Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 05:44:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779307.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_SRR1779307 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779307_1.fastq.gz SRR1779307_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 05:44:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779307.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,144,314
Mapped reads	13,455,743 / 95.13%
Unmapped reads	688,571 / 4.87%
Mapped paired reads	13,455,743 / 95.13%
Mapped reads, first in pair	6,802,386 / 48.09%
Mapped reads, second in pair	6,653,357 / 47.04%
Mapped reads, both in pair	13,281,866 / 93.9%
Mapped reads, singletons	173,877 / 1.23%
Secondary alignments	0
Supplementary alignments	35,377 / 0.25%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	461,708 / 3.26%
Duplication rate	3.19%
Clipped reads	434,268 / 3.07%

2.2. ACGT Content

Number/percentage of A's	330,754,335 / 30.89%
Number/percentage of C's	203,249,412 / 18.98%
Number/percentage of T's	329,693,541 / 30.79%
Number/percentage of G's	206,891,845 / 19.32%
Number/percentage of N's	283,499 / 0.03%

GC Percentage	38.3%

2.3. Coverage

Mean	0.346
Standard Deviation	1.4604

2.4. Mapping Quality

Mean Mapping Quality	52.97

2.5. Insert size

Mean	37,663.35
Standard Deviation	1,812,516.72
P25/Median/P75	151 / 208 / 290

2.6. Mismatches and indels

General error rate	0.36%
Mismatches	3,721,292
Insertions	76,979
Mapped reads with at least one insertion	0.57%
Deletions	99,552
Mapped reads with at least one deletion	0.73%
Homopolymer indels	46.8%

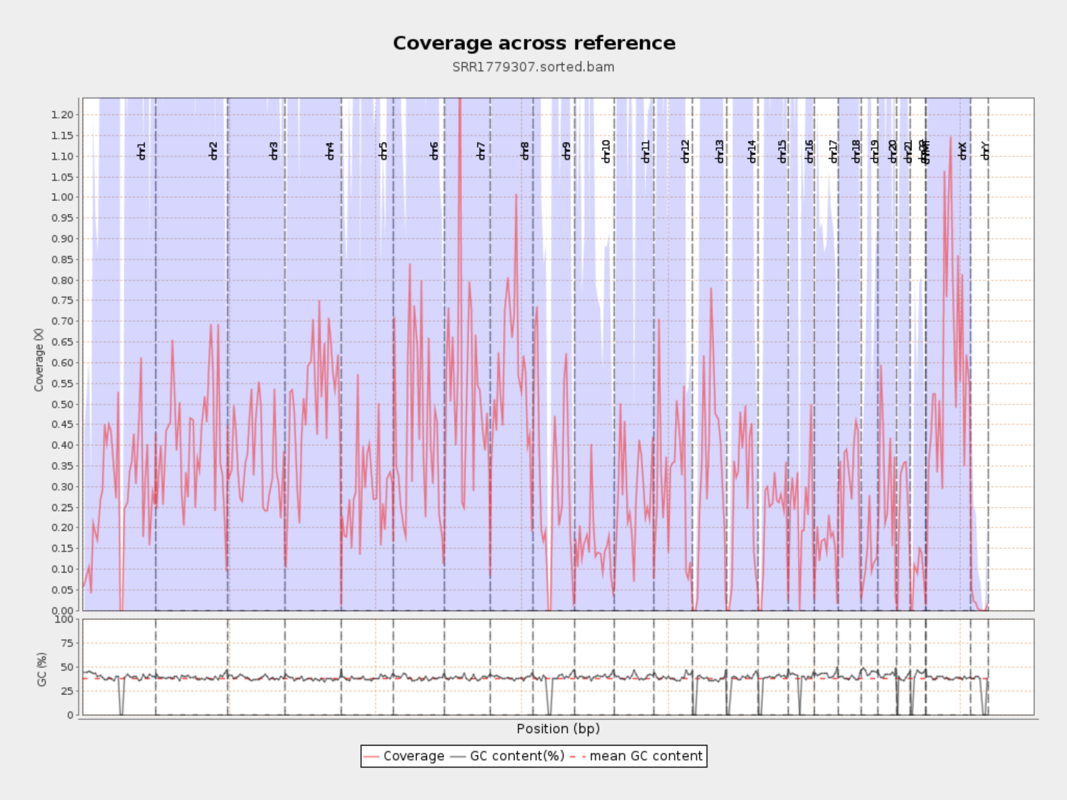
2.7. Chromosome stats

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

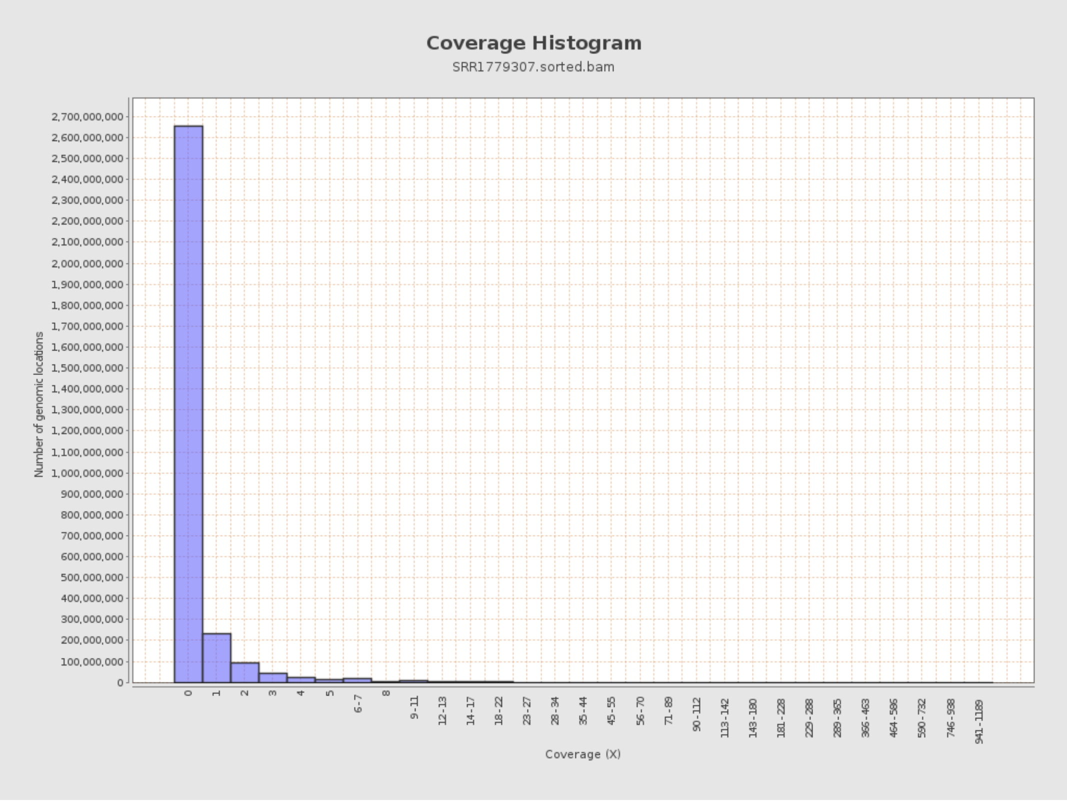
		bases	coverage	deviation
chr1	249250621	69813298	0.2801	1.6809
chr2	243199373	98882324	0.4066	1.429
chr3	198022430	72446702	0.3659	1.2152
chr4	191154276	96287000	0.5037	1.6306
chr5	180915260	52210024	0.2886	1.157
chr6	171115067	73773356	0.4311	1.7345
chr7	159138663	86921643	0.5462	2.0778
chr8	146364022	83765838	0.5723	1.6601
chr9	141213431	44646178	0.3162	1.3061
chr10	135534747	21531494	0.1589	1.4249
chr11	135006516	37977785	0.2813	1.1971
chr12	133851895	41159781	0.3075	1.1656
chr13	115169878	40074385	0.348	1.3598
chr14	107349540	29387596	0.2738	1.1899
chr15	102531392	23096917	0.2253	1.1112
chr16	90354753	21097217	0.2335	1.315
chr17	81195210	12890391	0.1588	0.734
chr18	78077248	25946200	0.3323	1.2492
chr19	59128983	7624131	0.1289	1.015
chr20	63025520	20386946	0.3235	1.2027
chr21	48129895	11912777	0.2475	0.948
chr22	51304566	4446350	0.0867	0.5146
chrMT	16571	1043	0.0629	0.3233
chrX	155270560	94033852	0.6056	2.2411

chrY	59373566	764530	0.0129	0.1876

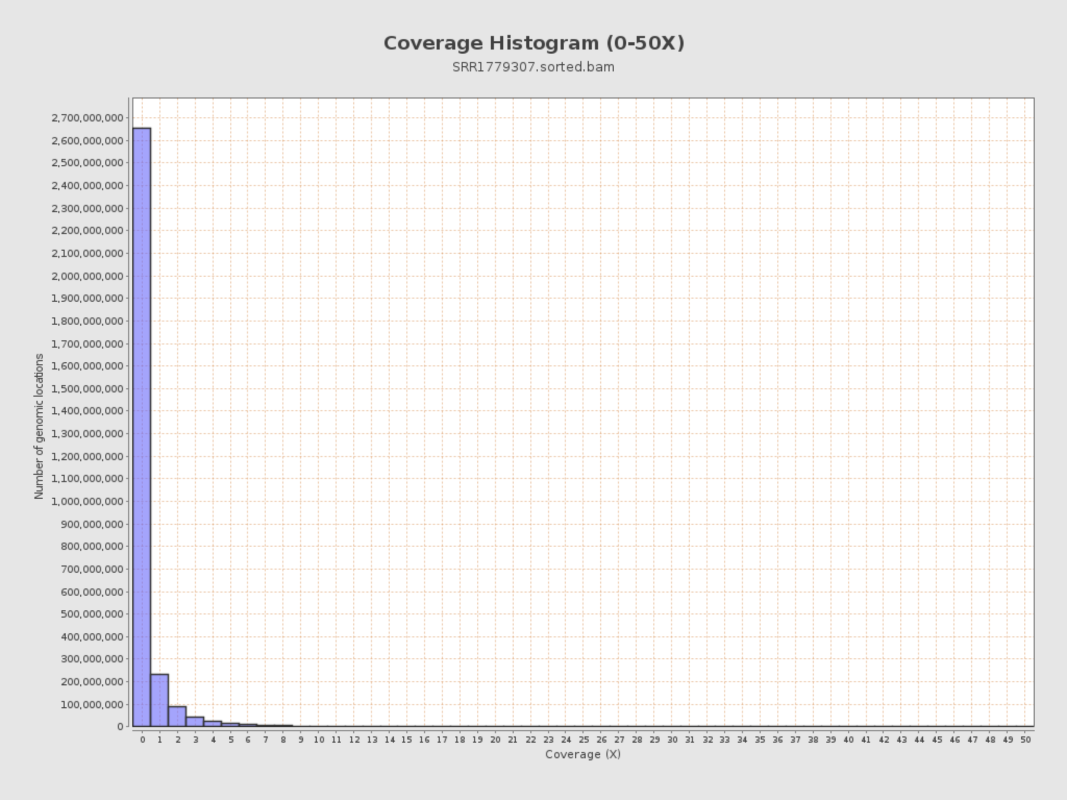
3. Results : Coverage across reference



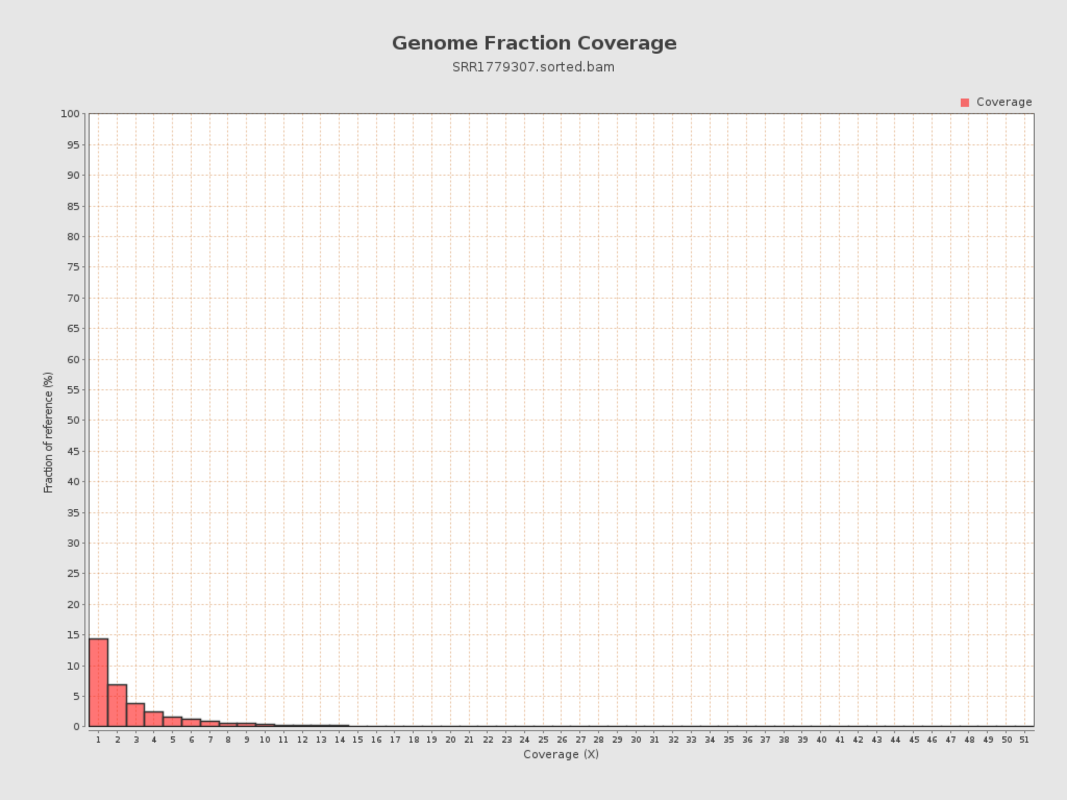
4. Results : Coverage Histogram



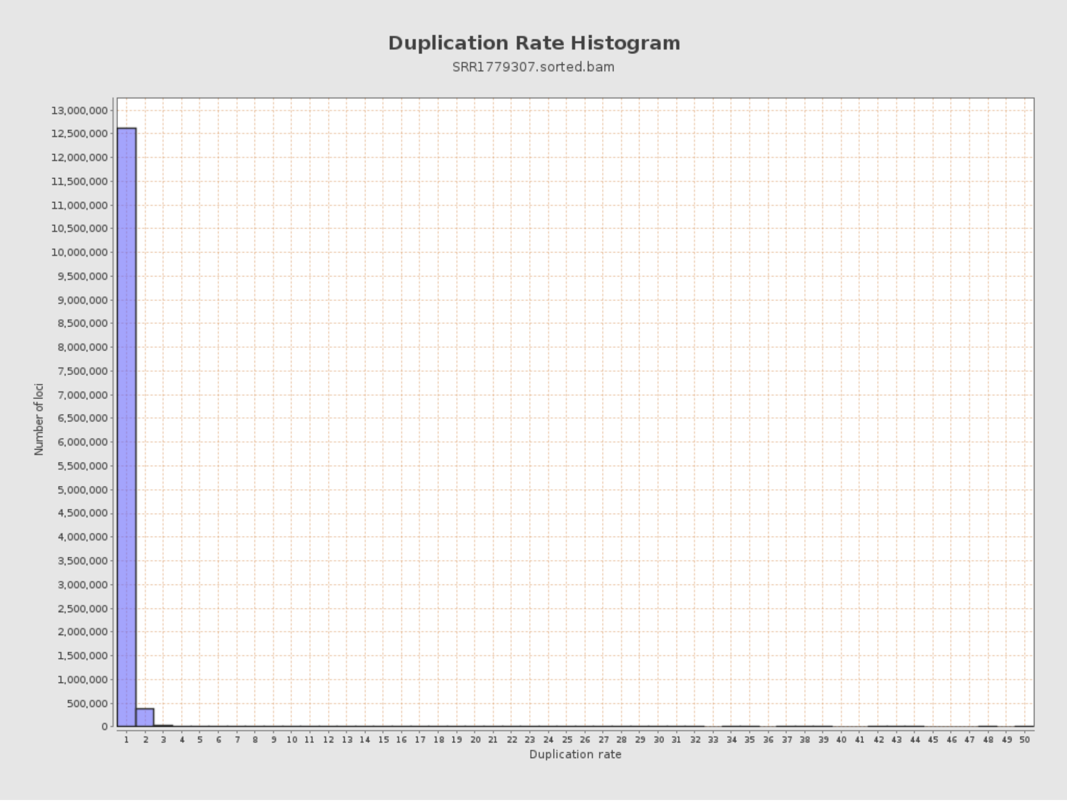
5. Results : Coverage Histogram (0-50X)



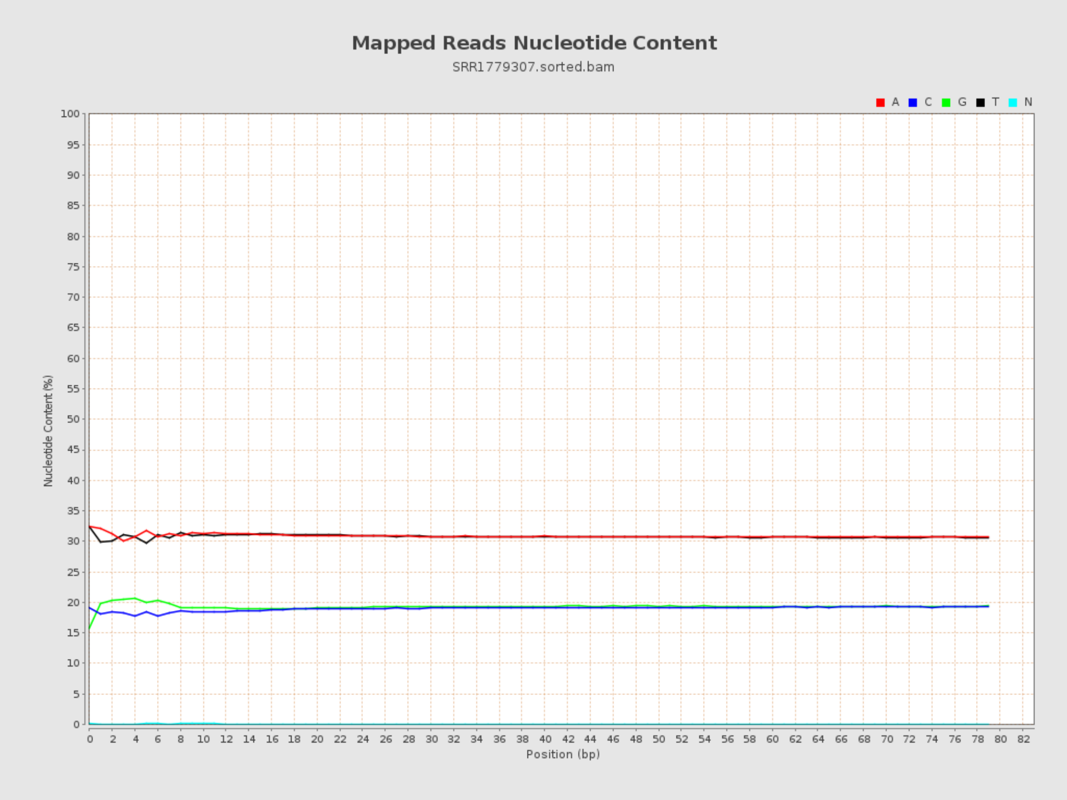
6. Results : Genome Fraction Coverage



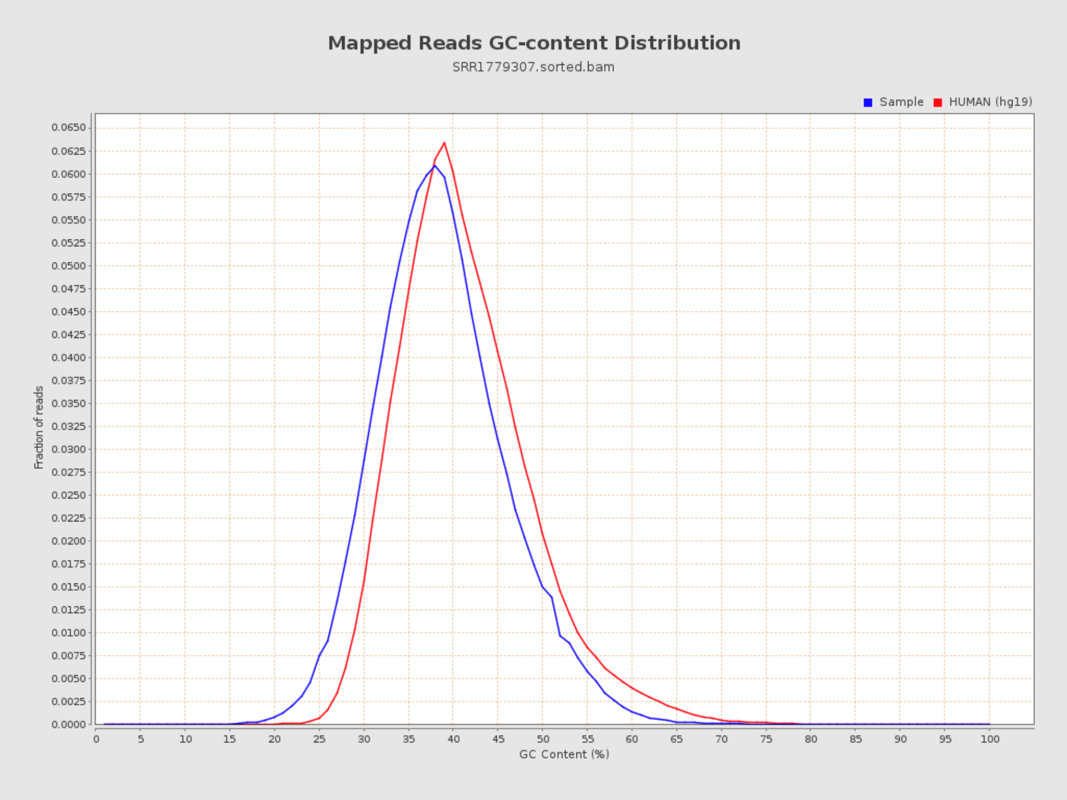
7. Results : Duplication Rate Histogram



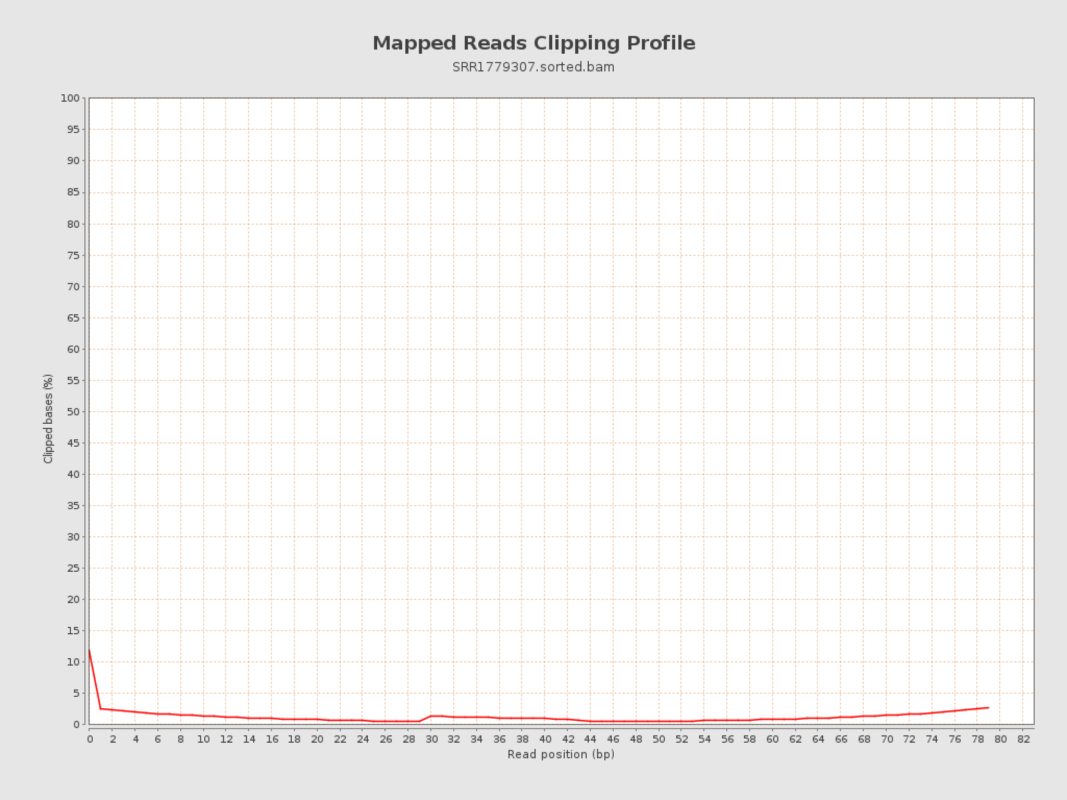
8. Results : Mapped Reads Nucleotide Content



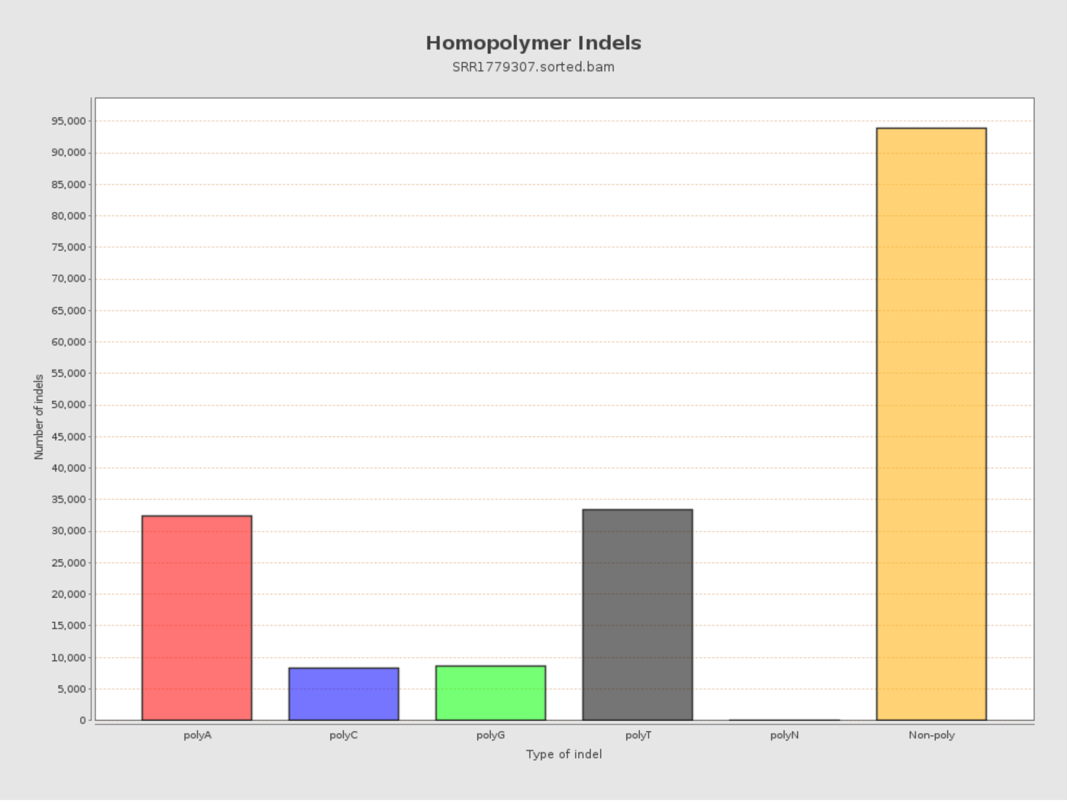
9. Results : Mapped Reads GC-content Distribution



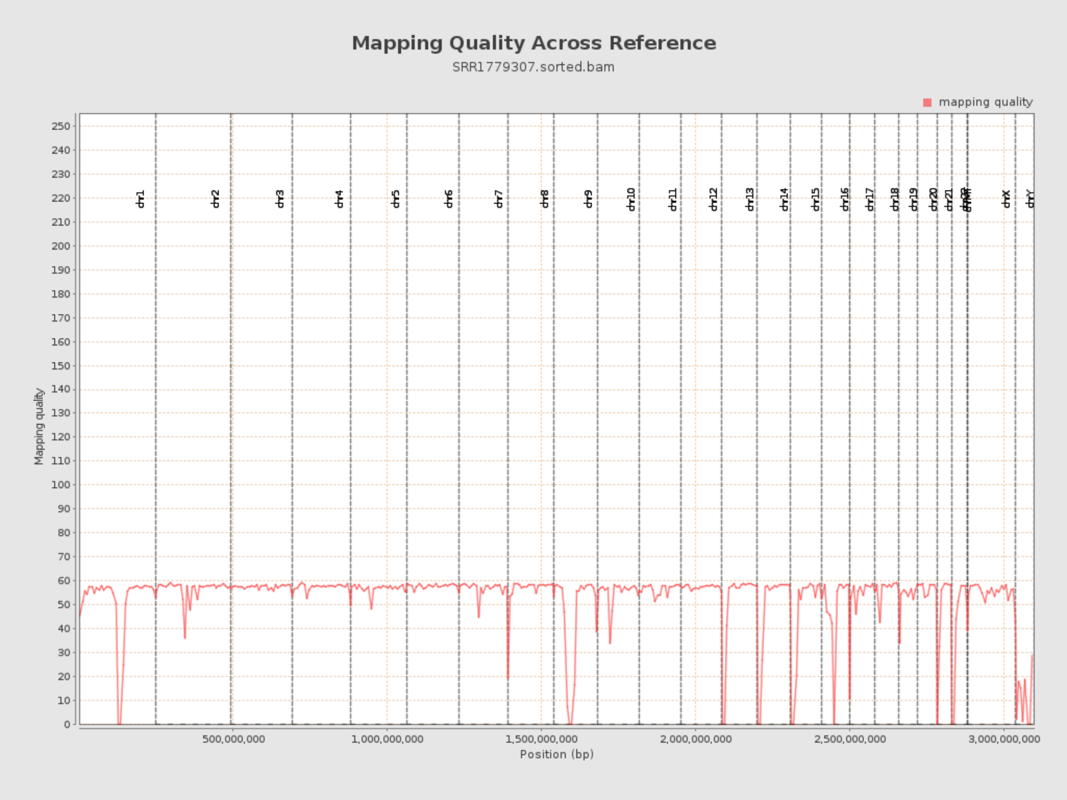
10. Results : Mapped Reads Clipping Profile



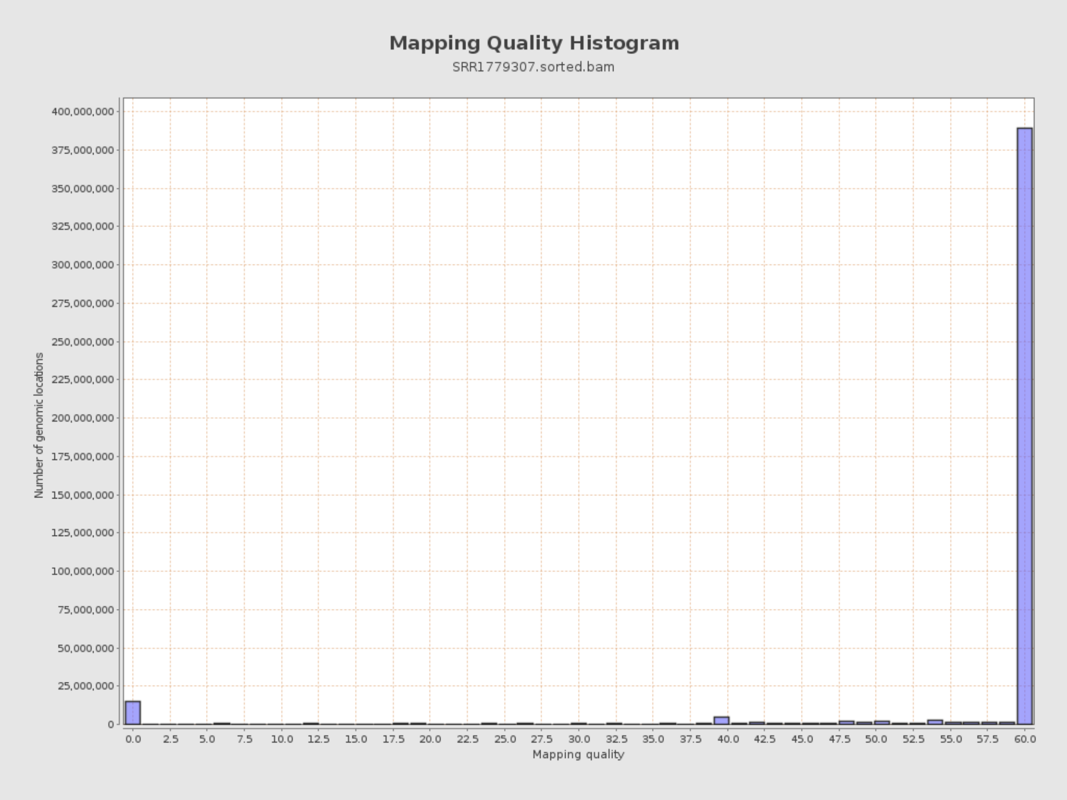
11. Results : Homopolymer Indels



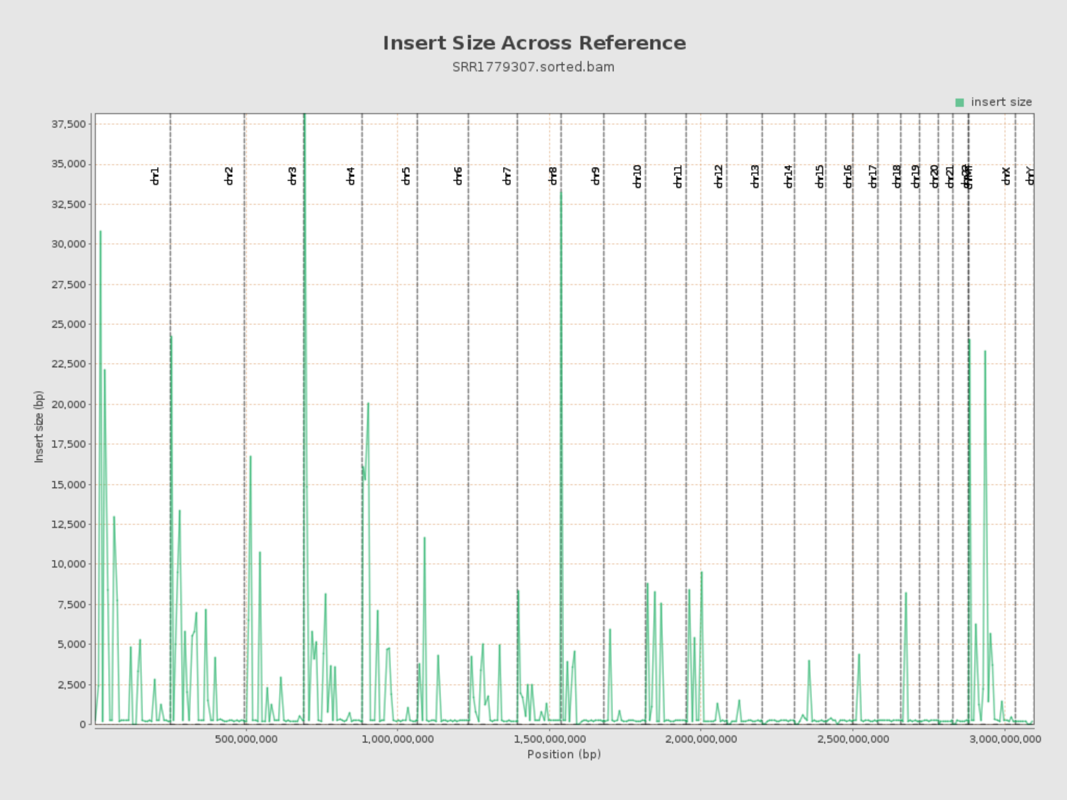
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram