Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 02:47:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926954.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_SRR926954 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926954_1.fastq.gz SRR926954_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 02:47:28 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926954.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,430,600
Mapped reads	8,150,174 / 96.67%
Unmapped reads	280,426 / 3.33%
Mapped paired reads	8,150,174 / 96.67%
Mapped reads, first in pair	4,088,302 / 48.49%
Mapped reads, second in pair	4,061,872 / 48.18%
Mapped reads, both in pair	8,022,816 / 95.16%
Mapped reads, singletons	127,358 / 1.51%
Secondary alignments	0
Supplementary alignments	123,201 / 1.46%
Read min/max/mean length	30 / 101 / 101.6
Duplicated reads (estimated)	474,219 / 5.62%
Duplication rate	5.08%
Clipped reads	3,017,699 / 35.79%

2.2. ACGT Content

Number/percentage of A's	202,519,983 / 27.12%
Number/percentage of C's	155,924,437 / 20.88%
Number/percentage of T's	203,732,636 / 27.28%
Number/percentage of G's	184,498,010 / 24.71%
Number/percentage of N's	40,093 / 0.01%

GC Percentage	45.59%

2.3. Coverage

Mean	0.2414
Standard Deviation	0.9107

2.4. Mapping Quality

Mean Mapping Quality	53.67

2.5. Insert size

Mean	139,092.03
Standard Deviation	3,713,393.27
P25/Median/P75	148 / 194 / 262

2.6. Mismatches and indels

General error rate	1.01%
Mismatches	7,387,426
Insertions	112,453
Mapped reads with at least one insertion	1.36%
Deletions	372,325
Mapped reads with at least one deletion	4.46%
Homopolymer indels	52.5%

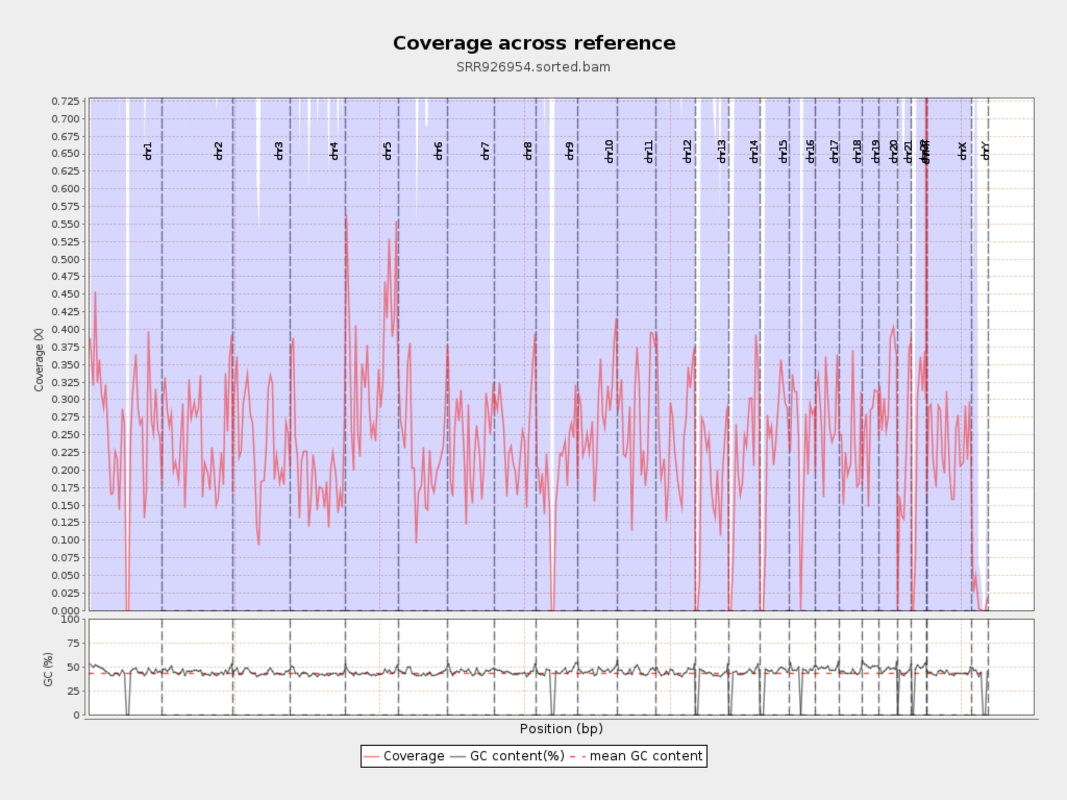
2.7. Chromosome stats

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

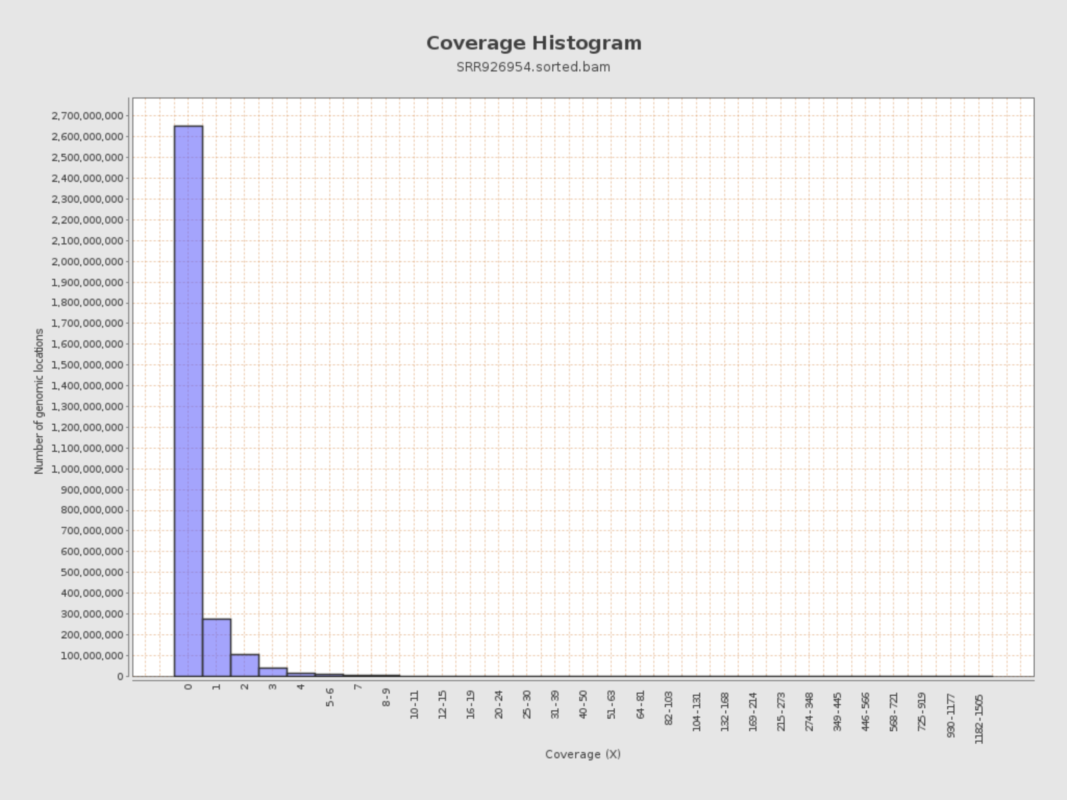
		bases	coverage	deviation
chr1	249250621	64128102	0.2573	1.1614
chr2	243199373	60292409	0.2479	1.5028
chr3	198022430	47862213	0.2417	0.7285
chr4	191154276	37949077	0.1985	0.8049
chr5	180915260	63964465	0.3536	0.9533
chr6	171115067	38575396	0.2254	0.7082
chr7	159138663	37973866	0.2386	0.7405
chr8	146364022	36908224	0.2522	0.7713
chr9	141213431	26329612	0.1865	0.7332
chr10	135534747	37879163	0.2795	0.896
chr11	135006516	37359533	0.2767	0.8842
chr12	133851895	33355345	0.2492	0.8112
chr13	115169878	20296290	0.1762	0.6171
chr14	107349540	22789059	0.2123	0.6981
chr15	102531392	22966318	0.224	0.7196
chr16	90354753	21845291	0.2418	0.9032
chr17	81195210	23315474	0.2872	0.8337
chr18	78077248	17797300	0.2279	0.8443
chr19	59128983	15622629	0.2642	0.8993
chr20	63025520	20425045	0.3241	0.8781
chr21	48129895	10071687	0.2093	1.3426
chr22	51304566	11577097	0.2257	0.7355
chrMT	16571	170374	10.2815	14.9784
chrX	155270560	36703968	0.2364	0.7222

chrY	59373566	1089521	0.0184	0.411

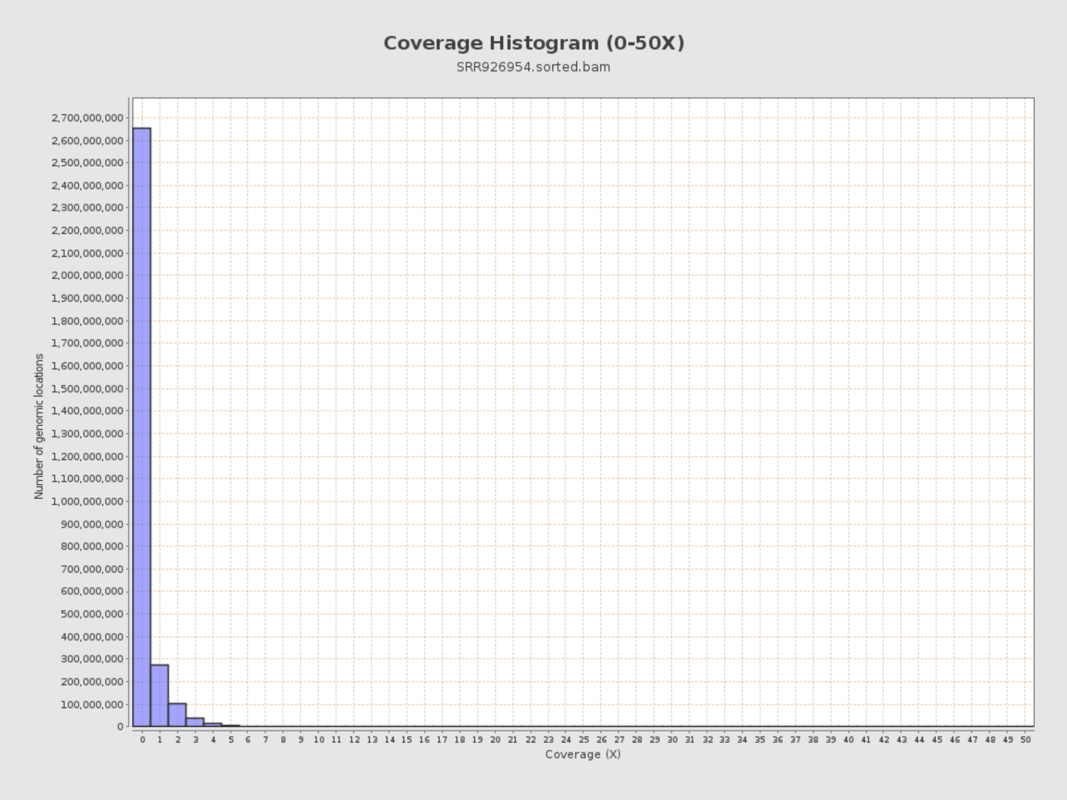
3. Results : Coverage across reference



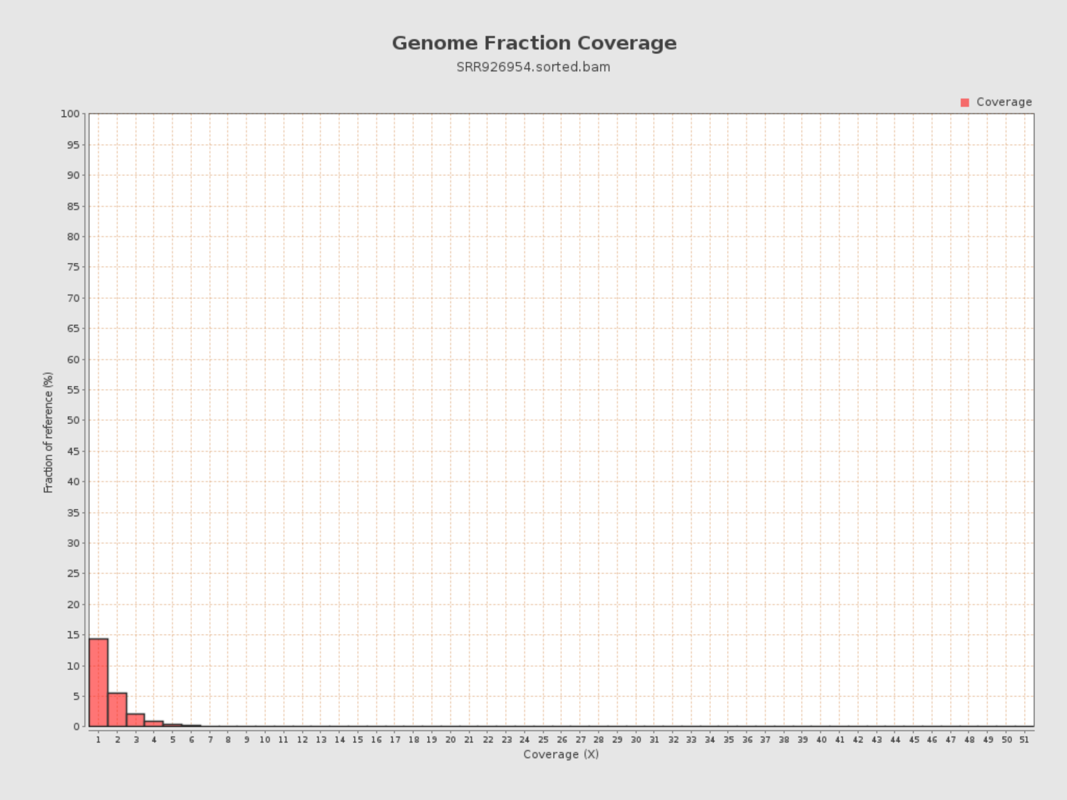
4. Results : Coverage Histogram



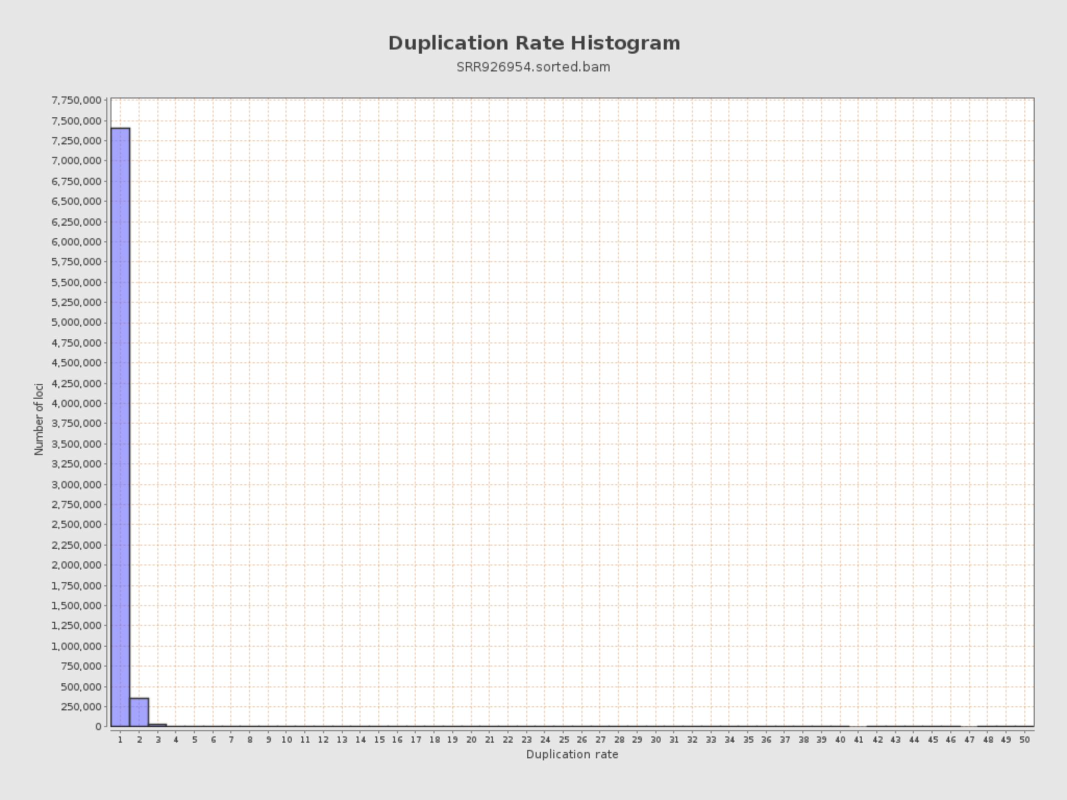
5. Results : Coverage Histogram (0-50X)



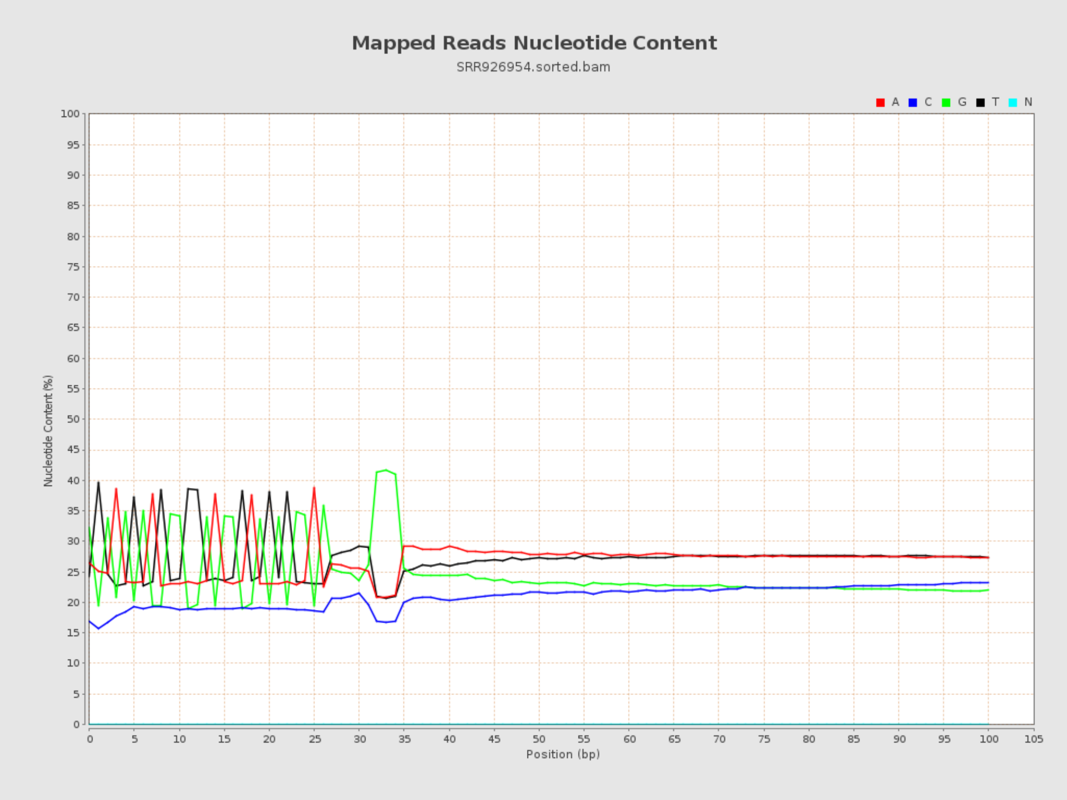
6. Results : Genome Fraction Coverage



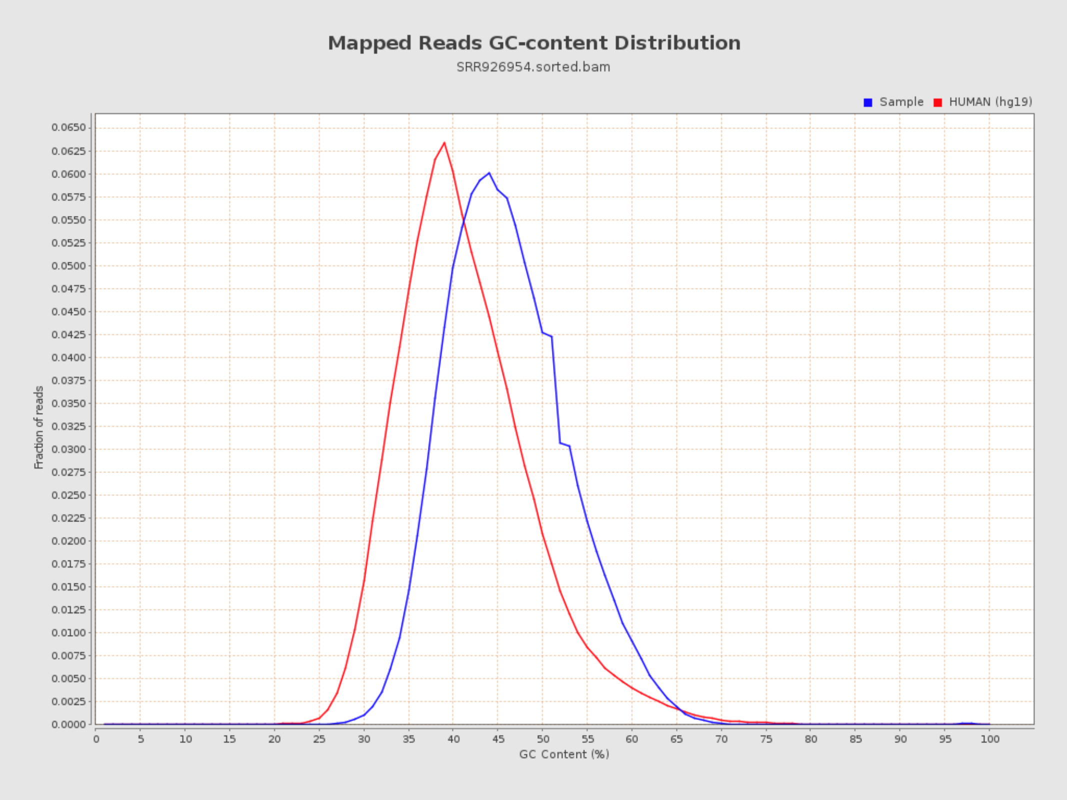
7. Results : Duplication Rate Histogram



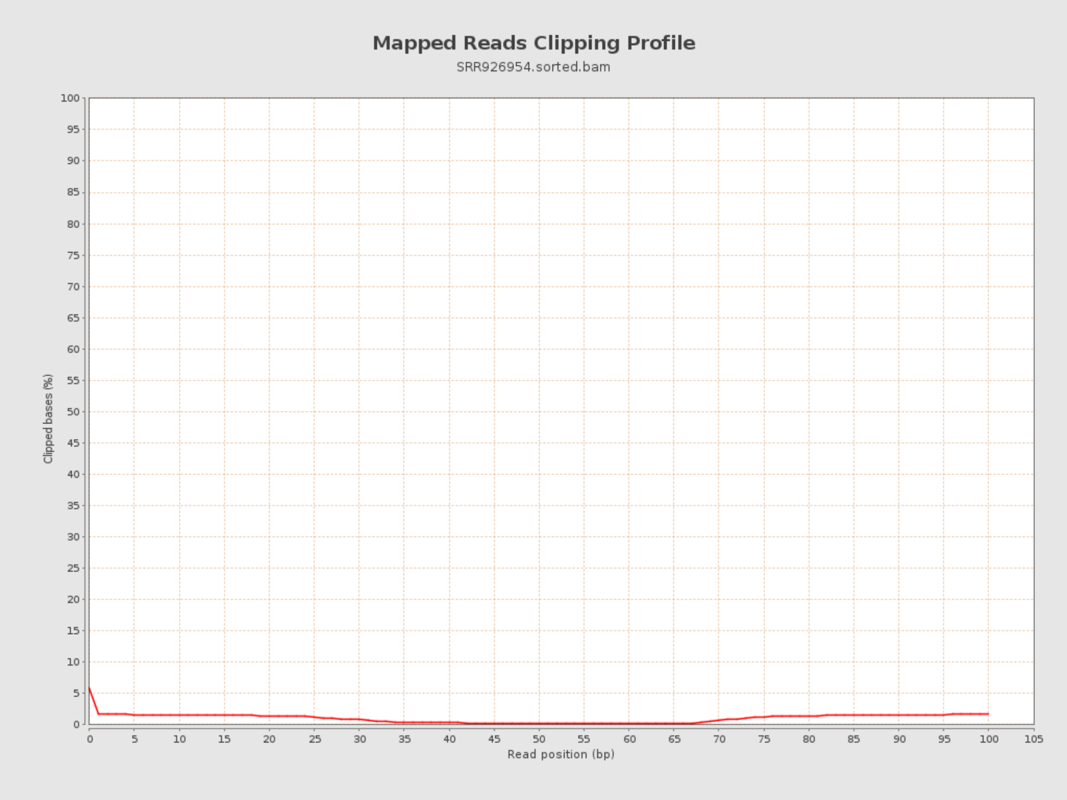
8. Results : Mapped Reads Nucleotide Content



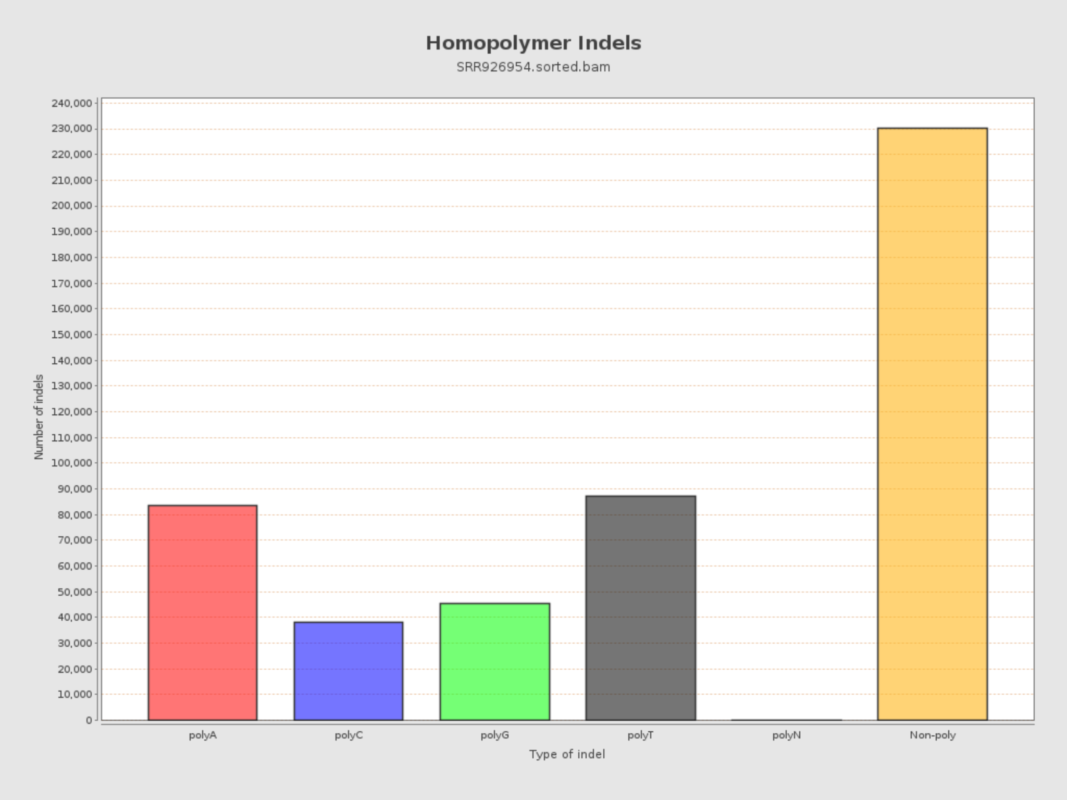
9. Results : Mapped Reads GC-content Distribution



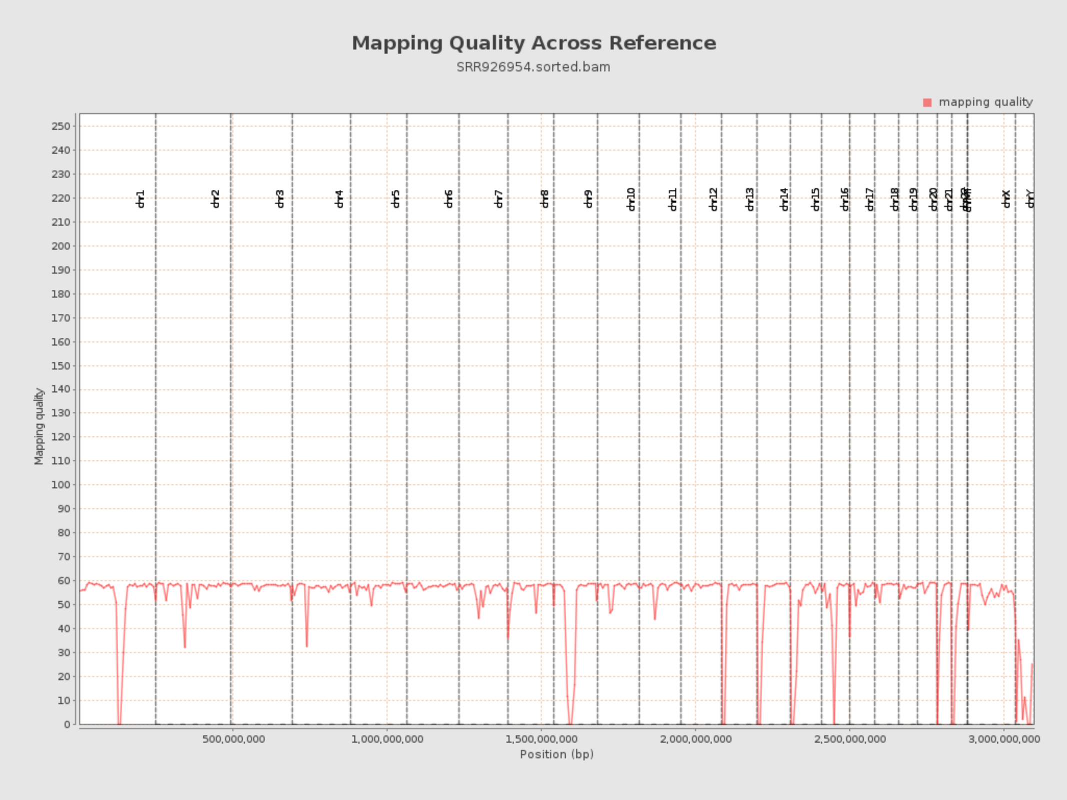
10. Results : Mapped Reads Clipping Profile



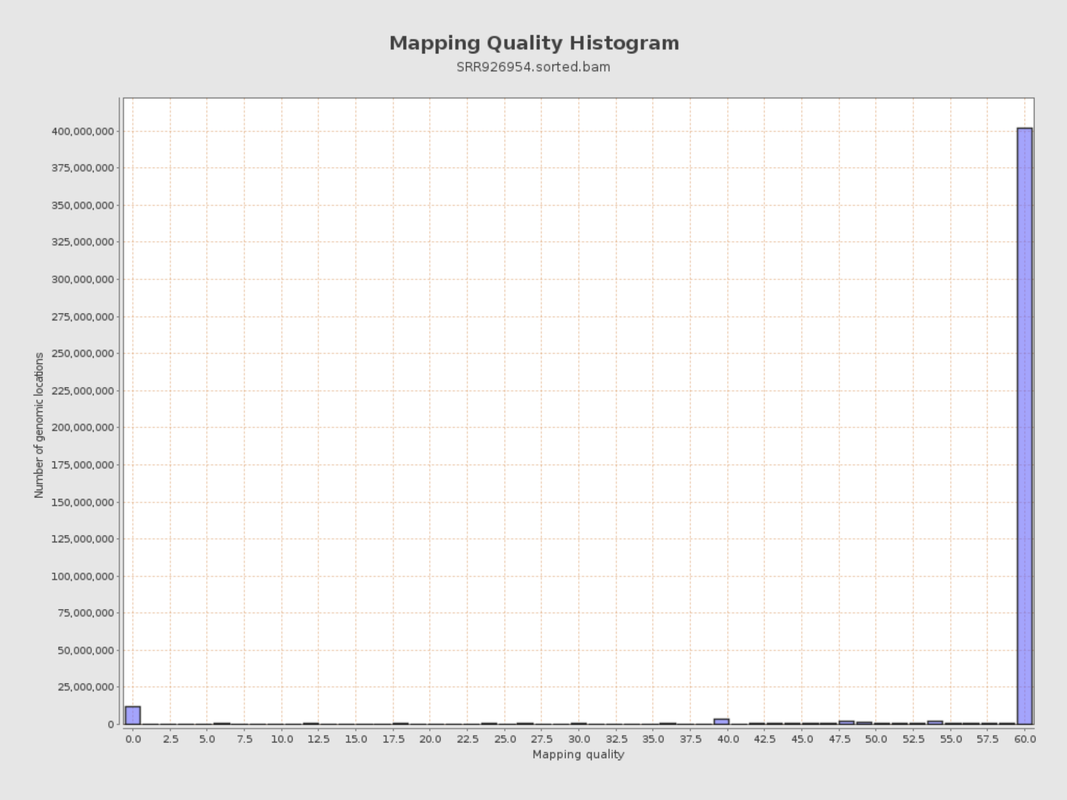
11. Results : Homopolymer Indels



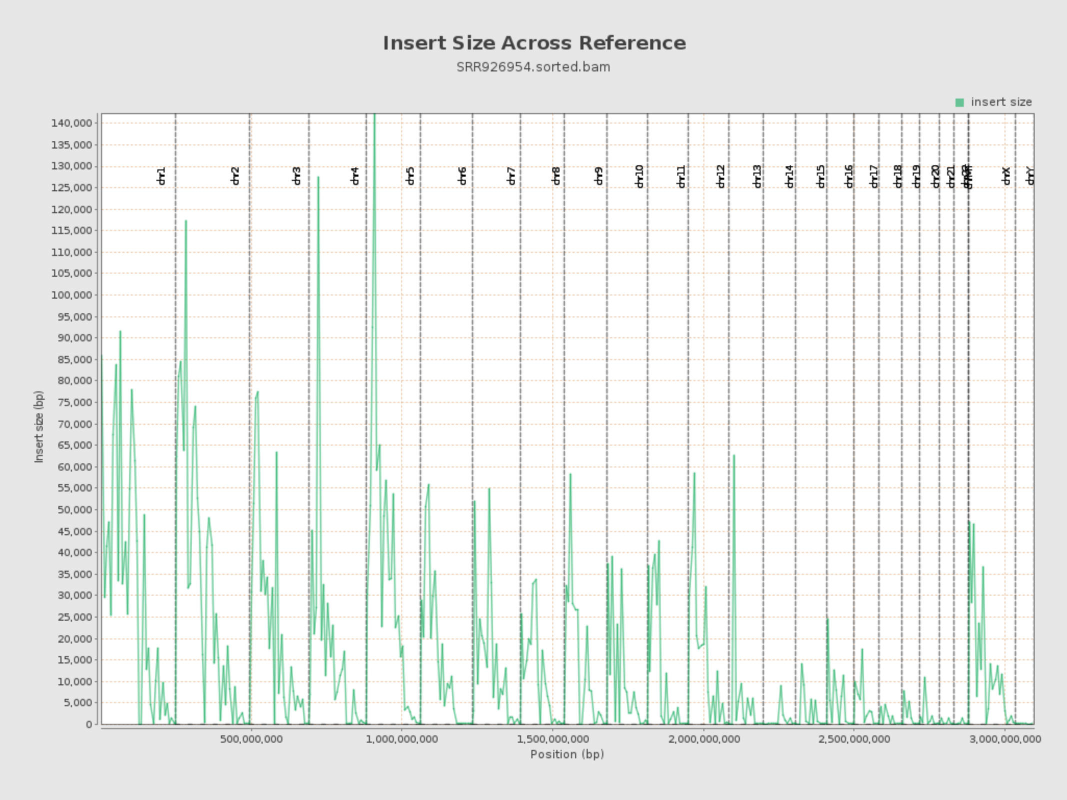
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram