**Figures**

*Figure 1:* (numberstats) Stats "flower" of bases by experiment - Ian and Steve. We could also include here panels that illustrate the integration points – signal vs element representations, IDR?

We may need more in here on the just the facts summaries, or in supplementary.

*Figure 2*: (selection) Multi-panel selection figure: Luke ward, Javier Herrero

 A: Mammalian constraint vs Hetreozygosity

 B: Something about Primate specific elements

 C: Motif IC content vs conservation

 D: Scatter plot of Motif correlation to conservation

*Figure 3*: The information content of ENCODE assays Ben Brown

 A: distribution of information content across bases (CDF?)

 B: comparison of information content over all bases vs conserved, non coding bases (bar chart?)

*Figure 4*: (promoter) Xianjun Dong, Chao Cheng

 A: Distribution of histone modifications over promoters, in LCP and HCP

 B: Distribution of TF density over promoters, in LCP HCP, TATA and something else pulled out?

 C: Quantitative model fit for LCP and HCP; histones

 D: Quantitative model fit for TFs? Currently not referred to in the text.

*Figure 5*: Patterns of chromatin modificiations at transcription factor binding sites. (tf\_anchored) Xianjun Dong, Ewan Birney

 Examples of TF/Chromatin association:

CTCF Proximal vs Distal

 TAF

 KAP

 ? One more?

*Figure 6*: (tf\_assoc) TF Associations: Anshul

 Co-association matrix of TFs by GSC statistics

 Example association

*Figure 7*: Patterns of chromatin modificiations at genomic repeat sequences (repeat\_anchored) Ian Dunham/Ewan Birney

 Likely to be similar to TF line above.

*Figure 8*: (segmentation) Steve Wilder/Michael Hoffman/Jason Ernst

A. Illustrative region with both segmentations and joint call

B. Association vs different types of elements

C. RNA segmentation; confusion plot of RNA vs Chromatin if it makes sense

 D. Methylation is referred to in the text.

*Figure 9*: (Self\_organised\_maps) Ali

 Example SOM map with 2 or 3 assays

 One GO term enrichment map

 All GO terms enrichment

*Figure 10*: (Experimental\_validation) : Chris/Ewan

 Experimental design figure

 Examples of in vitro plate, mouse, fish

 Enrichment over background of different methods vs different assays

*Figure 11*: (allele\_sp) Allele specific information: Tim Reddy and Bob Altschuler

A. Example locus

B. Example assay combination

C. Pairwise assay correlation

D. Pol2-->Cytoplasmic RNA progression

*Figure 12*: (gwas\_cancer) Variation association (GWAS) and Cancer. Ross/Belinda

A. Association of GWAS SNPs to Segmentation/DNaseI/TFs

B. Example locus

C. Exclusion of Somatic variants in Cancer

*Figure 13*: (personal\_genome) Personal genomes/rare disease. Joel/Mark

A. Example region with assay recalled on personal haplotypes

B. Diagram indicating the new set of variants prioritised by ENCODE

**Tables**

**Supplementary Figures**

Figure S1. Inter-laboratory variation is less than inter-sample variation. PCA analysis of U133plus 2 expression .