Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 00:44:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124882.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_SRR3124882 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124882_1.fastq.gz SRR3124882_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 00:44:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124882.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,548,150
Mapped reads	2,503,078 / 98.23%
Unmapped reads	45,072 / 1.77%
Mapped paired reads	2,503,078 / 98.23%
Mapped reads, first in pair	1,252,972 / 49.17%
Mapped reads, second in pair	1,250,106 / 49.06%
Mapped reads, both in pair	2,491,278 / 97.77%
Mapped reads, singletons	11,800 / 0.46%
Secondary alignments	0
Supplementary alignments	37,934 / 1.49%
Read min/max/mean length	30 / 151 / 151.71
Duplicated reads (estimated)	403,603 / 15.84%
Duplication rate	14.91%
Clipped reads	1,890,736 / 74.2%

2.2. ACGT Content

Number/percentage of A's	96,281,693 / 28.89%
Number/percentage of C's	67,312,069 / 20.19%
Number/percentage of T's	97,673,318 / 29.3%
Number/percentage of G's	72,016,617 / 21.61%
Number/percentage of N's	27,490 / 0.01%

GC Percentage	41.8%

2.3. Coverage

Mean	0.1078
Standard Deviation	1.3851

2.4. Mapping Quality

Mean Mapping Quality	53.34

2.5. Insert size

Mean	92,207.77
Standard Deviation	2,892,631.95
P25/Median/P75	136 / 169 / 215

2.6. Mismatches and indels

General error rate	1.19%
Mismatches	3,786,254
Insertions	65,904
Mapped reads with at least one insertion	2.47%
Deletions	133,288
Mapped reads with at least one deletion	5.1%
Homopolymer indels	45.65%

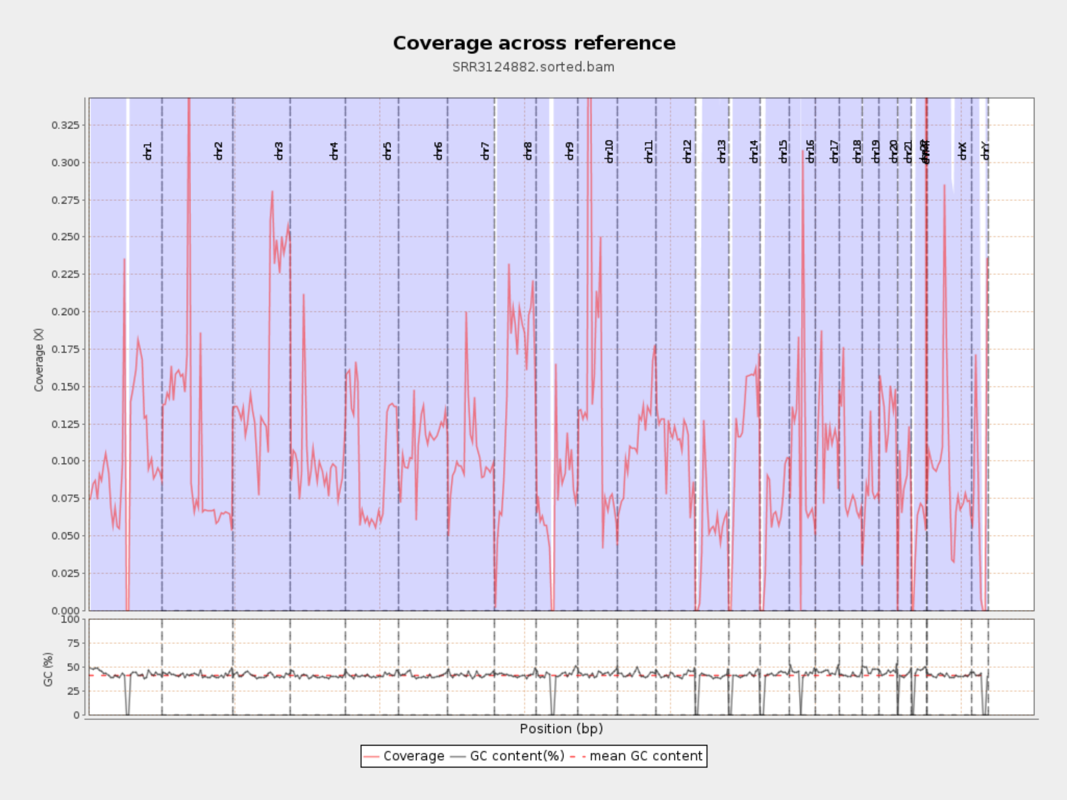
2.7. Chromosome stats

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

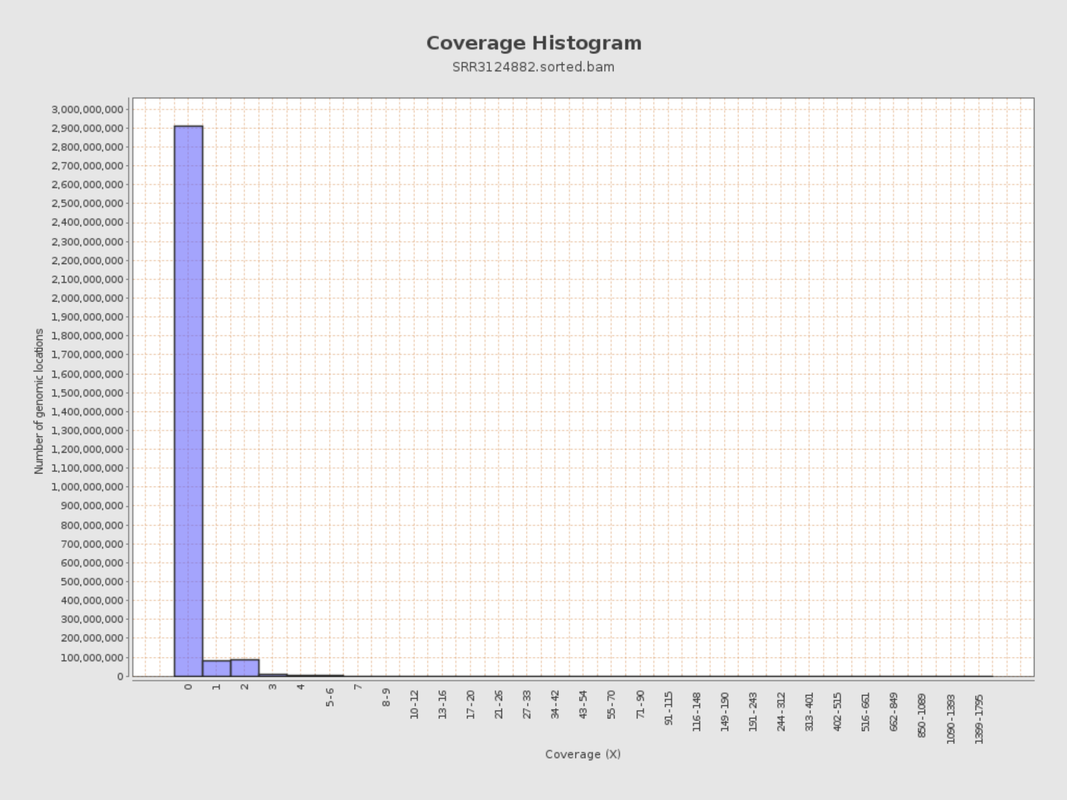
		bases	coverage	deviation
chr1	249250621	25127625	0.1008	1.3524
chr2	243199373	27534947	0.1132	2.1056
chr3	198022430	33481461	0.1691	0.6157
chr4	191154276	18703861	0.0978	0.8376
chr5	180915260	18559207	0.1026	0.4669
chr6	171115067	19129822	0.1118	0.764
chr7	159138663	16745334	0.1052	1.4523
chr8	146364022	22420195	0.1532	0.7312
chr9	141213431	10573750	0.0749	1.7996
chr10	135534747	20483479	0.1511	3.8766
chr11	135006516	15467006	0.1146	0.7943
chr12	133851895	15089694	0.1127	0.476
chr13	115169878	5926170	0.0515	0.3167
chr14	107349540	12458505	0.1161	0.5067
chr15	102531392	6384321	0.0623	0.35
chr16	90354753	9768598	0.1081	1.7551
chr17	81195210	9433985	0.1162	1.1263
chr18	78077248	7037158	0.0901	1.7922
chr19	59128983	4778210	0.0808	0.8528
chr20	63025520	8450606	0.1341	0.564
chr21	48129895	3997260	0.0831	0.6241
chr22	51304566	2436455	0.0475	0.333
chrMT	16571	283608	17.1147	10.8457
chrX	155270560	14690671	0.0946	0.5408

chrY	59373566	4619035	0.0778	1.8687

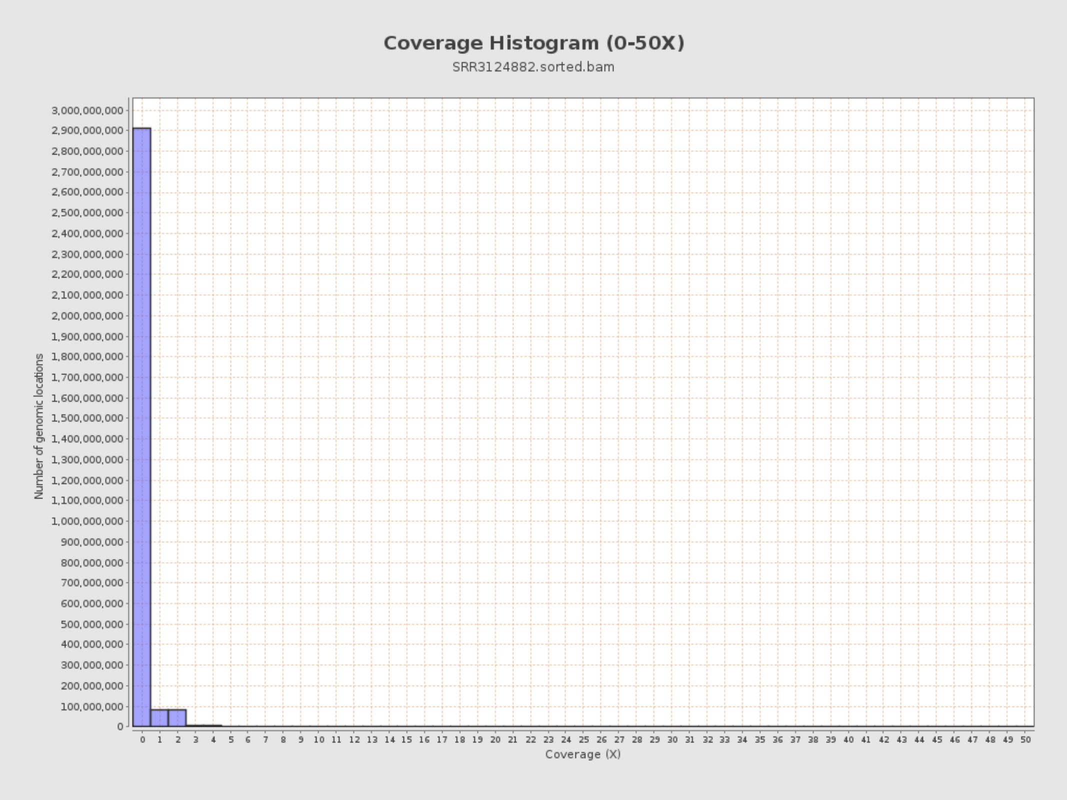
3. Results : Coverage across reference



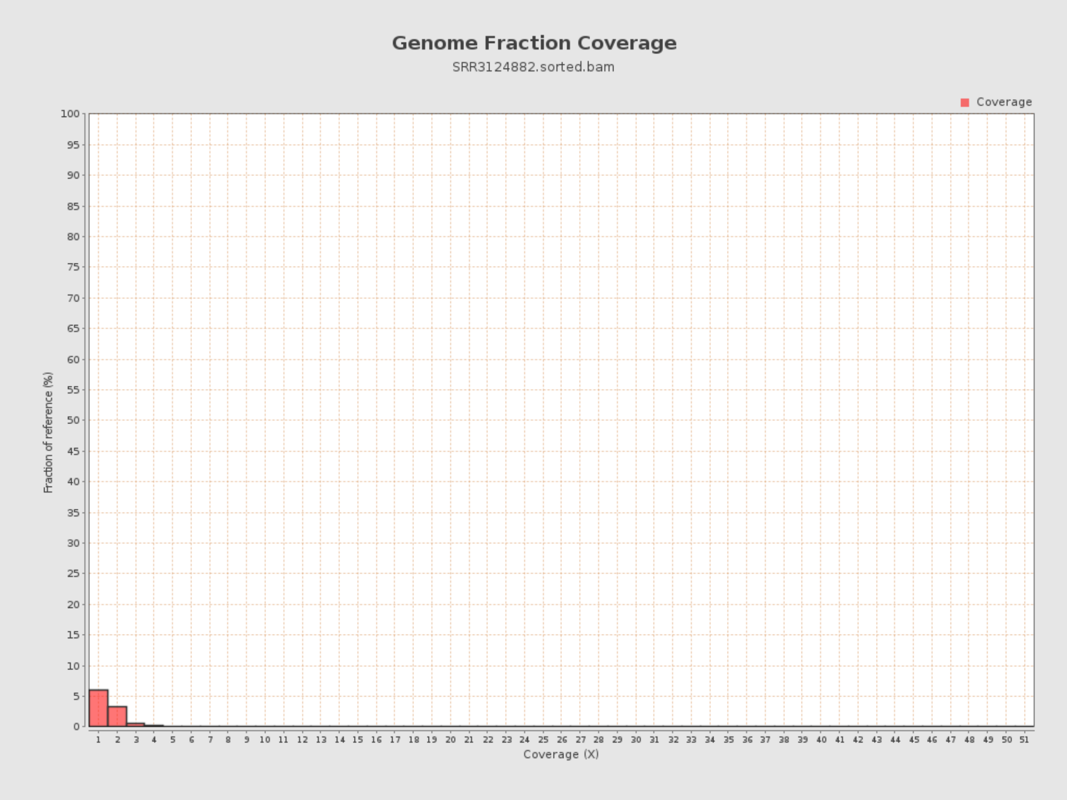
4. Results : Coverage Histogram



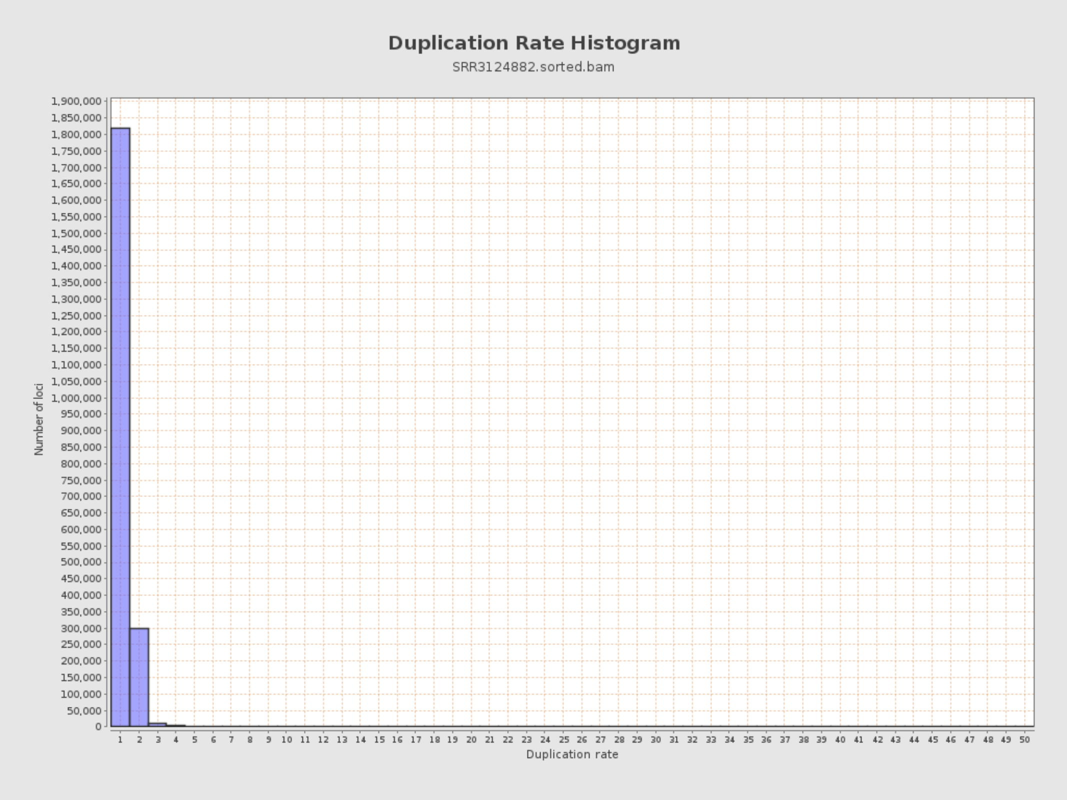
5. Results : Coverage Histogram (0-50X)



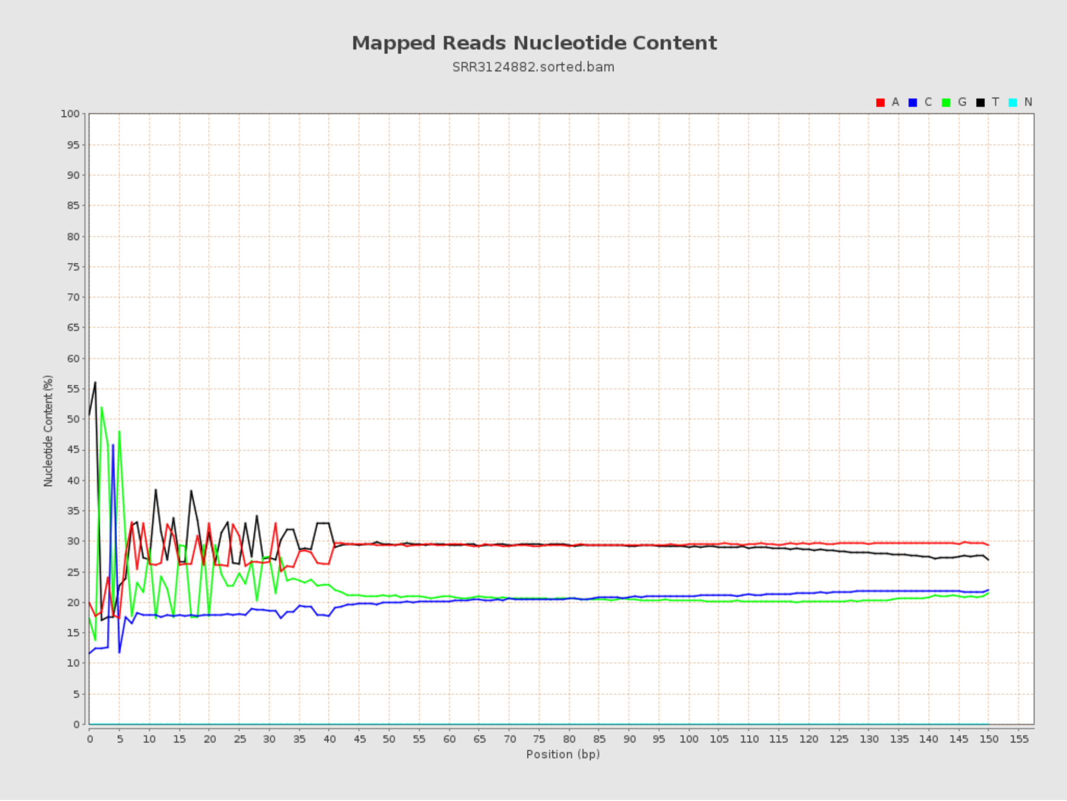
6. Results : Genome Fraction Coverage



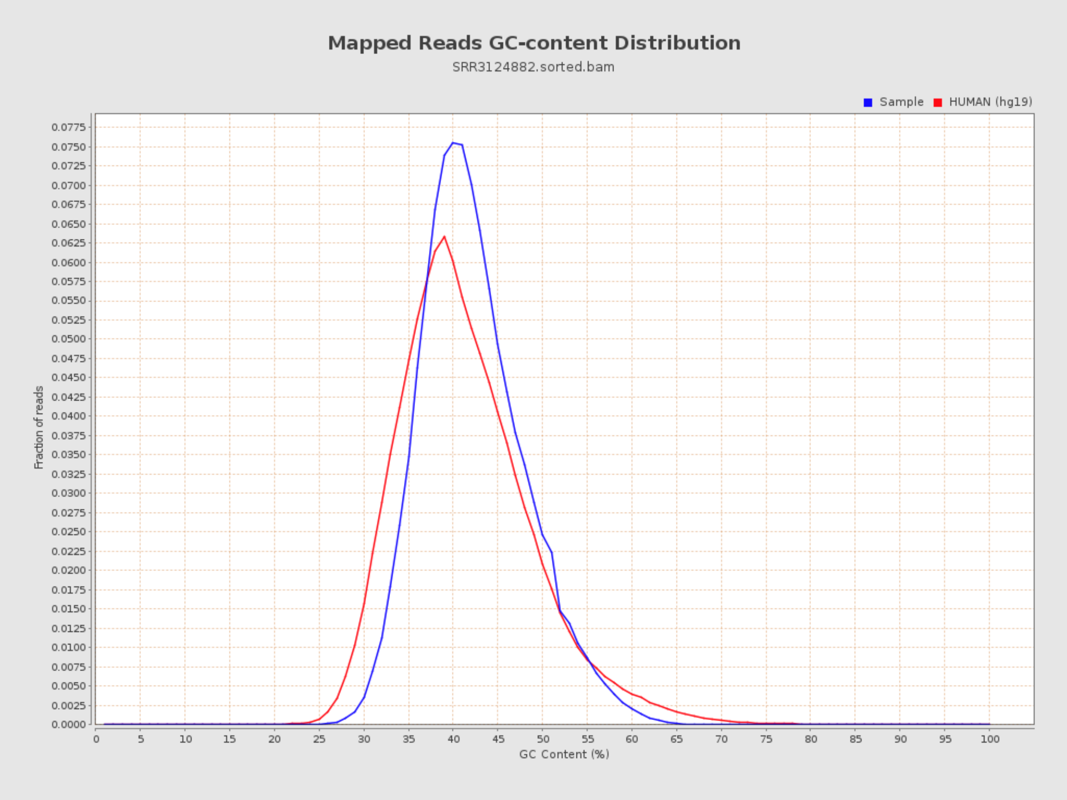
7. Results : Duplication Rate Histogram



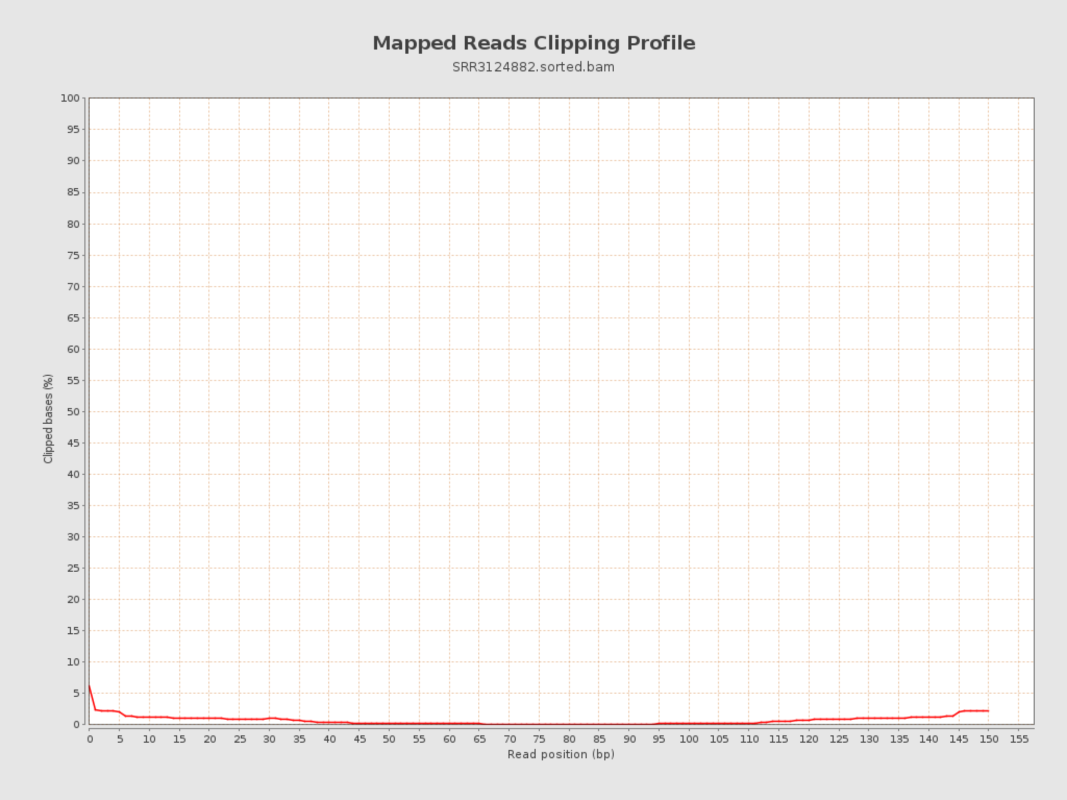
8. Results : Mapped Reads Nucleotide Content



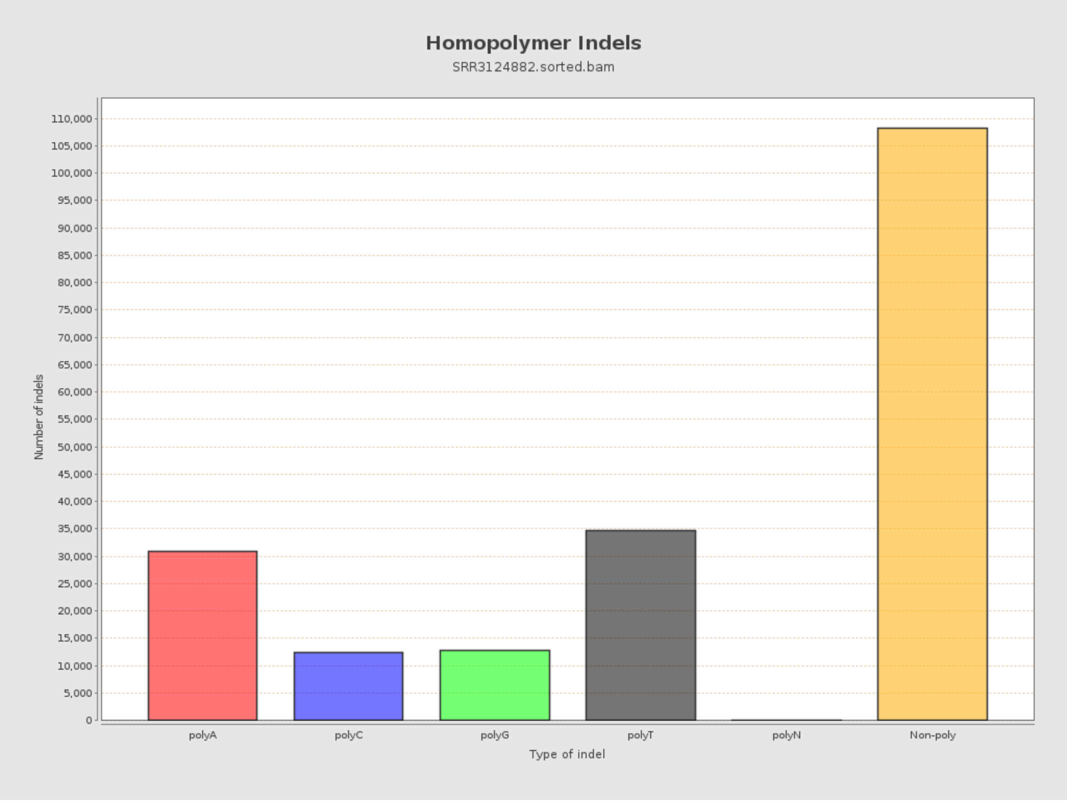
9. Results : Mapped Reads GC-content Distribution



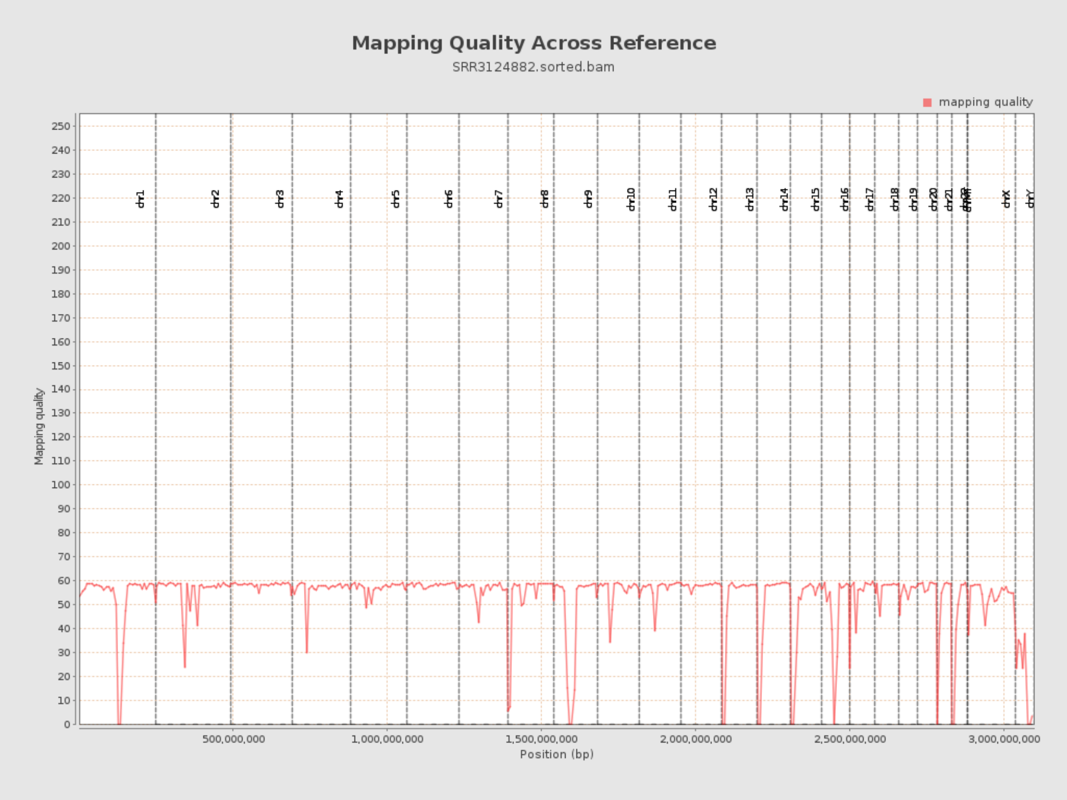
10. Results : Mapped Reads Clipping Profile



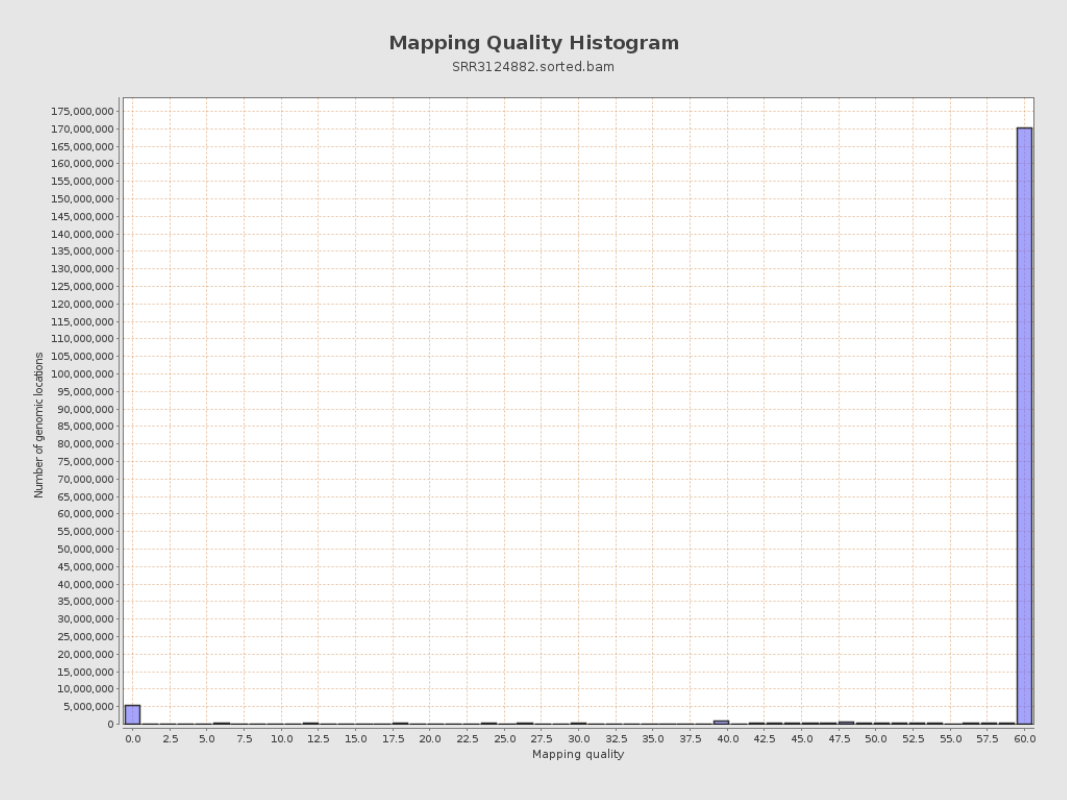
11. Results : Homopolymer Indels



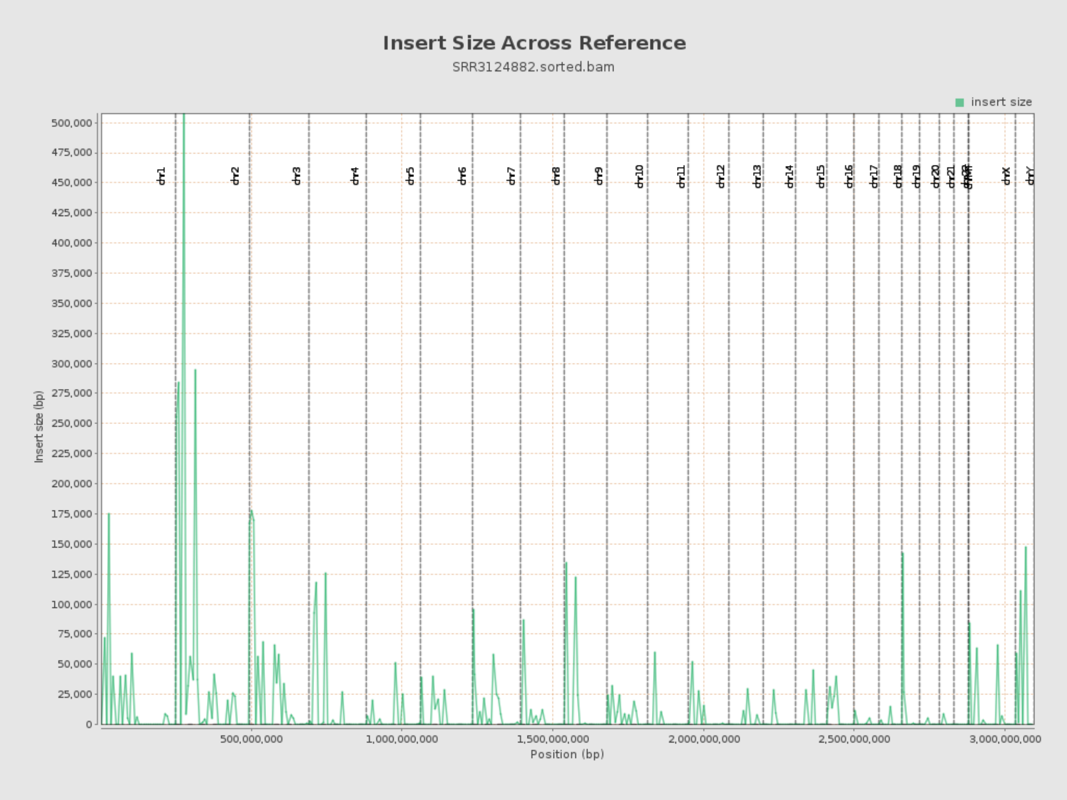
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram