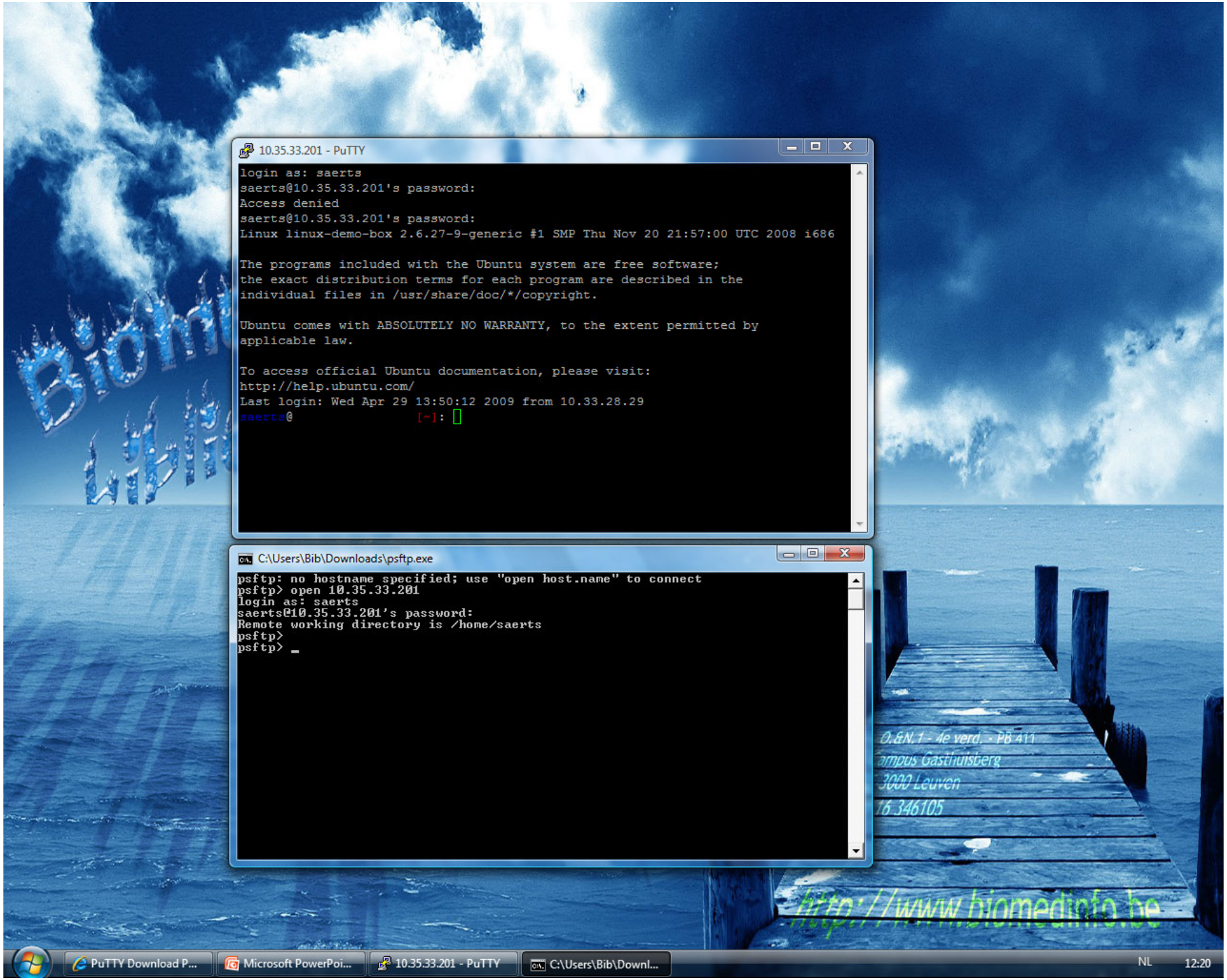

10.35.33.201 - PuTTY
login as: saerts
saerts@10.35.33.201's password:
Access denied
saerts@10.35.33.201's password:
Linux linux-demo-box 2.6.27-9-generic #1 SMP Thu Nov 20 21:57:00 UTC 2008 i686
The programs included with the Ubuntu system are free software;
the exact distribution terms for each program are described in the
individual files in /usr/share/doc/*/copyright.
Ubuntu comes with ABSOLUTELY NO WARRANTY, to the extent permitted by
applicable law.
To access official Ubuntu documentation, please visit:
http://help.ubuntu.com/
Last login: Wed Apr 29 13:50:12 2009 from 10.33.28.29
saerts@ [~]:
C:\Users\Bib\Downloads\psftp.exe
psftp: no hostname specified; use "open host.name" to connect
psftp> open 10.35.33.201
login as: saerts
saerts@10.35.33.201's password:
Remote working directory is /home/saerts
psftp>
psftp>
PuTTY Download P...
Microsoft PowerPoi...
10.35.33.201 - PuTTY
C:\Users\Bib\Downl...
NL
12:20

Human chr11:31,250,001-32,250,000 - UCSC Genome Browser v204 - Windows Internet Explorer provided by Powered By IT Groepdienst

File Edit View Favorites Tools Help

MGAS 762 Zoek Tijdschriften Boeken Databanken Nieuws [96 new] Ga naar

http://genome.ucsc.edu/cgi-bin/hgTracks ucsc genome

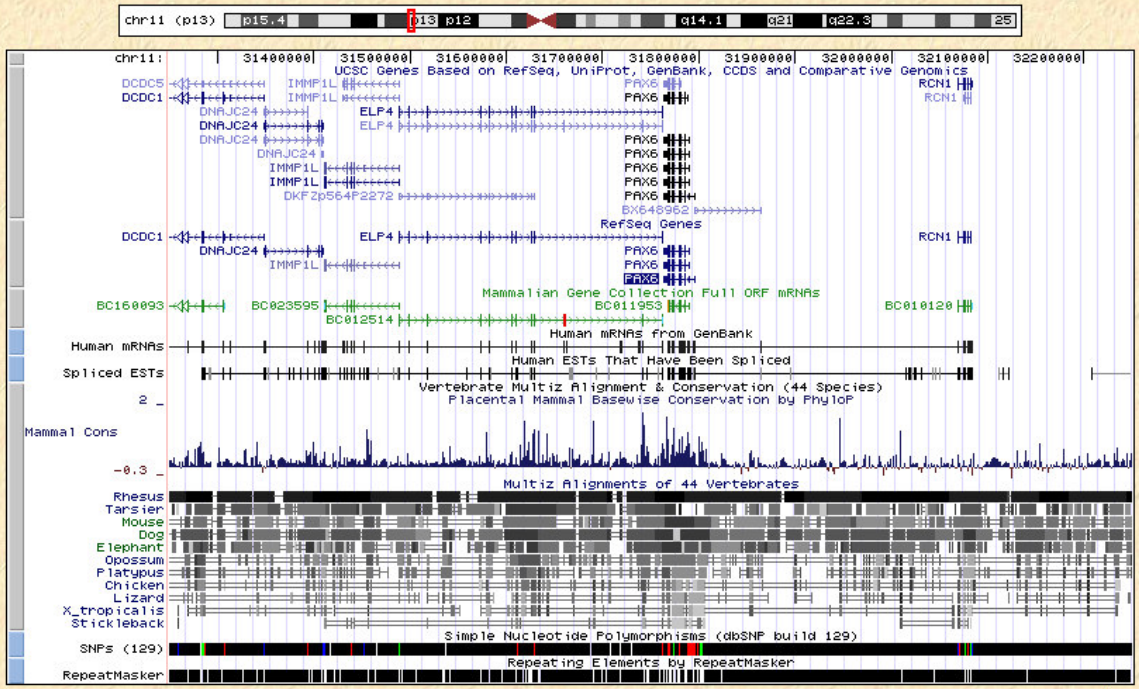
Page Tools

Home Genomes Blat Tables Gene Sorter PCR DNA Convert Ensembl NCBI PDF/PS Session Help

UCSC Genome Browser on Human Mar. 2006 Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x

position/search chr11:31,250,001-32,250,000 jump clear size 1,000,000 bp. configure



move start < 2.0 > Click on a feature for details. Click or drag in the base position track to zoom in. Click gray/blue bars on left for track options and descriptions. move end < 2.0 >

default tracks hide all add custom tracks configure reverse refresh

collapse all Use drop-down controls below and press refresh to alter tracks displayed. Tracks with lots of items will automatically be displayed in more compact modes. expand all

Mapping and Sequencing Tracks

refresh

Base Position	Chromosome Band	STS Markers	FISH Clones	Recomb Rate	Map Contigs
dense	hide	hide	hide	hide	hide
Assembly	Gap	Coverage	BAC End Pairs	Fosmid End Pairs	GC Percent

Done Internet | Protected Mode: On 100%

Human chr11:31,25... Microsoft PowerPoi... 10.35.33.201 - PuTTY C:\Users\Bib\Downl... NL 12:23

http://genome.ucsc.edu/cgi-bin/hgc?hgsid=131273568&g=htcGetDna2&table=&i=mixed&o=31250000&l=312 - Windows Internet Explorer pro

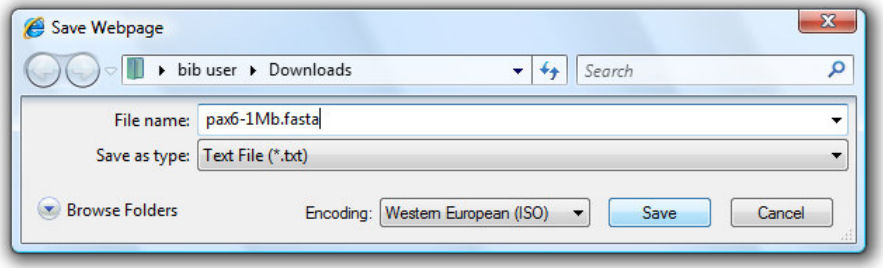
File Edit View Favorites Tools Help

MGAS 762 Zoek Tijdschriften Boeken Databanken Nieuws [96 new] Ga naar

http://genome.ucsc.edu/cgi-bin/hgc?hgsid=131273568&g=htcGetDna2&table=&i=mixed&o=31250000&l=31250000&r=32250000&getDnaPos=chr11%3A31%2C2 ucsc genome

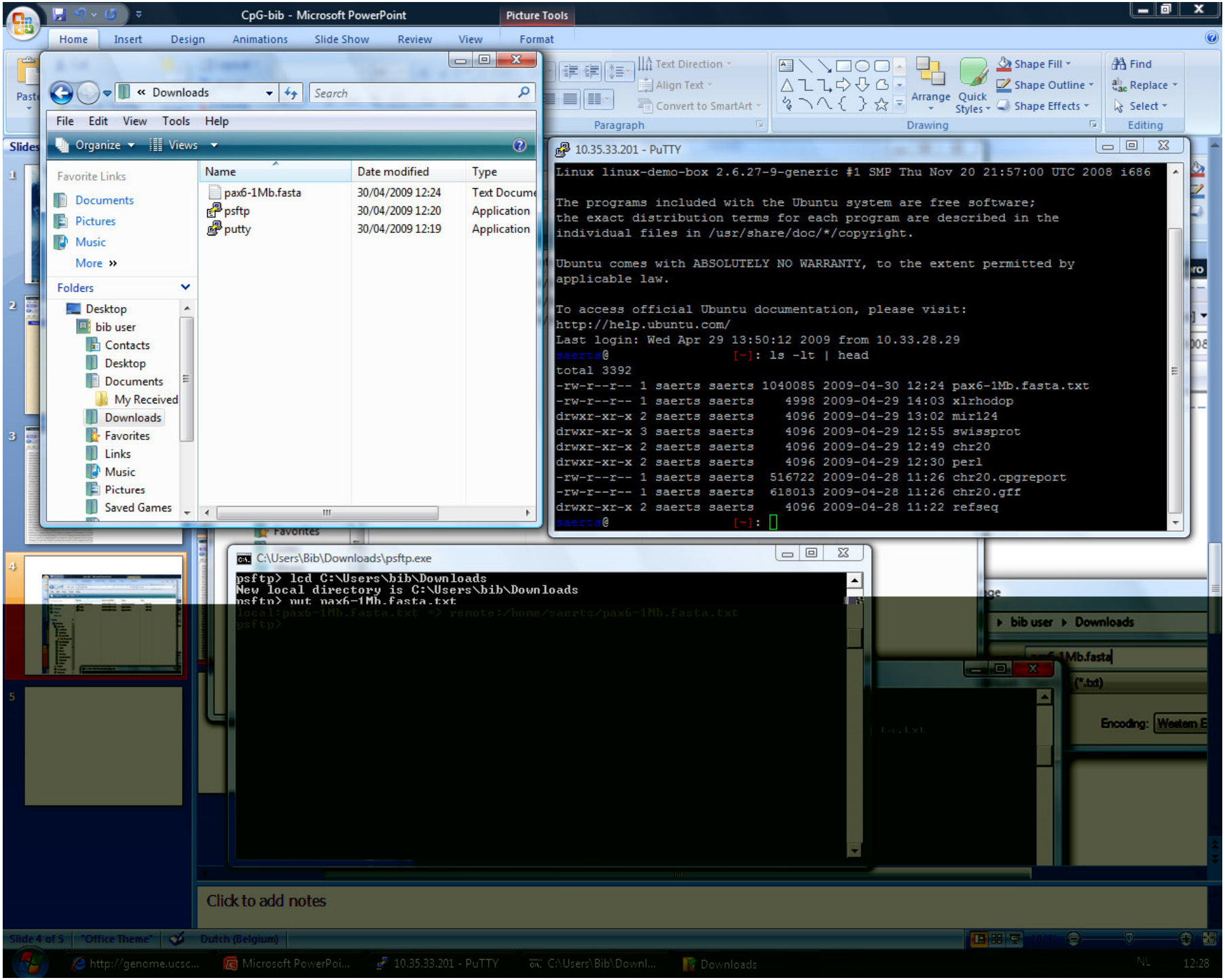
Page Tools

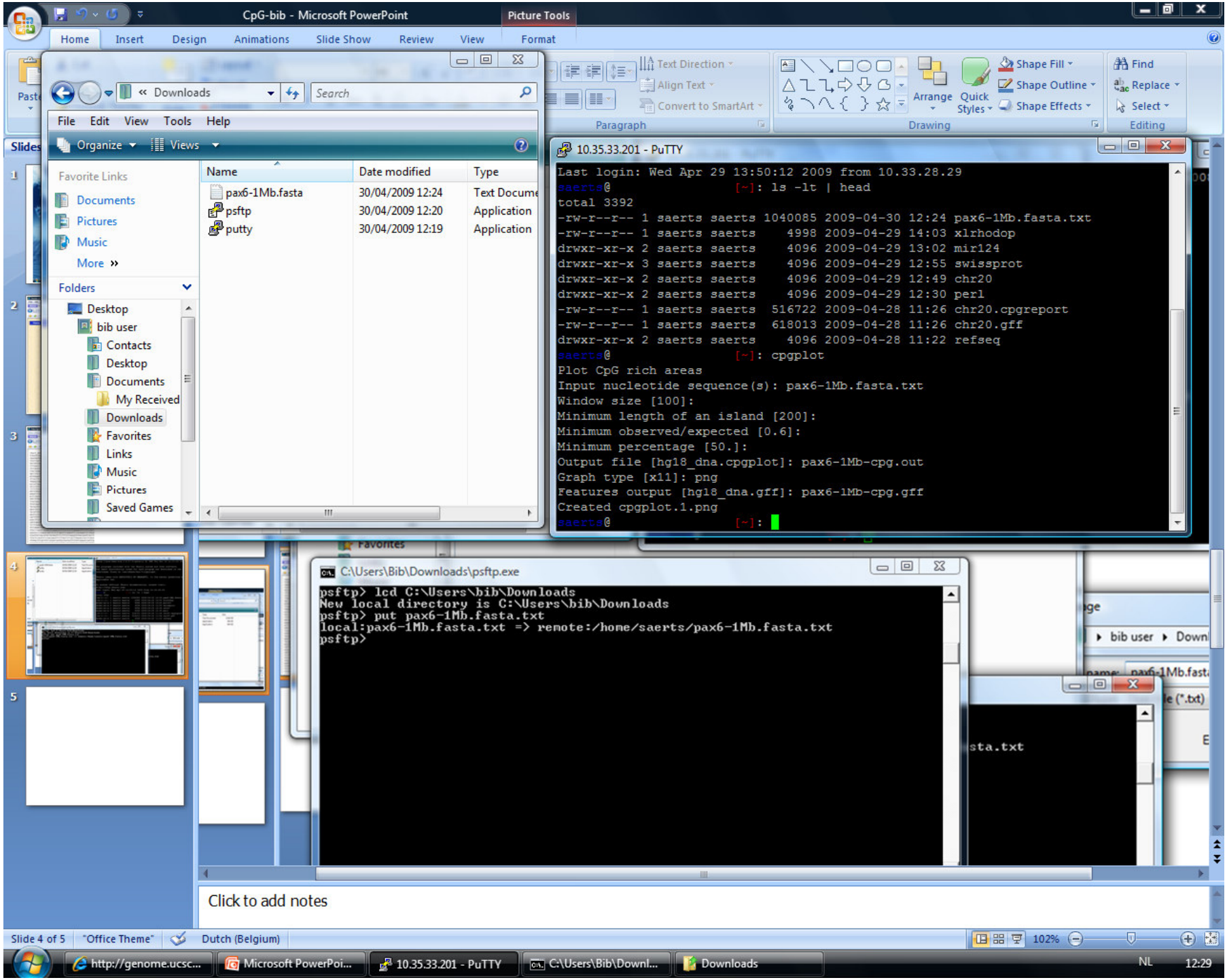
```
>hg18_dna range=chr11:31250001-32250000 5'pad=0 3'pad=0 strand=+ repeatMasking=none
TCAGGCCAGGCATGGTAGCTCATGCCTGTAATCCCAGCATTTTGGGAGGC
CAAGGAGGGCAGATCACGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACA
TGGTTGATTCCCCATCTCTACTAAAAATACAAAAATTAGCTGGGTGTGGT
GGCGGGCACCTGTAATCCCAGCTACTCAGGAGGCTGAGGCGGGAGAATCA
CTTGAACCCAGCAGGCGGAGGCTGCAGTGAGCCGAGATCGTGCCATTGCA
CTCCAGCCTGGTTGGCAGGGTGAGACTCCATCTAAAAAAAAAAAAAAAAA
CCACCAGAGCTGATAAGACGTTTTCACTATCACAAGAACAGCACGGGAAA
GACCTGCCACCATGACTCAATTACCTCCCATCAGGTCCCTCCCACAACAT
ATGGAAATTCAATATGAGATTTGGGTAGGGACATAGCCAAACCATATCAT
TTCACTTCTCAAATCTCATGACCCCTCCCAAATCTCATGTCCTCACATTT
TGAAACCAATCATGCCTTCCCGACAGTCCCTCAAAGTCTTAATTCATTTT
AGCATTAACTCAAAAGTCCACAGTCCAAAGTTTCATCTGAGACAAAGAAA
GTCCCTTCCACCTATGAGCCAGTAAATTAAAATAAAAAGCAAGTTAATTA
CTCTCTAGATAAAATGGGGGTACAGGCATTGGATAAATACAGTTGTTCCA
AATGGGAGAAACTGGAGAAAACAAATGGGCTACAGGCCCCATGCAAGTCT
AAAATCCAACAGGGTGGTCAAATCTTAAAACTCCAAAATGATCTCCTTTG
ACTCCATGTCTCACATACAGGTCATGCTGACGCAAGAAGGGGGTTCCCAT
GGTCTTGGGCAGTTCTACTCCTGCGGCTTTGCAGGGCACAGCCGCTGCTT
TCATGGGCTGGTGTTGAATGTCTGAAGCATTTCCAGATGCATGGTGCAAG
TTGTCAGTGGATCTACCATTTTGAGGTCTAGAGGATGGTGGTCCTCTTCT
TACAGGTCCACTAGGCAGTGCCCCAGTAGGAACTCTGTGTAGGGACTCAC
AAGCTGCCAAGGCTTGGGGCTTGCACCCTCTGAAGCCATGGCCTGAACTC
TACATTGGCCCCTTTCAGCCACGGCTGGAGCAGCTGGGATGCAGGGCACC
AAGTCCCTAGACTGCAATGTAGTATGGGACCCTGGGCCCGGCCCACGAAC
CATTTTTTCCTCCTAGGCCTCCAGGCTTGTGATGGGGGGCATTGCTGTGA
AGACTTCTGACATGCCCTGGAGACACTTTCCCCATTGTCTTGGGGATTAA
CATTCAGCTCCTCATTATTTATACAAATTTCTGCAGCCAGCTTGAATTTC
TCCTCAGAAAATGGGATTTTATTTTCTATTGAATTGTTAGGCTGTAAATT
TTCCAAACTTTTATGCTCTGCTTCCTTTATAAAACTGAATGCCTTTAACG
GTACCCAAGTCACATCTTGAATGCTTTGCTGCTTAGAAGTTTCTTCCACC
AGATACCCTAAATCATCTCTCTCAATTTCAAAGTTCCACAAATCTCTAGG
GCAGGGGCAACATACCACAAGTCTCTTTGCTAAAATATAACAAGTCACCT
TTGCTCCAGTTCCCAACAAGTTCCTTATCTCCATTTAAGACCACCTCAGC
CTGGACTTCATTGTCCATATCAGTATCAGCATTTTGGTCAAAGCCATTCA
ACAAGTCTCTAGGGAGCTCCAAACTTTCCAATTTTGTCCTATCTTCTTTT
GAGCTCTCCAAACTGTTCCAACCTCTAACTGTTACTCAGTTCGAAAGTCG
CTTCCACATTTTCAGGTATCTACAGCAGCACCCCACTCTTGGTACCAATT
TACTGTATTAGTCCATTTCACACTGCTGAGAAAGACATACCCAAGAATGG
GCAATTTATAAAAGAAAGAGGTTTAGTGGACTTACAGTTCCACATGGCTG
GGGAGGCTTCACACTCATGGTAGAAGGCAAATCGGAGCAAGTCATGTCTT
ACATGGATGGCAGCAAGCAGAGAGAGAGCTTGTGCAGGGAAACTCCTCCT
TATAAAACCATCAGATCGCATGAGACTAACTATCATGAGAACAGCATGTG
AAAGACCCATCCCCATGACTCAATTACCTCCCACCTGGGTGCCTCCCACA
ACATGTGGGAATTAAAGATGAGATTTGGGTGGGGACACAACCAAACCATA
TCAAGCATGAACAAATCCTGAGATACAAGAATCCACTATTTTTTCTCCTG
CTTTCTTGTCTTCTTCATAGGATCATGCATATTCATTCACTGGGGTTTAT
CAAGATAAGTTCTAGCCTTCTTTCTGCCCCTCTCTTAAGGCAATCTAAAT
GGTACCCCAACATTTCATCTTCCATTTACATACCGACAACTCCCAAATTG
ATATGTTTCTTTTATTCATCAATTCAAAATATTATTGACTACTAATATCT
CCCAAGTGCCTGGATATGGCAGTGAGCAAAACCAGCCAGGTTCTTGTTCT
```

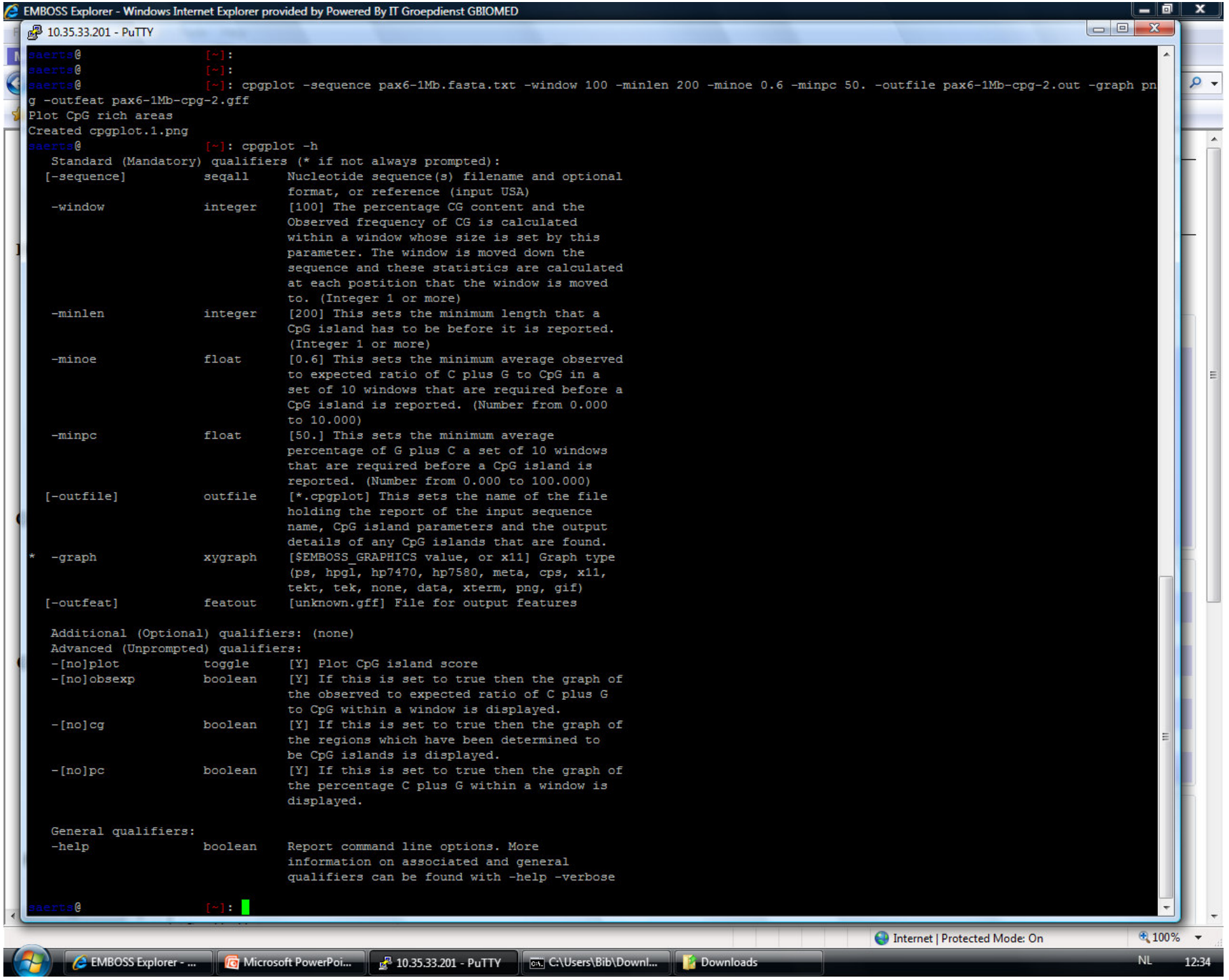


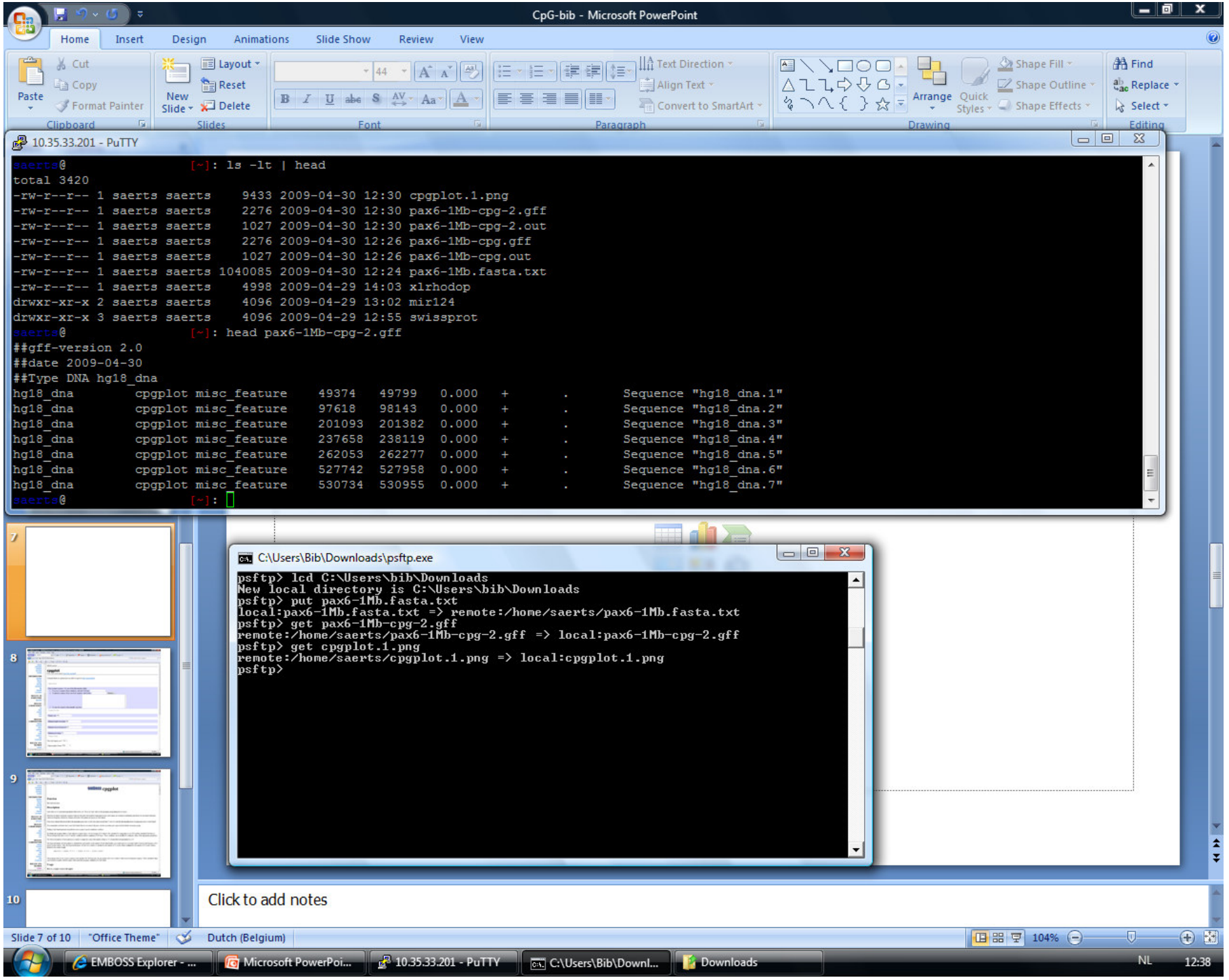
Done Internet | Protected Mode: On 100%

http://genome.ucsc... Microsoft PowerPoi... 10.35.33.201 - PuTTY C:\Users\Bib\Downl... NL 12:24


CpG-bib - Microsoft PowerPoint
Picture Tools
Home
Insert
Design
Animations
Slide Show
Review
View
Format
Downloads
Search
File Edit View Tools Help
Organize
Views
Favorite Links
Documents
Pictures
Music
More
Folders
Desktop
bib user
Contacts
Desktop
Documents
My Received
Downloads
Favorites
Links
Music
Pictures
Saved Games
Name
Date modified
Type
pax6-1Mb.fasta 30/04/2009 12:24 Text Docume
psftp 30/04/2009 12:20 Application
putty 30/04/2009 12:19 Application
10.35.33.201 - PuTTY
Linux linux-demo-box 2.6.27-9-generic #1 SMP Thu Nov 20 21:57:00 UTC 2008 i686
The programs included with the Ubuntu system are free software;
the exact distribution terms for each program are described in the
individual files in /usr/share/doc/*/copyright.
Ubuntu comes with ABSOLUTELY NO WARRANTY, to the extent permitted by
applicable law.
To access official Ubuntu documentation, please visit:
http://help.ubuntu.com/
Last login: Wed Apr 29 13:50:12 2009 from 10.33.28.29
saerts@ [~]: ls -lt | head
total 3392
-rw-r--r-- 1 saerts saerts 1040085 2009-04-30 12:24 pax6-1Mb.fasta.txt
-rw-r--r-- 1 saerts saerts 4998 2009-04-29 14:03 xlrhodop
drwxr-xr-x 2 saerts saerts 4096 2009-04-29 13:02 mir124
drwxr-xr-x 3 saerts saerts 4096 2009-04-29 12:55 swissprot
drwxr-xr-x 2 saerts saerts 4096 2009-04-29 12:49 chr20
drwxr-xr-x 2 saerts saerts 4096 2009-04-29 12:30 perl
-rw-r--r-- 1 saerts saerts 516722 2009-04-28 11:26 chr20.cpgreport
-rw-r--r-- 1 saerts saerts 618013 2009-04-28 11:26 chr20.gff
drwxr-xr-x 2 saerts saerts 4096 2009-04-28 11:22 refseq
saerts@ [~]:
C:\Users\Bib\Downloads\psftp.exe
psftp> lcd C:\Users\bib\Downloads
New local directory is C:\Users\bib\Downloads
psftp> put pax6-1Mb.fasta.txt
local:pax6-1Mb.fasta.txt => remote:/home/saerts/pax6-1Mb.fasta.txt
psftp>
bib user ▸ Downloads
Encoding:
Click to add notes
Slide 4 of 5
"Office Theme"
Dutch (Belgium)
http://genome.ucsc...
Microsoft PowerPoi...
10.35.33.201 - PuTTY
C:\Users\Bib\Downl...
Downloads
NL
12:28


CpG-bib - Microsoft PowerPoint
Picture Tools
Home
Insert
Design
Animations
Slide Show
Review
View
Format
Downloads
Search
File Edit View Tools Help
Organize
Views
Favorite Links
Documents
Pictures
Music
More
Folders
Desktop
bib user
Contacts
Desktop
Documents
My Received
Downloads
Favorites
Links
Music
Pictures
Saved Games
Name
Date modified
Type
pax6-1Mb.fasta 30/04/2009 12:24 Text Docume
psftp 30/04/2009 12:20 Application
putty 30/04/2009 12:19 Application
10.35.33.201 - PuTTY
Last login: Wed Apr 29 13:50:12 2009 from 10.33.28.29
saerts@ [~]: ls -lt | head
total 3392
-rw-r--r-- 1 saerts saerts 1040085 2009-04-30 12:24 pax6-1Mb.fasta.txt
-rw-r--r-- 1 saerts saerts 4998 2009-04-29 14:03 xlrhodop
drwxr-xr-x 2 saerts saerts 4096 2009-04-29 13:02 mir124
drwxr-xr-x 3 saerts saerts 4096 2009-04-29 12:55 swissprot
drwxr-xr-x 2 saerts saerts 4096 2009-04-29 12:49 chr20
drwxr-xr-x 2 saerts saerts 4096 2009-04-29 12:30 perl
-rw-r--r-- 1 saerts saerts 516722 2009-04-28 11:26 chr20.cpgreport
-rw-r--r-- 1 saerts saerts 618013 2009-04-28 11:26 chr20.gff
drwxr-xr-x 2 saerts saerts 4096 2009-04-28 11:22 refseq
saerts@ [~]: cpgplot
Plot CpG rich areas
Input nucleotide sequence(s): pax6-1Mb.fasta.txt
Window size [100]:
Minimum length of an island [200]:
Minimum observed/expected [0.6]:
Minimum percentage [50.]:
Output file [hg18_dna.cpgplot]: pax6-1Mb-cpg.out
Graph type [x11]: png
Features output [hg18_dna.gff]: pax6-1Mb-cpg.gff
Created cpgplot.1.png
saerts@ [~]:
C:\Users\Bib\Downloads\psftp.exe
psftp> lcd C:\Users\bib\Downloads
New local directory is C:\Users\bib\Downloads
psftp> put pax6-1Mb.fasta.txt
local:pax6-1Mb.fasta.txt => remote:/home/saerts/pax6-1Mb.fasta.txt
psftp>
Click to add notes
Slide 4 of 5
"Office Theme"
Dutch (Belgium)
102%
http://genome.ucsc...
Microsoft PowerPoi...
10.35.33.201 - PuTTY
C:\Users\Bib\Downl...
Downloads
NL
12:29


EMBOSS Explorer - Windows Internet Explorer provided by Powered By IT Groepdienst GBIOMED
10.35.33.201 - PuTTY
saerts@ [~]:
saerts@ [~]:
saerts@ [~]: cpgplot -sequence pax6-1Mb.fasta.txt -window 100 -minlen 200 -minoe 0.6 -minpc 50. -outfile pax6-1Mb-cpg-2.out -graph png -outfeat pax6-1Mb-cpg-2.gff
Plot CpG rich areas
Created cpgplot.1.png
saerts@ [~]: cpgplot -h
Standard (Mandatory) qualifiers (* if not always prompted):
[-sequence] seqall Nucleotide sequence(s) filename and optional format, or reference (input USA)
-window integer [100] The percentage CG content and the Observed frequency of CG is calculated within a window whose size is set by this parameter. The window is moved down the sequence and these statistics are calculated at each postition that the window is moved to. (Integer 1 or more)
-minlen integer [200] This sets the minimum length that a CpG island has to be before it is reported. (Integer 1 or more)
-minoe float [0.6] This sets the minimum average observed to expected ratio of C plus G to CpG in a set of 10 windows that are required before a CpG island is reported. (Number from 0.000 to 10.000)
-minpc float [50.] This sets the minimum average percentage of G plus C a set of 10 windows that are required before a CpG island is reported. (Number from 0.000 to 100.000)
[-outfile] outfile [*.cpgplot] This sets the name of the file holding the report of the input sequence name, CpG island parameters and the output details of any CpG islands that are found.
* -graph xygraph [$EMBOSS_GRAPHICS value, or x11] Graph type (ps, hpgl, hp7470, hp7580, meta, cps, x11, tekt, tek, none, data, xterm, png, gif)
[-outfeat] featout [unknown.gff] File for output features
Additional (Optional) qualifiers: (none)
Advanced (Unprompted) qualifiers:
-[no]plot toggle [Y] Plot CpG island score
-[no]obsexp boolean [Y] If this is set to true then the graph of the observed to expected ratio of C plus G to CpG within a window is displayed.
-[no]cg boolean [Y] If this is set to true then the graph of the regions which have been determined to be CpG islands is displayed.
-[no]pc boolean [Y] If this is set to true then the graph of the percentage C plus G within a window is displayed.
General qualifiers:
-help boolean Report command line options. More information on associated and general qualifiers can be found with -help -verbose
saerts@ [~]:
Internet | Protected Mode: On
100%
EMBOSS Explorer - ...
Microsoft PowerPoi...
10.35.33.201 - PuTTY
C:\Users\Bib\Downl...
Downloads
NL
12:34


CpG-bib - Microsoft PowerPoint
Home
Insert
Design
Animations
Slide Show
Review
View
Paste
Cut
Copy
Format Painter
Clipboard
New Slide
Layout
Reset
Delete
Slides
Font
Text Direction
Align Text
Convert to SmartArt
Paragraph
Arrange
Quick Styles
Shape Fill
Shape Outline
Shape Effects
Drawing
Find
Replace
Select
Editing
10.35.33.201 - PuTTY
saerts@ [~]: ls -lt | head
total 3420
-rw-r--r-- 1 saerts saerts 9433 2009-04-30 12:30 cpgplot.1.png
-rw-r--r-- 1 saerts saerts 2276 2009-04-30 12:30 pax6-1Mb-cpg-2.gff
-rw-r--r-- 1 saerts saerts 1027 2009-04-30 12:30 pax6-1Mb-cpg-2.out
-rw-r--r-- 1 saerts saerts 2276 2009-04-30 12:26 pax6-1Mb-cpg.gff
-rw-r--r-- 1 saerts saerts 1027 2009-04-30 12:26 pax6-1Mb-cpg.out
-rw-r--r-- 1 saerts saerts 1040085 2009-04-30 12:24 pax6-1Mb.fasta.txt
-rw-r--r-- 1 saerts saerts 4998 2009-04-29 14:03 xlrhodop
drwxr-xr-x 2 saerts saerts 4096 2009-04-29 13:02 mir124
drwxr-xr-x 3 saerts saerts 4096 2009-04-29 12:55 swissprot
saerts@ [~]: head pax6-1Mb-cpg-2.gff
##gff-version 2.0
##date 2009-04-30
##Type DNA hg18_dna
hg18_dna cpgplot misc_feature 49374 49799 0.000 + . Sequence "hg18_dna.1"
hg18_dna cpgplot misc_feature 97618 98143 0.000 + . Sequence "hg18_dna.2"
hg18_dna cpgplot misc_feature 201093 201382 0.000 + . Sequence "hg18_dna.3"
hg18_dna cpgplot misc_feature 237658 238119 0.000 + . Sequence "hg18_dna.4"
hg18_dna cpgplot misc_feature 262053 262277 0.000 + . Sequence "hg18_dna.5"
hg18_dna cpgplot misc_feature 527742 527958 0.000 + . Sequence "hg18_dna.6"
hg18_dna cpgplot misc_feature 530734 530955 0.000 + . Sequence "hg18_dna.7"
saerts@ [~]:
C:\Users\Bib\Downloads\psftp.exe
psftp> lcd C:\Users\bib\Downloads
New local directory is C:\Users\bib\Downloads
psftp> put pax6-1Mb.fasta.txt
local:pax6-1Mb.fasta.txt => remote:/home/saerts/pax6-1Mb.fasta.txt
psftp> get pax6-1Mb-cpg-2.gff
remote:/home/saerts/pax6-1Mb-cpg-2.gff => local:pax6-1Mb-cpg-2.gff
psftp> get cpgplot.1.png
remote:/home/saerts/cpgplot.1.png => local:cpgplot.1.png
psftp>
Click to add notes
Slide 7 of 10
"Office Theme"
Dutch (Belgium)
104%
EMBOSS Explorer - ...
Microsoft PowerPoi...
10.35.33.201 - PuTTY
C:\Users\Bib\Downl...
Downloads
NL
12:38

C:\Users\Bib\Downloads\psftp.exe

```
psftp> lcd C:\Users\bib\Downloads
New local directory is C:\Users\bib\Downloads
psftp> put pax6-1Mb.fasta.txt
local:pax6-1Mb.fasta.txt => remote:/home/saerts/pax6-1Mb.fasta.txt
psftp> get pax6-1Mb-cpg-2.gff
remote:/home/saerts/pax6-1Mb-cpg-2.gff => local:pax6-1Mb-cpg-2.gff
psftp> get cpgplot.1.png
remote:/home/saerts/cpgplot.1.png => local:cpgplot.1.png
psftp>
```

bib user ▸ Downloads

Search

File Edit View Tools Help

Organize Views Preview Print

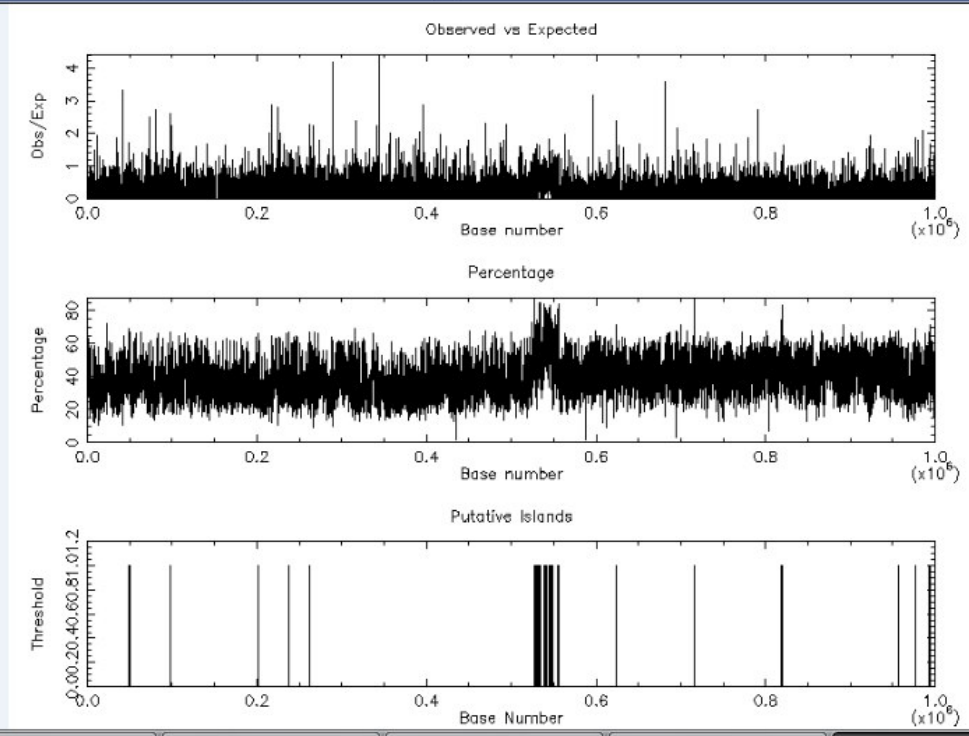
Favorite Links
- Documents
- Pictures
- Music
- More »

Folders
- Desktop
- bib user
  - Contacts
  - Desktop
  - Documents
  - My Received
  - Downloads
  - Favorites
  - Links

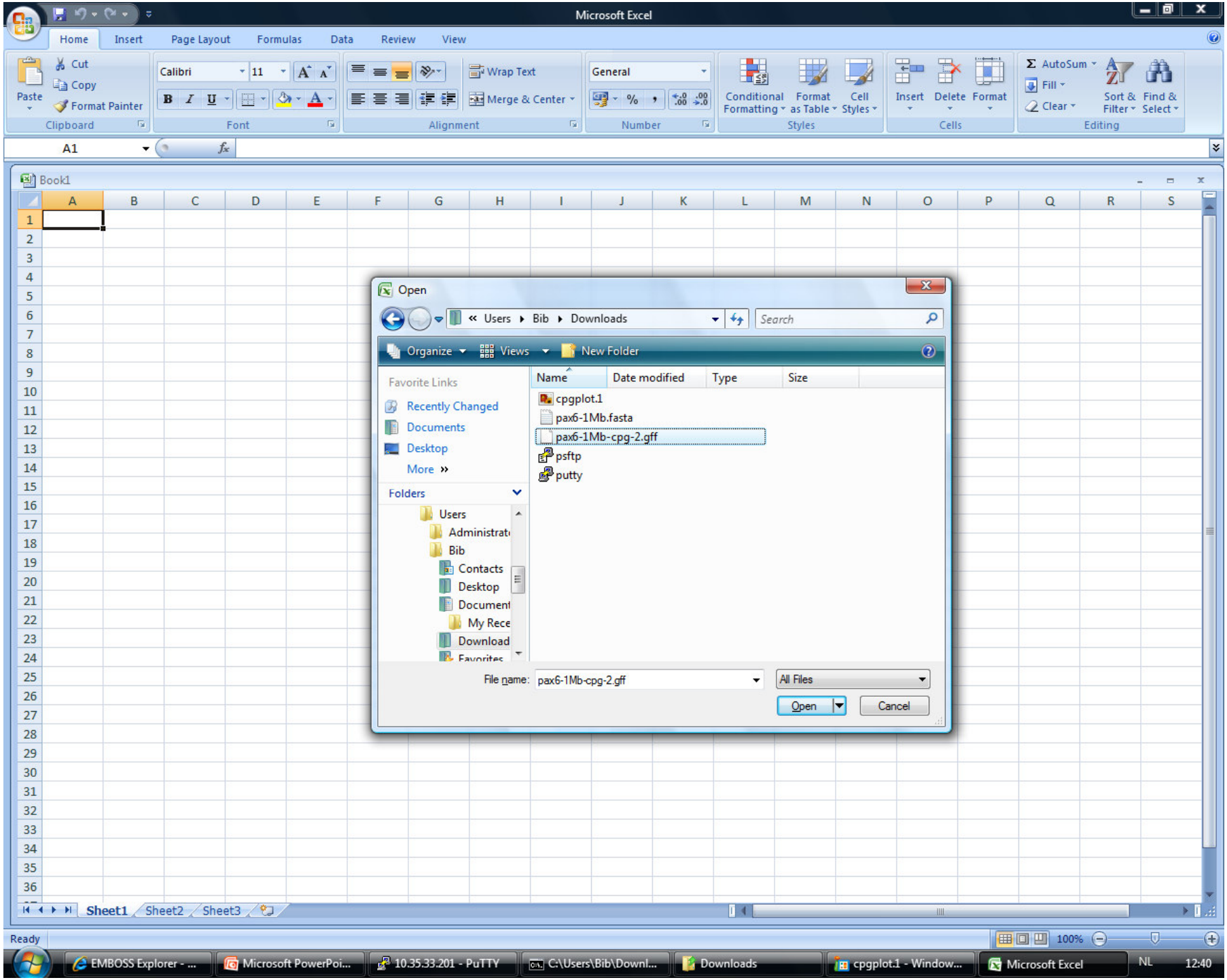
Name	Date modified	Type	Size
cpgplot.1	30/04/2009 12:38	PNG Image	10 KB
pax6-1Mb.fasta	30/04/2009 12:24	Text Document	1.016 KB
pax6-1Mb-cpg-2.gff	30/04/2009 12:37	GFF File	3 KB
psftp	30/04/2009 12:20	Application	300 KB
putty	30/04/2009 12:19	Application	444 KB

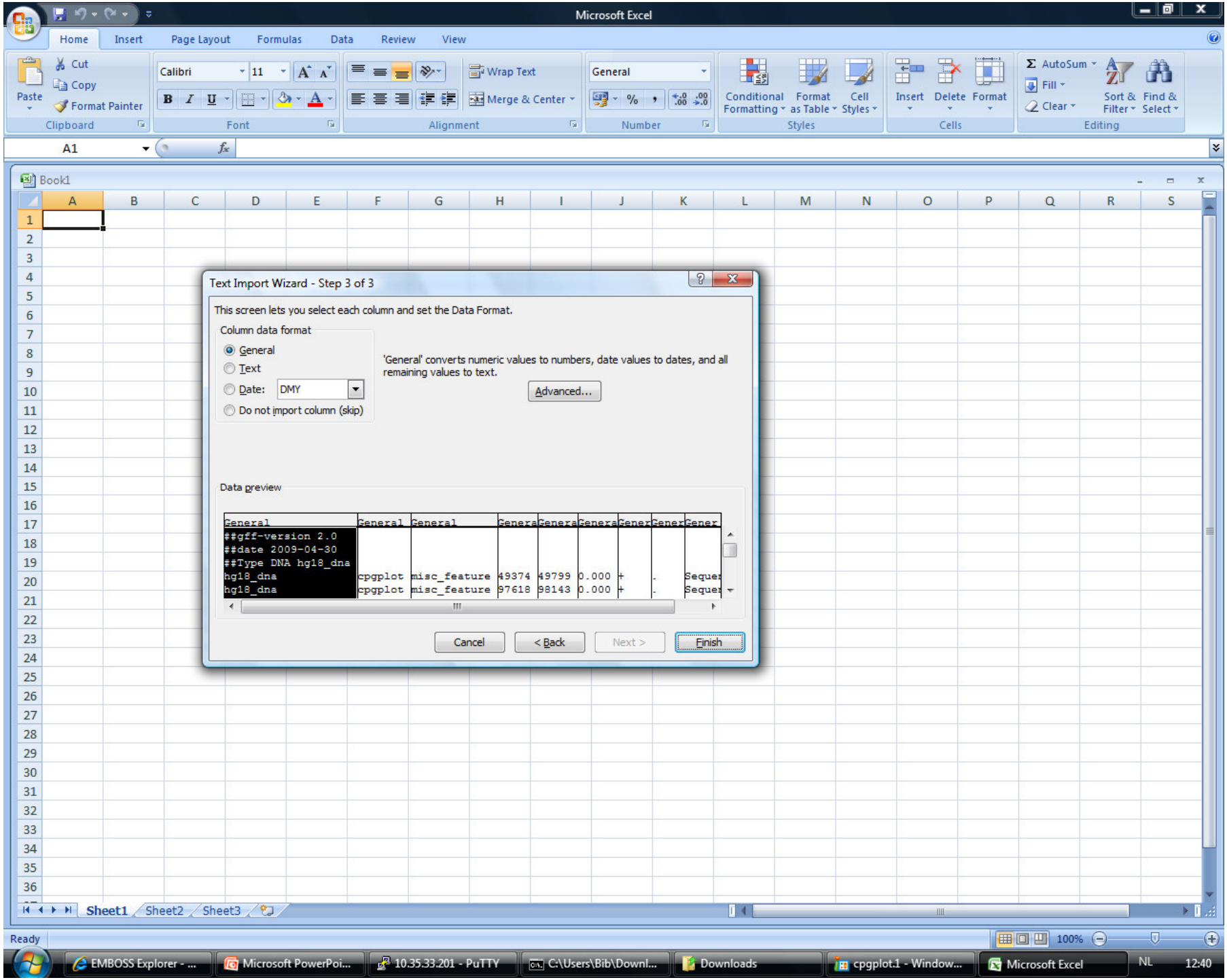
cpgplot.1 - Windows Photo Gallery

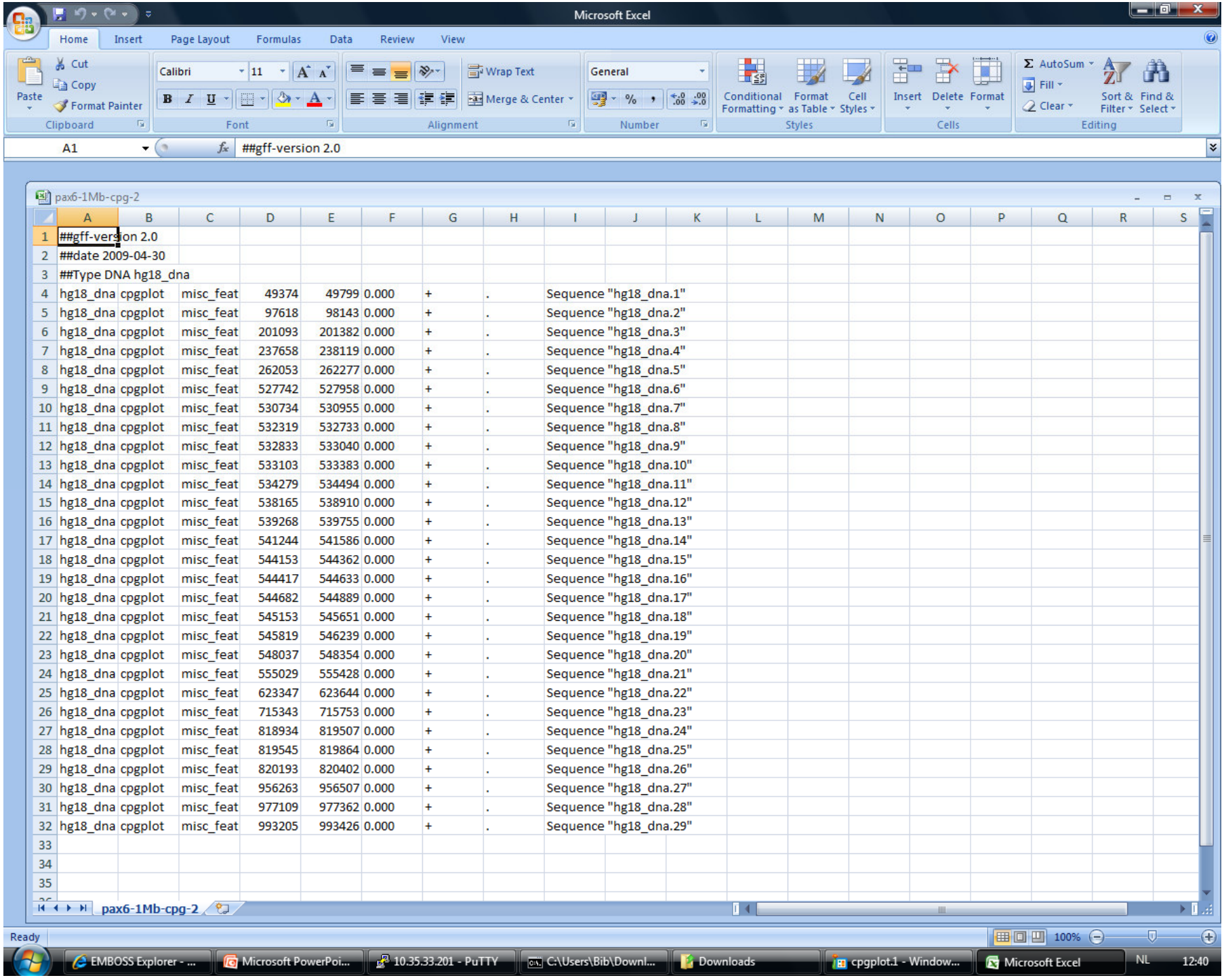
Add Folder To Gallery | File | Fix | Info | Print | E-mail | Burn | Make a Movie | Open

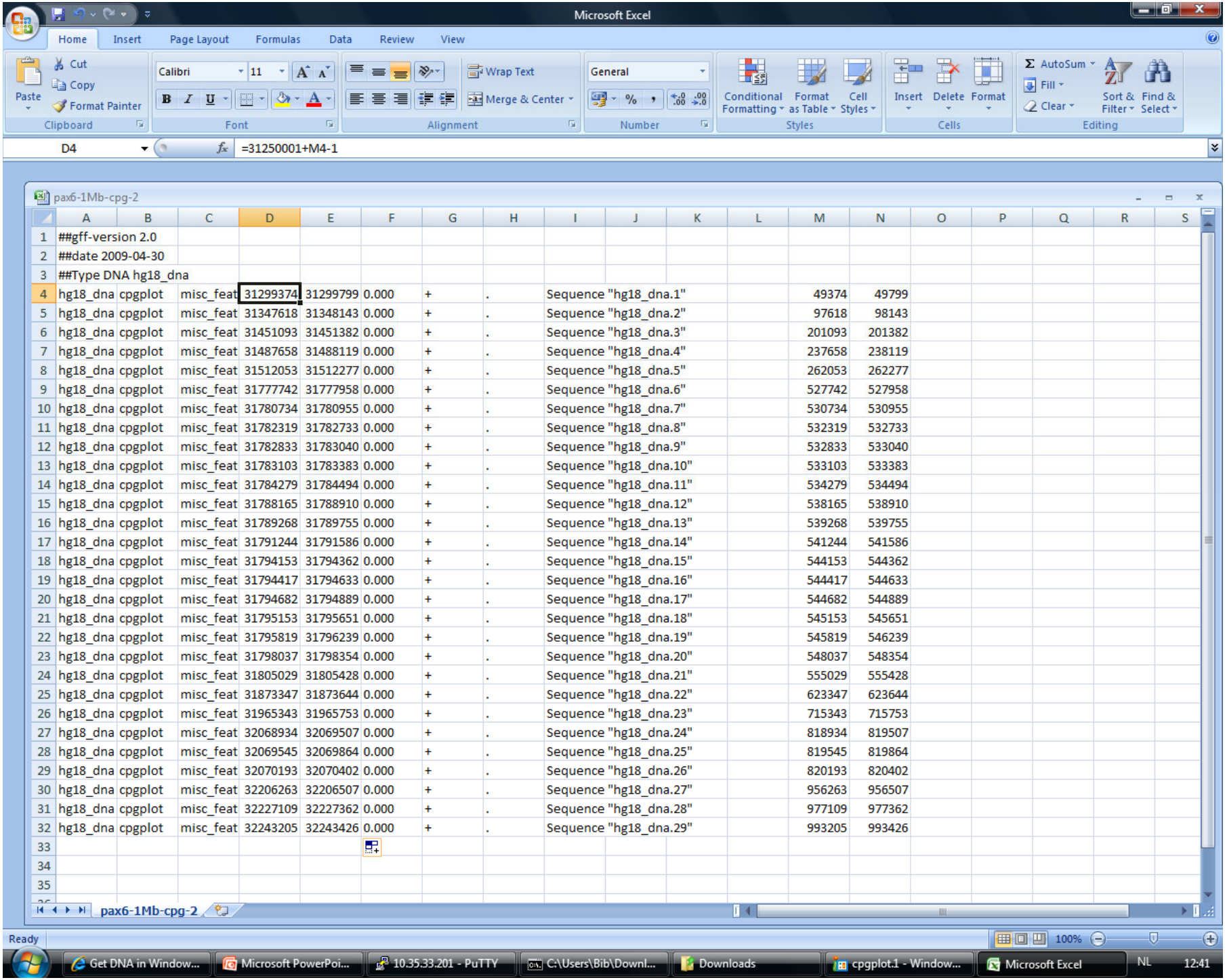


EMBOSS Explorer - ... | Microsoft PowerPoi... | 10.35.33.201 - PuTTY | C:\Users\Bib\Downl... | Downloads | cpgplot.1 - Window... | NL | 12:39

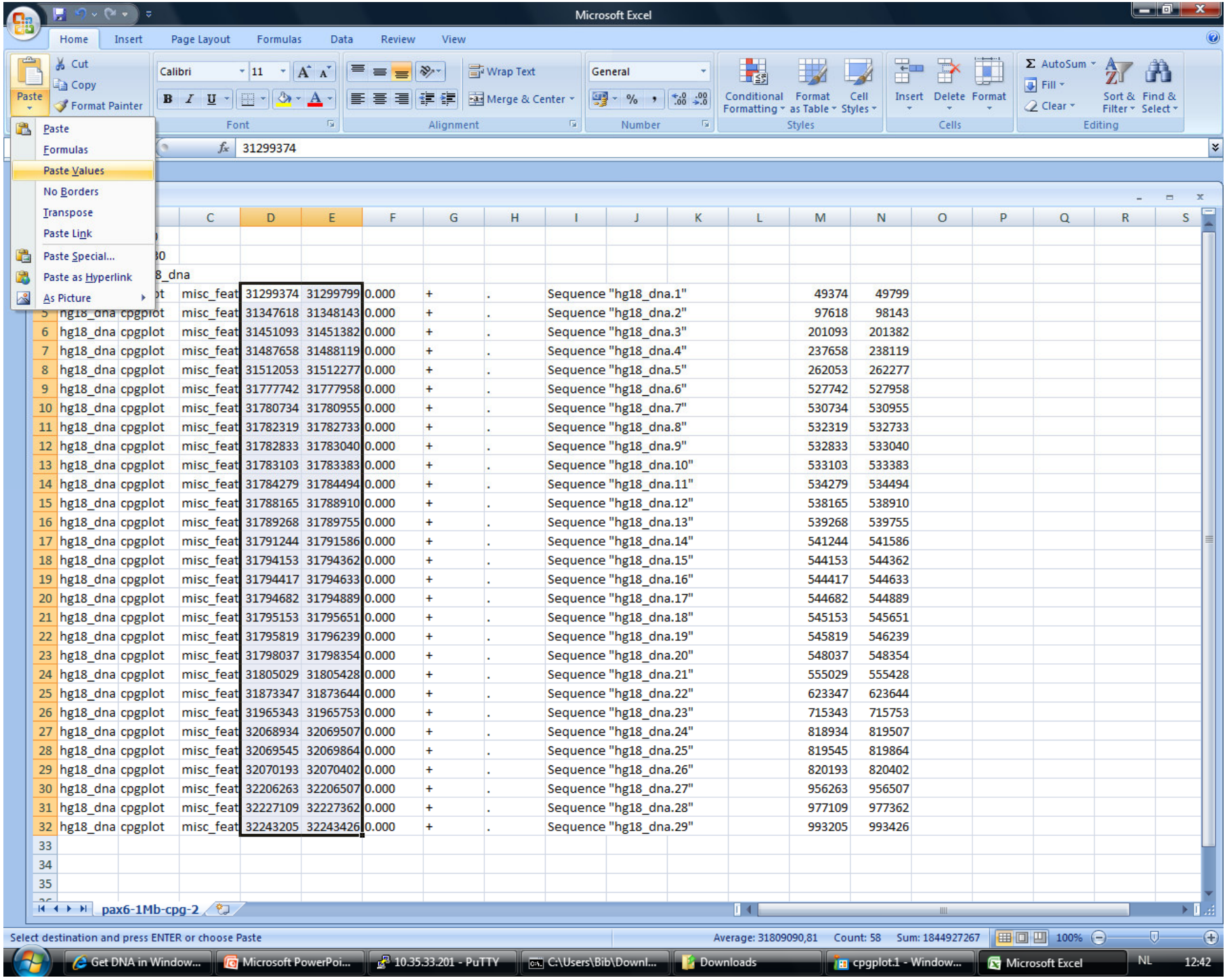

Microsoft Excel
Home
Insert
Page Layout
Formulas
Data
Review
View
Book1
Open
Users ▸ Bib ▸ Downloads
Search
Organize
Views
New Folder
Favorite Links
Recently Changed
Documents
Desktop
More »
Folders
Name
Date modified
Type
Size
cpgplot.1
pax6-1Mb.fasta
pax6-1Mb-cpg-2.gff
psftp
putty
File name: pax6-1Mb-cpg-2.gff
All Files
Open
Cancel
Sheet1
Sheet2
Sheet3
Ready
EMBOSS Explorer - ...
Microsoft PowerPoi...
10.35.33.201 - PuTTY
C:\Users\Bib\Downl...
Downloads
cpgplot.1 - Window...
Microsoft Excel
NL
12:40


Microsoft Excel
Home
Insert
Page Layout
Formulas
Data
Review
View
Paste
Cut
Copy
Format Painter
Clipboard
Calibri
11
Font
Wrap Text
Merge & Center
Alignment
General
Number
Conditional Formatting
Format as Table
Cell Styles
Styles
Insert
Delete
Format
Cells
AutoSum
Fill
Clear
Sort & Filter
Find & Select
Editing
A1
Book1
Text Import Wizard - Step 3 of 3
This screen lets you select each column and set the Data Format.
Column data format
General
Text
Date:
DMY
Do not import column (skip)
'General' converts numeric values to numbers, date values to dates, and all remaining values to text.
Advanced...
Data preview
General
##gff-version 2.0
##date 2009-04-30
##Type DNA hg18_dna
hg18_dna
hg18_dna
cpgplot
misc_feature
49374
49799
0.000
97618
98143
Cancel
< Back
Next >
Finish
Sheet1
Sheet2
Sheet3
Ready
100%
EMBOSS Explorer - ...
Microsoft PowerPoi...
10.35.33.201 - PuTTY
C:\Users\Bib\Downl...
Downloads
cpgplot.1 - Window...
Microsoft Excel
NL
12:40

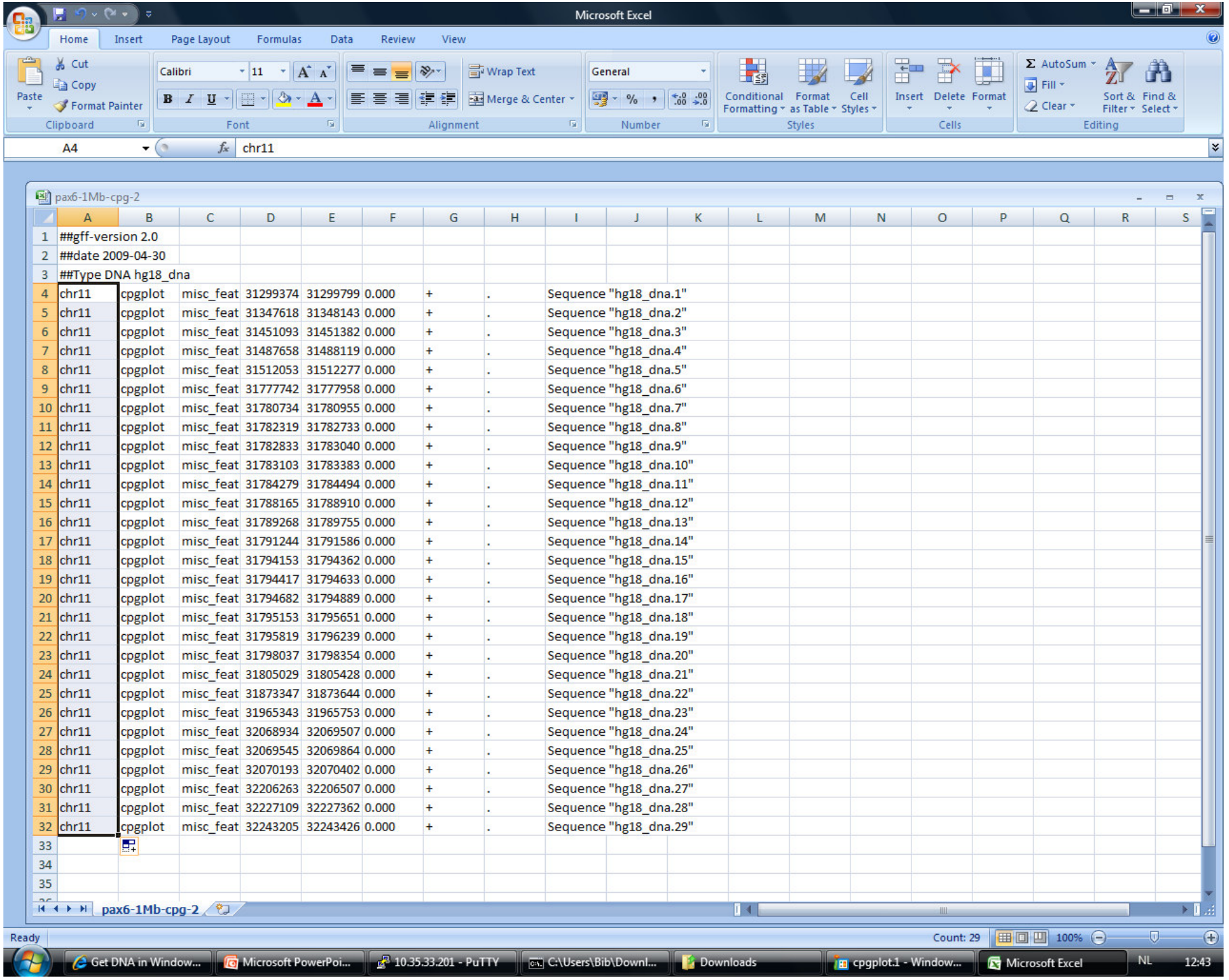

Microsoft Excel
Home
Insert
Page Layout
Formulas
Data
Review
View
Paste
Cut
Copy
Format Painter
Clipboard
Calibri
11
Font
Wrap Text
Merge & Center
Alignment
General
Number
Conditional Formatting
Format as Table
Cell Styles
Styles
Insert
Delete
Format
Cells
AutoSum
Fill
Clear
Sort & Filter
Find & Select
Editing
A1
##gff-version 2.0
pax6-1Mb-cpg-2
##gff-version 2.0
##date 2009-04-30
##Type DNA hg18_dna
hg18_dna cpgplot misc_feat 49374 49799 0.000 + . Sequence "hg18_dna.1"
hg18_dna cpgplot misc_feat 97618 98143 0.000 + . Sequence "hg18_dna.2"
hg18_dna cpgplot misc_feat 201093 201382 0.000 + . Sequence "hg18_dna.3"
hg18_dna cpgplot misc_feat 237658 238119 0.000 + . Sequence "hg18_dna.4"
hg18_dna cpgplot misc_feat 262053 262277 0.000 + . Sequence "hg18_dna.5"
hg18_dna cpgplot misc_feat 527742 527958 0.000 + . Sequence "hg18_dna.6"
hg18_dna cpgplot misc_feat 530734 530955 0.000 + . Sequence "hg18_dna.7"
hg18_dna cpgplot misc_feat 532319 532733 0.000 + . Sequence "hg18_dna.8"
hg18_dna cpgplot misc_feat 532833 533040 0.000 + . Sequence "hg18_dna.9"
hg18_dna cpgplot misc_feat 533103 533383 0.000 + . Sequence "hg18_dna.10"
hg18_dna cpgplot misc_feat 534279 534494 0.000 + . Sequence "hg18_dna.11"
hg18_dna cpgplot misc_feat 538165 538910 0.000 + . Sequence "hg18_dna.12"
hg18_dna cpgplot misc_feat 539268 539755 0.000 + . Sequence "hg18_dna.13"
hg18_dna cpgplot misc_feat 541244 541586 0.000 + . Sequence "hg18_dna.14"
hg18_dna cpgplot misc_feat 544153 544362 0.000 + . Sequence "hg18_dna.15"
hg18_dna cpgplot misc_feat 544417 544633 0.000 + . Sequence "hg18_dna.16"
hg18_dna cpgplot misc_feat 544682 544889 0.000 + . Sequence "hg18_dna.17"
hg18_dna cpgplot misc_feat 545153 545651 0.000 + . Sequence "hg18_dna.18"
hg18_dna cpgplot misc_feat 545819 546239 0.000 + . Sequence "hg18_dna.19"
hg18_dna cpgplot misc_feat 548037 548354 0.000 + . Sequence "hg18_dna.20"
hg18_dna cpgplot misc_feat 555029 555428 0.000 + . Sequence "hg18_dna.21"
hg18_dna cpgplot misc_feat 623347 623644 0.000 + . Sequence "hg18_dna.22"
hg18_dna cpgplot misc_feat 715343 715753 0.000 + . Sequence "hg18_dna.23"
hg18_dna cpgplot misc_feat 818934 819507 0.000 + . Sequence "hg18_dna.24"
hg18_dna cpgplot misc_feat 819545 819864 0.000 + . Sequence "hg18_dna.25"
hg18_dna cpgplot misc_feat 820193 820402 0.000 + . Sequence "hg18_dna.26"
hg18_dna cpgplot misc_feat 956263 956507 0.000 + . Sequence "hg18_dna.27"
hg18_dna cpgplot misc_feat 977109 977362 0.000 + . Sequence "hg18_dna.28"
hg18_dna cpgplot misc_feat 993205 993426 0.000 + . Sequence "hg18_dna.29"
pax6-1Mb-cpg-2
Ready
100%
EMBOSS Explorer - ...
Microsoft PowerPoi...
10.35.33.201 - PuTTY
C:\Users\Bib\Downl...
Downloads
cpgplot.1 - Window...
Microsoft Excel
NL
12:40

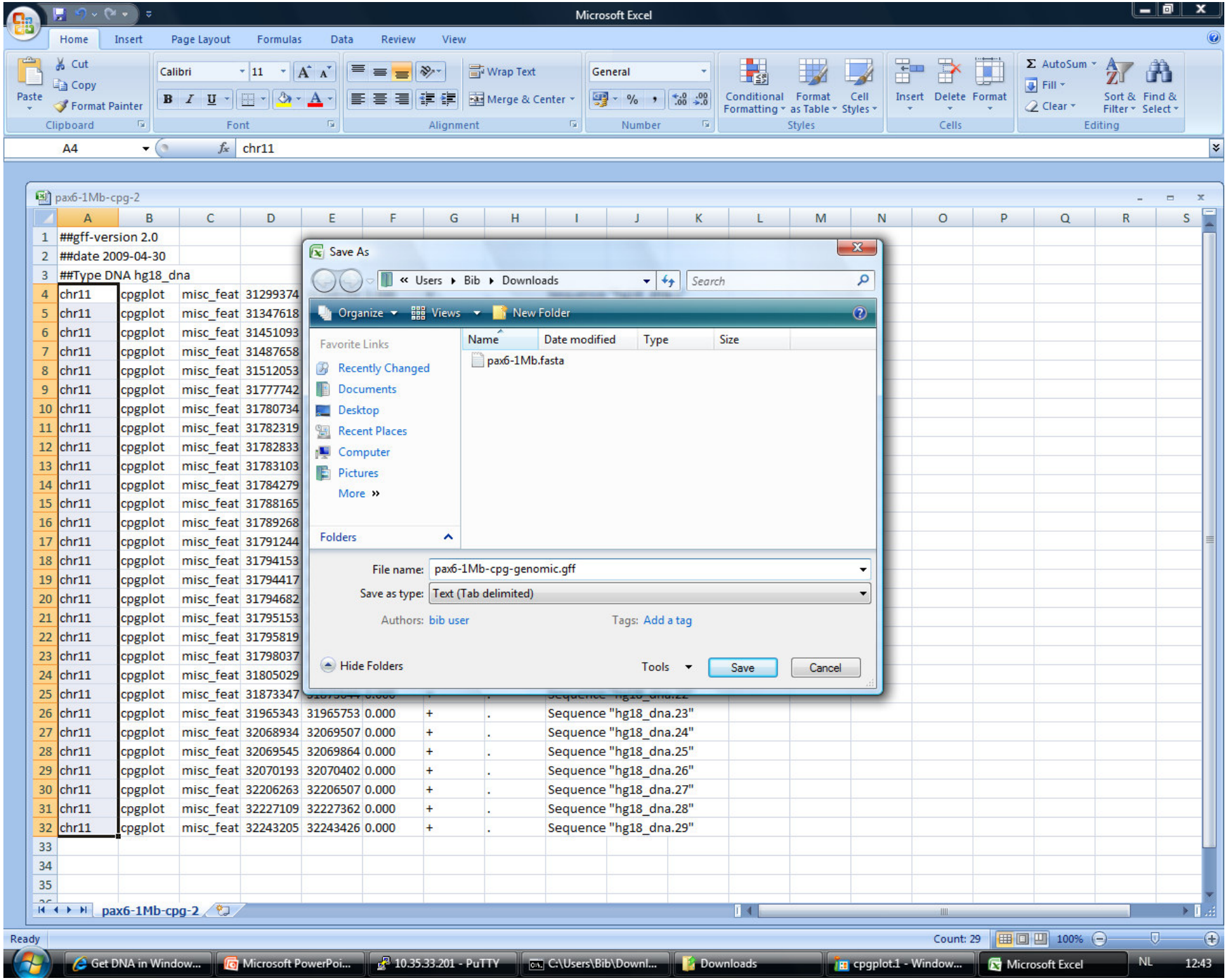


	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S
1	##gff-version 2.0																		
2	##date 2009-04-30																		
3	##Type DNA hg18_dna																		
4	hg18_dna	cpgplot	misc_feat	31299374	31299799	0.000	+	.	Sequence "hg18_dna.1"				49374	49799					
5	hg18_dna	cpgplot	misc_feat	31347618	31348143	0.000	+	.	Sequence "hg18_dna.2"				97618	98143					
6	hg18_dna	cpgplot	misc_feat	31451093	31451382	0.000	+	.	Sequence "hg18_dna.3"				201093	201382					
7	hg18_dna	cpgplot	misc_feat	31487658	31488119	0.000	+	.	Sequence "hg18_dna.4"				237658	238119					
8	hg18_dna	cpgplot	misc_feat	31512053	31512277	0.000	+	.	Sequence "hg18_dna.5"				262053	262277					
9	hg18_dna	cpgplot	misc_feat	31777742	31777958	0.000	+	.	Sequence "hg18_dna.6"				527742	527958					
10	hg18_dna	cpgplot	misc_feat	31780734	31780955	0.000	+	.	Sequence "hg18_dna.7"				530734	530955					
11	hg18_dna	cpgplot	misc_feat	31782319	31782733	0.000	+	.	Sequence "hg18_dna.8"				532319	532733					
12	hg18_dna	cpgplot	misc_feat	31782833	31783040	0.000	+	.	Sequence "hg18_dna.9"				532833	533040					
13	hg18_dna	cpgplot	misc_feat	31783103	31783383	0.000	+	.	Sequence "hg18_dna.10"				533103	533383					
14	hg18_dna	cpgplot	misc_feat	31784279	31784494	0.000	+	.	Sequence "hg18_dna.11"				534279	534494					
15	hg18_dna	cpgplot	misc_feat	31788165	31788910	0.000	+	.	Sequence "hg18_dna.12"				538165	538910					
16	hg18_dna	cpgplot	misc_feat	31789268	31789755	0.000	+	.	Sequence "hg18_dna.13"				539268	539755					
17	hg18_dna	cpgplot	misc_feat	31791244	31791586	0.000	+	.	Sequence "hg18_dna.14"				541244	541586					
18	hg18_dna	cpgplot	misc_feat	31794153	31794362	0.000	+	.	Sequence "hg18_dna.15"				544153	544362					
19	hg18_dna	cpgplot	misc_feat	31794417	31794633	0.000	+	.	Sequence "hg18_dna.16"				544417	544633					
20	hg18_dna	cpgplot	misc_feat	31794682	31794889	0.000	+	.	Sequence "hg18_dna.17"				544682	544889					
21	hg18_dna	cpgplot	misc_feat	31795153	31795651	0.000	+	.	Sequence "hg18_dna.18"				545153	545651					
22	hg18_dna	cpgplot	misc_feat	31795819	31796239	0.000	+	.	Sequence "hg18_dna.19"				545819	546239					
23	hg18_dna	cpgplot	misc_feat	31798037	31798354	0.000	+	.	Sequence "hg18_dna.20"				548037	548354					
24	hg18_dna	cpgplot	misc_feat	31805029	31805428	0.000	+	.	Sequence "hg18_dna.21"				555029	555428					
25	hg18_dna	cpgplot	misc_feat	31873347	31873644	0.000	+	.	Sequence "hg18_dna.22"				623347	623644					
26	hg18_dna	cpgplot	misc_feat	31965343	31965753	0.000	+	.	Sequence "hg18_dna.23"				715343	715753					
27	hg18_dna	cpgplot	misc_feat	32068934	32069507	0.000	+	.	Sequence "hg18_dna.24"				818934	819507					
28	hg18_dna	cpgplot	misc_feat	32069545	32069864	0.000	+	.	Sequence "hg18_dna.25"				819545	819864					
29	hg18_dna	cpgplot	misc_feat	32070193	32070402	0.000	+	.	Sequence "hg18_dna.26"				820193	820402					
30	hg18_dna	cpgplot	misc_feat	32206263	32206507	0.000	+	.	Sequence "hg18_dna.27"				956263	956507					
31	hg18_dna	cpgplot	misc_feat	32227109	32227362	0.000	+	.	Sequence "hg18_dna.28"				977109	977362					
32	hg18_dna	cpgplot	misc_feat	32243205	32243426	0.000	+	.	Sequence "hg18_dna.29"				993205	993426					
33																			
34																			
35																			



	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S
4	hg18_dna	cpgplot	misc_feat	31299374	31299799	0.000	+	.	Sequence "hg18_dna.1"				49374	49799					
5	hg18_dna	cpgplot	misc_feat	31347618	31348143	0.000	+	.	Sequence "hg18_dna.2"				97618	98143					
6	hg18_dna	cpgplot	misc_feat	31451093	31451382	0.000	+	.	Sequence "hg18_dna.3"				201093	201382					
7	hg18_dna	cpgplot	misc_feat	31487658	31488119	0.000	+	.	Sequence "hg18_dna.4"				237658	238119					
8	hg18_dna	cpgplot	misc_feat	31512053	31512277	0.000	+	.	Sequence "hg18_dna.5"				262053	262277					
9	hg18_dna	cpgplot	misc_feat	31777742	31777958	0.000	+	.	Sequence "hg18_dna.6"				527742	527958					
10	hg18_dna	cpgplot	misc_feat	31780734	31780955	0.000	+	.	Sequence "hg18_dna.7"				530734	530955					
11	hg18_dna	cpgplot	misc_feat	31782319	31782733	0.000	+	.	Sequence "hg18_dna.8"				532319	532733					
12	hg18_dna	cpgplot	misc_feat	31782833	31783040	0.000	+	.	Sequence "hg18_dna.9"				532833	533040					
13	hg18_dna	cpgplot	misc_feat	31783103	31783383	0.000	+	.	Sequence "hg18_dna.10"				533103	533383					
14	hg18_dna	cpgplot	misc_feat	31784279	31784494	0.000	+	.	Sequence "hg18_dna.11"				534279	534494					
15	hg18_dna	cpgplot	misc_feat	31788165	31788910	0.000	+	.	Sequence "hg18_dna.12"				538165	538910					
16	hg18_dna	cpgplot	misc_feat	31789268	31789755	0.000	+	.	Sequence "hg18_dna.13"				539268	539755					
17	hg18_dna	cpgplot	misc_feat	31791244	31791586	0.000	+	.	Sequence "hg18_dna.14"				541244	541586					
18	hg18_dna	cpgplot	misc_feat	31794153	31794362	0.000	+	.	Sequence "hg18_dna.15"				544153	544362					
19	hg18_dna	cpgplot	misc_feat	31794417	31794633	0.000	+	.	Sequence "hg18_dna.16"				544417	544633					
20	hg18_dna	cpgplot	misc_feat	31794682	31794889	0.000	+	.	Sequence "hg18_dna.17"				544682	544889					
21	hg18_dna	cpgplot	misc_feat	31795153	31795651	0.000	+	.	Sequence "hg18_dna.18"				545153	545651					
22	hg18_dna	cpgplot	misc_feat	31795819	31796239	0.000	+	.	Sequence "hg18_dna.19"				545819	546239					
23	hg18_dna	cpgplot	misc_feat	31798037	31798354	0.000	+	.	Sequence "hg18_dna.20"				548037	548354					
24	hg18_dna	cpgplot	misc_feat	31805029	31805428	0.000	+	.	Sequence "hg18_dna.21"				555029	555428					
25	hg18_dna	cpgplot	misc_feat	31873347	31873644	0.000	+	.	Sequence "hg18_dna.22"				623347	623644					
26	hg18_dna	cpgplot	misc_feat	31965343	31965753	0.000	+	.	Sequence "hg18_dna.23"				715343	715753					
27	hg18_dna	cpgplot	misc_feat	32068934	32069507	0.000	+	.	Sequence "hg18_dna.24"				818934	819507					
28	hg18_dna	cpgplot	misc_feat	32069545	32069864	0.000	+	.	Sequence "hg18_dna.25"				819545	819864					
29	hg18_dna	cpgplot	misc_feat	32070193	32070402	0.000	+	.	Sequence "hg18_dna.26"				820193	820402					
30	hg18_dna	cpgplot	misc_feat	32206263	32206507	0.000	+	.	Sequence "hg18_dna.27"				956263	956507					
31	hg18_dna	cpgplot	misc_feat	32227109	32227362	0.000	+	.	Sequence "hg18_dna.28"				977109	977362					
32	hg18_dna	cpgplot	misc_feat	32243205	32243426	0.000	+	.	Sequence "hg18_dna.29"				993205	993426					
33																			
34																			
35																			

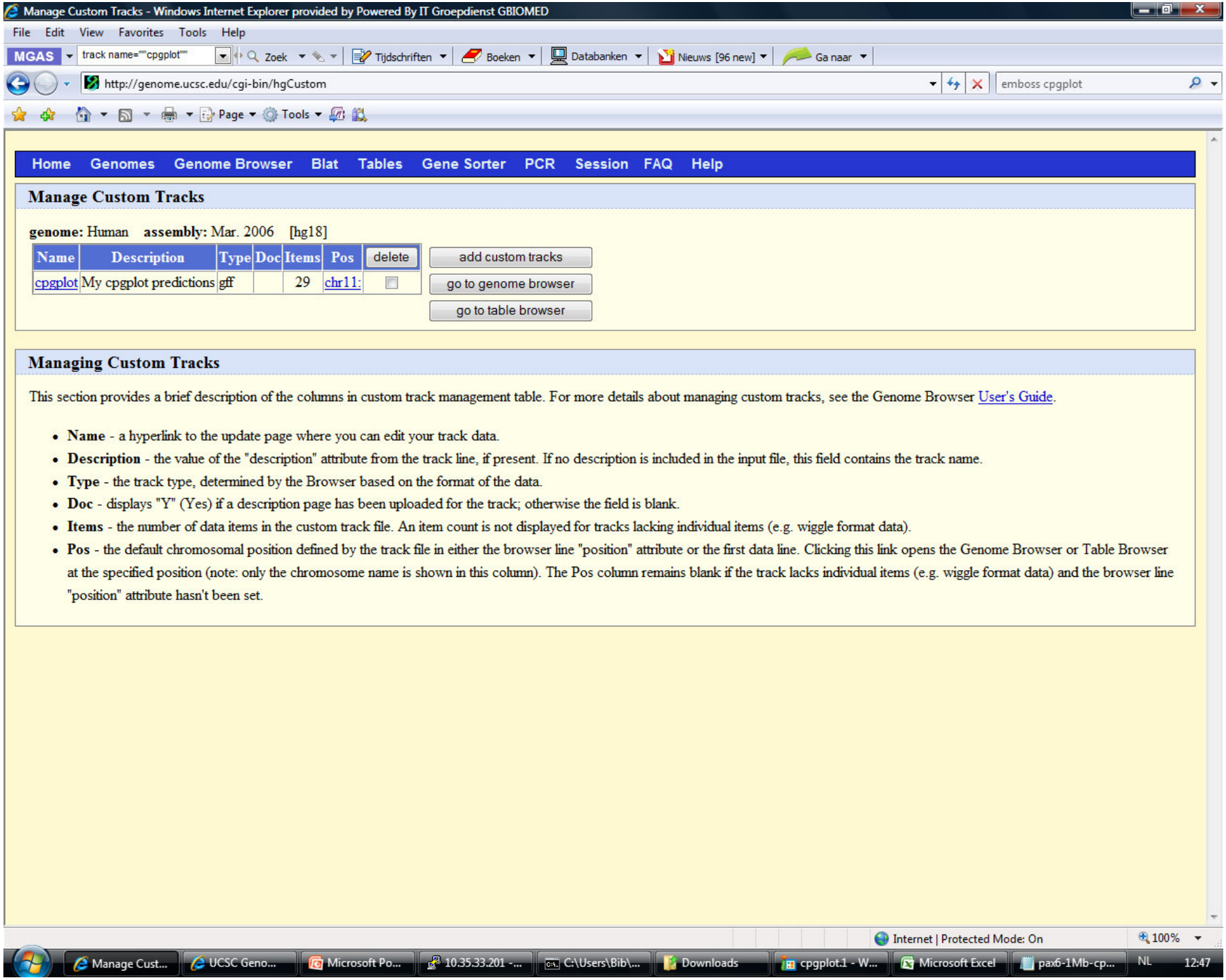

Microsoft Excel
Home
Insert
Page Layout
Formulas
Data
Review
View
Paste
Cut
Copy
Format Painter
Clipboard
Calibri
11
Font
Wrap Text
Merge & Center
Alignment
General
Number
Conditional Formatting
Format as Table
Cell Styles
Styles
Insert
Delete
Format
Cells
AutoSum
Fill
Clear
Sort & Filter
Find & Select
Editing
A4
chr11
pax6-1Mb-cpg-2
##gff-version 2.0
##date 2009-04-30
##Type DNA hg18_dna
chr11 cpgplot misc_feat 31299374 31299799 0.000 + . Sequence "hg18_dna.1"
chr11 cpgplot misc_feat 31347618 31348143 0.000 + . Sequence "hg18_dna.2"
chr11 cpgplot misc_feat 31451093 31451382 0.000 + . Sequence "hg18_dna.3"
chr11 cpgplot misc_feat 31487658 31488119 0.000 + . Sequence "hg18_dna.4"
chr11 cpgplot misc_feat 31512053 31512277 0.000 + . Sequence "hg18_dna.5"
chr11 cpgplot misc_feat 31777742 31777958 0.000 + . Sequence "hg18_dna.6"
chr11 cpgplot misc_feat 31780734 31780955 0.000 + . Sequence "hg18_dna.7"
chr11 cpgplot misc_feat 31782319 31782733 0.000 + . Sequence "hg18_dna.8"
chr11 cpgplot misc_feat 31782833 31783040 0.000 + . Sequence "hg18_dna.9"
chr11 cpgplot misc_feat 31783103 31783383 0.000 + . Sequence "hg18_dna.10"
chr11 cpgplot misc_feat 31784279 31784494 0.000 + . Sequence "hg18_dna.11"
chr11 cpgplot misc_feat 31788165 31788910 0.000 + . Sequence "hg18_dna.12"
chr11 cpgplot misc_feat 31789268 31789755 0.000 + . Sequence "hg18_dna.13"
chr11 cpgplot misc_feat 31791244 31791586 0.000 + . Sequence "hg18_dna.14"
chr11 cpgplot misc_feat 31794153 31794362 0.000 + . Sequence "hg18_dna.15"
chr11 cpgplot misc_feat 31794417 31794633 0.000 + . Sequence "hg18_dna.16"
chr11 cpgplot misc_feat 31794682 31794889 0.000 + . Sequence "hg18_dna.17"
chr11 cpgplot misc_feat 31795153 31795651 0.000 + . Sequence "hg18_dna.18"
chr11 cpgplot misc_feat 31795819 31796239 0.000 + . Sequence "hg18_dna.19"
chr11 cpgplot misc_feat 31798037 31798354 0.000 + . Sequence "hg18_dna.20"
chr11 cpgplot misc_feat 31805029 31805428 0.000 + . Sequence "hg18_dna.21"
chr11 cpgplot misc_feat 31873347 31873644 0.000 + . Sequence "hg18_dna.22"
chr11 cpgplot misc_feat 31965343 31965753 0.000 + . Sequence "hg18_dna.23"
chr11 cpgplot misc_feat 32068934 32069507 0.000 + . Sequence "hg18_dna.24"
chr11 cpgplot misc_feat 32069545 32069864 0.000 + . Sequence "hg18_dna.25"
chr11 cpgplot misc_feat 32070193 32070402 0.000 + . Sequence "hg18_dna.26"
chr11 cpgplot misc_feat 32206263 32206507 0.000 + . Sequence "hg18_dna.27"
chr11 cpgplot misc_feat 32227109 32227362 0.000 + . Sequence "hg18_dna.28"
chr11 cpgplot misc_feat 32243205 32243426 0.000 + . Sequence "hg18_dna.29"
pax6-1Mb-cpg-2
Ready
Count: 29
100%
Get DNA in Window...
Microsoft PowerPoi...
10.35.33.201 - PuTTY
C:\Users\Bib\Downl...
Downloads
cpgplot.1 - Window...
Microsoft Excel
NL
12:43

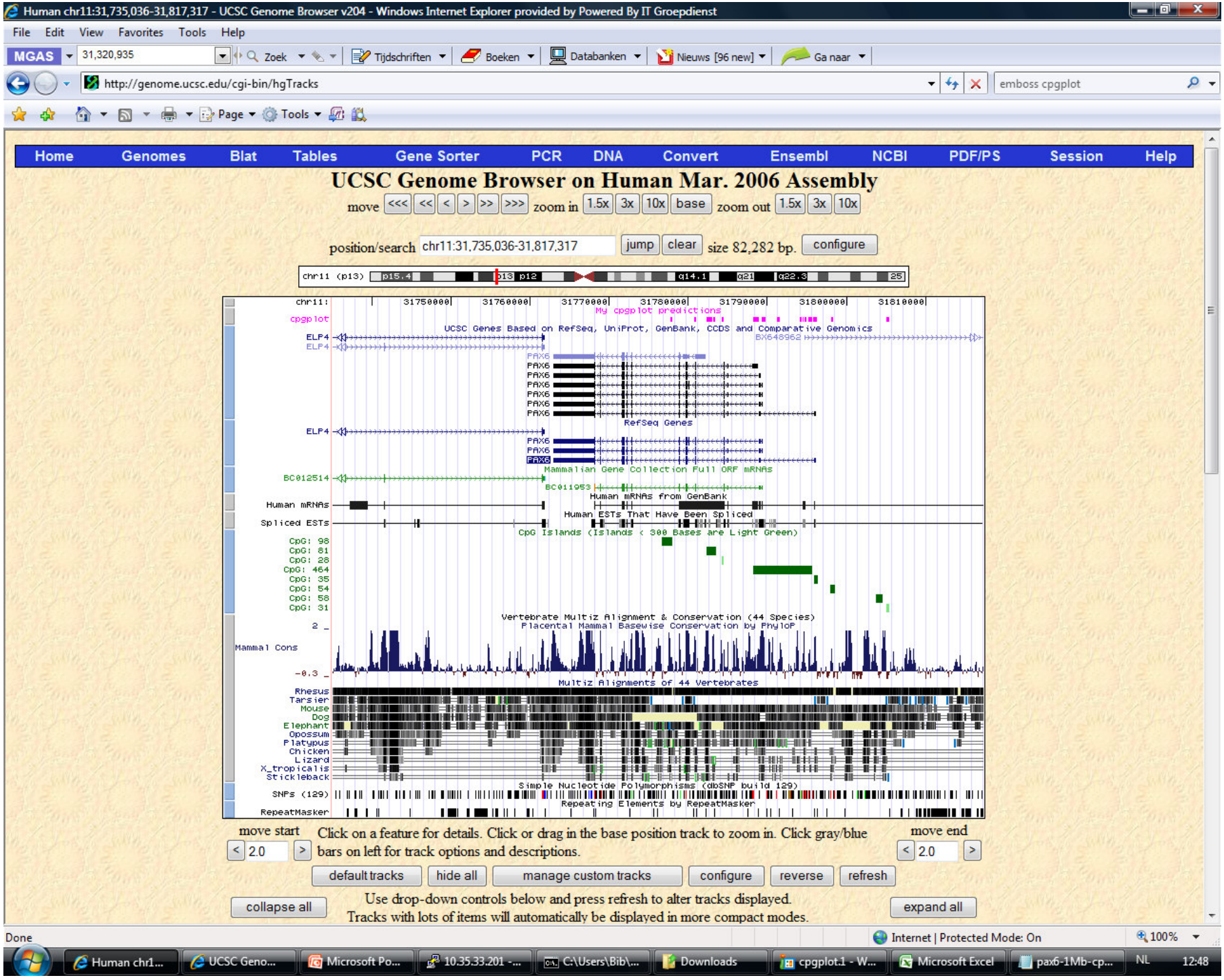

Microsoft Excel
Home
Insert
Page Layout
Formulas
Data
Review
View
Cut
Copy
Format Painter
Paste
Clipboard
Calibri
11
Font
Wrap Text
Merge & Center
Alignment
General
Number
Conditional Formatting
Format as Table
Cell Styles
Styles
Insert
Delete
Format
Cells
AutoSum
Fill
Clear
Sort & Filter
Find & Select
Editing
A4
chr11
pax6-1Mb-cpg-2
##gff-version 2.0
##date 2009-04-30
##Type DNA hg18_dna
chr11 cpgplot misc_feat 31299374
chr11 cpgplot misc_feat 31347618
chr11 cpgplot misc_feat 31451093
chr11 cpgplot misc_feat 31487658
chr11 cpgplot misc_feat 31512053
chr11 cpgplot misc_feat 31777742
chr11 cpgplot misc_feat 31780734
chr11 cpgplot misc_feat 31782319
chr11 cpgplot misc_feat 31782833
chr11 cpgplot misc_feat 31783103
chr11 cpgplot misc_feat 31784279
chr11 cpgplot misc_feat 31788165
chr11 cpgplot misc_feat 31789268
chr11 cpgplot misc_feat 31791244
chr11 cpgplot misc_feat 31794153
chr11 cpgplot misc_feat 31794417
chr11 cpgplot misc_feat 31794682
chr11 cpgplot misc_feat 31795153
chr11 cpgplot misc_feat 31795819
chr11 cpgplot misc_feat 31798037
chr11 cpgplot misc_feat 31805029
chr11 cpgplot misc_feat 31873347
chr11 cpgplot misc_feat 31965343 31965753 0.000 + . Sequence "hg18_dna.23"
chr11 cpgplot misc_feat 32068934 32069507 0.000 + . Sequence "hg18_dna.24"
chr11 cpgplot misc_feat 32069545 32069864 0.000 + . Sequence "hg18_dna.25"
chr11 cpgplot misc_feat 32070193 32070402 0.000 + . Sequence "hg18_dna.26"
chr11 cpgplot misc_feat 32206263 32206507 0.000 + . Sequence "hg18_dna.27"
chr11 cpgplot misc_feat 32227109 32227362 0.000 + . Sequence "hg18_dna.28"
chr11 cpgplot misc_feat 32243205 32243426 0.000 + . Sequence "hg18_dna.29"
pax6-1Mb-cpg-2
Save As
« Users ▸ Bib ▸ Downloads
Search
Organize
Views
New Folder
Favorite Links
Recently Changed
Documents
Desktop
Recent Places
Computer
Pictures
More »
Folders
Name
Date modified
Type
Size
pax6-1Mb.fasta
File name: pax6-1Mb-cpg-genomic.gff
Save as type: Text (Tab delimited)
Authors: bib user
Tags: Add a tag
Hide Folders
Tools
Save
Cancel
Ready
Count: 29
100%
Get DNA in Window...
Microsoft PowerPoi...
10.35.33.201 - PuTTY
C:\Users\Bib\Downl...
Downloads
cpgplot.1 - Window...
Microsoft Excel
NL
12:43

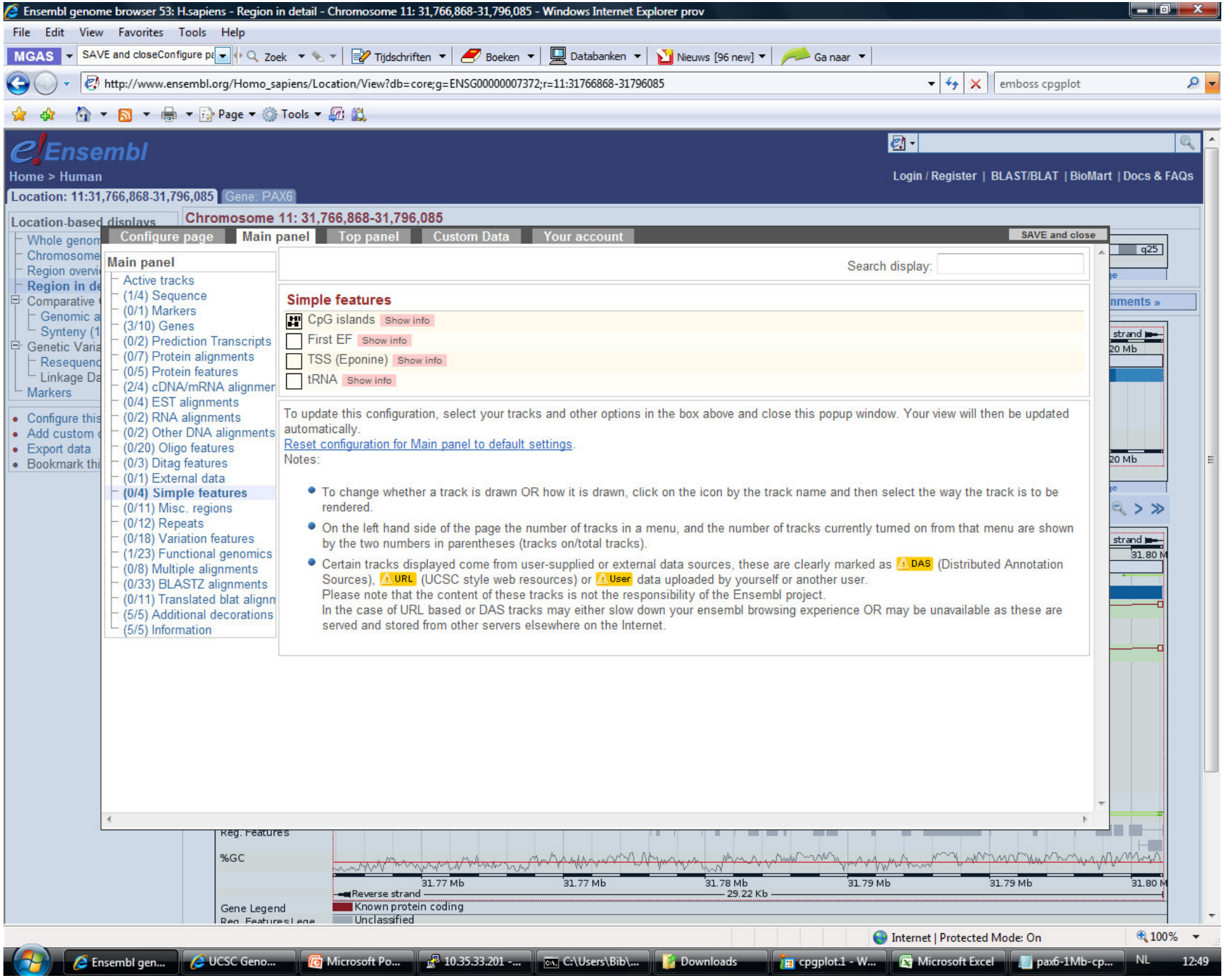
pax6-1Mb-cpg-genomic.gff - Notepad

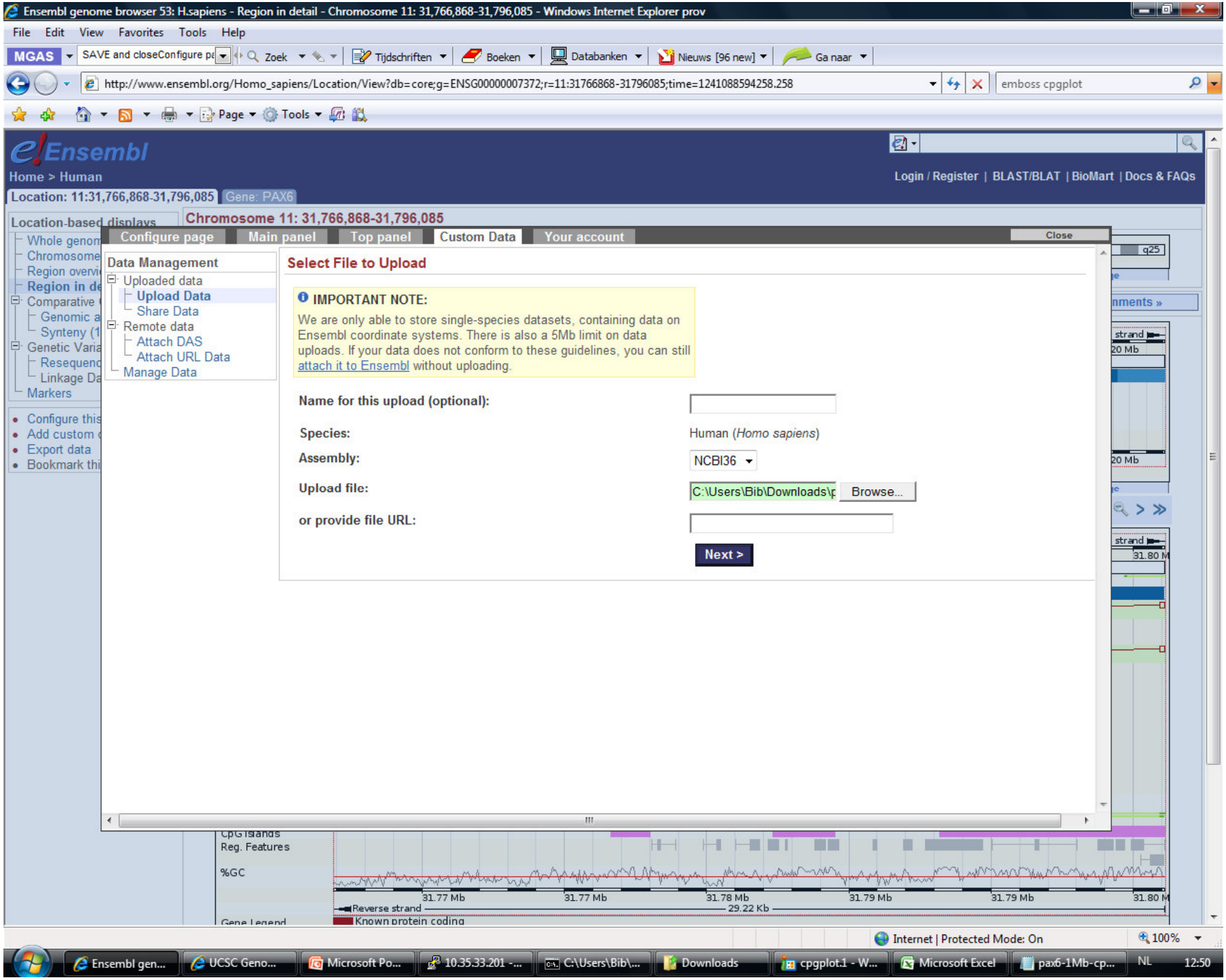
File Edit Format View Help

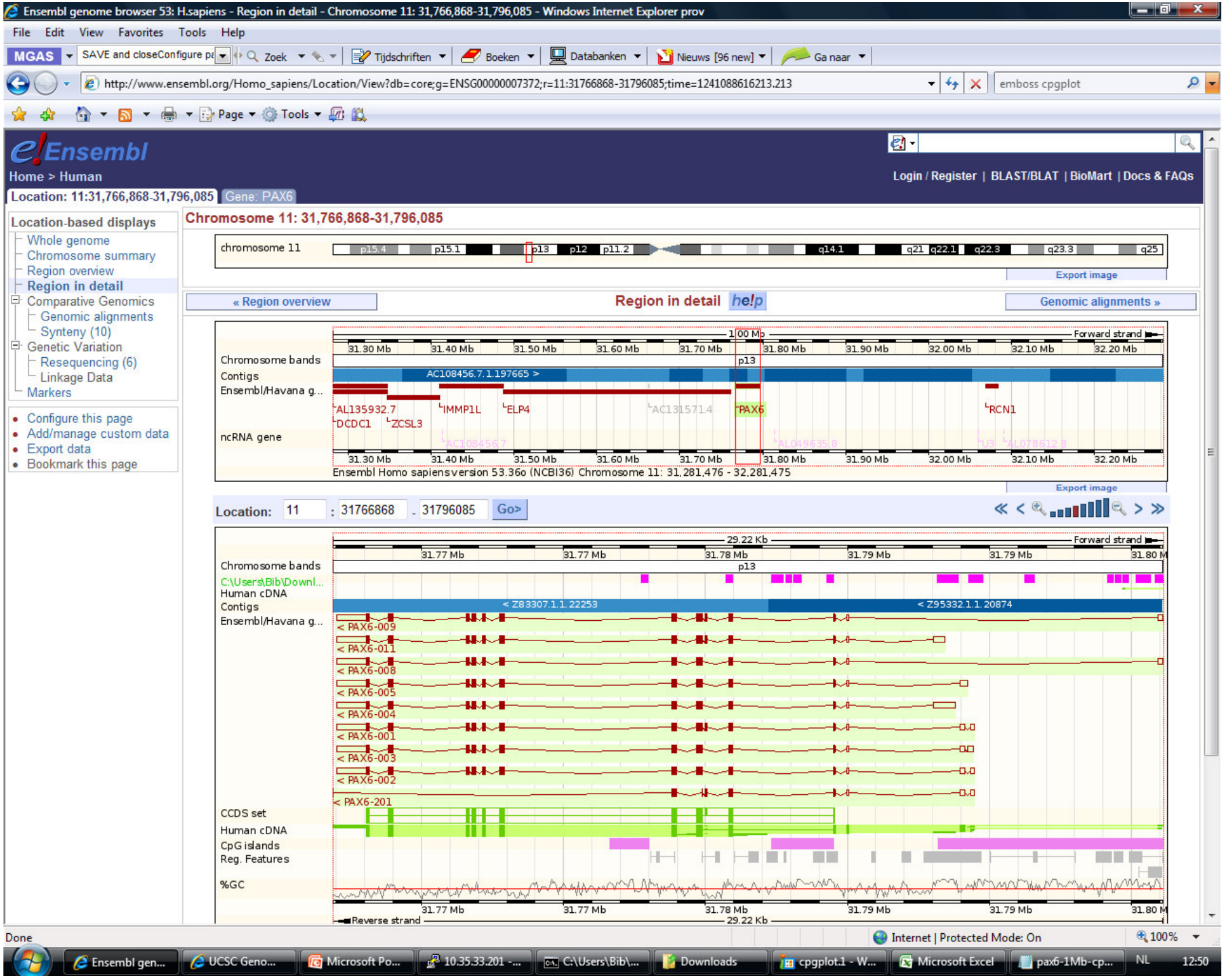
```
##gff-version 2.0
##date 2009-04-30
##Type DNA hg18_dna
track name="cpgplot" description="My cpgplot predictions" color=255,0,255
chr11   cpgplot misc_feature    31299374        31299799        0.000   +       .       "Sequence ""hg18_dna.1"""
chr11   cpgplot misc_feature    31347618        31348143        0.000   +       .       "Sequence ""hg18_dna.2"""
chr11   cpgplot misc_feature    31451093        31451382        0.000   +       .       "Sequence ""hg18_dna.3"""
chr11   cpgplot misc_feature    31487658        31488119        0.000   +       .       "Sequence ""hg18_dna.4"""
chr11   cpgplot misc_feature    31512053        31512277        0.000   +       .       "Sequence ""hg18_dna.5"""
chr11   cpgplot misc_feature    31777742        31777958        0.000   +       .       "Sequence ""hg18_dna.6"""
chr11   cpgplot misc_feature    31780734        31780955        0.000   +       .       "Sequence ""hg18_dna.7"""
chr11   cpgplot misc_feature    31782319        31782733        0.000   +       .       "Sequence ""hg18_dna.8"""
chr11   cpgplot misc_feature    31782833        31783040        0.000   +       .       "Sequence ""hg18_dna.9"""
chr11   cpgplot misc_feature    31783103        31783383        0.000   +       .       "Sequence ""hg18_dna.10"""
chr11   cpgplot misc_feature    31784279        31784494        0.000   +       .       "Sequence ""hg18_dna.11"""
chr11   cpgplot misc_feature    31788165        31788910        0.000   +       .       "Sequence ""hg18_dna.12"""
chr11   cpgplot misc_feature    31789268        31789755        0.000   +       .       "Sequence ""hg18_dna.13"""
chr11   cpgplot misc_feature    31791244        31791586        0.000   +       .       "Sequence ""hg18_dna.14"""
chr11   cpgplot misc_feature    31794153        31794362        0.000   +       .       "Sequence ""hg18_dna.15"""
chr11   cpgplot misc_feature    31794417        31794633        0.000   +       .       "Sequence ""hg18_dna.16"""
chr11   cpgplot misc_feature    31794682        31794889        0.000   +       .       "Sequence ""hg18_dna.17"""
chr11   cpgplot misc_feature    31795153        31795651        0.000   +       .       "Sequence ""hg18_dna.18"""
chr11   cpgplot misc_feature    31795819        31796239        0.000   +       .       "Sequence ""hg18_dna.19"""
chr11   cpgplot misc_feature    31798037        31798354        0.000   +       .       "Sequence ""hg18_dna.20"""
chr11   cpgplot misc_feature    31805029        31805428        0.000   +       .       "Sequence ""hg18_dna.21"""
chr11   cpgplot misc_feature    31873347        31873644        0.000   +       .       "Sequence ""hg18_dna.22"""
chr11   cpgplot misc_feature    31965343        31965753        0.000   +       .       "Sequence ""hg18_dna.23"""
chr11   cpgplot misc_feature    32068934        32069507        0.000   +       .       "Sequence ""hg18_dna.24"""
chr11   cpgplot misc_feature    32069545        32069864        0.000   +       .       "Sequence ""hg18_dna.25"""
chr11   cpgplot misc_feature    32070193        32070402        0.000   +       .       "Sequence ""hg18_dna.26"""
chr11   cpgplot misc_feature    32206263        32206507        0.000   +       .       "Sequence ""hg18_dna.27"""
chr11   cpgplot misc_feature    32227109        32227362        0.000   +       .       "Sequence ""hg18_dna.28"""
chr11   cpgplot misc_feature    32243205        32243426        0.000   +       .       "Sequence ""hg18_dna.29"""
```


Manage Custom Tracks - Windows Internet Explorer provided by Powered By IT Groepdienst GBIOMED
File Edit View Favorites Tools Help
MGAS track name=""cpgplot"" Zoek Tijdschriften Boeken Databanken Nieuws [96 new] Ga naar
http://genome.ucsc.edu/cgi-bin/hgCustom
emboss cpgplot
Page Tools
Home Genomes Genome Browser Blat Tables Gene Sorter PCR Session FAQ Help
Manage Custom Tracks
genome: Human assembly: Mar. 2006 [hg18]
Name Description Type Doc Items Pos delete
cpgplot My cpgplot predictions gff 29 chr11:
add custom tracks
go to genome browser
go to table browser
Managing Custom Tracks
This section provides a brief description of the columns in custom track management table. For more details about managing custom tracks, see the Genome Browser User's Guide.
Name - a hyperlink to the update page where you can edit your track data.
Description - the value of the "description" attribute from the track line, if present. If no description is included in the input file, this field contains the track name.
Type - the track type, determined by the Browser based on the format of the data.
Doc - displays "Y" (Yes) if a description page has been uploaded for the track; otherwise the field is blank.
Items - the number of data items in the custom track file. An item count is not displayed for tracks lacking individual items (e.g. wiggle format data).
Pos - the default chromosomal position defined by the track file in either the browser line "position" attribute or the first data line. Clicking this link opens the Genome Browser or Table Browser at the specified position (note: only the chromosome name is shown in this column). The Pos column remains blank if the track lacks individual items (e.g. wiggle format data) and the browser line "position" attribute hasn't been set.
Internet | Protected Mode: On
100%
Manage Cust... UCSC Geno... Microsoft Po... 10.35.33.201 -... C:\Users\Bib\... Downloads cpgplot.1 - W... Microsoft Excel pax6-1Mb-cp... NL 12:47

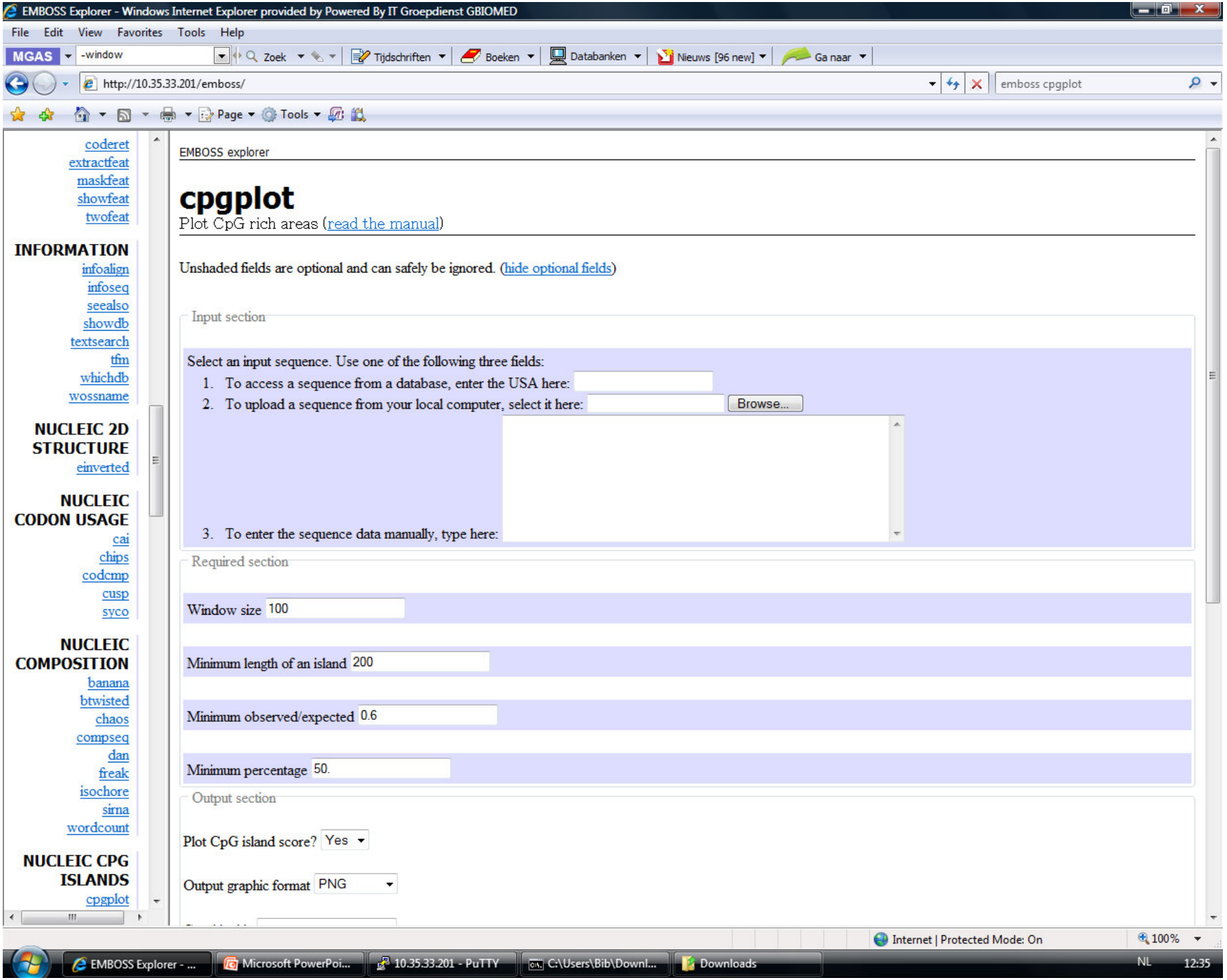

Human chr11:31,735,036-31,817,317 - UCSC Genome Browser v204 - Windows Internet Explorer provided by Powered By IT Groepdienst
http://genome.ucsc.edu/cgi-bin/hgTracks
Home Genomes Blat Tables Gene Sorter PCR DNA Convert Ensembl NCBI PDF/PS Session Help
UCSC Genome Browser on Human Mar. 2006 Assembly
move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x
position/search chr11:31,735,036-31,817,317 jump clear size 82,282 bp. configure
chr11 (p13)
chr11:
31750000
31760000
31770000
31780000
31790000
31800000
31810000
My cpgplot predictions
cpgplot
UCSC Genes Based on RefSeq, UniProt, GenBank, CCDS and Comparative Genomics
ELP4
PAX6
BX648962
RefSeq Genes
Mammalian Gene Collection Full ORF mRNAs
BC012514
BC011953
Human mRNAs from GenBank
Human mRNAs
Human ESTs That Have Been Spliced
Spliced ESTs
CpG Islands (Islands < 300 Bases are Light Green)
Vertebrate Multiz Alignment & Conservation (44 Species)
Placental Mammal Basewise Conservation by PhyloP
Mammal Cons
Multiz Alignments of 44 Vertebrates
Rhesus
Tarsier
Mouse
Dog
Elephant
Opossum
Platypus
Chicken
Lizard
X_tropicalis
Stickleback
Simple Nucleotide Polymorphisms (dbSNP build 129)
SNPs (129)
Repeating Elements by RepeatMasker
RepeatMasker
move start
move end
Click on a feature for details. Click or drag in the base position track to zoom in. Click gray/blue bars on left for track options and descriptions.
default tracks hide all manage custom tracks configure reverse refresh
collapse all
Use drop-down controls below and press refresh to alter tracks displayed.
Tracks with lots of items will automatically be displayed in more compact modes.
expand all
Done
Internet | Protected Mode: On
100%
Human chr1...
UCSC Geno...
Microsoft Po...
10.35.33.201 -...
C:\Users\Bib\...
Downloads
cpgplot.1 - W...
Microsoft Excel
pax6-1Mb-cp...
NL
12:48


Ensembl genome browser 53: H.sapiens - Region in detail - Chromosome 11: 31,766,868-31,796,085 - Windows Internet Explorer prov
File Edit View Favorites Tools Help
http://www.ensembl.org/Homo_sapiens/Location/View?db=core;g=ENSG00000007372;r=11:31766868-31796085
Home > Human
Location: 11:31,766,868-31,796,085
Gene: PAX6
Login / Register | BLAST/BLAT | BioMart | Docs & FAQs
Chromosome 11: 31,766,868-31,796,085
Configure page
Main panel
Top panel
Custom Data
Your account
SAVE and close
Search display:
Simple features
CpG islands Show info
First EF Show info
TSS (Eponine) Show info
tRNA Show info
To update this configuration, select your tracks and other options in the box above and close this popup window. Your view will then be updated automatically.
Reset configuration for Main panel to default settings.
Notes:
To change whether a track is drawn OR how it is drawn, click on the icon by the track name and then select the way the track is to be rendered.
On the left hand side of the page the number of tracks in a menu, and the number of tracks currently turned on from that menu are shown by the two numbers in parentheses (tracks on/total tracks).
Certain tracks displayed come from user-supplied or external data sources, these are clearly marked as DAS (Distributed Annotation Sources), URL (UCSC style web resources) or User data uploaded by yourself or another user.
Please note that the content of these tracks is not the responsibility of the Ensembl project.
In the case of URL based or DAS tracks may either slow down your ensembl browsing experience OR may be unavailable as these are served and stored from other servers elsewhere on the Internet.
Main panel
Active tracks
(1/4) Sequence
(0/1) Markers
(3/10) Genes
(0/2) Prediction Transcripts
(0/7) Protein alignments
(0/5) Protein features
(2/4) cDNA/mRNA alignmer
(0/4) EST alignments
(0/2) RNA alignments
(0/2) Other DNA alignments
(0/20) Oligo features
(0/3) Ditag features
(0/1) External data
(0/4) Simple features
(0/11) Misc. regions
(0/12) Repeats
(0/18) Variation features
(1/23) Functional genomics
(0/8) Multiple alignments
(0/33) BLASTZ alignments
(0/11) Translated blat alignn
(5/5) Additional decorations
(5/5) Information
Reg. Features
%GC
31.77 Mb
31.77 Mb
31.78 Mb
31.79 Mb
31.79 Mb
31.80 M
Reverse strand
29.22 Kb
Gene Legend
Known protein coding
Unclassified
Internet | Protected Mode: On
100%
Ensembl gen...
UCSC Geno...
Microsoft Po...
10.35.33.201 -...
C:\Users\Bib\...
Downloads
cpgplot.1 - W...
Microsoft Excel
pax6-1Mb-cp...
NL
12:49


Ensembl genome browser 53: H.sapiens - Region in detail - Chromosome 11: 31,766,868-31,796,085 - Windows Internet Explorer prov
File Edit View Favorites Tools Help
http://www.ensembl.org/Homo_sapiens/Location/View?db=core;g=ENSG00000007372;r=11:31766868-31796085;time=1241088594258.258
Home > Human
Login / Register | BLAST/BLAT | BioMart | Docs & FAQs
Location: 11:31,766,868-31,796,085
Gene: PAX6
Chromosome 11: 31,766,868-31,796,085
Configure page
Main panel
Top panel
Custom Data
Your account
Close
Data Management
Uploaded data
Upload Data
Share Data
Remote data
Attach DAS
Attach URL Data
Manage Data
Select File to Upload
IMPORTANT NOTE:
We are only able to store single-species datasets, containing data on Ensembl coordinate systems. There is also a 5Mb limit on data uploads. If your data does not conform to these guidelines, you can still attach it to Ensembl without uploading.
Name for this upload (optional):
Species:
Human (Homo sapiens)
Assembly:
NCBI36
Upload file:
Browse...
or provide file URL:
Next >
CpG Islands
Reg. Features
%GC
31.77 Mb
31.78 Mb
31.79 Mb
31.80 Mb
Reverse strand
29.22 Kb
Known protein coding
Internet | Protected Mode: On
100%


Ensembl genome browser 53: H.sapiens - Region in detail - Chromosome 11: 31,766,868-31,796,085 - Windows Internet Explorer prov
http://www.ensembl.org/Homo_sapiens/Location/View?db=core;g=ENSG00000007372;r=11:31766868-31796085;time=1241088616213.213
Home > Human
Login / Register | BLAST/BLAT | BioMart | Docs & FAQs
Location: 11:31,766,868-31,796,085
Gene: PAX6
Location-based displays
Whole genome
Chromosome summary
Region overview
Region in detail
Comparative Genomics
Genomic alignments
Synteny (10)
Genetic Variation
Resequencing (6)
Linkage Data
Markers
Configure this page
Add/manage custom data
Export data
Bookmark this page
Chromosome 11: 31,766,868-31,796,085
chromosome 11
Export image
« Region overview
Region in detail help
Genomic alignments »
Chromosome bands
Contigs
Ensembl/Havana g...
ncRNA gene
AL135932.7
IMMP1L
ELP4
PAX6
RCN1
DCDC1
ZCSL3
Ensembl Homo sapiens version 53.36o (NCBI36) Chromosome 11: 31,281,476 - 32,281,475
Location: 11 : 31766868 . 31796085 Go>
Human cDNA
CCDS set
CpG islands
Reg. Features
%GC
< PAX6-009
< PAX6-011
< PAX6-008
< PAX6-005
< PAX6-004
< PAX6-001
< PAX6-003
< PAX6-002
< PAX6-201
Done
Internet | Protected Mode: On
100%


Human chr11:31,735,036-31,817,317 - UCSC Genome Browser v204 - Windows Internet Explorer provided by Powered By IT Groepdienst
File Edit View Favorites Tools Help
http://genome.ucsc.edu/cgi-bin/hgTracks?insideX=115&revCmplDisp=0&hgsid=131273568&position=chr11%3A31735036-31817317&hgtgroup_user_close=0&hg
emboss cpgplot
Phenotype and Disease Associations refresh
Genes and Gene Prediction Tracks refresh
UCSC Genes pack
Old UCSC Genes hide
Alt Events hide
CCDS hide
RefSeq Genes pack
Other RefSeq hide
MGC Genes pack
ORFeome Clones hide
TransMap... hide
Vega Genes hide
Ensembl Genes hide
AceView Genes hide
SIB Genes hide
N-SCAN hide
CONTRAST hide
SGP Genes hide
Geneid Genes hide
Genscan Genes hide
Exoniphy hide
Augustus hide
RNA Genes hide
ACEScan hide
EvoFold hide
sno/miRNA hide
Pos Sel Genes hide
mRNA and EST Tracks refresh
Expression refresh
Regulation refresh
Broad Histone hide
CpG Islands full
hide
dense
squish
pack
full
EIO/JCVI NAS hide
Eponine TSS hide
FirstEF hide
GIS ChIP-PET hide
ORegAnno hide
SwitchGear TSS hide
TFBS Conserved hide
TS miRNA sites hide
Vista Enhancers hide
Yale TFBS hide
FOX2 CLIP-seq hide
LI/UCSD TAF1... hide
NKI Nuc Lamina... hide
Nucleosome Occupancy... hide
Uppsala ChIP... hide
Comparative Genomics refresh
Variation and Repeats refresh
Pilot ENCODE Regions and Genes refresh
Pilot ENCODE Transcription refresh
Pilot ENCODE Chromatin Immunoprecipitation refresh
Pilot ENCODE Chromatin Structure refresh
Pilot ENCODE Comparative Genomics and Variation refresh
refresh
Internet | Protected Mode: On
100%
Human chr1...
UCSC Geno...
Microsoft Po...
10.35.33.201 -...
C:\Users\Bib\...
Downloads
cpgplot.1 - W...
Microsoft Excel
pax6-1Mb-cp...
NL
12:48


EMBOSS Explorer - Windows Internet Explorer provided by Powered By IT Groepdienst GBIOMED
File Edit View Favorites Tools Help
http://10.35.33.201/emboss/
emboss cpgplot
coderet
extractfeat
maskfeat
showfeat
twofeat
INFORMATION
infoalign
infoseq
seealso
showdb
textsearch
tfm
whichdb
wossname
NUCLEIC 2D STRUCTURE
einverted
NUCLEIC CODON USAGE
cai
chips
codcmp
cusp
syco
NUCLEIC COMPOSITION
banana
btwisted
chaos
compseq
dan
freak
isochore
sirna
wordcount
NUCLEIC CPG ISLANDS
cpgplot
EMBOSS explorer
cpgplot
Plot CpG rich areas (read the manual)
Unshaded fields are optional and can safely be ignored. (hide optional fields)
Input section
Select an input sequence. Use one of the following three fields:
1. To access a sequence from a database, enter the USA here:
2. To upload a sequence from your local computer, select it here:
Browse...
3. To enter the sequence data manually, type here:
Required section
Window size 100
Minimum length of an island 200
Minimum observed/expected 0.6
Minimum percentage 50.
Output section
Plot CpG island score? Yes
Output graphic format PNG
Internet | Protected Mode: On
100%
EMBOSS Explorer - ...
Microsoft PowerPoi...
10.35.33.201 - PuTTY
C:\Users\Bib\Downl...
Downloads
NL
12:35

EMBOSS Explorer - Windows Internet Explorer provided by Powered By IT Groepdienst GBIOMED
File Edit View Favorites Tools Help
MGAS -window Zoek Tijdschriften Boeken Databanken Nieuws [96 new] Ga naar
http://10.35.33.201/emboss/ emboss cpgplot
Page Tools

coderet
extractfeat
maskfeat
showfeat
twofeat

INFORMATION
infoalign
infoseq
seealso
showdb
textsearch
tfm
whichdb
wossname

NUCLEIC 2D STRUCTURE
einverted

NUCLEIC CODON USAGE
cai
chips
codcmp
cusp
syco

NUCLEIC COMPOSITION
banana
btwisted
chaos
compseq
dan
freak
isochore
sirna
wordcount

NUCLEIC CPG ISLANDS
cpgplot

emboss cpgplot

Function

Plot CpG rich areas

Description

CpG refers to a C nucleotide immediately followed by a G. The 'p' in 'CpG' refers to the phosphate group linking the two bases.

Detection of regions of genomic sequences that are rich in the CpG pattern is important because such regions are resistant to methylation and tend to be associated with genes which are frequently switched on. Regions rich in the CpG pattern are known as CpG islands.

It has been estimated that about half of all mammalian genes have a CpG-rich region around their 5' end. It is said that all mammalian house-keeping genes have a CpG island!

Non-mammalian vertebrates have some CpG islands that are associated with genes, but the association gets equivocal in the farther taxonomic groups.

Finding a CpG island upstream of predicted exons or genes is good contributory evidence.

By default, this program defines a CpG island as a region where, over an average of 10 windows, the calculated % composition is over 50% and the calculated Obs/Exp (i.e. Observed/Expected) ratio is over 0.6 and the conditions hold for a minimum of 200 bases. These conditions can be modified by setting the values of the appropriate parameters.

The Observed number of CpG patterns in a window is simply the count of the number of times a 'C' is found followed immediately by a 'G'.

The Expected number of CpG patterns is calculated for each window as the number of CpG dinucleotides you would expect to see in that window based on the frequency of C's and G's in that window. Thus, the Expected frequency of CpG's in a window is calculated as the number of 'C's in the window multiplied by the number of 'G's in the window, divided by the window length.

```
Expected = (number of C's  * number of G's) / window length
```

This program reads in one or more sequences and calculates the Obs/Exp ratio, the percentage CpG over a window which is moved along the sequence. These calculated values can be plotted, together with the regions which match this program's definition of a CpG island.

Usage

Here is a sample session with cpgplot

Done
Internet | Protected Mode: On
100%
EMBOSS Explorer - ... Microsoft PowerPoi... 10.35.33.201 - PuTTY C:\Users\Bib\Downl... Downloads
NL 12:35