Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 06:25:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779309.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_SRR1779309 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779309_1.fastq.gz SRR1779309_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 06:25:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779309.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,686,288
Mapped reads	16,062,455 / 96.26%
Unmapped reads	623,833 / 3.74%
Mapped paired reads	16,062,455 / 96.26%
Mapped reads, first in pair	8,078,751 / 48.42%
Mapped reads, second in pair	7,983,704 / 47.85%
Mapped reads, both in pair	15,938,712 / 95.52%
Mapped reads, singletons	123,743 / 0.74%
Secondary alignments	0
Supplementary alignments	44,179 / 0.26%
Read min/max/mean length	30 / 80 / 80.1
Duplicated reads (estimated)	551,984 / 3.31%
Duplication rate	3.18%
Clipped reads	519,368 / 3.11%

2.2. ACGT Content

Number/percentage of A's	394,182,349 / 30.84%
Number/percentage of C's	243,258,684 / 19.03%
Number/percentage of T's	392,869,201 / 30.73%
Number/percentage of G's	247,657,855 / 19.37%
Number/percentage of N's	337,620 / 0.03%

GC Percentage	38.4%

2.3. Coverage

Mean	0.413
Standard Deviation	1.6035

2.4. Mapping Quality

Mean Mapping Quality	53.04

2.5. Insert size

Mean	36,106.42
Standard Deviation	1,794,675.41
P25/Median/P75	157 / 210 / 286

2.6. Mismatches and indels

General error rate	0.36%
Mismatches	4,474,359
Insertions	94,409
Mapped reads with at least one insertion	0.58%
Deletions	123,072
Mapped reads with at least one deletion	0.76%
Homopolymer indels	46.74%

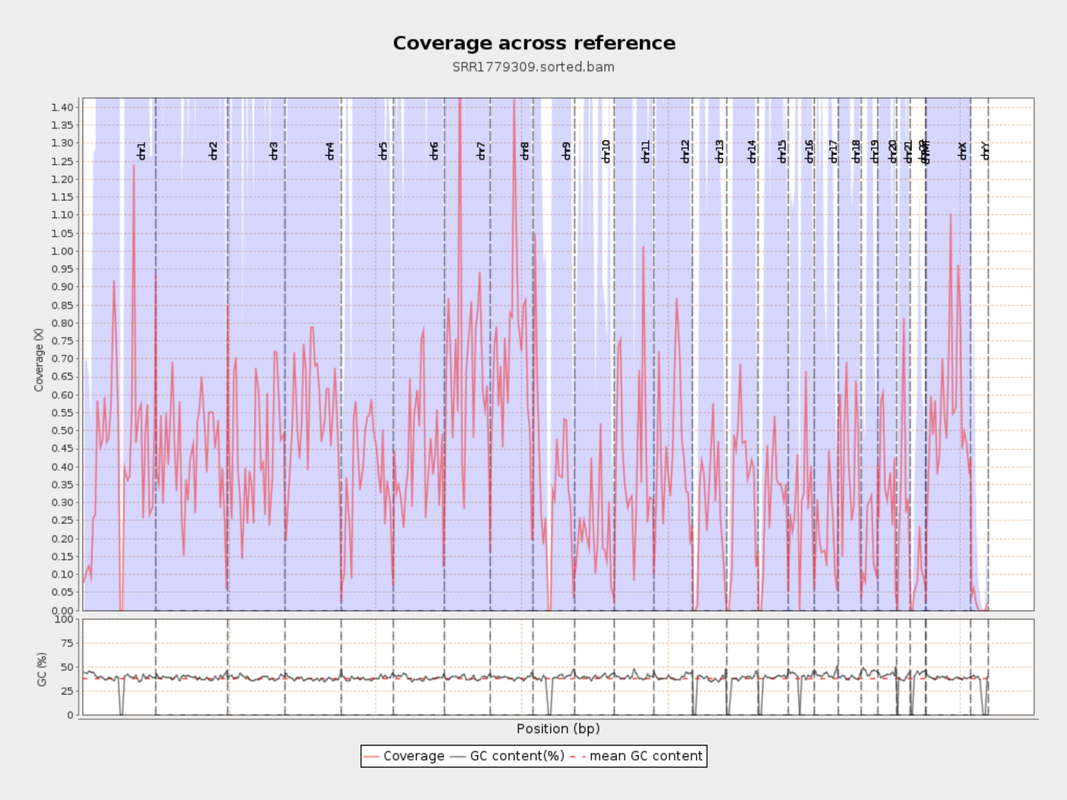
2.7. Chromosome stats

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

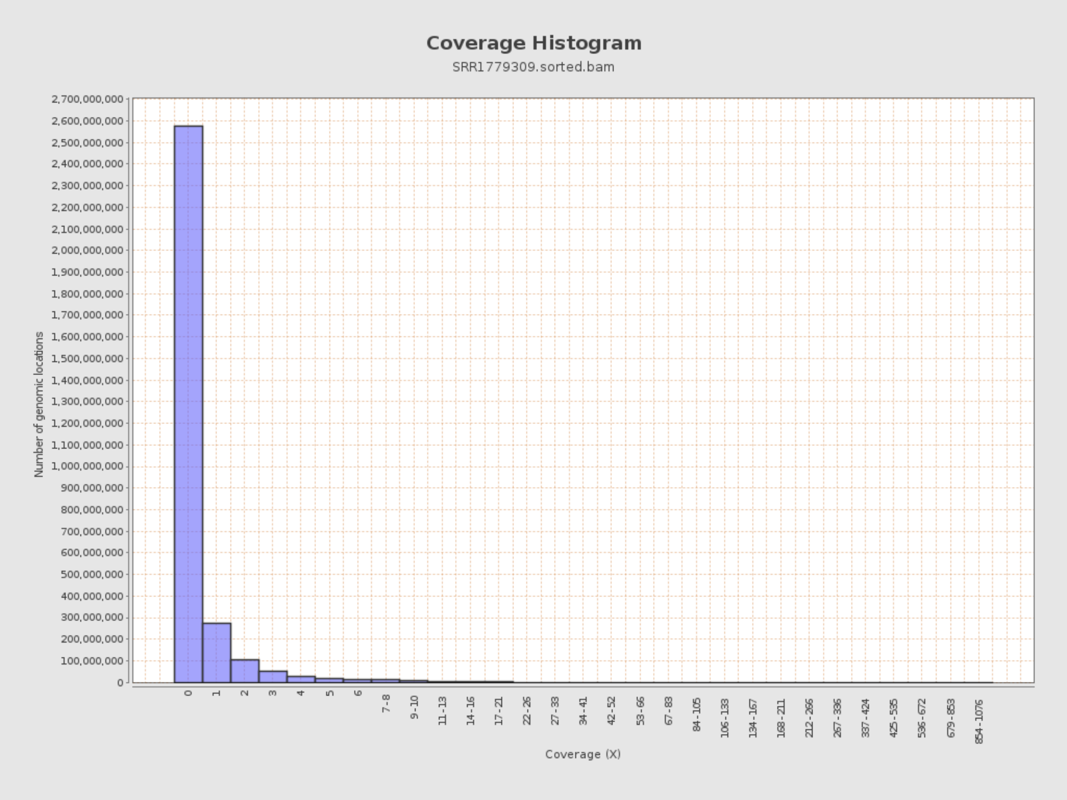
		bases	coverage	deviation
chr1	249250621	107634308	0.4318	1.9615
chr2	243199373	104767282	0.4308	1.4766
chr3	198022430	89019806	0.4495	1.5829
chr4	191154276	104537751	0.5469	1.7892
chr5	180915260	66028697	0.365	1.257
chr6	171115067	75377395	0.4405	1.5075
chr7	159138663	108839440	0.6839	2.1612
chr8	146364022	105464762	0.7206	1.9847
chr9	141213431	50312621	0.3563	1.4585
chr10	135534747	28597849	0.211	1.8903
chr11	135006516	58316031	0.4319	1.5218
chr12	133851895	58465598	0.4368	1.4372
chr13	115169878	31423809	0.2728	1.1061
chr14	107349540	37908161	0.3531	1.2739
chr15	102531392	30122722	0.2938	1.2154
chr16	90354753	25890213	0.2865	1.192
chr17	81195210	17554799	0.2162	0.9483
chr18	78077248	34095043	0.4367	1.6562
chr19	59128983	11150647	0.1886	1.1121
chr20	63025520	23868020	0.3787	1.2004
chr21	48129895	15210890	0.316	1.3397
chr22	51304566	4537063	0.0884	0.5137
chrMT	16571	434	0.0262	0.1667
chrX	155270560	88337665	0.5689	2.2344

chrY	59373566	1098485	0.0185	0.3223

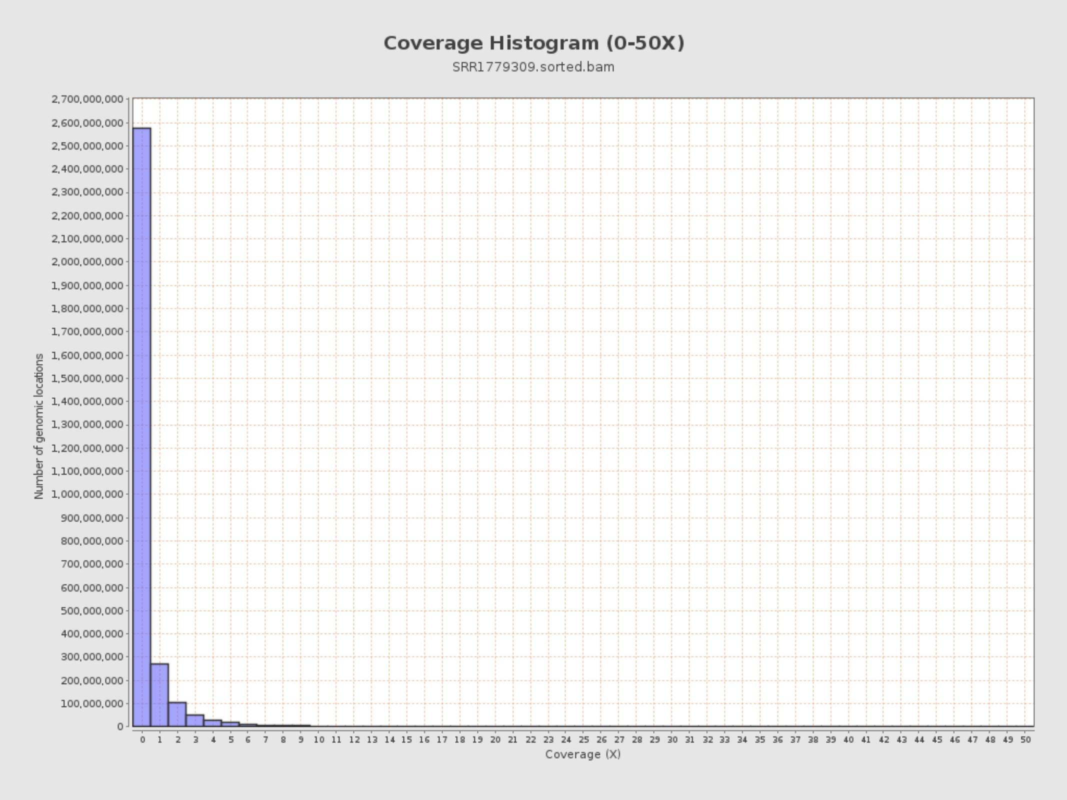
3. Results : Coverage across reference



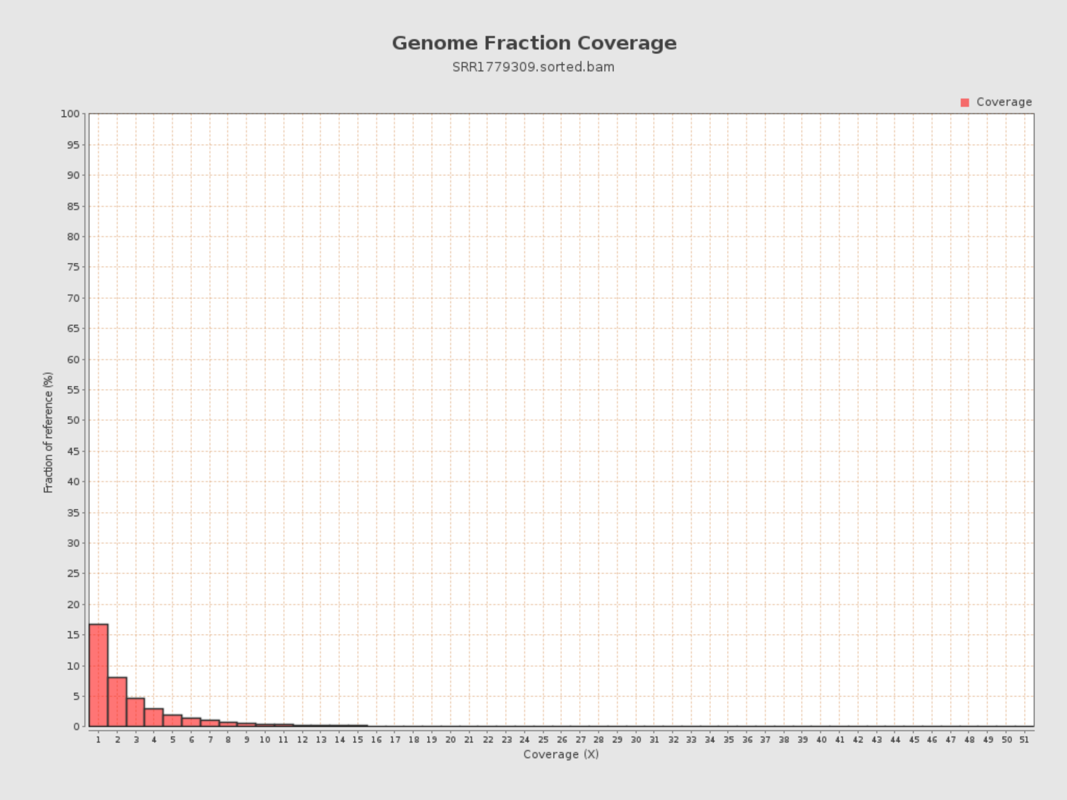
4. Results : Coverage Histogram



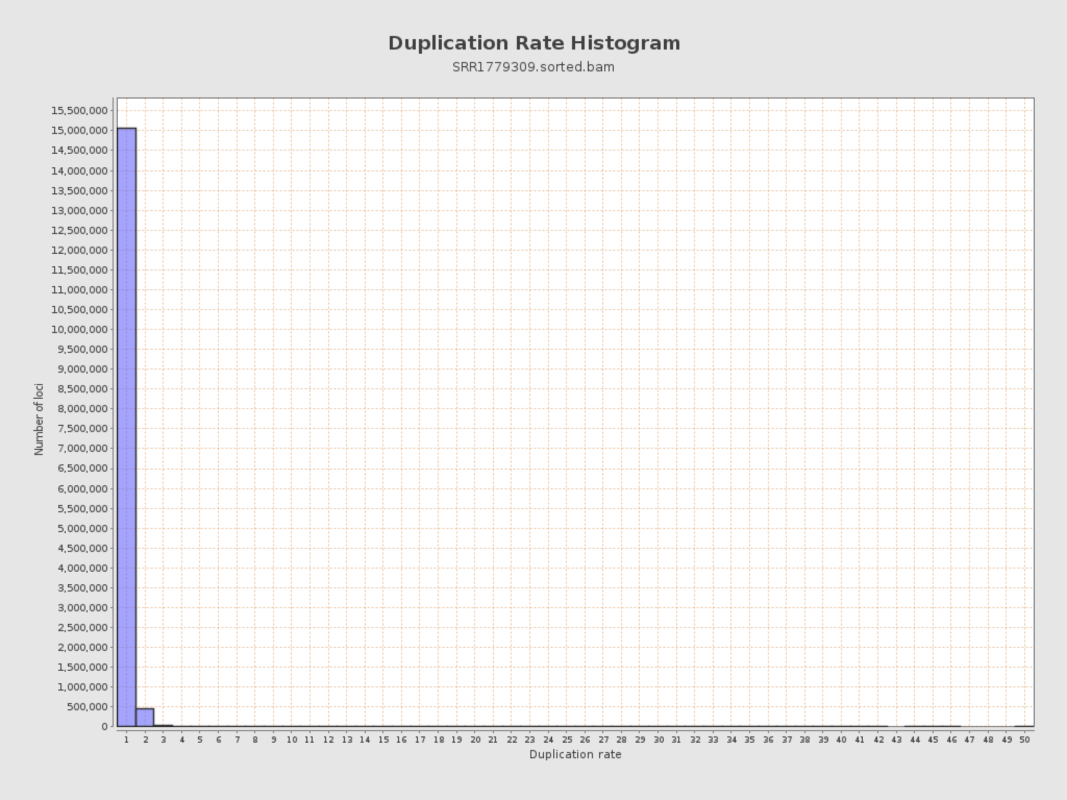
5. Results : Coverage Histogram (0-50X)



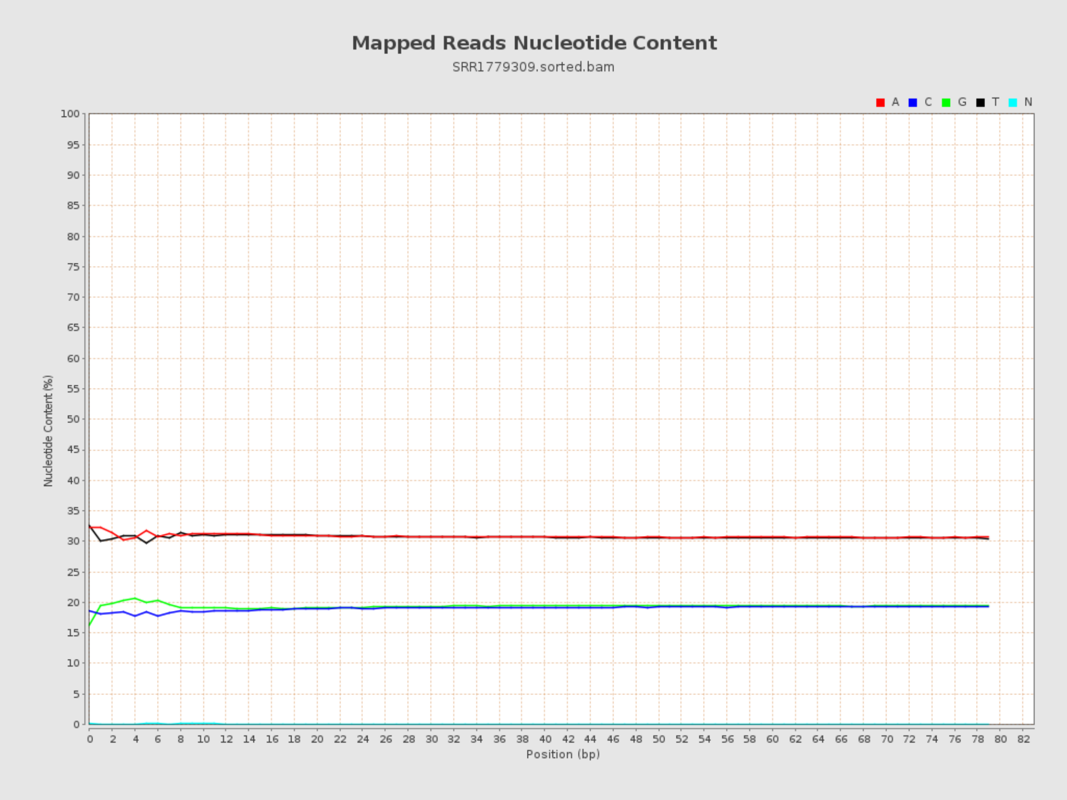
6. Results : Genome Fraction Coverage



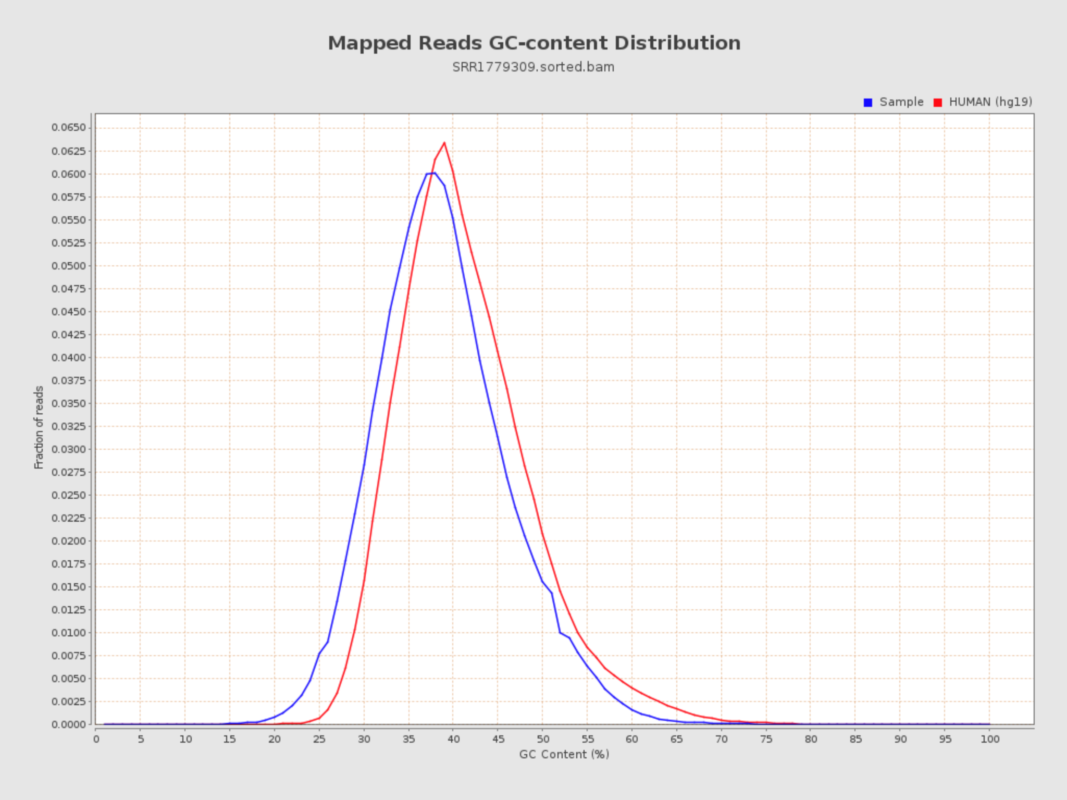
7. Results : Duplication Rate Histogram



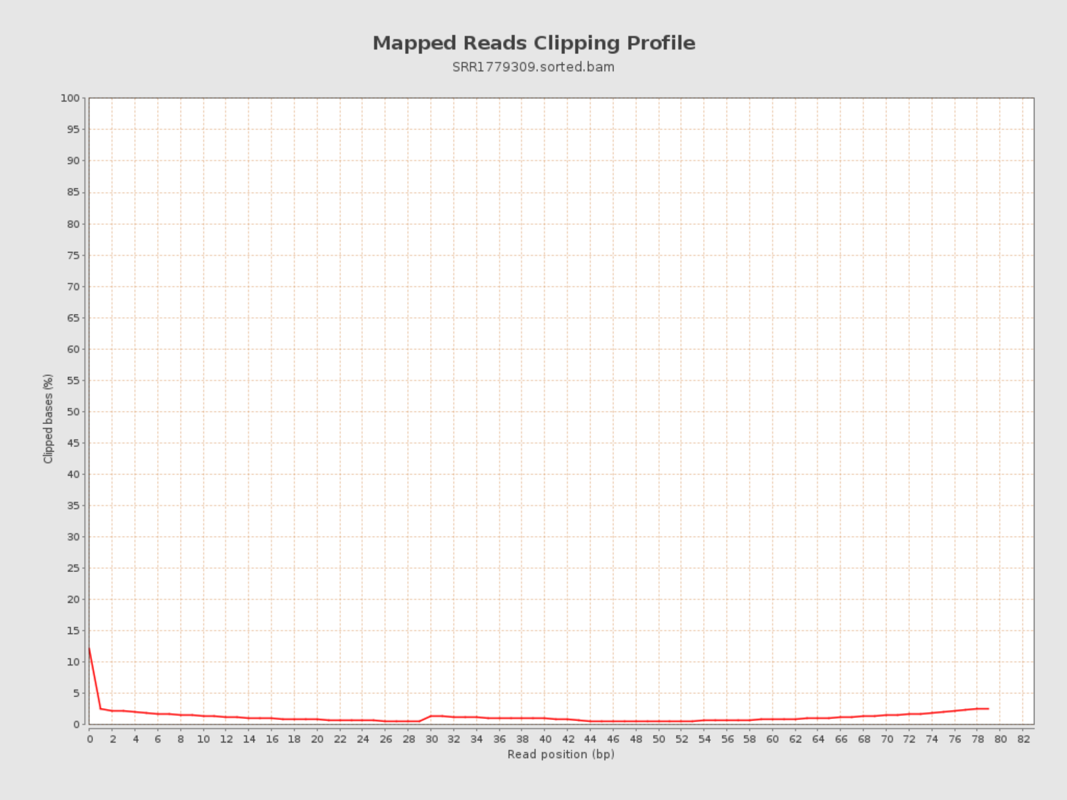
8. Results : Mapped Reads Nucleotide Content



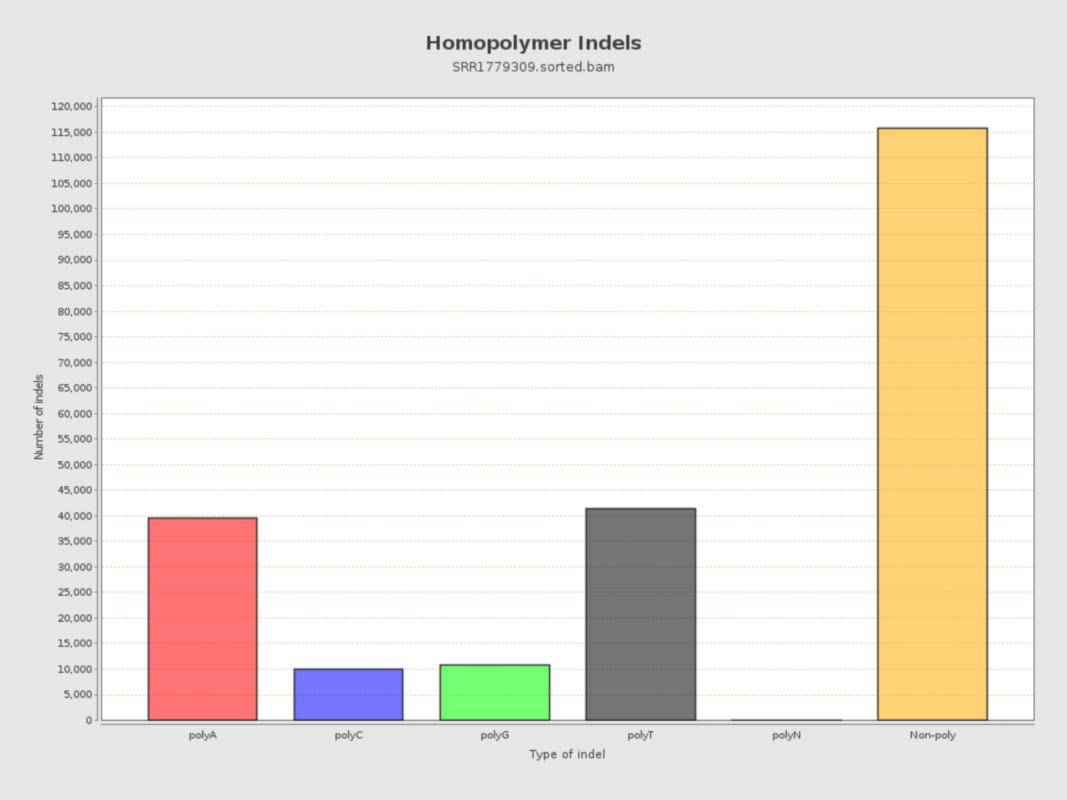
9. Results : Mapped Reads GC-content Distribution



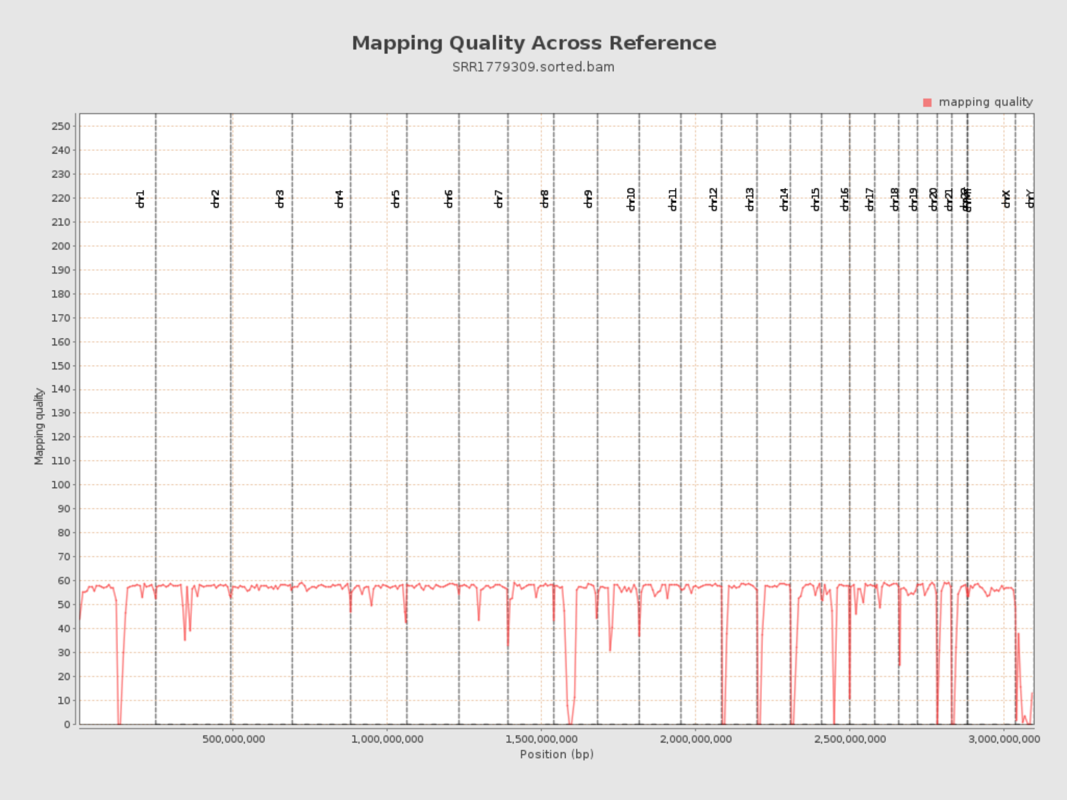
10. Results : Mapped Reads Clipping Profile



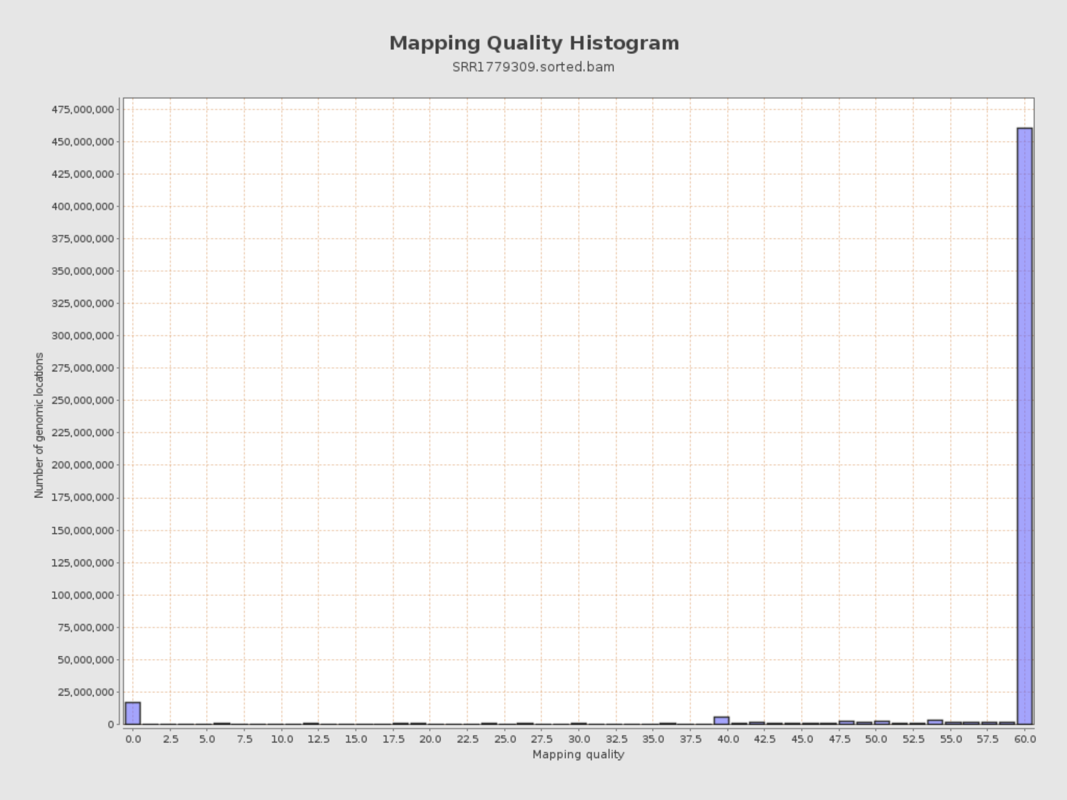
11. Results : Homopolymer Indels



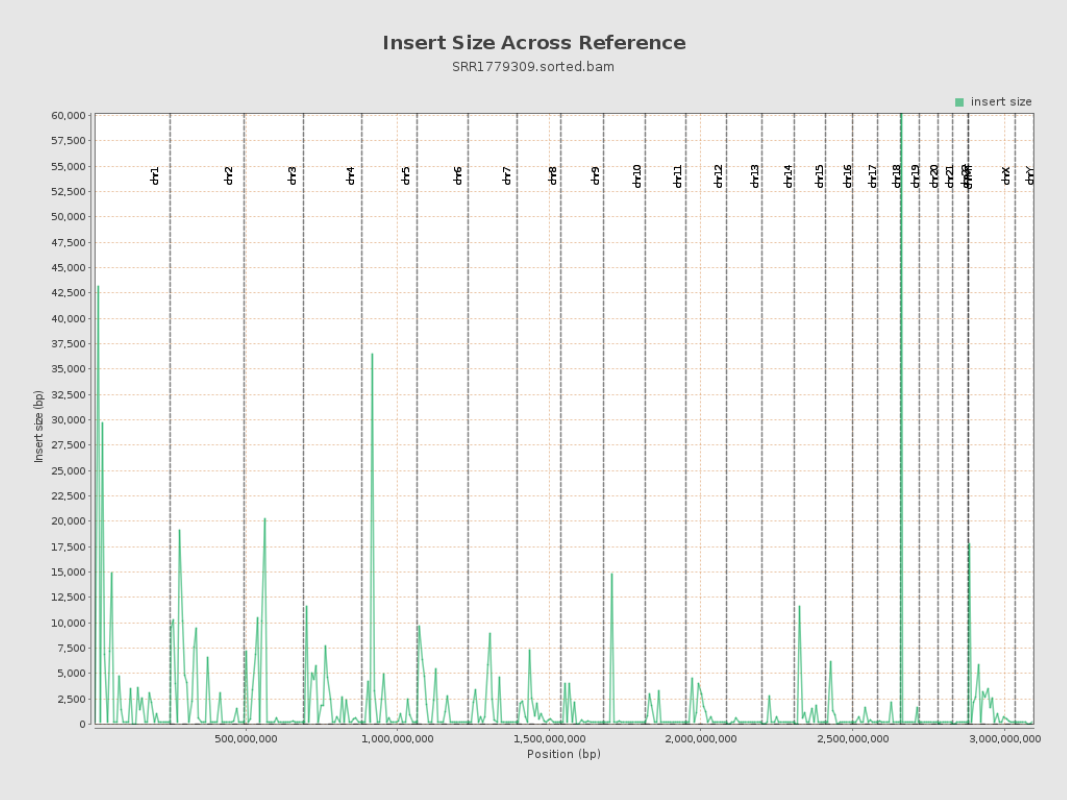
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram