

# 2018専門実習 課題

種子の縦横比・粒長・粒幅のGWASの結果について、  
原因 遺伝子を探索を行い、  
その遺伝子の役割について考察してください。

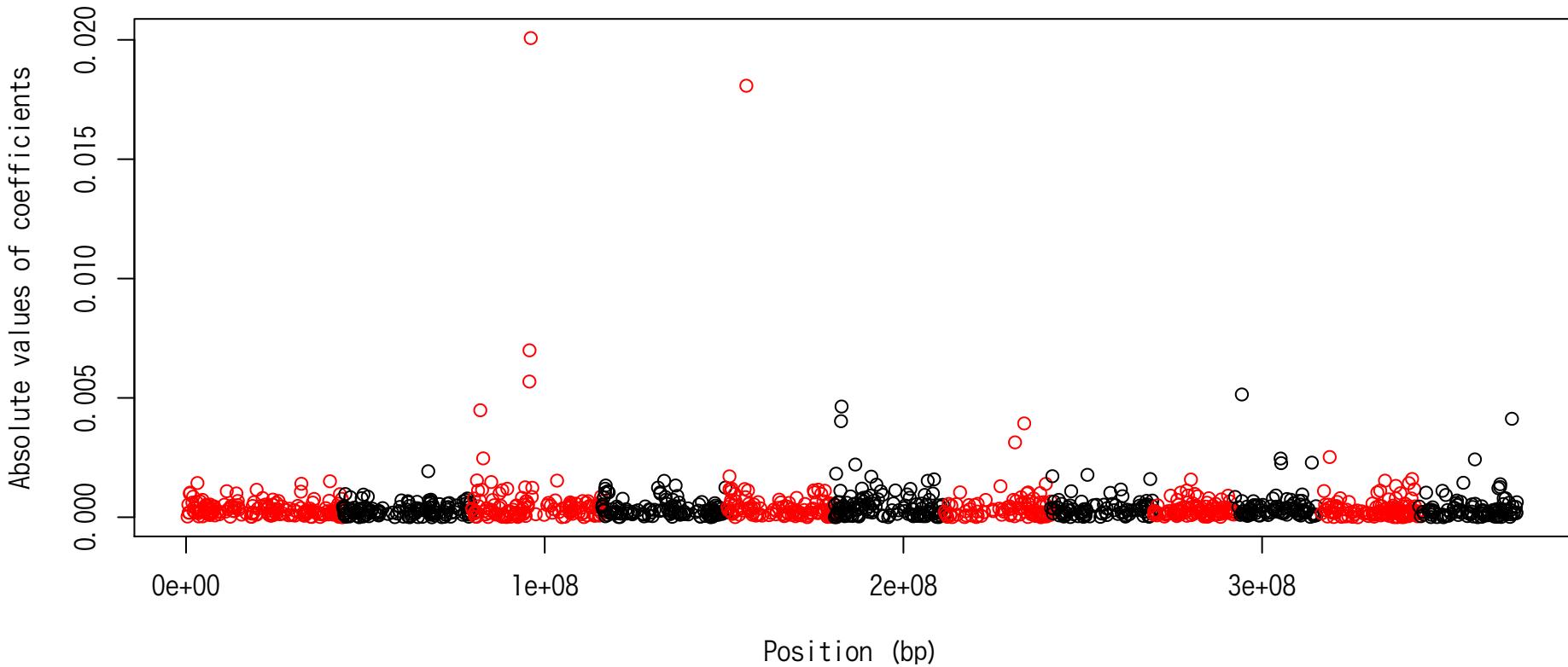


Rice Diversity.

Part of the image collection of the <a href="http://www.irri.org" rel="nofollow">International Rice Research Institute (IRRI)</a>.

# チュートリアルであつかったGWAS 縦横比

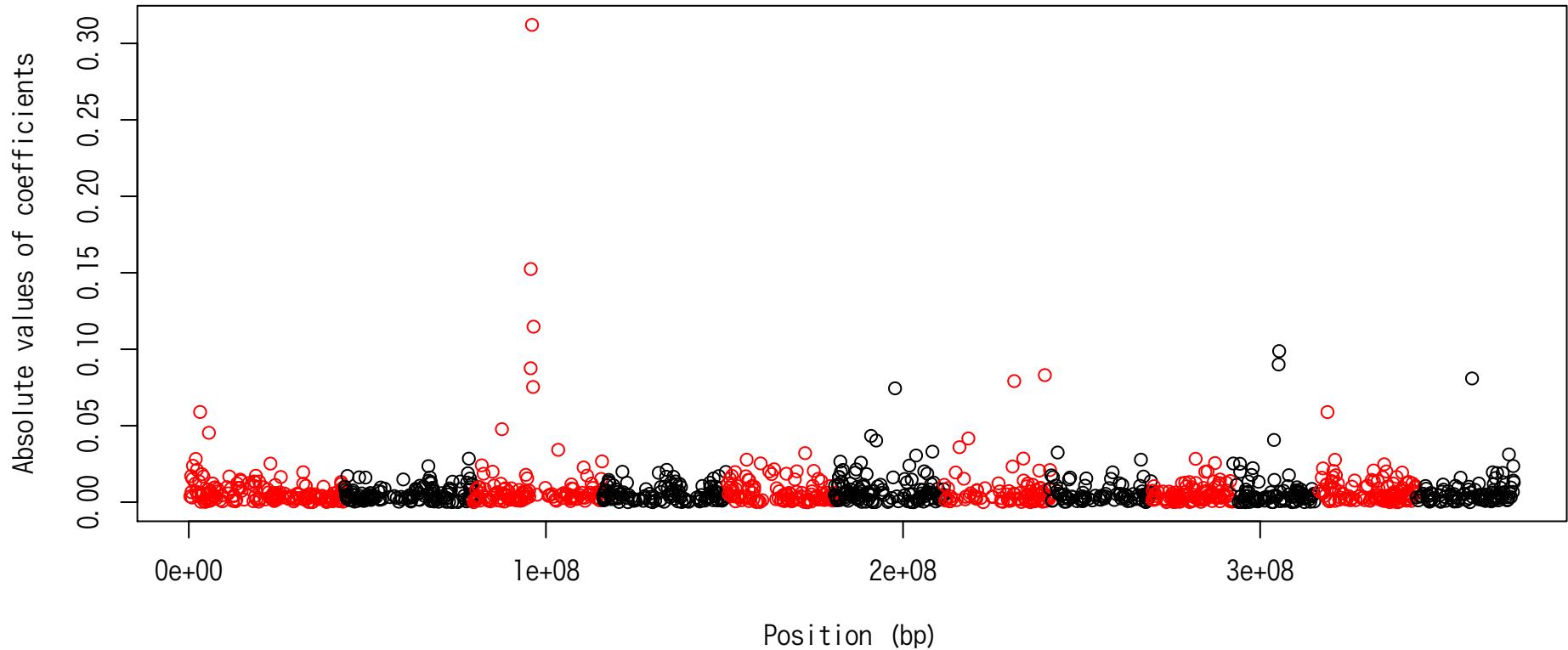
GWAS – BayesB – Seed. width/Seed. length



marker	chr	pos	abs.fmBB.ETA.MRK.b.
id3008333	3	16,621,452	0.020073506
id5002699	5	5,273,692	0.0180782
id3008139	3	16,272,206	0.006993685
id3008127	3	16,247,306	0.005685386
id10000498	10	2,043,939	0.00514448
id6001632	6	bit.ly/gwas100110 2,160,757	0.004639277

# GWAS Seed length

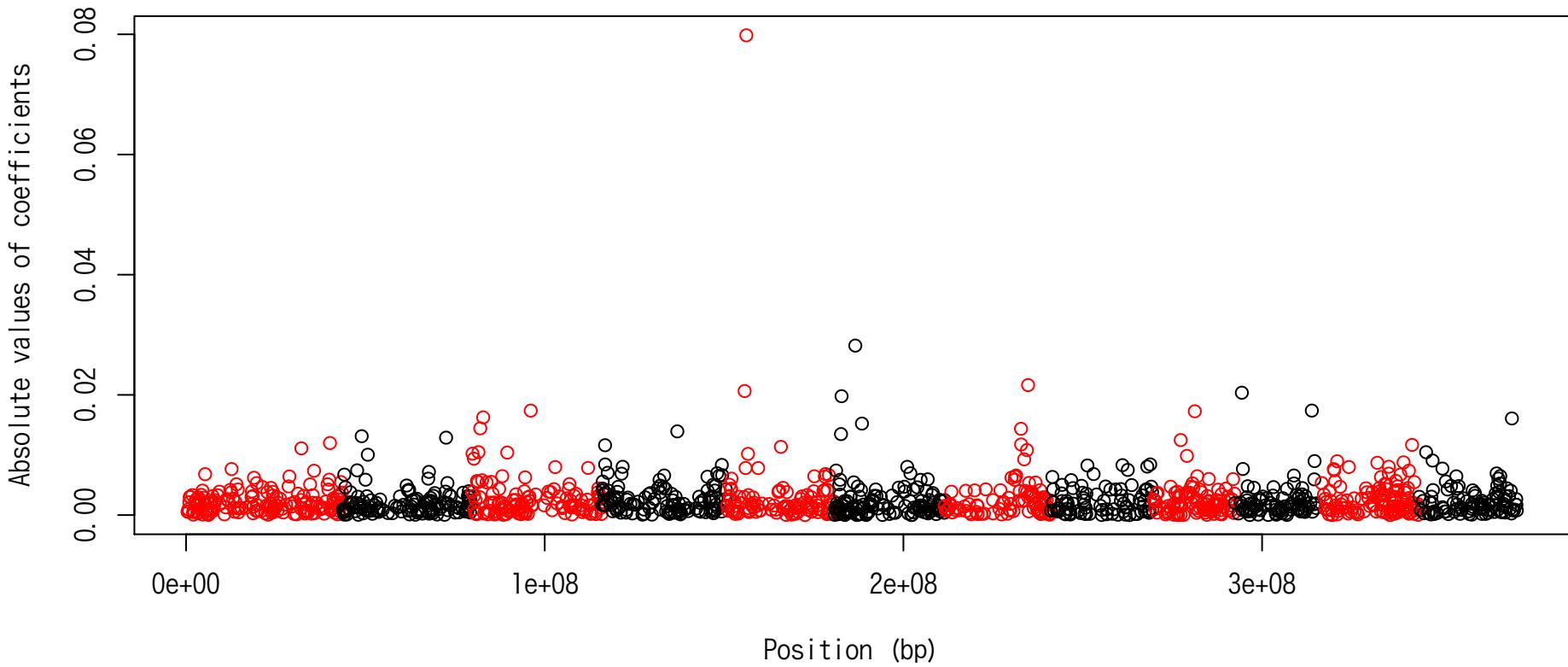
GWAS – BayesB – Seed. length



marker	chr	pos	abs.fmBB.ETA.MRK.b.
id3008333	3	16,621,452	0.31211751
id3008139	3	16,272,206	0.15244834
id3008459	3	17,047,630	0.11475756
id10003501	10	13,008,071	0.09877811
id10003462	10	12,850,534	0.09005561
id3008127	3	16,247,306	0.08758173

# GWAS Seed width

GWAS – BayesB – Seed. width



marker	chr	pos	abs.fmBB.ETA.MRK.b.
id5002699	5	5,273,692	0.07983603
id6003829	6	5,994,007	0.02820405
id7004106	7	23,250,996	0.02163568
id5002528	5	4,797,494	0.02064282
id10000498	10	2,043,939	0.02036695
id6001632	6	2,160,757	0.01978717

# イネの粒長、粒重、形に関する遺伝子

Locus / Gene	RAP ID	Chr	start	end	reference
DWARF61 / OsBRI1	Os01g0718300	chr01	29,927,587	29,931,452	Zhao et al 2013 Plant Science
GW2	Os02g0244100	chr02	8,115,223	8,121,651	Song et al 2007 Nat Gen
GS2	Os02g0701300	chr02	28,863,274	28,866,997	Zhang et al 2013 Crop Journal
PGL2	Os02g0747900	chr02	31,423,973	31,424,983	Heang and Sassa 2012 Breeding Sci
smg1 / OsMKK4	Os02g0787300	chr02	33,442,070	33,443,948	Duan et al 2014 Plant J
PGL1	Os03g0171300	chr03	3,814,378	3,823,216	Heang and Sassa 2012 PLoS One
GS3	Os03g0407400	chr03	16,729,501	16,735,109	Fan et al 2006 TAG; Mao et al 2010 PNAS
qGL3 / OsPPKL1	Os03g0646900	chr03	25,042,427	25,045,410	Hu et al 2012 JIPB
GIF1	Os04g0413500	chr04	20,422,171	20,426,921	Wang et al 2008 Nat Gen
DWARF11	Os04g0469800	chr04	23,467,167	23,471,592	Tanabe et al 2005 Plant Cell
APG	Os05g0139100	chr05	2,246,835	2,248,876	Heang and Sassa 2012 PLoS One
SGL / SRS3	Os05g0154700	chr05	3,207,517	3,210,183	Wu et al 2014 Plant Cell Rep
GS5	Os05g0158500	chr05	3,439,304	3,443,769	Li et al 2011 Nat Genet
GW5	Os05g0187500	chr05	5,365,121	5,366,701	Shomura et al 2008 Nat Genet
D1 / RGA1	Os05g0333200	chr05	15,609,569	15,613,588	Ashikari et al 1999 PNAS
BU1	Os06g0226500	chr06	6,556,697	6,557,748	Tanaka et al 2009 Plant Phys
GW6/OsgIHAT1/ GW6a	Os06g0650300	chr06	26,591,905	26,593,464	Song et al 2015 PNAS
GL7 / GW7 / qSS7 / GS7	Os07g0603300	chr07	24,664,328	24,669,321	Shao et al 2012 TAG; Wang Y et al 2015 Nat Gen; Wang S et al 2015 Nat Gen
SRS1/DEP2	Os07g0616000	chr07	25,381,698	25,389,532	Abe et al 2010 Genes Genet Syst
OsFIE1	Os08g0137250	chr08	2,095,644	2,100,604	Folsom et al 2014 Plant Phys
GW8 / OsSPL16	Os08g0531600	chr08	26,501,167	26,506,198	Wang et al 2012 Nat Gen
DEP1	Os09g0441900	chr09	16,411,151	16,415,851	Huang et al 2009 Nat Gen
SG1	Os09g0459200	chr09	17,350,940	17,352,413	Nakagawa 2012 Plant Phys
SRS5	Os11g0247300	chr11	7,960,531	7,963,375	Segami et al 2012 Rice

# GW5について調べる

<https://shigen.nig.ac.jp/rice/oryzabase/gene/advanced/search>

The screenshot shows the Oryzabase gene search interface. At the top, there is a navigation bar with links for '更新情報', 'ご意見・ご要望', 'サイトマップ', 'Japanese | English', and search fields for 'Search' and 'for'. Below the navigation bar is a menu bar with links for 'Home', 'About', '系統', '分譲/寄託依頼', 'イネの基礎', '研究基盤情報', '遺伝子', '研究支援ツール', and 'ダウンロード'. The main content area has a title '遺伝子 - 検索' and a sub-section '検索 - 遺伝子'. It features a 'キーワード検索' section with a text input field containing 'GW5', a 'Search' button, and a 'Clear' button. A red callout box with an arrow points to the 'GW5' input field, containing the text 'GW5と入力する'. Below this are several other search fields: 'CGSNL 遺伝子シンボル', 'CGSNL 遺伝子名', 'タンパク質名', '染色体' (with a dropdown menu), '対立遺伝子', 'RAP ID', and '解説'. The '解説' field contains a list of categories: '001\_生化学的性質 (5364)', '002\_栄養器官 (1)', and '003\_生殖器官 (1)'.

# GW5の情報が表示される

更新情報 ご意見・ご要望 サイトマップ Japanese | English

Search 全体 for  GO!

Google Custom Search

Home About 系統 分譲/寄託依頼 イネの基礎 研究基盤情報 遺伝子 研究支援ツール ダウンロード

## 遺伝子 - 詳細

検索 リスト ダウンロード trait classification

フィードバックはこちら

### 詳細 - 遺伝子

Basic Information	
CGSNL 遺伝子シンボル	GW5
遺伝子シンボルシノニム	qSW5/GW5, GSE5
CGSNL 遺伝子名	GRAIN WIDTH 5
遺伝子名シノニム	GRAIN SIZE ON CHROMOSOME 5
タンパク質名	
対立遺伝子	gse5-cr
染色体番号	5
解説	LOC_Os05g09520. a Plasma Membrane-Associated Protein with IQ Domains.
形質クラス	種子 - 形態学的な特徴 - 粒形 QTLの特性 - 収穫と生産性
発現	
Sequence/Locus	
cDNA Accession No.	-
RAP ID	Os05g0187500
Links	Oryzabase Chromosome View ( IRGSP 1.0 / Build5 ) RAP-DB ( IRGSP 1.0 / Build5 ) Related IDs List ( IRGSP 1.0 / Build5 )
INSD Accession List (Test version)	-
マップ	
位置情報(cM)	
リンクエージマップ	Classical linkage map
文献	
Duan P., Xu J., Zeng D., Zhang B., Geng M., Zhang G., Huang K., Huang L., Xu R., Ge S., Qian Q., Li Y. Mol Plant 2017 10(5) 685-694 Natural Variation in the Promoter of GSE5 Contributes to grain size Diversity in Rice.	
Du Y., He W., Deng C., Chen X., Gou L., Zhu F., Guo W., Zhang J., Wang T. PLoS ONE 2016 11(3) e0150458	

# RAP-DBでもGW5について調べる

<http://rapdb.dna.affrc.go.jp/index.html>

The Rice Annotation Project (RAP) was conceptualized in 2004 upon the completion of the *Oryza sativa* ssp. *japonica* cv. Nipponbare genome sequencing by the **International Rice Genome Sequencing Project** with the aim of providing the scientific community with an accurate and timely annotation of the rice genome sequence. One of the major objectives of this project is to facilitate a comprehensive analysis of the genome structure and function of rice on the basis of the annotation.

**What's New**

**26/November/2018** NEW NEWS

- We have updated CGSNL annotation and manual curation data (see [update 2018-11-26.txt](#)).

**29/March/2018**

- We have updated CGSNL annotation and manual curation data (see [update 2018-03-](#)

**GW5と入力する**

Expressing OsTCL1 in Arabidopsis inhibited trichome formation and promoted root hair formation, however, the function of OsTCL1 in

# Os05t0187500-01の詳細を調べる

The screenshot shows the rap-db GBrowse Details View for the gene **Os05t0187500-01**. The top navigation bar includes links for Home, News, About, Browser, Tools, Download, Documents, Publications, and Links. Below the navigation is a search bar with 'Keywords' and 'Search' buttons, along with an 'Advanced' link.

The main content area displays the gene's details:

- Locus:** Os05g0187500
- Description:** IQ calmodulin-binding motif family protein, Positive regulator of brassinosteroid signalling, Regulation of grain width and weight
- RAP-DB Gene Symbol Synonym(s):** GW5, qSW5/GW5, GSE5
- RAP-DB Gene Name Synonym(s):** GRAIN WIDTH 5
- CGSNL Gene Symbol:** GW5
- CGSNL Gene Name:** GRAIN WIDTH 5
- Oryzabase Gene Symbol Synonym(s):** qSW5/GW5, GSE5
- Oryzabase Gene Name Synonym(s):** GRAIN SIZE ON CHROMOSOME 5

A red box highlights a literature reference:

**Literature**  
**PMID: 28394310**

# GW5の文献情報を入手

PubMed の利用

<https://www.ncbi.nlm.nih.gov/pubmed>

The screenshot shows the PubMed search interface with the query "gw5 rice" entered in the search bar. The search results are displayed under the heading "Search results" with 19 items found. The results list two articles:

1. Tian P, Liu J, Mou C, Shi C, Zhang H, Zhao Z, Lin Q, Wang J, Wang J, Zhang X, Guo X, Cheng Z, Zhu S, Ren Y, Lei C, Wang H, Wan J. GW5-Like, a homolog of GW5, negatively regulates grain width, weight and salt resistance in rice. *J Integr Plant Biol.* 2018 Nov 19. doi: 10.1111/jipb.12745. [Epub ahead of print] PMID: 30450718 [Similar articles](#)
2. Volante A, Desiderio F, Tondelli A, Perrini R, Orasen G, Biselli C, Riccardi P, Vattari A, Cavalluzzo D, Urso S, Ben Hassen M, Fricano A, Piffanelli P, Cozzi P, Biscarini F, Sacchi GA, Cattivelli L, Valè G. Genome-Wide Analysis of japonica Rice Performance under Limited Water and Permanent Flooding Conditions. *Front Plant Sci.* 2017 Oct 30;8:1862. doi: 10.3389/fpls.2017.01862. eCollection 2017. PMID: 29163588 [Free PMC Article](#) [Similar articles](#)

On the right side of the search results, there is a "Search details" panel with the search query: gw5[All Fields] AND ("oryza"[MeSH Terms] OR "oryza"[All Fields] OR "rice"[All Fields]). Below this panel, a note states: "論理演算子(AND, NOT, OR)を用いた検索も可能".

Annotations in red boxes highlight the following areas:

- A red box surrounds the "Sort by" dropdown menu, which is set to "Most Recent".
- A red box surrounds the "Find related data" section, which includes a "Database: Select" dropdown and a "Find items" button.
- A large red box surrounds the "Search details" panel and the explanatory text below it.

検索ボックスに、思いつく用語をキーワードとして入力し、「Search」をクリック

# PubMed の利用

The screenshot shows the PubMed search interface with the query 'gw5 rice'. The search results are displayed in a summary format with 20 items per page, sorted by 'Best Match'. A red box highlights the 'Best Match' sorting option in the dropdown menu. The first result is a study titled 'GW5 acts as a transcriptional regulator of the grain width pathway to regulate grain width and weight in rice.' by Liu J, Chen J, Wang H, Wan J, published in Nat Plants. 2017 Apr;10(3):17043. PMID: 28394310.

This screenshot shows the full article page for the study mentioned above. The page includes the abstract, author information, and a 'Comment in' section. On the right side, there are sections for 'Full text links' (genetics), 'Save items' (with an 'Add to Favorites' button), and 'Similar articles'. A red box highlights the 'Similar articles' section, which lists related studies such as 'Inference of the japonica rice domestication process from the distribution' [Plant Cell Physiol. 2008] and 'Control of rice grain-filling and yield by a gene with a potential signature of doi' [Nat Genet. 2008].

# 文献検索の方法

- PubMed

<https://www.ncbi.nlm.nih.gov/pubmed>



TOGO TV

2010-02-27 PubMedの使い方～基本編～

<https://tогotv.dbcls.jp/20100227.html>

- Google Scholar

<https://scholar.google.co.jp>

TOGO TV

研究者のためのGoogle活用術

～Google Scholarを中心に～ 2017

<http://tогotv.dbcls.jp/20170605.html>



# PGSB barley genome database

<http://pgsb.helmholtz-muenchen.de/plant/barley/>

**PGSB** Plant Genome and Systems Biology

PGSB Home PlantsDB Databases PlantsDB Tools BLAST/Search Publications Contact/Cite & Imprint

PlantsDB Search

Barley Project

About Genome View Gene Annotation Genome Zipper Comparative Map Viewer Download

Welcome to the PGSB barley genome database

 Barley is an annual cereal grain from the Family of Poaceae and it has been cultivated for more than 7000 years. In former times barley grains were even used as currency by the Sumerian and Babylonian cultures. Nowadays barley is a major animal feed crop. It serves as an essential base for malting and brewing and to a lesser extend as component in bread and health food. Barley is widely adaptable to various climatic and soil conditions, because of its tolerance towards cold, drought, alkali, salinity. Regarding produced quantity and cultivated area barley ranks worldwide as number four after maize, rice and wheat.

 The barley genome is diploid, contains 7 chromosomes and has a size of 5.1 Gb. The growing sequence data and subsequent analyses are a valuable resource for comparative cereal genomics and help plant breeders to develop new improved crop varieties.

**nature.com** The new reference barley genome assembly sequence has been published in Nature (<http://www.nature.com/nature/journal/v544/n7651/full/nature22043.html>) in April 2017 by members of the International Barley Sequencing Consortium (IBSC). Read more from the [international press release](#).

The 2017 barley reference genome assembly and gene predictions, as described in Mascher, Gundlach et al., 2017 Nature, are now available for download from PlantsDB: [barley download center](#).

A user training video about the use of genome resources for barley has been produced in the frame of the transPLANT project. You can watch it here: [barley user training video](#).

THE BARLEY GENOME GOES OKTOBERFEST!  
This video shows the cooperation of Gatersleben (IPK) and Munich (PGSB) in barley research to cope with climate change.

# PGSB barley genome database

キーワード検索



About Genome View Gene Annotation Genome Zipper Comparative Map Viewer Download

## Gene Annotation

This site provides access to the barley gene annotation described in the [Nature 2012 paper](#) (IBSC, 2012). You can search gene models by their identifier or functional description. IPK also provides a BLAST server where you can search your own sequences against the barley gene models: <http://webblast.ipk-gatersleben.de/barley/viroblast.php>

## Search for Genetic Elements

by name/id (case sensitive)

by free text

Your input: e.g. "MLOC\_58956.3", "Histone H2"

amylase

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## Search for Genetic Elements

Name	Type	Description	Size	Start	Stop	Strand
AK364918	transcript_IBSC	Beta-amylase Monomeric				
AK375808	transcript_IBSC	alpha-amylase inhibitor				
HORVU1Hr1G055140.2	transcript_IBSC	beta-amylase 1				
HORVU1Hr1G038950.1	transcript_IBSC	beta-amylase 1				
HORVU1Hr1G038950.4	transcript_IBSC	beta-amylase 1				
HORVU2Hr1G043920.4	transcript_IBSC	beta-amylase 5				
HORVU2Hr1G043920.7	transcript_IBSC	beta-amylase 5 Alpha-				

# PGSB barley genome database



About Genome View Gene Annotation Genome Zipper Comparative Map Viewer Download

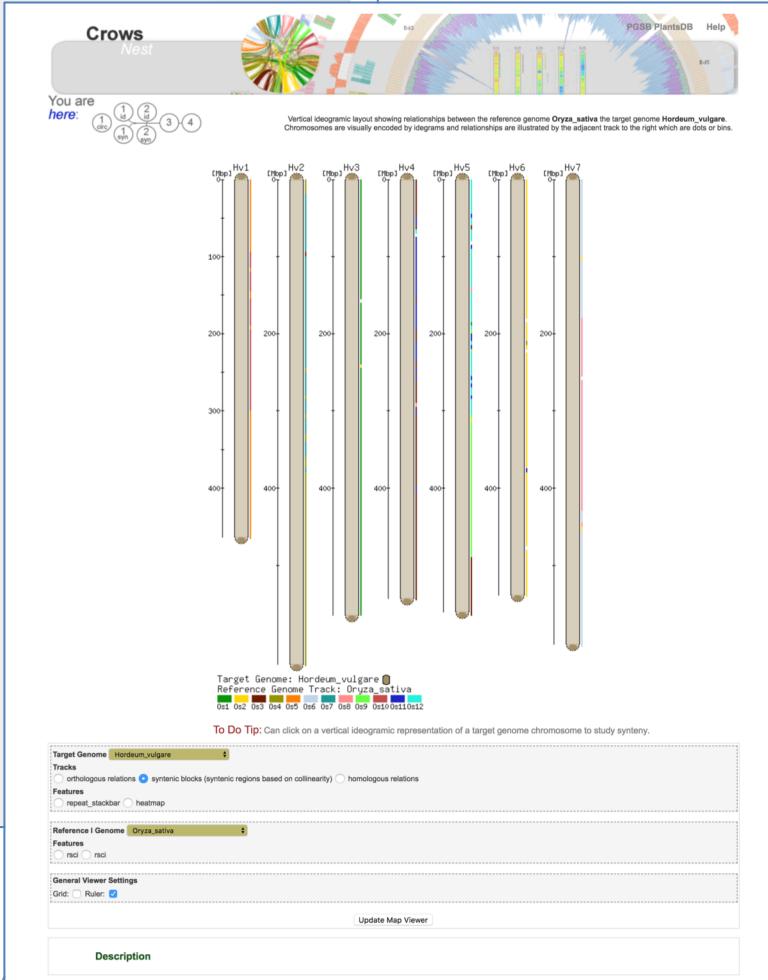
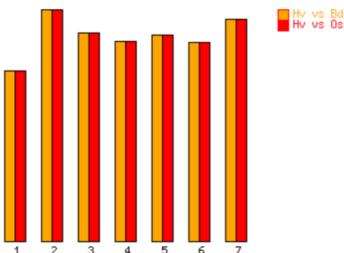
## Comparative Genome View

PGSB Comparative Genome Map Viewer allows you to visualize synteny relationships between different maps. The Viewer consists of four levels to visualize synteny from the macro to the micro level. Currently synteny of the genome *Hordeum vulgare* has been calculated to *Brachypodium distachyon* and *Oryza sativa*.

To enter the top level view of the PGSB Comparative Map Viewer choose one of the following links:

- [Hordeum vulgare vs Brachypodium distachyon](#)
- [Hordeum vulgare vs Oryza sativa](#)

In order to browse synteny relations of one chromosome to another genome (chromosome - whole genome synteny) please choose on one of the chromosomes below.



## Comparative Genome