

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 15:31:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777250.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1777250 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777250_1.fastq.gz SRR1777250_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 15:31:01 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777250.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,612,898
Mapped reads	18,491,385 / 99.35%
Unmapped reads	121,513 / 0.65%
Mapped paired reads	18,491,385 / 99.35%
Mapped reads, first in pair	9,247,287 / 49.68%
Mapped reads, second in pair	9,244,098 / 49.67%
Mapped reads, both in pair	18,447,228 / 99.11%
Mapped reads, singletons	44,157 / 0.24%
Secondary alignments	0
Supplementary alignments	609,676 / 3.28%
Read min/max/mean length	30 / 101 / 102.29
Duplicated reads (estimated)	10,098,256 / 54.25%
Duplication rate	35.15%
Clipped reads	9,305,515 / 49.99%

2.2. ACGT Content

Number/percentage of A's	433,856,807 / 25.82%
Number/percentage of C's	351,218,839 / 20.9%
Number/percentage of T's	489,745,661 / 29.15%
Number/percentage of G's	405,353,317 / 24.12%
Number/percentage of N's	58,241 / 0%

GC Percentage	45.03%
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2.3. Coverage

Mean	0.543
Standard Deviation	8.3534

2.4. Mapping Quality

Mean Mapping Quality	53.85
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2.5. Insert size

Mean	405,945.43
Standard Deviation	6,332,747.38
P25/Median/P75	152 / 197 / 252

2.6. Mismatches and indels

General error rate	0.45%
Mismatches	7,407,746
Insertions	100,916
Mapped reads with at least one insertion	0.53%
Deletions	355,703
Mapped reads with at least one deletion	1.9%
Homopolymer indels	49.54%

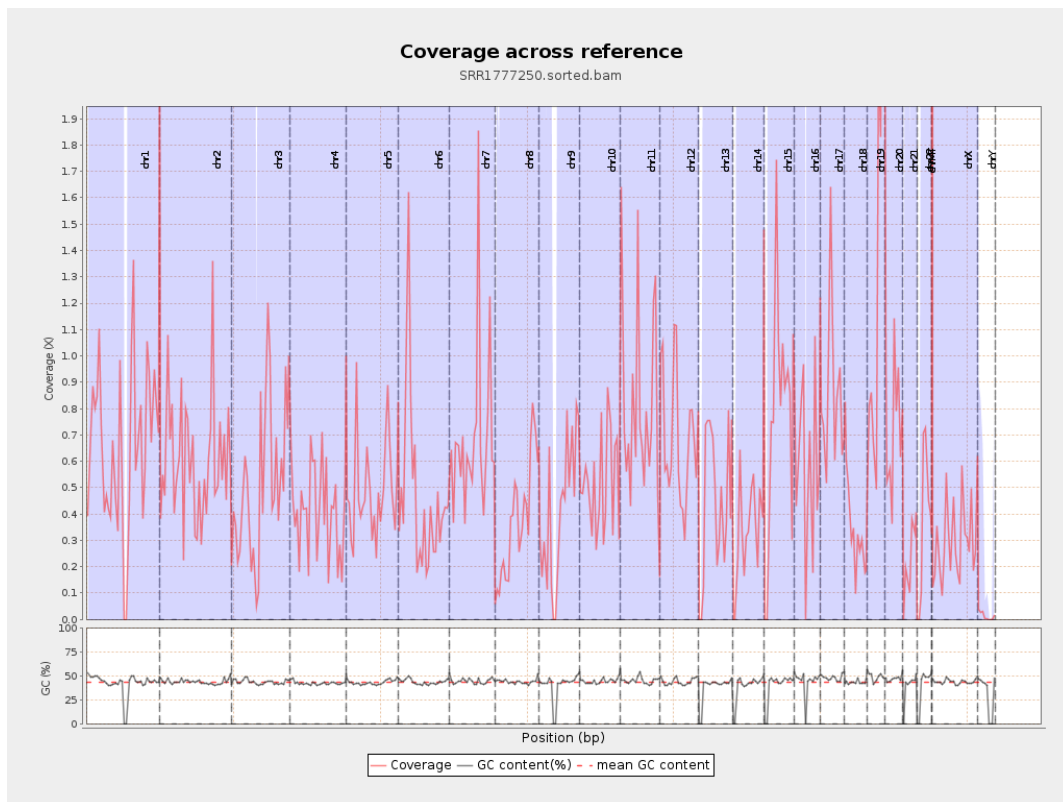
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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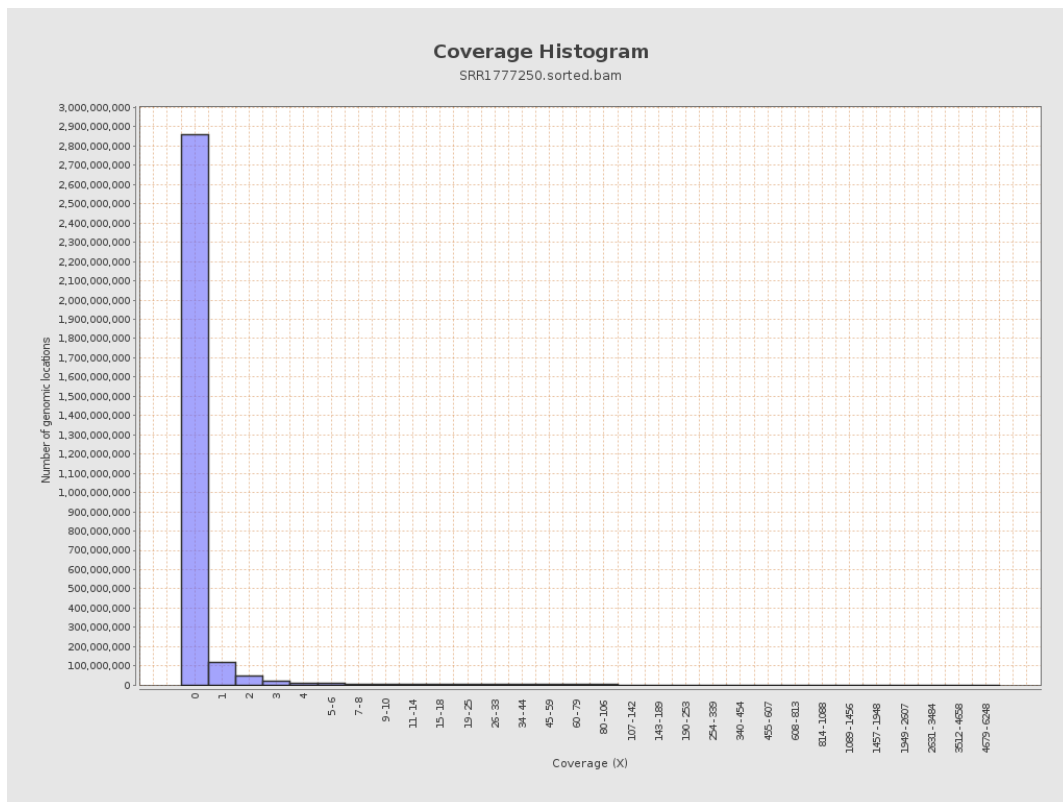
		bases	coverage	deviation
chr1	249250621	166935788	0.6698	10.5391
chr2	243199373	147138105	0.605	8.3591
chr3	198022430	101123726	0.5107	7.8695
chr4	191154276	79580715	0.4163	6.6837
chr5	180915260	89103499	0.4925	7.7303
chr6	171115067	78539131	0.459	7.4613
chr7	159138663	109113544	0.6857	11.6794
chr8	146364022	56228648	0.3842	6.2556
chr9	141213431	58055128	0.4111	6.3854
chr10	135534747	69615105	0.5136	7.6958
chr11	135006516	112015364	0.8297	10.7481
chr12	133851895	91706611	0.6851	9.211
chr13	115169878	50539432	0.4388	7.0825
chr14	107349540	36450069	0.3395	6.0777
chr15	102531392	76772496	0.7488	9.9966
chr16	90354753	52992926	0.5865	8.1301
chr17	81195210	70824612	0.8723	10.0849
chr18	78077248	26365096	0.3377	6.1413
chr19	59128983	84190156	1.4238	14.0298
chr20	63025520	46834235	0.7431	9.5914
chr21	48129895	10941673	0.2273	4.0061
chr22	51304566	19131694	0.3729	5.6878
chrMT	16571	469366	28.3245	17.8621
chrX	155270560	45415057	0.2925	5.5736

chrY	59373566	777923	0.0131	0.5296
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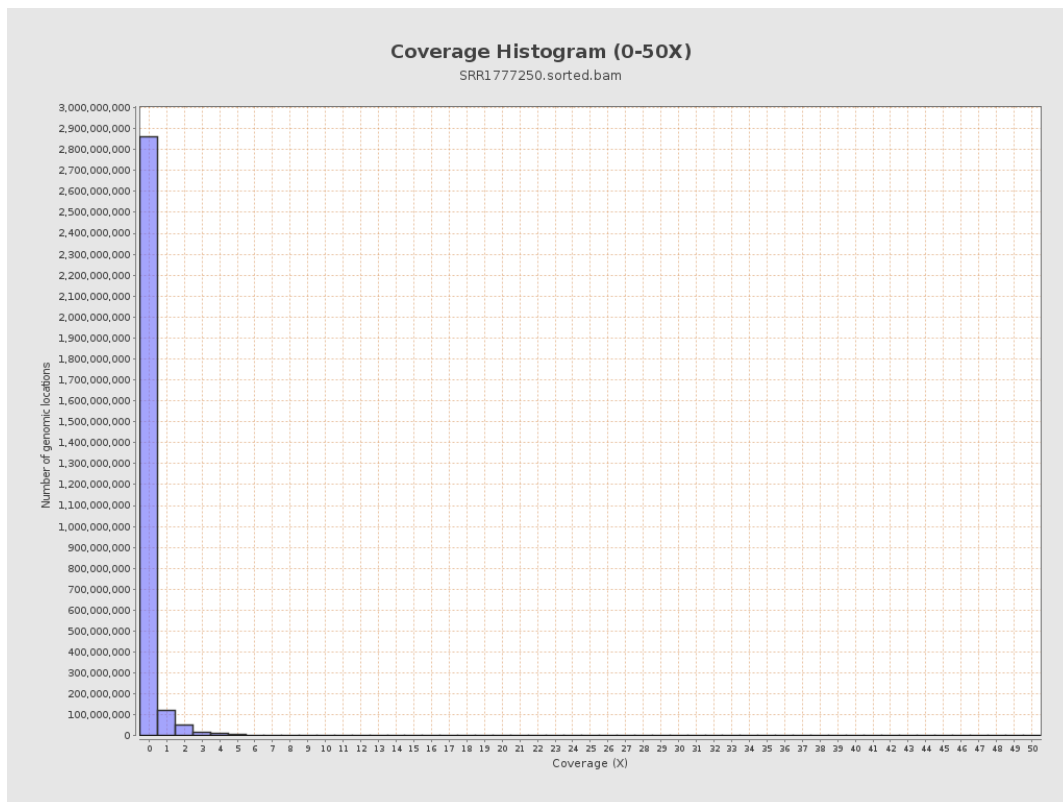
3. Results : Coverage across reference



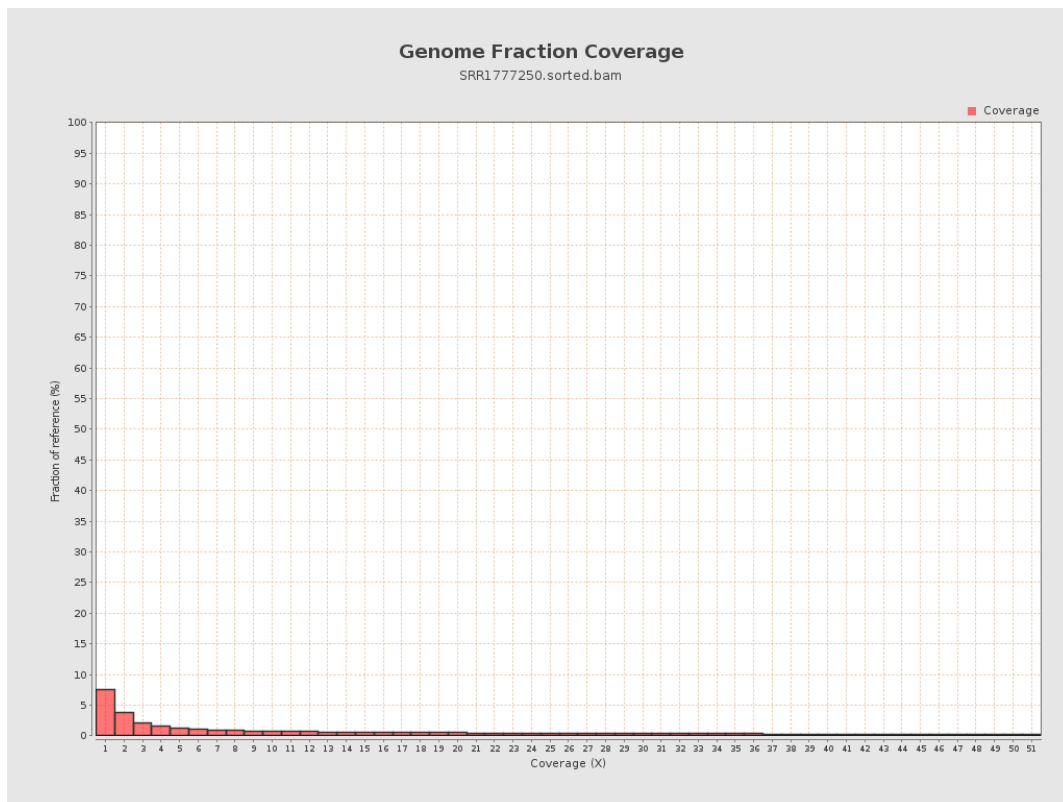
4. Results : Coverage Histogram



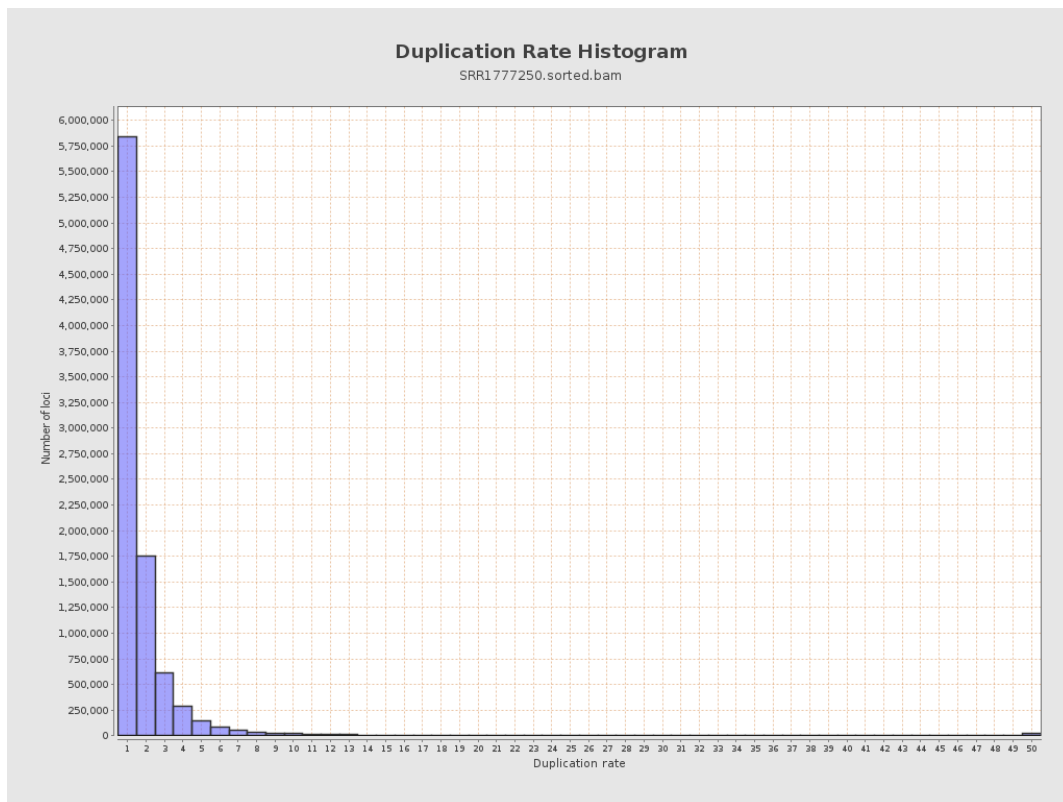
5. Results : Coverage Histogram (0-50X)



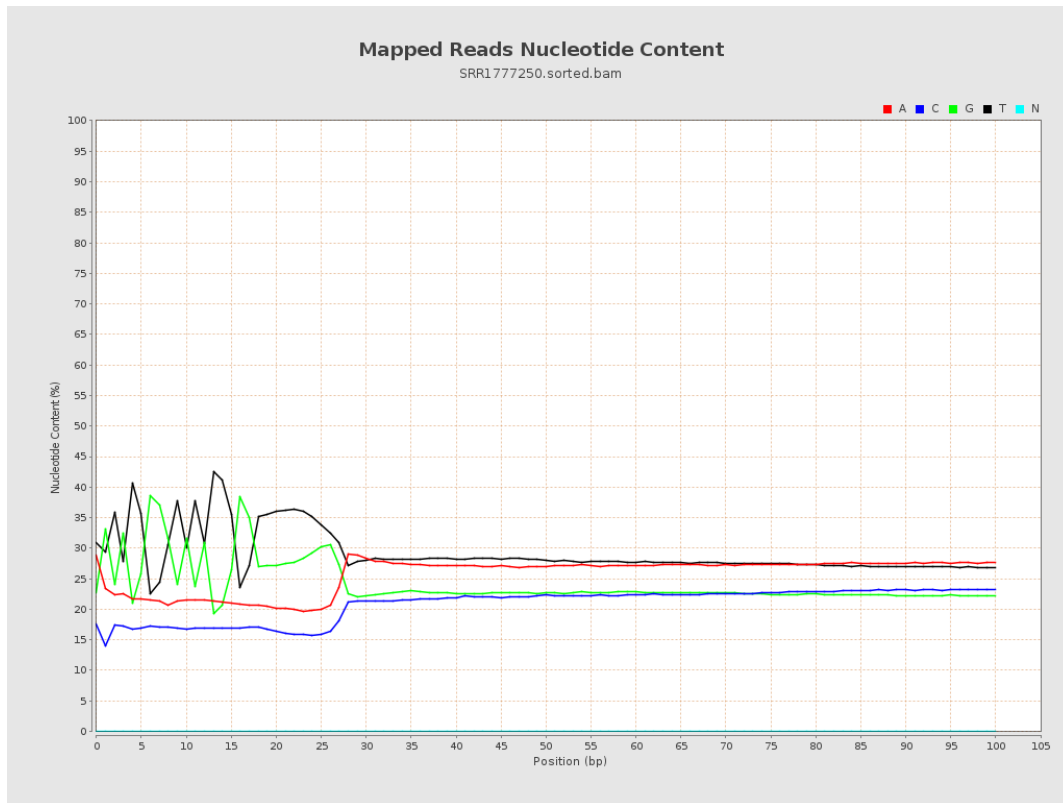
6. Results : Genome Fraction Coverage



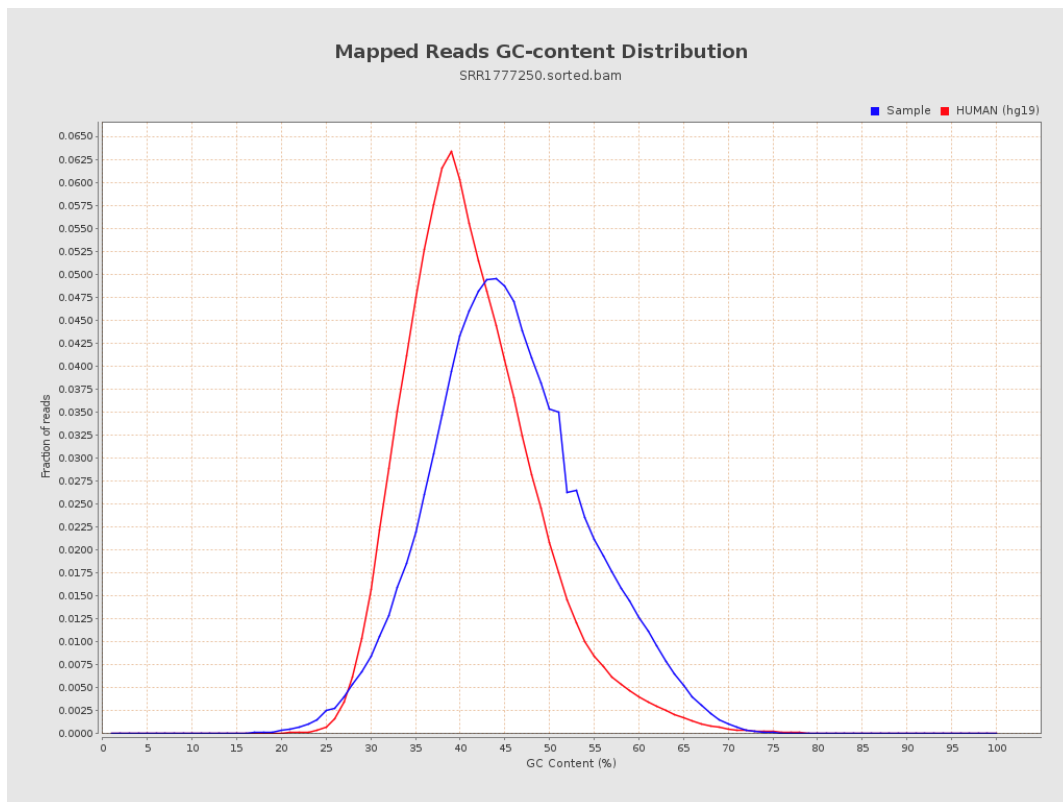
7. Results : Duplication Rate Histogram



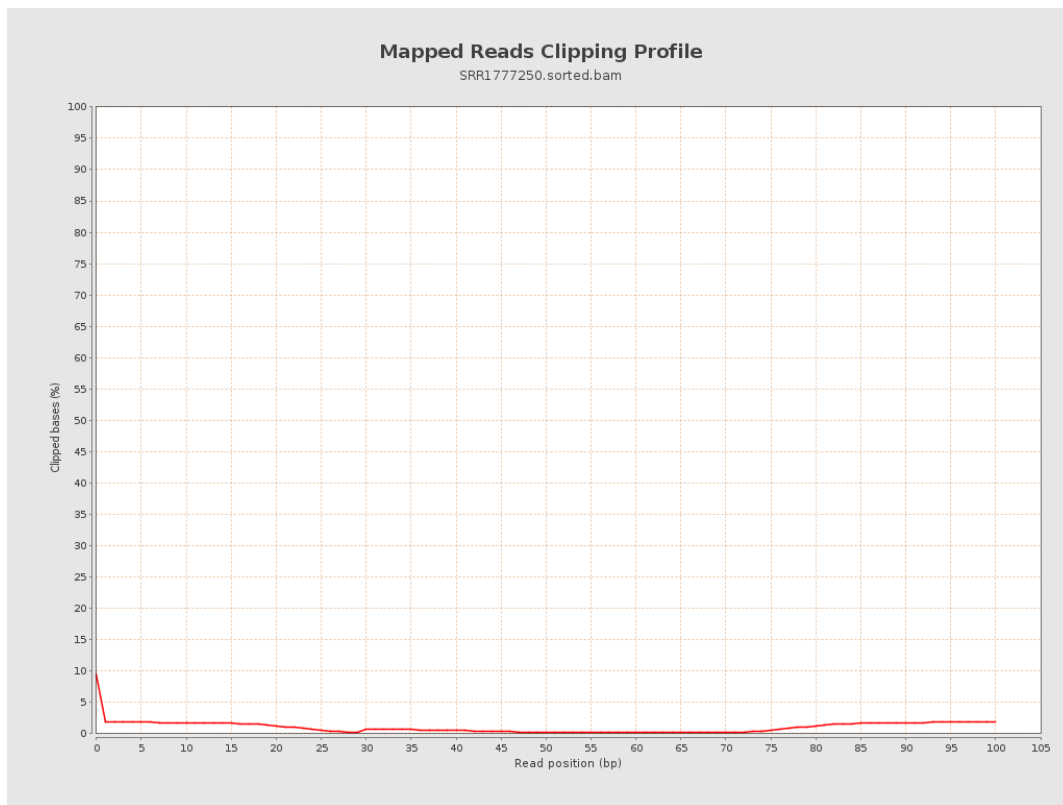
8. Results : Mapped Reads Nucleotide Content



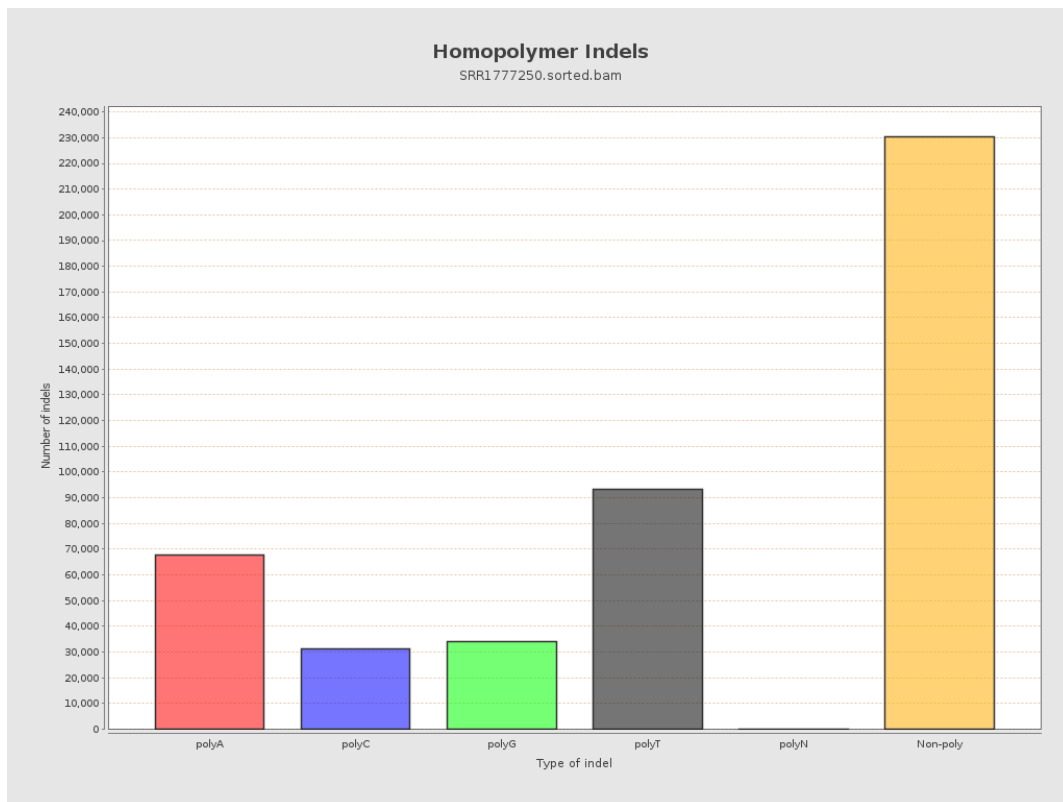
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



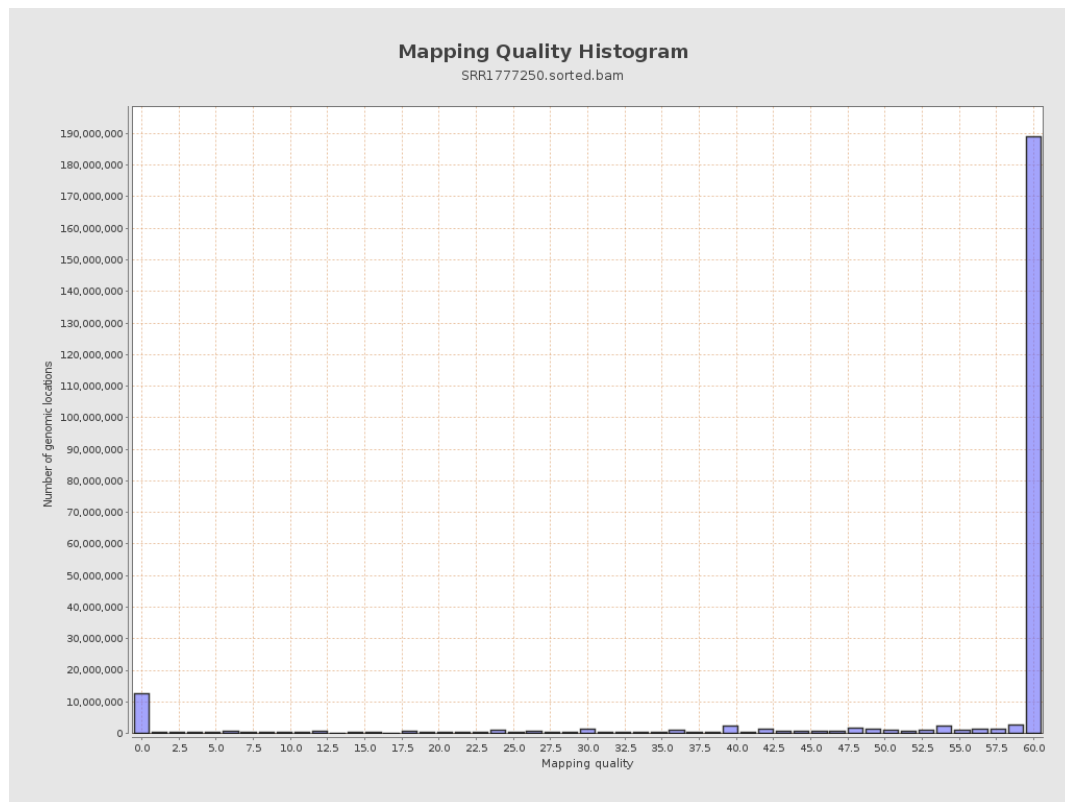
11. Results : Homopolymer Indels



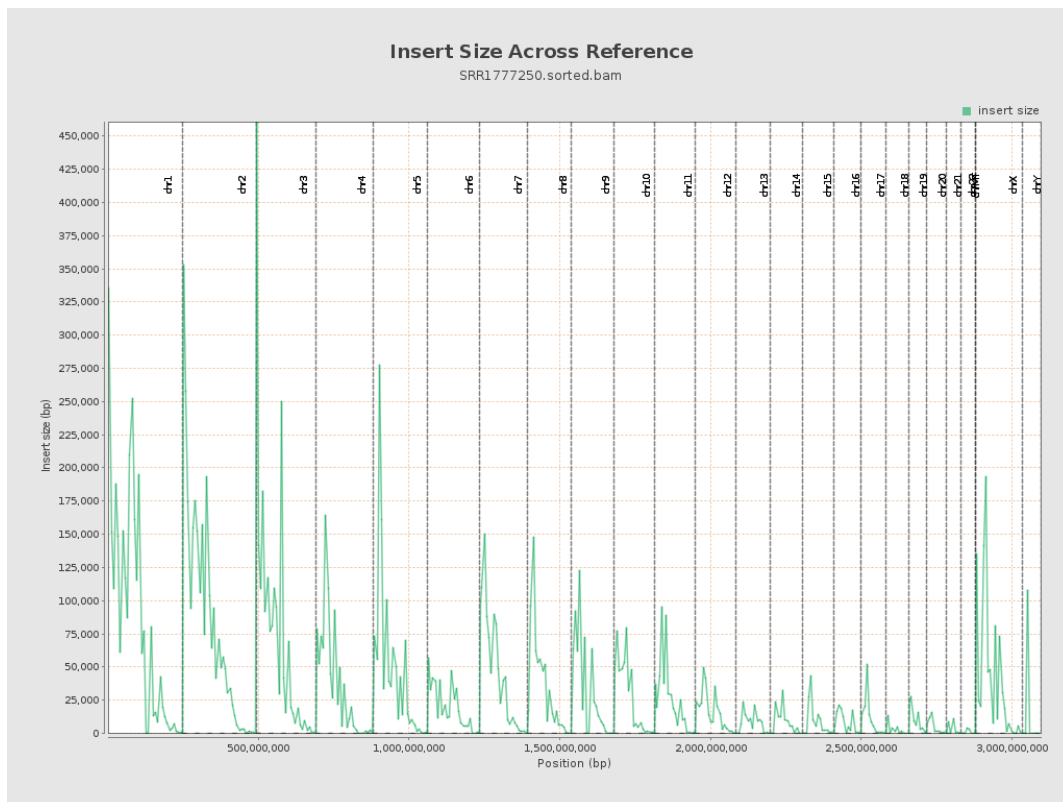
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

