRPMAALPPPAGRNHSPLPPPQTNHEEPSRSRNH KTAKLPAPSIDRSTKPLDRSLAPFDREPFTLGKKPPFSDKPSIPAGR SLGEHLPKIQKPPLPPTTERHERSSPLPGKPPVPKHGWGPDRREND EDDVHQRLPQPALLPMSSNTFPSRSTKPSPMNPLPSSHMPGAFSES NSSFPQSASLPPYFSQGSPNRPPIRAEGRNFLPLPNKPRPPSPAEEEN SLNEEWYVSYITRPEAEAALRKINQDGTFLVRDSSKKTTPNYVLM VLYKDKVYNIQIRYQKESQVYLLGTGLRGKEDFLSVSDIIDYFRKM PLLLIDGKNRGSRYQCTLTHAAGYPGNS
SLP-76 224-244 deletion (ΔGADS)	GSGGGGSALRNVPRSEVLGWDPDSLADYFKKLNKYDCEKAVKK YHIDGARFLNLTENDIQKFKLRVPILSKLSQEINKNEERRSIFTRKP QVPRFPEETESHEEDNGGWSSFEEDDYESPNDQDGEDDGDYESP NEEEEAPVEDDADYEPPPSNDEEALQNSILPAKPPFNSNSMYIDRPP SGKTPQQPPVPPQRPMAALPPPAGRNHSPLPPPQTNHEEPSRSRRS LAPFDREPFTLGKKPPFSDKPSIPAGRSLGEHLPKIQKPPLPPTTERH ERSSPLPGKPPVPKHGWGPDRRENDEDDVHQRLPQPALLPMSS NTFPSRSTKPSPMNPLPSSHMPGAFSESNSSFPQSASLPPYFSQGSPN RPPIRAEGRNFLPLPNKPRPPSPAEEENSLNEEWYVSYITRPEAEA LRKINQDGTFLVRDSSKKTTPNYVLMVLYKDKVYNIQIRYQKES QVYLLGTGLRGKEDFLSVSDIIDYFRKMPLLLIDGKNRGSRYQCTL THAAGYPGNS
Notch+Gal4- VP64	ILDYSFTGGAGRDIPPPQIEEACELPECQVDAGNKVCNLQCNNHAC GWDGGDCSLNFNDPWKNCTQSLQCWKYFSDGHCDQGCNSAECWGLD DGFDCQLTEGQCNPYDQYCKDHFSDGHCDQGCNSAECWGLD CAEHVPERLAAGTLVLVLLPPDQLRNNSFHFLRELSHVLHTNVVF KRDAQGQQMIFPYYGHEELRKHPIKRSTVGWATSSLLPGTSGGR QRRELDPMDIRGSIVYLEIDNRQCVQSSSQCFQSATDVA AFLGALA SLGSLNIPYKIEAVKSEPVEPPLPSQLHLMYVAAAFAVLLFFVGCV LLSRKRRRMKLLSSIEQACDICRLKCLKSKEKPKCAKCLKNNWE CRYSKTKRSPLTRAHLTEVESRLERLEQLFLIFPREDLDMILKMD SLQDIKALLTGLFVQDNVNKDAVTDRLASVETDMPLTLRQHRISAT SSSESSNKGQRQLTVSAAAGSGSGGSDALDDFDLDMLGSDAL DDFDLDMLGSDALDDFDLDMLGSDALDDFDLDMLGSDALDDFDLDMLGSDAL