INFORMATICS GENOMICS PROTEOMICS METABOLOMICS

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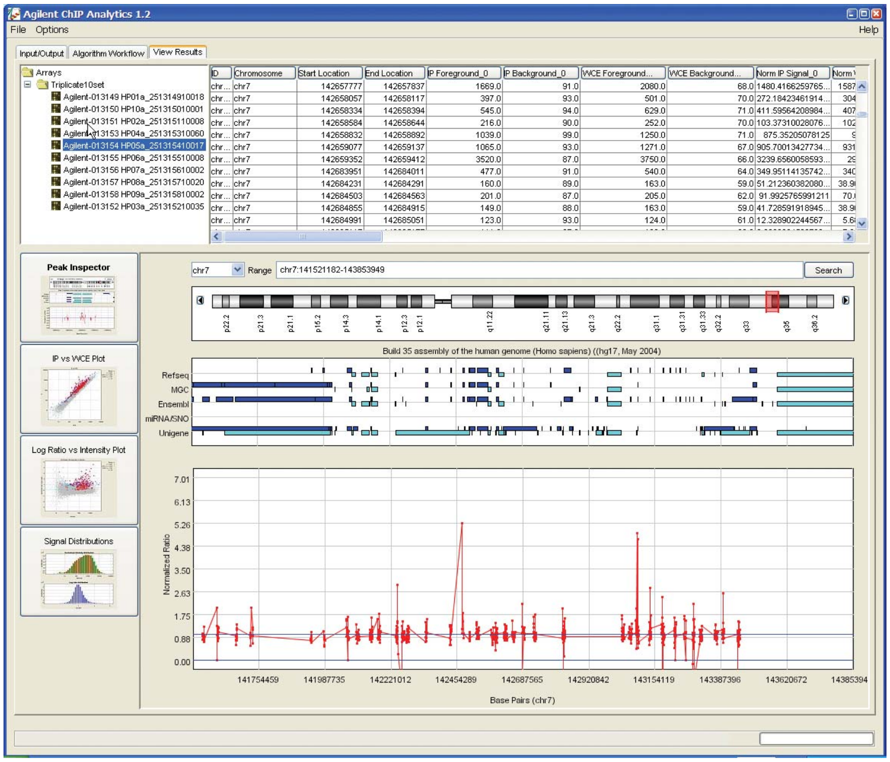
Agilent ChIP Analytics 1.2 Software

ChIP Analytics 1.2 software is an easy-to-use application for analyzing data from Agilent ChIP-on-chip microarrays. It accepts data output from Agilent Feature Extraction software or AXON GenePix® software and analyzes the significance of protein binding events without extensive processing and manipulation. The software takes advantage of the high-speed statistical analysis functions that include user-configurable heuristics for binding event identification based on p-values and adjacent probes, as well as inter- and intra-array intensity normalization and error modeling.

Features and Benefits at a Glance

- New visualization capabilities with reference genome, QC plots, and binding event data
- Peak detection algorithm for convenient visualization of binding sites
- Simultaneous analysis of sets of microarrays and experiments
- Output reports containing probe, sequence, and gene detail
- UCSC track report option allows visualization of binding event data in the UCSC Genome Browser
- Support for multiple biological and technical replicates



Arrays
- Triplicate10set
  - Agilent-013149 HP01a_251314910018
  - Agilent-013150 HP10a_251315010001
  - Agilent-013151 HP02a_251315110008
  - Agilent-013153 HP04a_251315310060
  - Agilent-013154 HP05a_251315410017
  - Agilent-013155 HP06a_251315510008
  - Agilent-013156 HP07a_251315610002
  - Agilent-013157 HP08a_251315710020
  - Agilent-013158 HP09a_251315810002
  - Agilent-013152 HP03a_251315210035

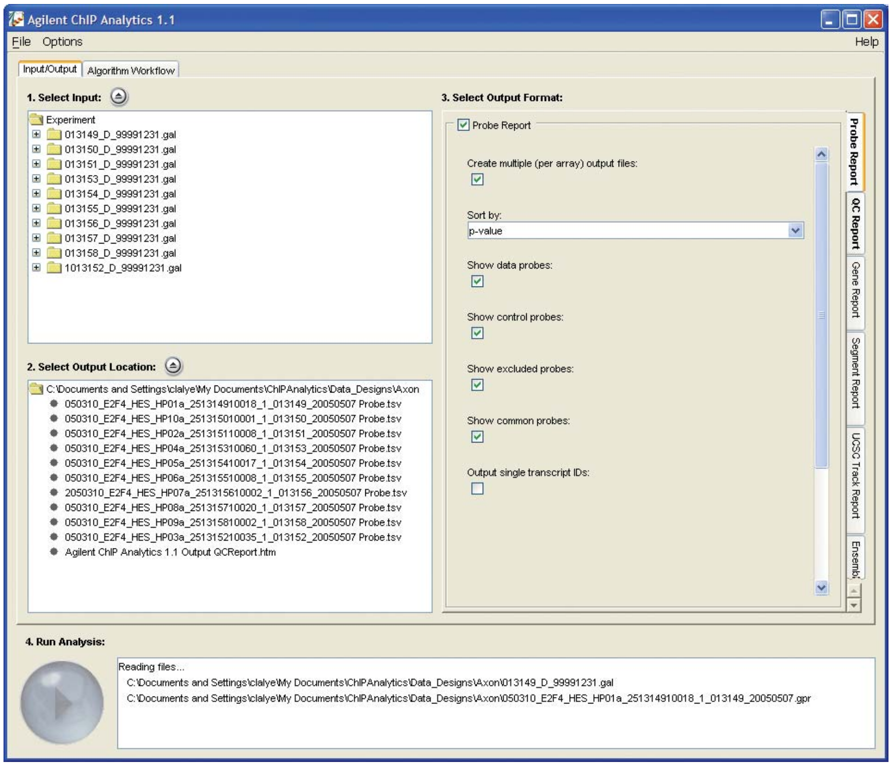
ID	Chromosome	Start Location	End Location	IP Foreground_0	IP Background_0	WCE Foreground...	WCE Background...	Norm IP Signal_0	Norm
chr...	chr7	142657777	142657837	1669.0	91.0	2080.0	68.0	1480.416259765...	1587
chr...	chr7	142658057	142658117	397.0	93.0	501.0	70.0	272.18423461914...	304
chr...	chr7	142658334	142658394	545.0	94.0	629.0	71.0	411.59564208984...	407
chr...	chr7	142658584	142658644	216.0	90.0	252.0	70.0	103.37310028076...	102
chr...	chr7	142658832	142658892	1039.0	99.0	1250.0	71.0	875.35205078125	9
chr...	chr7	142659077	142659137	1065.0	93.0	1271.0	67.0	905.70013427734...	931
chr...	chr7	142659352	142659412	3520.0	87.0	3750.0	66.0	3239.6560058593...	29
chr...	chr7	142683951	142684011	477.0	91.0	540.0	64.0	349.95114135742...	340
chr...	chr7	142684231	142684291	160.0	89.0	163.0	59.0	51.212360382080...	38.9
chr...	chr7	142684503	142684563	201.0	87.0	205.0	62.0	91.9925765991211	70.
chr...	chr7	142684855	142684915	149.0	88.0	163.0	59.0	41.728591918945...	38.9
chr...	chr7	142684991	142685051	123.0	93.0	124.0	61.0	12.328902244567...	5.6

chr7 Range chr7:141521182-143853949

Figure 1. The peak detection visualization feature allows inspection of the regions of interest and a display of nearby genomic features.

Simultaneous Analysis of Sets of Microarrays with Annotations

Overview of ChIP Analytics workflow and inputs and outputs. Software supports use of multiple biological and technical replicates.



1. Select Input:

Experiment
- 013149_D_99991231.gal
- 013150_D_99991231.gal
- 013151_D_99991231.gal
- 013153_D_99991231.gal
- 013154_D_99991231.gal
- 013155_D_99991231.gal
- 013156_D_99991231.gal
- 013157_D_99991231.gal
- 013158_D_99991231.gal
- 1013152_D_99991231.gal

2. Select Output Location:

C:\Documents and Settings\claye\My Documents\ChIPAnalytics\Data_Designs\Axon
- 050310_E2F4_HES_HP01a_251314910018_1_013149_20050507 Probe.tsv
- 050310_E2F4_HES_HP10a_251315010001_1_013150_20050507 Probe.tsv
- 050310_E2F4_HES_HP02a_251315110008_1_013151_20050507 Probe.tsv
- 050310_E2F4_HES_HP04a_251315310060_1_013153_20050507 Probe.tsv
- 050310_E2F4_HES_HP05a_251315410017_1_013154_20050507 Probe.tsv
- 050310_E2F4_HES_HP06a_251315510008_1_013155_20050507 Probe.tsv
- 2050310_E2F4_HES_HP07a_251315610002_1_013156_20050507 Probe.tsv
- 050310_E2F4_HES_HP08a_251315710020_1_013157_20050507 Probe.tsv
- 050310_E2F4_HES_HP09a_251315810002_1_013158_20050507 Probe.tsv
- 050310_E2F4_HES_HP03a_251315210035_1_013152_20050507 Probe.tsv
- Agilent ChIP Analytics 1.1 Output QCReport.htm

3. Select Output Format:

☑ Probe Report

Create multiple (per array) output files: ☑

Sort by: p-value

Show data probes: ☑

Show control probes: ☑

Show excluded probes: ☑

Show common probes: ☑

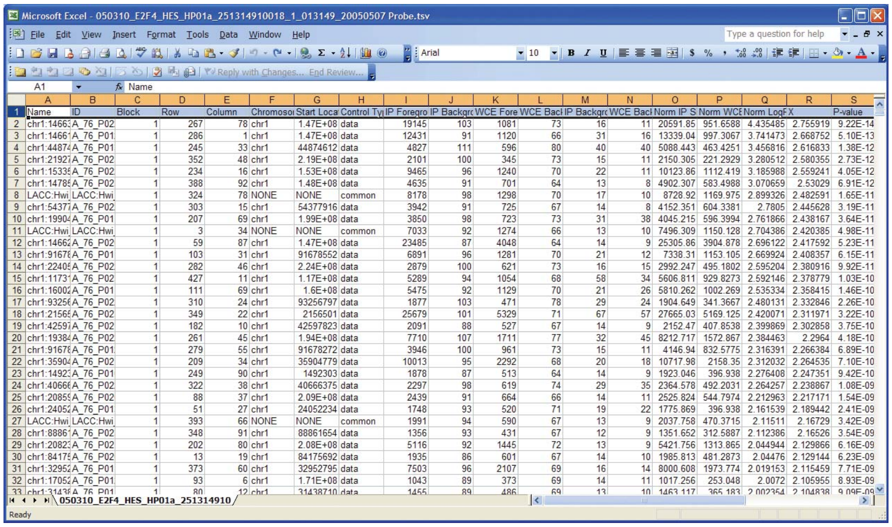
Output single transcript IDs: ☐

4. Run Analysis:

```
Reading files...
  C:\Documents and Settings\claye\My Documents\ChIPAnalytics\Data_Designs\Axon\013149_D_99991231.gal
  C:\Documents and Settings\claye\My Documents\ChIPAnalytics\Data_Designs\Axon\050310_E2F4_HES_HP01a_251314910018_1_013149_20050507.gpr
```

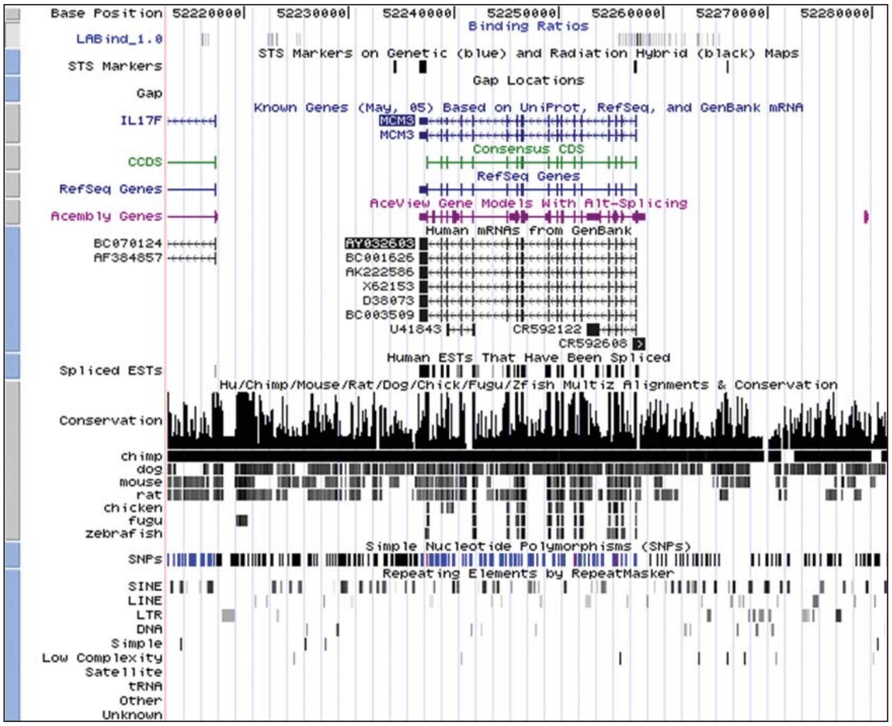
Output Reports Containing Probe, Sequence, and Gene Detail

Output allows identification of probes, genes, and genomic loci that exhibit significant binding. ChIP Analytics reports its findings in file formats that can be easily loaded into other analysis software.

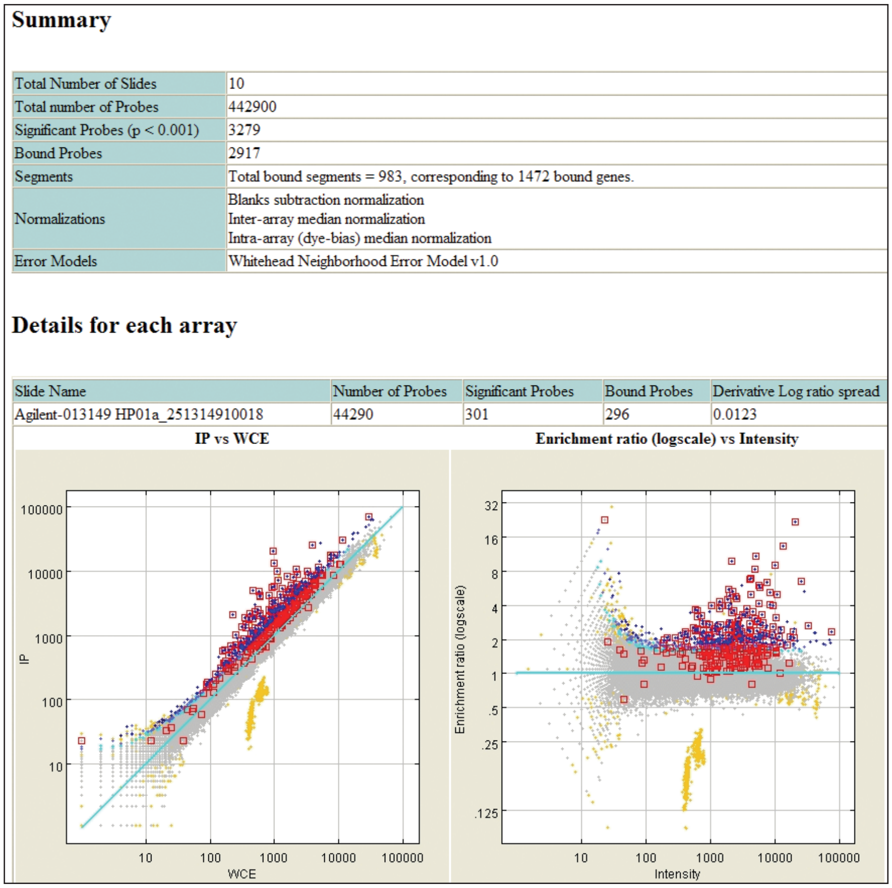


	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S
1	Name	ID	Block	Row	Column	Chromosoı	Start Loca	Control Tyı	IP Foregro	IP Backgrc	WCE Fore	WCE Bacl	IP Backgrc	WCE Bacl	Norm IP S	Norm WCE	Norm LogF	X	P-value
2	chr1:14663	A_76_P02	1	267	78	chr1	1.47E+08	data	19145	103	1081	73	16	11	20591.85	951.6588	4.435485	2.755919	9.22E-14
3	chr1:14661	A_76_P01	1	286	1	chr1	1.47E+08	data	12431	91	1120	66	31	16	13339.04	997.3067	3.741473	2.668752	5.10E-13
4	chr1:44874	A_76_P01	1	245	33	chr1	44874612	data	4827	111	596	80	40	40	5088.443	463.4251	3.456816	2.616833	1.38E-12
5	chr1:21927	A_76_P02	1	352	48	chr1	2.19E+08	data	2101	100	345	73	15	11	2150.305	221.2929	3.280512	2.580355	2.73E-12
6	chr1:15335	A_76_P02	1	234	16	chr1	1.53E+08	data	9465	96	1240	70	22	11	10123.86	1112.419	3.185988	2.559241	4.05E-12
7	chr1:14785	A_76_P02	1	388	92	chr1	1.48E+08	data	4635	91	701	64	13	8	4902.307	583.4988	3.070659	2.53029	6.91E-12
8	LACC:Hwi_	LACC:Hwi_	1	324	78	NONE	NONE	common	8178	98	1298	70	17	10	8728.92	1169.975	2.899326	2.482591	1.65E-11
9	chr1:54377	A_76_P02	1	303	15	chr1	54377916	data	3942	91	725	67	14	8	4152.351	604.3381	2.7805	2.445628	3.19E-11
10	chr1:19904	A_76_P01	1	207	69	chr1	1.99E+08	data	3850	98	723	73	31	38	4045.215	596.3994	2.761866	2.438167	3.64E-11
11	LACC:Hwi_	LACC:Hwi_	1	3	34	NONE	NONE	common	7033	92	1274	66	13	10	7496.309	1150.128	2.704386	2.420385	4.98E-11
12	chr1:14662	A_76_P02	1	59	87	chr1	1.47E+08	data	23485	87	4048	64	14	9	25305.86	3904.878	2.696122	2.417592	5.23E-11
13	chr1:91678	A_76_P01	1	103	31	chr1	91678552	data	6891	96	1281	70	21	12	7338.31	1153.105	2.669924	2.408357	6.15E-11
14	chr1:22405	A_76_P02	1	282	46	chr1	2.24E+08	data	2879	100	621	73	16	15	2992.247	495.1802	2.595204	2.380916	9.92E-11
15	chr1:11731	A_76_P02	1	427	11	chr1	1.17E+08	data	5289	94	1054	68	58	34	5606.811	929.8273	2.592146	2.378779	1.03E-10
16	chr1:16002	A_76_P01	1	111	69	chr1	1.6E+08	data	5475	92	1129	70	21	26	5810.262	1002.269	2.535334	2.358415	1.46E-10
17	chr1:93256	A_76_P02	1	310	24	chr1	93256797	data	1877	103	471	78	29	24	1904.649	341.3667	2.480131	2.332846	2.26E-10
18	chr1:21565	A_76_P02	1	349	22	chr1	2156501	data	25679	101	5329	71	67	57	27665.03	5169.125	2.420071	2.311971	3.22E-10
19	chr1:42597	A_76_P02	1	182	10	chr1	42597823	data	2091	88	527	67	14	9	2152.47	407.8538	2.399869	2.302858	3.75E-10
20	chr1:19384	A_76_P02	1	261	45	chr1	1.94E+08	data	7710	107	1711	77	32	45	8212.717	1572.867	2.384463	2.2964	4.18E-10
21	chr1:91678	A_76_P01	1	279	55	chr1	91678272	data	3946	100	961	73	15	11	4146.94	832.5775	2.316391	2.266384	6.89E-10
22	chr1:35904	A_76_P02	1	209	34	chr1	35904779	data	10013	95	2292	68	20	18	10717.98	2158.35	2.312032	2.264535	7.10E-10
23	chr1:14923	A_76_P01	1	249	90	chr1	1492303	data	1878	87	513	64	14	9	1923.046	396.938	2.276408	2.247351	9.42E-10
24	chr1:40666	A_76_P02	1	322	38	chr1	40666375	data	2297	98	619	74	29	35	2364.578	492.2031	2.264257	2.238867	1.08E-09
25	chr1:20859	A_76_P02	1	88	37	chr1	2.09E+08	data	2439	91	664	66	14	11	2525.824	544.7974	2.212963	2.217171	1.54E-09
26	chr1:24052	A_76_P01	1	51	27	chr1	24052234	data	1748	93	520	71	19	22	1775.869	396.938	2.161539	2.189442	2.41E-09
27	LACC:Hwi_	LACC:Hwi_	1	393	66	NONE	NONE	common	1991	94	590	67	13	9	2037.758	470.3715	2.11511	2.16729	3.42E-09
28	chr1:88861	A_76_P02	1	348	91	chr1	88861654	data	1356	93	431	67	12	9	1351.652	312.5887	2.112386	2.16526	3.54E-09
29	chr1:20823	A_76_P02	1	202	80	chr1	2.08E+08	data	5116	92	1445	72	13	9	5421.756	1313.865	2.044944	2.129866	6.16E-09
30	chr1:84175	A_76_P02	1	13	19	chr1	84175692	data	1935	86	601	67	14	10	1985.813	481.2873	2.04476	2.129144	6.23E-09
31	chr1:32952	A_76_P01	1	373	60	chr1	32952795	data	7503	96	2107	69	16	14	8000.608	1973.774	2.019153	2.115459	7.71E-09
32	chr1:17052	A_76_P01	1	93	6	chr1	1.71E+08	data	1043	89	373	69	14	11	1017.256	253.048	2.0072	2.105955	8.93E-09
33	chr1:31438	A_76_P01	1	80	12	chr1	31438710	data	1455	89	486	69	13	10	1463.117	365.183	2.002354	2.104838	9.09E-09

Option of UCSC Track Report
Compatibility with the UCSC Genome Browser view allows you to easily visualize binding data (shown here is a May 2004 human reference sequence based on NCBI Build 35).



QC Report
Shown here is an example of the convenient, at-a-glance visualization for key experimental elements. The QC report shows a plot of the immunoprecipitated extract (IP) vs. the whole cell extract (WCE) and allows identification of enriched vs. unenriched targets.



Summary

Total Number of Slides	10
Total number of Probes	442900
Significant Probes (p < 0.001)	3279
Bound Probes	2917
Segments	Total bound segments = 983, corresponding to 1472 bound genes.
Normalizations	Blanks subtraction normalization Inter-array median normalization Intra-array (dye-bias) median normalization
Error Models	Whitehead Neighborhood Error Model v1.0

Details for each array

Slide Name	Number of Probes	Significant Probes	Bound Probes	Derivative Log ratio spread
Agilent-013149 HP01a_251314910018	44290	301	296	0.0123

Specifications

Product number (commercial use)	**G4477AA, option CML**
Product number (academic/non-profit use)	**G4477AA, option NFP**
License type and duration	**One year, single workstation**
Operating system	**Windows® 2000** **Windows® XP SP2** **Mac OS X**
RAM	**Minimum 512 MB (1 GB or more preferred)**
Hard disk space	**200 MB (software)** **2 GB or more (design files and Feature Extraction data files)**
Additional software	**Internet Explorer 6.0 or later** **Adobe® Reader 4.0 or later** **Java 1.4.2_08 or better**
CPU	**2.0 GHz processor or faster**

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Printed in the U.S.A. April 26, 2006
5989-4360EN