1. ChIP-seq prediction
   - Several people complained they have to evaluate the in vitro models on ChIP-seq binding, where it is clearly a much more complex and noisy signal. The consensus is that ChIP-seq peaks do not necessarily contain a binding site and should not be used for this evaluation.
   - Gary Stormo suggested a new criteria to gauge ChIP-seq prediction: median relative predicted affinity of positive peaks.
   - Gary also showed a proof from a past paper that stricter motif (= higher information content) have better AUC when predicting ChIP-seq binding (in concordance with what we observed). This explains the good performance of Jussi’s models which are quite strict.
   - Raluca Gordan suggested using as negative peaks all unbound accessible sites (which limits the datasets that can be used, since both ChIP-seq and DNase I are required) and also taking more peaks (not just top 500).

2. HT-SELEX methods comparison
   - Gary Stormo wants an HT-SELEX DREAM challenge (the problem: it is difficult to get someone’s unpublished data for a challenge).
   - Harmen Bussemaker (two new PWM methods for SELEX), Todd Riley (featureREDUCE), Gary Stromo (BEEML), Alexandre Morozov (biophysical model) would like someone to test their method on HT-SELEX data. Should we ‘raise this glove’? They can send in their PWMs, and I have the pipeline to evaluate them. The problem is that they already know what the evaluation is going to be like (PBM prediction) – so maybe this won’t work as they can ‘cheat’ and train the model on PBM data.

3. ShortCAKE
   - Polly Fordyce used it to generate her oligo library.
   - Alexandre Morozov used it to generate simulated MITOMI data.
   - People are moving to SELEX and customPBMs, so it seems that universal designs are less and less used.

4. Polly Fordyce
   - She is unhappy with using MatrixREDUCE on her MITOMI data. The motifs are not clear.
   - I made a pitch about our AmadeusPBM – we’ll see if she bites it. If so, I can provide her with the same scripts I developed for Doron to analyze MITOMI and run it in Amadeus.
   - Any conflict of interest in collaborating with her? I know she and Doron are competing. Do we need to ask Doron first?

5. HTS-IBIS
   - Currently, we evaluate the performance using PBM and ChIP-seq.
   - As noted before, the ChIP-seq evaluation should be different. The 300bp sequences downstream are not real control.
• As for PBM, maybe using $R^2$ and larger sets of positive would should our advantage, since Jussi’s strict motifs should be only good at identifying high-affinity sites, while ours should capture the variability better.
• I will try and report with new results.