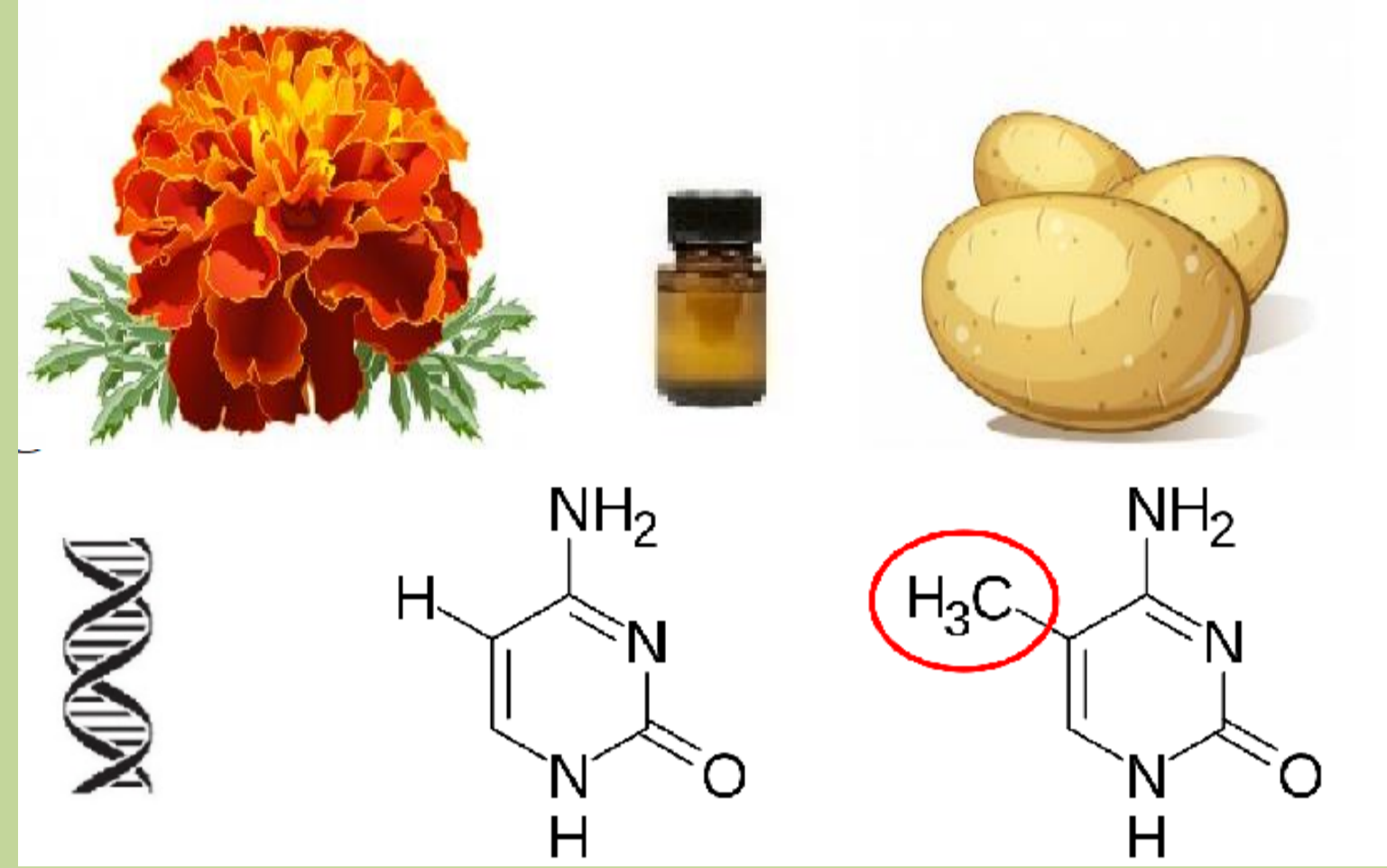


# HYPOTHESIS



- Potato plants exposed to French Marigold essential oil (EO) exhibit change in DNA methylation pattern.
- Repeated EO exposure cause prolonged alternations in DNA methylation affecting various potato defense responses.

# METHODOLOGY



- Potato plants were exposed to French Marigold EO for 3 consecutive days for 8 h each day and samples were collected 10 days after EO removal.
- **Whole-Genome Bisulfite Sequencing (WGBS)** was used to identify differentially methylated (DM) DNA sequences among control and EO-exposed plants.
- Various genetic features each at methylation ratio of 0.25 between control and treated samples were analyzed in **R programming language**.
- Functional annotation clustering of DM genes was performed with **DAVID database**.

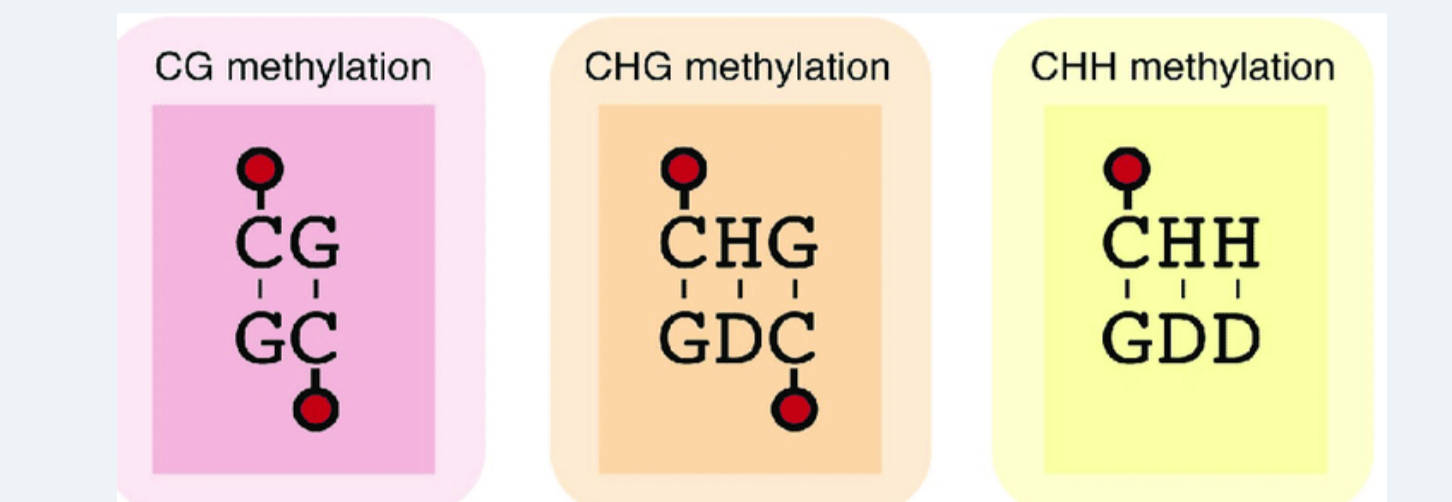
# CONCLUSION

- Potato plants repeatedly exposed to French Marigold EO had hypomethylated genes involved in various defense response mechanisms.
- Since hypomethylation is associated with increased gene expression, exposed potato plants could possibly have enhanced defense response to biotic stress.



# French Marigold essential oil affected DNA methylation in potato

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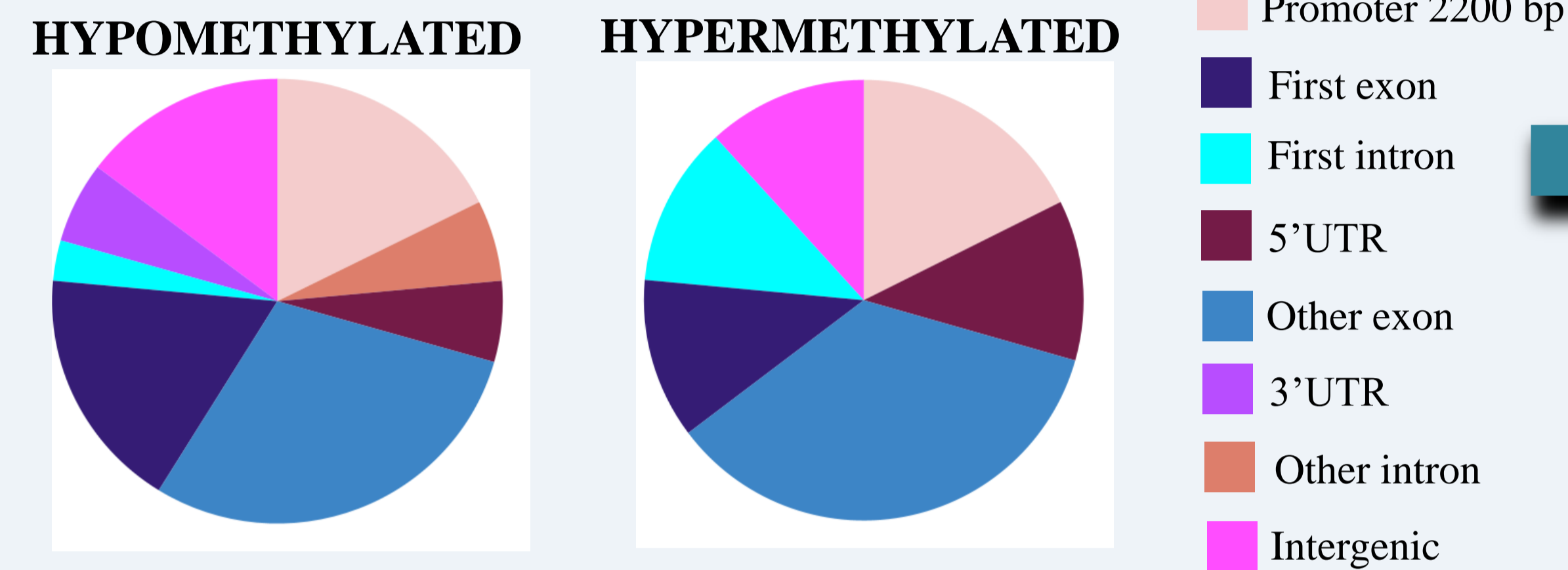


**Number of analyzed cytosines**  
(minimum number of reads = 10)

|     | Control  | Treatment |
|-----|----------|-----------|
| CG  | 12091859 | 4803772   |
| CHG | 2509     | 865       |
| CHH | 1223     | 357       |

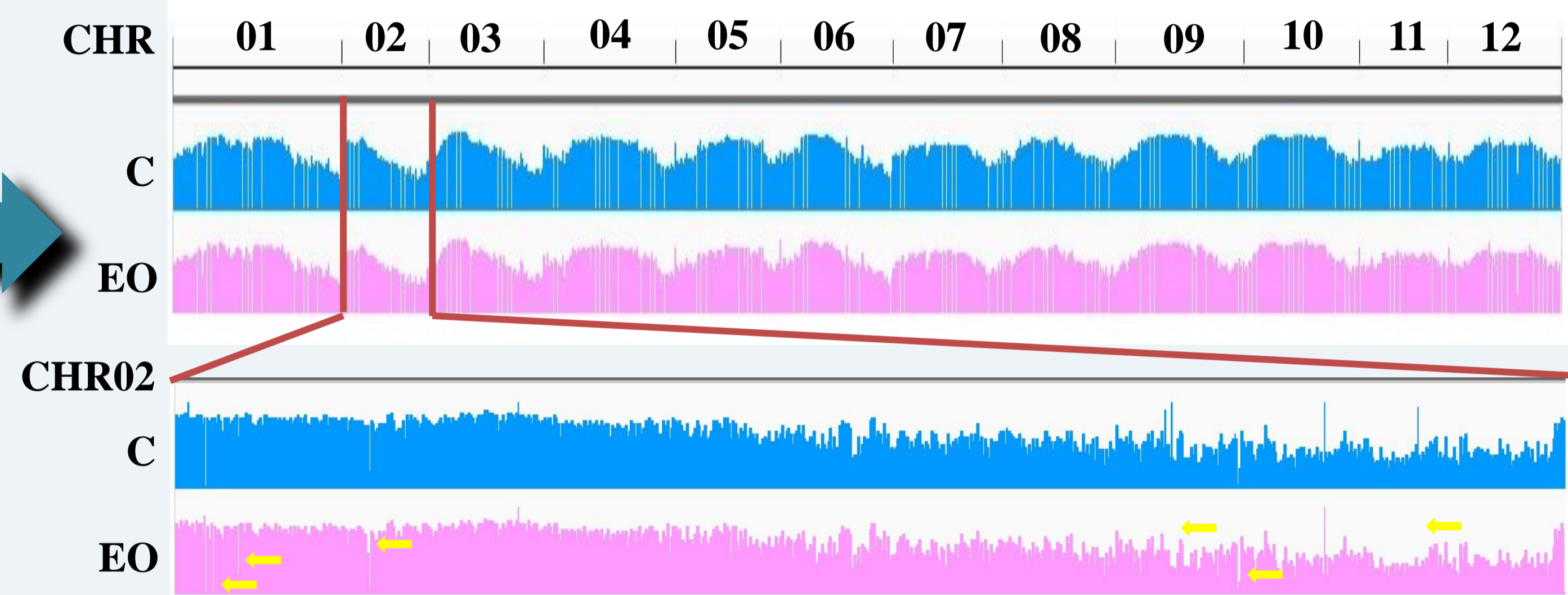
Differential methylation is predominant in **CG context** in comparison to CHG and CHH context (H = A, T or C)

## Proportion of hypo- and hypermethylated genetic features between control and EO-exposed potato



The average methylation level of the whole genome was **72.29%** in control and **69.23%** in exposed samples

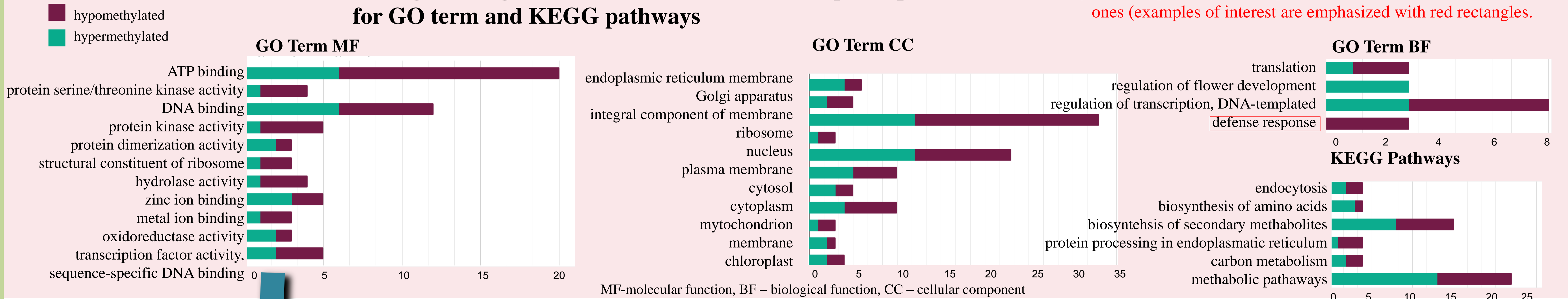
## DNA methylation profiles in the CG cytosine context for WGBS analysis of control and EO-exposed potato



Chromosome 2 has the biggest difference in methylation proportion between control and EO-exposed plants.

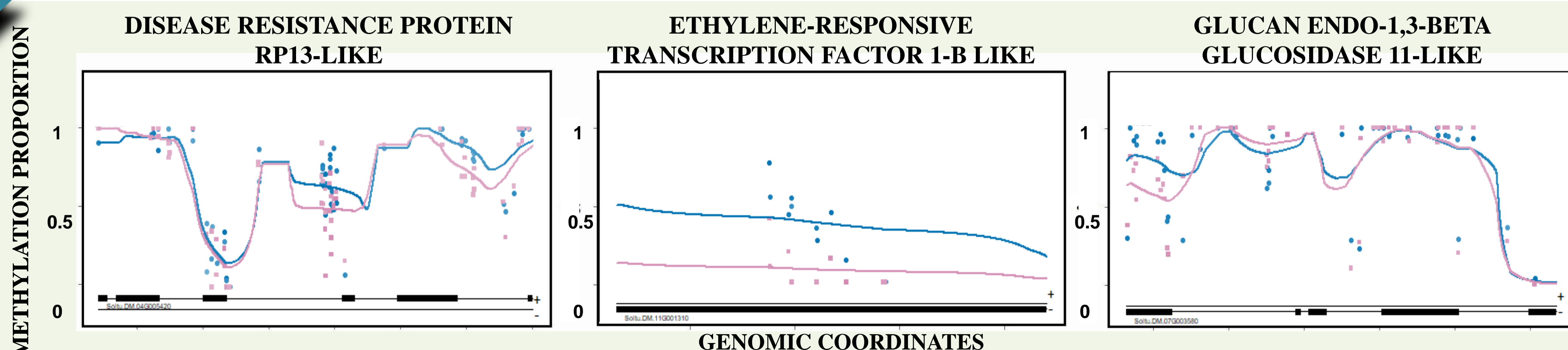
In general, hypomethylated sequences outnumbered hypermethylated ones (examples of interest are emphasized with red rectangles).

## Functional annotation clustering of DM genes between control and EO-exposed plants for GO term and KEGG pathways



## Differential methylation of genes involved in defense responses between control and EO-exposed potato

- control
- treatment



Local methylation profiles displaying the methylation at DM genes involved in various defense responses in potato. Each point on the graph represents methylation proportion of individual cytosines, in potato control (blue) or EO-exposed (pink). Black boxes represent exons.