

Introduction - Studies and Statistics

IMG contains methylomics data from various studies. These data can be explored starting with the landing page illustrated in Figure 1.

Methylomics Experiments

Experiments | Stats by Chemistry | Explore Motifs | Stats by Function

Select All | Clear All

Filter column: Unique Motifs | Filter text: | Apply ?

Export | Page 1 of 5 << first < prev 1 2 3 4 5 next > last >> 100

Column Selector | Select Page | Deselect Page

Select	ID	Experiment Name	Chemistry Type	Total Samples	Unique Motifs	Domain	Genome
<input type="checkbox"/>	49	Leptolyngbya_sp_PCC_6406_native_C2	native C2	1	18	B	Leptolyngbya_sp_PCC_6406
<input type="checkbox"/>	130	Marinobacter_sp_P6-C4	P6-C4	1	17	B	Marinobacter_sp_LVR2A5A20
<input type="checkbox"/>	137	Methanosarcina_sp_SMA-21_P4-C2	P4-C2	1	16	A	Methanosarcina_soligelidi_SMA-21
<input type="checkbox"/>	274	Synechococcus_sp_P6-C4	P6-C4	1	15	B	Synechococcus_sp_PCC_7002
<input type="checkbox"/>	148	Marinobacter_sp_LV10R510-11A_P6-C4	P6-C4	1	14	B	Marinobacter_sp_LV10R510-11A
<input type="checkbox"/>	330	Olsenella_umbonata_P6-C4	P6-C4	1	14	B	Olsenella_umbonata_DSM_22620
<input type="checkbox"/>	405	Bradyrhizobium_erythrophlei_P6-C4	P6-C4	1	14	B	Bradyrhizobium_erythrophlei_GAS138
<input type="checkbox"/>	211	Corynebacterium_mycetoides_P6-C4	P6-C4	1	13	B	Corynebacterium_mycetoides_DSM_20632
<input type="checkbox"/>	275	Cyanotheca_sp_ATCC_51142_P6-C4	P6-C4	1	13	B	Cyanotheca_sp_BH68_ATCC_51142
<input type="checkbox"/>	301	Nonlabens_sp_Hel1_33_55_P6-C4	P6-C4	1	13	B	Nonlabens_sp_Hel1_33_55
<input type="checkbox"/>	326	Arthrobacter_woluensis_P6-C4	P6-C4	1	13	B	Arthrobacter_woluensis_DSM_10495
<input type="checkbox"/>	333	Corynebacterium_timonense_P6-C4	P6-C4	1	13	B	Corynebacterium_timonense_DSM_45434
<input type="checkbox"/>	386	Kosakonia_oryzae_P6-C4	P6-C4	1	13	B	Kosakonia_oryzae_D4
<input type="checkbox"/>	422	Pseudovibrio_P6-C4	P6-C4	1	13	B	Pseudovibrio_sp_Tun.PHSC04-5.14
<input type="checkbox"/>	457	Synechococcus_sp_P6-C4	P6-C4	1	13	B	Synechococcus_sp_7002

Figure 1. Methylomics landing page – Experiments tab

The *Experiments* tab on the landing page lists all the methylomics studies in IMG, the genome for the study, the chemistry type used, total samples, and the number of unique motifs (Fig. 1).

The *Stats by Chemistry* tab lists the present motif modifications and the frequency of modification of each motif for each chemistry type (Fig. 2).

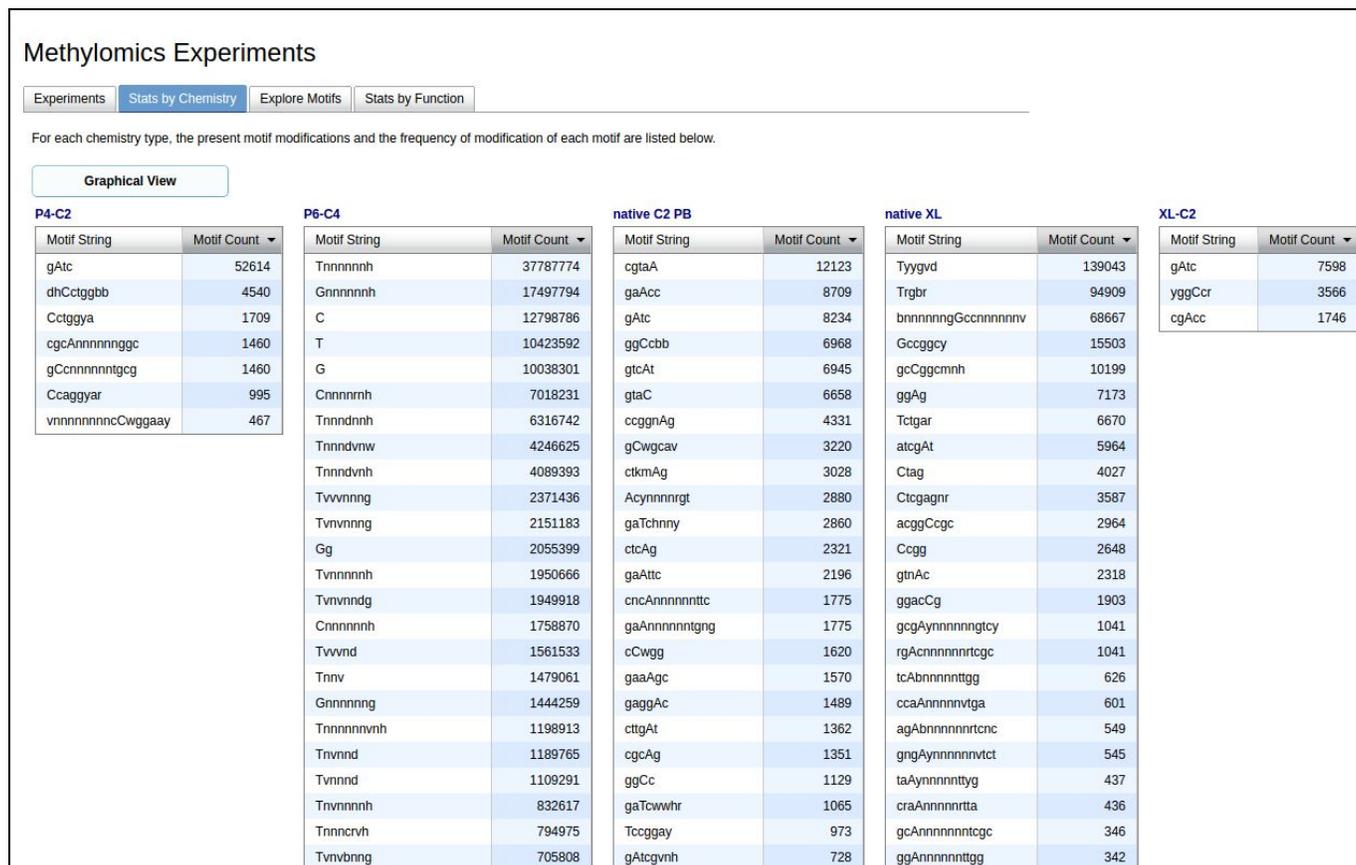


Figure 2. Methylomics landing page – Stats by Chemistry tab – table view

Stats by Chemistry can also be displayed graphically – see Fig. 2b below – by clicking on “Graphical View”.

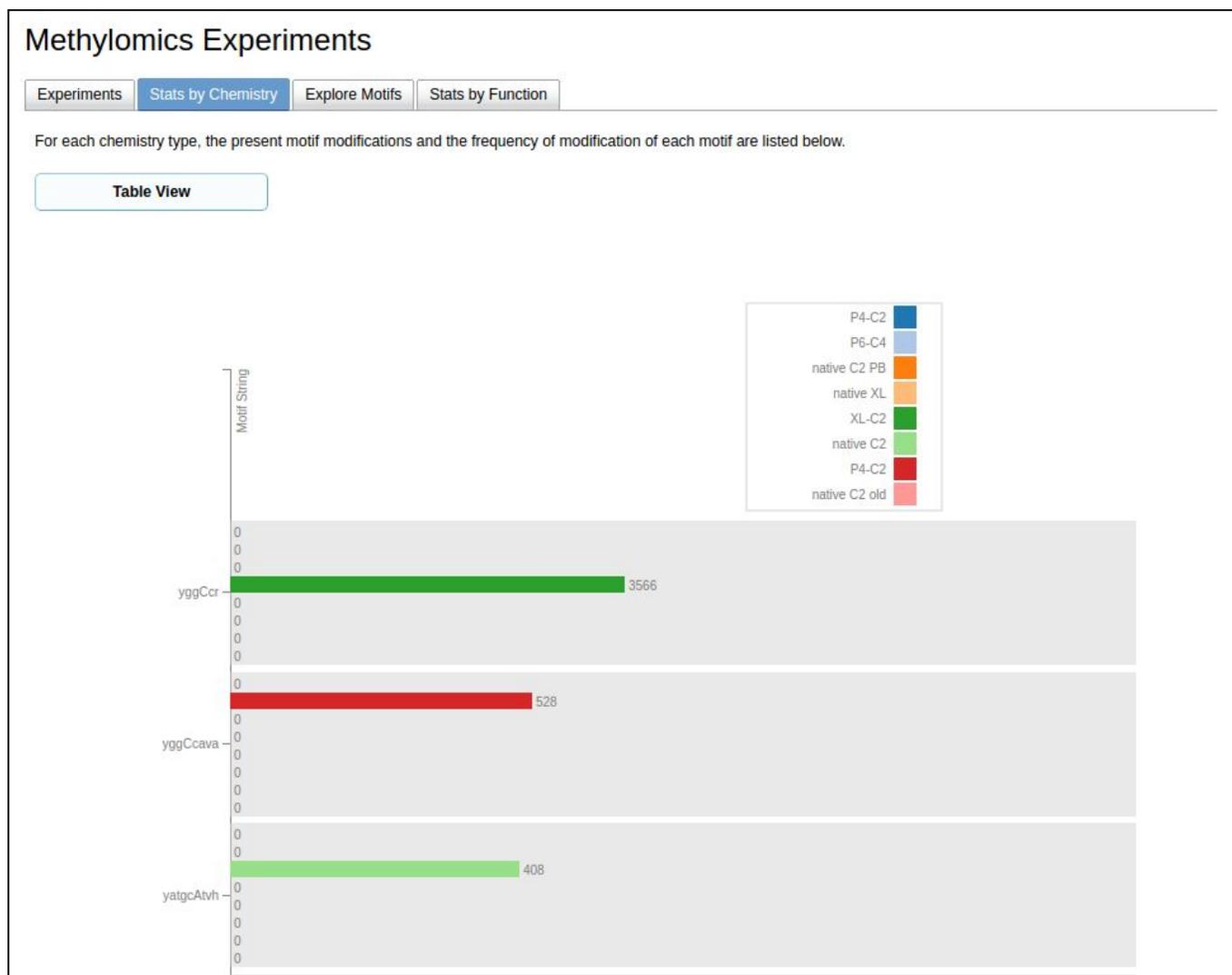


Figure 2b. Stats by Chemistry tab – graphical view

The *Explore Motifs* tab - each motif can be observed in multiple genomes under various experimental conditions (Fig. 3). Choose *Stats by Motifs* to see a chart displaying the fraction modified for each selected motif (Fig. 3b). Choose *Generate Tree* to view the occurrence of motifs in the context of the taxonomic lineage of the genomes in which they are observed (Fig. 3c).

Methylomics Experiments

Experiments Stats by Chemistry **Explore Motifs** Stats by Function

Each motif can be observed in multiple genomes under various experimental conditions. Choose [Stats by Motifs](#) to see a chart displaying the fraction modified for each selected motif. You may select all motifs for this function. Choose [Motifs by Taxonomy](#) to view the occurrence of motifs in the context of the taxonomic lineage of the genomes in which they are observed. You may select up to 7 motifs for this function.

Select All Clear All

- A
- AAAAGAGGB
- AAAAGTTNC
- AAAT
- AAAYNNNNNGTTA
- AAAYNNNNNTGGC
- AAAYNNNNNTCNYC
- AACACC
- AACATC
- AACCA
- AACGAC
- AACNNNNCTWC
- AACNNNNNGTCC
- AACNNNNNGTGC
- AACNNNNNTAC
- AAGAAG
- AAGAYC
- AAGCAG
- AAGGAC
- AAGGTAVYD
- AAGNNNNCTGC
- AAGNNNNNTCAC
- AAGNNNNNTGGA
- AAGNNNNNTGGC
- AAGNNNNNTGGG
- AAGNNNNRTCC
- AAGNNNTACA
- AAGNNRTGG
- AATAYNNNNNCTC
- AATT

Generate Tree Stats by Motifs

Figure 3. Methylomics landing page – Explore Motifs tab

Methylation modification fraction for selected motifs

Each motif can be observed in multiple genomes under various experimental conditions. The chart below displays the fraction modified for each selected motif.

[View input file](#)

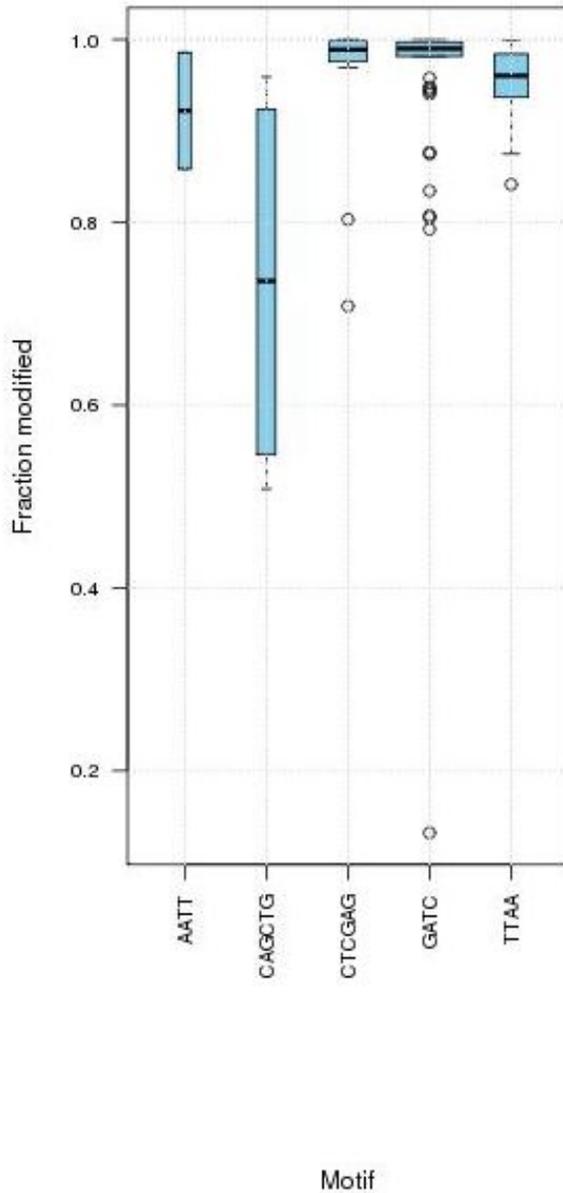


Figure 3b. Explore Motifs – Stats by Motifs

Radial Tree Distribution ?

Radial Tree Export

In the current view, the tree is rendered by **family** and colored by **phylum**. To change these settings, click on the "Customize Tree" button. Clicking on a node in the tree brings up the details for that node on the right of the tree.

- 1. ■ AATT
- 2. ■ CAGCTG
- 3. ■ CTCGAG
- 4. ■ GATC
- 5. ■ TTA

Customize Tree

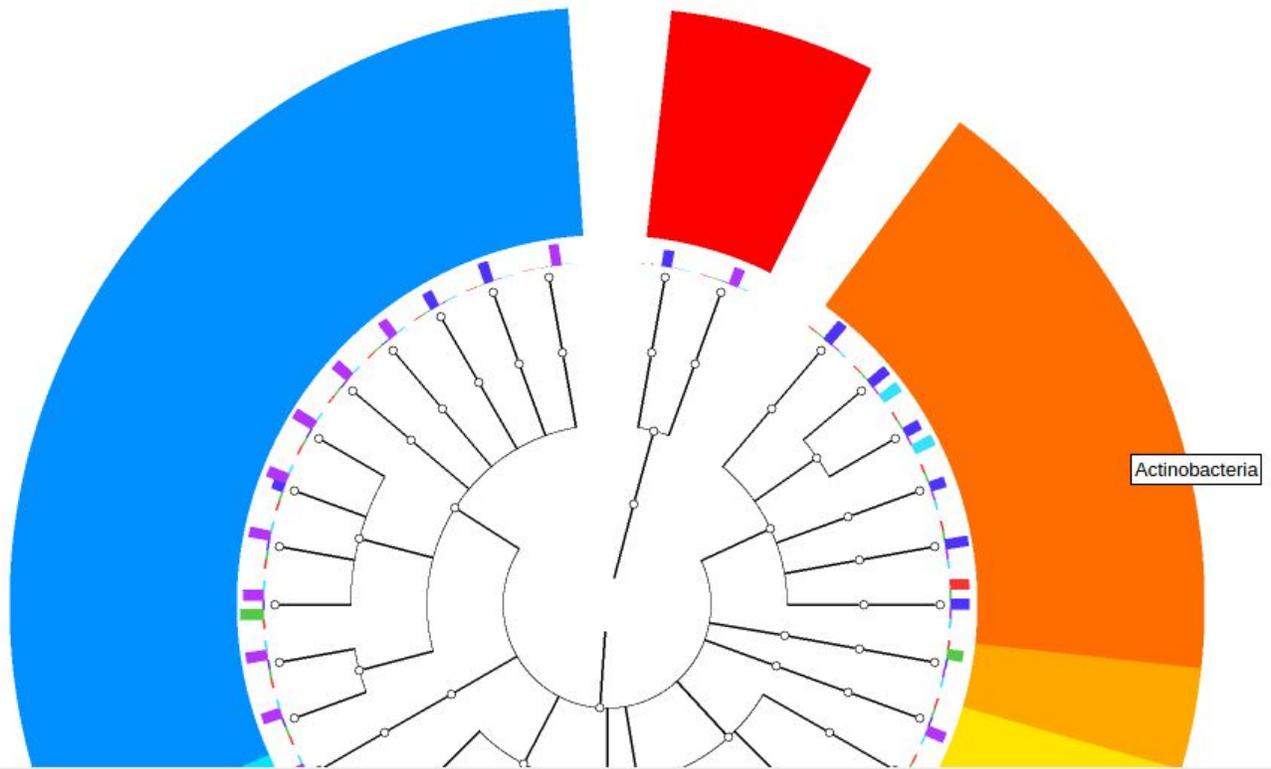


Figure 3c. Explore Motifs – Motifs by Taxonomy

The *Stats by Function* tab displays the modification count for a given function for each experiment in a heat map (Fig. 4).

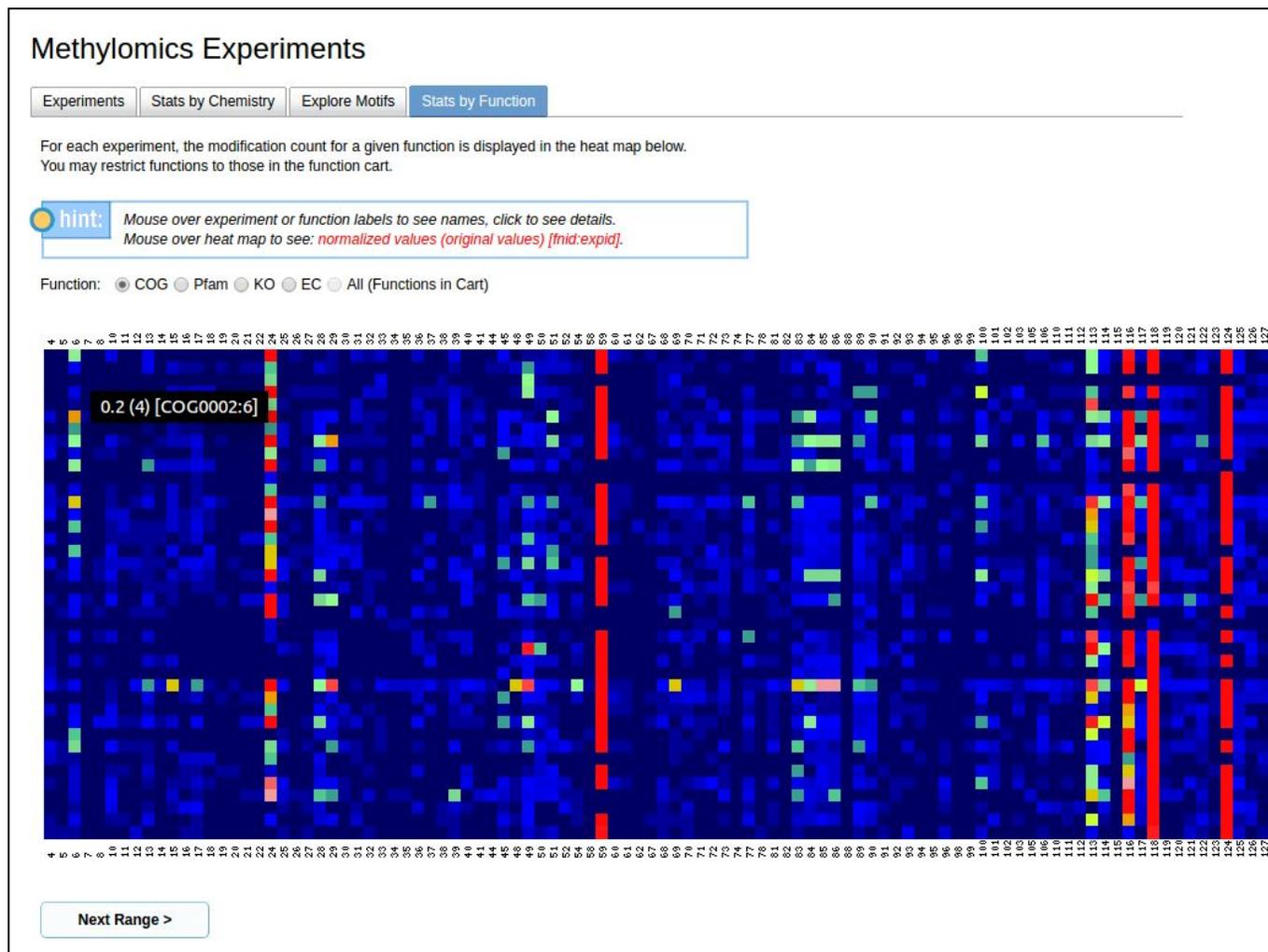


Figure 4. Methyloomics landing page - Stats by Function tab

Individual Methylomics Study Details

There are 2 ways to get to an individual experiment page. The first way is from the genome details page (Fig. 5b). If a genome has associated methylomics studies, there will be a link to “Methylomics Experiments” at the top of the details page. The second way is from the main Methylomics landing page by clicking on an Experiment name (Fig. 1).

Methylomics Experiment ? 📖

Genome: [Meiothermus ruber 21, DSM 1279](#)
 Experiment: [Meiothermus_ruber_DSM1279_native_C2](#)

Select Samples View in GBrowse

Select	Sample ID	Sample Name	Unique Motifs
<input type="checkbox"/>	6	Meiothermus_ruber_DSM1279_native_C2	10

Select All Clear All

Figure 5. Example of a Methylomics Study – Experiment page

Meiothermus ruber 21, DSM 1279

Add to Genome Cart Browse Genome BLAST Genome Download Data

About Genome

- Overview
- Statistics
- Methylomics Experiments
- Genes

Overview

Study Name (Proposal Name)	A Genomic Encyclopedia of Bacteria and Archaea (GEBA)
Organism Name	Meiothermus ruber 21, DSM 1279
Taxon ID	646564545
NCBI Taxon ID	504728
GOLD ID in IMG Database	Study ID: Gs0000008 Project ID: Gp0001170
GOLD Analysis Project Id	Ga0001338
GOLD Analysis Project Type	Genome Analysis
Submission Type	Primary
JGI Analysis Product Name	Microbial Improved Draft Isolate Genome
JGI Analysis Project Type	Genome Analysis
External Links	JGI Portal ; NCBI/RefSeq:NC_013946
Lineage	Bacteria ; Deinococcus-Thermus ; Deinococci ; Thermales ; Thermaceae ; Meiothermus ; Meiothermus ruber
Sequencing Status	Finished
Sequencing Center	DOE Joint Genome Institute (JGI)

Figure 5b. Genome Detail page

To view the detailed table (Fig. 6) of all the base modifications for a given sample, click on the sample name from the study page (Fig. 5). The Chromosome Viewer button links to the chromosome viewer displaying areas of methylation (Fig. 7).

Base Modifications

Sample: *Meiothermus_ruber_DSM1279_native_C2*

[Chromosome Viewer](#)

[Meiothermus_ruber_DSM1279_native_C2](#)

Filter column: ID Filter text: Apply

Export Page 1 of 564 << first < prev 1 2 3 4 5 6 7 8 9 10 next > last >> 100

Column Selector Select Page Deselect Page

Select	ID	Motif Context	Motif String	Start Coord	End Coord	Methylation Coord	Strand	Score	Coverage	Scaffold ID
<input type="checkbox"/>	16911	CTCGCTTCGAGCTCAAGGTAATCCAGGAAAGCCTGTTACG	aAtt	273	276	274	+		28	646564567
<input type="checkbox"/>	16912	CCTGAACAGGCTTTCCTGGAATTACCTTGAGCTCGAAGCGA	aAtt	273	276	275	-		36	646564567
<input type="checkbox"/>	16913	TCCAAGTACATCTTCGAGAATTTGTGGTGGGGCAGAACA	aAtt	373	376	374	+		31	646564567
<input type="checkbox"/>	16914	TTGTTCTGCCCCACCACAAAATTCTCGAAGATGACTTGGG	aAtt	373	376	375	-		38	646564567
<input type="checkbox"/>	16915	TGGAGTACATCGCCAGGCAAATTACCTCCAACATCCGCGAG	aAtt	939	942	940	+		42	646564567
<input type="checkbox"/>	16916	GCTCGCGGATGTTGGAGGTAATTTGCCTGGCGATGTACTCC	aAtt	939	942	941	-		36	646564567
<input type="checkbox"/>	16917	AGGTCGTGATTCTCTGTCAAATTGCCATGTACCTGATCCGC	aAtt	1179	1182	1180	+		46	646564567
<input type="checkbox"/>	16918	CGCGGATCAGGTACATGGCAATTTGACGAGGAATCACGACC	aAtt	1179	1182	1181	-		43	646564567
<input type="checkbox"/>	16919	CCCATGCCTCGTACCAGAAATTTGGGCGAGTCTTCGATGGG	aAtt	1227	1230	1228	+		49	646564567
<input type="checkbox"/>	16920	GCCCATCGAAGAACTGCCCAATTTCCGGTAGCGAGGCATGG	aAtt	1227	1230	1229	-		45	646564567
<input type="checkbox"/>	16921	CTTCTCGTATCGGCTGGTAATTAATAACATAATCACCCAG	aAtt	1388	1391	1389	+		45	646564567
<input type="checkbox"/>	16922	CCTGGTGATTATGTTATTTAATTACCCAGCCGATACGAGAA	aAtt	1388	1391	1390	-		48	646564567
<input type="checkbox"/>	16923	AGGCCTGGAAGTGTGGATAAATTAATAGCCCTGTGGATAA	aAtt	1427	1430	1428	+		49	646564567
<input type="checkbox"/>	16924	GTTATCCACAGGGCTAATTAATTTATCCACAGTCCAGGCC	aAtt	1427	1430	1429	-		46	646564567
<input type="checkbox"/>	16925	CTGGAAGTGTGGATAAATTAATAGCCCTGTGGATAACTCT	aAtt	1431	1434	1432	+		46	646564567
<input type="checkbox"/>	16926	CAGAGTTATCCACAGGGCTAATTAATTTATCCACAGTTCCA	aAtt	1431	1434	1433	-		45	646564567
<input type="checkbox"/>	16927	TTGTCCACAGGTTATGCACAATTTCCACACCTTTTATCCA	aAtt	1562	1565	1563	+		52	646564567
<input type="checkbox"/>	16928	GTGGATAAAAGGTGTGGAAATTTGCATAACCTGTGGACA	aAtt	1562	1565	1564	-		43	646564567

Figure 6. Base modifications for a sample

Chromosome Viewer - METHYLATION

Genome: [Meiothermus ruber 21, DSM 1279](#)

Scaffold: [Meiothermus ruber DSM 1279 chromosome: NC_013946](#)

(3097457bp, gc=0.63, coordinates 1-500000)

Switch coloring to:

hint: Mouse over a gene to see details.
Methylated bases are marked by dots, RNAs in **black**, Pseudo genes in white
My Gene in cyan or dashes
Gene(s) with protein is marked by a purple bar
Gene(s) in Gene Cart is marked by a blue bar
||||| CRISPR array

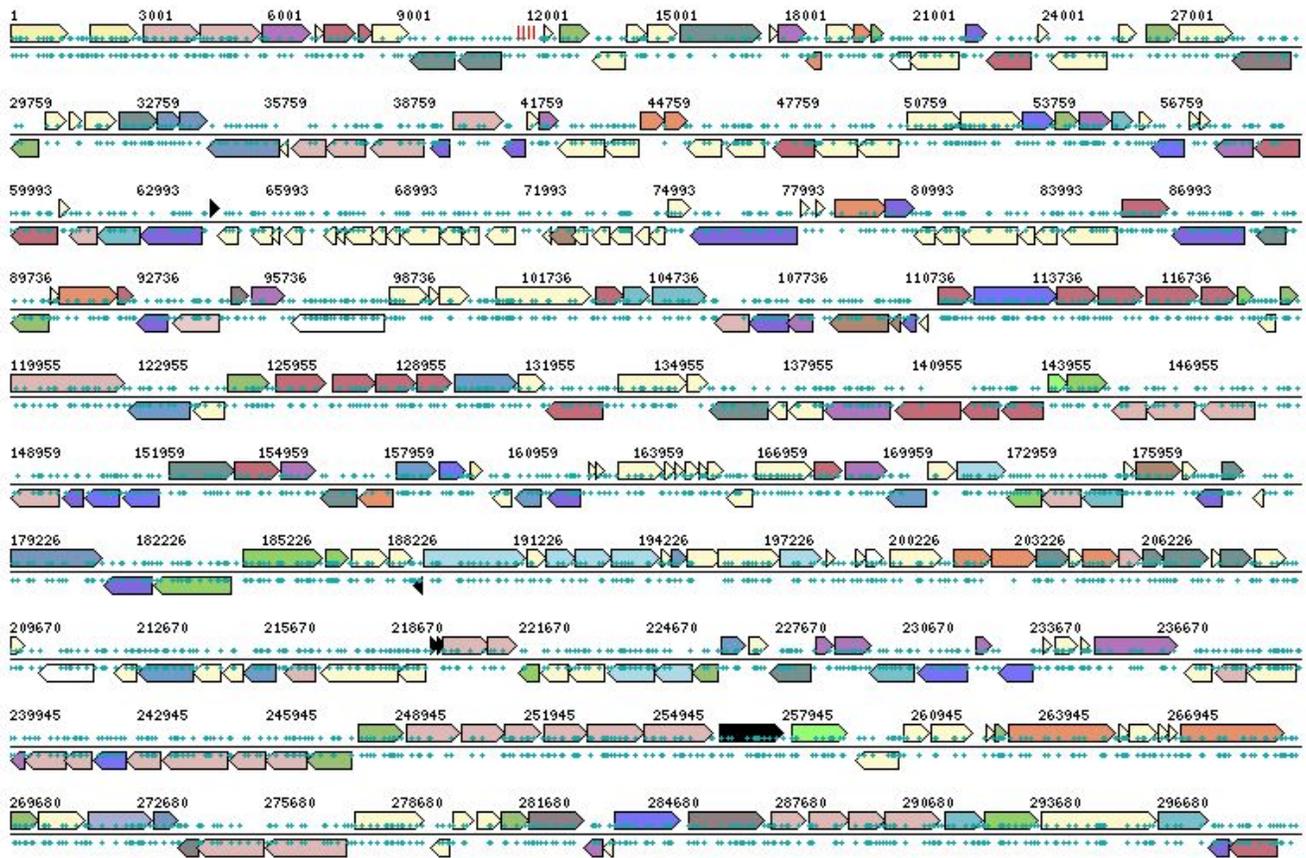


Figure 7. Chromosome Viewer – methylation display

To view the summary of motifs for an individual study, click on the count of unique motifs for a given sample from the study page (Fig. 5).

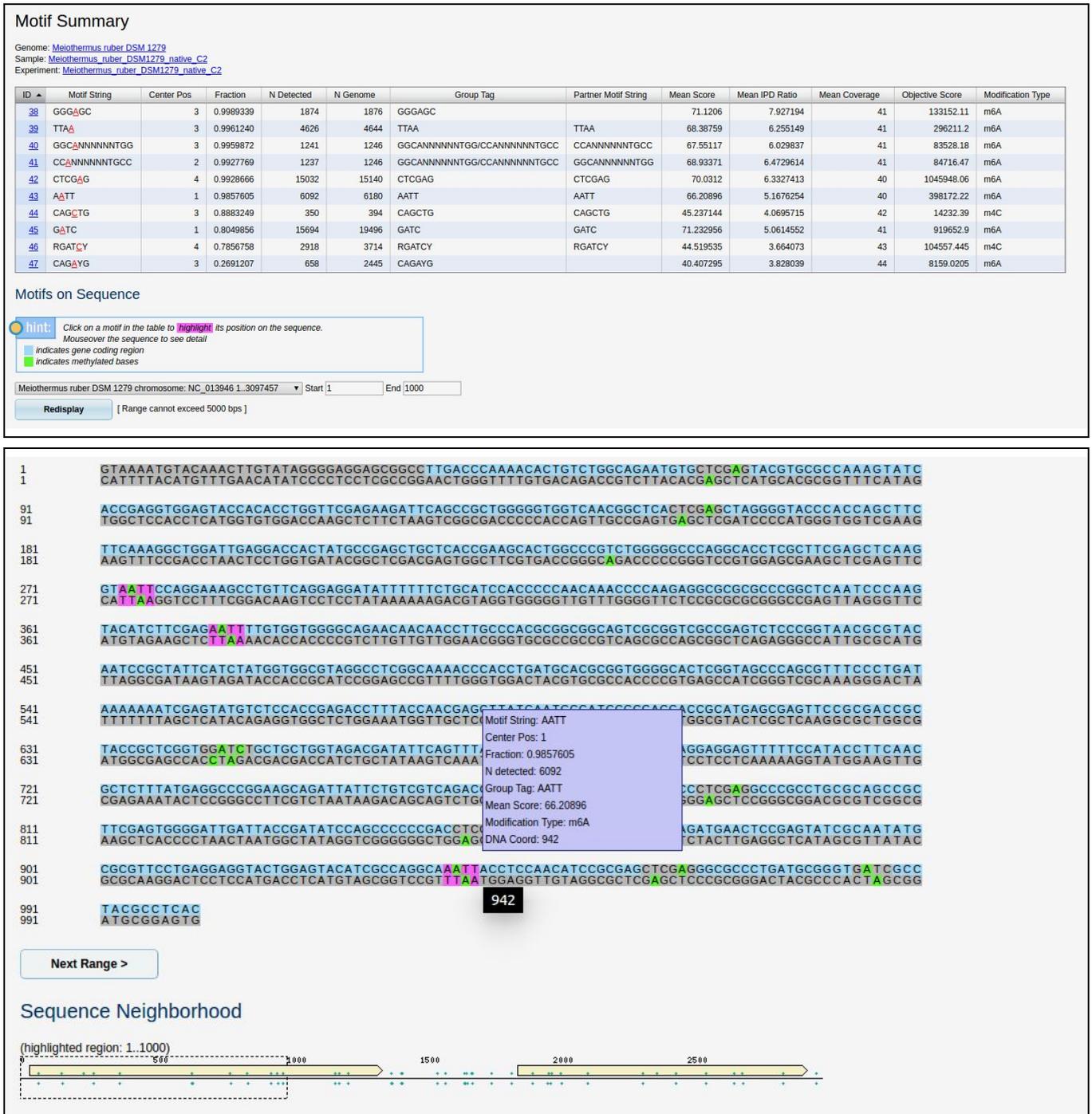


Figure 8. Motif Summary for a methylomics sample

The Motif Summary displays all the details of the motifs for the selected sample in a table. Below the table is a detailed chromosome sequence and a gene neighborhood for the current

sequence range. Clicking on any given motif in the table will highlight that motif on the chromosome sequence.