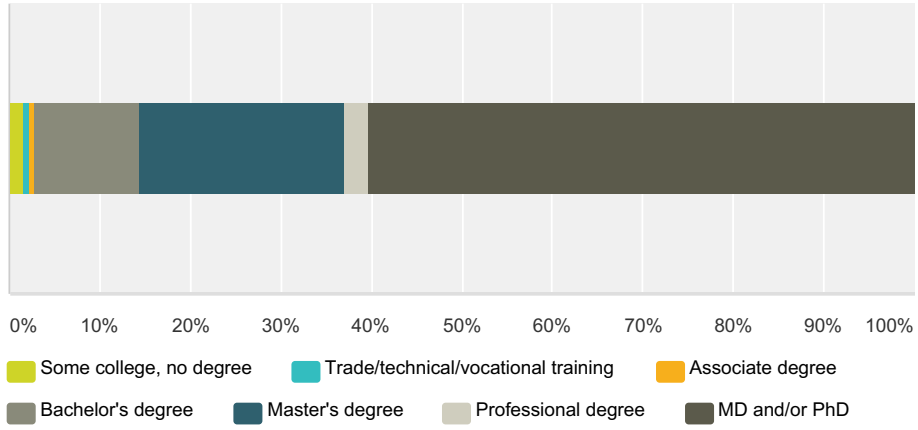# 2016 UCSC Genome Browser User Feedback Survey Report

Summary of Responses & Open-Ended Responses

Q1 What is your highest level of education/degree?

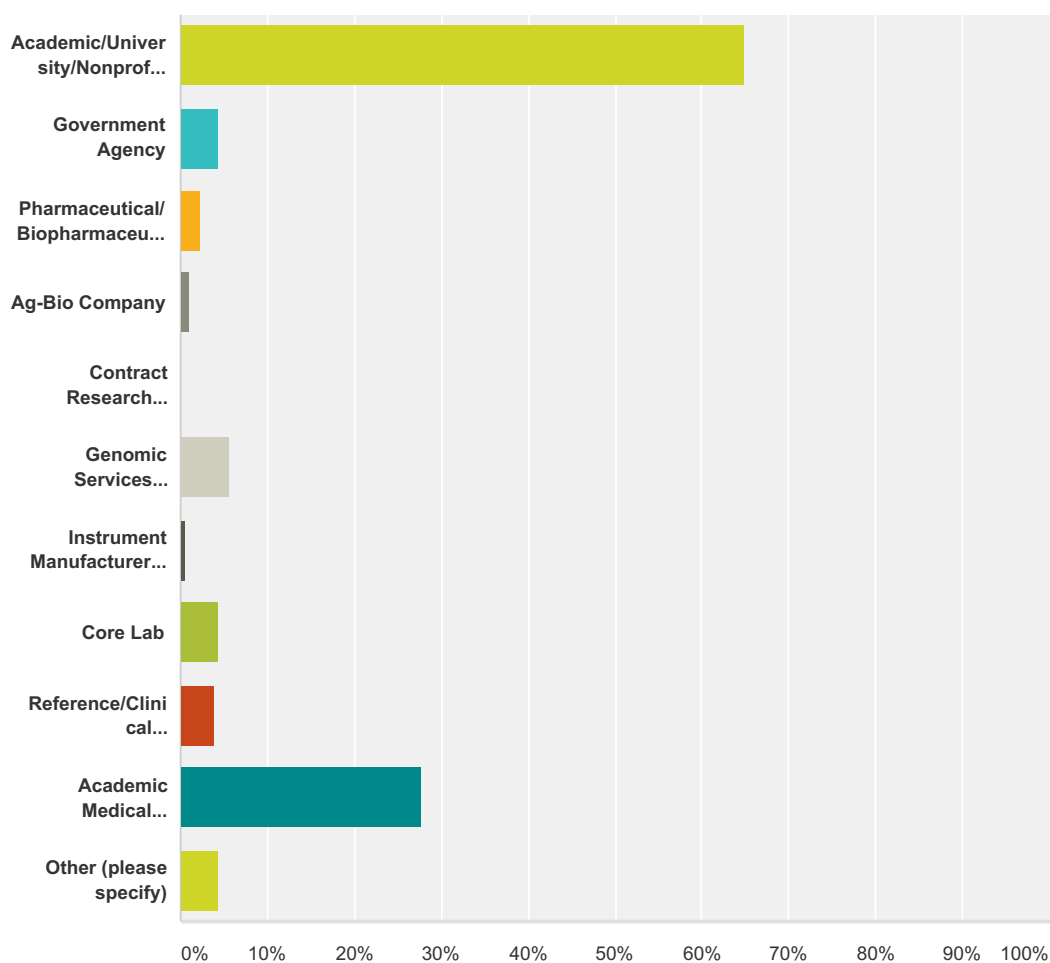Answered: 181   Skipped: 2

Answer Choices	Responses	
Some college, no degree	**1.66%**	3
Trade/technical/vocational training	**0.55%**	1
Associate degree	**0.55%**	1
Bachelor's degree	**11.60%**	21
Master's degree	**22.65%**	41
Professional degree	**2.76%**	5
MD and/or PhD	**60.22%**	109
Total		**181**

Q2 Where do you work? (Check all that apply)

Answered: 180   Skipped: 3

Answer Choices	Responses	
Academic/University/Nonprofit Research Institute	65.00%	117
Government Agency	4.44%	8
Pharmaceutical/Biopharmaceutical Company	2.22%	4
Ag-Bio Company	1.11%	2
Contract Research Organization	0.00%	0
Genomic Services Provider	5.56%	10
Instrument Manufacturer/Vendor	0.56%	1
Core Lab	4.44%	8
Reference/Clinical Lab/Hospital CLIA Lab	3.89%	7
Academic Medical Center/Hospital	27.78%	50

	Other (please specify)	4.44%	8
Total Respondents: 180			

#	Other (please specify)	Date
1	Student	7/19/2016 6:09 PM
2	UNIVERSIDAD DE GUADALAJARA	7/18/2016 8:00 PM
3	Biotech	7/18/2016 12:35 AM
4	own business	7/15/2016 4:42 PM
5	Biotech	7/14/2016 6:52 PM
6	Informatics Company	7/14/2016 11:20 AM
7	translational bioinformatics company	7/14/2016 9:02 AM
8	Genome Sequencing Center	7/13/2016 3:58 PM

Q3 What best describes your currentposition? (Check all that apply)

Answered: 168   Skipped: 15
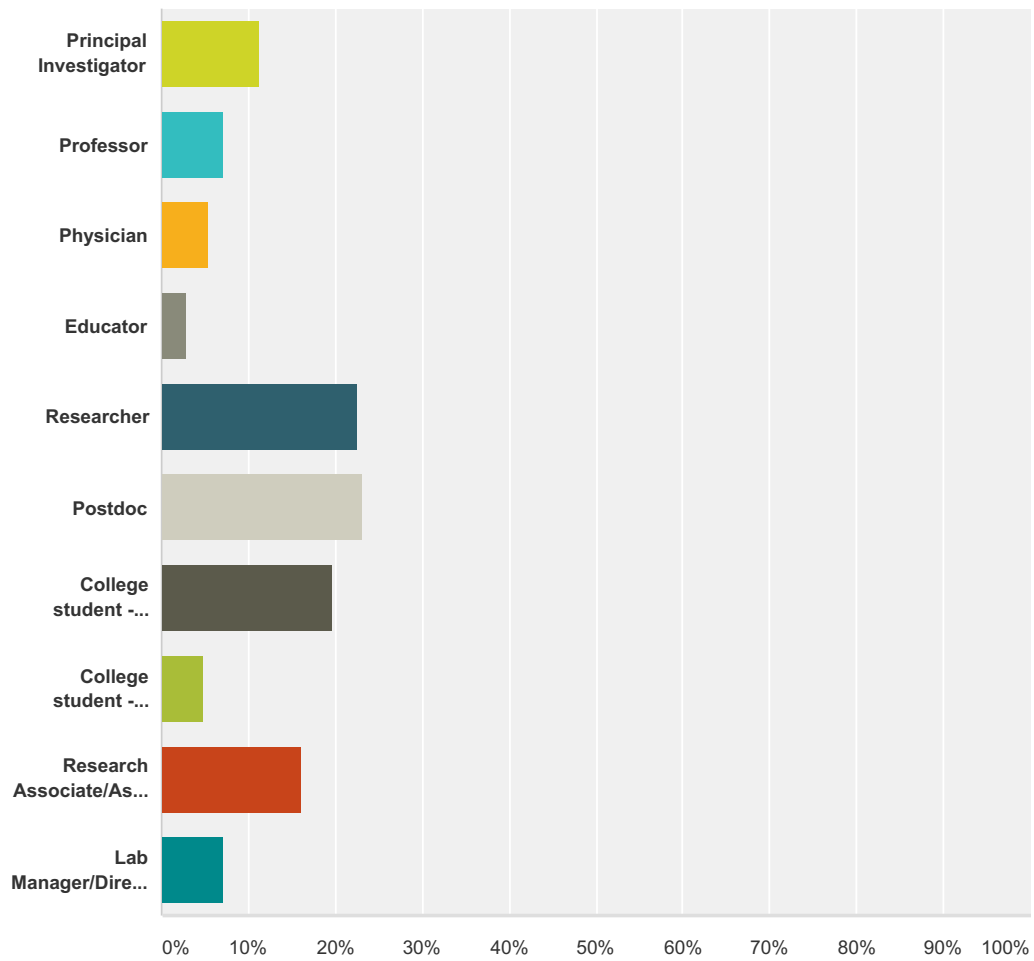
Answer Choices	Responses	
Principal Investigator	11.31%	19
Professor	7.14%	12
Physician	5.36%	9
Educator	2.98%	5
Researcher	22.62%	38
Postdoc	23.21%	39
College student - graduate	19.64%	33
College student - undergradutate	4.76%	8
Research Associate/Assistant	16.07%	27
Lab Manager/Director	7.14%	12

#	Other (please specify)	Date
	Total Respondents: 168	
1	engineer?	7/21/2016 12:53 AM
2	Senior Cytogenetics Analist	7/19/2016 12:18 PM
3	PhD Student	7/19/2016 12:41 AM
4	PhD Student	7/16/2016 3:27 PM
5	Systems Administrator	7/15/2016 5:00 PM
6	Ph.D. Student	7/14/2016 10:08 AM
7	industry scientist	7/14/2016 9:02 AM
8	PhD student	7/14/2016 7:24 AM
9	PhD student	7/14/2016 6:32 AM
10	Group leader - software development	7/14/2016 1:16 AM
11	Scientist	7/13/2016 9:31 PM
12	MD/PhD student	7/13/2016 4:12 PM
13	Research engineer	7/13/2016 1:39 PM
14	Research/staff scientist	7/13/2016 1:14 PM
15	System Adminstrator	7/13/2016 12:52 PM
16	IT/DBA	7/13/2016 12:36 PM

Q4 What are your professional interests? (Check all that apply)

Answered: 180   Skipped: 3
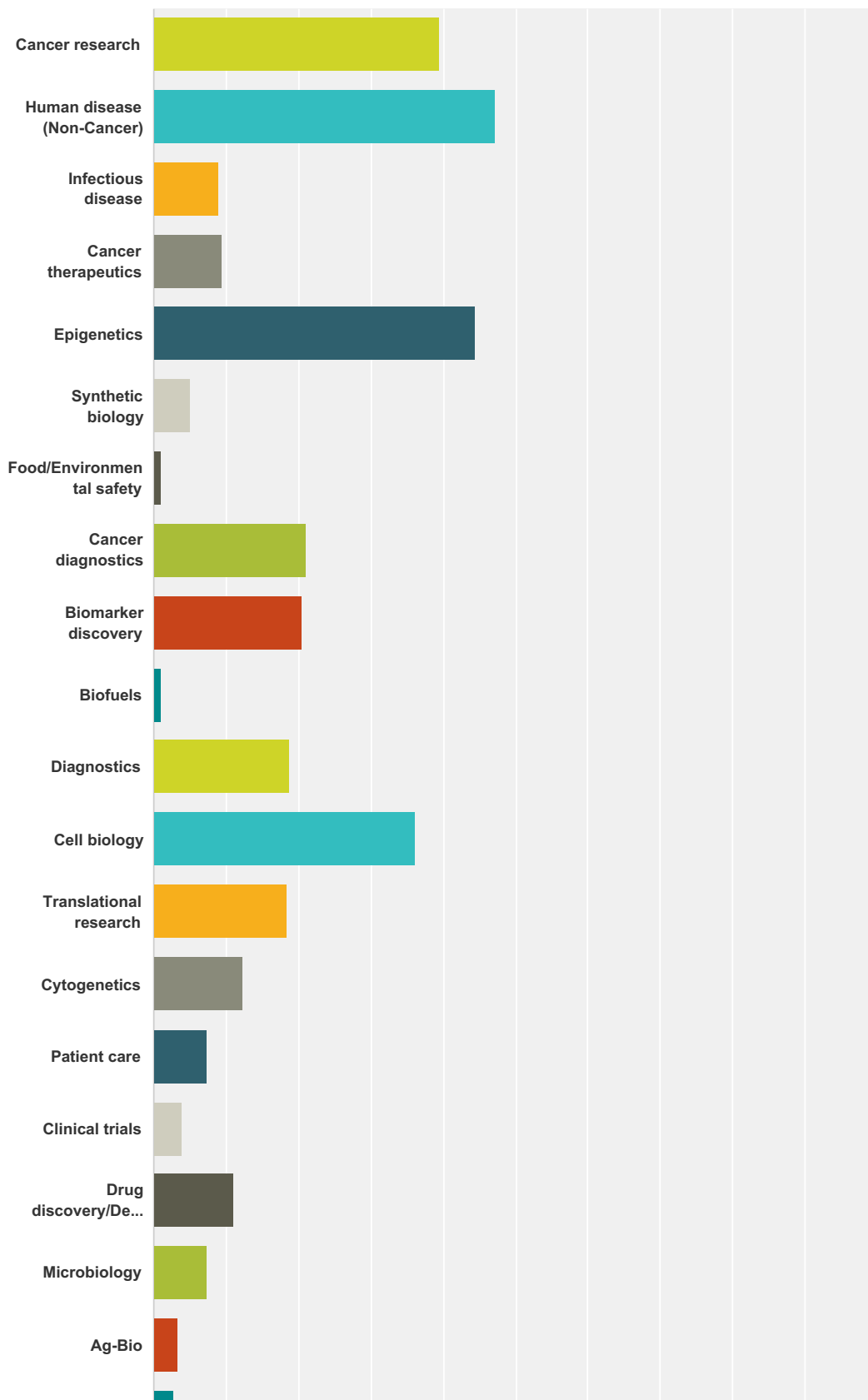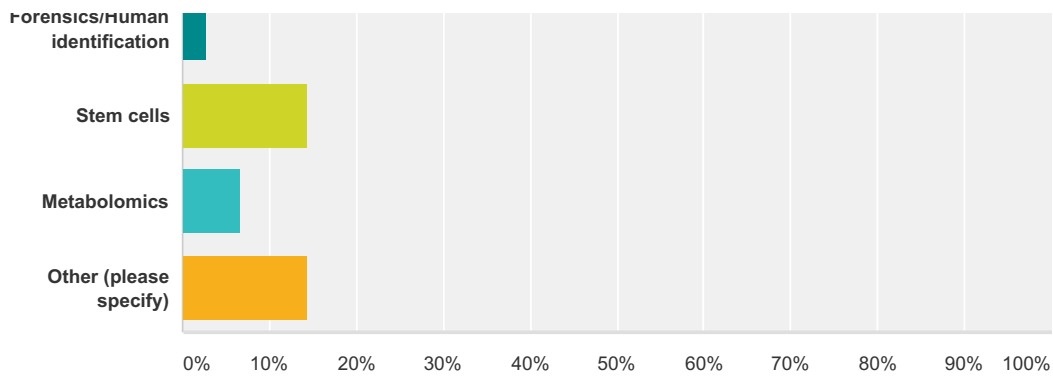
Answer Choices	Responses	
Cancer research	**39.44%**	71
Human disease (Non-Cancer)	**47.22%**	85
Infectious disease	**8.89%**	16
Cancer therapeutics	**9.44%**	17
Epigenetics	**44.44%**	80
Synthetic biology	**5.00%**	9
Food/Environmental safety	**1.11%**	2
Cancer diagnostics	**21.11%**	38
Biomarker discovery	**20.56%**	37
Biofuels	**1.11%**	2
Diagnostics	**18.89%**	34
Cell biology	**36.11%**	65
Translational research	**18.33%**	33
Cytogenetics	**12.22%**	22
Patient care	**7.22%**	13
Clinical trials	**3.89%**	7
Drug discovery/Development	**11.11%**	20
Microbiology	**7.22%**	13
Ag-Bio	**3.33%**	6
Forensics/Human identification	**2.78%**	5
Stem cells	**14.44%**	26
Metabolomics	**6.67%**	12
Other (please specify)	**14.44%**	26
Total Respondents: 180		

#	Other (please specify)	Date

1	Complex traits in models	8/2/2016 1:11 PM
2	Evolution	7/27/2016 2:43 PM
3	Phylogenetics, Evolution, Phylogenomics, Transposable Elements	7/26/2016 9:31 AM
4	Bioinformatics	7/26/2016 4:17 AM
5	Psychiatric	7/22/2016 3:30 PM
6	Human genetics	7/20/2016 1:25 AM
7	bioinformatics	7/19/2016 2:19 PM
8	Genomics	7/18/2016 3:14 PM
9	Bioinformatics	7/18/2016 2:24 AM
10	Computer Science	7/15/2016 5:00 PM
11	Immunology	7/15/2016 8:40 AM
12	Disease model mouse	7/15/2016 1:08 AM
13	Developmental Genetics	7/14/2016 9:51 AM
14	neuroscience	7/14/2016 9:25 AM
15	Genetics	7/14/2016 8:20 AM
16	Parasites, Genomics, Phylogenetics	7/14/2016 1:49 AM
17	Genetics	7/14/2016 1:39 AM
18	Transcription/Translation	7/14/2016 1:27 AM
19	Evolution	7/14/2016 1:16 AM
20	Structural Variation	7/13/2016 10:02 PM
21	evolution	7/13/2016 6:18 PM
22	Evolutionary Biology	7/13/2016 4:54 PM
23	computational biology	7/13/2016 3:12 PM
24	Genomics, developmental biology	7/13/2016 1:39 PM
25	Ethical, Legal, Social Issues (ELSI)	7/13/2016 1:14 PM
26	brain diseases	7/13/2016 11:56 AM

Q5 Which of these tasks do you perform regularly?(Check all that apply)

Answered: 179   Skipped: 4
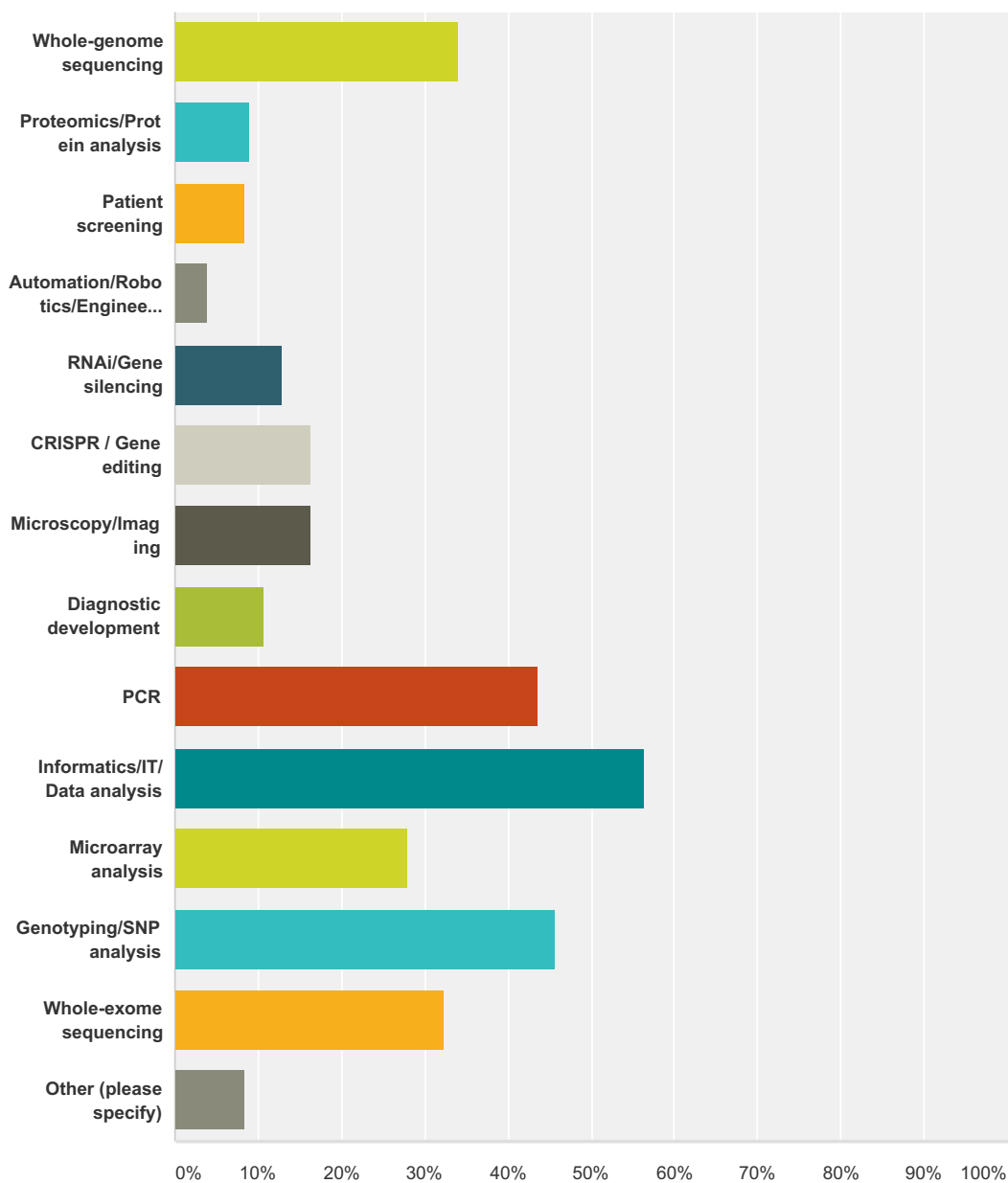
Answer Choices	Responses	
Whole-genome sequencing	**34.08%**	61
Proteomics/Protein analysis	**8.94%**	16
Patient screening	**8.38%**	15
Automation/Robotics/Engineering	**3.91%**	7
RNAi/Gene silencing	**12.85%**	23

CRISPR / Gene editing	**16.20%**	29
Microscopy/Imaging	**16.20%**	29
Diagnostic development	**10.61%**	19
PCR	**43.58%**	78
Informatics/IT/Data analysis	**56.42%**	101
Microarray analysis	**27.93%**	50
Genotyping/SNP analysis	**45.81%**	82
Whole-exome sequencing	**32.40%**	58
Other (please specify)	**8.38%**	15
Total Respondents: 179		

#	Other (please specify)	Date
1	RNASEQ, atacseq	8/2/2016 1:11 PM
2	Amplicon Sequencing	7/27/2016 5:55 AM
3	all RNA methods	7/26/2016 9:00 AM
4	RNAseq analysis	7/26/2016 4:17 AM
5	transfection	7/25/2016 9:53 PM
6	FISH	7/20/2016 9:38 PM
7	gene cloning	7/18/2016 11:55 AM
8	splicing modulation (exon skipping)	7/18/2016 8:36 AM
9	NGS analysis	7/18/2016 2:24 AM
10	karyotyping	7/17/2016 1:56 AM
11	RNASeq, ATACSeq	7/15/2016 8:40 AM
12	Chip-seq	7/14/2016 9:51 AM
13	transcriptomics	7/14/2016 9:25 AM
14	Software development, database design	7/14/2016 1:16 AM
15	RNAseq	7/13/2016 1:30 PM

Q6 What computer platform do you generally use? (Check all that apply)

Answered: 180   Skipped: 3
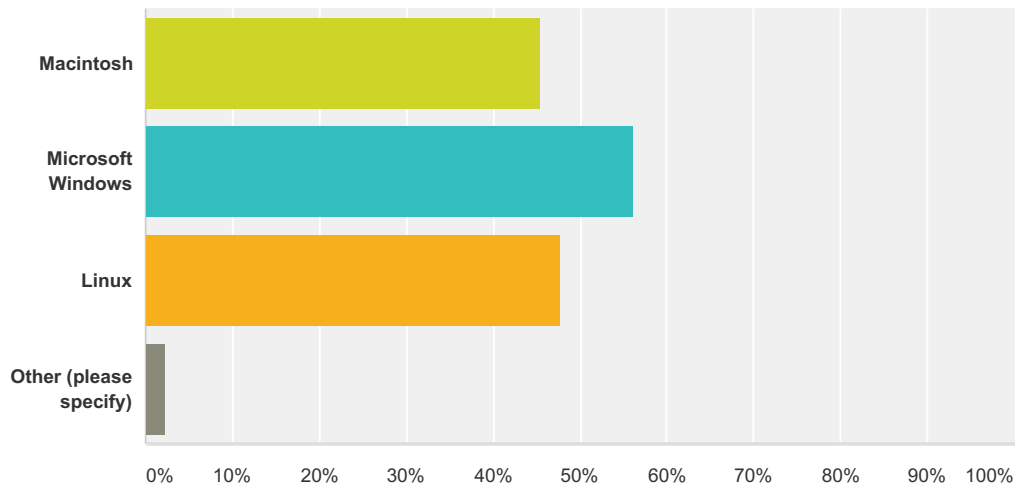
Answer Choices	Responses	
Macintosh	45.56%	82
Microsoft Windows	56.11%	101
Linux	47.78%	86
Other (please specify)	2.22%	4
Total Respondents: 180		

#	Other (please specify)	Date
1	SGE High Performance Cluster	7/15/2016 8:40 AM
2	Proprietary OS	7/14/2016 11:20 AM
3	Unix	7/14/2016 8:20 AM
4	ChromeOS	7/14/2016 1:49 AM

Q7 What internet browser/s do you regularly use?(Check all that apply)

Answered: 180   Skipped: 3
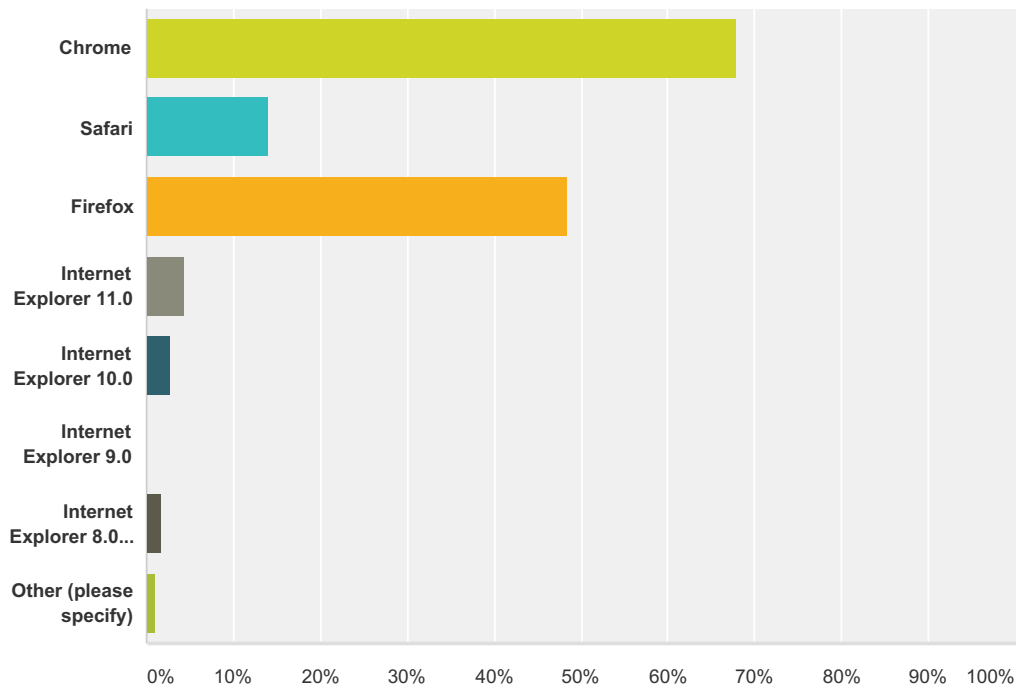
Answer Choices	Responses	
Chrome	**67.78%**	122
Safari	**13.89%**	25
Firefox	**48.33%**	87
Internet Explorer 11.0	**4.44%**	8
Internet Explorer 10.0	**2.78%**	5
Internet Explorer 9.0	**0.00%**	0
Internet Explorer 8.0 or older	**1.67%**	3
Other (please specify)	**1.11%**	2
Total Respondents: 180		

#	Other (please specify)	Date
1	chromiuim, opera	7/21/2016 10:19 AM
2	Microsoft Edge 25.10586.0.0	7/14/2016 10:08 AM

Q8 Which of these websites/tools do you use?

Answered: 161   Skipped: 22
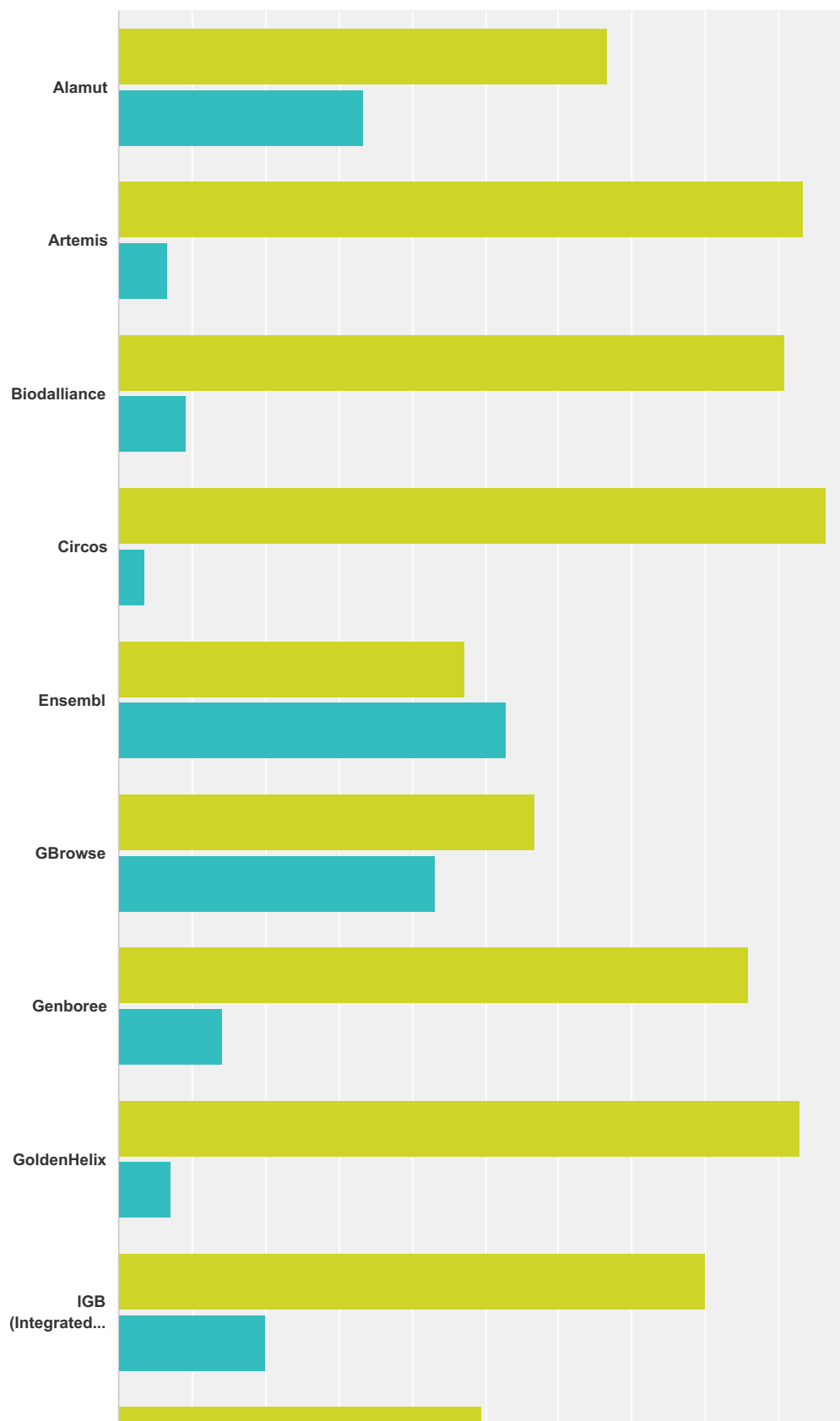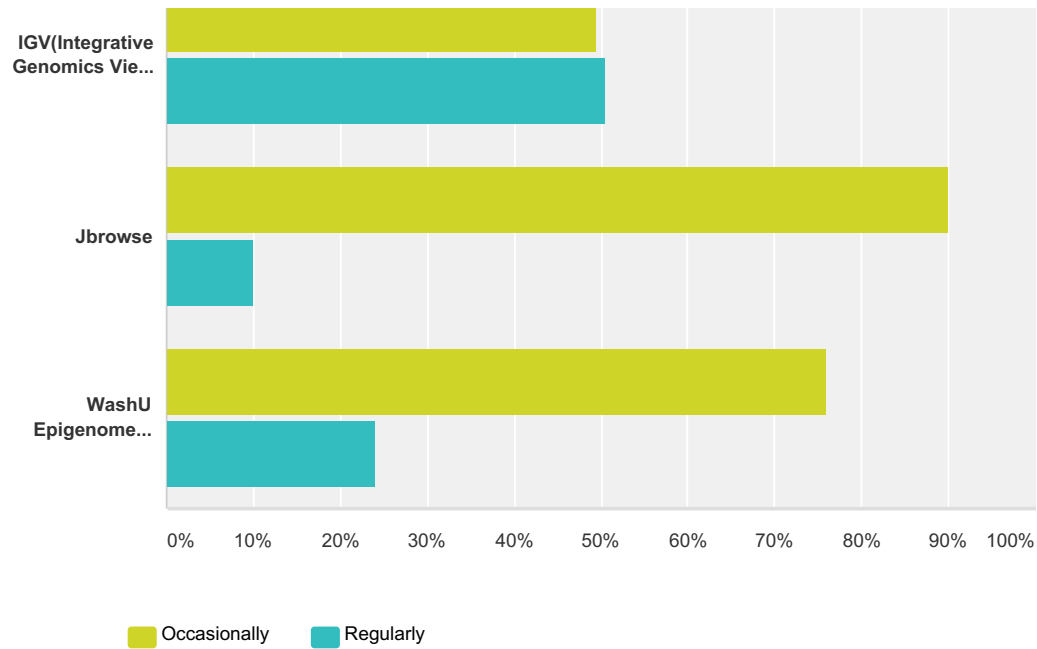
	Occasionally	Regularly	Total
Alamut	**66.67%** 12	**33.33%** 6	18
Artemis	**93.33%** 14	**6.67%** 1	15
Biodalliance	**90.91%** 10	**9.09%** 1	11
Circos	**96.55%** 28	**3.45%** 1	29
Ensembl	**47.18%** 67	**52.82%** 75	142
GBrowse	**56.76%** 21	**43.24%** 16	37
Genboree	**85.71%** 12	**14.29%** 2	14
GoldenHelix	**92.86%** 13	**7.14%** 1	14
IGB (Integrated Genome Browser)	**80.00%** 28	**20.00%** 7	35
IGV(Integrative Genomics Viewer - Broad Institute)	**49.46%** 46	**50.54%** 47	93
Jbrowse	**90.00%** 18	**10.00%** 2	20
WashU Epigenome Browser	**76.00%** 19	**24.00%** 6	25

#	Other (please describe)	Date
1	R, Python, NCBI, Tablet	7/27/2016 7:41 AM
2	NCBI / UCSC	7/26/2016 9:00 AM

3	http://dgv.tcag.ca/gb2/gbrowse	7/26/2016 12:08 AM
4	Galaxy suite	7/18/2016 11:55 AM
5	usegalaxy.org	7/18/2016 2:24 AM
6	ncbi, ucsc	7/15/2016 4:42 PM
7	GEO	7/15/2016 8:40 AM
8	MMDBJ	7/15/2016 1:08 AM
9	Kegg and TogoWS	7/14/2016 11:20 AM
10	genecards	7/14/2016 10:08 AM
11	NCBI	7/14/2016 4:32 AM
12	BRAINEAC	7/14/2016 2:20 AM
13	NCBI PubMed and associated databases (e.g. "Gene")	7/13/2016 3:58 PM
14	Galaxy, BioMart	7/13/2016 3:33 PM

Q9 For the tools listed above, whichfeatures from these would you like to see incorporated into the UCSC Browser?

Answered: 57   Skipped: 126

#	Responses	Date
1	ensembl is much easier to look at a particular trancript and it's related information. So, looking at something you know you want to look at. UCSC is better for looking at a region where you don't know what you're looking for.	8/5/2016 11:38 AM
2	Splice site strength predictions	7/28/2016 4:48 AM
3	WashU Epigenome Browser: Visualization of Hi-C and 4C-seq	7/27/2016 7:28 AM
4	equal	7/27/2016 5:55 AM
5	WashUEpigenome Browser	7/26/2016 3:01 PM
6	--more datasets as in the washU epigenome browser --ease of extracting subsets of datasets in relation to a custom dataset	7/26/2016 8:33 AM
7	Make an easier interface of Epigenome Browser tracks with ENCODE tracks	7/25/2016 9:53 PM
8	GWAS SNP	7/24/2016 6:53 PM
9	NA	7/24/2016 5:07 AM
10	Epigenome browser	7/23/2016 4:11 AM
11	a easy way to export SNPs	7/22/2016 3:30 PM
12	ARABIDOPSIS GENOME	7/21/2016 10:19 AM
13	Ensembl BioMart like data selection and download	7/21/2016 8:19 AM
14	Variant annotation. Would be nice if selecting region on chromosome within a gene there would be opportunity to see what cDNA, protein positions are intersected if any	7/21/2016 6:35 AM
15	well, none. I use IGV mainly to load BAM, which can only be done locally, so unless you provide a local version of your browser... and biodalliance as it can be easily implemented in in-house apps.	7/21/2016 12:53 AM
16	To download sequences	7/19/2016 6:09 PM
17	better exporting of ensemble homology data (eg. ORCA tracks)	7/18/2016 11:55 AM
18	ease of use...	7/18/2016 10:01 AM
19	splicing site prediction. Reference gene search (based on public data)	7/18/2016 8:36 AM
20	Align other species to Human reference	7/17/2016 2:30 AM
21	NA	7/16/2016 7:36 PM
22	bamfile coverage, ability to load genomes	7/15/2016 10:34 AM
23	-nucleotide positions on transcript, to be able to give a c. position to a SNV for example -colored ATGC letters in the first track, to be able to recognise a nucleotide pattern easier	7/15/2016 9:24 AM
24	Alamut,Ensembl	7/15/2016 6:57 AM
25	No idea, have no found any browser/webtool except UCSCgb worth the time to explore..	7/15/2016 2:12 AM
26	Microsatellite information	7/15/2016 1:08 AM
27	Sashimi plot	7/14/2016 9:00 PM
28	Getting cDNA and UTR sequences for gene's is much easier in ensembl	7/14/2016 11:48 AM
29	Mostly I'm fine with the UCSC Browser amount of information, but I would like the "in silico PCR" tool to be able to examine mRNA sequences, which essentially means exon/exon junctions, rather than genomic DNA only.	7/14/2016 10:51 AM
30	Easier to load(host) custom datasets	7/14/2016 9:51 AM

31	-	7/14/2016 7:24 AM
32	quickly connected gene information with the ncbi protein/gene/mRNA databases	7/14/2016 6:32 AM
33	Great (http://bejerano.stanford.edu/great/public/html/) NIH David (https://david-d.ncifcrf.gov/)	7/14/2016 6:25 AM
34	Yes	7/14/2016 4:23 AM
35	Alamut	7/14/2016 2:32 AM
36	IGV, Circos	7/14/2016 1:56 AM
37	REST API	7/14/2016 1:54 AM
38	Although the number of genomes and accompanying information in the UCSC Browser is already very comprehensive, it would be great if even more genomes could be added such as protozoa, plants and microbial (although I'm aware of http://microbes.ucsc.edu/), etc so that the UCSC Browser becomes the first port of call.	7/14/2016 1:27 AM
39	Circular-genome view of Circos	7/13/2016 9:47 PM
40	grns	7/13/2016 9:38 PM
41	UCSC browser is too old-school (using technology of 2000s, and we have stopped using it).	7/13/2016 9:15 PM
42	fast visualization of annotation track	7/13/2016 6:18 PM
43	Washu Epigenome Browser	7/13/2016 3:39 PM
44	IGV	7/13/2016 3:37 PM
45	Ensembl 1000Genome haplotypes	7/13/2016 3:33 PM
46	Highlight multiple coordiantes	7/13/2016 3:18 PM
47	A way to use personal BigWig files from behind a firewall.	7/13/2016 2:43 PM
48	ability to view bam pileups, VCF files in conjunction with gene structure	7/13/2016 2:40 PM
49	fast browsing (e.g. WashU Epigenomics Browser); sashimi plot to visualize the splicing junctions (in IGV)	7/13/2016 1:30 PM
50	Hi-C viewer (as a heatmap). I'd like to be able to upload my own interaction matrix and visualize it in a heatmap form using the genome browser. There are other tools which can do this, but having it integrated in the browser would be a big plus in the light of the advances in 3D genome biology.	7/13/2016 1:21 PM
51	Direct FASTA upload	7/13/2016 1:01 PM
52	the ability to load GWAS results into the genome browser and see them against the genome as (like a manhattan plot above, and gene locations below and matched to the manhattan plot). It would also be nice to export such an image	7/13/2016 12:53 PM
53	None -- they stink, UCSC is way better and more flexible	7/13/2016 12:52 PM
54	ENSEMBL: has a nice REST API, with VEP IGV: java webstart allowing to use local files.	7/13/2016 12:49 PM
55	Hide introns for transcripts	7/13/2016 12:27 PM
56	I only use UCSC Regularly	7/13/2016 12:13 PM
57	from IGV, you can copy and paste in tab delimited coordinates and they will be auto corrected to coordinates, e.g. these all work: For the UCSC human genome browser: 11[tab]46878268[tab]46940173 chr11[tab]46878268[tab]46940173 11:46878268-46940173 should all autocorrect/resolve to chr11:46878268-46940173	7/13/2016 11:56 AM

Q10 How interested would you be in a mobile version of the UCSC Genome Browser?

Answered: 174   Skipped: 9
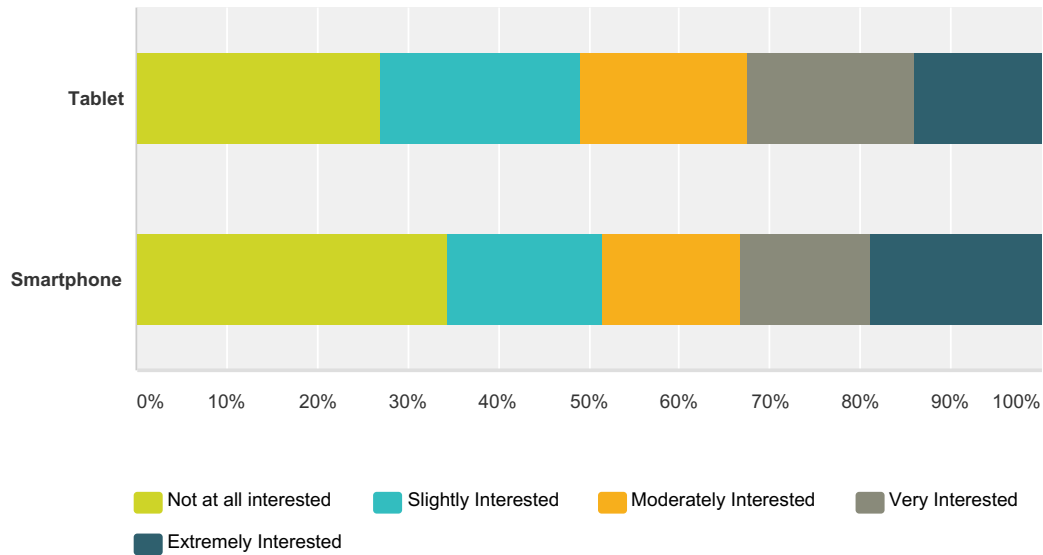
	Not at all interested	Slightly Interested	Moderately Interested	Very Interested	Extremely Interested	Total
Tablet	**26.99%** 44	**22.09%** 36	**18.40%** 30	**18.40%** 30	**14.11%** 23	163
Smartphone	**34.55%** 57	**16.97%** 28	**15.15%** 25	**14.55%** 24	**18.79%** 31	165

#	Comments	Date
1	I don't typically do real work on my mobil device	7/27/2016 7:41 AM
2	Smartphones are just too small to visualize that amount of data in my opinon	7/27/2016 7:28 AM
3	I would prefer you to make it easier to setup on local	7/26/2016 9:00 AM
4	my phone will not support. its a blackberry.	7/25/2016 6:01 AM
5	A tablet version might be interestng but I don't have any (and no plans to get one). Smartphone no.	7/21/2016 12:53 AM
6	i think it no more useful in mobile version	7/20/2016 9:38 PM
7	I am working with large datasets. Not recommanded to tablet and smartphone.	7/20/2016 2:53 AM
8	It's difficult to analyze data with mobile device like smartphone.	7/18/2016 3:14 PM
9	YES PLEASE	7/18/2016 11:55 AM
10	I can get ucsc browser on my i pad and cell	7/15/2016 4:42 PM
11	Yes please ! Androïd first !	7/15/2016 9:24 AM
12	Don't do it! Nobody who takes their genomics seriously will be browsing the genome on a f-ing tablet.	7/15/2016 2:12 AM
13	I would be very excited about a UCSC Genome Browser mobile version, because I check the website very often, and sometimes I don't have a handy laptop!	7/14/2016 10:51 AM
14	UCSC will be bit heavy for mobiles	7/14/2016 1:56 AM
15	YES PLEASE	7/13/2016 10:02 PM

| 16 | i do all my browser work on my desktop PC - can't imagine having a browser emergency need on the road | 7/13/2016 1:14 PM |
| 17 | Generally I think more efforts should be put to improve the browser on computer but not mobile devices | 7/13/2016 12:27 PM |

Q11 If we were to implement an API for the
UCSC Genome Browser, what would be
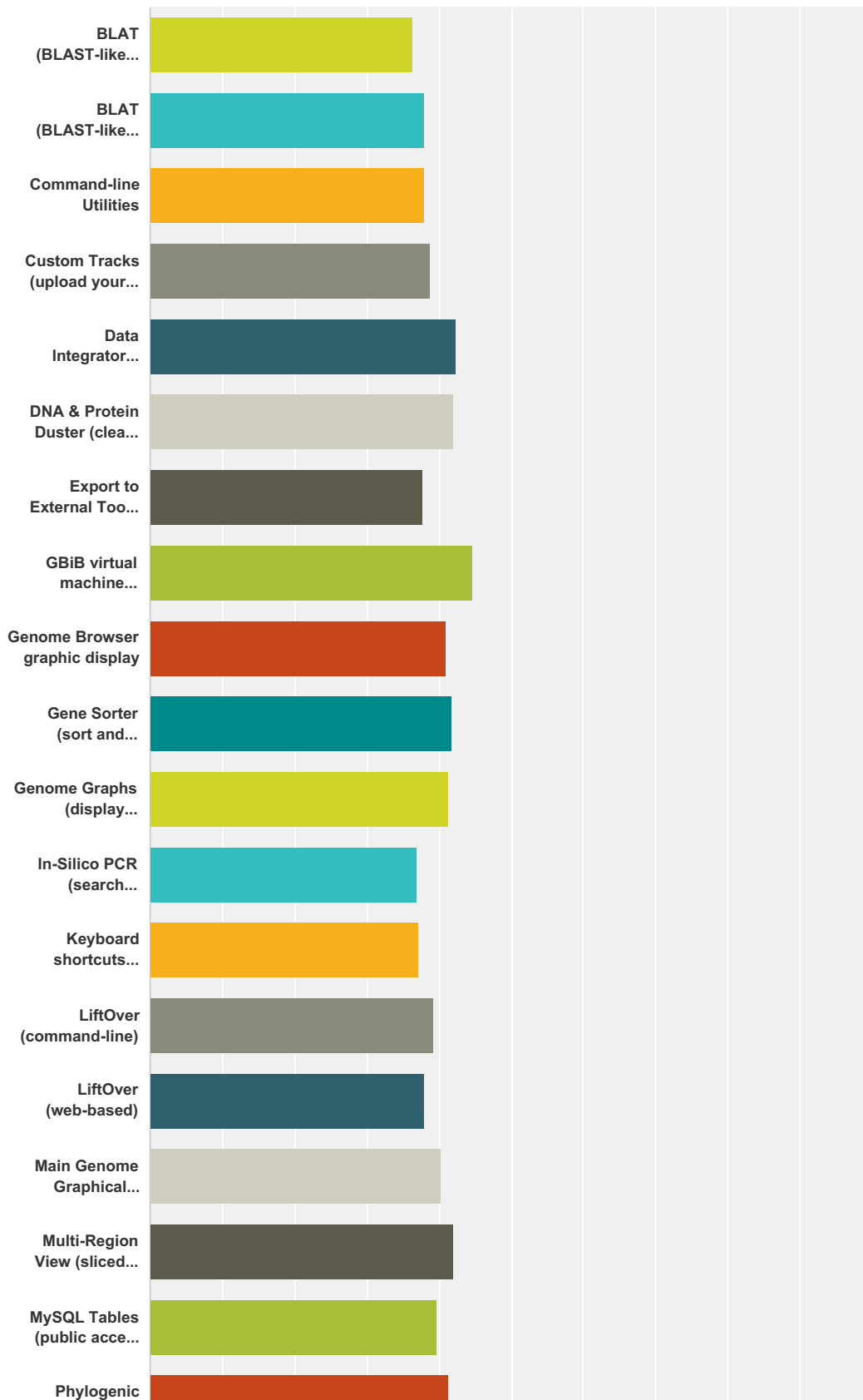most useful to you, and how would you use
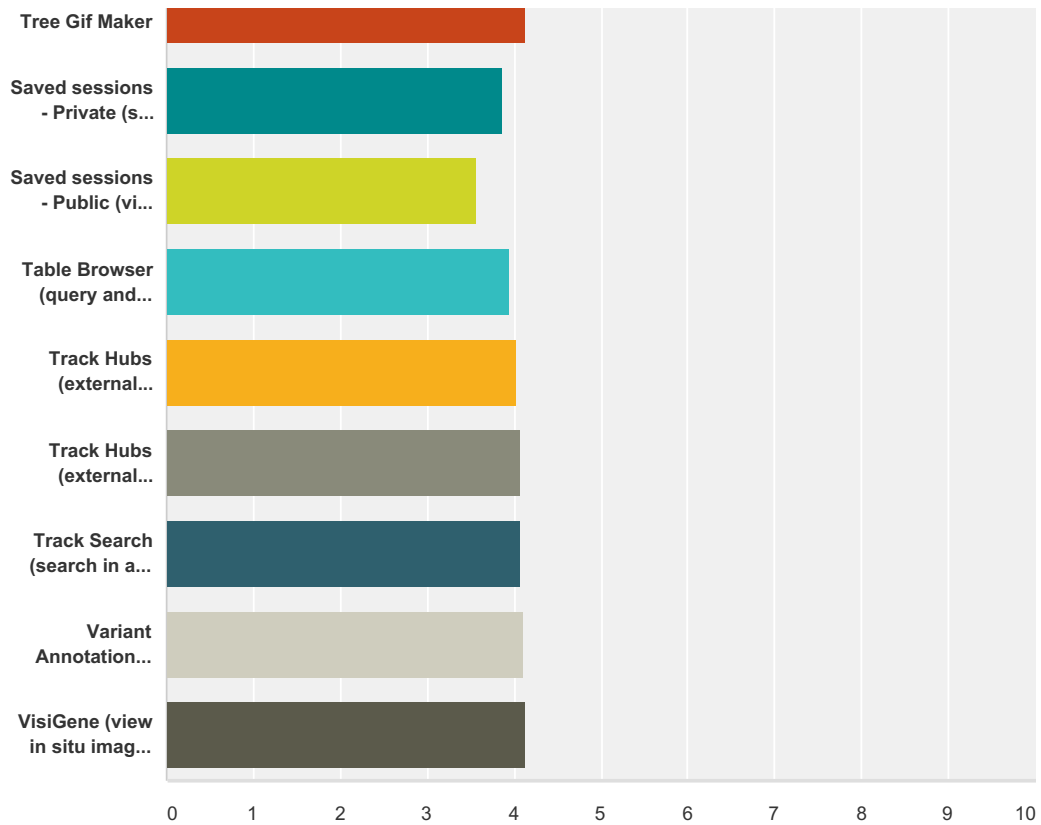it?

Answered: 49   Skipped: 134

#	Responses	Date
1	I wouldn't, I'm not that skilled.	8/5/2016 11:38 AM
2	Representing genomewide haplotypes/diplotypes for thousands of individuals. Especially for non models via track hubs.	8/2/2016 1:11 PM
3	During casual conversation about genetics.	7/27/2016 2:43 PM
4	It would certainly be useful. I would love to be able to integrate the downloading of specific regions into my command-line pipelines so that it isn't a manual step.	7/27/2016 7:41 AM
5	no comment	7/27/2016 5:55 AM
6	A way to query and pull down RefSeq gene promoter regions and other genome sequences. Being able to provide a publically accessible, programmatic, and standardized way to obtain sequences used in analyses would help in data reproducibility. Having to resort to flat files when different genome browsers produce different formats (index-0 vs index-1, etc) is annoying.	7/26/2016 10:00 AM
7	Facility to serve BigWig RNAseq data on own genome maps	7/26/2016 4:17 AM
8	pass	7/25/2016 6:01 AM
9	I DON'T kNOW	7/24/2016 6:53 PM
10	Examination of data during meetings	7/24/2016 5:07 AM
11	Primer design tool, unique FISH probe designer where you choose probe length, and the software gives you unique sequences in the genome.	7/23/2016 4:11 AM
12	- most useful type of API: REST - most useful operations: download of datasets based on metadata, download of annotation tracks; operations that allow to retrieve coherent datasets (e.g., given a list of gene/transcript identifiers, retrieve all coordinates for assembly version X and corresponding sequence data); operations that allow to map identifiers to their most recent version	7/21/2016 8:19 AM
13	Variant annotation	7/21/2016 6:35 AM
14	I regularly use perl script to connect to the mysql public database which is quite well described. Something really useful would be a module that could compute conservation at amino-acid level using MultiZ alignment for particular positions, e.g. I have a missense and my app would like to know how the concerned aa is conserved across species (without using a predictor).	7/21/2016 12:53 AM
15	I would like to enter a specific gene and open it directly in the Genome Browser	7/19/2016 6:09 PM
16	I seldom use API.	7/18/2016 3:14 PM
17	viewing data from galaxy histories, eg. Chip-seq wiggle tracks and other deep sequencing. GEO dataset integration?	7/18/2016 11:55 AM
18	browser check variant in meeting	7/18/2016 4:34 AM
19	uploading local data	7/18/2016 2:24 AM
20	Access to information of a given gene, transcript or protein from any track available (for instance, conservation scores, common SNPs, related publication articles, etc.)	7/17/2016 7:35 PM
21	Most useful if available in R, where I would use it to explore public datasets in relation to our own.	7/17/2016 4:54 PM
22	I would not be using an APU	7/17/2016 2:30 AM
23	NA	7/16/2016 7:36 PM
24	maybe, not sure how I would use it yet	7/15/2016 4:42 PM

25	Don't know if I need things to be all that different from how they are now. Maybe make it easier to find full tracks in your ftp-jungle.. But it's not that bad once you've done it a few times.	7/15/2016 2:12 AM
26	I want to incorporate the UCSC Genome Browser in my cloud platform specific on one aspect of bio-info-analysis via the API. GIVE MOST CONVENIENCE TO USERS.	7/15/2016 12:32 AM
27	See third party REST API at http://togows.org/help/ (external API section).	7/15/2016 12:15 AM
28	Directly import data into R for further analysis	7/14/2016 9:00 PM
29	I cannot choose about the contents, but I think a way to meke it lighter and quicker would be to allow the visitors to select in advance (prior to the search) the argument-tiles.	7/14/2016 10:51 AM
30	It would be very helpful. Because in that case, we can work in offline also.	7/14/2016 10:08 AM
31	Not sure. Nothing urgently missing from UCSC GB services. Maybe return pictures of a region given assembly, tracks of interest, etc. Maybe our customers would use this to help orient themselves to the genome while browsing their variants in our software	7/14/2016 9:02 AM
32	-	7/14/2016 7:24 AM
33	Don't know yet	7/14/2016 6:32 AM
34	Genomic feature API that is compatible with the Ensembl offerings and GA4GH	7/14/2016 1:54 AM
35	accessing track functionality, like extracting translations from bigGenePred+fasta, slicing of data	7/14/2016 1:49 AM
36	Map Bed regions to features on the genome	7/14/2016 12:06 AM
37	For plotting and I would use it all the time. Python please!	7/13/2016 10:02 PM
38	python API for downloading annotation data in a given genomic region	7/13/2016 6:18 PM
39	create sessions with custom data	7/13/2016 3:37 PM
40	Import SRA (GEO) experiments from public repositories to analyze allele specific expression, allele specific methylation	7/13/2016 3:33 PM
41	SNP Annotation	7/13/2016 3:13 PM
42	A way to combine local data and UCSC tracks in graphics and tables from within R.	7/13/2016 2:43 PM
43	an R package for UCSC Genome Browser data access; API for capturing UCSC screen shot.	7/13/2016 1:30 PM
44	Extraction of portions of a table or genome, rather than using the full file available via goldenPath and gbdb.	7/13/2016 12:52 PM
45	A Web API ? something like NCBI eutils where each mysql database would be available. Ah, and allowing CORS request.	7/13/2016 12:49 PM
46	python;R; for implemention. I would use it to retrieve data (for instance gene coordinates and tracks) needed during for my scritpts.	7/13/2016 12:48 PM
47	We have developed the Exomiser (http://www.sanger.ac.uk/science/tools/exomiser) and the Human Phenotype Ontology and it would be great to be able to fetch a view of genomic context via API that would look something like the main Genome Browser and to display it on tools like Exomiser.	7/13/2016 12:32 PM
48	Gene Ontology	7/13/2016 12:27 PM
49	I will	7/13/2016 12:13 PM

Q12 How useful are the following tools/features to you?

Answered: 172   Skipped: 11

- BLAT (BLAST-like...
- BLAT (BLAST-like...
- Command-line Utilities
- Custom Tracks (upload your...
- Data Integrator...
- DNA & Protein Duster (clea...
- Export to External Too...
- GBiB virtual machine...
- Genome Browser graphic display
- Gene Sorter (sort and...
- Genome Graphs (display...
- In-Silico PCR (search...
- Keyboard shortcuts...
- LiftOver (command-line)
- LiftOver (web-based)
- Main Genome Graphical...
- Multi-Region View (sliced...
- MySQL Tables (public acce...
- Phylogenic

Bar chart (vertical axis labels, left to right value ~4):
- Tree Gif Maker
- Saved sessions - Private (s...
- Saved sessions - Public (vi...
- Table Browser (query and...
- Track Hubs (external...
- Track Hubs (external...
- Track Search (search in a...
- Variant Annotation...
- VisiGene (view in situ imag...

Horizontal axis: 0 1 2 3 4 5 6 7 8 9 10

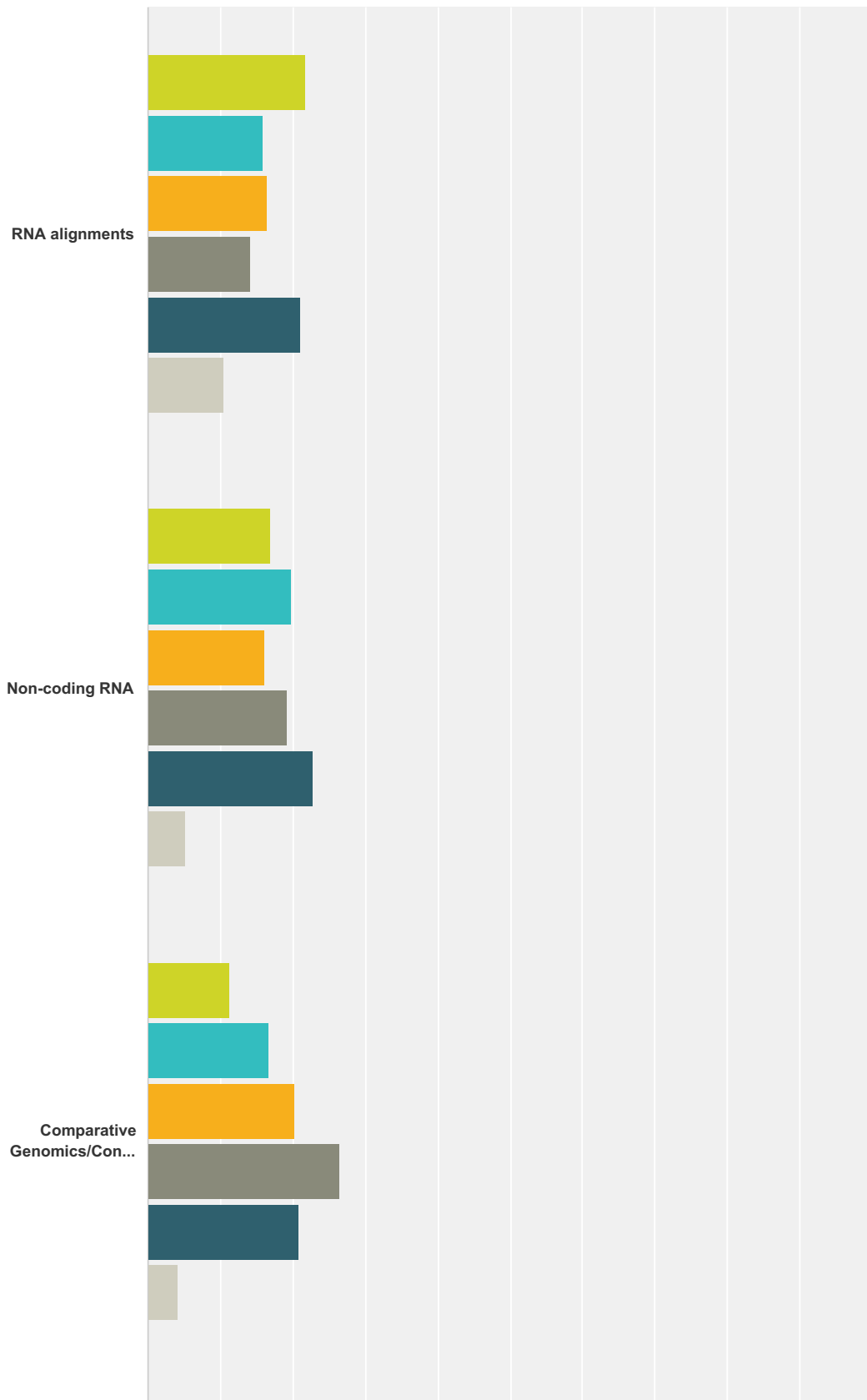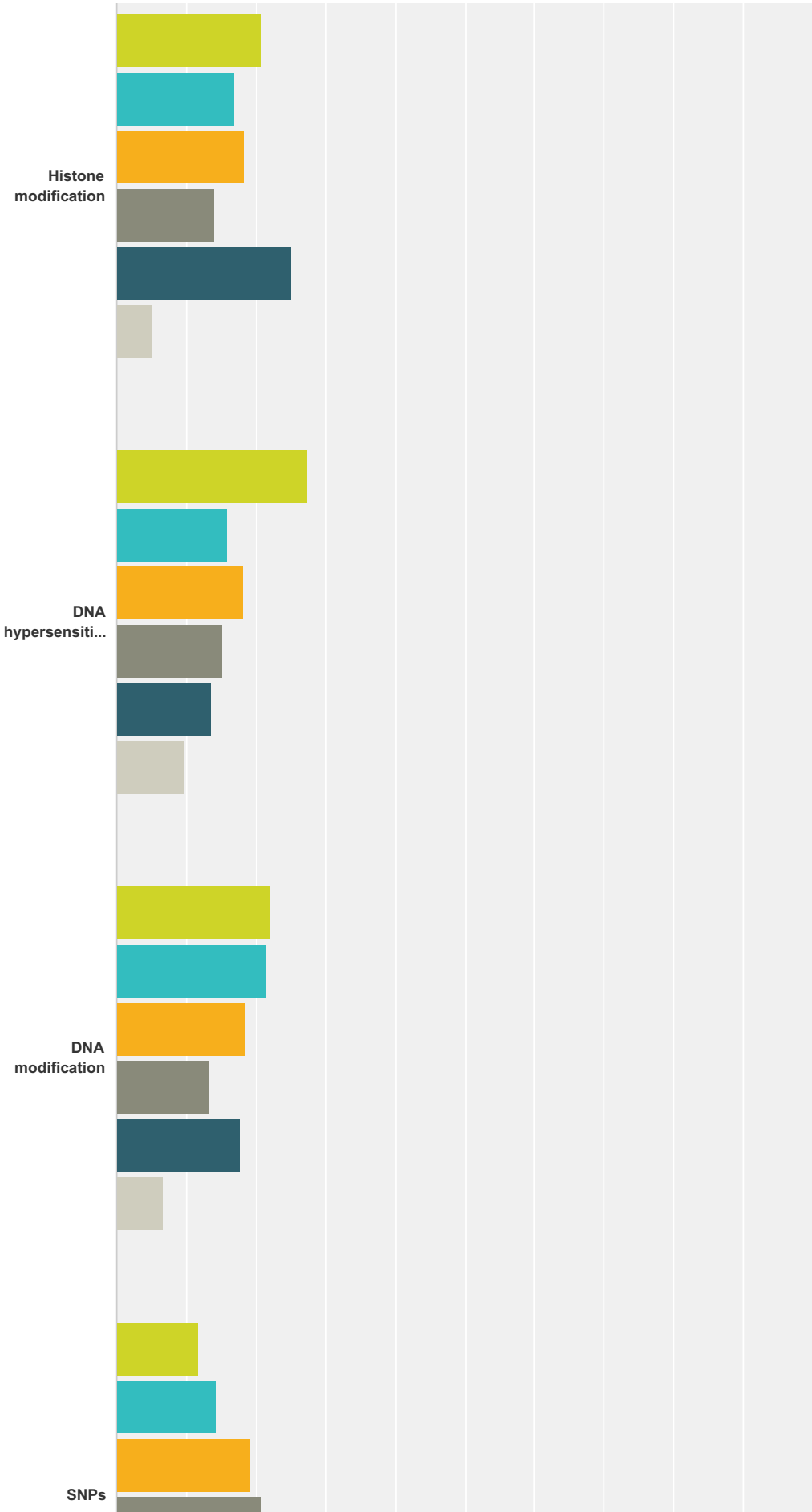|	Not at all useful	Slightly useful	Very useful	Unsure/unfamiliar with tool	Total	Weighted Average
BLAT (BLAST-like alignment tool) -Command-line utility	12.00% 18	21.33% 32	45.33% 68	21.33% 32	150	3.64
BLAT (BLAST-like alignment tool) - Web-based	4.35% 7	8.70% 14	81.37% 131	5.59% 9	161	3.81
Command-line Utilities	11.19% 16	15.38% 22	51.05% 73	22.38% 32	143	3.80
Custom Tracks (upload your data to view in browser)	3.23% 5	9.03% 14	79.35% 123	8.39% 13	155	3.89
Data Integrator (combine and export data from multiple tracks)	5.59% 8	10.49% 15	53.15% 76	30.77% 44	143	4.24
DNA & Protein Duster (cleans sequence output)	15.44% 21	18.38% 25	14.71% 20	51.47% 70	136	4.20
Export to External Tools (e.g. view browser region at NCBI, Ensembl)	6.52% 9	25.36% 35	44.20% 61	23.91% 33	138	3.78
GBiB virtual machine (virtual machineof the UCSC Genome Browser)	13.64% 18	14.39% 19	13.64% 18	58.33% 77	132	4.47
Genome Browser graphic display	2.07% 3	6.21% 9	77.93% 113	13.79% 20	145	4.09
Gene Sorter (sort and filter genes by similarity)	12.12% 16	17.42% 23	26.52% 35	43.94% 58	132	4.17
Genome Graphs (display genome-wide data sets)	6.52% 9	12.32% 17	52.17% 72	28.99% 40	138	4.14

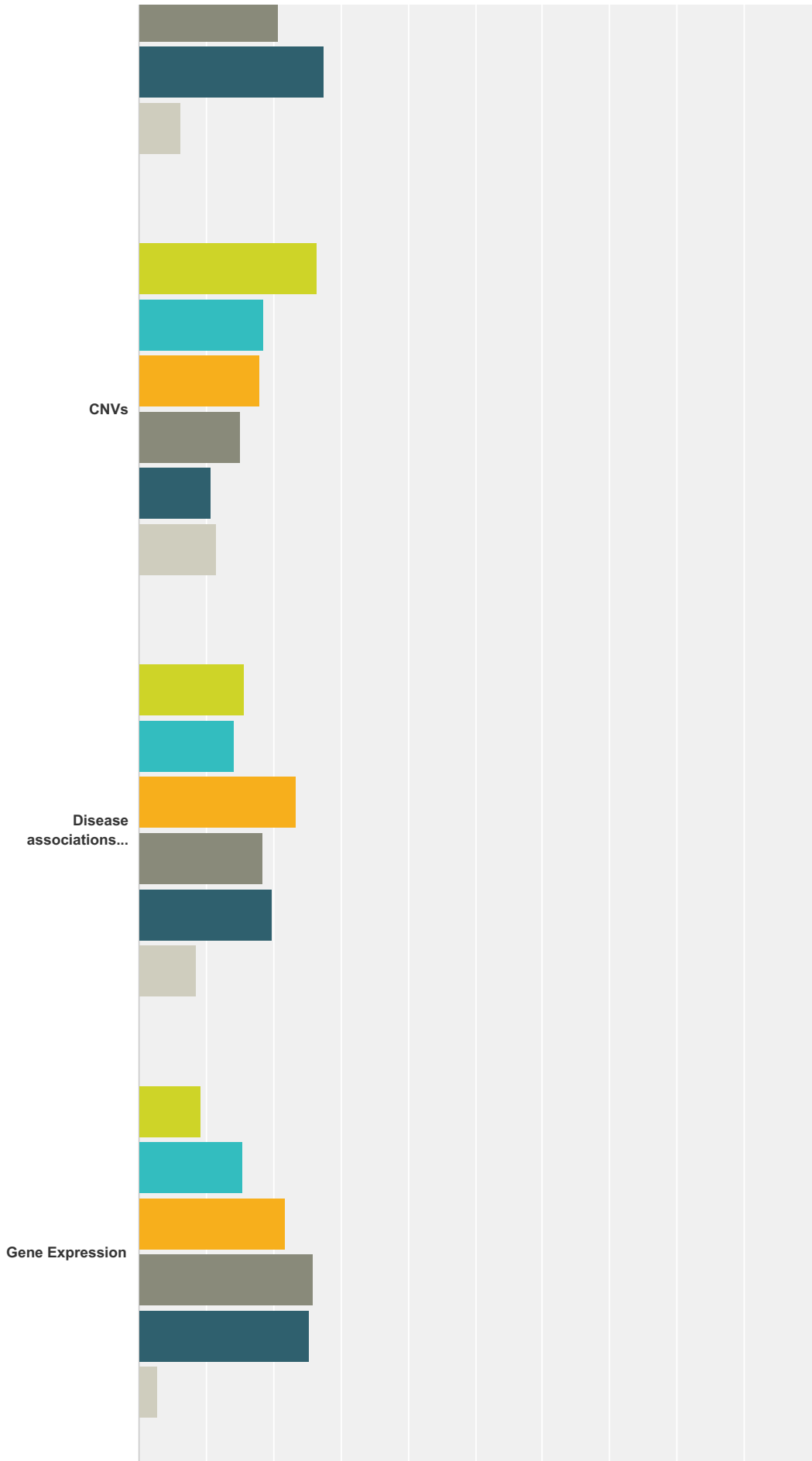| Feature						
In-Silico PCR (search sequence with primer pairs)	**12.41%** 17	**19.71%** 27	**44.53%** 61	**23.36%** 32	137	3.70
Keyboard shortcuts (keyboard shortcuts to popular navigation)	**13.43%** 18	**26.12%** 35	**28.36%** 38	**32.09%** 43	134	3.72
LiftOver (command-line)	**13.48%** 19	**15.60%** 22	**39.01%** 55	**31.91%** 45	141	3.92
LiftOver (web-based)	**11.27%** 16	**16.20%** 23	**49.30%** 70	**23.24%** 33	142	3.80
Main Genome Graphical Viewer (view assembly tracks, etc.)	**2.94%** 4	**9.56%** 13	**72.06%** 98	**15.44%** 21	136	4.03
Multi-Region View (sliced view to see exon only, gene only, etc.)	**5.26%** 7	**14.29%** 19	**48.87%** 65	**31.58%** 42	133	4.19
MySQL Tables (public access to tables via MySQL)	**12.77%** 18	**18.44%** 26	**33.33%** 47	**35.46%** 50	141	3.96
Phylogenic Tree Gif Maker	**13.18%** 17	**24.03%** 31	**12.40%** 16	**50.39%** 65	129	4.13
Saved sessions - Private (save your browser configuration)	**5.07%** 7	**17.39%** 24	**59.42%** 82	**18.12%** 25	138	3.86
Saved sessions - Public (view public sessions and make yours public)	**12.31%** 16	**23.85%** 31	**43.08%** 56	**20.77%** 27	130	3.57
Table Browser (query and download track tables)	**3.47%** 5	**13.89%** 20	**65.97%** 95	**16.67%** 24	144	3.95
Track Hubs (external tracks and assemblies) - Public	**8.82%** 12	**13.97%** 19	**48.53%** 66	**28.68%** 39	136	4.03
Track Hubs (external tracks and assemblies) - Private	**8.70%** 12	**13.04%** 18	**48.55%** 67	**29.71%** 41	138	4.07
Track Search (search in all tracks)	**5.26%** 7	**13.53%** 18	**55.64%** 74	**25.56%** 34	133	4.08
Variant Annotation Integrator (variant cell integration and predictions)	**9.42%** 13	**14.49%** 20	**41.30%** 57	**34.78%** 48	138	4.12
VisiGene (view in situ images, cellular images, etc.)	**15.79%** 21	**15.79%** 21	**22.56%** 30	**45.86%** 61	133	4.13

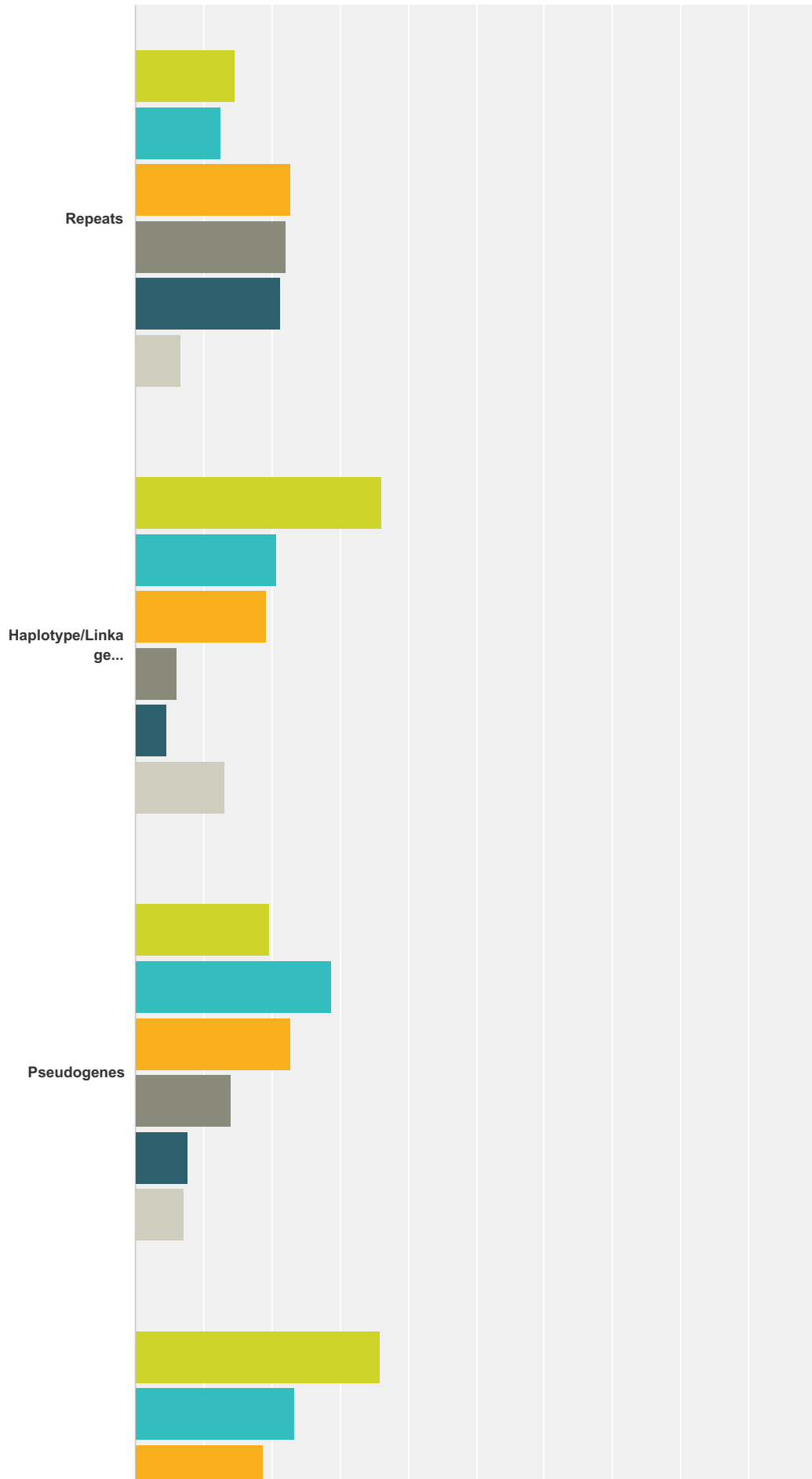| #	Comments	Date
1	its taking to portuguese family, kurdish patients	7/25/2016 6:01 AM
2	Massively improved documentation?	7/15/2016 5:00 PM
3	I love the UCSC Genome Browser, please do not remove any features!	7/14/2016 10:51 AM
4	unclear difference between 'Genome Browser graphic display' and 'Main Genome Graphical Viewer'	7/14/2016 9:02 AM
5	Table Browser is a must!	7/13/2016 3:33 PM
6	Liftover is hard to use without a tutorial.	7/13/2016 3:18 PM
7	I <3 the public mysql server	7/13/2016 12:49 PM

Q13 How often do you use the following UCSC Genome Browser data sets?

Answered: 163   Skipped: 20

RNA alignments

Non-coding RNA

Comparative Genomics/Con...

Histone modification

DNA hypersensiti...

DNA modification

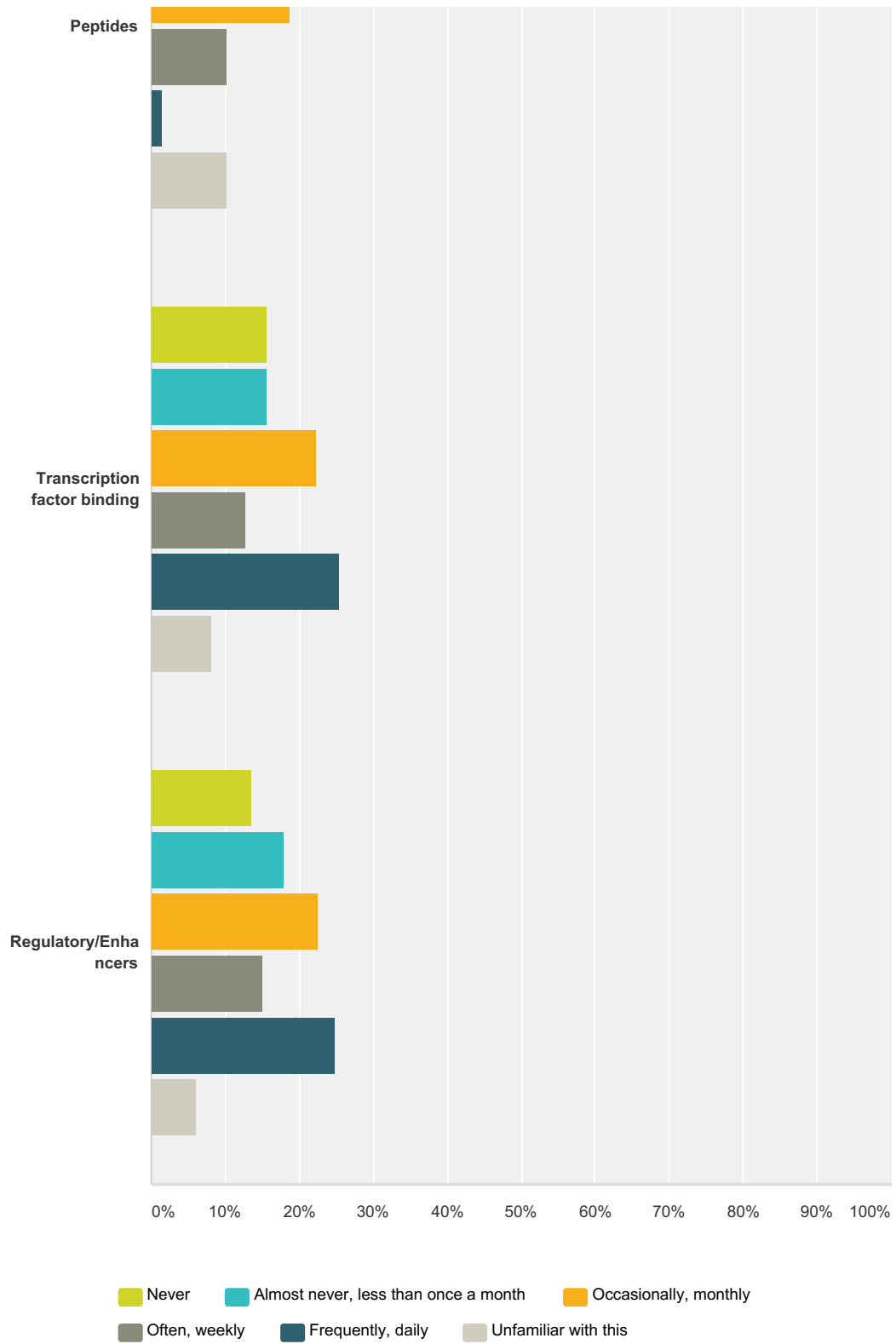**SNPs**

CNVs

Disease associations...

Gene Expression

	Never	Almost never, less than once a month	Occasionally, monthly	Often, weekly	Frequently, daily	Unfamiliar with this	Total
RNA alignments	**21.80%** 29	**15.79%** 21	**16.54%** 22	**14.29%** 19	**21.05%** 28	**10.53%** 14	133
Non-coding RNA	**16.91%** 23	**19.85%** 27	**16.18%** 22	**19.12%** 26	**22.79%** 31	**5.15%** 7	136

Comparative Genomics/Conservation	**11.19%** 16	**16.78%** 24	**20.28%** 29	**26.57%** 38	**20.98%** 30	**4.20%** 6	143
Histone modification	**20.59%** 28	**16.91%** 23	**18.38%** 25	**13.97%** 19	**25.00%** 34	**5.15%** 7	136
DNA hypersensitivity	**27.27%** 36	**15.91%** 21	**18.18%** 24	**15.15%** 20	**13.64%** 18	**9.85%** 13	132
DNA modification	**22.22%** 30	**21.48%** 29	**18.52%** 25	**13.33%** 18	**17.78%** 24	**6.67%** 9	135
SNPs	**11.72%** 17	**14.48%** 21	**19.31%** 28	**20.69%** 30	**27.59%** 40	**6.21%** 9	145
CNVs	**26.43%** 37	**18.57%** 26	**17.86%** 25	**15.00%** 21	**10.71%** 15	**11.43%** 16	140
Disease associations/Variants	**15.60%** 22	**14.18%** 20	**23.40%** 33	**18.44%** 26	**19.86%** 28	**8.51%** 12	141
Gene Expression	**9.09%** 13	**15.38%** 22	**21.68%** 31	**25.87%** 37	**25.17%** 36	**2.80%** 4	143
Repeats	**14.71%** 20	**12.50%** 17	**22.79%** 31	**22.06%** 30	**21.32%** 29	**6.62%** 9	136
Haplotype/Linkage disequilibrium	**36.15%** 47	**20.77%** 27	**19.23%** 25	**6.15%** 8	**4.62%** 6	**13.08%** 17	130
Pseudogenes	**19.53%** 25	**28.91%** 37	**22.66%** 29	**14.06%** 18	**7.81%** 10	**7.03%** 9	128
Peptides	**35.94%** 46	**23.44%** 30	**18.75%** 24	**10.16%** 13	**1.56%** 2	**10.16%** 13	128
Transcription factor binding	**15.67%** 21	**15.67%** 21	**22.39%** 30	**12.69%** 17	**25.37%** 34	**8.21%** 11	134
Regulatory/Enhancers	**13.53%** 18	**18.05%** 24	**22.56%** 30	**15.04%** 20	**24.81%** 33	**6.02%** 8	133

#	Comments (other datasets you use)	Date
1	We want to easily have these tracks for other systems! It would be great if there were a book (like the O'Reilly series) on how to build your own	8/2/2016 1:11 PM
2	Drosophila stuff	7/27/2016 2:43 PM
3	ENCODE	7/27/2016 7:28 AM
4	Custom RNA-seq and ChIP-seq tracks/hubs	7/26/2016 2:46 AM
5	Hub Epigenome Tracks	7/25/2016 9:53 PM
6	I use the tracks of publication	7/20/2016 2:53 AM
7	Very helpful and useful!	7/15/2016 12:20 PM
8	DNA methylation	7/15/2016 2:12 AM
9	COSMIC, publications	7/14/2016 9:02 AM
10	mouse ref seq	7/14/2016 8:20 AM
11	CGI, segmental duplications: daily	7/13/2016 3:33 PM

Q14 Which genome assemblies do you use? (See our assembly gateway page for all assemblies)

Answered: 167   Skipped: 16
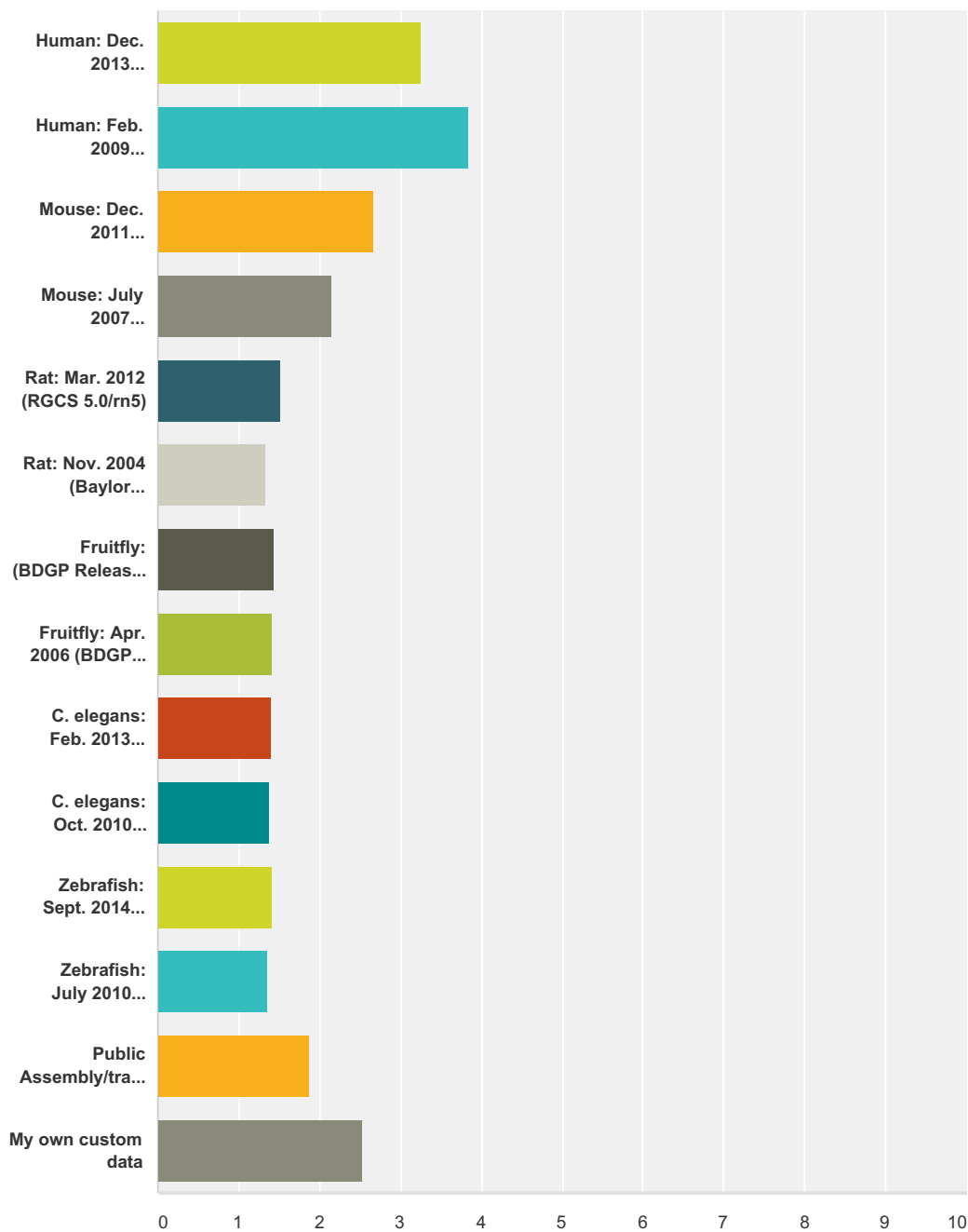
	Never	Almost never, less than once per month	Occasionally, monthly	Often, weekly	Frequently, daily	Total	Weighted Average
Human: Dec. 2013 (GRCh38/hg38)	**13.42%** 20	**17.45%** 26	**22.82%** 34	**22.15%** 33	**24.16%** 36	149	3.26
Human: Feb. 2009 (GRCh37/hg19)	**12.99%** 20	**3.90%** 6	**14.29%** 22	**23.38%** 36	**45.45%** 70	154	3.84

Mouse: Dec. 2011 (GRCm38/mm10)	**32.58%** 43	**19.70%** 26	**12.12%** 16	**19.70%** 26	**15.91%** 21	132	2.67
Mouse: July 2007 (NCBI37/mm9)	**49.59%** 61	**17.89%** 22	**11.38%** 14	**10.57%** 13	**10.57%** 13	123	2.15
Rat: Mar. 2012 (RGCS 5.0/rn5)	**65.55%** 78	**22.69%** 27	**6.72%** 8	**3.36%** 4	**1.68%** 2	119	1.53
Rat: Nov. 2004 (Baylor 3.4/rn4)	**74.36%** 87	**21.37%** 25	**2.56%** 3	**0.00%** 0	**1.71%** 2	117	1.33
Fruitfly: (BDGP Release 6 + 1SO1 Mr/dm6)	**73.11%** 87	**15.13%** 18	**6.72%** 8	**3.36%** 4	**1.68%** 2	119	1.45
Fruitfly: Apr. 2006 (BDGP R5/dm3)	**77.59%** 90	**12.93%** 15	**3.45%** 4	**3.45%** 4	**2.59%** 3	116	1.41
C. elegans: Feb. 2013 (WBcel235/ce11)	**75.86%** 88	**12.93%** 15	**8.62%** 10	**0.86%** 1	**1.72%** 2	116	1.40
C. elegans: Oct. 2010 (WS220/ce10)	**77.39%** 89	**13.91%** 16	**5.22%** 6	**1.74%** 2	**1.74%** 2	115	1.37
Zebrafish: Sept. 2014 (GRCz/danRer10)	**73.50%** 86	**16.24%** 19	**7.69%** 9	**0.85%** 1	**1.71%** 2	117	1.41
Zebrafish: July 2010 (Zv9/danRer7)	**77.59%** 90	**12.93%** 15	**6.03%** 7	**2.59%** 3	**0.86%** 1	116	1.36
Public Assembly/track hub	**56.14%** 64	**18.42%** 21	**13.16%** 15	**7.02%** 8	**5.26%** 6	114	1.87
My own custom data	**43.10%** 50	**12.07%** 14	**12.93%** 15	**12.07%** 14	**19.83%** 23	116	2.53

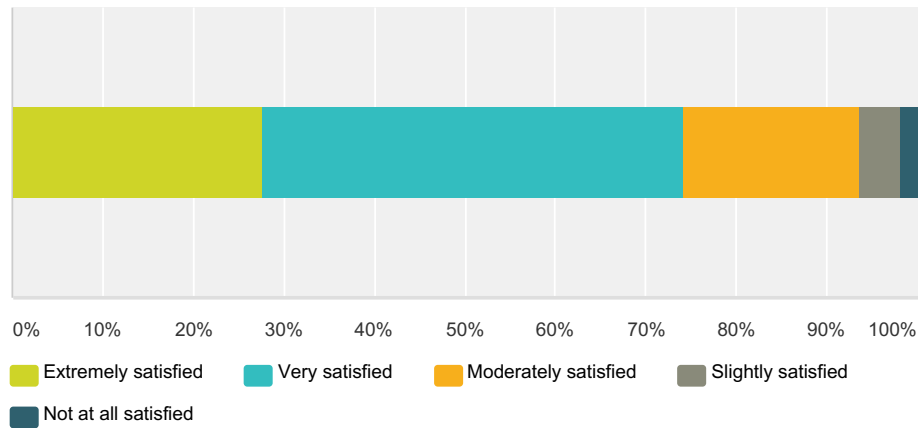| #	Please specify public track assembly/track hub, custom data, or other data:	Date
1	I put in patient microarray regions most frequently.	7/26/2016 11:44 AM
2	Roadmap Browser Chromatin state segmentation Bisulfite-seq	7/25/2016 9:53 PM
3	All primate genomes and the yeast genome (SacCer2).	7/18/2016 3:14 PM
4	Viewing data from my own Galaxy histories or GEO datasets	7/18/2016 11:55 AM
5	We maintain a partial UCSC GenBrowse mirror where we DB-load/track-ra configure tracks for our 1700+ NGS datasets.	7/17/2016 4:54 PM
6	Very important!	7/15/2016 12:20 PM
7	more gtf file support, gtf files for different species, also more clear annotation file information	7/15/2016 10:34 AM
8	Lizard (anoCar2), chicken (galGal4)	7/13/2016 4:54 PM
9	Custom tracks (not public): methylome, DMR, imprinted genes	7/13/2016 3:33 PM
10	I'm working only with plant genomes, so UCSC Genome Browser is not my main toolbox.	7/13/2016 1:39 PM
11	Dog Sep. 2011 (Broad CanFam3.1/canFam3) Assembly	7/13/2016 12:53 PM

Q15 Please list any data or assemblies you would like to see added to theBrowser.

Answered: 26   Skipped: 157

#	Responses	Date
1	Better viz of gene structure. Too much redundancy of isoforms. I think things everyday to be honest but have forgotten them now.	7/27/2016 2:43 PM
2	S. pombe	7/27/2016 3:29 AM
3	Tribolium	7/26/2016 4:17 AM
4	primer design	7/24/2016 6:53 PM
5	SECIS and Selenoproteins prediction	7/24/2016 5:07 AM
6	It's an impossible request... but I am going to write it down anyway: instead of more and more biol. data, I would like to see "confidence tracks" that allow me to get a rough idea how reliable/trustworthy certain measurements are. What is the noise and what is the true signal in the data?	7/21/2016 8:19 AM
7	None	7/20/2016 7:30 PM
8	I would like to see RNA based more data on your Browser.	7/20/2016 3:01 PM
9	Datasets for addgene > locating regions that have already been cloned into available vectors	7/18/2016 11:55 AM
10	TCGA	7/17/2016 11:20 PM
11	Camelus dromedarius	7/17/2016 2:30 AM
12	NA	7/16/2016 7:36 PM
13	To make copies as good quality photo for use in papers.	7/16/2016 3:27 PM
14	more plant species, more species from NCBI modified to fit UCSC genome (chromosome) naming.	7/15/2016 10:34 AM
15	mitochondrial DNA	7/14/2016 10:51 AM
16	Any reptile	7/14/2016 9:51 AM
17	nematostella vectensis	7/14/2016 8:25 AM
18	eQTLs	7/14/2016 7:24 AM
19	dbNSFP general score from all predictions	7/14/2016 4:32 AM
20	Protozoa, bacteria, plants.	7/14/2016 1:27 AM
21	more RefSeq (i.e., painted turtle, minke whale) or Ensembl (i.e. dolphin) gene prediction annotations for non-model organisms for which only Augustus and GenScan are currently available on the UCSC Table Browser	7/13/2016 4:54 PM
22	RNA-seq reads from GTEX SNPs from GTEX Methylome from human oocytes	7/13/2016 3:33 PM
23	Chicken galGal5 & Japanese quail (cotJap1)	7/13/2016 1:52 PM
24	Plants: Arabidopsis, Maize, Amborella...	7/13/2016 1:39 PM
25	Plasmodium falciparum and friends	7/13/2016 12:52 PM
26	Hi-C	7/13/2016 12:27 PM

Q16 How satisfied are you with the overall UCSC Genome Browser response time/speed?

Answered: 170   Skipped: 13

Legend: Extremely satisfied | Very satisfied | Moderately satisfied | Slightly satisfied | Not at all satisfied

Answer Choices	Responses	
Extremely satisfied	27.65%	47
Very satisfied	46.47%	79
Moderately satisfied	19.41%	33
Slightly satisfied	4.71%	8
Not at all satisfied	1.76%	3
Total		**170**

#	Comments	Date
1	The browser is fantastic and I know the team will come up with great new tools.	7/26/2016 11:44 AM
2	You do a great job! Thank you so much for letting me have 57 sessions that I can keep refering to and updating!	7/25/2016 9:53 PM
3	I come from China, and I think it is so slow.	7/24/2016 6:53 PM
4	the european mirror was a great improvment	7/21/2016 12:53 AM
5	no more change its face	7/20/2016 9:38 PM
6	It's generally good but can be slow at times	7/20/2016 10:25 AM
7	need to indicate color key to be more helpful	7/19/2016 12:27 PM
8	Unbelievable fast given the amount of data! No comparison with other tools.	7/17/2016 4:54 PM
9	awesome program	7/15/2016 4:42 PM
10	Thanks!	7/15/2016 12:20 PM
11	much slower than IGV	7/14/2016 9:25 AM
12	It's very very veeery slow.	7/14/2016 7:24 AM
13	Resource is awesome but it only lacks in run time	7/14/2016 1:56 AM
14	problems with the R functions in ENCODE explorer	7/13/2016 9:38 PM
15	It's extremely slow.	7/13/2016 9:31 PM

| 16 | I am extremelly happy to have free-acess to this incredibly user-friendly interface thta you folks have created! | 7/13/2016 3:33 PM |
| 17 | a bit slow in retrieving data for display | 7/13/2016 11:56 AM |

Q17 Please describe anything we can do to improve your experience (data desired, UI changes, navigation, documentation, training, etc).

Answered: 58 Skipped: 125

#	Responses	Date
1	they way you choose which tracks are displayed is kind of... rough. And a bit... ugly.	8/5/2016 11:38 AM
2	A book on how to host a genome for a no model via track hubs. Assuming one has a genome(s), RNASEQ, SNP genotyping, ATACseq, histone marks , etc.	8/2/2016 1:11 PM
3	Default window size and tracks displayed can be a bit naff. Annoying when useful tracks from old assembly aren't included in new one. Otherwise I have been in love with ucsc gb since I first found it. More ergonomic, aesthetic that the competitors, with interesting range of tracks.	7/27/2016 2:43 PM
4	Honestly, I don't use it much. I find the user interface really unintuitive and the documentation is not nearly as helpful as I would like and I think is sometimes out of date. But it is often the only tool where I can get the data I need, so sometimes there I am.	7/27/2016 7:41 AM
5	The link to ENCODE tracks disappeared with the site redesign. I cannot find it except through an obscure help files link.	7/27/2016 7:28 AM
6	Ability to change viewing ranges of all tracks in a single hub in one go (at the moment have to either alter the trackdb.txt for the hub, or go through one by one - very terious!).	7/27/2016 3:29 AM
7	Freshen and clean up the UI a bit. NCBI and Ensembl have done a good job of making the UI more straightforward for new people.	7/26/2016 10:00 AM
8	There is a tiny bug in the BLAT implementation: When I, for example, give BLAT two different introns of a gene in a "multi-fasta sequence", and I press "submit" and then click on the first entry, I will see both intron sequences aligned to the gene. However, when I use the same two sequences, but click on "I'm feeling lucky", I will then see only the first of the two sequences aligned to the genome. Maybe this is intentional, but it confused me a bit, when I first noticed this behaviour.	7/26/2016 9:31 AM
9	have a better UI for things like data integrator, and have it available for more tracks than it currently is.	7/26/2016 8:33 AM
10	Modernize the appearance of the UI. Include both FBgn numbers and gene abbreviations for Drosophila.	7/26/2016 4:17 AM
11	It would be very useful to be able to adjust the display configuration of multiple custom tracks at once rather than having to do each track individually (i.e. track height, data view scaling, vertical viewing range, etc)	7/26/2016 2:46 AM
12	It would eliminate a minor aggravation if when I paste coordinates from another source and leave in a final empty space, the Browser was able to interpret that as just a space without giving an error message. It would be good to have documentation for the Roadmap tracks samples etc. similar in quantity and quality to those of ENCODE. There is some kind of error in the code of the Psoas muscle bisulfite-seq track so that it cannot display certain regions and that track (not any of the other bisulfite-seq tracks) times out. It would be very helpful if you can fix it.	7/25/2016 9:53 PM
13	dont take us to european families or patients. v r nt interested.	7/25/2016 6:01 AM
14	improve GUI	7/21/2016 10:19 AM
15	the main window has a old-fashion style but you know it.	7/21/2016 12:53 AM
16	You may encourage authors to upload their raw data that are available on Track Hubs. Or, if possible, you may insert raw data from GEO or anywhere into your Hubs.	7/20/2016 3:01 PM
17	In my opinion, UCSC is the best genome browser. If possible, please make the table description file more clear in the golden path directory.	7/18/2016 3:14 PM
18	Keep up the great work!!	7/18/2016 11:55 AM
19	More training sessions, nearby my city, or at least, webinars. A "hot line" (chat, or whatever) to quickly solve issues	7/18/2016 8:36 AM

20	When setting up the browser, documentation for local installation was rather confusing, especially how to add custom tracks into a local MySQL DB and how to configure the trackDB.ra files. It took quite some time to figure this out, so a short Tutorial with detailed steps and maybe an example track to add for the trackDB.ra file would be very helpful, as the current documentation only made sense after the tasks were accomplished.	7/18/2016 7:34 AM
21	keep going- you are doing a great job! Thank you very much	7/18/2016 2:24 AM
22	More documentation on maintaining mirrors.	7/17/2016 4:54 PM
23	More non human genomes	7/17/2016 2:30 AM
24	easy integration of public and private data, better visualization	7/16/2016 7:36 PM
25	It is impossible upload some chip-seq files, sometimes it is necessary to modify them. Big files take a lot of time to upload. As a desire I would like to see more interface modification options. Thank you for your work.	7/16/2016 10:00 AM
26	Installation documentation needs improvement.	7/15/2016 5:00 PM
27	Maybe it is possible but i haven't found yet : i often would like to download a personnal custom track that i have in a session. It seems possible with the table browser, but a simple button in the modify section for the custom track would be very useful. Thank you for your awesome browser ! François from France	7/15/2016 9:24 AM
28	marking more than on SNPs in a region e.g we now have the option to highlight one SNP but would be much easier to see all the linked SNPs highlighted which i do now manually.	7/15/2016 7:35 AM
29	Recently the browser window has started to jump around quite a bit after zoom out-zoom in, i.e 10x out followed by 10x in is not centered on same point. Very annoying!!	7/15/2016 2:12 AM
30	Can i still use hg19 version?	7/15/2016 12:32 AM
31	I want to ask about qPCR track in mouse genome browser. When "Click here for primer details: XXXXX" in the qPCR track, I cold see primer sequences. However, now I cannot find details. Please improve qPCR track. Thank you.	7/14/2016 10:10 PM
32	Modern/cleaner UI. Make it easier to find a number of frequent tools	7/14/2016 11:48 AM
33	I love you guys. Your website is amazing and I would be lost without it.	7/14/2016 11:38 AM
34	Please, can you design a translated version of the UCSC Genome Browser? I use it a lot with college students and PhD students, along with my research job, but most of them cannot fully understand the potential of the website because they are not fluent in English. If could have an Italian version of the website I think they would consult it so much more.	7/14/2016 10:51 AM
35	I have a workflow where I have all my custom tracks first set to autoscale to see interesting regions. But then I have the task of making all the tracks the same y-axis. This is a hurdle because I have to right-click on each track and manually change the y-axis scale. This can be very tedious and time-consuming. After all that, I will have change back to auto-scale to see another genomic region, then use a constant y-axis value. If there's any way to automatically set the y-axis scale to the same value for all tracks - this would be desired.	7/14/2016 9:27 AM
36	ability to embed it in other page with examples of navigating within it	7/14/2016 8:25 AM
37	Daily users of graphical interface need drop down menus that require the least possible amount of scrolling. I'm annoyed with recent changes that put useless graphics all over the place and make it much harder to see/scroll through the menus of functional tools! Please put useless graphics to the right side out of the way of getting work done. Thanks!	7/14/2016 8:20 AM
38	Make it fast.	7/14/2016 7:24 AM
39	better and more up to date documentation on track specs. easier registration of public hubs	7/14/2016 1:49 AM
40	As we maintain a partial mirror of the UCSC Genome Browser (http://gwips.ucc.ie) it would be very useful if there was more structured information on the Kent source tree such as architecture etc. And also an easy way to determine differences in functionality between the different genome versions so that we can add new functionality in a more modular way.	7/14/2016 1:27 AM
41	I can't find a direct link to the ENCODE data on the new home page.	7/14/2016 1:02 AM
42	Make it easier to upload many files into custom tracks at once. Keep up the great work Jim and the rest of yall!	7/13/2016 10:02 PM
43	Make it faster.	7/13/2016 9:31 PM
44	When I click on a gene's transcript, I would like it to come up in its own window rather than taking me off the page. I don't seem to be able to make that happen.	7/13/2016 3:58 PM
45	Sometimes the documentation is a bit unclear and complex like the reciprocal best chains, liftovers , chains.	7/13/2016 3:39 PM

46	Data Integrator tool runs very slowly (almost demotivating) from Brazil. A video-guide on how to format file for multi-region view would be very handy. In the Table browser tool, it would be interesting to have a tool that allows subtracting data values (filter) from any two tables (the opposite of integrating or the overlap/not overlap filter). Say, for example, differentially data points values from two tables.	7/13/2016 3:33 PM
47	Please allow users to highlight multiple regions and make Liftover easier to use.	7/13/2016 3:18 PM
48	Make the coordinates in the browser consistent with coordinate tables (i.e. so that both start from either 0 or 1, as opposed to having one set with 0 and another starting at 1)	7/13/2016 3:12 PM
49	1. chicken galGal5 reference genome with Ensembl annotation 2. Japanese quail cotJap1 reference genome 3. phastCons track for chicken galGal4, galGal5, and cotJap1	7/13/2016 1:52 PM
50	response speed; more data visualization design (e.g. how to display circular RNA, splicing junctions; how to group bigwig files with other format e.g. bigBed); easy to share the URL (e.g. to shorten it);	7/13/2016 1:30 PM
51	As explained above, visualization of the Hi-C data.	7/13/2016 1:21 PM
52	i would like to have a url that shows the "describe table schema" from table browser. currently when you click on that there doesn't appear to be a shareable/portable url	7/13/2016 1:14 PM
53	Thanks	7/13/2016 1:07 PM
54	The Genome Browser does a bad job of preventing cross-site scripting and sql injection attacks. Content is displayed verbatim from the URL onto the page, and there is little done to control direct mysql queries from the posted content. Either do a much better job of filtering and validating data expected and entered, or provide an exhaustive list of all variables accepted by the executables and their intended value ranges. Our site has been threatened with shutdown several times by our security department, and I have been forced to hack the code to prevent possible misuse.	7/13/2016 12:52 PM
55	- kent source code on github - REST API	7/13/2016 12:49 PM
56	UCSC is really an AWESOME tool that is extremely helpful. I am limited more by my own lack of time than by shortcomings at the Browser. I realise this kind of comment is not that useful to you, sorry :-0.	7/13/2016 12:32 PM
57	Webinars discussing advanced track usage	7/13/2016 11:56 AM
58	from IGV, you can copy and paste in tab delimited coordinates and they will be auto corrected to coordinates, e.g. these all work: For the UCSC human genome browser: 11[tab]46878268[tab]46940173 chr11[tab]46878268[tab]46940173 11:46878268-46940173 should all autocorrect/resolve to chr11:46878268-46940173	7/13/2016 11:56 AM