Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 18:02:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777269.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_SRR1777269 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777269_1.fastq.gz SRR1777269_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 18:01:59 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777269.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	56,564,284
Mapped reads	56,128,483 / 99.23%
Unmapped reads	435,801 / 0.77%
Mapped paired reads	56,128,483 / 99.23%
Mapped reads, first in pair	28,067,779 / 49.62%
Mapped reads, second in pair	28,060,704 / 49.61%
Mapped reads, both in pair	55,948,990 / 98.91%
Mapped reads, singletons	179,493 / 0.32%
Secondary alignments	0
Supplementary alignments	2,044,951 / 3.62%
Read min/max/mean length	30 / 101 / 102.48
Duplicated reads (estimated)	25,586,000 / 45.23%
Duplication rate	37.32%
Clipped reads	7,388,630 / 13.06%

2.2. ACGT Content

Number/percentage of A's	1,564,733,861 / 27.81%
Number/percentage of C's	1,248,669,496 / 22.19%
Number/percentage of T's	1,553,058,320 / 27.6%
Number/percentage of G's	1,259,378,635 / 22.38%
Number/percentage of N's	237,762 / 0%

GC Percentage	44.58%

2.3. Coverage

Mean	1.8177
Standard Deviation	16.2413

2.4. Mapping Quality

Mean Mapping Quality	54.57

2.5. Insert size

Mean	338,640.85
Standard Deviation	5,695,311.97
P25/Median/P75	182 / 233 / 295

2.6. Mismatches and indels

General error rate	0.27%
Mismatches	13,868,444
Insertions	1,015,132
Mapped reads with at least one insertion	1.78%
Deletions	371,158
Mapped reads with at least one deletion	0.65%
Homopolymer indels	51.89%

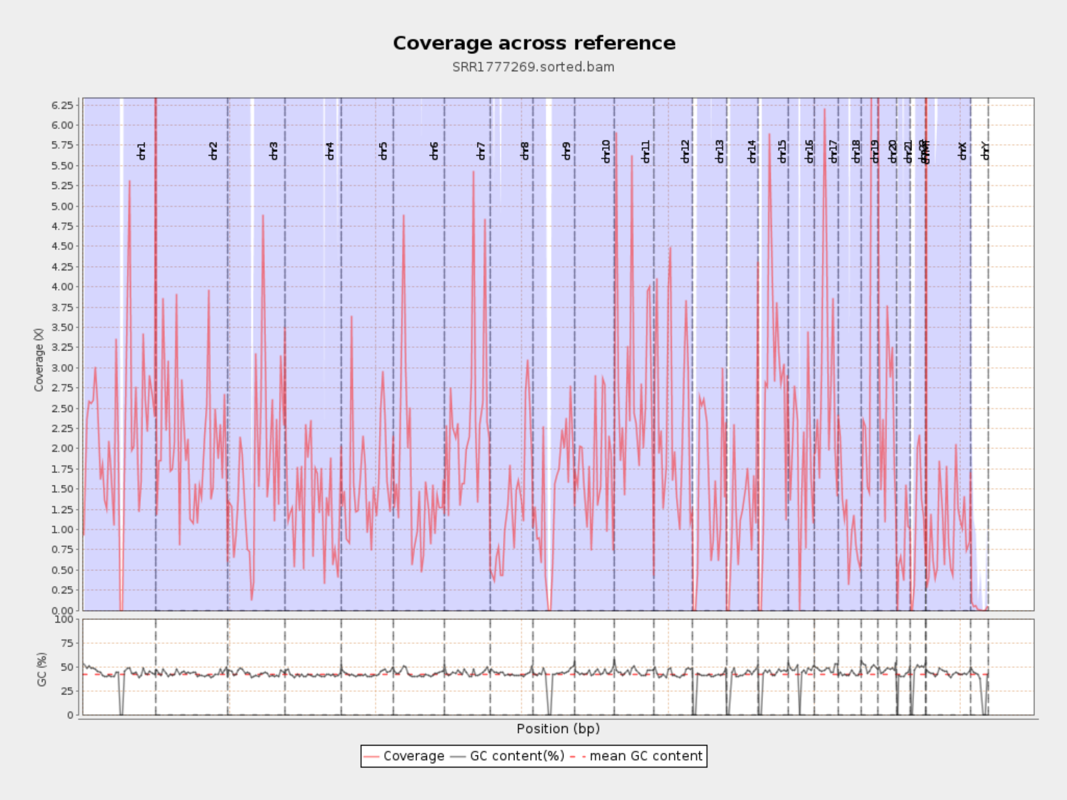
2.7. Chromosome stats

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

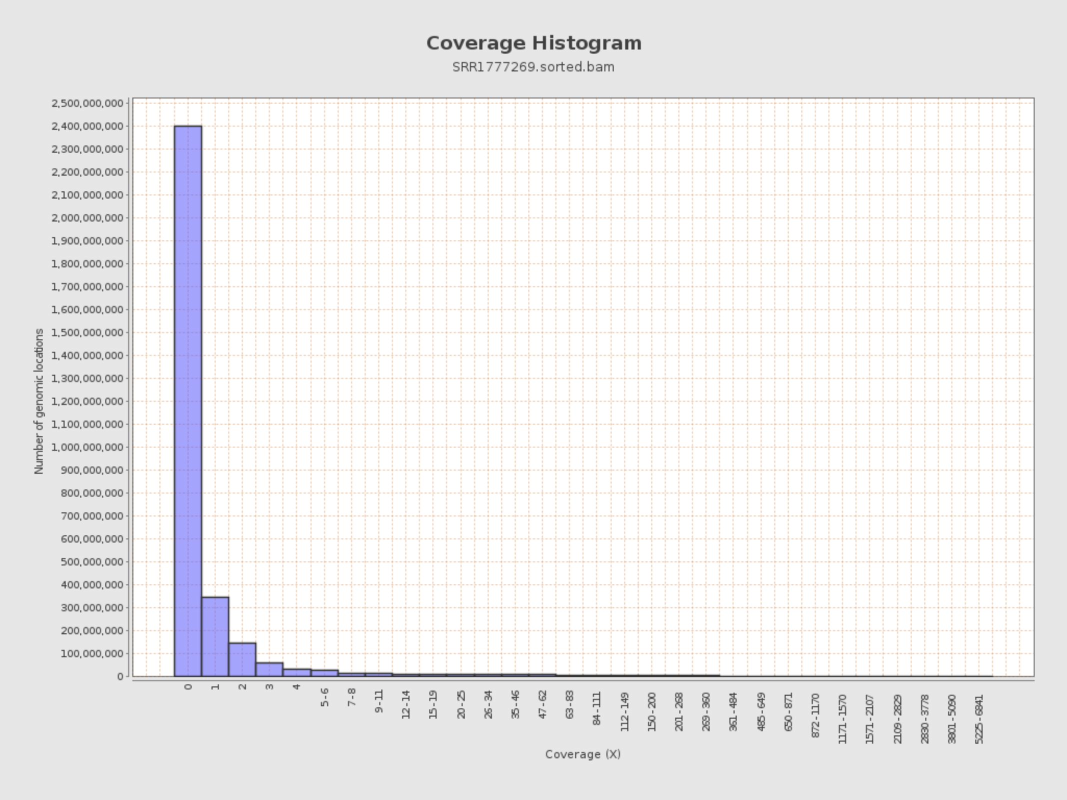
		bases	coverage	deviation
chr1	249250621	554147977	2.2233	18.2533
chr2	243199373	499338808	2.0532	16.7325
chr3	198022430	349567494	1.7653	16.3805
chr4	191154276	252427687	1.3205	12.6263
chr5	180915260	297061026	1.642	14.3655
chr6	171115067	264630401	1.5465	13.6703
chr7	159138663	373420685	2.3465	20.3603
chr8	146364022	192762688	1.317	13.8128
chr9	141213431	193590713	1.3709	13.2152
chr10	135534747	236277905	1.7433	14.7649
chr11	135006516	383578052	2.8412	22.5683
chr12	133851895	321849049	2.4045	18.2087
chr13	115169878	168410541	1.4623	14.7613
chr14	107349540	123640171	1.1518	11.5299
chr15	102531392	265212745	2.5866	21.4712
chr16	90354753	160124127	1.7722	14.2525
chr17	81195210	237959162	2.9307	21.9258
chr18	78077248	87915010	1.126	11.045
chr19	59128983	264125884	4.4669	28.6602
chr20	63025520	152390786	2.4179	18.4093
chr21	48129895	37409111	0.7773	9.7815
chr22	51304566	55543010	1.0826	9.6207
chrMT	16571	2344059	141.4555	47.7062
chrX	155270560	151370652	0.9749	10.3218

chrY	59373566	1825275	0.0307	0.9064

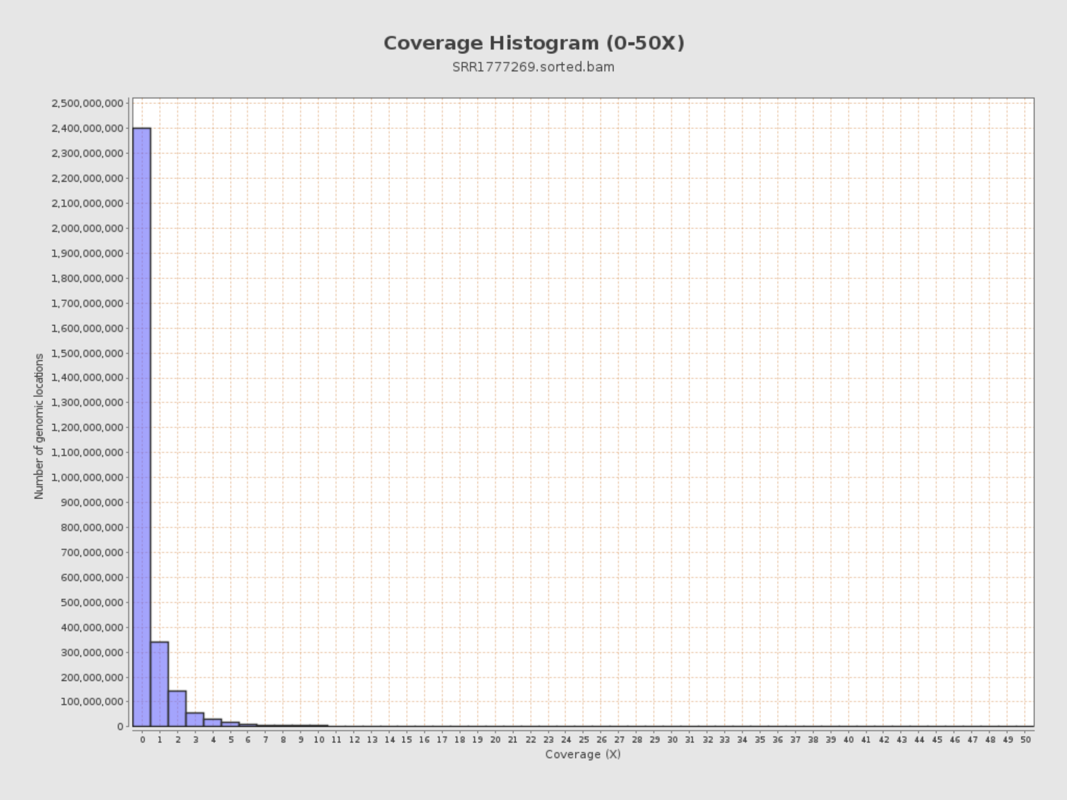
3. Results : Coverage across reference



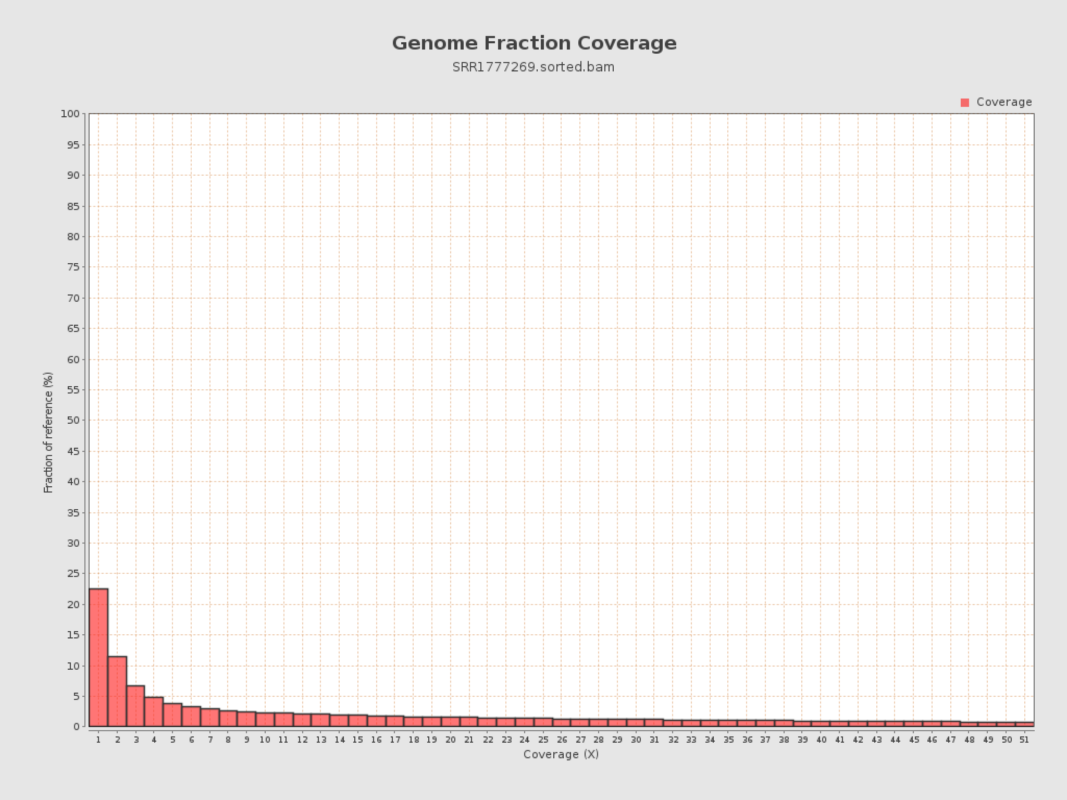
4. Results : Coverage Histogram



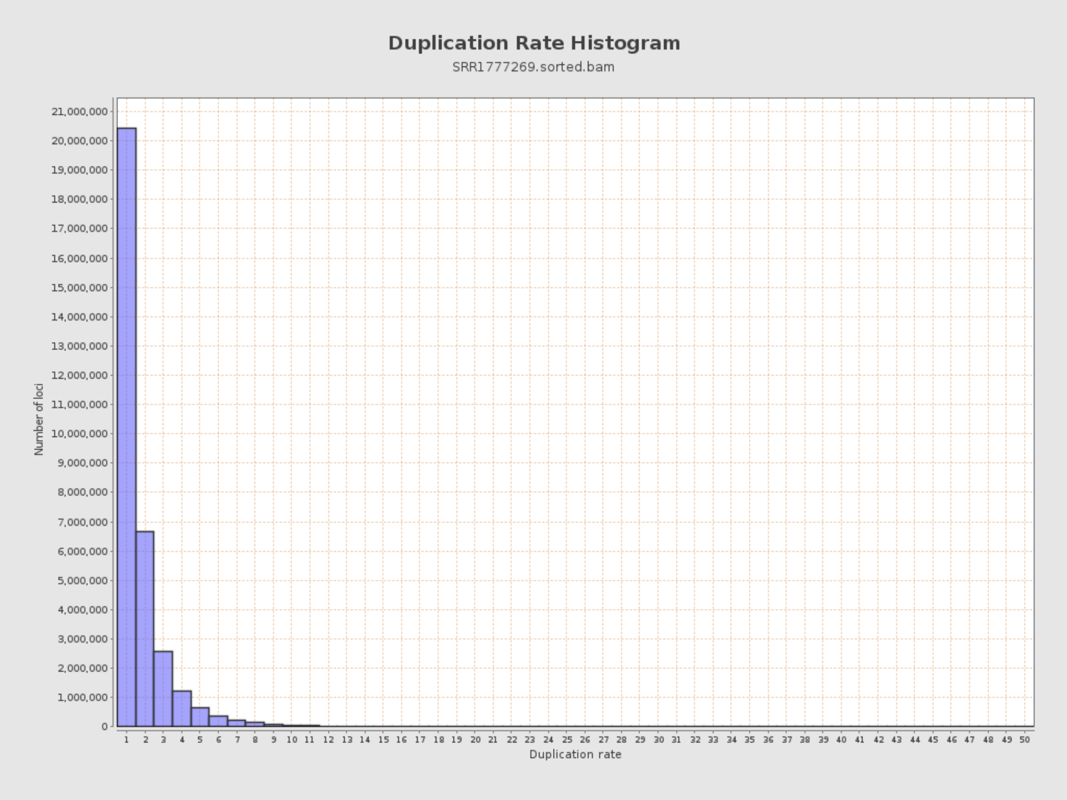
5. Results : Coverage Histogram (0-50X)



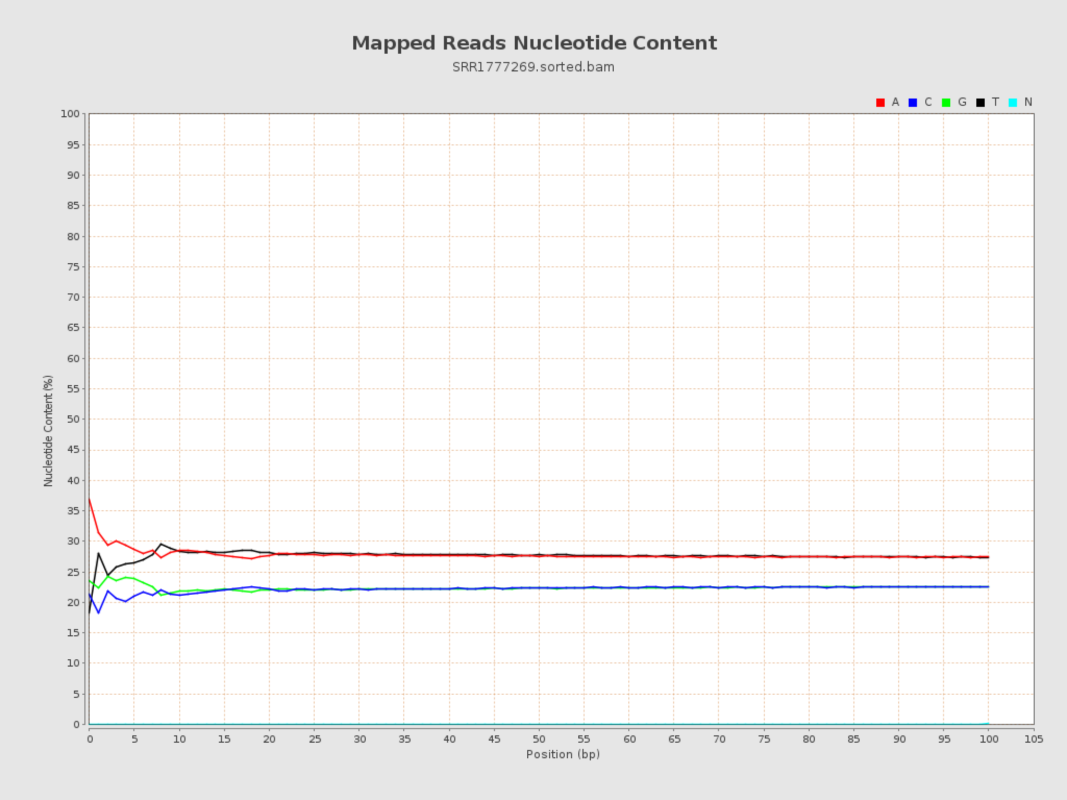
6. Results : Genome Fraction Coverage



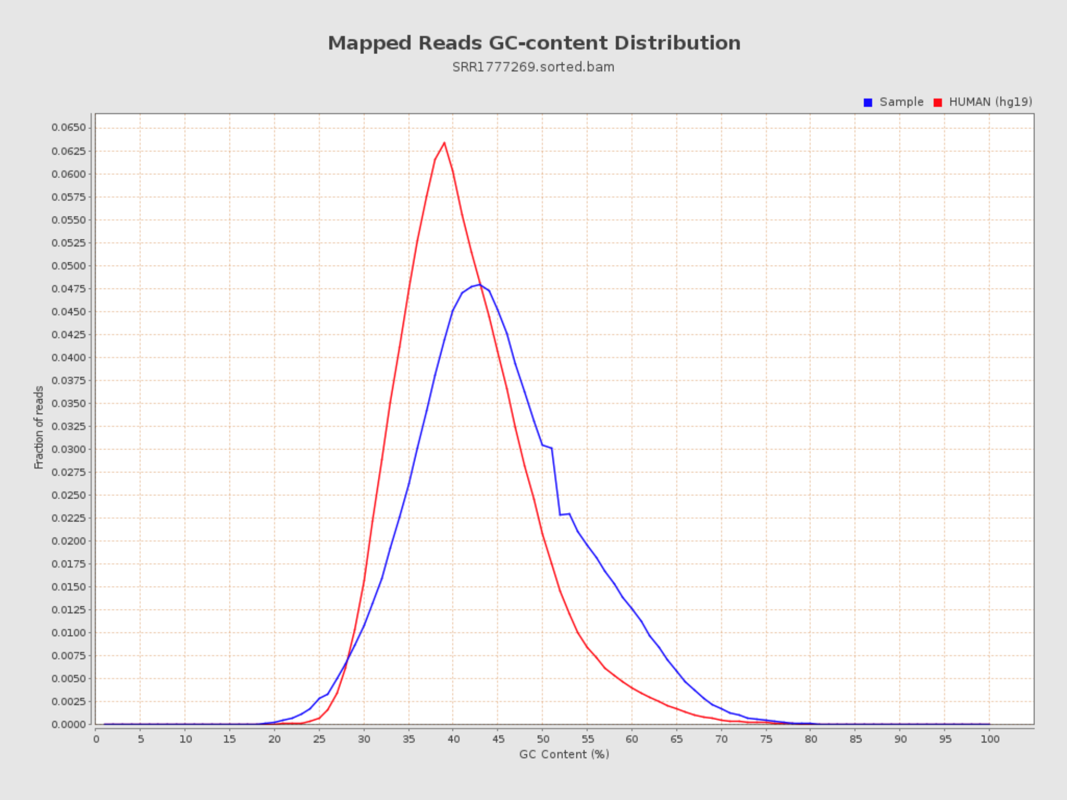
7. Results : Duplication Rate Histogram



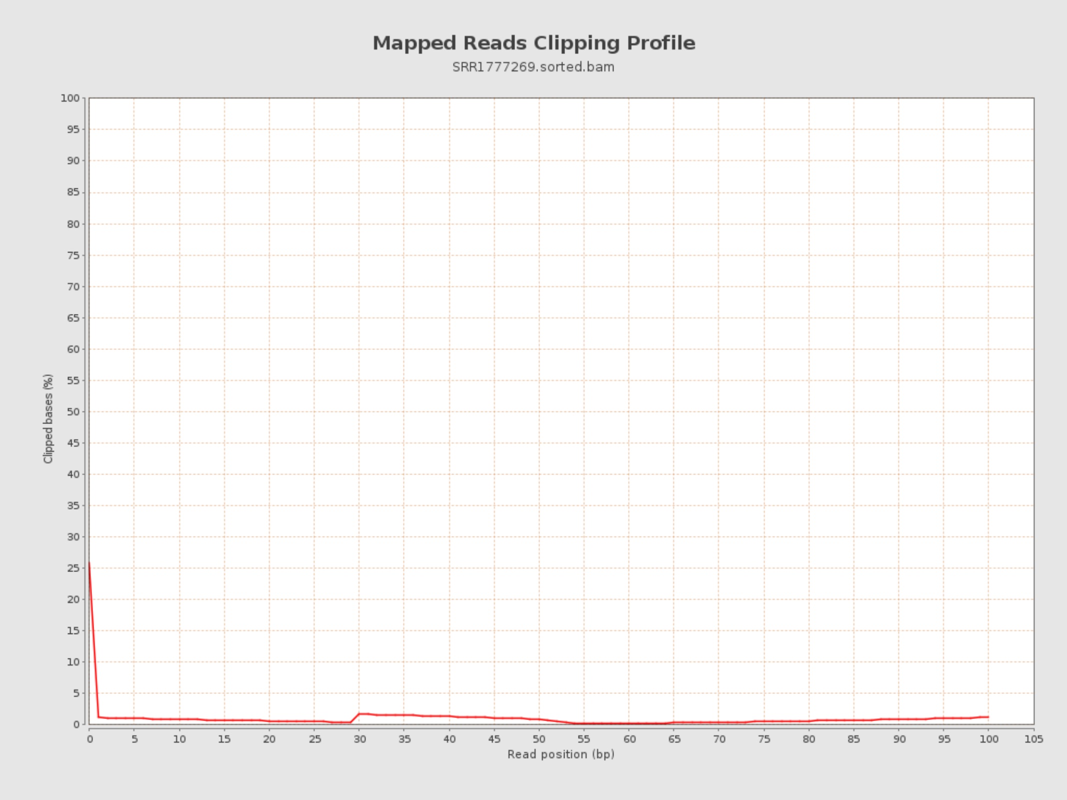
8. Results : Mapped Reads Nucleotide Content



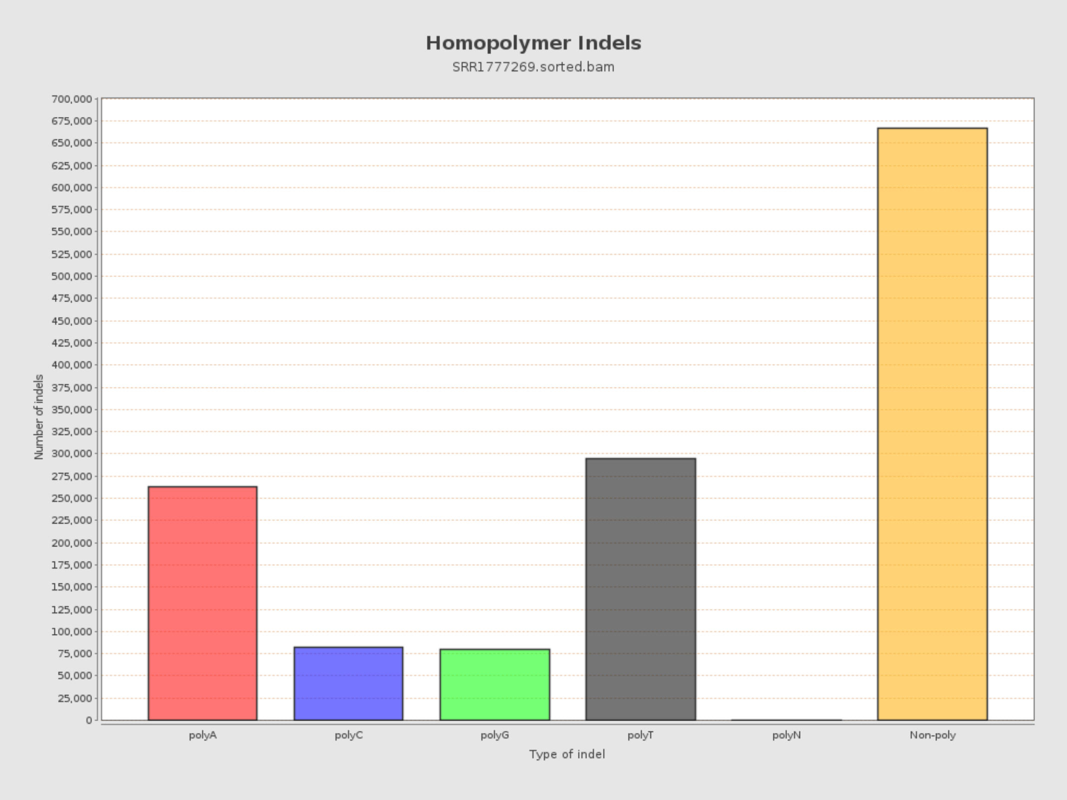
9. Results : Mapped Reads GC-content Distribution



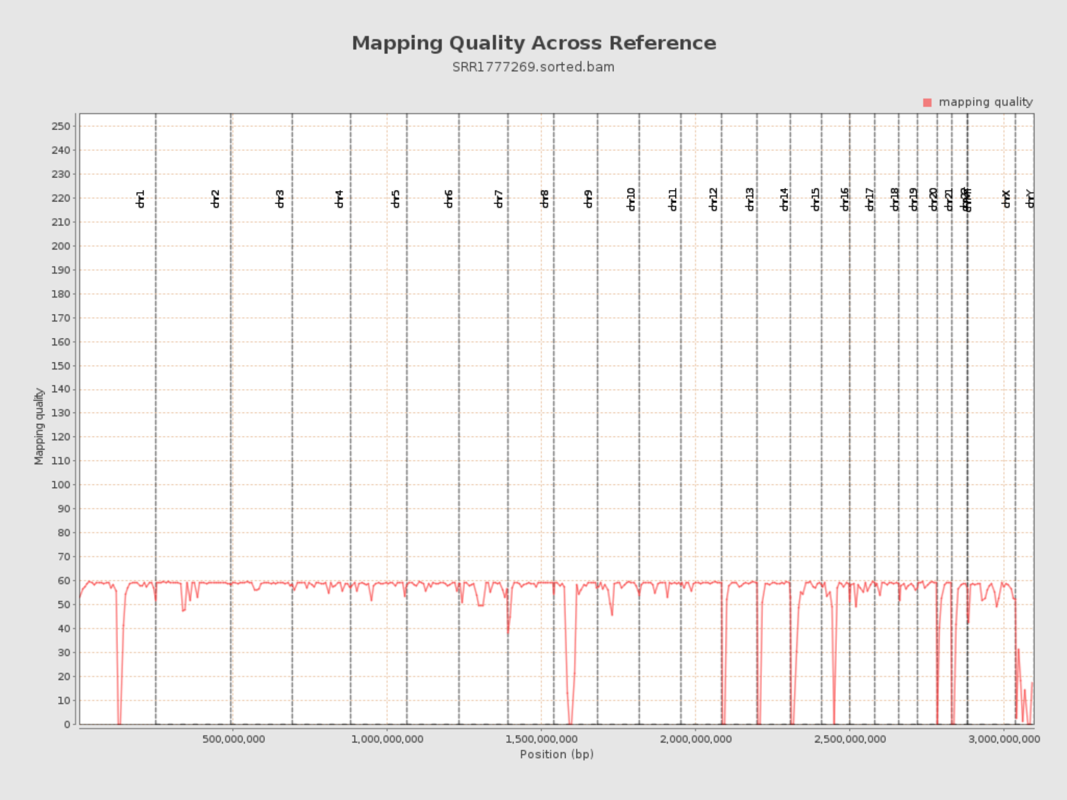
10. Results : Mapped Reads Clipping Profile



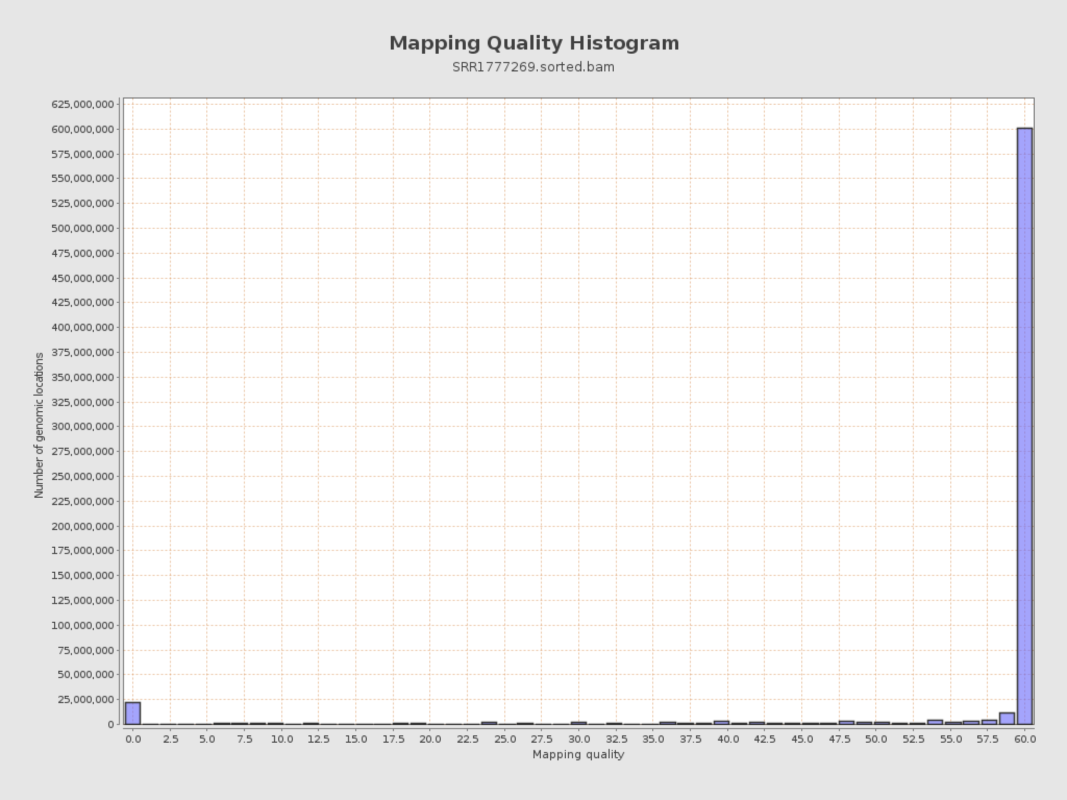
11. Results : Homopolymer Indels



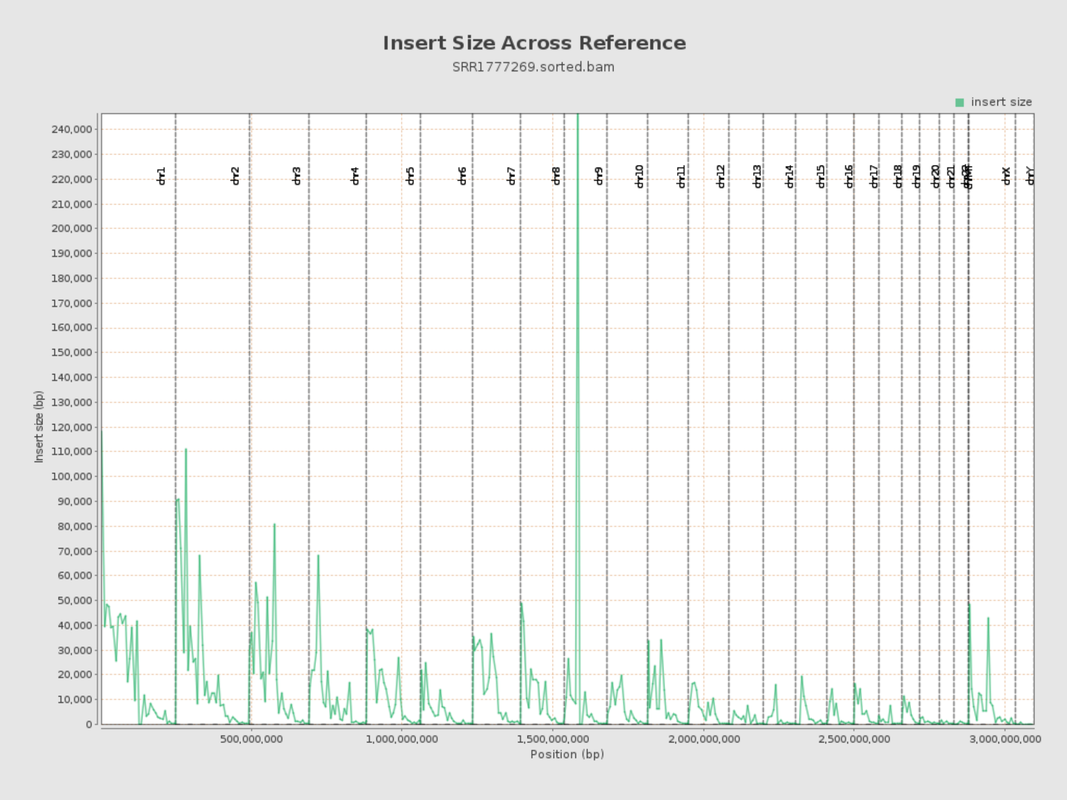
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram