Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 01:04:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124885.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_SRR3124885 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124885_1.fastq.gz SRR3124885_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 01:04:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124885.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,369,188
Mapped reads	6,149,661 / 96.55%
Unmapped reads	219,527 / 3.45%
Mapped paired reads	6,149,661 / 96.55%
Mapped reads, first in pair	3,095,351 / 48.6%
Mapped reads, second in pair	3,054,310 / 47.95%
Mapped reads, both in pair	6,045,404 / 94.92%
Mapped reads, singletons	104,257 / 1.64%
Secondary alignments	0
Supplementary alignments	6,174 / 0.1%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	351,072 / 5.51%
Duplication rate	3.43%
Clipped reads	1,910,274 / 29.99%

2.2. ACGT Content

Number/percentage of A's	118,161,699 / 28.75%
Number/percentage of C's	76,114,329 / 18.52%
Number/percentage of T's	122,558,035 / 29.82%
Number/percentage of G's	94,153,307 / 22.91%
Number/percentage of N's	3,731 / 0%

GC Percentage	41.43%

2.3. Coverage

Mean	0.1328
Standard Deviation	1.2263

2.4. Mapping Quality

Mean Mapping Quality	51.95

2.5. Insert size

Mean	79,839.63
Standard Deviation	2,733,938.44
P25/Median/P75	161 / 215 / 292

2.6. Mismatches and indels

General error rate	0.73%
Mismatches	2,940,156
Insertions	45,042
Mapped reads with at least one insertion	0.73%
Deletions	116,120
Mapped reads with at least one deletion	1.87%
Homopolymer indels	49.78%

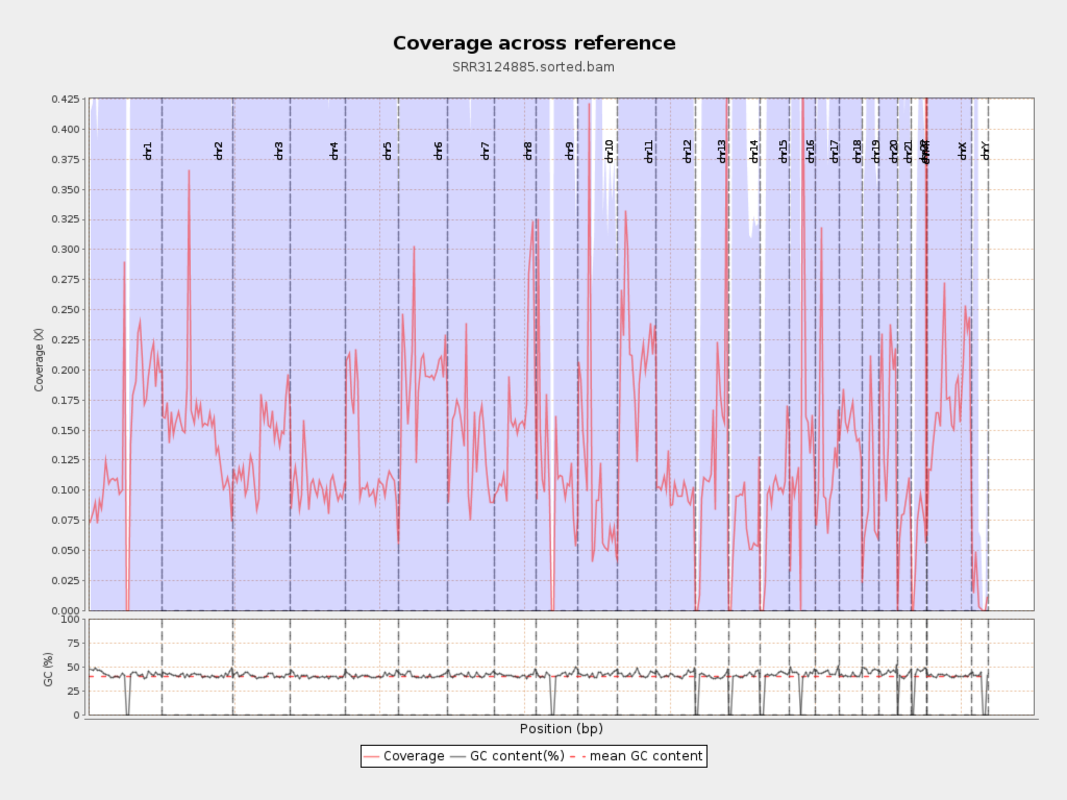
2.7. Chromosome stats

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

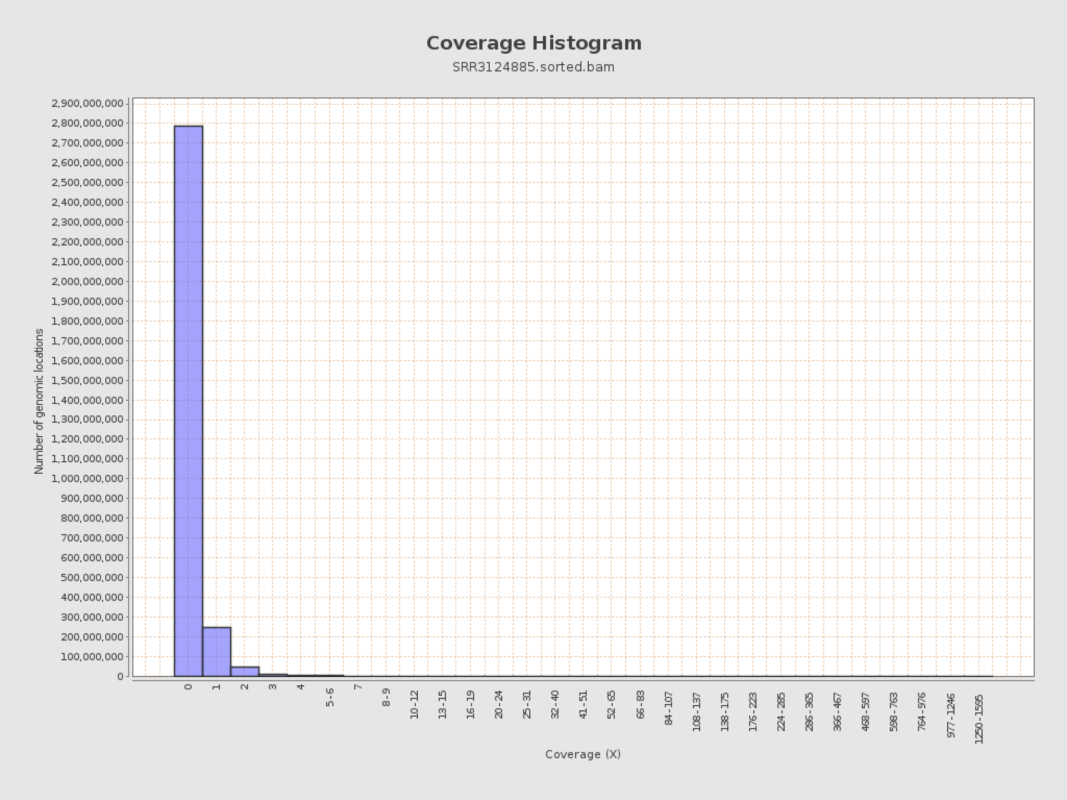
		bases	coverage	deviation
chr1	249250621	35247554	0.1414	1.7649
chr2	243199373	37520504	0.1543	1.3043
chr3	198022430	26792577	0.1353	0.4541
chr4	191154276	19504715	0.102	0.5364
chr5	180915260	22665402	0.1253	0.4314
chr6	171115067	33182366	0.1939	1.2837
chr7	159138663	21871202	0.1374	1.818
chr8	146364022	24241974	0.1656	0.6424
chr9	141213431	15656856	0.1109	1.1906
chr10	135534747	15088785	0.1113	2.4715
chr11	135006516	28636085	0.2121	1.1306
chr12	133851895	13307059	0.0994	0.393
chr13	115169878	15209857	0.1321	0.4881
chr14	107349540	6843187	0.0637	0.3976
chr15	102531392	8970626	0.0875	0.3563
chr16	90354753	12887454	0.1426	2.0729
chr17	81195210	9861488	0.1215	1.7927
chr18	78077248	12103418	0.155	1.8326
chr19	59128983	5699949	0.0964	1.3177
chr20	63025520	10865434	0.1724	0.5348
chr21	48129895	3600104	0.0748	0.4143
chr22	51304566	2912229	0.0568	0.2819
chrMT	16571	109503	6.6081	4.2373
chrX	155270560	27653037	0.1781	0.8843

chrY	59373566	728679	0.0123	0.531

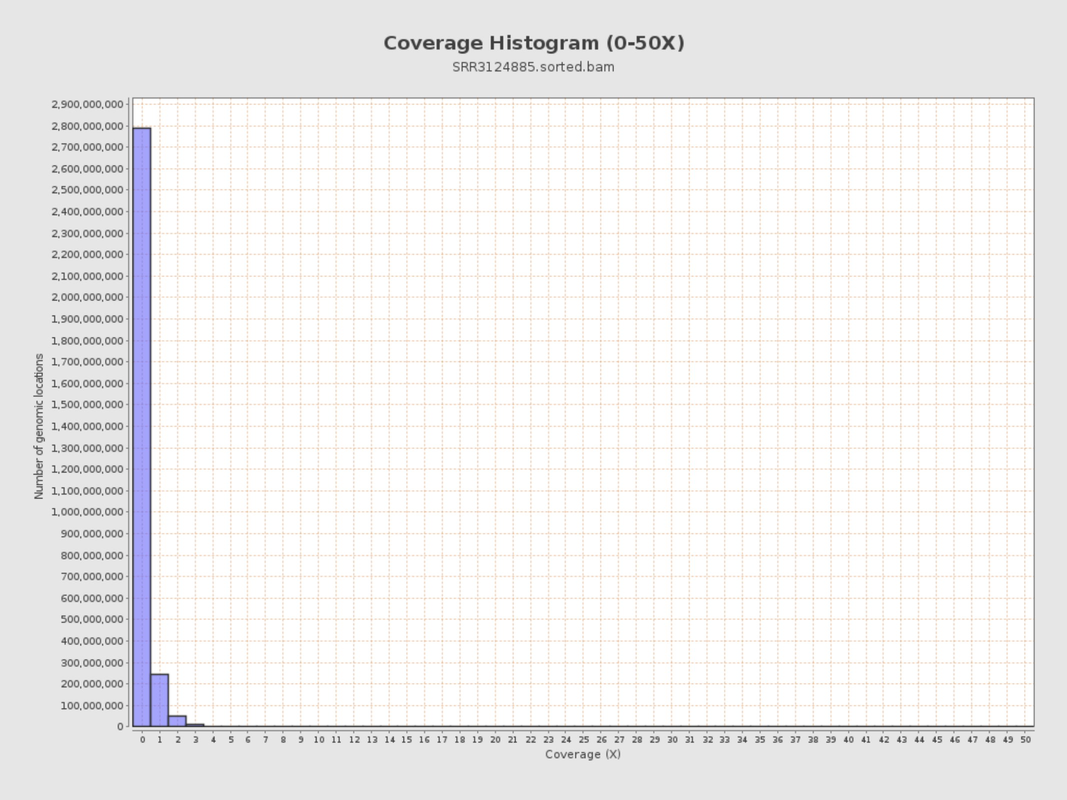
3. Results : Coverage across reference



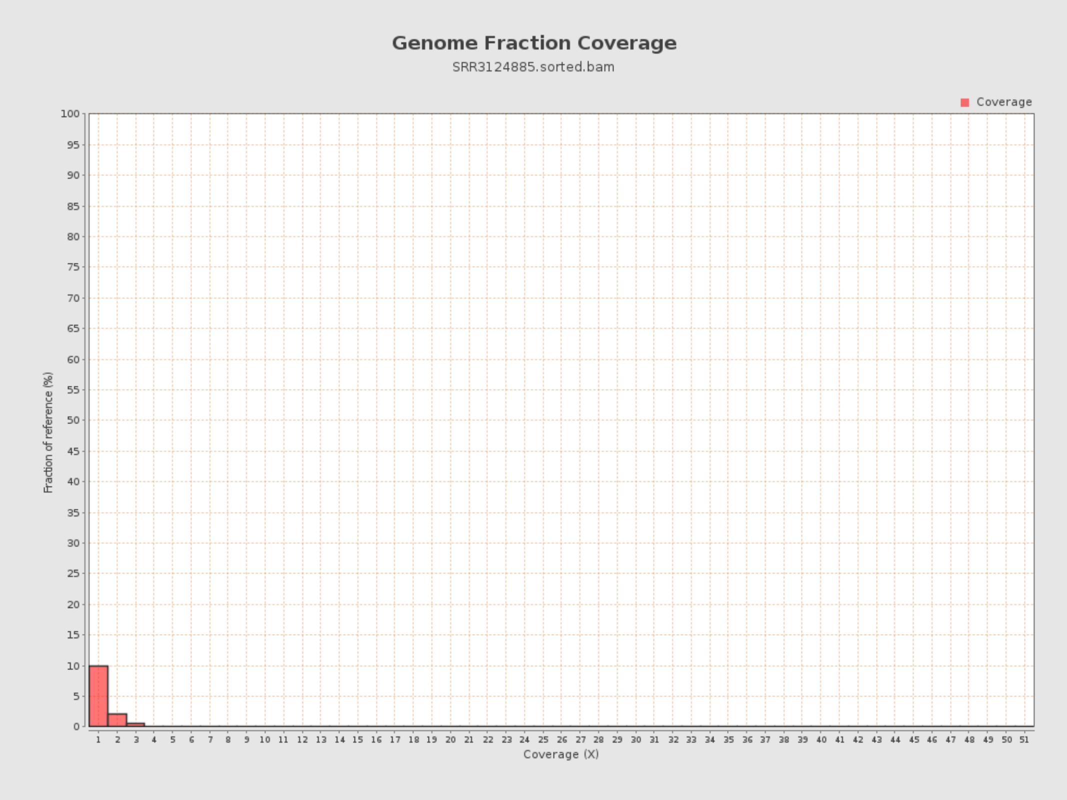
4. Results : Coverage Histogram



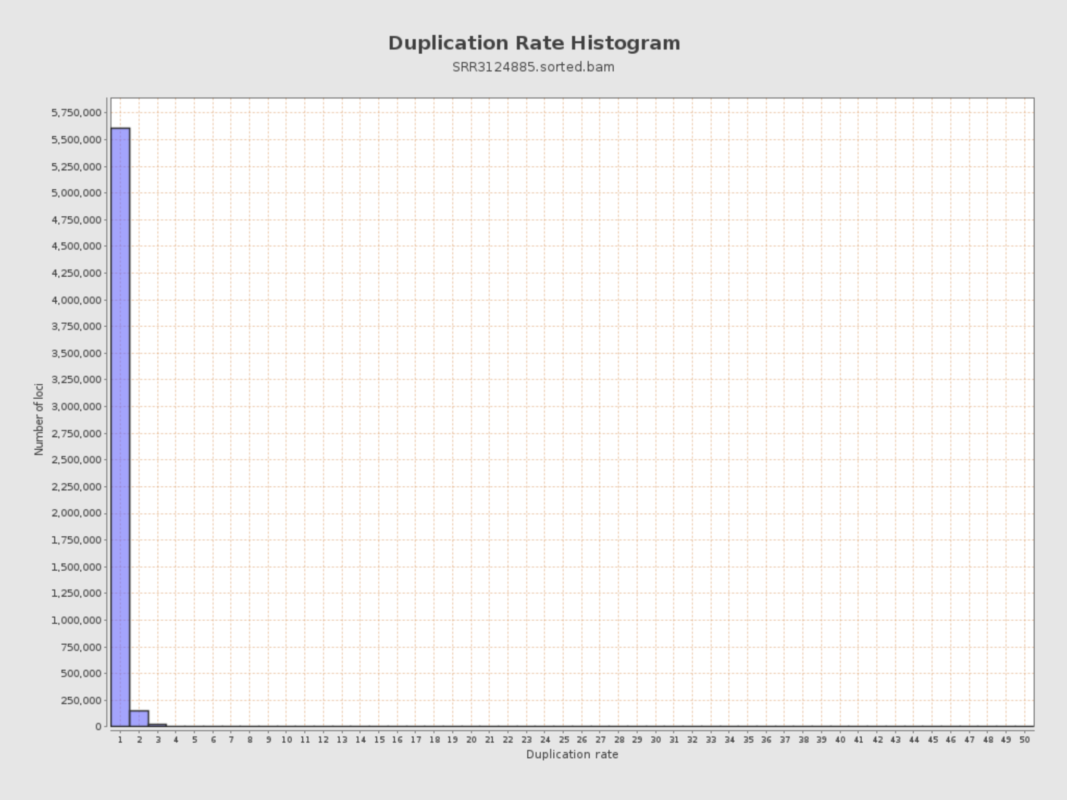
5. Results : Coverage Histogram (0-50X)



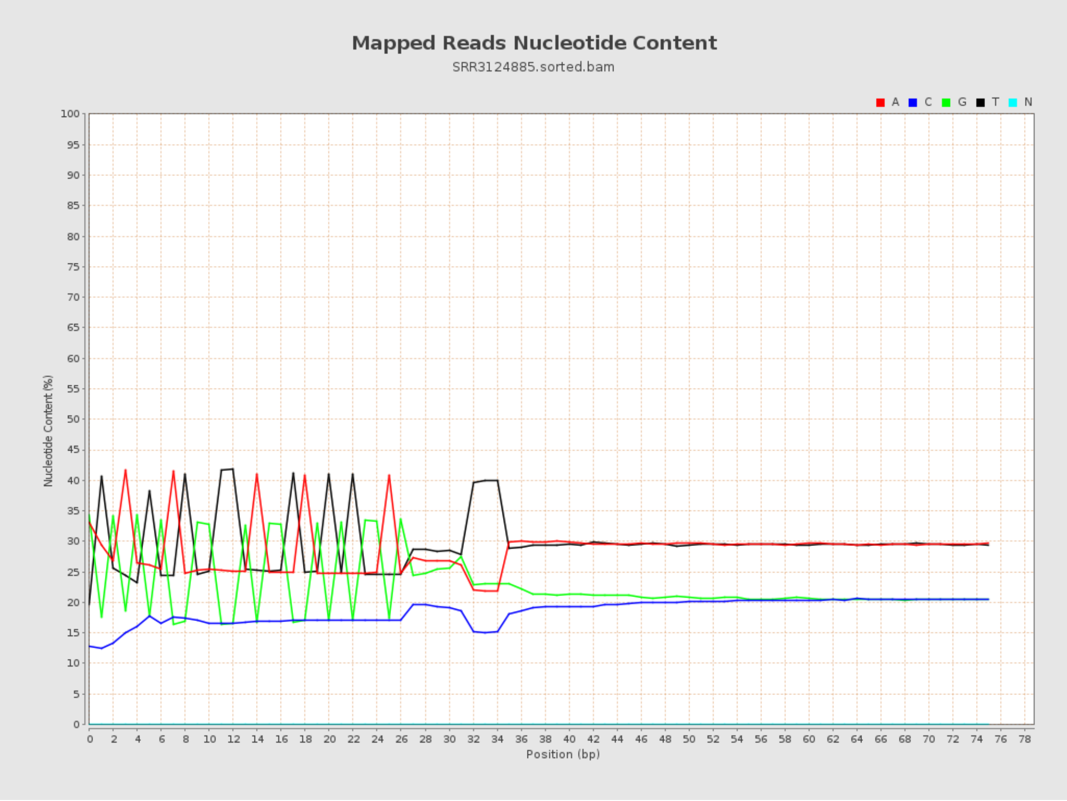
6. Results : Genome Fraction Coverage



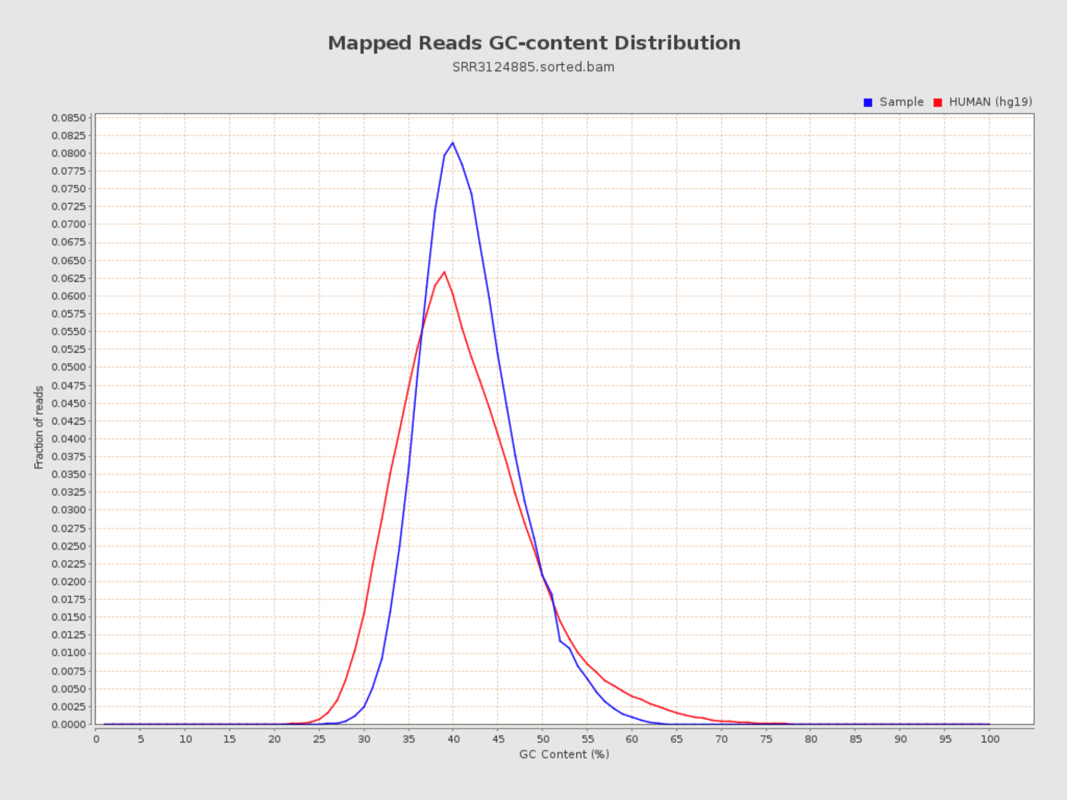
7. Results : Duplication Rate Histogram



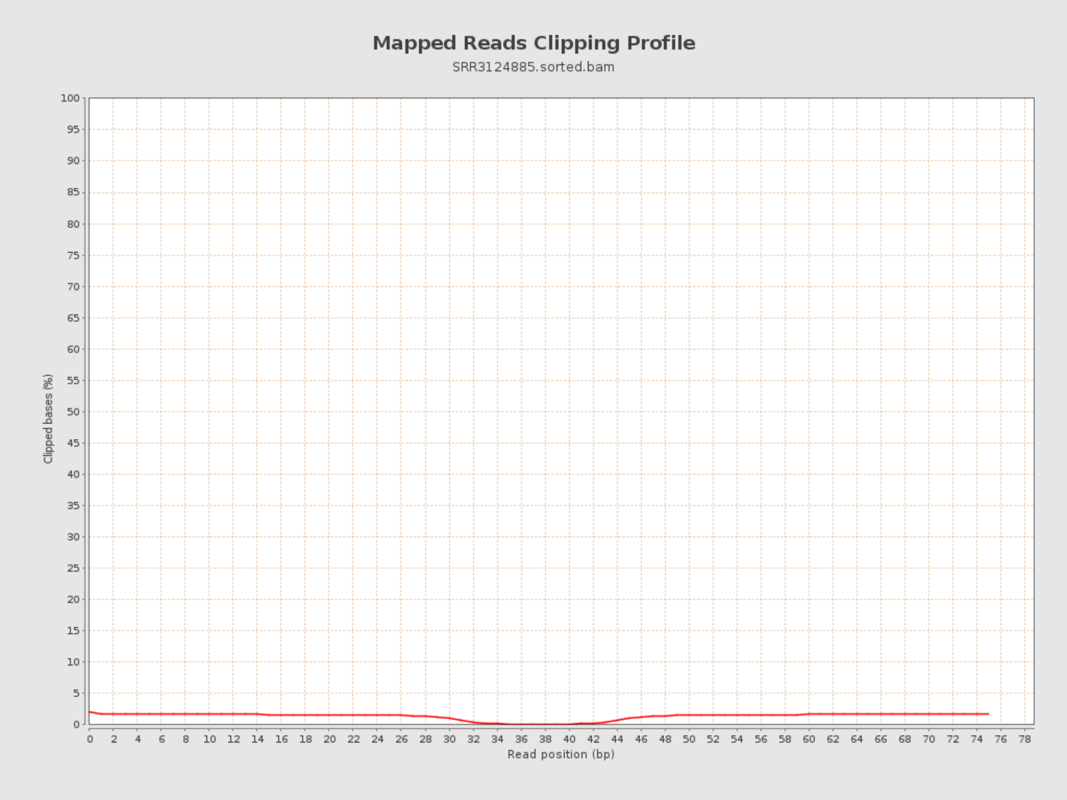
8. Results : Mapped Reads Nucleotide Content



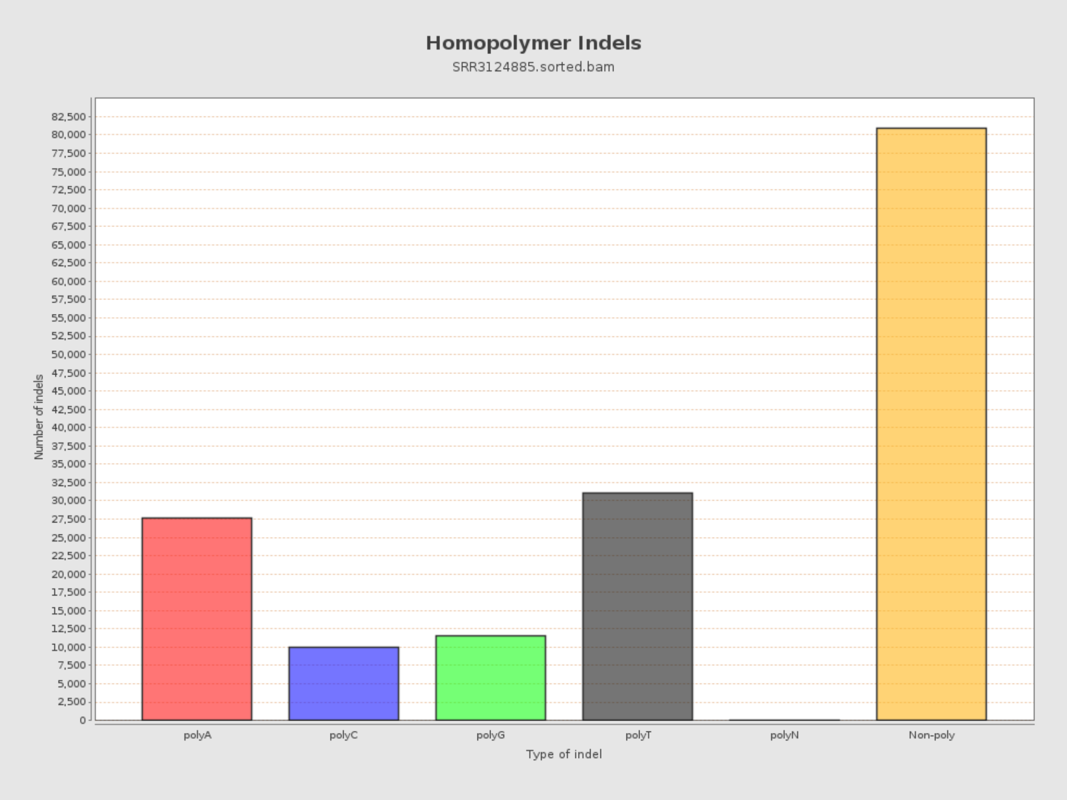
9. Results : Mapped Reads GC-content Distribution



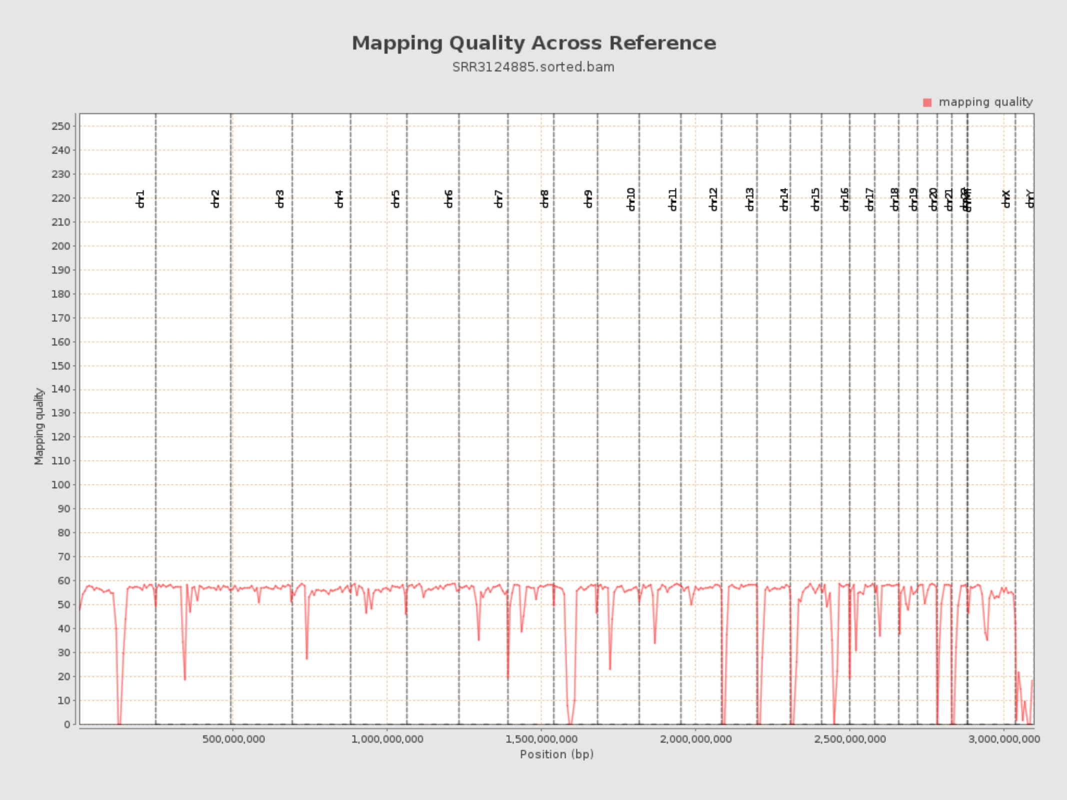
10. Results : Mapped Reads Clipping Profile



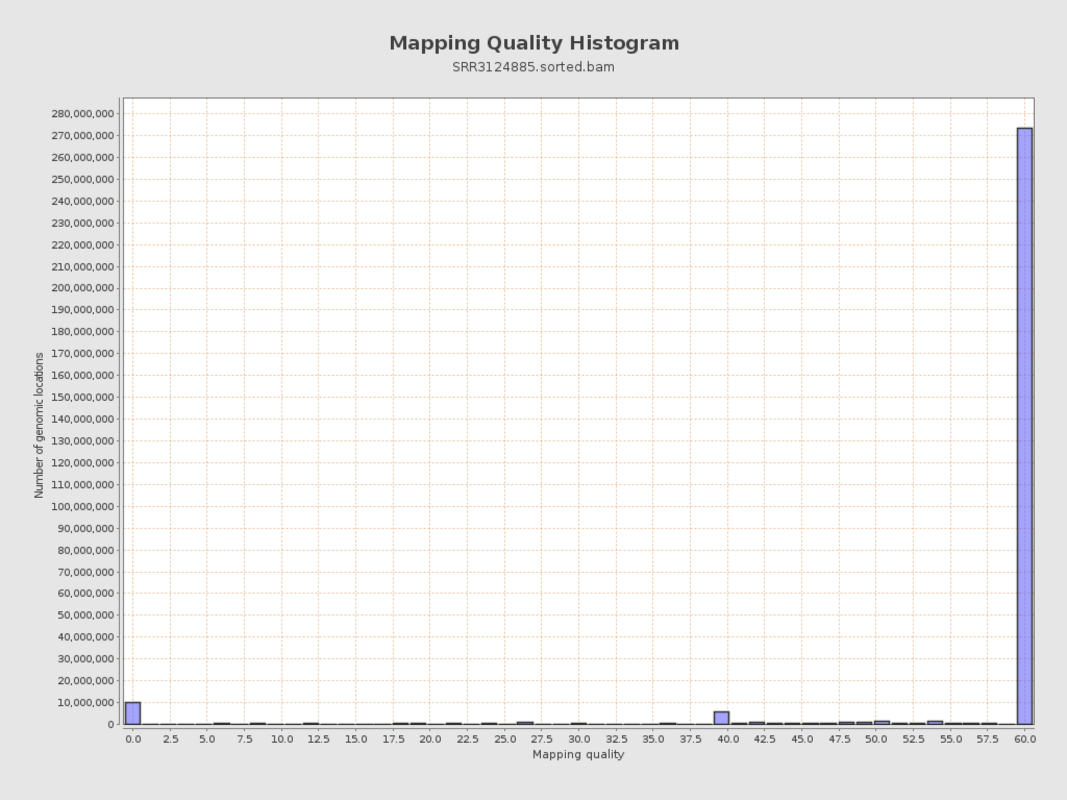
11. Results : Homopolymer Indels



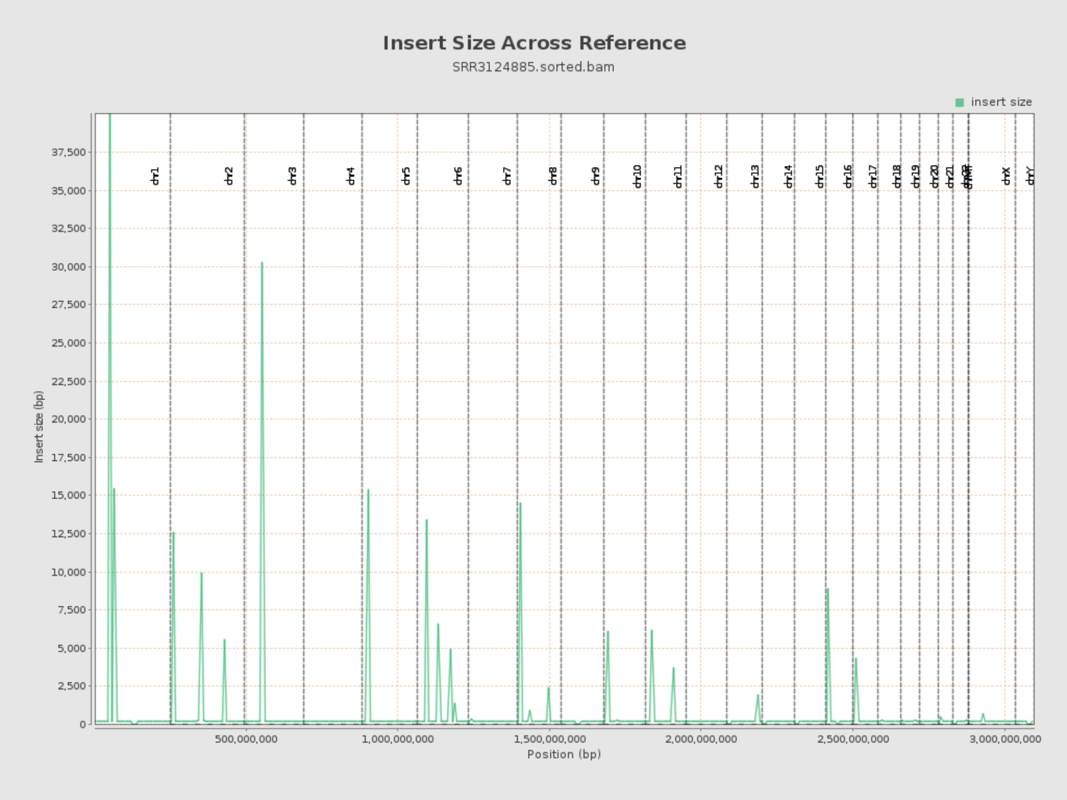
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram