Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 09:32:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124953.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_SRR3124953 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124953_1.fastq.gz SRR3124953_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 09:32:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124953.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,649,326
Mapped reads	6,237,107 / 93.8%
Unmapped reads	412,219 / 6.2%
Mapped paired reads	6,237,107 / 93.8%
Mapped reads, first in pair	3,186,635 / 47.92%
Mapped reads, second in pair	3,050,472 / 45.88%
Mapped reads, both in pair	6,048,250 / 90.96%
Mapped reads, singletons	188,857 / 2.84%
Secondary alignments	0
Supplementary alignments	7,753 / 0.12%
Read min/max/mean length	30 / 76 / 76.04
Duplicated reads (estimated)	536,315 / 8.07%
Duplication rate	5.17%
Clipped reads	2,868,616 / 43.14%

2.2. ACGT Content

Number/percentage of A's	107,822,297 / 27.85%
Number/percentage of C's	68,024,822 / 17.57%
Number/percentage of T's	117,892,423 / 30.45%
Number/percentage of G's	93,463,320 / 24.14%
Number/percentage of N's	3,192 / 0%

GC Percentage	41.71%

2.3. Coverage

Mean	0.1251
Standard Deviation	1.6864

2.4. Mapping Quality

Mean Mapping Quality	51.68

2.5. Insert size

Mean	25,271.86
Standard Deviation	1,457,666.81
P25/Median/P75	148 / 199 / 276

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	2,406,707
Insertions	39,687
Mapped reads with at least one insertion	0.63%
Deletions	101,019
Mapped reads with at least one deletion	1.6%
Homopolymer indels	48.99%

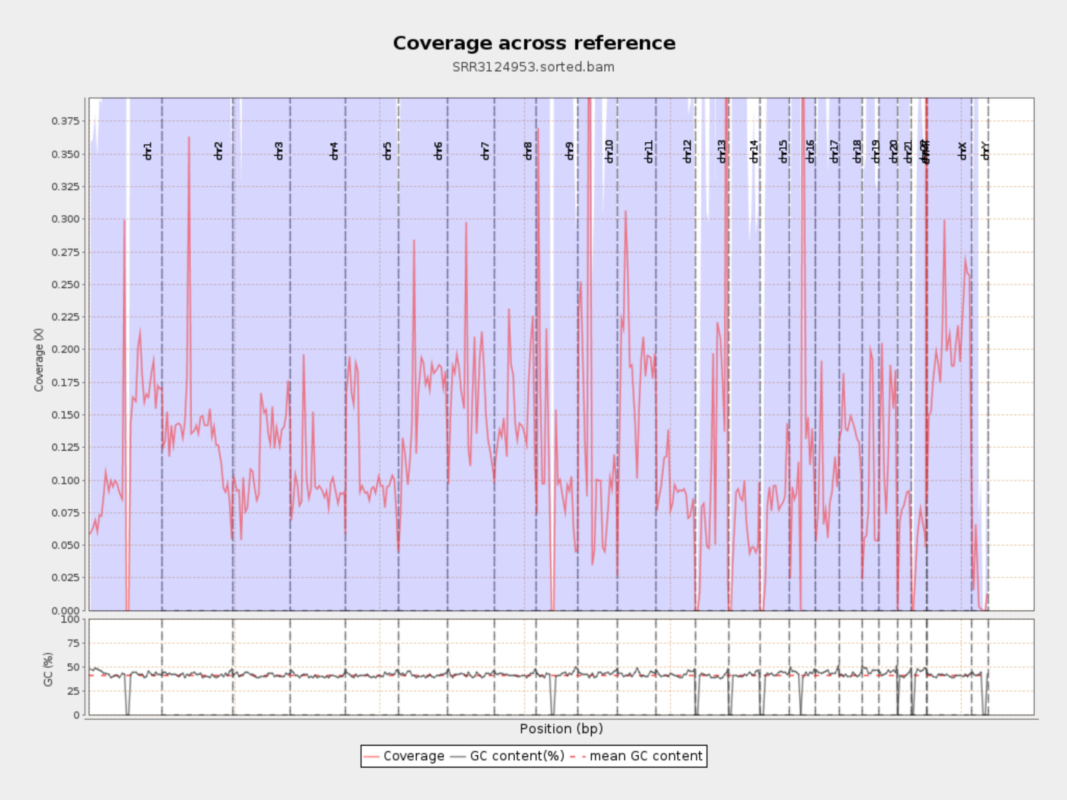
2.7. Chromosome stats

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

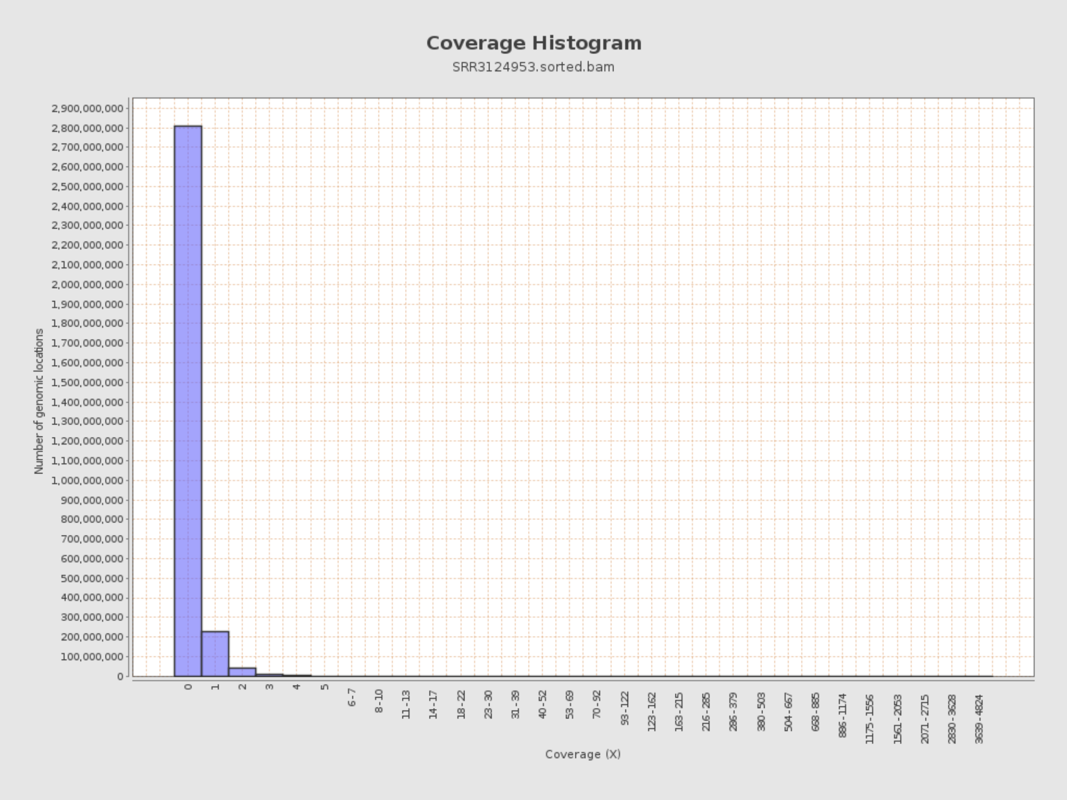
		bases	**coverage**	**deviation**
chr1	249250621	31027897	0.1245	1.899
chr2	243199373	33625057	0.1383	1.6336
chr3	198022430	23484695	0.1186	0.4789
chr4	191154276	18538972	0.097	2.9611
chr5	180915260	20535690	0.1135	0.5934
chr6	171115067	27308106	0.1596	1.2126
chr7	159138663	26543037	0.1668	2.287
chr8	146364022	22527377	0.1539	0.7045
chr9	141213431	15250042	0.108	1.8707
chr10	135534747	18213950	0.1344	3.9097
chr11	135006516	25116434	0.186	1.3499
chr12	133851895	12269890	0.0917	0.3876
chr13	115169878	15376255	0.1335	0.5853
chr14	107349540	6269915	0.0584	0.5401
chr15	102531392	7615718	0.0743	0.3458
chr16	90354753	12124820	0.1342	2.6519
chr17	81195210	7485683	0.0922	1.1533
chr18	78077248	10967515	0.1405	2.0261
chr19	59128983	5533982	0.0936	1.4267
chr20	63025520	8987869	0.1426	0.5015
chr21	48129895	3381314	0.0703	0.4552
chr22	51304566	2350955	0.0458	0.264
chrMT	16571	227099	13.7046	9.2368
chrX	155270560	31658662	0.2039	0.964

chrY	59373566	935243	0.0158	0.7414

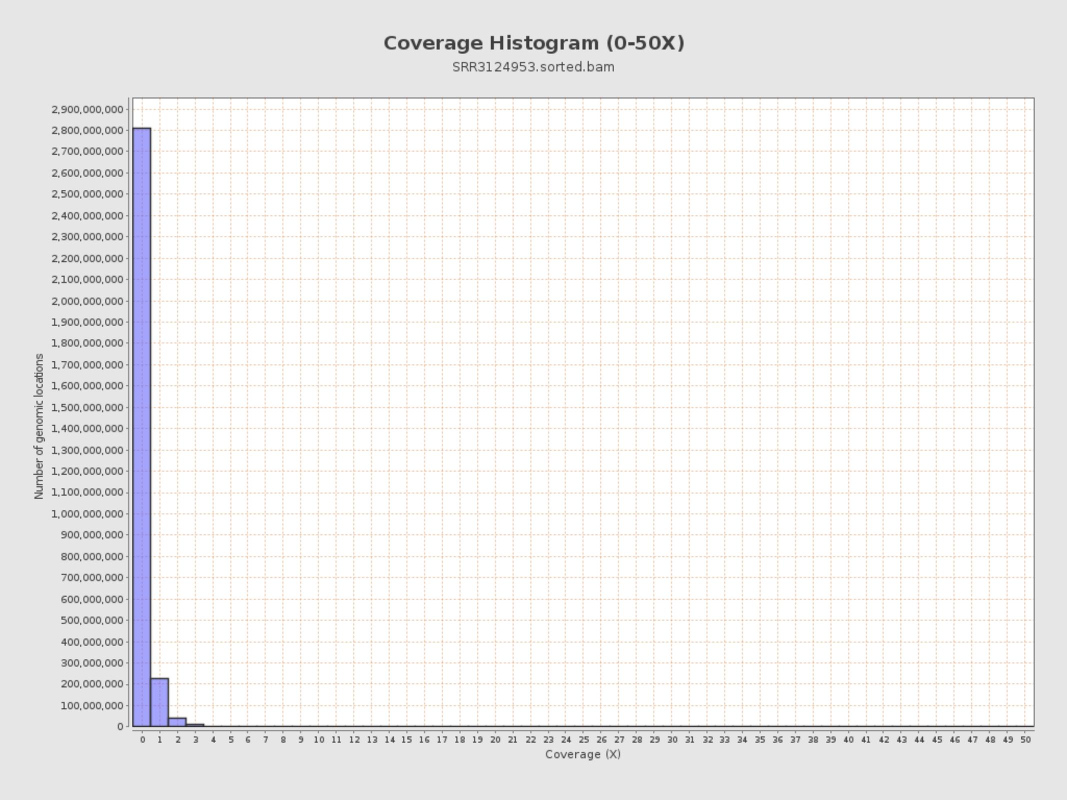
3. Results : Coverage across reference



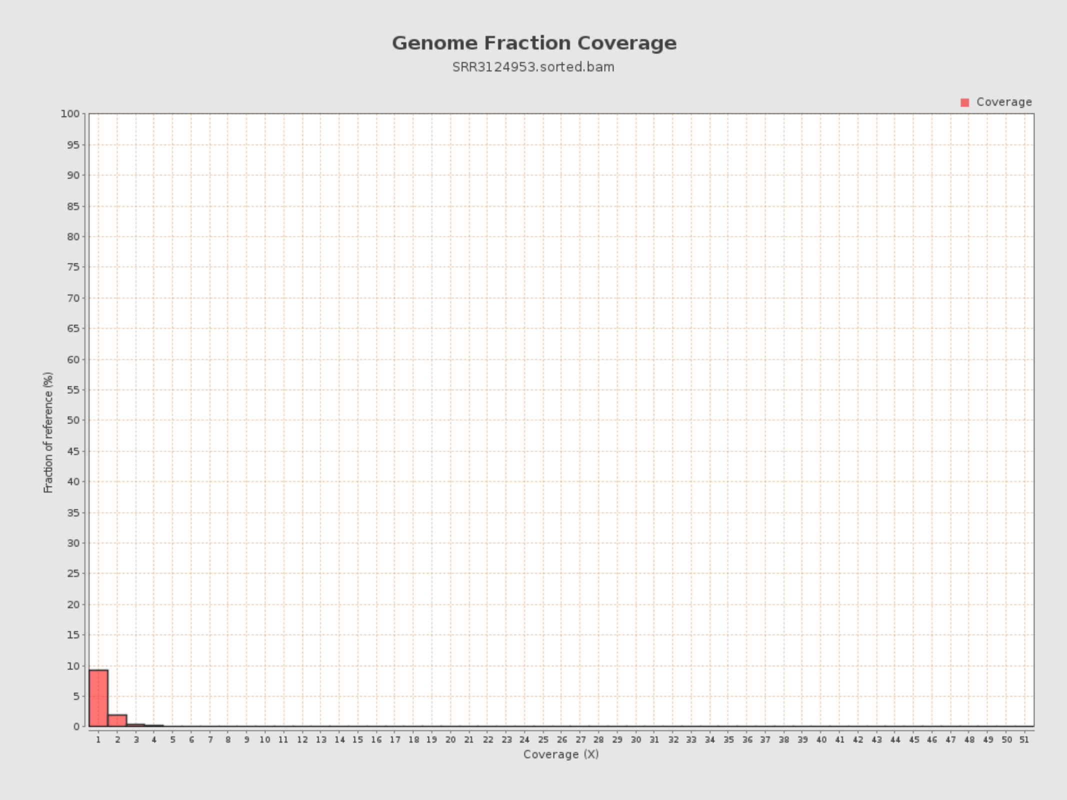
4. Results : Coverage Histogram



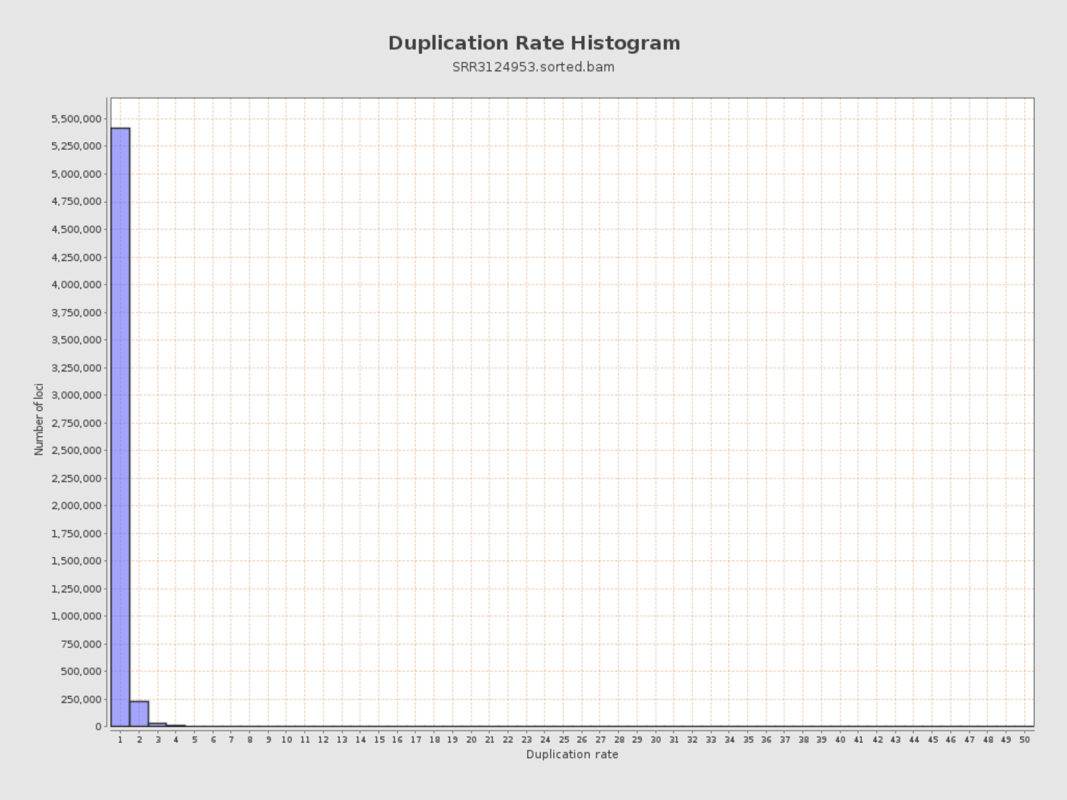
5. Results : Coverage Histogram (0-50X)



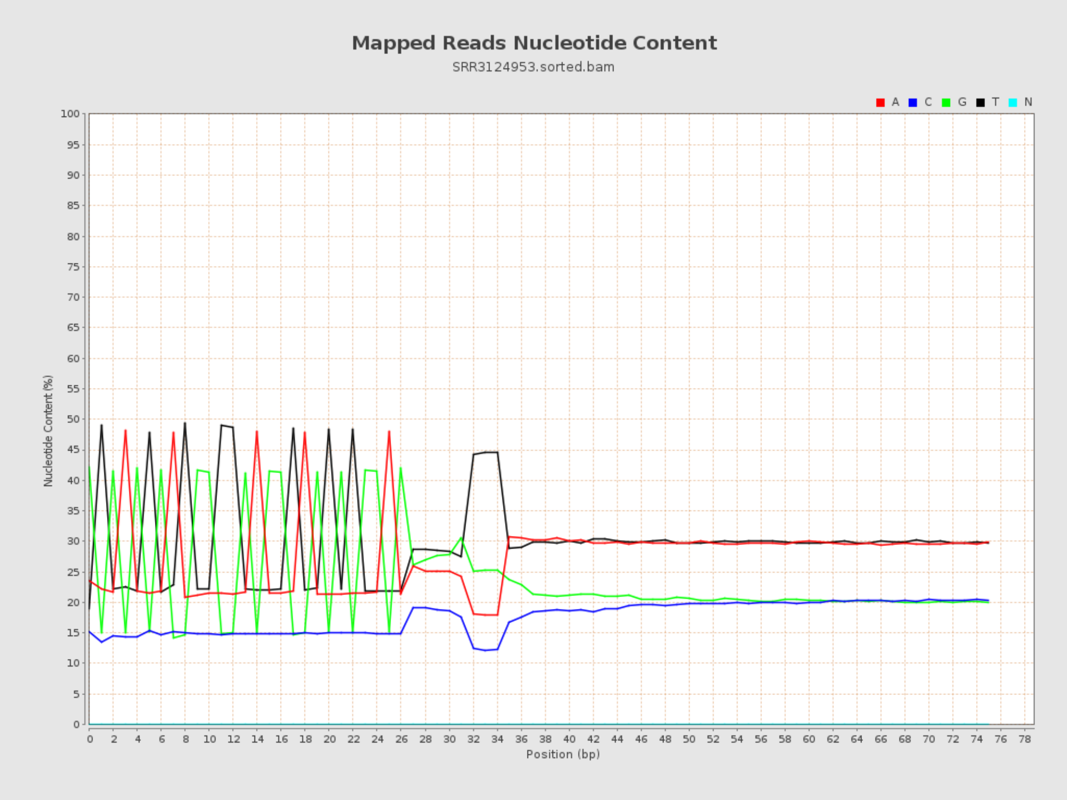
6. Results : Genome Fraction Coverage



7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content



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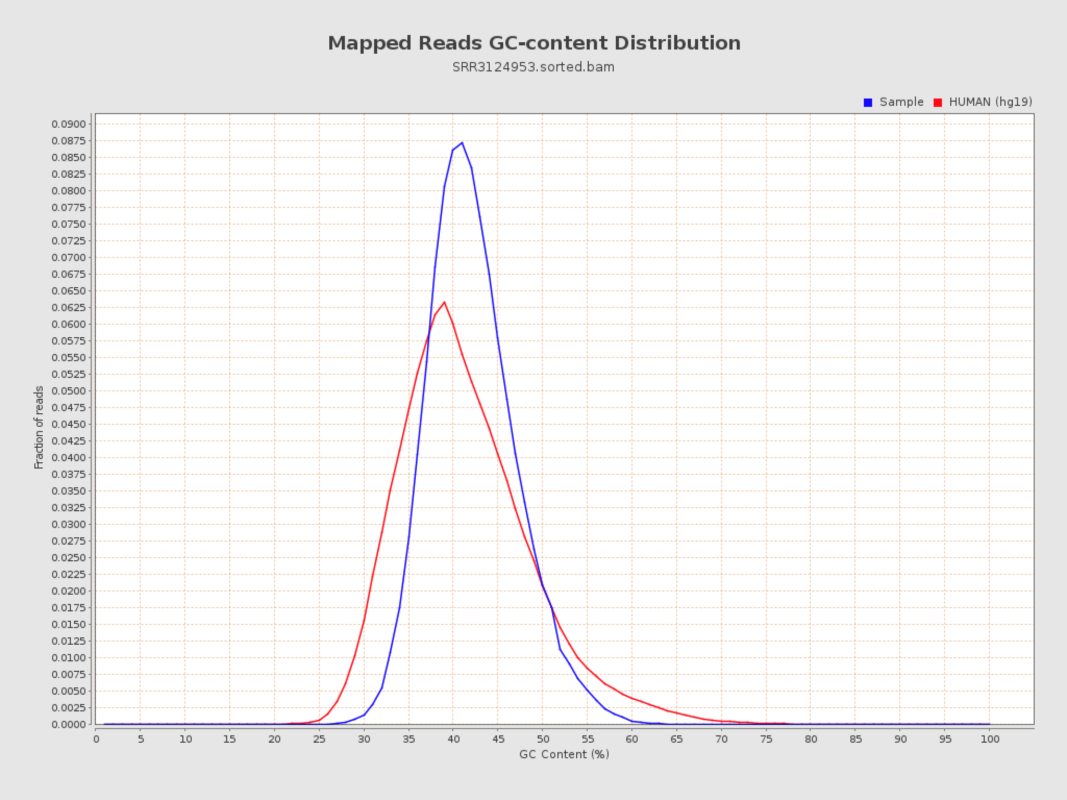
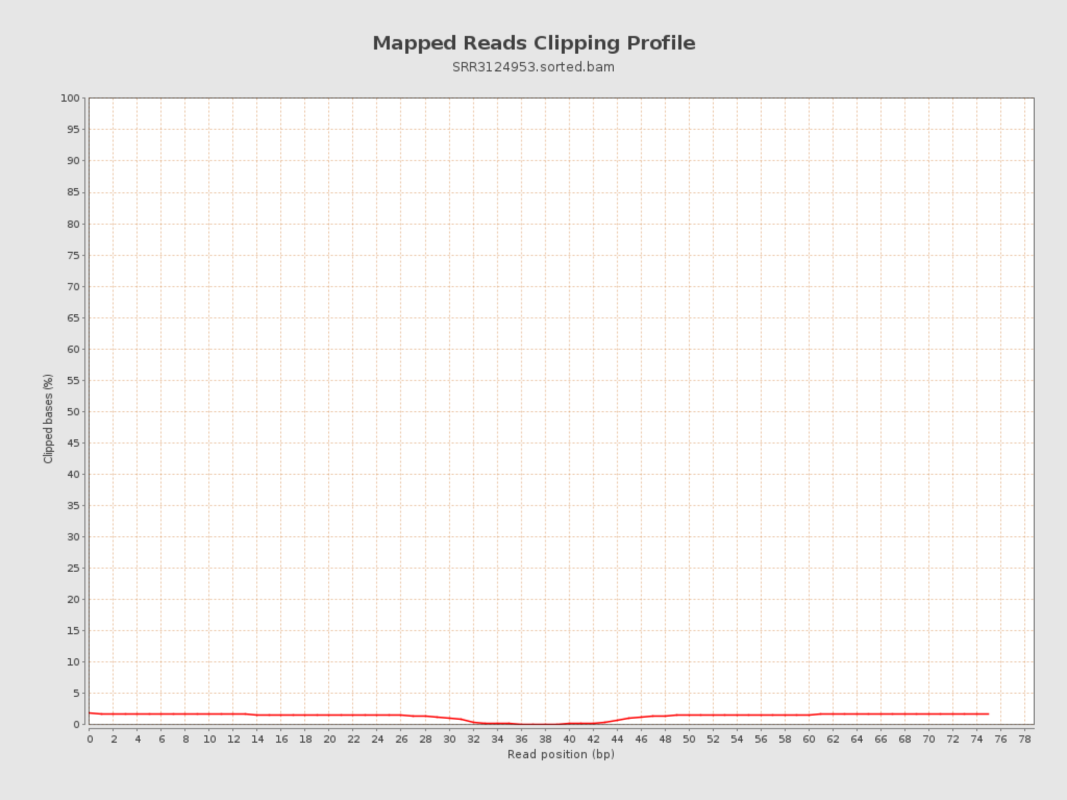
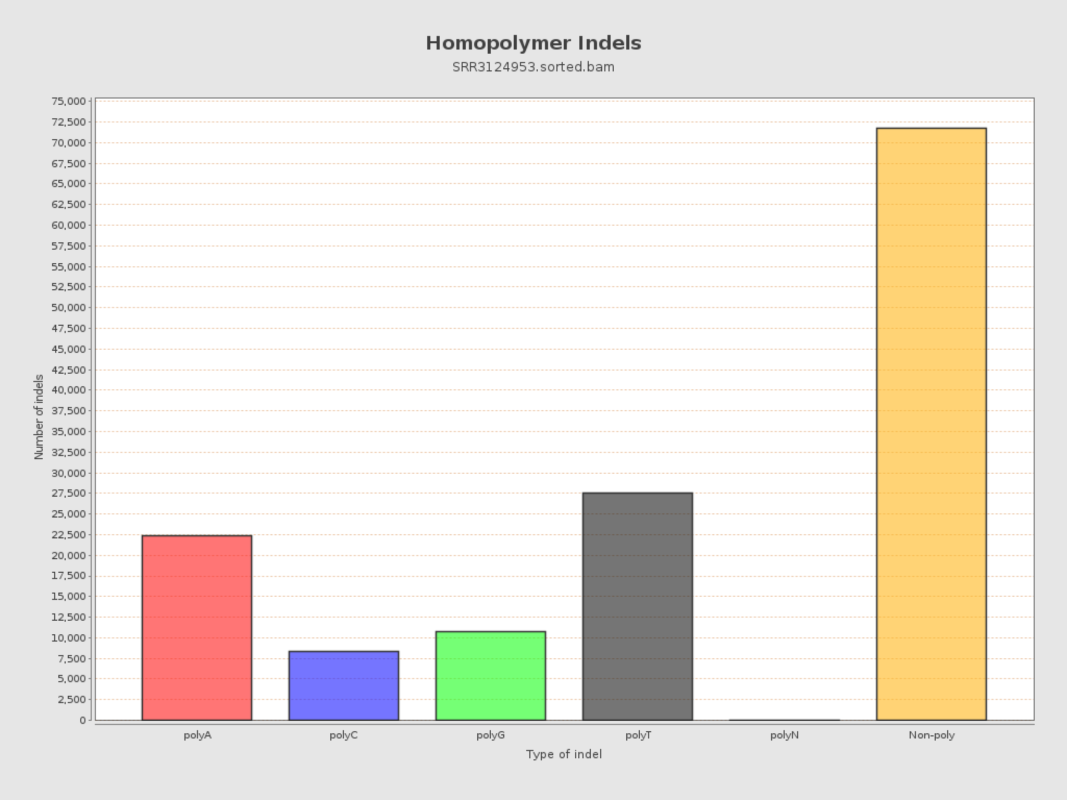
9. Results : Mapped Reads GC-content Distribution



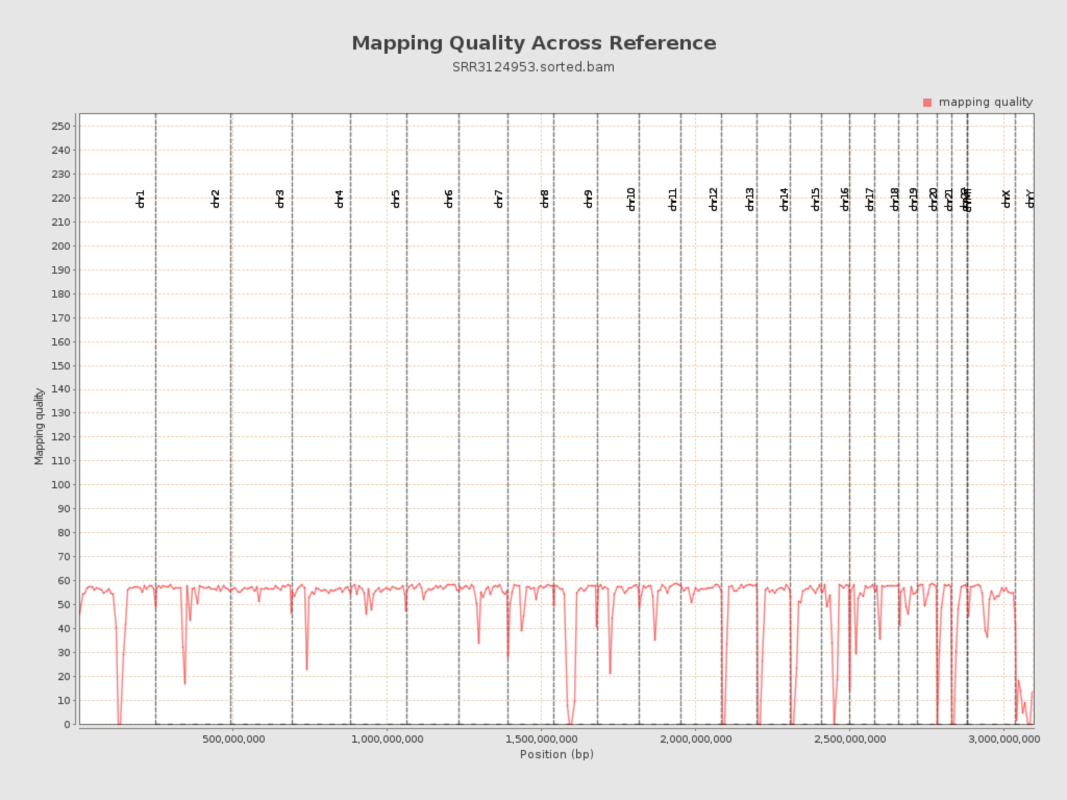
10. Results : Mapped Reads Clipping Profile



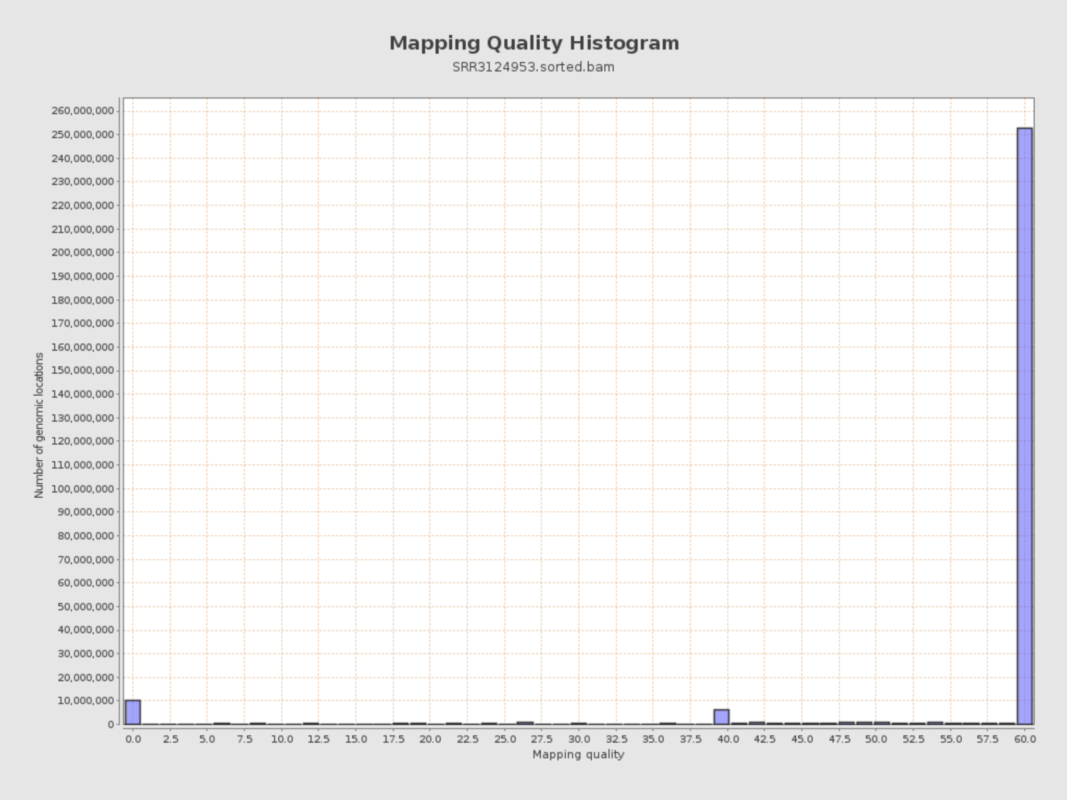
11. Results : Homopolymer Indels



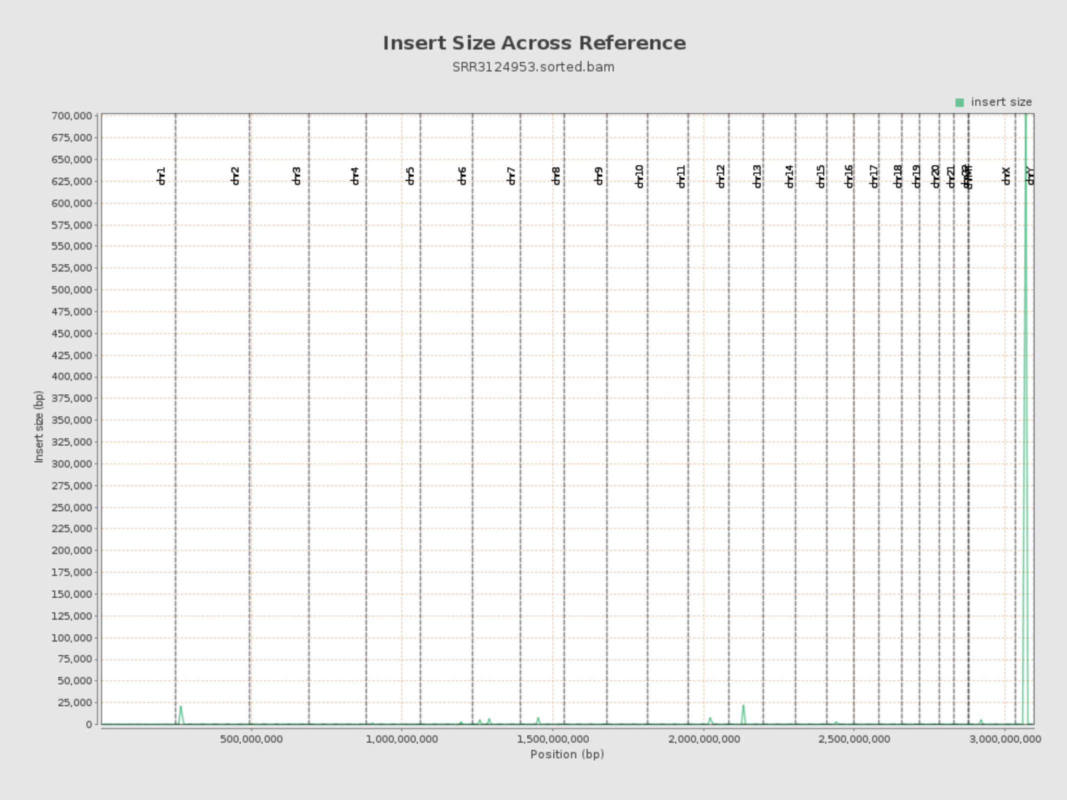
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram