Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/08 04:46:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124848.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_SRR3124848 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124848_1.fastq.gz SRR3124848_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 08 04:46:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124848.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	89,272,918
Mapped reads	68,446,323 / 76.67%
Unmapped reads	20,826,595 / 23.33%
Mapped paired reads	68,446,323 / 76.67%
Mapped reads, first in pair	34,366,661 / 38.5%
Mapped reads, second in pair	34,079,662 / 38.17%
Mapped reads, both in pair	66,178,712 / 74.13%
Mapped reads, singletons	2,267,611 / 2.54%
Secondary alignments	0
Supplementary alignments	1,558,902 / 1.75%
Read min/max/mean length	30 / 150 / 150.83
Duplicated reads (estimated)	30,227,470 / 33.86%
Duplication rate	34.65%
Clipped reads	52,265,339 / 58.55%

2.2. ACGT Content

Number/percentage of A's	2,383,757,996 / 29.47%
Number/percentage of C's	1,599,679,192 / 19.78%
Number/percentage of T's	2,374,469,839 / 29.36%
Number/percentage of G's	1,730,288,088 / 21.39%
Number/percentage of N's	119,209 / 0%

GC Percentage	41.17%

2.3. Coverage

Mean	2.6147
Standard Deviation	38.7174

2.4. Mapping Quality

Mean Mapping Quality	52.82

2.5. Insert size

Mean	93,014.26
Standard Deviation	2,932,383.47
P25/Median/P75	110 / 152 / 213

2.6. Mismatches and indels

General error rate	1.22%
Mismatches	94,655,678
Insertions	1,469,997
Mapped reads with at least one insertion	2%
Deletions	2,665,364
Mapped reads with at least one deletion	3.73%
Homopolymer indels	43.02%

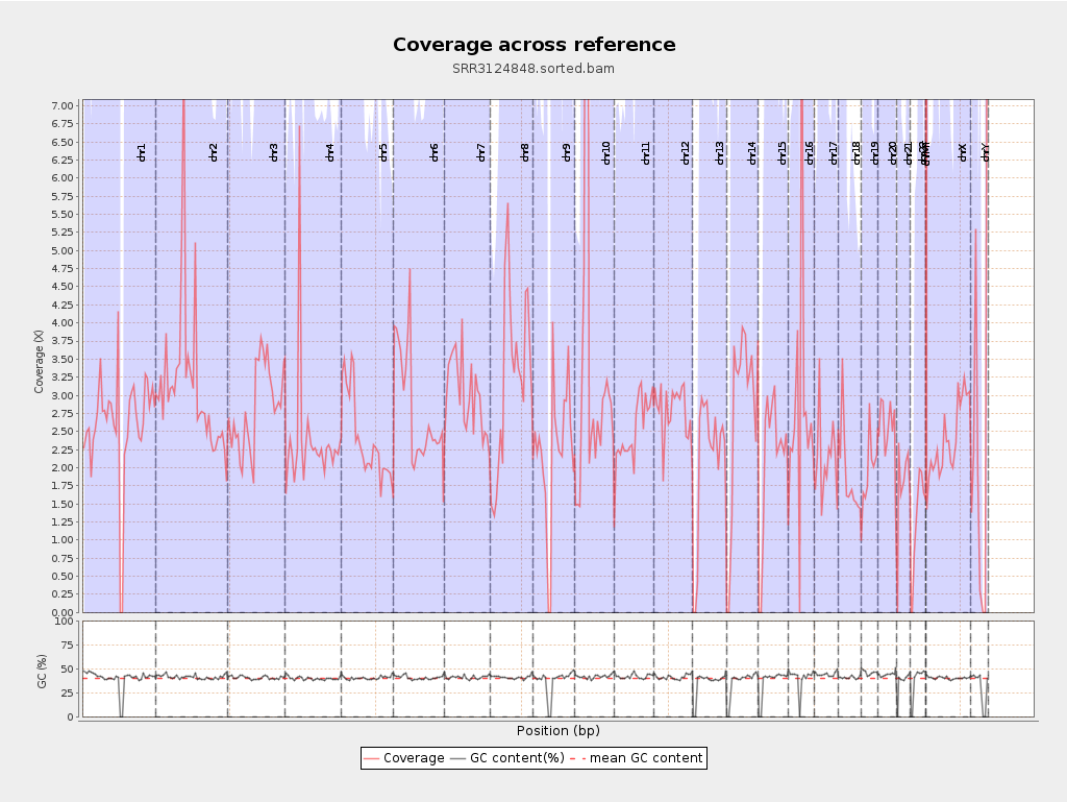
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

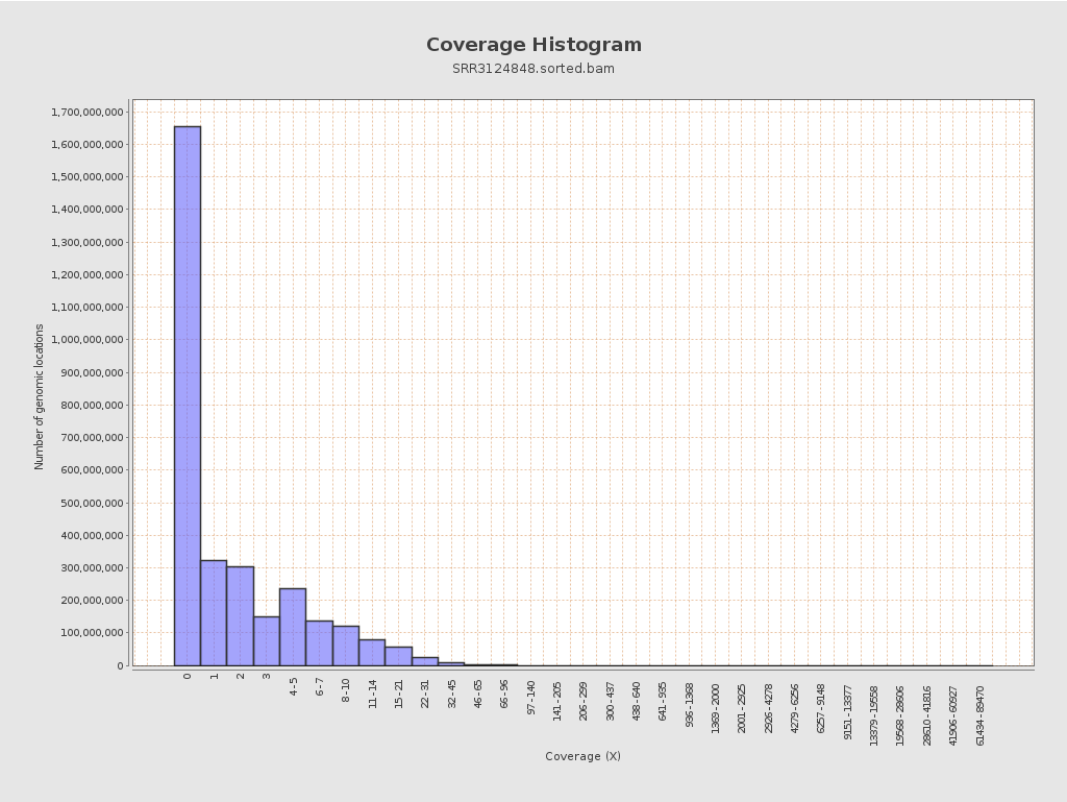
		bases	coverage	deviation
chr1	249250621	646229611	2.5927	30.2734
chr2	243199373	767339019	3.1552	47.6081
chr3	198022430	559606822	2.826	7.473
chr4	191154276	454777216	2.3791	27.9212
chr5	180915260	433004263	2.3934	8.4718
chr6	171115067	480127156	2.8059	15.6065
chr7	159138663	476132574	2.9919	26.034
chr8	146364022	473342663	3.234	10.782
chr9	141213431	317765830	2.2503	36.1842
chr10	135534747	466380880	3.441	137.1247
chr11	135006516	339976675	2.5182	14.8219
chr12	133851895	373736635	2.7922	5.927
chr13	115169878	242179419	2.1028	4.6945
chr14	107349540	299715100	2.792	7.8365
chr15	102531392	214538181	2.0924	5.5028
chr16	90354753	261244575	2.8913	51.4978
chr17	81195210	174926072	2.1544	27.3415
chr18	78077248	151143502	1.9358	37.8818
chr19	59128983	117829188	1.9927	17.3432
chr20	63025520	162455074	2.5776	21.6115
chr21	48129895	85890160	1.7845	16.1488
chr22	51304566	64695313	1.261	5.8916
chrMT	16571	3585030	216.3436	114.0111
chrX	155270560	373012417	2.4023	9.4623

chrY	59373566	154597340	2.6038	65.1417

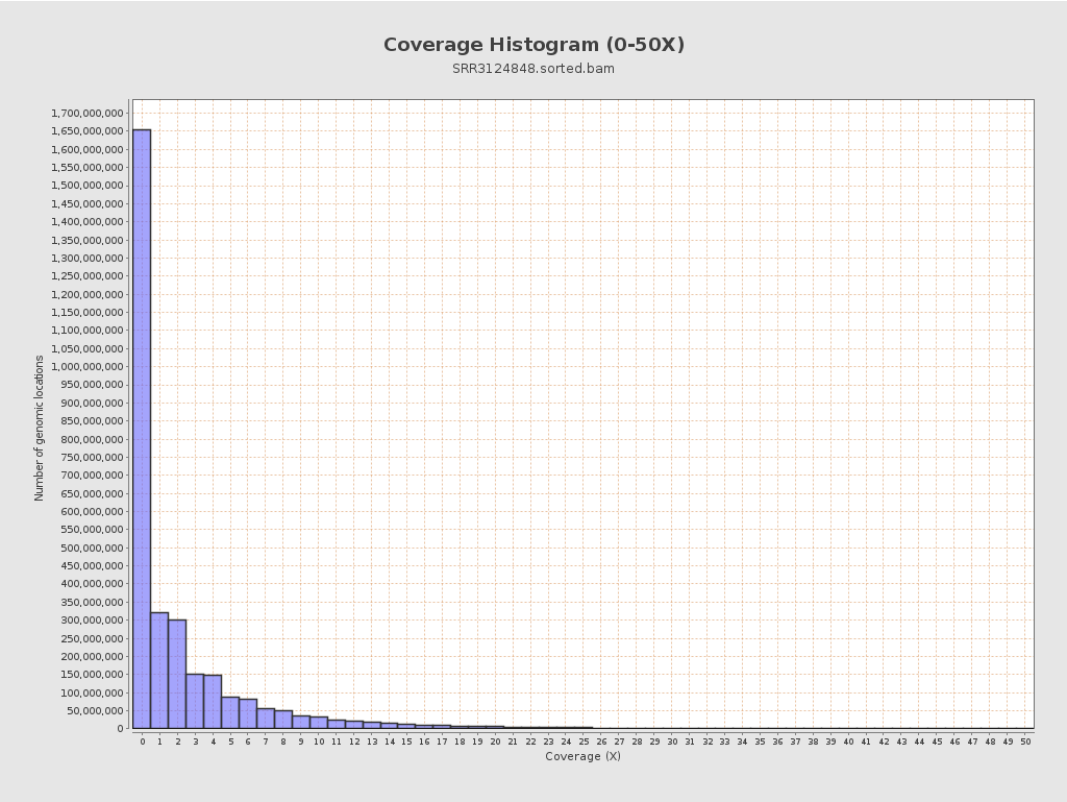
3. Results : Coverage across reference



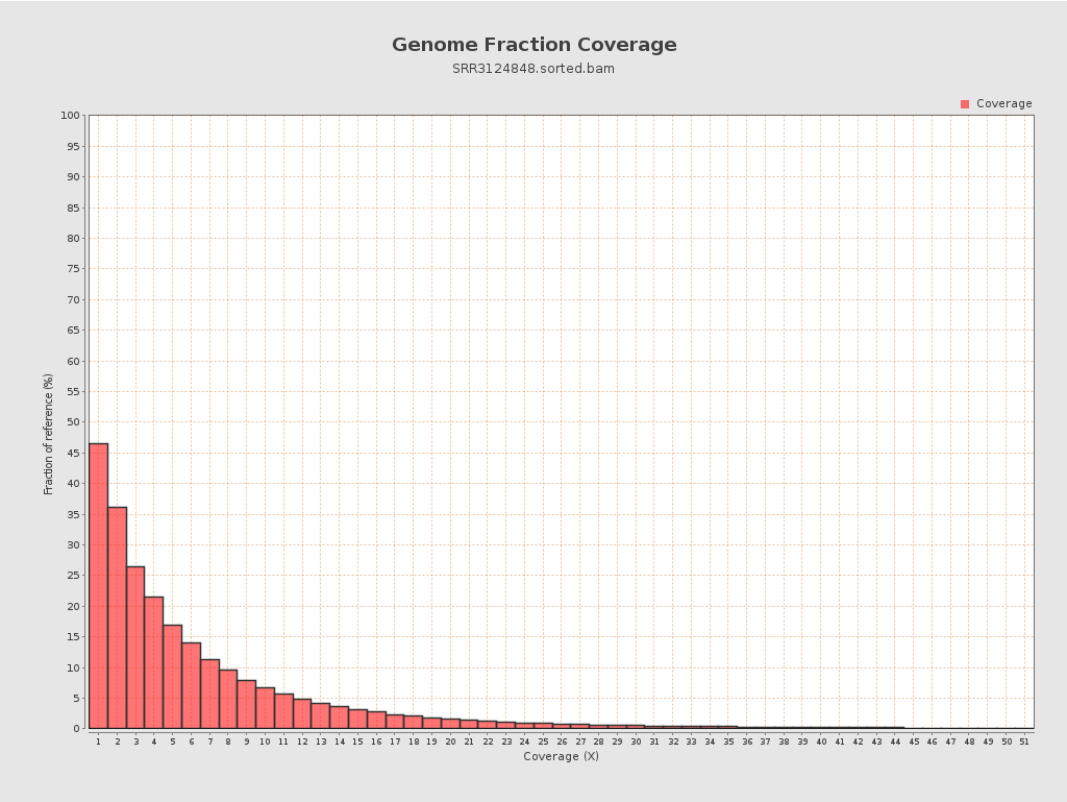
4. Results : Coverage Histogram



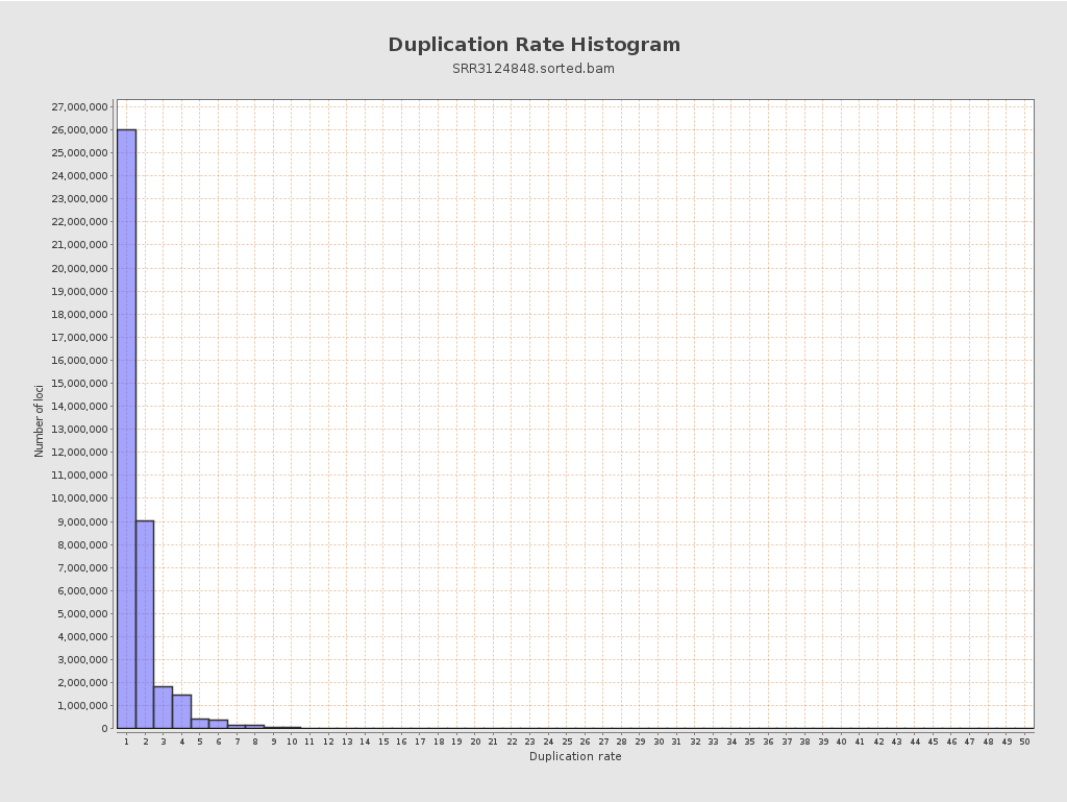
5. Results : Coverage Histogram (0-50X)



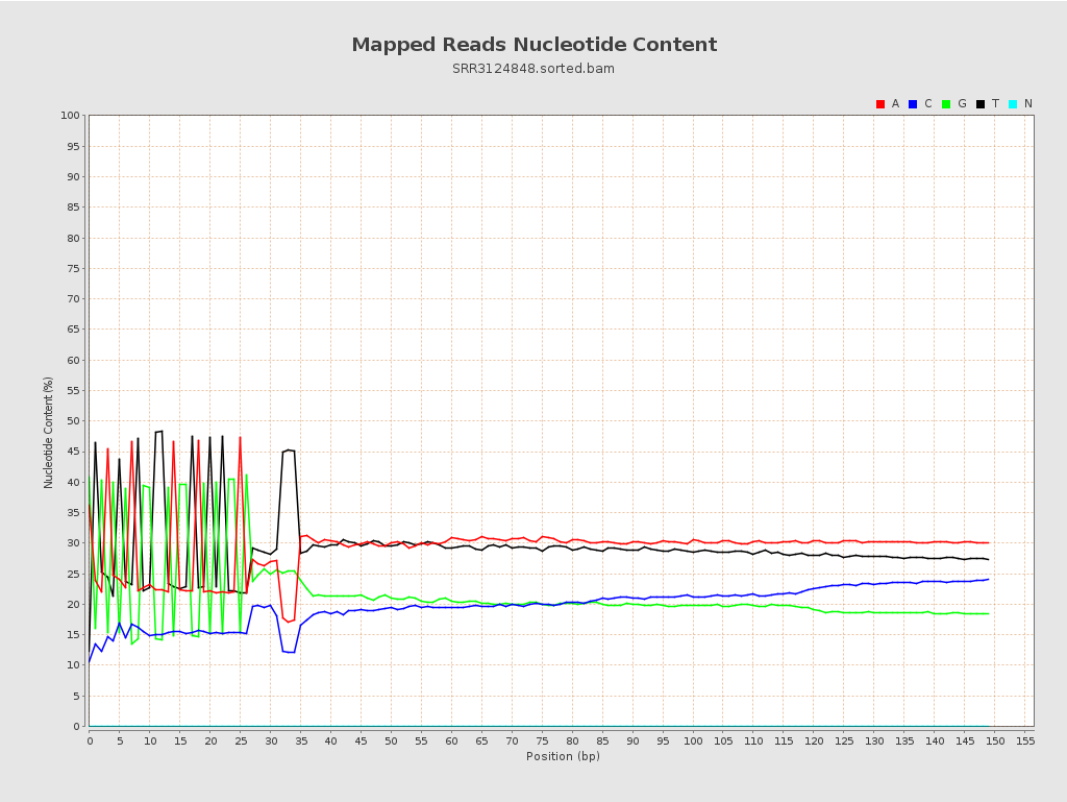
6. Results : Genome Fraction Coverage



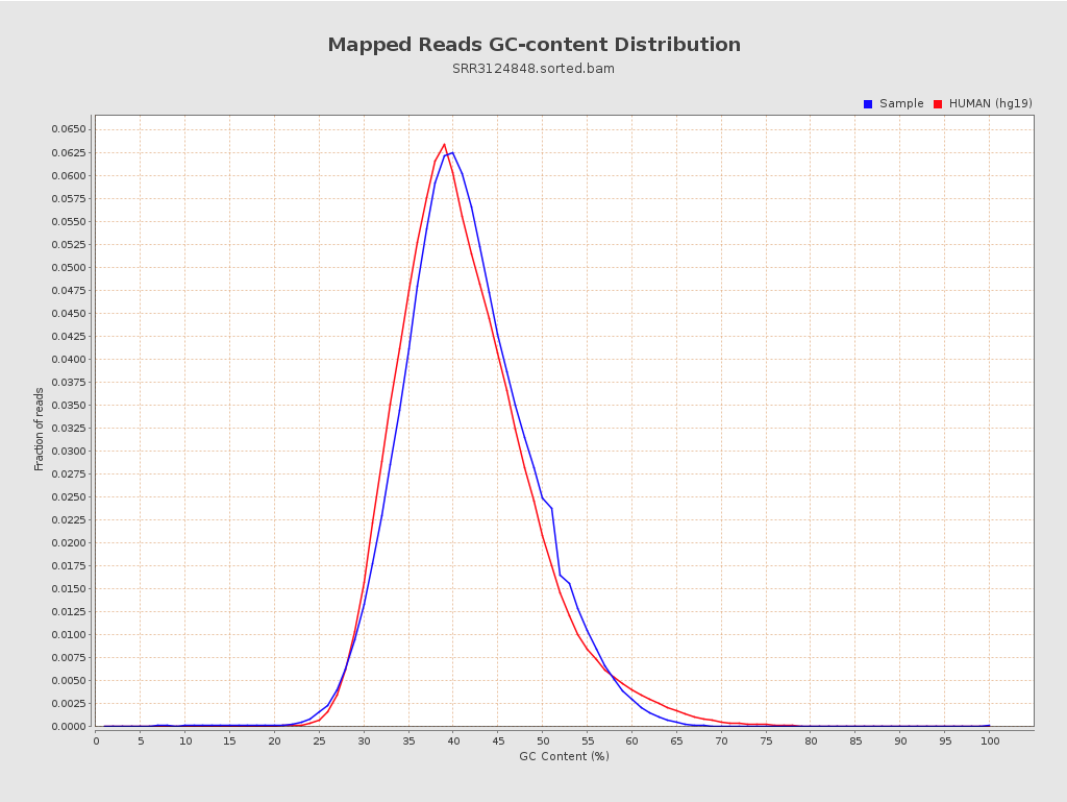
7. Results : Duplication Rate Histogram



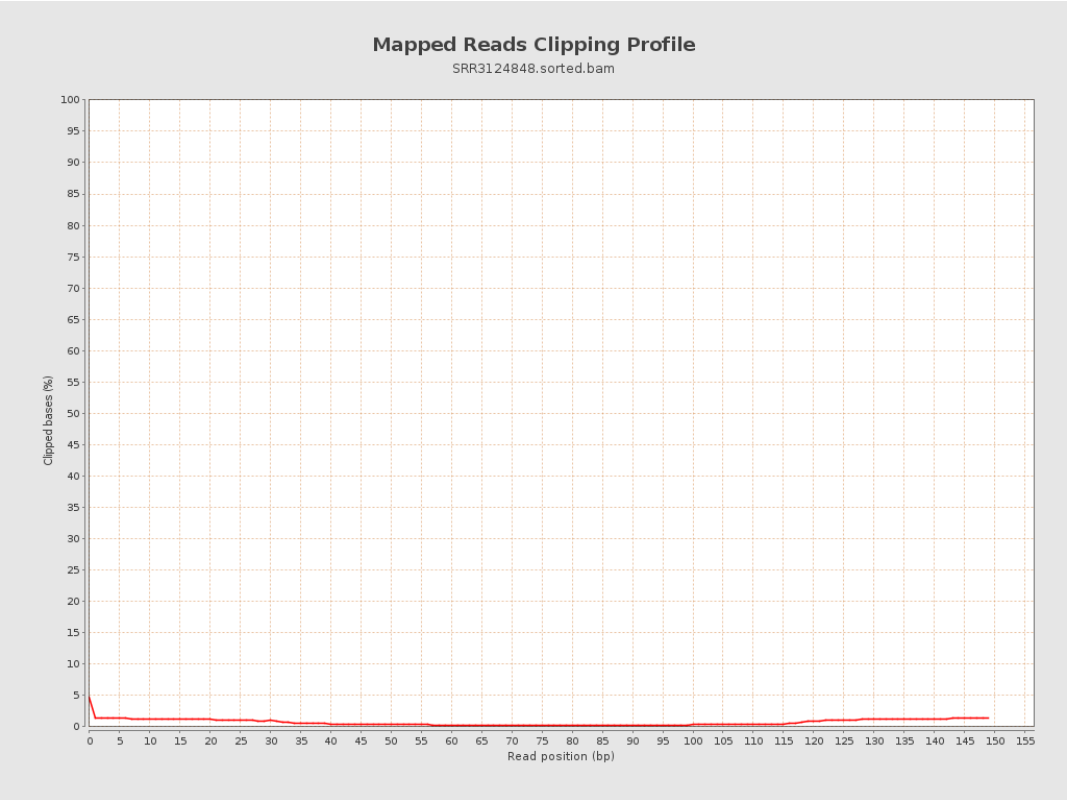
8. Results : Mapped Reads Nucleotide Content



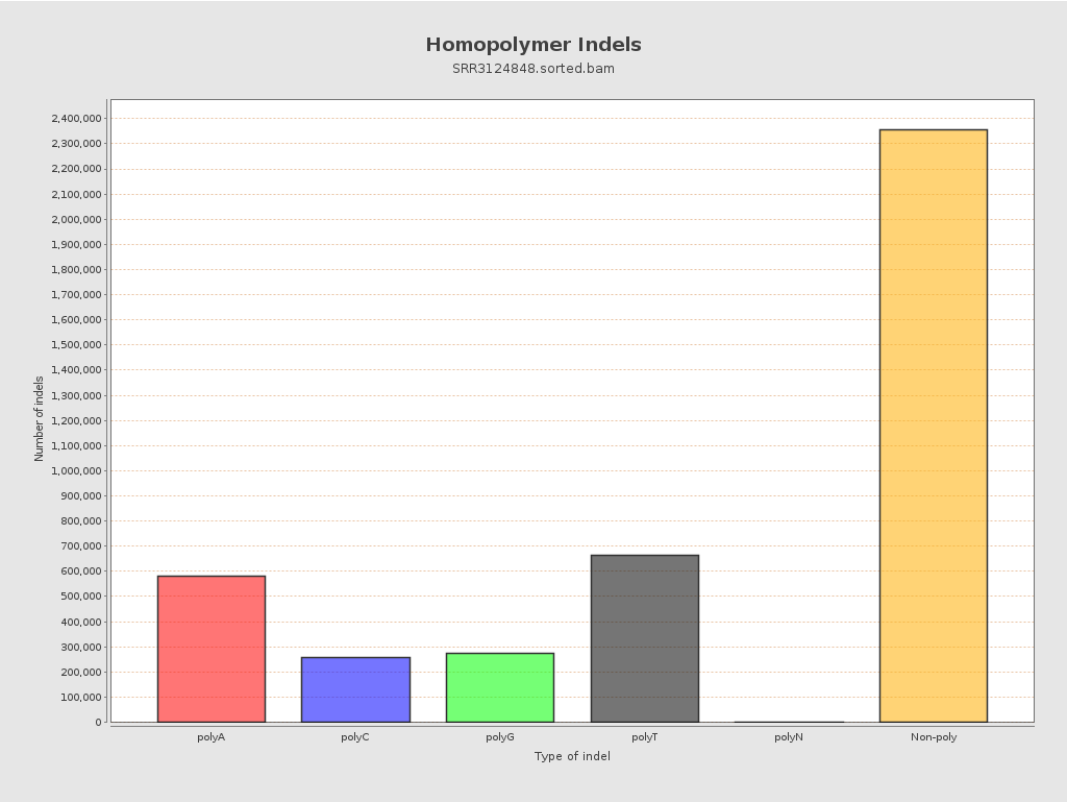
9. Results : Mapped Reads GC-content Distribution



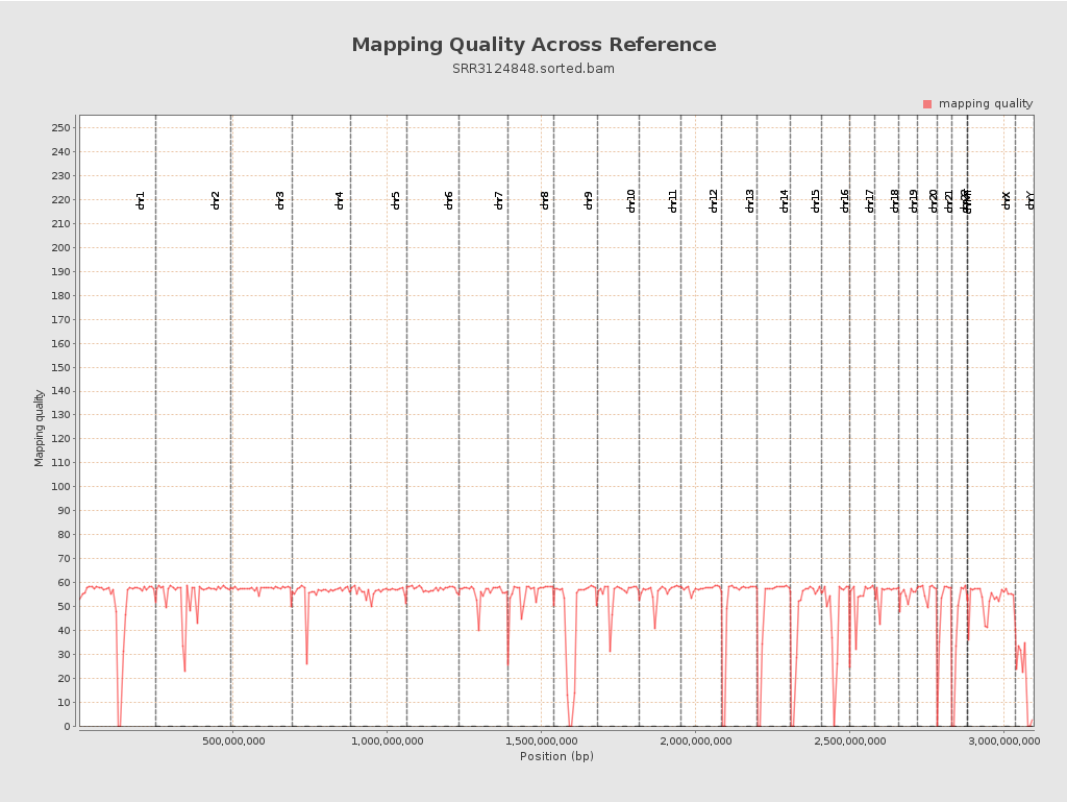
10. Results : Mapped Reads Clipping Profile



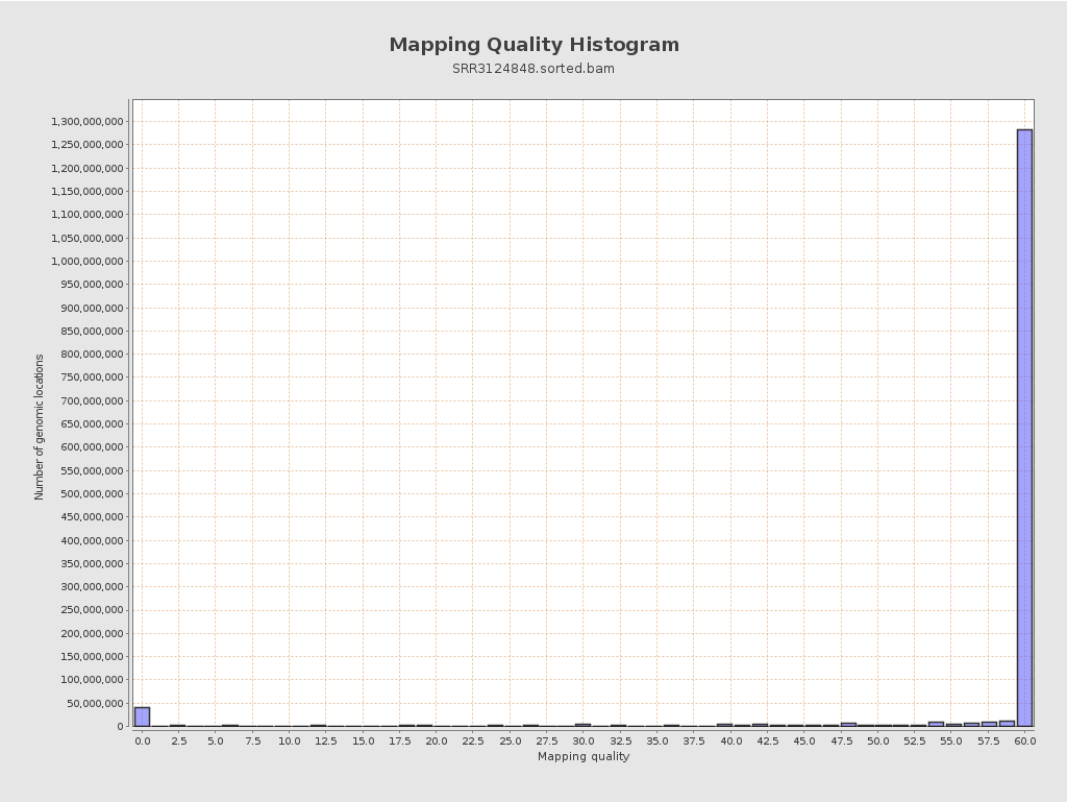
11. Results : Homopolymer Indels



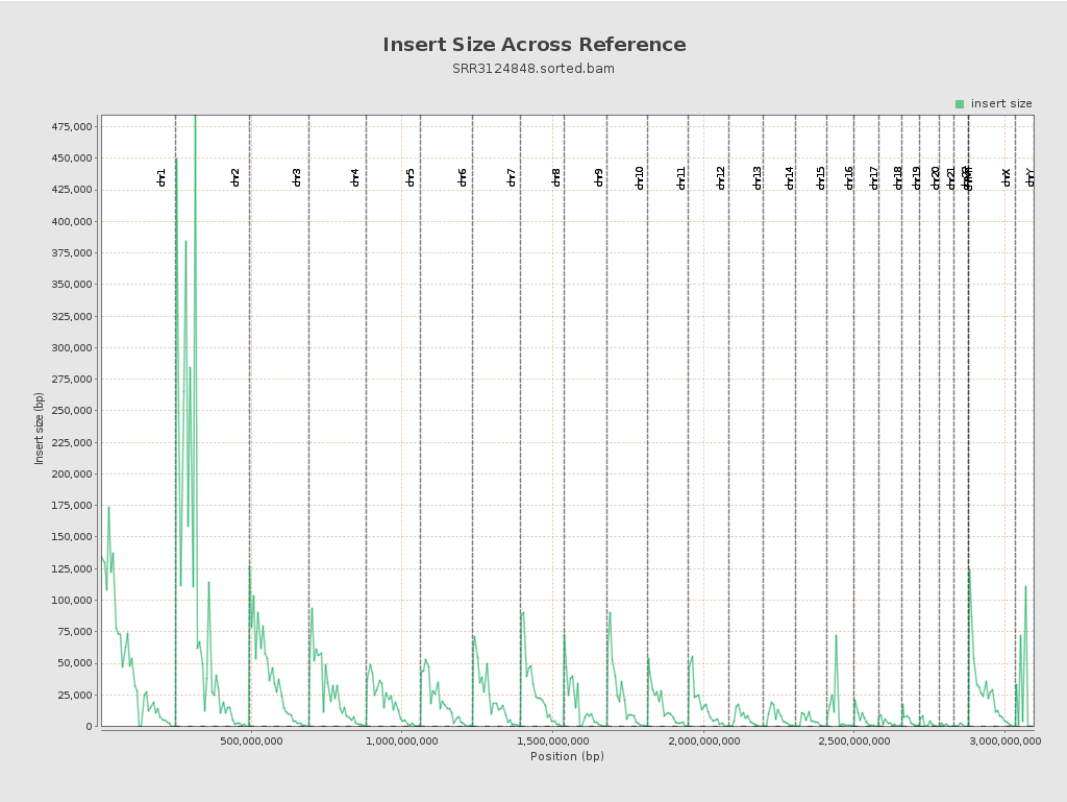
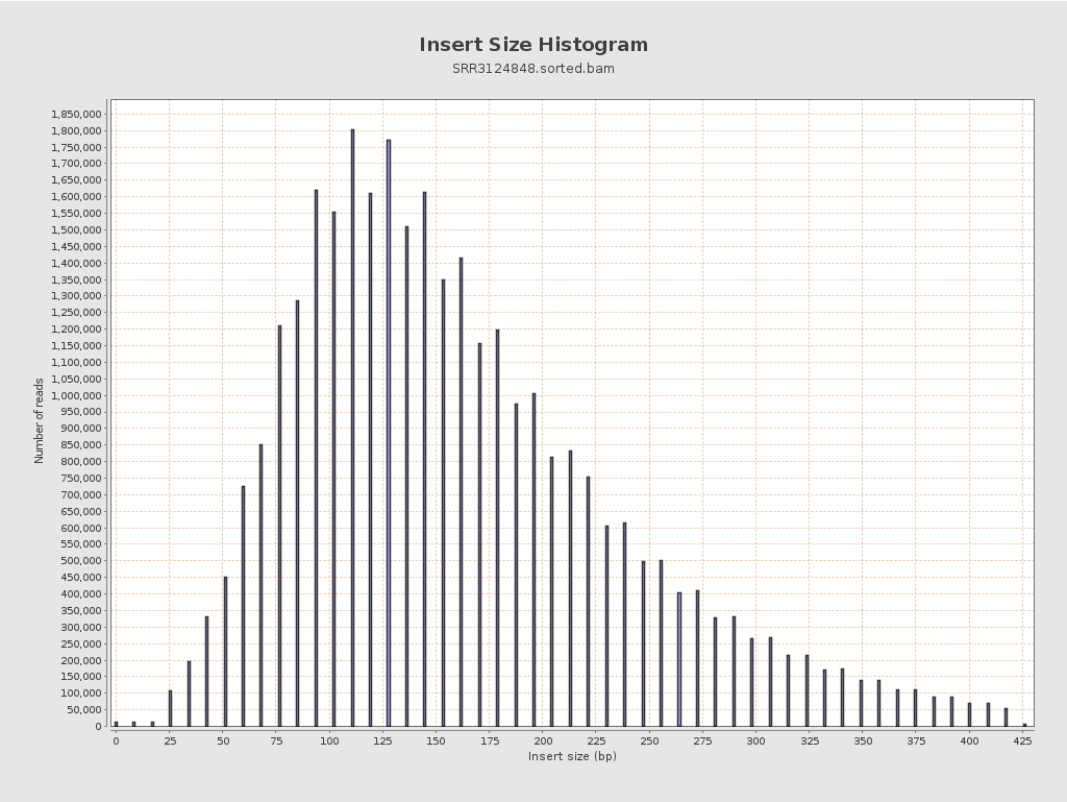
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram