Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/02 10:15:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504640.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_SRR504640 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504640_1.fastq.gz SRR504640_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Jan 02 10:15:51 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504640.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	438,671,610
Mapped reads	399,305,174 / 91.03%
Unmapped reads	39,366,436 / 8.97%
Mapped paired reads	399,305,174 / 91.03%
Mapped reads, first in pair	204,377,088 / 46.59%
Mapped reads, second in pair	194,928,086 / 44.44%
Mapped reads, both in pair	386,232,908 / 88.05%
Mapped reads, singletons	13,072,266 / 2.98%
Secondary alignments	0
Supplementary alignments	3,168,036 / 0.72%
Read min/max/mean length	30 / 100 / 100.27
Duplicated reads (estimated)	108,851,517 / 24.81%
Duplication rate	24.06%
Clipped reads	228,698,662 / 52.13%

2.2. ACGT Content

Number/percentage of A's	8,172,746,578 / 25.61%
Number/percentage of C's	7,275,813,180 / 22.8%
Number/percentage of T's	8,319,274,260 / 26.07%
Number/percentage of G's	7,646,541,288 / 23.96%
Number/percentage of N's	499,976,206 / 1.57%

GC Percentage	46.76%

2.3. Coverage

Mean	10.3118
Standard Deviation	25.4028

2.4. Mapping Quality

Mean Mapping Quality	53.04

2.5. Insert size

Mean	63,201.93
Standard Deviation	2,449,505.91
P25/Median/P75	314 / 348 / 384

2.6. Mismatches and indels

General error rate	0.92%
Mismatches	286,057,698
Insertions	4,168,198
Mapped reads with at least one insertion	1.02%
Deletions	4,056,734
Mapped reads with at least one deletion	0.99%
Homopolymer indels	35.07%

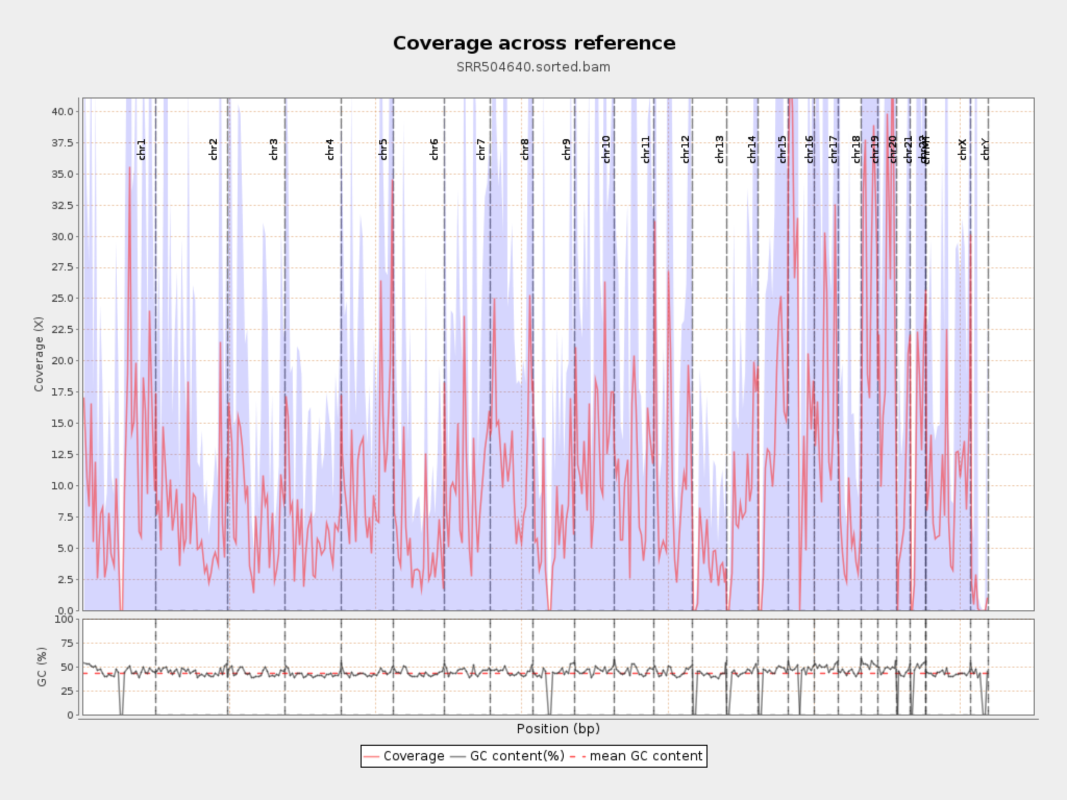
2.7. Chromosome stats

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

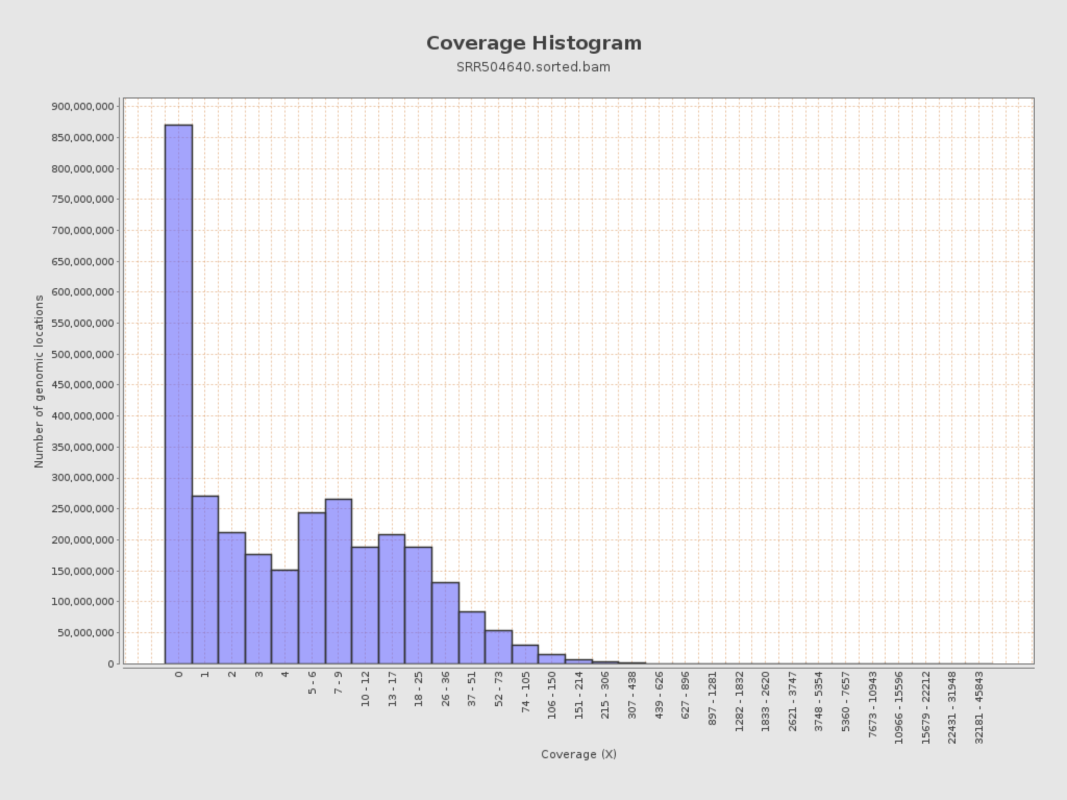
		bases	coverage	deviation
chr1	249250621	2694502401	10.8104	22.3383
chr2	243199373	1793960082	7.3765	36.9685
chr3	198022430	1578356771	7.9706	15.7638
chr4	191154276	1231445615	6.4422	11.3897
chr5	180915260	2164091594	11.9619	20.0565
chr6	171115067	844250149	4.9338	11.0868
chr7	159138663	1638549606	10.2964	18.5013
chr8	146364022	1857659195	12.692	33.4614
chr9	141213431	880531027	6.2355	13.9226
chr10	135534747	1840589330	13.5802	22.7471
chr11	135006516	1411486293	10.4549	19.9887
chr12	133851895	1527561711	11.4123	23.719
chr13	115169878	416406789	3.6156	7.1261
chr14	107349540	962938335	8.9701	18.5008
chr15	102531392	1299299190	12.6722	23.8184
chr16	90354753	1892366474	20.9437	33.6316
chr17	81195210	1414438635	17.4202	30.529
chr18	78077248	430633260	5.5155	43.9423
chr19	59128983	1660235498	28.0782	56.39
chr20	63025520	1600998635	25.4024	36.1279
chr21	48129895	483957072	10.0552	19.5053
chr22	51304566	651376456	12.6963	26.9828
chrMT	16571	369348	22.2888	18.4589
chrX	155270560	1600425268	10.3073	18.5583

chrY	59373566	45791449	0.7712	26.6351

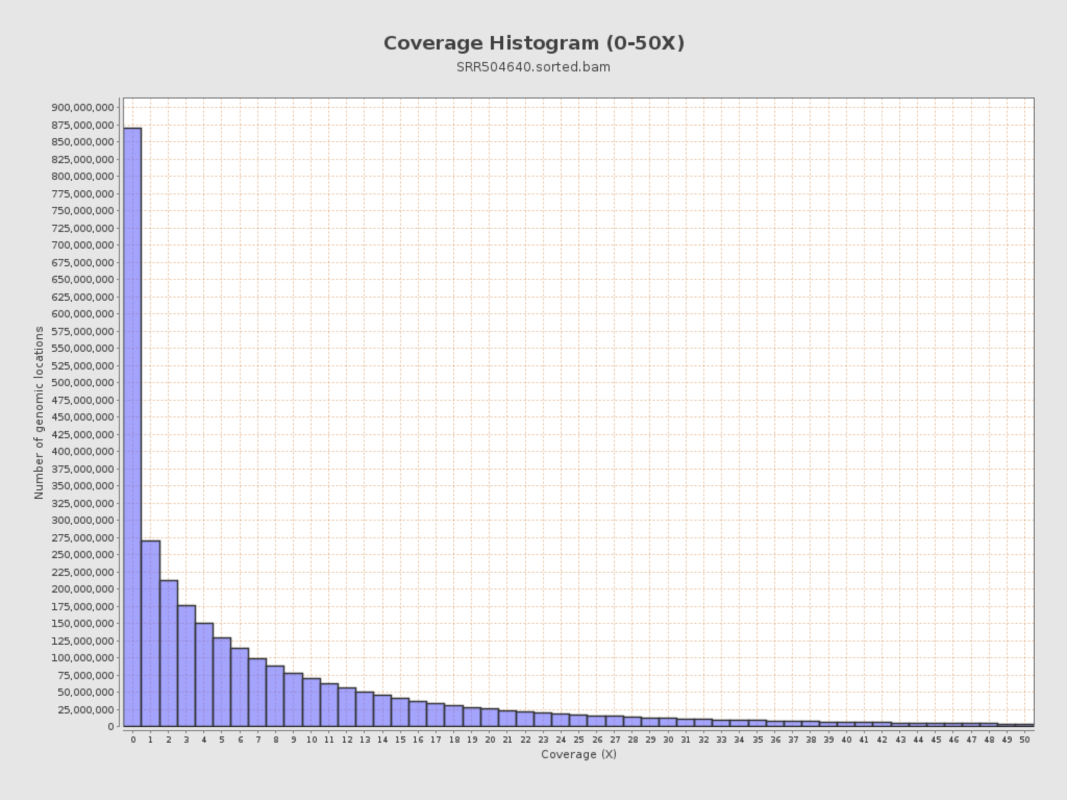
3. Results : Coverage across reference



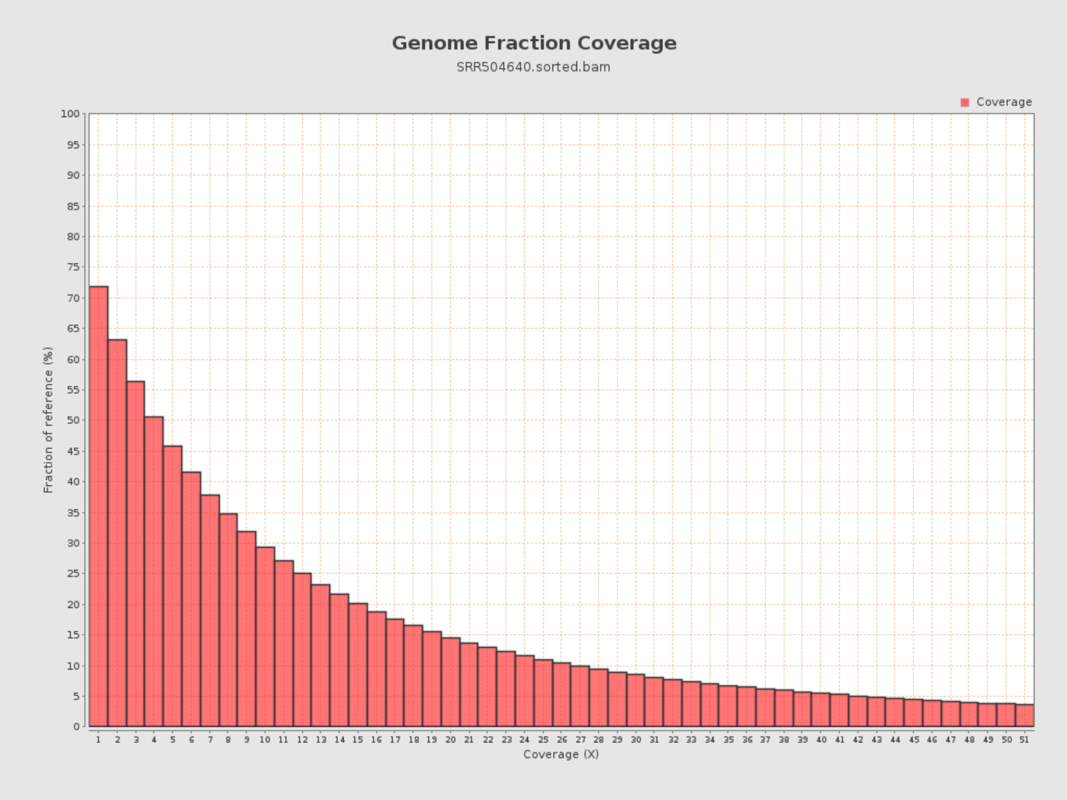
4. Results : Coverage Histogram



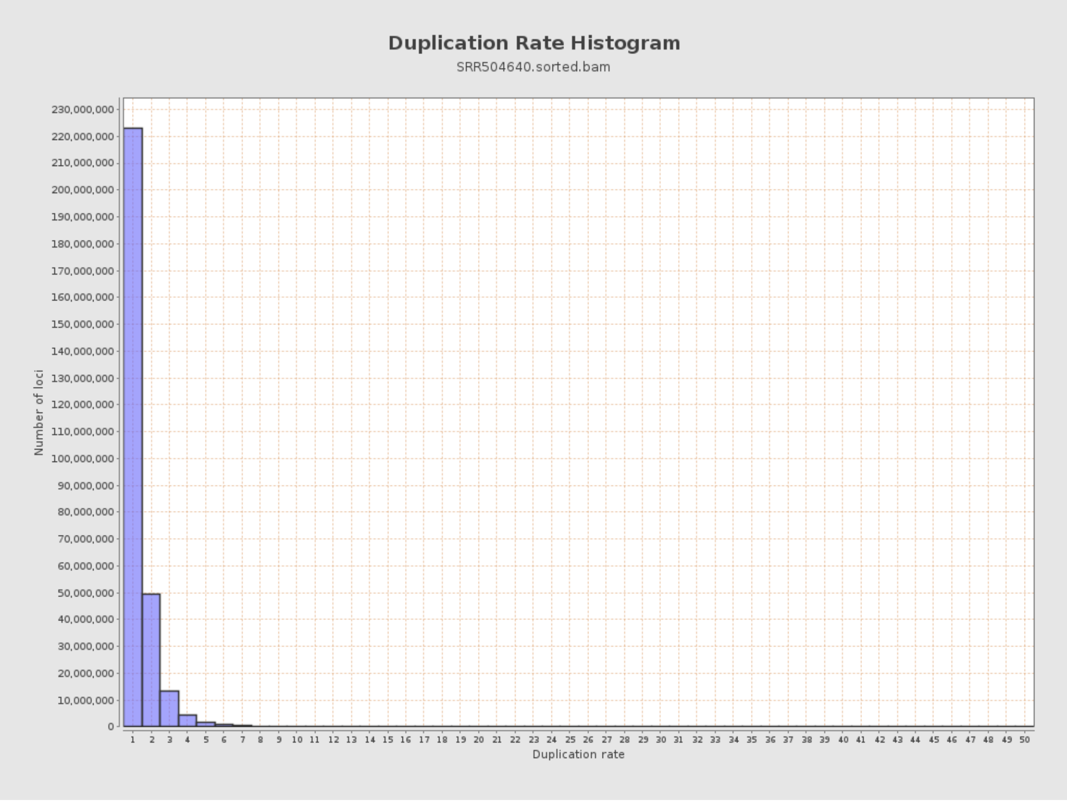
5. Results : Coverage Histogram (0-50X)



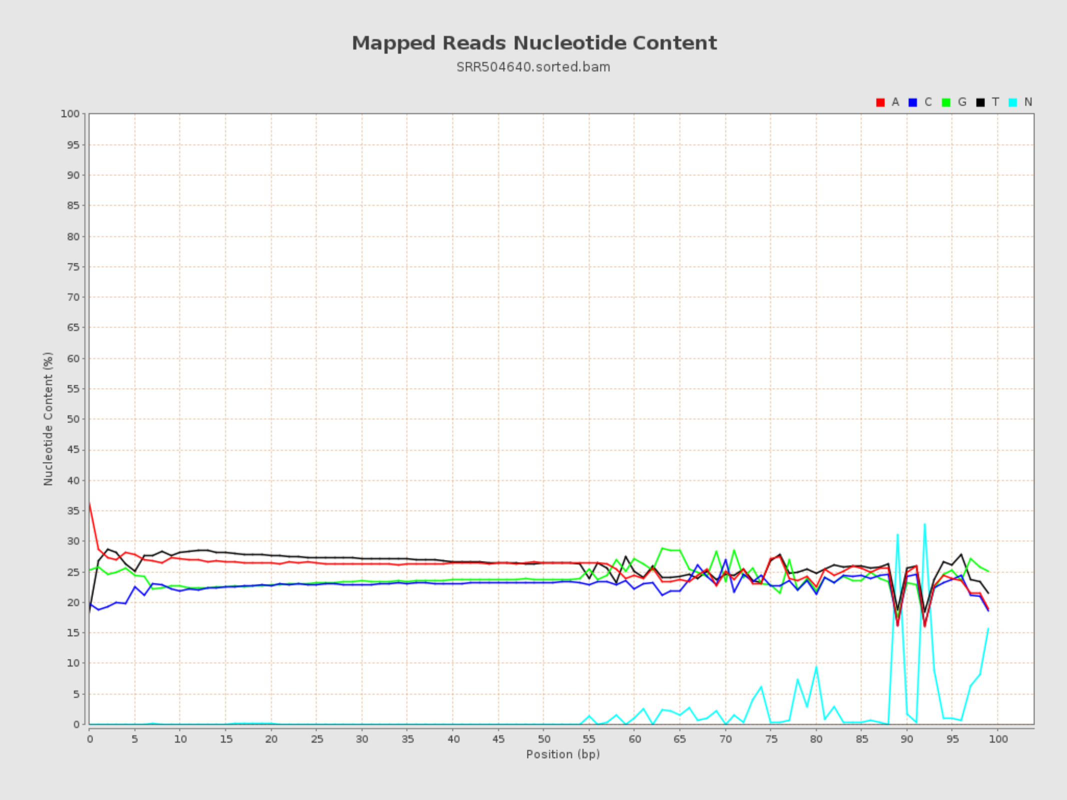
6. Results : Genome Fraction Coverage



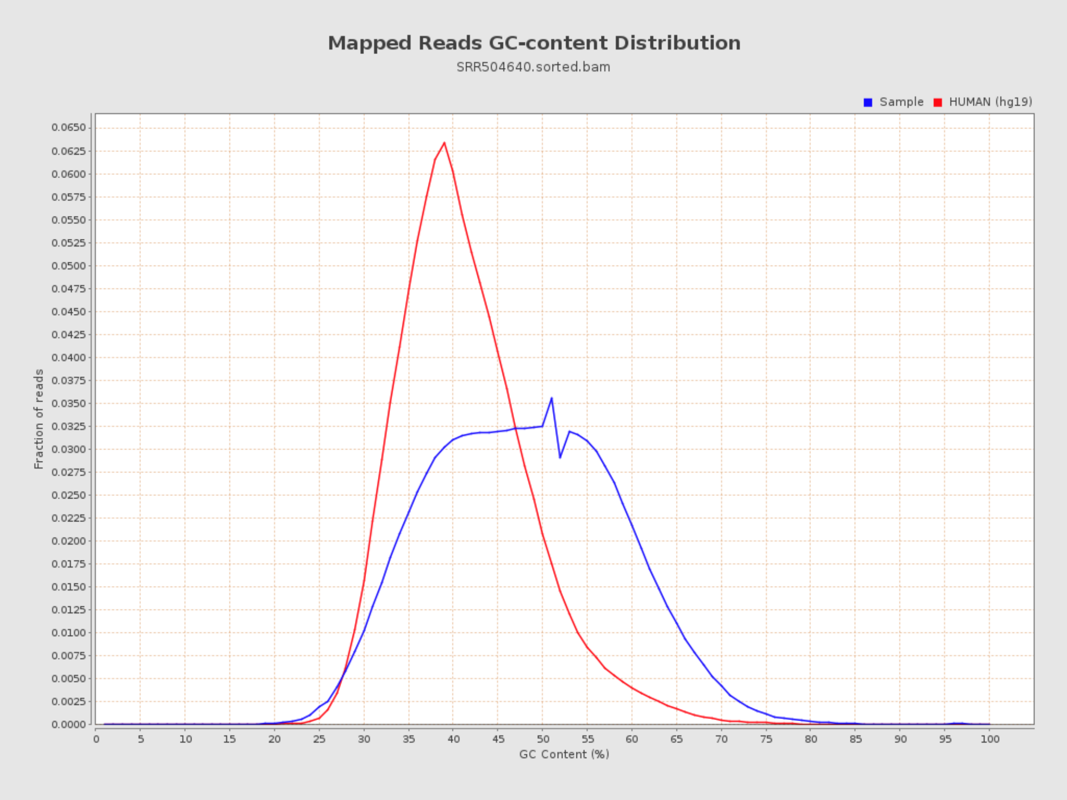
7. Results : Duplication Rate Histogram



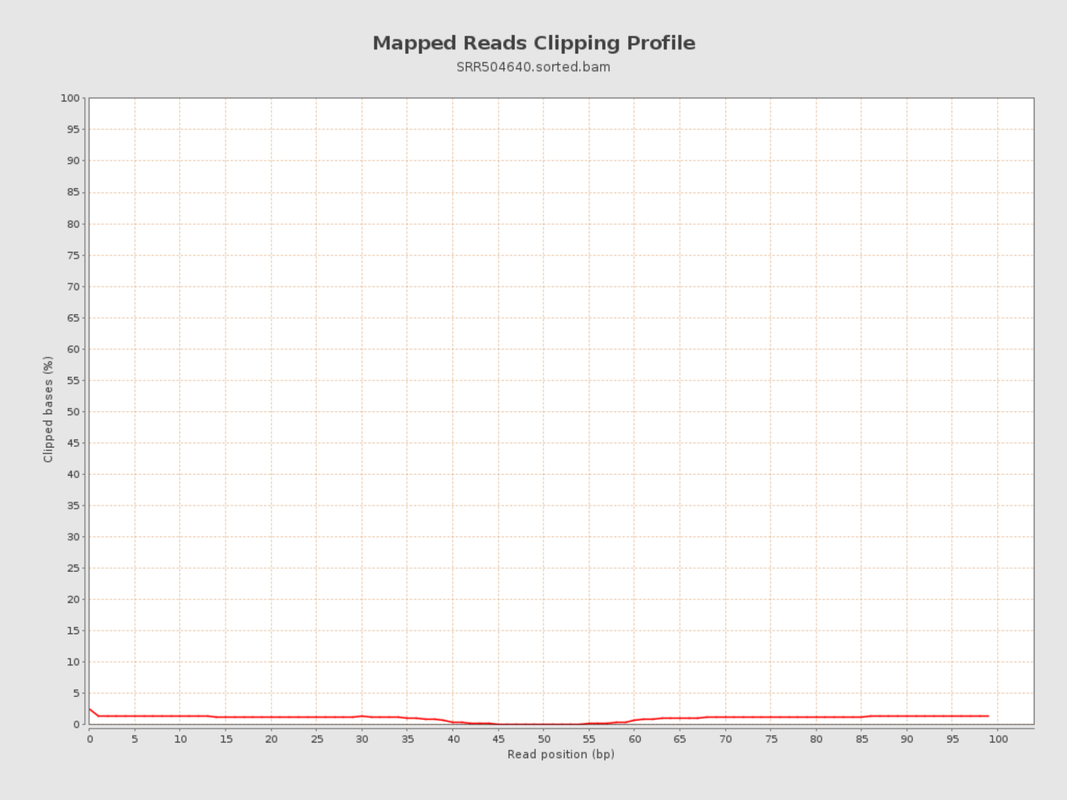
8. Results : Mapped Reads Nucleotide Content



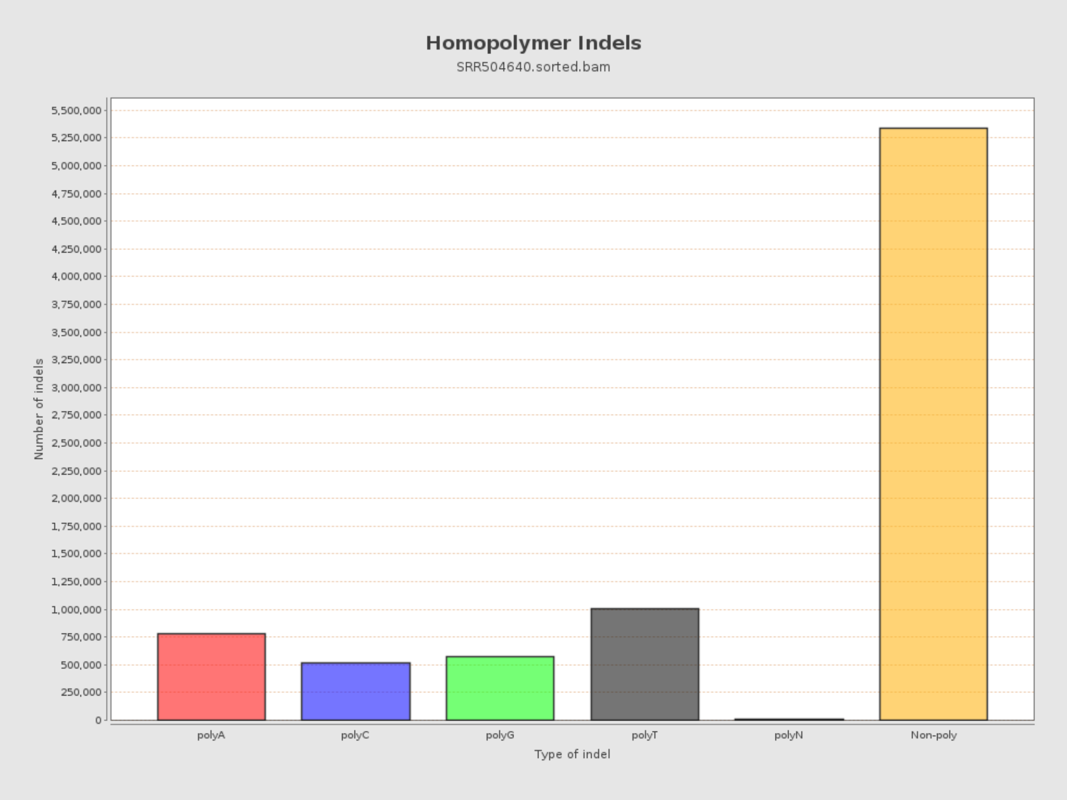
9. Results : Mapped Reads GC-content Distribution



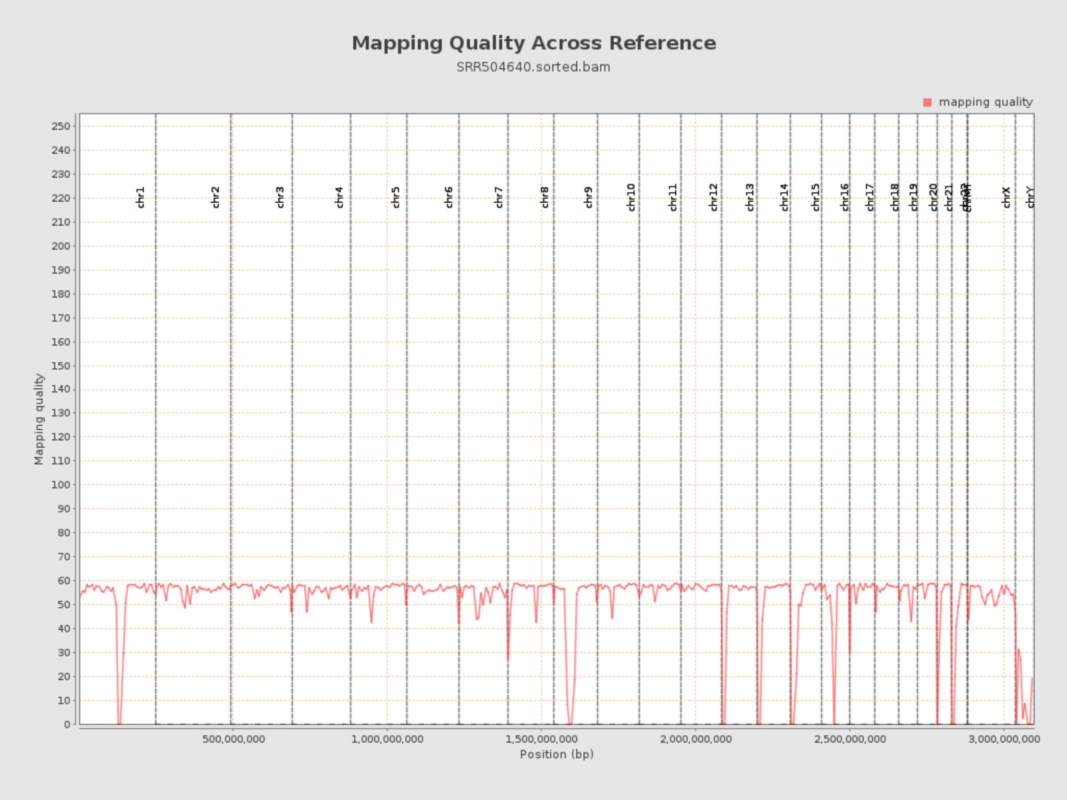
10. Results : Mapped Reads Clipping Profile



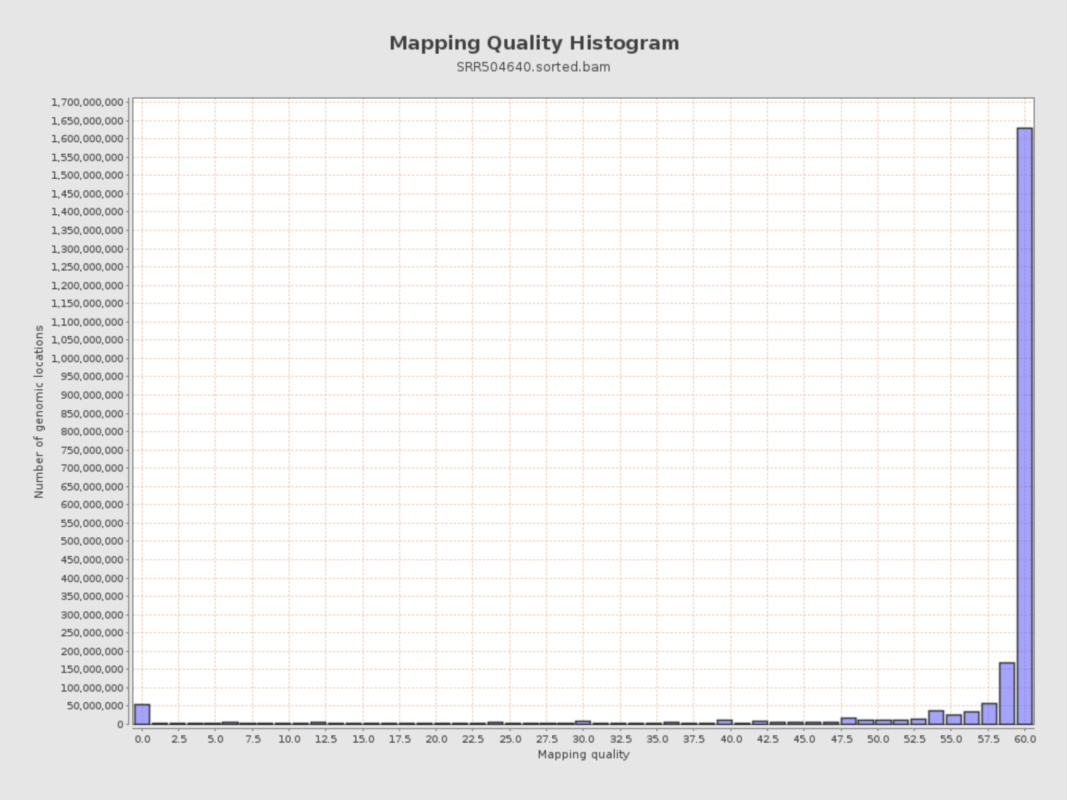
11. Results : Homopolymer Indels



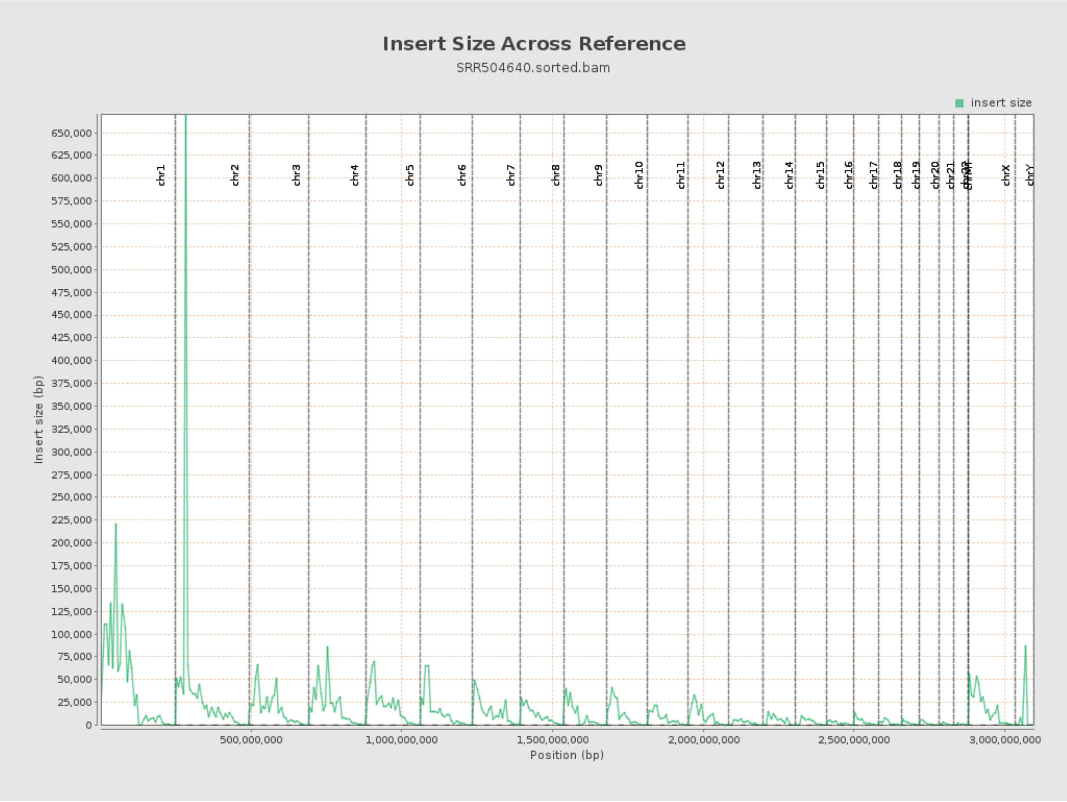
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram