Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 01:25:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124888.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_SRR3124888 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124888_1.fastq.gz SRR3124888_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 01:25:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124888.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,728,386
Mapped reads	6,507,445 / 96.72%
Unmapped reads	220,941 / 3.28%
Mapped paired reads	6,507,445 / 96.72%
Mapped reads, first in pair	3,269,652 / 48.59%
Mapped reads, second in pair	3,237,793 / 48.12%
Mapped reads, both in pair	6,410,664 / 95.28%
Mapped reads, singletons	96,781 / 1.44%
Secondary alignments	0
Supplementary alignments	6,137 / 0.09%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	429,577 / 6.38%
Duplication rate	4.03%
Clipped reads	2,033,919 / 30.23%

2.2. ACGT Content

Number/percentage of A's	123,006,218 / 28.26%
Number/percentage of C's	82,469,427 / 18.95%
Number/percentage of T's	128,014,118 / 29.41%
Number/percentage of G's	101,775,121 / 23.38%
Number/percentage of N's	4,041 / 0%

GC Percentage	42.33%

2.3. Coverage

Mean	0.1407
Standard Deviation	1.4207

2.4. Mapping Quality

Mean Mapping Quality	51.71

2.5. Insert size

Mean	36,906.31
Standard Deviation	1,814,036.27
P25/Median/P75	154 / 201 / 270

2.6. Mismatches and indels

General error rate	0.71%
Mismatches	3,002,530
Insertions	44,384
Mapped reads with at least one insertion	0.68%
Deletions	113,226
Mapped reads with at least one deletion	1.72%
Homopolymer indels	49.75%

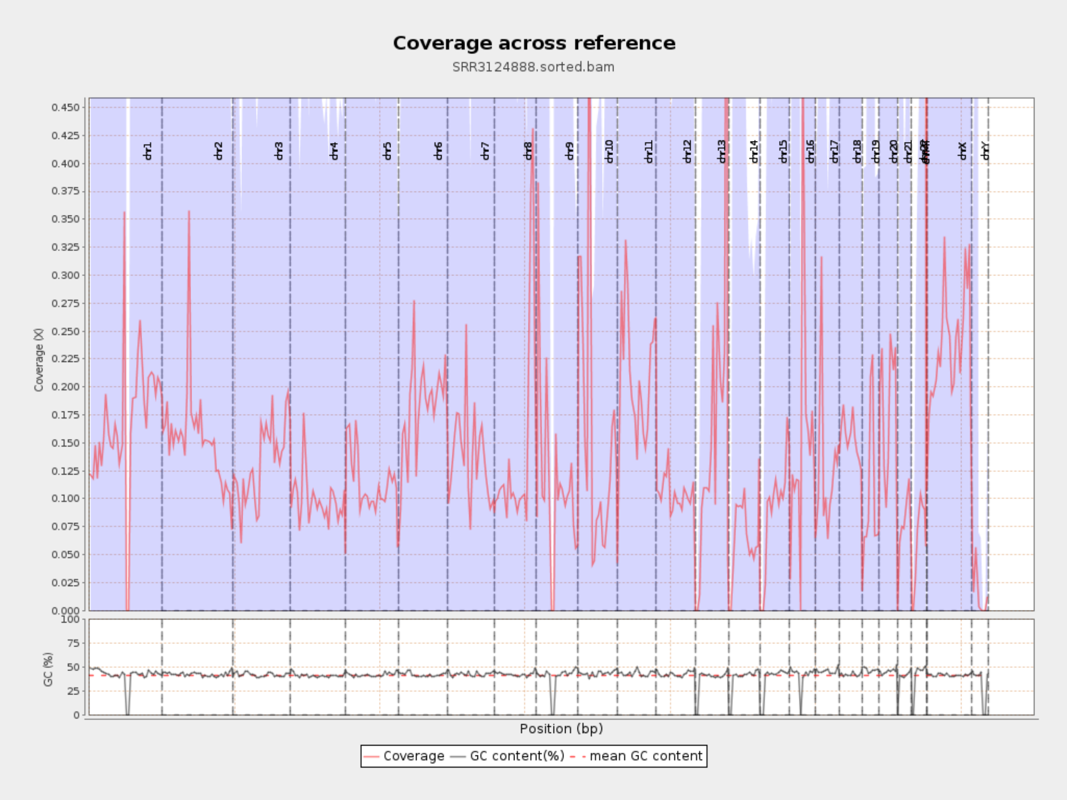
2.7. Chromosome stats

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

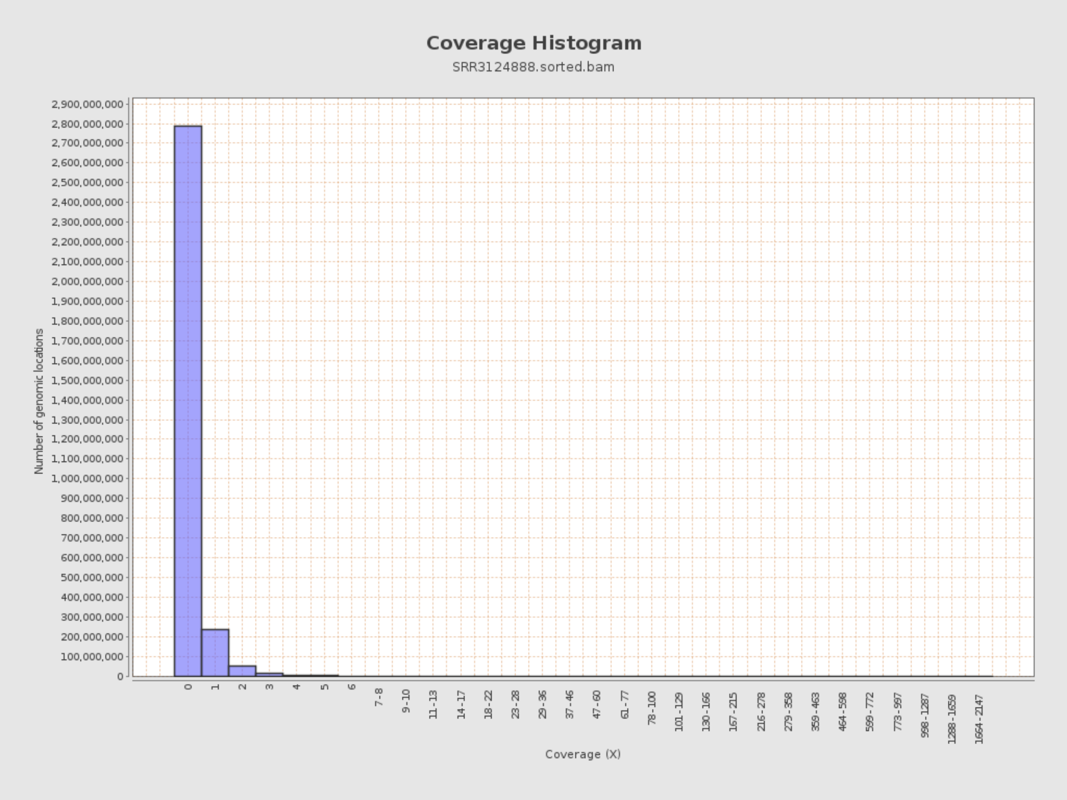
		bases	coverage	deviation
chr1	249250621	41933067	0.1682	1.7222
chr2	243199373	37566354	0.1545	1.2937
chr3	198022430	26113538	0.1319	0.504
chr4	191154276	18897539	0.0989	0.6081
chr5	180915260	20736513	0.1146	0.4234
chr6	171115067	30993133	0.1811	1.0693
chr7	159138663	22064814	0.1387	1.7772
chr8	146364022	21303779	0.1456	0.6112
chr9	141213431	16791229	0.1189	1.1565
chr10	135534747	21805854	0.1609	4.2745
chr11	135006516	27714309	0.2053	0.9748
chr12	133851895	13942765	0.1042	0.4099
chr13	115169878	21065930	0.1829	0.7669
chr14	107349540	6750063	0.0629	0.3896
chr15	102531392	9109218	0.0888	0.3853
chr16	90354753	13672829	0.1513	2.2593
chr17	81195210	10029965	0.1235	1.7372
chr18	78077248	12160816	0.1558	1.8795
chr19	59128983	6265474	0.106	1.0987
chr20	63025520	11429127	0.1813	0.5681
chr21	48129895	3597388	0.0747	0.4249
chr22	51304566	3130066	0.061	0.3058
chrMT	16571	532653	32.1437	17.2317
chrX	155270560	36915936	0.2378	0.9347

chrY	59373566	914894	0.0154	0.701

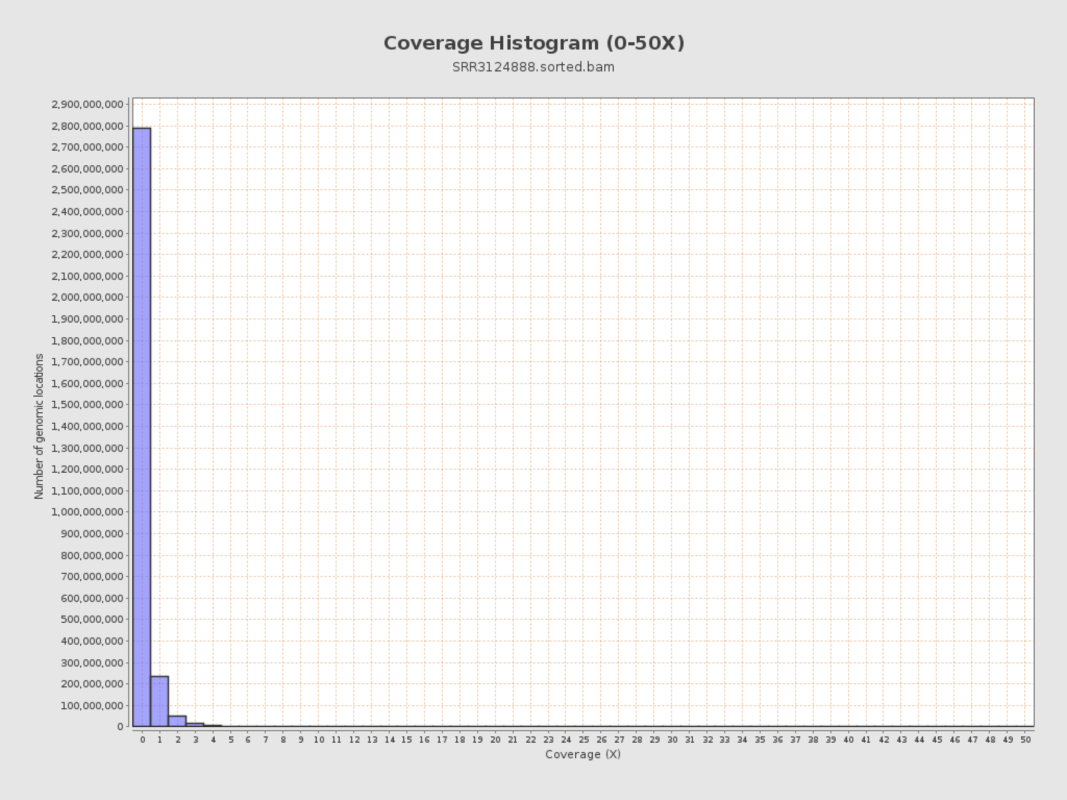
3. Results : Coverage across reference



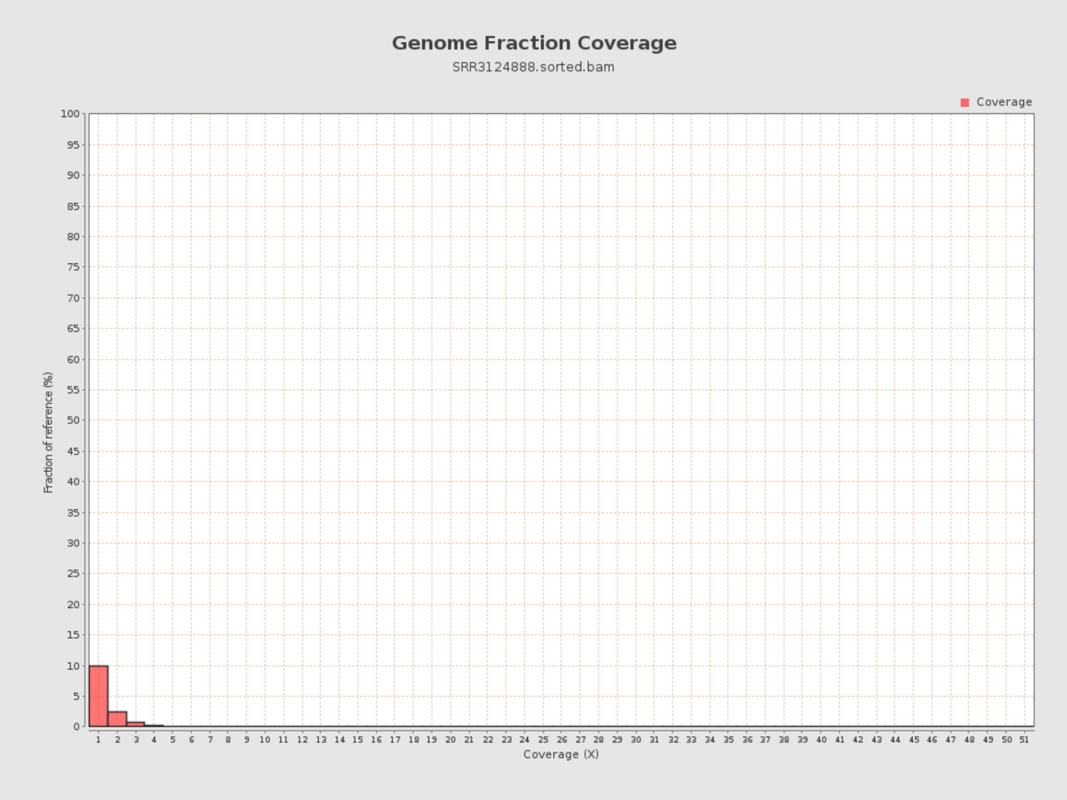
4. Results : Coverage Histogram



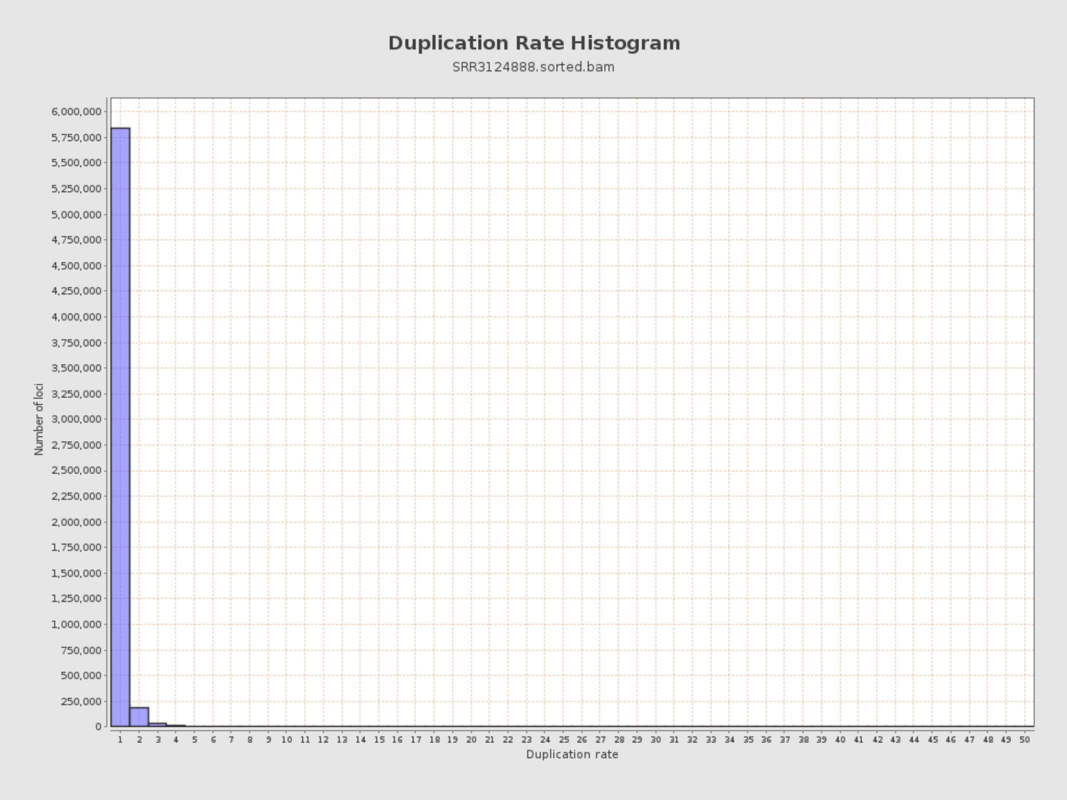
5. Results : Coverage Histogram (0-50X)



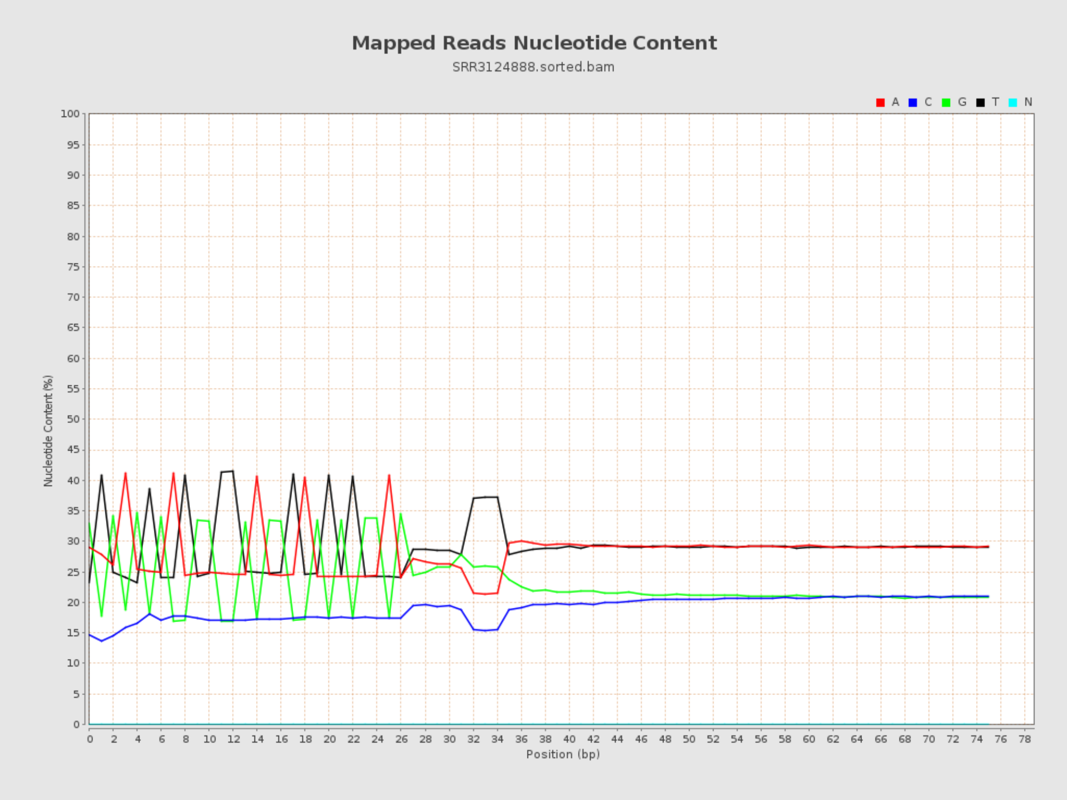
6. Results : Genome Fraction Coverage



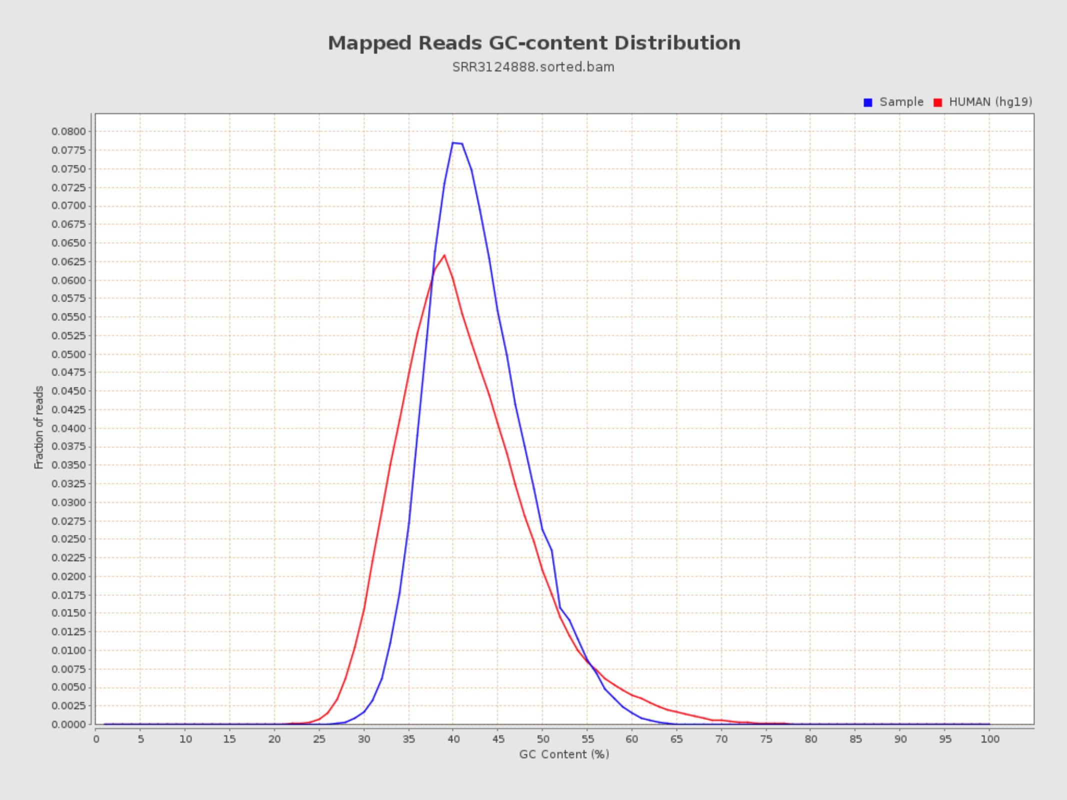
7. Results : Duplication Rate Histogram



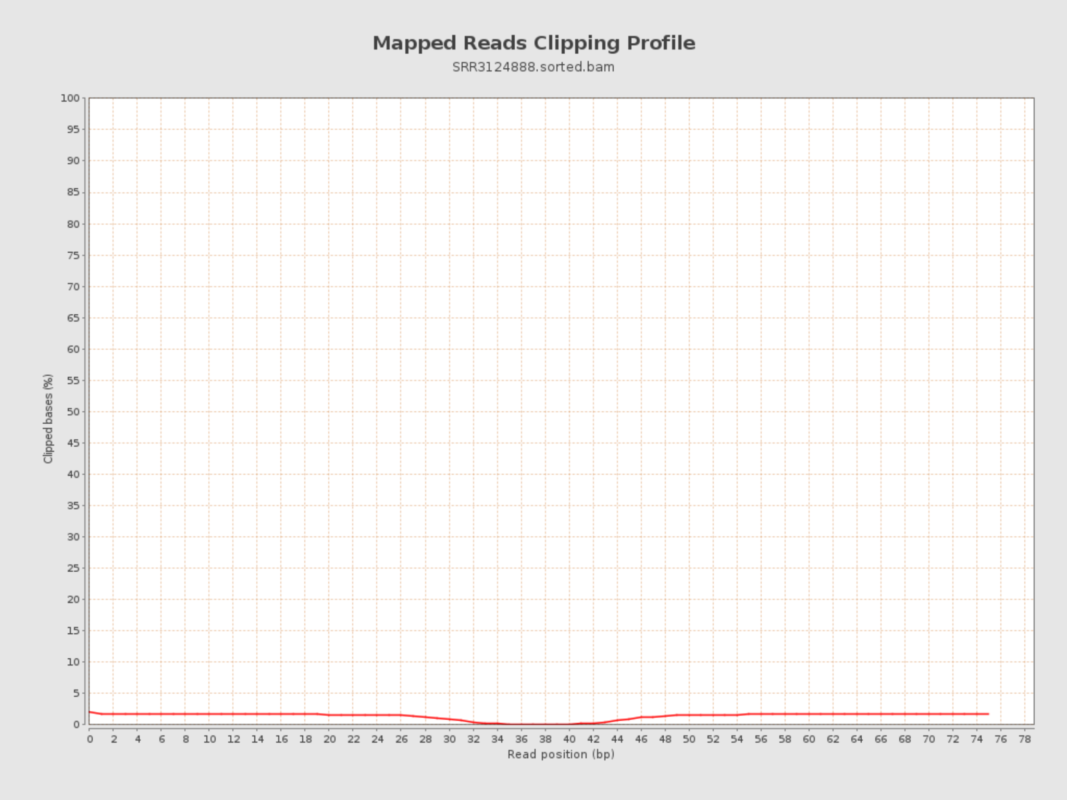
8. Results : Mapped Reads Nucleotide Content



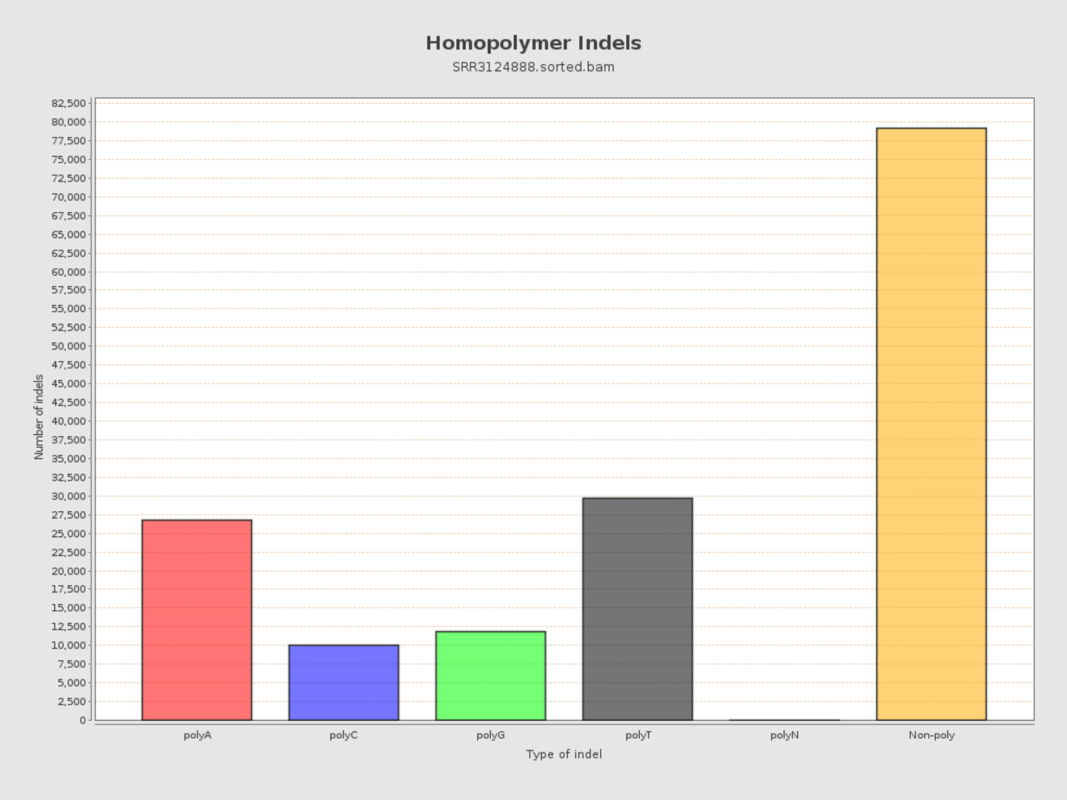
9. Results : Mapped Reads GC-content Distribution



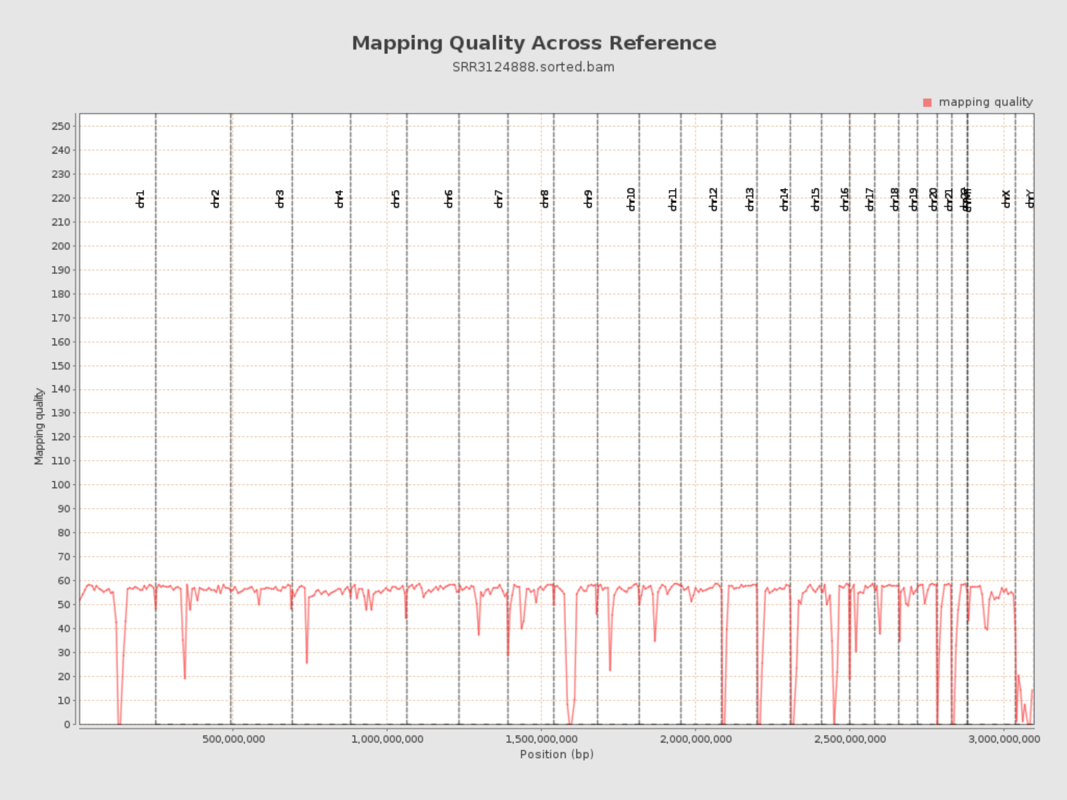
10. Results : Mapped Reads Clipping Profile



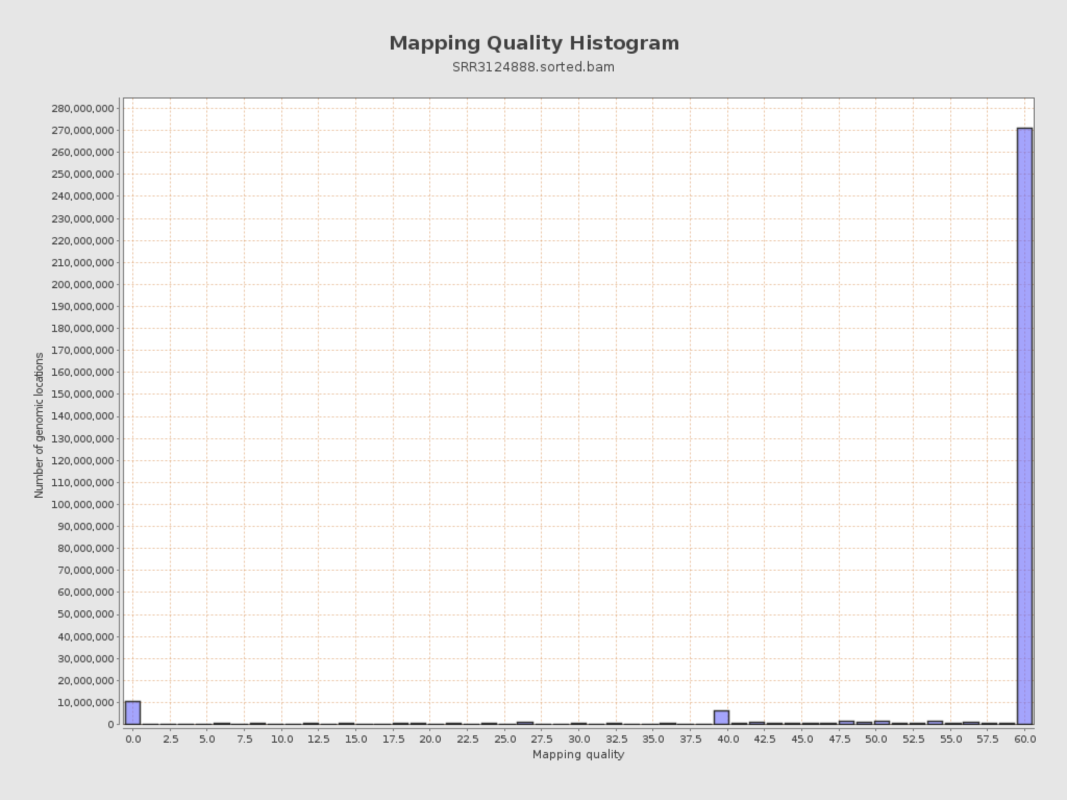
11. Results : Homopolymer Indels



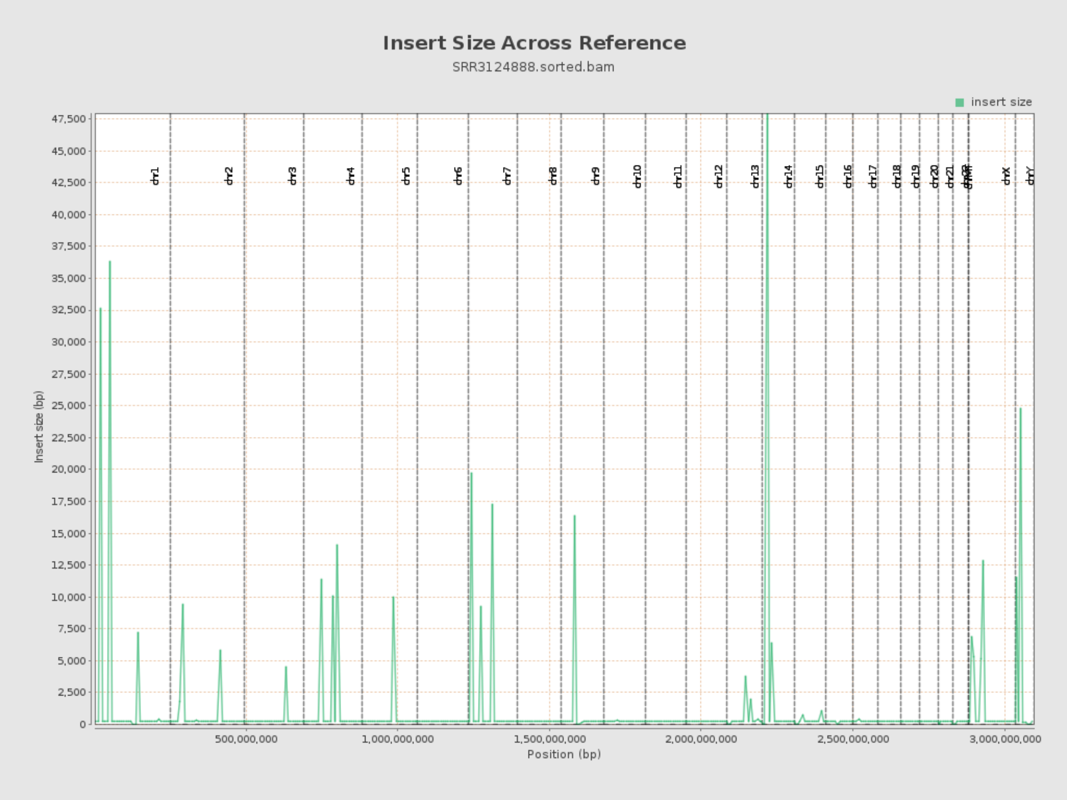
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram