

Recommended settings for copy number analysis using Axion[®] CNV Summary Tools Software and Nexus Copy Number[™] Software

Nexus Copy Number Software, Version 7.0 (Discovery Edition) from BioDiscovery.
Based on Build Version: 8154

Highlighted settings have been optimized.

Step Name	Operation
Combine Replicates Within Array	None
Systematic Correction	User must first specify "Quadratic Correction" from the pull down menu and select the appropriate "Systematic Correction" file using the browse button
Recenter Probes	None
Combine Replicates Between Arrays	None
Analysis	SNP-FASST2 Segmentation

Parameter Name	Value
Significance Threshold	1.0E-8
Max Contiguous Probe Spacing(Kbp)	1000.0
Min number of probes per segment	3
High Gain	0.75
Gain	0.12
Loss	-0.18
Big Loss	-1.1
Male Sex Chromosomes Big Loss	-1.0
3:1 Sex chromosome gain	1.2
4:1 Sex chromosome gain	1.7
Homozygous Frequency Threshold	0.8
Homozygous Value Threshold	0.7
Heterozygous Imbalance Threshold	0.4
Minimum LOH Length(KB)	500
Minimum SNP Probe Density (Probes/MB)	0.0
Robust Variance Sample QC Calculation: Percent outliers to remove	3.0