Transcription factor modulation upon prostate cancer stimulus with KB698 Treatment

By Harrison E. Smith

QC

Downstream CHIP-seq data was processed through the Genialis platform

Collection title : Kronos_AR_&_FOXA1

Alignment : BWA ALN + batch mode on (Aquas parameters)

    Build : hg19
    Quality threshold : 5
    Seed length : 32
    (Default remaining settings)

Peak calling : MACS2 batch + batch mode on (Aquas parameters)

    Promoter regions Bed file : HG19_TSS_ALL_-1000_+1000.bed
    Use TagAlign files : Yes
    Quality filtering threshold : 30
    Background : Pooled Input
    (Default remaining settings)

QC

Alignment Quality

	FriP	Peak count	# Reads in promotors	Fraction reads in Promoters
Treat_FOXA1	0.17	50332	671070	0.044
Control_FOXA1	0.046	23062	725856	0.029
Treat_AR	0.14	46018	1925153	0.085
Control_AR	0.086	37057	1484441	0.06

	Total reads	Total mapped reads	% Mapped
Treat_FOXA1	39225299	34444571	87.81%
Control_FOXA1	45886429	43290108	94.34%
Treat_AR	48498882	45126663	93.05%
Control_AR	44073133	40871557	92.74%

Meme-CHIP motif discovery

Meme-CHIP was used to extract the motifs from the top 1000 peaks in each sample respectively

Narrow peak files were extracted and loaded on to Rstudio to sort and isolate the top 1000 peaks

The files were then converted into fasta files to use as the meme-chip input

```
$ bedtools getfasta [OPTIONS] -fi <input FASTA> -bed <BED/GFF/VCF>
```

Files were then uploaded to Meme-Chip with default parameters

Meme-CHIP motif discovery

Treated FOXA1 CHIP
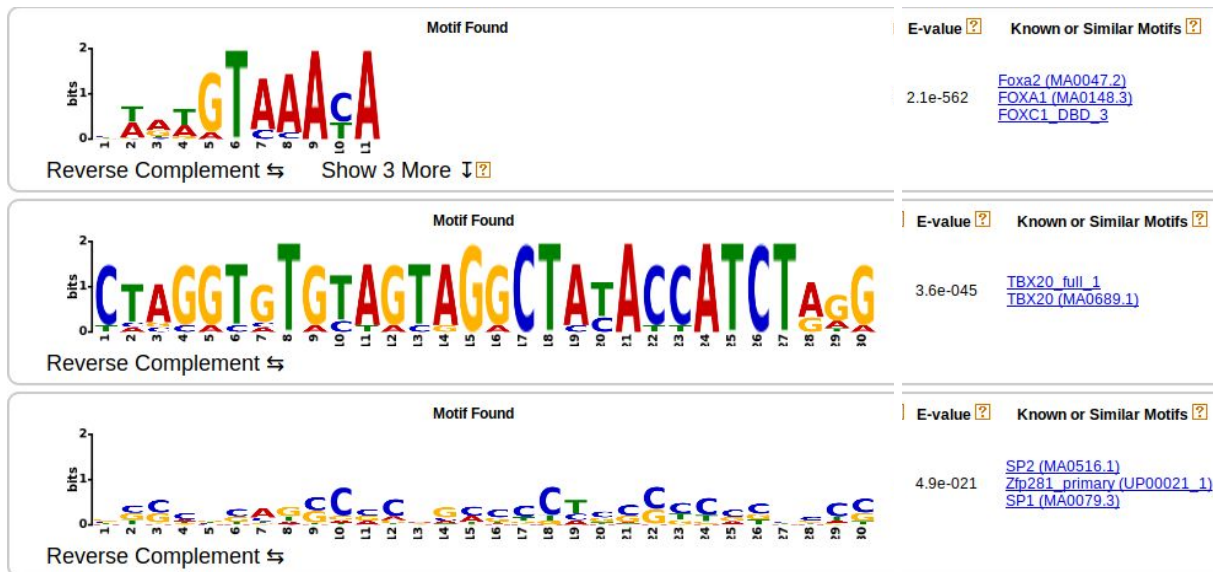
Meme-CHIP motif discovery

Control FOXA1 CHIP
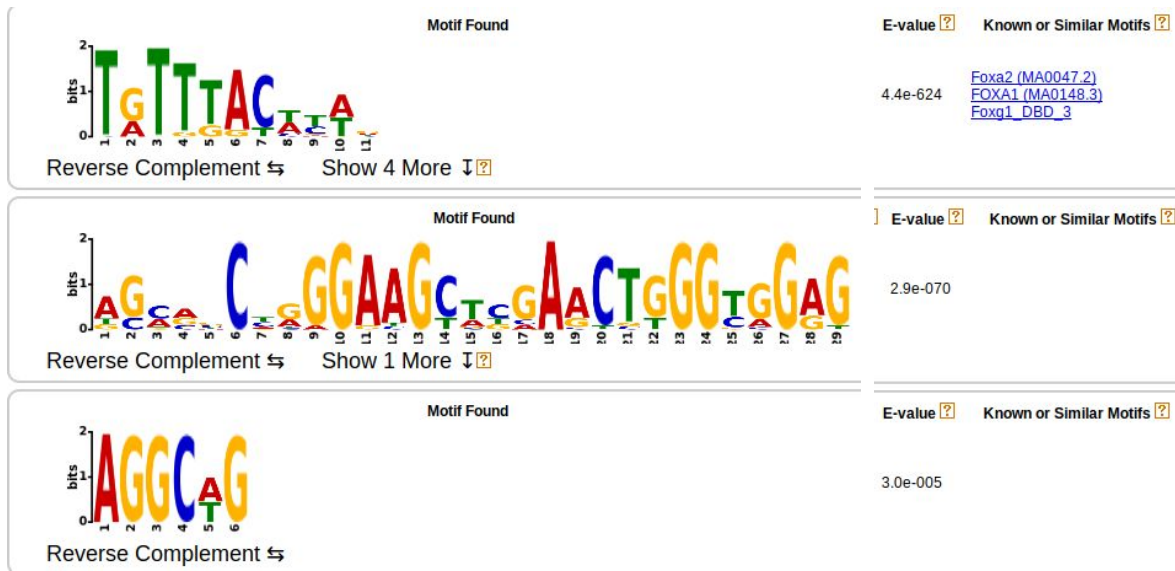
Meme-CHIP motif discovery

Treated AR CHIP
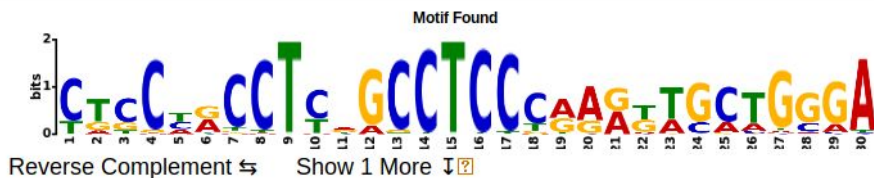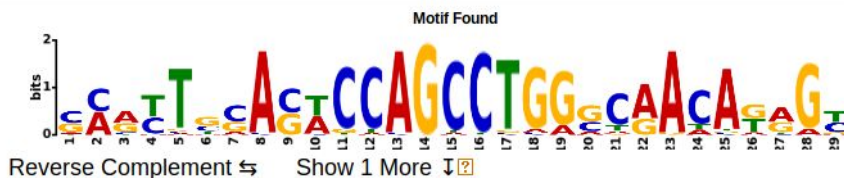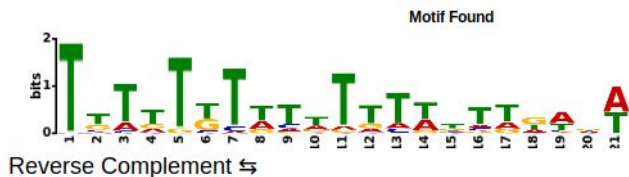
Meme-CHIP motif discovery

Control AR CHIP
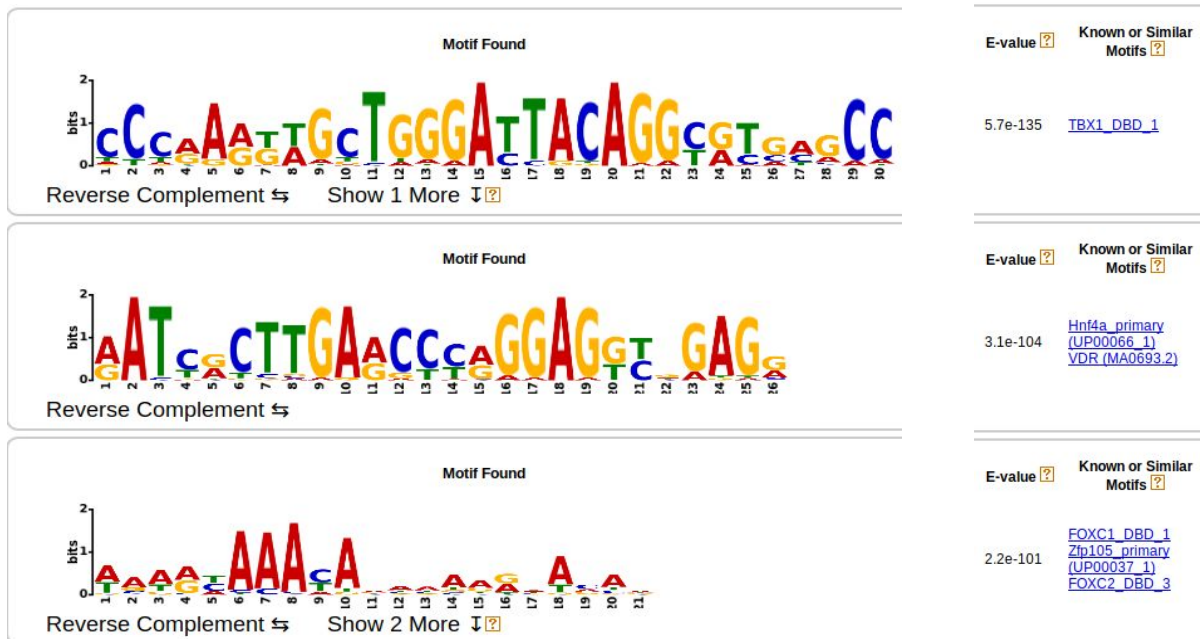
Bam Plots   SOD1
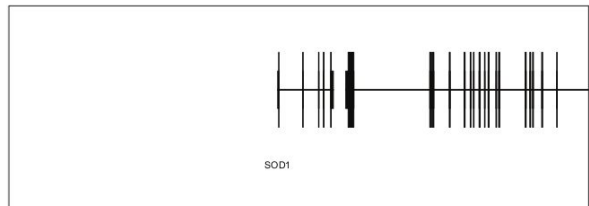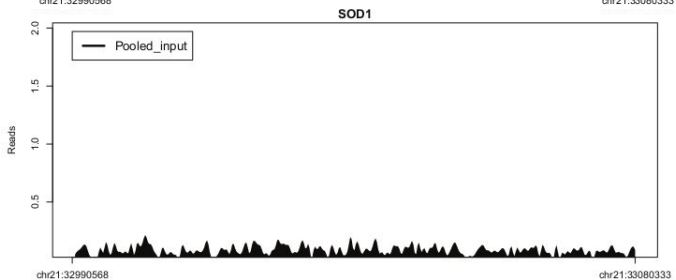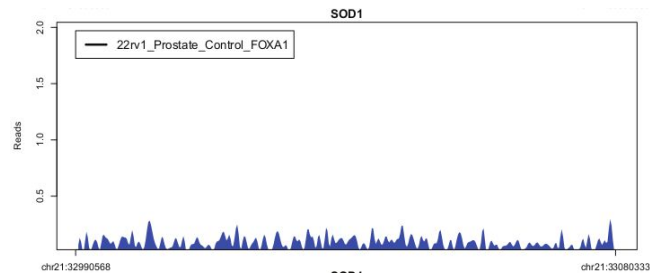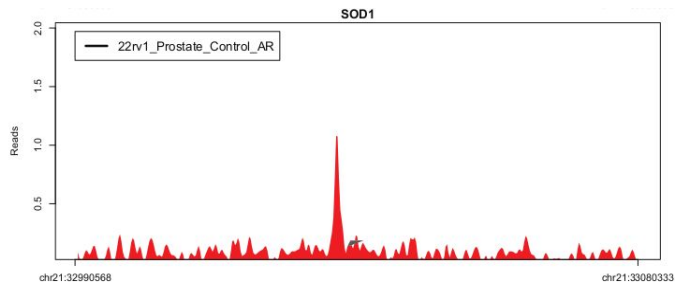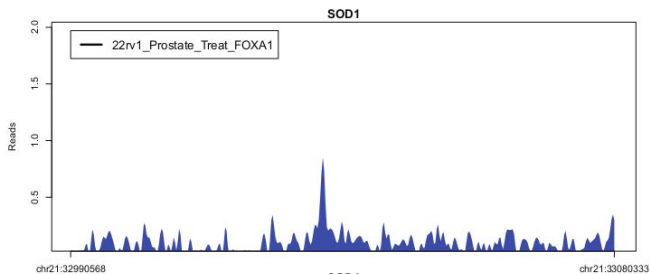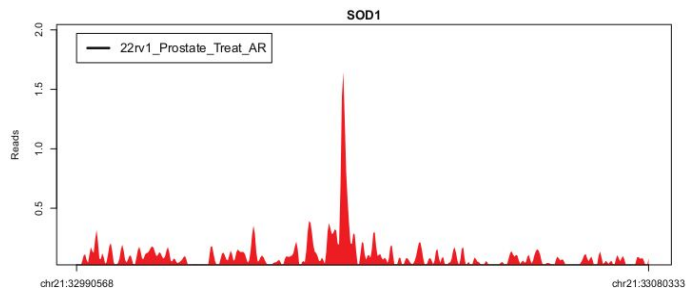
Bam Plots   FOXA1
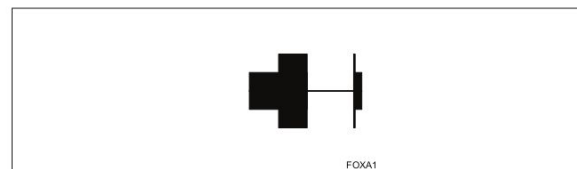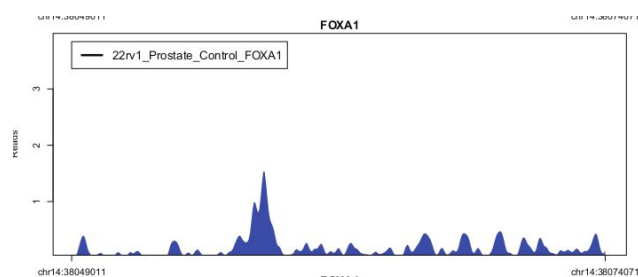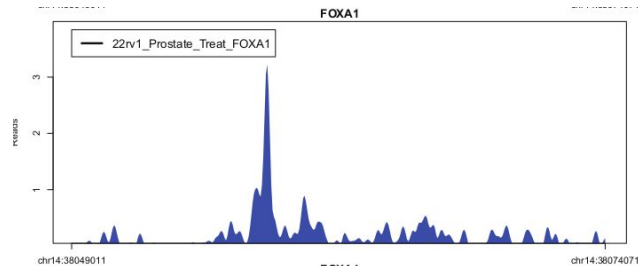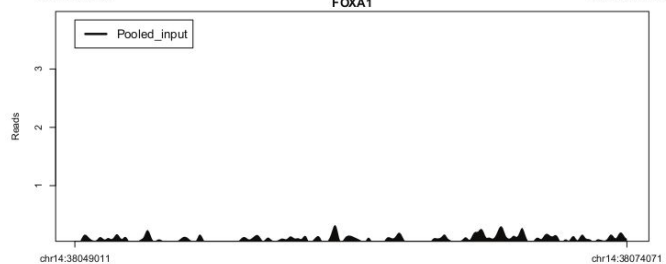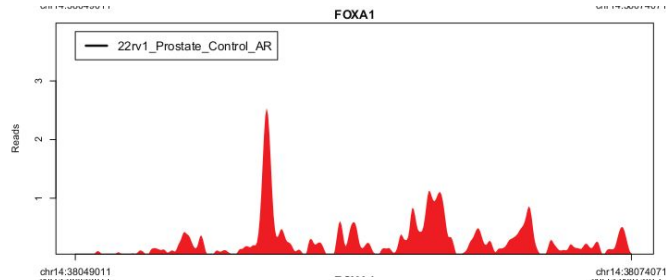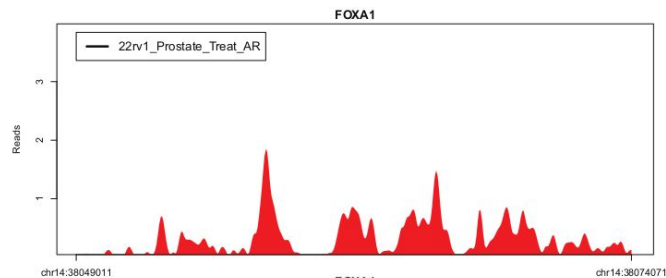
Bam Plots   TP53
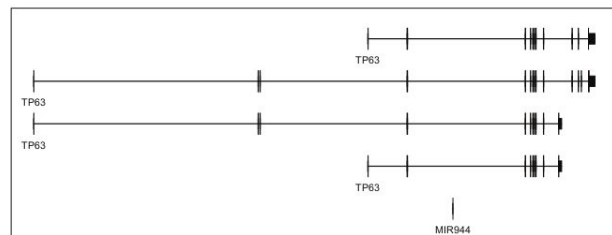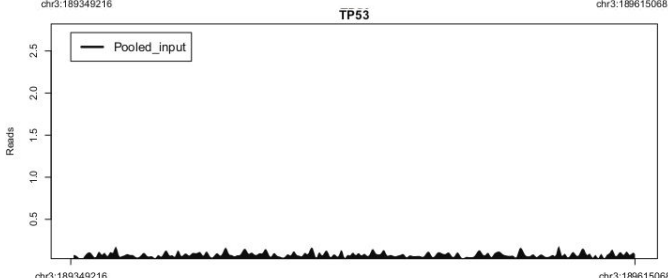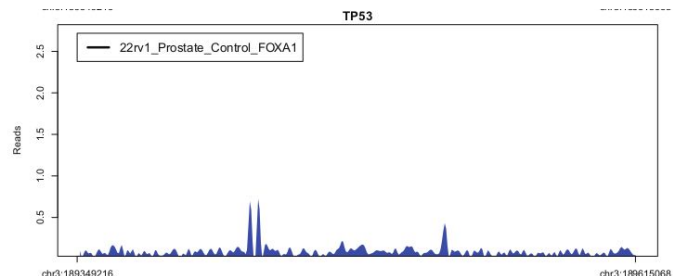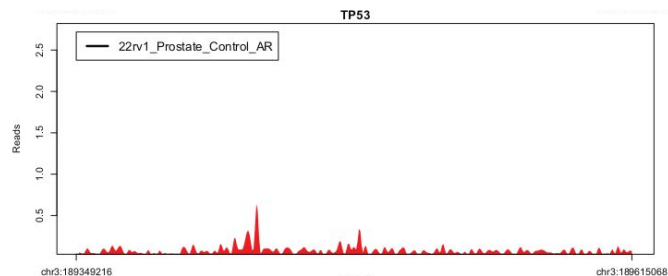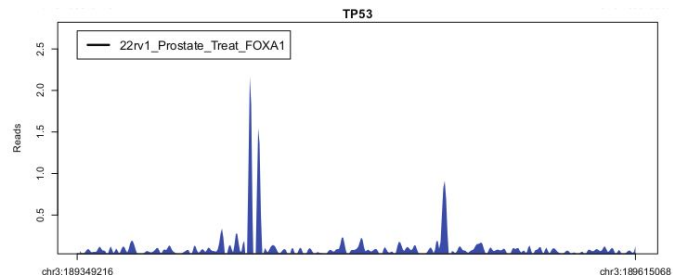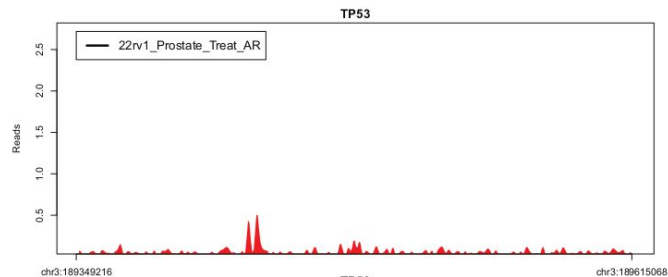
Bam Plots   MYC
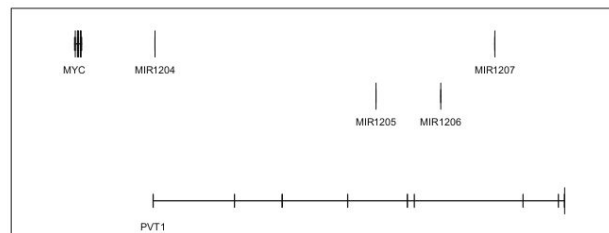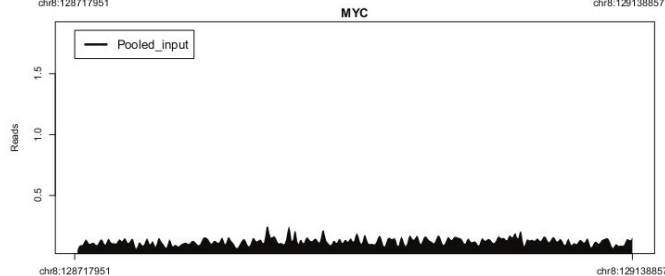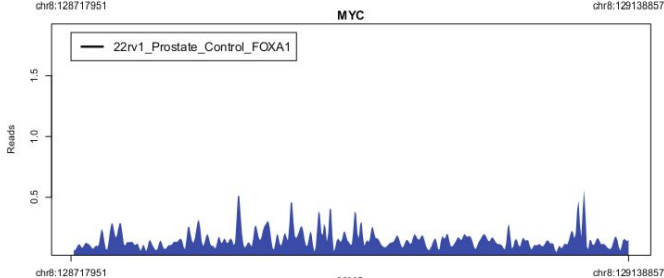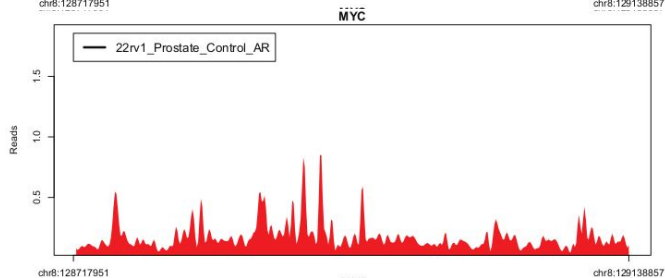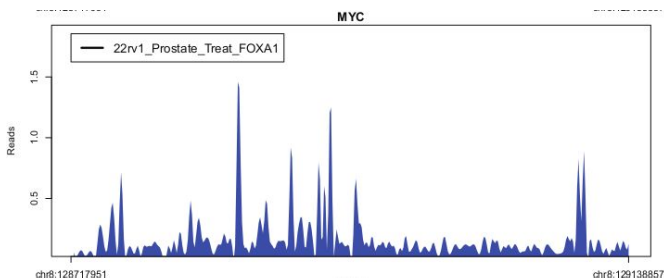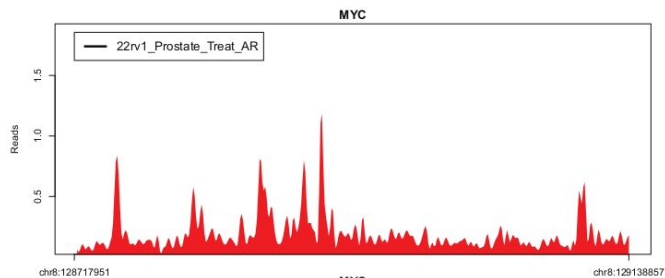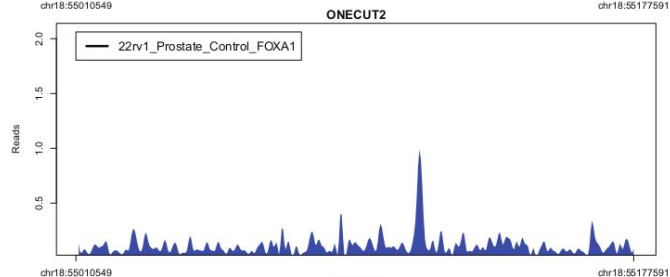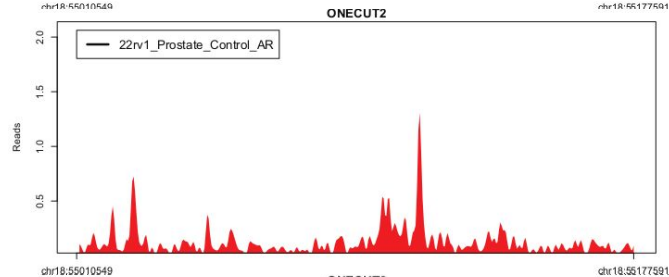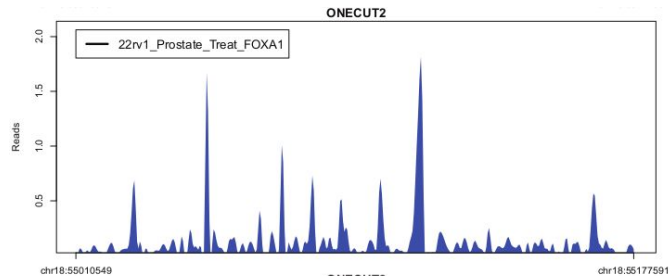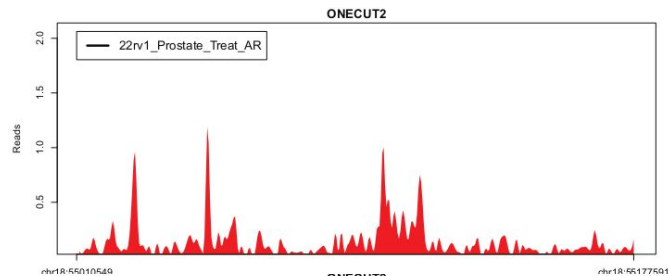
Bam Plots   TMPRSS2
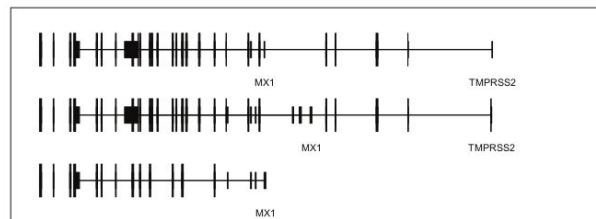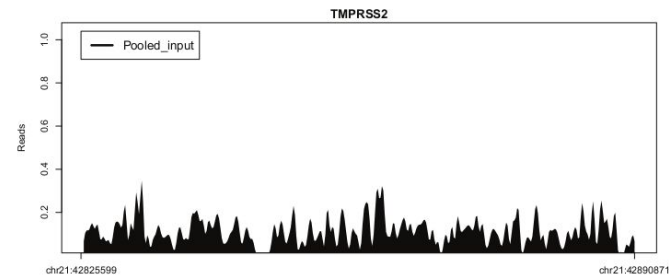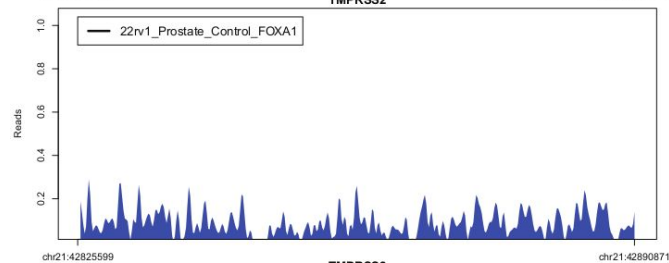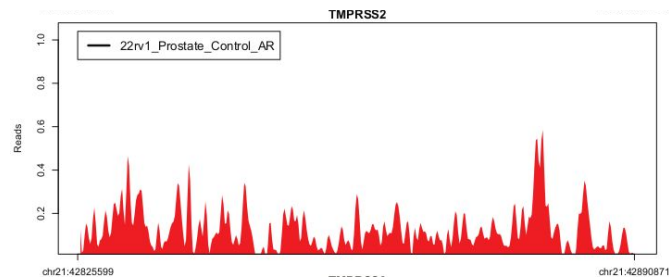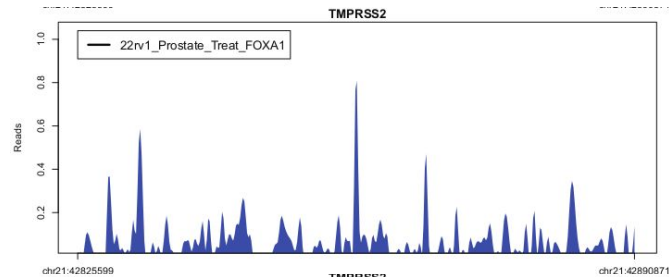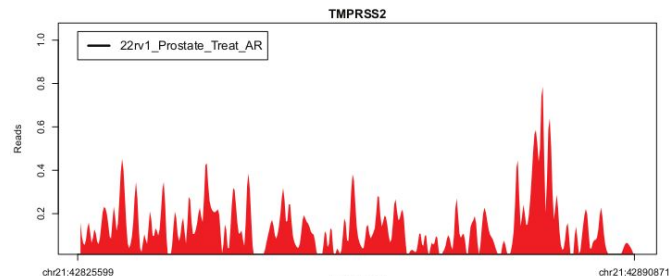
Bam Plots ONECUT2
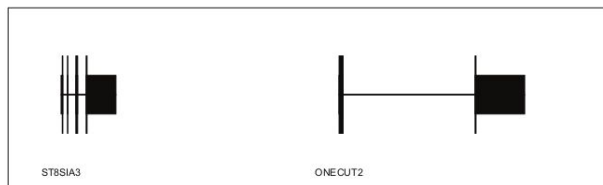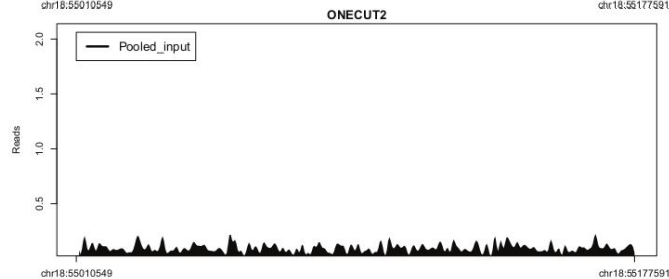
UCSC Genome Browser (link)

http://torta.bcmt.bcm.edu/cgi-bin/hgTracks?db=hg19&lastVirtModeType=default&lastVirtModeExtraState=&virtModeType=default&virtMode=0&nonVirtPosition=&position=chr21%3A32990568%2D33080333&hgsid=644_VmV8XA3tCsxG8S34EeGjTa8Dv731