Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 18:57:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777270.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_SRR1777270 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777270_1.fastq.gz SRR1777270_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 18:57:56 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777270.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	55,627,034
Mapped reads	55,203,436 / 99.24%
Unmapped reads	423,598 / 0.76%
Mapped paired reads	55,203,436 / 99.24%
Mapped reads, first in pair	27,605,587 / 49.63%
Mapped reads, second in pair	27,597,849 / 49.61%
Mapped reads, both in pair	55,026,860 / 98.92%
Mapped reads, singletons	176,576 / 0.32%
Secondary alignments	0
Supplementary alignments	2,011,365 / 3.62%
Read min/max/mean length	30 / 101 / 102.48
Duplicated reads (estimated)	24,944,161 / 44.84%
Duplication rate	37.01%
Clipped reads	7,268,345 / 13.07%

2.2. ACGT Content

Number/percentage of A's	1,537,466,482 / 27.79%
Number/percentage of C's	1,229,465,493 / 22.22%
Number/percentage of T's	1,526,032,447 / 27.58%
Number/percentage of G's	1,240,167,971 / 22.41%
Number/percentage of N's	208,855 / 0%

GC Percentage	44.63%

2.3. Coverage

Mean	1.7877
Standard Deviation	15.9492

2.4. Mapping Quality

Mean Mapping Quality	54.57

2.5. Insert size

Mean	338,999.13
Standard Deviation	5,710,154.63
P25/Median/P75	183 / 233 / 295

2.6. Mismatches and indels

General error rate	0.27%
Mismatches	13,721,859
Insertions	1,002,525
Mapped reads with at least one insertion	1.79%
Deletions	368,508
Mapped reads with at least one deletion	0.66%
Homopolymer indels	51.9%

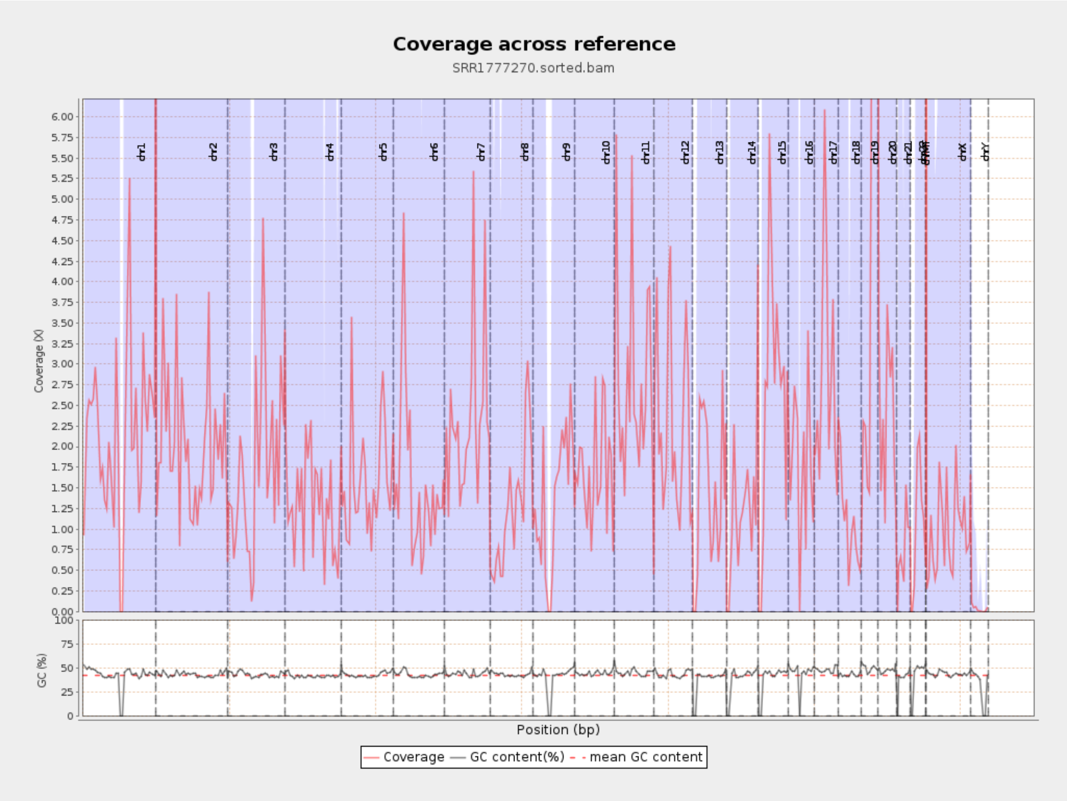
2.7. Chromosome stats

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

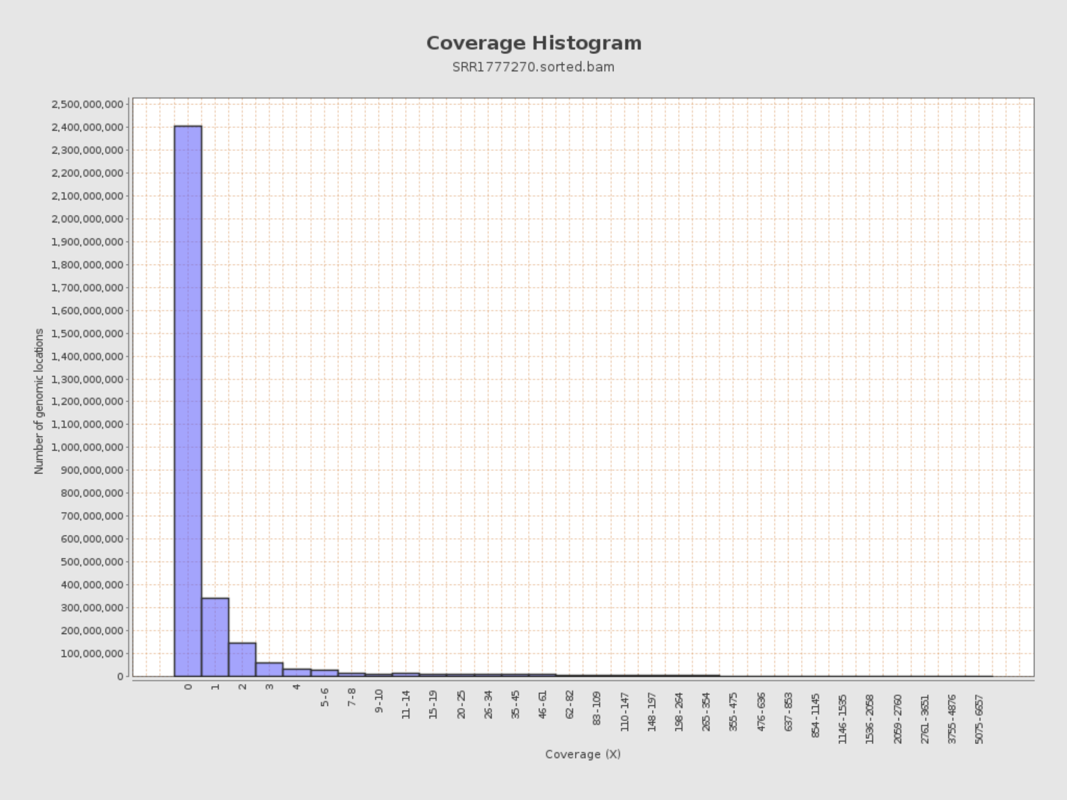
		bases	**coverage**	**deviation**
chr1	249250621	545379880	2.1881	17.929
chr2	243199373	490626404	2.0174	16.4313
chr3	198022430	343523812	1.7348	16.0641
chr4	191154276	248006501	1.2974	12.3867
chr5	180915260	292051270	1.6143	14.0994
chr6	171115067	260191872	1.5206	13.4111
chr7	159138663	367380233	2.3086	19.993
chr8	146364022	189065314	1.2917	13.5625
chr9	141213431	190387435	1.3482	13.0238
chr10	135534747	232262567	1.7137	14.4934
chr11	135006516	377310508	2.7948	22.152
chr12	133851895	316819015	2.3669	17.9309
chr13	115169878	164631072	1.4295	14.4186
chr14	107349540	121186164	1.1289	11.2551
chr15	102531392	260738387	2.543	21.0843
chr16	90354753	157945707	1.7481	14.0288
chr17	81195210	234268757	2.8853	21.5164
chr18	78077248	86410372	1.1067	10.8074
chr19	59128983	260861363	4.4117	28.2199
chr20	63025520	150178131	2.3828	18.1138
chr21	48129895	37072074	0.7703	9.6235
chr22	51304566	54594710	1.0641	9.4326
chrMT	16571	2324994	140.305	47.101
chrX	155270560	149102857	0.9603	10.1559

chrY	59373566	1853238	0.0312	0.9303

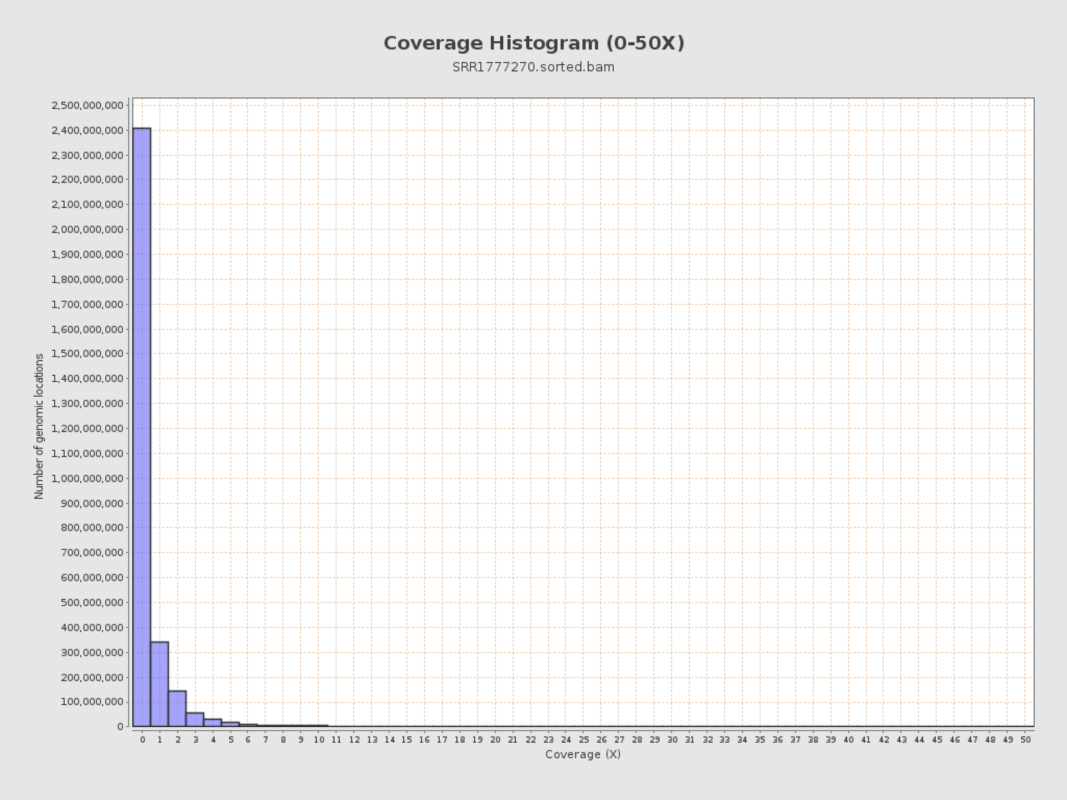
3. Results : Coverage across reference



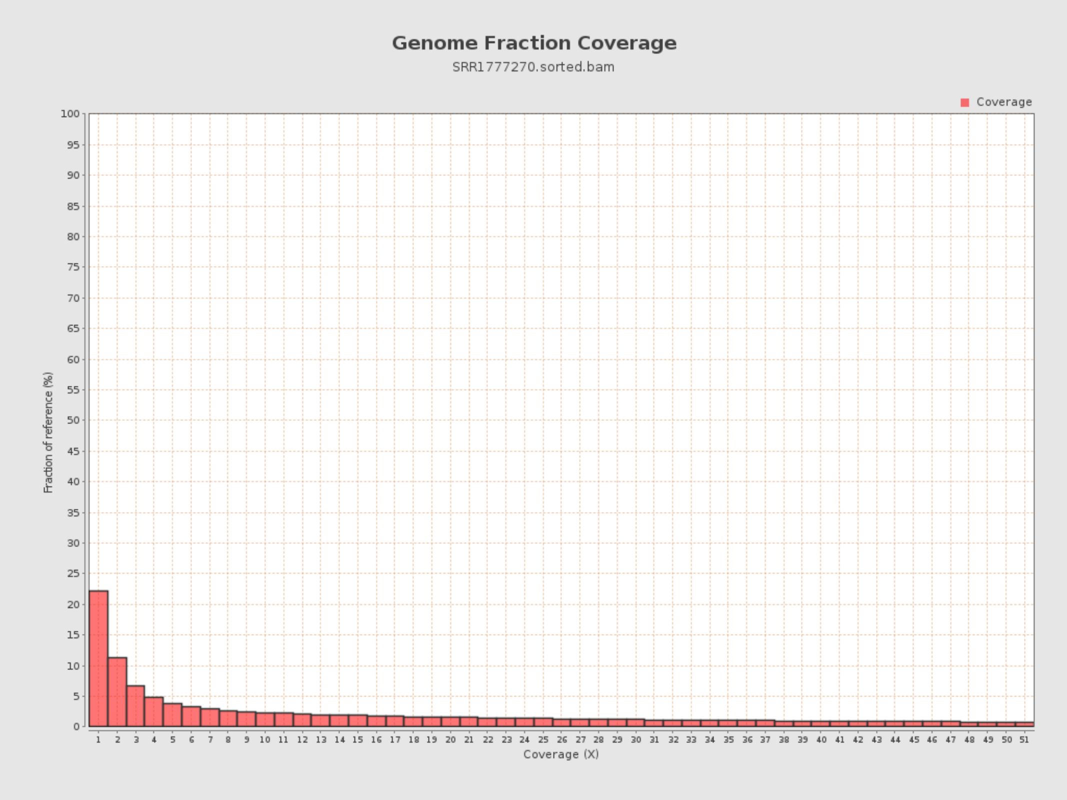
4. Results : Coverage Histogram



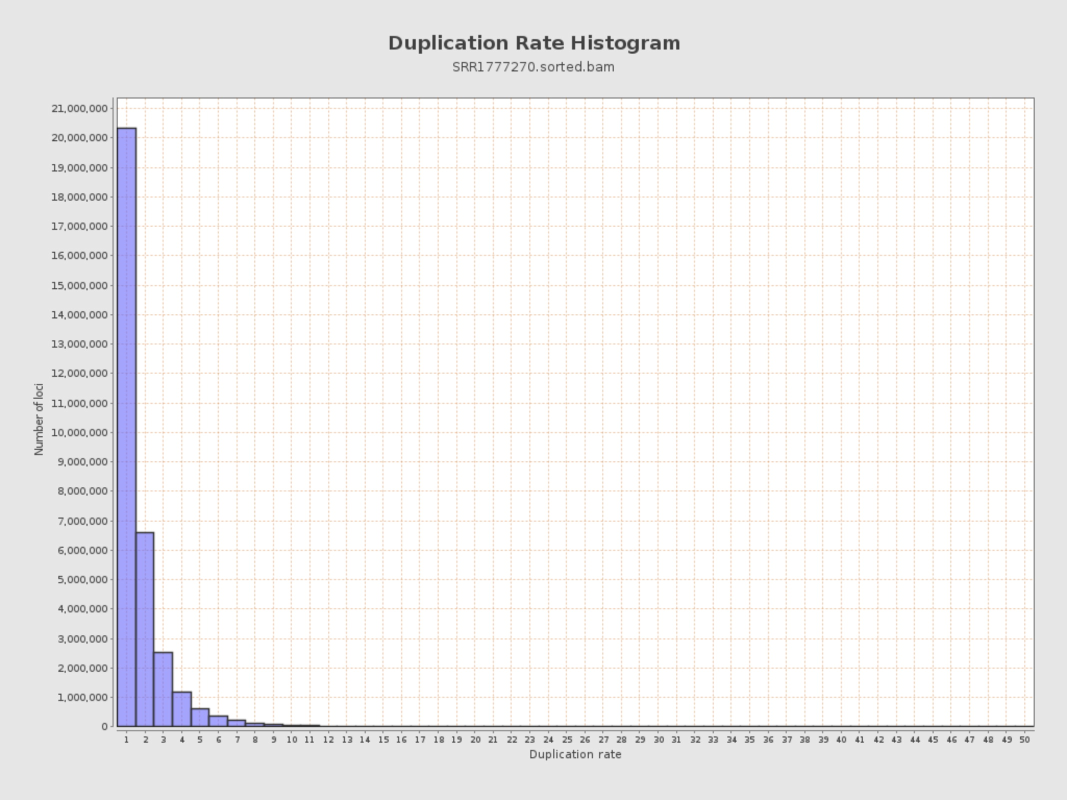
5. Results : Coverage Histogram (0-50X)



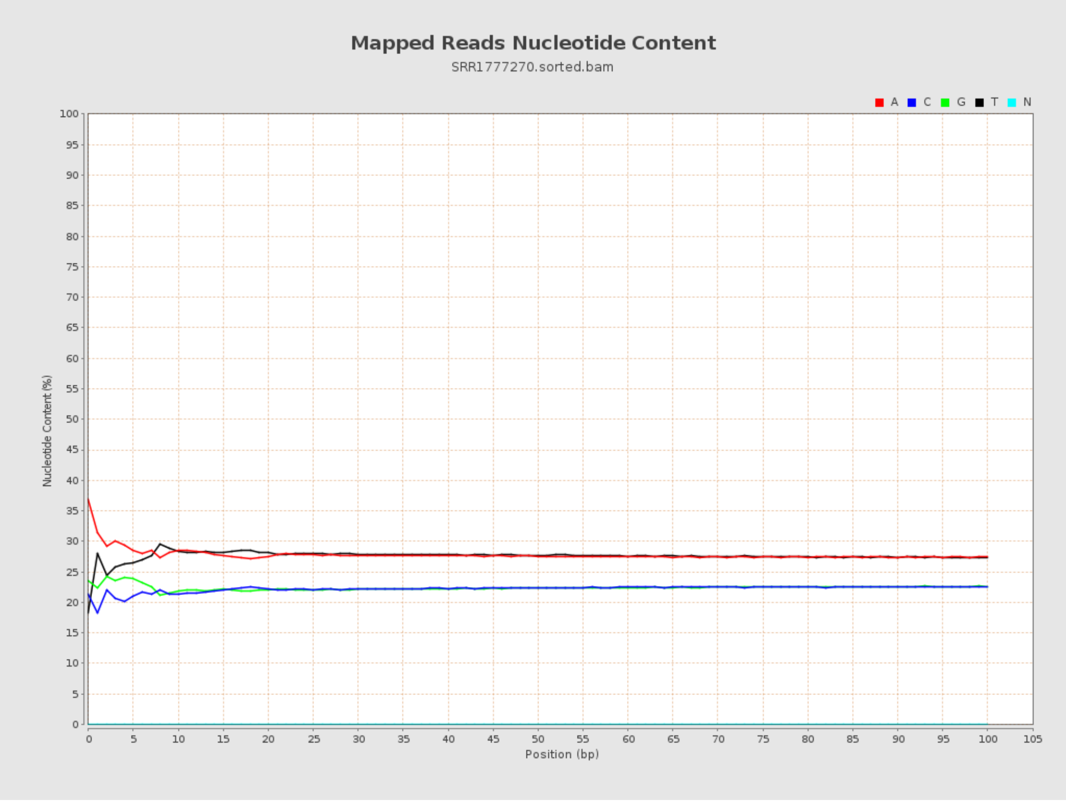
6. Results : Genome Fraction Coverage



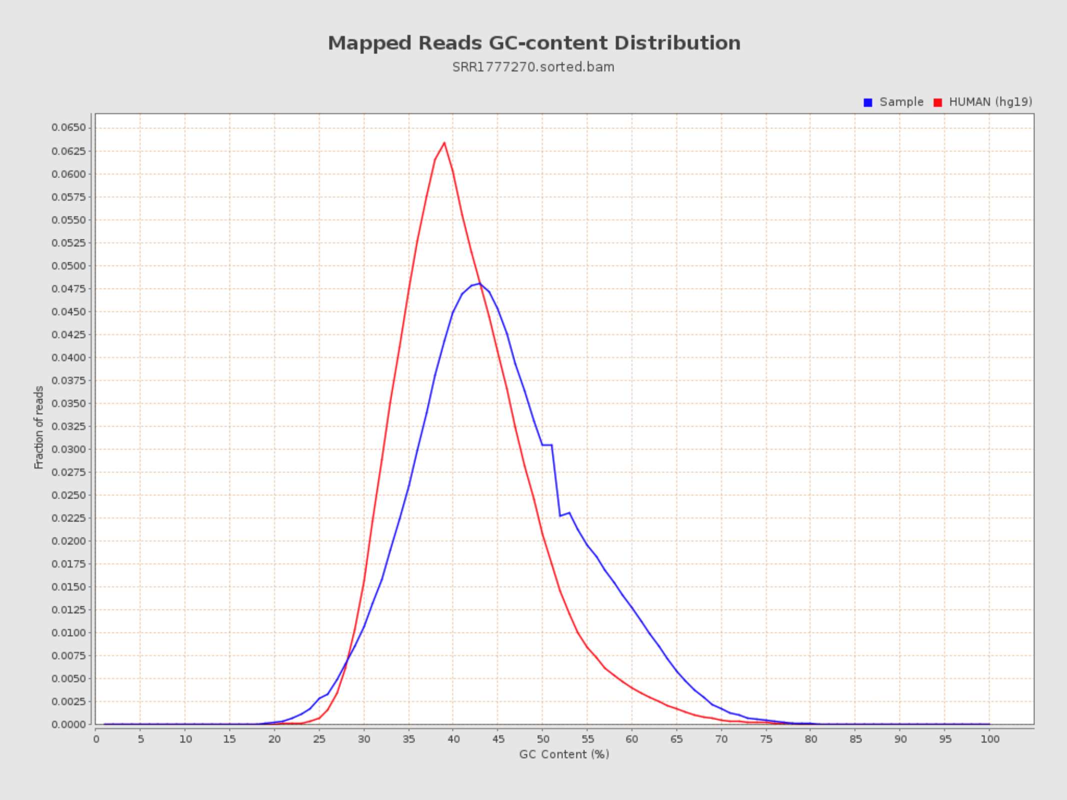
7. Results : Duplication Rate Histogram



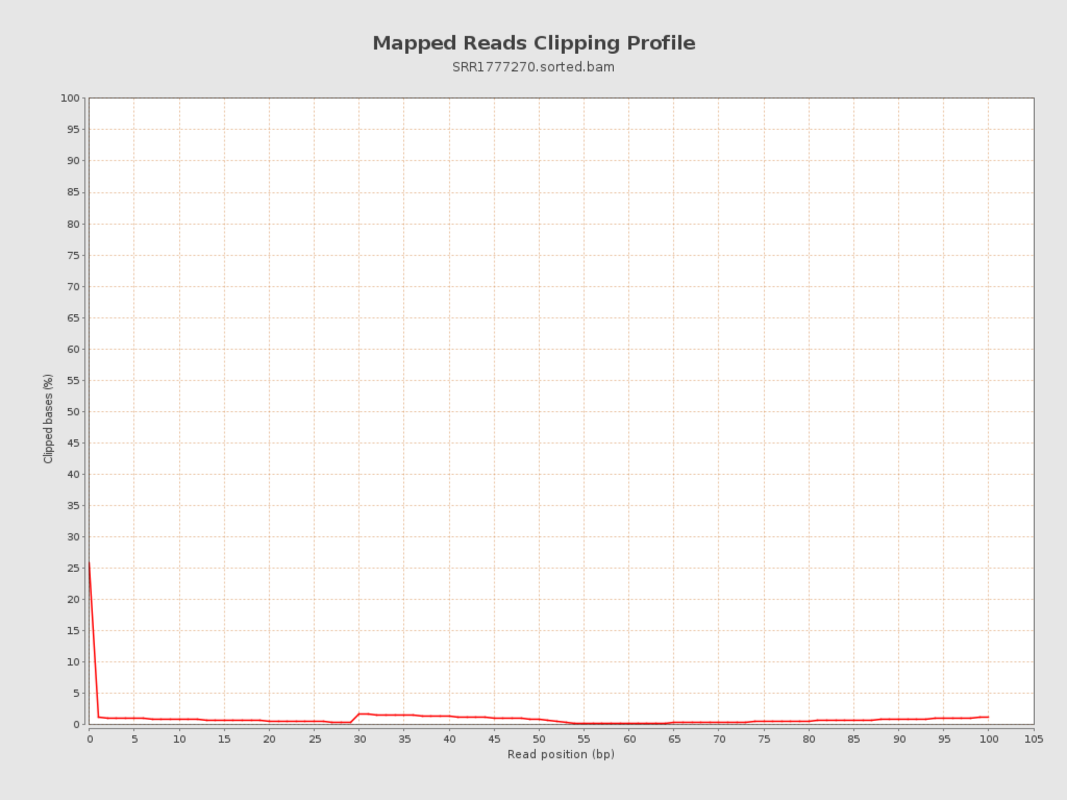
8. Results : Mapped Reads Nucleotide Content



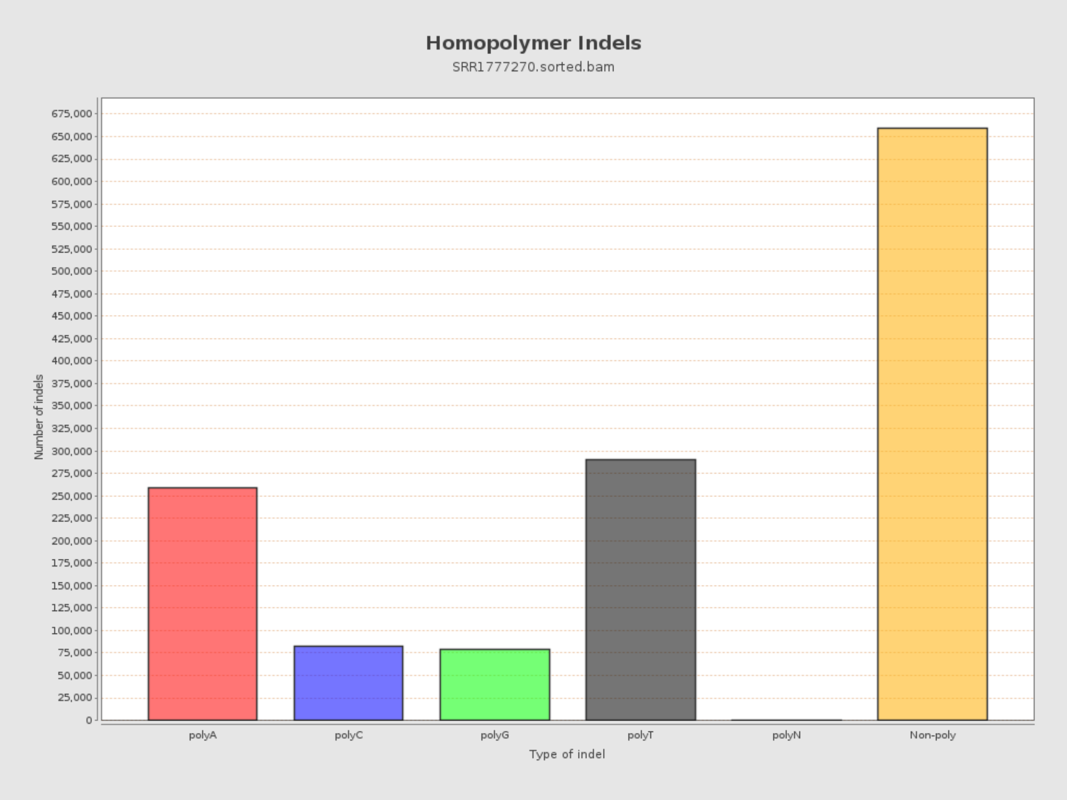
9. Results : Mapped Reads GC-content Distribution



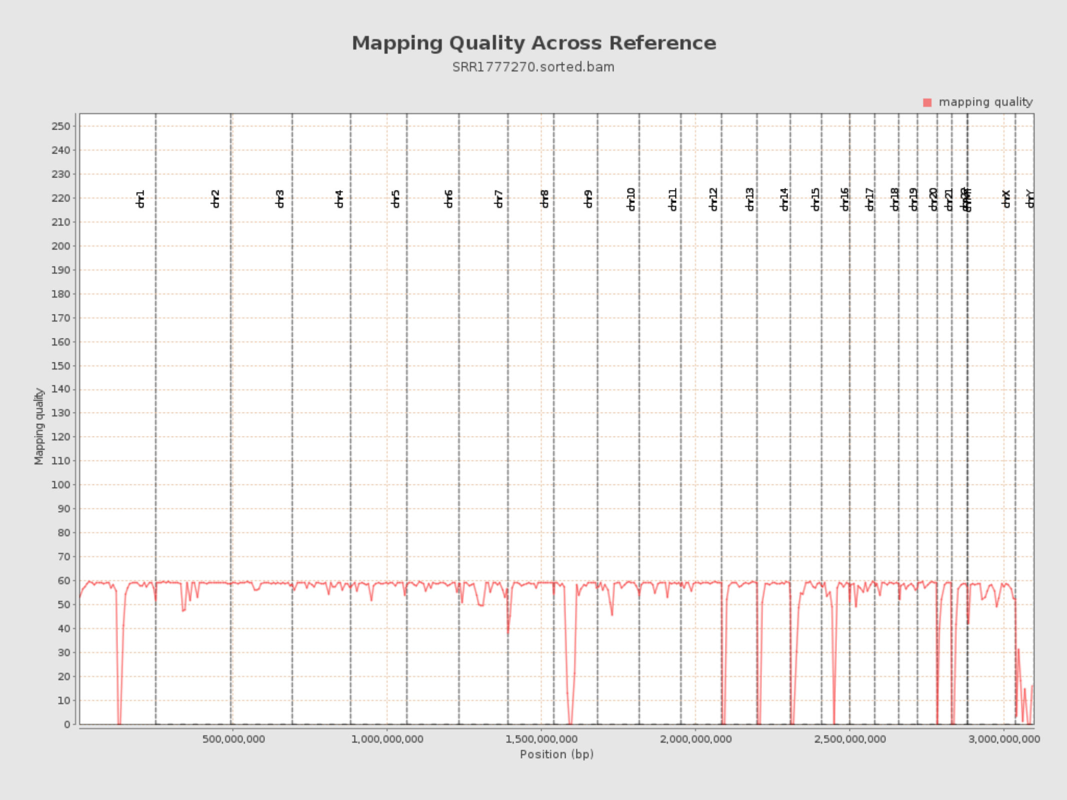
10. Results : Mapped Reads Clipping Profile



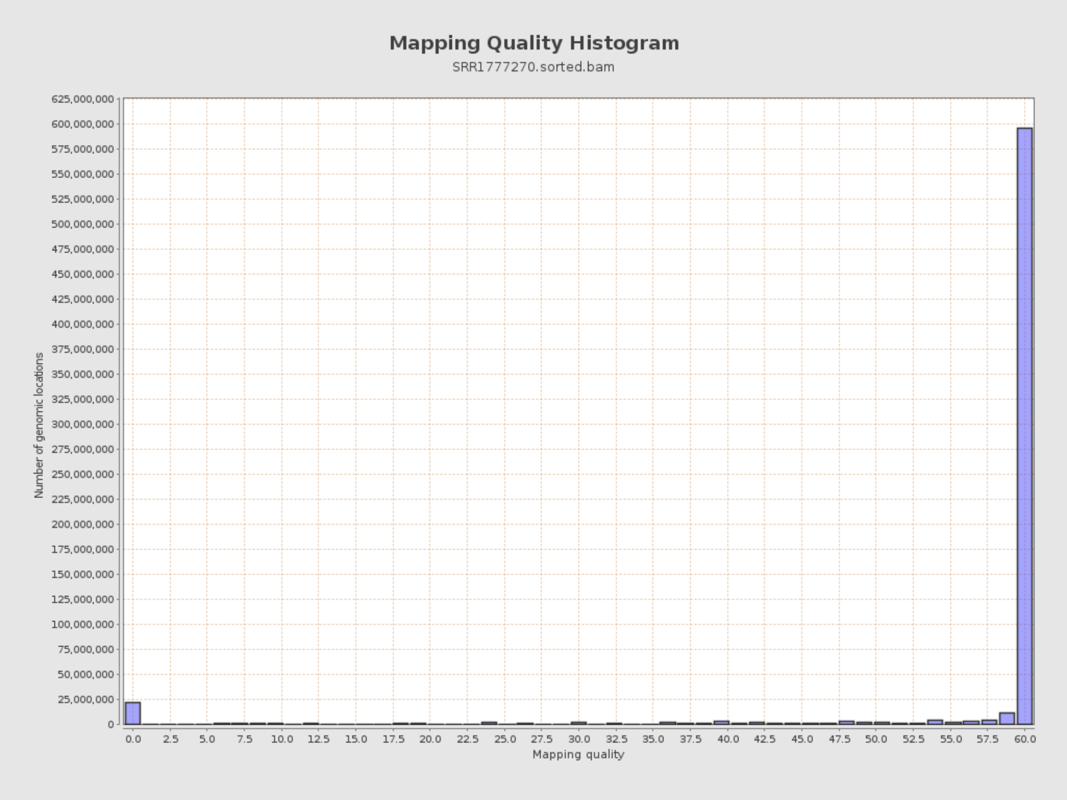
11. Results : Homopolymer Indels



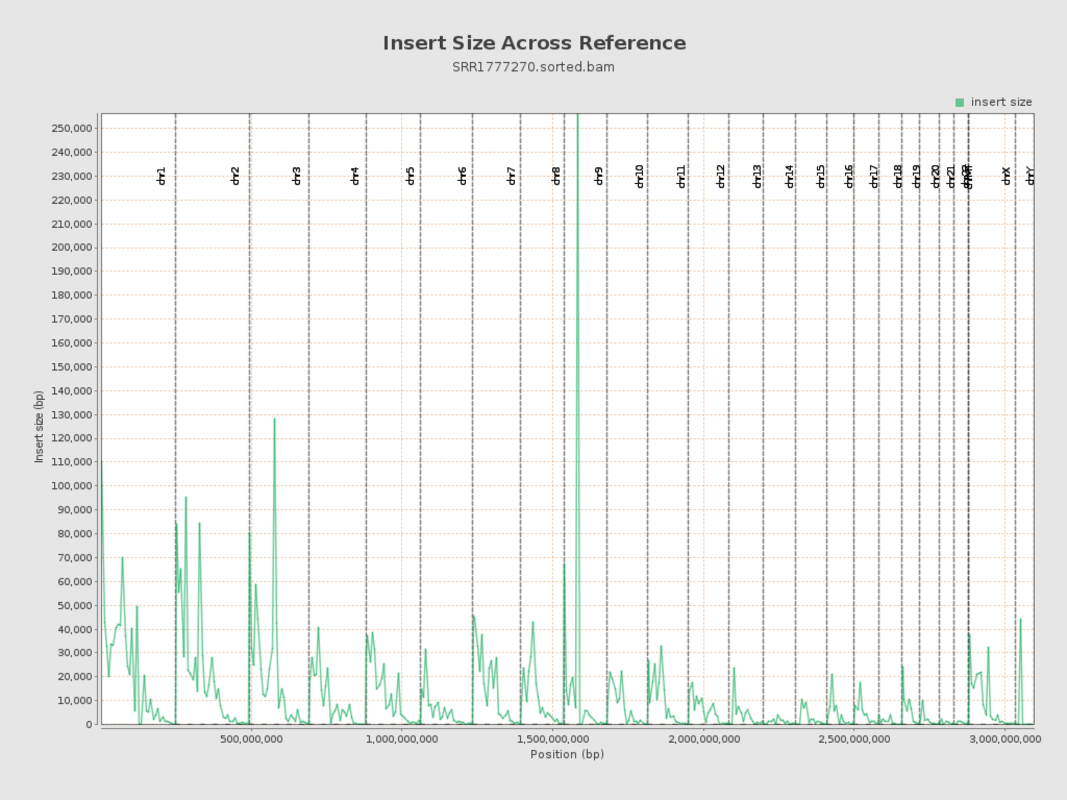
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram