Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/01 12:51:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504636.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_SRR504636 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504636_1.fastq.gz SRR504636_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 01 12:51:49 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504636.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	330,459,032
Mapped reads	286,827,988 / 86.8%
Unmapped reads	43,631,044 / 13.2%
Mapped paired reads	286,827,988 / 86.8%
Mapped reads, first in pair	143,935,571 / 43.56%
Mapped reads, second in pair	142,892,417 / 43.24%
Mapped reads, both in pair	284,322,010 / 86.04%
Mapped reads, singletons	2,505,978 / 0.76%
Secondary alignments	0
Supplementary alignments	3,100,685 / 0.94%
Read min/max/mean length	30 / 100 / 100.39
Duplicated reads (estimated)	86,966,064 / 26.32%
Duplication rate	24.72%
Clipped reads	25,079,681 / 7.59%

2.2. ACGT Content

Number/percentage of A's	7,098,393,368 / 25.1%
Number/percentage of C's	6,922,345,279 / 24.47%
Number/percentage of T's	7,134,401,367 / 25.22%
Number/percentage of G's	7,078,484,032 / 25.03%
Number/percentage of N's	51,734,562 / 0.18%

GC Percentage	49.5%

2.3. Coverage

Mean	9.1392
Standard Deviation	35.8869

2.4. Mapping Quality

Mean Mapping Quality	53.62

2.5. Insert size

Mean	39,985
Standard Deviation	1,907,618.06
P25/Median/P75	329 / 366 / 411

2.6. Mismatches and indels

General error rate	0.83%
Mismatches	229,546,124
Insertions	3,031,002
Mapped reads with at least one insertion	1.03%
Deletions	2,699,990
Mapped reads with at least one deletion	0.91%
Homopolymer indels	36.92%

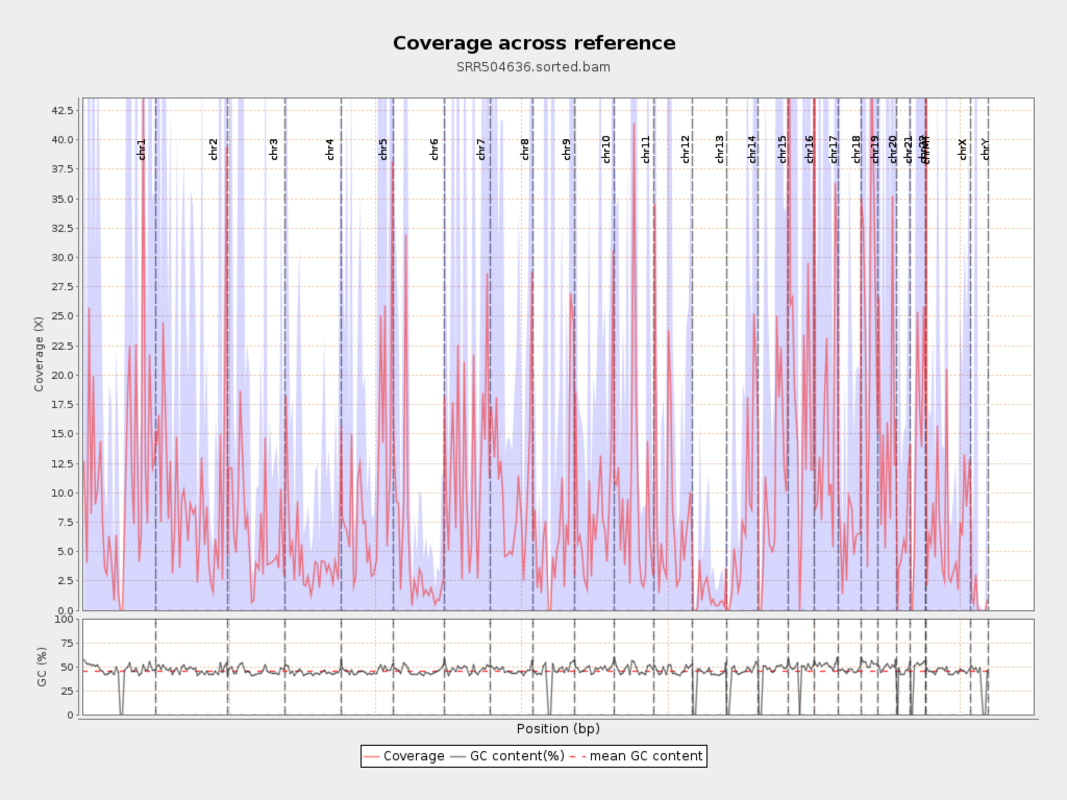
2.7. Chromosome stats

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

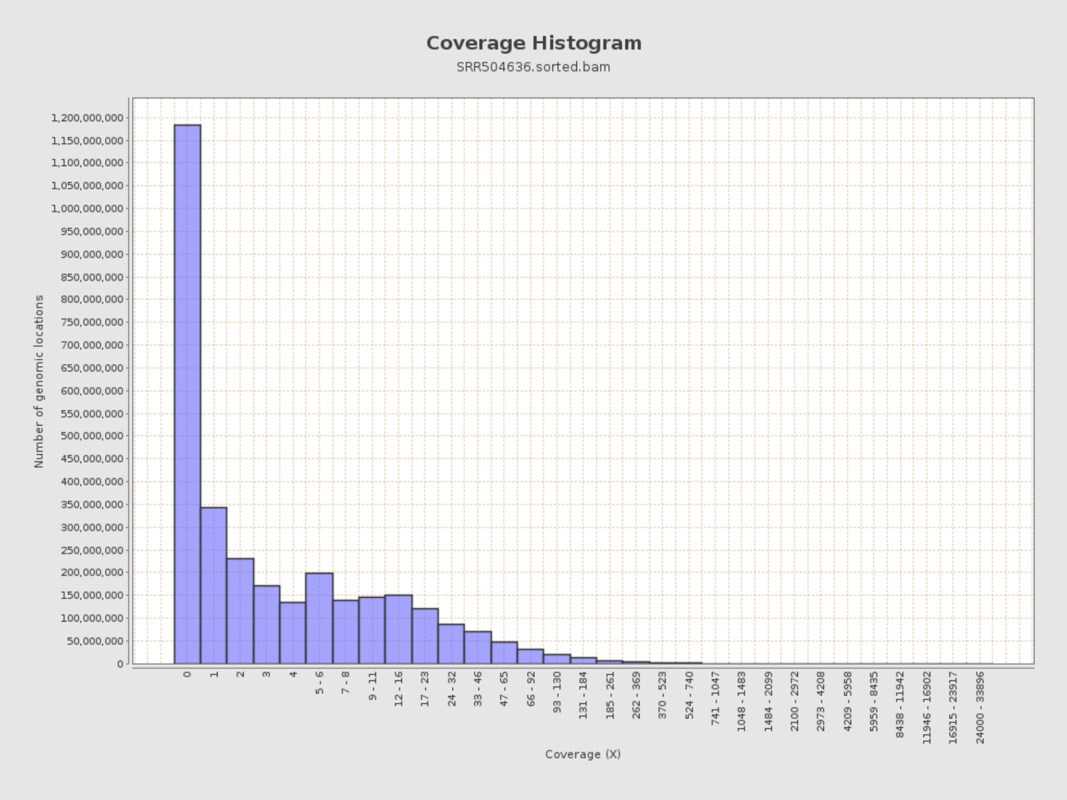
		bases	coverage	deviation
chr1	249250621	2719119820	10.9092	35.3154
chr2	243199373	2294946835	9.4365	27.6756
chr3	198022430	1340695781	6.7704	22.988
chr4	191154276	875615492	4.5807	14.2573
chr5	180915260	1905762551	10.534	29.8416
chr6	171115067	814733492	4.7613	17.4694
chr7	159138663	1948155943	12.2419	31.4232
chr8	146364022	1506256797	10.2912	26.919
chr9	141213431	979380703	6.9355	66.2189
chr10	135534747	1148507827	8.4739	27.0453
chr11	135006516	1322648796	9.7969	33.5671
chr12	133851895	1190966857	8.8976	26.4564
chr13	115169878	130929306	1.1368	5.3041
chr14	107349540	873267777	8.1348	22.0126
chr15	102531392	1031045050	10.0559	28.2576
chr16	90354753	1831043527	20.265	50.4852
chr17	81195210	1223631391	15.0702	39.5857
chr18	78077248	485392095	6.2168	67.7451
chr19	59128983	1534817570	25.9571	106.7315
chr20	63025520	967843278	15.3564	46.2011
chr21	48129895	303133841	6.2982	20.6058
chr22	51304566	708293262	13.8057	33.9938
chrMT	16571	2720561	164.176	64.2678
chrX	155270560	1111316687	7.1573	17.2659

chrY	59373566	41869704	0.7052	31.299

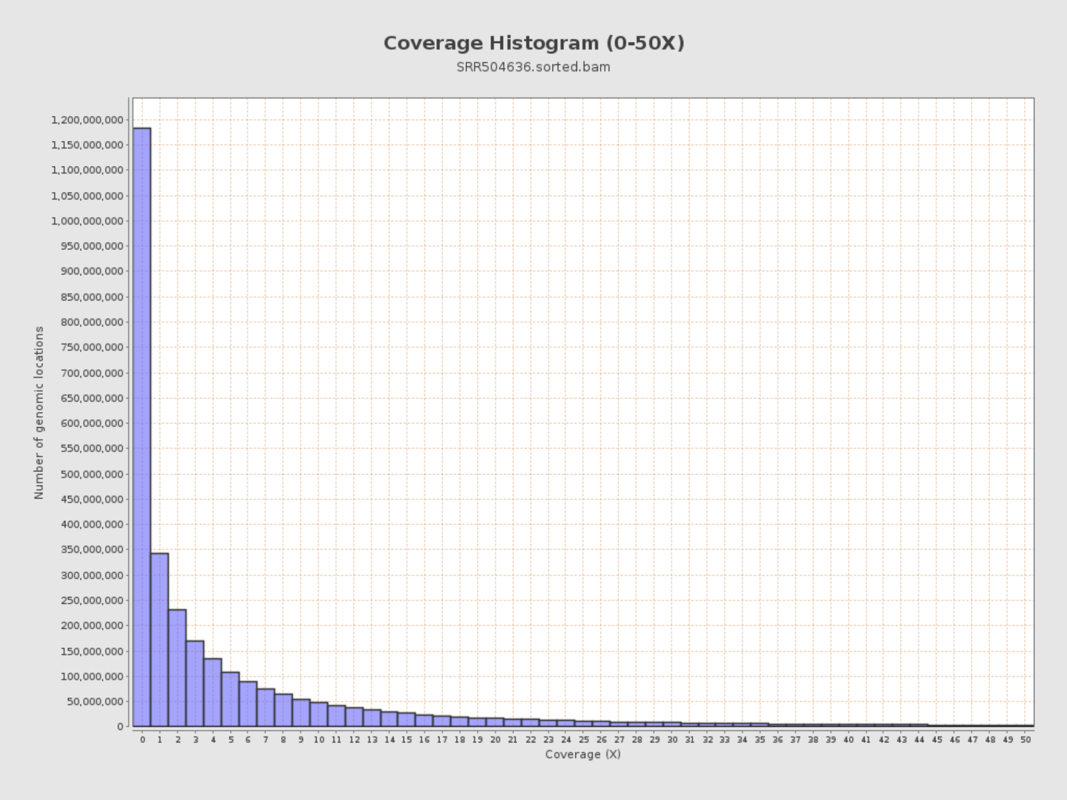
3. Results : Coverage across reference



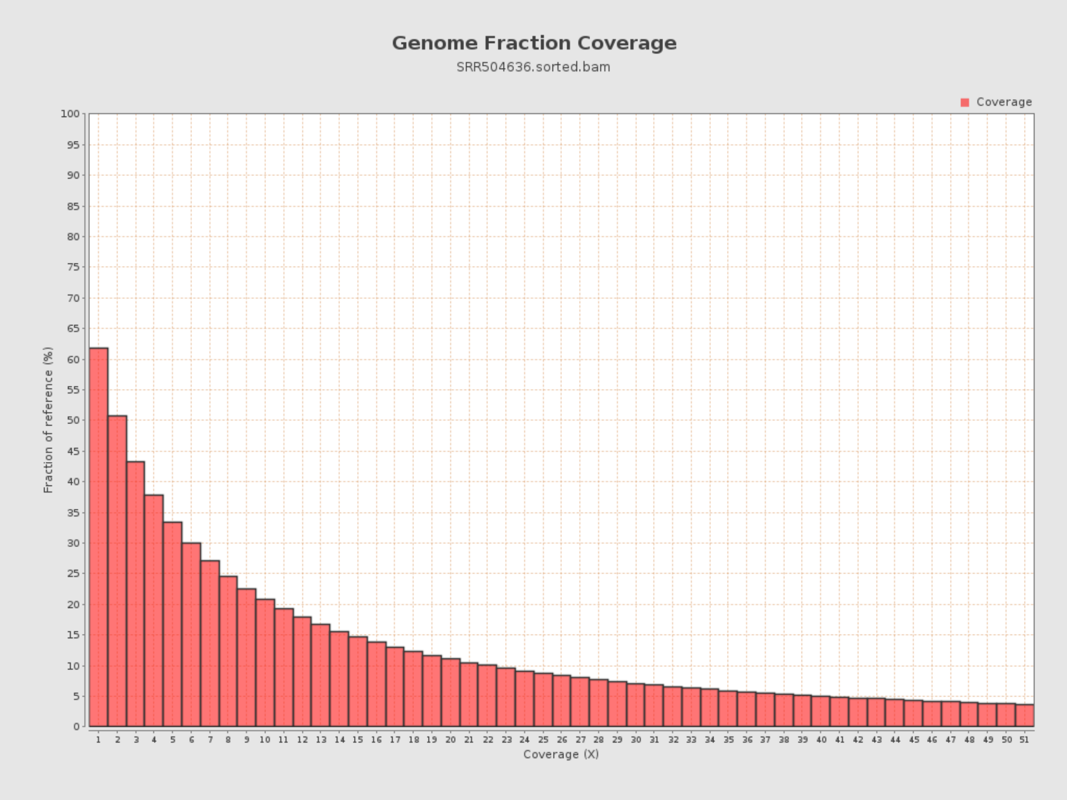
4. Results : Coverage Histogram



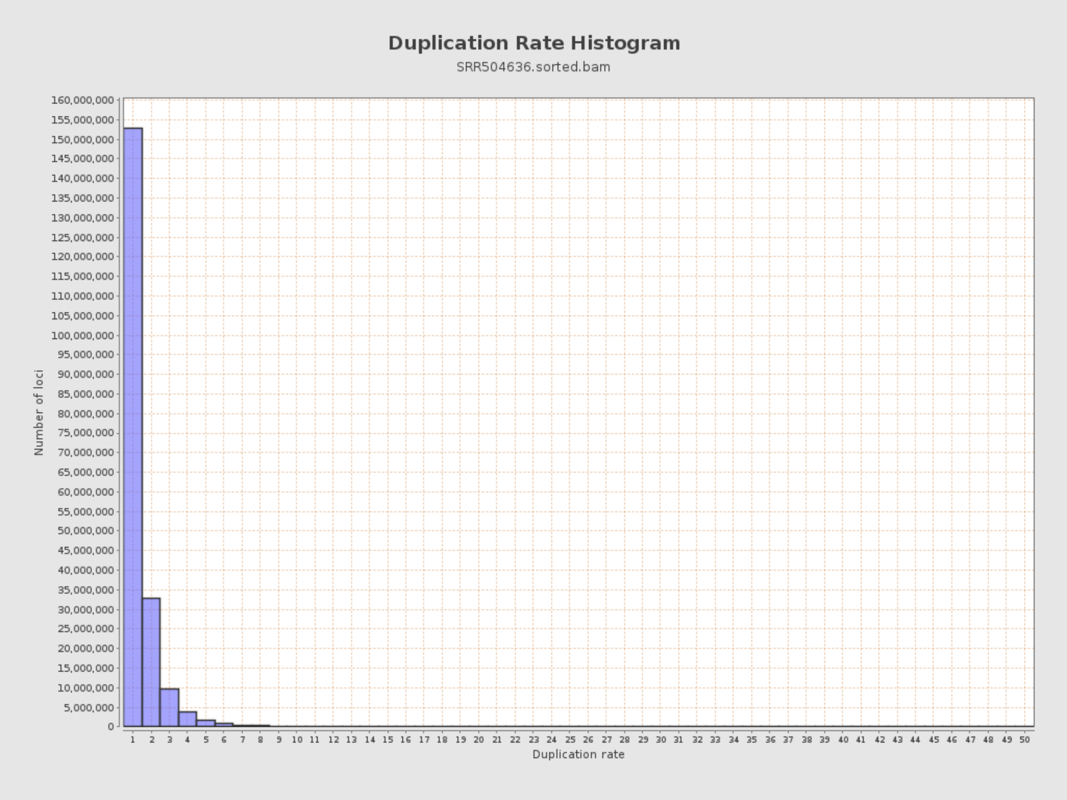
5. Results : Coverage Histogram (0-50X)



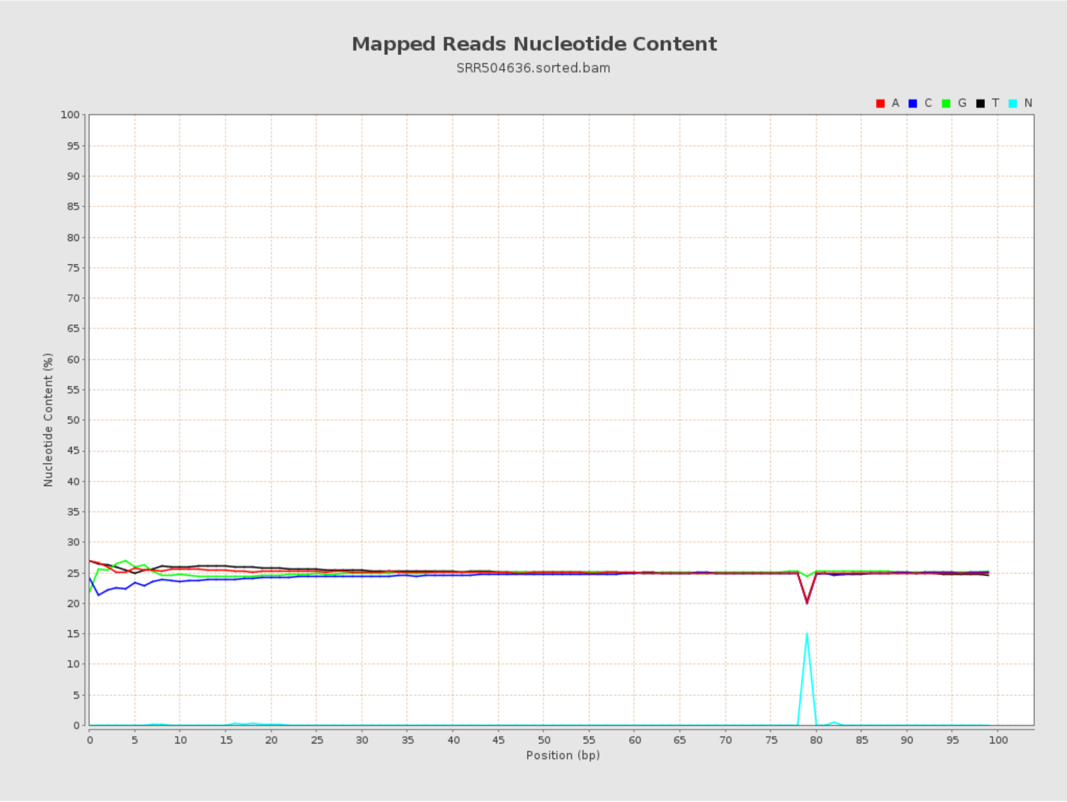
6. Results : Genome Fraction Coverage



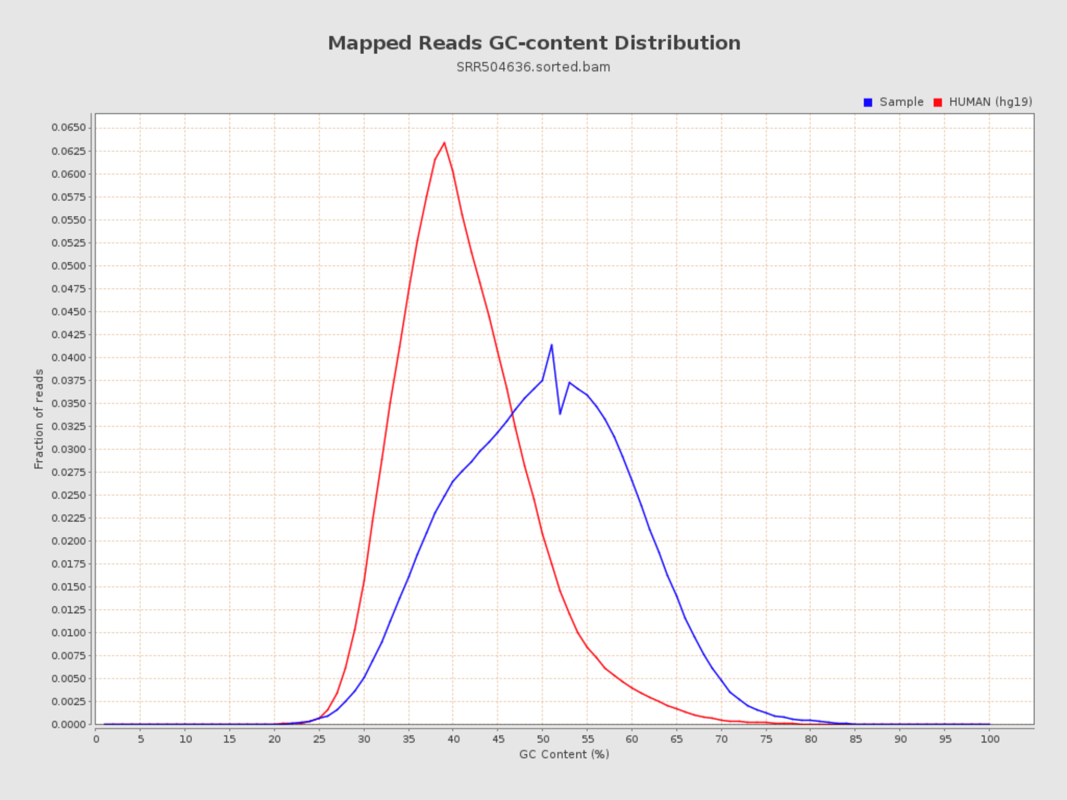
7. Results : Duplication Rate Histogram



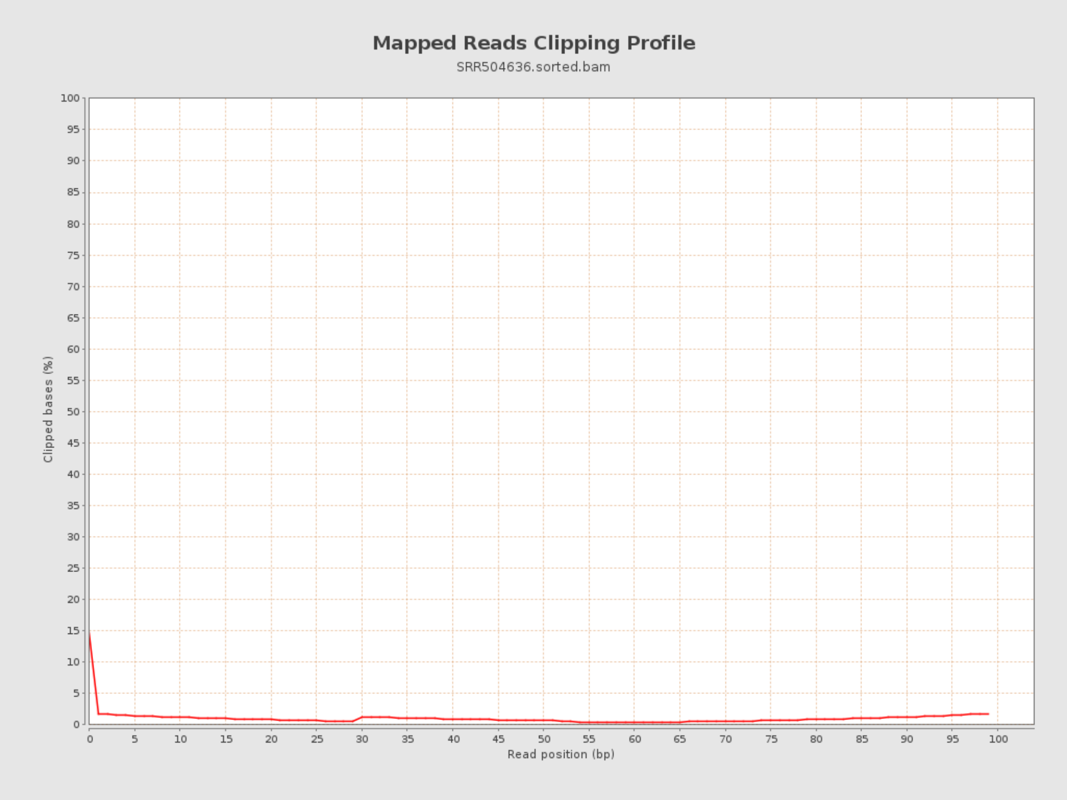
8. Results : Mapped Reads Nucleotide Content



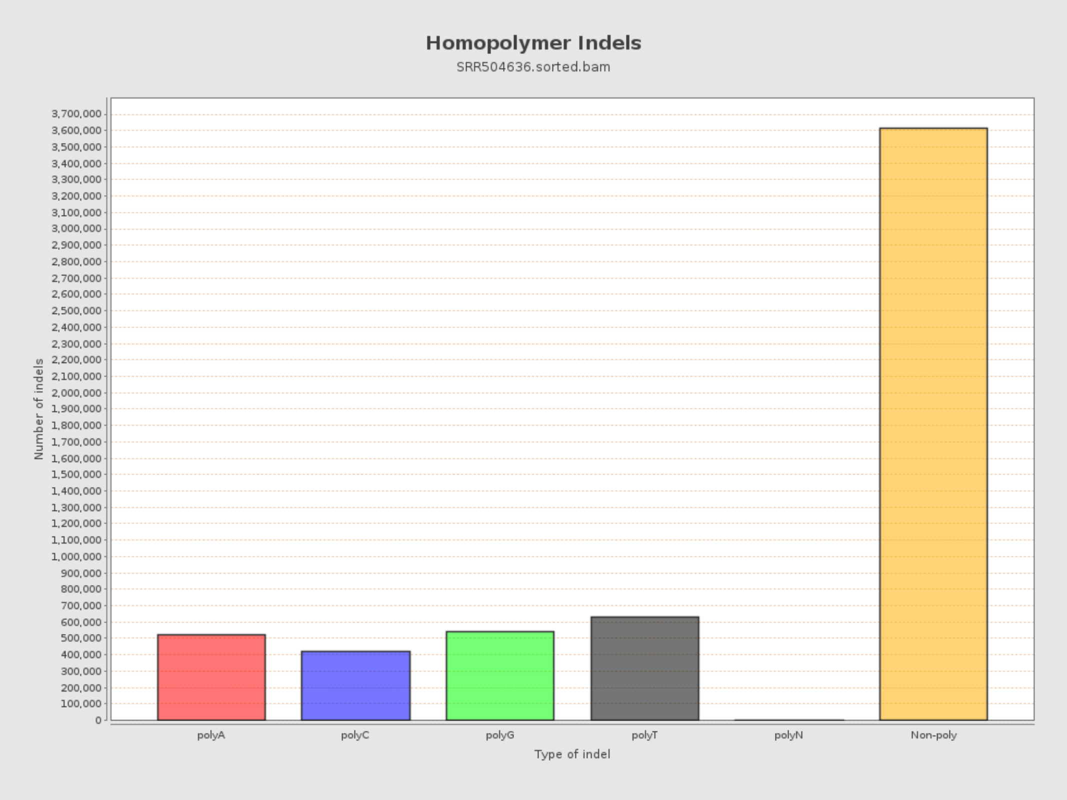
9. Results : Mapped Reads GC-content Distribution



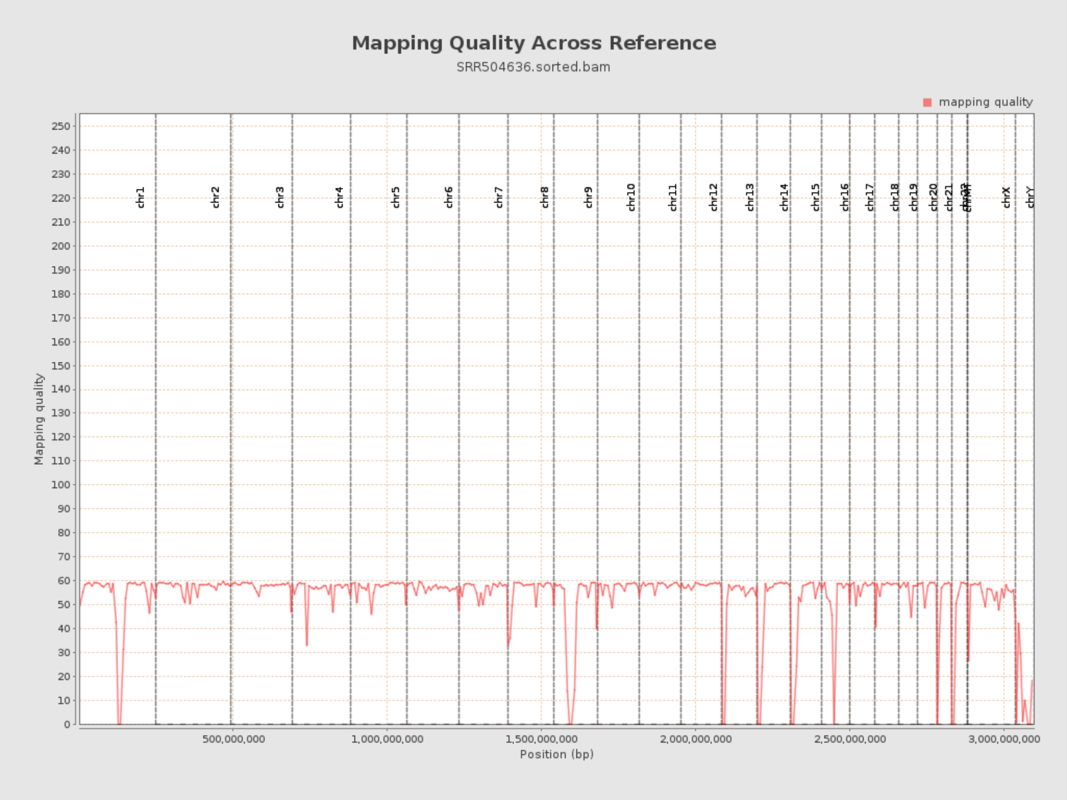
10. Results : Mapped Reads Clipping Profile



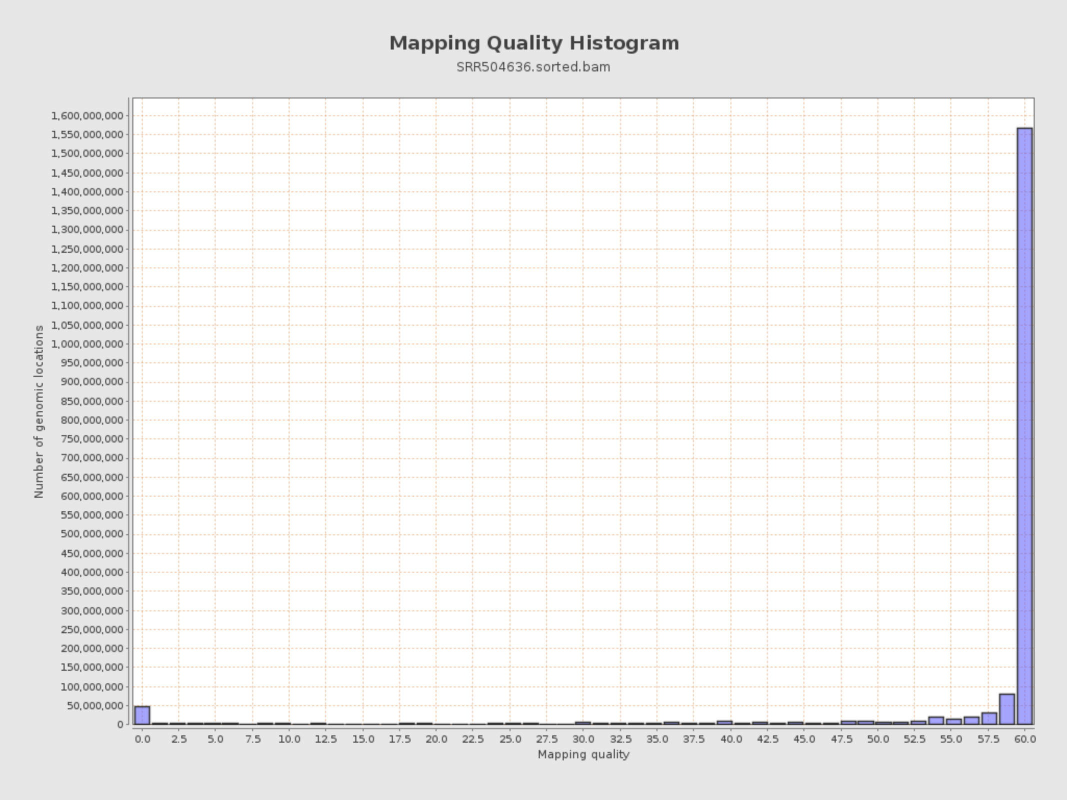
11. Results : Homopolymer Indels



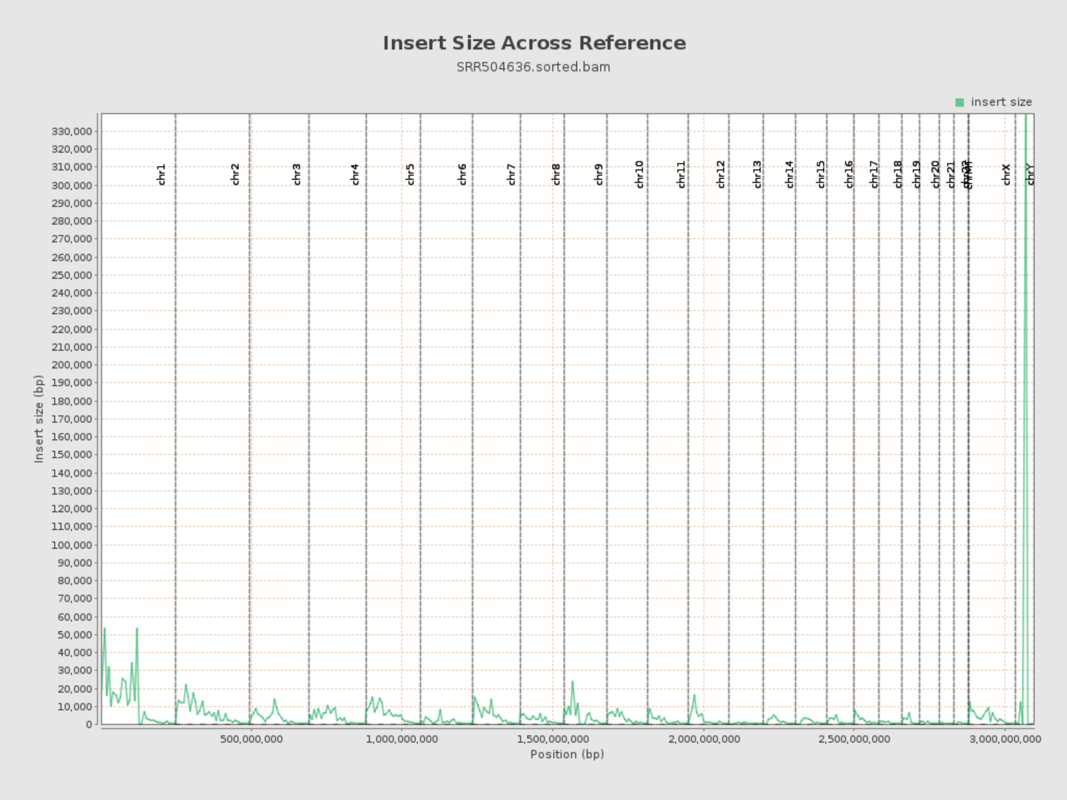
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram