

## Additional File 12

Family 1: Positively selected sites found. Sequence is CSEP0228

1 2 3 4 5 6 7

Positive selection Purifying selection

1 11 21 31 41  
M S C A I A I L L N T V G R L V V T G L D N G L S H Y G V Y N V P L T Y Q F L V P E E K L G I H V S

51 61 71 81 91  
T S Q I T Q P D T H V V A Y C S I I N N L S Q L V D I I T K D I P D I T R S P K L S D S E Y V D L E

101 111 121 131 141  
T K C R S Y V E R K S L A T L E L S M S E L K K D G H C T D D N L A S L N F Q G I L G V S G N Y S C

151 161 171 181 191  
F A A P V E S P S F N I T A D E P I R L E S F L S E G E L L R D R G L V I R P N A M A W F Q G H L H

201 211 221 231 241  
I F E Q R V S D D D D H T W W Y P L T S I G Q E D T N A P I I V E F I Y Q A I P Q I S W F M N V I I

251 261 271 281 291  
G F N K L M V T T S L P G L M L N A S Q E E S S K T Y Q N R N P E N L D H P K Y I Y D E E F L E R R

301 311 321 331 341  
K D Y I Q F K F C K D T S K L L N N L G L P T S E Y D E S F G C H V P K Y M S D E E S I G Q L K M I

351 361 371 381 391  
K L P P Q S D T S L P A E T F T R Q P G E G W L C D E R D L W A D G P P K K A P S I S R K L Q

Additional File 13. Continued: Family 2: Positively selected sites found. Sequence is CSEP0006

1 11 21 31 41  
MWINLCVTLISWLIILQVSCDNIPDSDMYLPDGTNGFVCDLDFYSIDHVR

51 61 71 81 91  
EAAKKGVEAF FYKRKVDKFP KTFEDTQLYN VKSDILLSWP IISSGLFYR

101 111 121 131 141  
TPGNSRLIIN TRGQIMGIVV ISFQKPSHKI SYNKCI PVRR SLEENKNGQS

151 161 171 181 191  
LLNECWGLAT PTFGYNCGSK FFPKSILDKM IGPDAIKNYQ QRLSGRNKLS

201 211 221 231 241  
CLIKYTGDEF SGVDLYWYPL HQKLSDKRLA GPSSRF RVVF DISNSEFKGI

251 261 271 281 291  
IDVENRNKKC VTVWDVSSIS SNNIYISSST LNLDKVG DGH WPQTCFGHKL

301 311 321 331 341  
KSKIMWLYLE FALKYWMSTL NESNP NLPLT SQKFIYSWFI RPGETNKDSS

351 361 371 381 391  
NHVFAIAYNT KHNNYKLYLM KTRNVKVDVH NPCLEFS TDD IDRLRKHIGD

401 411  
KHNPEESLSI DR

Additional File 12. Continued: Family 3: Positively selected sites found. Sequence is CSEP0217

1 11 21 31 41  
MKTSFALYLA LTTLQVGIKG SVIGENDYIC GTDVITAANI FKSIDKACHT

51 61 71 81 91  
LYHSRKVIRY PADYDASATF FISDARLEFSW PLMKDERIFN TGRAGNIRLI

101 111 121 131 141  
IDSSCRFIGI IQKTINQPDQ RCFRPMKLPR DMVDSSNPLP GRLPVLRGYS

151 161 171 181 191  
CGGIVFDSVQ VEKVRQETLK EFQRWNSLNH QISLTTLRVV QELYGSMVFL

201 211 221 231 241  
LPKKTPTSPT QLLRLADYSC FIVIDSNHKT LGMVSRSIDN WDKCDELWEM

251 261 271 281 291  
EPERHHIHHP QKNSVGETVFEGLTDYECGP FKFLRETINS HMQIACTIFQ

301 311 321 331 341  
KIQMSSAHFQ RGRLCSAQID TDTGSFEVWK FPLQLPERDL ITEHILSSNN

351 361 371 381 391  
CVIMLDEQCY FHGVYMYSKK TKEKCNQLFP QYVQETLDYE DEISDLSWVD

401  
EMIVDWSSPLK

Additional File 12. Continued: Family 4: Positively selected sites found. Sequence is CSEP0154

1 11 21 31 41  
MRLSRIAMIF QSASFCTISL AARFMVHPHE DSKVFFCDME FEQETYARID

51 61 71 81 91  
REKI IDTGTI QTLNEELNRL VADTTDQRFV QFYD TDNGGY EYFNFPTRFR

101 111 121 131 141  
KRYDGN DLAI TEYIMVIDQQ GRPCSMMSK TLV LKGIRNR RIVQRSYSLC

151 161  
AVGTKYSPQW RQI

Family 5: Positively selected sites found. Sequence is CSEP0118

1 11 21 31 41  
MKIFSPASTA ALACL LLVVP VALAVGYFQC SHDERFSLAY IQHKDSQCEA

51 61 71 81 91  
RHAKDDEPRG PNGEVYRTH IMTVPRVGFV VYYIIQVIDD SPTYRLYEDL

101 111 121  
SNEWEP CVYQ ETNKHTDS DS DESDI

Additional File 12. Continued: Family 6: Positively selected sites found. Sequence is CSEP0015

1 11 21 31 41  
MRPLAL LTAI PVFYSVYVAG DNAYHCS DSE GNTNTTYDQA LLEGSVK DTC

51 61 71 81 91  
LPNSELSAAQ LAANVEAKKY PQVWVDSQDY GFNGTVLLWK YQGNSSSEGLD

101 111 121 131 141  
ESDALIFTDN ACNIMGLVQK SKGFYTICKG AHEHFDEKVI TNTMHKKNVQR

151 161 171 181 191  
RWIFGND DDD NDEDEEVNKL HGFAGSSSDN AITLSPNIER EYDNYNRGRK

201 211 221 231 241  
GWSYSRKVPK YLFPDPPPTL QQADDDTSSY ASTDYGTASQ SFSSTNGDDS

251 261 271 281 291  
SQYNEGSEYD YGSQYQGGSS SSYQKSRSKK KGFVSGLFGS SRKQRYLPAT

301 311 321 331 341  
ADFPSTRNPP KPDLSRGRPS GKIIITPGCP TRPPPNDGYT MRPYRPTFEY

351 361 371 381 391  
GPDGTILLIT DKVTTMDKVT TMDKVITMDK IIPNQCYNIR IIFLKWVDAH

401 411 421  
DTRQDSFKKI SKDLVTLCFR FSRVAVFL

Additional File 12. Continued: Family 7: No positively selected sites found! Sequence is CSEP0058

1 11 21 31 41  
MRFFLFILAL MVAGFMAVPT GPYIVRRTNK KTAHTKFLET VDGFRWQDKV

51 61 71 81 91  
DTWTEKTRIT IENVLEKIST FYTDKFGKKA GSIPKPSGSK SLSPAVHDAS

101 111 121 131 141  
HSNHTKRFLQ QDPFGYRLDG EKTFSYYNKK SKVHLDHLFR EYQNSA

Family 8: Positively selected sites found. Sequence is CSEP0058

1 11 21 31 41  
MKFISTATTA ALAGILLAP ATYGNRYK ELSDPVSEAD VIKMVS DRTL

51 61 71 81 91  
EKNADIHPKV PTGESHKSYM FMKR TYANRP RITAYLVQVY GDPKEYQLSL

101 111  
HAGGRWHLCS LEDES

Additional File 12. Continued: Family 9: No positively selected sites found. Sequence is CSEP0290

1 11 21 31 41  
MQIFILFLAL FMTGLMAVPI SIHGIGSLSH RNIGDVNPNI IENPNSVNNV

51 61 71 81 91  
KIFGNGVDRT DLMQQIASTK ESNRFLGENN ADVGTSLSLT NDNFPVTRSG

101 111 121 131 141  
GYLSALTYNP TRVMGGVAPP RKHAKRALYQ SPSGFQLDGK HRFPYYNQRS

151 161 171 181  
IRRVNGLVND HKILSTNRRL RRPSVQRKPL LLNKEKSSSP

Family 10: Positively selected sites found. Sequence is CSEP0029

1 11 21 31 41  
MRFFNMAFIL QSAALFLPAL ASYKISHTNE EEKKFMCYNR AIYARDYWEE

51 61 71 81 91  
KLYADRLVQT KQKTEISMKD ITNISWPTNK SDLVLYDDNN ALHYFHMILT

101 111 121 131 141  
SIADSVNIRG QTVLIRYSLL IDNYGRVCSI VMHEQGASES ETRLLHDVIP

151  
ELTHPFCVLF G

Additional File 12. Continued: Family 11: Positively selected sites found. Sequence is CSEP0047

1 11 21 31 41  
MKFPVSLVTI AISTVALAYC VPPSSQPTLP EGQEVISNSL KVPGENALEY

51 61 71 81 91  
CSSEFLSYPI RLFNVAIKPT IPTINEQVEV FVDGFTGIPL SPEVQLRVFD

101 111 121 131 141  
WASGRDLSEP INFFKYMNSI NAQVPDHSVGO FRLFFRFKPE PTILYSGQIG

151 161  
IELNYRKDFK LLCVKTPIRI F

Family 12: Positively selected sites found. Sequence is CSEP0092

1 11 21 31 41  
MKFLHSTEIT TILSLFASLC ATQGVNDGYP MYNCRGVIFY SDSVTNSAAR

51 61 71 81 91  
AHRLKMGEGIN GYPQKLNSEFN ADGPPPHRIF PMVRDEDVYS GGIESFYFVI

101 111 121  
VDRSGQQQGV AYSVADGYMP CQTIVNPEY



Additional File 12. Continued: Family 13: Positively selected sites found. Sequence is CSEP0125

1 11 21 31 41  
MKIFSLISLA AILSHLTPAI ANQNYKCHDQ IIGPIPLMES VNNAFKYYNE

51 61 71 81 91  
EAKPGPADKL FIPSAFDLKI KYKDGTFDVK IEVGANSQKQ IIVVKAYCQG

101 111 121  
KTFDCTPTNE PPTYNKLQPK AENTKM

Family 14: No positively selected sites found in the protein. Sequence is CSEP0364

1 11 21 31 41  
MSIFISIFFL ISCLTLVYPI NGMKIERRFI GSVHKG YQCN KKKHNM YDIE

51 61 71 81 91  
PTLKSACKAY IKRKQKKWFF IYFINRTVFK RFSESKRFGF PPDTQITPVL

101 111 121 131  
PKGLGKISLY VMLTLISSGI YWQTPRIFIC VEA

Additional File 12. Continued: Family 15: Positively selected sites found. Sequence is CSEP0418

1 11 21 31 41  
MKNLYHTFRC QSILLKAIFFM LLLTSANASL TLQYVKRSME PGYHCHNKLY

51 61 71 81 91  
SFGIEIKVRK LACKAFLSTR DDARRPIVRQ EYINVENLIY EWSLPANPTI

101 111 121 131 141  
NPTIHPTDQT RKYTGKIIFN NRCELIDVAC YERKTKQEYL CQKVSQVSS

151 161 171 181 191  
TTS GDDKVLE EPFVQCGSLA LKTEEIREYA RSKSFDSLLE FHEVRETLGR

201 211 221 231 241  
IDGPWKRALF SKELIIRHRS NDILYEIVVD KHDEVVGMVV THHISRKLTS

251 261 271 281 291  
AEAHDGEI IK GPRKAKLKKH TIRLVCFHFK TFPLLRPALI SDVSNPLKRR

301  
ALV

Additional File 12. Continued: Family 16: Positively selected sites found. Sequence is CSEP0343

1 11 21 31 41  
MKLFTISGAA KLFFILAPVI AMPDNYHSGS TPVPDQDNDF SFYCPDQIY

51 61 71 81 91  
NKNYLISVVQ EARQIMRDSY TQYVYPSTFN HFNYDIIGEL WHYPLTGNDK

101 111 121 131 141  
PMKFSCFARF LKLINGFNVL VSYGAQDFVV FNTNNDIAGV AHRKSVNGRS

151  
IFEPCSLLG

Family 18: Positively selected sites found. Sequence is CSEP0229

1 11 21 31 41  
MKLLSMTAVA LLIEFSVSIH LSEDDGAFIN EPKLPVLDNFGMDCYSDKT

51 61 71 81 91  
YGQITVKSAA AEAYTNTCNS PGQMERCTFD RFPMENLFLH PIGGGYVSHL

101 111 121 131 141  
GVPAQHYYII NSAGQFLAGM LKYETHGNLV SALCRFTPYT AFLSYAESRR

151 161 171 181  
LNTQGDRNYY GSQYGQAGQQ PPIGSNRRSH SGY

Additional File 12. Continued: Family 17: No positively selected sites found in the protein. Sequence is CSEP0225

1 11 21 31 41  
MHNILLSSFL VLLHTYLHIT GSSASPTSNG KSKLGLSTDD FVCNGEYVSS

51 61 71 81 91  
SIVRQSIDAA WKALEFTTQPN DVYVNHVEDT RIEGGTSKTL FSGPIPIHGD

101 111 121 131 141  
YGLPDEGFKT IARVVFD FQR HLVGIIITIHK NGVRHCREII GASNPASFDA

151 161 171 181 191  
NLHDLLGYKC ANEVFDYRYV ASSYTEAYNE LSNGSIRPGG YPKIIDRPGS

201 211 221 231 241  
PHGAQFSWPL LPYSKLYNHG DATYNEFISF TDSIETLSVY YTDNYREHIC

251 261 271 281 291  
PAIWTNKTPA LSNPDFLMKH YRAPESSDSL IHCHGKSFEP HFVADNIKIA

301 311 321 331 341  
KRAHEFRSKH KLDLLFPEPI GDESASPGQS NWLWPLRIQE DFHQVRQRSI

351 361 371 381 391  
EYFLVLDGSF EFVGVFSFEN KNYSPCLSEG SKNLSHDMPQ DYLPQ

Additional File 12. Continued: Family 19: Positively selected sites found. Sequence is CSEP0139

1 11 21 31 41  
MKVLLAASTA GLAAFLLLVPTAYGLHYFKC NSRRIFAYSV IVGYTDSATY

51 61 71 81 91  
EQIQAGDPHF AGGHTYGAYR FTDYLPD GSP RNYLVQMVNV NPY YRLFESS

101 111  
GGRWHICTME GS

Family 20: Positively selected sites found. Sequence is CSEP0063

1 11 21 31 41  
MKIQNMKWFIALMFTPKFAY ADYVFNCYGL DVTRELIRRAYLLSMNGYVP

51 61 71 81 91  
DYPVITSISY LYNNEPIGIF PILGDD ETSI AAELYRPF LI WSQSFLDWGV

101 111 121  
YFLGDNGYEI CYKNPAYNGY TFRQIAFGNL

Additional File 12. Continued: Family 21: Positively selected sites found. Sequence is CSEP0064

1 11 21 31 41  
MRPFQLLSAL AIFINLEAVE AAAYWDCDGT EIPERNVRAA VVLAFFNYRKE  
51 61 71 81 91  
SFHGYPATFI IGSTFSGVGE VRQFPVEDSD ANWQGGAVKY YILTNKRGSY  
101 111  
LEVFSVSG NKC TFVEG

Family 22: Positively selected sites found. Sequence is CSEP0180

1 11 21 31 41  
MRLPLASFI ALMSHLISVS AEYKYVCP SK IKETTARIDM LRNDISSGSI  
51 61 71 81 91  
TEGVLIITSS GLRVLT YIFD RKIIDGVAYD FMVTVNYRDK LTRVYEKES E  
101 111  
HTRICELIFV LD

Additional File 12. Continued: Family 23: Positively selected sites found. Sequence is CSEP0248

1 11 21 31 41  
MKNLSFVSLA LFLSHLMPVL AVKNYTCGGV VVPAKTIKSE IEKKFDTIPL  
51 61 71 81 91  
LDGQTYVAAA ECGKTVFEVN PPRNGGSPLS VEIAFNRYRQE VMSITATRDN  
101  
ETVDCK

Family 24: Positively selected sites found. Sequence is CSEP0111

1 11 21 31 41  
MRFPHLVHLS VIFGFFTFES AAYYTCPSGI LIQNDTVRSR AQEIMNLSGVQ  
51 61 71 81 91  
LDVHRTPGQV EMSNITFYGS KAGGDLWFETS DFNPPITTEN TFKISISYPG  
101 111 121  
EEIVLTFEQK FGSGSQEGTC DVSVEM

Additional File 12. Continued: Family 25: Positively selected sites found. Sequence is CSEP0012

1 11 21 31 41  
MRTATLLAFV GTWLGSLAGI VRFEPEYLCG NDVHIPVSDV NNSLNLFQEQ

51 61 71 81 91  
AINCQQGFNI GSPGYLYDGK PKNRASVSTA MHAFGFD FID LNIDHWYEYI

101 111 121 131  
IVYDIDFKLQ KFEAVRLRGS KERKVLKCEY DPRYQD

Family 27: Positively selected sites found. Sequence is CSEP0034

1 11 21 31 41  
MRFSSLAIVC QIASIFVTSK AWAILNHIDE QTKRFNC DGV YVRYNEFASR

51 61 71 81 91  
QTRLVKSTD DRNSRAWSLV VQQLLNKPM GEEDPSVMFR DDASAHLTYI

101 111 121 131 141  
KLDDLTKLDN YGSQSLRTDY VVAIDGSNRA CAVILRRQDQ AWDHSWMGEP

151  
TFQFCTIY



Additional File 12. Continued: Family 26: Positively selected sites found. Sequence is CSEP0403

1 11 21 31 41  
MQFTVRQSTT KFRRLHIILF LTISVIGLTL QADISGYICD DLVVPYDKVV

51 61 71 81 91  
EVAKKASEFV KSVDGRYRFP ALLEDTQLFG VEGQNMFEVVP FRRFDSMRS G

101 111 121 131 141  
GNKGRDRIVL DASGNFKGVV YDTNDGNVHP MPTYRKCRPF LDDKHLELEK

151 161 171 181 191  
YIDDGYQISG FACGSNFLDR DVE TNLYNEC IRYISLPQKI KDKYKFPCR

201 211 221 231 241  
YAFQKINELW FQYNTNKNYD NKQTKVINSF MATFNNRCEF LNIKRISRVI

251 261 271 281 291  
THEEPCSYTW TAI PSAEATM TDSLFDVQSK NYKISDEFYA CKSYIFRITS

301 311 321 331 341  
IQNHMFHIFS LLLSNEPSSI EHMMHRQGEL LLWPMTLPER HEPRINHPLT

351 361 371 381 391  
FSIGFDRSNQ FSGIYFVTGS EWTWKKAKPC PNFNLLLESRL KARGSG

Additional File 12. Continued: Family 28: Positively selected sites found. Sequence is CSEP0234

1 11 21 31 41  
MIAWTVLSIL ALLPLCF AKP ALRKSHT E L F RCNLKYISMV QAQEAVKLG C

51 61 71 81 91  
NQMEVAPPAS LFPASFSGSE LFGLVGVGLF TWPVFPSKNV LRE DYGLNRV

101 111 121 131 141  
VFDSSCRLVG LIHIKPTGPE CCLHLMEIED LKMTHELK VY DTRWDSLQLY

151 161 171 181 191  
GYRFDD ELYL KNSVEEFVKE NFQSFRRNPS IKNALSMYPN LEQFTKFEIR

201 211 221 231 241  
TRPIELGPNG IQQA AVRFNR RLIIINSNKEI IGICRKS DNV WKPFAELRIL

251 261 271 281 291  
NDVYK LKVIS ARGPERGYEG LHGMNHNGIQ VSTAMLRSHL LMACKVLMER

301 311 321 331  
NMG T N T N D E N SMLAKMESTS DRLIFTWPLR MPENFVHGM

Additional File 12. Continued: Family 29: Positively selected sites found. Sequence is CSEP0059

1 11 21 31 41  
MKFLSAASMA T L S G L L L S A T A H A A D P Y F E C S M N T A V S F S G I I F Y E Q S H E Y

51 61 71 81 91  
L D A E P G D P E G P N G E I Y P A R R F T R V R R D G S D V L I L I Q S L D E Y P L R R A Y E K T

101 111  
E Q G W R L C P F H K P

Family 30: Positively selected sites found. Sequence is CSEP0070

1 11 21 31 41  
M R T S T L L R C L F T W L V T A I T T V Q C Q N D Y H C S N N I V V K G D V I Q R A L N D I S T D

51 61 71 81 91  
S T S T L Y A A G T L Y V N D V F V N R W W K E M I V P E S Y Y V G G T D T S Y R L I Y D D N K F V

101 111 121  
R S I Q L V Y H F R L G I R I S Q C T E V I E E

Additional File 12. Continued: Family 31: Positively selected sites found. Sequence is CSEP0105

1 11 21 31 41  
MHSNRLLSCLGIWLSIIGLVQCITEYYCGNNVVISQELIQSVSEIAISE

51 61 71 81 91  
LRAGVTWHTSLSGIIYRGNLCGLPNPTYRWFIQQSEDENS EVVMKYFLLV

101 111 121  
SASCEVQGVISTGWRKKLGEDDTWCTEA

Family 32: Positively selected sites found. Sequence is CSEP0106

1 11 21 31 41  
MKFSNTASMAALAGLSLLIPAVHGTLMFDCGNDARFLTSTVMEYLSIATA

51 61 71 81 91  
ASIEDDDPPYAQQQVNGAYRFTKNINNVNRTELVQSTNIHPFYRFFEITS

101 111  
GHYECPLKEHYA

Additional File 12. Continued: Family 33: Positively selected sites found. Sequence is CSEP0195

1 11 21 31 41  
MRSYINIIICL AIIAIIIFAA PNNTLSLHRP VLSAMDKRNI GKDHTGYQCG

51 61 71 81 91  
STKHKMNKIL DAIQMACPDP AQSDSEWFYSY NDSGFPKTFS EAQRLGLPKD

101 111 121 131 141  
TMITPVRGGF FDQLQFHYAA FEPVTCKLRG VIRQKDNKKD GVFQLCQYTT

151 161  
WPLSWTDPFH PG

Family 34: Positively selected sites found. Sequence is CSEP0371

1 11 21 31 41  
MKTFFQFASIV AGLSFLKTTI AAGDDYITLG MTSIKVQHIH SVARDMWTMD

51 61 71 81 91  
IDYYKSEYQG RYPAFWGNVR GKPARKEYPLL YEGKVWTHGS FMYVYVATED

101 111  
LSYIRLYYEG TESCDREVPSP

Additional File 12. Continued: Family 35: Positively selected sites found. Sequence is CSEP0380

1 11 21 31 41  
MKFLN TVSAS ALSALI LGSV VQGY VLKCS T GKEFD NQTMD ELASK AEYQY

51 61 71 81 91  
GHES YPLG PD GEKCK AYEFN SQLP NSQS SL ISAYS ATDHS HLAR ATIPYL

101 111 121  
VQVC DSMES Y RLF EWYDYRW VKCD