

微生物所测试技术论坛
第十八讲

生物信息学基础与 微生物基因组分析

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提纲

- 生物信息学概述
- 微生物基因组学分析
- 系统发生与进化分析

生物信息学

Bioinformatics is the application of computer science and information technology to the field of biology and medicine. Bioinformatics deals with algorithms, databases and information systems, web technologies, artificial intelligence and soft computing, information and computation theory, software engineering, data mining, image processing, modeling and simulation, signal processing, discrete mathematics, control and system theory, circuit theory, and statistics, for generating new knowledge of biology and medicine, and improving & discovering new models of computation. *(from Wikipedia)*

算法和软件

- In mathematics and computer science, an algorithm is an effective method expressed as a finite list of well-defined instructions for calculating a function. Algorithms are used for calculation, data processing, and automated reasoning. In simple words an algorithm is a **step-by-step procedure for calculations.** (*from Wikipedia*)
- Software is a set of **programs, procedures, algorithms** and its **documentation.**

算法很难？！怎么办？

- 对于一般的生物信息学应用需求，不一定需要了解算法的本质
- 软件是算法的表现形式，先接触软件再了解算法
- 和身边的生物信息学家探讨，应该采用什么样的软件
- 目前免费的生物信息学算法（软件）能够解决绝大部分生物信息学的需求
- 当现有的工具无法满足你的需求时：
 - 改良现有算法（如，改变参数，进行微调等）
 - 发明新的算法

数据库与应用平台

- NCBI Home
- Site Map (A-Z)
- All Resources
- Chemicals & Bioassays
- Data & Software
- DNA & RNA
- Domains & Structures
- Genes & Expression
- Genetics & Medicine
- Genomes & Maps
- Homology
- Literature
- Proteins
- Sequence Analysis
- Taxonomy
- Training & Tutorials
- Variation

Welcome to NCBI

The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information.


[About the NCBI](#) | [Mission](#) | [Organization](#) | [Research](#) | [RSS Feeds](#)

Get Started

- [Tools](#): Analyze data using NCBI software
- [Downloads](#): Get NCBI data or software
- [How-To's](#): Learn how to accomplish specific tasks at NCBI
- [Submissions](#): Submit data to GenBank or other NCBI databases

Genomic Structural Variation

dbVar archives large scale genomic variation data and associates defined variants with phenotypic information.



II 1 2 3 4 5 6 7

Popular Resources

- [BLAST](#)
- [Bookshelf](#)
- [Gene](#)
- [Genome](#)
- [Nucleotide](#)
- [OMIM](#)
- [Protein](#)
- [PubChem](#)
- [PubMed](#)
- [PubMed Central](#)
- [SNP](#)

NCBI News

NCBI will continue to operate SRA
13 Oct 2011
Subsequent to an announcement in February 2011 that NCBI was planning to phase out the

New NCBI News Issue
07 Sep 2011
New Feature Highlighter in the sequence databases and Simple Object Access Protocol

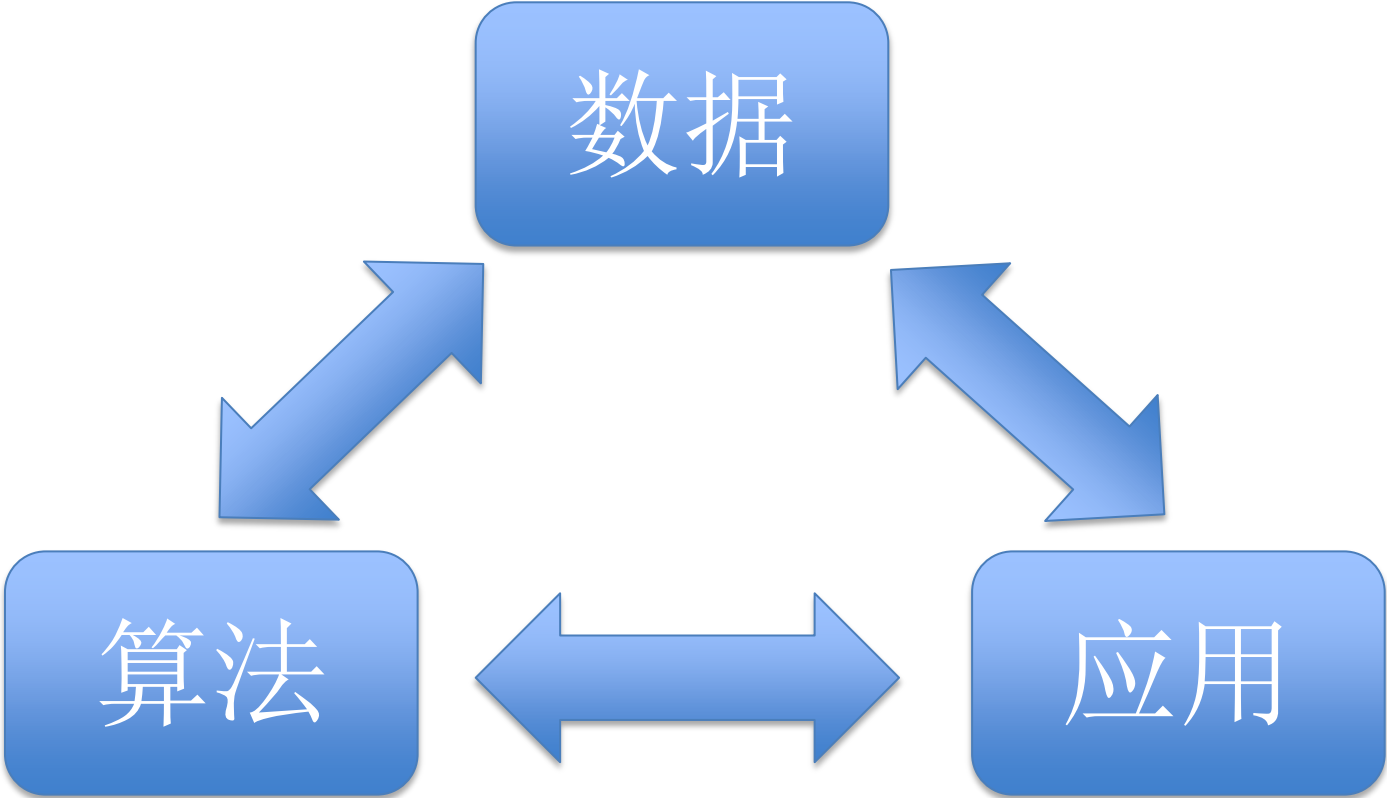
[More...](#)

数据库和网站是生物信息学最常见的应用形式之一

- 建立和使用针对特定领域的生物信息学数据库和信息平台（网站）是生物信息学的研究工作之一
- 建立数据标准是构建数据库的核心工作之一
- 数据库和信息平台（网站）是为生物学工作者服务的，要充分考虑他们的需求和使用习惯
- 数据库和平台建设要面向特定的生物学需求

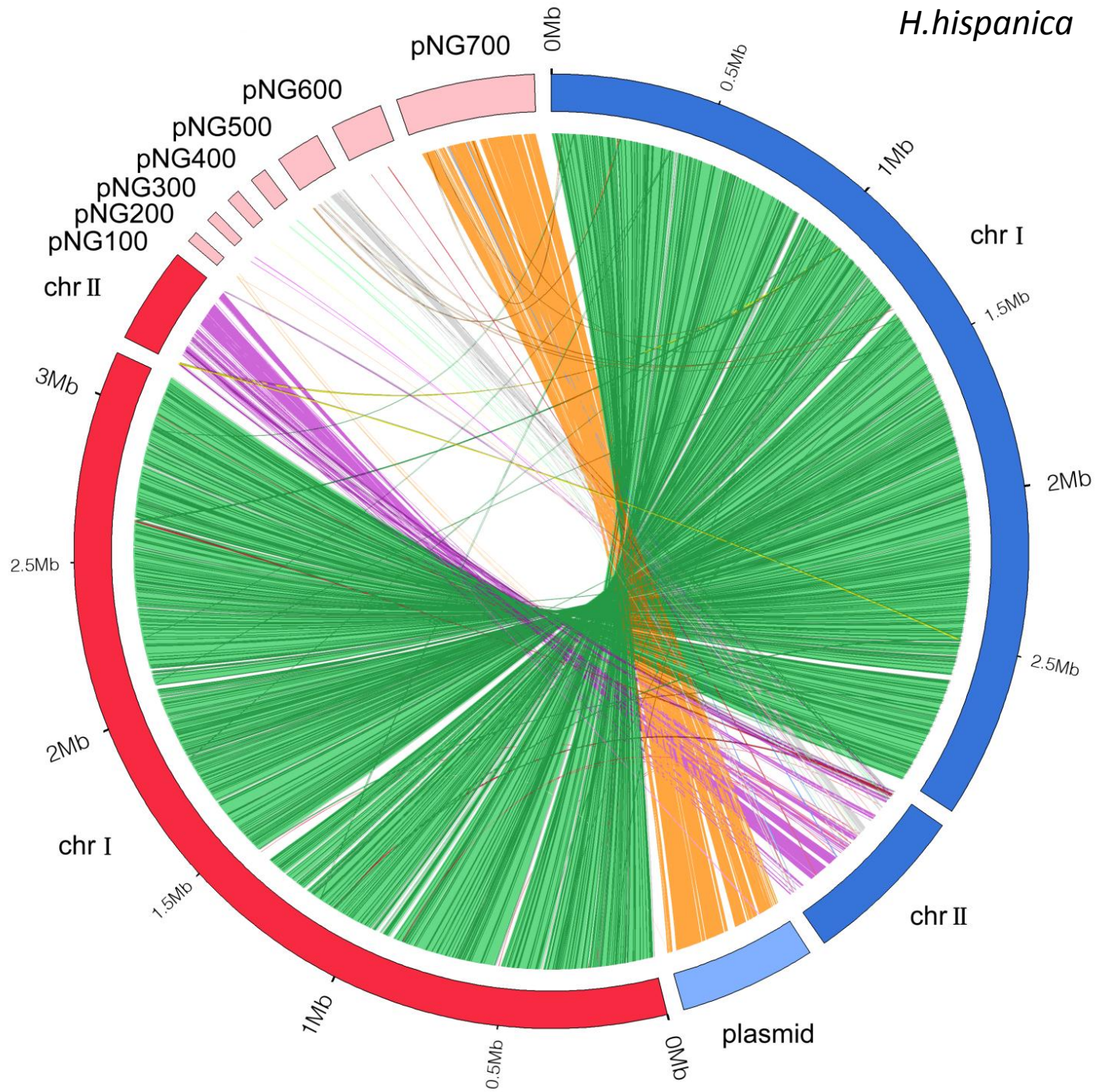
Applied bioinformatics

- Applying bioinformatics skills onto biological researches
 - Sequence analysis
 - Phylogenetics
 - Protein domain analysis
 - Data mining
 - Genome analysis
 -

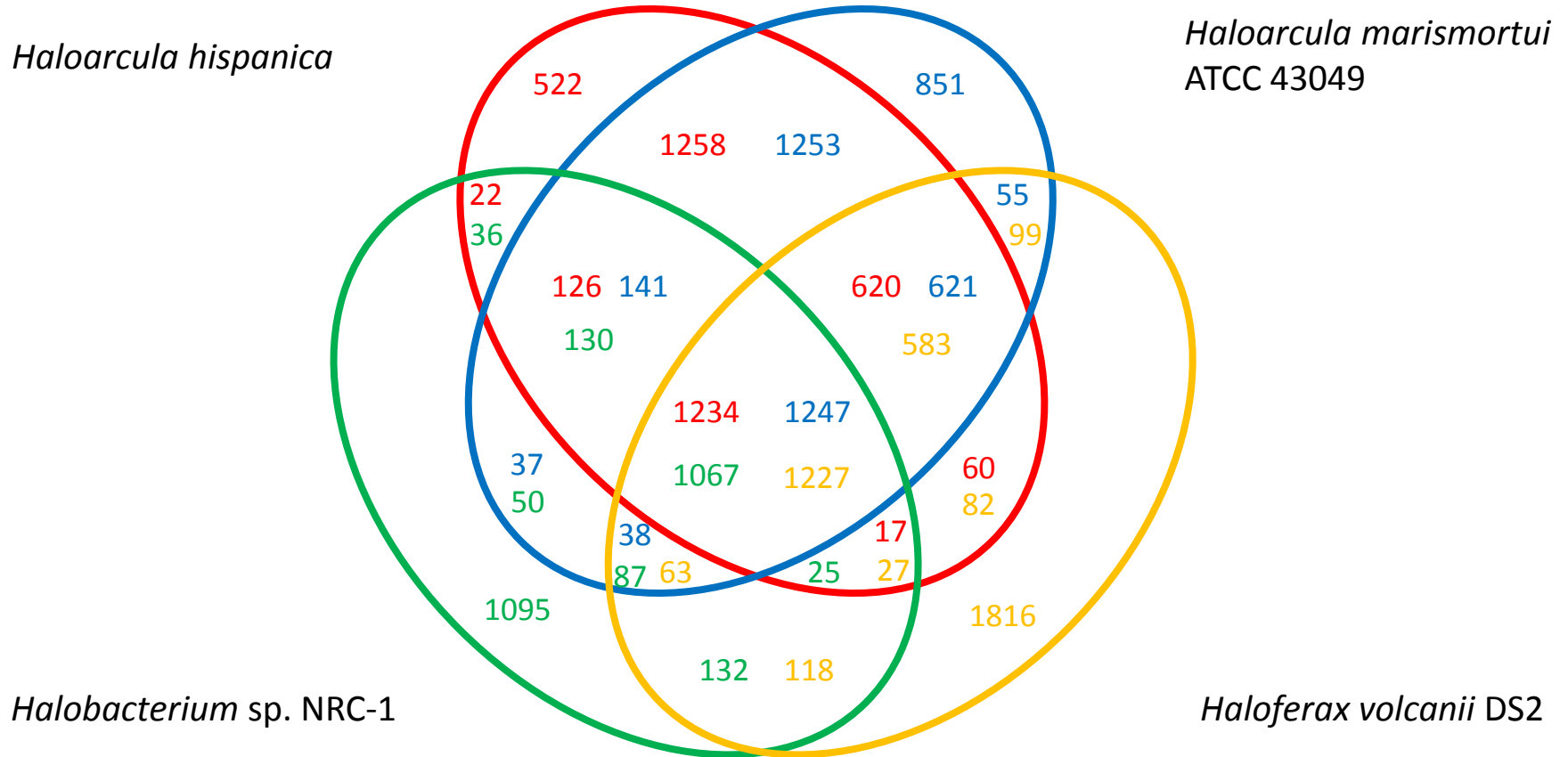


微生物基因组分析

H. hispanica



Venn diagram display of homologous proteins between four haloarchaea

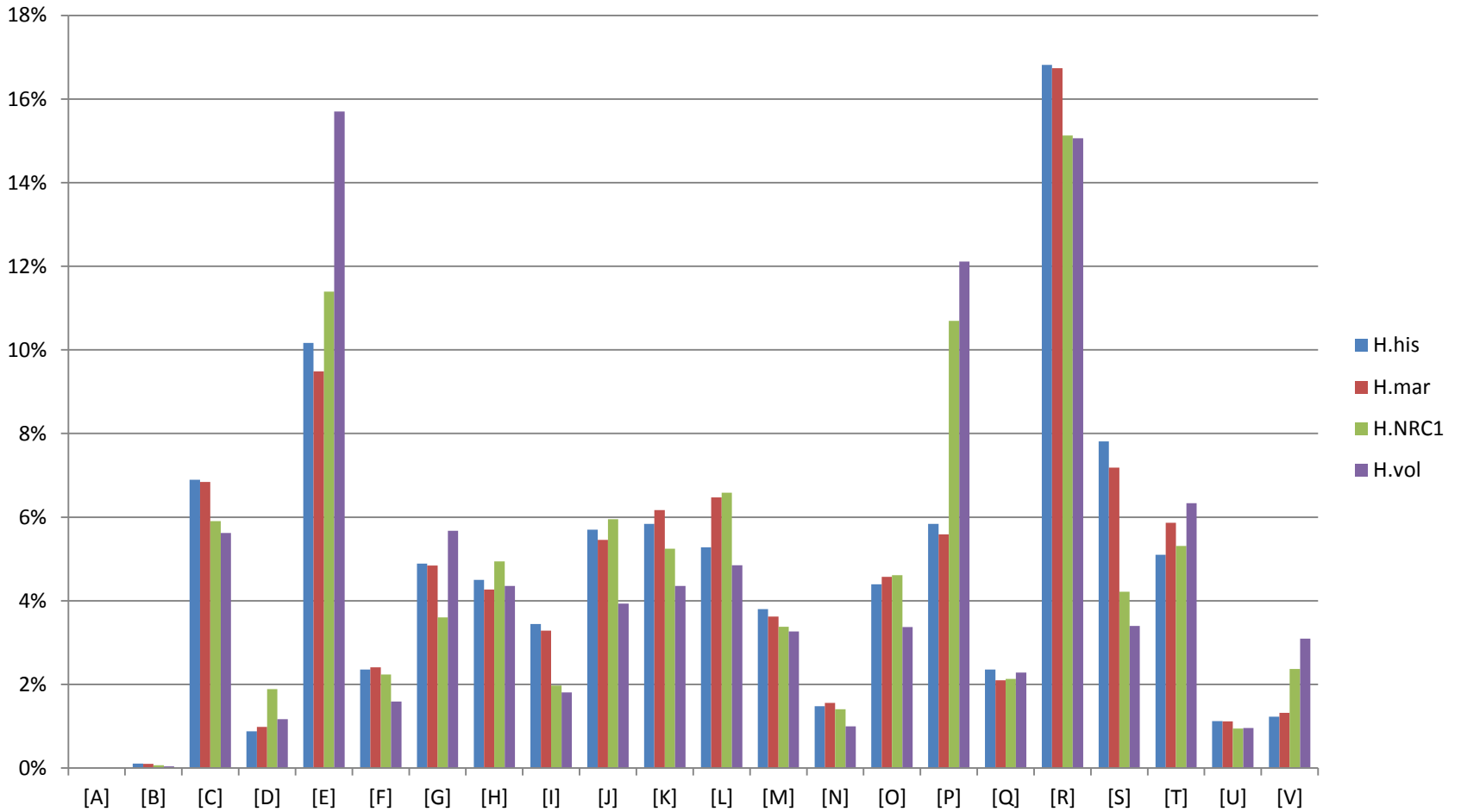


Coverage $\geq 60\%$
 Similarity $\geq 60\%$
 E-value $\leq 1e-5$

COGs annotation

| COGs_function | <i>H. hispanica</i> | <i>H. marismortui</i> | <i>H. sp. NRC-1</i> | <i>H. volcanii</i> |
|-------------------------------------------------------------------|---------------------|-----------------------|---------------------|--------------------|
| [A] RNA processing and modification | 0 | 0 | 1 | 1 |
| [B] Chromatin structure and dynamics | 3 | 3 | 3 | 3 |
| [C] Energy production and conversion | 196 | 202 | 269 | 423 |
| [D] Cell cycle control, cell division, chromosome partitioning | 25 | 29 | 86 | 88 |
| [E] Amino acid transport and metabolism | 289 | 280 | 519 | 1182 |
| [F] Nucleotide transport and metabolism | 67 | 71 | 102 | 120 |
| [G] Carbohydrate transport and metabolism | 139 | 143 | 164 | 427 |
| [H] Coenzyme transport and metabolism | 128 | 126 | 225 | 328 |
| [I] Lipid transport and metabolism | 98 | 97 | 90 | 136 |
| [J] Translation, ribosomal structure and biogenesis | 162 | 161 | 271 | 296 |
| [K] Transcription | 166 | 182 | 239 | 328 |
| [L] Replication, recombination and repair | 150 | 191 | 300 | 365 |
| [M] Cell wall/membrane/envelope biogenesis | 108 | 107 | 154 | 246 |
| [N] Cell motility | 42 | 46 | 64 | 75 |
| [O] Posttranslational modification, protein turnover, chaperones | 125 | 135 | 210 | 254 |
| [P] Inorganic ion transport and metabolism | 166 | 165 | 487 | 912 |
| [Q] Secondary metabolites biosynthesis, transport and catabolism | 67 | 62 | 97 | 172 |
| [R] General function prediction only | 478 | 494 | 689 | 1134 |
| [S] Function unknown | 222 | 212 | 192 | 256 |
| [T] Signal transduction mechanisms | 145 | 173 | 242 | 477 |
| [U] Intracellular trafficking, secretion, and vesicular transport | 32 | 33 | 43 | 72 |
| [V] Defense mechanisms | 35 | 39 | 108 | 233 |

COGs annotation



Gene gain and loss(compare with the *H.marismortui* genome)

-CELLULAR PROCESSES AND SIGNALING

Gains

| | |
|-----------------------|----------------------------------------------------------------------------------------------------------------------------------------|
| Hhis_chr1_orf00123 | [M] COG2843 Putative enzyme of poly-gamma-glutamate biosynthesis (capsule formation) |
| Hhis_chr1_orf00955 | [M] COG2335 Secreted and surface protein containing fasciclin-like repeats |
| Hhis_chr1_orf01616 | [M] COG1732 Periplasmic glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein) |
| Hhis_chr1_orf02648 | [M] COG0399 Predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis |
| Hhis_chr1_orf03002 | [O] COG1404 Subtilisin-like serine proteases |
| Hhis_chr2_orf00071 | [V] COG1002 Type II restriction enzyme, methylase subunits |
| Hhis_chr2_orf00190 | [V] COG3440 Predicted restriction endonuclease |
| Hhis_chr2_orf00287 | [T] COG2337 Growth inhibitor |
| Hhis_chr2_orf00345 | [V] COG0286 Type I restriction-modification system methyltransferase subunit |
| Hhis_plasmid_orf00272 | [D] COG2846 Regulator of cell morphogenesis and NO signaling |

Losses

| | |
|-----------------------|-----------------------------------------------------------------------------------------------|
| Hmar_chr1_YP_136008 | [O] COG0755 ABC-type transport system involved in cytochrome c biogenesis, permease component |
| Hmar_chr1_YP_136002 | [O] COG0785 Cytochrome c biogenesis protein |
| Hmar_chr1_YP_136005 | [O] COG1138 Cytochrome c biogenesis factor |
| Hmar_pNG600_YP_134345 | [O] COG2020 Putative protein-S-isoprenylcysteine methyltransferase |
| Hmar_chr1_YP_136011 | [O] COG2332 Cytochrome c-type biogenesis protein CcmE |
| Hmar_chr1_YP_136004 | [O] COG2386 ABC-type transport system involved in cytochrome c biogenesis, permease component |
| Hmar_chr1_YP_136912 | [V] COG1401 GTPase subunit of restriction endonuclease |
| Hmar_chr1_YP_136477 | [V] COG1619 Uncharacterized proteins, homologs of microcin C7 resistance protein MccF |
| Hmar_pNG600_YP_134389 | [V] COG1715 Restriction endonuclease |
| Hmar_chr1_YP_136547 | [V] COG2746 Aminoglycoside N3'-acetyltransferase |
| Hmar_chr1_YP_136913 | [V] COG4268 McrBC 5-methylcytosine restriction system component |

Genome Island

