

EASANA® Visualization Module Quick Reference Card

1- Screenshot

EASANA FAST DB® Client Edition Probe Data

Project name: **TISSUES (cerebellum vs. others)** / Chip: huex (human) / 11 samples
EASANA expiration: Unknown

Release: 2011_2 (Jun. 2011) Welcome Frederic - [logout](#)

Gene: **GSHG0021765** Save session

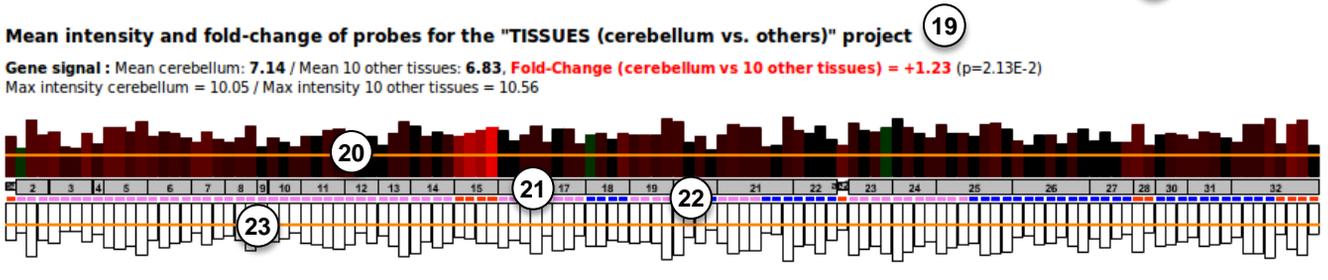
Project: huex (human) TISSUES (cerebellum vs. others)

Probe Selection: **120 probes**

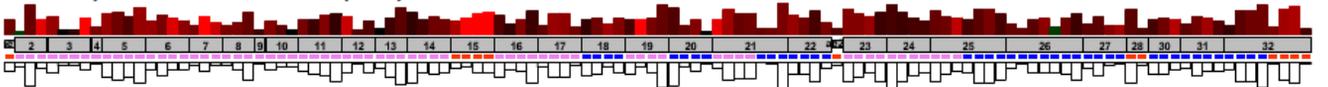
High-Specificity Constitutive
 Exonic Expressed

Display ESTs: OFF
 Relative colors: OFF
 SI colors: OFF
 Relative scale (Z): ON

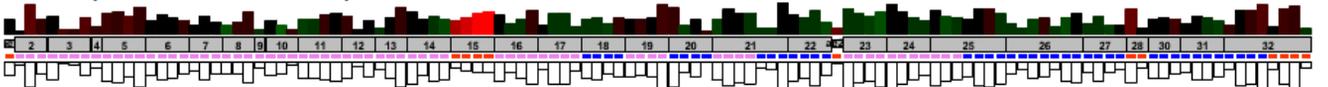
1- Polybromo 1
2- Release
3- Welcome Frederic
4- logout
5- FAST DB® Client Edition
6- Probe Data
7- Gene
8- Project
9- Probe Selection
10- Refresh
11- Display ESTs
12- Relative colors
13- SI colors
14- Relative scale (Z)
15- Human icon
16- Gene structure diagram
17- Zoomed-in gene structure diagram
18- Gene structure diagram with red highlights



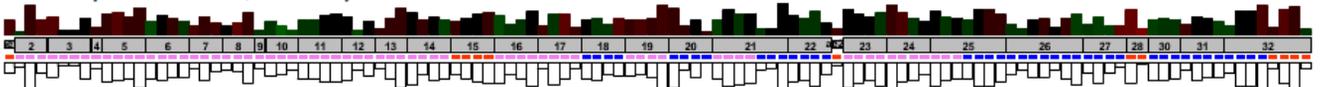
Mean cerebellum: **7.14** / Mean kidney: **6.27** ; **Fold-Change (cerebellum vs kidney) = +1.82**
Max intensity cerebellum = 10.05 / Max intensity kidney = 9.20



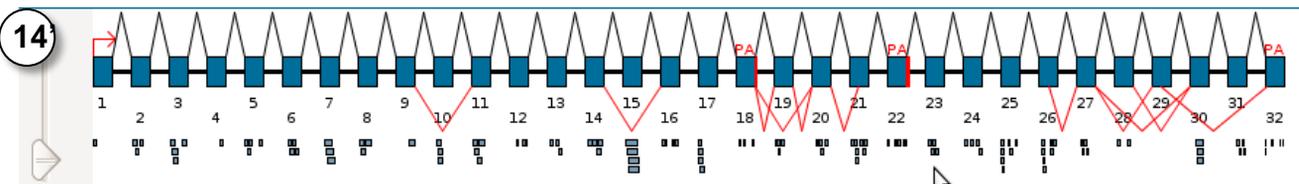
Mean cerebellum: **7.14** / Mean liver: **7.10** ; **Fold-Change (cerebellum vs liver) = +1.03**
Max intensity cerebellum = 10.05 / Max intensity liver = 9.93



Mean cerebellum: **7.14** / Mean muscle: **7.08** ; **Fold-Change (cerebellum vs muscle) = +1.04**
Max intensity cerebellum = 10.05 / Max intensity muscle = 9.99



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EASANA[®] Visualization Module

Quick Reference Card

2- Legend

1	Gene name and project information
2	EASANA [®] version
3	Click on this link to logout.
4	“transfer icon”: access to the “file manager tool”; “envelope icon”: send an email to us.
5	FAST DB [®] Client Edition to get information regarding splicing of gene products.
6	Probe data: get information regarding probe (Affymetrix IDs, localization, intensities, regulation...).
7	Search another gene using any kind of keywords (need to be “validated”, see 10).
8	Change for another project for which you want to display the probe intensity in EASANA [®] (need to be “validated”, see 10).
9	Possibility to filter probes based on different kind of criteria (need to be “validated”, see 10).
10	“REFRESH” button to validate choice from 7 and/or 8 and/or 9.
11	Possibility to include information from EST data (depending on EASANA [®] version).
12	Switch color mode (default is <i>absolute</i> : a given color corresponds to a precise fold-change; <i>relative</i> : all color is relative to the highest fold-change).
13	Switch color mode to Splicing Index (default is expression).
14	Switch scale mode (default is <i>relative</i> : length of exons and introns are proportional; <i>off</i> : all exons have the same length: see 14’).
15	Pictogram indicating the specie used for the project (Human/Mouse)
16	Exon/intron structure of the gene (blue boxes correspond to exon and horizontal lines to introns).
17	Alternative events are displayed in red. In this example, exon 19 is known to be skipped.
18	Rectangles under the exon/intron gene structure correspond to probe localization.
19	This track under the gene structure represents the mean of the replicated experiments. Project name, experimental conditions, mean fold-change and p-value at the gene level are indicated here (not always the same value than in the results from the EASANA [®] analysis module: to be faster, visualization makes mean of all the gene probe intensities in the different replicates).
20	Each bar corresponds to one probe (Note that these tracks are not at the same scale than the gene structure graphics!). Bar height corresponds to probe intensities (bars above correspond to condition2 (Cerebellum), and white bars below to condition1 (Other tissues)). Bar color corresponds to fold-change of probe intensities between condition2 and condition1. Red bars correspond to up-regulated probes, green bars to down-regulated probes, and black bars correspond to probes whose intensity is the same between the two experimental conditions.
21	As noted previously (20), the scale of these tracks is not the same than the gene structure on the top of the page. The grey track between bars showing intensity in the two conditions allows to retrieve the exonic localization of probes.
22	Color under probes indicates the “constitutive level”: blue means that this region is shared by at least 75% of transcripts; purple means that this region is shared by more at least 50% of transcripts (and less than 75%); red means that this region is shared by less than 50% of transcripts.
23	We defined high-quality and low-quality probes that can be excluded from the visualization using the corresponding filters (9). For example, some probes target a genomic region that is identical to other chromosomal localizations: these probes are represented as a red-bordered dark-grey rectangle.

EASANA[®] Visualization Module

Quick Reference Card

3- Interpretation

Gene level:

Most probes are red, indicating that this gene is more expressed in cerebellum cells compared to cells from the 10 other tissues.

Fold-Change (cerebellum vs 10 other tissues) = +1.23 (p=2.13E-2)

The mean fold-change indicated by the EASANA[®] visualization module is x1.23 (see figure above).

Exon level:

Probes targeting exon 15 are more red than the other probes, indicating that this exon is more included in transcripts from cerebellum cells compared to transcripts from the 10 other tissues cells. Moreover, exon 15 is already known to be a cassette exon.

Cerebellum vs. Kidney

Gene level: gene is more expressed in cerebellum;
Exon level: exon 15 is more included in cerebellum.

Cerebellum vs. Liver

Gene level: there is no variation at the gene level;
Exon level: exon 15 is more included in cerebellum.

Cerebellum vs. Muscle

Gene level: there is no variation at the gene level;
Exon level: there is no variation at the exon level.

EASANA® Visualization Module Quick Reference Card

4- FAST DB® Client Edition

EASANA FAST DB® Client Probe Data Release: 2011_2 (Jun. 2011) Welcome Frederic - [logout](#)

Polybromo 1
Project name: TISSUES (cerebellum vs. others) / Chip: huex (human)
[chr3\(-\): 52579882-52719852](#)
EASANA expiration: Unknown

The EASANA® visualization module is a user-friendly interface allowing to display microarray data in their genomic context.
Display data for any gene => **Check** results from analysis => **Share** data with your collaborators
Click [here](#) for more information about EASANA®

FAST DB options: **Gene View**

Gene: GSHG0021765 **Size:** 139970 bp **Chromosome:** chr3

Alternative splicing

Transcription initiation and first exon(s)	
First exon(s)	
Exon 1	1

Transcription termination and last exon(s)	
Last exon(s)	
Exon 18	1
Exon 22	1
Exon 32	15

Alternative Splice sites	
Exon(s) skipping	
Exon 14->16	10
Exon 18->20	1
Exon 27->29	11

Gene View

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FAST DB options: **Transcripts View**

18 Transcripts

Gene: GSHG0021765 **Size:** 139970 bp **Chromosome:** chr3

Go Annotations

- biological process:**
 - GO:0006338 (chromatin remodeling)
 - GO:0006355 (regulation of transcription, DNA-dependent)
 - GO:0007067 (mitosis)
 - GO:0009285 (negative regulation of cell proliferation)
- molecular function:**
 - GO:0003677 (DNA binding)
 - GO:0003682 (chromatin binding)
 - GO:0005515 (protein binding)
- cellular component:**
 - GO:0000228 (nuclear chromosome)
 - GO:0005634 (nucleus)

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FAST DB options: **Gene annotations**

Symbols: PBPM1
Stable Id: GSHG0021765
Name: Polybromo 1

Previous symbols: BAF180, PB1

Synonyms: CCDS: [CCDS2859.1](#)
CCDS: [CCDS2860.1](#)
CCDS: [CCDS43099.1](#)
Ensembl: [ENSG00000163939](#)
Entrez: [55193](#)
FASTDB1.0: [8132](#)
HJAY: [HJ0301259](#)
Hugo: [HGNC-30064](#)
OMIM: [606083](#)
Pubmed: [11078522](#)
Pubmed: [11483580](#)
RefSeq: [NM_018165](#)
Ucsc: [uc003der.2](#)
Uniprot: [Q86U86](#)
VEGA: [OTTHUMG00000152663](#)

EASANA FAST DB® Client Probe Data Release: 2011_2 (Jun. 2011) Welcome Frederic - [logout](#)

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FAST DB options: **Transcripts View**

18 Transcripts

Gene: GSHG0021765 **Size:** 139970 bp **Chromosome:** chr3

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FAST DB options: **Transcripts View**

18 Transcripts

Gene: GSHG0021765 **Size:** 139970 bp **Chromosome:** chr3

Transcripts: AF197569, BC115009, BC115010, BC115011

Gene annotations

Transcripts View

EASANA® Visualization Module

Quick Reference Card

5- Probe Data



Polybromo 1

Project name: TISSUES (cerebellum vs. others) / Chip: huex (human) / 11 samples

EASANA expiration: Unknown

EASANA®

FAST DB® Client Edition

Probe Data

Release 2011_2 (Jun. 2011)

Welcome Frederic - [logout](#)

Gene [Save session](#)

Project

Probe Selection: 120 probes

High-Specificity Constitutive
 Exonic Expressed

[Refresh](#)

Display ESTs OFF

Relative colors OFF

SI colors OFF

Relative scale (?) ON



human

Probe ID	Probeset ID	Transcript Cluster ID	Chromosomal localization	FAST DB localization	FAST DB exon number	Sequence
1139439	2676304	2676219	chr3(-) 52719834-52719858	GSHG0021765 -5 - 19	ae1	GGCCGGAGGAGCAATAGCAGCAGCC
3177974	2676295	2676219	chr3(-) 52713693-52713717	GSHG0021765 6136 - 6160	e2	AGAGAAGAAGAGCTACCTCCCTTC
2000155	2676295	2676219	chr3(-) 52713674-52713698	GSHG0021765 6155 - 6179	e2	CCCTTCAGCAGTGTGACGGGGAC
3238778	2676295	2676219	chr3(-) 52713642-52713666	GSHG0021765 6187 - 6211	e2	ATGGGCACCATCTGTGTCACACC
1444063	2676294	2676219	chr3(-) 52712581-52712605	GSHG0021765 7248 - 7272	e3	GTGCCATGAACCTATAATACCATC
5381775	2676294	2676219	chr3(-) 52712567-52712591	GSHG0021765 7262 - 7286	e3	ATAATACCATCCGAGACTATAAGGA
5722217	2676294	2676219	chr3(-) 52712563-52712587	GSHG0021765 7266 - 7290	e3	TACCATCCGAGACTATAAGGATGAA
5353403	2676294	2676219	chr3(-) 52712521-52712545	GSHG0021765 7308 - 7332	e3	TGAGCTCTCATTAGGGCACCAAAG
682177	2676292	2676219	chr3(-) 52702528-52702552	GSHG0021765 17301 - 17325	e4	TTCCAGCTCTTTTTAACAATGCAA
310396	2676289	2676219	chr3(-) 52696263-52696287	GSHG0021765 23566 - 23590	e5	TTCTCTGAATATAAAGCCGTTGC
1009760	2676289	2676219	chr3(-) 52696246-52696270	GSHG0021765 23583 - 23607	e5	CCGCTTGCAAACCTCTGGGATTTGTA
5377088	2676289	2676219	chr3(-) 52696233-52696257	GSHG0021765 23596 - 23620	e5	CTGGGATTTGTACCTTCGAACAAGA
1592567	2676289	2676219	chr3(-) 52696158-52696182	GSHG0021765 23671 - 23695	e5	TGGGCAAGACAATCAGGGCACAATG
412270	2676286	2676219	chr3(-) 52692270-52692294	GSHG0021765 27559 - 27583	e6	TTCTTGAGCCATAGTTGTAGCTAC
4265604	2676286	2676219	chr3(-) 52692255-52692279	GSHG0021765 27574 - 27598	e6	TTGTAGCTACAATCCATCAGGACG
3022047	2676286	2676219	chr3(-) 52692244-52692268	GSHG0021765 27585 - 27609	e6	AATCCATCAGGACGCTCTCATTAGCG
4644832	2676286	2676219	chr3(-) 52692226-52692250	GSHG0021765 27603 - 27627	e6	ATTAGCGAACTTTTCAGAAACTGC
771042	2676284	2676219	chr3(-) 52685784-52685808	GSHG0021765 34045 - 34069	e7	GCAATAATTAAGGAGCCTATAGATC

Export to CSV 

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