

Figure S1. Comparison of RNA-Seq and qPCR results. The horizontal axis is the result of RNA-Seq, and the vertical axis is the result of qPCR. The number on the coordinate axis represents the log₂ value of each gene expression ratio of gregarious and solitary armyworms.

Gene	log ₂ FC(G/S, RNA-Seq)	log ₂ FC(G/S, qPCR)
TRINITY_DN11213_c0_g4	-1.23264	-1.29826
TRINITY_DN1026_c5_g1	-1.61120	-1.13386
TRINITY_DN11743_c0_g1	-1.26588	-1.12059
TRINITY_DN876_c3_g1	-2.72646	-3.29073
TRINITY_DN2583_c0_g1	1.39784	1.16565
TRINITY_DN1017_c0_g1	5.61830	4.13641
TRINITY_DN1037_c0_g2	14.1709	9.21950

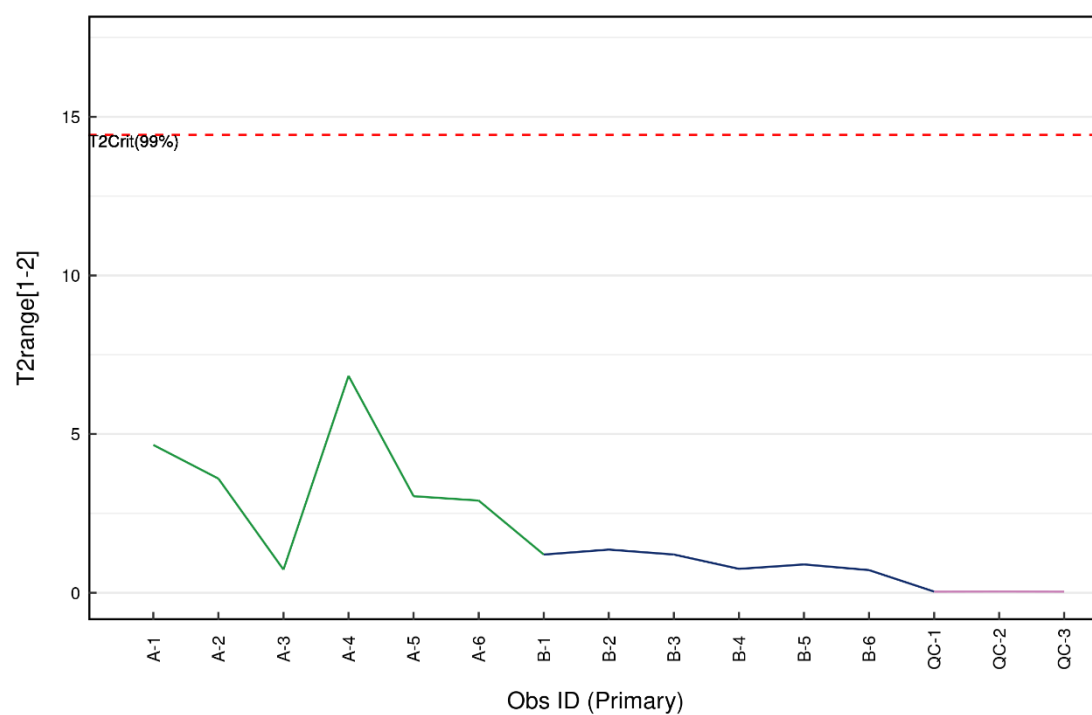


Figure S2A. Hotelling T2 range line plot of negative ion mode population samples.

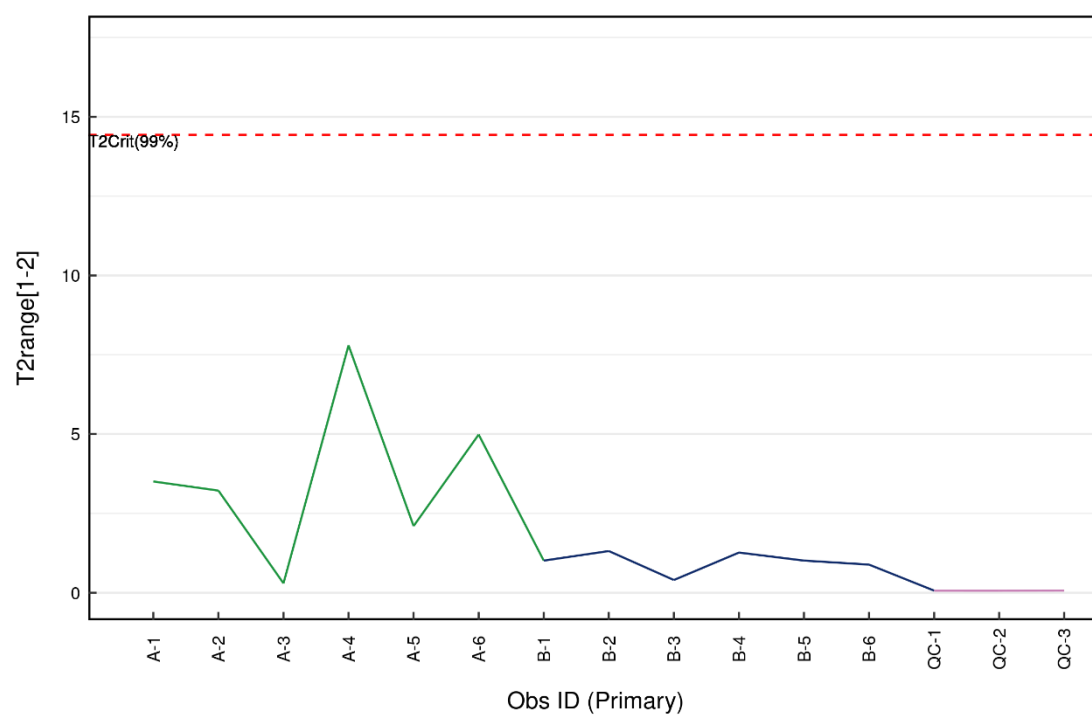


Figure S2B. Hotelling T2 range line plot of positive ion mode population samples.

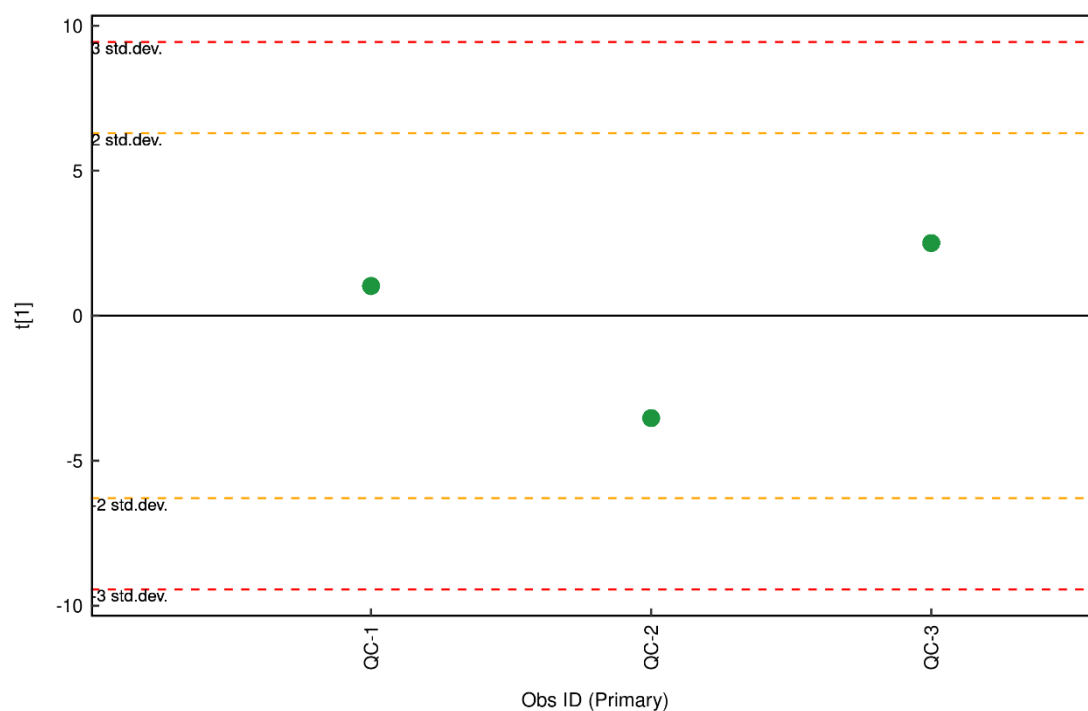


Figure S2C. MCC map of QC samples in negative ion mode.

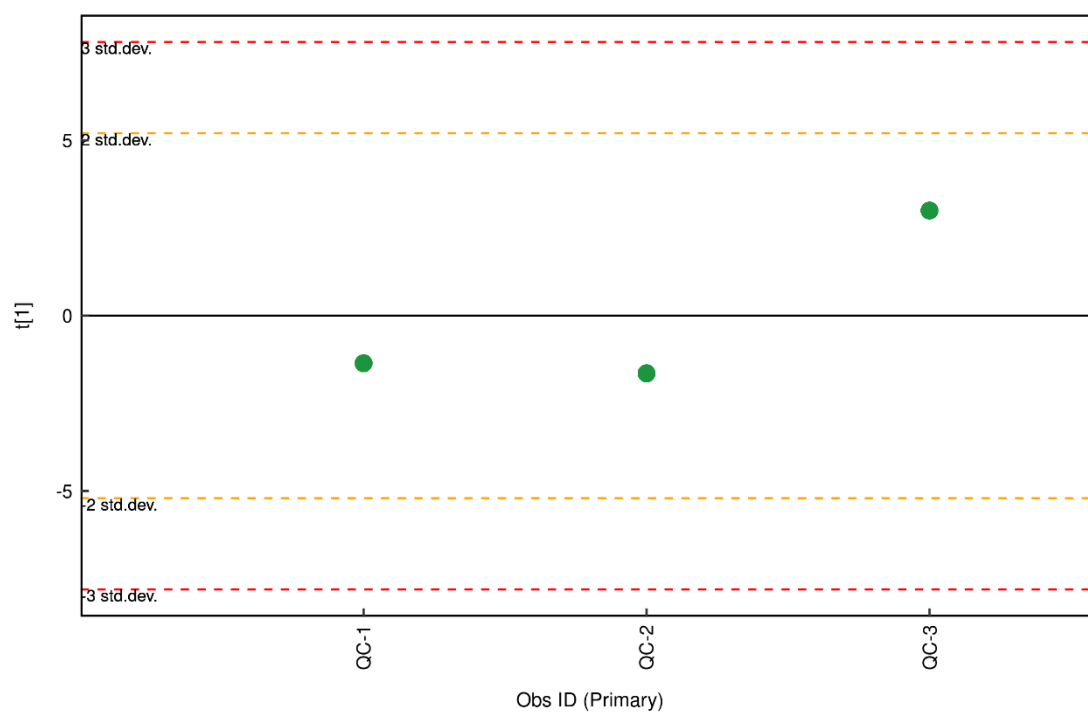


Figure S2D. MCC map of QC samples in positive ion mode.

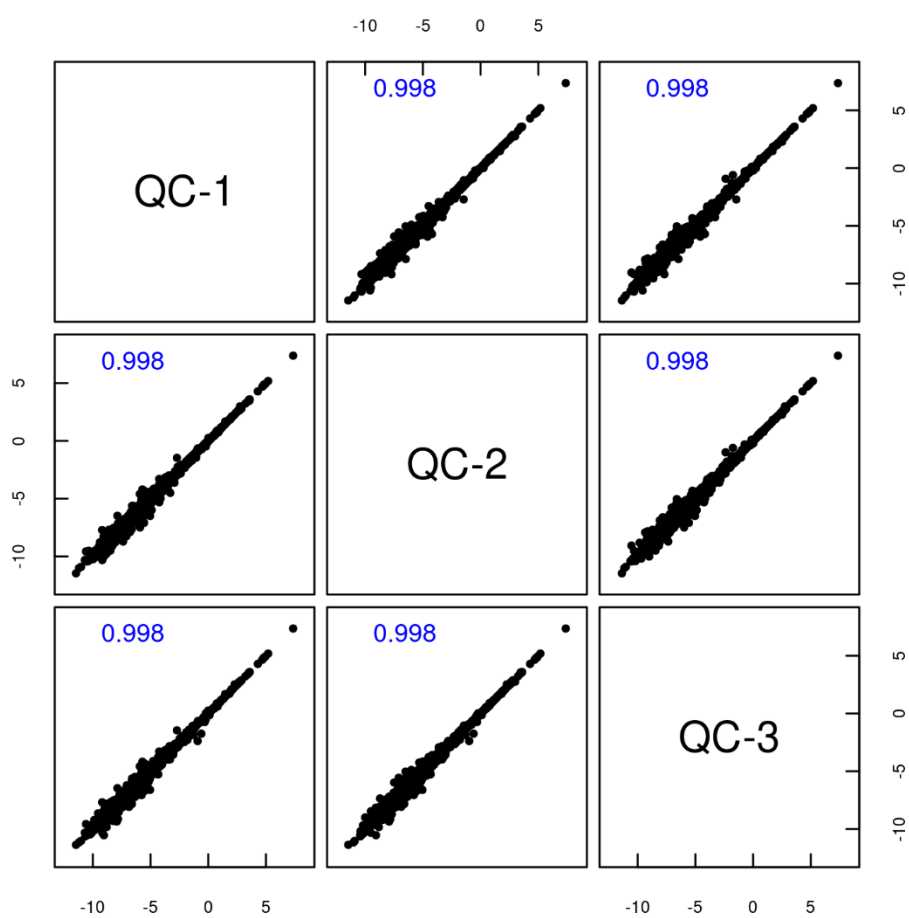


Figure S2E. Correlation map of QC samples in negative ion mode.

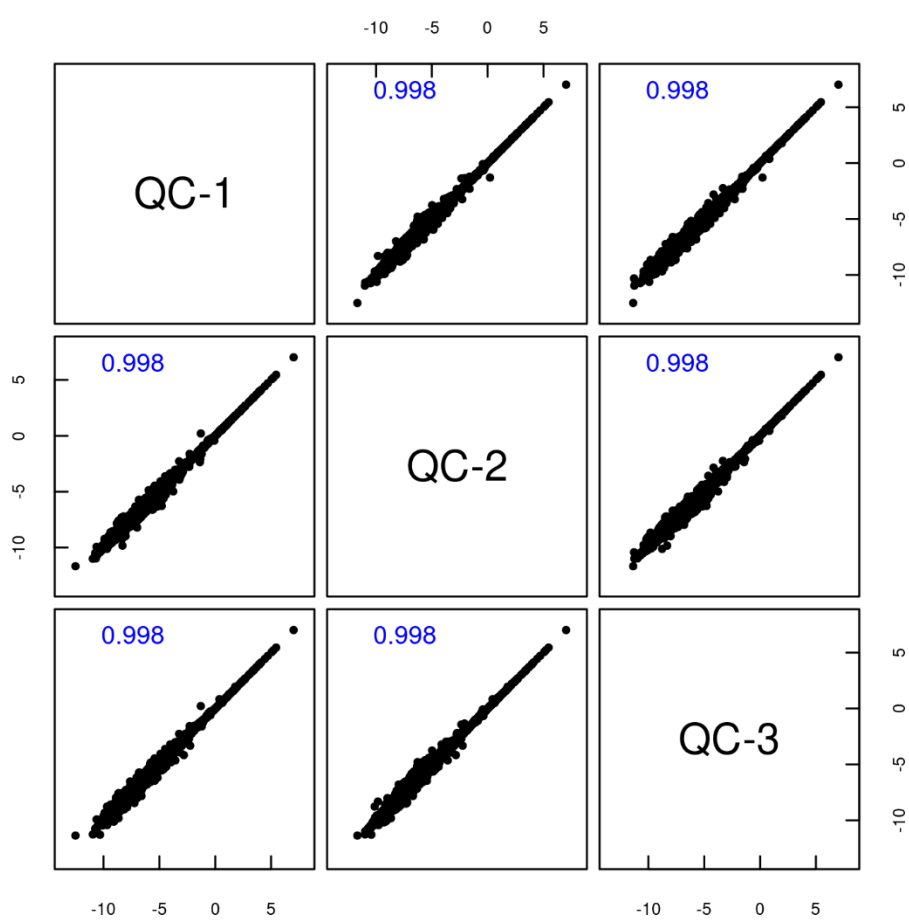


Figure S2F. Correlation map of QC samples in positive ion mode.

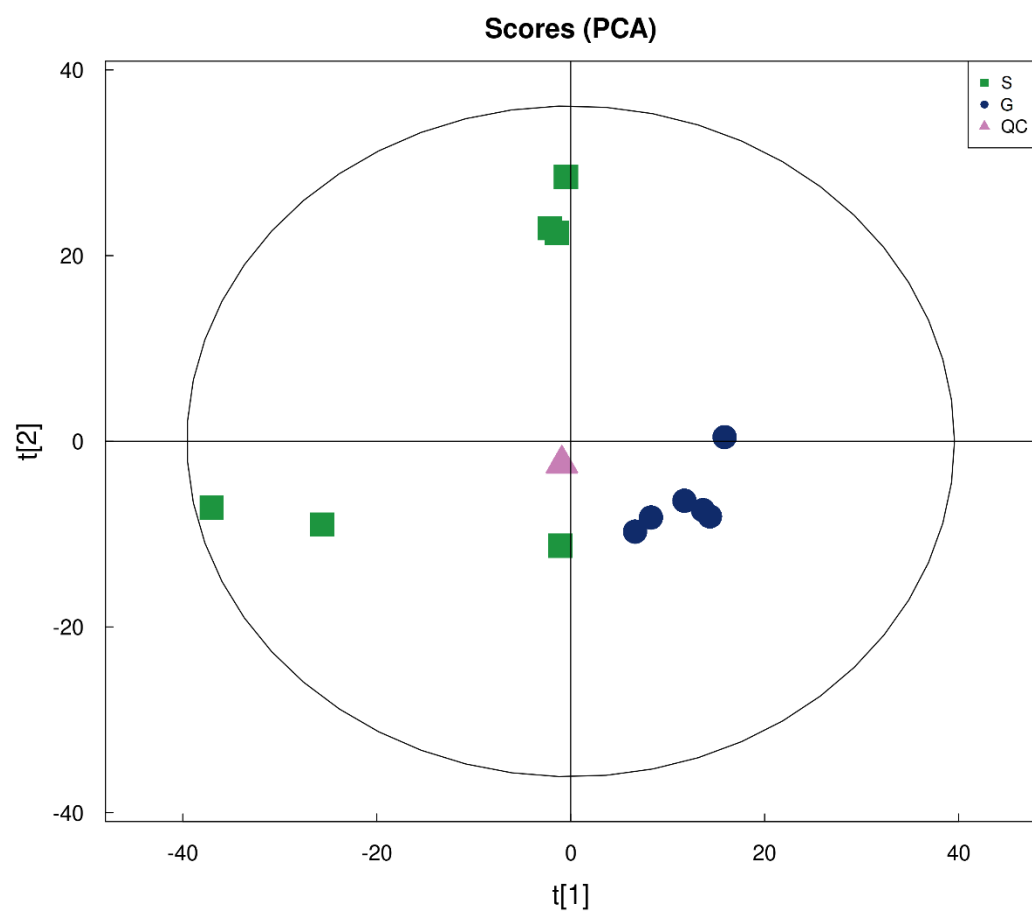


Figure S2G. PCA analysis of negative ion mode population samples.

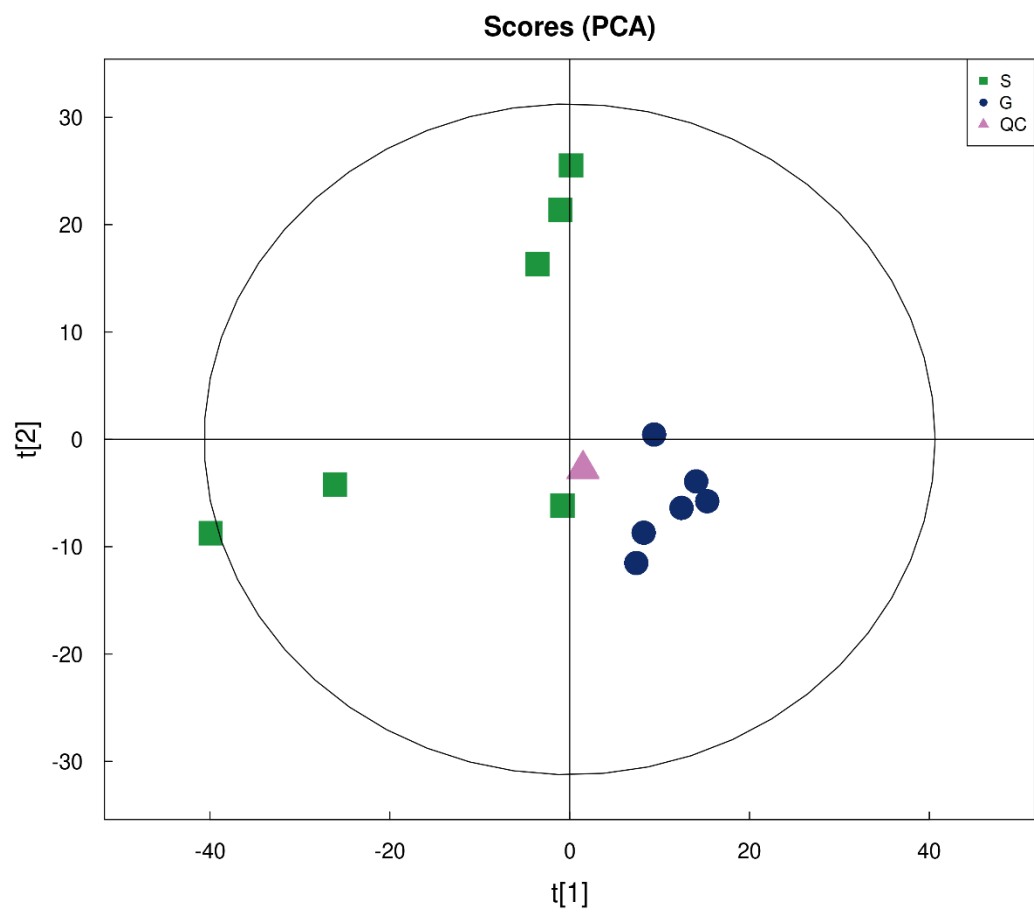


Figure S2H. PCA analysis of positive ion mode population samples.

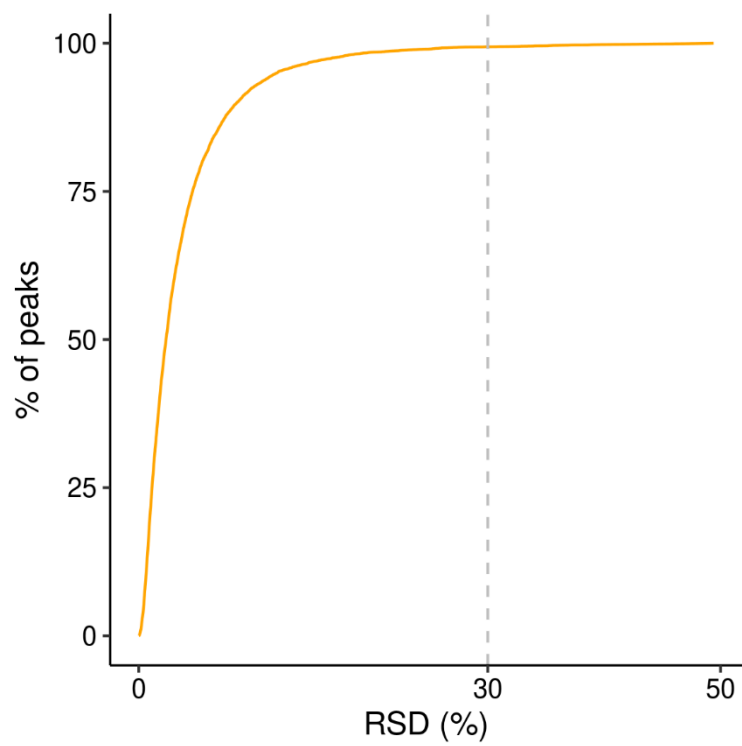


Figure S2I. Relative standard deviation of QC samples in negative ion mode.

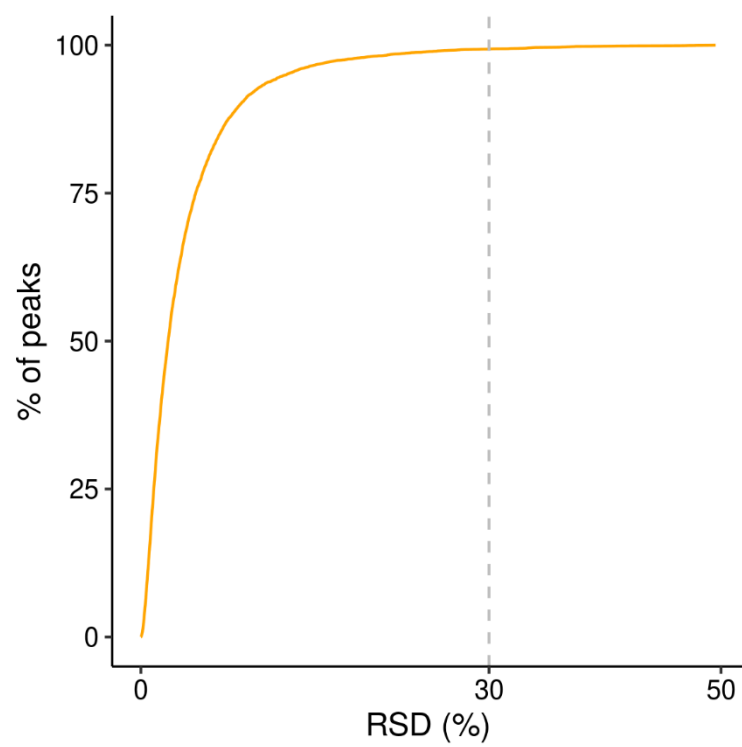


Figure S2J. Relative standard deviation of QC samples in positive ion mode.