Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 02:14:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779156.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_SRR1779156 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779156_1.fastq.gz SRR1779156_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 02:14:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779156.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,135,270
Mapped reads	5,926,619 / 96.6%
Unmapped reads	208,651 / 3.4%
Mapped paired reads	5,926,619 / 96.6%
Mapped reads, first in pair	2,981,790 / 48.6%
Mapped reads, second in pair	2,944,829 / 48%
Mapped reads, both in pair	5,863,908 / 95.58%
Mapped reads, singletons	62,711 / 1.02%
Secondary alignments	0
Supplementary alignments	34,397 / 0.56%
Read min/max/mean length	30 / 101 / 101.22
Duplicated reads (estimated)	79,056 / 1.29%
Duplication rate	1.15%
Clipped reads	366,318 / 5.97%

2.2. ACGT Content

Number/percentage of A's	180,355,392 / 30.48%
Number/percentage of C's	114,975,457 / 19.43%
Number/percentage of T's	179,278,266 / 30.29%
Number/percentage of G's	116,963,622 / 19.76%
Number/percentage of N's	240,658 / 0.04%

GC Percentage	39.19%

2.3. Coverage

Mean	0.1912
Standard Deviation	0.6888

2.4. Mapping Quality

Mean Mapping Quality	53.62

2.5. Insert size

Mean	73,043.94
Standard Deviation	2,604,701.56
P25/Median/P75	167 / 222 / 300

2.6. Mismatches and indels

General error rate	0.45%
Mismatches	2,565,597
Insertions	50,149
Mapped reads with at least one insertion	0.83%
Deletions	62,095
Mapped reads with at least one deletion	1.03%
Homopolymer indels	46.54%

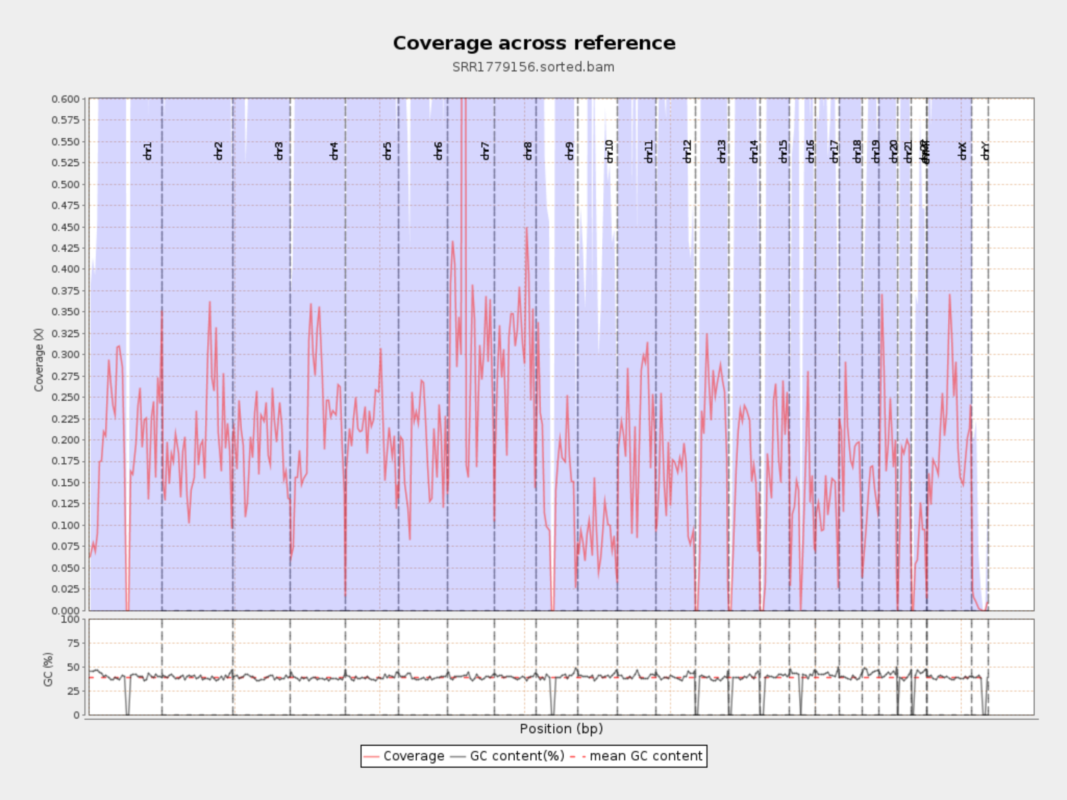
2.7. Chromosome stats

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

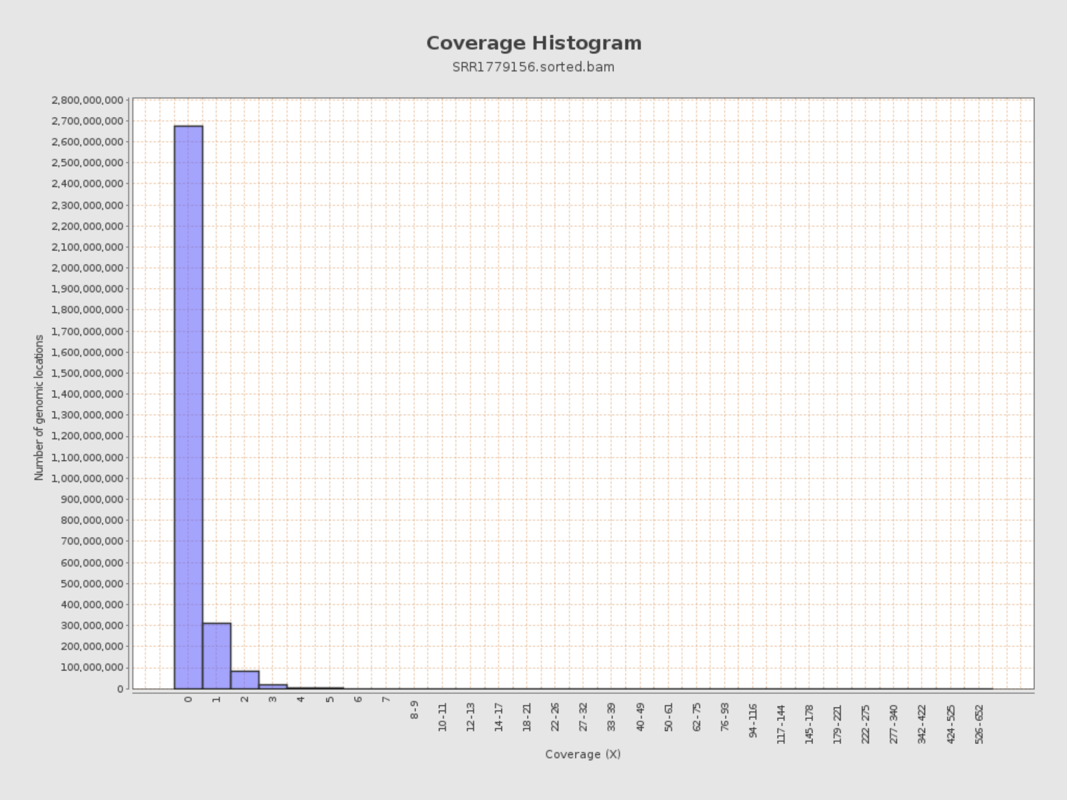
		bases	coverage	deviation
chr1	249250621	47892547	0.1921	0.8284
chr2	243199373	47923136	0.1971	0.6079
chr3	198022430	39020275	0.197	0.5434
chr4	191154276	42693962	0.2233	0.5928
chr5	180915260	38199419	0.2111	0.5644
chr6	171115067	32421929	0.1895	0.5444
chr7	159138663	60091226	0.3776	1.561
chr8	146364022	44730923	0.3056	0.6973
chr9	141213431	21447616	0.1519	0.5101
chr10	135534747	11730427	0.0865	0.9737
chr11	135006516	28624572	0.212	0.5731
chr12	133851895	19987780	0.1493	0.4776
chr13	115169878	24150204	0.2097	0.58
chr14	107349540	16665078	0.1552	0.4931
chr15	102531392	16580175	0.1617	0.5164
chr16	90354753	11167624	0.1236	0.4336
chr17	81195210	9480694	0.1168	0.4454
chr18	78077248	15018427	0.1924	0.5568
chr19	59128983	7380043	0.1248	0.5559
chr20	63025520	13848636	0.2197	0.6
chr21	48129895	6941278	0.1442	0.4756
chr22	51304566	3431865	0.0669	0.3178
chrMT	16571	238	0.0144	0.119
chrX	155270560	32113142	0.2068	0.5844

chrY	59373566	412019	0.0069	0.1256

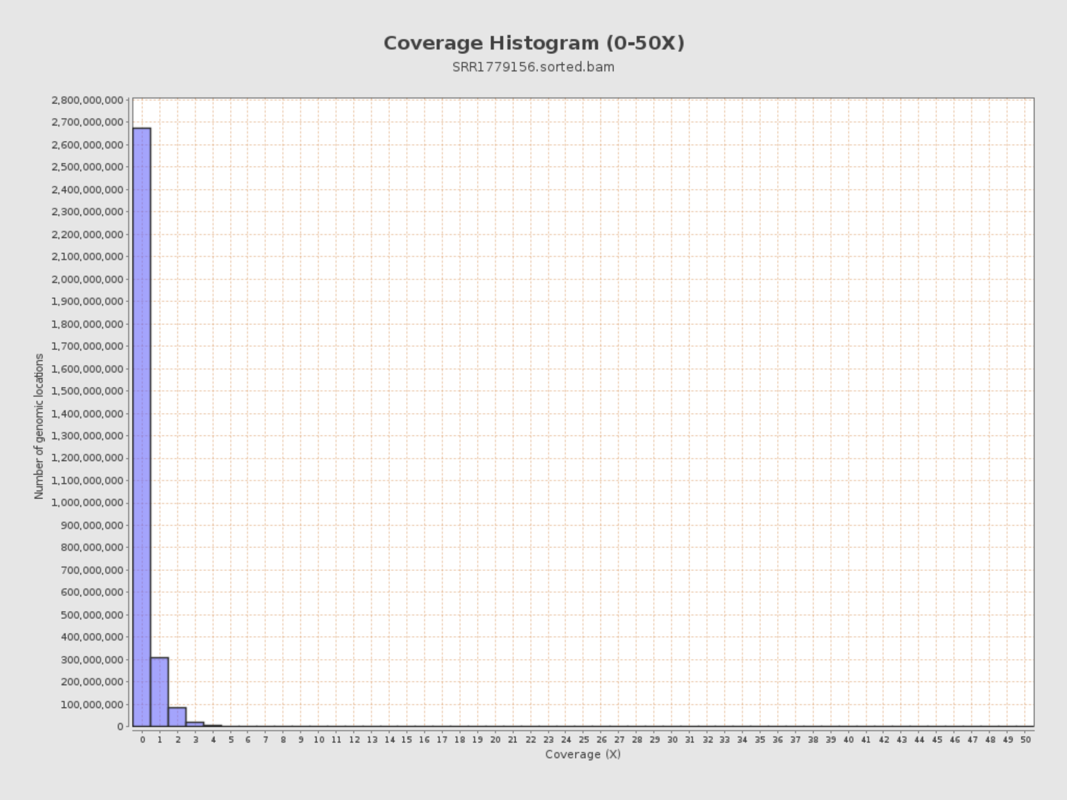
3. Results : Coverage across reference



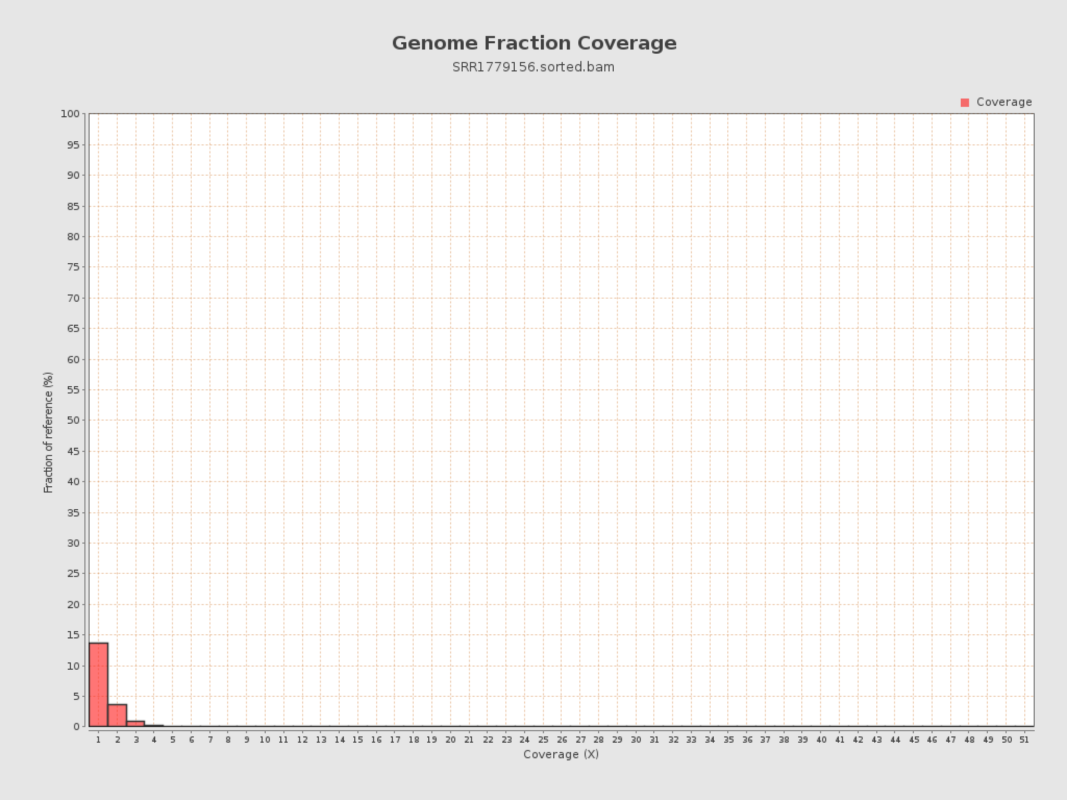
4. Results : Coverage Histogram



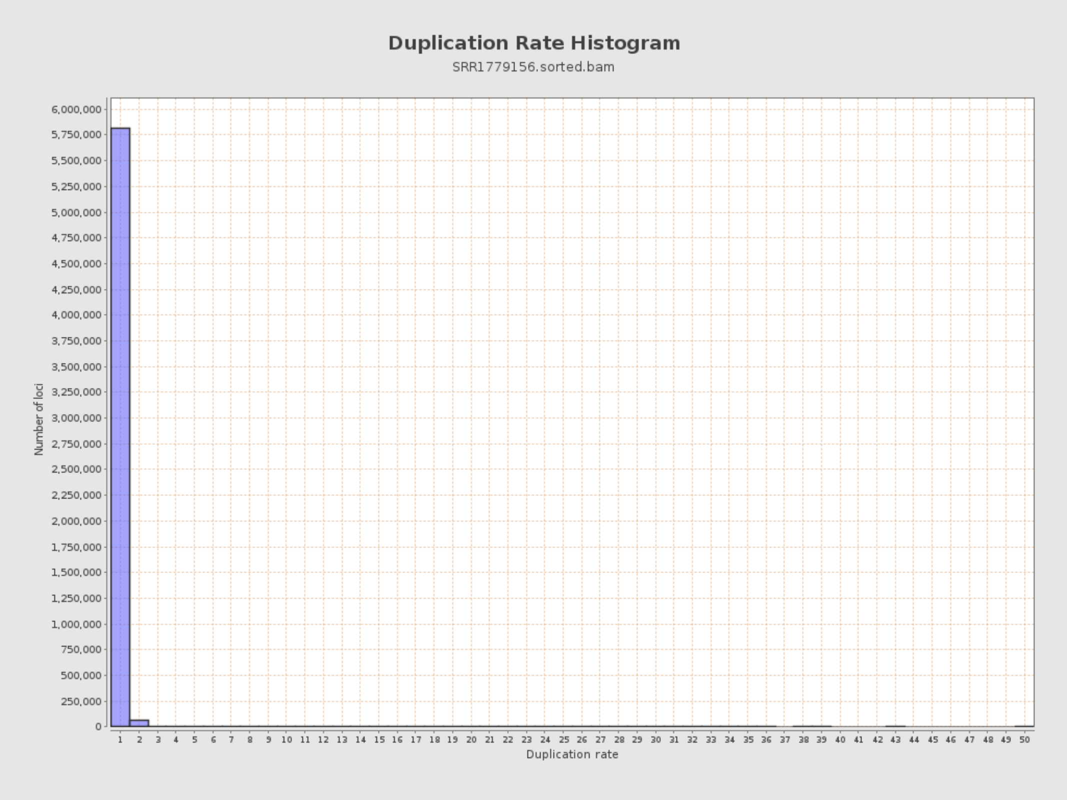
5. Results : Coverage Histogram (0-50X)



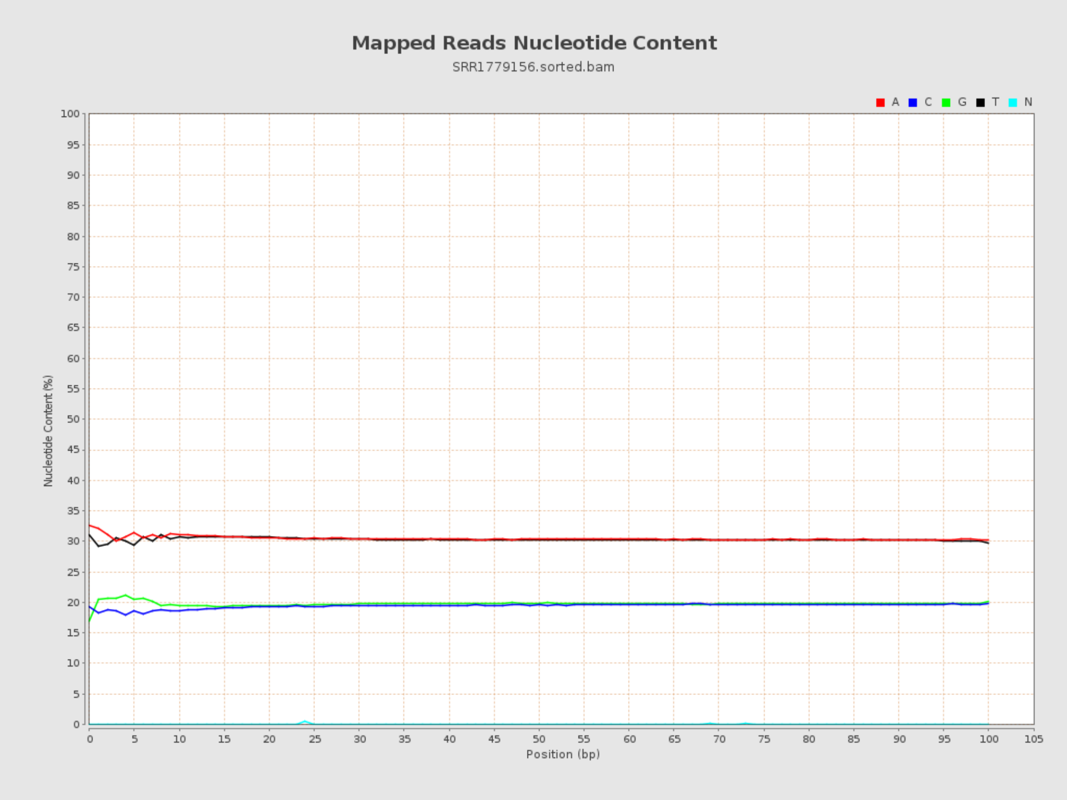
6. Results : Genome Fraction Coverage



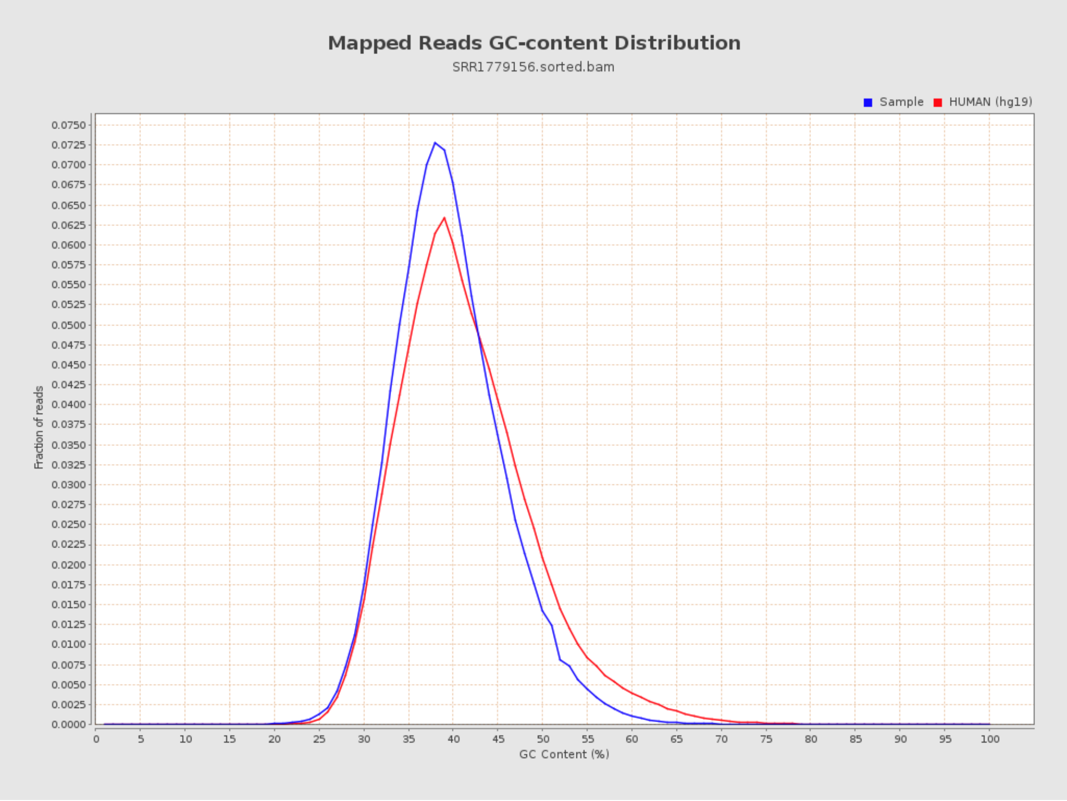
7. Results : Duplication Rate Histogram



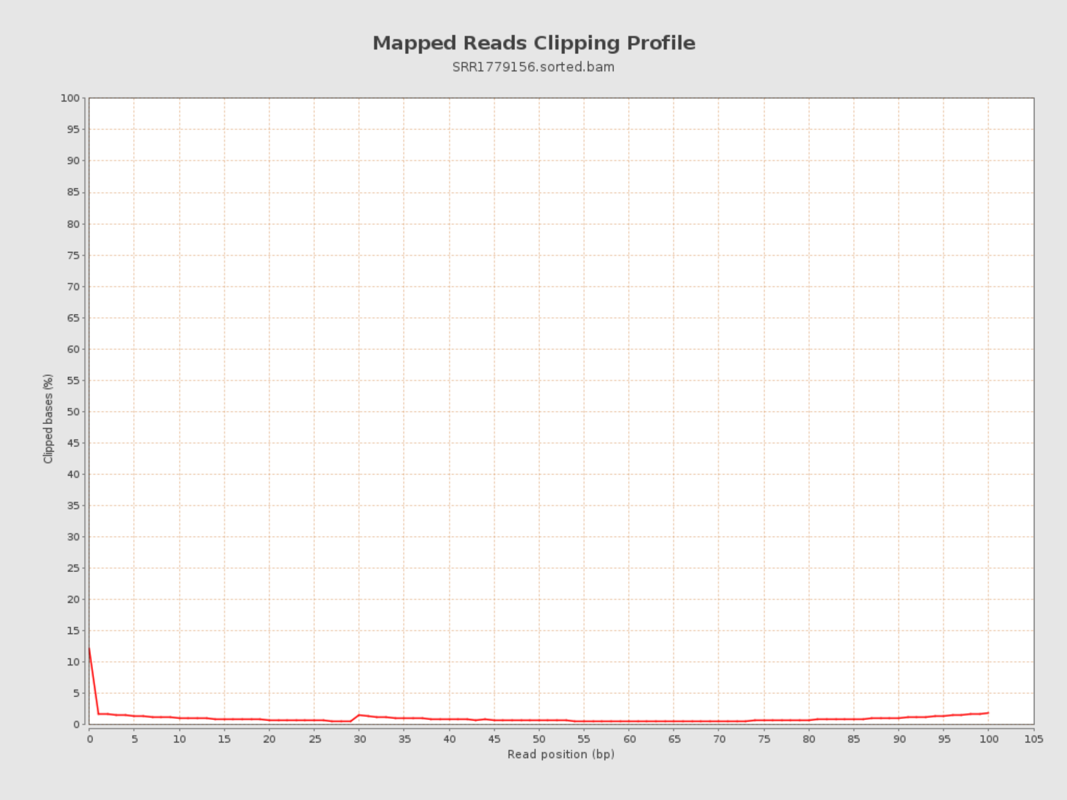
8. Results : Mapped Reads Nucleotide Content



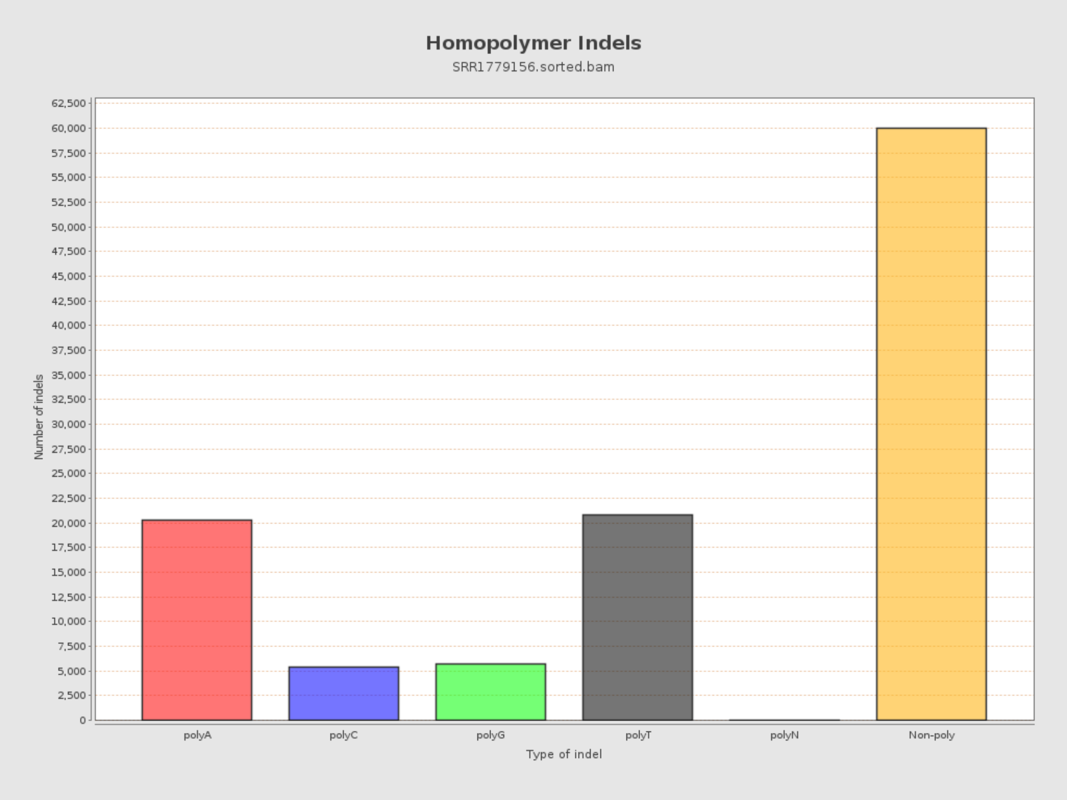
9. Results : Mapped Reads GC-content Distribution



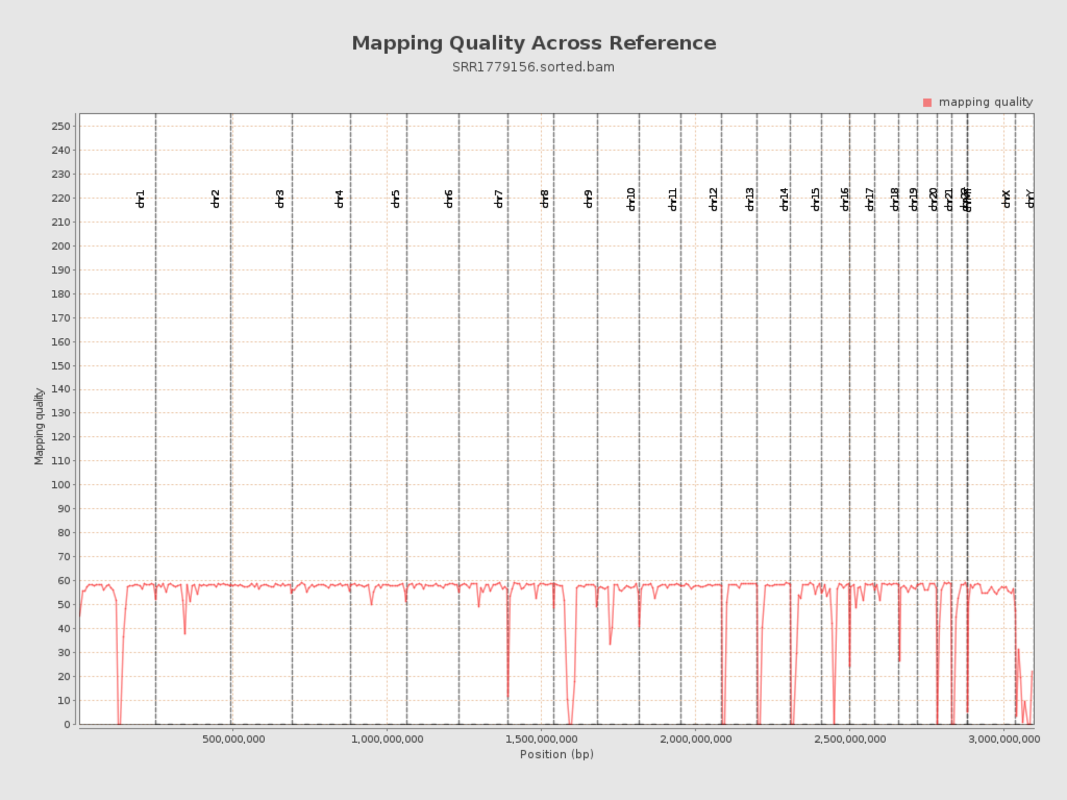
10. Results : Mapped Reads Clipping Profile



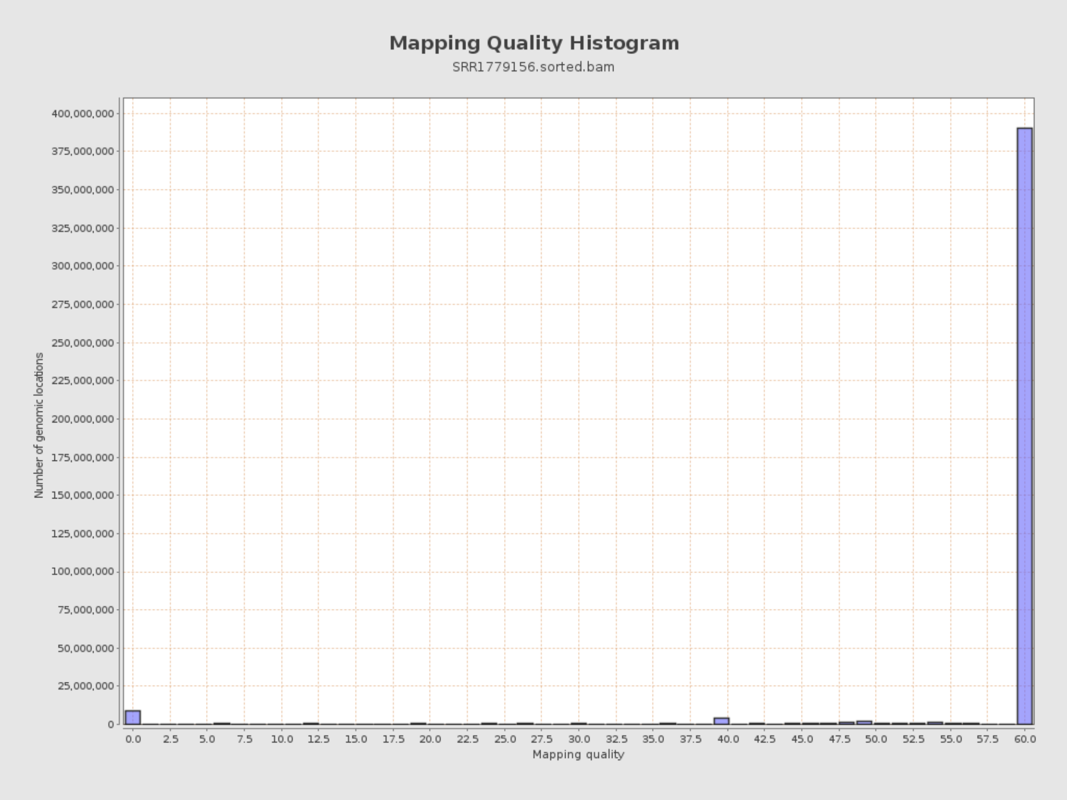
11. Results : Homopolymer Indels



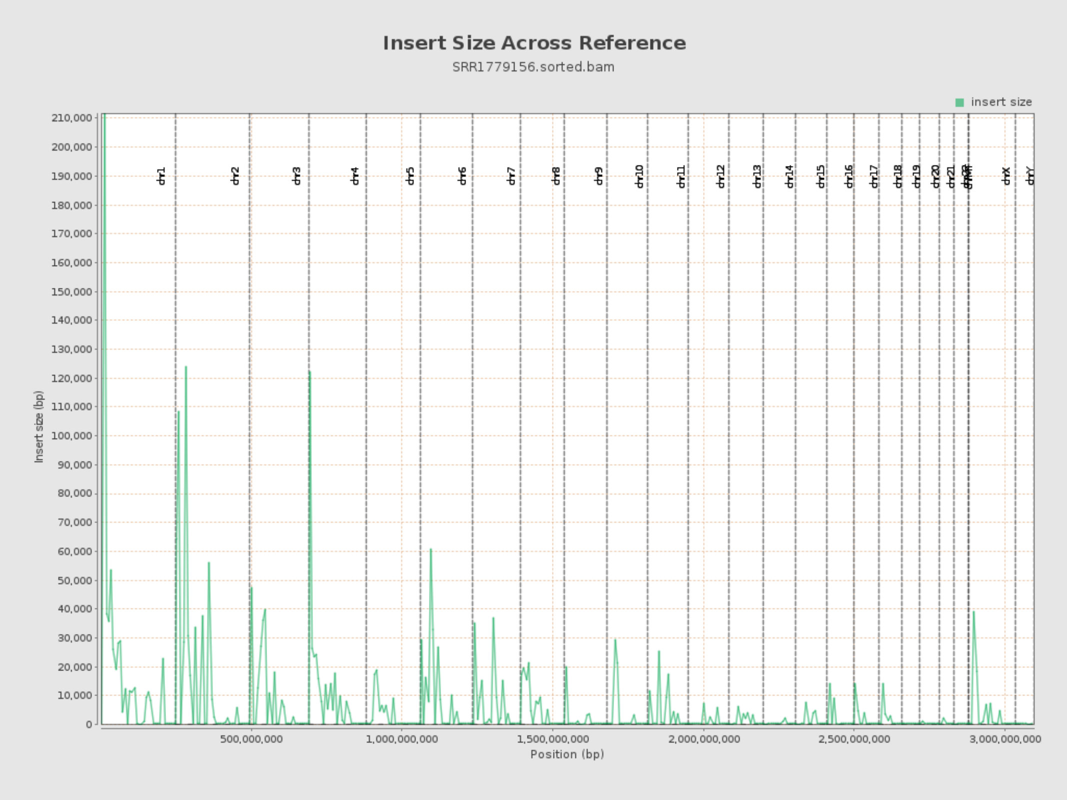
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram