Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/11 17:40:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438262.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_SRR8438262 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438262_1.fastq.gz SRR8438262_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 11 17:40:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438262.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	912,266,718
Mapped reads	908,973,964 / 99.64%
Unmapped reads	3,292,754 / 0.36%
Mapped paired reads	908,973,964 / 99.64%
Mapped reads, first in pair	454,771,475 / 49.85%
Mapped reads, second in pair	454,202,489 / 49.79%
Mapped reads, both in pair	907,313,014 / 99.46%
Mapped reads, singletons	1,660,950 / 0.18%
Secondary alignments	0
Supplementary alignments	14,648,062 / 1.61%
Read min/max/mean length	30 / 149 / 118.84
Duplicated reads (estimated)	394,194,629 / 43.21%
Duplication rate	41.82%
Clipped reads	211,979,114 / 23.24%

2.2. ACGT Content

Number/percentage of A's	31,668,888,801 / 30.76%
Number/percentage of C's	20,055,792,108 / 19.48%
Number/percentage of T's	30,790,168,492 / 29.9%
Number/percentage of G's	20,445,982,847 / 19.86%
Number/percentage of N's	264,241 / 0%

GC Percentage	39.34%

2.3. Coverage

Mean	33.2671
Standard Deviation	386.3011

2.4. Mapping Quality

Mean Mapping Quality	53.19

2.5. Insert size

Mean	141,775.07
Standard Deviation	3,812,460.92
P25/Median/P75	81 / 132 / 207

2.6. Mismatches and indels

General error rate	0.31%
Mismatches	299,216,074
Insertions	14,791,840
Mapped reads with at least one insertion	1.61%
Deletions	10,103,945
Mapped reads with at least one deletion	1.1%
Homopolymer indels	47.94%

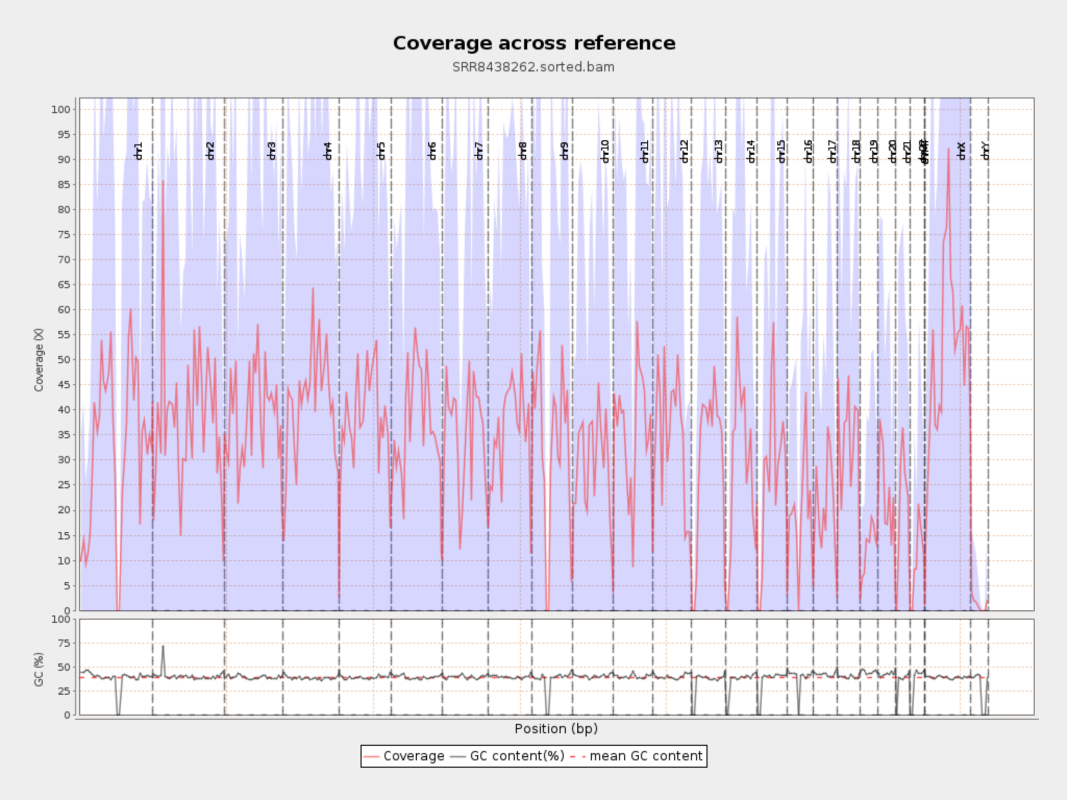
2.7. Chromosome stats

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

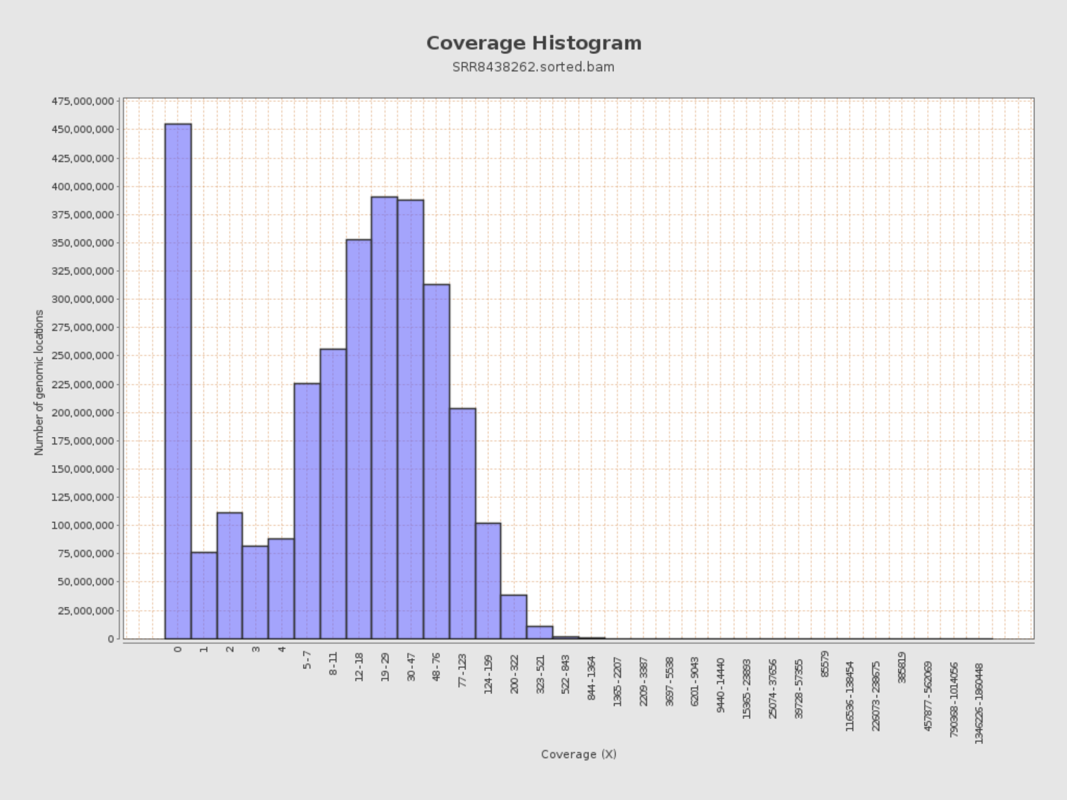
		bases	coverage	deviation
chr1	249250621	8217617314	32.9693	53.1452
chr2	243199373	9351639562	38.4526	1,367.1844
chr3	198022430	7711385924	38.942	51.9416
chr4	191154276	7981137019	41.7523	53.9743
chr5	180915260	6936578816	38.3416	52.059
chr6	171115067	6508883447	38.038	53.4486
chr7	159138663	5551067018	34.882	50.2511
chr8	146364022	5325301527	36.384	49.0531
chr9	141213431	4538401882	32.1386	55.0037
chr10	135534747	4087655261	30.1595	44.6732
chr11	135006516	4818128104	35.6881	51.7476
chr12	133851895	4599644789	34.3637	49.699
chr13	115169878	3519844160	30.5622	46.4169
chr14	107349540	3102487881	28.9008	46.6998
chr15	102531392	2780374112	27.1173	48.3259
chr16	90354753	1674529231	18.5328	31.7012
chr17	81195210	1662638430	20.4771	36.3592
chr18	78077248	2676978135	34.2863	47.5863
chr19	59128983	744714398	12.5947	24.9022
chr20	63025520	1443591700	22.9049	37.7404
chr21	48129895	1046353447	21.7402	40.1587
chr22	51304566	508981687	9.9208	24.9569
chrMT	16571	17059	1.0294	2.1791
chrX	155270560	8123929511	52.3211	74.4792

chrY	59373566	72810117	1.2263	8.4985

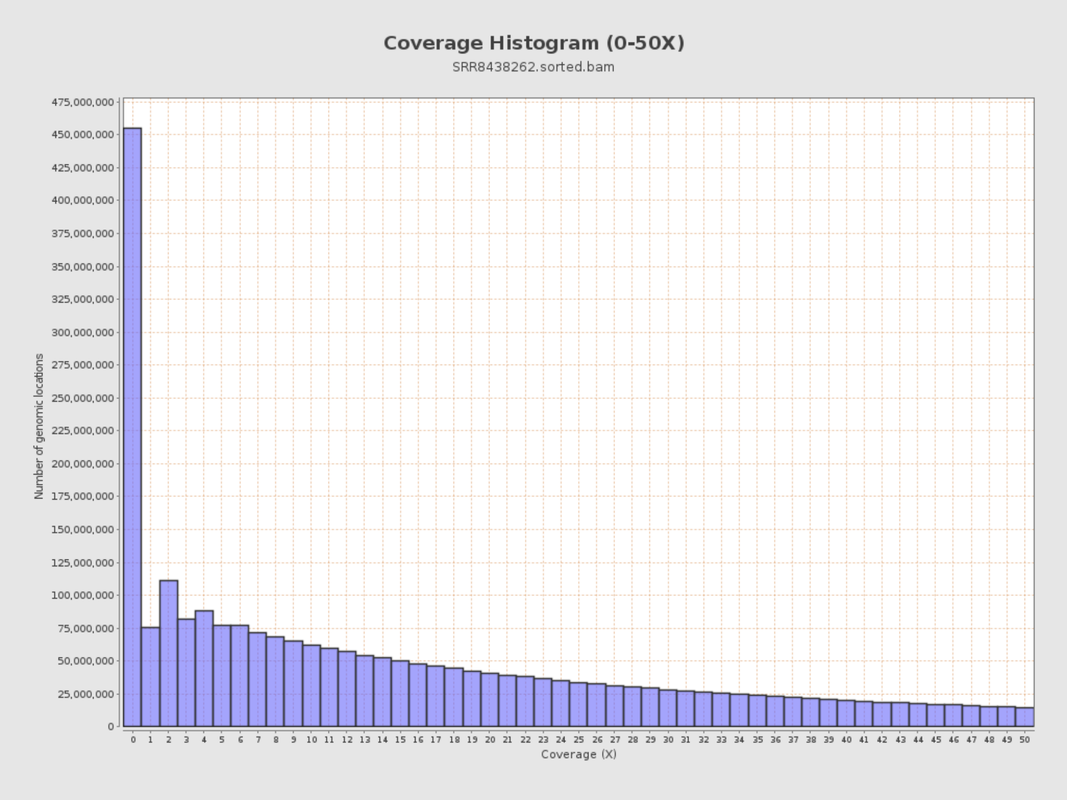
3. Results : Coverage across reference



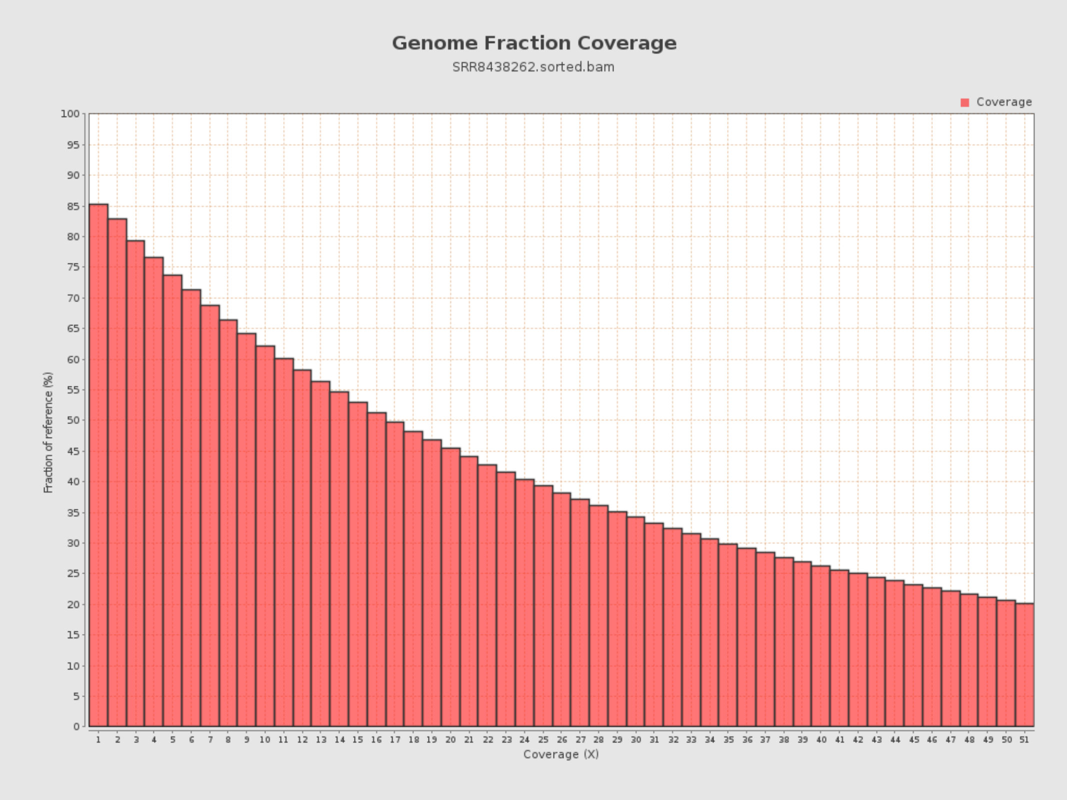
4. Results : Coverage Histogram



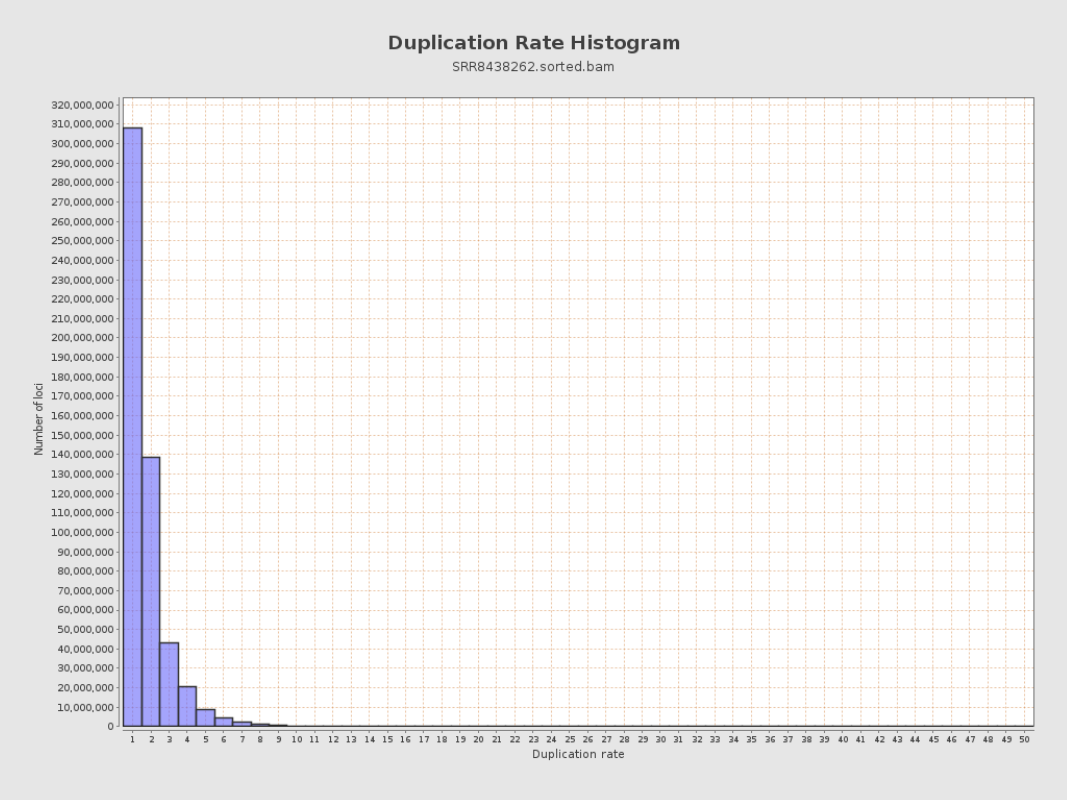
5. Results : Coverage Histogram (0-50X)



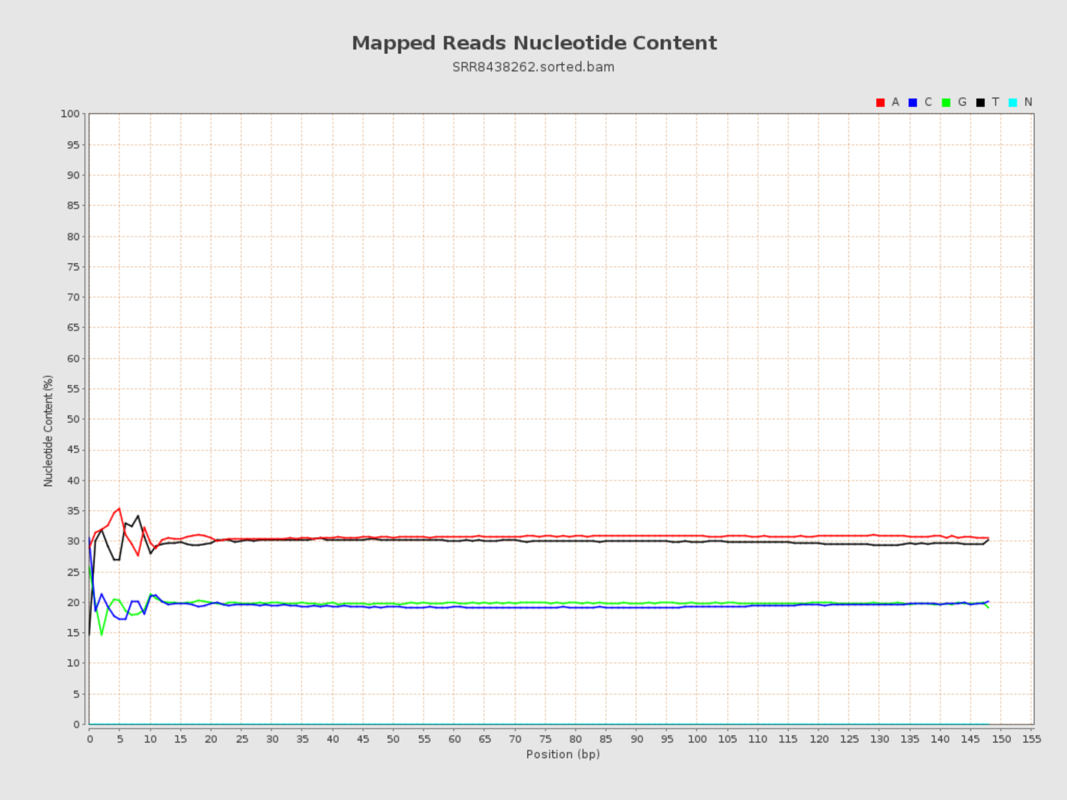
6. Results : Genome Fraction Coverage



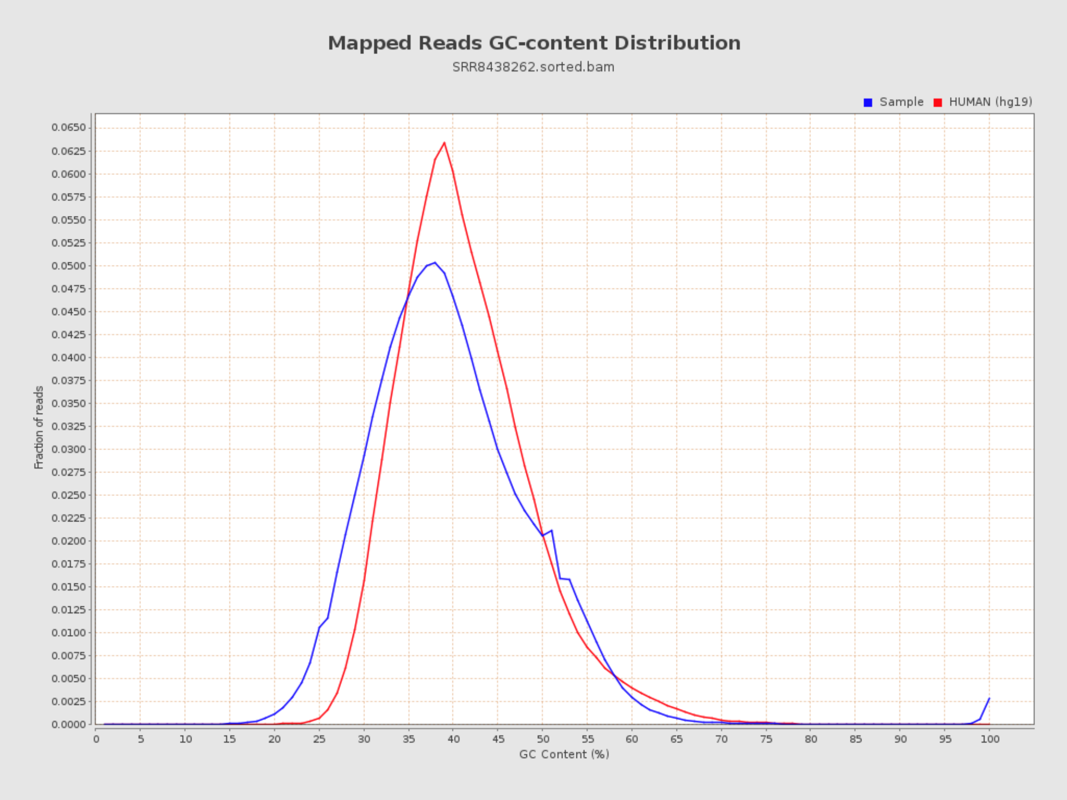
7. Results : Duplication Rate Histogram



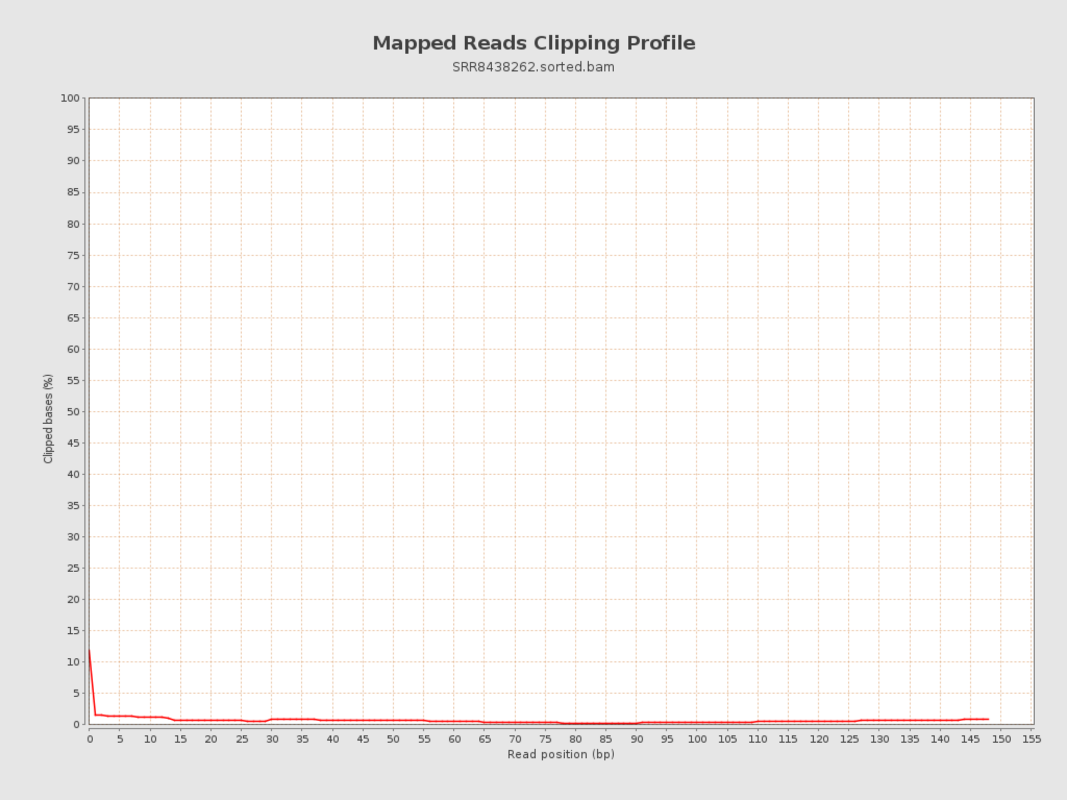
8. Results : Mapped Reads Nucleotide Content



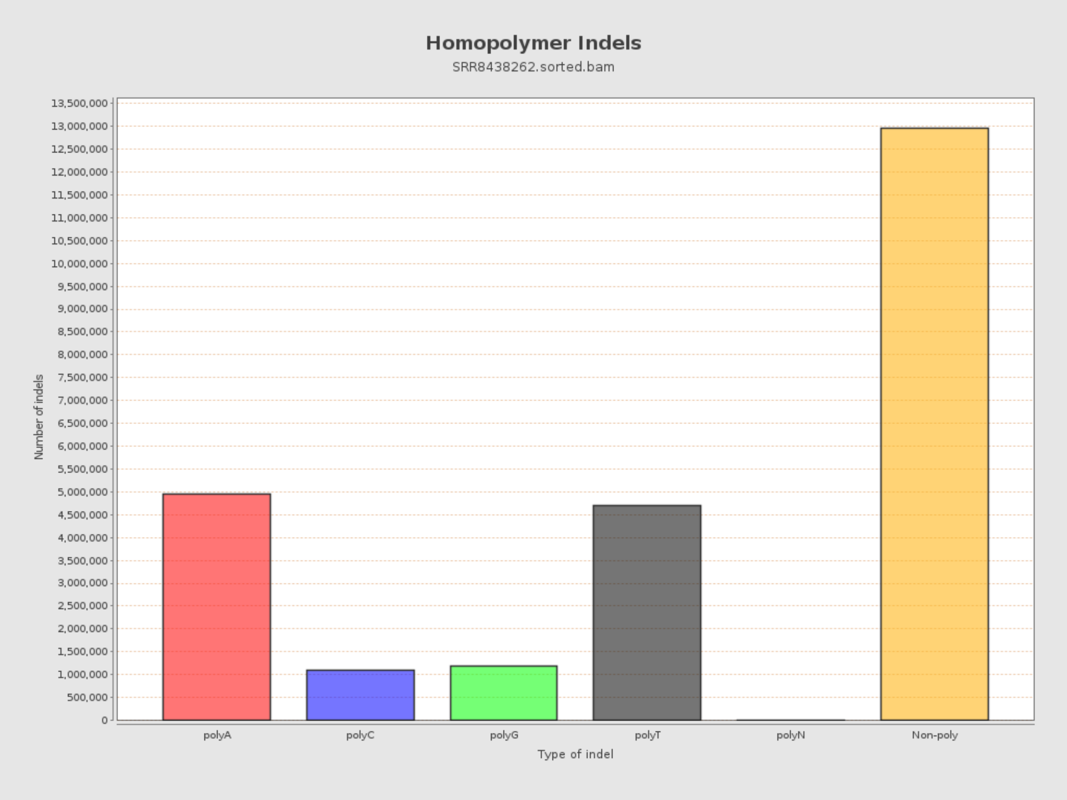
9. Results : Mapped Reads GC-content Distribution



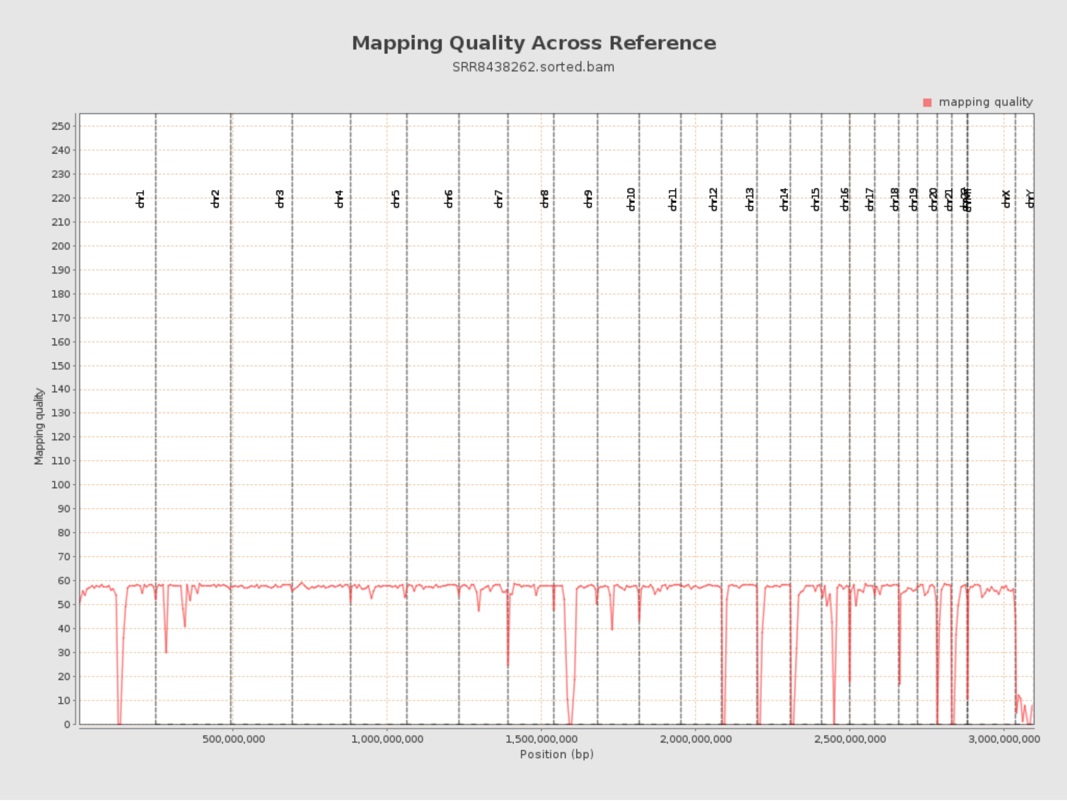
10. Results : Mapped Reads Clipping Profile



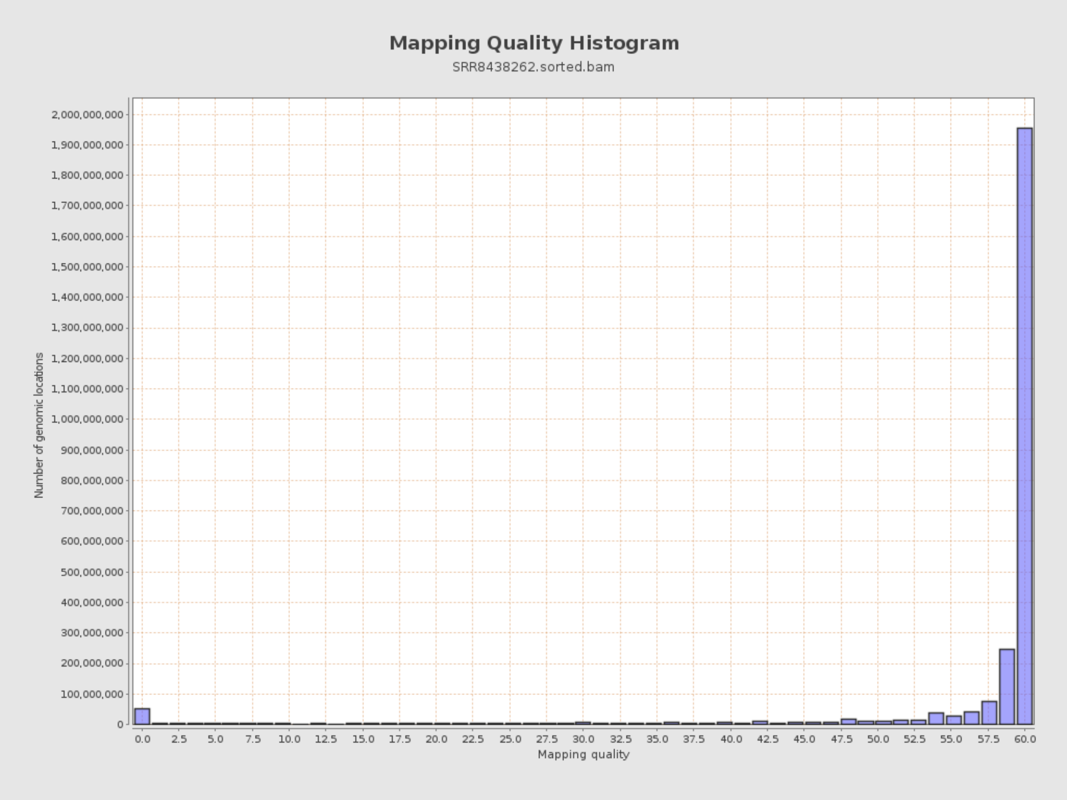
11. Results : Homopolymer Indels



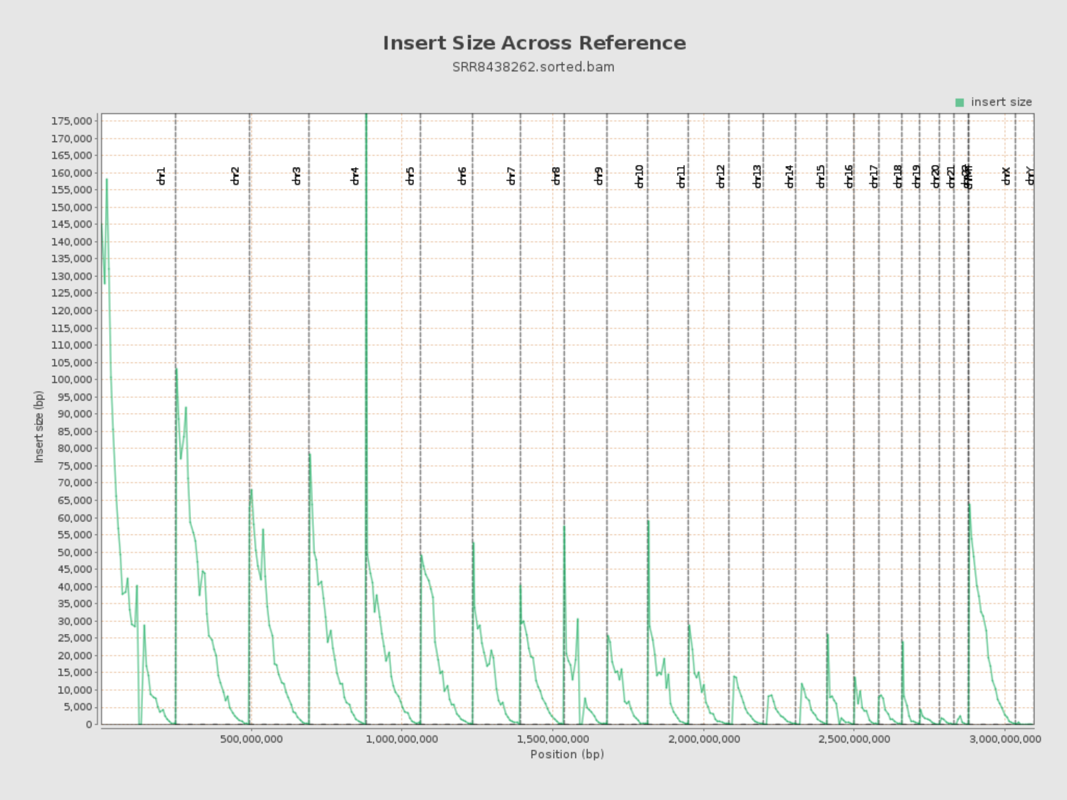
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram