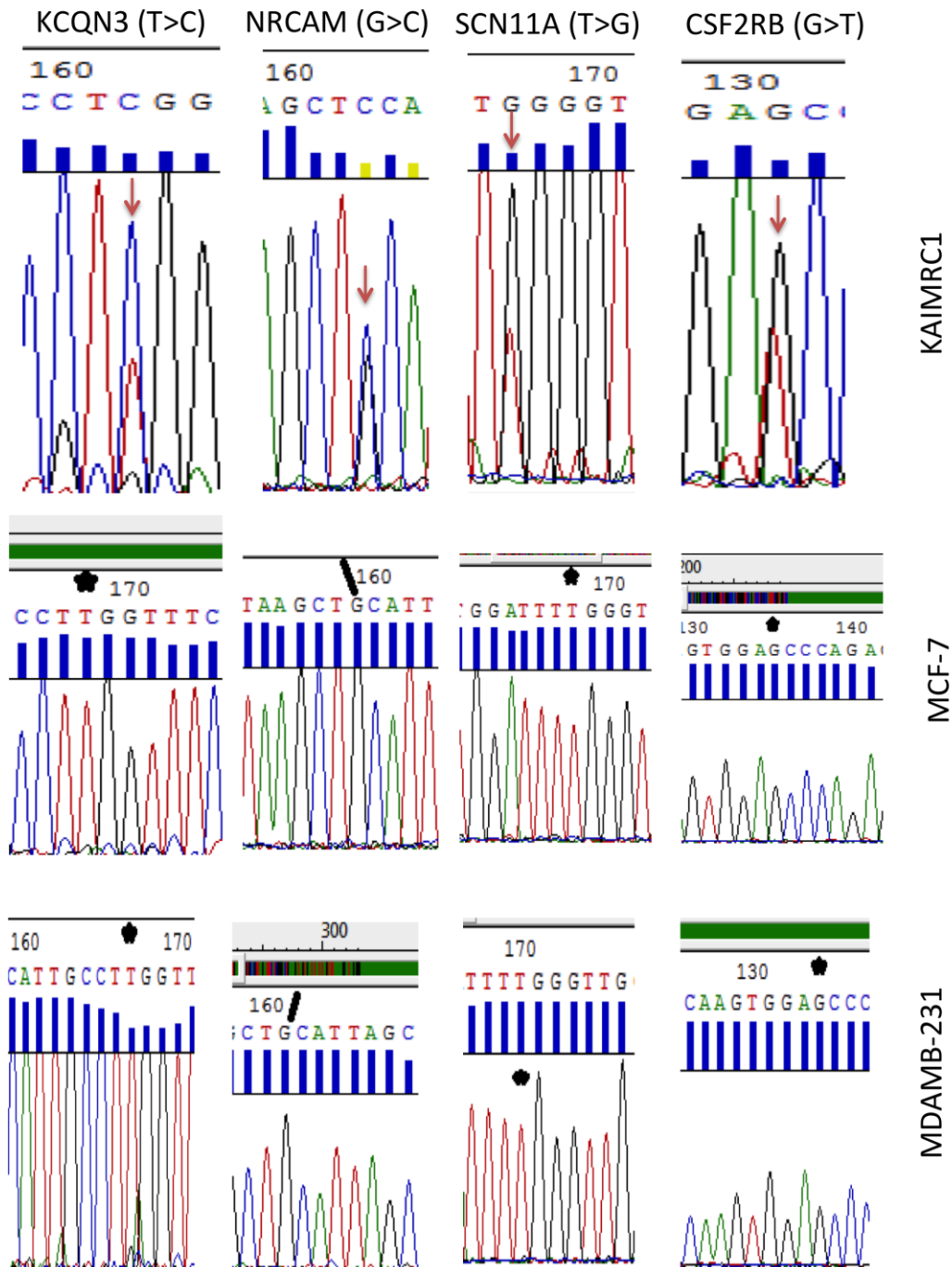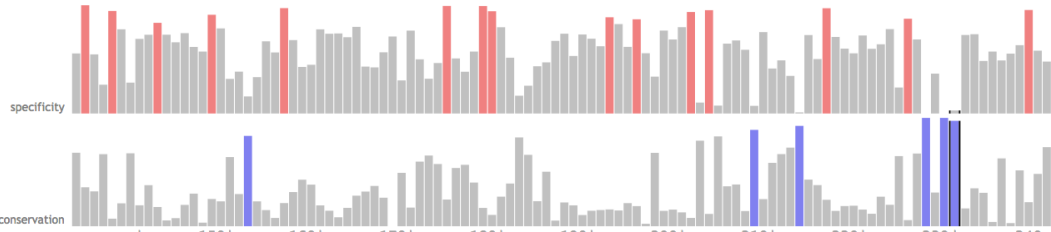# Supplemental Figures

Figure S1: Validation of mutations in genes KCQN3, NRCAM, SCN11A, and CSF2RB across breast cancer cell lines using Sanger sequencing protocol. The rightmost panel shows CSF2RB mutation (G>T) in KAIMRC1 cells but not in MDA-MB-231 and MCF-7 cells. The red arrow and asterisks point site of changes.

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variant : IL3RB_HUMAN S230I

msa columns order: by specificity ▾ submit

specificity

conservation

| | 150| 160| 170| 180| 190| 200| 210| 220| 230| 240|

```
IL3RB_HUMAN/133-240   1 PPEPRDLQISTDQDHFLLTWSVALGSPQSHWLSPGDLEFEVVYKRLQDSWEDAAILLSNTSQATLGPEHLMPSSTYVARVRTRLAPGSRLSGRPSKWSPEVCWDSQPG
tr F7IKP3 F7IKP3_CALJA  1 PPAPKDLQISTHQDHFLLTWSVALGVPQSQWLSQGDLEFEVVYKRLQDSWEDAASLLSNASQATLGLEHLMPSSTYMARVRTRLASGSRLSGRPSPWSQEFYWNSQPG
tr F7DHE0 F7DHE0_HORSE  1 PPAPKELQITNARDHFLLTWSMALGDSQSHWLS--NLEFEVVYRRLQDSWEDAPTLLSDSFQAILGPEHLLPSSTYVARVRARLAPGSGLSGRPSQWSPEVRWDSQPG
tr H0WSU8 H0WSU8_OTOGA  1 PPAPQDLQISAIGEHFLLSWNVTLGGPQPHWLSQEDLEFEVVYRRLQDPWEDAPSLRSNTSQVVLGPSHLMPSSTYVARVRTFLVPGSDFSGRPSEWSPEVRWDSQPG
tr G1LTB8 G1LTB8_AILME  1 APEPKDLINTTGDRFLLTWTVALPGPQSHWLS--SLEYEVVYKRLQDSWEEASTLQVNSSQAILEPEHLLPSSTYVARVRTHLAPSSGLSGRPSPWSPEVLWHSQRG
tr F1SKK0 F1SKK0_PIG    1 PPAPRGLHVSAAQGCFLLSWTVAHEGPQSHWLS--SLEFEVVYKRLQDSWEDAHTIHSGSPQVTLGPEHLLPSSTYVARVRTHLAPSSGLSGRPSPWSPEVHWVSQRG
tr E2RIM5 E2RIM5_CANFA  1 PPAPKDLLIDTTGDRFLLTWAVALPDSQGHWLS--SLEVEVVYKRLQDSWEEASTLHLNSSRAVLGPEHLVPSSTYVARVRTHLASNSGLSGRPSQWSPEVRWHSQTG
tr G3SXI4 G3SXI4_LOXAF  1 PPEPEDLEVSHAGDGFLLTWRAHLGGLQSRWLSERHLESELVYRRLQDSWEEASTLYSSSSQAVLGPEHLVPSSTYVARVRTFLAPGAGHSGKPSQWSPEVRWHSQTG
tr Q9Z1A0 Q9Z1A0_CAVPO  1 PPPPQDVQINTSGDQVLLTWSVALGPGHTSWLSQRDLEFEVVYRRLQDSWEEASTLHSNSSQAALGPEFLFLPSSTYVARVRTRLARGSGFSGRPSQWSPEVSWSSQPG
tr G1TK65 G1TK65_RABIT  1 PPPPTDLQISSRGGGFLLSWSVDLGESQRPWLSREDLEFEVLFRRLHDSWEEATSLLSNSSQATLGPEHLTPNSPYVARVRTRLAPGVAFSGRPSEWSSEIQWDSQSG
tr F1MXH7 F1MXH7_BOVIN  1 PPTPKDLNITATRESLLLLFWSIAHEGFQSHWLS--SLEFEVVYRRLQDSWEDALTIHSKSPQAILELKDLQPSSTYVEVKIRSF--PGEYFSGYWSDWSKTVLWSTH--
tr G3INB9 G3INB9_CRIGR  1 PPPPKDINISPSGDHFLLKWSVPLGDAWVPWLSQEDLQFEVSYKRLQDSWEDAPSLHTSNLWATLEPKLLLPSNTYVARVRTQLSPGSTLSGKPSRWSPEVQWDSQPG
tr Q3U2T6 Q3U2T6_MOUSE  1 PPLPKNVSISSSEDRFLLKWSVSLGDAQVSWLSSKDIEFEVAYKRLQDSWEDAYSLHTSSKFQVNFEPKLFLPSIYAARVRTRLSPGSSLSGRPSRWSPEVQWDSQPG
tr Q78ZF5 Q78ZF5_RAT    1 PPPPKDISISPSGDHFLLKWSVPLGDAQVSLLSQKDIQFEVAYKQLQDSWEDASSLHTCNLWVTLEPKLFLPSNIYVARVRAQLAPGSSLSGRPSEWSPEVHWDSPTE
tr G3UFG8 G3UFG8_LOXAF  1 PPEPEDLQVSHAGDGFLLTWRAHLGGLQSRWLSERHLESELVYRRLQDSWEEASTLLPHLTVGEEVQARLLRAPCAGPG----------VAPSTGFSGKPSKWSPEVRWDSQPG
tr F7F5T7 F7F5T7_ORNAN  1 PPAPKQLKVKSIGEGFLLSWNVSTEMP----LQ--DLEFEVLYKRQRDSWEDASSYILNRTQMILN-DTLIPGSTYVARIRTRLAPSSTLSGRPSAWSPEETWQSQAG
tr G5BAV8 G5BAV8_HETGA  1 SLDKNGYFSFQPDRLLHIQRTVTLAGADRYSYSEGDLEFEVVYKRLHESWENASTLHSSSSQVTLGPELLLPSSTYVSHLLRLAPHSSFSGRPSQWSREVHWDSQPG
tr H0ZK65 H0ZK65_TAEGU  2 PLPPQNLSVSSMTSDFLLTWKTTDRSQG---LE--NLDYEVTYKRKEWESWEEAASLLSNTTHCSLSREDLVPGSSYVARVRARPGQASNFSGQYSKWSMEVSWKTPEG
tr F1NCG4 F1NCG4_CHICK  2 PLPPQNLSIRESSGDFLLTWTSPDGSQGLG----SALEYEVAYRKREWESWEKAASLLSNTTRCHLSH--LIPGSRYVARVRARPEQGRGFSGHYSEWSTDVSWETPEG
tr G1KSA1 G1KSA1_ANOCA  2 -LPPQNLVVNITEDDSFLIWEAGI---RNNWL-ENSLDFEVTYKRFWESWEESSSLVSNASQCLL--QHLVPGNTYVARVRSKPGRTSQFVGHYSDWSSVVIWDTPEG
tr F1NCG4 F1NCG4_CHICK  2 ---PPSVELMKSQE-YELRWKKH-----SLRYGFIKQKYQVAYKREWESWEKAASLLSNTTHCHL--SHLIPGSRYVARVRAR--PEQDYQGYWSEWSEEFIWET---
tr G1NJ15 G1NJ15_MELGA  2 PLPPQNLSVRESSGAFLLTWTAPDG-SQG--L-GNALEYEVAYKRDWESWEDSLEMHLYSFSVFIPPLHLIPGSRYIARVRARPEQDRGFSGQYSEWSTDVSWETAEG
tr F6VPW1 F6VPW1_MONDO  3 PPTPKNLQITKNGT-----------QNHQASS---VLMFEVAYKR-WESWEEAFTKSSSTSHVTFGHDHLIPDNR-----RAKTS-----GERSSPWSSEVSWESQEG
tr G3WKI4 G3WKI4_SARHA  3 PPAPENLKIMKNGT-----------QSLQEFL---GLKFKVAYKR-WESWEEASTMDSSEAHVLLEYDHLIPNDP-----RAISS-----AGYSSPWSHEFSWNSQEG
tr F7FJP7 F7FJP7_MONDO  3 PEAPFDLNITYRKADFVLTFSTTHS--WNDYV--KELIHDIAYHQEQSDWT---HIRSSYPHITLLERKLQPSSTYEVKIRSF--PGEYFSGYWSDWSPTVYFRTPL-
tr H9GEL3 H9GEL3_ANOCA  3 PEAPFNLKITYLEKEYLVDFSSRHG--PKTYLS-GKLMHELAYRQESTPWTNIES--QYTPLKILG-KKLQPSSRYEMRVRSKPH-GGYFEGTWSEWSSS---------
tr H0ZK68 H0ZK68_TAEGU  4 --------------TSNLTWSLNI---SSHYLD-GRREYQVRYRHVSQSWEEAANLPIEQDQDMWANFERLSPNSKYEAAVRARPSARSRYNGIWSDWSKPVLWRT---
tr F1NDV9 F1NDV9_CHICK  4 --PEDLQVFSKAKTYNLTWSLNI---SSHYLS-GERQYEVRYRTTSQSWEEAETFIISQDQMWAPFERLSPNMKYEAAVRAKPGASSTCRGVWSDWSKTVLWSTH--
tr Q6UA82 Q6UA82_CANFA  4 ------------------------------LEFEARKRSPGHSWEEASLMALRQNQQWISLETLTPDTLYEFQVRVRAQRGS--HKTWSPWSQPLAFRTRP-
tr F6RXT4 F6RXT4_MONDO  4 ------------------------------LVFEARYRIQGKPWEEAAVLSIKQDQRWVCIEKLSPDTEYEFQVRVRGKPERTS--AAVWSPWSQTLVFRTKP-
tr G3WNS2 G3WNS2_SARHA  4 --ALSNLSLNQQEEAYNVSWEVPV---YSHYL-EGHLIFEVRYQIQGNSWEKATTLPITQDQRWVYLEKLSPNTKYELQVRGK--SKKNGSSGWSPWSPTLIFQTKP-
tr G1PZN0 G1PZN0_MYOLU  5 --PPSDLQSNVSSDSCVLSLG--LEPLAS--LLSYELAFKRQEEAWEQGSH--VGVTWLILEAVELDPGSTYEARLRVQMANEERYEGPWSNSRPVSFLS---
tr H0VUF3 H0VUF3_CAVPO  5 --PPSDLQSNTSSGSCVLTWSISPP--LEPMAT--LLSYELAFKRQEETWERAQYKDIGVTWIVLEAIELDPGSTYEARLRVQMATEERYEGQWSWSNWSQSVCFSSP--
tr G1SXF3 G1SXF3_RABIT  5 --PPSDLQSNISSGSCVLTWSVSLA--LEPLTT--LLSYELAFKRQEEAWEGAQHKDVGVTRITLEAIELDPGSTYEARLRVQMATEERYEGQWSWSQSVCFRPP--
tr G5BXZ1 G5BXZ1_HETGA  5 --PPSDLQSNVSSDSCVLTWSISPA--LEPMAA--LLSYELAFKRQEEAWEQAQHDIGVTLLTLEAVELDPGSTYEARLRVQMAMEECHEGQWSWSQSVCFFSP--
tr F6PIK9 F6PIK9_HORSE  5 --PPSDLQSNVSSDSCVLTWSITPA--LEPLTS--LLTYELAFKRQEEAWEQAQHKDVGVTLILEAVELDPGTTYEARLRVQMATEDRYEGQWSWSQSQVRFPS---
tr G1L9A1 G1L9A1_AILME  5 --SPSGLQRNISSDYCVLTWSVSPV--VEHLTS--VLSCELAFKEQEEAWEQARHHIVGVTQLTLETVELDPGSHYEARLVQVQKATELRCEGQWSWSQFACFPT---
tr H2ZZ29 H2ZZ29_LATCH  5 PHPPHNLSVKTTDANFLLAWETEYARDPTGVL-WGAVQYEVSYKRSWETWDDSTFLNEDTPQMELNGLLLDPGVEYSARVRAKPRGDQGFRGHWSEWSPSAMWQSAT-
tr F1RGX9 F1RGX9_PIG    5 --PSDVQSNVSSDHCVLTWSISPA--LEPLAS--LLSYELAFKRQEEAWEARRRDIGVTWLKLEAAELDPGSSYEARLRVQMVTEERYEGQWSWSLPVRFPAP--
tr E2QZT2 E2QZT2_CANFA  5 --PPLDLQSNVSSGSCVLTWGVSLA--LEPLAA--ILSYELAFKRQEEAWEQARHRDVGVTRLTLEAVELDPGSSYEARLRVQMATEQHYEGQWSWSQSVCFPP---
tr G3TPN5 G3TPN5_LOXAF  5 --PPSALQSNVSSDYCVLTWSISPA--LEPMAG--LLTYELAFKRQEETWEQARHKDVGVTWLILEAMELDPGSTYEARLRVQMAQEERYEGQWSWSLPVCFLTP--
tr F1MTF9 F1MTF9_BOVIN  5 --PPSDLQSNVSSEHCVLTWSISPA--LEPLAM--LLSYELAFKRQEEAWEWARHKDVGVTWLKLEAAELDPGSAYEARLRVQMAMEERYEGVWSDWSQVCFAAP--
tr I3M006 I3M006_SPETR  5 --PPSDLHSNISSGSCVLTWISPA--LEPMTT--LLSYELAFKRQEEAWEQARHKDVGVTWLILEAIELDPGSTYEARLRVRMAVEERHEGQWSWSQSVCFPSP--
tr H2ZZ29 H2ZZ29_LATCH  5 -PPPFNLSVSELLDNFKVEWKKALPYP------HMQQKYELQFKKQAEAWEFSETLDQDTTDMLLPKMLLDSGSSYVMRVRTKMLKTLSYDGPWSQEAKWETK--
tr H0WXY0 H0WXY0_OTOGA  5 --PPSDLHSNISSGYCILTWNISPA--LEPMTT--LLSYELAFKRQEEAWAQHKDVGVTWLILEAIELDPGFTYEARLRVQMATGALYSGQWSWSHPVCCSSP--
tr Q5U4K2 Q5U4K2_XENLA  5 -PPPRWLMSDKLKDTVILSWKSPVPST--FHL---TMLYQIAYRRQWEGWKDSASNVTKELNVSLSPRLFVSGSTYIFRVRTLPHDGEQPKGSWKSKELTMKIPEG
tr G1Q8J5 G1Q8J5_MYOLU  6 --APDSLEVTQEGSTCNVTWTVPQA---SHYL-ERHLEFEVRTRSLDRSWEEASLLKQNQQWIFL--ETLAPDTAYELQVRVRAQRGSLL--TWSPWSQPLAFRTRP-
tr Q8CBU1 Q8CBU1_MOUSE  6 --APHSLQVLHIDTRCNISWKVSQ---VSHYI-EPYLEFEARRRLLGHSWEDASVLSLKQRQQWLFLEMLIPSTSYEVQVRVK--AQRNNTGTWSPWSQLTFRTRP-
tr I3LD35 I3LD35_PIG    6 --PPNSLQVAHIGTRCNITWNLSQ---FSHYL-QSYVEFEVRTRSPGLSWEEGLL--SRGSHCXL--ETLAPDTPYELQVRVK--PQLGHQKAWSWSGPLL------
tr I3N1D4 I3N1D4_SPETR  6 --APDSLQVLEVGTTCNVTWRTSL---VSHYI-ESYLEFQVRTRTPGHSWEEAALLSLKRQQQQWIWLEQLTPRTPYELQVRAK--PRRGDHTVWSWSRPLAFRTRP-
tr F1N409 F1N409_BOVIN  6 --PPHSLQVVRIETRCNITWTVSQ---VSHYI-QNDVEFEARLRYADHSWEDARLLTLRQNQQWISLENLAPGTEYELQVRAK--PRLGSHEVWSHWSQPLAFRTVP-
tr G9K5M5 G9K5M5_MUSPF  6 --APDLLQITHVGTKCINTWNFSP---SSHYI-ESYLEFEARLRLQNQQWICLETLTPGTLYEFQVRVRK--AHLGSHKAWSPWSQPLAFRTKP-
tr F1SKK0 F1SKK0_PIG    7 -MAPPTLNLTKDREGYILHWKEE-----KMNYPHIGYIFQVQYKKDADSWEETKTVLQKGHSMSLPP--LEPATRYQARVRVKPDPGS-YNGTWSKWSKEQSWDTE--
tr G3SXI4 G3SXI4_LOXAF  7 -MDRPTLNVTKDGDSYMLRWETQ-----KQYYGHIRHSFEVQYRKDTDSWEESKTTLENTYNMPLLP--LEPSTRYWARVRVKPSLSS-YNGIWSEWSEELSWDTE--
tr F1MXH7 F1MXH7_BOVIN  7 -MAPPTLNVTKGRDGYILHWREE-----KMSYSHIACIFQVQYKKEGASWEDTKTDFQNAHTMSLPP--LEPASRYQARVRVKPDPGN-YNGIWSEWSEARSWDTD--
tr Q3U2T6 Q3U2T6_MOUSE  7 -MEPPTLNLTKNRDSYSLHWETQ-----KMAYSFIEHTFQVQYKKKSDSWEDSKTNLDRAHSMDLSQ--LEPDTSYCARVRVKPISN--YDGIWSKWSEEYTWKTD--
tr F7DHE0 F7DHE0_HORSE  7 -MPPPKLNVTRSTDGYVLLWKAE-----EMMYKHIGHTFQVQYKKDTASWEDSKTSLQNAHSMSLPW--LEPSTKYQARVRVKPTPGG-YNGVWSEWSEERSWGTE--
tr Q9Z1A0 Q9Z1A0_CAVPO  7 -MAAPTLNVTKDGDTYSLRWVTE-----KMYYSHIENTFEIQYRTAGDRWENSKTTLKNAHNMPLPP--LEPATTYLARVRVKPSPGGAYNGIWSEWSEEQRWTTD--
tr G3UFG8 G3UFG8_LOXAF  7 -MGCPTLNVTKDGDSYLHWEAD-----KD----LAPNFEVQYRKDTALWKEAKTALQNTYSLWLSG--LEPSTRYWARVRVKPTPAI-YNGIWSEWSEECFWDTE--
tr G1LTB8 G1LTB8_AILME  7 -MAQPALNVTKSRDGYTLHWTAK-----EMFYKHIQHTFQVQYKKDAASWEESKTTLQNAHSMSLPP--LEPSTRYWARVRVKPTPSG-YNGIWSEWSEECFWDTE--
tr E2RIM5 E2RIM5_CANFA  7 -MARPTLNVTKNRDGYTLHWEAD-----EMFYKHIQHTFQVQYRKDTVSWEKSVMKLENAHSMSLPP--LEPSTRYQARVRVRTSRTG-YNGIWSEWSEEHFWDTD--
sp P32927 IL3RB_HUMAN   7 -MAPPSLNVTKDGDSYSLRWETM-----KMRYEHIDHTFEIQYRKDTATWKDSKTTLQNAHSMALPA--LEPSTRYWARVRVRTSRTG-YNGIWSEWSEARSWDTP--
tr F7IKP3 F7IKP3_CALJA  7 -FTLSPL----------WGWSGT----STKMQSDRHNFETEFRSCTNP-QDSKTTLPNAHSMTPLA--LEPSTMYWARVRVKTSRSG-YKGIWSEWSQWSWDTE--
tr Q78ZF5 Q78ZF5_RAT    7 -MNPPTLNLTKNRDSYSLHWETQ-----KMSYPFIQHAFQVQYKKKLDRWEDSKTNLNHAHSMDLPQ--LEPGTSYCARVRVKTIPE--YKGLWSEWSNECTWTTD--
tr H2TYM5 H2TYM5_TAKRU  8 --------------NALLTWKYPPGDLQYGWI--TLVYELQYRREAENWKVKPS--LWETHLEL--LS-LPVGDYVVRVRCRSK----NSQLWKWSSAVL------
tr Q63968 Q63968_9MURI  8 --------------------------------RTGYNGIWSEWSEAHS-------MAL--PALEPSTRYWARVRTS-RTGYNGIWSEWSEARSWDTE--
tr G3PSA4 G3PSA4_GASAC  8 -------------AALLSWSYPPGDLRYGWI--TLVYELQYRREPDAWKVKHP--LREPQVEL--LG-LPAGDYVVRVRCRSQ----NSGLWSWSAAMP------
tr Q6UAQ2 Q6UAQ2_TETNG  8 -------------NALLSWRYPPGDLQYGWI--TLVYELQYRRDAGNWKVKPS--LREPQVEL--LS-LPVGDYVVRVRCRSK----NSPLWKWSALMP------
tr A8WH92 A8WH92_DANRE  8 ------------SNVSWSKGSNFP----KSIKKHEFQLQFKDAHTSWEMAKPQLSQENYTQLNHDLLTVGEEYQARVRKPVEDGHFRGEWSEWSPAVSWRSEIG
tr I3J6V4 I3J6V4_ORENI  8 -------------NALISWTYPPAHVQYGWI--TLVYELQYRREPDNWKVKHP--LREPQVEL--LG-LPVDDYVVRVRCRPQ----HSKLWSDWSATLL------
tr G4RJE0 G4RJE0_ONCMY  8 ----PGSPVI---INGTNATWSAG--SPLSFKIY--EYEFQVKVKREDQLWGEAQSLTRL------KQEPW--DGIHHIRVRVKPTQ--PPSSHWSEWSTTASWTSE--
tr I3JPI3 I3JPI3_ORENI  9 PNPPQHVNVTEKDNNWIVKWTEPNKSE------KHGLYYQVLYYRKQD--ENSSTLLDFTSWTLLG-KSLAPLQVYQVKVRSLVVPGSKYEGIPSEWSTDPVEWTTNEG
tr F1R4Q0 F1R4Q0_DANRE  9 PKQPFNLTIRNIDGGFNLTWDV-------------LIYRVRVLS-KSSPEKENILQQNQQSMVILSEKLQPGLQHVADQVAVNPEW-FPSMWSEWSDSVEWGVE--
tr G3W556 G3W556_SARHA 10 PRAPRNLIYSQGSDVFFLTWDNNYP-PDHFLIE--ELQYMVEIQKKKDTTT--QFEKIYSSLNLTFLAYHLENKSTYTARVRSKVSD-QTYTGQWSDWSPTVEWF----
tr H3AGM7 H3AGM7_LATCH 10 PKRPENLTIE---TKMRLSWKNPYD--DGSFLS-DELIFQVHYKKKGDPEKNAIENVSATTEYVIISNDLEPGVNVTAKVRVRS----EEYKTDWSDWSEEVEFHS----
tr H0XTC8 H0XTC8_OTOGA 10 PRAPGNLTVHTNSDTLLLTWSNPYP-PGTFLHS--ELAYMVNVSREHNSS-DF--RIYNVTVLRITASTLKHGVSYTARVRAW---AESYNSNWSEWSPGIRWL----
tr Q3U905 Q3U905_MOUSE 10 PLAPDNLTLHTNSDEWLLTWNNLYP-SNNLLYK--DLISMVNISREDNPA-EF--IVYNVPRLSFPINILMSGVYYTARVRVR---SQILTGTWSEWSSPSITWY----
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Figure S2: Conservation of amino acid residues in protein IL3RB_HUMAN. S230 is highly conserved across vertebrates. This diagram is the output from "mutationassessor" program.