Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/06 02:24:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124836.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_SRR3124836 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124836_1.fastq.gz SRR3124836_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 06 02:24:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124836.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	66,333,856
Mapped reads	62,965,476 / 94.92%
Unmapped reads	3,368,380 / 5.08%
Mapped paired reads	62,965,476 / 94.92%
Mapped reads, first in pair	31,759,533 / 47.88%
Mapped reads, second in pair	31,205,943 / 47.04%
Mapped reads, both in pair	61,919,574 / 93.35%
Mapped reads, singletons	1,045,902 / 1.58%
Secondary alignments	0
Supplementary alignments	3,194,890 / 4.82%
Read min/max/mean length	30 / 150 / 152.42
Duplicated reads (estimated)	22,837,970 / 34.43%
Duplication rate	23.29%
Clipped reads	40,459,125 / 60.99%

2.2. ACGT Content

Number/percentage of A's	2,378,020,229 / 29.01%
Number/percentage of C's	1,568,849,956 / 19.14%
Number/percentage of T's	2,458,199,580 / 29.98%
Number/percentage of G's	1,793,158,759 / 21.87%
Number/percentage of N's	337,790 / 0%

GC Percentage	41.01%

2.3. Coverage

Mean	2.6504
Standard Deviation	35.6025

2.4. Mapping Quality

Mean Mapping Quality	52.8

2.5. Insert size

Mean	330,887.24
Standard Deviation	5,546,271.42
P25/Median/P75	181 / 237 / 301

2.6. Mismatches and indels

General error rate	1.48%
Mismatches	116,804,966
Insertions	1,493,286
Mapped reads with at least one insertion	2.21%
Deletions	3,110,710
Mapped reads with at least one deletion	4.73%
Homopolymer indels	44.17%

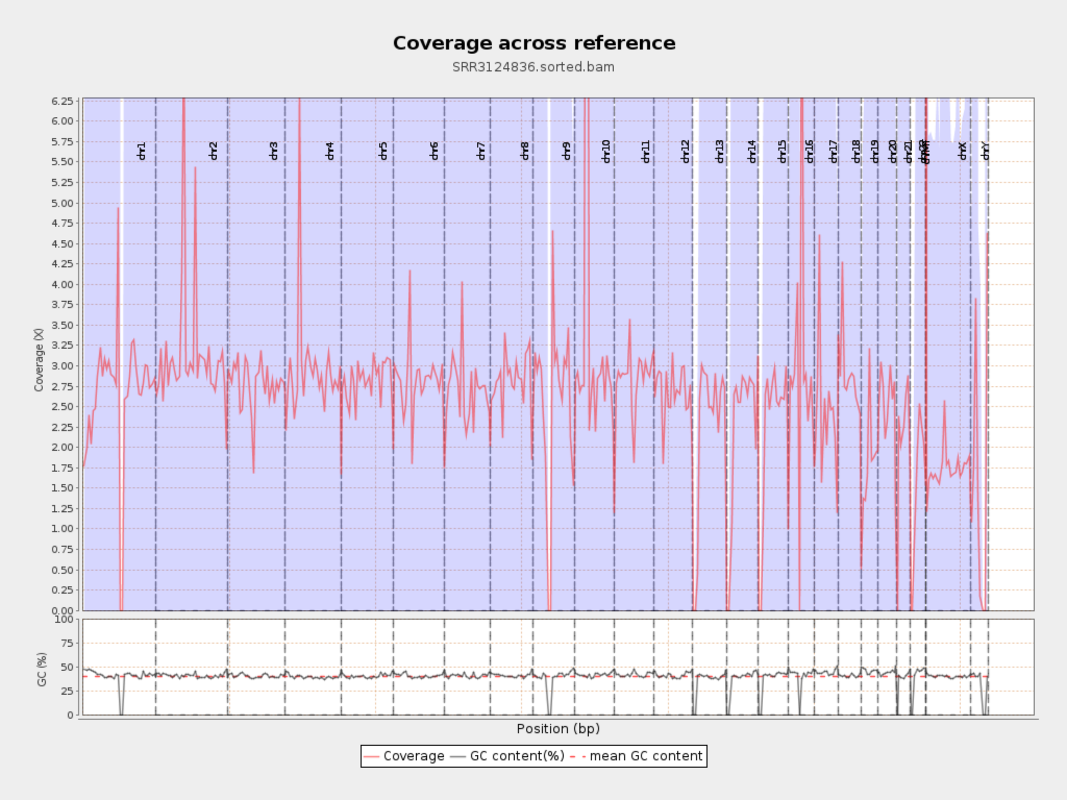
2.7. Chromosome stats

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

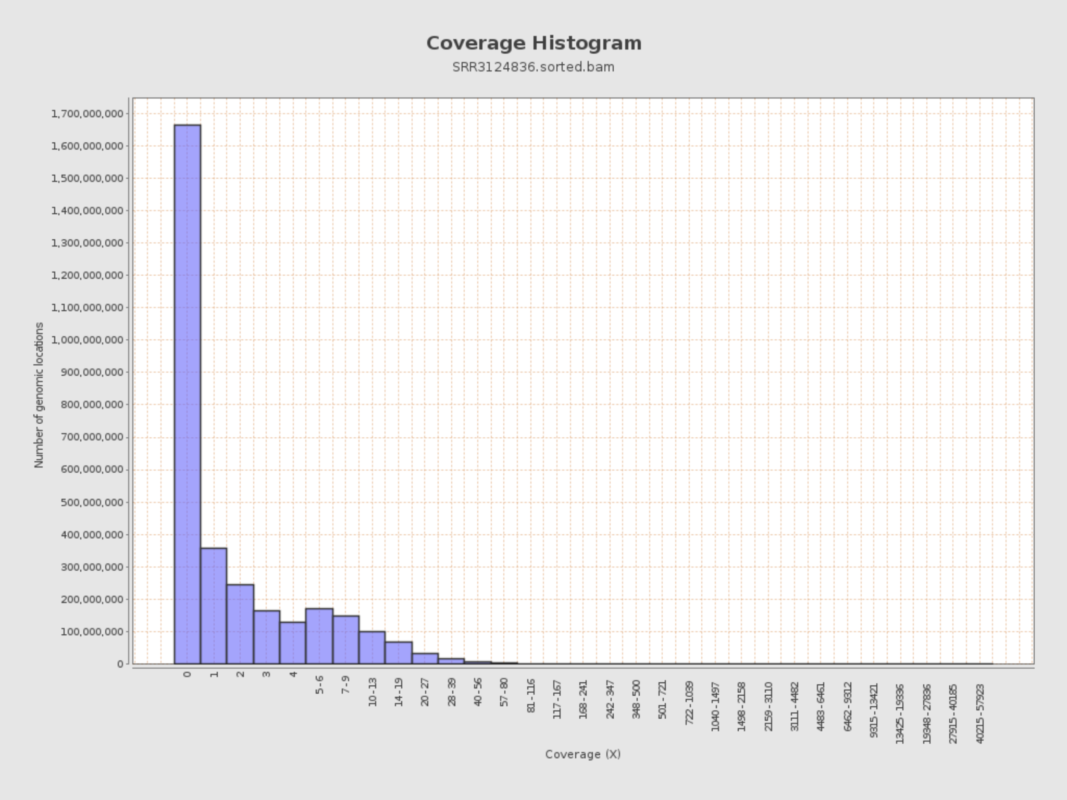
		bases	coverage	deviation
chr1	249250621	660866031	2.6514	36.9852
chr2	243199373	774322340	3.1839	38.8479
chr3	198022430	549181093	2.7733	6.487
chr4	191154276	570561697	2.9848	24.3496
chr5	180915260	508193561	2.809	6.3616
chr6	171115067	485081118	2.8348	15.9404
chr7	159138663	429079971	2.6963	28.4446
chr8	146364022	412652189	2.8194	8.7054
chr9	141213431	359592544	2.5464	48.751
chr10	135534747	473574130	3.4941	116.7312
chr11	135006516	382251555	2.8314	25.9217
chr12	133851895	358857224	2.681	14.3655
chr13	115169878	255674120	2.22	4.8292
chr14	107349540	237360495	2.2111	6.2113
chr15	102531392	225150370	2.1959	7.8435
chr16	90354753	273306101	3.0248	46.6374
chr17	81195210	200115360	2.4646	35.606
chr18	78077248	227679222	2.9161	43.5821
chr19	59128983	108257382	1.8309	20.2582
chr20	63025520	162503985	2.5784	9.0485
chr21	48129895	102949428	2.139	12.1009
chr22	51304566	78037961	1.5211	5.5235
chrMT	16571	2998178	180.9292	86.5139
chrX	155270560	269648814	1.7366	8.7682

chrY	59373566	97002437	1.6338	39.0862

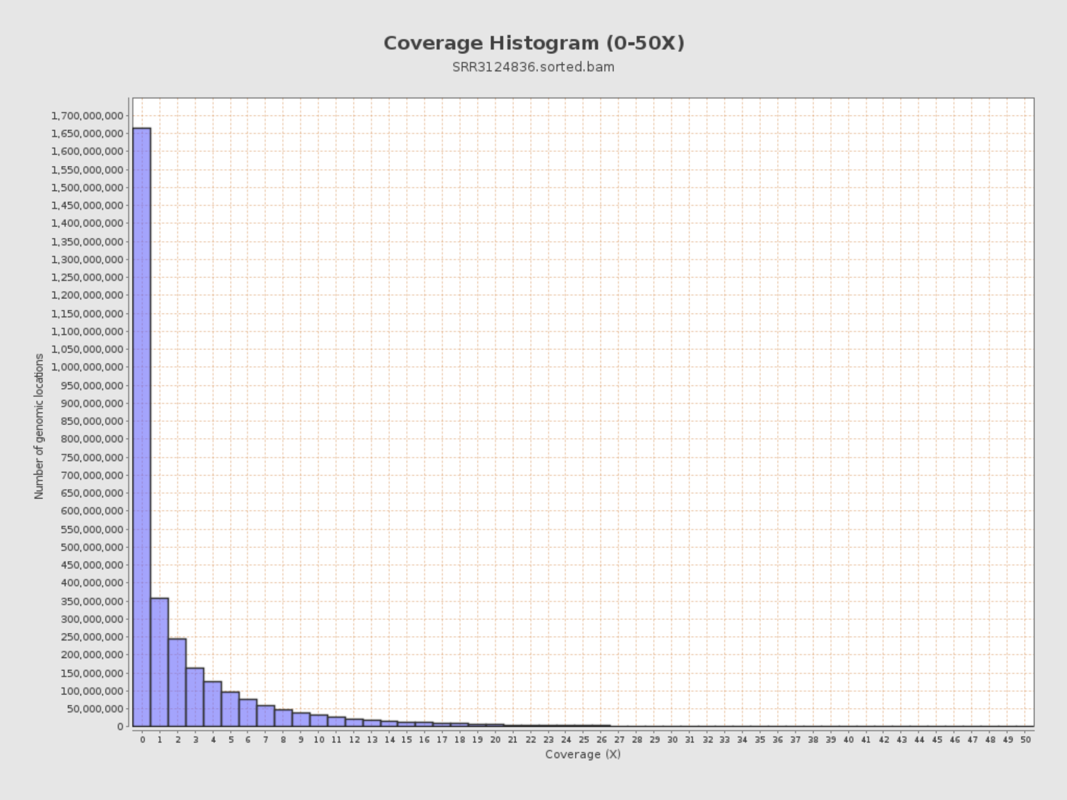
3. Results : Coverage across reference



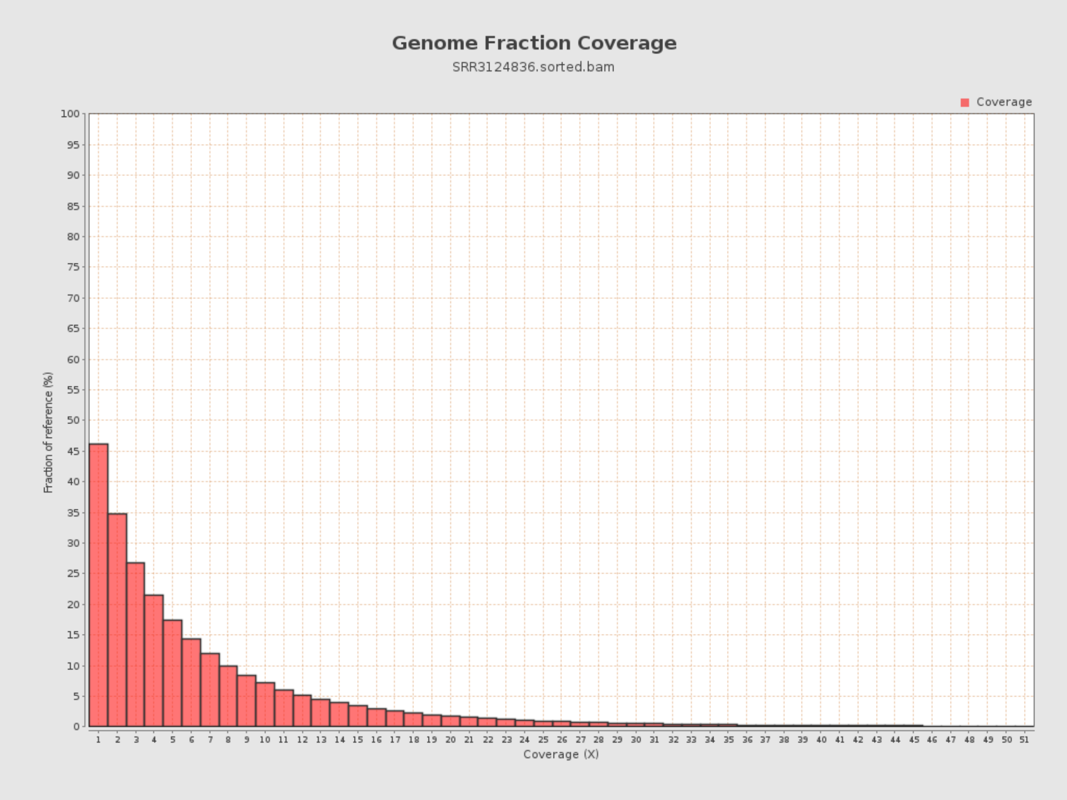
4. Results : Coverage Histogram



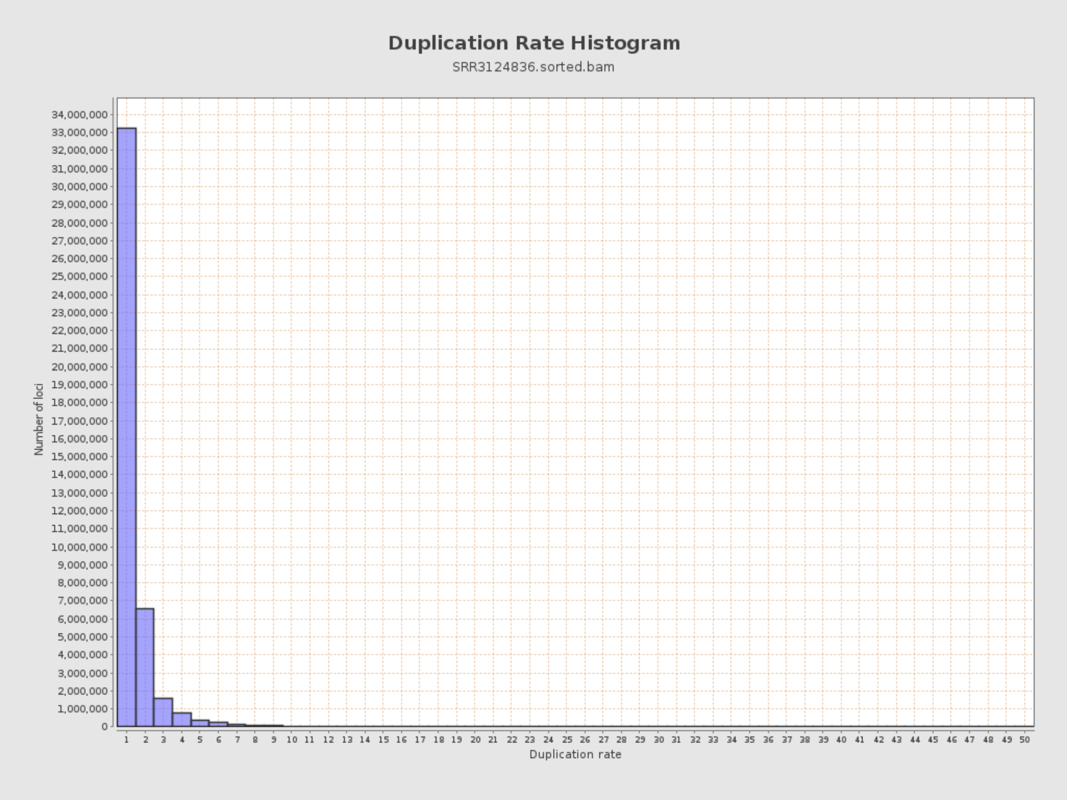
5. Results : Coverage Histogram (0-50X)



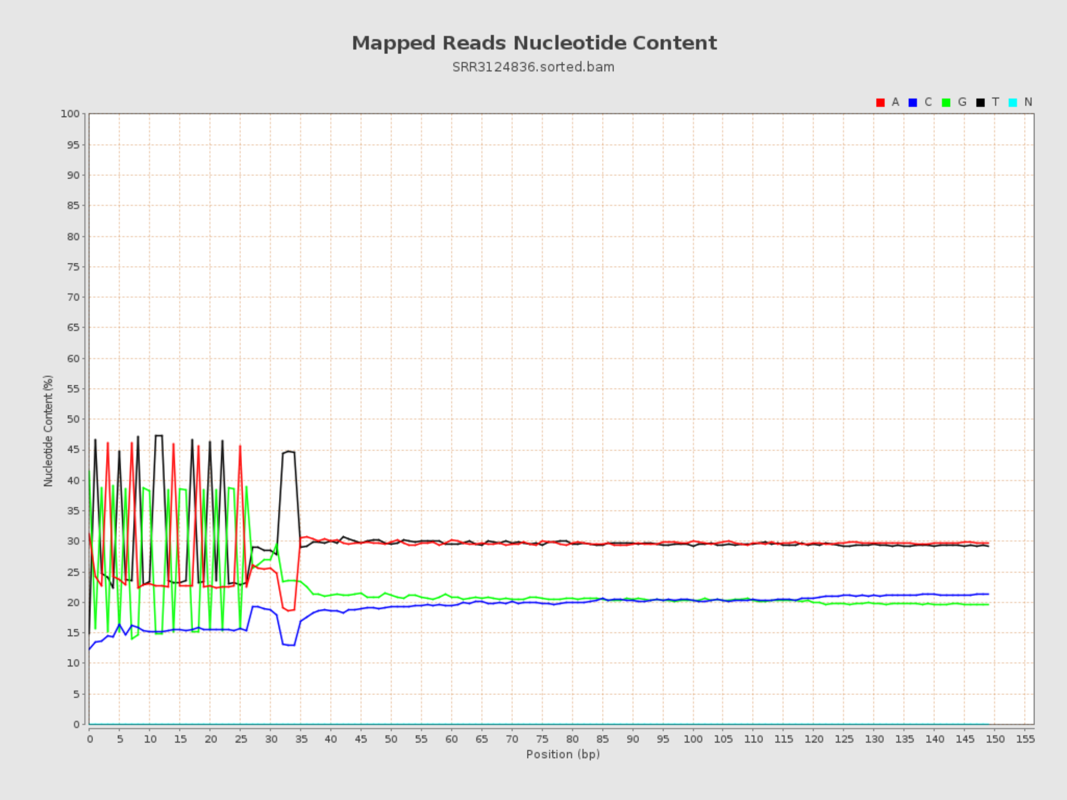
6. Results : Genome Fraction Coverage



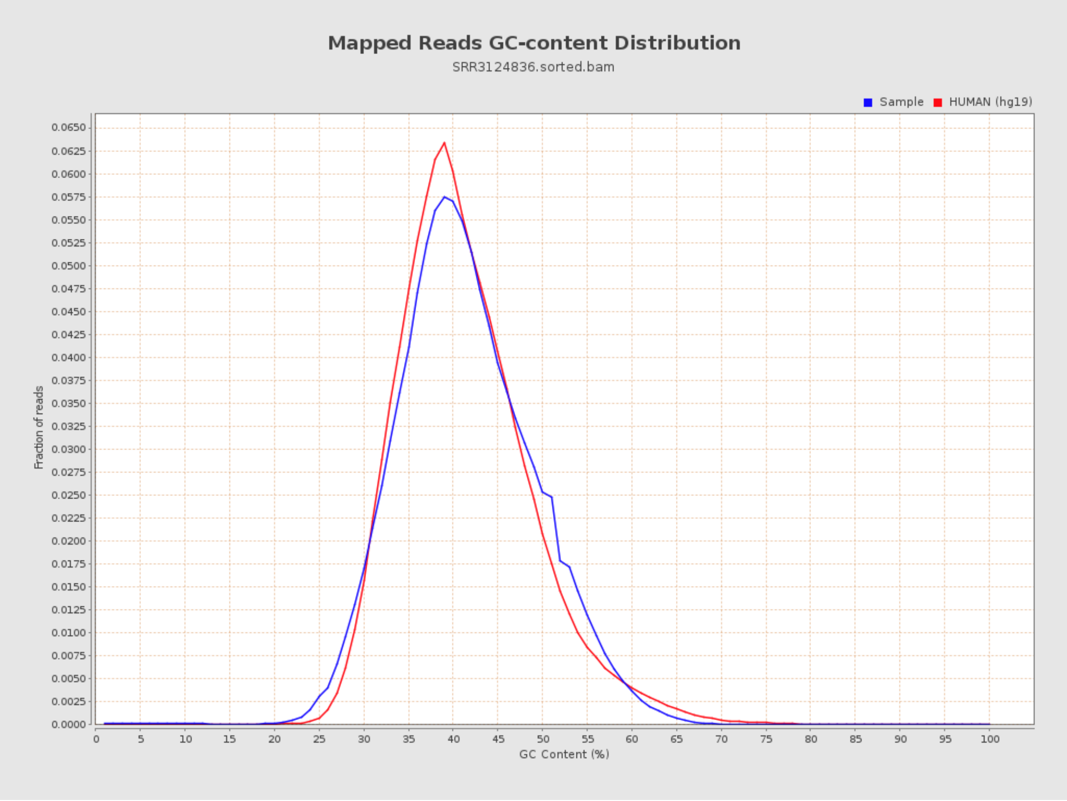
7. Results : Duplication Rate Histogram



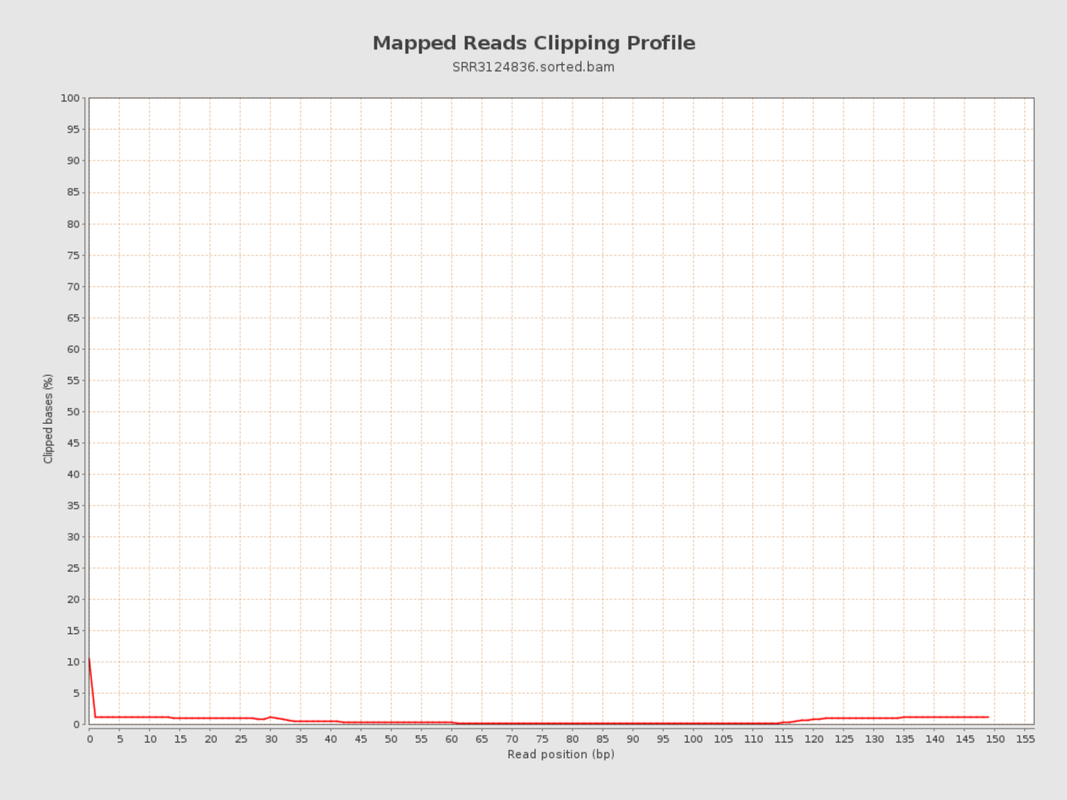
8. Results : Mapped Reads Nucleotide Content



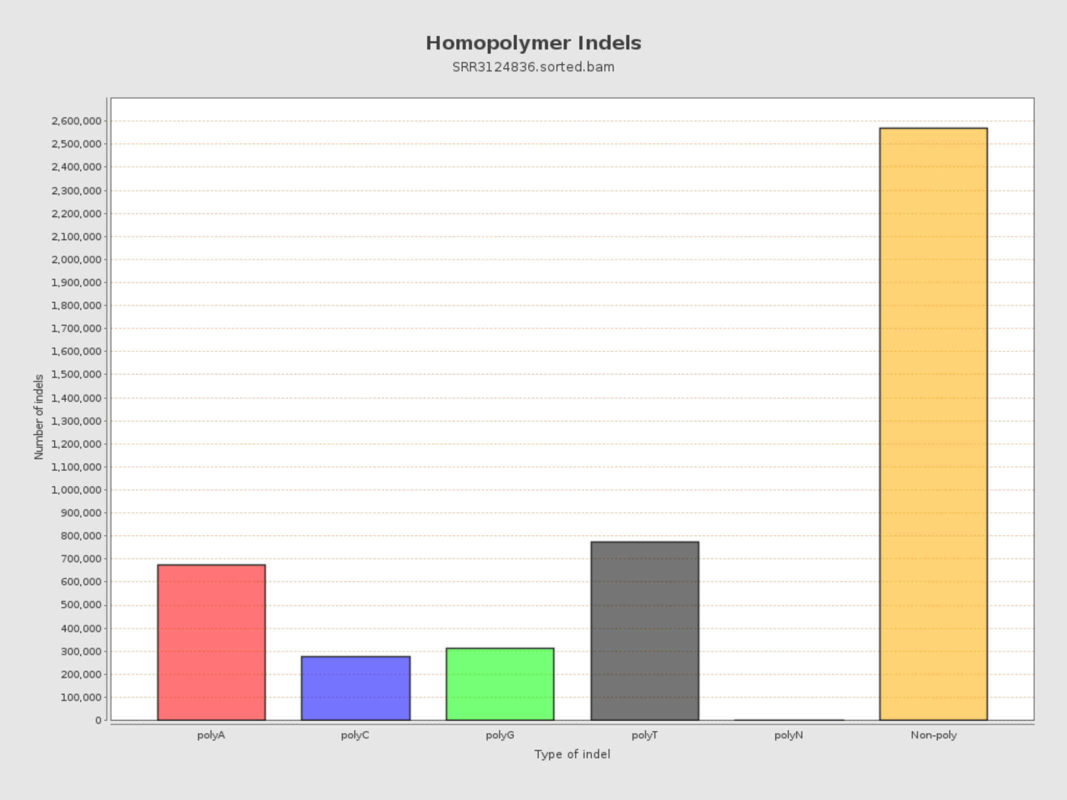
9. Results : Mapped Reads GC-content Distribution



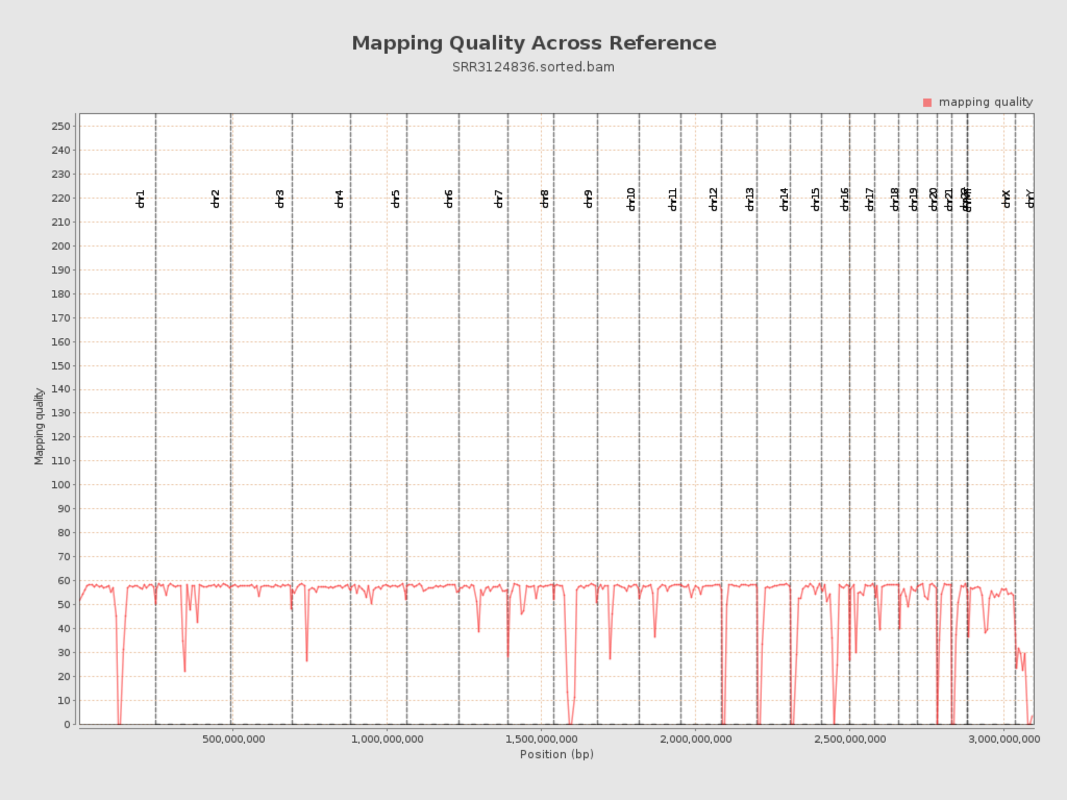
10. Results : Mapped Reads Clipping Profile



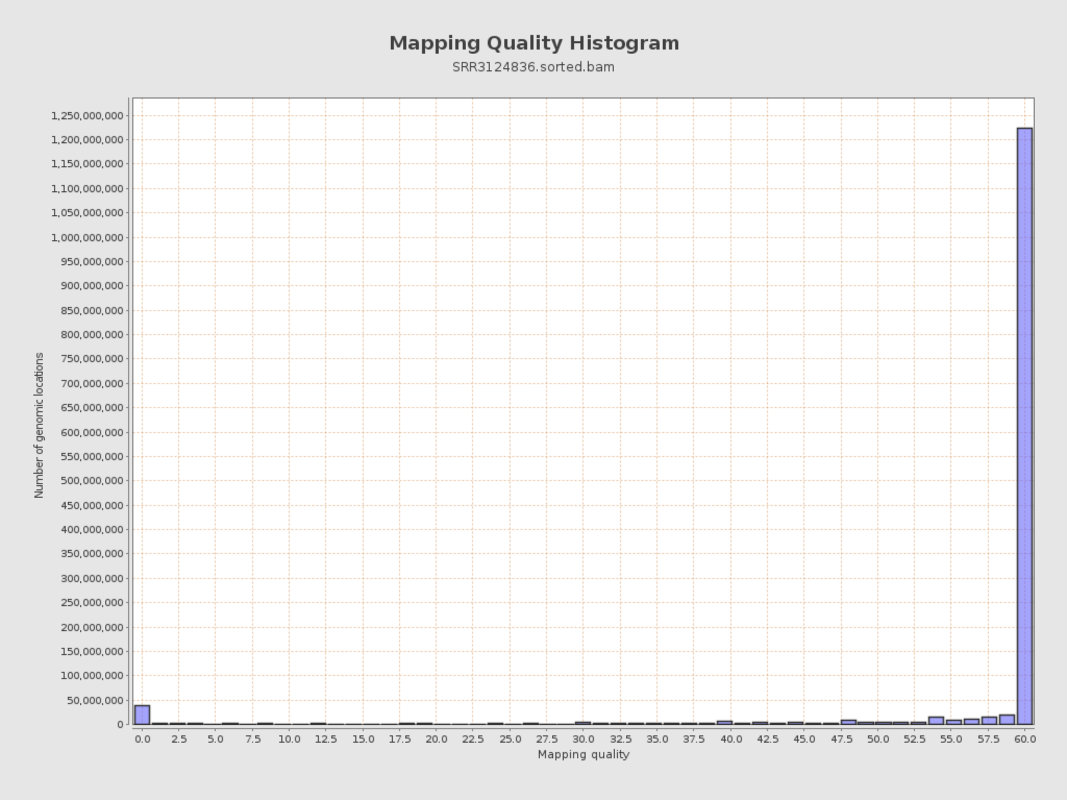
11. Results : Homopolymer Indels



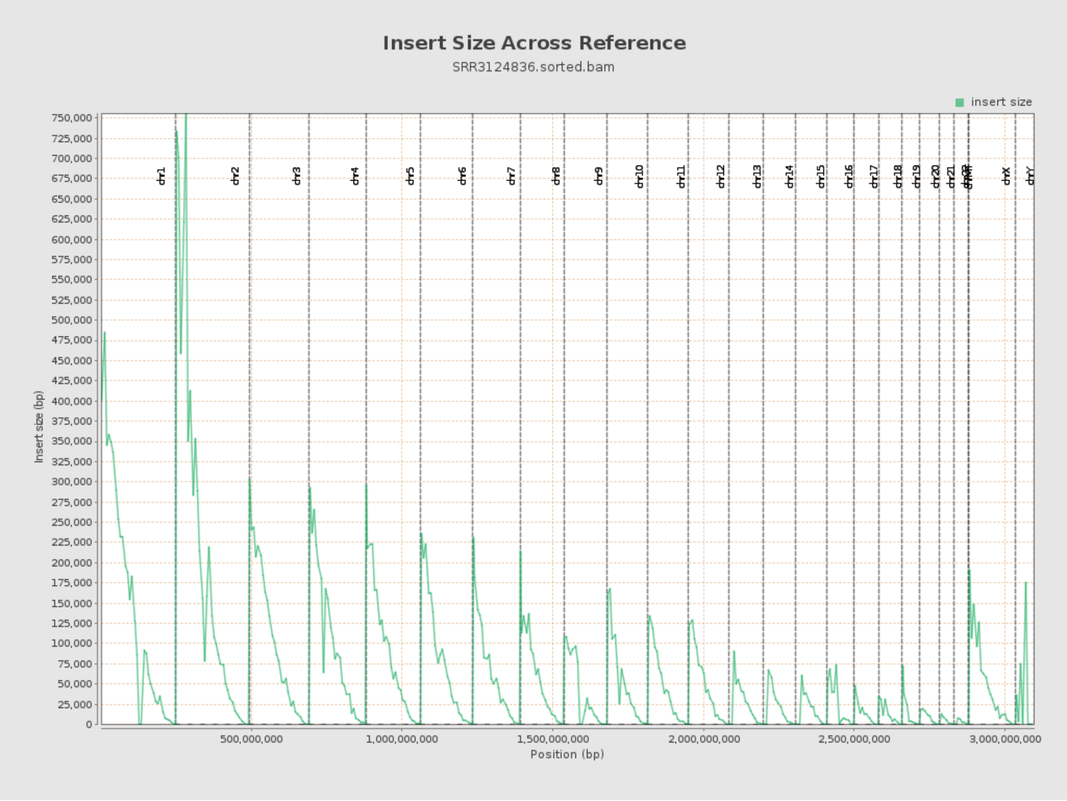
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram