

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 15:12:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777249.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_SRR1777249 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777249_1.fastq.gz SRR1777249_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 15:11:59 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777249.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,889,854
Mapped reads	18,764,951 / 99.34%
Unmapped reads	124,903 / 0.66%
Mapped paired reads	18,764,951 / 99.34%
Mapped reads, first in pair	9,384,025 / 49.68%
Mapped reads, second in pair	9,380,926 / 49.66%
Mapped reads, both in pair	18,720,868 / 99.11%
Mapped reads, singletons	44,083 / 0.23%
Secondary alignments	0
Supplementary alignments	619,620 / 3.28%
Read min/max/mean length	30 / 101 / 102.29
Duplicated reads (estimated)	10,300,802 / 54.53%
Duplication rate	35.4%
Clipped reads	9,430,679 / 49.92%

2.2. ACGT Content

Number/percentage of A's	440,896,472 / 25.85%
Number/percentage of C's	356,109,567 / 20.88%
Number/percentage of T's	497,440,502 / 29.17%
Number/percentage of G's	410,868,377 / 24.09%
Number/percentage of N's	63,847 / 0%

GC Percentage	44.97%
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2.3. Coverage

Mean	0.5511
Standard Deviation	8.485

2.4. Mapping Quality

Mean Mapping Quality	53.85
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2.5. Insert size

Mean	406,131.54
Standard Deviation	6,331,736.71
P25/Median/P75	152 / 197 / 252

2.6. Mismatches and indels

General error rate	0.45%
Mismatches	7,482,818
Insertions	102,144
Mapped reads with at least one insertion	0.53%
Deletions	360,936
Mapped reads with at least one deletion	1.89%
Homopolymer indels	49.4%

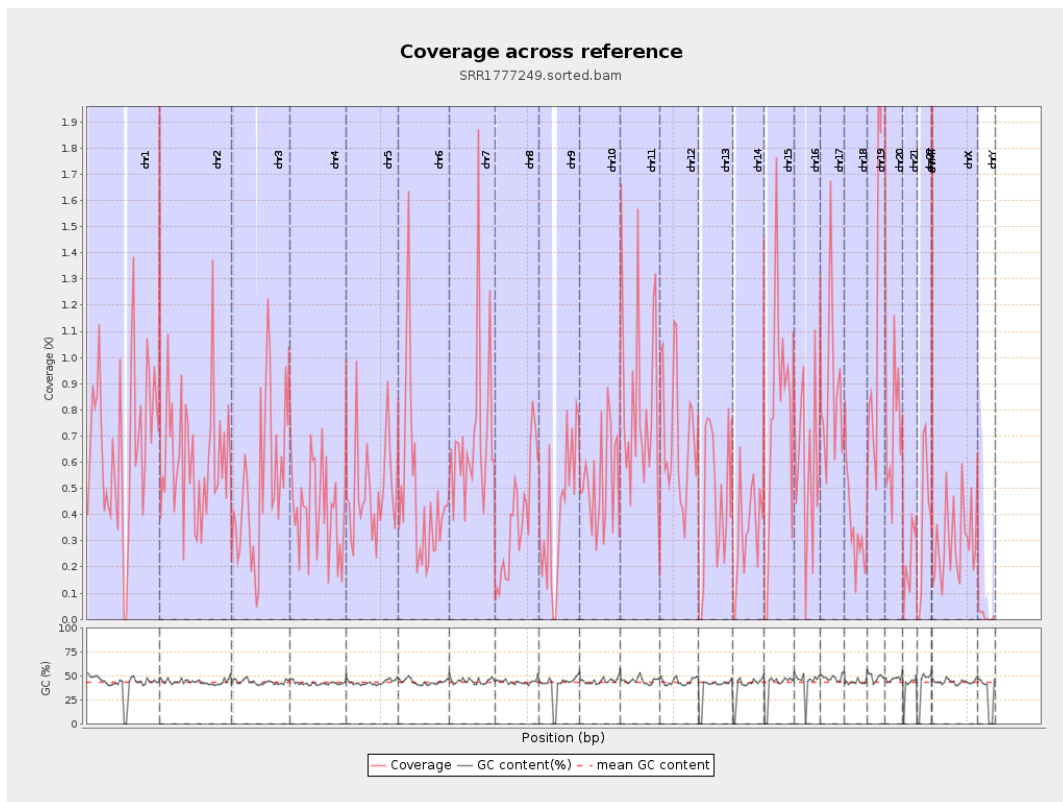
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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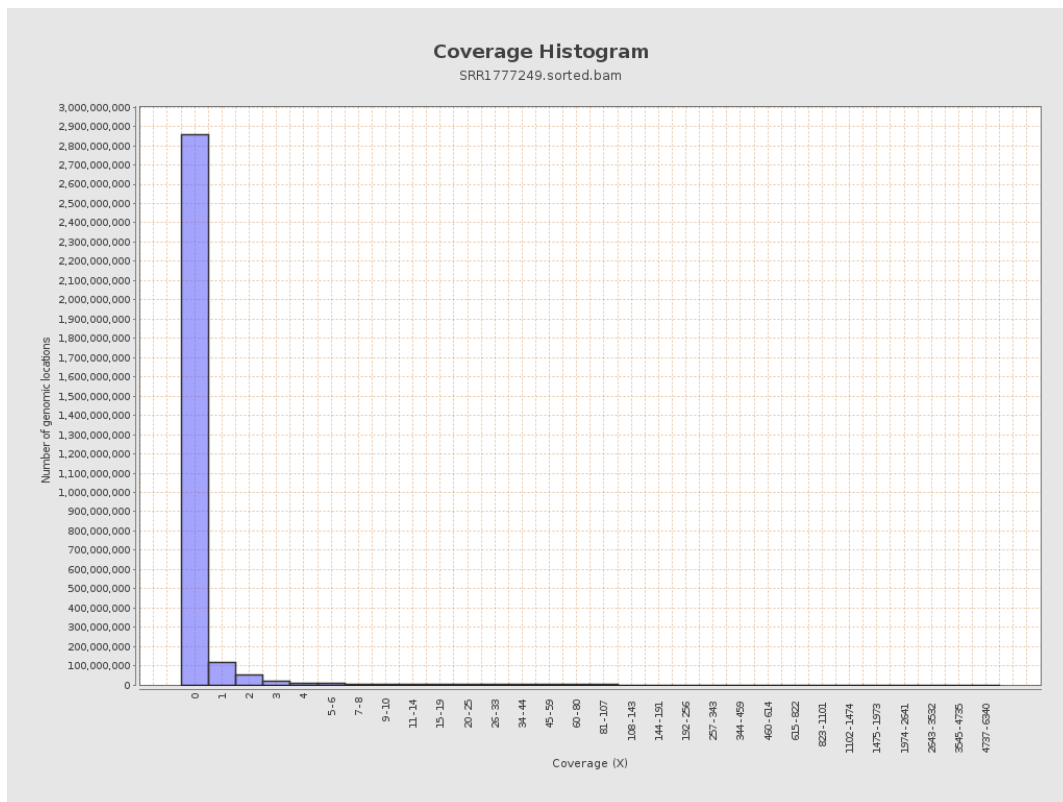
		bases	coverage	deviation
chr1	249250621	169619498	0.6805	10.731
chr2	243199373	149160280	0.6133	8.4797
chr3	198022430	102870895	0.5195	8.0175
chr4	191154276	80983634	0.4237	6.788
chr5	180915260	90304950	0.4992	7.8506
chr6	171115067	80159625	0.4685	7.6272
chr7	159138663	111129500	0.6983	11.7687
chr8	146364022	57291018	0.3914	6.3593
chr9	141213431	58531800	0.4145	6.4721
chr10	135534747	70556782	0.5206	7.8408
chr11	135006516	113626515	0.8416	10.9207
chr12	133851895	93238099	0.6966	9.3743
chr13	115169878	51158531	0.4442	7.1934
chr14	107349540	36924834	0.344	6.1637
chr15	102531392	77839710	0.7592	10.1466
chr16	90354753	53706338	0.5944	8.2005
chr17	81195210	71811333	0.8844	10.2405
chr18	78077248	26936761	0.345	6.2653
chr19	59128983	85151697	1.4401	14.2579
chr20	63025520	47233290	0.7494	9.7514
chr21	48129895	11074039	0.2301	4.0447
chr22	51304566	19262721	0.3755	5.7727
chrMT	16571	469310	28.3212	18.5669
chrX	155270560	46195827	0.2975	5.696

chrY	59373566	778877	0.0131	0.5259
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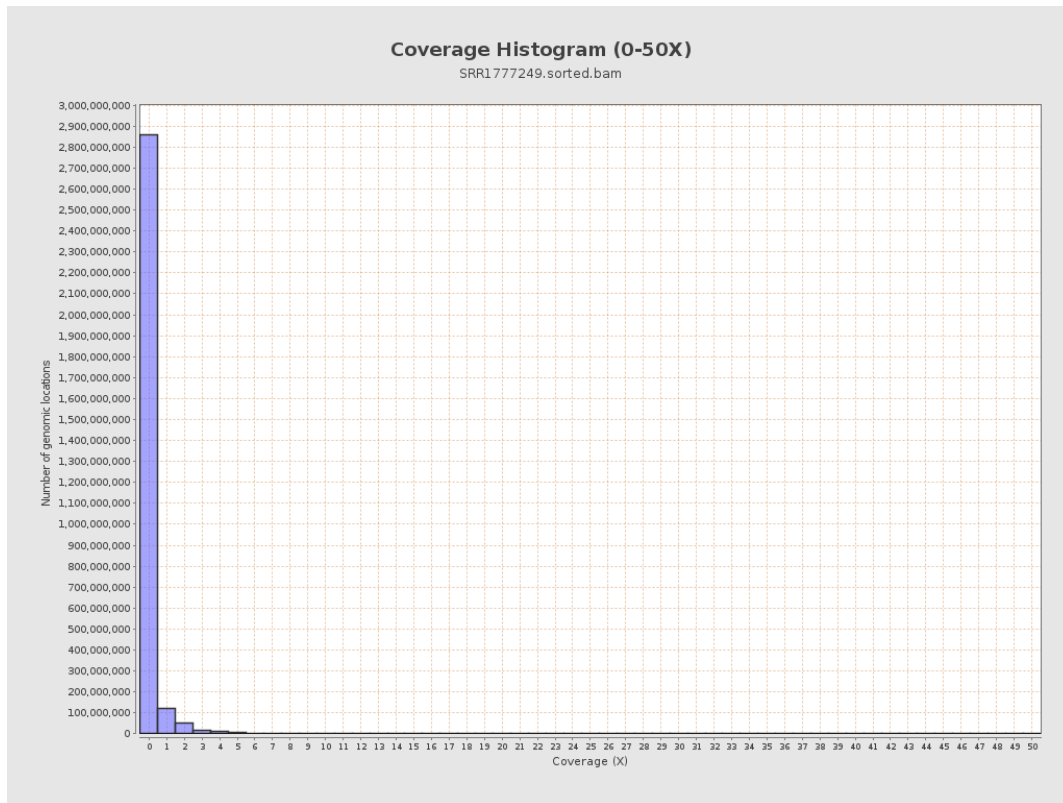
3. Results : Coverage across reference



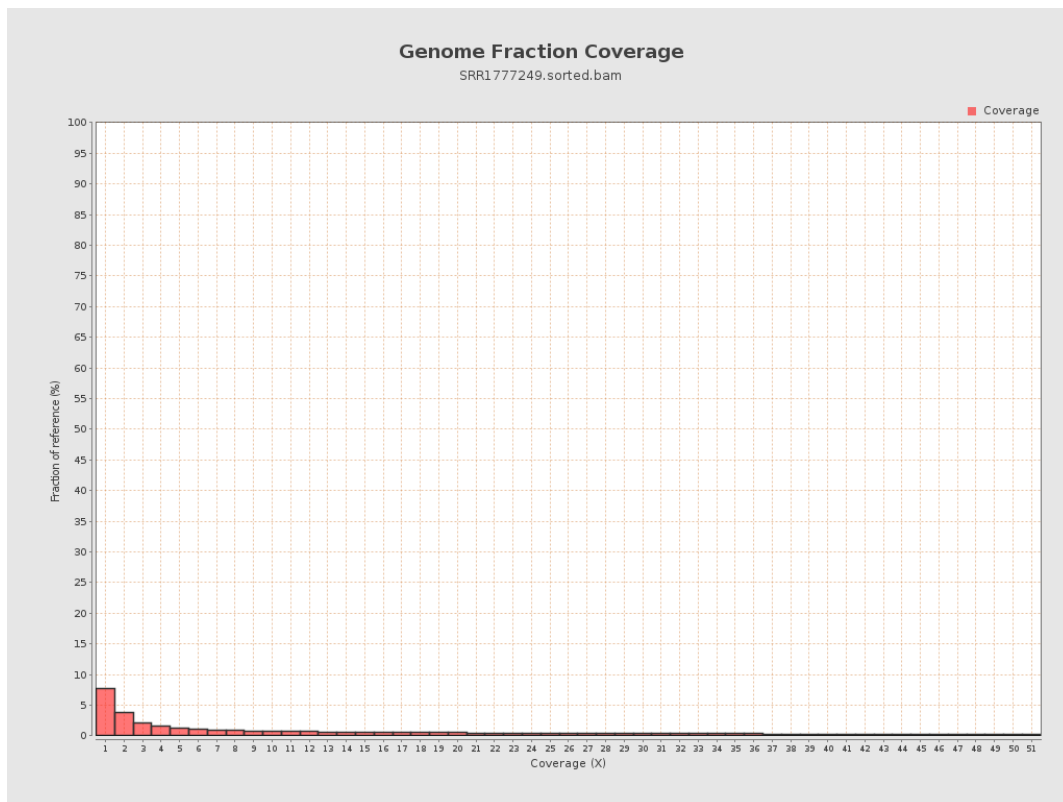
4. Results : Coverage Histogram



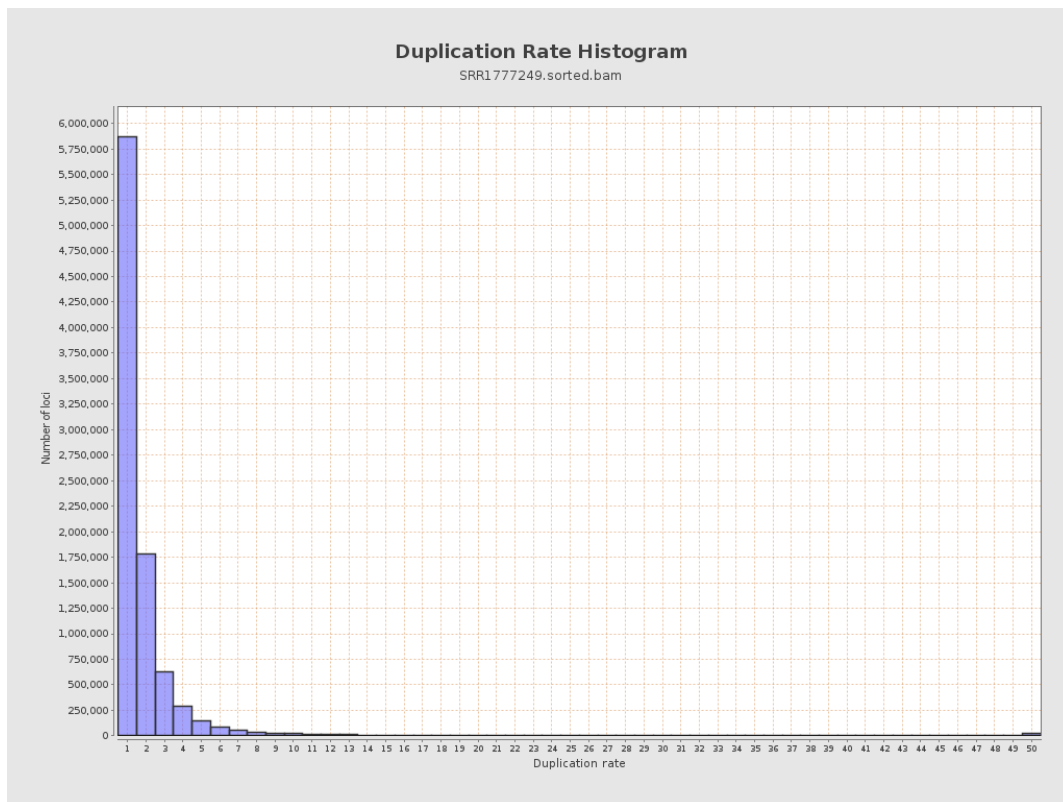
5. Results : Coverage Histogram (0-50X)



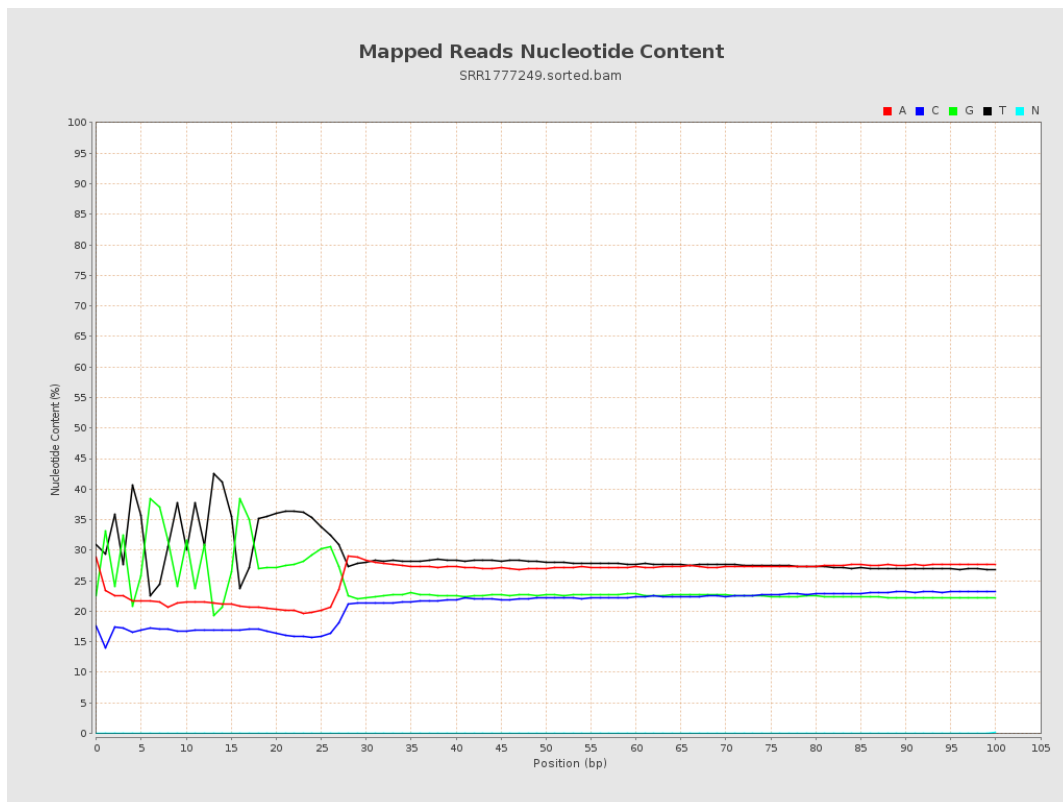
6. Results : Genome Fraction Coverage



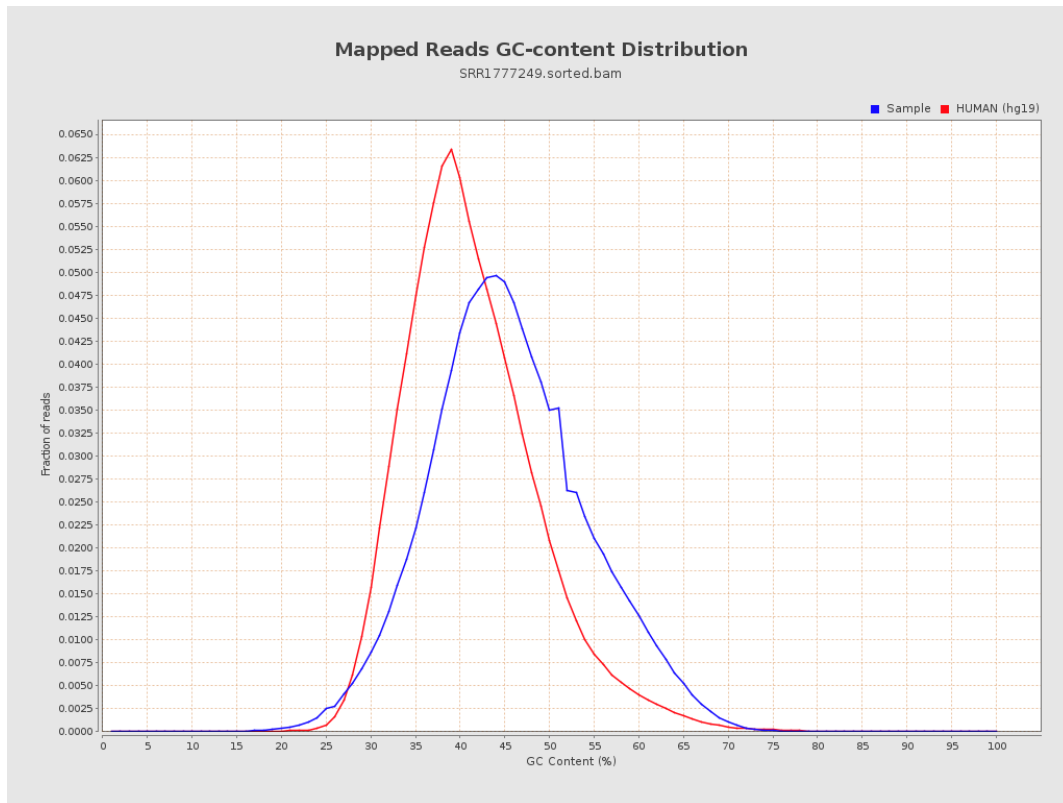
7. Results : Duplication Rate Histogram



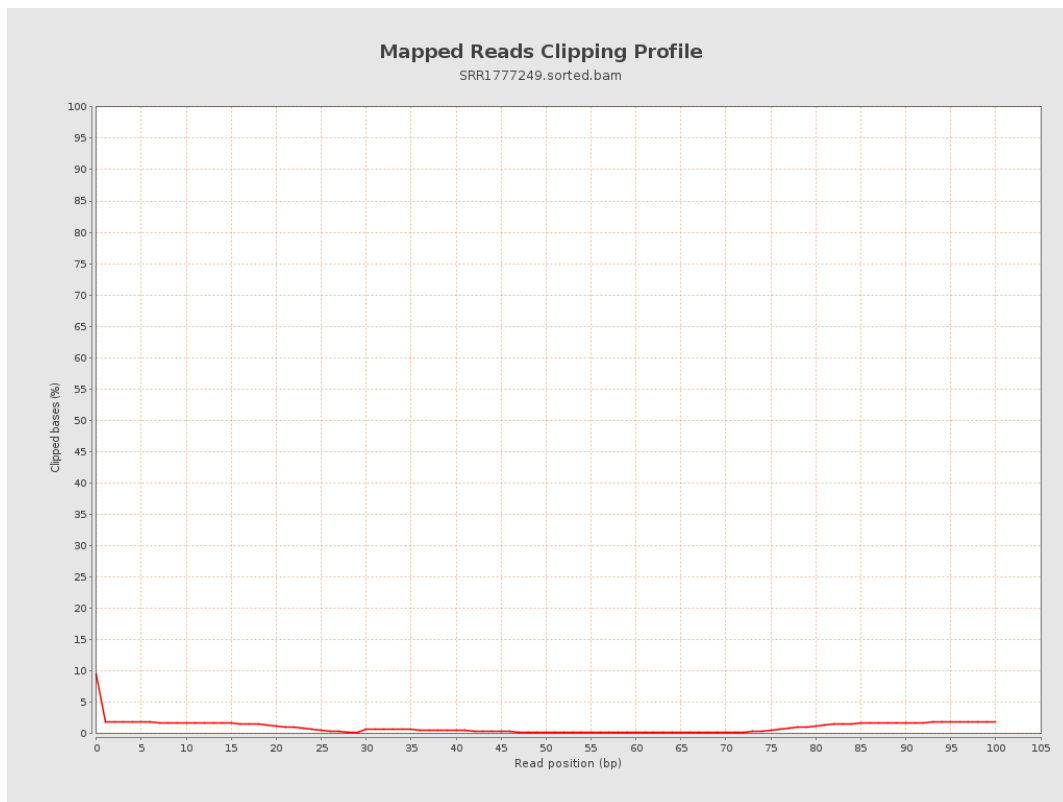
8. Results : Mapped Reads Nucleotide Content



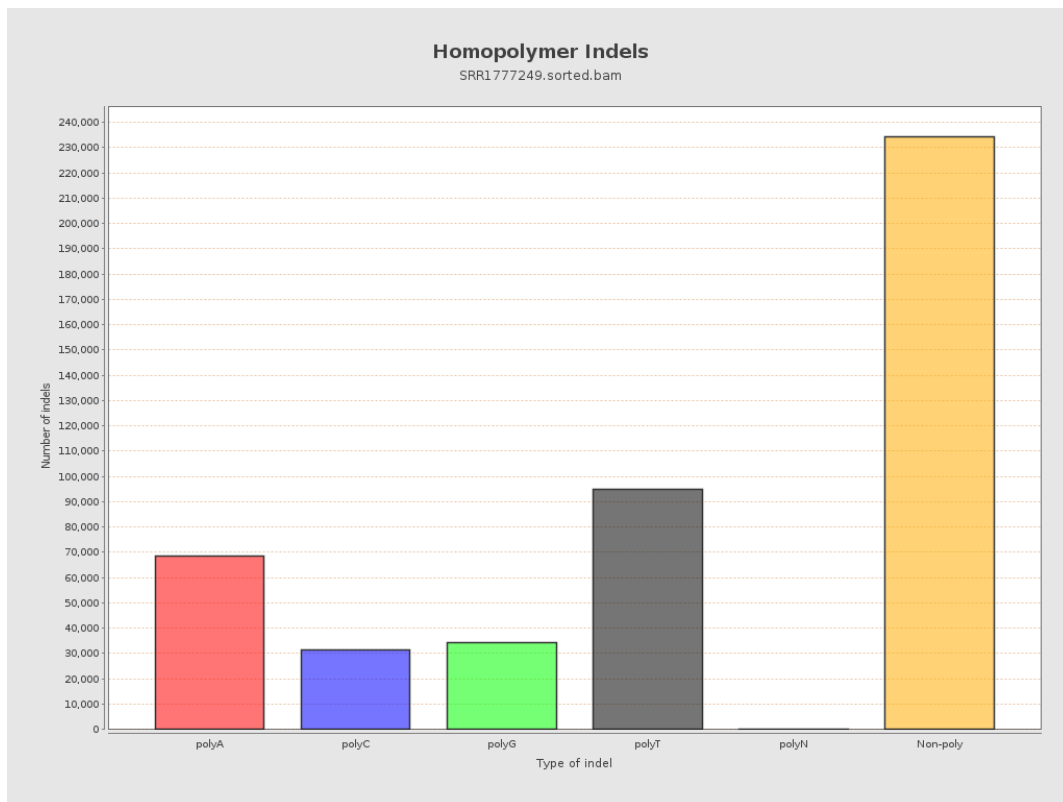
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



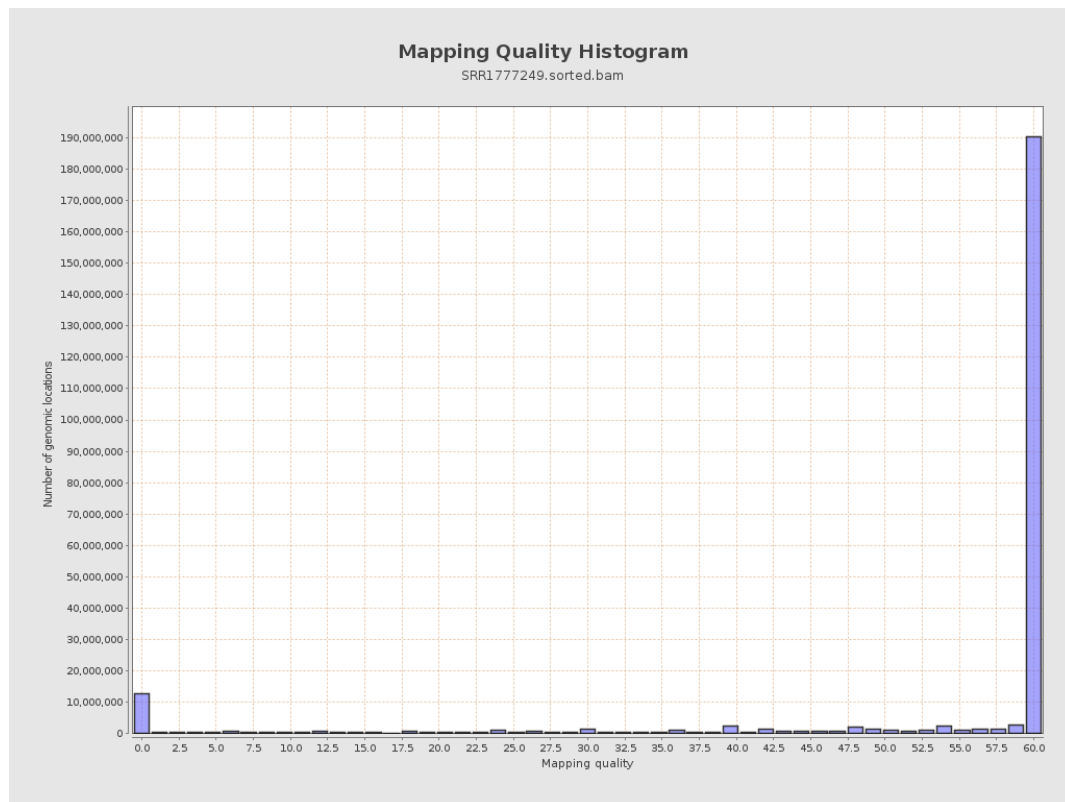
11. Results : Homopolymer Indels



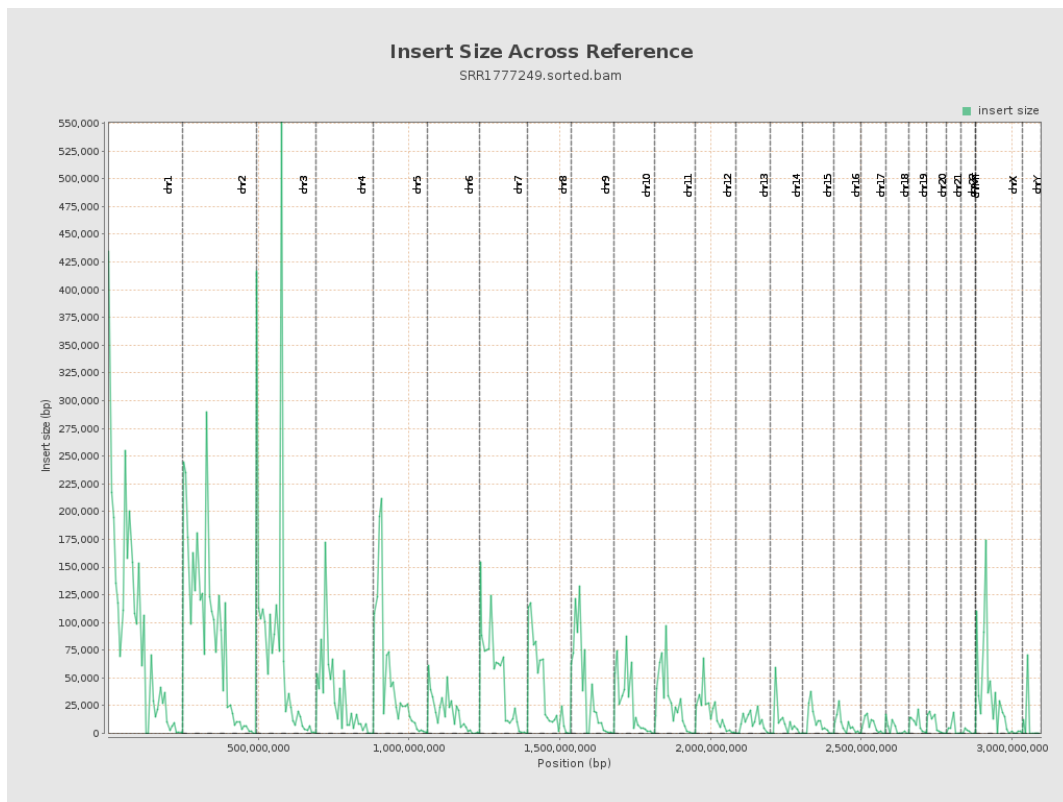
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

