Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/06 14:39:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438255.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_SRR8438255 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438255_1.fastq.gz SRR8438255_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 06 14:39:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438255.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	653,579,140
Mapped reads	651,418,446 / 99.67%
Unmapped reads	2,160,694 / 0.33%
Mapped paired reads	651,418,446 / 99.67%
Mapped reads, first in pair	325,914,479 / 49.87%
Mapped reads, second in pair	325,503,967 / 49.8%
Mapped reads, both in pair	649,863,308 / 99.43%
Mapped reads, singletons	1,555,138 / 0.24%
Secondary alignments	0
Supplementary alignments	11,420,108 / 1.75%
Read min/max/mean length	28 / 151 / 145.77
Duplicated reads (estimated)	261,415,149 / 40%
Duplication rate	37.39%
Clipped reads	116,204,233 / 17.78%

2.2. ACGT Content

Number/percentage of A's	28,502,519,728 / 30.29%
Number/percentage of C's	18,772,292,148 / 19.95%
Number/percentage of T's	27,137,773,893 / 28.84%
Number/percentage of G's	19,678,377,220 / 20.91%
Number/percentage of N's	704,329 / 0%

GC Percentage	40.87%

2.3. Coverage

Mean	30.4031
Standard Deviation	82.4403

2.4. Mapping Quality

Mean Mapping Quality	55.06

2.5. Insert size

Mean	40,002.92
Standard Deviation	1,938,583.11
P25/Median/P75	200 / 263 / 362

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	482,475,905
Insertions	12,051,304
Mapped reads with at least one insertion	1.82%
Deletions	10,691,375
Mapped reads with at least one deletion	1.61%
Homopolymer indels	48.41%

2.7. Chromosome stats

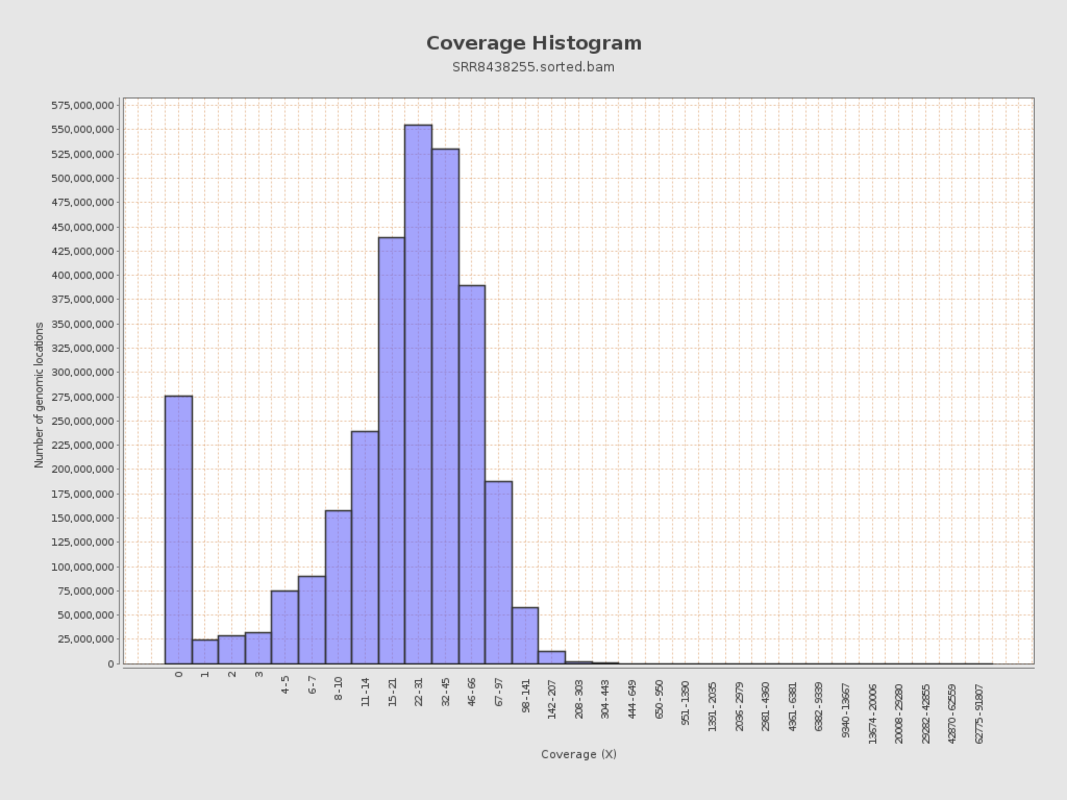
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	coverage	deviation
chr1	249250621	7622368467	30.5811	30.9762
chr2	243199373	8407815556	34.5717	94.4794
chr3	198022430	6901887260	34.8541	91.3204
chr4	191154276	6401801628	33.4902	27.5218
chr5	180915260	6150655170	33.9974	28.2086
chr6	171115067	5996746487	35.0451	28.5547
chr7	159138663	4929226892	30.9744	25.594
chr8	146364022	5008225738	34.2176	27.3938
chr9	141213431	3927653610	27.8136	32.4942
chr10	135534747	4118006604	30.3834	39.2832
chr11	135006516	4345108094	32.1844	27.5446
chr12	133851895	4278197862	31.9622	26.2334
chr13	115169878	3305274496	28.6991	26.9904
chr14	107349540	3142824304	29.2766	29.875
chr15	102531392	2673454994	26.0745	26.7441
chr16	90354753	2579768314	28.5516	46.7824
chr17	81195210	2343049241	28.857	33.9516
chr18	78077248	2564559781	32.8464	27.852
chr19	59128983	1405503440	23.7701	112.2251
chr20	63025520	2001321750	31.7541	29.1544
chr21	48129895	1279189605	26.5779	48.6505
chr22	51304566	996134523	19.4161	26.2809
chrMT	16571	450665478	27,196.0339	10,442.8877
chrX	155270560	2839016463	18.2843	20.9863

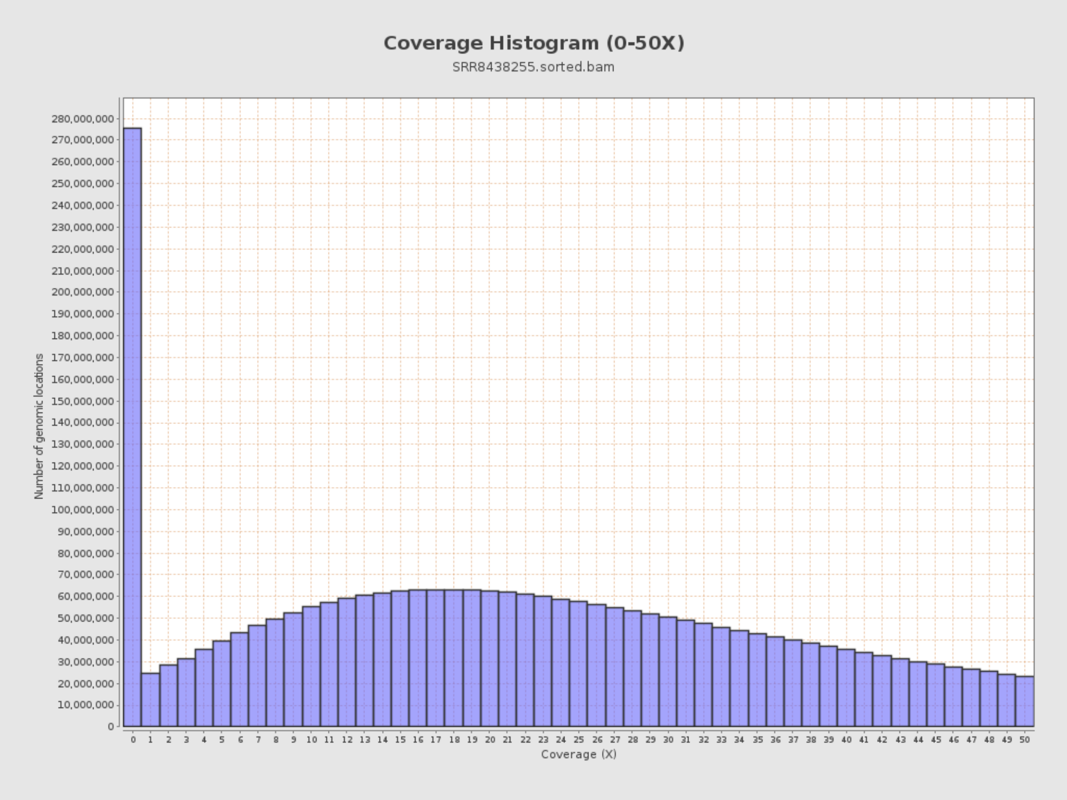
chrY	59373566	450264501	7.5836	26.4473

3. Results : Coverage across reference

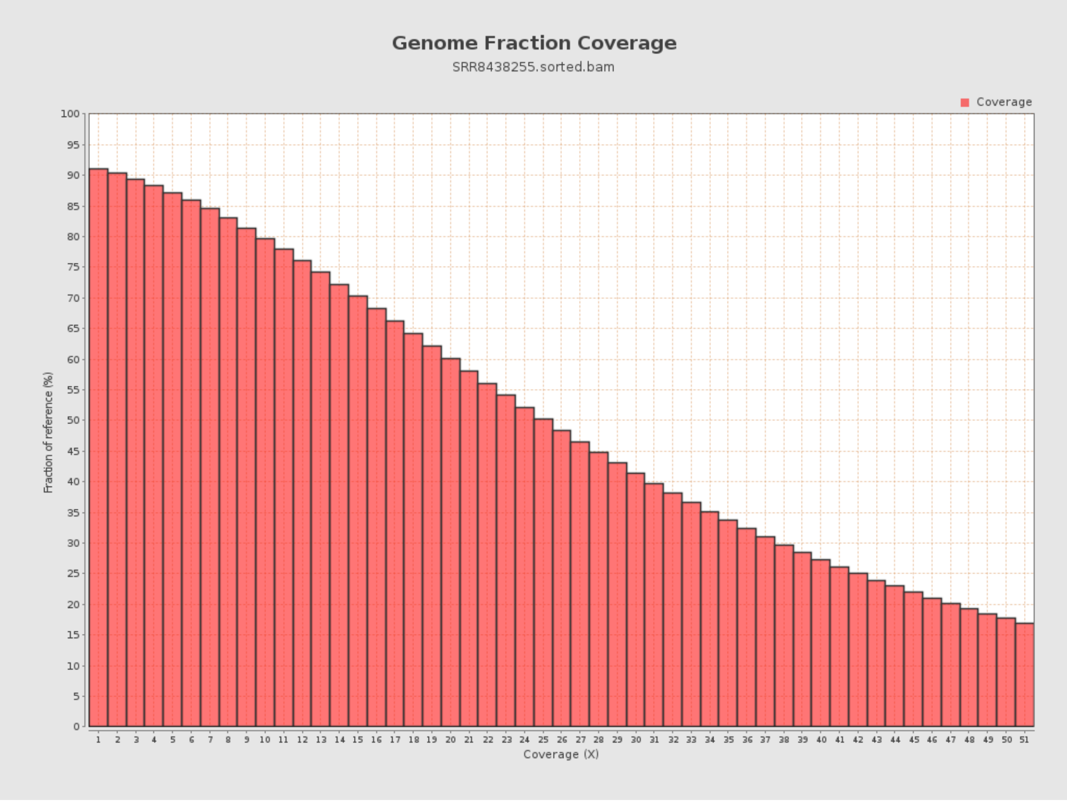
4. Results : Coverage Histogram



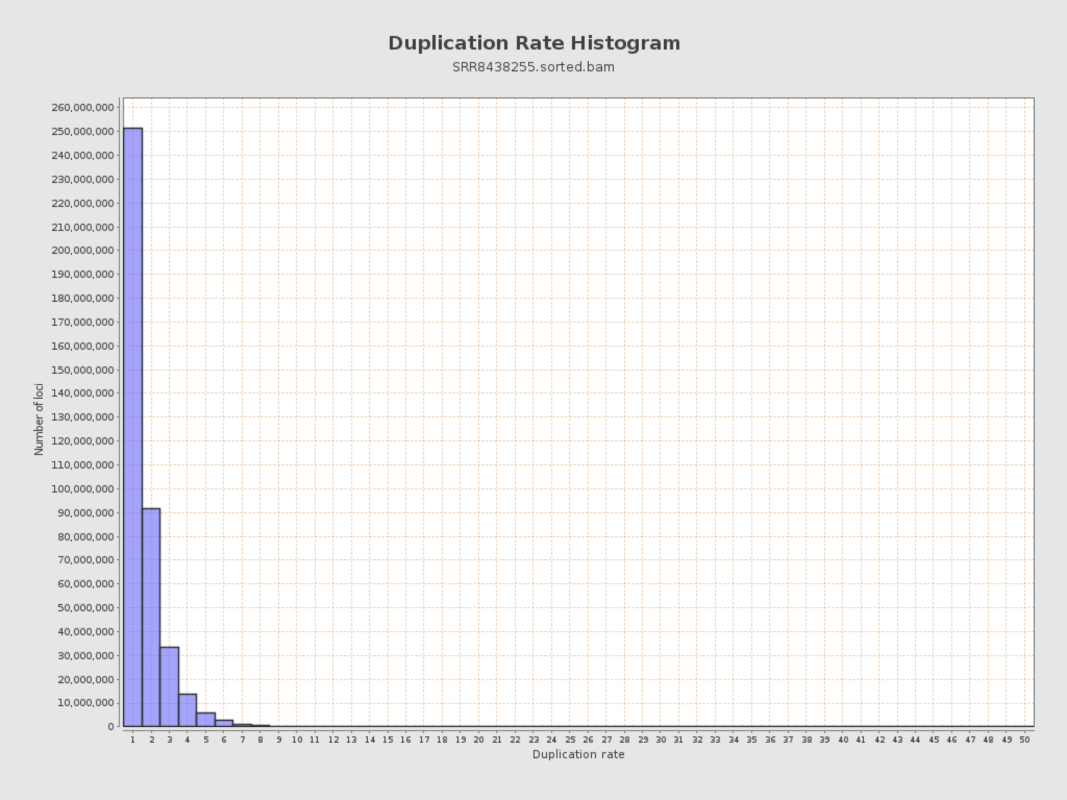
5. Results : Coverage Histogram (0-50X)



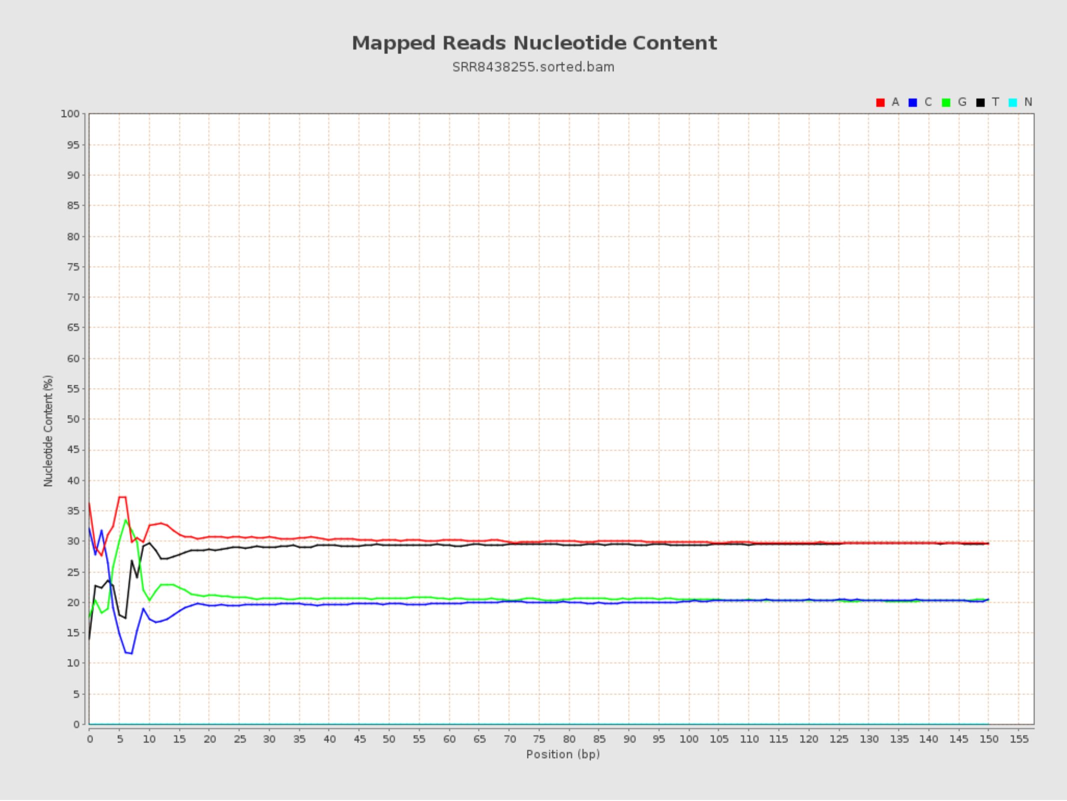
6. Results : Genome Fraction Coverage



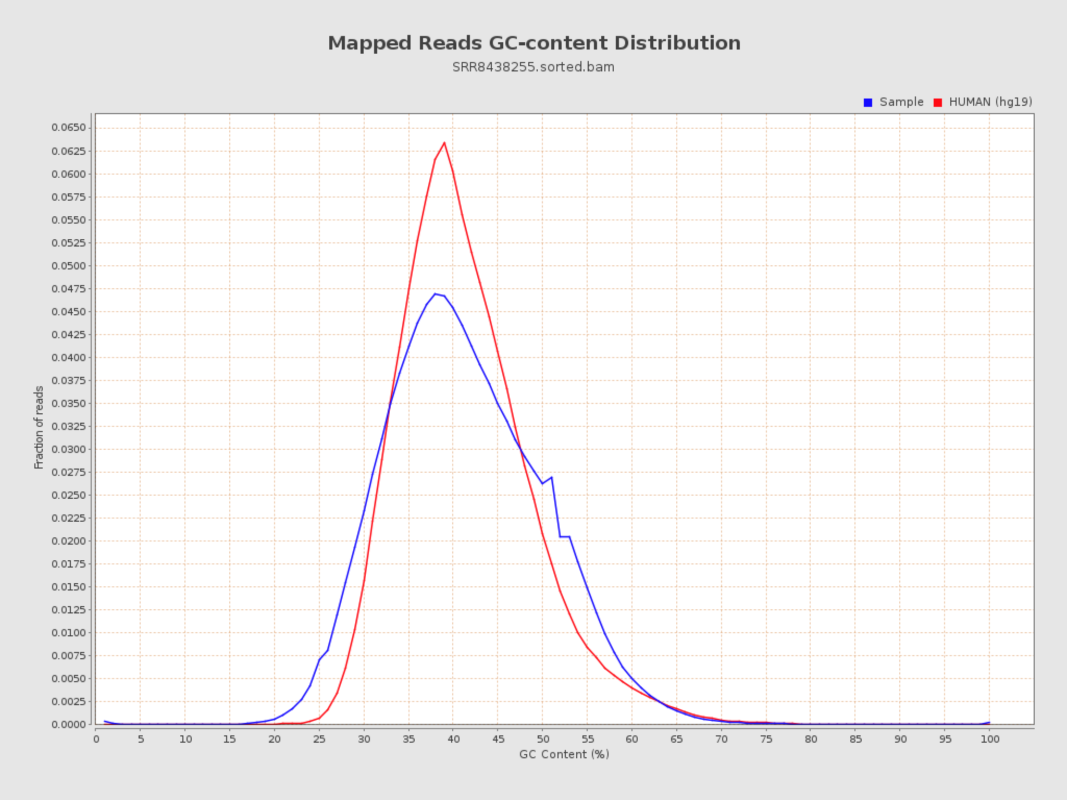
7. Results : Duplication Rate Histogram



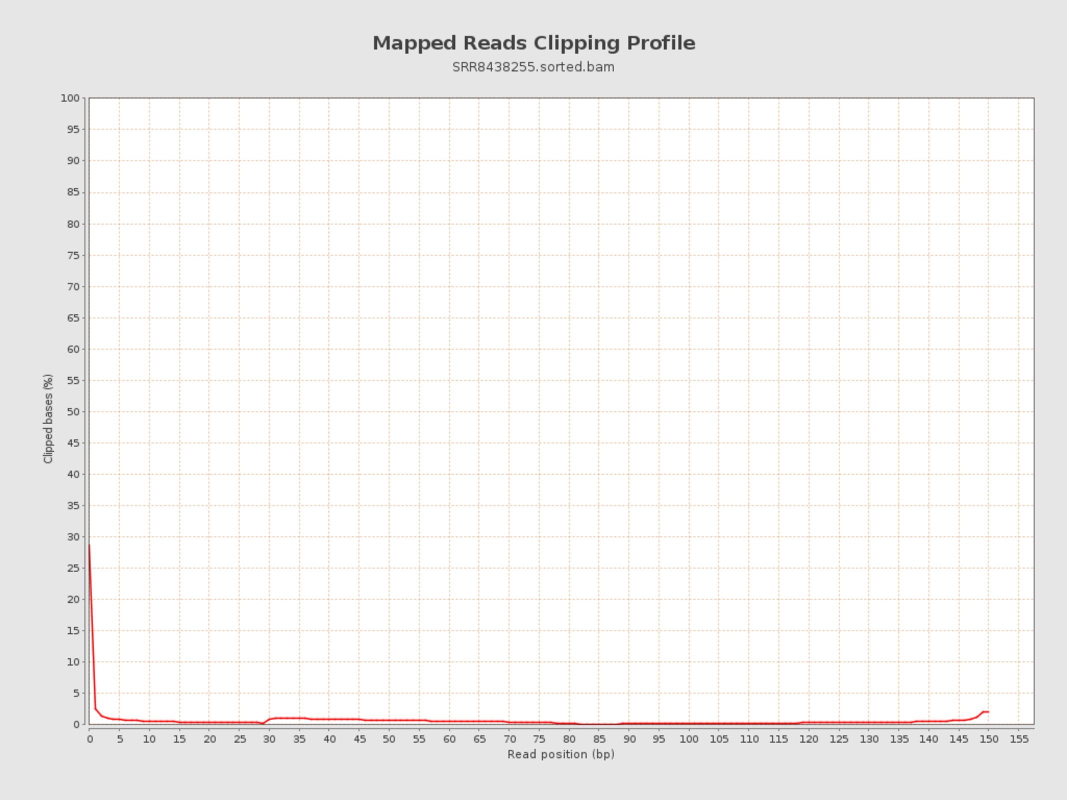
8. Results : Mapped Reads Nucleotide Content



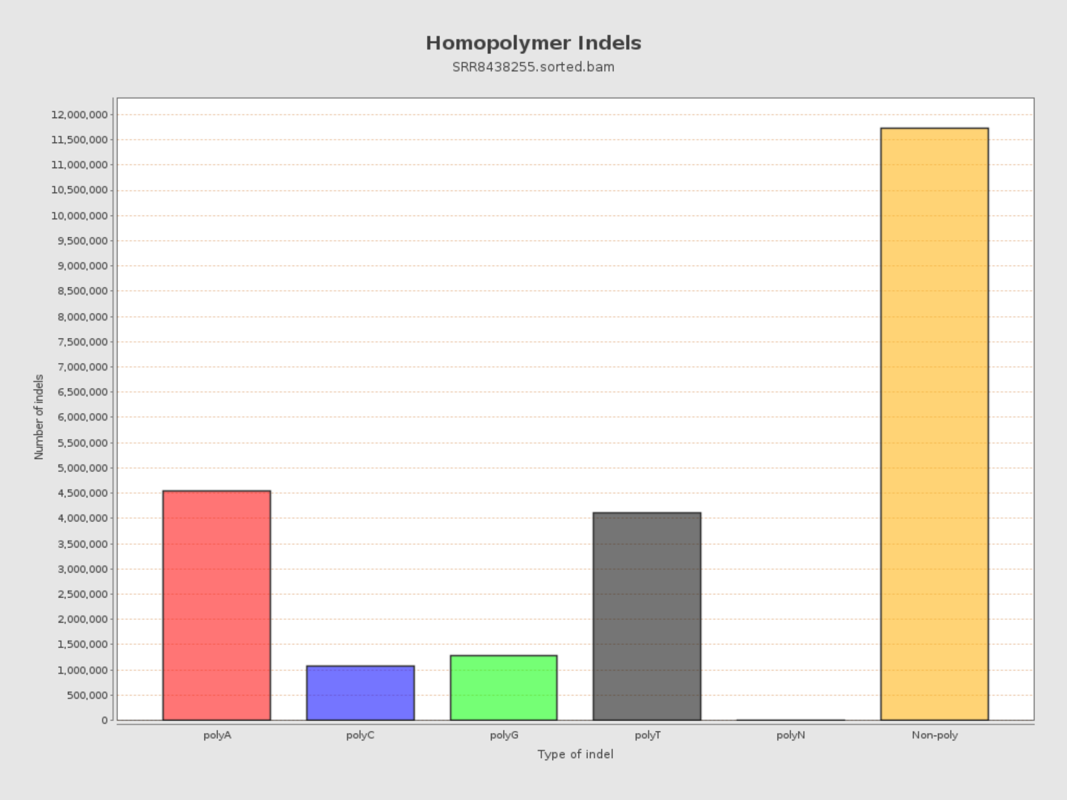
9. Results : Mapped Reads GC-content Distribution



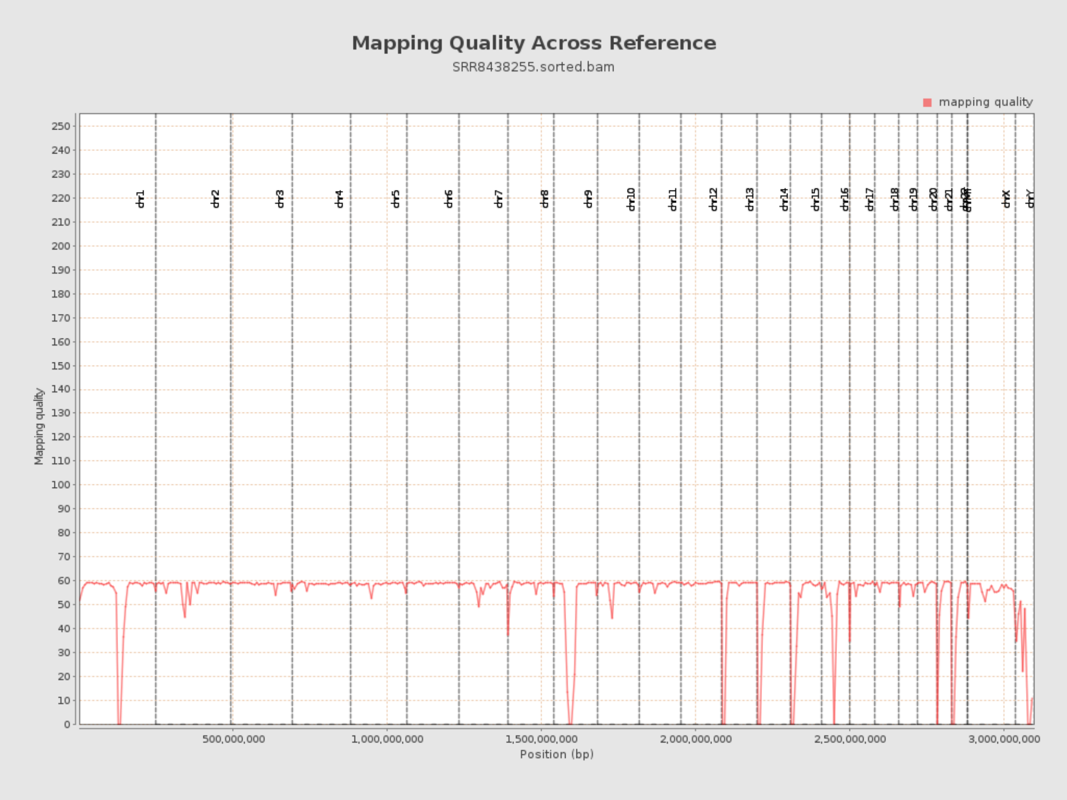
10. Results : Mapped Reads Clipping Profile



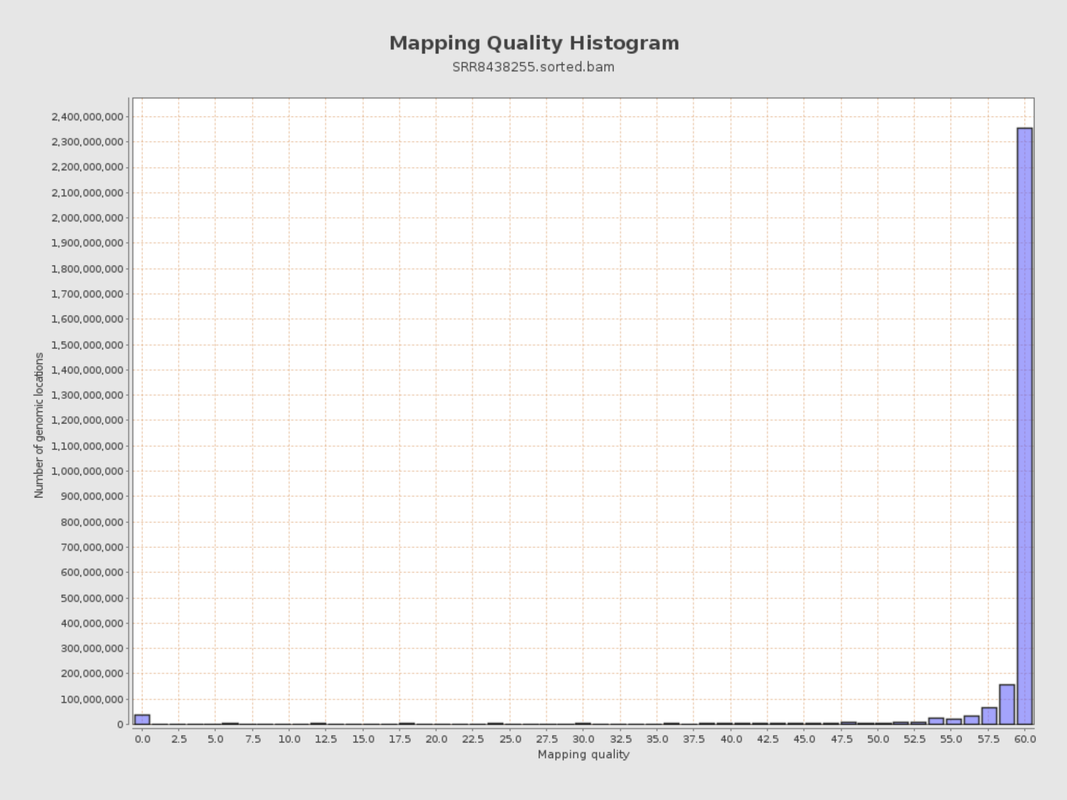
11. Results : Homopolymer Indels



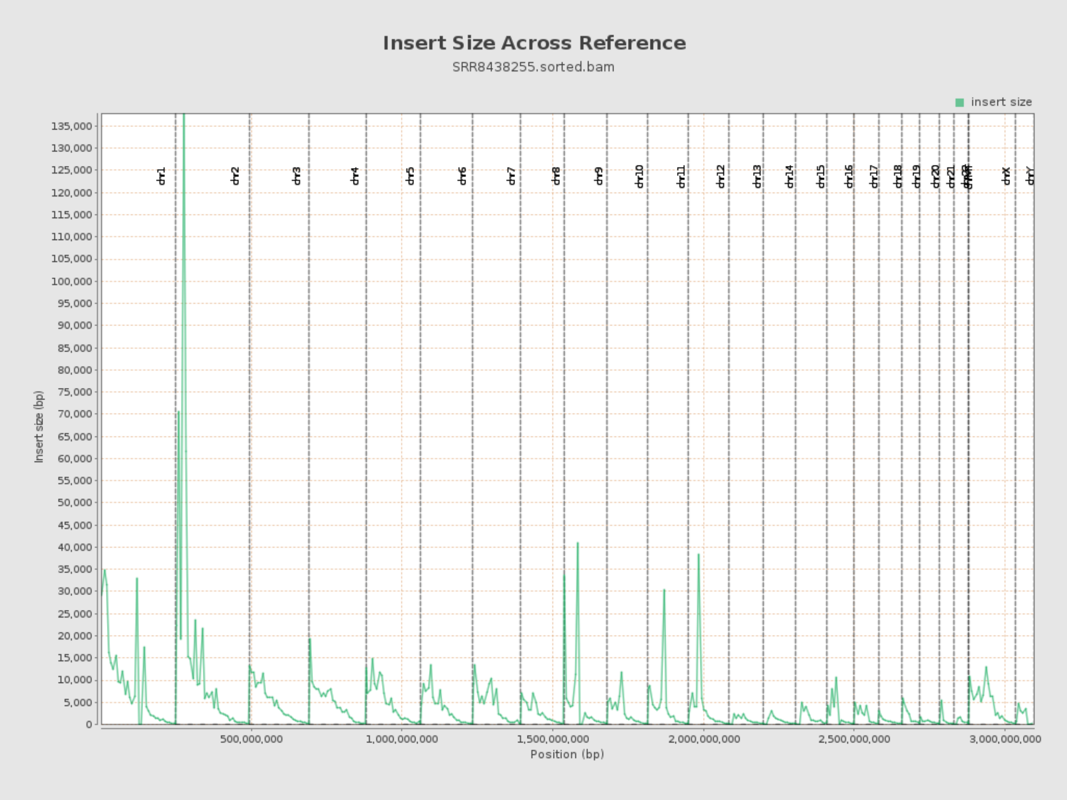
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram