Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/21 15:18:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504596.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_SRR504596 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504596_1.fastq.gz SRR504596_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 21 15:18:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504596.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	364,671,172
Mapped reads	348,913,207 / 95.68%
Unmapped reads	15,757,965 / 4.32%
Mapped paired reads	348,913,207 / 95.68%
Mapped reads, first in pair	174,584,715 / 47.87%
Mapped reads, second in pair	174,328,492 / 47.8%
Mapped reads, both in pair	345,965,020 / 94.87%
Mapped reads, singletons	2,948,187 / 0.81%
Secondary alignments	0
Supplementary alignments	1,018,060 / 0.28%
Read min/max/mean length	30 / 100 / 100.11
Duplicated reads (estimated)	76,794,945 / 21.06%
Duplication rate	18.03%
Clipped reads	54,696,666 / 15%

2.2. ACGT Content

Number/percentage of A's	9,521,361,583 / 28.41%
Number/percentage of C's	7,187,358,030 / 21.45%
Number/percentage of T's	9,426,271,120 / 28.13%
Number/percentage of G's	7,364,645,828 / 21.98%
Number/percentage of N's	9,385,592 / 0.03%

GC Percentage	43.43%

2.3. Coverage

Mean	10.8279
Standard Deviation	95.3997

2.4. Mapping Quality

Mean Mapping Quality	53.37

2.5. Insert size

Mean	34,124.92
Standard Deviation	1,752,241.81
P25/Median/P75	132 / 188 / 246

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	186,301,201
Insertions	3,387,822
Mapped reads with at least one insertion	0.93%
Deletions	4,157,302
Mapped reads with at least one deletion	1.15%
Homopolymer indels	40.41%

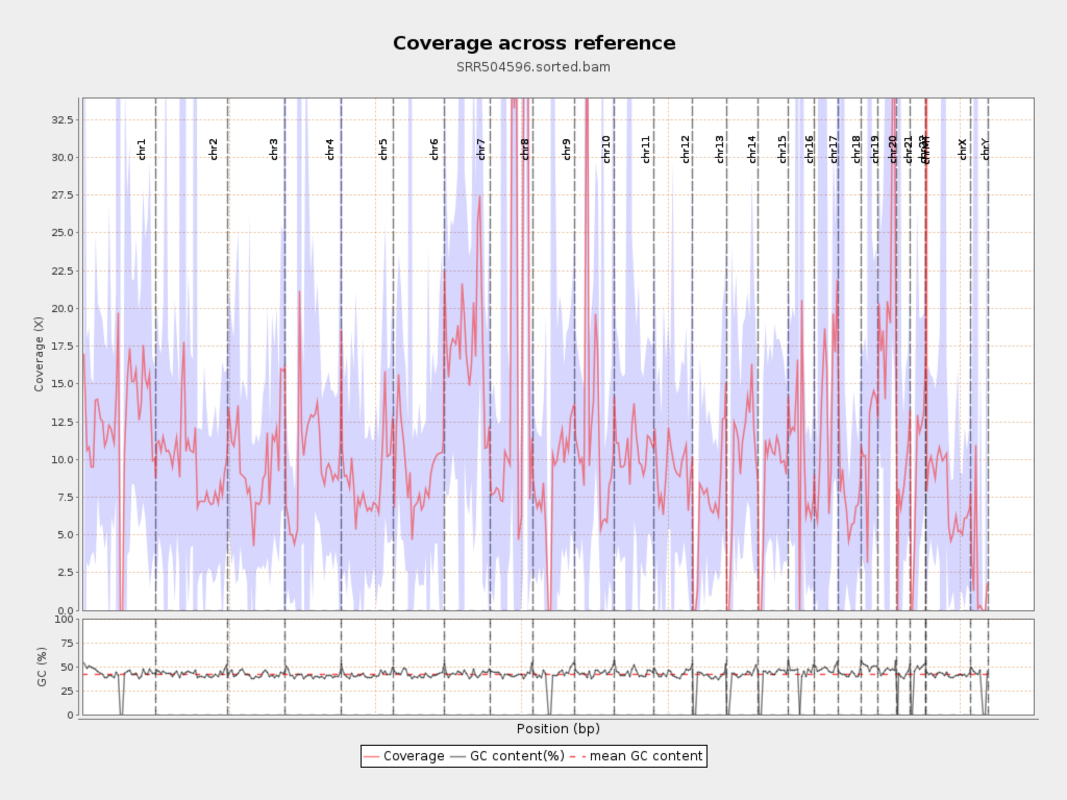
2.7. Chromosome stats

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

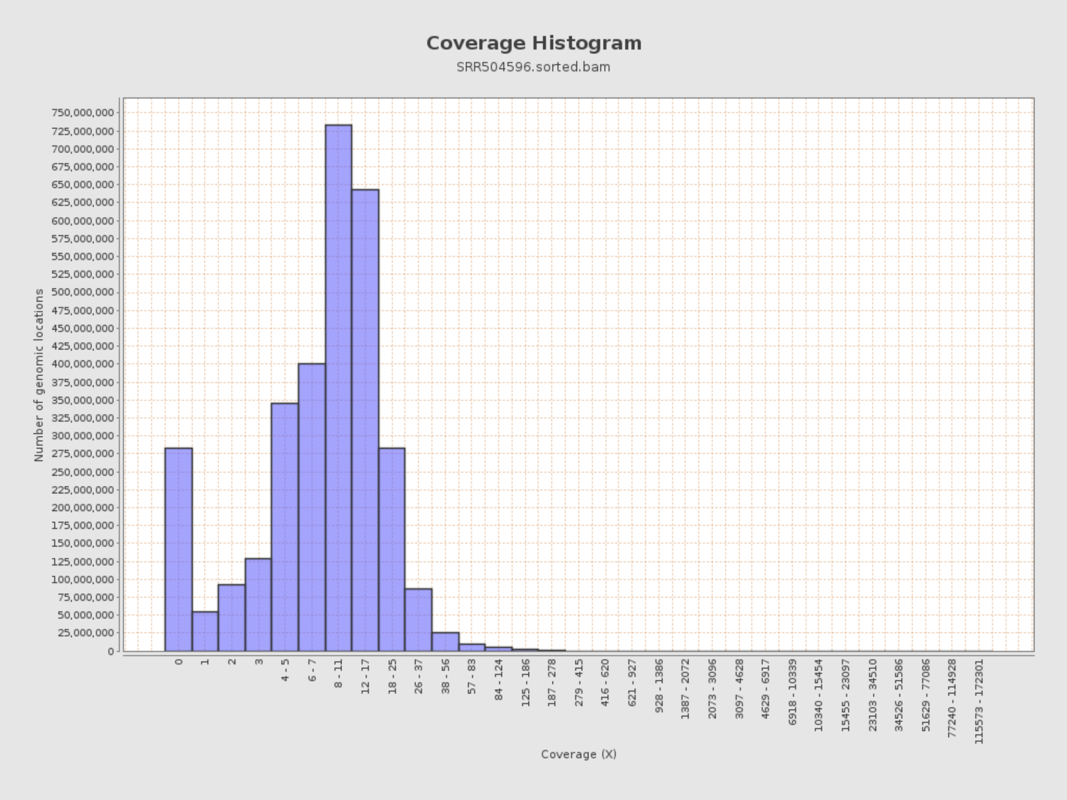
		bases	coverage	deviation
chr1	249250621	3118128053	12.51	173.0609
chr2	243199373	2366526861	9.7308	57.6503
chr3	198022430	1981862752	10.0083	16.5716
chr4	191154276	1899223195	9.9356	114.4001
chr5	180915260	1583088398	8.7504	10.272
chr6	171115067	1570781895	9.1797	22.6115
chr7	159138663	2827866375	17.7698	137.3831
chr8	146364022	2947042490	20.135	67.1582
chr9	141213431	1208431198	8.5575	60.9038
chr10	135534747	1631621129	12.0384	258.4859
chr11	135006516	1439079073	10.6593	38.8477
chr12	133851895	1252583884	9.358	9.0452
chr13	115169878	813961785	7.0675	6.5148
chr14	107349540	1087549980	10.1309	9.5329
chr15	102531392	875590320	8.5397	7.3241
chr16	90354753	931473592	10.3091	73.5238
chr17	81195210	1039979014	12.8084	45.1519
chr18	78077248	571818967	7.3238	94.4147
chr19	59128983	670431237	11.3385	89.3207
chr20	63025520	1409029956	22.3565	29.2587
chr21	48129895	402260656	8.3578	40.2655
chr22	51304566	452229333	8.8146	9.465
chrMT	16571	119926369	7,237.1232	1,547.8824
chrX	155270560	1190582369	7.6678	18.7397

chrY	59373566	128697060	2.1676	116.0726

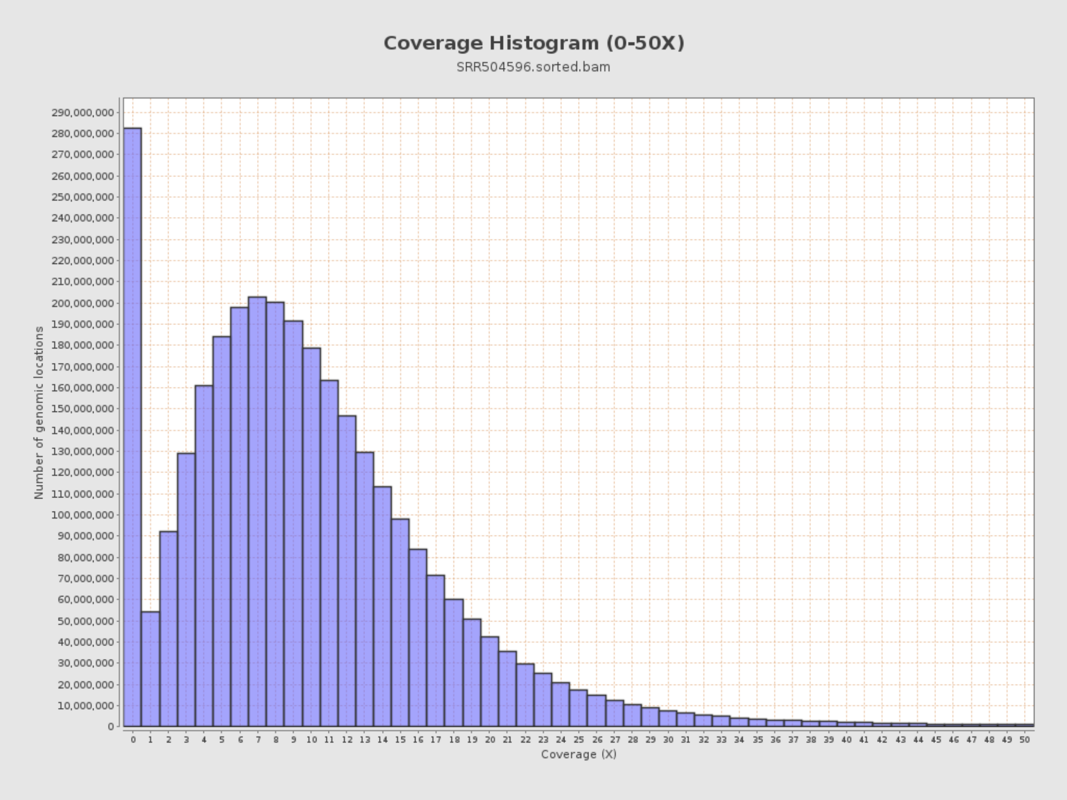
3. Results : Coverage across reference



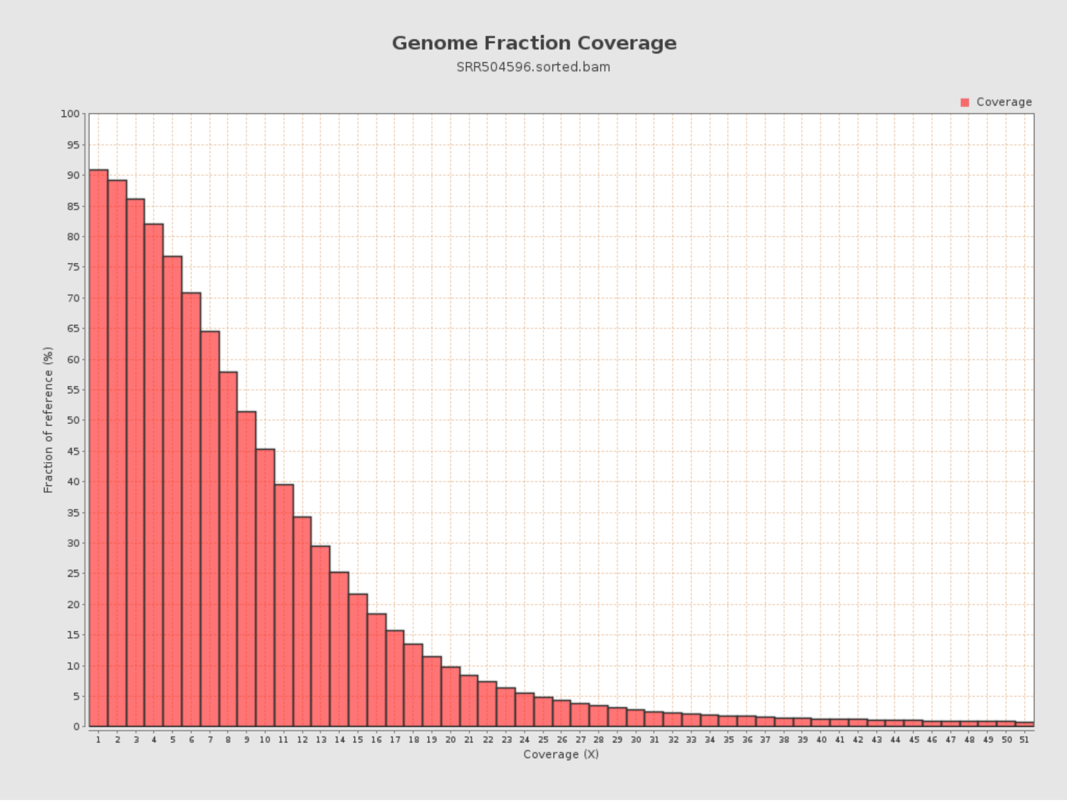
4. Results : Coverage Histogram



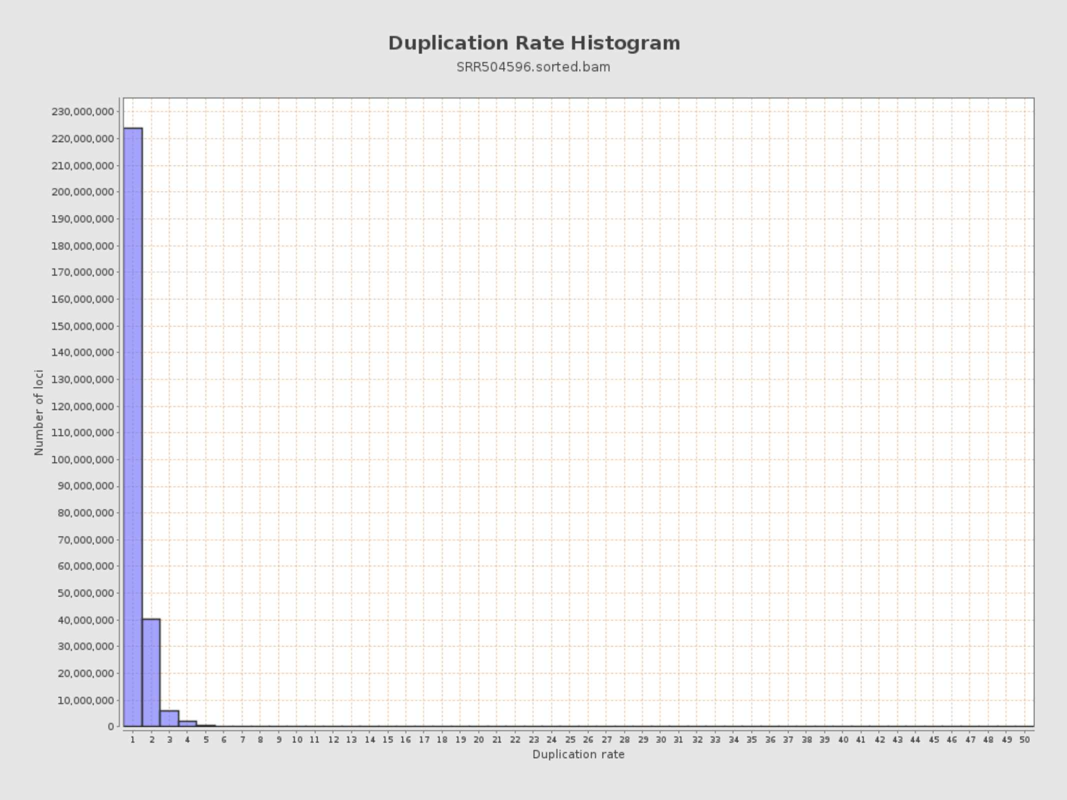
5. Results : Coverage Histogram (0-50X)



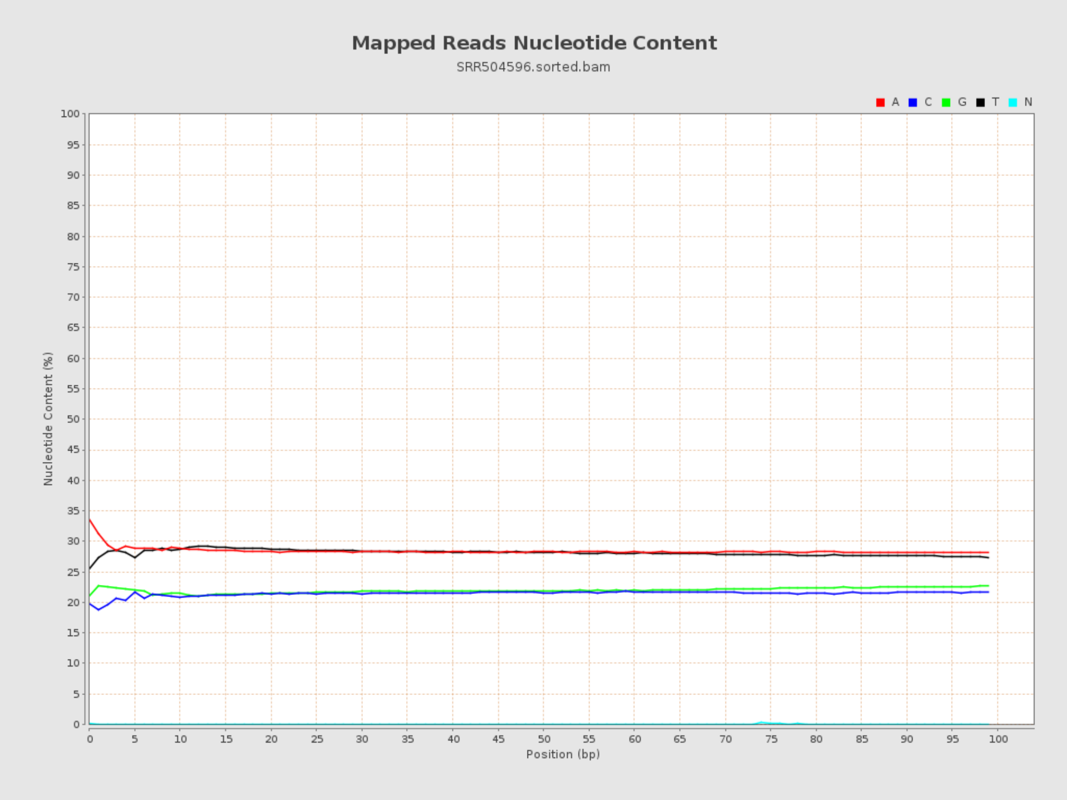
6. Results : Genome Fraction Coverage



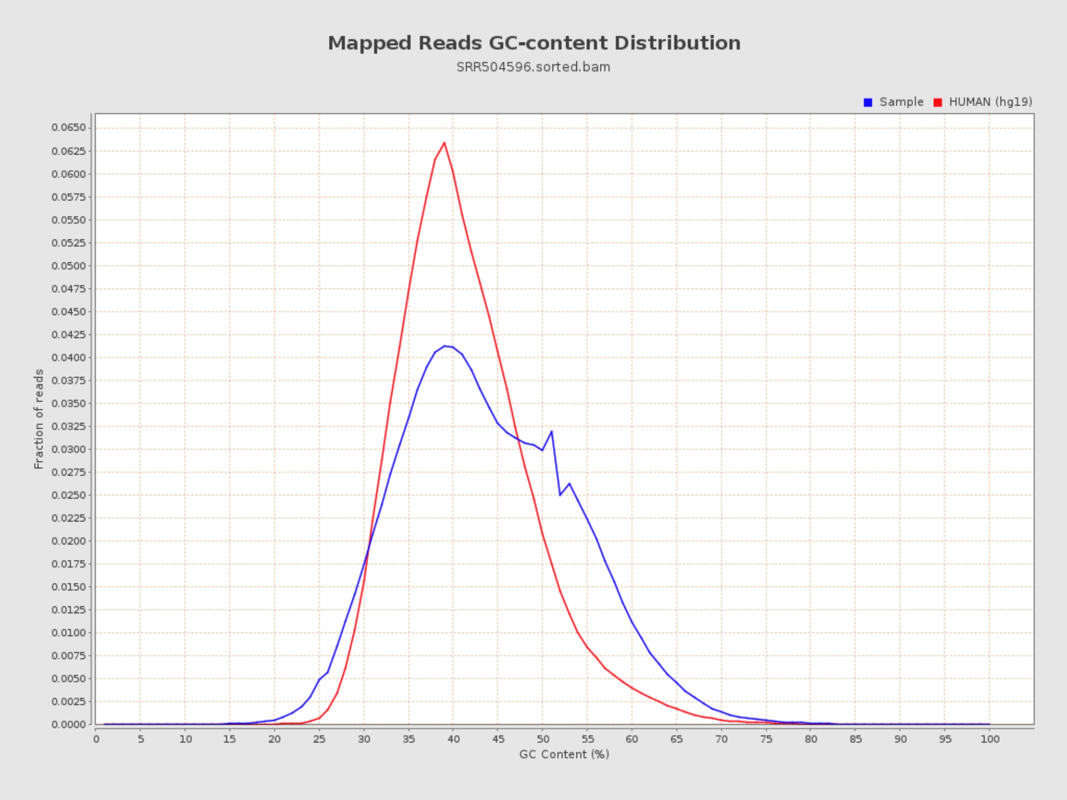
7. Results : Duplication Rate Histogram



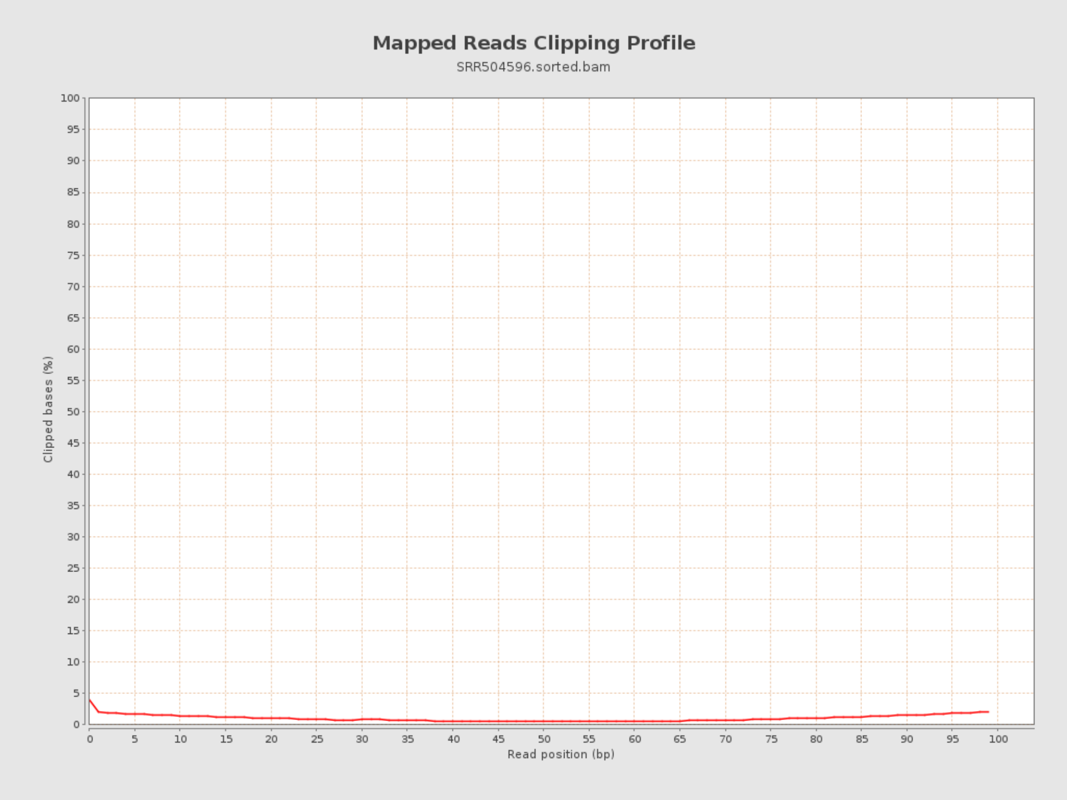
8. Results : Mapped Reads Nucleotide Content



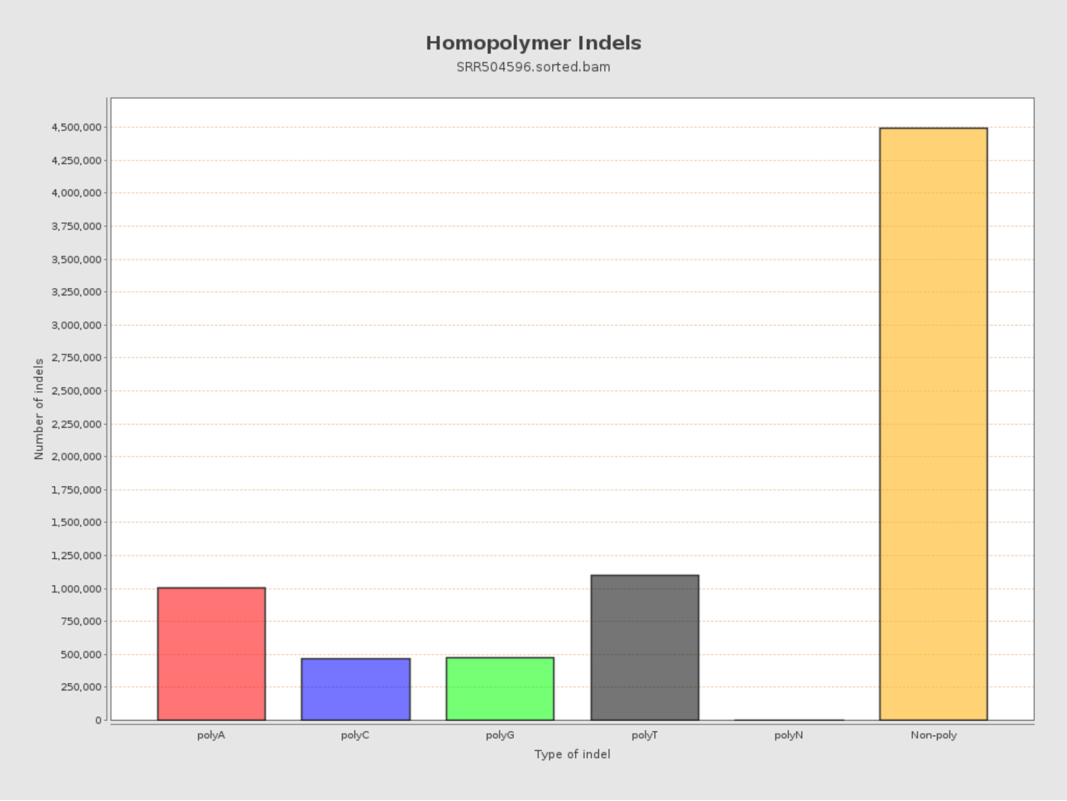
9. Results : Mapped Reads GC-content Distribution



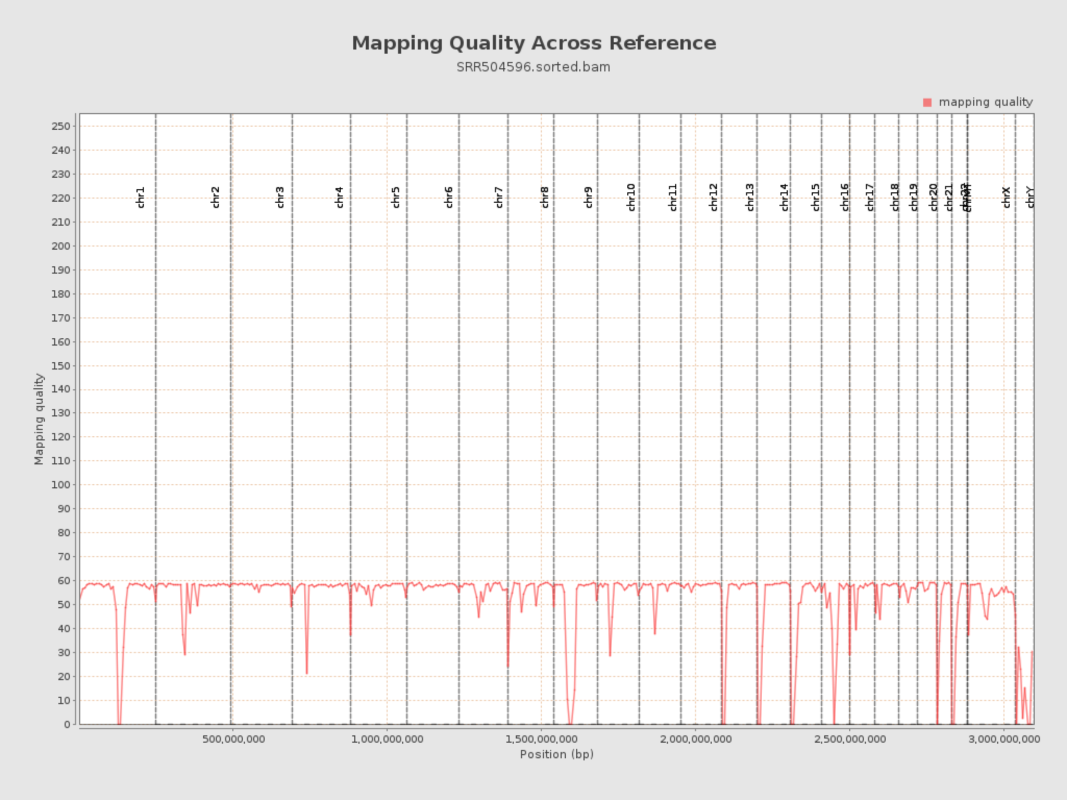
10. Results : Mapped Reads Clipping Profile



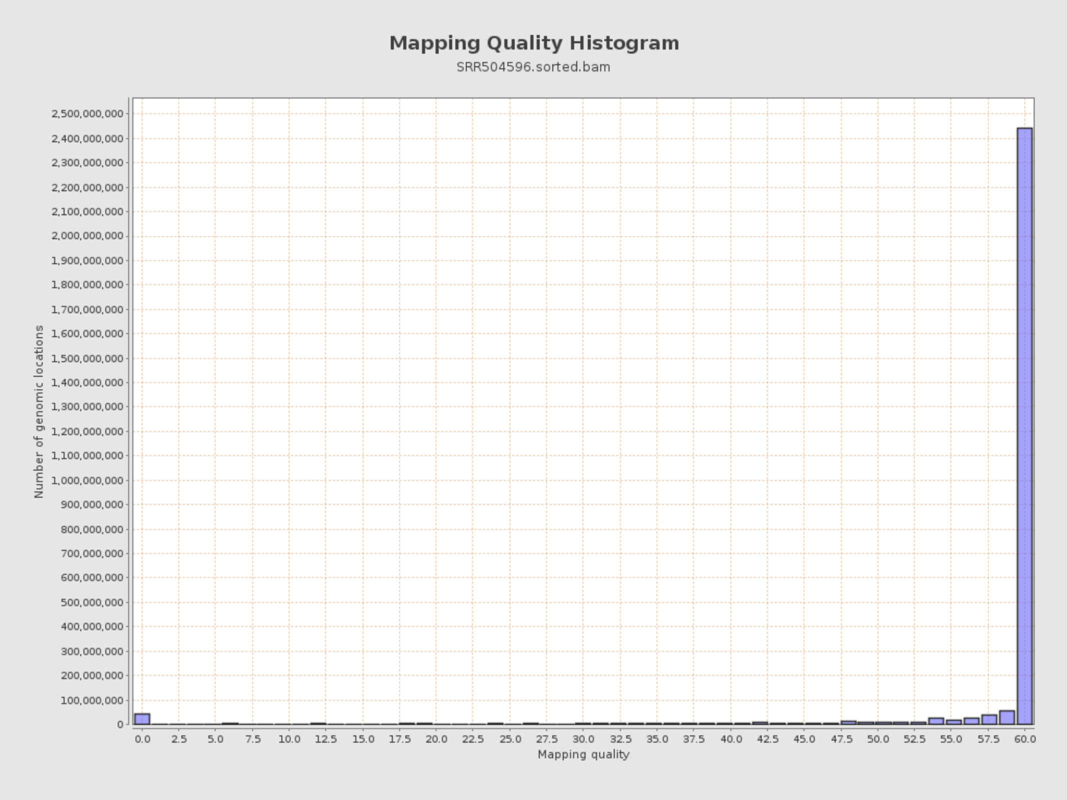
11. Results : Homopolymer Indels



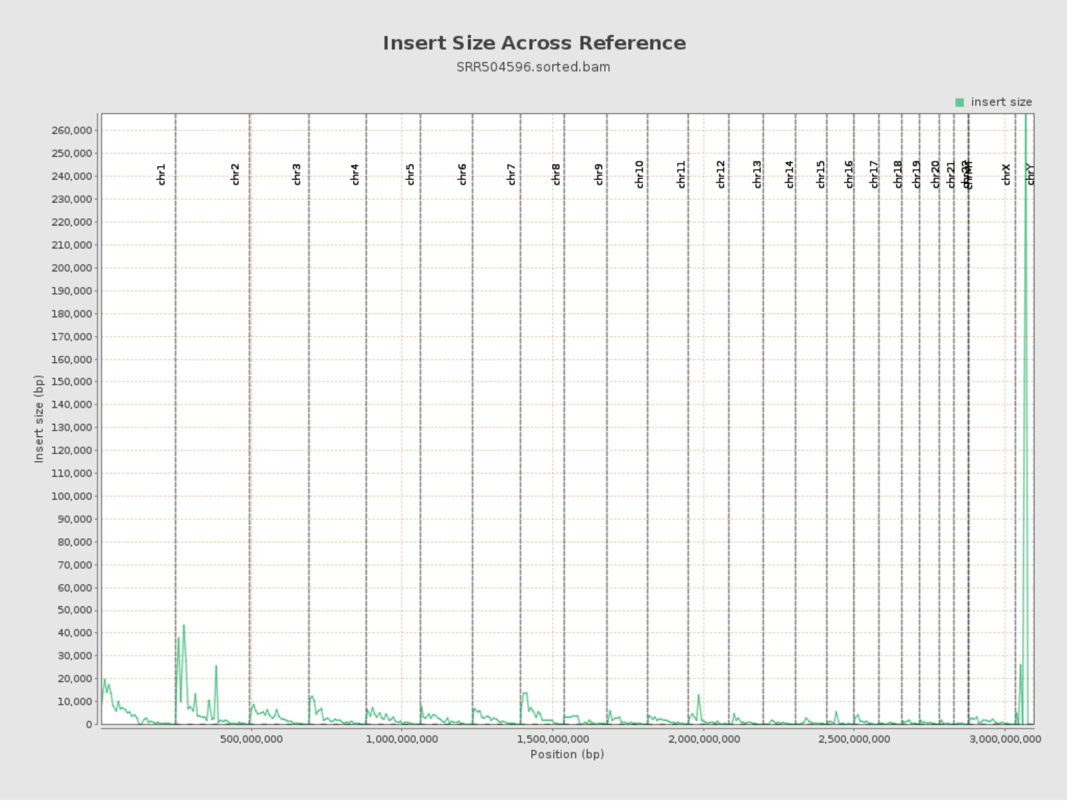
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram