Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 13:32:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124985.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_SRR3124985 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124985_1.fastq.gz SRR3124985_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 13:32:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124985.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,932,142
Mapped reads	4,699,101 / 95.28%
Unmapped reads	233,041 / 4.72%
Mapped paired reads	4,699,101 / 95.28%
Mapped reads, first in pair	2,396,517 / 48.59%
Mapped reads, second in pair	2,302,584 / 46.69%
Mapped reads, both in pair	4,573,870 / 92.74%
Mapped reads, singletons	125,231 / 2.54%
Secondary alignments	0
Supplementary alignments	17,224 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	372,243 / 7.55%
Duplication rate	4.42%
Clipped reads	2,462,267 / 49.92%

2.2. ACGT Content

Number/percentage of A's	79,440,119 / 27.76%
Number/percentage of C's	50,256,634 / 17.56%
Number/percentage of T's	86,632,824 / 30.28%
Number/percentage of G's	69,806,939 / 24.4%
Number/percentage of N's	1 / 0%

GC Percentage	41.96%

2.3. Coverage

Mean	0.0925
Standard Deviation	1.3144

2.4. Mapping Quality

Mean Mapping Quality	51.5

2.5. Insert size

Mean	78,767.74
Standard Deviation	2,649,353.31
P25/Median/P75	127 / 171 / 236

2.6. Mismatches and indels

General error rate	0.81%
Mismatches	2,233,613
Insertions	39,684
Mapped reads with at least one insertion	0.83%
Deletions	93,627
Mapped reads with at least one deletion	1.97%
Homopolymer indels	46.11%

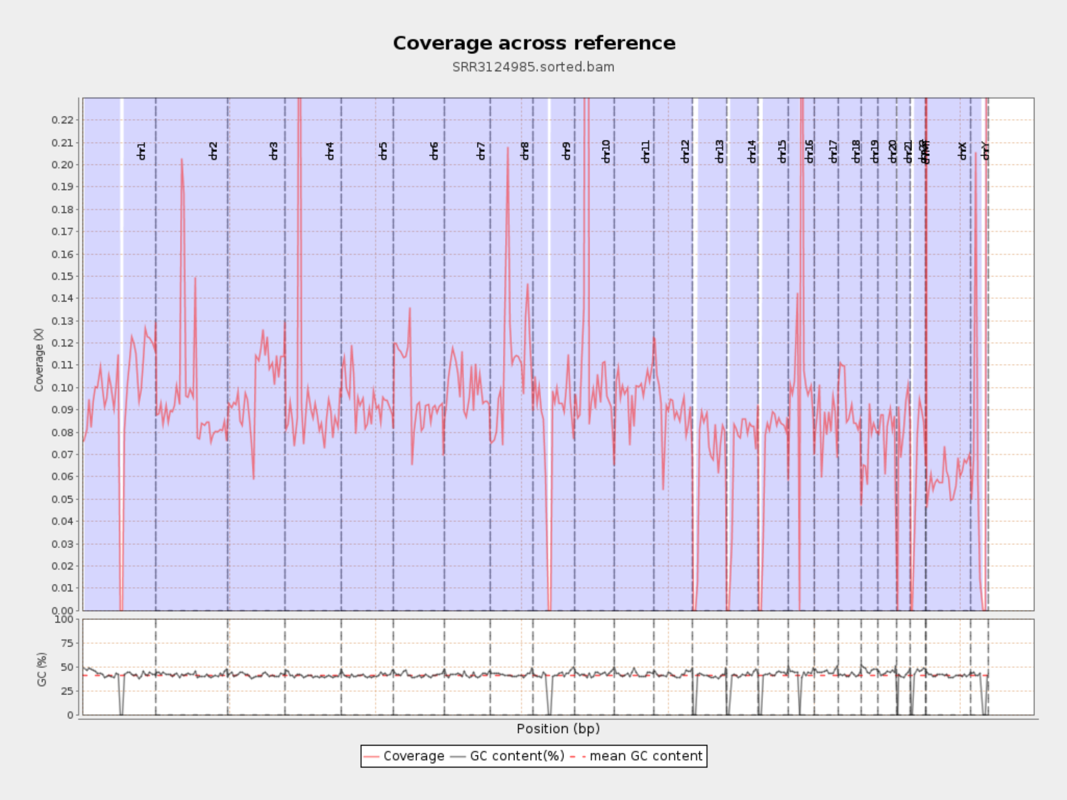
2.7. Chromosome stats

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

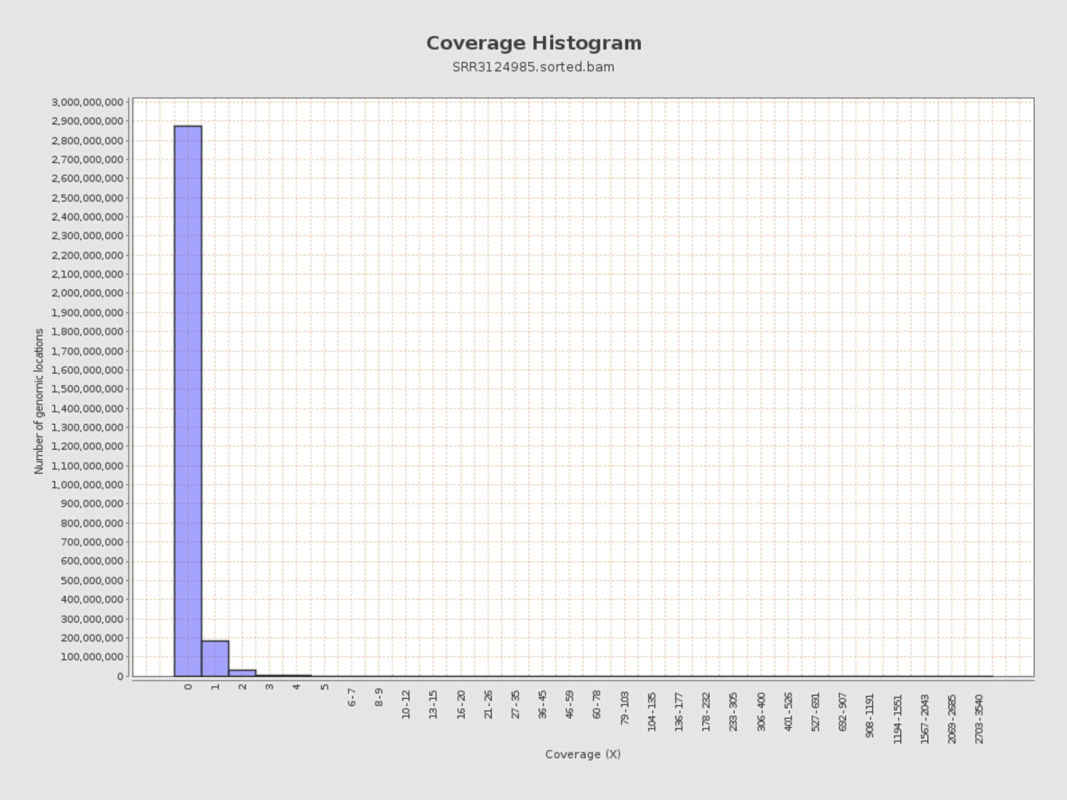
		bases	coverage	deviation
chr1	249250621	24225390	0.0972	0.5662
chr2	243199373	23231277	0.0955	1.3876
chr3	198022430	19973691	0.1009	0.4601
chr4	191154276	18828026	0.0985	1.3506
chr5	180915260	17071646	0.0944	0.3789
chr6	171115067	16771413	0.098	0.4601
chr7	159138663	15962955	0.1003	0.6157
chr8	146364022	16441612	0.1123	0.4456
chr9	141213431	11694883	0.0828	0.6925
chr10	135534747	18330424	0.1352	4.8498
chr11	135006516	13274790	0.0983	0.4691
chr12	133851895	12102684	0.0904	0.3622
chr13	115169878	7473600	0.0649	0.2955
chr14	107349540	7254975	0.0676	0.3741
chr15	102531392	6981428	0.0681	0.3134
chr16	90354753	10558619	0.1169	2.0288
chr17	81195210	6852293	0.0844	0.5602
chr18	78077248	7297673	0.0935	0.9666
chr19	59128983	4349724	0.0736	0.5437
chr20	63025520	5077441	0.0806	0.5611
chr21	48129895	3798568	0.0789	0.6863
chr22	51304566	3066324	0.0598	0.3425
chrMT	16571	130160	7.8547	5.3676
chrX	155270560	9301575	0.0599	0.3596

chrY	59373566	6239130	0.1051	2.4675

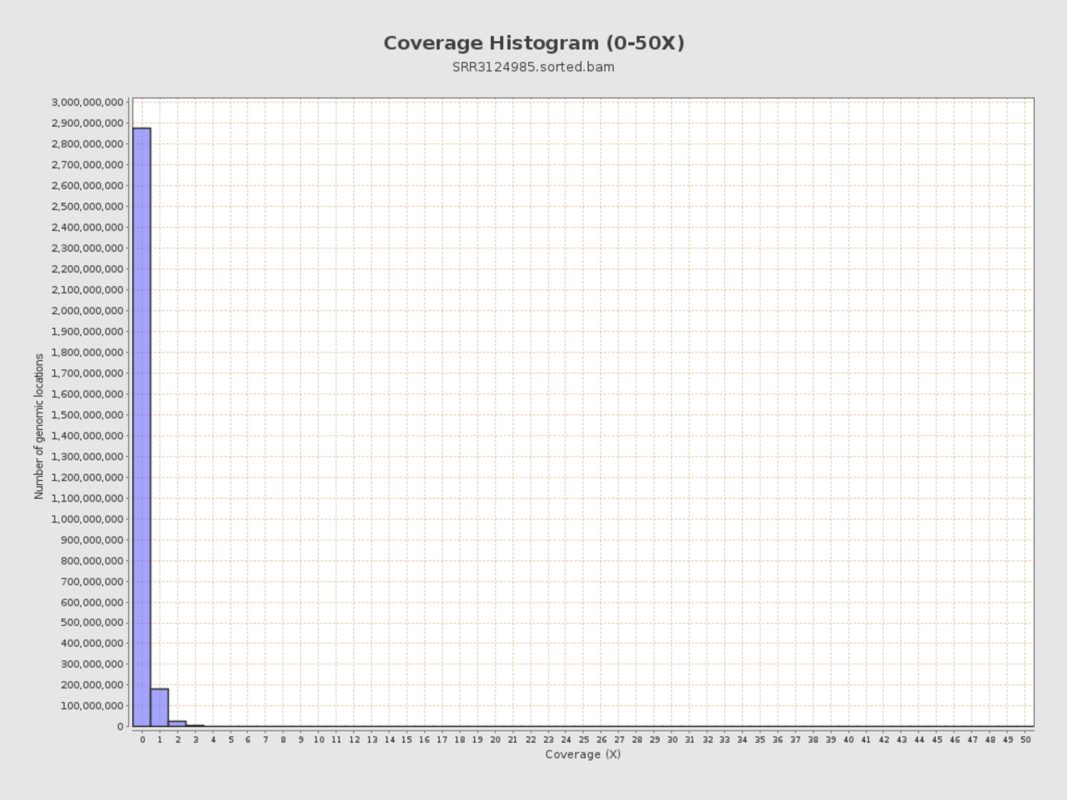
3. Results : Coverage across reference



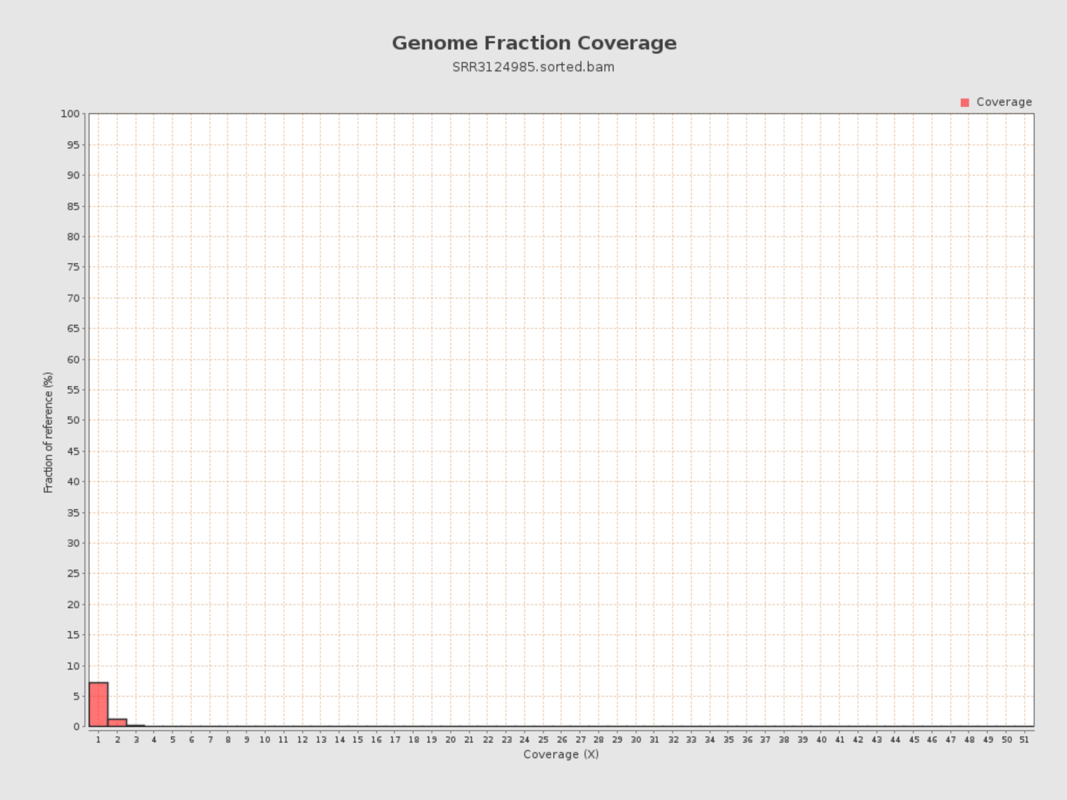
4. Results : Coverage Histogram



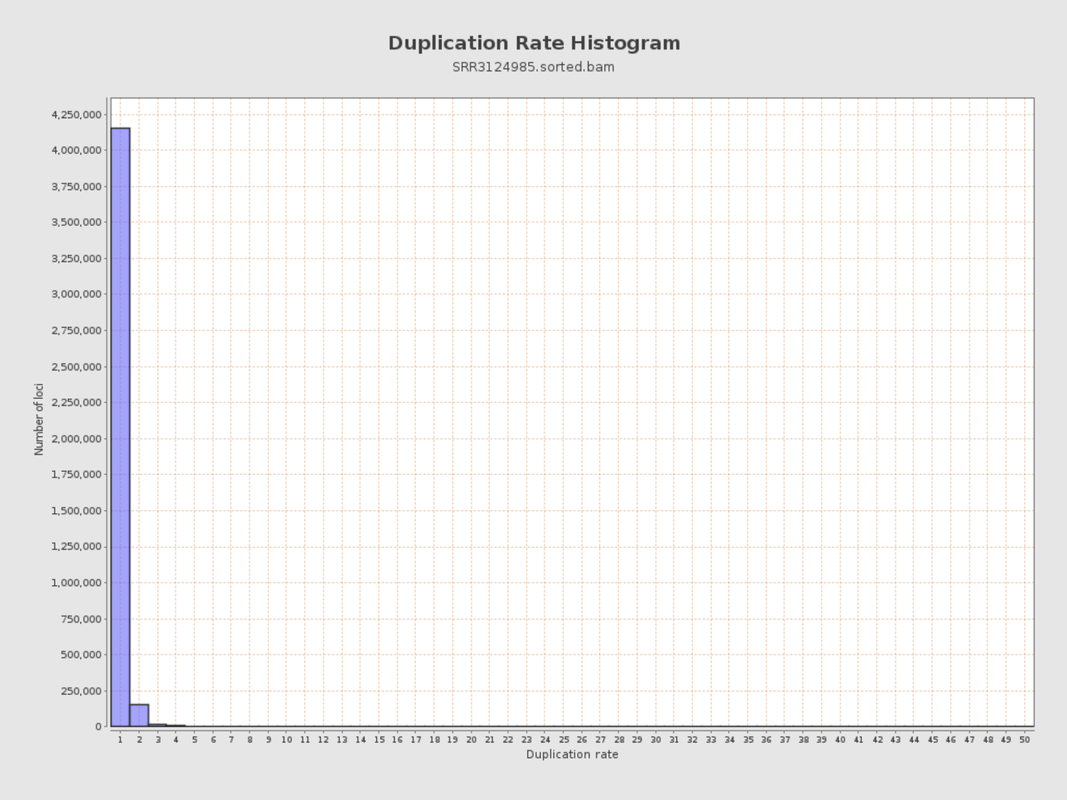
5. Results : Coverage Histogram (0-50X)



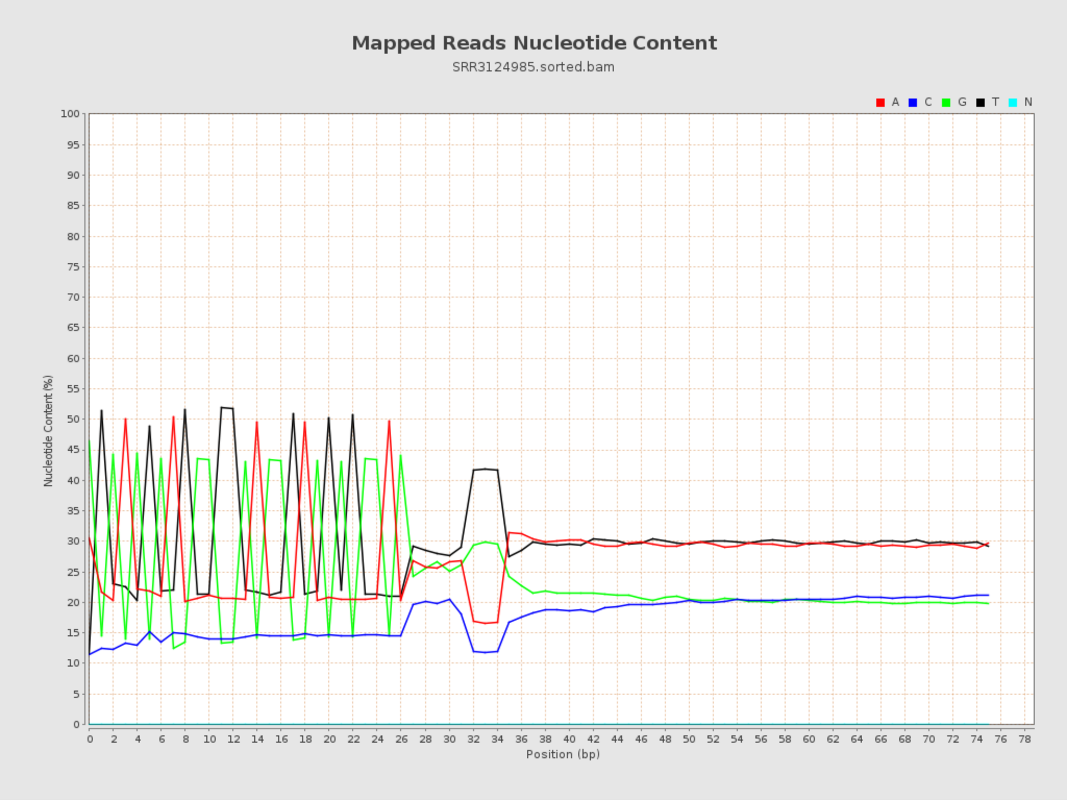
6. Results : Genome Fraction Coverage



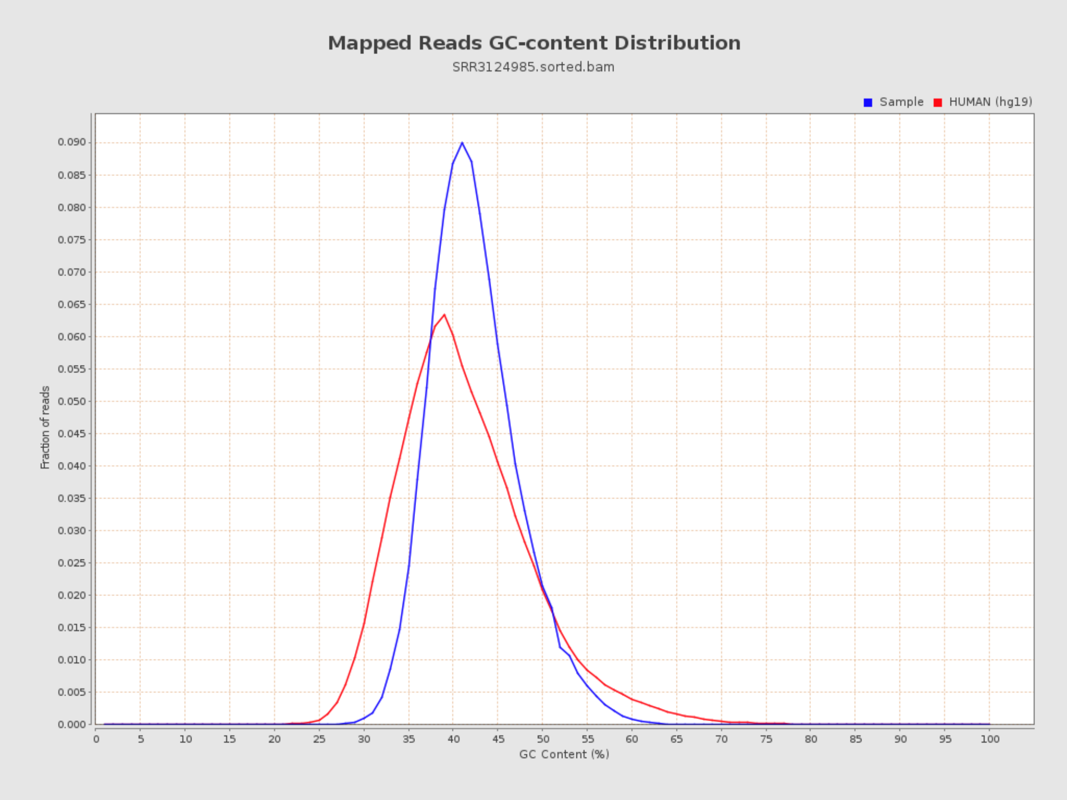
7. Results : Duplication Rate Histogram



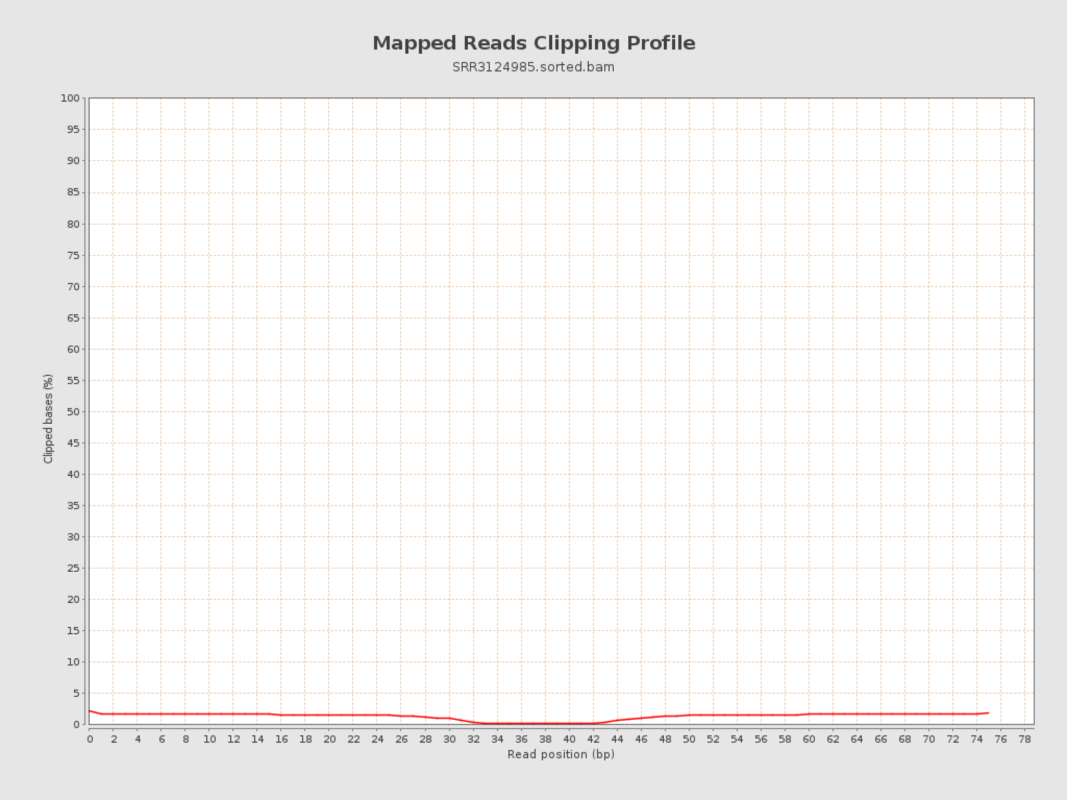
8. Results : Mapped Reads Nucleotide Content



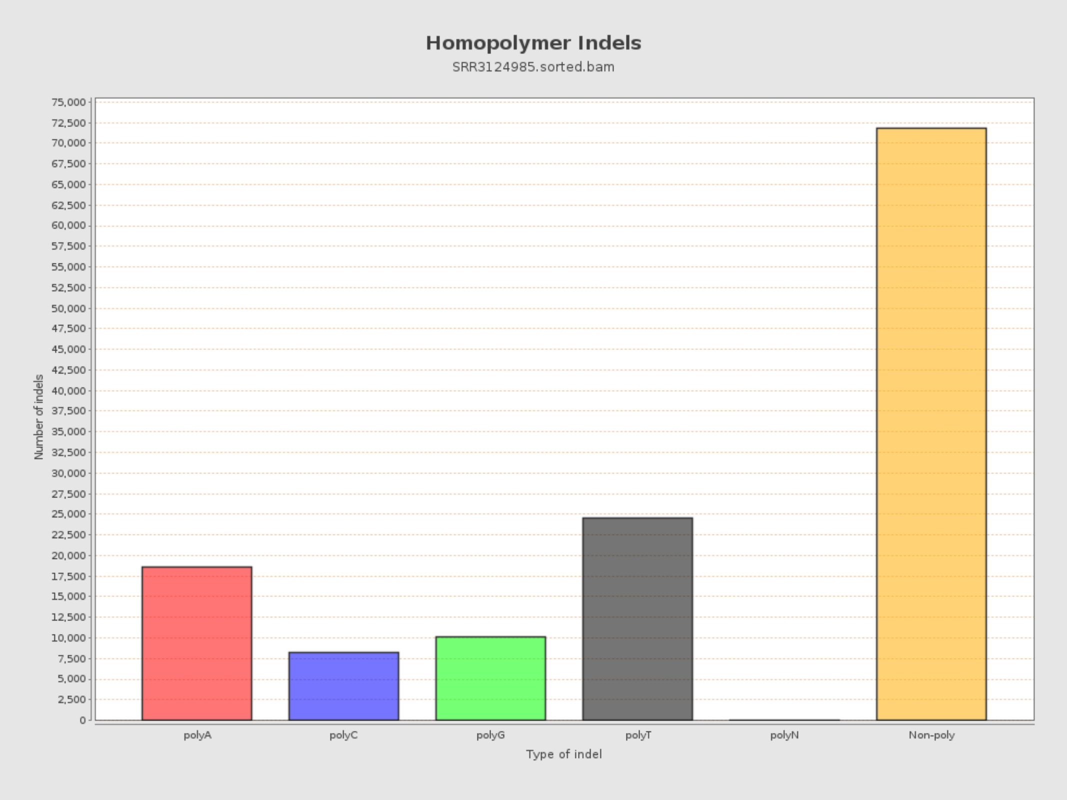
9. Results : Mapped Reads GC-content Distribution



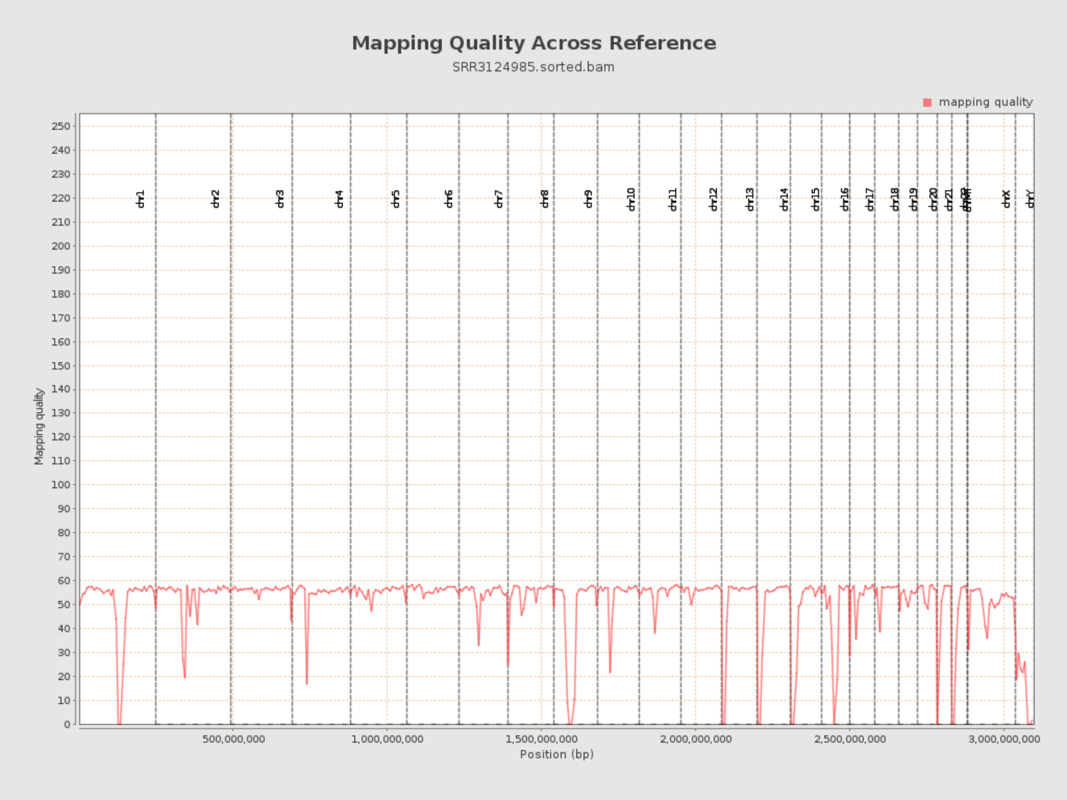
10. Results : Mapped Reads Clipping Profile



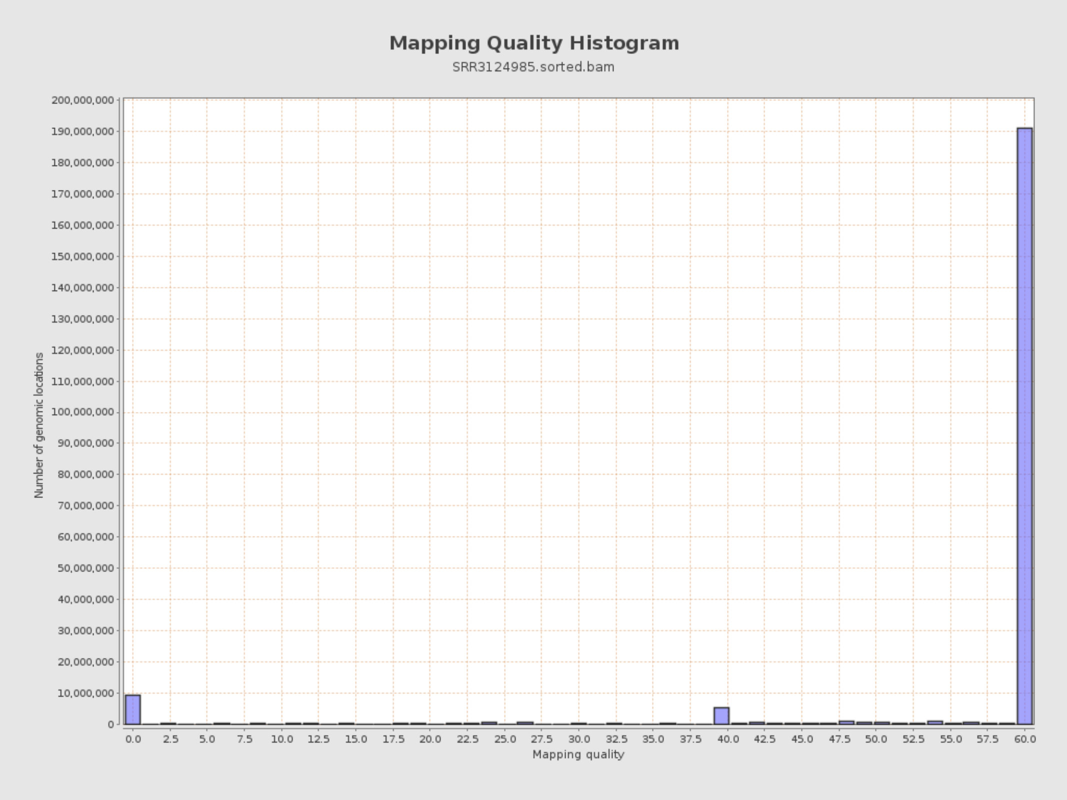
11. Results : Homopolymer Indels



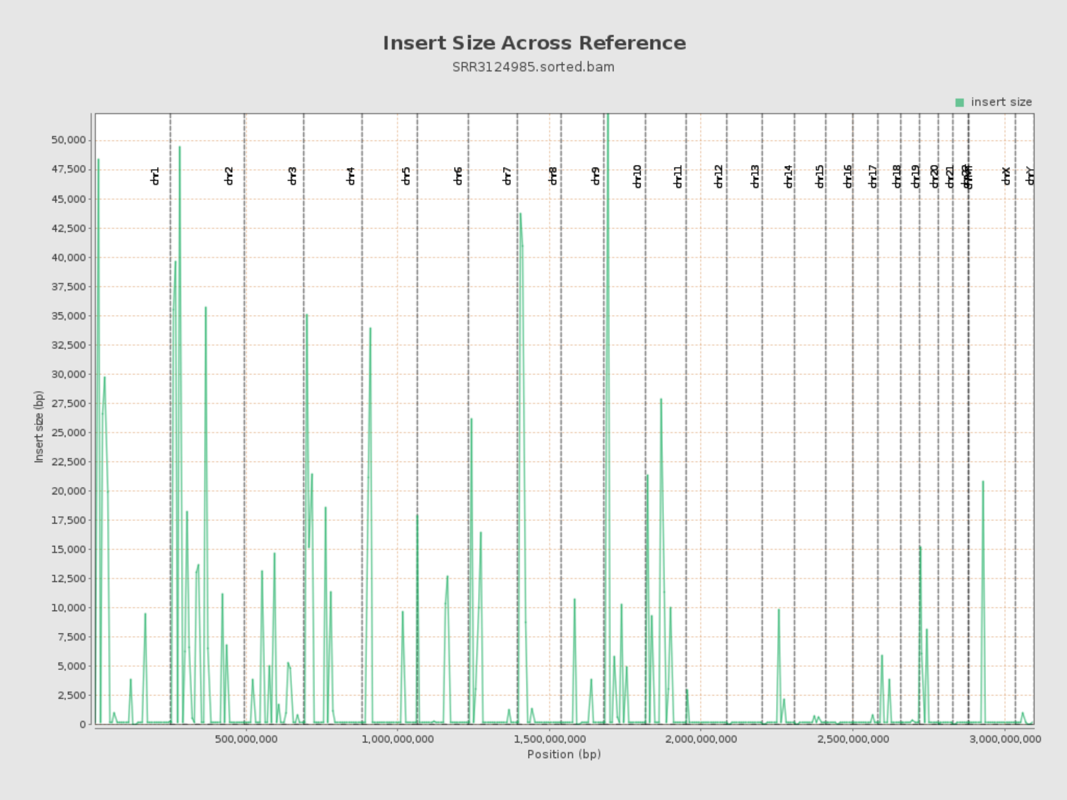
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram