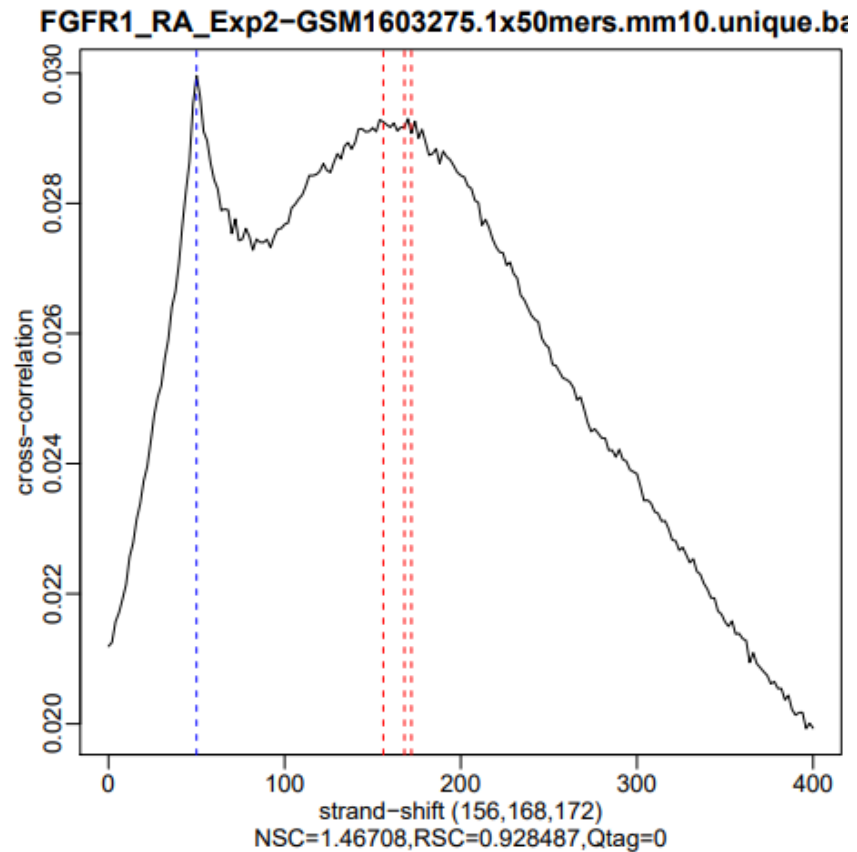
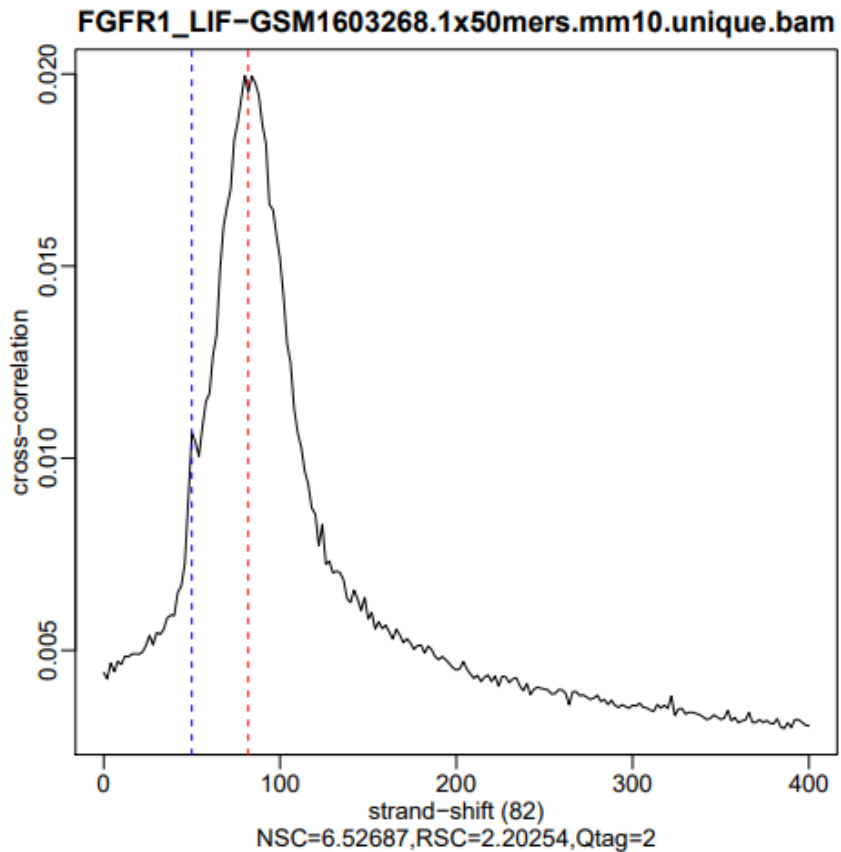


Dataset stats

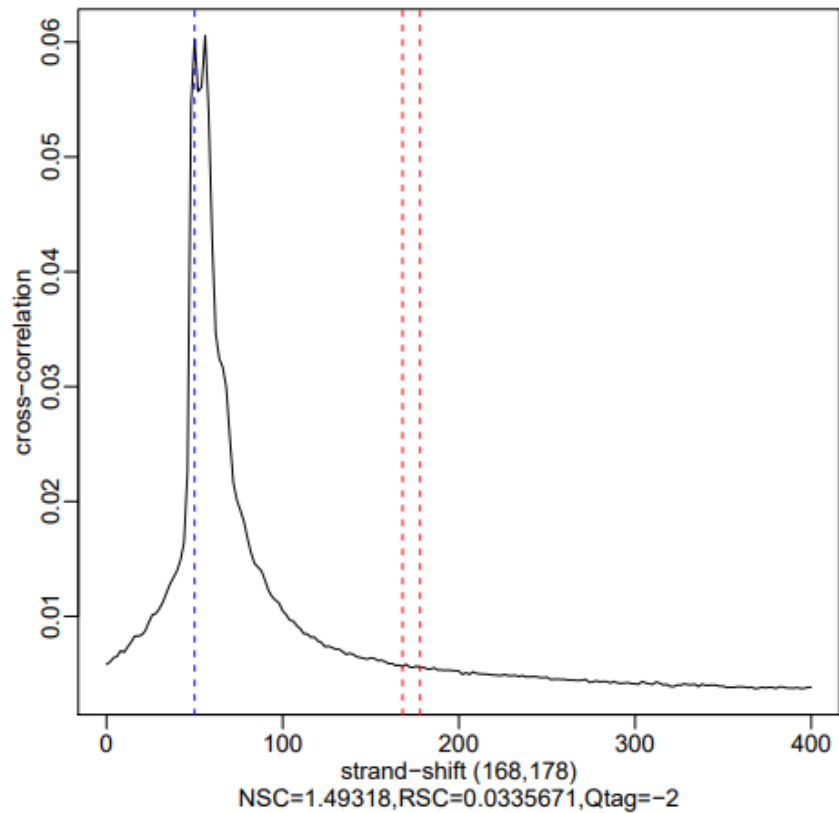
Species	#	Read Length	Raw fragments	Unique	Complexity	MACS2 NumPeaks	MACS2 RPM	MACS2 PseudoRep NumPeaks	MACS2 RPM	NSC	RSC	QC
hg38_no_haps	FGFR1_LIF-GSM1603268	1x50	202,601,919	118,417,973	0.04	176	6,146			6.527	2.203	2
hg38_no_haps	FGFR1_RA_Exp2-GSM1603275	1x50	26,459,306	15,571,797	0.85	745	10,546			1.467	0.928	0
hg38_no_haps	FGFR1_RA-GSM1603271	1x50	171,546,555	55,730,457	0.14	4	22			1.493	0.034	-2
hg38_no_haps	H3.3_RA-GSM1603274	1x50	187,356,177	43,030,732	0.05					2.637	0.111	-2
hg38_no_haps	Nur77_LIF-GSM1603270	1x50	200,979,400	119,703,622	0.08	4	22			10.564	1.244	1
hg38_no_haps	Nur77_RA-GSM1603273	1x50	199,297,844	99,530,481	0.07	1	3			12.051	0.949	0
hg38_no_haps	RXRa_LIF-GSM1603269	1x50	202,874,068	126,368,008	0.11	0	0			4.810	1.177	1
hg38_no_haps	RXRa_RA-GSM1603272	1x50	197,808,527	79,944,508	0.04	659	17,715			1.875	0.079	-2
chrM	FGFR1_LIF-GSM1603268	1x50	202,601,919	7,413	0.20							
chrM	FGFR1_RA_Exp2-GSM1603275	1x50	26,459,306	1,049	0.44							
chrM	FGFR1_RA-GSM1603271	1x50	171,546,555	68,630	0.38							
chrM	H3.3_RA-GSM1603274	1x50	187,356,177	186	0.46							
chrM	Nur77_LIF-GSM1603270	1x50	200,979,400	7,228	0.22							
chrM	Nur77_RA-GSM1603273	1x50	199,297,844	744	0.31							
chrM	RXRa_LIF-GSM1603269	1x50	202,874,068	10,545	0.23							
chrM	RXRa_RA-GSM1603272	1x50	197,808,527	562	0.33							

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

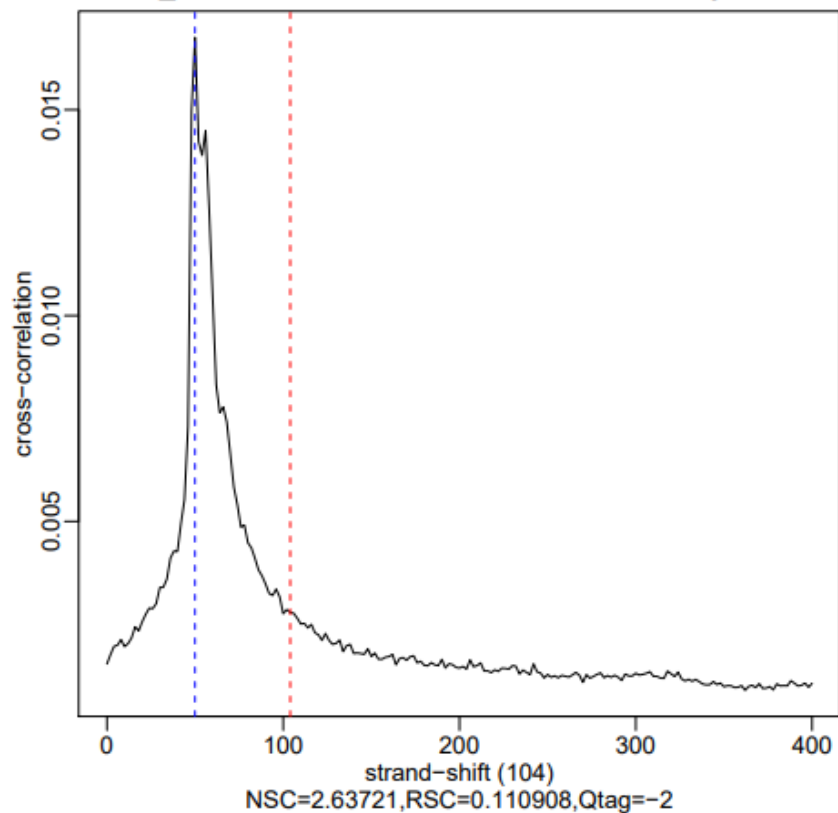
Cross-correlation QC



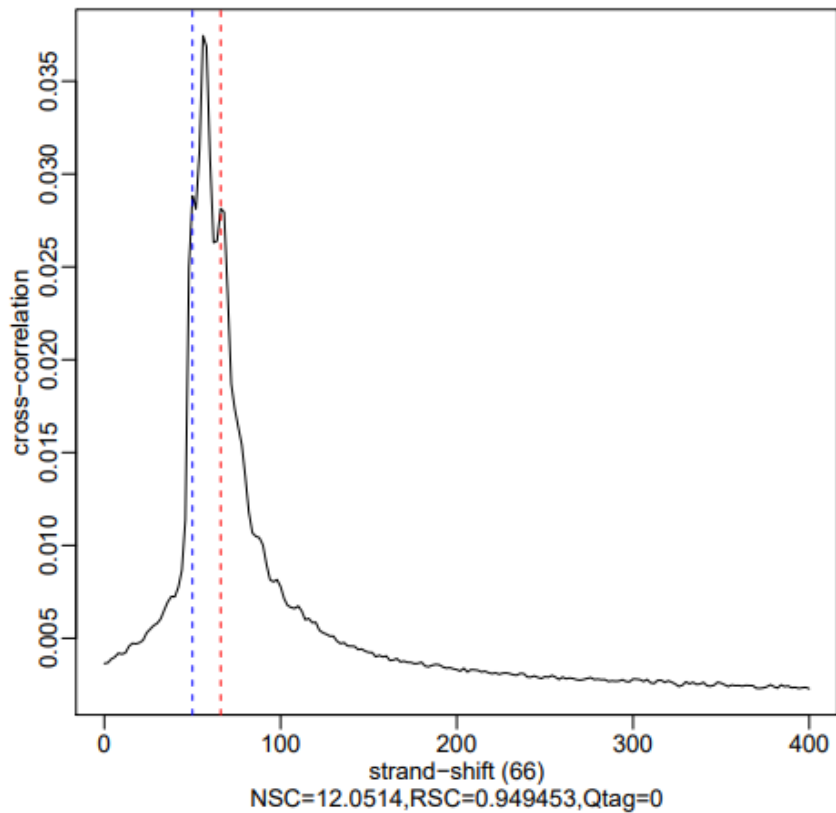
FGFR1_RA-GSM1603271.1x50mers.mm10.unique.bam



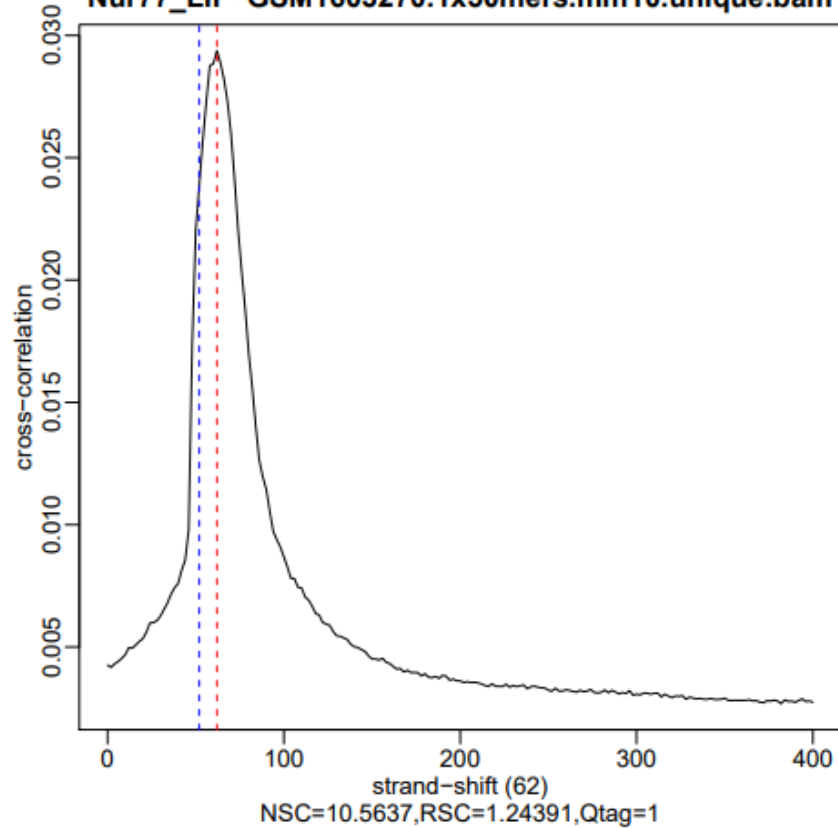
H3.3_RA-GSM1603274.1x50mers.mm10.unique.bam



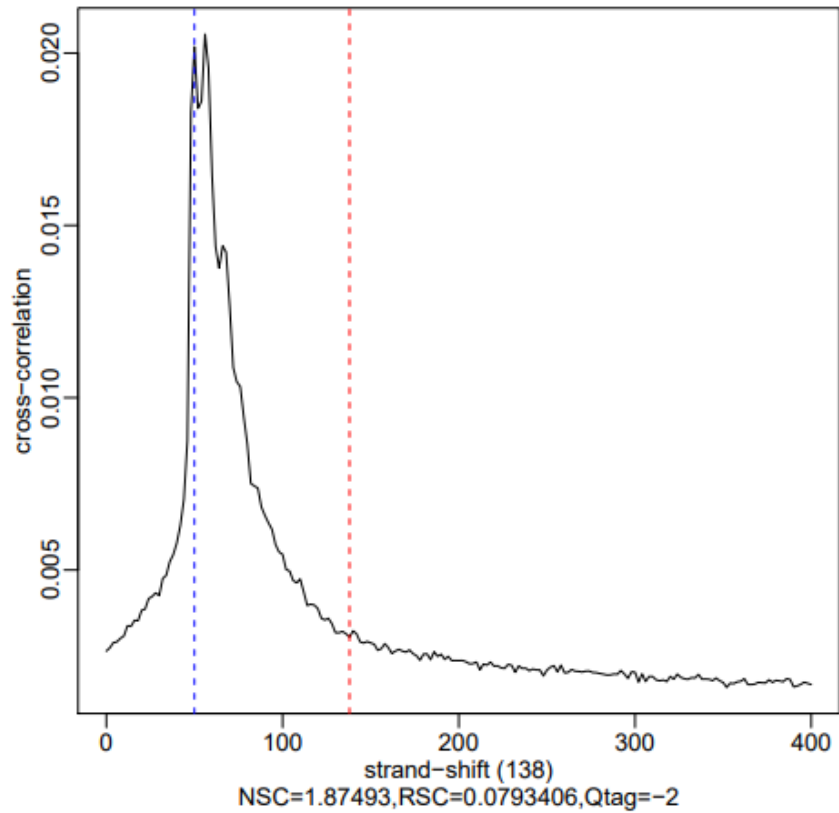
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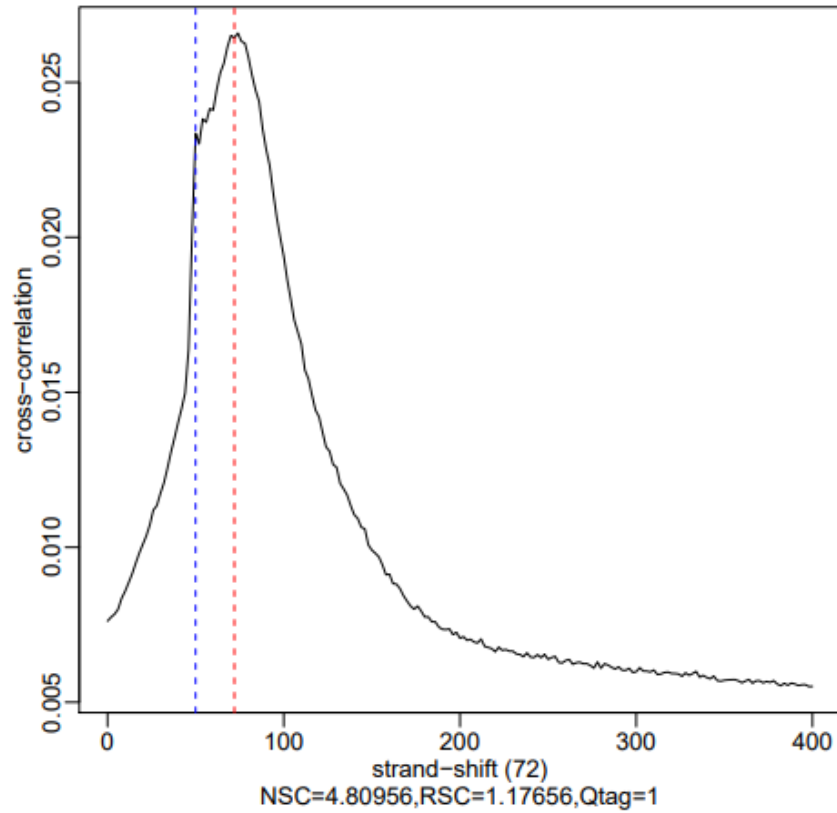
Nur77_LIF-GSM1603270.1x50mers.mm10.unique.bam



RXRa_RA-GSM1603272.1x50mers.mm10.unique.bam



RXRa_LIF-GSM1603269.1x50mers.mm10.unique.bam



chrM

5 kb | mm10
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

FGFR1_LIF-GSM1603268.1x50mers.chrM.unique.bigWig

RXRa_LIF-GSM1603269.1x50mers.chrM.unique.bigWig

Nur77_LIF-GSM1603270.1x50mers.chrM.unique.bigWig

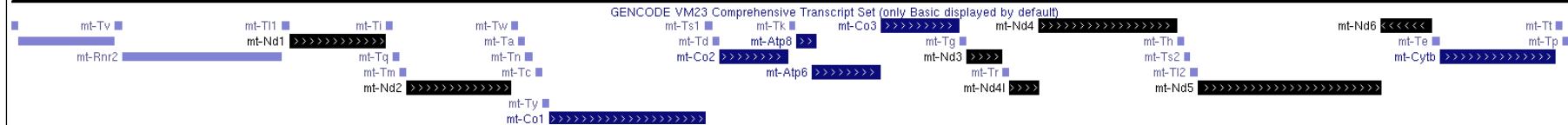
FGFR1_RA-GSM1603271.1x50mers.chrM.unique.bigWig

RXRa_RA-GSM1603272.1x50mers.chrM.unique.bigWig

Nur77_RA-GSM1603273.1x50mers.chrM.unique.bigWig

H3.3_RA-GSM1603274.1x50mers.chrM.unique.bigWig

FGFR1_RA_Exp2-GSM1603275.1x50mers.chrM.unique.bigWig



chrM stranded

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

FGFR1_LIF-GSM1603268.1x50mers.chrM.unique.plus.bigWig

FGFR1_RA-GSM1603271.1x50mers.chrM.unique.plus.bigWig

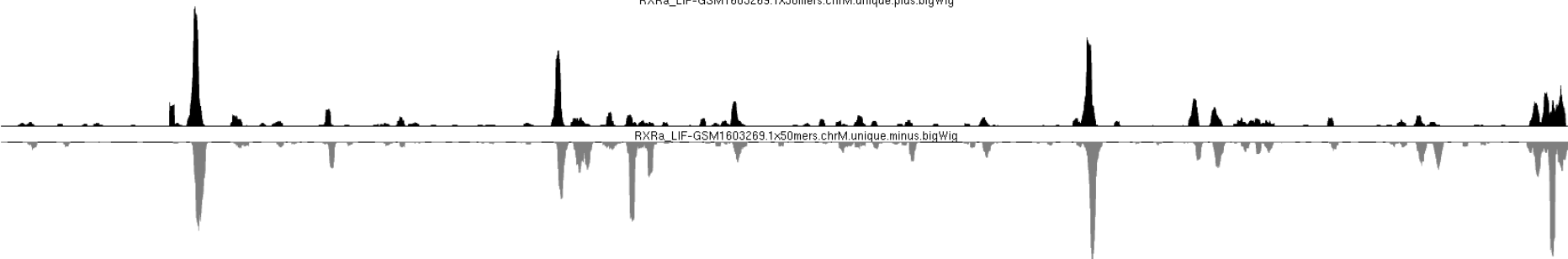
FGFR1_RA-GSM1603271.1x50mers.chrM.unique.minus.bigWig

GENCODE VM23 Comprehensive Transcript Set (only Basic displayed by default)

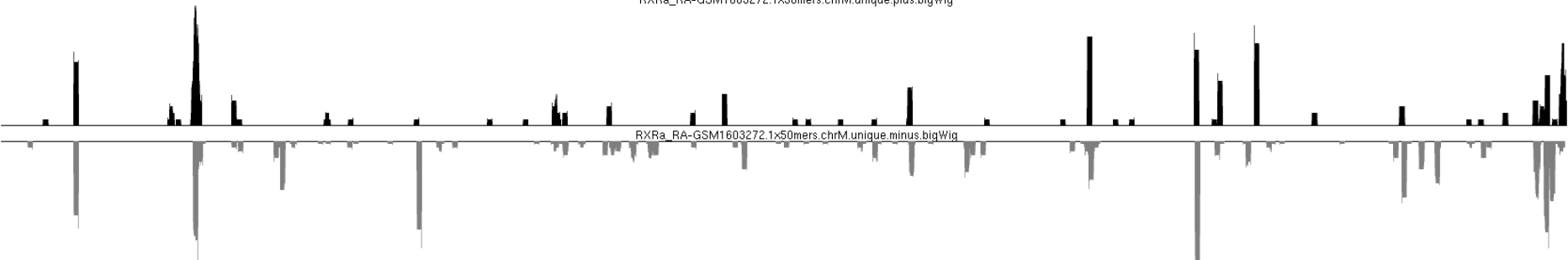


setup on ? - >

5 kb | mm10
 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|
 RXRa_LIF-GSM1603269.1x50mers.chrM.unique.plus.bigWig



RXRa_RA-GSM1603272.1x50mers.chrM.unique.plus.bigWig



GENCODE VM23 Comprehensive Transcript Set (only Basic displayed by default)

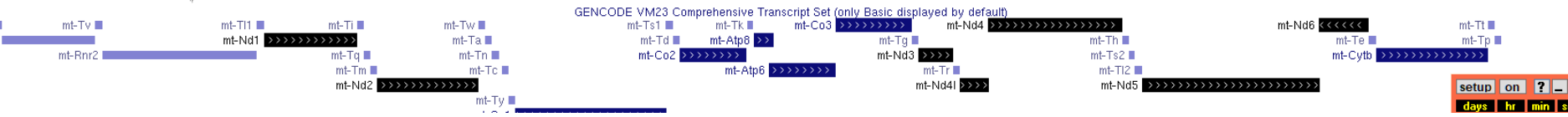
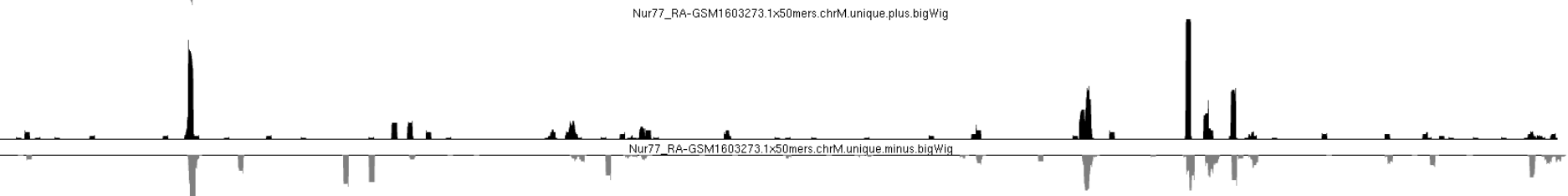
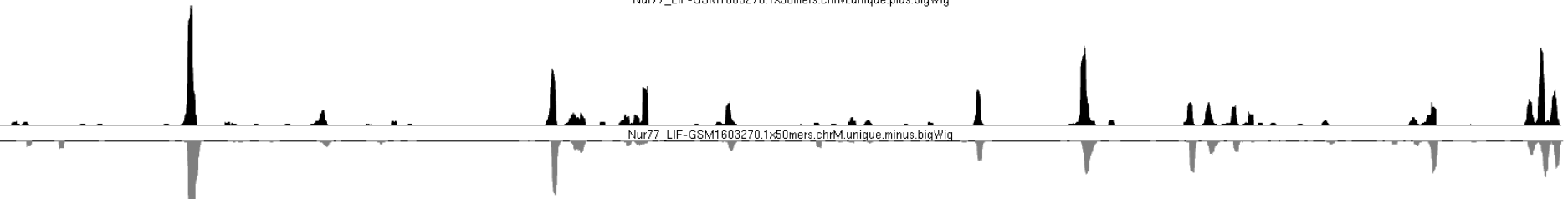


setup on ?

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

5 kb | mm10

Nur77_LIF-GSM1603270.1x50mers.chrM.unique.plus.bigWig



setup on ? -

days hr min sec

