**Figure 1.**

Contrasts and p-values were calculated using GenStat:

matrix [rows=!t('CarcinomaVsControl','BenignVsControl','CarcinomaVsBenign');\ columns=3] Contr;\

values=!(0,-1,1, 1,-1,0, -1,0,1)

for y=logIL1b,logIL10,logIL13,logIL6,logIL12,\

logRANTES,logEOTAXIN,logIL17, logMIP1A,logGMCSF,logMIP1B,logMCP1,\

logIL15,logIL5,logIFNG,logIFNA,logIL1RA,logTNFA,logIL2,logIL7,\

logIP10,logIL2R,logMIG,logIL4,logIL8,logTNFRII,logMDC,logTGFB1;\

yind=1...28

delete [redef=y] cont1,cont2,cont3, se\_cont1,se\_cont2,se\_cont3,\

tstat1,tstat2,tstat3, pval1,pval2,pval3, rdf,\

effdiff, se\_effdiff

blocks PID

treatments comparison(Status; 3; Contr)

anova [fprob=y; pr=aovt,means,contrasts] y

akeep [aovtable=atab] terms=Status; contrast=effdiff;\ secontrasts=se\_effdiff

aplot

scalar rdf

calc rdf = atab['d.f.']$[6]

calc cont1 = effdiff[1]

calc se\_cont1 = se\_effdiff[1]

calc tstat1 = cont1/se\_cont1

calc pval1 = 2\*cut(abs(tstat1); #rdf)

calc cont2 = effdiff[2]

calc se\_cont2 = se\_effdiff[2]

calc tstat2 = cont2/se\_cont2

calc pval2 = 2\*cut(abs(tstat2); #rdf)

calc cont3 = effdiff[3]

calc se\_cont3 = se\_effdiff[3]

calc tstat3 = cont3/se\_cont3

calc pval3 = 2\*cut(abs(tstat3); #rdf)

for co=cont1,cont2,cont3; se=se\_cont1,se\_cont2,se\_cont3;\

ts=tstat1,tstat2,tstat3; pv=pval1,pval2,pval3; \

CN=C1,C2,C3; SC=SE1,SE2,SE3; TT=TS1,TS2,TS3; PVL=PV1,PV2,PV3

calc CN$[#yind] = co

calc SC$[#yind] = se

calc TT$[#yind] = ts

calc PVL$[#yind] = pv

endfor

endfor

calc mlpv1 = -log10(PV1)

calc mlpv2 = -log10(PV2)

calc mlpv3 = -log10(PV3)

Volcano plot used standard plot, points and lines functions in R:

plot(TD$C1,TD$mlpv1, col=1, cex=1.2, pch=19, cex.axis=0.9, cex.lab=1.3, xlim=c(-2,5),ylim=c(0,20), xlab=expression(paste("Contrast (",log[2]," scale)")), ylab=expression(paste(-log[10],"(P-value)")))

points(TD$C2,TD$mlpv2, col=1, cex=1.2, pch=21)

points(TD$C3,TD$mlpv3, col="darkgray", cex=1.2, pch=19)

lines(c(-1,-1), c(0,20), lty=4)

lines(c(1,1), c(0,20), lty=4)

lines(c(-2,5), c(cutoff,cutoff), lty=3)

lines(c(-2,5), c(cutoff2,cutoff2), lty=2)

points(x=notable1[,"Contrast\_1"],y=notable1[,"C1\_MinusLogP"], pch=19, col=1, cex=1.5)

text(x=notable1[,"Contrast\_1"],y=notable1[,"C1\_MinusLogP"], labels=substring(rownames(notable1),4), pos=2, offset=0.4, cex=0.9, srt=0)

points(x=notable2[,"Contrast\_2"],y=notable2[,"C2\_MinusLogP"], pch=21, col=1, cex=1.5)

text(x=notable2[,"Contrast\_2"],y=notable2[,"C2\_MinusLogP"], labels=substring(rownames(notable2),4), pos=2, offset=0.4, cex=0.9, srt=0)

points(x=notable3[,"Contrast\_3"],y=notable3[,"C3\_MinusLogP"], pch=19, col="darkgray", cex=1.5)

text(x=notable3[,"Contrast\_3"],y=notable3[,"C3\_MinusLogP"], labels=substring(rownames(notable3),4), pos=2, offset=0.4, cex=0.9, srt=0)

legend(xy.coords(x=c(1.1, 3.4), y=c(17.5,13)), legend=c("Malignant vs Healthy Control","Benign vs Healthy Control","Malignant vs Benign"), pch=c(19,21,19), col=c(1,1,"darkgray"), pt.cex=1.5, cex=1.0 )

legend(xy.coords(x=c(3.5,4.75), y=c(3.75,1.5)), legend=c("P=0.0001","P=0.05"), lty=c(2,3), cex=0.8, text.font=3)