Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 07:35:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124936.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_SRR3124936 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124936_1.fastq.gz SRR3124936_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 07:35:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124936.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,215,734
Mapped reads	4,162,467 / 98.74%
Unmapped reads	53,267 / 1.26%
Mapped paired reads	4,162,467 / 98.74%
Mapped reads, first in pair	2,084,496 / 49.45%
Mapped reads, second in pair	2,077,971 / 49.29%
Mapped reads, both in pair	4,147,744 / 98.39%
Mapped reads, singletons	14,723 / 0.35%
Secondary alignments	0
Supplementary alignments	47,739 / 1.13%
Read min/max/mean length	30 / 151 / 151.56
Duplicated reads (estimated)	628,011 / 14.9%
Duplication rate	13.75%
Clipped reads	3,016,467 / 71.55%

2.2. ACGT Content

Number/percentage of A's	164,616,478 / 29.23%
Number/percentage of C's	113,560,676 / 20.17%
Number/percentage of T's	165,964,855 / 29.47%
Number/percentage of G's	118,988,309 / 21.13%
Number/percentage of N's	24,994 / 0%

GC Percentage	41.29%

2.3. Coverage

Mean	0.182
Standard Deviation	2.4645

2.4. Mapping Quality

Mean Mapping Quality	53.74

2.5. Insert size

Mean	59,535.58
Standard Deviation	2,335,722.56
P25/Median/P75	138 / 169 / 213

2.6. Mismatches and indels

General error rate	1.42%
Mismatches	7,753,070
Insertions	100,981
Mapped reads with at least one insertion	2.32%
Deletions	195,858
Mapped reads with at least one deletion	4.54%
Homopolymer indels	45.65%

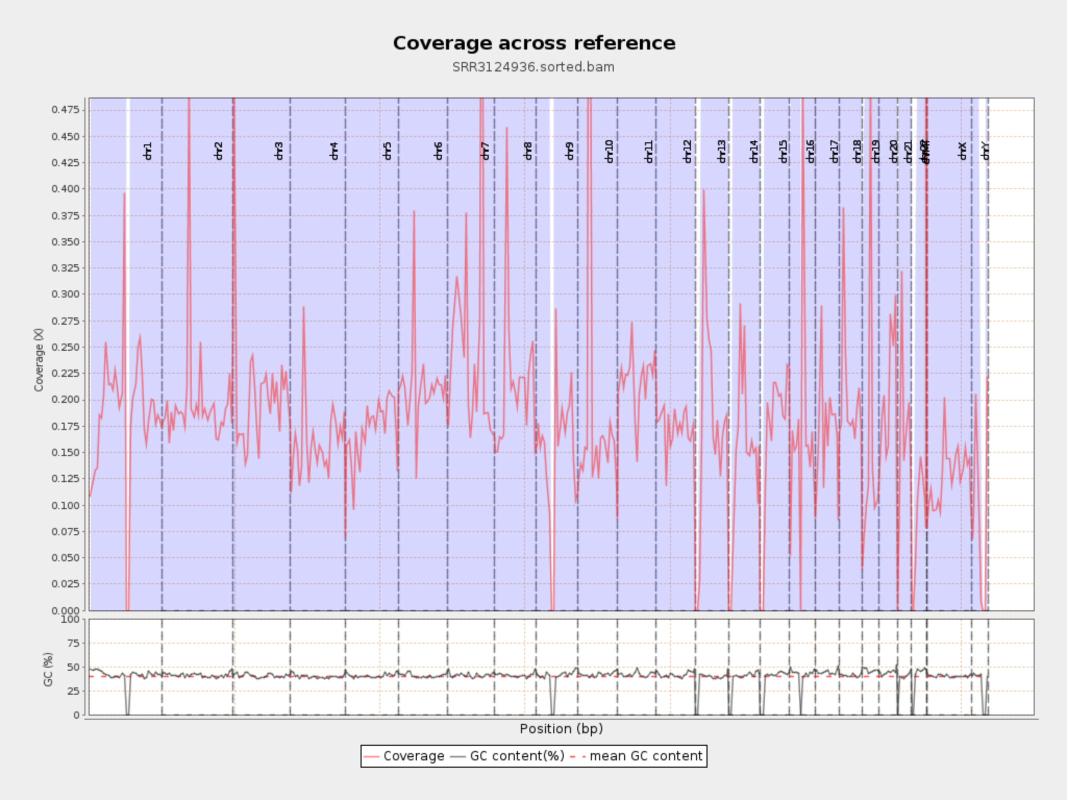
2.7. Chromosome stats

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

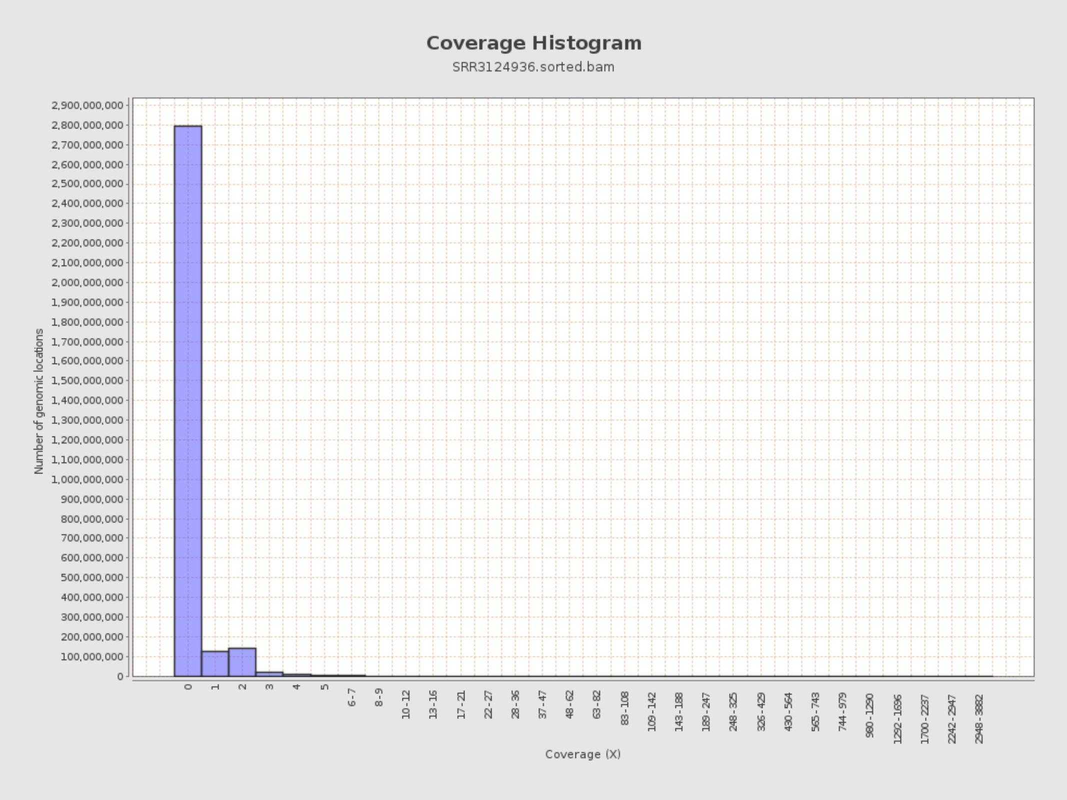
		bases	coverage	deviation
chr1	249250621	46563651	0.1868	3.6874
chr2	243199373	48390652	0.199	2.1882
chr3	198022430	41209619	0.2081	0.7123
chr4	191154276	30419098	0.1591	1.2045
chr5	180915260	31041411	0.1716	0.5946
chr6	171115067	36473485	0.2132	1.9517
chr7	159138663	41450824	0.2605	3.5807
chr8	146364022	31366063	0.2143	0.9167
chr9	141213431	21214018	0.1502	3.218
chr10	135534747	25954684	0.1915	6.9073
chr11	135006516	29157965	0.216	2.0428
chr12	133851895	23086435	0.1725	0.59
chr13	115169878	19698371	0.171	0.599
chr14	107349540	15779235	0.147	0.5833
chr15	102531392	16883855	0.1647	0.5905
chr16	90354753	14979408	0.1658	2.4927
chr17	81195210	13983897	0.1722	2.3853
chr18	78077248	16184069	0.2073	3.0548
chr19	59128983	9236046	0.1562	1.8218
chr20	63025520	12991233	0.2061	0.7655
chr21	48129895	7965271	0.1655	0.8422
chr22	51304566	4248477	0.0828	0.4115
chrMT	16571	132120	7.973	5.2691
chrX	155270560	19902347	0.1282	0.8191

chrY	59373566	5213730	0.0878	1.8452

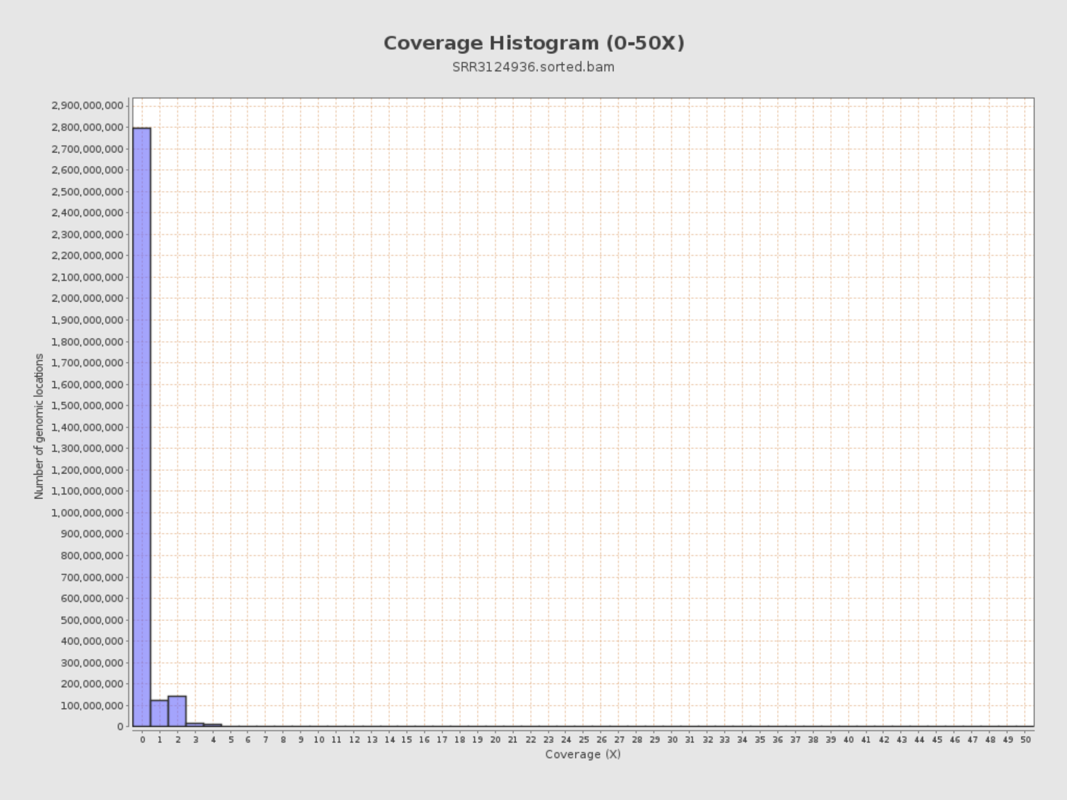
3. Results : Coverage across reference



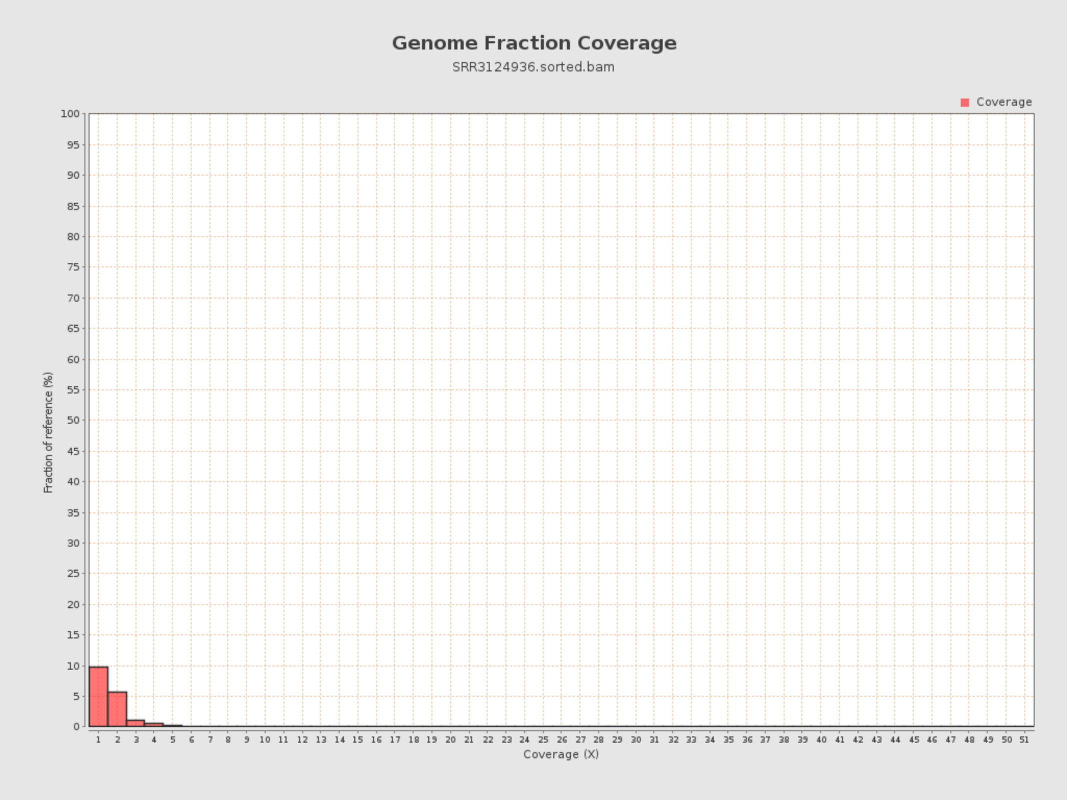
4. Results : Coverage Histogram



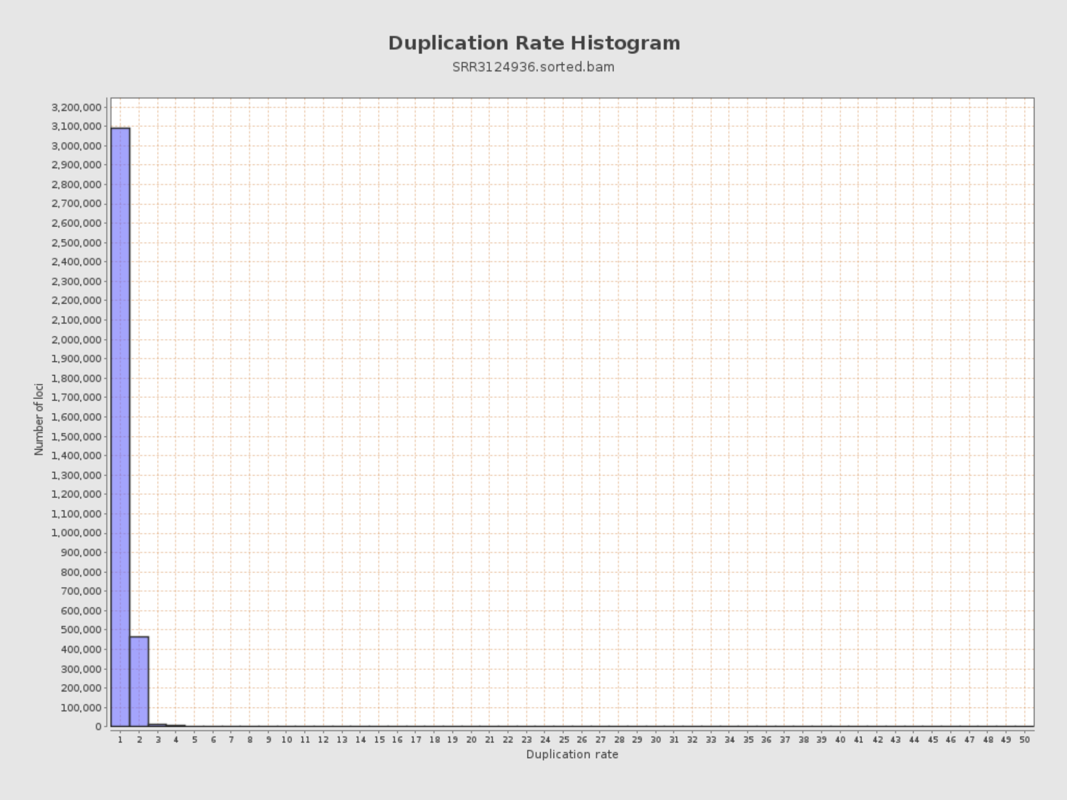
5. Results : Coverage Histogram (0-50X)



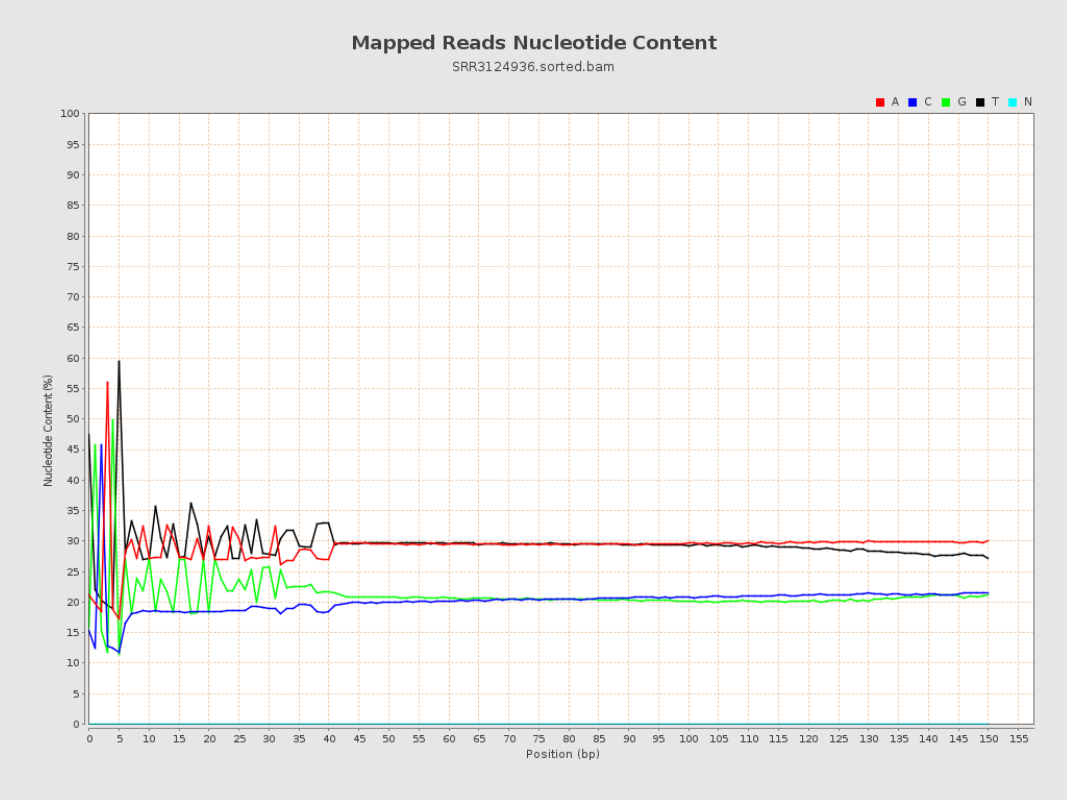
6. Results : Genome Fraction Coverage



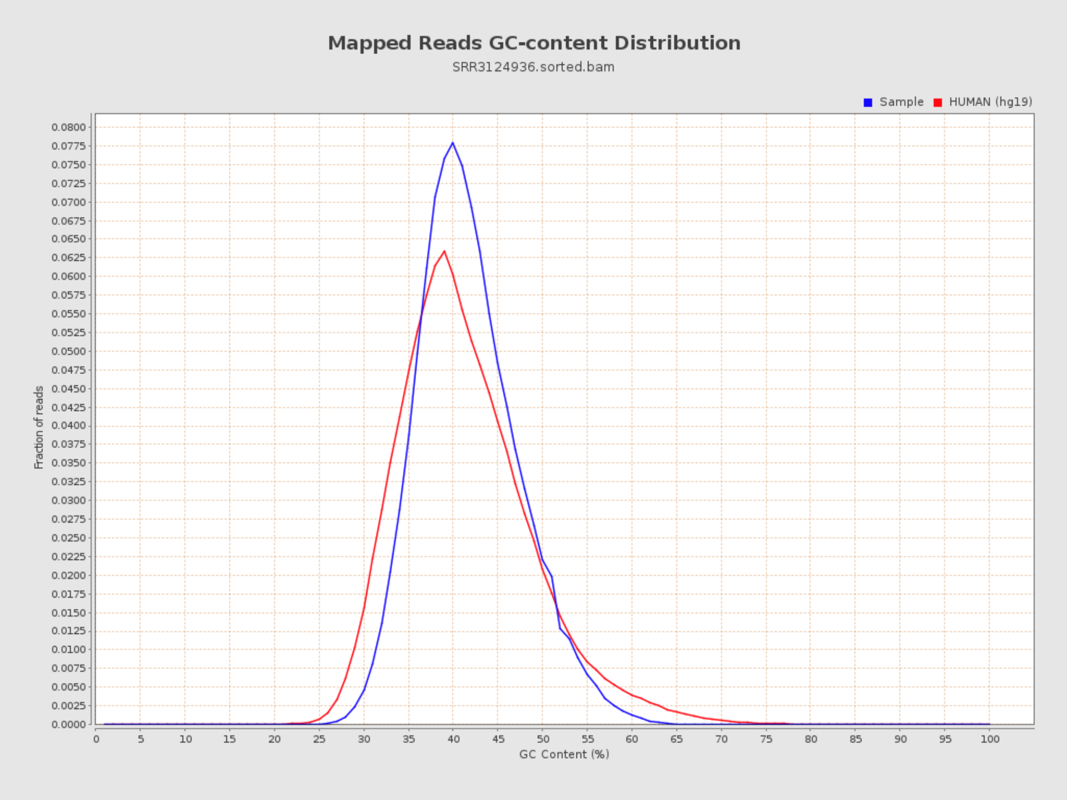
7. Results : Duplication Rate Histogram



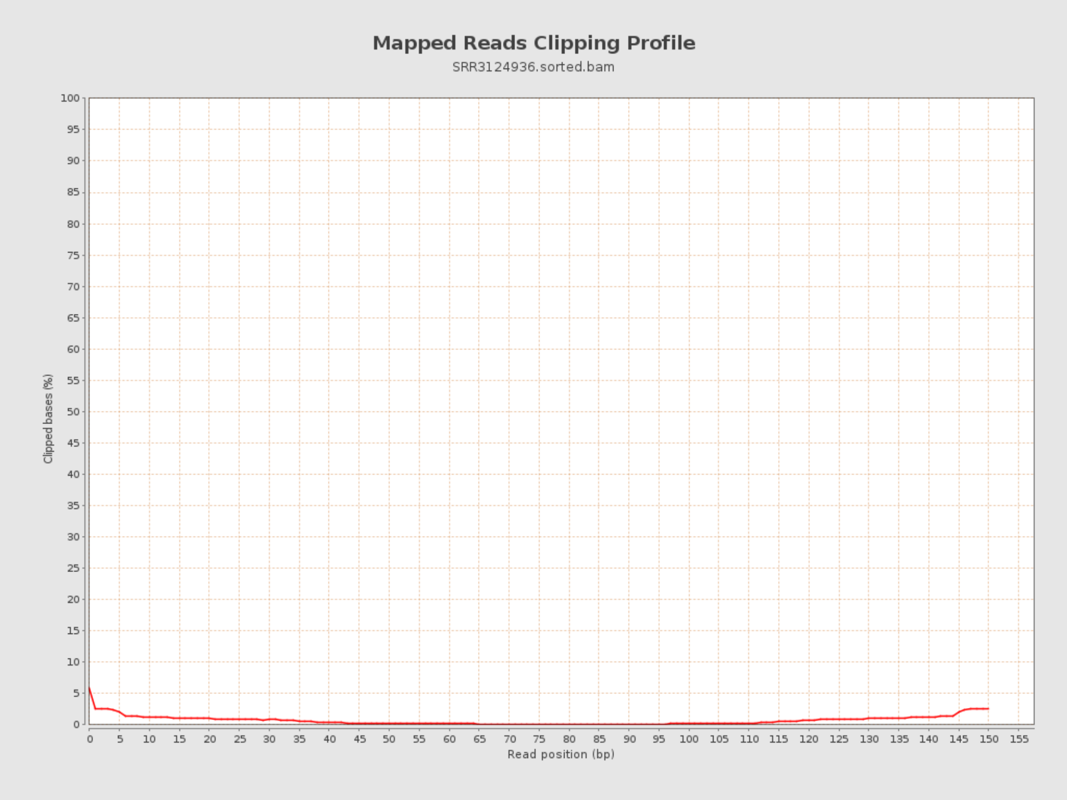
8. Results : Mapped Reads Nucleotide Content



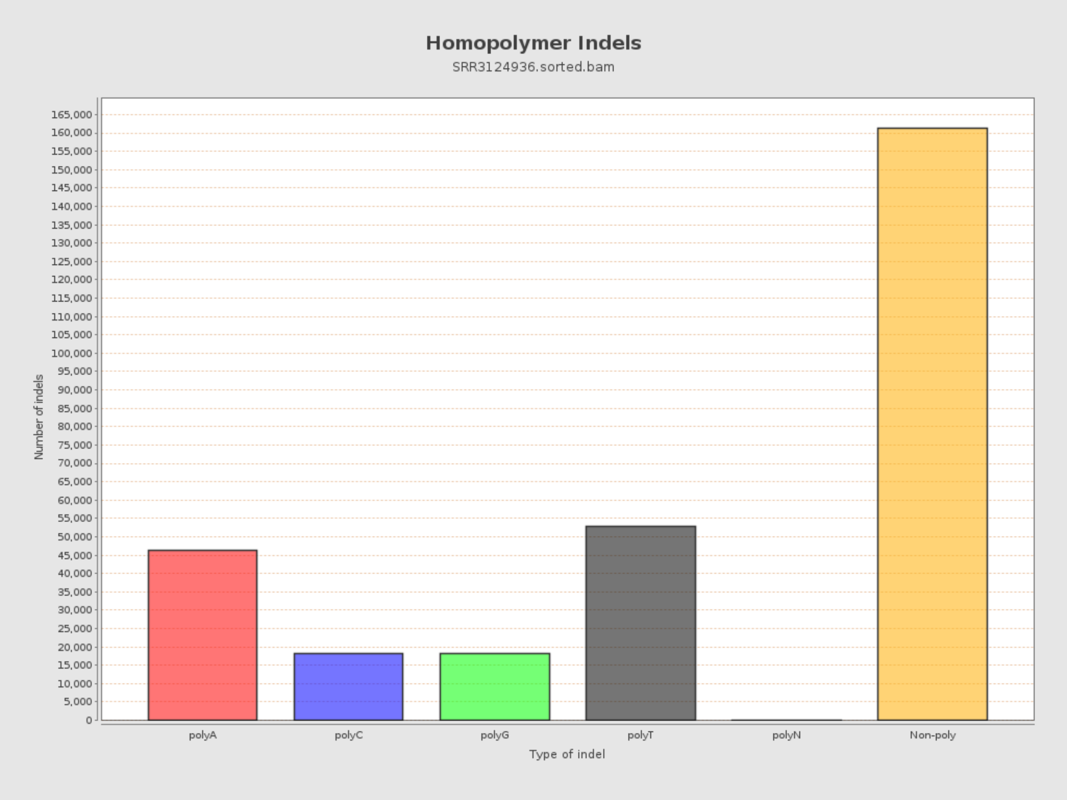
9. Results : Mapped Reads GC-content Distribution



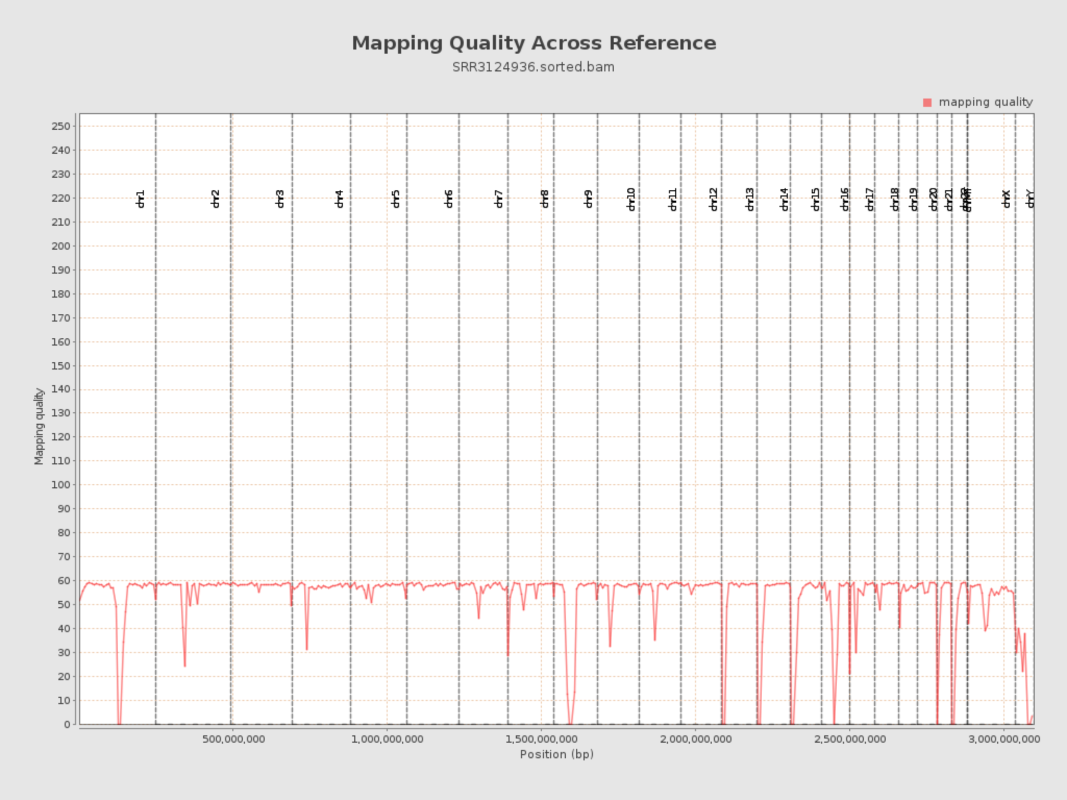
10. Results : Mapped Reads Clipping Profile



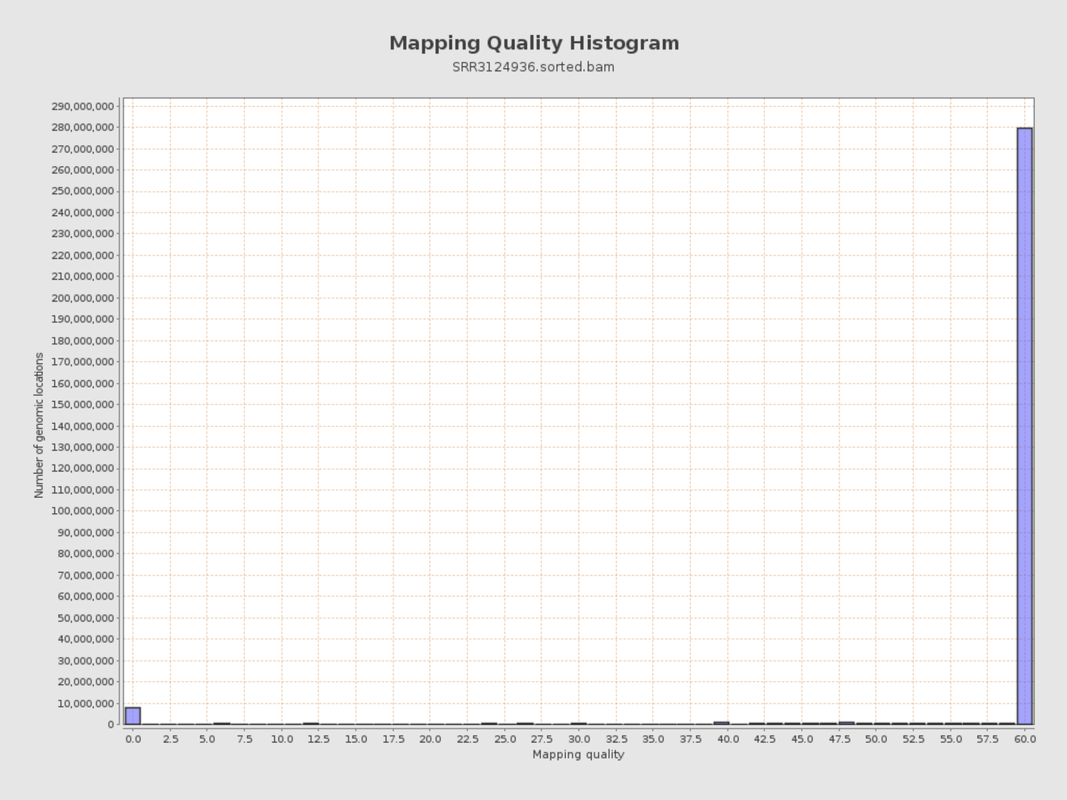
11. Results : Homopolymer Indels



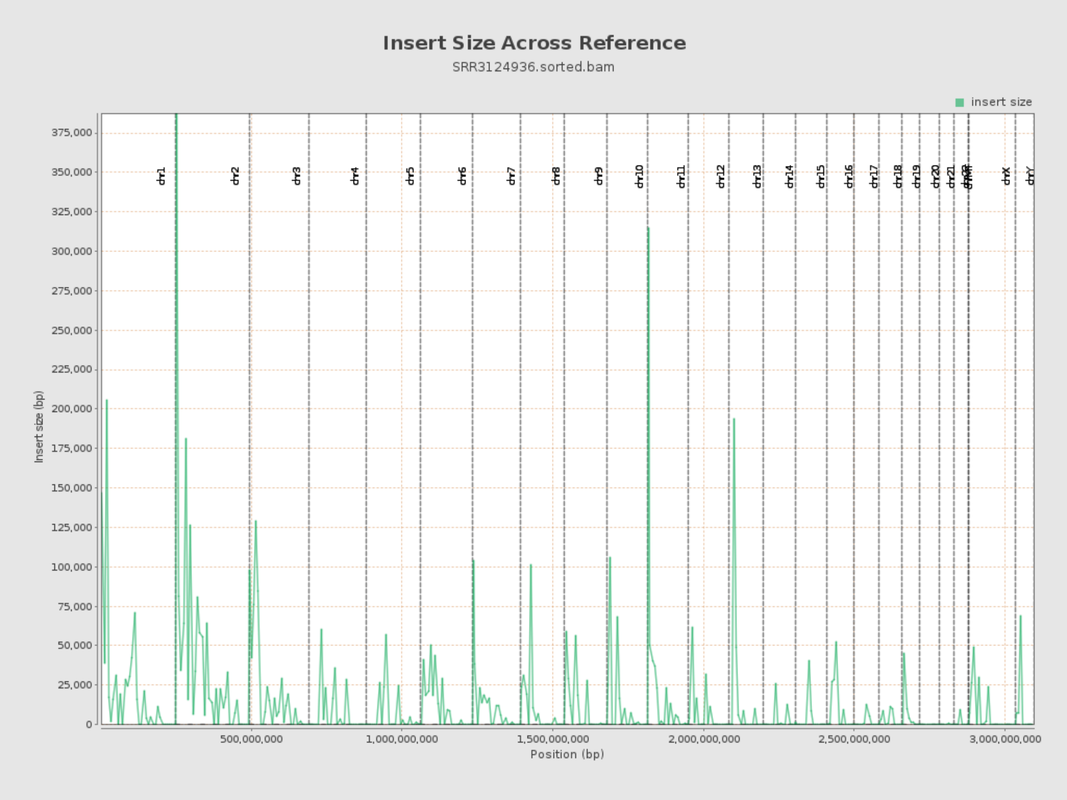
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram