

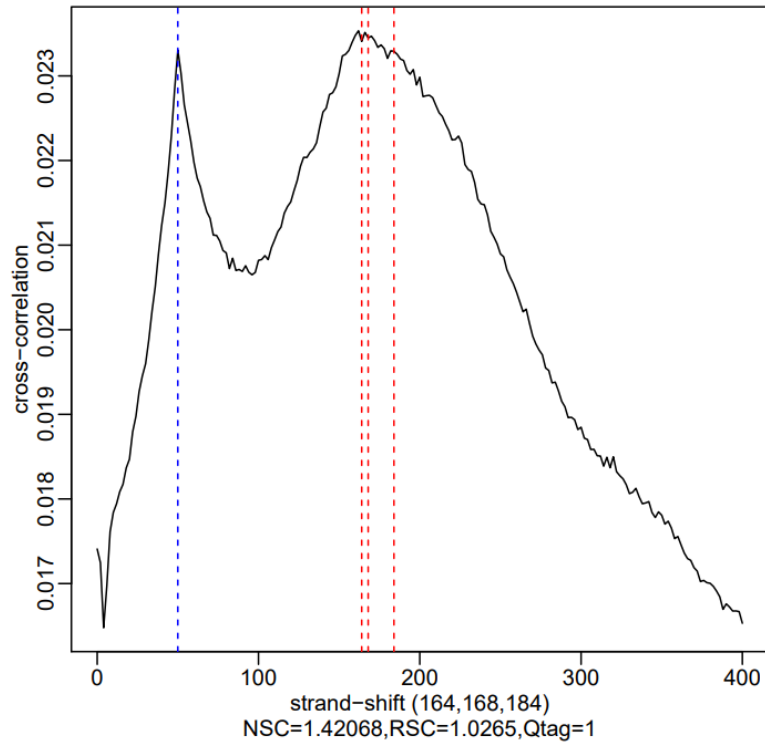
Dataset stats

Species	#	Read Length	Raw fragments	Unique	Complexity	MACS2 NumPeaks	MACS2 RPM	MACS2 PseudoRep NumPeaks	MACS2 RPM	NSC	RSC	QC
hg38_no_haps	Control_4_FGFR1_GSM2439179	1x50	36,740,346	29,580,521	0.55	28,791	79,988			1.421	1.027	1
hg38_no_haps	Control_4_input-GSM2439178	1x50	33,997,437	28,653,506	0.98					1.163	0.469	-1
hg38_no_haps	Patient_3_FGFR1_GSM2439181	1x50	33,294,331	24,257,330	0.37	45,814	244,833			1.508	2.687	2
hg38_no_haps	Patient_3_NOTCH-GSM2439182	1x50	24,586,311	28,803,228	0.17	31,943	145,485			3.570	6.144	2
hg38_no_haps	Patient_3_input-GSM2439180	1x50	34,700,795	20,740,325	0.98					1.142	0.305	-1
chrM	Control_4_FGFR1_GSM2439179	1x50	36,740,346	624,038	0.04							
chrM	Control_4_input-GSM2439178	1x50	33,997,437	159,490	0.18							
chrM	Patient_3_FGFR1_GSM2439181	1x50	33,294,331	123,458	0.16							
chrM	Patient_3_NOTCH-GSM2439182	1x50	24,586,311	57,429	0.13							
chrM	Patient_3_input-GSM2439180	1x50	34,700,795	125,139	0.23							

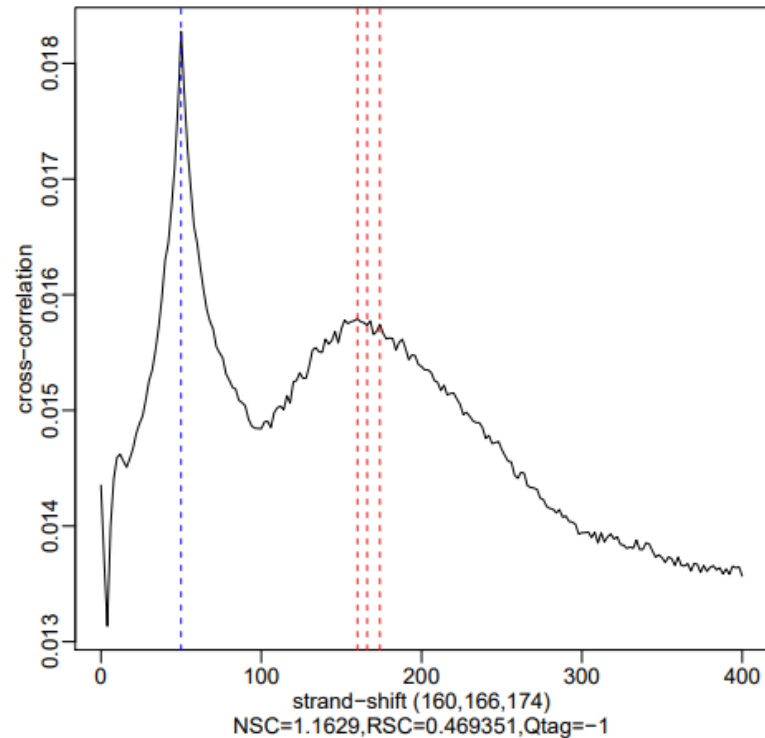
Aligned against the genome as well as against chrM alone
(due to NUMTs, some of chrM is not uniquely mappable)

Cross-correlation QC

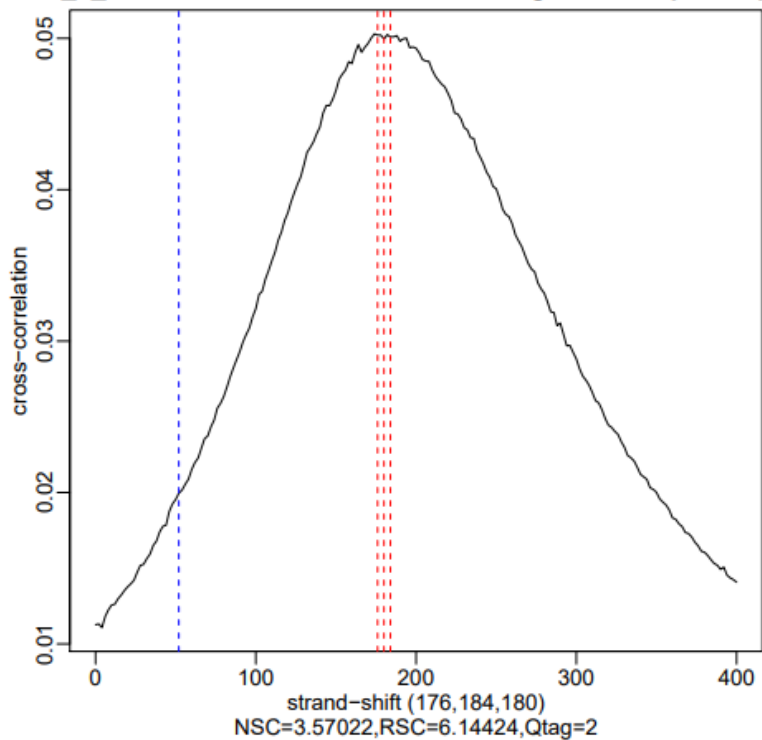
Control_4_FGFR1_GSM2439179.1x50mers.hg38-no-haps.uniq



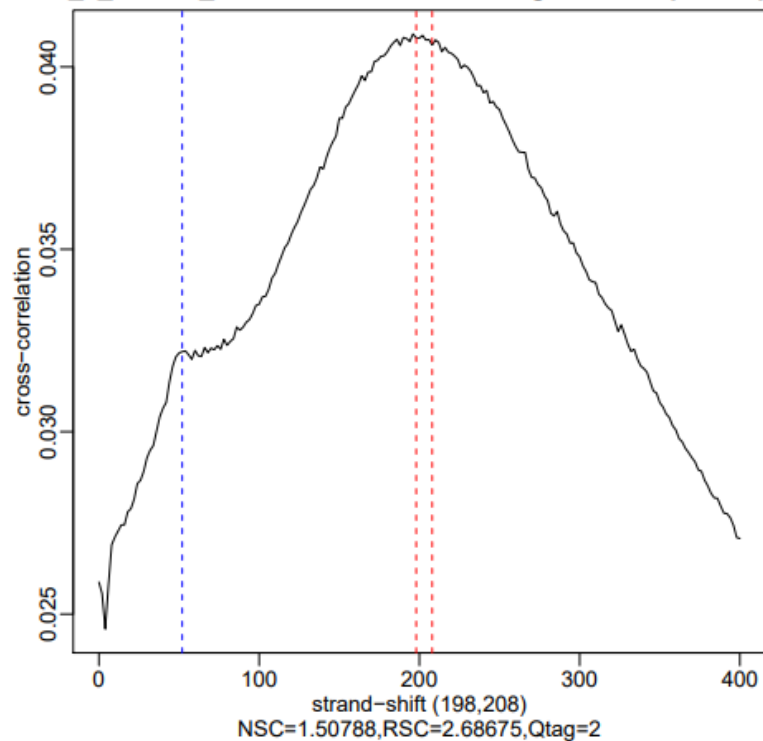
Control_4_input-GSM2439178.1x50mers.hg38-no-haps.uniq



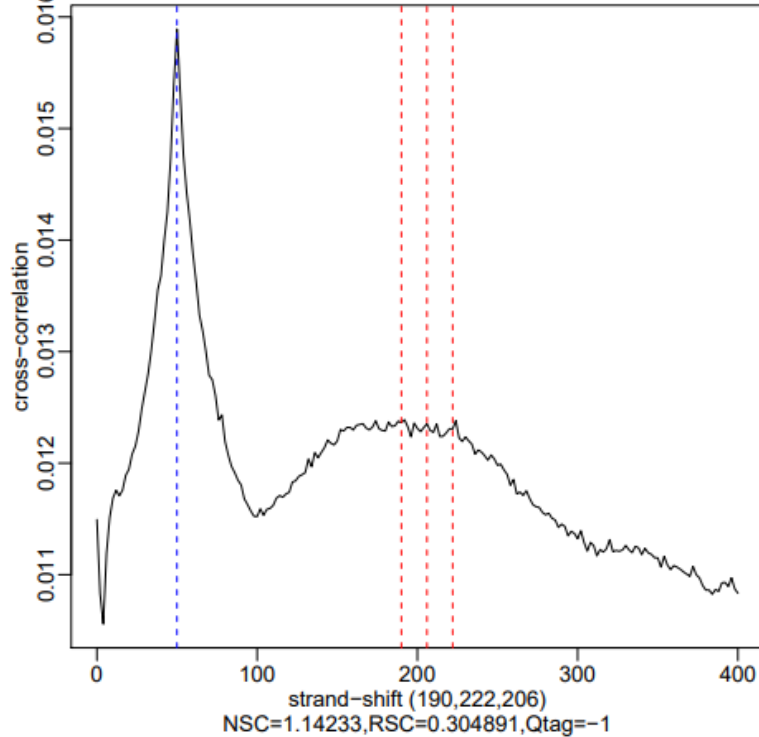
Patient_3_NOTCH-GSM2439182.1x50mers.hg38-no-haps.uniq



Patient_3_FGFR1_GSM2439181.1x50mers.hg38-no-haps.uniq



Patient_3_input-GSM2439180.1x50mers.hg38-no-haps.unique



This is basic QC to make sure the ChIP shows good enrichment overall

It does

Peak overlap

#DataSet:

	Region	Control_4_FGFR1_GSM2439179	Patient_3_FGFR1_GSM2439181	Patient_3_NOTCH-GSM2439182
Control_4_FGFR1_GSM2439179	28791	1.00	0.79	0.62
Patient_3_FGFR1_GSM2439181	45814	0.43	1.00	0.46
Patient_3_NOTCH-GSM2439182	31943	0.58	0.75	1.00

chrM

5 kb | hg38
500| 1,000| 1,500| 2,000| 2,500| 3,000| 3,500| 4,000| 4,500| 5,000| 5,500| 6,000| 6,500| 7,000| 7,500| 8,000| 8,500| 9,000| 9,500| 10,000| 10,500| 11,000| 11,500| 12,000| 12,500| 13,000| 13,500| 14,000| 14,500| 15,000| 15,500| 16,000| 16,500
Control_4_FGFR1_GSM2439179.1x50mers.chrM.unique.RPM.bigWig



Control_4_input-GSM2439178.1x50mers.chrM.unique.RPM.bigWig



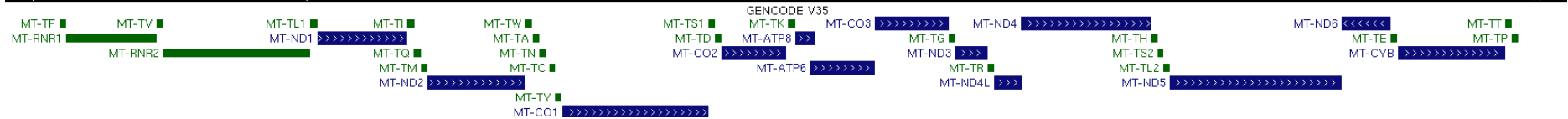
Patient_3_FGFR1_GSM2439181.1x50mers.chrM.unique.RPM.bigWig



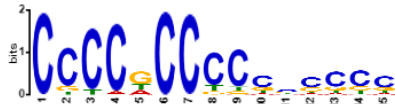
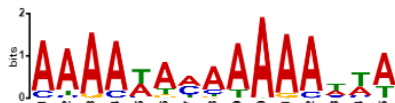



Patient_3_input-GSM2439180.1x50mers.chrM.unique.RPM.bigWig





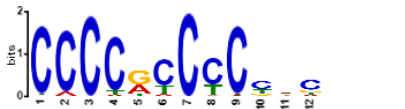
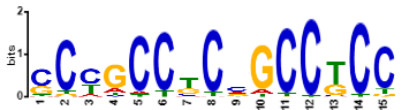

Patient_3_NOTCH-GSM2439182.1x50mers.chrM.unique.RPM.bigWig






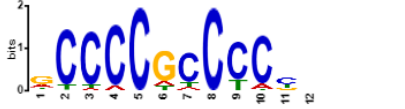

MEME-ChIP, Control FGFR1

<p>Motif Found</p>  <p>Reverse Complement ⇄ Show 6 More ⓘ</p>	<p>Discovery/Enrichment Program ⓘ</p> <p>MEME</p>	<p>E-value ⓘ</p> <p>3.3e-089</p> <p>Known or Similar Motifs ⓘ</p> <p>SP2 (MA0516.1) Zfp281_primary (UP00021_1) SP1 (MA0079.3)</p>	<p>Distribution ⓘ</p> <p>Not Centrally Enriched</p>	<p>SpaMo & FIMO ⓘ</p> <ul style="list-style-type: none"> Motif Spacing Analysis Motif Sites in GFF3
<p>Motif Found</p>  <p>Reverse Complement ⇄ Show 4 More ⓘ</p>	<p>Discovery/Enrichment Program ⓘ</p> <p>MEME</p>	<p>E-value ⓘ</p> <p>8.3e-051</p> <p>Known or Similar Motifs ⓘ</p> <p>Srf_secondary (UP00077_2) ZNF384 (MA1125.1) CPEB1_full</p>	<p>Distribution ⓘ</p> <p>Not Centrally Enriched</p>	<p>SpaMo & FIMO ⓘ</p> <ul style="list-style-type: none"> Motif Spacing Analysis Motif Sites in GFF3
<p>Motif Found</p>  <p>Reverse Complement ⇄ Show 1 More ⓘ</p>	<p>Discovery/Enrichment Program ⓘ</p> <p>MEME</p>	<p>E-value ⓘ</p> <p>4.7e-030</p> <p>Known or Similar Motifs ⓘ</p>	<p>Distribution ⓘ</p> <p>Not Centrally Enriched</p>	<p>SpaMo & FIMO ⓘ</p> <ul style="list-style-type: none"> Motif Spacing Analysis Motif Sites in GFF3
<p>Motif Found</p>  <p>Reverse Complement ⇄</p>	<p>Discovery/Enrichment Program ⓘ</p> <p>STREME</p>	<p>E-value ⓘ</p> <p>6.7e-014</p> <p>Known or Similar Motifs ⓘ</p> <p>CTCF (MA0139.1) CTCF_full CTCF_L (MA1102.1)</p>	<p>Distribution ⓘ</p> <p>Not Centrally Enriched</p>	<p>SpaMo & FIMO ⓘ</p> <ul style="list-style-type: none"> Motif Spacing Analysis Motif Sites in GFF3
<p>Motif Found</p>  <p>Reverse Complement ⇄ Show 1 More ⓘ</p>	<p>Discovery/Enrichment Program ⓘ</p> <p>STREME</p>	<p>E-value ⓘ</p> <p>2.2e-011</p> <p>Known or Similar Motifs ⓘ</p> <p>ELK1_DBD_2 ELK1 (MA0028.2) ETV3_DBD</p>	<p>Distribution ⓘ</p> <p>Not Centrally Enriched</p>	<p>SpaMo & FIMO ⓘ</p> <ul style="list-style-type: none"> Motif Spacing Analysis Motif Sites in GFF3

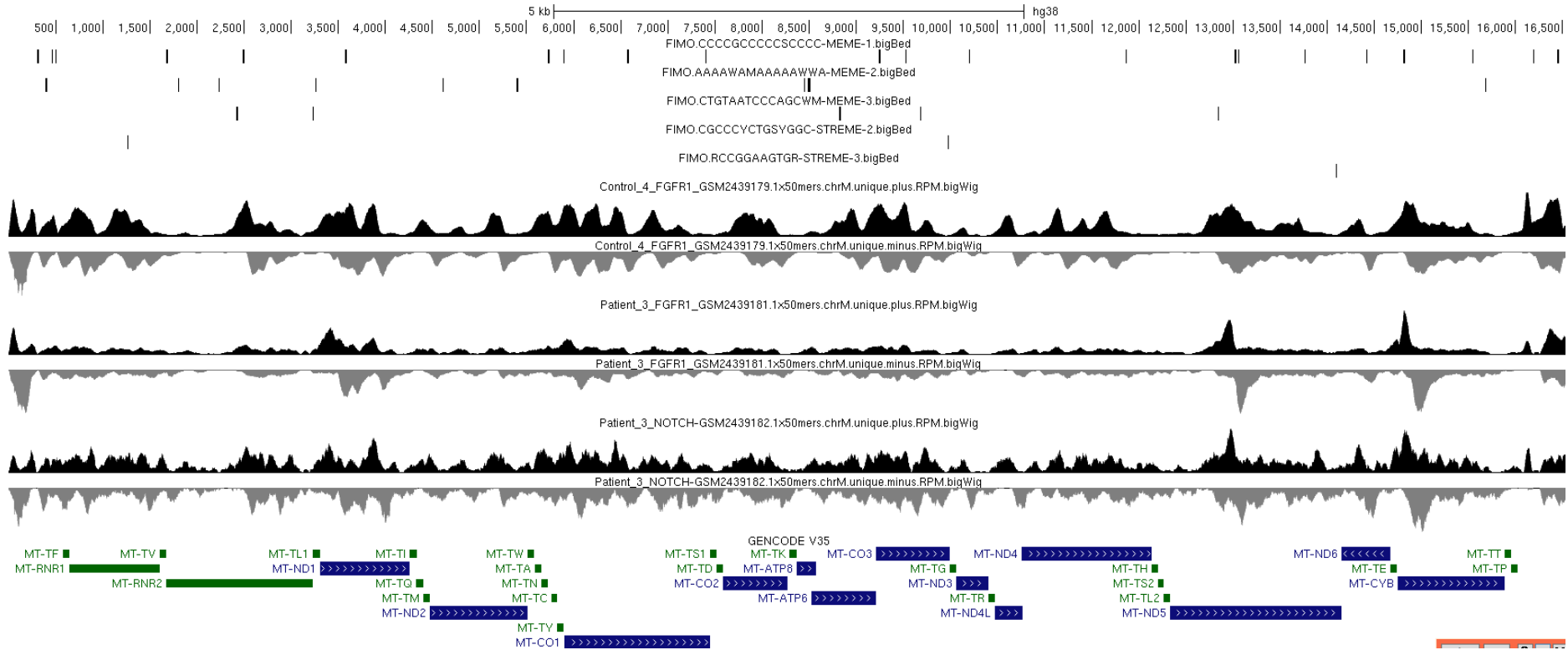
MEME-ChIP, Patient FFGFR1

Motif Found	Discovery/Enrichment Program	E-value	Known or Similar Motifs	Distribution	SpaMo & FIMO
 <p>Reverse Complement ⇄ Show 1 More ↓</p>	MEME	5.7e-111	ONECUT3_DBD ONECUT3 (MA0757.1) ONECUT1_DBD	Not Centrally Enriched	<ul style="list-style-type: none"> Motif Spacing Analysis Motif Sites in GFF3
 <p>Reverse Complement ⇄ Show 1 More ↓</p>	MEME	2.2e-082		Not Centrally Enriched	<ul style="list-style-type: none"> Motif Spacing Analysis Motif Sites in GFF3
 <p>Reverse Complement ⇄ Show 2 More ↓</p>	STREME	6.1e-063	SP1 (MA0079.3) SP2 (MA0516.1) SP1_DBD	Not Centrally Enriched	<ul style="list-style-type: none"> Motif Spacing Analysis Motif Sites in GFF3
 <p>Reverse Complement ⇄ Show 3 More ↓</p>	MEME	1.7e-048	ZNF263 (MA0528.1) Zfx (MA0146.2) ETV6_full_1	Not Centrally Enriched	<ul style="list-style-type: none"> Motif Spacing Analysis Motif Sites in GFF3
 <p>Reverse Complement ⇄</p>	STREME	7.0e-033		Not Centrally Enriched	<ul style="list-style-type: none"> Motif Spacing Analysis Motif Sites in GFF3

MEME-CHIP, Patient NOTCH

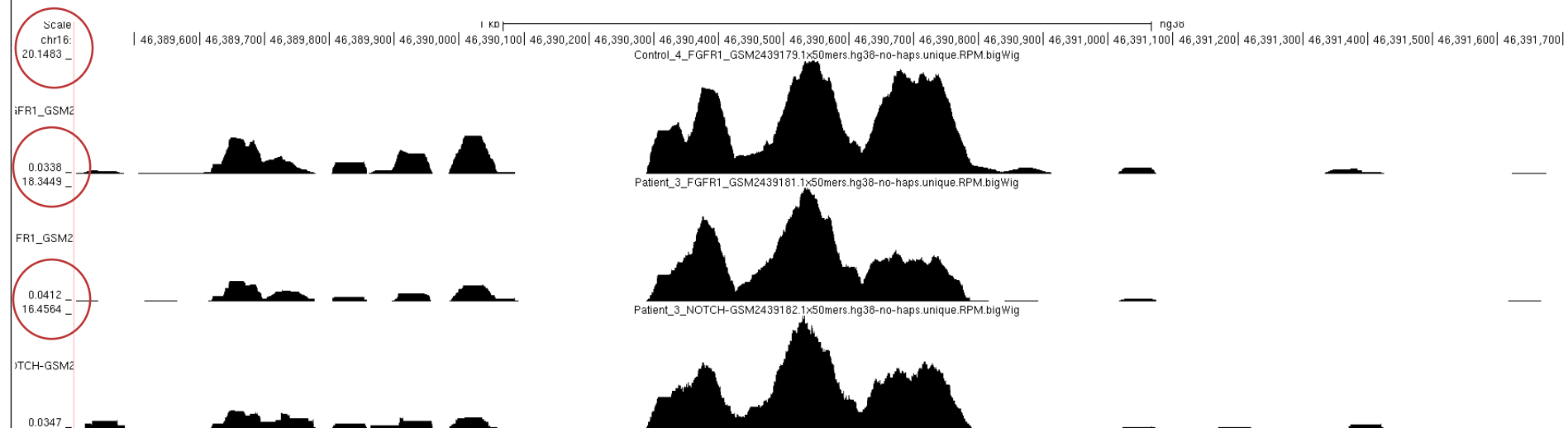
<p>Motif Found</p>  <p>Reverse Complement ⇄ Show 3 More ↗</p>	<p>Discovery/Enrichment Program ?</p> <p>MEME</p>	<p>E-value ?</p> <p>8.7e-081</p>	<p>Known or Similar Motifs ?</p> <p>ZNF384 (MA1125.1)</p>	<p>Distribution ?</p> <p>Not Centrally Enriched</p>	<p>SpaMo & FIMO ?</p> <ul style="list-style-type: none"> Motif Spacing Analysis Motif Sites in GFF3
<p>Motif Found</p>  <p>Reverse Complement ⇄ Show 1 More ↗</p>	<p>Discovery/Enrichment Program ?</p> <p>MEME</p>	<p>E-value ?</p> <p>2.3e-057</p>	<p>Known or Similar Motifs ?</p>	<p>Distribution ?</p> <p>Not Centrally Enriched</p>	<p>SpaMo & FIMO ?</p> <ul style="list-style-type: none"> Motif Spacing Analysis Motif Sites in GFF3
<p>Motif Found</p>  <p>Reverse Complement ⇄ Show 5 More ↗</p>	<p>Discovery/Enrichment Program ?</p> <p>MEME</p>	<p>E-value ?</p> <p>5.5e-041</p>	<p>Known or Similar Motifs ?</p> <p>KLF4 (MA0039.3)</p>	<p>Distribution ?</p> <p>Not Centrally Enriched</p>	<p>SpaMo & FIMO ?</p> <ul style="list-style-type: none"> Motif Spacing Analysis Motif Sites in GFF3
<p>Motif Found</p>  <p>Reverse Complement ⇄ Show 2 More ↗</p>	<p>Discovery/Enrichment Program ?</p> <p>STREME</p>	<p>E-value ?</p> <p>8.1e-037</p>	<p>Known or Similar Motifs ?</p> <p>SPI (MA0079.3) SPI_DB KLF16 (MA0741.1)</p>	<p>Distribution ?</p> <p>Not Centrally Enriched</p>	<p>SpaMo & FIMO ?</p> <ul style="list-style-type: none"> Motif Spacing Analysis Motif Sites in GFF3
<p>Motif Found</p>  <p>Reverse Complement ⇄</p>	<p>Discovery/Enrichment Program ?</p> <p>STREME</p>	<p>E-value ?</p> <p>2.4e-020</p>	<p>Known or Similar Motifs ?</p>	<p>Distribution ?</p> <p>Not Centrally Enriched</p>	<p>SpaMo & FIMO ?</p> <ul style="list-style-type: none"> Motif Spacing Analysis Motif Sites in GFF3

peaks and motifs

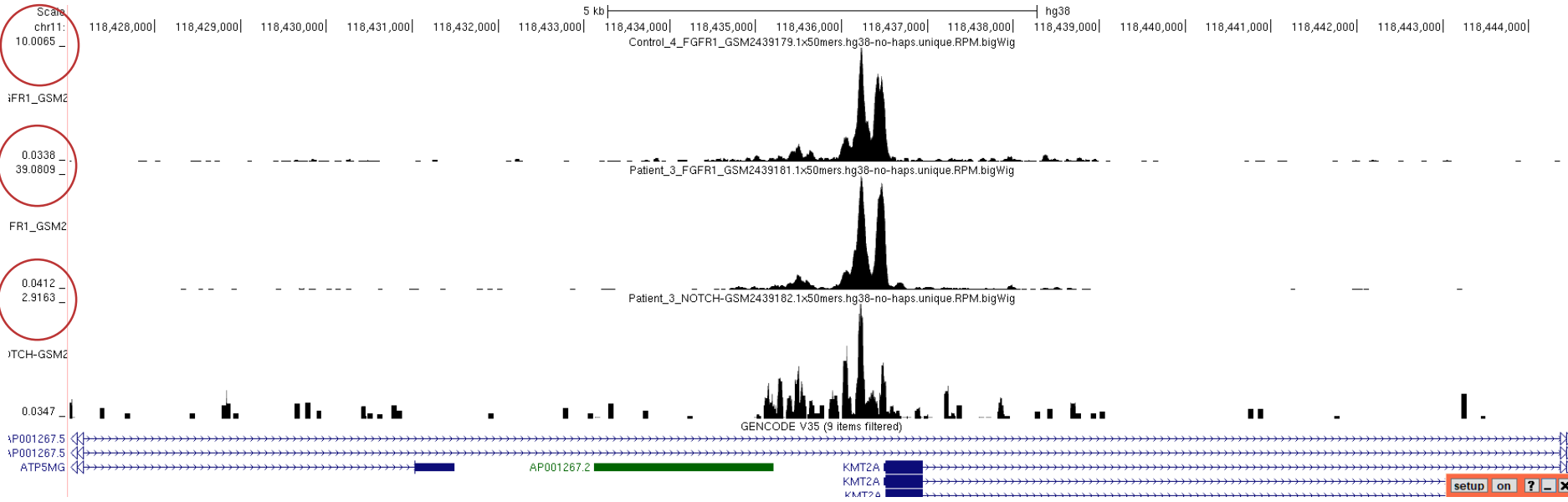


The top motif is seen in quite a few of the peaks, but not all of them

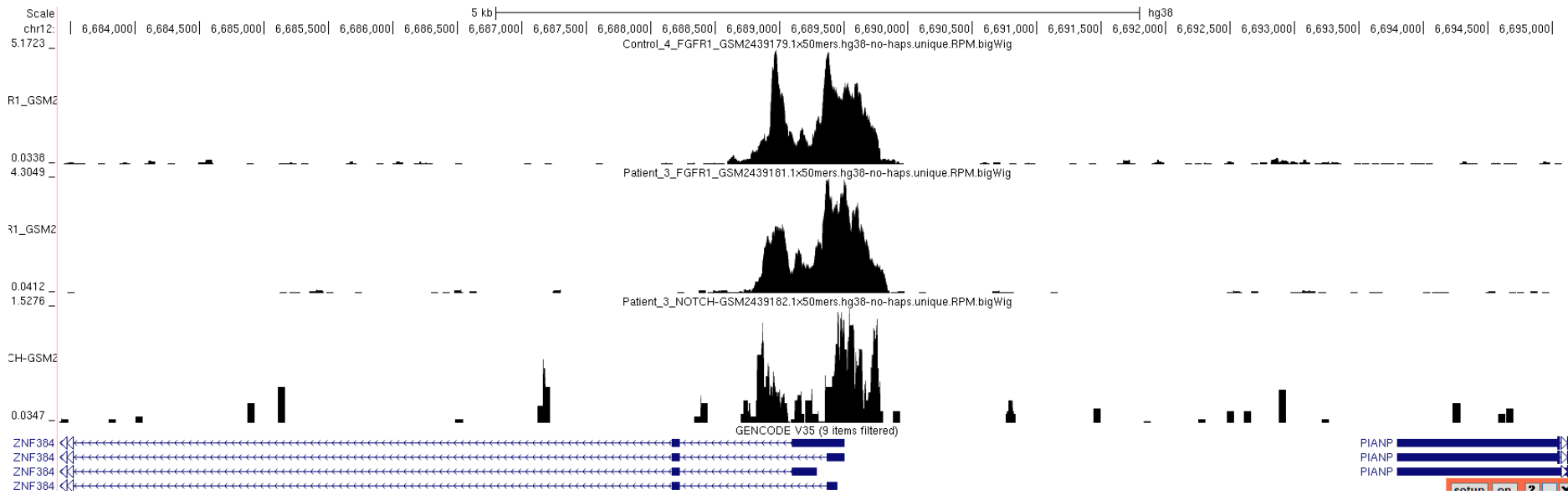
Top nuclear peaks (Control FGFR1)



This is likely an artifact



This is real



This is real too

Peak levels on chrM are several-fold higher than the top 3 nuclear peaks, i.e. they are unlikely to be due to NUMTs

Circos plot

Control FGFR1

Patient FGFR1

Patient NOTCH

