**Rob’s Notes on Meeting with USACIL**

03/17 – 03/18/2015

(non-prioritized and supplemental to USACIL document)

1. Add presets to specify whether to filter or not to filter: stutter, adenylation, plus stutter
2. Extended locus issues:
   1. Create options to extend loci that are more user friendly, e.g. “edge-to-edge"
   2. Move specification from ladder file to lab settings (use ladder file as default?)
   3. Extended locus doesn’t include stutter or adenylation
   4. Display info about ambiguous extended locus alleles in one place, in unified manner
   5. Verify consistency of OL designation in extended loci
3. Pull-up issues:
   1. As part of inter-channel pattern-based pull-up analysis, note that pull-up does not have stutter
   2. Pull-up with excessive residual in multi-allelic locus is not reliable – often causes real peaks to not be called (another example of why systems approach is needed)
   3. Need setting to suppress “primary pull-up artifact when irrelevant
   4. Amend pull-up to identify primary peak(s) (or channel(s))
   5. Similarly, amend primary peak(s) to identify peak(s) (or channel(s)) pulled up
4. Allele call issues:
   1. Artifact recognition for craters: when are craters called/not called; what happens when a crater is combined with another artifact (e.g. stutter)
   2. Suppress stutter-crater? Stutter/poor morphology?
5. General:
   1. A run with nested folders caused Osiris to use a ladder that was not in the same folder as the sample, but not when the folders were run separately?
   2. Multiple peaks with the same call are an issue in V2.3. Is it fixed in V2.4?
   3. V2.3 gave rise to a peak with a negative allele call (bp = 0). Is this bug fixed?
6. Possible improvements to discuss:
   1. Hints file for user to select peaks to ignore or to include in ILS’s and ladder loci – this would become effective on rerunning the analysis
   2. “info” option for peaks (loci?) that would provide information that is not an artifact, such as “peak could belong to locus on left” or “height of peak after correcting for pull-up = (approx.) …” These would not need to be cleared by the analyst
   3. Under “Curve Fit” heading on sample thresholds tab, include two different settings for each of the two options there, one for normalization and the other for analysis. This would allow greater sensitivity for normalization to get the best possible base line and lesser sensitivity for the analysis, if desired.