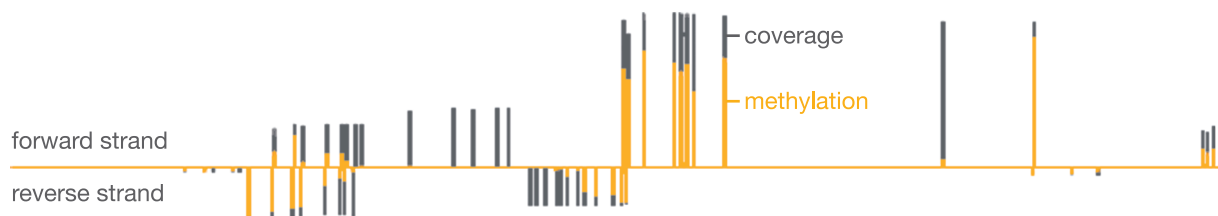


# DNA methylation



## Methylation patterns and their effect on expression



### Mapping

Genomatix mapping technology makes analyzing DNA methylation data (from bisulfite treated DNA) as simple as mapping any other sequencing data. Due to our algorithm's capability to align reads with sophisticated base sensitive T->C conversion, no specific libraries or additional processing is required.

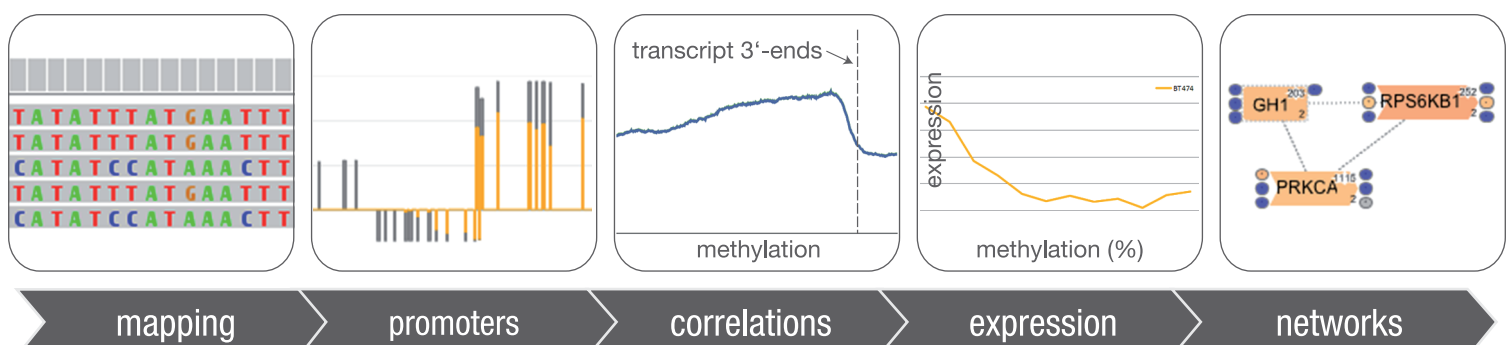
### Methylation patterns

The graphic above shows the methylation patterns of the gene PRKD1 in a T47D breast cancer cell line, shown. After mapping, the coverage and methylation figures for all CpGs can be provided by the software. For promoter based analysis, statistics are generated for each promoter annotated in our comprehensive annotation database (EIDorado). As methylation patterns are known to effect gene expression, these statistics can give indications about methylation based gene regulation.

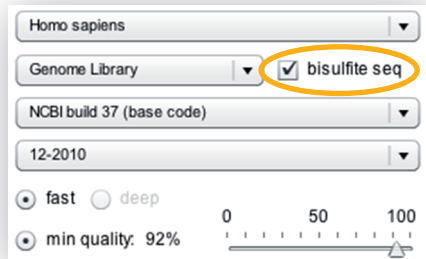
### Data integration

Comparing expression and methylation data allows to investigate the global and local effects of promoter methylation. The expression plot (below) shows decreased expression with increased methylation. The Genomatix Pathways System (GePS) allows to include methylation data into the network analysis. In the "networks" icon you can see three genes that are colored according to their expression value, and - in addition - are surrounded by colored circles that provide the average methylation value of their promoters.

#### workflow



## User interface, mapping and comparison

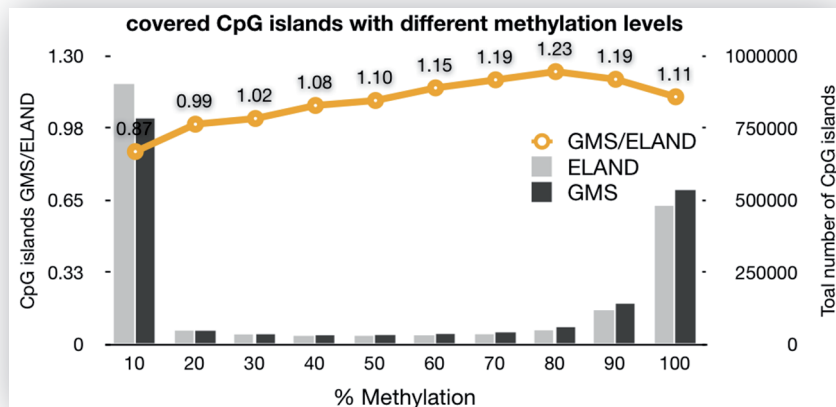


### Mapping

Genomatix technology makes analyzing DNA methylation data as simple as mapping DNA-Seq data. Just check the "bisulfite seq" box (see left) and you're done. This will activate our base sensitive T->C conversion algorithm while mapping the reads to the genome. All other settings like alignment quality and the number of insertions/deletions/mutations can be specified as usual.

### Comparing the Genomatix Mapping Approach

To compare our base sensitive T->C conversion approach on the Genomatix Mining Station (GMS) against global T->C conversion strategies, we used a dataset provided by Illumina in the iDEA challenge 2011. This comparison shows that we can map more reads with methylation states over 30%, when mapping them to the complete human genome (based on the ELAND mappings provided with the iDEA challenge 2011 data).



mapping statistics DNA methylation (bisulfite)		
	unique	all
BT-474	57%	65%
MCF7	51%	59%
MCF 10A	56%	64%
T47D	50%	59%

### Mapping statistics

Mapping statistics of four breast cancer cell lines from the Illumina iDEA challenge 2011. Mapping bisulfite sequencing data is technically more difficult, especially for unmethylated reads. In these reads all 'C's have been converted into 'T's. This leads to a loss of information and consequently to an increased number of ambiguous hits.



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### About us

Genomatix is one of the world's leading suppliers of technologies to analyze and interpret genomic data. As well as laying the groundwork for microarray experiments and NGS data sequencing analyses, our hardware and software solutions help answer the typical questions posed by systems biology. Our approach: combine multiple lines of evidence to perform an integrated meta-analysis.