Supervised detection of the same peaks jointly across several ChIP-seq samples
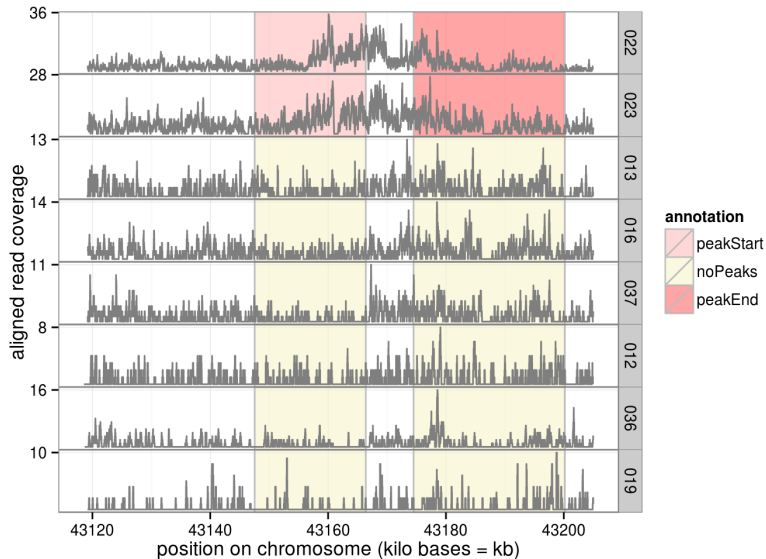
Toby Dylan Hocking
toby.hocking@mail.mcgill.ca
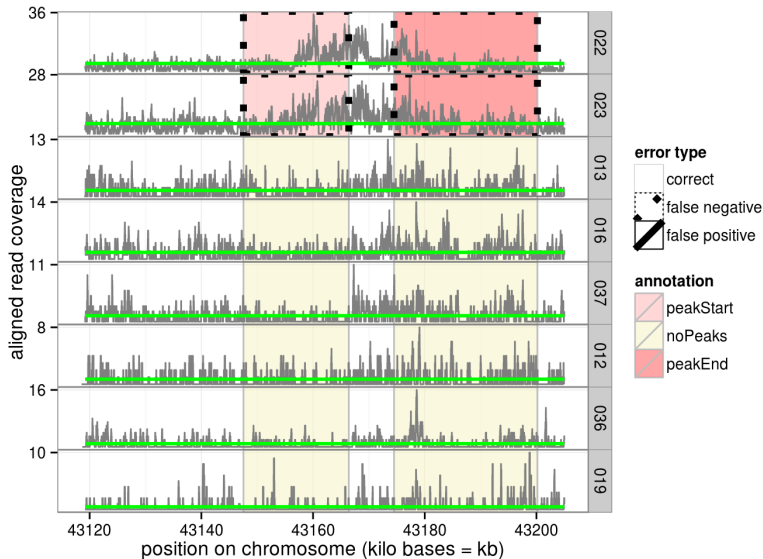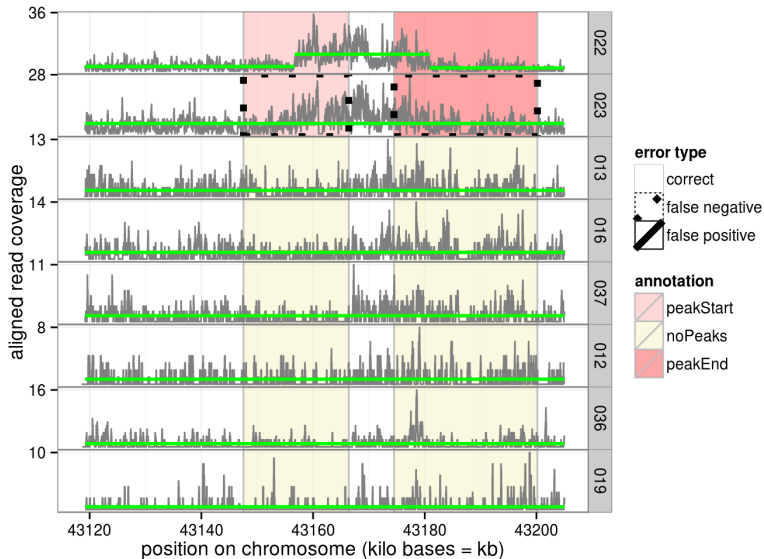joint work with Guillem Rigaill and Guillaume Bourque
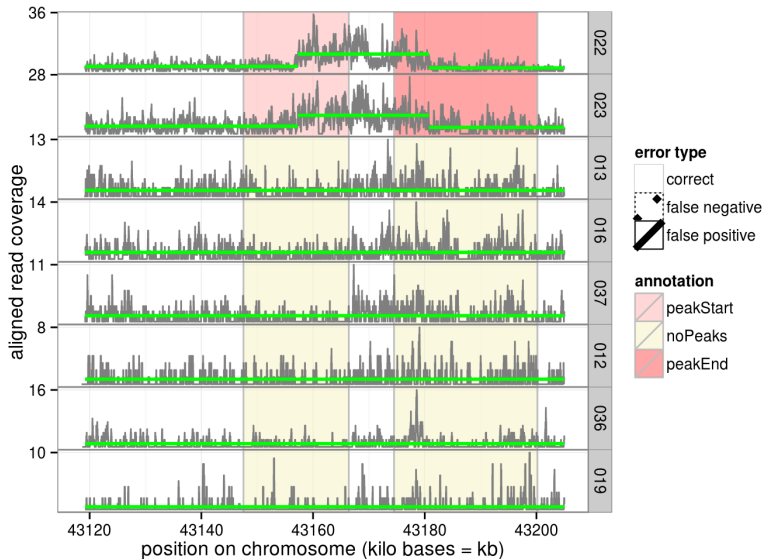
2 April 2015

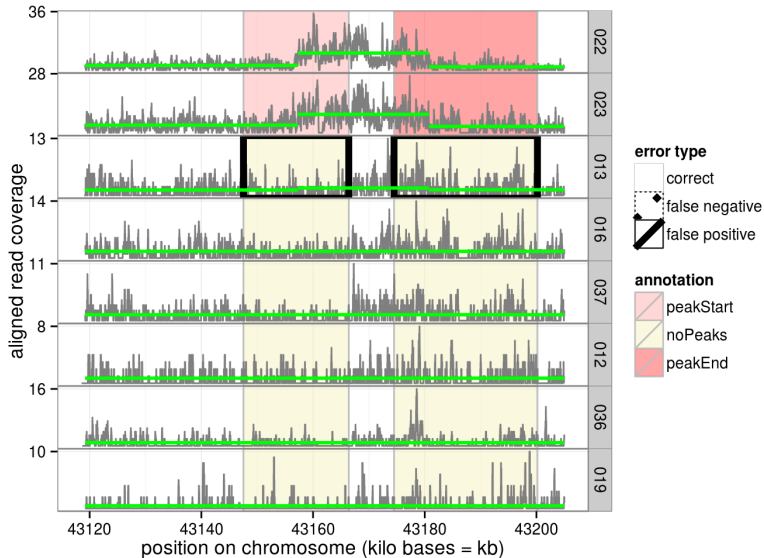# H3K36me3 data and labels

PeakSegJoint model with 0 peaks
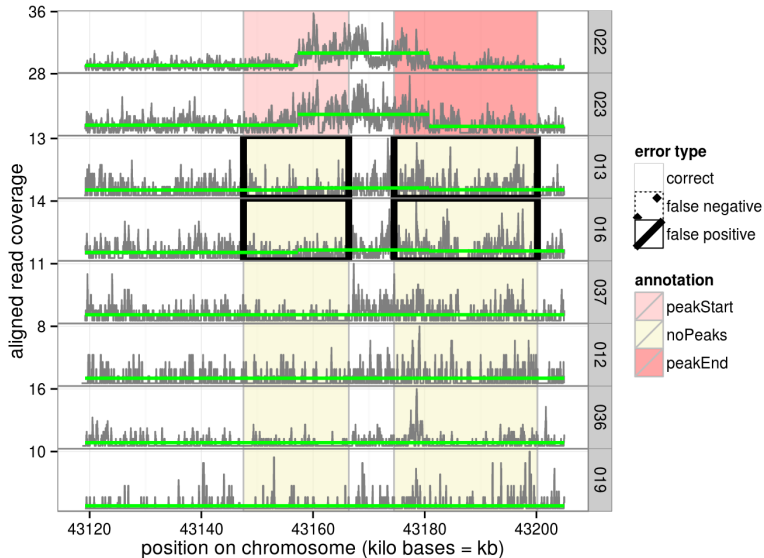
PeakSegJoint model with 1 peak
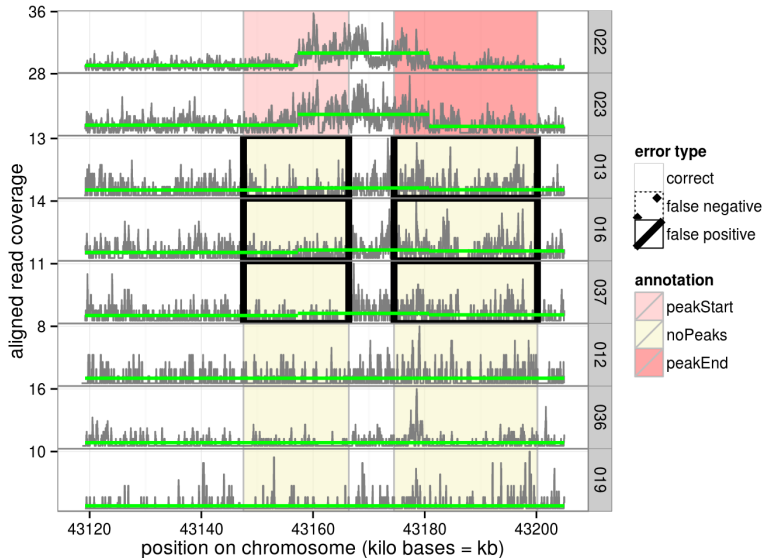
PeakSegJoint model with 2 peaks
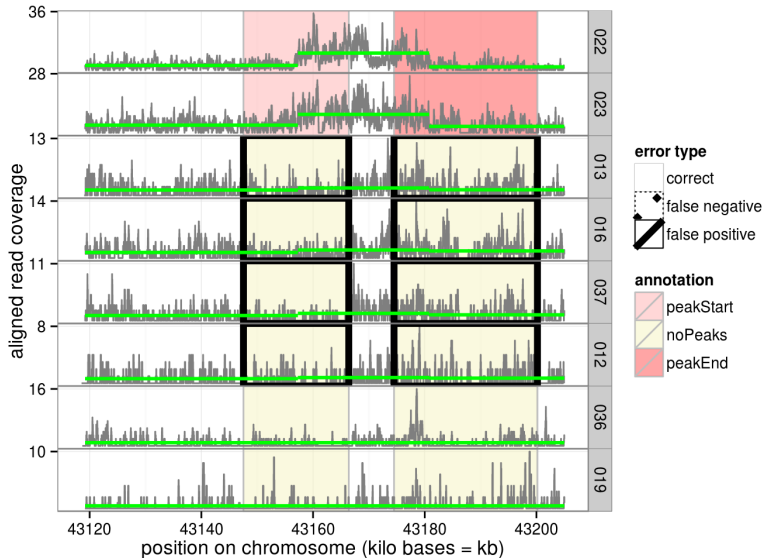
PeakSegJoint model with 3 peaks
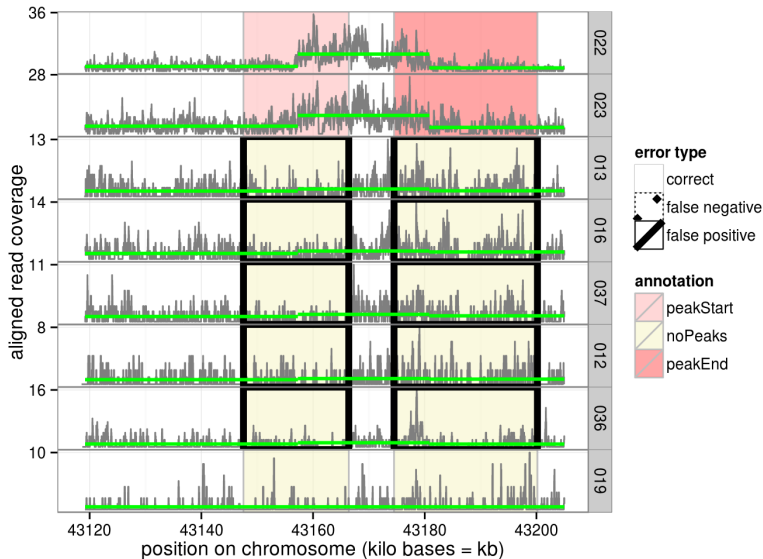
PeakSegJoint model with 4 peaks
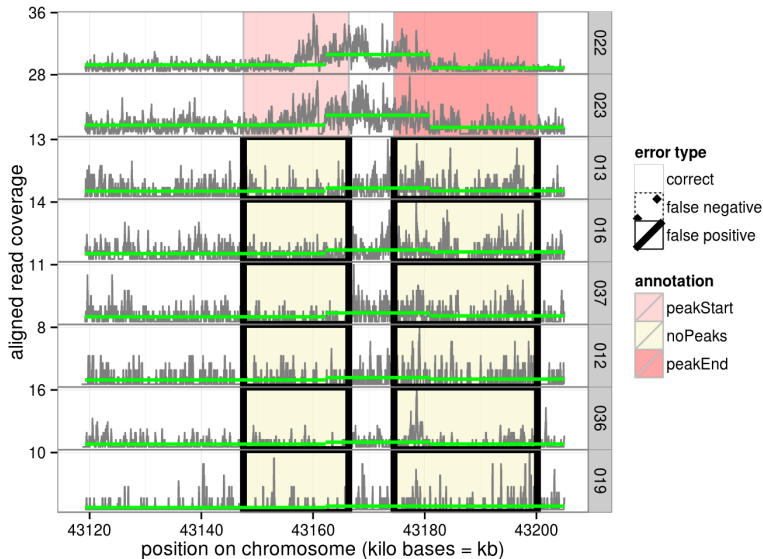
PeakSegJoint model with 5 peaks
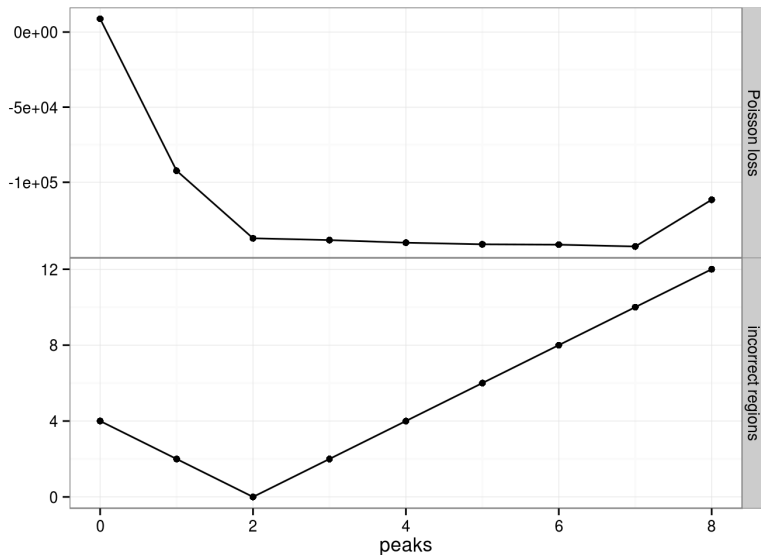
PeakSegJoint model with 6 peaks

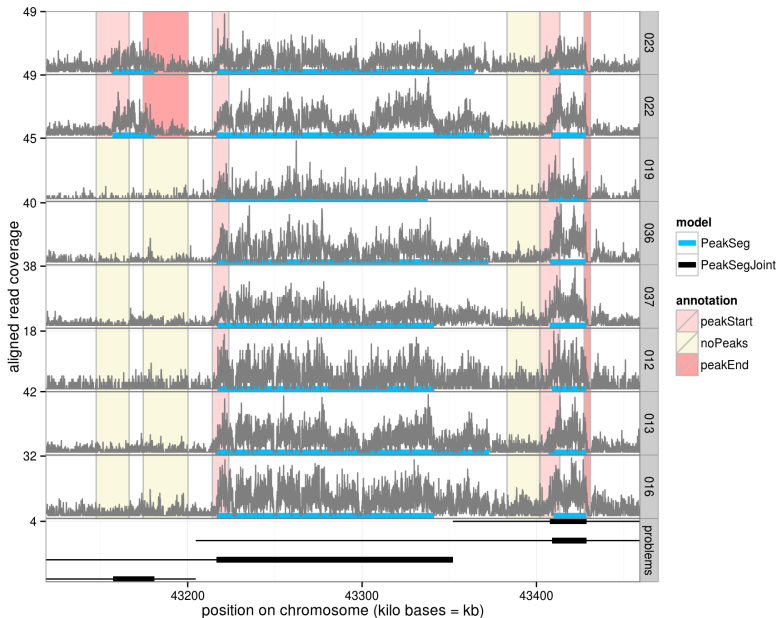# PeakSegJoint model with 7 peaks

PeakSegJoint model with 8 peaks

Select model with minimal number of incorrect regions

Comparison of PeakSeg and Joint model

Comparing timings to segment 8 samples

Segment each sample (PeakSeg):

seconds	sample.id
0.80	McGill0023
0.80	McGill0022
0.80	McGill0019
0.82	McGill0036
0.81	McGill0037
0.81	McGill0012
0.82	McGill0013
0.80	McGill0016
6.47	total

Segment each genomic region (PeakSegJoint):

	data	seconds
chr21:42909696-43204608	23595	0.05
chr21:43057152-43352064	162129	0.14
chr21:43204608-43499520	206437	0.18
chr21:43352064-43646976	67903	0.08
total		0.45