Partek® Genomics Suite™

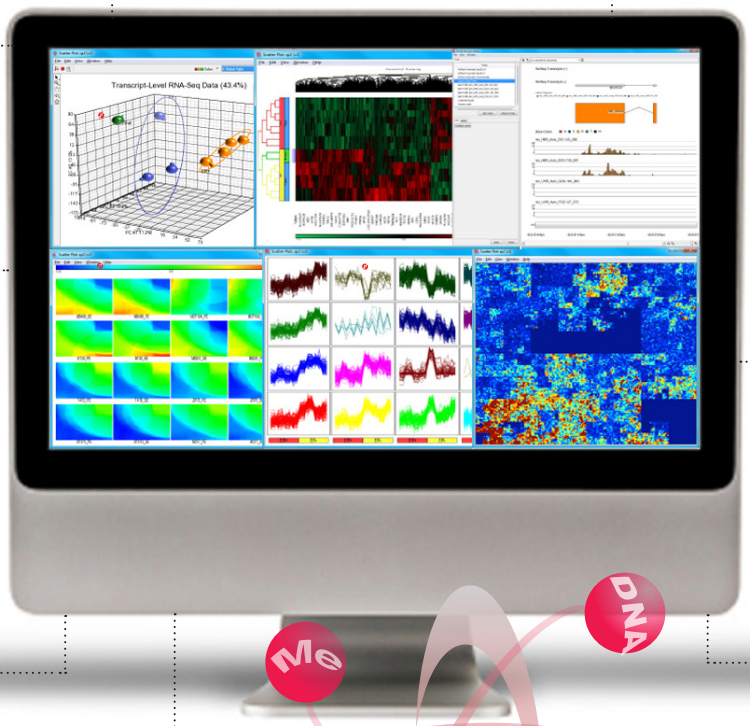
The Most Trusted Genomics Software Worldwide

Partek® Genomics Suite™ is the software scientists worldwide have come to trust for their genomic data analysis & visualization needs. In 2011 alone, it was cited in over 400 peer-reviewed publications. It's fast, agile, & memory efficient, allowing you to analyze large data sets right from your desktop. With its user-friendly interface, comprehensive workflows, & ability to support all qPCR, microarray, & next generation sequencing technologies, Partek Genomics Suite gives biologists, bioinformaticists, & statisticians a single, integrated solution for trustworthy results. Get your free trial today & see what Partek Genomics Suite can do for you.

Easily import & analyze all your qPCR, next generation sequencing, & microarray data on a single platform

Powerful statistics & interactive visualizations provide fast, comprehensive data analysis

An intuitive interface speeds adaptation when you're a novice user & accelerates your work when you're an expert user



Choose the platform that works best for your environment: Windows®, Linux®, or Macintosh®

Detect differentially expressed genes & fold changes across different groups, time points, & any experiment factor or design for meaningful biological discovery

Convenient data access tools help you identify & annotate important biomarkers & construct & validate predictive diagnostic systems enabling you to better determine an accurate diagnosis & prognosis

Import wizard & workflows for all major assays streamline your analysis & gives novice users the confidence they need

Increase your collaboration by sharing your findings with others within your organization through information-rich graphical displays

Supports all core assays allowing you to discover & validate on a single platform

Partek Genomics Suite Workflows

Partek Genomics Suite has workflows for the following assays to provide you one platform for all your genomic data analysis needs & to simplify the process & speed to biological discovery.

Next Generation Sequencing*

	Illumina	AB/SOLiD	Ion Torrent	Roche 454	PacBio
RNA-Seq					
Differential Gene Expression	•	•	•	•	•
Alternative Splicing	•	•	•	•	•
sRNA-Seq (miRNA)	•	•	•	•	•
Fusion Transcripts	•	•	•		
Coding SNPs/eQTL	•	•	•	•	•
DNA-Seq (SNPs/InDels)					
C&idate Genes	•	•	•	•	•
Exome	•	•	•	•	
Whole Genome	•	•			
Copy Number	•	•	•	•	•
ChIP-Seq	•	•	•	•	
DNA-Methylation	•	•	•	•	

Microarray

	Affymetrix	Illumina	Agilent	Nimblegen	Custom
Gene Expression	•	•	•	•	•
Exon/Alternative Splicing	•		•		
Micro RNA	•	•	•	•	•
Tiling	•		•	•	•
Association/Trio	•	•			
Allele Specific CN	•	•			
LOH	•	•	•		
Copy Number (CN)	•	•	•	•	•
ChIP-ChIP	•		•	•	•
DNA-Methylation	•	•	•	•	

qPCR

	TaqMan	NanoString
Gene Expression	•	•
Micro RNA	•	•

*Partek Flow is required for alignment & quantification. BAM files or zipped project files are imported into Partek Genomics Suite

Partek®
turning data into discovery®

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