Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/22 13:39:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504601.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_SRR504601 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504601_1.fastq.gz SRR504601_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 22 13:39:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504601.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	423,713,276
Mapped reads	364,698,182 / 86.07%
Unmapped reads	59,015,094 / 13.93%
Mapped paired reads	364,698,182 / 86.07%
Mapped reads, first in pair	182,646,858 / 43.11%
Mapped reads, second in pair	182,051,324 / 42.97%
Mapped reads, both in pair	362,690,082 / 85.6%
Mapped reads, singletons	2,008,100 / 0.47%
Secondary alignments	0
Supplementary alignments	2,003,393 / 0.47%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	88,739,623 / 20.94%
Duplication rate	21.71%
Clipped reads	17,930,178 / 4.23%

2.2. ACGT Content

Number/percentage of A's	9,548,853,620 / 26.38%
Number/percentage of C's	8,471,926,180 / 23.4%
Number/percentage of T's	9,580,590,267 / 26.47%
Number/percentage of G's	8,591,518,747 / 23.73%
Number/percentage of N's	6,910,494 / 0.02%

GC Percentage	47.14%

2.3. Coverage

Mean	11.6966
Standard Deviation	24.1854

2.4. Mapping Quality

Mean Mapping Quality	53.98

2.5. Insert size

Mean	29,242.01
Standard Deviation	1,659,578.2
P25/Median/P75	180 / 213 / 267

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	192,610,664
Insertions	2,722,270
Mapped reads with at least one insertion	0.73%
Deletions	3,642,898
Mapped reads with at least one deletion	0.97%
Homopolymer indels	40.43%

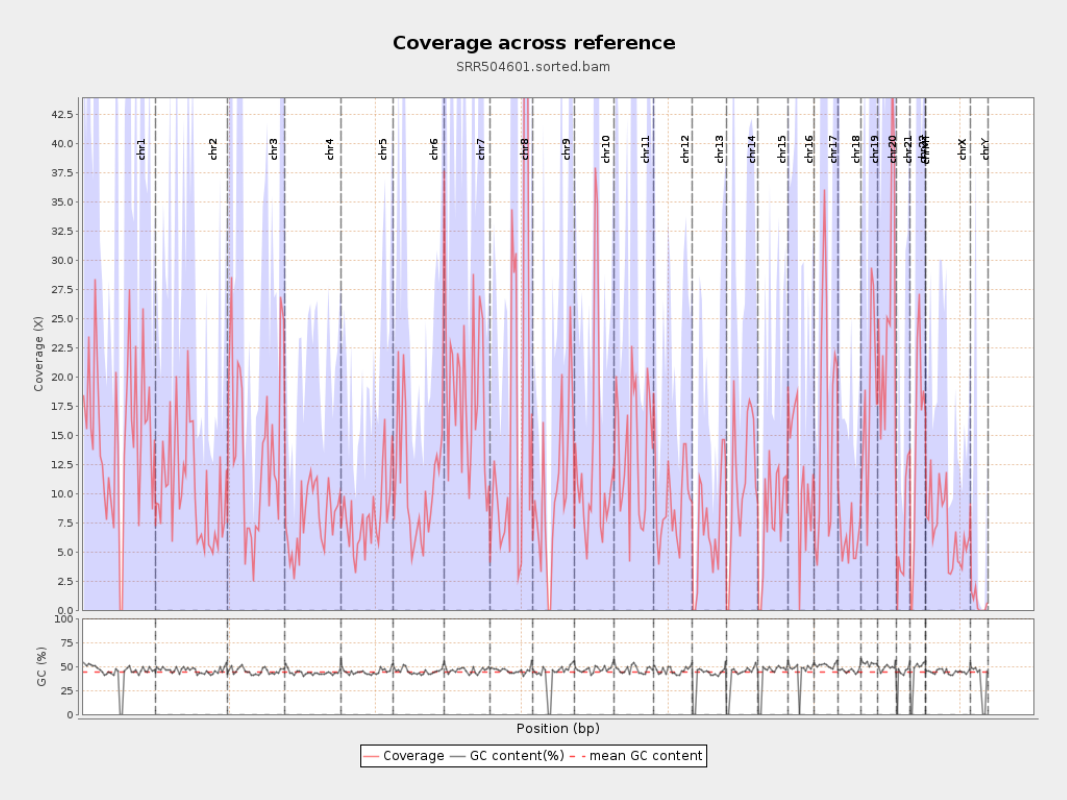
2.7. Chromosome stats

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

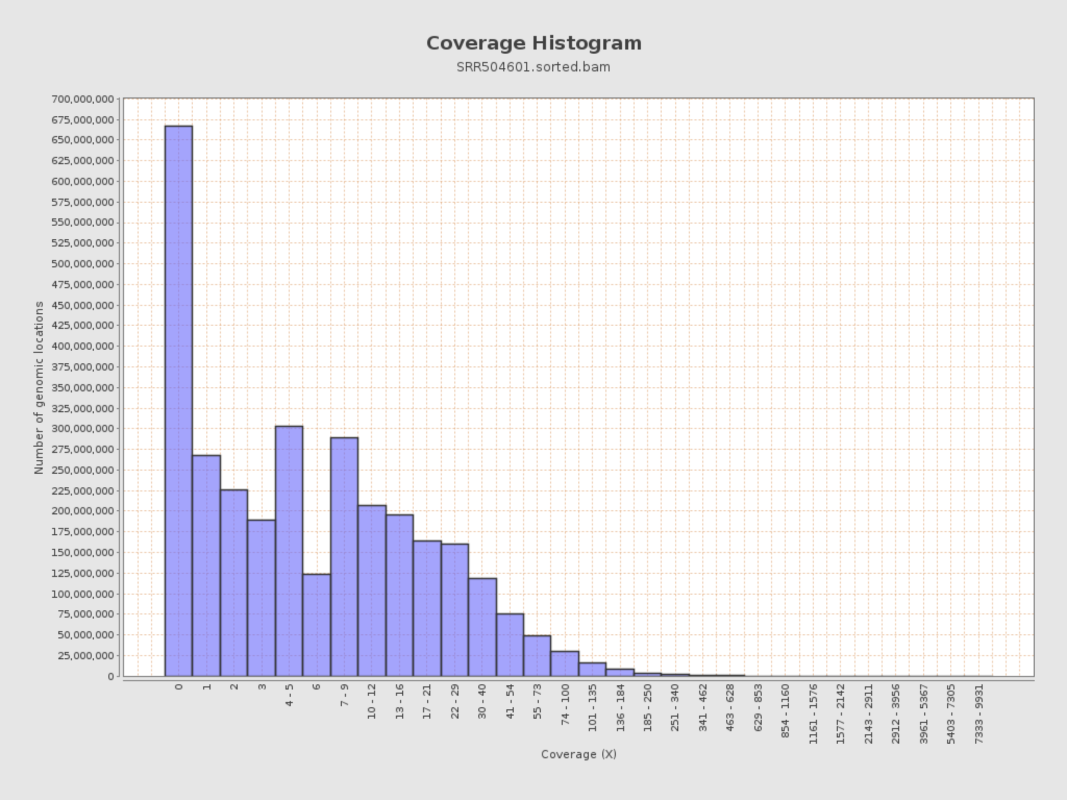
		bases	coverage	deviation
chr1	249250621	3715881565	14.9082	25.144
chr2	243199373	2483259994	10.2108	18.2481
chr3	198022430	2682998619	13.549	22.3786
chr4	191154276	1517206628	7.9371	12.5799
chr5	180915260	1474048639	8.1477	13.7012
chr6	171115067	1851131424	10.8181	17.6317
chr7	159138663	2946151784	18.5131	27.5161
chr8	146364022	2764968033	18.891	46.4142
chr9	141213431	1423928649	10.0835	19.6823
chr10	135534747	1704303035	12.5747	23.7517
chr11	135006516	1845947524	13.673	23.1815
chr12	133851895	1234860593	9.2256	15.4797
chr13	115169878	823053547	7.1464	13.4024
chr14	107349540	1209512763	11.2671	19.5749
chr15	102531392	806765702	7.8685	14.7236
chr16	90354753	1056660929	11.6946	20.0853
chr17	81195210	1311128592	16.1479	49.6279
chr18	78077248	473602350	6.0658	28.3582
chr19	59128983	1064456692	18.0023	31.2552
chr20	63025520	1628265926	25.835	38.536
chr21	48129895	343581419	7.1386	18.0585
chr22	51304566	743719293	14.4962	26.9491
chrMT	16571	232586	14.0357	10.9831
chrX	155270560	1066990740	6.8718	12.119

chrY	59373566	36521556	0.6151	14.6582

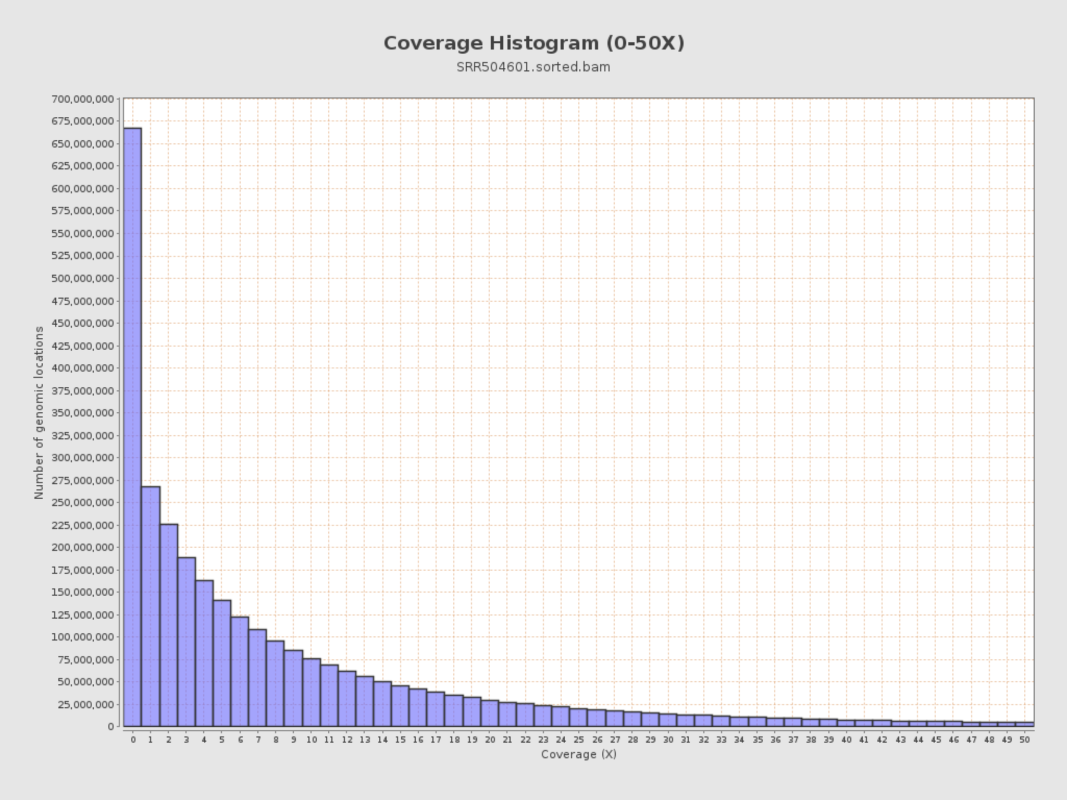
3. Results : Coverage across reference



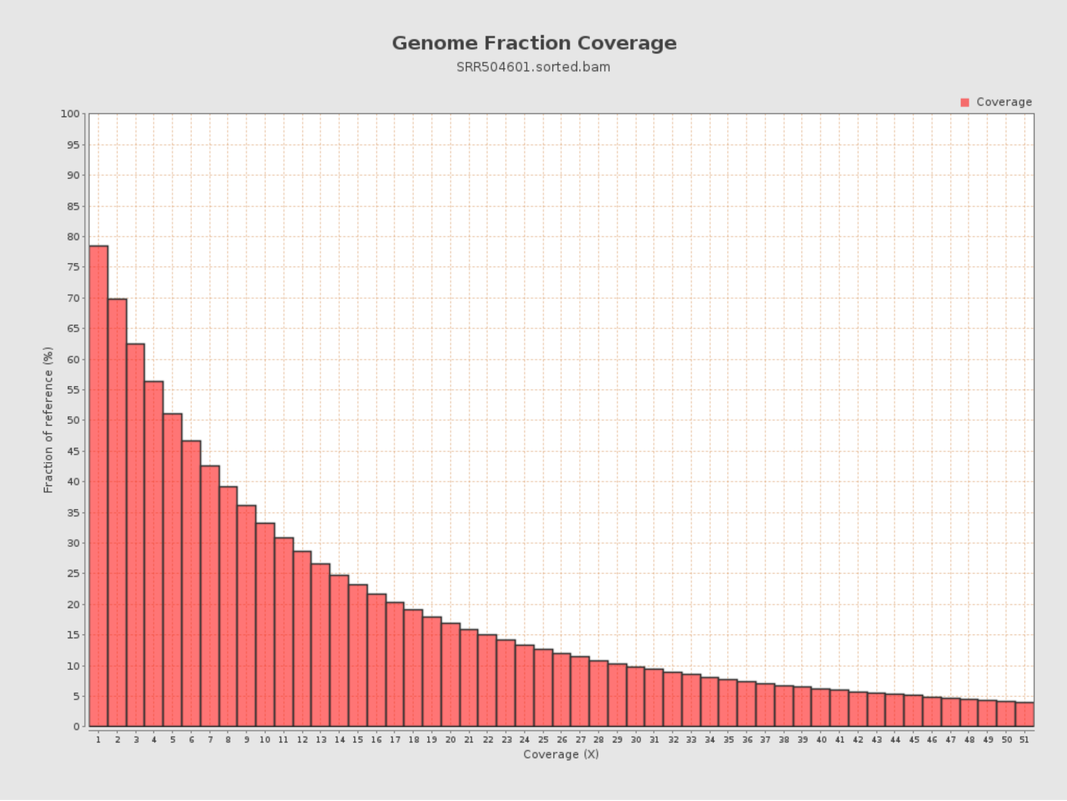
4. Results : Coverage Histogram



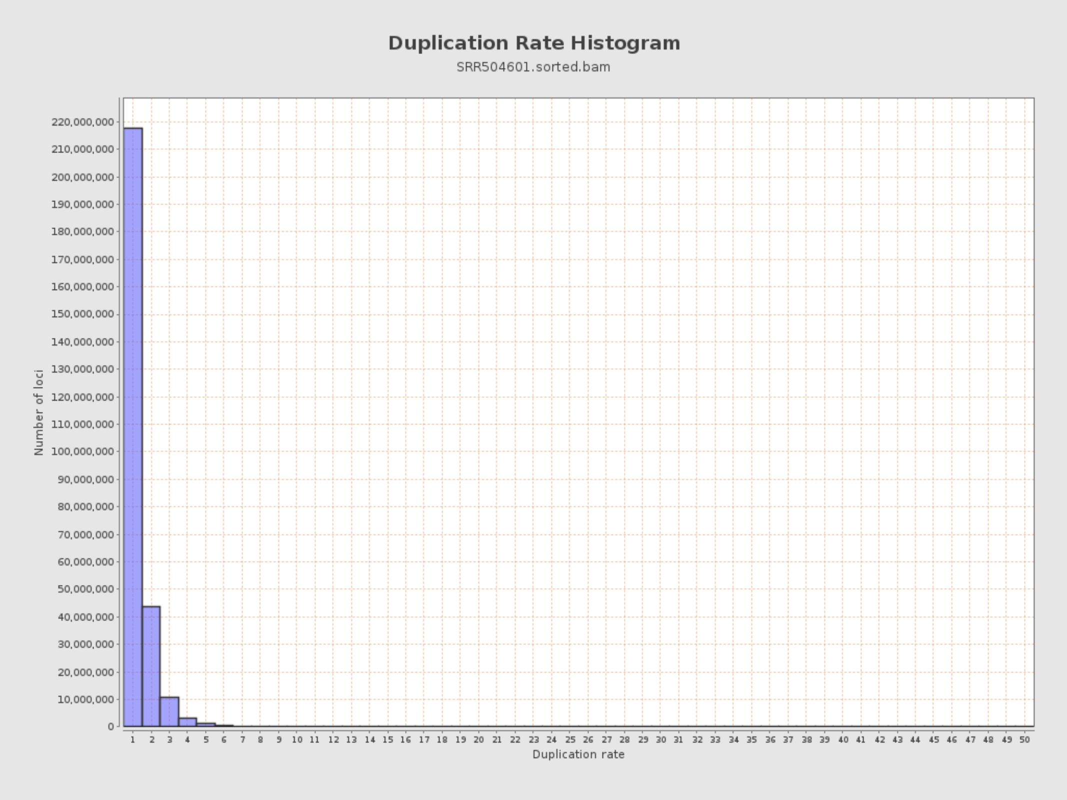
5. Results : Coverage Histogram (0-50X)



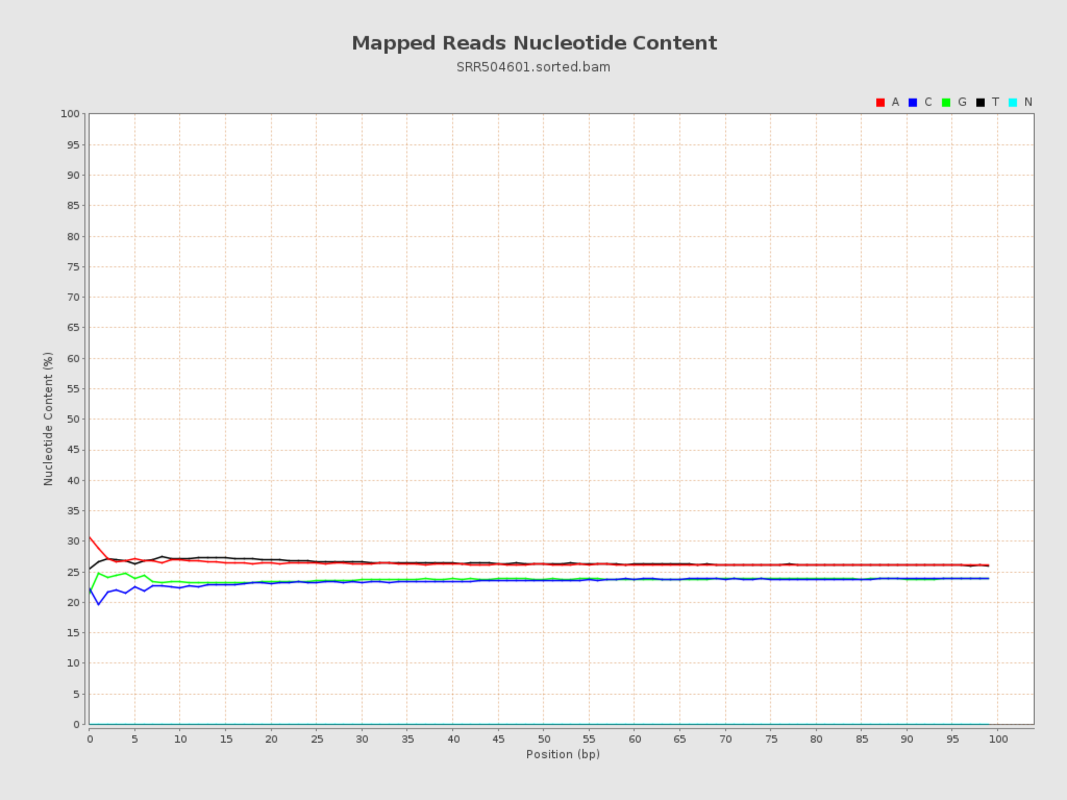
6. Results : Genome Fraction Coverage



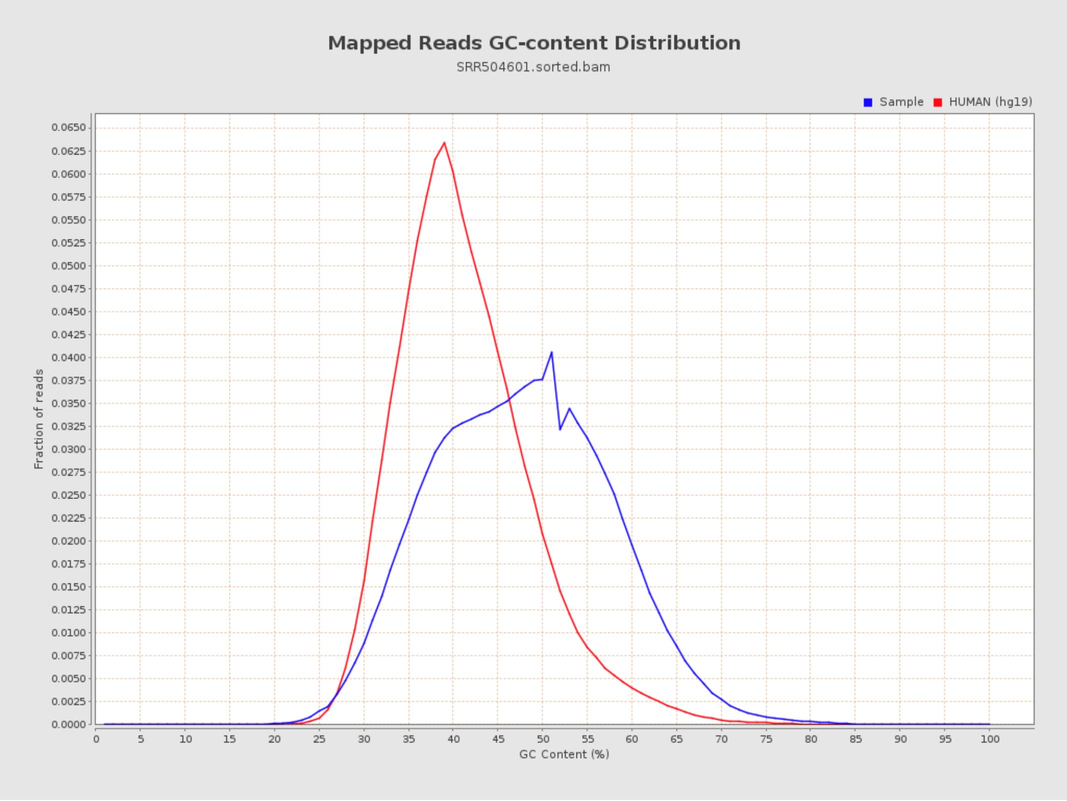
7. Results : Duplication Rate Histogram



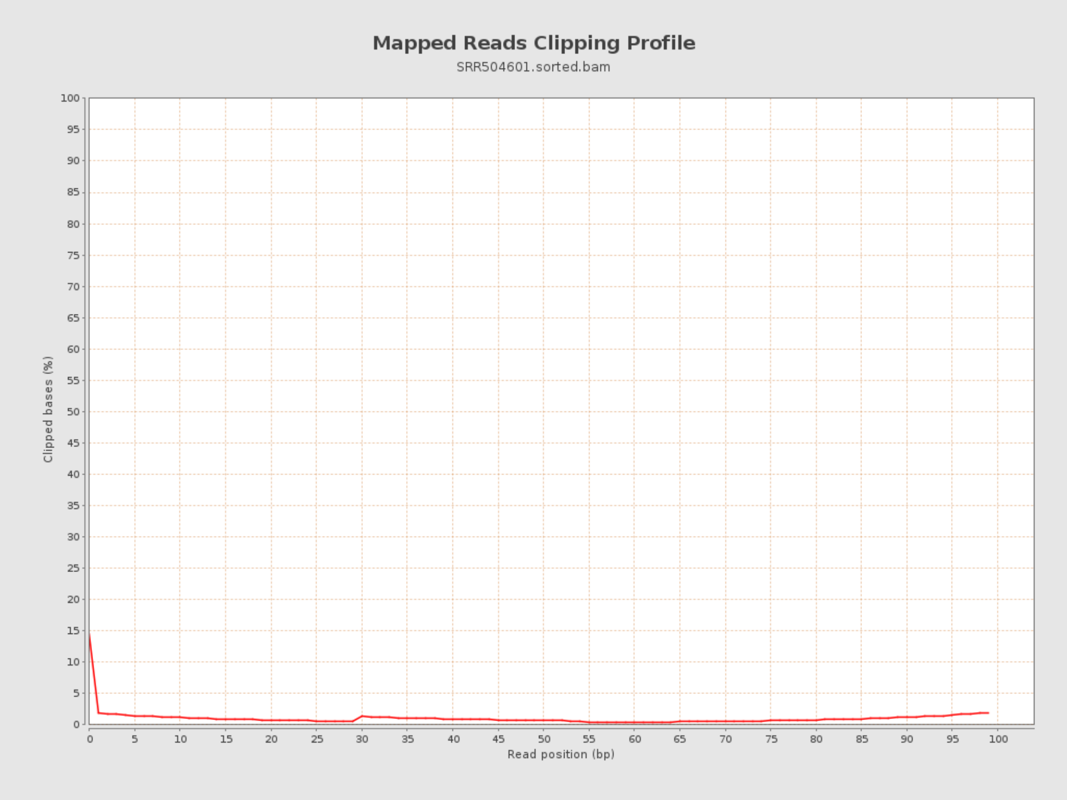
8. Results : Mapped Reads Nucleotide Content



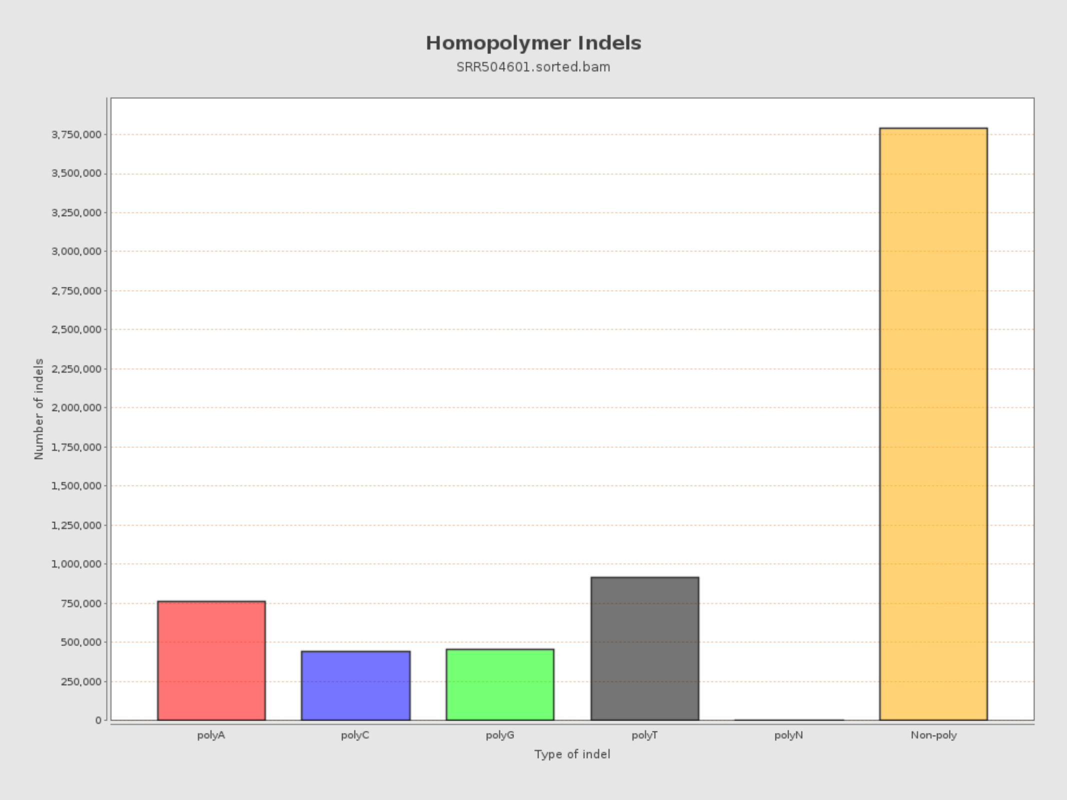
9. Results : Mapped Reads GC-content Distribution



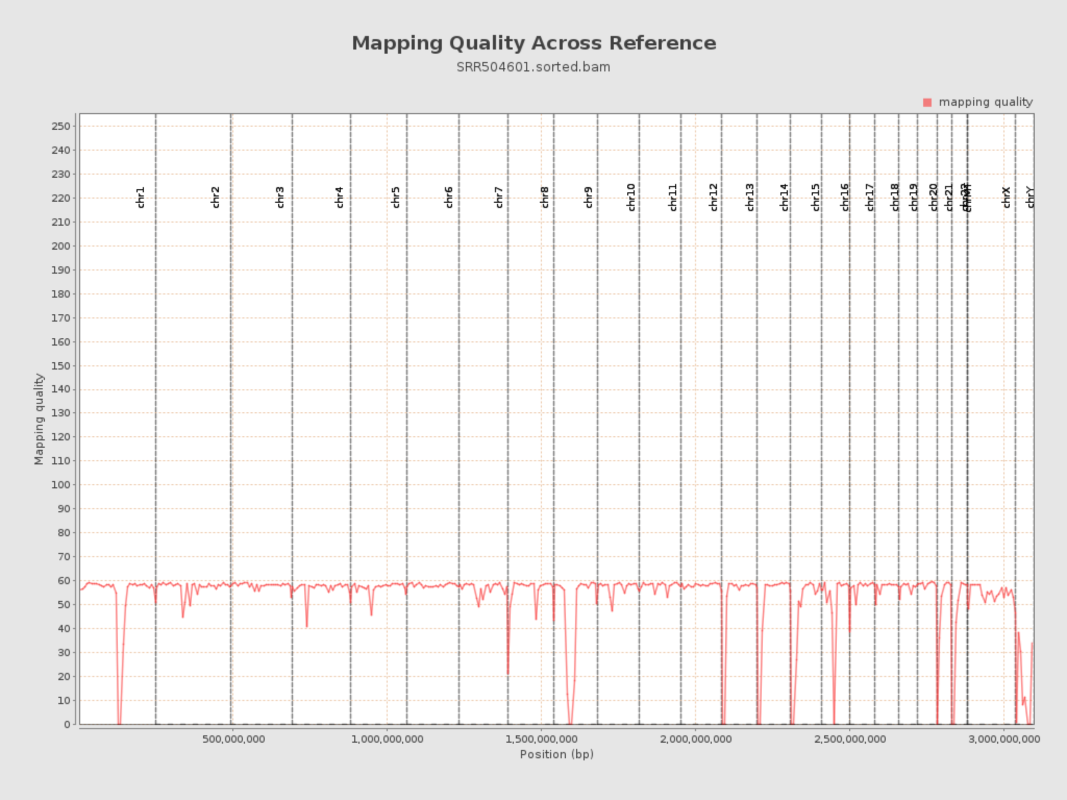
10. Results : Mapped Reads Clipping Profile



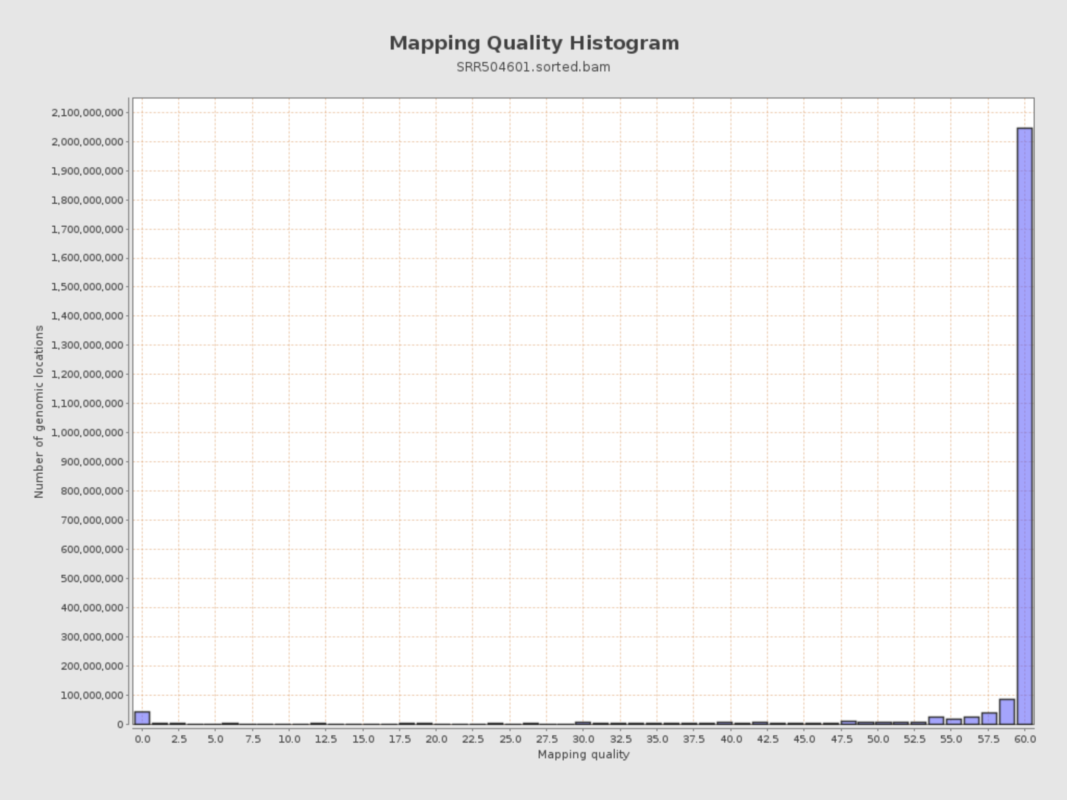
11. Results : Homopolymer Indels



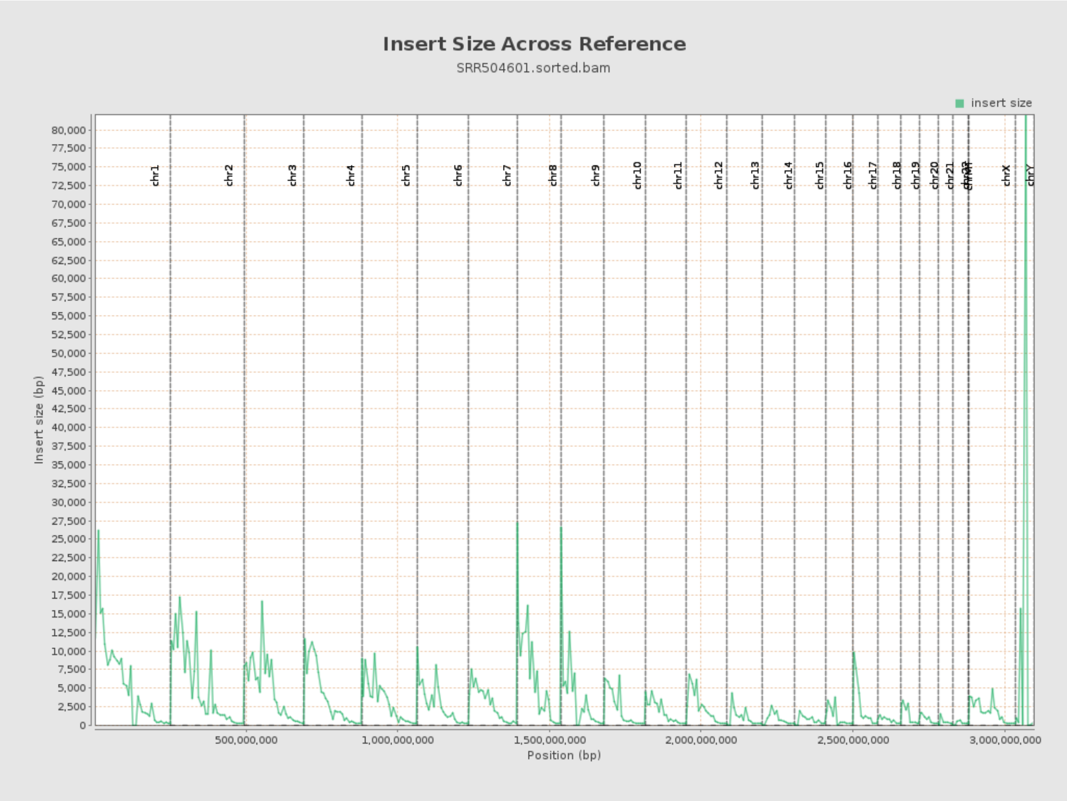
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram