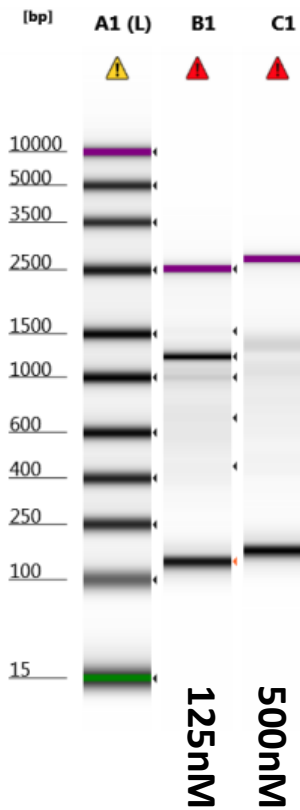
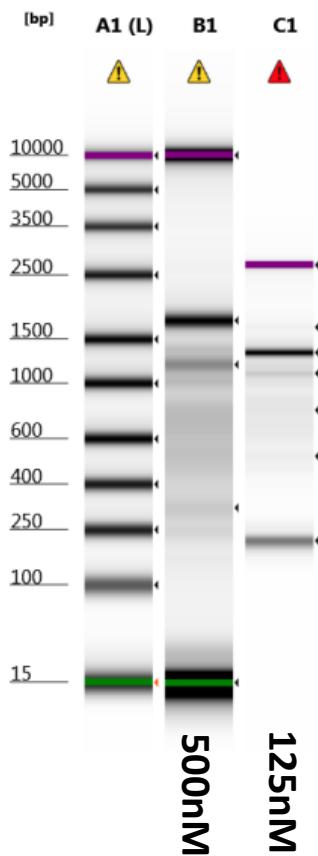


# D5000 TapeStation

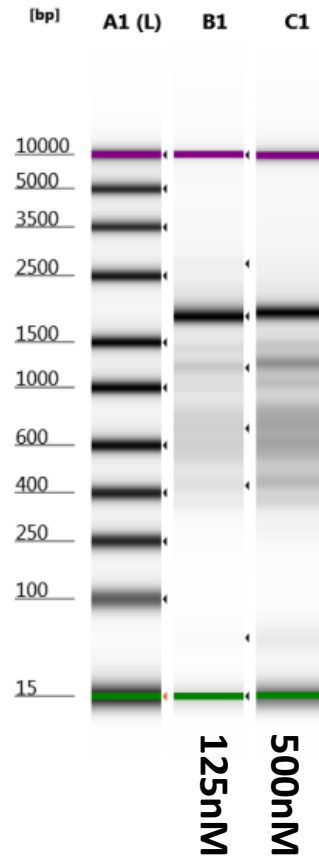
crosslinked  
samples:



3h Proteinase K,  
before clean-up



3h Proteinase K,  
post clean-up



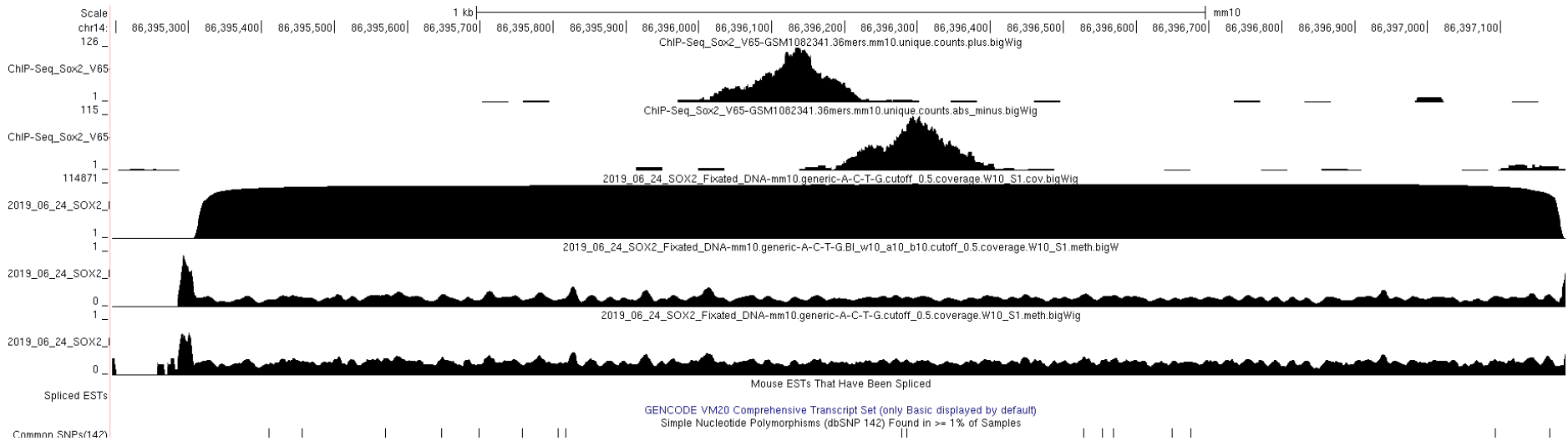
## Mapping stats

Species	Assay	#	Mapping	Base Contexts	Reads	Total Bases	Mean Read Length	Median Read Length
<b>Mus musculus</b>	<b>CLAPP</b>	2019_06_24_SOX2_Fixated_DNA-mm10	<b>Tombo 1.3 denovo</b>	<b>generic-A-C-T-G</b>	2,122,224	1,343,998,193	633	523

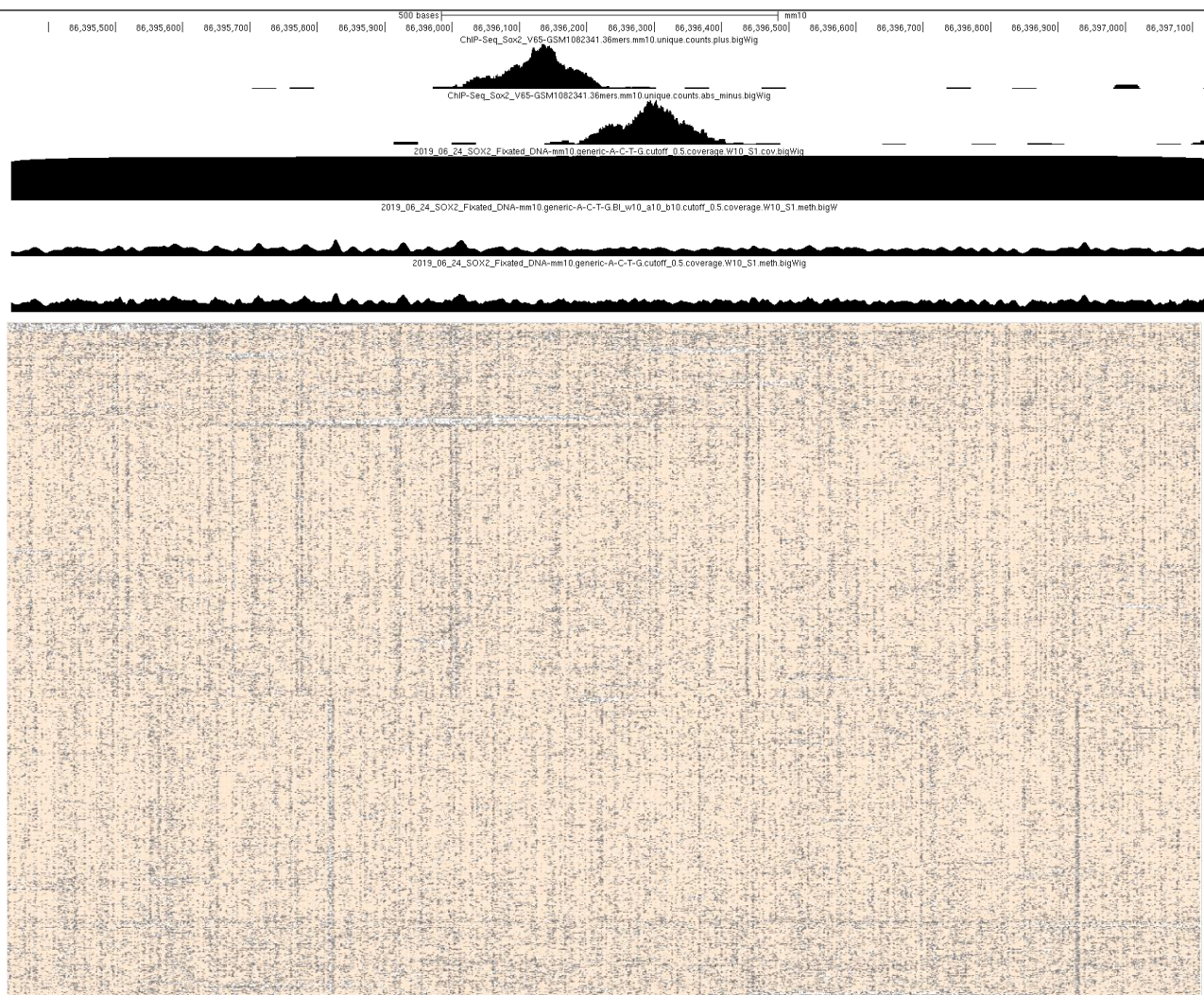
Note:

242,138 reads mapped to the amplified regions

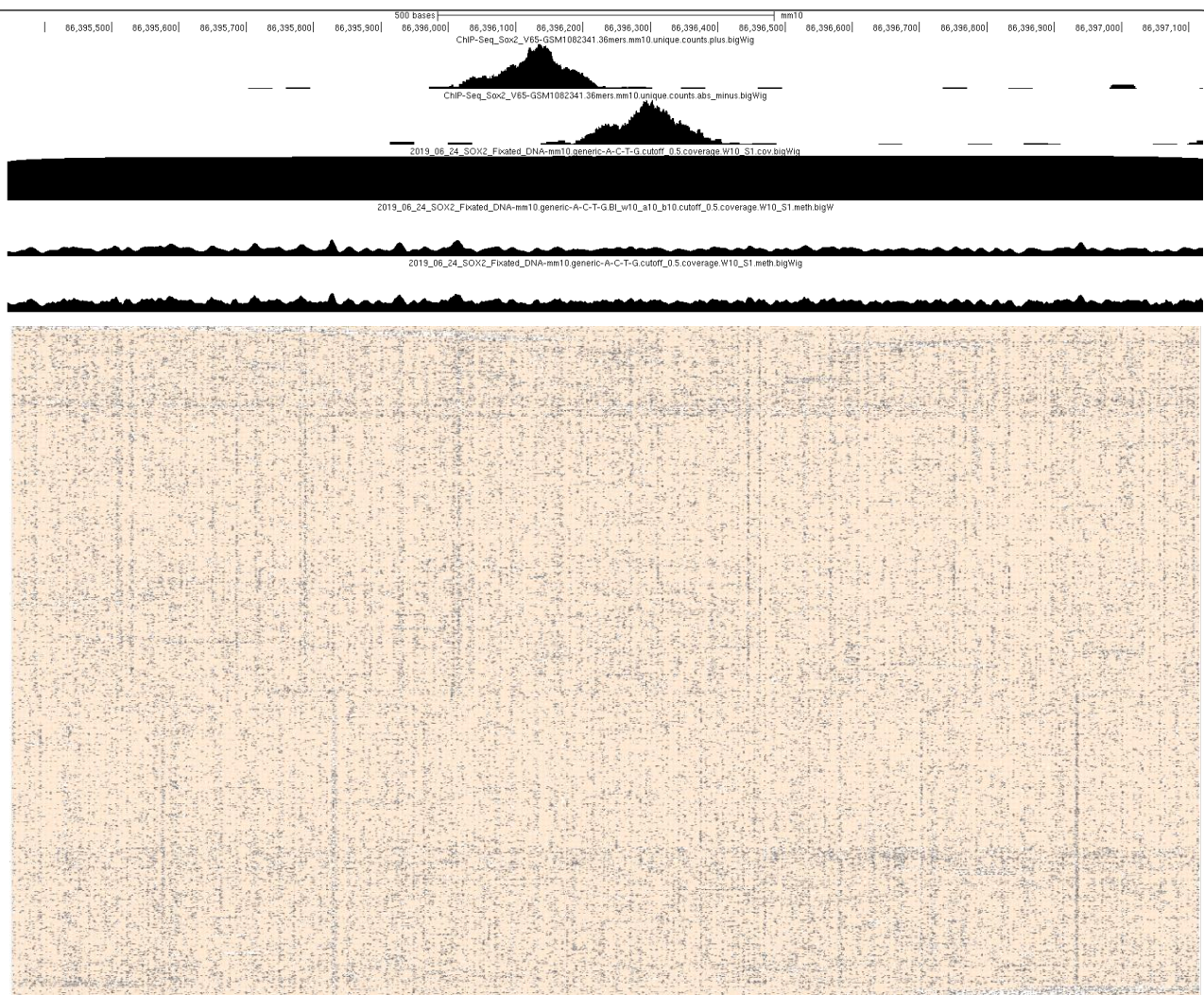
1,880,086 reads mapped elsewhere



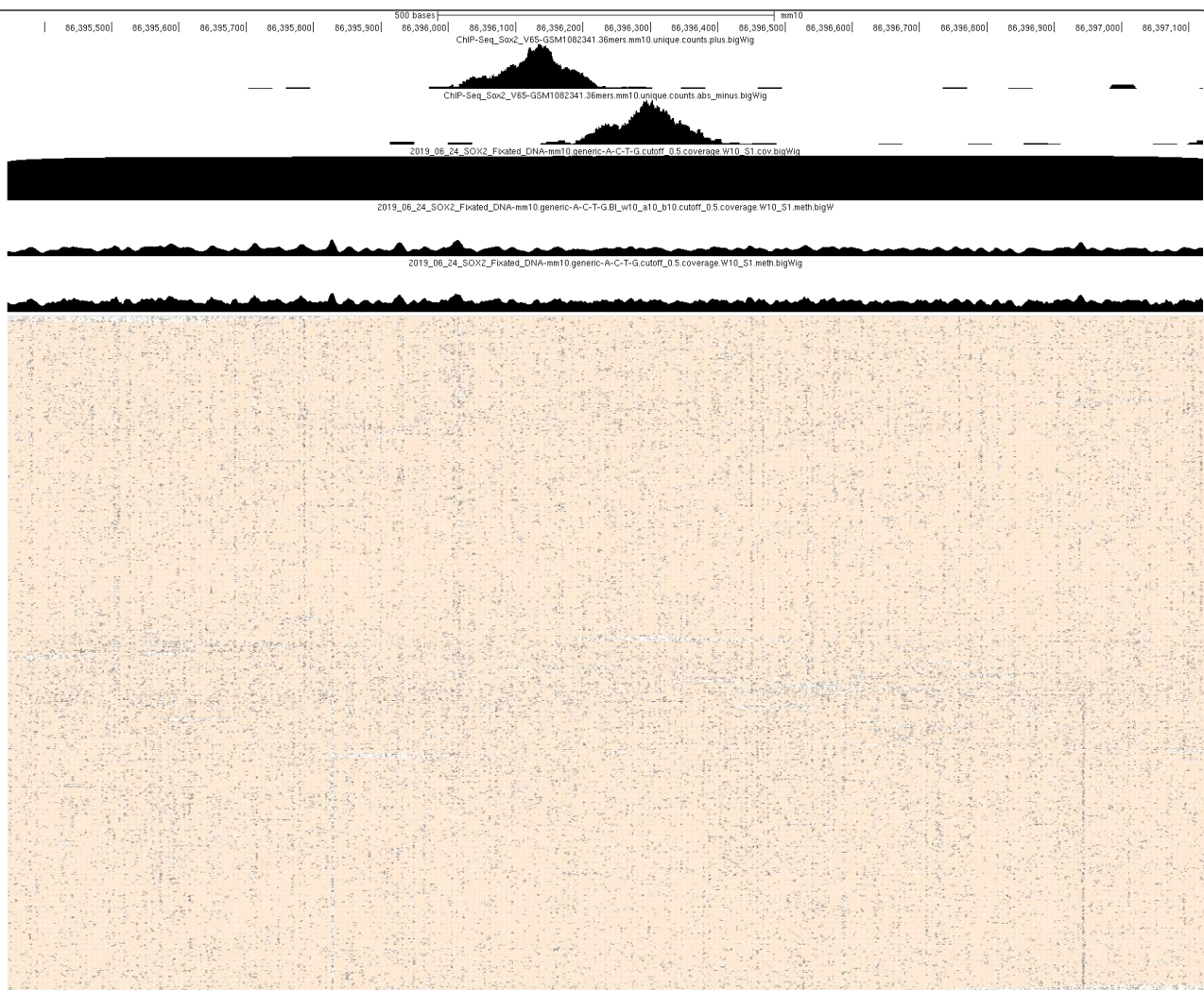
Single-molecule (1000  
reads subsample)  
 $p=0.5$  binarization

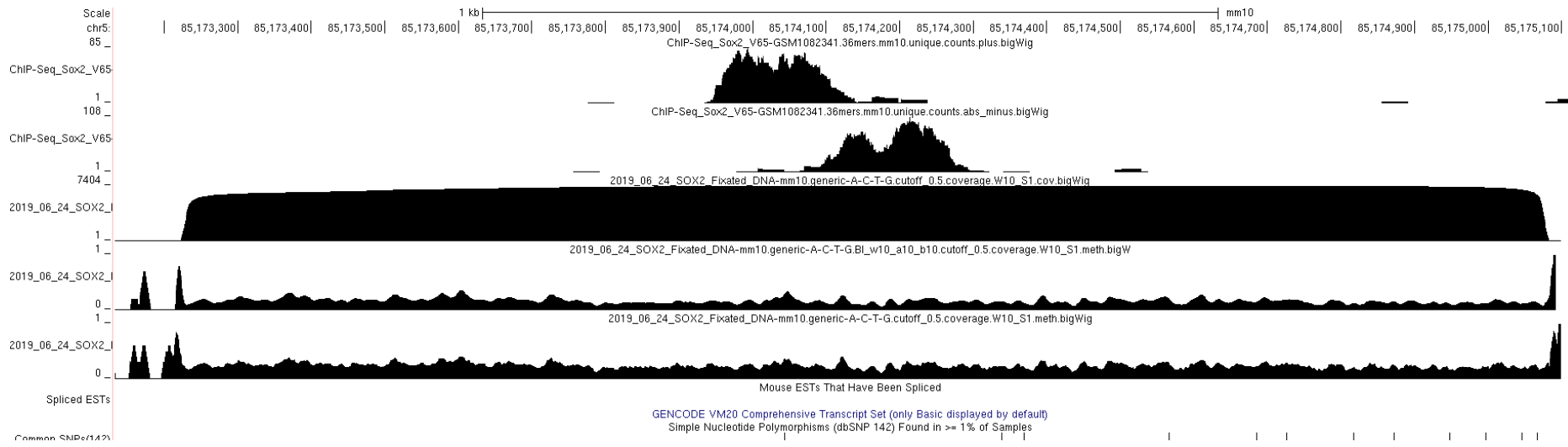


Single-molecule (1000  
reads subsample)  
 $p=0.3$  binarization

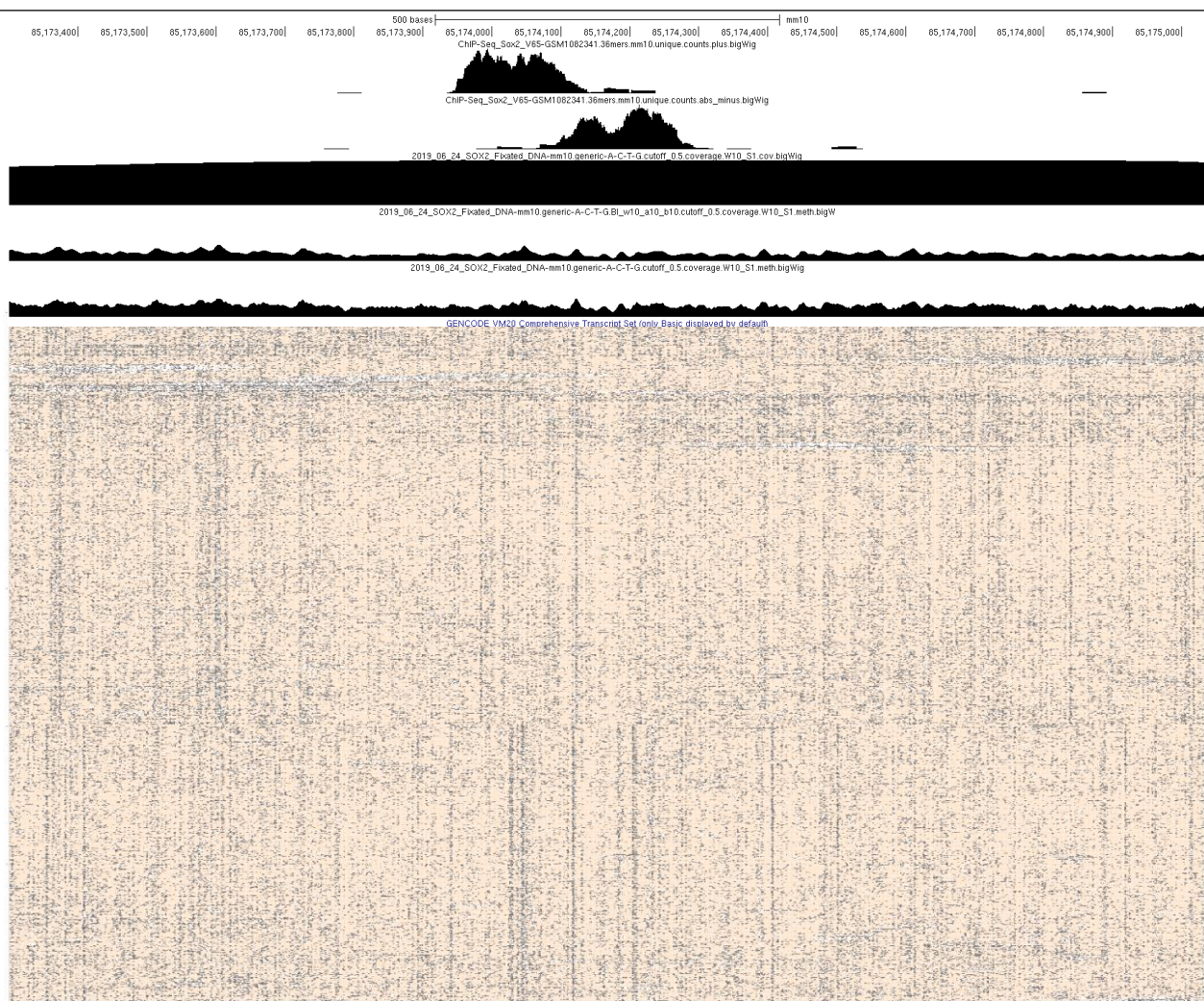


Single-molecule (1000  
reads subsample)  
 $p=0.1$  binarization

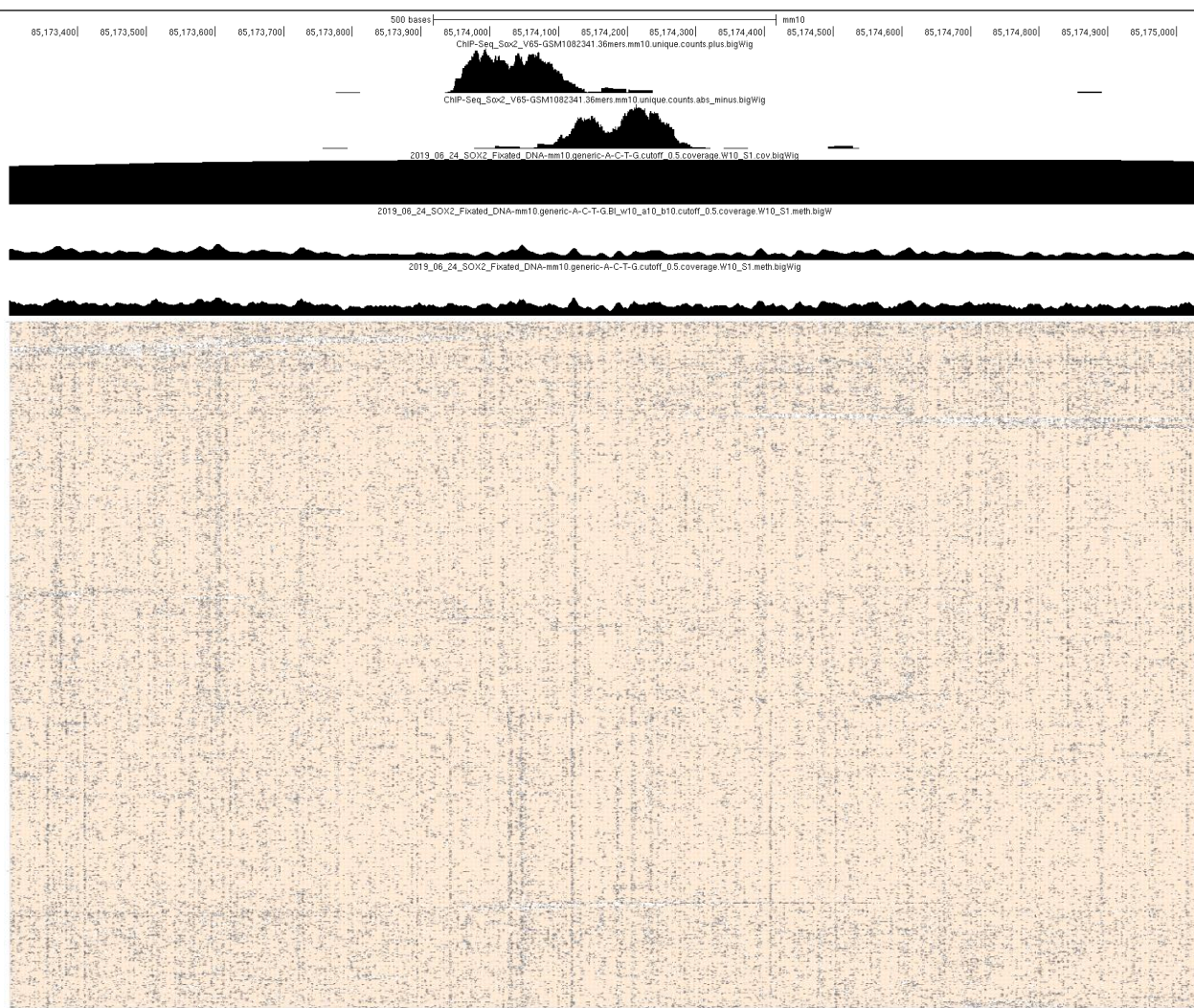




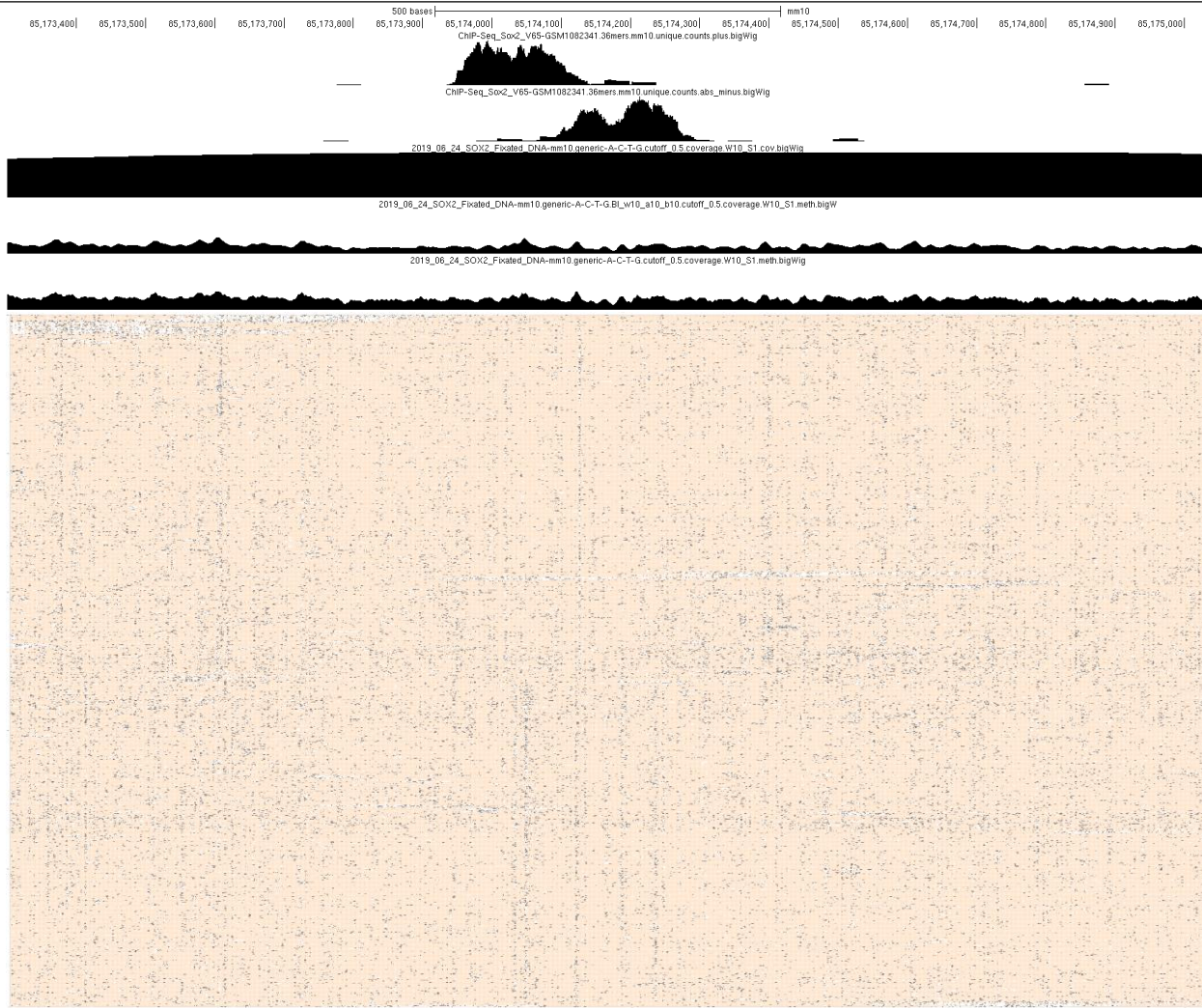
Single-molecule (1000  
reads subsample)  
 $p=0.5$  binarization

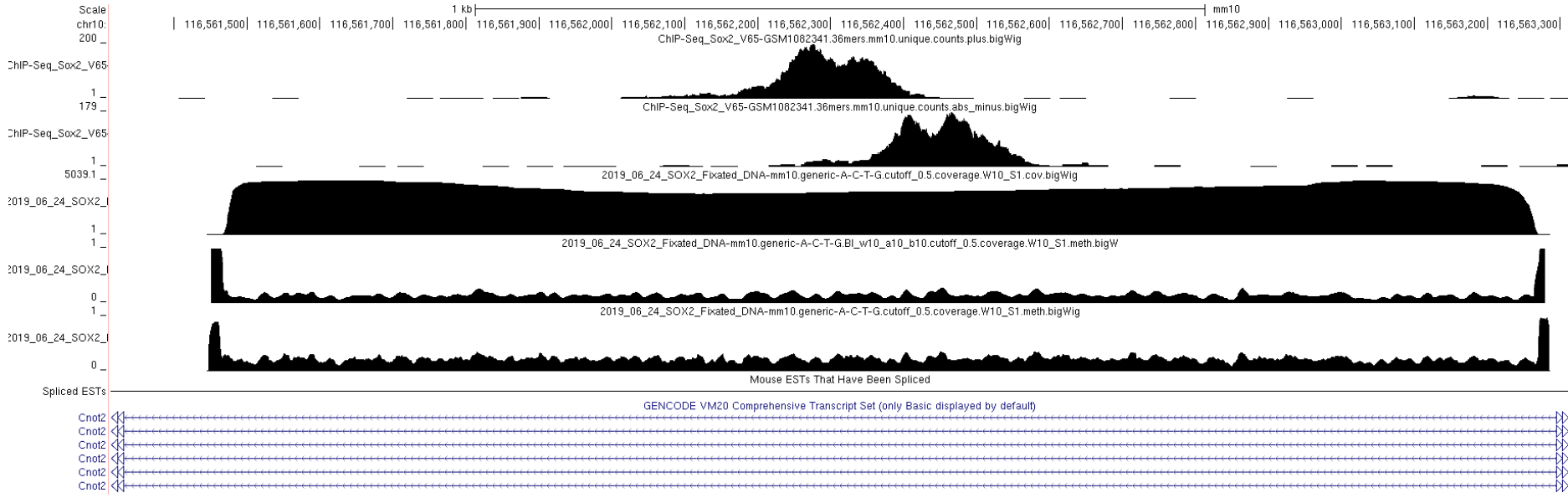


Single-molecule (1000  
reads subsample)  
 $p=0.3$  binarization

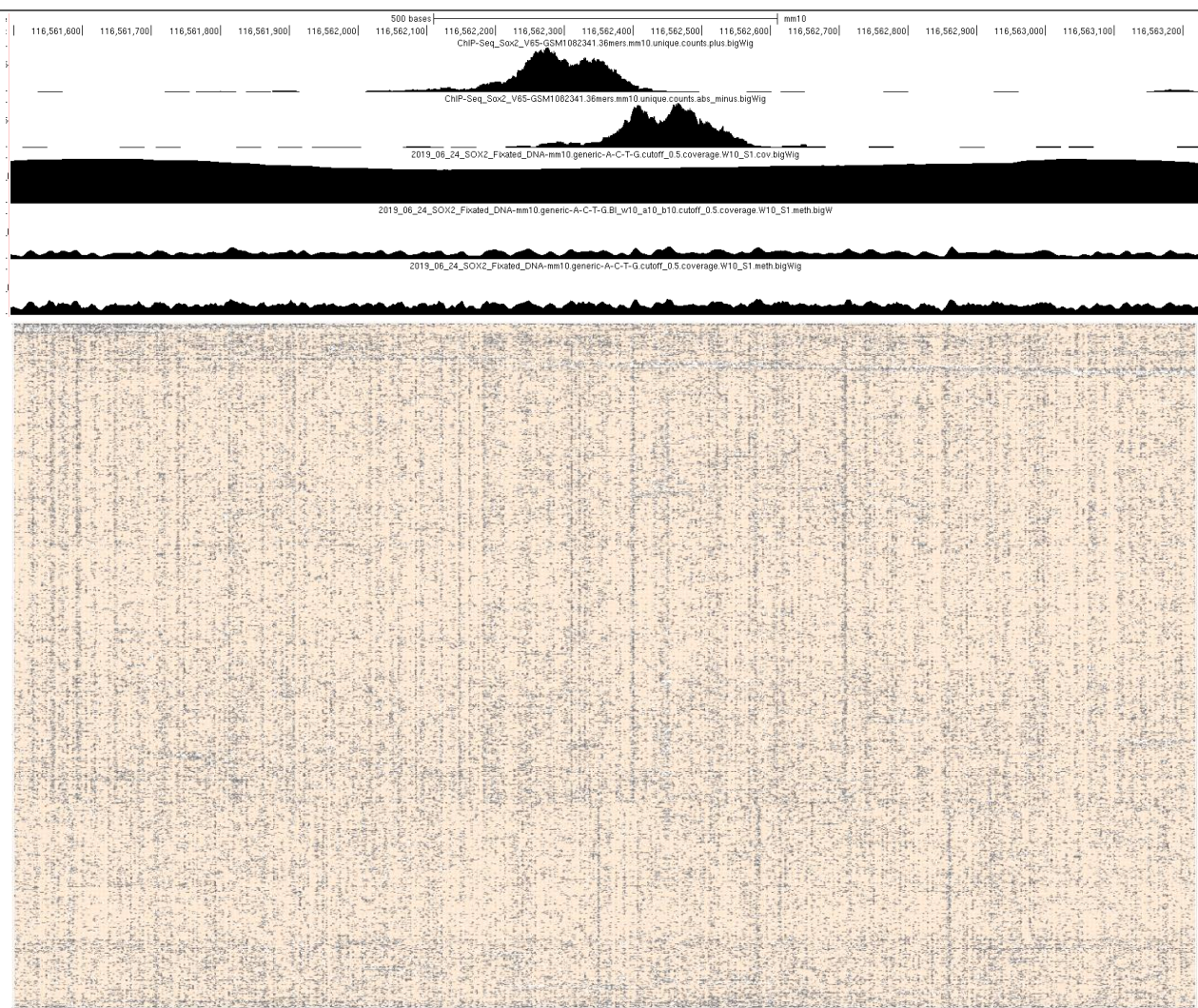


Single-molecule (1000  
reads subsample)  
 $p=0.1$  binarization

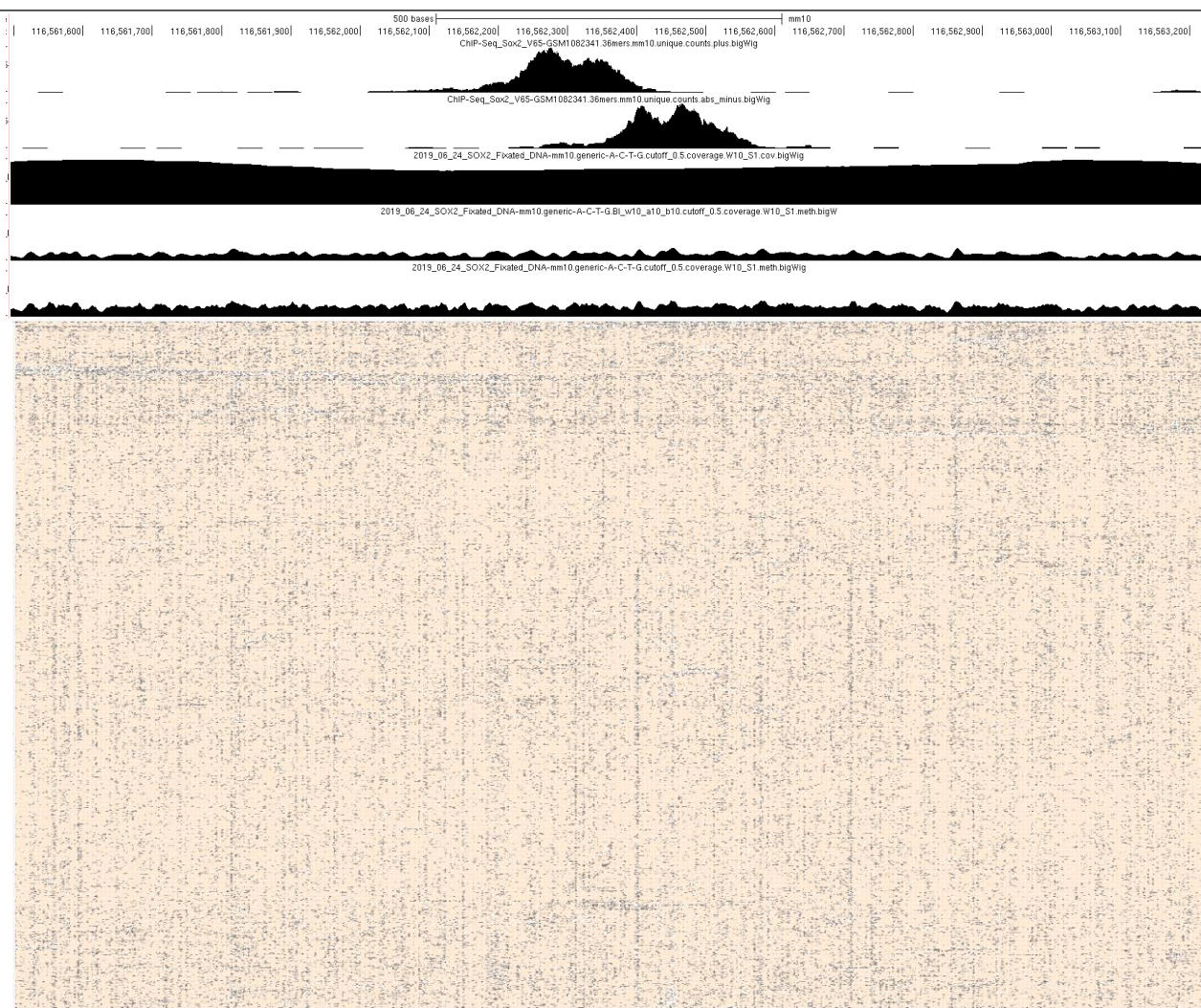




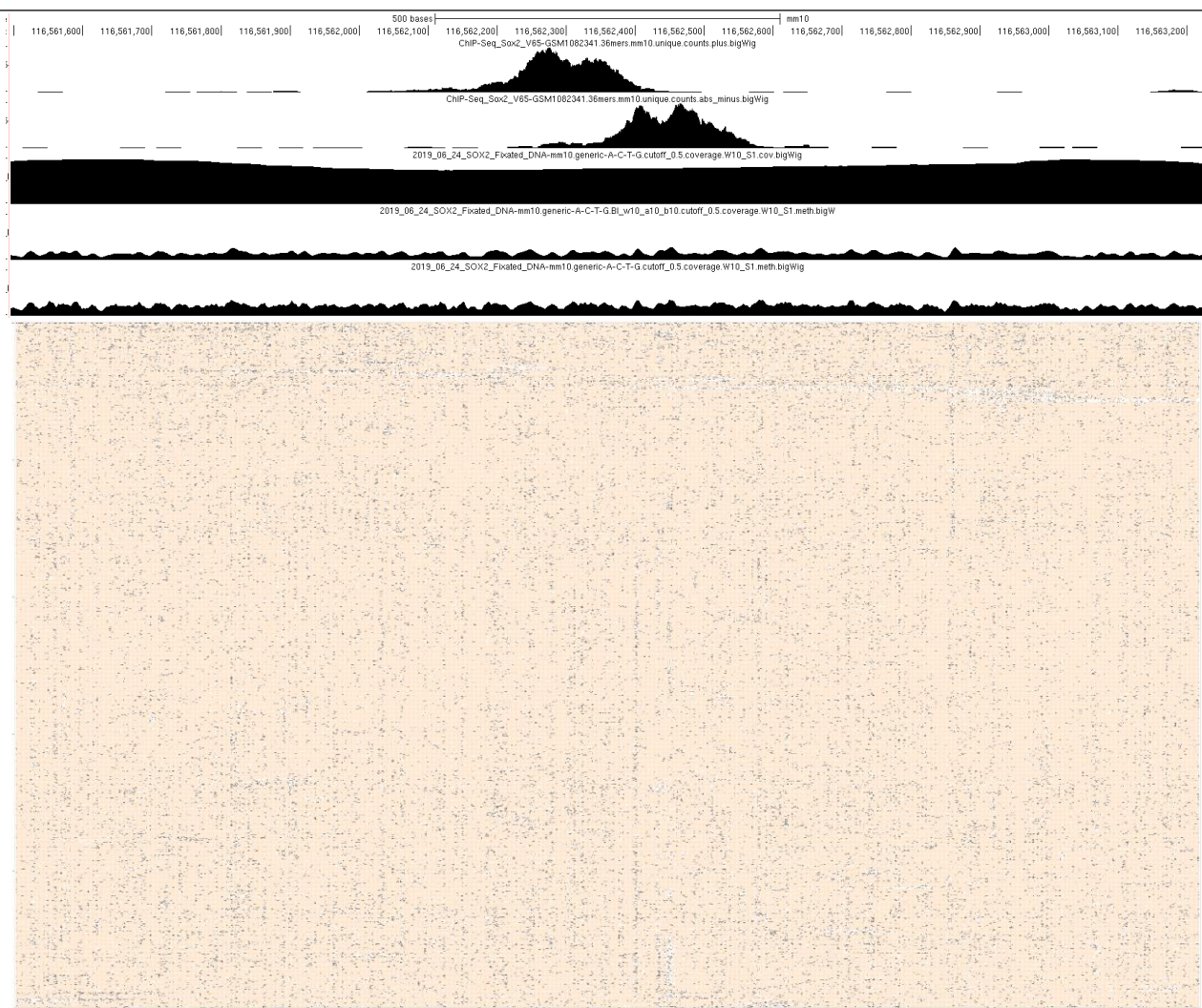
Single-molecule (1000  
reads subsample)  
 $p=0.5$  binarization

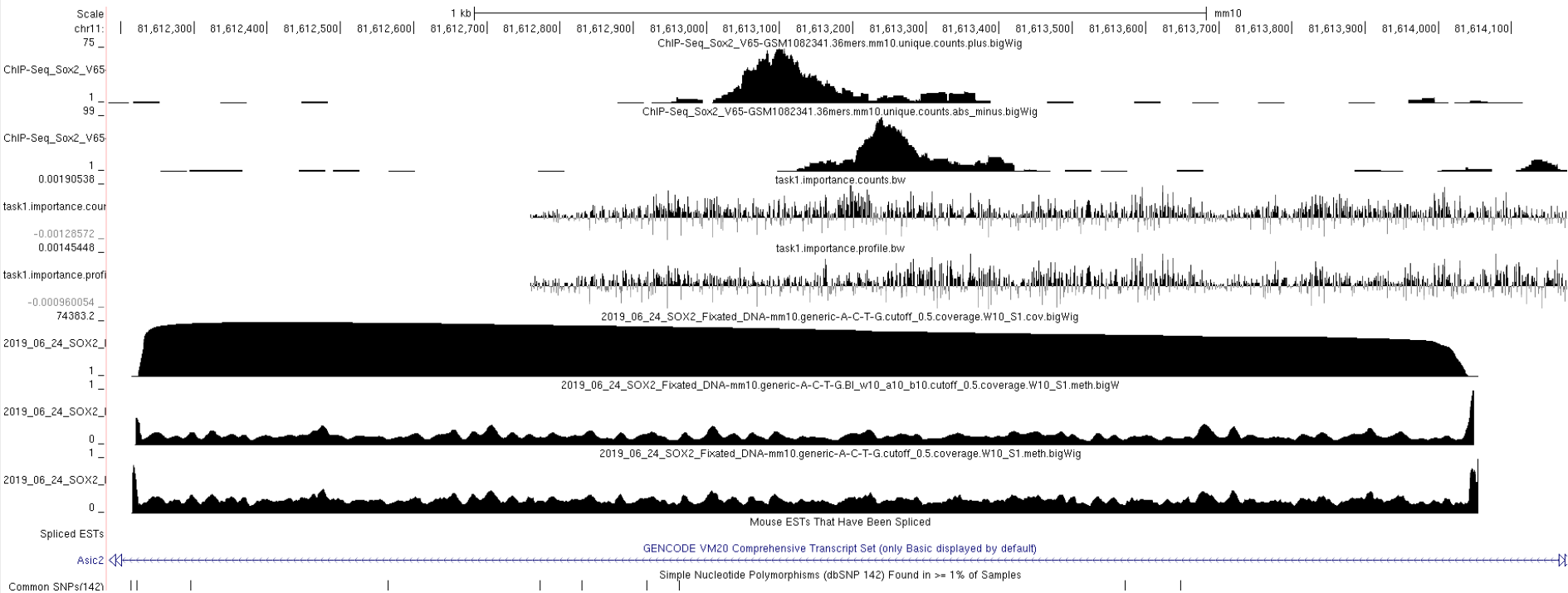


Single-molecule (1000  
reads subsample)  
 $p=0.3$  binarization

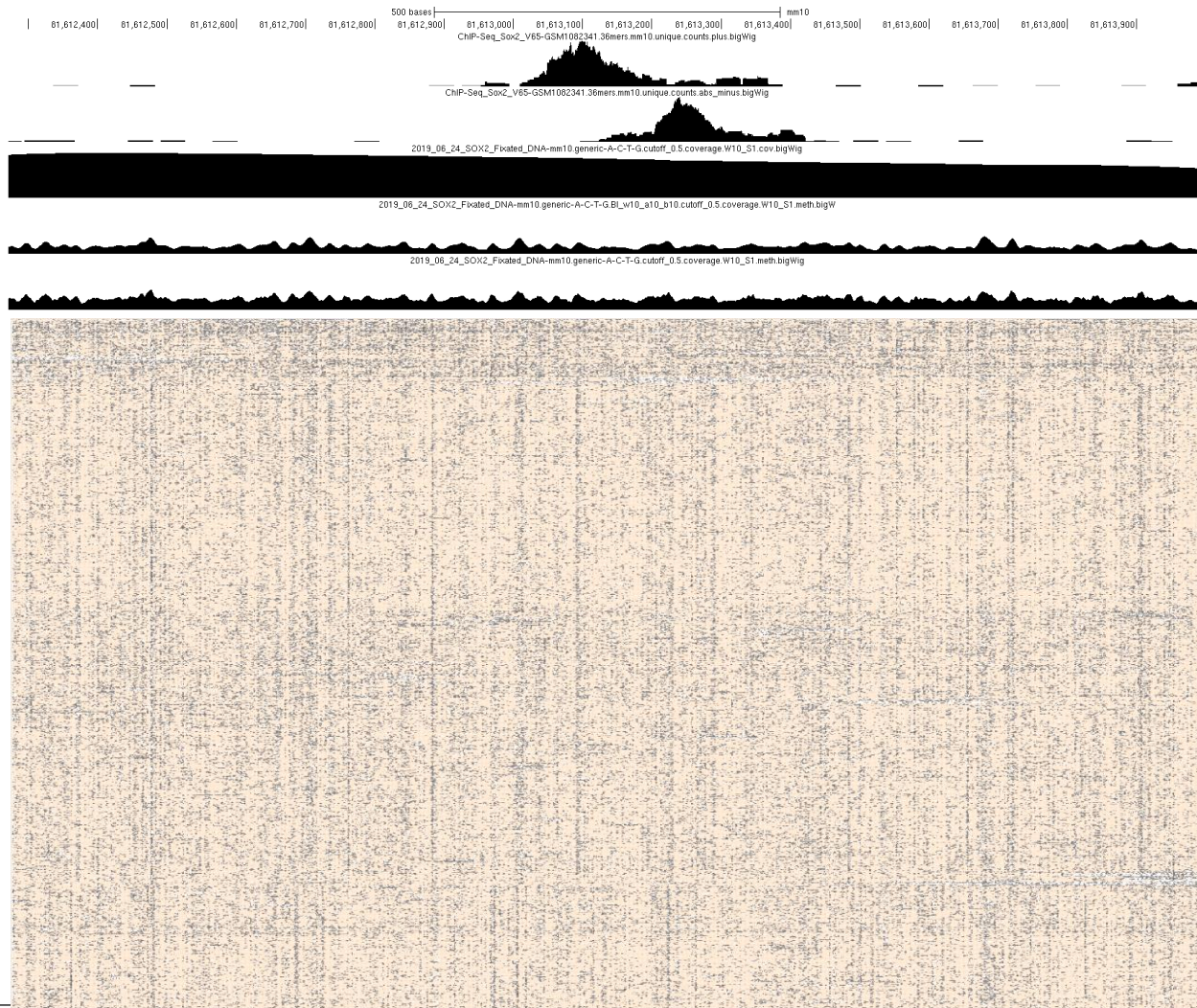


Single-molecule (1000  
reads subsample)  
 $p=0.1$  binarization





Single-molecule (1000  
reads subsample)  
 $p=0.5$  binarization





Single-molecule (1000  
reads subsample)  
 $p=0.5$  binarization

