

# DNA Methylation Patterns in *Crassostrea gigas*

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- **Epigenetics** describes DNA modifications that change gene expression without altering the underlying nucleotide sequence.
- **DNA methylation** in organisms is extremely diverse, variable among species, and can change genome function under external influences.

**The objective of this study is to use the Pacific Oyster as a model organism to characterize the distribution and identify potential functions of DNA methylation.**

## Approach

- **High-throughput Bisulfite Sequencing** was used to examine genome DNA methylation in sperm cells of the Pacific oyster.

## Mapping to the Oyster Genome

1670 Scaffolds - 502 Mbp



**Citation**  
In accordance with our terms of use, please cite the dataset as:  
Zhang, Qi, Feng, X., Guo, X., Li, L., Lu, H., Xu, F., Yang, P., Zhang, L., Wang, X., Qi, H., Zhu, Y., Yang, L., Huang, Z. (2012). Genomic data from the Pacific oyster (*Crassostrea gigas*). GigaScience. <http://dx.doi.org/10.5524/100030>

**Bisulfite Treated Library [Sperm]**  
171 million - 72bp paired-end reads

## Bisulfite Sequence Mapping Program (BSMAP)

- A short reads mapping software for bisulfite sequencing reads
- Total number of aligned reads:  
Pairs: 85 million  
Singles: 32.4 million

## Galaxy Workflow

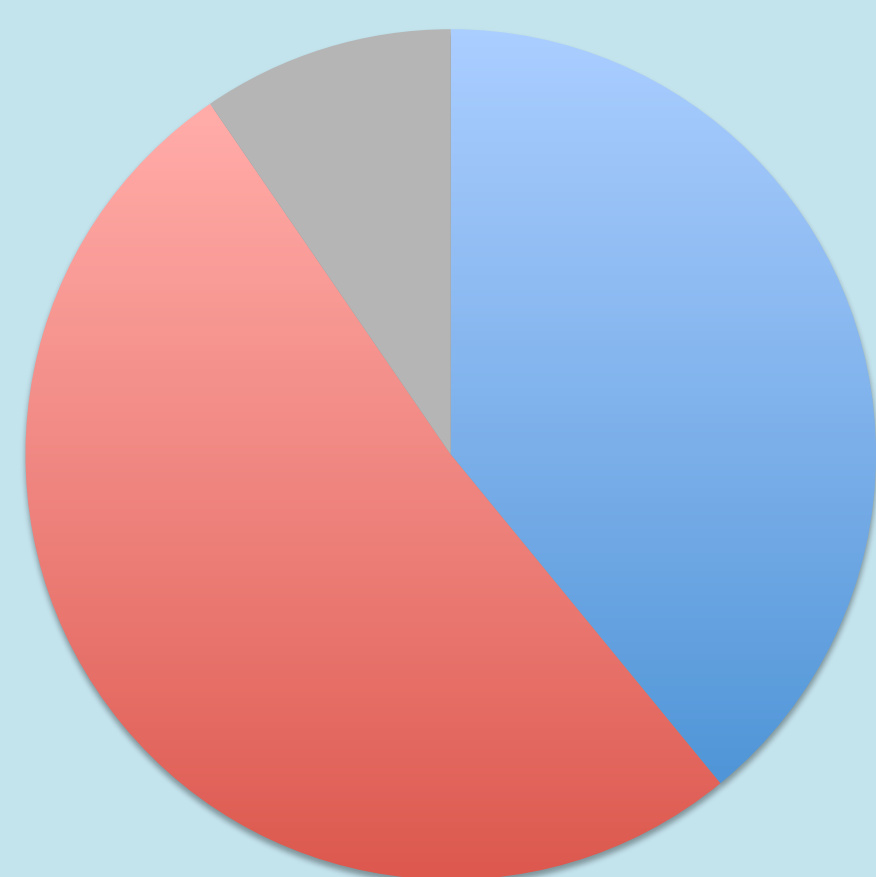
1 million \*Methylated CpGs  
2.9 million Unmethylated CpGs  
\*5x coverage / 50% methylation

## Methylated CpGs

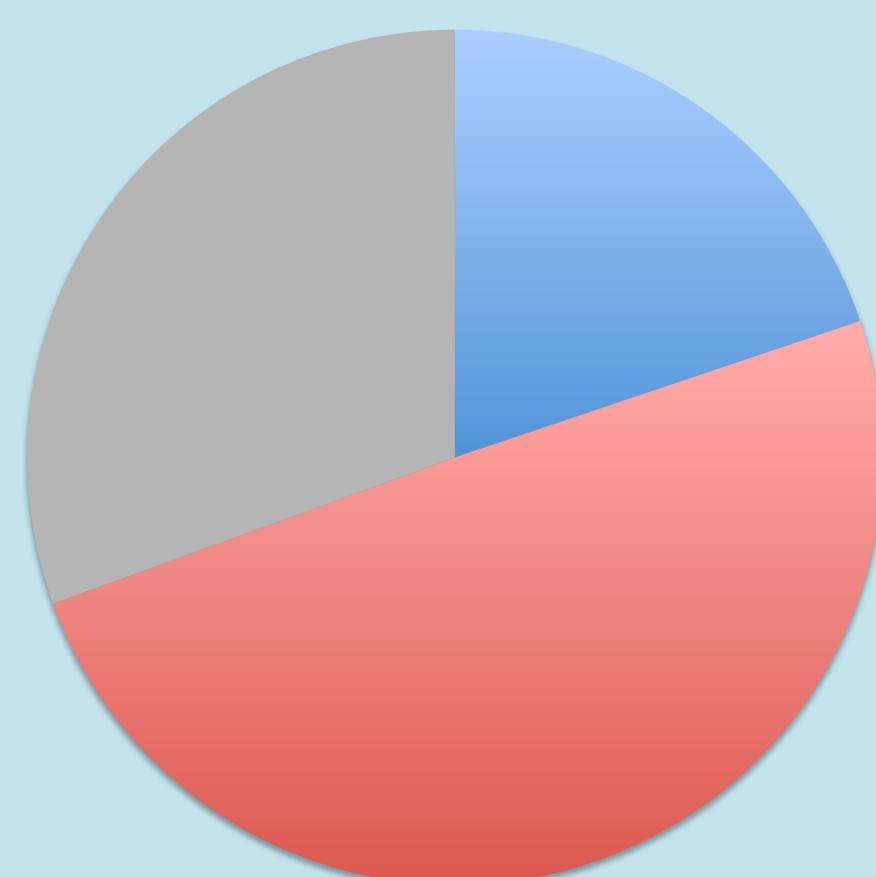
Total	949,478
mRNA	736,195
Exons	306,956
Introns	403,503
Repeat regions	5,961
Transposable elements	28,334
Promoter region	275
High expression windows	40,653

## Distribution of CpGs Across the Genome

### Methylated CpGs

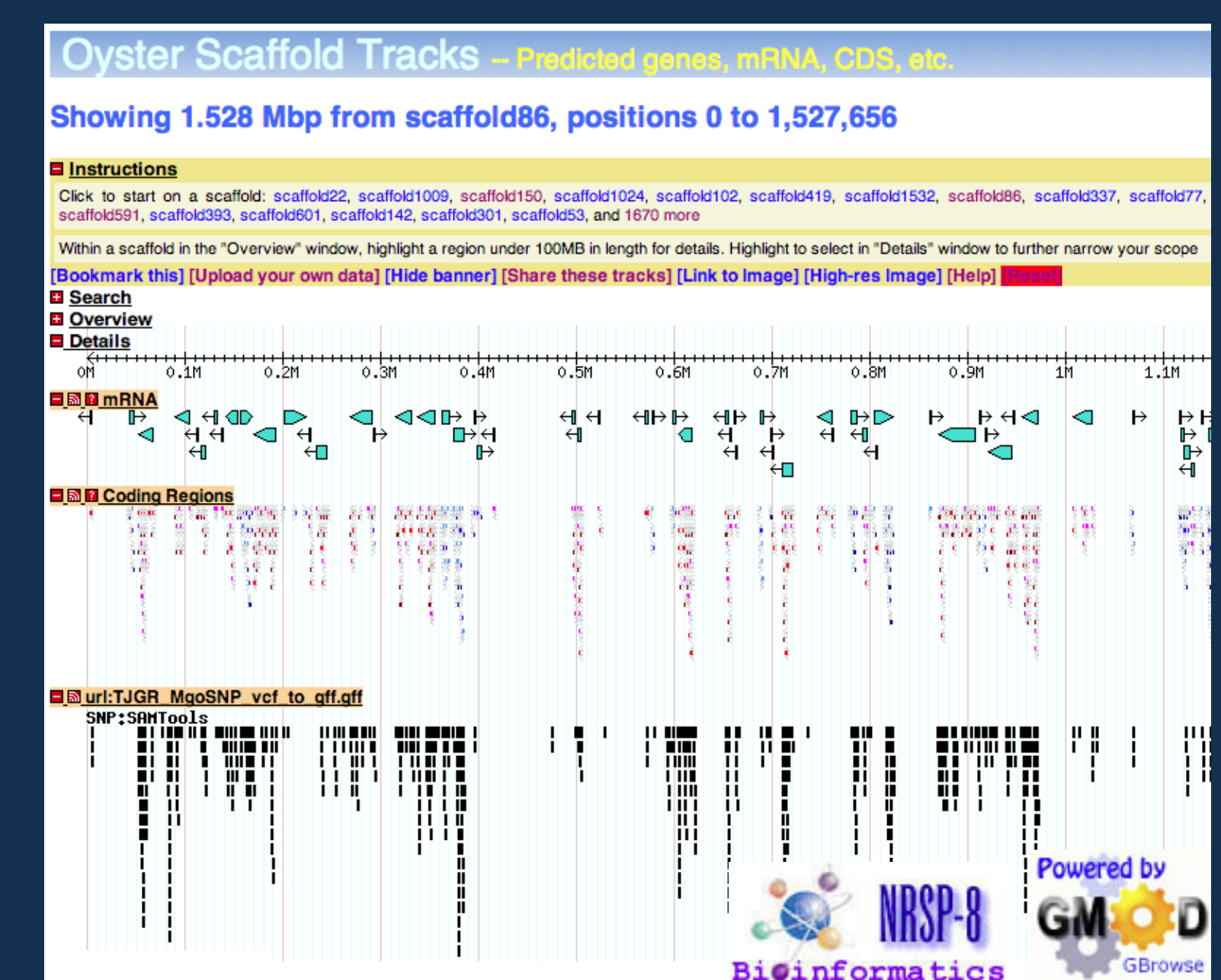
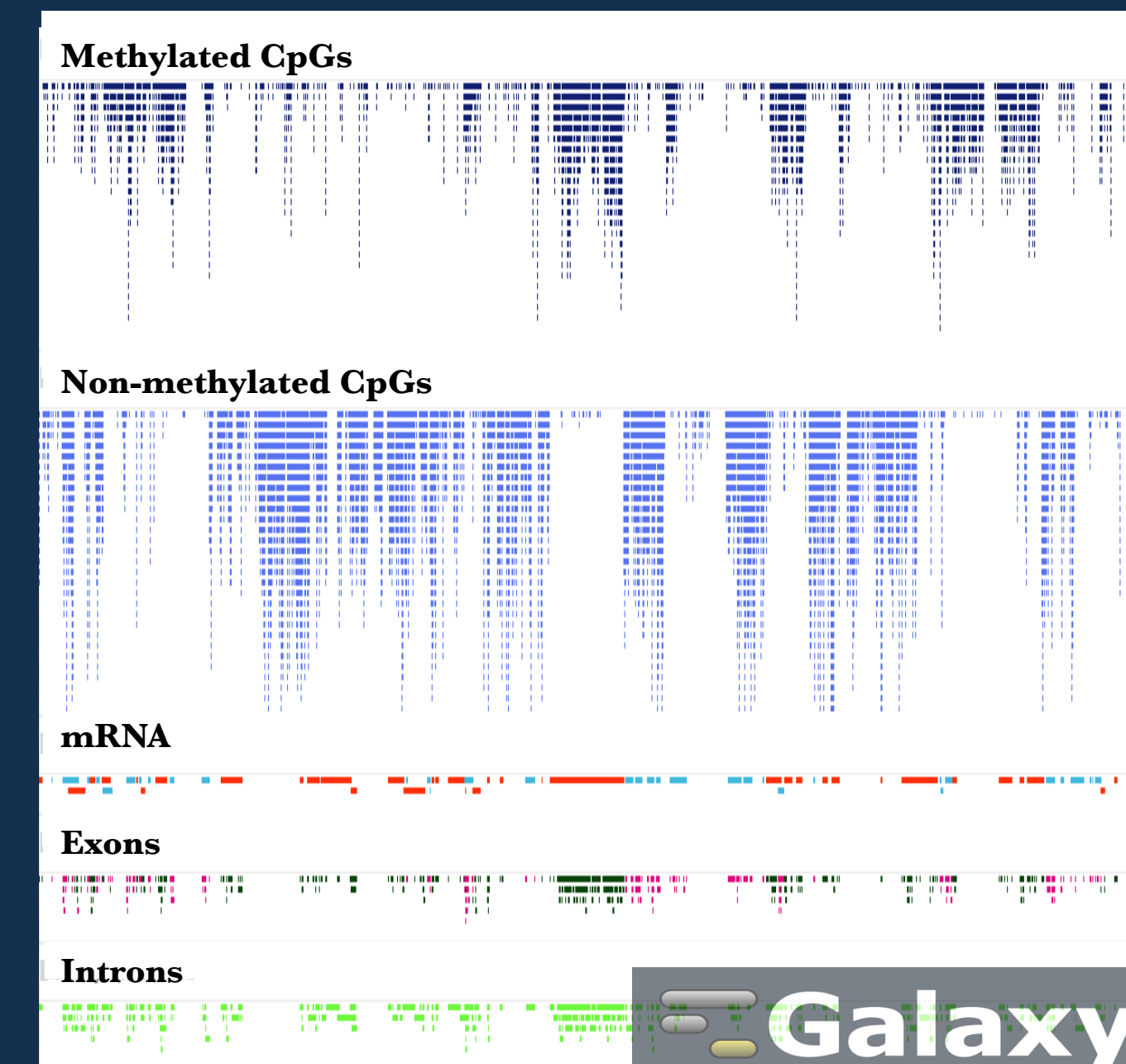


### All CpGs

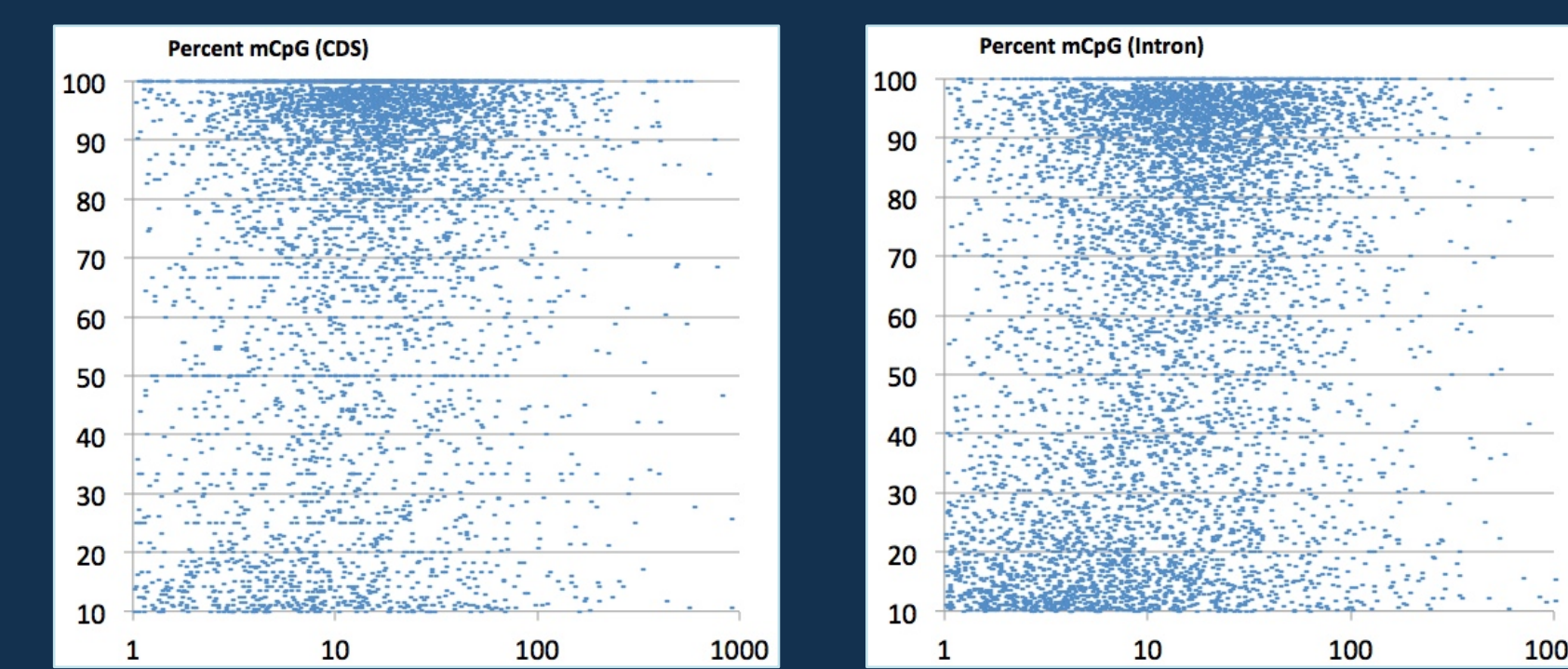


Exons  
Introns  
Other

## Genomic Visualization Tools



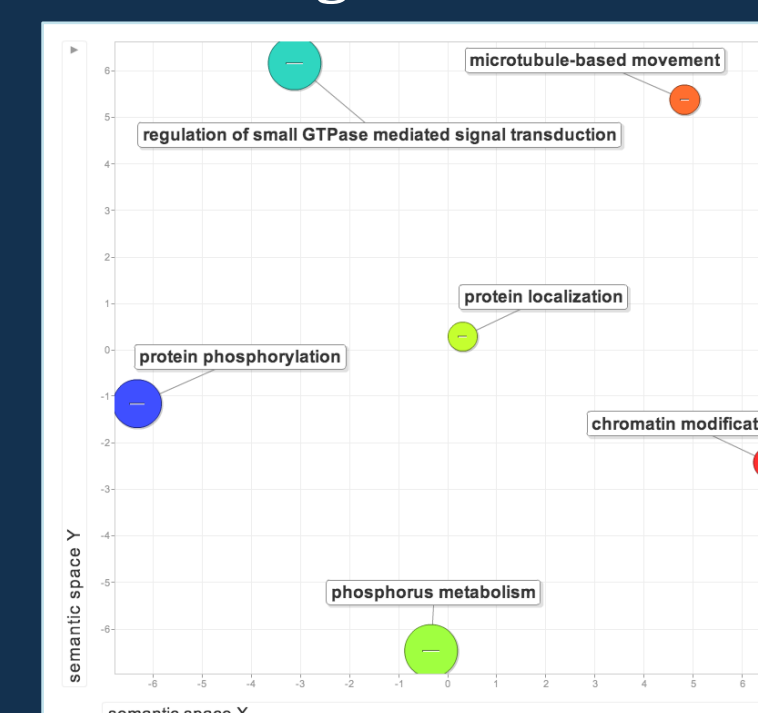
## Gene Body Methylation and Expression



Gene Expression in Male Gonad (RPKM) - Zhang et al 2012

## Gene Ontology and Enrichment Analysis

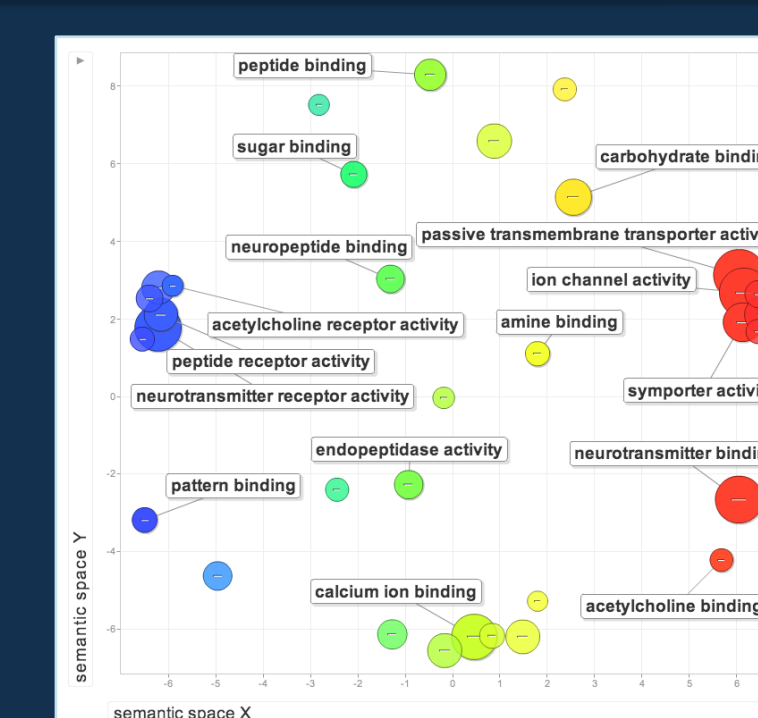
### Biological Process



### Molecular Function



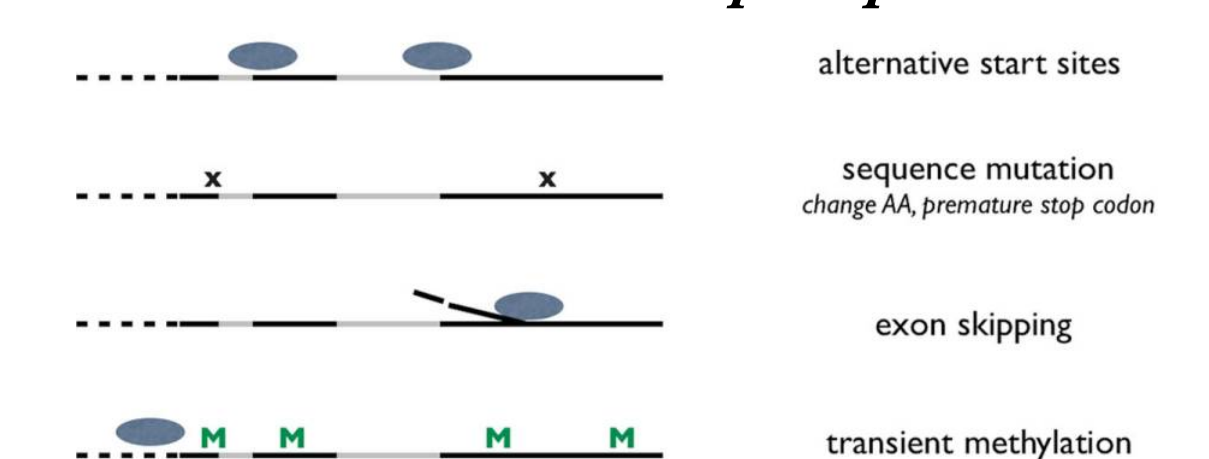
Genes that were predominantly (80%) **methylated**



Genes that were predominantly (80%) **unmethylated**

- DNA methylation is dispersed throughout the oyster genome, occurring primarily in expressed portions.
- Sparsely methylated genes are associated with inducible expression.

**Theory: Absence of methylation contributes to increased adaptive potential.**



## Additional Information

Supporting data including genomic feature tracks, links to software, an electronic version of this poster, and other resources are available at: <http://goo.gl/pqBE4>

