cn1Cvs.cn1P

DCLRE1B: p.Val525= снр73 p.Tyr1 SMTR2: p.Ser546Phe3 PCDHB13: p.Ala397= PROKR2: p.Val180= FNBP FI P5. n Glu262= Synonymous mutations GTPBP1: p.Pro58(Functional mutations ZNF442: p.Asp79His Cancer genes PDE10A: p.Ala275= SLC27A6: D.Asn533# CHL1: p.Leu1089IlefsTer2 FLRT2: p.His565= SPINIMA OVal MANSCT: p.Gin60= Ter15 IMPACT: p.Leu72Trp ITLN1: p.Ser156Tyr F5: p.Asp1464His SNTG2: p.Alay20Val KCNA6: p.Leu301TrpfsTer73 LHX5: p.Asp152Asn A2ML1: p.Val224Leu Pro177Leu PCDH12: p.Pro957= NLRP5: p.Lys236Asn HOXD9; p,Ala2/20N#/ NFE2L2: p.Asp29Gly POLDI: p.Ala890Pro providente. ZXX606: p.Pro6= DVL1: p.Trp532GlyfsTer142 PLCL1: p.Me1083Thr TMEM184B: p.Ser14= CMTR2:/p/@lu569Ter INTS1: p.Glu293Val H2BC14: p.Asp69His SORCS///p/Vals/986/Ju/ FBXL16: p.Ser239Cys T/SSK6: p.Asp154Tyr MYH1: p.Asp4Tyr SRRG: p.Ser224Arg CDC198: p.Asp210Asr OR6F1: p.5E/242=//p.Glu62# Met 1234 Met /ZMF653; p| Trp573Ter CDH8: p.Ser761Tyr ADAMTSL1: p.Ser450= n Ala103Glu NUP210: p.Val81Met MECOM; p.Met241 TTN: p.Asp15698Glu VPS11: p.Pro601Leu COL21A1: p.Ala157 p.Ala243Ser DOK1: p.Arg616Leu ALG2: p.Ala243Ser DOK1: p.Ala86Ser ZFHX4
A1: p.Pro1227Thr CXXC5: p.Val49Met ZFHX4
CPALPP1: p.Asp225Asn XPNPEP1: p.Asp100
TTN: p.Pro25788Ala SLC28A2: p.Ala168Val //ZFHX4: p.\$\dagge\n2158Glu COL22A1: p.Pro1227Thr Cn l: p.Asp225Asn/ XPNPEP1:/p.Asp100His SLC28A2: p.Ala168Val GA6L2: p.Gly616del/ RGS/12: p.Leu252Phe GOLGA61/2: p.Gly616de/// STX2: p.Arg113Trp/ MUC1/6: p.Thr14102= APBB2: p.Pro294=// 75997Glu TTN: p.Tyr17132= ////NSUN2:/p.As/n2/18/Asp PLCL1: p.Lys997Glu HNRNPA1: p.Gly283Arg TRPV4: p.A./a266Ser// SLC5A11: p.Ala224= SIGLEC1: p. \(\tilde{\text{gln}} \) 1441Lys/ SNHGŽ8: p,Pro348= PHKB: p.Asn1075Ser // SLC13A1: p.Lleu3: SS56Arg // SRIN3A: p.Arg102FNF216: p.Pro663Leu // SRIN3A: p.Pro378Gln CVD2: p.Thr SLC/13A1: p.Leu353Phe LIG1: p.Gly178Arg IL20: p.Lys56Arg 0.2 TRAPPC9: p.Glu934Thrfs/Ter4 PLCXD3: p.Thr250Asn RYR3: p.Glu41Lys // MRP\$22: p.Arg2/63His CNTN2: p.Pro366AlafsTer26 ØNECUT3: p.Pro157Gln ENTPD6: p.Ser227Leu DMWD: p.Asp124ArgfsTer10 /POLE: p.Val464= EPHA5: p.Arg783GlufsTer7 CDH26: p.Val57= ARHGEF17: p.Gly276 Ser277insProArg / AKR1B10: p.Phe312SerfsTer22 FAT2: p.Arg1937Gln 0.0 0.2 8.0 0.6 0.41.0

CCF of cn1C (CIS+AIS)