Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 00:26:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777243.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_SRR1777243 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777243_1.fastq.gz SRR1777243_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 00:26:46 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777243.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,384,766
Mapped reads	12,185,195 / 98.39%
Unmapped reads	199,571 / 1.61%
Mapped paired reads	12,185,195 / 98.39%
Mapped reads, first in pair	6,115,017 / 49.38%
Mapped reads, second in pair	6,070,178 / 49.01%
Mapped reads, both in pair	12,105,412 / 97.74%
Mapped reads, singletons	79,783 / 0.64%
Secondary alignments	0
Supplementary alignments	120,334 / 0.97%
Read min/max/mean length	30 / 101 / 101.39
Duplicated reads (estimated)	953,789 / 7.7%
Duplication rate	4.66%
Clipped reads	1,934,103 / 15.62%

2.2. ACGT Content

Number/percentage of A's	348,600,041 / 29.2%
Number/percentage of C's	249,184,218 / 20.88%
Number/percentage of T's	342,444,639 / 28.69%
Number/percentage of G's	253,390,717 / 21.23%
Number/percentage of N's	54,305 / 0%

GC Percentage	42.1%

2.3. Coverage

Mean	0.3857
Standard Deviation	5.0486

2.4. Mapping Quality

Mean Mapping Quality	53.29

2.5. Insert size

Mean	249,130.72
Standard Deviation	4,947,844.49
P25/Median/P75	127 / 173 / 234

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	5,788,243
Insertions	126,665
Mapped reads with at least one insertion	1.01%
Deletions	151,707
Mapped reads with at least one deletion	1.21%
Homopolymer indels	42.54%

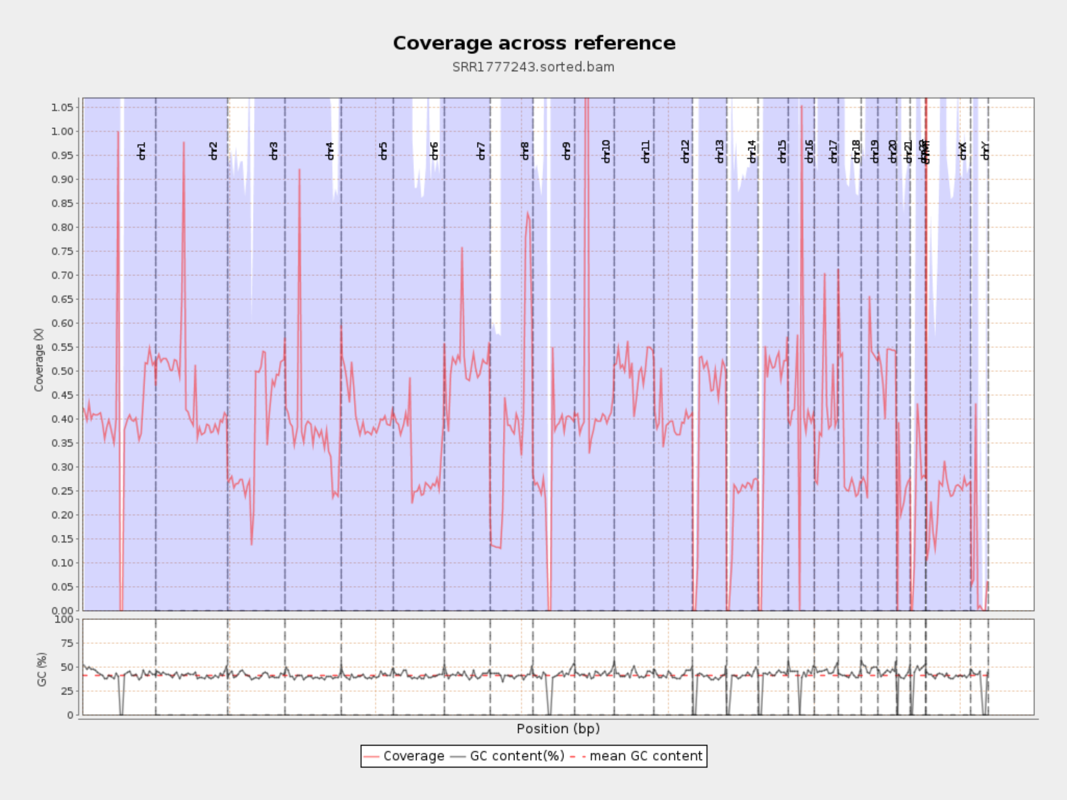
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

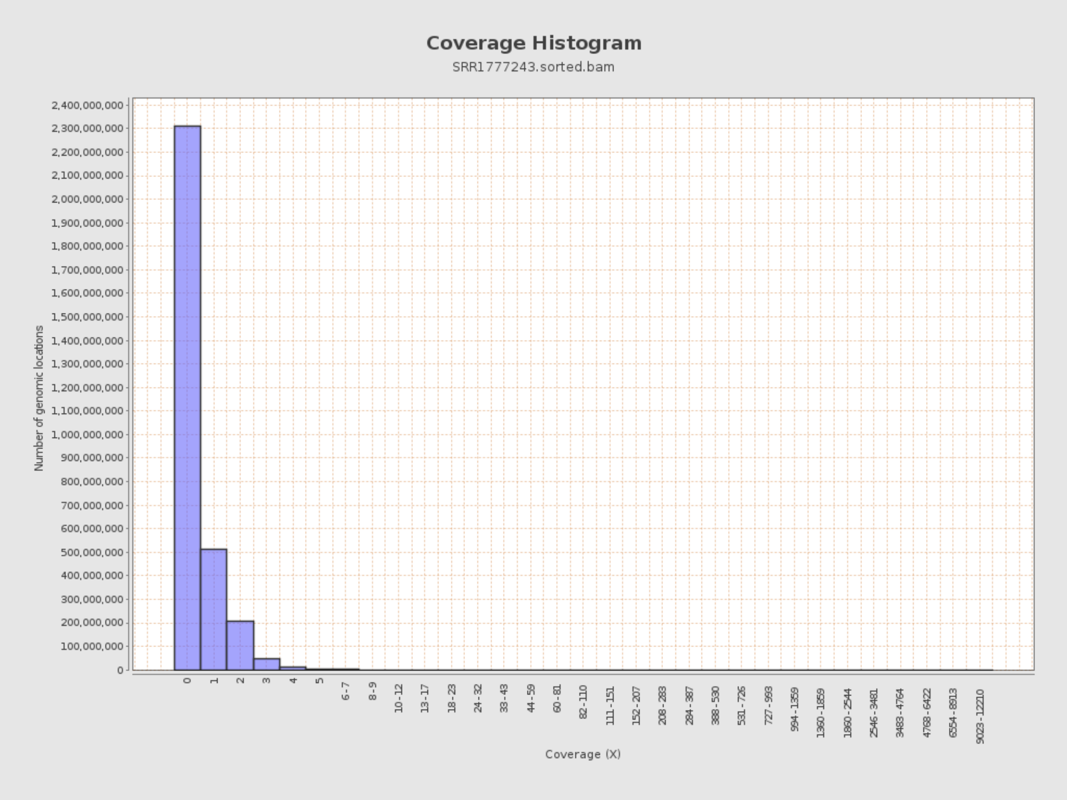
		bases	coverage	deviation
chr1	249250621	102111379	0.4097	12.4477
chr2	243199373	112584745	0.4629	3.3153
chr3	198022430	73782420	0.3726	1.0818
chr4	191154276	72237608	0.3779	4.2411
chr5	180915260	74928359	0.4142	0.8162
chr6	171115067	53588723	0.3132	1.5481
chr7	159138663	82033059	0.5155	4.9723
chr8	146364022	56809522	0.3881	2.7387
chr9	141213431	44258404	0.3134	4.27
chr10	135534747	64511845	0.476	11.1333
chr11	135006516	68401425	0.5067	2.3597
chr12	133851895	52936967	0.3955	0.9516
chr13	115169878	47788889	0.4149	0.7814
chr14	107349540	23252881	0.2166	0.6196
chr15	102531392	43590117	0.4251	0.8113
chr16	90354753	39616369	0.4385	4.5494
chr17	81195210	33081645	0.4074	1.5729
chr18	78077248	25844503	0.331	4.5126
chr19	59128983	25343974	0.4286	6.0446
chr20	63025520	32293181	0.5124	1.2602
chr21	48129895	11746938	0.2441	1.8083
chr22	51304566	11765015	0.2293	0.6122
chrMT	16571	605072	36.5139	7.1922
chrX	155270560	36248970	0.2335	1.1231

chrY	59373566	4680173	0.0788	5.2082

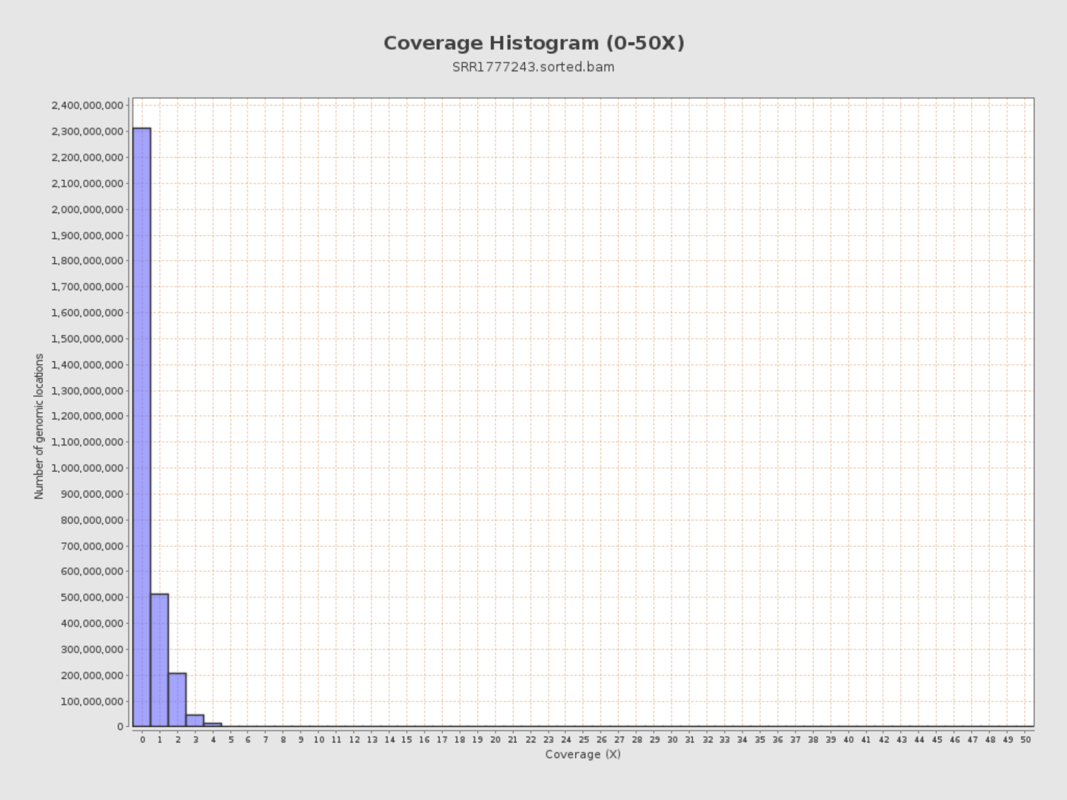
3. Results : Coverage across reference



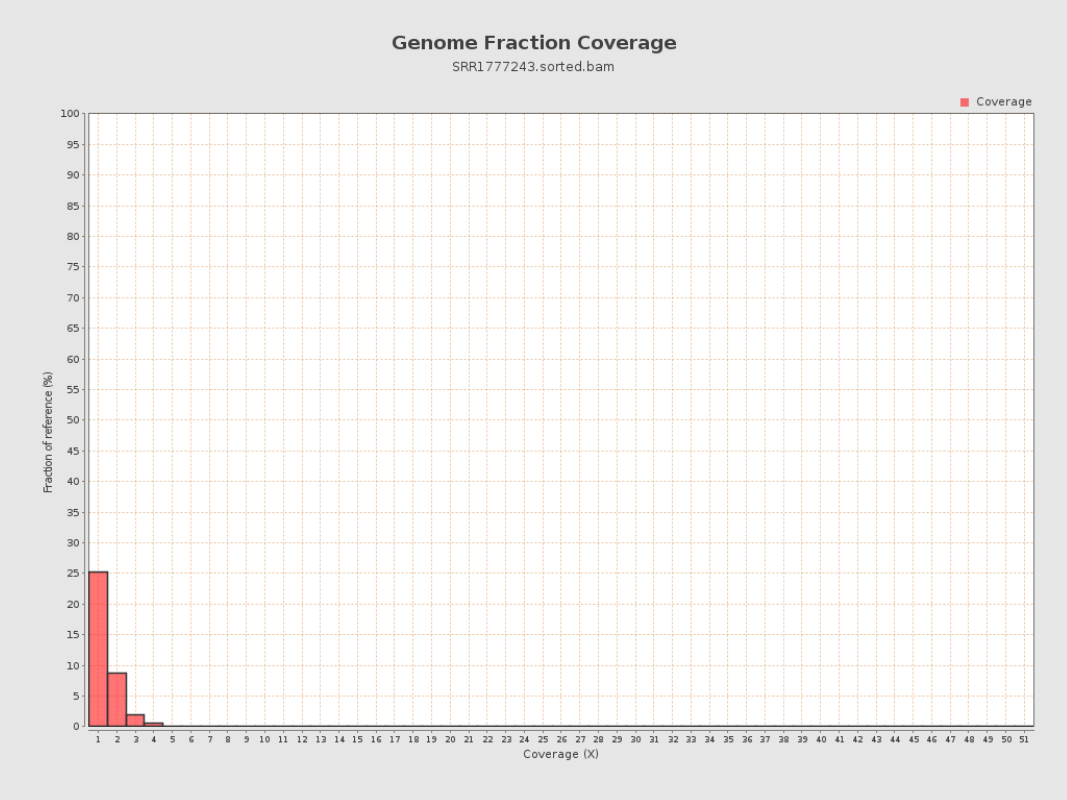
4. Results : Coverage Histogram



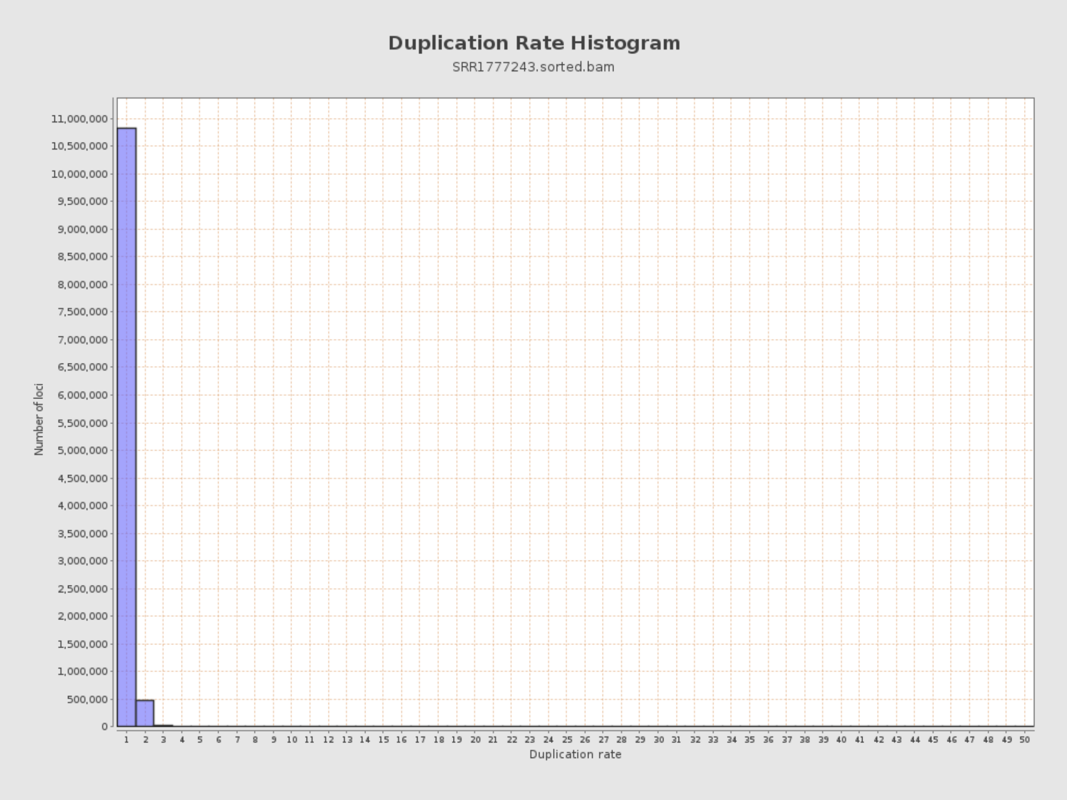
5. Results : Coverage Histogram (0-50X)



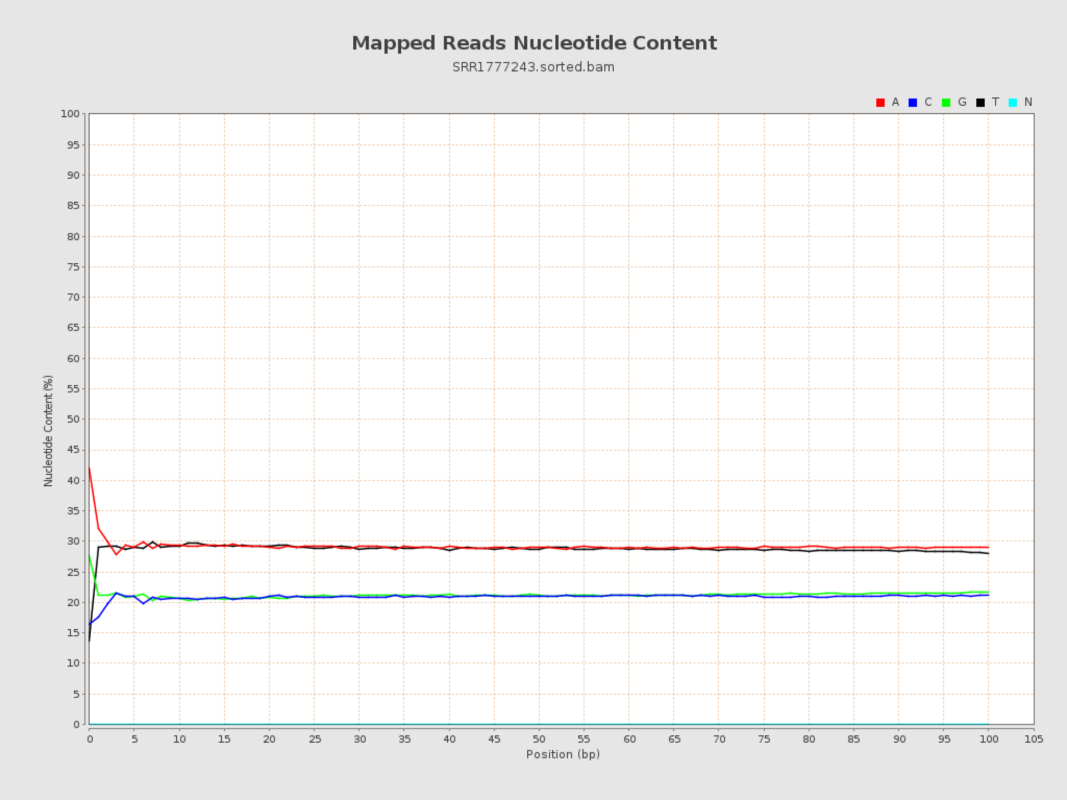
6. Results : Genome Fraction Coverage



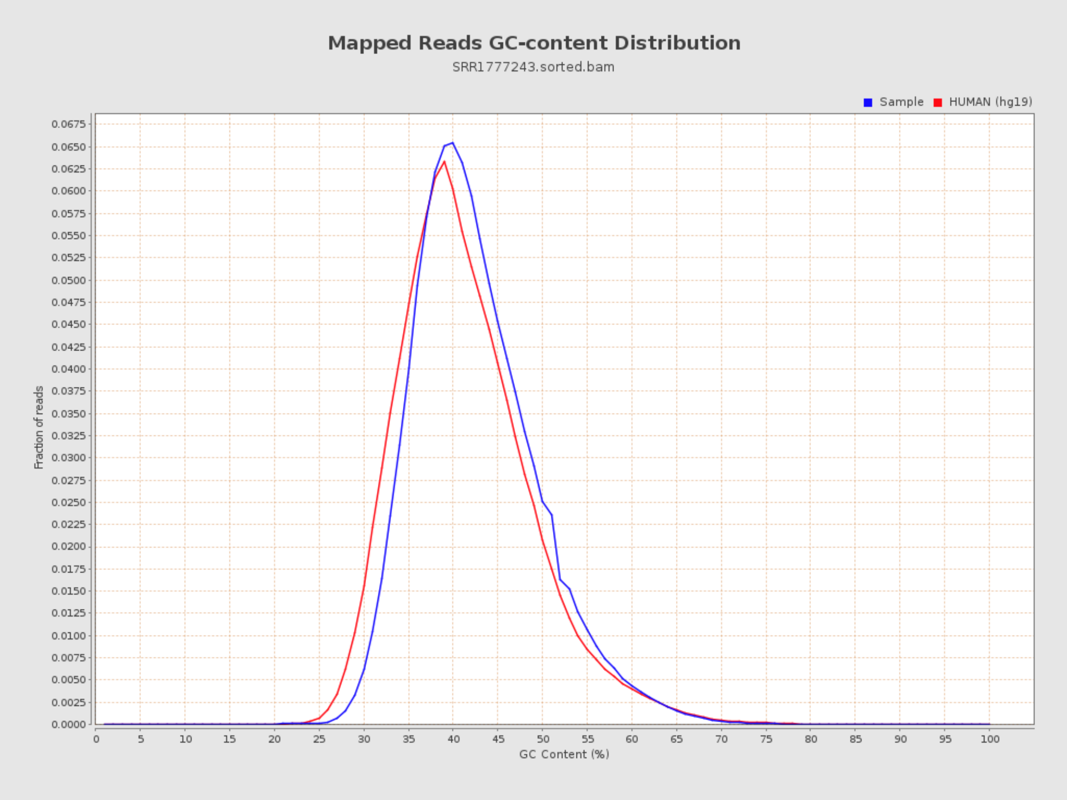
7. Results : Duplication Rate Histogram



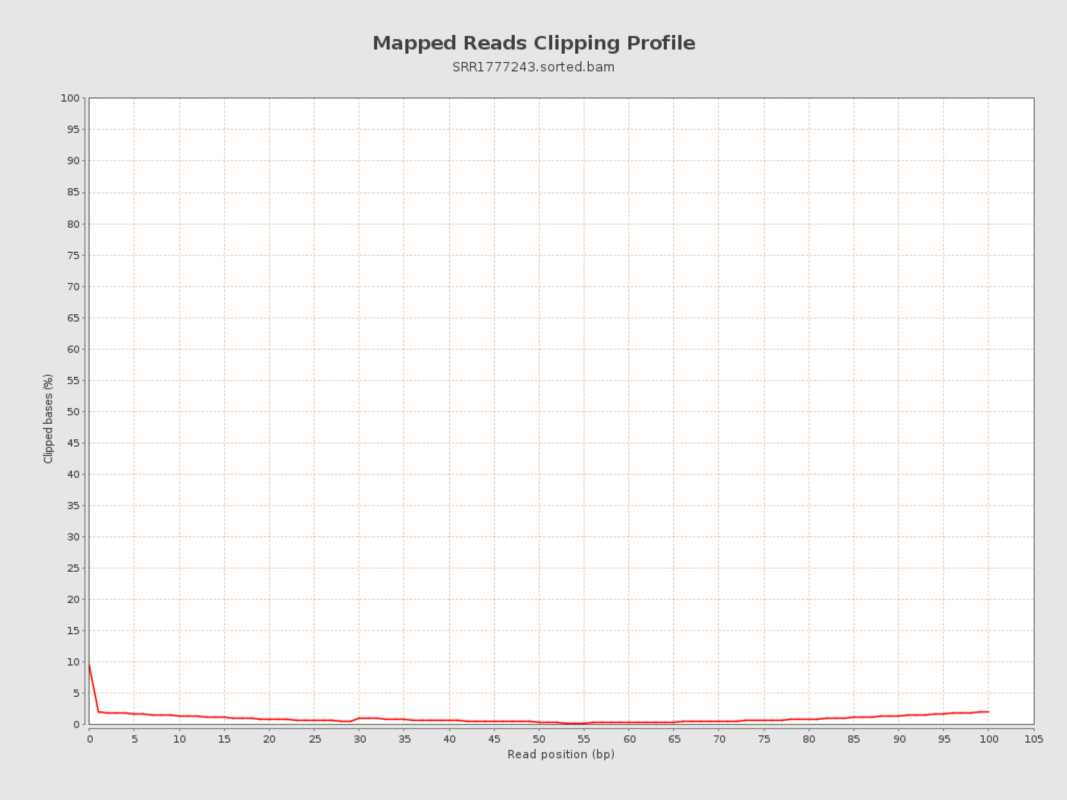
8. Results : Mapped Reads Nucleotide Content



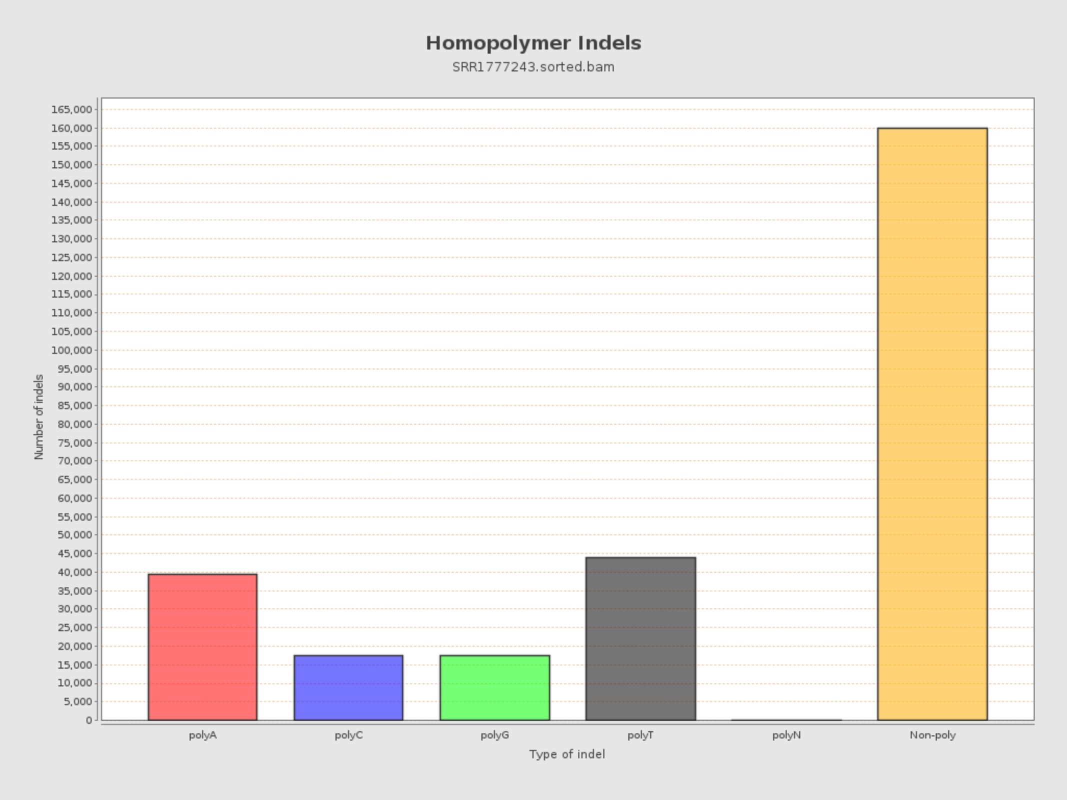
9. Results : Mapped Reads GC-content Distribution



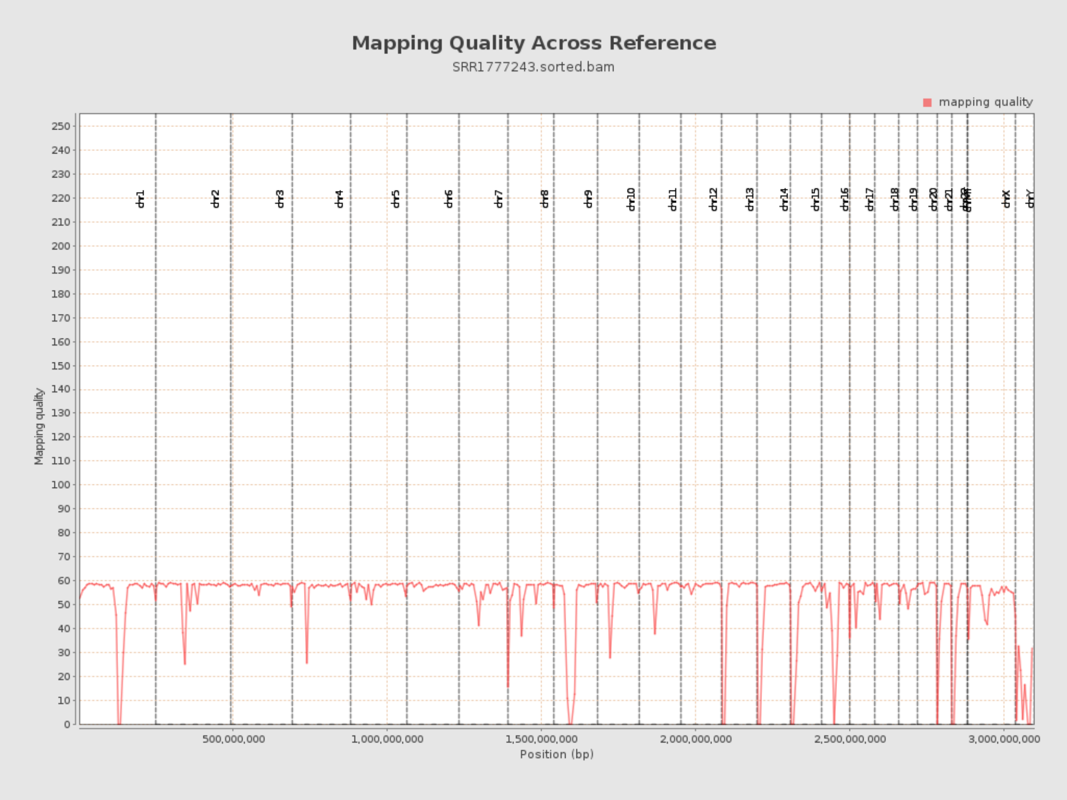
10. Results : Mapped Reads Clipping Profile



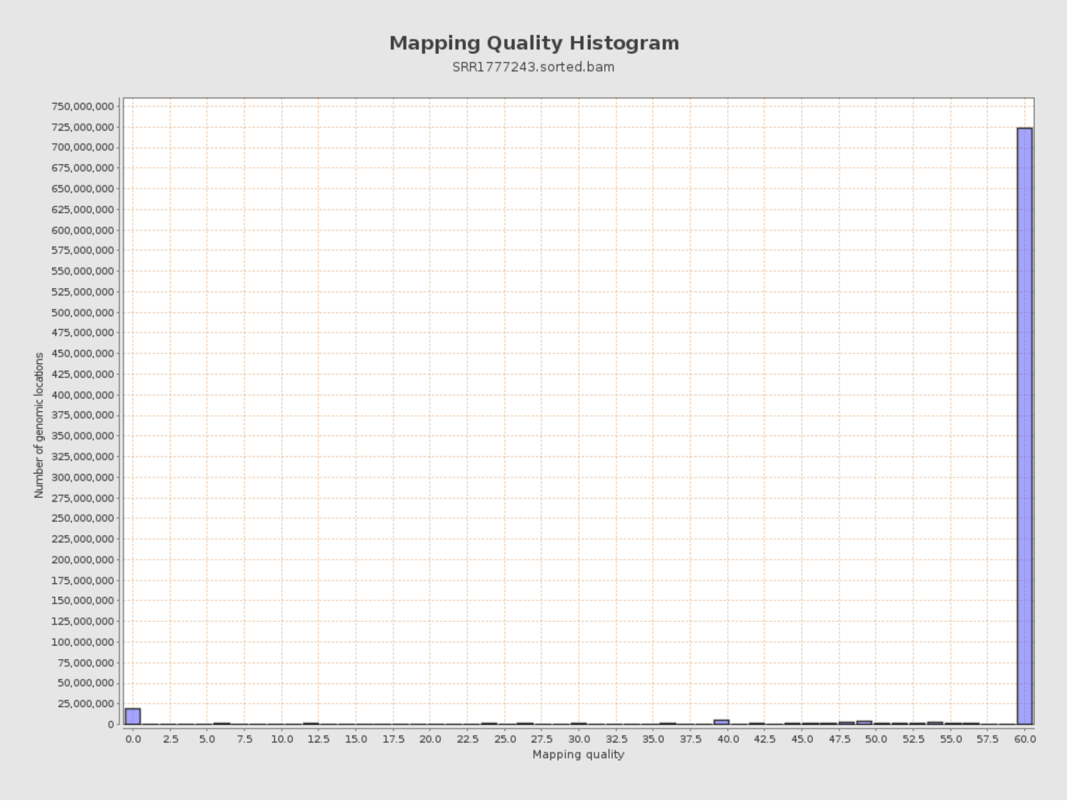
11. Results : Homopolymer Indels



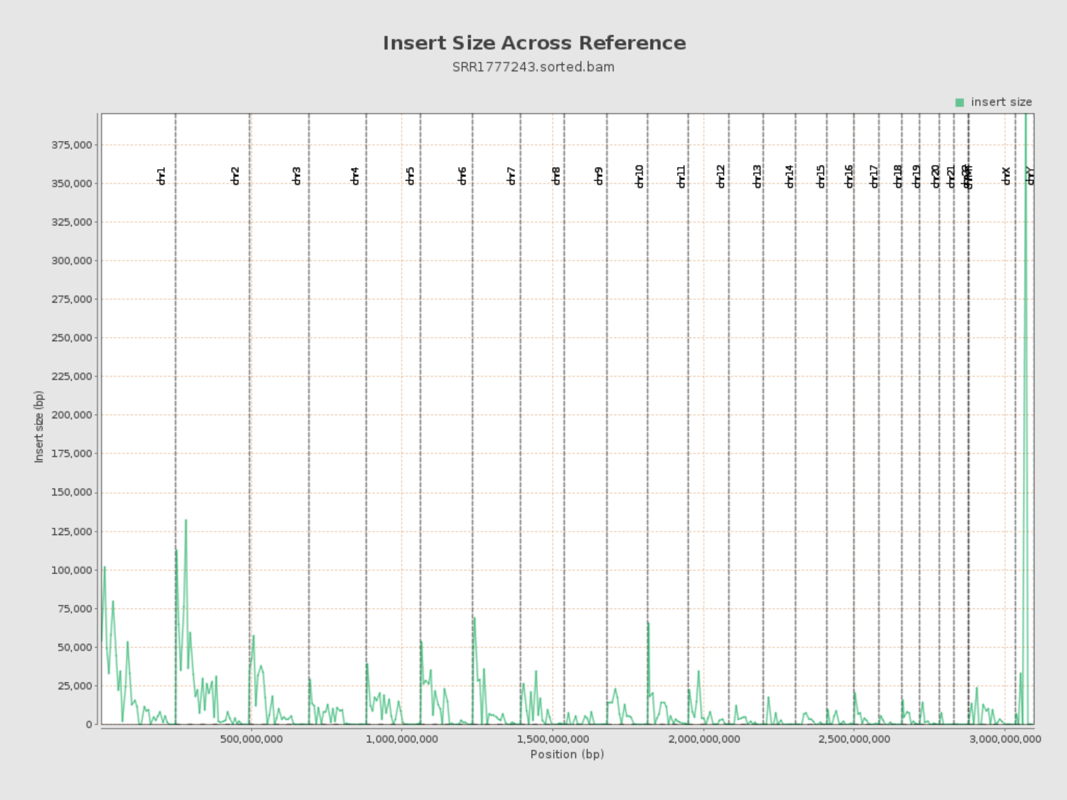
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram