

GensearchNGS : Integrating OMICs analysis and visualization

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Introduction

Analysis of NGS data has become more and more diverse, making it necessary to combine information from multiple datasources to properly analyse a sample.

The previously presented GensearchNGS-Viewer focused mainly on the analysis and display of DNaseq data.

We present our latest work of integrating more OMICs data sources, notably RNAseq and bisulfite sequencing data.

We integrated the support for standard fileformats for those datasources, like BAM files, as well as the support for basic data analysis.

The result is an integrated solution to analyse multiple OMICs datasources, making it easier to understand the biological process happening in a sample.

The rest of the poster gives an overview of the features added related to RNAseq and bisulfite sequencing data.

Features

RNAseq

- Expression analysis statistics
- Expression comparison
- Optimized spliced reads display

Bisulfite sequencing

- Region specific methylation analysis
- Visualization of bisulfite sequencing alignments
- Interactive visualization filters
- Min/Max methylation
- SNP specific reads

Availability

GensearchNGS is a multi-platform desktop application developed in Java. It is available for Windows, Linux and OSX.

A demo version of GensearchNGS can be downloaded at:

<http://VIZBI2016.phenosystems.com>

The demo version has very few restrictions, notably related to the creation and loading of analysis projects.

Figure 1: Bisulfite sequencing visualization

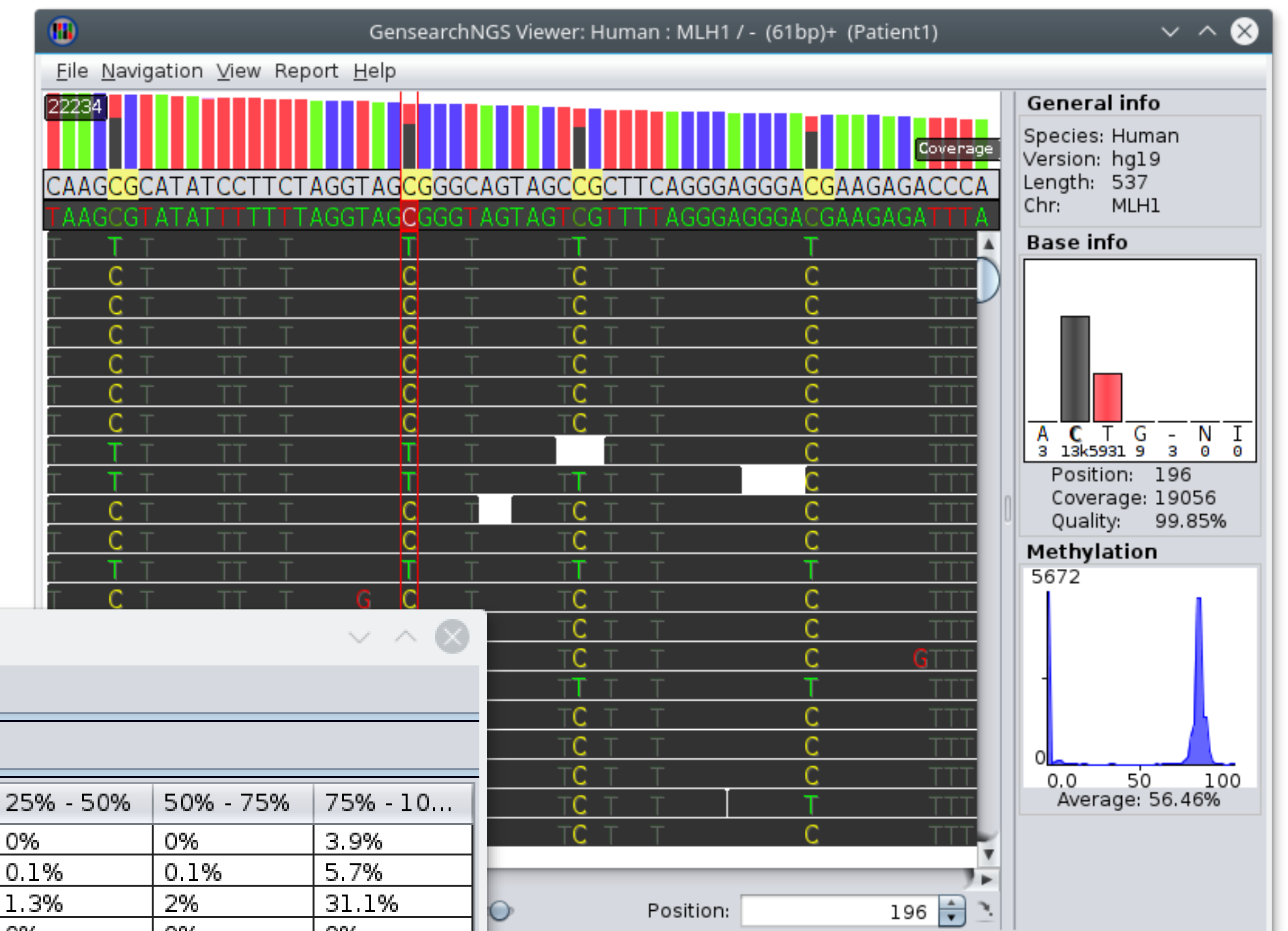


Figure 2: Region specific statistics

Name	CpG meth.	Other me...	Avg. read...	0% - 25%	25% - 50%	50% - 75%	75% - 10...
ATM Ex1	4.4%	2.7%	4.6%	96.1%	0%	0%	3.9%
ATM Prom	6.3%	6.2%	6.5%	94.2%	0.1%	0.1%	5.7%
BRCA1	34.4%	5.1%	34.7%	65.7%	1.3%	2%	31.1%
ESR1	0.8%	0%	0.7%	100%	0%	0%	0%
GTL2	15.5%	16.7%	16.4%	83.5%	1.3%	0.9%	14.4%
LINE1	83.6%	4.7%	83.5%	0%	1.8%	19.3%	78.9%
MEG3 Prom	55.5%	12.3%	55.9%	43.7%	0.4%	0.3%	55.6%
MEST	31.3%	2.2%	32%	66.4%	0.2%	4.1%	29.3%
MLH1	55.4%	3.8%	54.4%	32.6%	0%	7.7%	59.8%
NF1							
PEG3	2.3%	7.1%	2.2%	98.5%	0%	0%	1.5%
PTEN	0.5%	3%	0.5%	100%	0%	0%	0%
RAD51C	25.9%	2.1%	25.1%	76.3%	0%	0%	23.7%
RB1	1%	1.2%	1%	100%	0%	0%	0%
SHANK3							
TP53 CTCF							
TP53 Ex1	13.9%	5%	13.7%	86.6%	0%	0%	13.4%

Figure 3: Statistic comparison

Region	Patient 1	Patient 2	Patient 3	Patient 4
LINE1	6.9%	12.9%	22.2%	22.2%
PTEN	91.7%		42.5%	
ATM Prom	52.4%	99.1%	22.2%	44.1%
MEG3 Prom	16.5%	51.3%	1.5%	50.2%
ATM Ex1	43%	29.7%	19.2%	62.8%
NF1				
RAD51C	84.8%	18%	77.4%	
MLH1	13.3%	51.3%	63.2%	64.6%
ESR1	63.9%		27.4%	
GTL2	54.6%	83%	72.5%	86.2%
BRCA1	30.1%	57.3%	19.1%	91.3%
MEST	81.6%	27.4%	47.8%	46.7%
RB1	19.1%		13.2%	10.9%
SHANK3				
TP53 Ex1	27.7%	48.2%	98%	82.9%
TP53 CTCF				
PEG3	24.4%	59.2%	86.6%	49.1%

Figure 4: RNAseq spliced alignment visualization

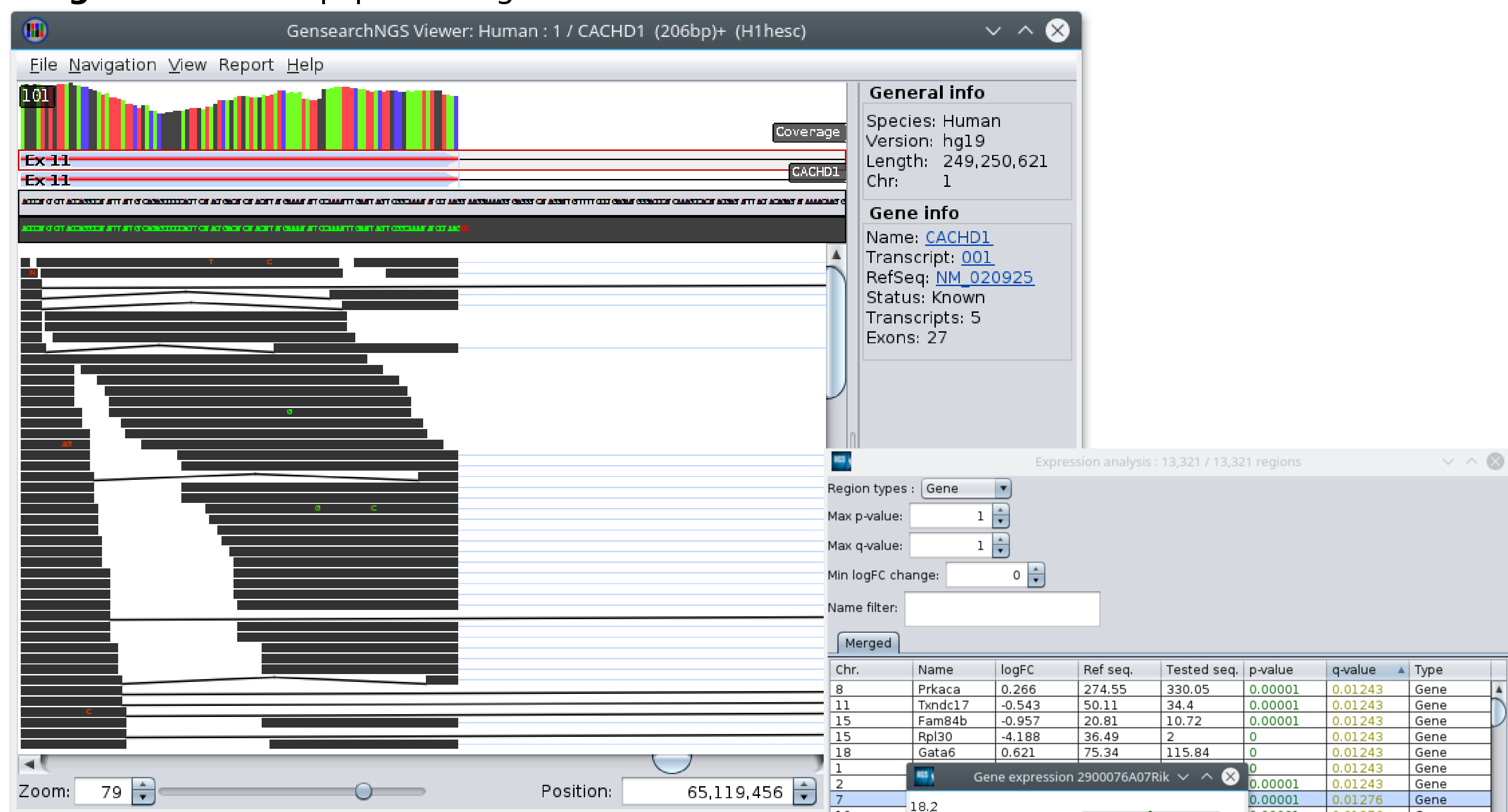


Figure 4: Expression analysis

Chr.	Name	logFC	Ref. seq.	Tested seq.	p-value	q-value	Type
8	Prkaca	0.266	274.55	330.05	0.00001	0.01243	Gene
11	Tundcl7	-0.543	50.11	34.4	0.00001	0.01243	Gene
15	Fam84b	-0.957	20.81	18.72	0.00001	0.01243	Gene
15	Rpl9	-4.188	36.49	2	0	0.01243	Gene
18	Gata6	0.621	75.34	115.84	0	0.01243	Gene
1					0.00001	0.01243	Gene
2					0.00001	0.01243	Gene
7					0.00001	0.01276	Gene
10					0.00001	0.01276	Gene
9					0.00001	0.01284	Gene
6					0.00001	0.01284	Gene
18					0.00001	0.01333	Gene
6					0.00003	0.01347	Gene
6					0.00003	0.01347	Gene
6					0.00002	0.01347	Gene
7					0.00002	0.01347	Gene
8					0.00002	0.01347	Gene
8	Irf5	-3.127	14.46	1.66	0.00002	0.01347	Gene
9	Cnc1	-0.663	11.56	7.9	0.00002	0.01347	Gene
10	Atp5d	0.681	547.53	878.01	0.00002	0.01347	Gene
11	Narf	0.5	128.29	181.45	0.00002	0.01347	Gene
11	Ybx2	1.556	20.51	68.33	0.00003	0.01347	Gene
11	Trim16	-1.323	15.07	6.02	0.00002	0.01347	Gene

Figure 5: Expression comparison

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Website GensearchNGS:
<http://VIZBI2016.phenosystems.com/>

Personal website:
<http://beat.wolf.home.hefr.ch/>



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