Shannon Human Splicing Pipeline Server Documentation

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Account creation and types of accounts

Registering a new account

You can create a new account from the Shannon pipeline server home page (http://shannonpipeline.cytognomix.com) by clicking the button “Register a new account”. An account creation screen will appear. Upon successful submission of the account creation form an e-mail will be sent to the e-mail address you provided. Clicking the activation link in this e-mail will grant you trial access to the server. Two types of accounts are available, a trial account and a subscription based account. Differences between the two account types are described below.

Trial account

This is the account type you will be assigned upon standard account creation. You can run the pipeline any *reasonable* number of times to test and evaluate the resource. Basic server functionality is identical to subscription accounts, with the exception of the number of results reported. While viewing results, you are presented with are a reduced subset of the full results. Trial users see fewer than 2% of leaky and inactivating variants and the maximum number of variants returned is capped. We hope you find the trial output useful and see enough potential in Shannon pipeline functionality to consider subscribing.

Subscription

We thank you for considering purchasing a subscription. Your contributions allow us to keep the server running and improve the resource. A subscribe button is adjacent to the “Register a new account” button on the server home page. Clicking it will navigate your browser to a page describing the Shannon pipeline along with subscription pricing. Short-term subscriptions are currently available through PayPal, which provides the latest pricing. Other payment mechanisms are available by contacting us at info@cytognomix.com. Subscribers gain the ability to view full Shannon pipeline output. Jobs submitted by subscribers are priority queued in front of trial users to ensure subscribers are not delayed by trial user submissions. For users who wish to run the Shannon pipeline locally or incorporate it into an existing pipeline, a standalone version of the pipeline may suit your needs. For more information on these options please visit the Subscription webpage.

Quick start and overview of site functionality

This section contains basic information on how to run the plugin, view your results, and check your messages. We assume you have registered and signed in to the Shannon pipeline server. Following these instructions will guide you through your first run and provide an overview of server functionality. After signing in you will see a page with three tabs at the top of your screen labeled “Execute a new analysis”, “View completed analyses”, and “View messages”.

Running the pipeline with sample data

In the event you don’t not currently have a VCF file you would like to examine, sample data can be executed in order to see how results are presented on the server. To execute a sample job, simply navigate to the “Execute a new analysis” tab (see the screenshot below) and click the button “Try a sample run”.

Running the pipeline using a VCF file

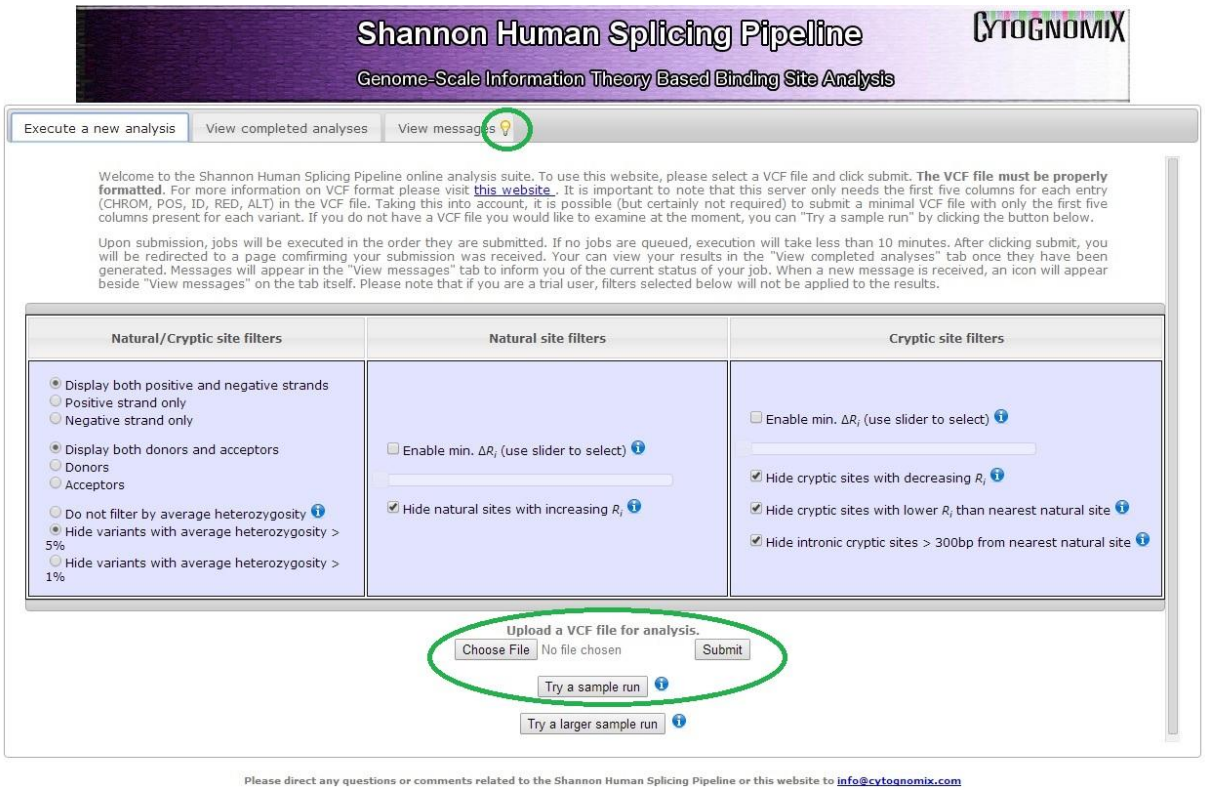
The Shannon pipeline server accepts files in VCF format for analysis. Information on this file format can be found here. VCF files adhering to this format are understood by the server, however only the first five columns of each variant entry are taken into account. Other columns are ignored and may be left out while generating your own files in VCF format. For example the following data is an acceptable variant entry in a VCF file:

22	17237440	Dataset1_Group5	C	T

Note: The ID field (3rd column above) in a VCF file can be used as a label to facilitate separating multiple samples after a run. To label all variants from a sample, place the name of the sample in the ID field in a VCF file. Do this for all samples and place them in the same VCF file. When results are reported, the ID of each variant is preserved.

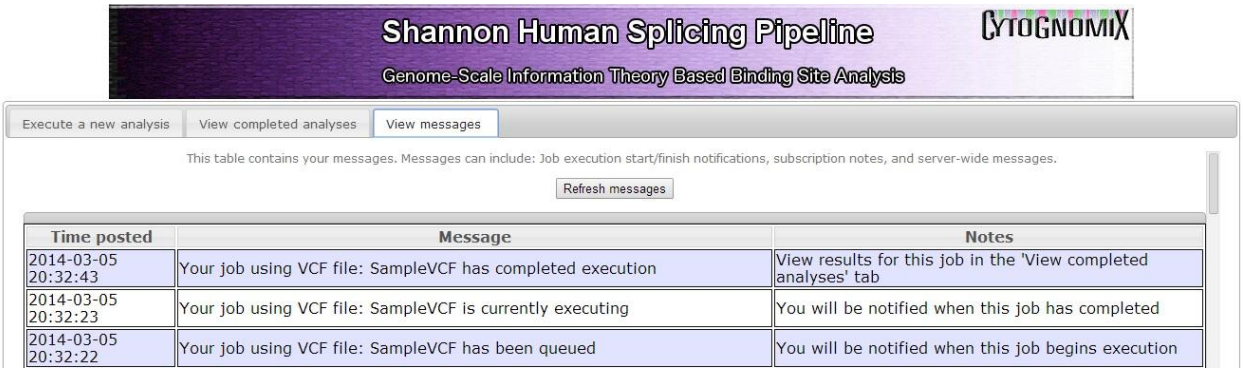
The number of variants in a VCF file is limited to 2,500,000. If a VCF file is submitted with a larger number of variants than this maximum, an error message will appear. To examine a VCF file with greater than 2,500,000 variants, it must be split into multiple files and submitted separately.

When you have your VCF file ready, navigate to the “Execute a new analysis” tab (see the screenshot below). Your data can be submitted to the server by clicking on “Choose File”, browsing your computer for the VCF file, then clicking “Submit”.



After your job has been submitted

Upon clicking submit, your job will be queued on our server. If no other users are currently executing a job, it will begin execution immediately. The “View messages” tab will contain updates related to your job submission. For example, a message will be posted when the job first becomes queued, begins executing, and has finished. When you have received a new message a light bulb will appear beside “View messages” in the tab itself (see the “View messages” tab in the screenshot above to for an example of this icon). When you navigate to the “View messages” tab, the light bulb will disappear indicating you have read your new messages. An example of messages you will find in your messages tab can be found in the screenshot below.

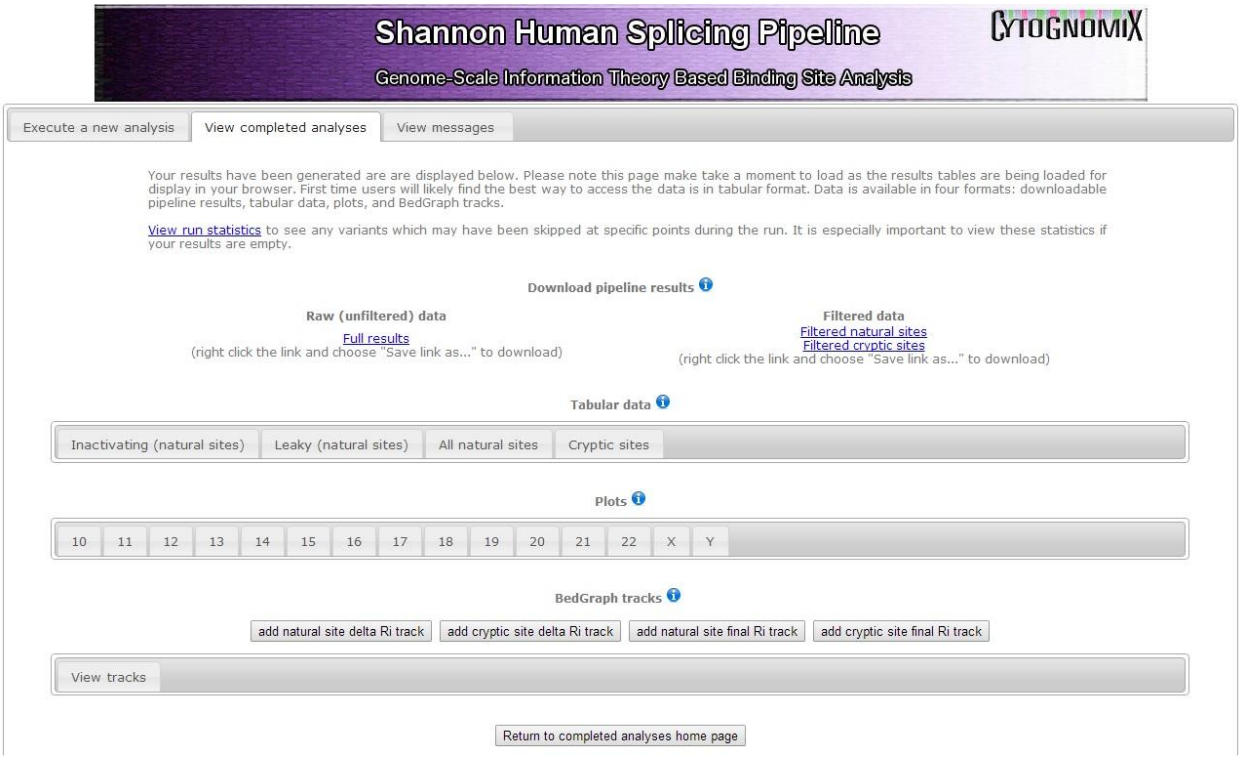


Jobs will generally take several minutes to execute. A job analyzing the maximum number of variants will execute in approximately 15 minutes. You do not have to wait online while your job is executing. Completed jobs are saved on the server for 30 days. Thus, you can submit your job and return later to view your results.

Viewing results

Completed jobs can be found in the “View completed analysis” tab (see screenshot below). Click on “View results of run” to view results for the selected run.

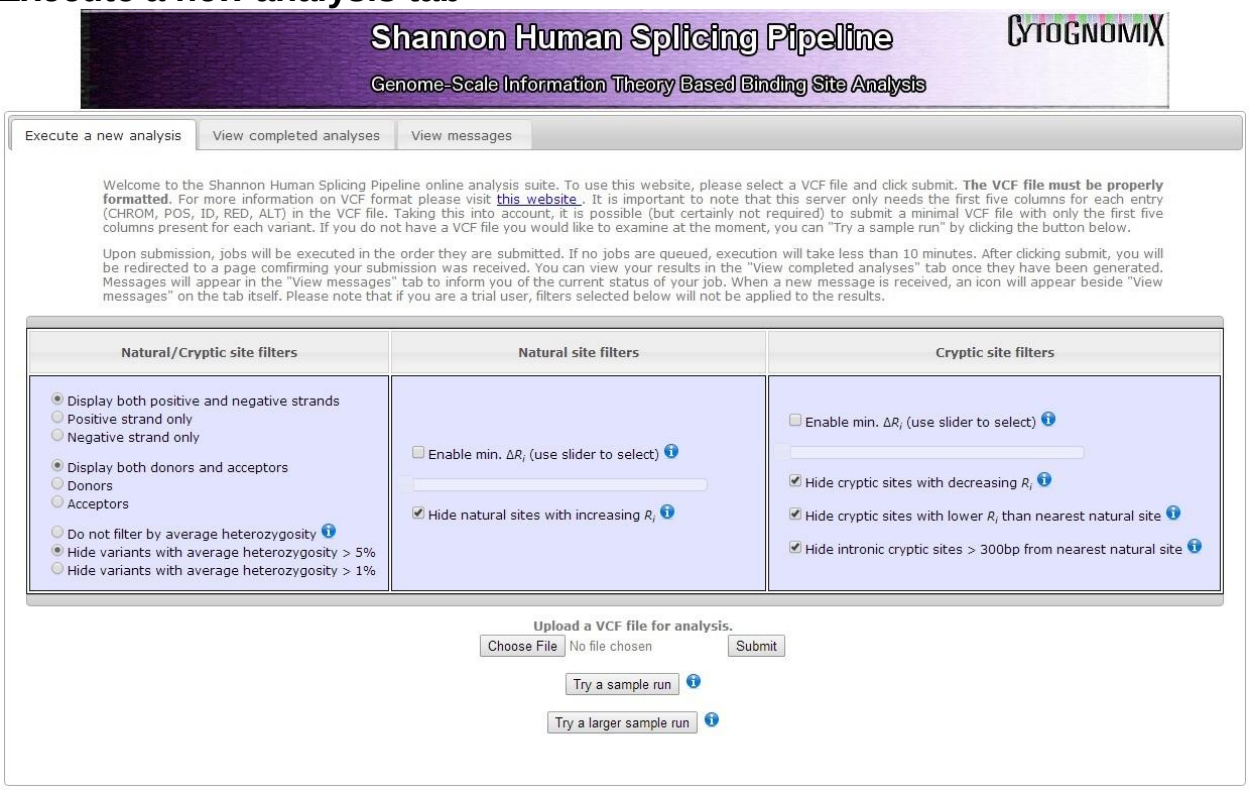
The screenshot below shows a typical results page. For more information about any of the types of data reported (downloading raw pipeline results, tabular data, plots, or BedGraph tracks) please refer to the appropriate sections within this document.



Navigating the Shannon pipeline server

After logging in, you are presented with three tabs on the Shannon pipeline server home page. All server functionality can be found within these tabs.

Execute a new analysis tab



Filters

Nine filters are currently available to help further reduce pipeline results to a tractable number of potentially deleterious variants or to hone in on specific types of variants. Default filters are depicted in the screenshot and were selected to greatly reduce the number of variants in pipeline results while removing as few relevant variants as possible. Reasoning behind the selection of these particular default values is discussed in greater detail in our 2013 paper.

Strand
Default value: display both positive and negative strands.
Some targeted analyses may only be interested in variants on either the positive or negative strand.

Splice site type
Default value: display both donors and acceptors.
Use this filter to display only donor or acceptor sites.

Average heterozygosity
Default value: hide variants with average heterozygosity > 5%
dbSNP135 is examined to determine if a variant has been assigned an rsID. Although a variant may be a known variant in dbSNP, a known variant with low average heterozygosity may be potentially pathogenic. Generally, known variants with high average heterozygosity will not be of interest and thus this filter is set to hide variants with average heterozygosity > 5%.

Natural site ΔR_i
Default value: not used
To make use of this filter, the checkbox labeled "Enable min. ΔR_i" must be checked. Doing so will enable the slider below the checkbox which can be dragged to select the minimum ΔR_i for filtering. This minimum limit applies to both positive and negative ΔR_i values. For example, to view only those variants which increase natural splice site R_i by three or more bits or reduce natural splice site R_i by three or more bits, set the slider to 3.
Note: the slider begins at a value of 1.0 as splice sites with $\Delta R_i < 1.0$ are not reported by the pipeline.

Hide natural sites with increasing R_i
Default value: yes
An increase in natural site strength will likely serve only to widen the existing gap in R_i between the natural and nearby cryptic sites.

Cryptic site ΔR_i
Default value: not used
To make use of this filter, the checkbox labeled "Enable min. ΔR_i" must be checked. Doing so will enable the slider below the checkbox which can be dragged to select the minimum ΔR_i for filtering. This minimum limit applies to both positive and negative ΔR_i values. For example, to view only those variants which increase cryptic splice site R_i by three or more bits or reduce cryptic splice site R_i by three or more bits, set the slider to 3.
Note: the slider begins at a value of 1.0 as splice sites with $\Delta R_i < 1.0$ are not reported by the pipeline.

Hide cryptic sites with decreasing R_i
Default value: yes
A decrease in cryptic site strength will likely serve only to widen the existing gap in R_i between the cryptic site and any nearby natural sites.

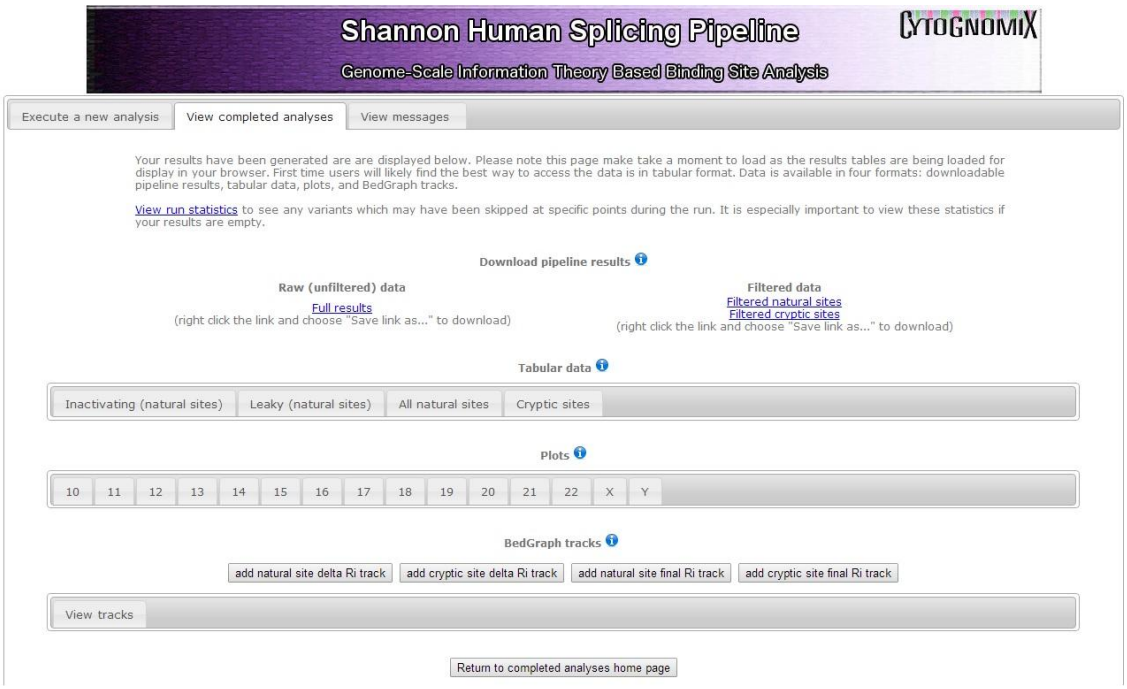
Hide cryptic sites with lower R_i than nearest natural site
Default value: yes
Generally, if a cryptic site has not increased in strength to an R_i greater than a nearby natural site it will not be of interest.

Hide intronic cryptic sites > 300bp from nearest natural site
Default value: yes
Cryptic sites more distant than 300bp from a natural site are unlikely to form a viable exon.

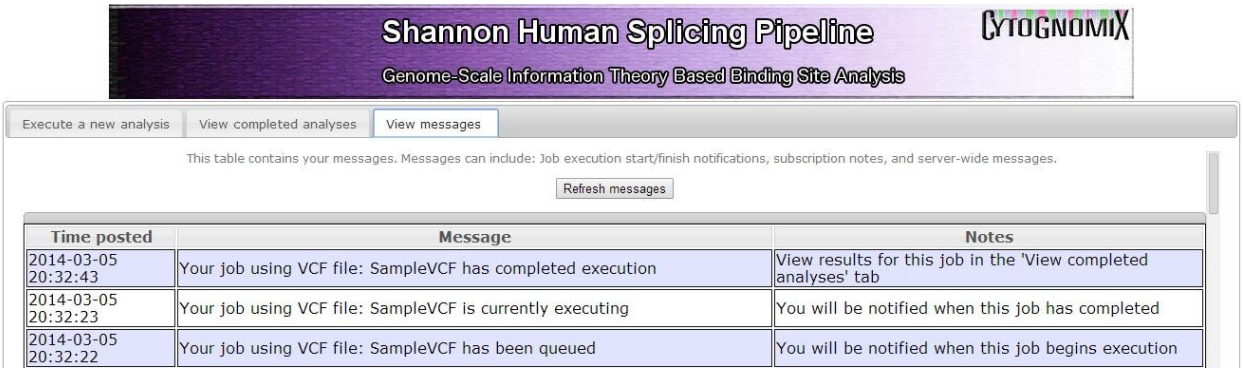
View completed analyses tab

Information related to each job you have submitted to the Shannon pipeline server is displayed here. The “VCF filename” and “Start time” fields can be used to identify the job you wish to examine. Jobs are ordered by start time. To view job results click the hyperlink “View results of run”. Times are displayed in Greenwich Mean Time (GMT). Jobs are removed from our servers at the “Delete time”. The “Job status” field is set to one of three states 1) Queued, 2) Executing, or 3) Finished. The option to view results will appear only if the job is in a “Finished” state.

After clicking “View results of run” a results page will appear in the same tab (see the screenshot below). For more information about any of the types of data reported (downloading raw pipeline results, tabular data, plots, or BedGraph tracks) please refer to the appropriate sections in this document. The hyperlink “View run statistics” will open a new tab in your browser and display the number of variants examined in the run. The number of variants unable to be examined by the server will also be displayed. The vast majority of the time, variants are unable to be examined due to an improperly formatted VCF file or a reference nucleotide which does not match the reference genome. If variants were indeed unable to be examined, a hyperlink will be provided to view the list of variants skipped along with the reason why the server could not examine each variant.



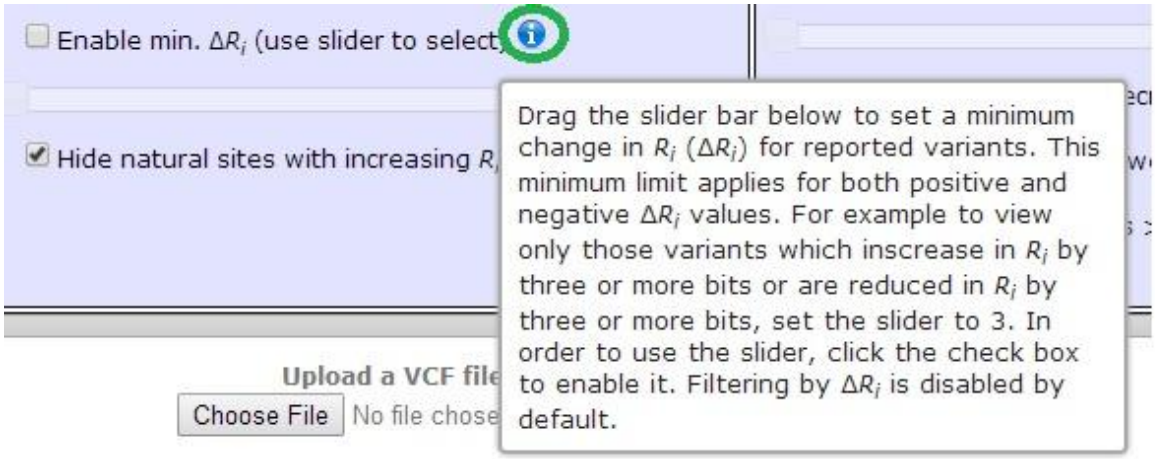
View messages tab and messaging system



The server provides a messaging system to inform you of changes in your submitted job status, account information, and server-wide notices. When you have received a new message a light bulb will appear beside “View messages” in the tab itself to inform you a new message has been received. Navigating to the “View messages” tab will remove the light bulb indicating you have read your new messages. The messaging system allows you to focus on submitting additional jobs or other tasks while your job is being processed. It is important to note it is not necessary to remain on the Shannon server website while your job is executing if it is inconvenient to do so. Your jobs are saved for 30 days after submission and can be viewed at a later date. The system generates a reminder message w in advance of deletion of previously generated results.

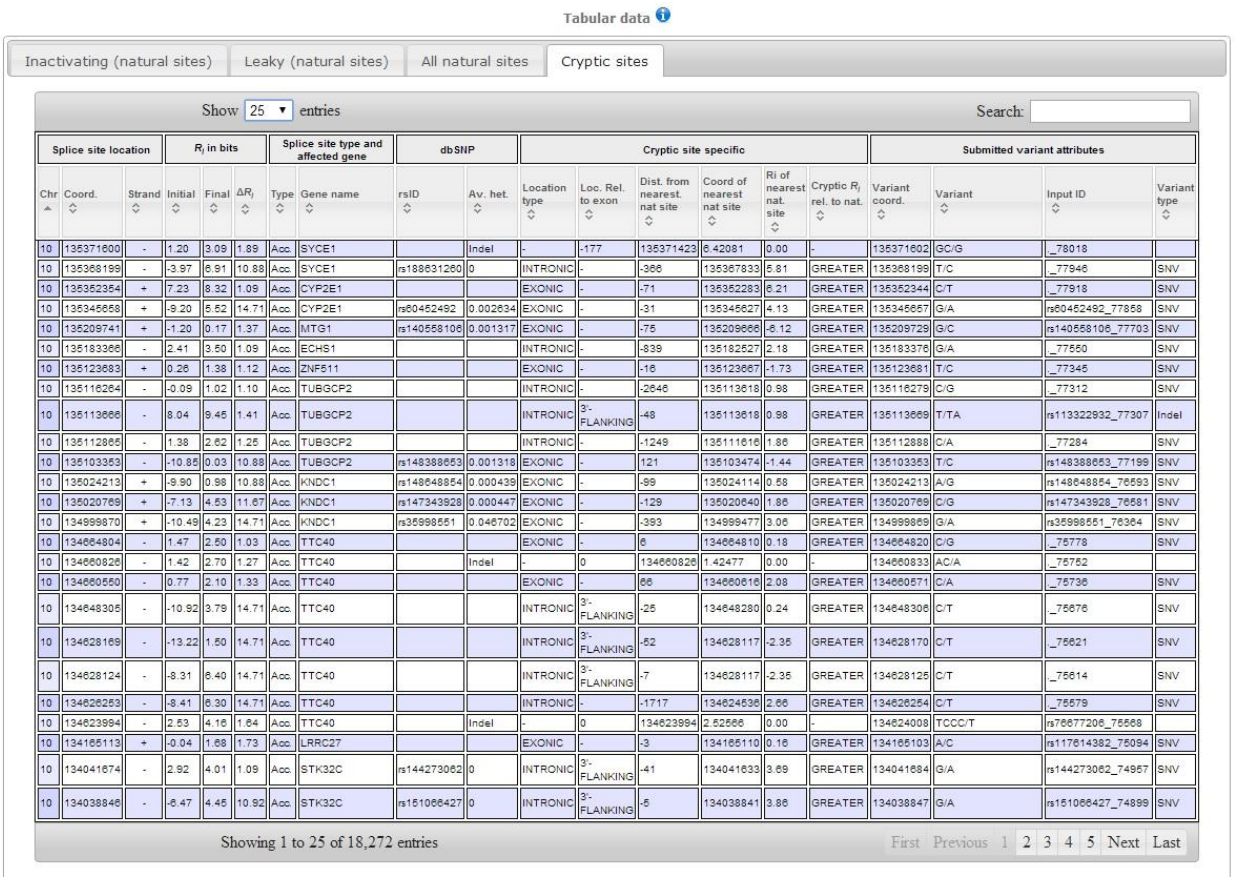
Getting additional help and bug reporting

Blue “information” icons can be found on most pages on the Shannon pipeline server. Hovering the mouse over one of these icons will cause additional information to be displayed in the form of a tooltip. An example of one of these icons and its related tooltip can be found in the screenshot below.



For additional assistance with the use of the server or to report a software bug, please contact info@cytognomix.com.

Tabular data


Tabular data

Inactivating (natural sites) | Leaky (natural sites) | All natural sites | Cryptic sites

Show 25 entries Search:

Splice site location			R_i in bits			Splice site type and affected gene		dbSNP		Cryptic site specific						Submitted variant attributes			
Chr	Coord.	Strand	Initial	Final	ΔR_i	Type	Gene name	rsID	Av. het.	Location type	Loc. Rel. to exon	Dist. from nearest nat site	Coord of nearest nat site	Ri of nearest nat. site	Cryptic R_i rel. to nat.	Variant coord.	Variant	Input ID	Variant type
10	135371600	-	1.20	3.09	1.89	Acc.	SYCE1		Indel	-	-177	135371423	6.42081	0.00	-	135371602	GC/G	_78018	
10	135368199	-	-3.97	6.91	10.88	Acc.	SYCE1	rs188631260	0	INTRONIC	-	-366	135367833	5.81	GREATER	135368199	T/C	_77946	SNV
10	135352354	+	7.23	8.32	1.09	Acc.	CYP2E1			EXONIC	-	-71	135352283	6.21	GREATER	135352344	C/T	_77918	SNV
10	135345658	+	-9.20	5.52	14.71	Acc.	CYP2E1	rs60452492	0.002634	EXONIC	-	-31	135345627	4.13	GREATER	135345657	G/A	rs60452492_77858	SNV
10	135209741	+	-1.20	0.17	1.37	Acc.	MTG1	rs140558106	0.001317	EXONIC	-	-75	135209666	-5.12	GREATER	135209729	G/C	rs140558106_77703	SNV
10	135183366	-	2.41	3.50	1.09	Acc.	ECHS1			INTRONIC	-	-839	135182527	2.18	GREATER	135183376	G/A	_77550	SNV
10	135123683	+	0.26	1.38	1.12	Acc.	ZNF511			EXONIC	-	-16	135123667	-1.73	GREATER	135123681	T/C	_77345	SNV
10	135116264	-	-0.09	1.02	1.10	Acc.	TUBGCP2			INTRONIC	-	-2646	135113618	0.98	GREATER	135116279	C/G	_77312	SNV
10	135113666	-	8.04	9.45	1.41	Acc.	TUBGCP2			INTRONIC	3'-FLANKING	-48	135113618	0.98	GREATER	135113669	T/TA	rs113322932_77307	Indel
10	135112865	-	1.38	2.62	1.25	Acc.	TUBGCP2			INTRONIC	-	-1249	135111616	1.86	GREATER	135112888	C/A	_77284	SNV
10	135103353	-	-10.85	0.03	10.88	Acc.	TUBGCP2	rs148388653	0.001318	EXONIC		121	135103474	-1.44	GREATER	135103353	T/C	rs148388653_77199	SNV
10	135024213	+	-9.90	0.98	10.88	Acc.	KNDC1	rs148648854	0.000439	EXONIC	-	-99	135024114	0.58	GREATER	135024213	A/G	rs148648854_76593	SNV
10	135020769	+	-7.13	4.53	11.67	Acc.	KNDC1	rs147343928	0.000447	EXONIC	-	-129	135020640	1.86	GREATER	135020769	C/G	rs147343928_76581	SNV
10	134999870	+	-10.49	4.23	14.71	Acc.	KNDC1	rs35998551	0.046702	EXONIC	-	-393	134999477	3.06	GREATER	134999869	G/A	rs35998551_76364	SNV
10	134664804	-	1.47	2.50	1.03	Acc.	TTC40			EXONIC	-	6	134664810	0.18	GREATER	134664820	C/G	_75778	SNV
10	134660826	-	1.42	2.70	1.27	Acc.	TTC40		Indel	-	0	134660826	1.42477	0.00	-	134660833	AC/A	_75752	
10	134660550	-	0.77	2.10	1.33	Acc.	TTC40			EXONIC	-	66	134660616	2.08	GREATER	134660571	C/A	_75736	SNV
10	134648305	-	-10.92	3.79	14.71	Acc.	TTC40			INTRONIC	3'-FLANKING	-25	134648280	0.24	GREATER	134648306	C/T	_75676	SNV
10	134628169	-	-13.22	1.50	14.71	Acc.	TTC40			INTRONIC	3'-FLANKING	-52	134628117	-2.35	GREATER	134628170	C/T	_75621	SNV
10	134628124	-	-8.31	6.40	14.71	Acc.	TTC40			INTRONIC	3'-FLANKING	-7	134628117	-2.35	GREATER	134628125	C/T	_75614	SNV
10	134626253	-	-8.41	6.30	14.71	Acc.	TTC40			INTRONIC	-	-1717	134624536	2.66	GREATER	134626254	C/T	_75579	SNV
10	134623994	-	2.53	4.16	1.64	Acc.	TTC40		Indel	-	0	134623994	2.52566	0.00	-	134624008	TCCC/T	rs76677206_75568	
10	134165113	+	-0.04	1.68	1.73	Acc.	LRRC27			EXONIC		-3	134165110	0.16	GREATER	134165103	A/C	rs117614382_75094	SNV
10	134041674	-	2.92	4.01	1.09	Acc.	STK32C	rs144273062	0	INTRONIC	3'-FLANKING	-41	134041633	3.69	GREATER	134041684	G/A	rs144273062_74957	SNV
10	134038846	-	-6.47	4.45	10.92	Acc.	STK32C	rs151066427	0	INTRONIC	3'-FLANKING	-5	134038841	3.86	GREATER	134038847	G/A	rs151066427_74899	SNV

Showing 1 to 25 of 18,272 entries First Previous 1 2 3 4 5 Next Last

Types of tabular data

Tabular output is generated based on filters selected on the job submission page. Variants which do not meet the filtering criteria will not appear in tabular data and must be found in the raw pipeline output (full output). Four types of tables can be viewed in the tabular data section, these are:

1. Inactivating (natural sites)
Includes natural splice sites with an initial R_i greater than 1.6 bits and which drop below that value after the variant is introduced.

2. Leaky (natural sites)
Leaky sites are those natural splice sites which experience a drop in R_i after the variant is introduced but do not fall below an R_i of 1.6 bits.

3. All natural sites
All natural sites with ΔR_i of at least 1.0 bit are included here.

4. Cryptic sites
All cryptic sites with ΔR_i of at least 1.0 bit are included here.

Description of column headers

Each row in the table represents a single variant. The meaning of each column is described below:

1. Chr
Chromosome where the splice site is located.

2. Coord
Genomic coordinate of the splice site experiencing a change in R_i.

3. Strand
Displayed as "+" for positive and "-" for negative strand.

4. Initial
R_i of the splice site using the reference genome (hg19/GRCh37).

5. Final
R_i of the splice site after introducing the variant specified in the input VCF file.

6. ΔR_i
The change in R_i before and after introducing the variant.

7. Type
The site is either an acceptor or a donor. Displayed as "Acc." or “Don.".

8. Gene Name
Name of the gene closest to the location of the variant. If multiple genes overlap the genomic coordinate of the variant, they will all be appear in a comma delimited list.

9. rsID
If the variant is found in dbSNP135 its rsID is displayed here. Otherwise the field is blank.

10. Av. het
If the variant has an rsID in dbSNP135, its average heterozygosity is displayed. Otherwise the field is blank.

Columns displayed only for cryptic site variants

11. Location type
If the cryptic site is found within a known exon in RefSeq it is “EXONIC”. If it is not, it is “INTRONIC”.

12. Loc. Rel. to exon
If variant is downstream relative to the nearest exon it is "3'-FLANKING". Otherwise it is "5'-FLANKING".

13. Dist. From nearest nat site
The number of base pairs separating the cryptic splice site from its nearest natural site of the same phase (donor, acceptor).

14. Coord of nearest nat site
The genomic coordinate of the natural site closest to the cryptic site.

15. R_i of nearest nat site
The R_i of the natural site closest to the cryptic site.

16. Cryptic R_i rel. to nat
If a cryptic site has a higher final R_i than the nearest natural site we denote it "GREATER", otherwise it is "LESS".

Additional columns displayed for all variants
17. Variant coord
The genomic coordinate of the variant as specified in the input VCF file.

18. Variant
Reference and alternate nucleotides as specified in the input VCF file. Ex: A/G

19. Input ID
The ID column from the input VCF file. An additional "_" followed by a number is appended to ensure each ID is unique.

20. Variant type
A variant is either an SNV (single nucleotide variant) or an Indel (insertion or deletion).

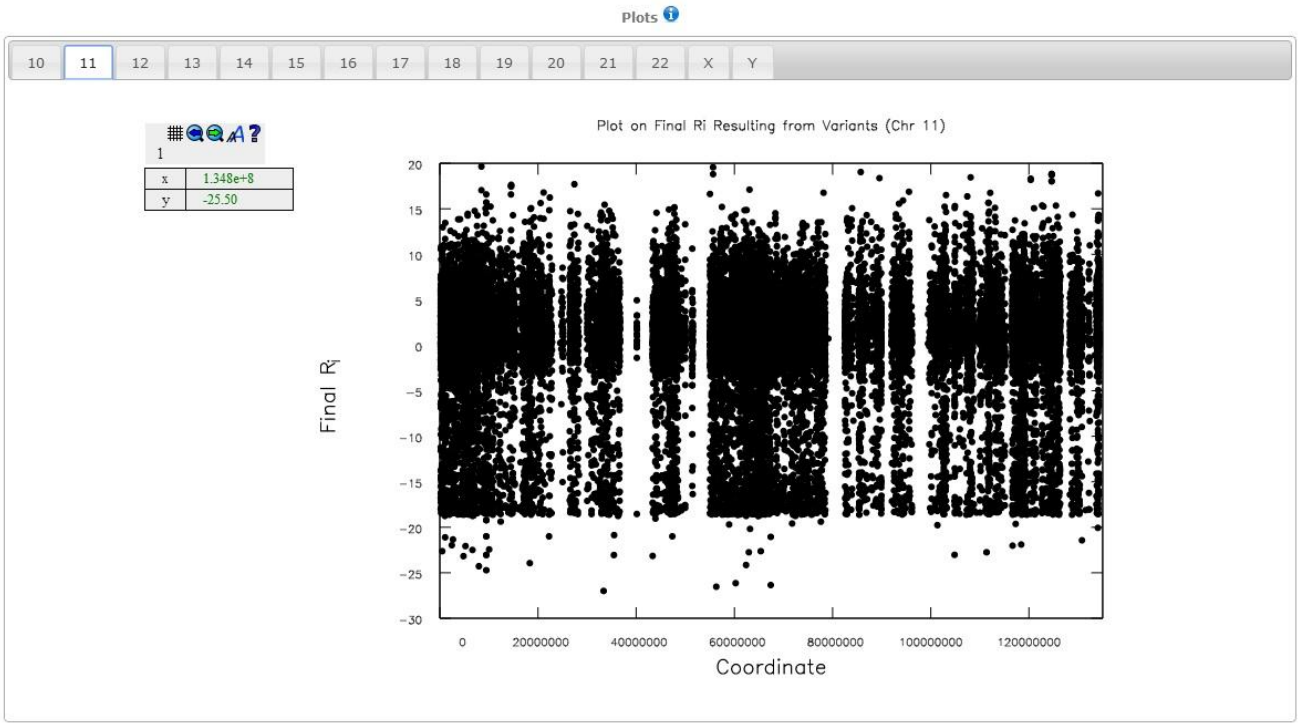
Table functions

A dropdown box ("Show x entries") can be utilized to alter the number of variants displayed on the same page of the table. Ten, 25, 50, or 100 variants can be displayed at once. The search bar located at the upper-right of the table allows real-time searching for specific letters/numbers. Those variants matching a search term will be preserved while those which do not will be temporarily removed from the table. Pages of the table can be browsed by using the paging options located at the lower-right of the table.

Table load times

Tables with a large number of variants will take a moment to load in your browser. To ensure tables load in a relatively timely manner, tables cannot display greater than 100,000 variants simultaneously. To obtain data unable to be displayed within a table because of this restriction, please download the raw pipeline output.

Plots



An example of a plot generated by the pipeline.

Scatter plots provide a visual representation of the final R_i for each variant.

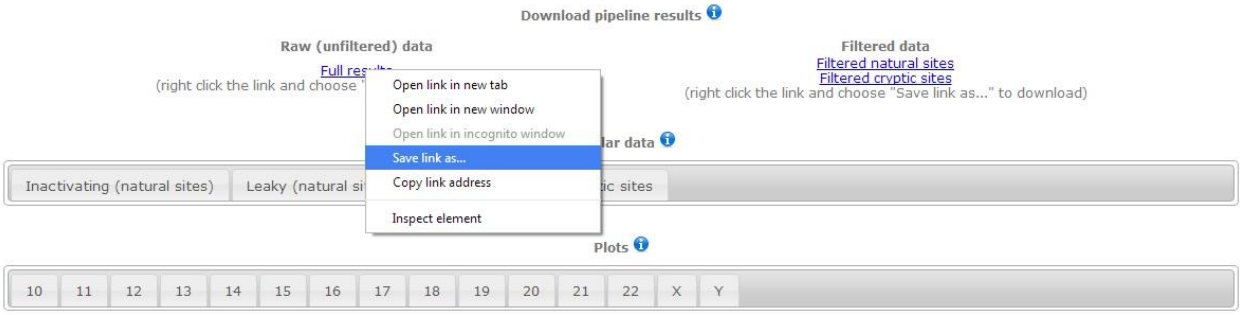
Plot functions

Hovering the mouse over a plot point will produce a tool-tip containing the variant ID specified in the input VCF file. This ID can be used to find a variant of interest in the tabular output or raw pipeline output.

To zoom in to a specified location, hold right click and draw a box within the plot. Upon releasing right click, the plot will zoom to the boxed location. To zoom out, make use of the box to the left of the main plot. Clicking the icon of a magnifying glass with an arrow pointing left will zoom out to the previous level of zoom.

Clicking a location on the plot will display the genomic coordinate of the location followed by the final R_i.

Downloading pipeline output



Three types of files are available for download. “Full results” contains the unfiltered raw pipeline output. Therefore any filters chosen before your job was submitted will not be represented here. Filters can be performed manually using a scripting language or spreadsheet software. “Filtered natural sites” and “Filtered cryptic sites” mirror the tabular data.

How to download or view the pipeline output

Pipeline output files can be downloaded by right clicking on the appropriate output file and clicking “Save link as..” (or equivalent in your browser). To view the output online, simply click on the link and the output will appear in a new browser tab.

Differences between raw pipeline output and “tidy” output

There are two formats in which pipeline output can be downloaded. Differences between these two formats are largely cosmetic. Column headers are present in “tidy” output. The “tidy” format can be used directly as input for Veridical. Within raw pipeline output, positive strand is represented by a “0” and negative strand is represented by “1”. R_i values are not rounded to two decimal places and there is no ΔR_i field in raw pipeline output. Acceptor sites are denoted “ACCEPTOR” instead of “Acc.”. Similarly, donor sites are denoted “DONOR” instead of “Don.”. The chromosome field contains a preceding “chr” in the raw output.

Column order in “tidy” pipeline output

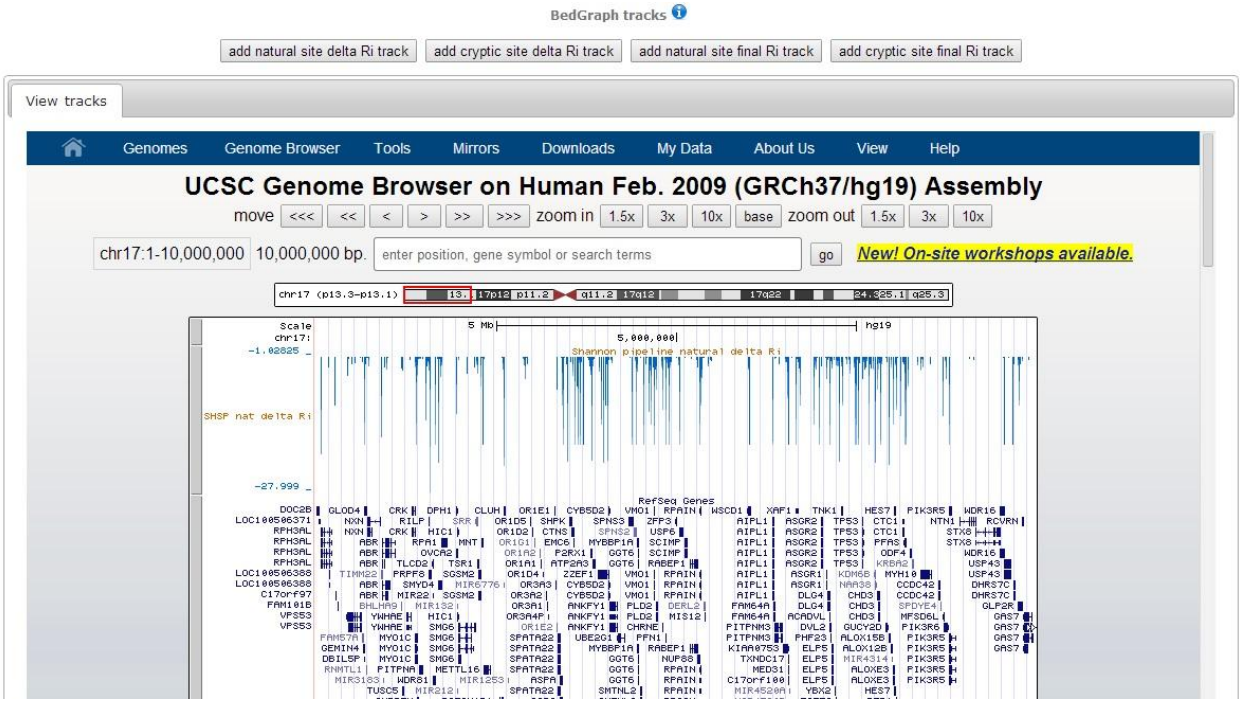
1. Chromosome
2. Splice site coord
3. Strand (+ or -)
4. Initial R_i (rounded to two decimal places)
5. Final R_i (rounded to two decimal places)
6. ΔR_i (rounded to two decimal places)
7. Splice site type (donor or acceptor)
8. Gene name
9. CRYPTICSITE or NATURALSITE
10. Location type (intronic or exonic)
11. Loc. Rel. to exon (5’-flanking or 3’-flanking)
12. Dist. From nearest natural site
13. Coord of nearest natural site

14. R_i of nearest natural site (rounded to two decimal places)
15. Cryptic site R_i relative to nearest natural site R_i
16. rsID
17. Average heterozygosity
18. Input variant coord
19. Input variant nucleotides
20. Input ID
21. Variant type

Column order in raw pipeline output

1. Input ID
2. Splice site coord
3. Strand (0 represents positive strand. 1 represents negative strand)
4. Initial R_i
5. Final R_i
6. Input variant coord
7. Input variant nucleotides
8. Chromosome
9. Splice site type (donor or acceptor)
10. Gene name
11. CRYPTICSITE or NATURALSITE
12. Location type (intronic or exonic)
13. Loc. Rel. to exon (5'-flanking or 3'-flanking)
14. Dist. From nearest natural site
15. Coord of nearest natural site
16. R_i of nearest natural site
17. Cryptic site R_i relative to nearest natural site R_i
18. rsID
19. Average heterozygosity
20. Variant type

BedGraph Tracks



Four BedGraph tracks are generated each time the pipeline is executed, these are:

1. ΔR_i of all natural sites.
2. ΔR_i of all cryptic sites.
3. Final R_i of all natural sites.
4. Final R_i of all cryptic sites.

How to view tracks

The BedGraph tracks are automatically submitted to the UCSC Genome Browser and can be viewed there within a frame on the pipeline results page. Clicking the buttons labelled “add natural site delta R_i track”, etc. will upload the selected track to the UCSC Genome Browser. Any custom tracks previously uploaded from this site will also be visible. To remove tracks, click the button “manage custom tracks” on UCSC directly beneath the genome browser window, check the appropriate checkboxes of tracks to be removed and click delete. Uploading a new track will replace an older track of the same name. For example, if you uploaded the cryptic site delta R_i track from a previous run on this server, uploading it again by clicking the button “add cryptic site delta R_i track” will replace it.

Note: The UCSC Genome Browser is a separate resource managed by UCSC. As such, we are not responsible for maintaining this resource. As the functionality of the UCSC Genome Browser is quite extensive, it cannot be properly discussed in this document. For an introduction to the genome browser please visit this tutorial written by OpenHelix.

FAQ

This FAQ will be updated with answers to common questions.

Q: How fast is the Shannon human splicing pipeline server?
A: The length of time needed to examine a VCF file is related to the number of different chromosomes in the VCF file being examined. As a general rule, if all chromosomes are present, a run will take at least 5 minutes. (3,000,000 variants in ~15min). Examining only chromosome 22 even with a large number of variants will take less than 1min.

Q: How does the Shannon pipeline annotate the gene name field for a variant location overlapped by more than one gene?
A: The gene name field will contain multiple genes separated by commas.

Q: I performed an analysis on a VCF file I uploaded and I'm getting empty results. What can I do?
A: In this situation it is important to make use of the "View run statistics" hyperlink on the results page. It is likely the server could not properly parse the VCF file you uploaded. Inside the "View run statistics" link, you can find more information about how many variants were unable to be examined by the server and a description of why they were skipped.

Terms of use

You are welcome to use the Shannon human splicing mutation pipeline server (SMPS) as our guest. Guest (trial) access requires a valid email address and affiliation to test and evaluate the resource.

This resource is covered by US Patent #5867402 and other patents pending.

Subscriptions to obtain full pipeline results and increased job queue priority are available from Cytognomix. Pricing is tiered according to licensee, seat quantity, and license duration.

This resource is intended for research purposes only and is not intended for use in clinical diagnostics or selection of therapy. The technology has been peer reviewed in multiple scientific journals and has been widely cited. The results produced by this resource are based on these publications. No other warranty or guaranty is granted based on the results generated by the SMPS.

Analyses submitted by subscribers are executed before those submitted by trial users.

Disk space is limited on the Shannon human splicing pipeline sever. We reserve the right to remove uploaded VCF files or pipeline results in advance of the standard deletion schedule in the event files exceed our capacity to store them. Users will be notified by email in advance of file deletions that occur on non-standard deletion schedules.

Executing the same variants on the pipeline server repeatedly or other actions which may be disruptive to the server's functionality is considered to be a serious violation of these Terms of Use and is prohibited. This is a shared resource with finite resources. Any attempt to circumvent the limitations of trial server access or any failure to adhere to these restrictions will result in permanent suspension/removal of your account, and/or notification of administrators or officers at your institution or company. Uploading malicious code or other more serious attacks upon the website will incur legal liability for you and your employer for any damages sustained by Cytognomix.

Publications or presentations that use or describe results produced by this resource should reference the server web address (http://shannonpipeline.cytognomix.com), and Shirley et al. "Interpretation, stratification and evidence for sequence variants affecting mRNA splicing in complete human genome sequences.", Genomics Proteomics Bioinformatics, 11:77-85, 2013 DOI: 10.1016/j.gpb.2013.01.008.

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