Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 01:17:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124887.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_SRR3124887 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124887_1.fastq.gz SRR3124887_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 01:17:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124887.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,715,428
Mapped reads	5,505,268 / 96.32%
Unmapped reads	210,160 / 3.68%
Mapped paired reads	5,505,268 / 96.32%
Mapped reads, first in pair	2,767,767 / 48.43%
Mapped reads, second in pair	2,737,501 / 47.9%
Mapped reads, both in pair	5,418,766 / 94.81%
Mapped reads, singletons	86,502 / 1.51%
Secondary alignments	0
Supplementary alignments	6,744 / 0.12%
Read min/max/mean length	30 / 76 / 76.04
Duplicated reads (estimated)	273,247 / 4.78%
Duplication rate	3.29%
Clipped reads	1,841,910 / 32.23%

2.2. ACGT Content

Number/percentage of A's	102,213,478 / 28.06%
Number/percentage of C's	68,824,679 / 18.89%
Number/percentage of T's	106,820,001 / 29.32%
Number/percentage of G's	86,470,270 / 23.73%
Number/percentage of N's	3,233 / 0%

GC Percentage	42.62%

2.3. Coverage

Mean	0.1177
Standard Deviation	0.8636

2.4. Mapping Quality

Mean Mapping Quality	51.83

2.5. Insert size

Mean	58,145.09
Standard Deviation	2,325,455.6
P25/Median/P75	154 / 201 / 263

2.6. Mismatches and indels

General error rate	0.7%
Mismatches	2,478,535
Insertions	41,708
Mapped reads with at least one insertion	0.75%
Deletions	101,147
Mapped reads with at least one deletion	1.82%
Homopolymer indels	48.98%

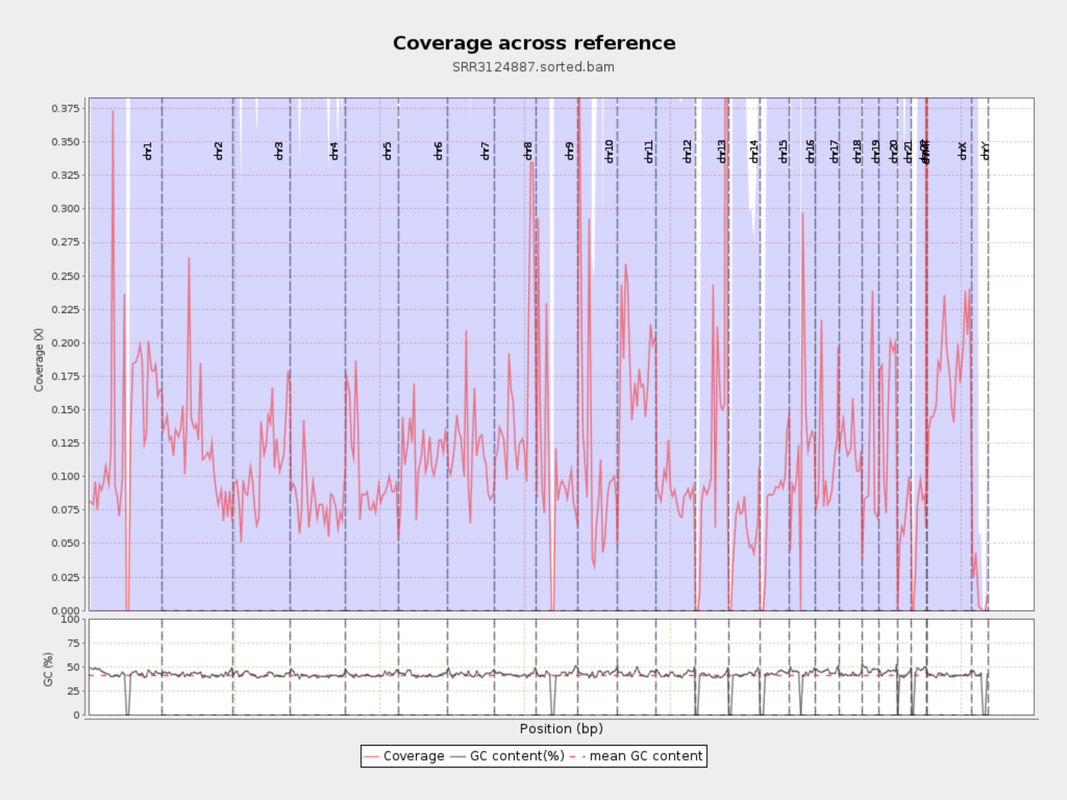
2.7. Chromosome stats

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

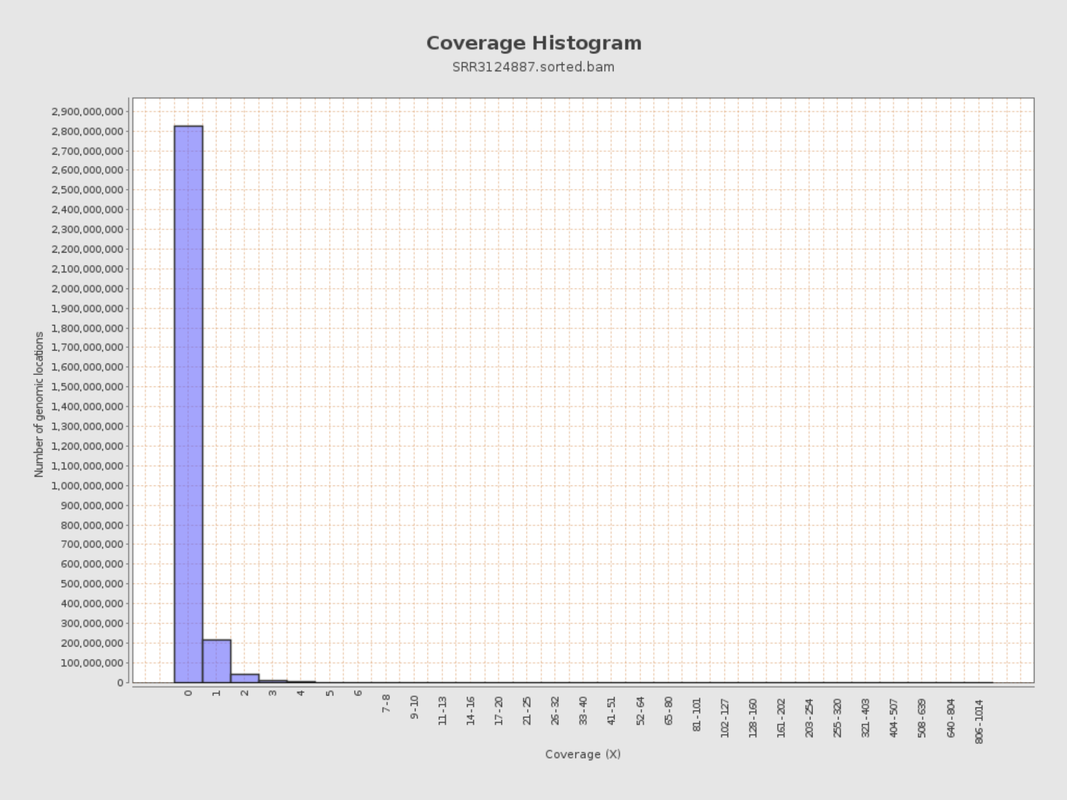
		bases	coverage	deviation
chr1	249250621	33502043	0.1344	1.0914
chr2	243199373	29940108	0.1231	1.0492
chr3	198022430	21645366	0.1093	0.3994
chr4	191154276	15369905	0.0804	0.5228
chr5	180915260	18479328	0.1021	0.3916
chr6	171115067	19943221	0.1165	0.6861
chr7	159138663	18782199	0.118	1.1451
chr8	146364022	23493734	0.1605	0.5861
chr9	141213431	14325303	0.1014	0.8196
chr10	135534747	16624304	0.1227	1.7471
chr11	135006516	24356771	0.1804	0.7252
chr12	133851895	11877002	0.0887	0.3601
chr13	115169878	21344007	0.1853	0.9511
chr14	107349540	5816295	0.0542	0.3289
chr15	102531392	7963590	0.0777	0.337
chr16	90354753	10774727	0.1192	1.2848
chr17	81195210	8952181	0.1103	1.1084
chr18	78077248	9699068	0.1242	1.3107
chr19	59128983	6561405	0.111	0.8004
chr20	63025520	9889464	0.1569	0.5156
chr21	48129895	3091606	0.0642	0.3623
chr22	51304566	3008465	0.0586	0.3011
chrMT	16571	329728	19.8979	12.6227
chrX	155270560	27896628	0.1797	0.7129

chrY	59373566	819653	0.0138	0.6844

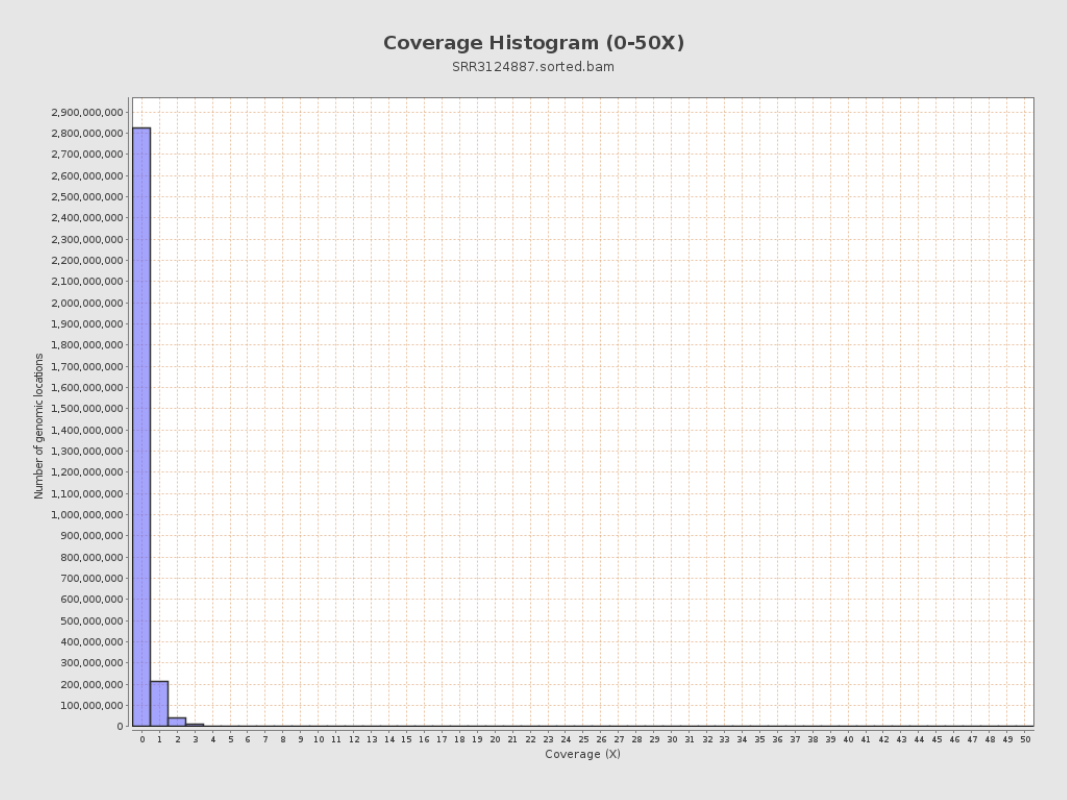
3. Results : Coverage across reference



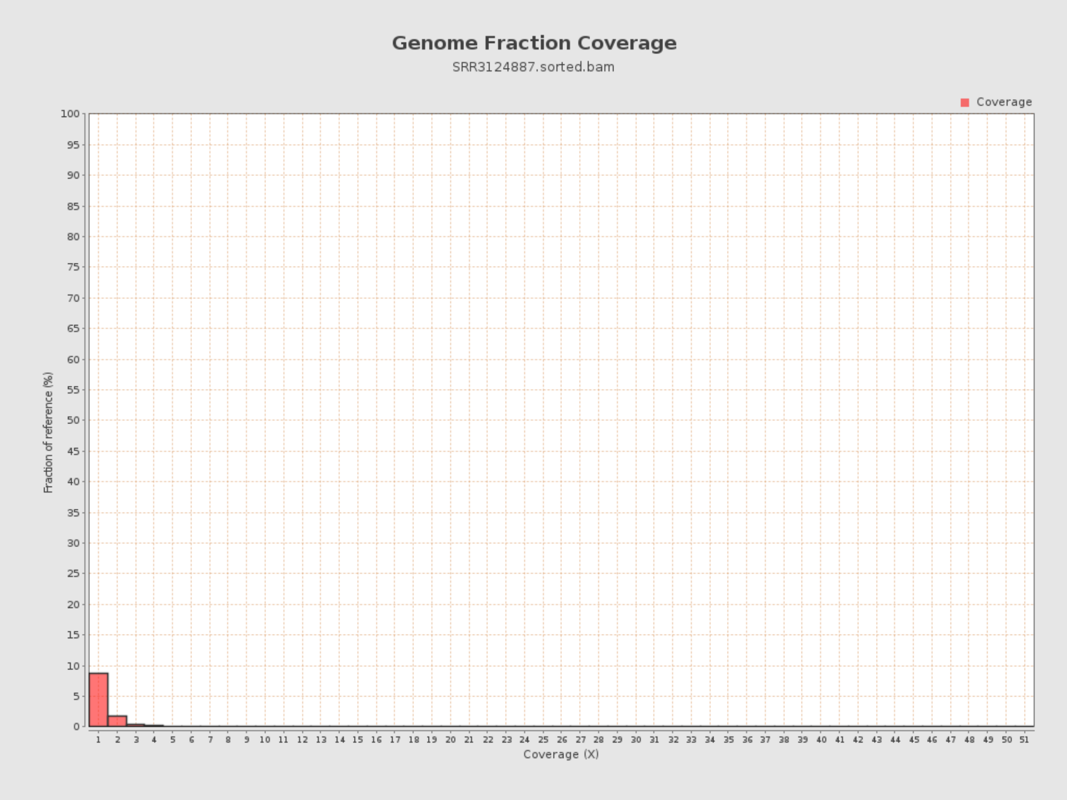
4. Results : Coverage Histogram



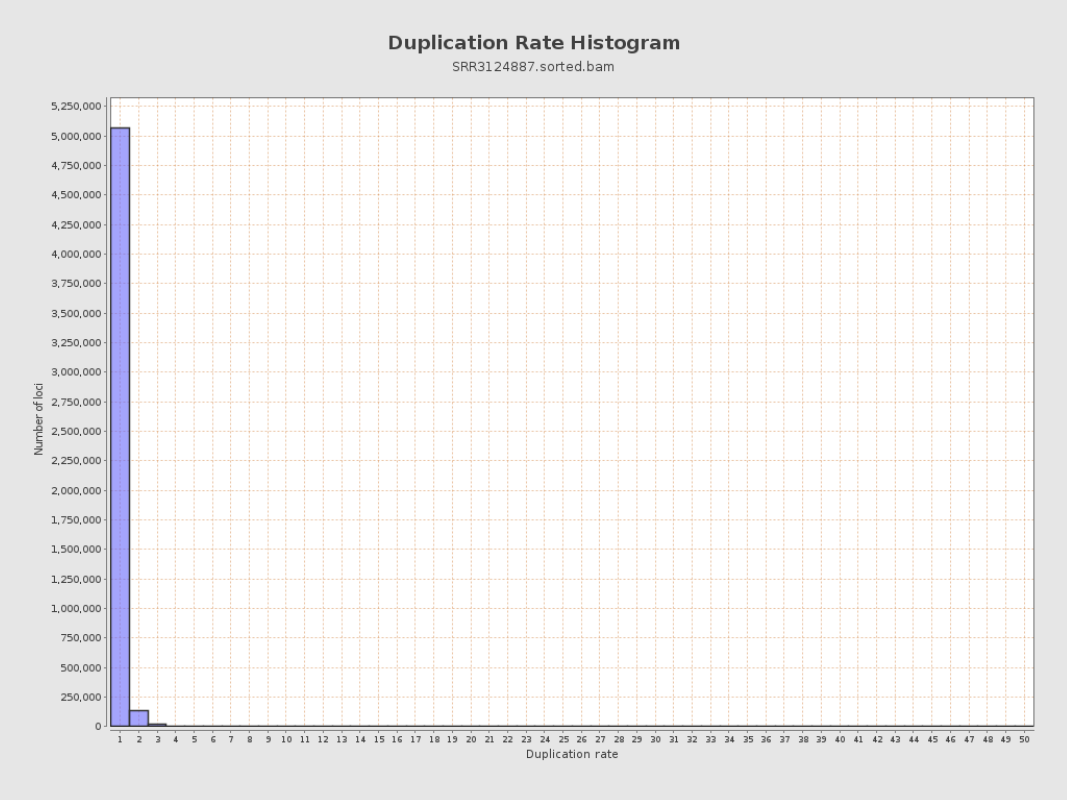
5. Results : Coverage Histogram (0-50X)



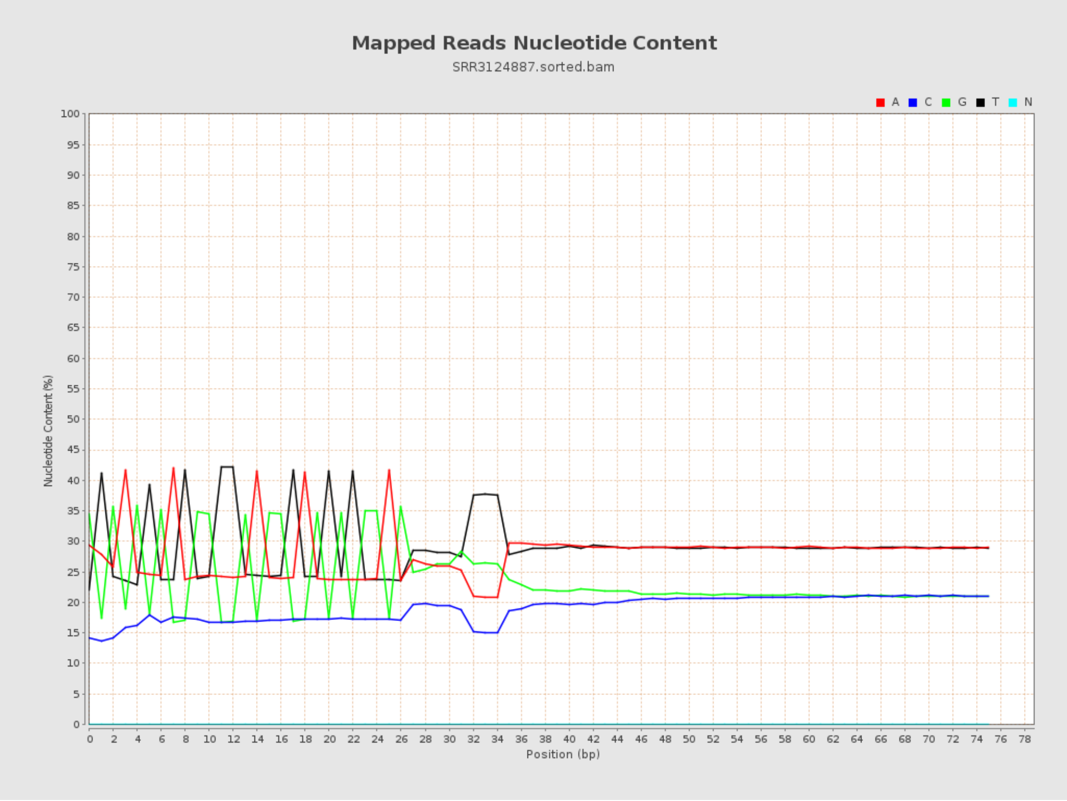
6. Results : Genome Fraction Coverage



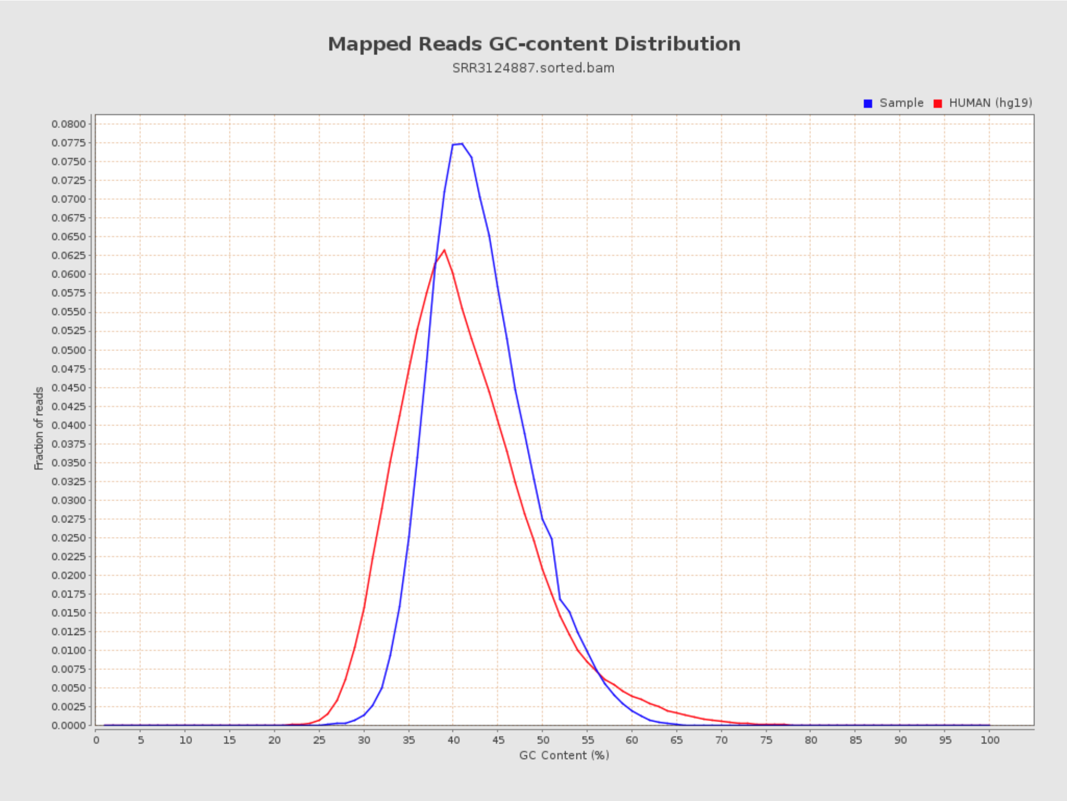
7. Results : Duplication Rate Histogram



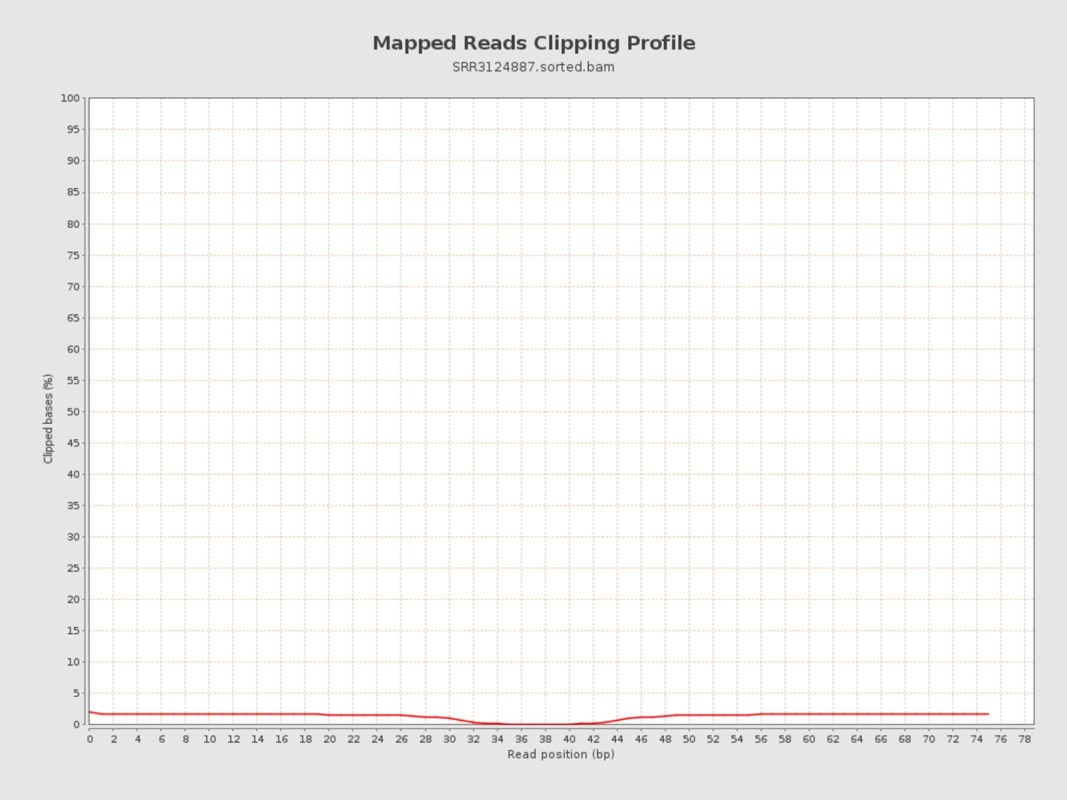
8. Results : Mapped Reads Nucleotide Content



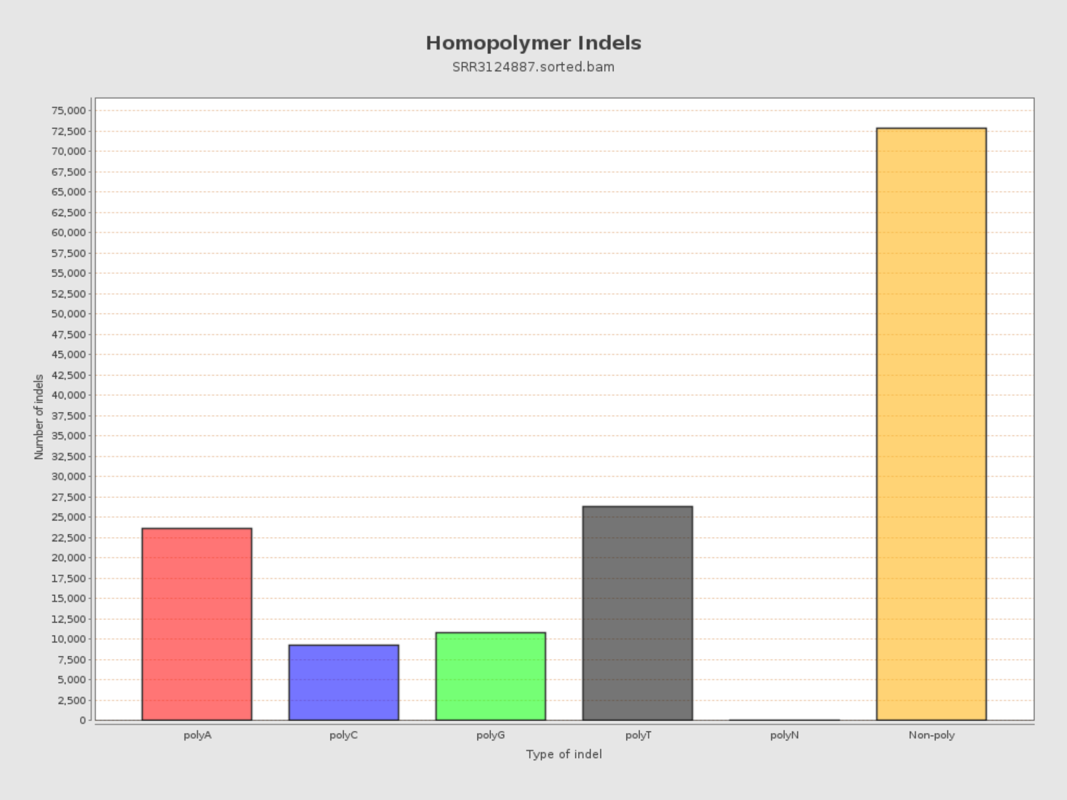
9. Results : Mapped Reads GC-content Distribution



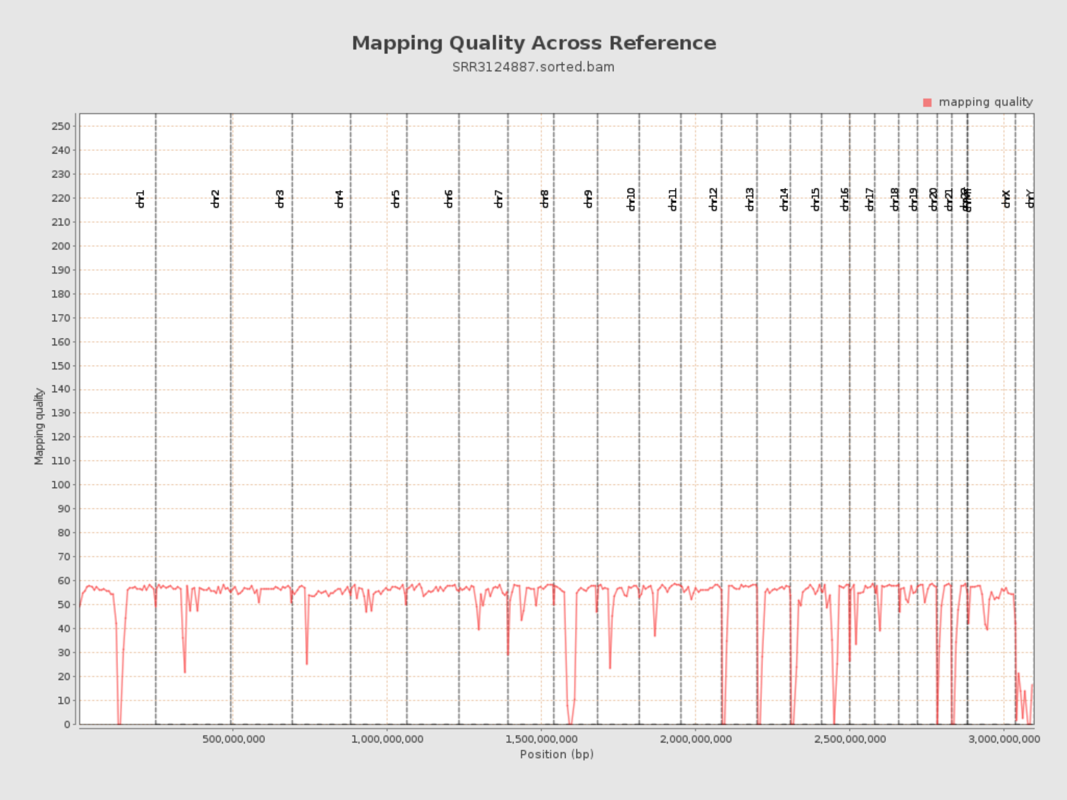
10. Results : Mapped Reads Clipping Profile



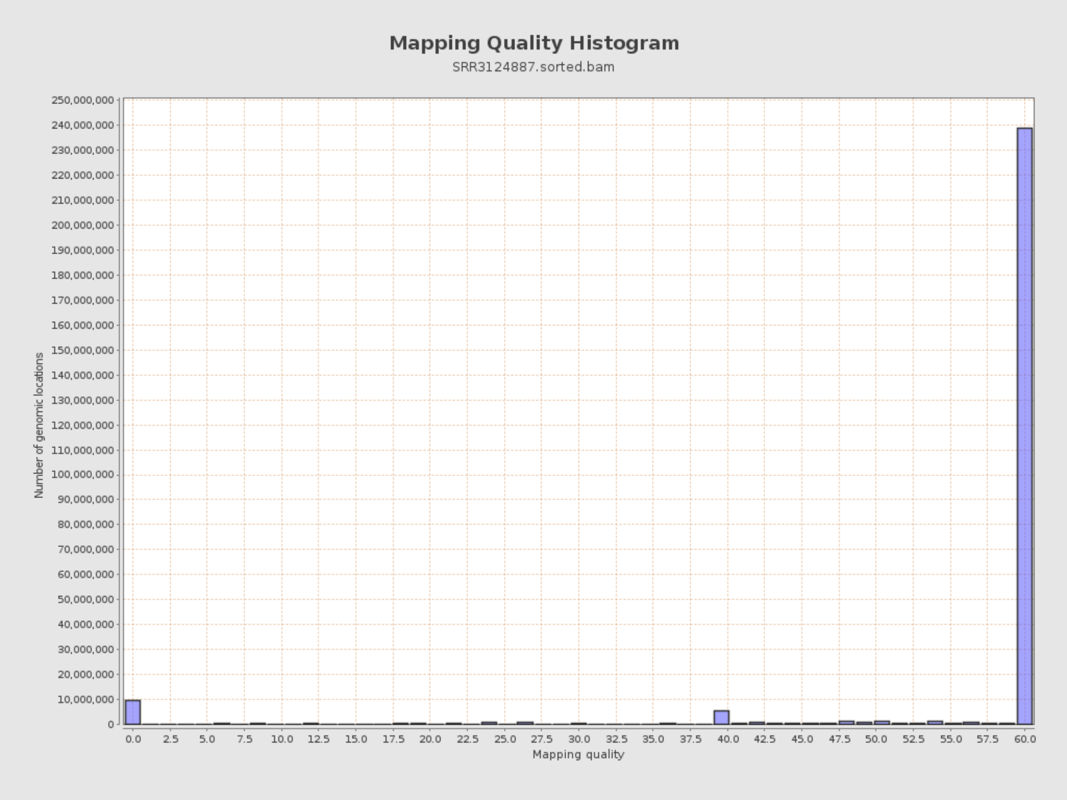
11. Results : Homopolymer Indels



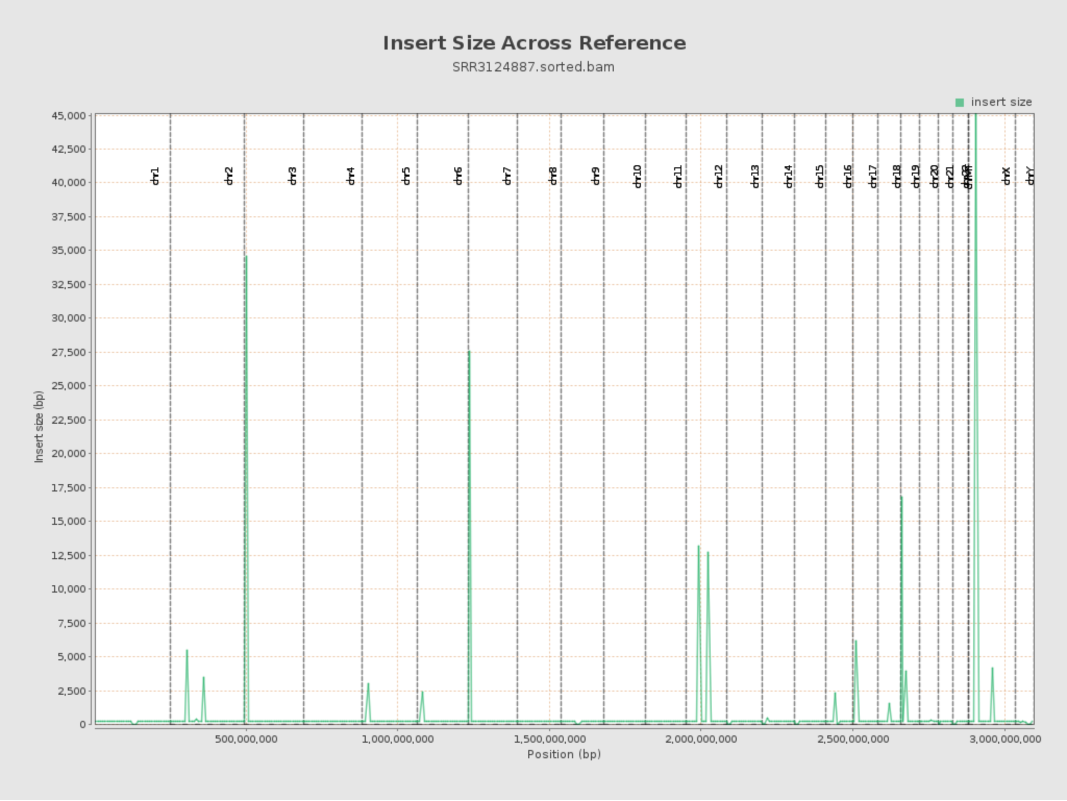
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram