

## SUPPLEMENTAL MATERIAL

**Supplementary Figure 1:** Larger image for Figure 1: Step 1, top image.

The image shows the UCSC Genome Bioinformatics website. At the top, there is a yellow header with the text "UCSC Genome Bioinformatics". Below this is a blue navigation bar with links: Genomes, Blat, Tables, Gene Sorter, PCR, VisiGene, Proteome, Session, FAQ, and Help. On the left side, there is a vertical menu with links: Genome Browser, ENCODE, Blat, Table Browser, Gene Sorter, In Silico PCR, Genome Graphs, Galaxy, VisiGene, and Proteome. The main content area has a light blue background and is titled "About the UCSC Genome Bioinformatics Site". It contains two paragraphs of text. The first paragraph welcomes users and mentions the ENCODE project. The second paragraph describes the tools available on the site, such as the Genome Browser, Gene Sorter, Blat, Table Browser, VisiGene, and Genome Graphs. At the bottom of the main content area, there is a paragraph about the development and maintenance of the site by the Genome Bioinformatics Group at UCSC, and a link to a public mailing list.

**Supplementary Figure 2:** Larger image for Figure 1: Step 1, middle image.

The image shows the "Human Genome Graphs" tool interface. It features a light blue header with the title "Human Genome Graphs". Below the header, there are several input fields and buttons. The "clade" field is set to "Mammal", the "genome" field is set to "Human", and the "assembly" field is set to "Mar. 2006". There are two "graph" fields, both set to "- nothing -", and two "in" fields, one set to "blue" and the other to "red". Below these fields are several buttons: "upload", "import", "configure", "correlate", "significance threshold:" followed by a text input field containing "0", "browse regions", and "sort genes".

**Supplementary Figure 3:** Larger image for Figure 1: Step 1, bottom image.

### Upload Data to Genome Graphs

**name of data set:**

**description:**

**file format:**

**markers are:**

**column labels:**

**display min value:**  **max value:**

**label values:**

**draw connecting lines between markers separated by up to**  **bases.**

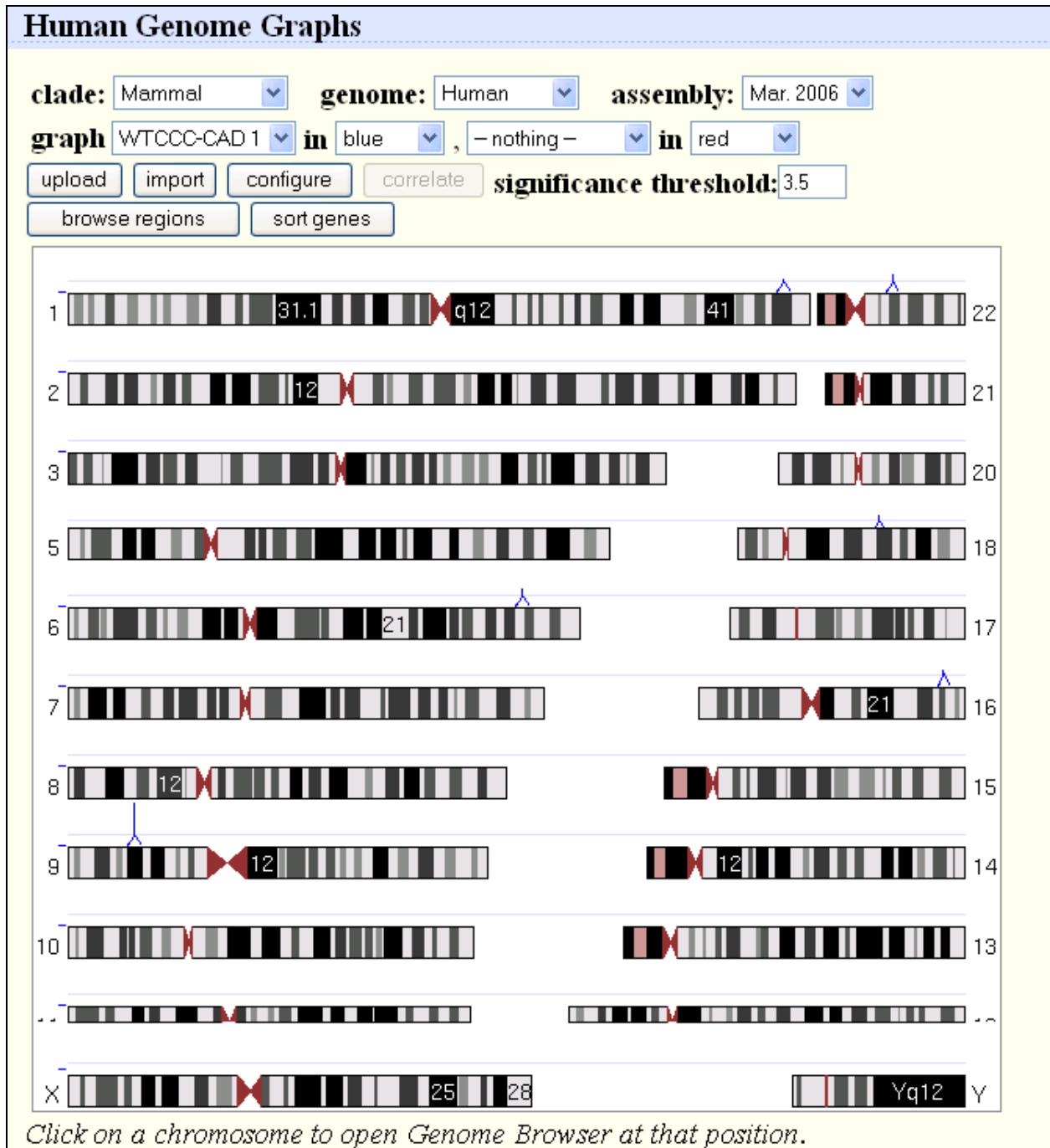
**file name:**

or

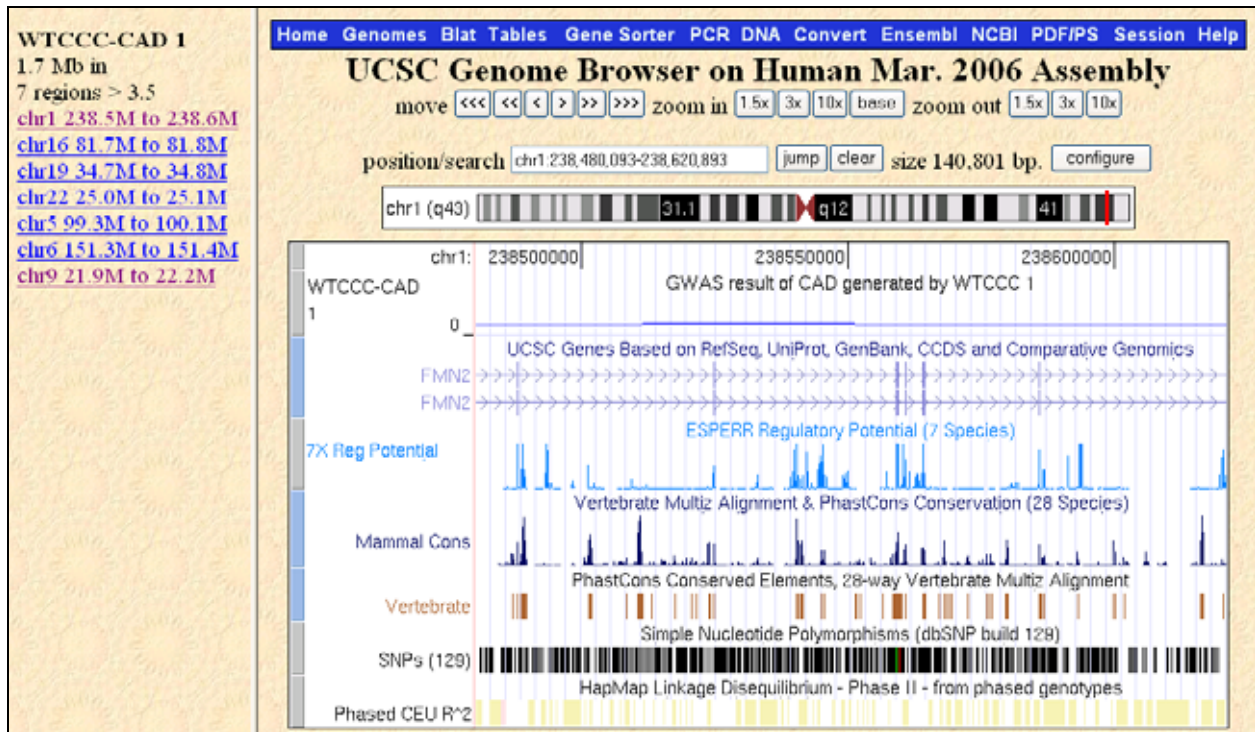
**Paste URLs or data:**

rs11799950	0.000
rs7531591	3.510
rs17672135	3.983
rs1889867	3.510
rs2118978	0.000
rs40175	0.000
rs492938	3.510

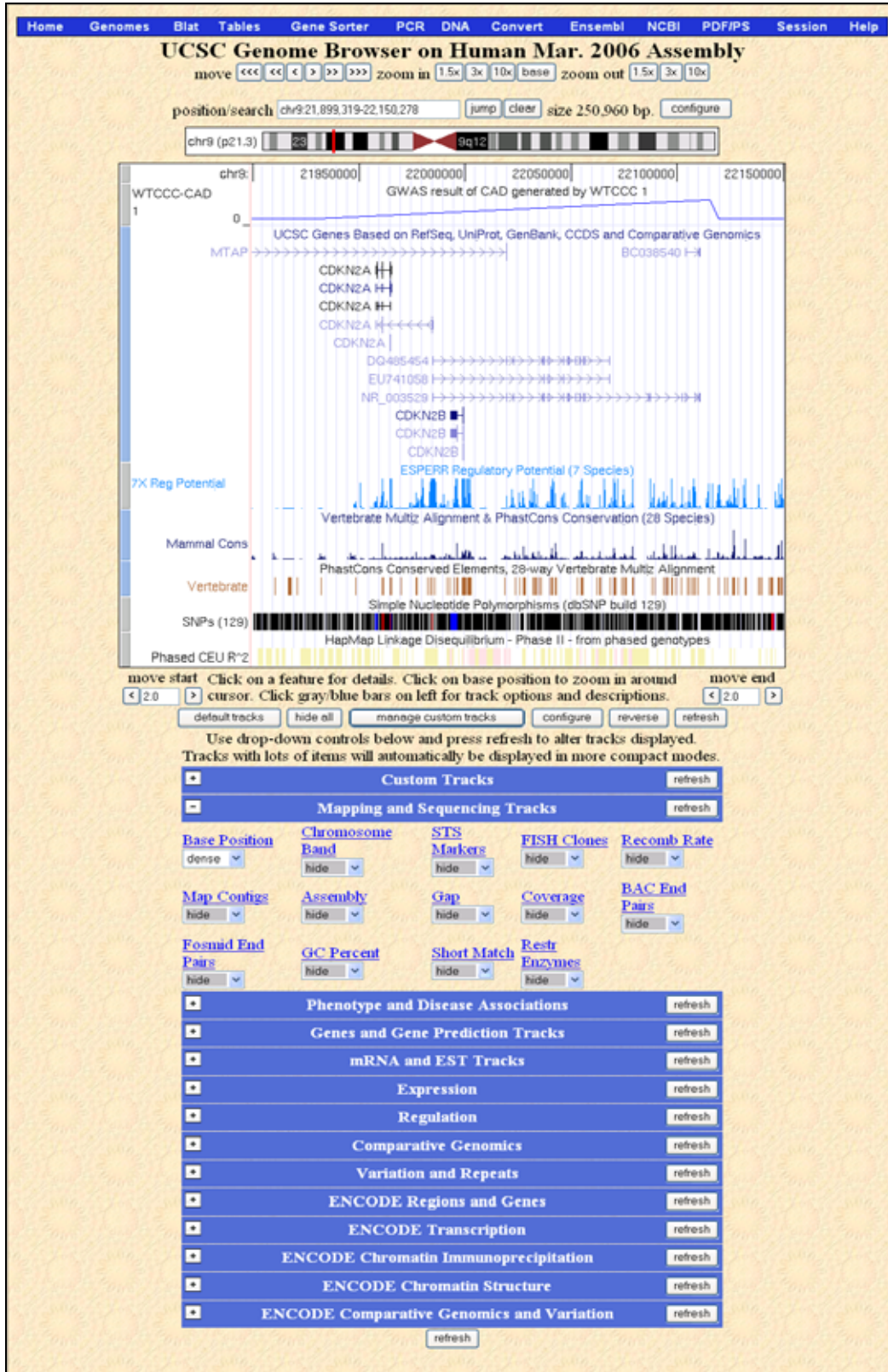
Supplementary Figure 4: Larger image for Figure 1: Step 2, top image.



Supplementary Figure 5: Larger image for Figure 1: Step 2, bottom image.



Supplementary Figure 6: Larger image for Figure 1: Step 3.





**Supplementary Figure 7:** Larger image for Figure 1: Step 2, top image.

Human Gene CDKN2A (uc003zpk.1) Description and Page Index					
<p><b>Description:</b> cyclin-dependent kinase inhibitor 2A isoform 1</p> <p><b>RefSeq Summary (NM_000077):</b> This gene generates several transcript variants which differ in their first exons. At least three alternatively spliced variants encoding distinct proteins have been reported, two of which encode structurally related isoforms known to function as inhibitors of CDK4 kinase. The remaining transcript includes an alternate first exon located 20 Kb upstream of the remainder of the gene; this transcript contains an alternate open reading frame (ARF) that specifies a protein which is structurally unrelated to the products of the other variants. This ARF product functions as a stabilizer of the tumor suppressor protein p53 as it can interact with, and sequester, MDM1, a protein responsible for the degradation of p53. In spite of the structural and functional differences, the CDK inhibitor isoforms and the ARF product encoded by this gene, through the regulatory roles of CDK4 and p53 in cell cycle G1 progression, share a common functionality in cell cycle G1 control. This gene is frequently mutated or deleted in a wide variety of tumors, and is known to be an important tumor suppressor gene. [provided by RefSeq].</p> <p><b>Strand:</b> - <b>Genomic Size:</b> 7288 <b>Exon Count:</b> 3 <b>Coding Exon Count:</b> 3</p>					
<b>Page Index</b>	Sequence and Links	UniProt Comments	Genetic Associations	CTD	Microarray
RNA Structure	Protein Structure	Other Species	GO Annotations	mRNA Descriptions	Pathways
Other Names	Model Information	Methods			

**Supplementary Figure 8:** Larger image for Figure 1: Step 1, middle image.

Genetic Association Studies of Complex Diseases and Disorders	
<p><b>Genetic Association Database:</b> <a href="#">CDKN2A</a></p> <p><b>CDC HuGE Published Literature:</b> <a href="#">CDKN2A</a></p> <p><b>Positive Disease Associations:</b> <a href="#">adult T-cell leukemia</a> , <a href="#">bladder cancer</a> , <a href="#">breast cancer melanoma</a> , <a href="#">diabetes, type 2</a> , <a href="#">diabetes, type 2 hypertension lipoprotein</a> , <a href="#">esophageal squamous cell carcinoma</a> , <a href="#">familial melanoma</a> , <a href="#">lung carcinoma</a> , <a href="#">melanoma</a> , <a href="#">myocardial infarct</a> , <a href="#">neurofibromatosis 1</a> , <a href="#">oligodendrogliomas</a> , <a href="#">ovarian cancer</a> , <a href="#">pancreatic cancer</a> , <a href="#">physical function</a></p> <p><b>Related Studies:</b></p> <ol style="list-style-type: none"> <li> <p><b>adult T-cell leukemia</b></p> <p>Fujiwara H et al. 1999, Alteration of p16 (CDKN2) gene is associated with interleukin-2-induced tumor cell growth in adult T-cell leukemia., Experimental hematology. 1999 Jun;27(6):1004-9. [PubMed <a href="#">10378889</a>]</p> </li> <li> <p><b>bladder cancer</b></p> <p>Sakano, S. et al. 2003, Clinical course of bladder neoplasms and single nucleotide polymorphisms in the CDKN2A gene., International journal of cancer. Journal international du cancer. 2003 Mar;104(1):98-103. [PubMed <a href="#">12532425</a>]</p> <p><i>Our results corroborate the earlier findings that single base mutation is not the prime mode of inactivation of the CDKN2A gene in bladder cancer. Further, the results indicate, a role for the 3' UTR polymorphisms in the CDKN2A gene in tumor invasiveness.</i></p> </li> <li> <p><b>breast cancer melanoma</b></p> <p>Debniak, T. et al. 2006, MC1R common variants, CDKN2A and their association with melanoma and breast cancer risk, Int J Cancer 2006. [PubMed <a href="#">16988943</a>]</p> </li> </ol>	

**Supplementary Figure 9:** Larger image for Figure 1: Step 4, bottom image.

# Association Database

H I J K L M N O P Q R S T U V W X Y Z

**All View    Search for All    Record found: 2**

ed	CDC Index	1 - GAD 2 - CDC	Year	Assoc? YorN	Gene Symbol	OMIM	Gene Expert	Broad Phenotype (Disease)	Disease Expert	MeSH Disease Ter
		CDC	2007	Y	CDKN2A	<a href="#">600160</a>		myocardial infarct		Coronary A
		CDC	2007		CDKN2A	<a href="#">600160</a>		atherosclerosis, generalized m		Myocardial

Result Page: **1**

National Institute

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**Supplemental Data:** Demonstration data set.

SNP	$-\log_{10}P$
rs11799950	0.000
rs7531591	3.510
rs17672135	3.983
rs1889867	3.510
rs2118978	0.000
rs40175	0.000
rs492938	3.510
rs383830	5.243
rs34162536	3.510
rs455144	0.000
rs11961921	0.000
rs36082661	3.510
rs6922269	5.199
rs505358	3.510
rs34091791	0.000
rs10124918	0.000
rs2811716	3.510
rs1333049	13.747
rs7020996	3.510
rs13300968	0.000
rs11860434	0.000
rs11648346	3.510
rs8055236	5.012
rs16959735	3.510
rs4782691	0.000
rs7339484	0.000
rs8100086	3.510
rs7250581	5.040
rs4805440	3.510
rs10403126	0.000
rs10610555	0.000
rs28643474	3.510
rs688034	5.161
rs5761483	3.510
rs11913617	0.000