**Spring 2014 Genomics Exam #1**
**Genomic Sequences & Variations**

There is no time limit on this test, though I don't want you to spend too much time on it. I have tried to design an exam that will take less time that exams in the past. You do not need to read any additional papers other than the ones I send to you. There are 4 pages, including this cover sheet, for this test. You are not allowed discuss the test with anyone until all exams are turned in at 11:30 am on Wednesday February 10. **ELECTRONIC COPIES OF YOUR EXAM ANSWERS ARE DUE BY 11:30 am ON WEDNESDAY FEBRUARY 10**. You may use a calculator, a ruler, your notes, the book, and the internet. You may work on this exam in as many blocks of time as you want. Submit your electronic version before 11:30 am (eastern time zone).

The **answers to the questions must be typed in a Word file and emailed to me as an attachment**. Be sure to backup your test answers just in case (I suggest a thumb drive or other removable storage). You will need to capture screen images as a part of your answers which you may do without seeking permission since your test answers will not be in the public domain. Remember to explain your thoughts in *your* own words and use screen shots to support your answers. Screen shots without ***your*** words are worth very few points. Support your answers with data using screen shots liberally.

*DO NOT READ or DOWNLOAD ANY NEW PAPERS FOR THIS EXAM. You may search and read abstracts. RELY ON YOUR EXPERIENCE, AND YOUR SKILLS. Spell out your logic for each answer.*

**-3 pts if you do not follow this direction.**
**Please do not write or type your name on any page other than this cover page.**
Staple all your pages (INCLUDING THE TEST PAGES) together when finished with the exam.

Name (please type):

Write out the full pledge and sign (electronic signature is ideal):

How long did this exam take you to complete?

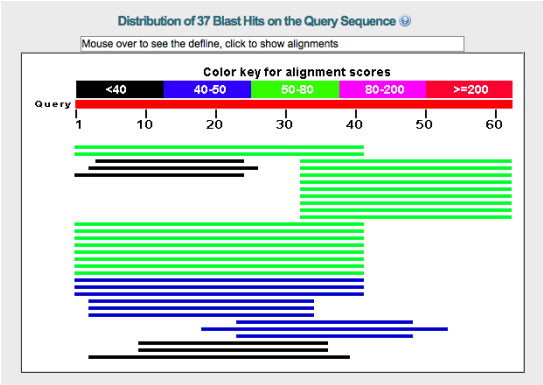
**10 pts**

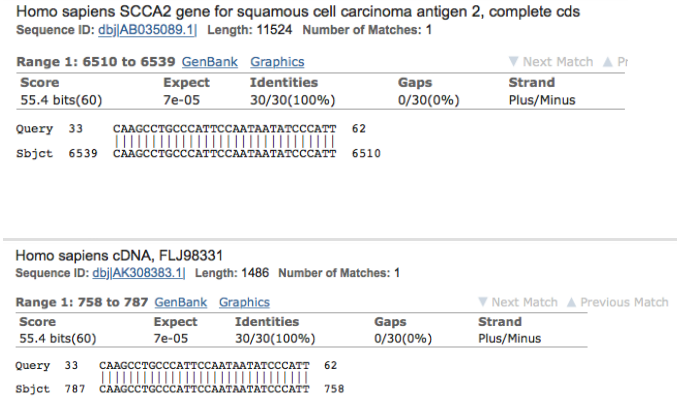
1) Below I have provided you with a sequence of DNA that was emailed to me from a former student who is a physician at a university hospital. This physician has asked for my advice about what is going on given the atypical nature of this sequence.

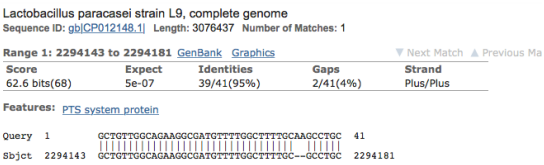
GCTGTTGGCAGAAGGCGATGTTTTGGCTTTTGCAAGCCTGCCCATTCCAATAATATCCCATT

Compose a one paragraph (100 word maximum) response to this curious physician. You MUST include screen shots of your data and document (your source) how you found the answer in order for insurance to pay for the patient's treatment.

From BLAST:




Horizontal gene transfer from *Lactobacillus paracasei* into human gene SCCA2 (should have tracked down the source of FLJ98331 cDNA). Disrupt gene and causes cancer.

**10 pts**

2) Here is a peptide from a proteomics project. What is this protein's function? Cite your source(s) of information and include a hyperlink for my verification. You are allowed to copy and paste your answer for this question. DKYYYTRKILGSTLACARASALCLNFNSTLILLPVCRNLL

From BLAST, found this protein/gene: NADPH oxidase 1 (NOX1). Go to NCBI Gene database and use GO terms to define function. Most importantly, noting that via alternative mRNA splicing, it is both an NADPH oxidase and a H+ ion transporter which are two unrelated molecular processes.

http://www.ncbi.nlm.nih.gov/gene/27035

Gene Ontology Provided by GOA

| Function | Evidence Code | Pubs |
|---|---|---|
| NADP binding | IC | PubMed |
| Rac GTPase binding | IPI | PubMed |
| metal ion binding | IEA | |
| protein binding | IPI | PubMed |
| superoxide-generating NADPH oxidase activity | IC | PubMed |
| superoxide-generating NADPH oxidase activity | TAS | PubMed |
| voltage-gated proton channel activity | IDA | PubMed |

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| Process | Evidence Code | Pubs |
|---|---|---|
| NADP metabolic process | IC | PubMed |
| angiogenesis | IMP | PubMed |
| cell migration | IMP | PubMed |
| cellular response to hyperoxia | IEA | |
| cellular stress response to acidic pH | IDA | PubMed |
| extracellular matrix organization | IEA | |
| hydrogen peroxide metabolic process | IDA | PubMed |
| inflammatory response | TAS | PubMed |
| intracellular pH elevation | IDA | PubMed |
| oxidation-reduction process | IDA | PubMed |
| oxygen metabolic process | IEA | |
| positive regulation of JNK cascade | IEA | |
| positive regulation of cell proliferation | IDA | PubMed |
| positive regulation of integrin biosynthetic process | IMP | PubMed |
| positive regulation of oxidative stress-induced intrinsic apoptotic signaling pathway | IEA | |
| positive regulation of smooth muscle cell proliferation | ISS | PubMed |
| positive regulation of vascular endothelial growth factor production | IEP | PubMed |
| proton transport | IDA | PubMed |
| regulation of blood pressure | TAS | PubMed |
| regulation of ion transmembrane transport | IEA | |
| regulation of systemic arterial blood pressure by renin-angiotensin | IEA | |
| respiratory burst | TAS | PubMed |
| signal transduction | TAS | PubMed |
| small GTPase mediated signal transduction | TAS | |
| superoxide anion generation | IDA | PubMed |

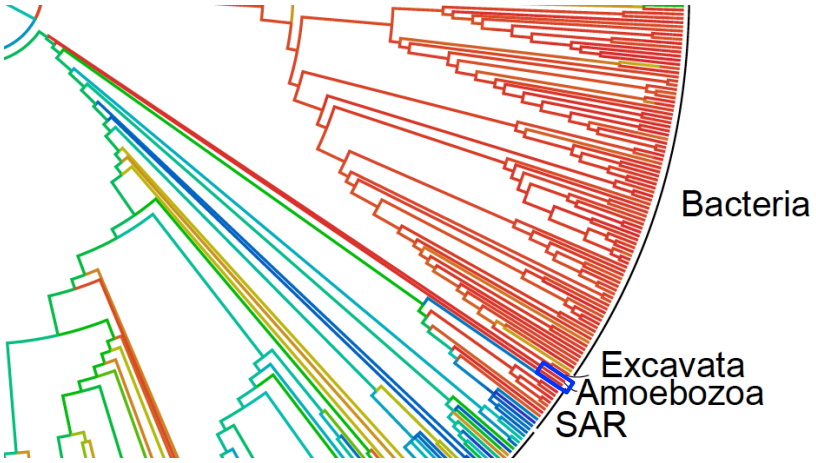
Items 1 - 25 of 26 < Prev Page 1 of 2 Next >

| Component | Evidence Code | Pubs |
|---|---|---|
| NADPH oxidase complex | IDA | PubMed |
| cell junction | IEA | |
| early endosome | IDA | PubMed |
| integral component of membrane | IC | PubMed |
| invadopodium membrane | IDA | PubMed |
| plasma membrane | TAS | |

**10 pts**

3) Included with your exam packet is a PDF file (Question_3.pdf) of an evolutionary tree showing the relatedness of the entire tree of life (down to operational taxonomic units (OTUs)). Draw a box for two terminal branches that are each other's closest relative but have very many SNPs. To generate your answer, zoom way in on two terminal branches, take a screen shot and insert your evidence here. The box you draw should be around the two ends of the branches.

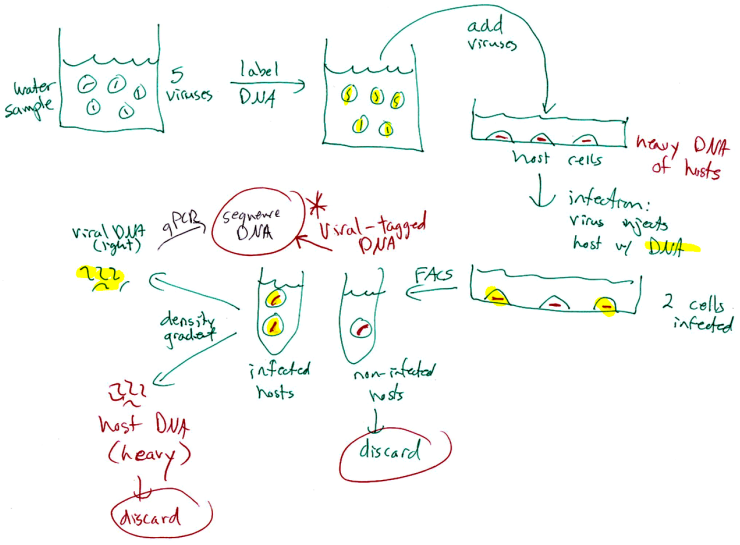
The goal was to find two branches where they have very long lines (many SNPs) and no branches off of their long lines. See blue box as an example.




**15 pts**

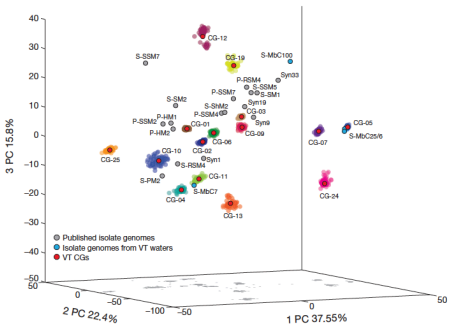
4) Illustrate the steps for this method called viral tagging as described here: in water samples containing mixed and unknown viruses, the viral DNA is labeled non-specifically with a fluorescent dye. Viruses are mixed with a host cell that contains its own genome pre-labeled with isotopically heavy DNA. The virus-infected cells are collected by fluorescence-activated flow cytometry. Isotopically light viral DNA is separated from heavy host DNA using a density gradient, and the infecting viral DNA is quantitatively amplified to produce viral-tagged DNA. Viral-tagged DNA can be sequenced at this point. You can draw on a piece of paper and scan it, or draw it electronically in your favorite program. Include your drawing with your answers. Label the steps and relevant features of your diagram. Print neatly if you do this by hand.

Must have these general steps with labels.




**15 pts**

5) PCA plot showing the genetic relationship of cultivated viruses and viral-tagged viruses all of which can infect one species of cyanobacteria host. Viruses in the plot are from a single seawater sample, plus all published cyanophage genomes previously sequenced. Principal component (PC) analysis of population-level variation the data for each viral *Candidatus* genome (CG; genus name for cyanobacteria viruses) recovered from the viral-tagged samples (colored 'clouds'; cloud colors are arbitrary to aid in discriminating populations). VT = viral tagged.

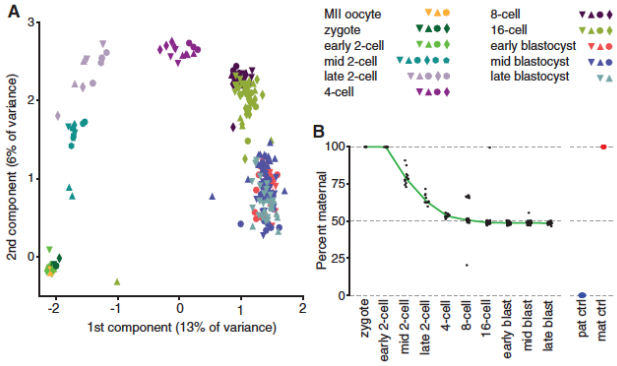



Describe three conclusions based on this figure alone. Limit each answer to a maximum of 50 words and support each with data from this figure.

1. greater diversity in VT isolates then in previously sequenced viruses
2. variations among each VT CGs (clouds)
3. subpopulations (see 3 strains on far right side).
4. and several others

**15 pts**

6) Single-cell mRNA transcripts during preimplantation mouse development. (A) Single-cell transcriptomes projected onto the first two principal components. Cells from different stages and embryos are designated by colors and symbols. (B) The percentage (by mass) of maternal RNA observed in single-cells (black dots; median is in green) at different stages of development and in controls from pure maternal (genotype called *CAST*, red) and paternal (genotype called *C57*, blue)

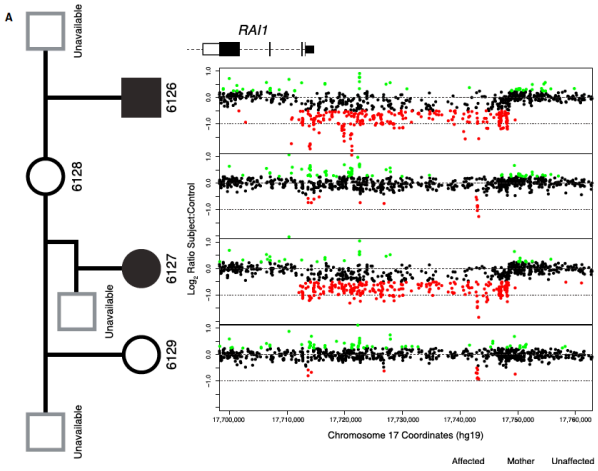


backgrounds. The eight-cell stage outlier cells with maternal bias are all from one embryo.

a) What biological process is recapitulated in panel A based on PCA analysis? Support your answer with data from this figure. Limit your answer to a maximum of 60 words.
development of egg through preimplentation embryo
b) Describe the type of early embryo allele transcriptional regulation revealed in panel B. Support your answer with data from this figure. Limit your answer to a maximum of 60 words.
starts 100% maternal (oocyte) and converts to 50:50 maternal and paternal alleles (mid-2 cell to early 8 cell stages)

**15 pts**

7) Family 1 was referred for assessment of two children with a rare recessive genetic disease and a common mother but two different fathers as shown. Comparative genome hybridization (CGH) validated for clinical diagnosis was used with DNA from two of the children.




a) Describe the molecular cause of this disease. Support your answer with data from this figure. Limit your answer to a maximum of 60 words.
40 kb deletion from one chromosome ($\log_2 = -0.5$)
hemizygous disease
b) How could two children in the same family contract this rare recessive disease? Support your answer with data from this figure. Limit your answer to a maximum of 60 words.
mother mosaic in ovaries so that some eggs wt, some with deletion. She did not have the disease, so she could not have deletion in all her somatic cells.

**10 pts**

8) Last question. I am attaching a manuscript that was accepted for publication. I would like you to review the manuscript and give me your overall opinion of the research presented. Focus on the data and use the data in the manuscript to support your evaluation. Do not look up any information online about this paper or stenosporic acid. Judge the manuscript only on its own merits using your prior experience of reading papers. Limit your evaluation to a maximum of 200 words. Support your opinion with data.

This was part of a global experiment about 3 years ago to see if for profit journals would accept manuscripts that should have been rejected. Figure 2 lacks vehicle control and was not dose dependent. Figure 3 lacked control of radiation but no drug. Grammar was the least of its problems, but that was pretty bad too. http://science.sciencemag.org/content/342/6154/60.full