Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 16:07:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777255.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_SRR1777255 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777255_1.fastq.gz SRR1777255_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 16:07:49 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777255.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,445,112
Mapped reads	20,284,519 / 99.21%
Unmapped reads	160,593 / 0.79%
Mapped paired reads	20,284,519 / 99.21%
Mapped reads, first in pair	10,144,128 / 49.62%
Mapped reads, second in pair	10,140,391 / 49.6%
Mapped reads, both in pair	20,213,758 / 98.87%
Mapped reads, singletons	70,761 / 0.35%
Secondary alignments	0
Supplementary alignments	824,577 / 4.03%
Read min/max/mean length	30 / 101 / 102.62
Duplicated reads (estimated)	7,962,831 / 38.95%
Duplication rate	31.06%
Clipped reads	3,225,427 / 15.78%

2.2. ACGT Content

Number/percentage of A's	548,572,817 / 27.34%
Number/percentage of C's	453,465,278 / 22.6%
Number/percentage of T's	547,064,945 / 27.27%
Number/percentage of G's	457,255,417 / 22.79%
Number/percentage of N's	75,110 / 0%

GC Percentage	45.39%

2.3. Coverage

Mean	0.6485
Standard Deviation	33.1015

2.4. Mapping Quality

Mean Mapping Quality	54.53

2.5. Insert size

Mean	246,708.38
Standard Deviation	3,575,720.96
P25/Median/P75	179 / 226 / 283

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	7,127,638
Insertions	477,371
Mapped reads with at least one insertion	2.24%
Deletions	337,743
Mapped reads with at least one deletion	1.5%
Homopolymer indels	36.31%

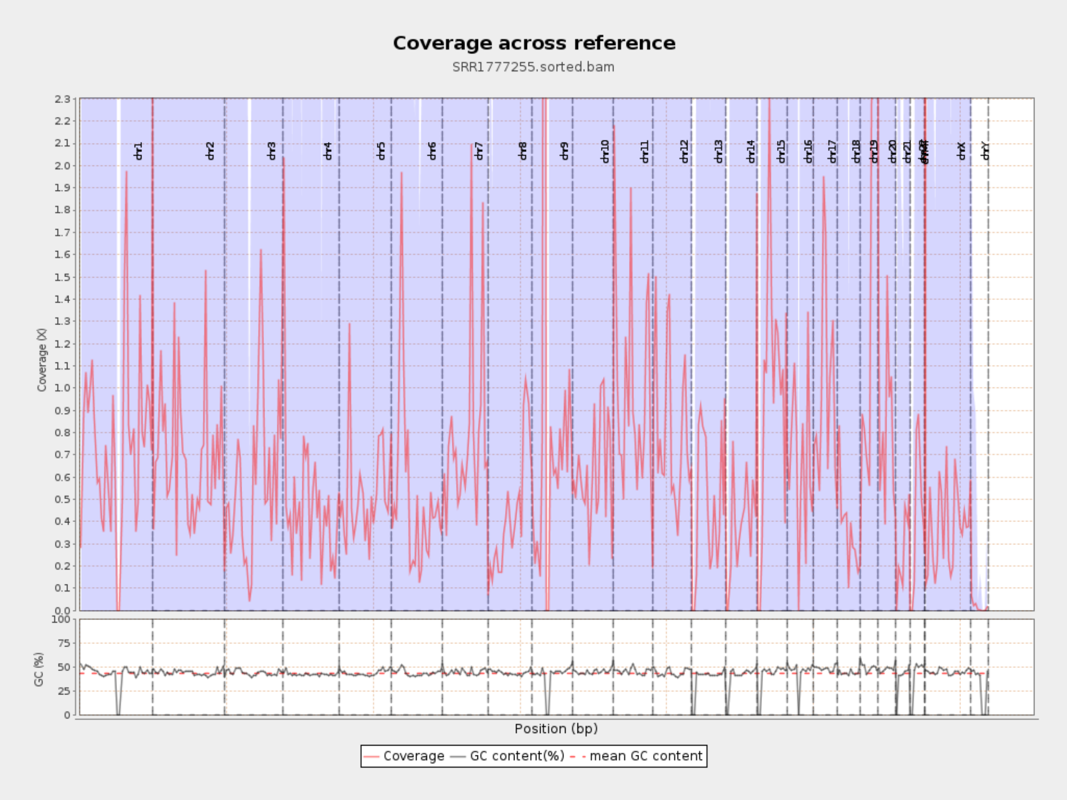
2.7. Chromosome stats

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

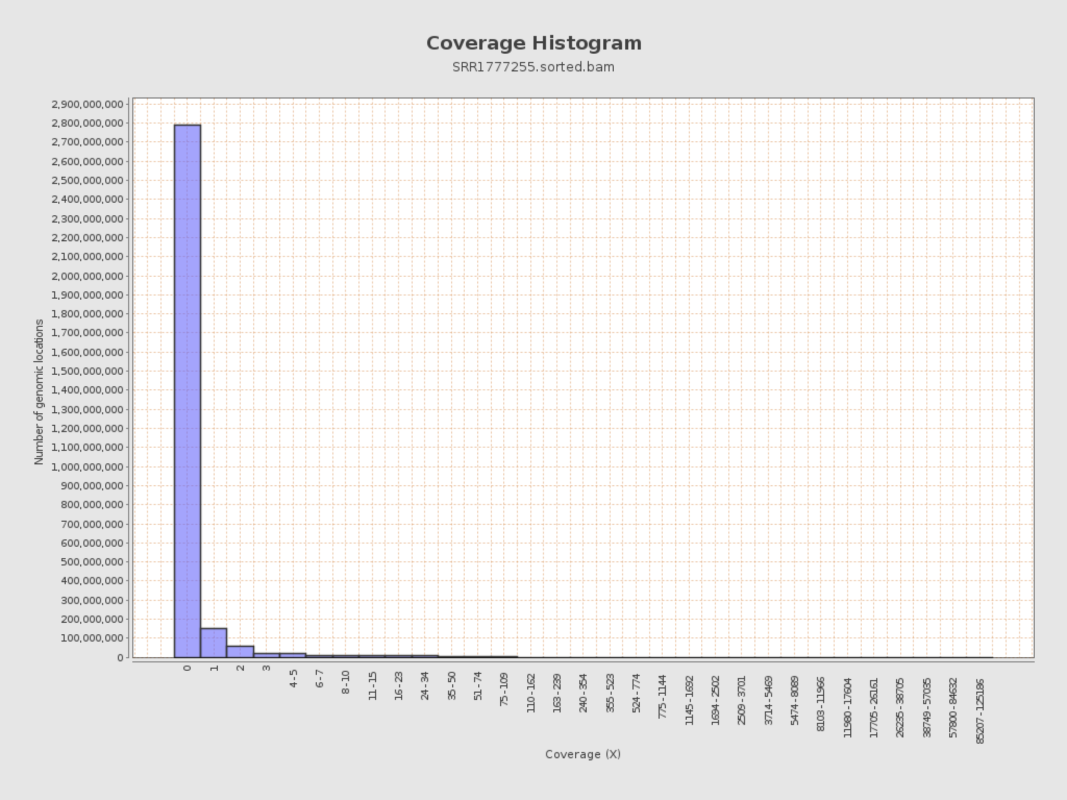
		bases	coverage	deviation
chr1	249250621	189997374	0.7623	6.3601
chr2	243199373	170858953	0.7025	6.2007
chr3	198022430	115875018	0.5852	5.5378
chr4	191154276	90910952	0.4756	22.377
chr5	180915260	95205253	0.5262	4.9686
chr6	171115067	87247849	0.5099	4.9786
chr7	159138663	124404435	0.7817	9.4876
chr8	146364022	65323709	0.4463	5.0599
chr9	141213431	134611515	0.9532	150.2417
chr10	135534747	84787910	0.6256	5.7645
chr11	135006516	133586145	0.9895	8.1768
chr12	133851895	108801930	0.8129	6.6215
chr13	115169878	54004384	0.4689	5.1121
chr14	107349540	41335299	0.3851	3.9519
chr15	102531392	97924124	0.9551	8.3165
chr16	90354753	59172378	0.6549	5.3623
chr17	81195210	81404678	1.0026	7.7514
chr18	78077248	29410130	0.3767	5.3362
chr19	59128983	97040985	1.6412	11.6304
chr20	63025520	52634170	0.8351	6.7811
chr21	48129895	12897725	0.268	3.4302
chr22	51304566	21355166	0.4162	3.951
chrMT	16571	753458	45.4685	21.177
chrX	155270560	57007440	0.3671	4.4021

chrY	59373566	937939	0.0158	0.7506

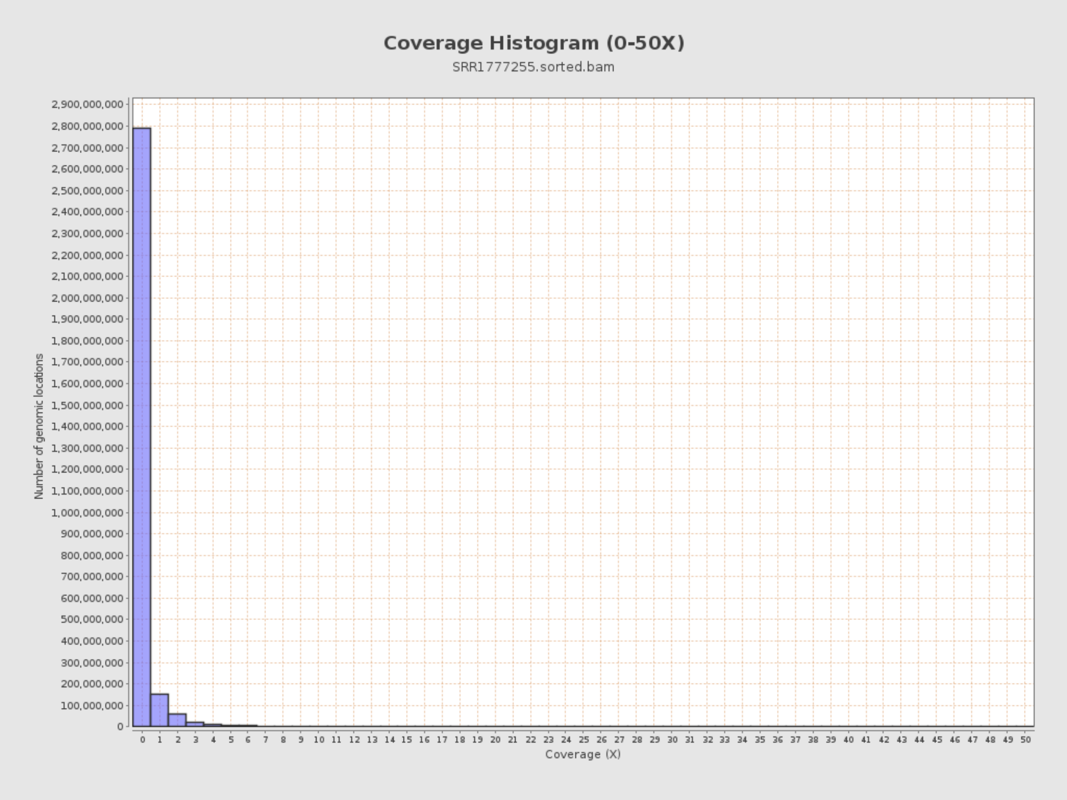
3. Results : Coverage across reference



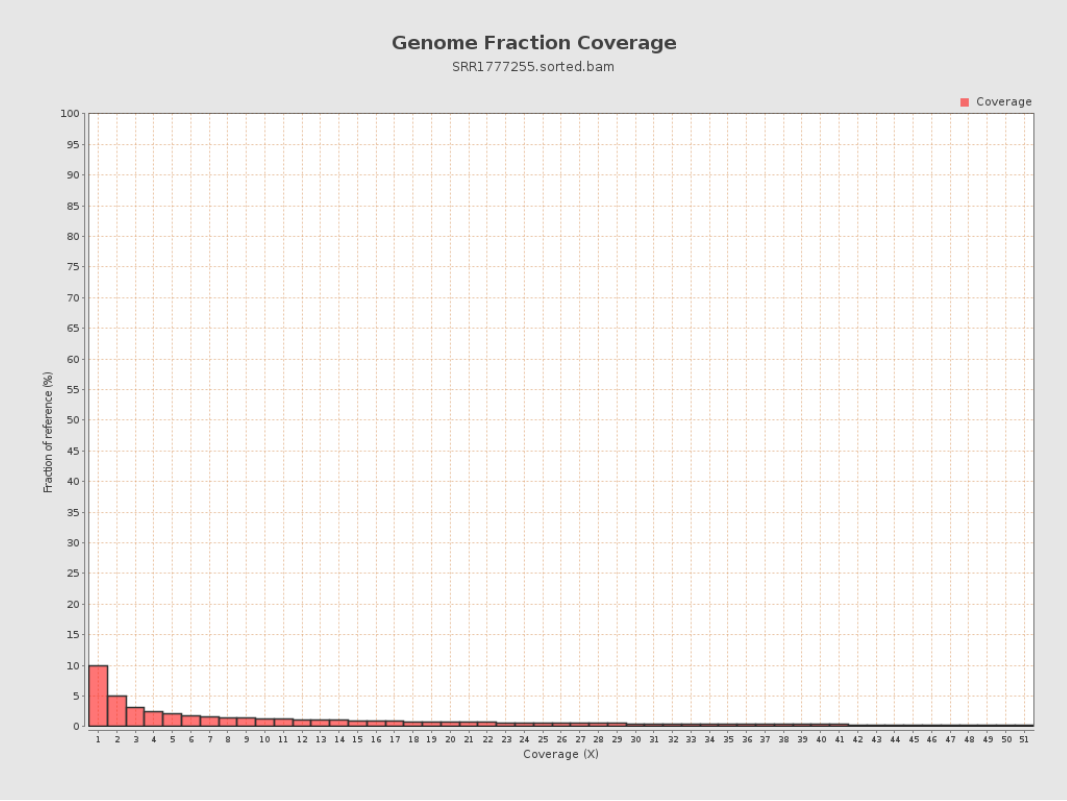
4. Results : Coverage Histogram



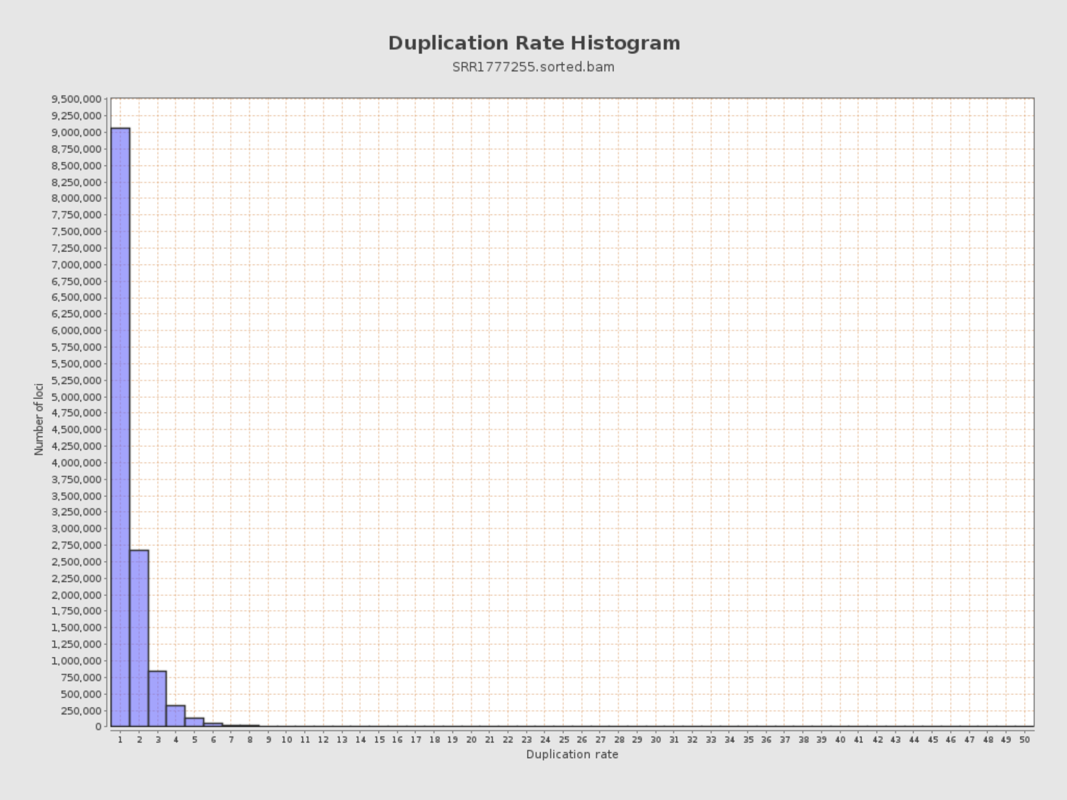
5. Results : Coverage Histogram (0-50X)



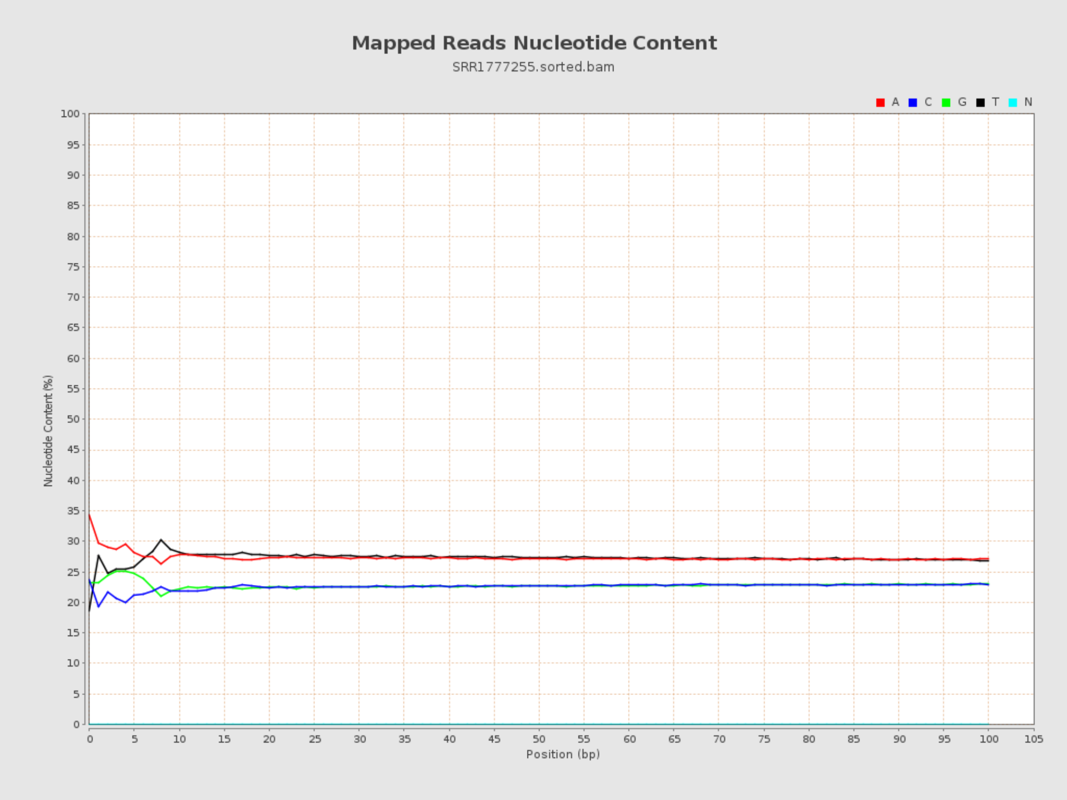
6. Results : Genome Fraction Coverage



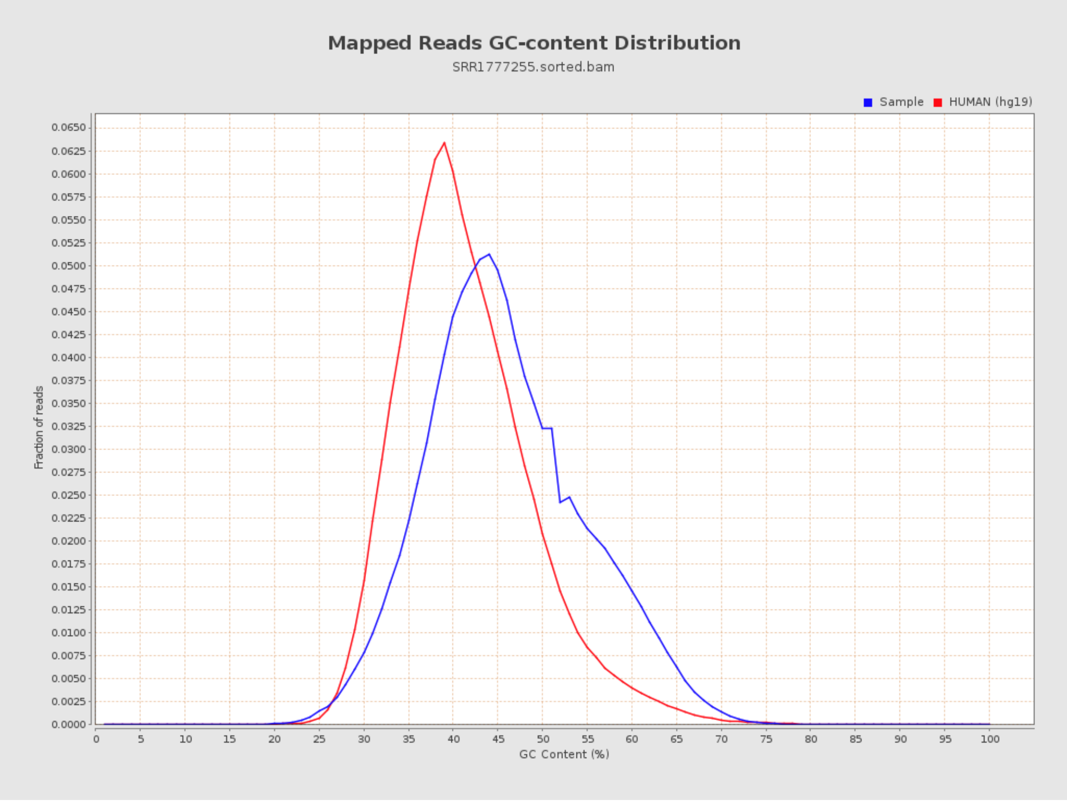
7. Results : Duplication Rate Histogram



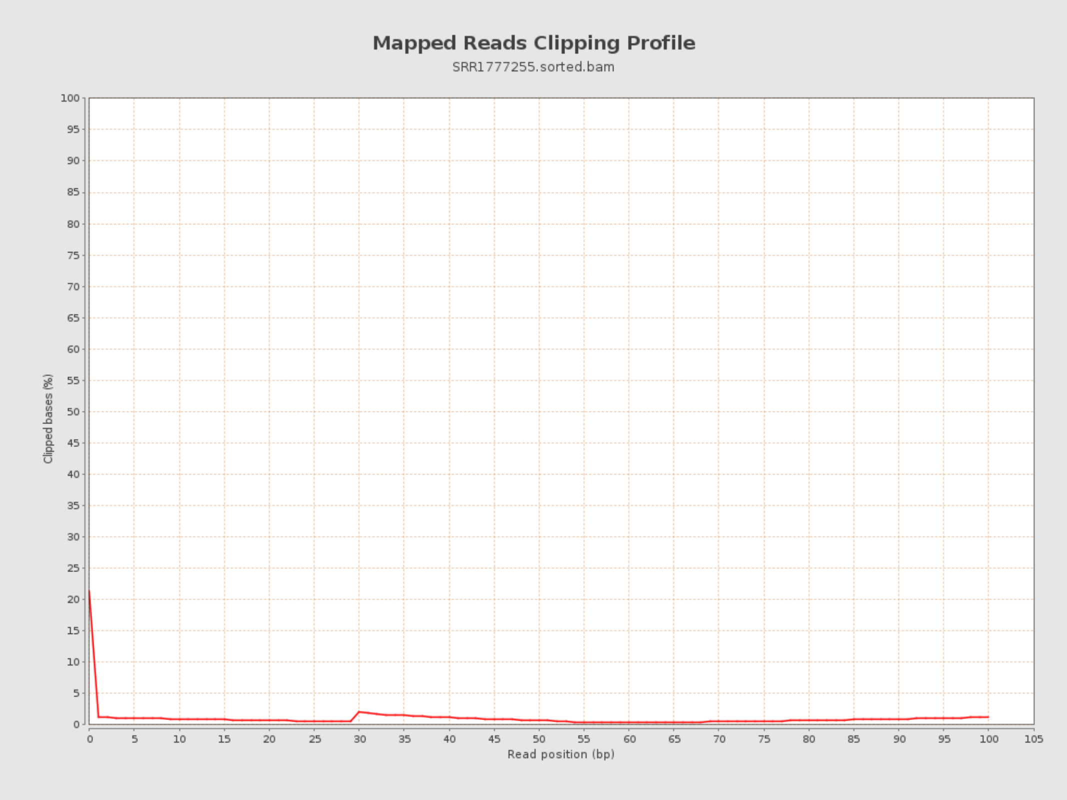
8. Results : Mapped Reads Nucleotide Content



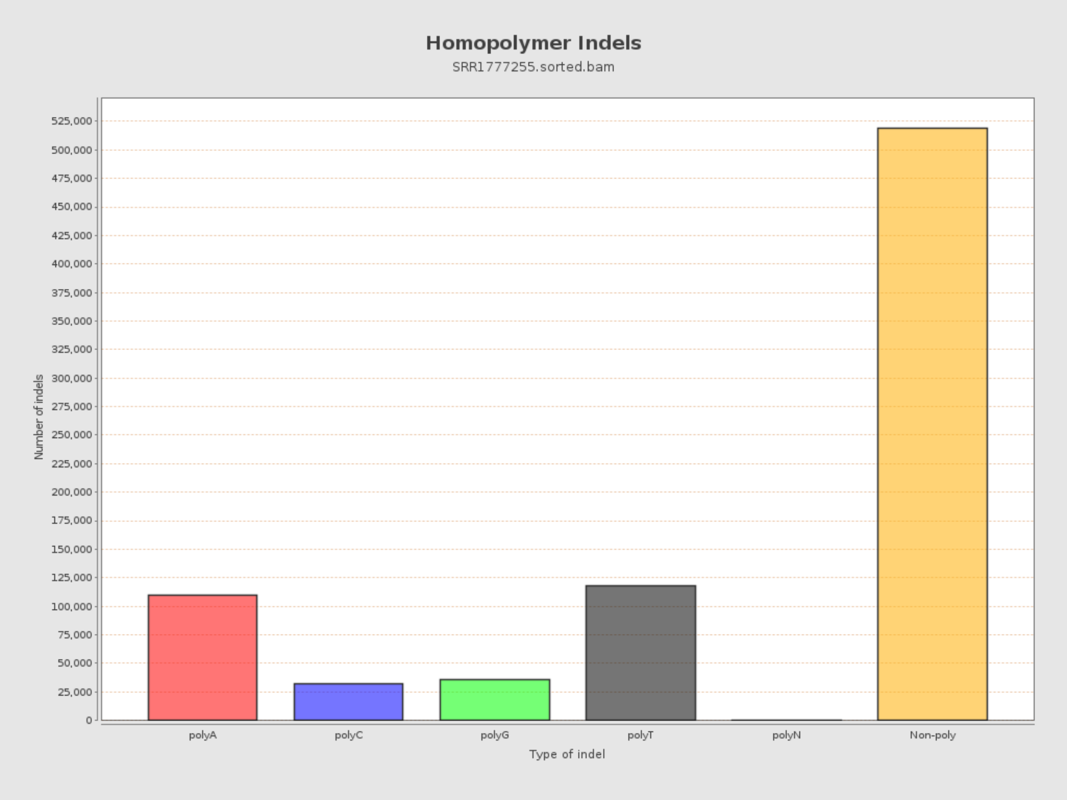
9. Results : Mapped Reads GC-content Distribution



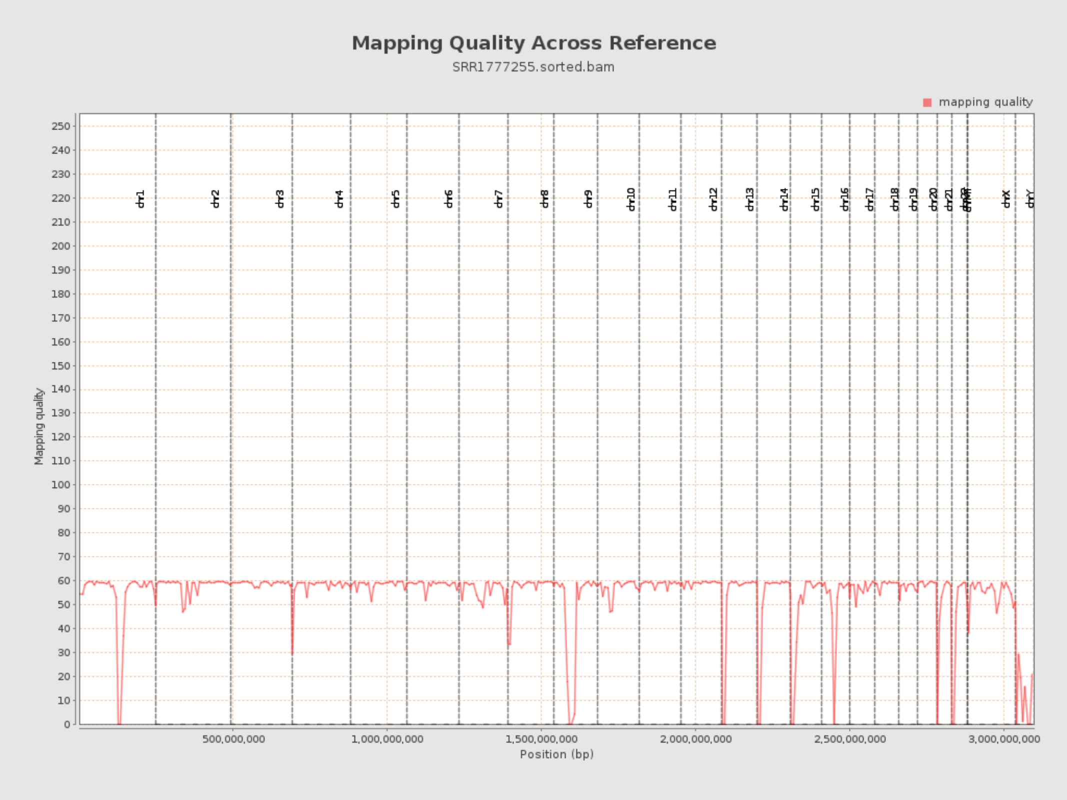
10. Results : Mapped Reads Clipping Profile



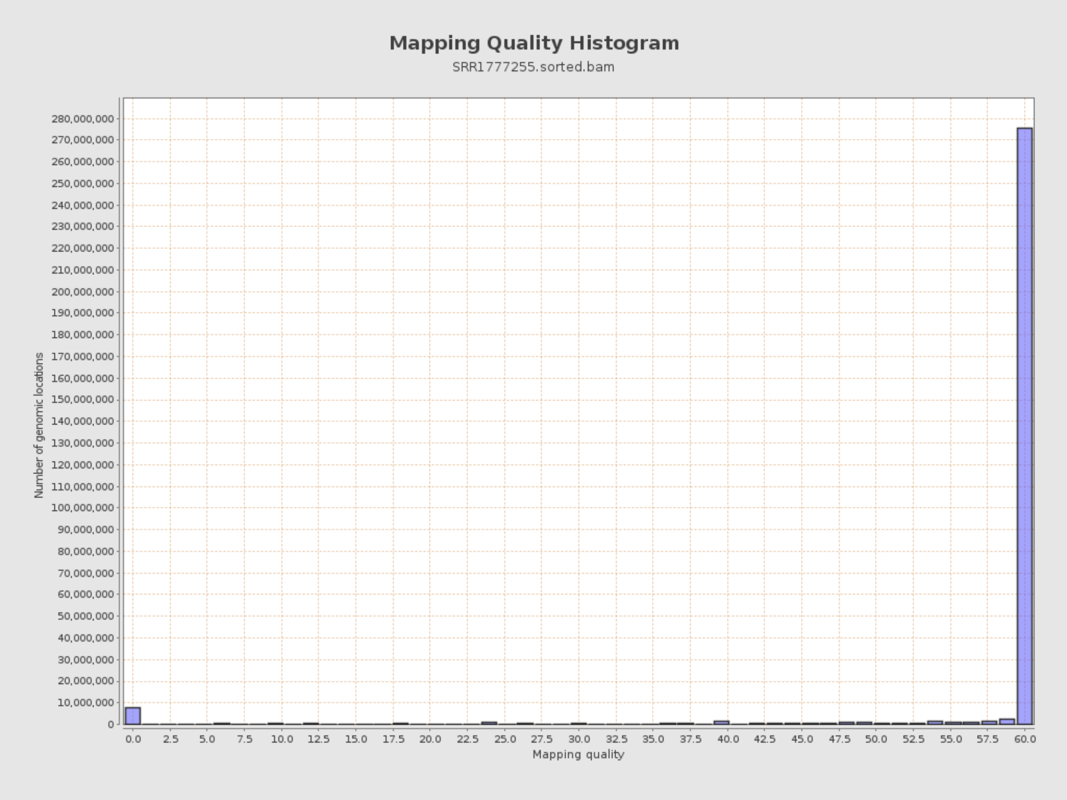
11. Results : Homopolymer Indels



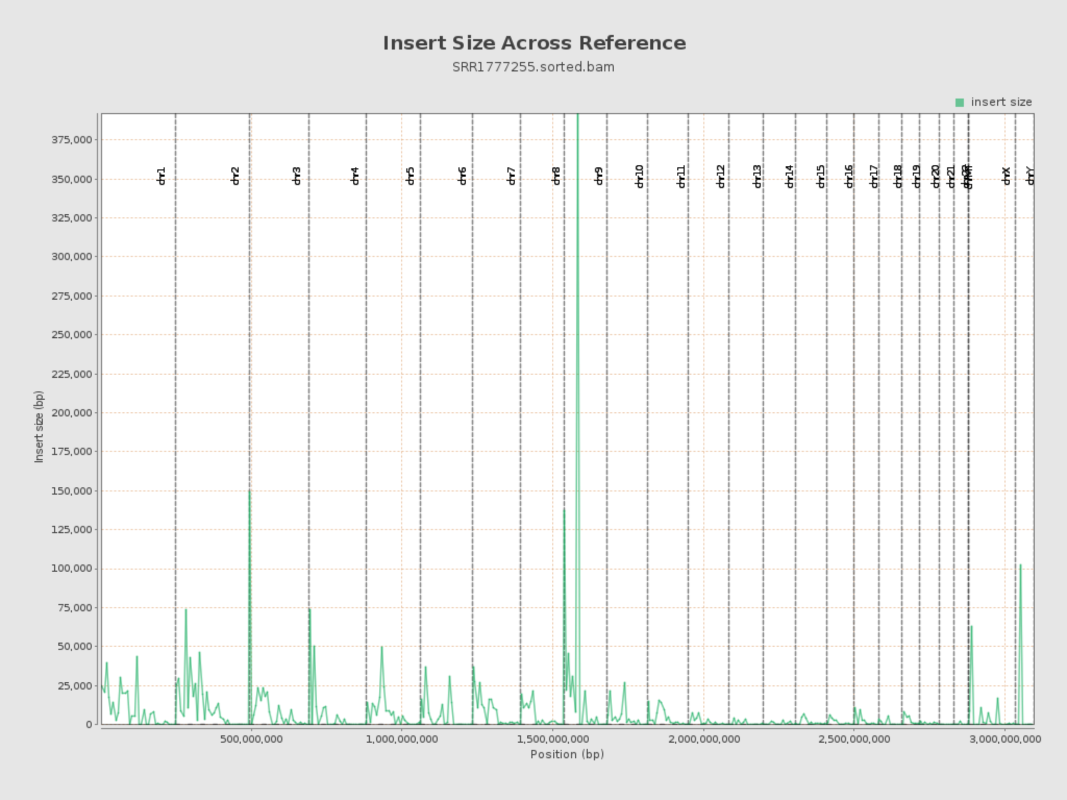
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram