	Category	Priority	Complexity	Time (hours)
Pogvue 23rd December 2008				
************** Fix the display bug!!!!!!! *************************	basic function	0	2	3
Fix yscroll	basic function	0	2	3
Feature height proportional to score	basic function	1	1	1
Names of repeats	basic function	1	1	1
Distinguish tracks	beauty	1	1	1
Scale with commas	beauty	1	1	1
More single key zoom levels	ease of use	1	1	1
Make arrow keys work	ease of use	1	1	1
Goto middle,start,end	ease of use	1	1	1
Logos for the alignment	basic function	1	1	2
Graph display	basic function	1	1	2
Fetch graphs - only fetch on sequence fetch in bottom panel	basic function	1	1	2
Move tracks	ease of use	1	1	2
Delete tracks	ease of use	1	1	2
Gene info display - description, pid etc, publications, GO, expression,	basic function	1	1	3
Indel density (basic - not tree based)	basic function	1	1	3
UTRs on genes	basic function	1	1	3
Strand displayed better - arrows etc	basic function	1	1	3
Fix AlignmentPanel	basic function	1	2	8
Printing postscript	basic function	1	2	3
Drag to select search region	basic function	1	2	3
Show chromosome and coords and no. base pairs in view	beauty	1	2	3
Better labels	beauty	1	2	3
Chromoview - context	beauty	1	3	3
Bumping of labels	beauty	1	2	4
Read maf	basic function	1	3	8
Better gene display	beauty	1	2	3
Transparent overlay for bottom panel	beauty	1	3	4
zoom to whole gene,	ease of use	2	1	1
zoom to promoter,	ease of use	2	1	1
Tab to next feature	ease of use	2	1	1
Search panel for motifs	basic function	2	1	2
Clearer fonts	beauty	2	1	2
Column demarcation?	beauty	2	1	2
Quality scores in alignments	basic function	2	2	3
Gaps in alignments - real or otherwise	basic function	2	3	8
Colours - more transparency - find good examples of displaying data. Guardian,TED T	beauty	2	3	8
Progress bars - on loading, sequence fetching, searching	ease of use	2	3	8
menus and palettes	ease of use	2	3	8
Scale logos by score	beauty	3	1	3
Feature search	basic function	3	2	3
Quickview for sequence.	ease of use	3	3	8
Logos by clade	improved display	3	3	8
Drag select to zoom	ease of use	3	3	8
Bookmarking	ease of use	3	3	16
Translation of genes	improved display	3	3	16
Sequence and tree display	improved display	3	3	3
Tree display for features	Ease of use	3	3	3
Make obvious the bottom panel is blow up of the top panel	beauty	3	3	4
Add gff features	basic function	4	1	2
Alignment statistics - percent identity, coverage, feature density etc.	basic function	4	1	3
Pwm generation from features	basic function	4	2	4
Alignment coverage shadow.	basic function	4	3	8
Make more use of colour and size - size by score	beauty	4	3	8
Diced data - with gffs. Can we do this on the fly?	basic function	4	4	8
Gene squeeze.	improved display	4	4	16
Position of mutations on tree	basic function	4	4	16
Position of indels on tree	basic function	4	4	16
Gene comparison - cartoon comparison	improved display	4	4	16
animations????? Root to human motif changes?	beauty	5	5	0
Human - Rodent - Hedgehog - Dolphin motif changes.	beauty	5	5	0
Separators between tracks	beauty	5	1	4
Linkouts	ease of use	5	1	3
Save to file	basic function	5	2	3
List tracks	ease of use	5	2	3
Change track colours	ease of use	5	2	3
Colour sequence by clade	improved display	5	2	3
Kmer frequencies	basic function	5	3	3
Fade to grey when waiting for new data?	ease of use	5	3	8
Default analysis of genes - conserved splice sites, conserved start and stop, TATA bo	basic function	5	1	8
Domain display	basic function	5	4	16
Fade in and out - when changing regions?	beauty	5	4	#VALUE!
Fancy damped scrolling	beauty	5	4	#VALUE!
'Adenosine!', 'Cytosine!', 'Thymine!', 'Guanine' - bugger!	fun	10	3	0
Structure display	basic function	10	10	0
Auto-zoom -	ease of use	?	?	0
Distribution plots	??			0
Transfac summary	????			0
Simplify and clarify - not quite sure how to do this	hmmm			0
				#VALUE!