Respondents = 195

Track	Definitely Appear	Definitely Appear (%)
Transcript **(in the current default set of tracks)**	185	94.87%
Gene Span **(in the current default set of tracks)**	172	88.21%
Transgenic Insertion Site **(in the current default set of tracks)**	136	69.74%
cDNA **(in the current default set of tracks)**	133	68.21%
CDS	105	53.85%
Developmental stage subsets, unique reads (modENCODE Transcription Group) **(in the current default set of tracks)**	87	44.62%
NCBI Gnomon, 2006 **(in the current default set of tracks)**	86	44.10%
Orthologs (OrthoDB) **(in the current default set of tracks)**	79	40.51%
mRNA	64	32.82%
Estimated Cytological Band	63	32.31%
D melanogaster proteins	53	27.18%
Point Mutation	49	25.13%
Transgenic Insertions in stocks, Bloomington	48	24.62%
Regulatory Region	48	24.62%
Transcription Start Sites (embryonic)	44	22.56%
Enhancer	44	22.56%
Natural TE (only visible below 300Kb) **(in the current default set of tracks)**	38	19.49%
PhyloCSF (CONGO) **(in the current default set of tracks)**	37	18.97%
Repeat region **(in the current default set of tracks)**	36	18.46%
RNA-seq exon junctions	36	18.46%
VDRC RNAi amplicons	36	18.46%
TRiP RNAi amplicons	36	18.46%
Transgenic Insertions in stocks, Kyoto	34	17.44%
Transgenic Insertions in stocks, Harvard	32	16.41%
Silencer	32	16.41%
Deleted segment	32	16.41%
DRSC RNAi amplicons	27	13.85%
Sequence Variant	26	13.33%
CNS and adult head, stranded	26	13.33%
Bloomington Deficiency Kit: deleted segment	26	13.33%
Protein Binding Site	24	12.31%
Developmental stage subsets (Baylor)	24	12.31%
EST	23	11.79%
Stock Center Aberration: deleted segment	23	11.79%
Indels	22	11.28%
Imaginal disc and other carcass, stranded	22	11.28%
3-frame translation (forward)	21	10.77%

Fat body and salivary glands, stranded	21	10.77%
Tissue culture cells, stranded (modENCODE Transcription Group)	21	10.77%
Gonads and male accessory glands, stranded	20	10.26%
L3 CNS neuron, stranded	20	10.26%
Duplicated segment	20	10.26%
TFBS HOT spot analysis	19	9.74%
NIG-Fly RNAi amplicons	19	9.74%
Rescue Fragment	18	9.23%
Digestive system, stranded	18	9.23%
L3 CNS neuroblast, stranded	17	8.72%
Other proteins	16	8.21%
RNA Editing Sites	16	8.21%
Stock Center Aberration: duplicated segment	15	7.69%
PeptideAtlas peptides	14	7.18%
Putative Brain Enhancers (Pfeiffer et al)	14	7.18%
Restriction Sites	14	7.18%
Aberration Junction	13	6.67%
Bloomington Deficiency Kit: gap filling or haploinsufficiency flanking segment	13	6.67%
HFA RNAi amplicons	13	6.67%
Affymetrix v1	12	6.15%
Affymetrix v2	12	6.15%
BKNA RNAi amplicons	12	6.15%
DNA/GC Content	11	5.64%
Uncharacterized Change in Nucleotide Sequence	11	5.64%
Origin of Replication	11	5.64%
Tiling BAC (only visible below 300Kb)	11	5.64%
3-frame translation (reverse)	10	5.13%
Insulator class I	10	5.13%
Insulator class II	10	5.13%
Chromatin Domains (5-state model, Kc cells)	10	5.13%
Chromatin Domains (9-state model, S2 cells)	10	5.13%
DGRC-1 amplicons	10	5.13%
Treatments/Conditions, stranded	10	5.13%
CONTRAST	9	4.62%
TFBS zinc finger domain	9	4.62%
TFBS BTB/POZ domain	9	4.62%
TFBS homeodomain	8	4.10%
TFBS helix-loop-helix domain	8	4.10%
TFBS other	7	3.59%
Chromatin Domains (9-state model, BG3 cells)	7	3.59%

DGRC-2 oligos	7	3.59%
other aligned sequences	5	2.56%
PROBLEMATIC: Sindbis Virus Infected, stranded	5	2.56%
Complex Substitution	4	2.05%
PROBLEMATIC: New treatments subsets, stranded	4	2.05%