Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/23 01:32:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438278.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_SRR8438278 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438278_1.fastq.gz SRR8438278_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 23 01:32:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438278.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	572,213,834
Mapped reads	570,459,742 / 99.69%
Unmapped reads	1,754,092 / 0.31%
Mapped paired reads	570,459,742 / 99.69%
Mapped reads, first in pair	285,337,537 / 49.87%
Mapped reads, second in pair	285,122,205 / 49.83%
Mapped reads, both in pair	569,211,290 / 99.48%
Mapped reads, singletons	1,248,452 / 0.22%
Secondary alignments	0
Supplementary alignments	8,929,915 / 1.56%
Read min/max/mean length	28 / 151 / 144.53
Duplicated reads (estimated)	248,752,162 / 43.47%
Duplication rate	40.62%
Clipped reads	105,339,296 / 18.41%

2.2. ACGT Content

Number/percentage of A's	24,490,806,544 / 29.97%
Number/percentage of C's	16,522,487,306 / 20.22%
Number/percentage of T's	23,388,751,039 / 28.62%
Number/percentage of G's	17,305,923,254 / 21.18%
Number/percentage of N's	506,702 / 0%

GC Percentage	41.4%

2.3. Coverage

Mean	26.4015
Standard Deviation	97.4001

2.4. Mapping Quality

Mean Mapping Quality	54.96

2.5. Insert size

Mean	41,077.09
Standard Deviation	1,998,954.97
P25/Median/P75	179 / 233 / 323

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	413,221,188
Insertions	10,290,782
Mapped reads with at least one insertion	1.78%
Deletions	9,247,238
Mapped reads with at least one deletion	1.6%
Homopolymer indels	48.71%

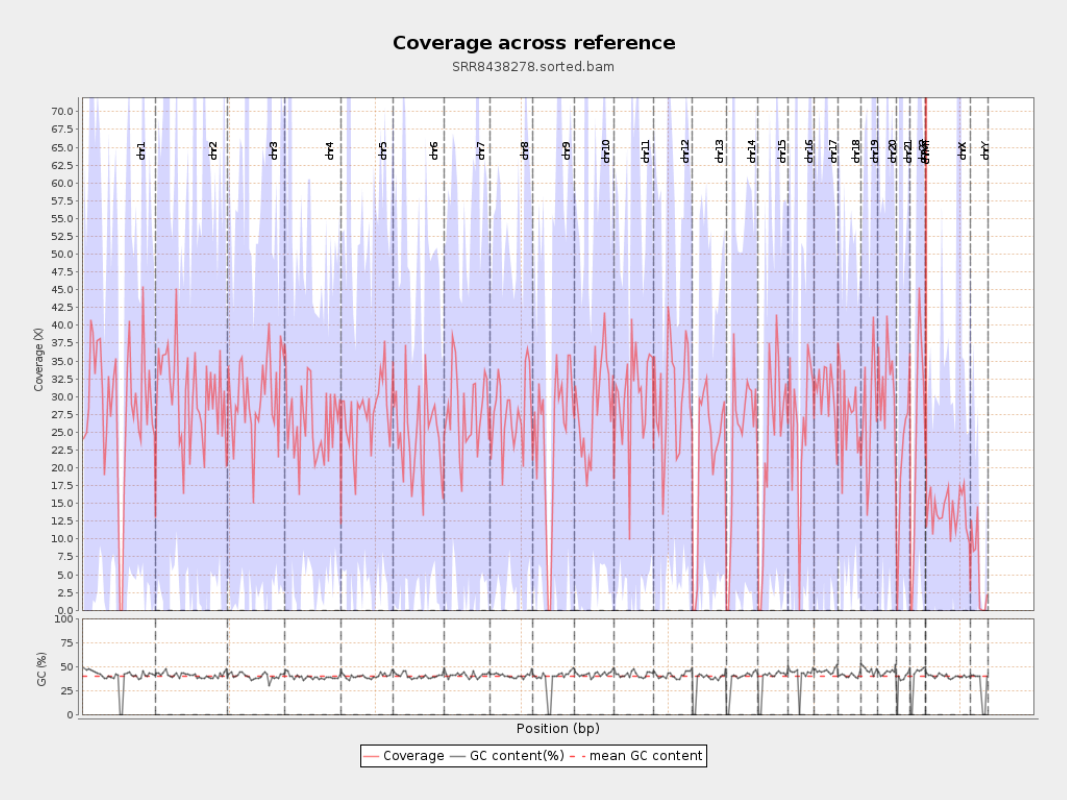
2.7. Chromosome stats

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

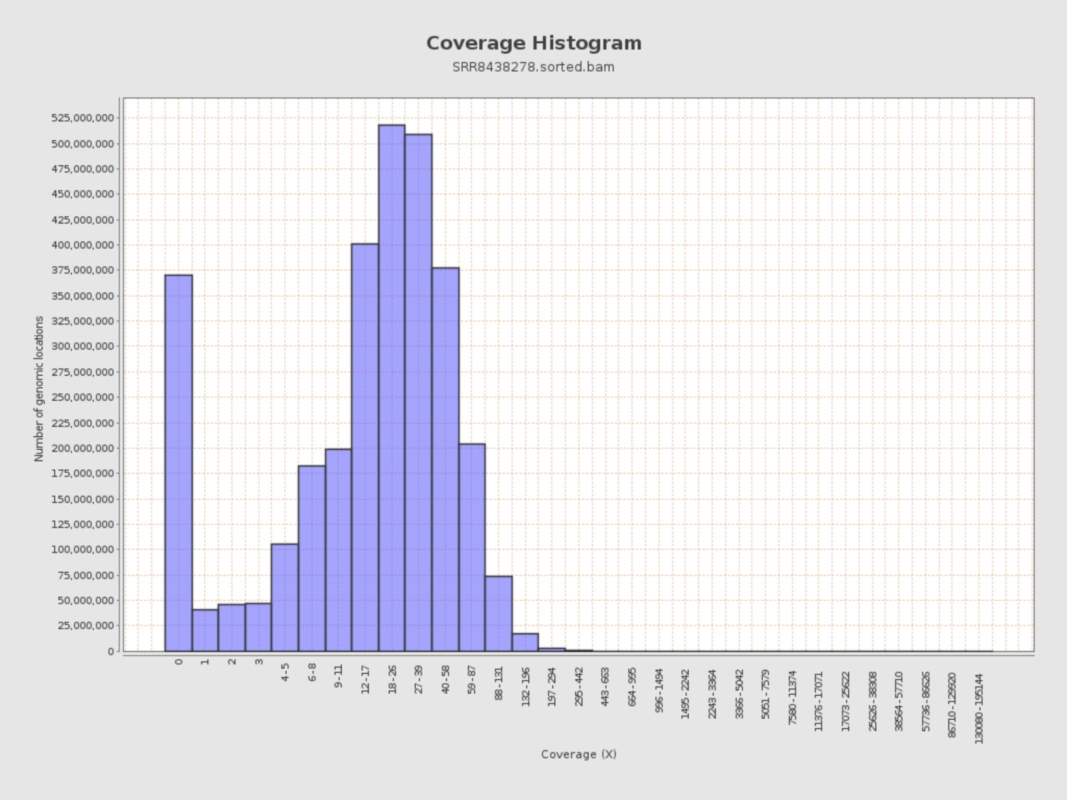
		bases	coverage	deviation
chr1	249250621	7014012800	28.1404	30.1059
chr2	243199373	7331037039	30.1441	130.108
chr3	198022430	5891327799	29.7508	222.0737
chr4	191154276	4986823872	26.088	34.8983
chr5	180915260	5051373626	27.9212	49.9574
chr6	171115067	4242696296	24.7944	26.2259
chr7	159138663	4421207776	27.7821	32.4027
chr8	146364022	4064239690	27.768	26.9832
chr9	141213431	3478477894	24.6328	31.2957
chr10	135534747	3936424814	29.0437	43.8654
chr11	135006516	4064775392	30.108	29.2286
chr12	133851895	4082610842	30.501	28.9149
chr13	115169878	2536111354	22.0206	23.4076
chr14	107349540	2626580734	24.4676	31.9922
chr15	102531392	2383505565	23.2466	28.6213
chr16	90354753	2338480708	25.8811	37.2341
chr17	81195210	2502996716	30.8269	33.6667
chr18	78077248	2154126044	27.5897	24.4153
chr19	59128983	1598570361	27.0353	322.5047
chr20	63025520	2011208448	31.911	31.6124
chr21	48129895	990549043	20.5807	120.4905
chr22	51304566	1253203076	24.4267	32.9325
chrMT	16571	288909969	17,434.6732	6,725.2525
chrX	155270560	2151822863	13.8585	36.9308

chrY	59373566	329919877	5.5567	15.6017

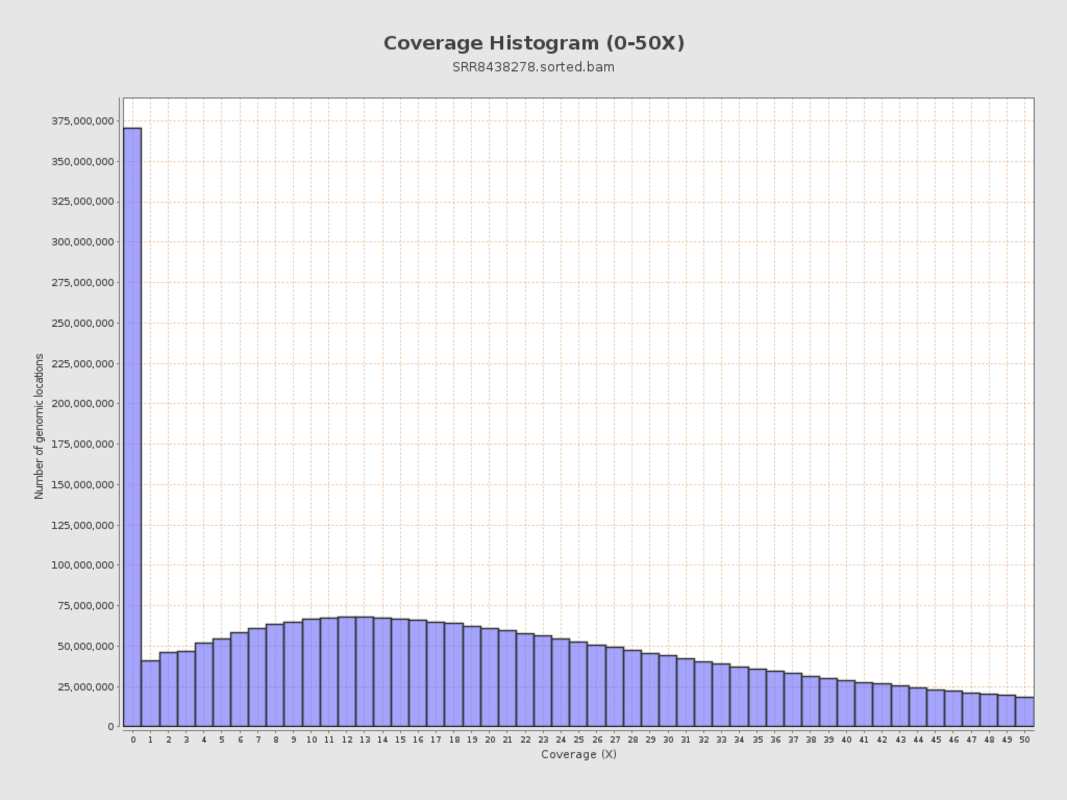
3. Results : Coverage across reference



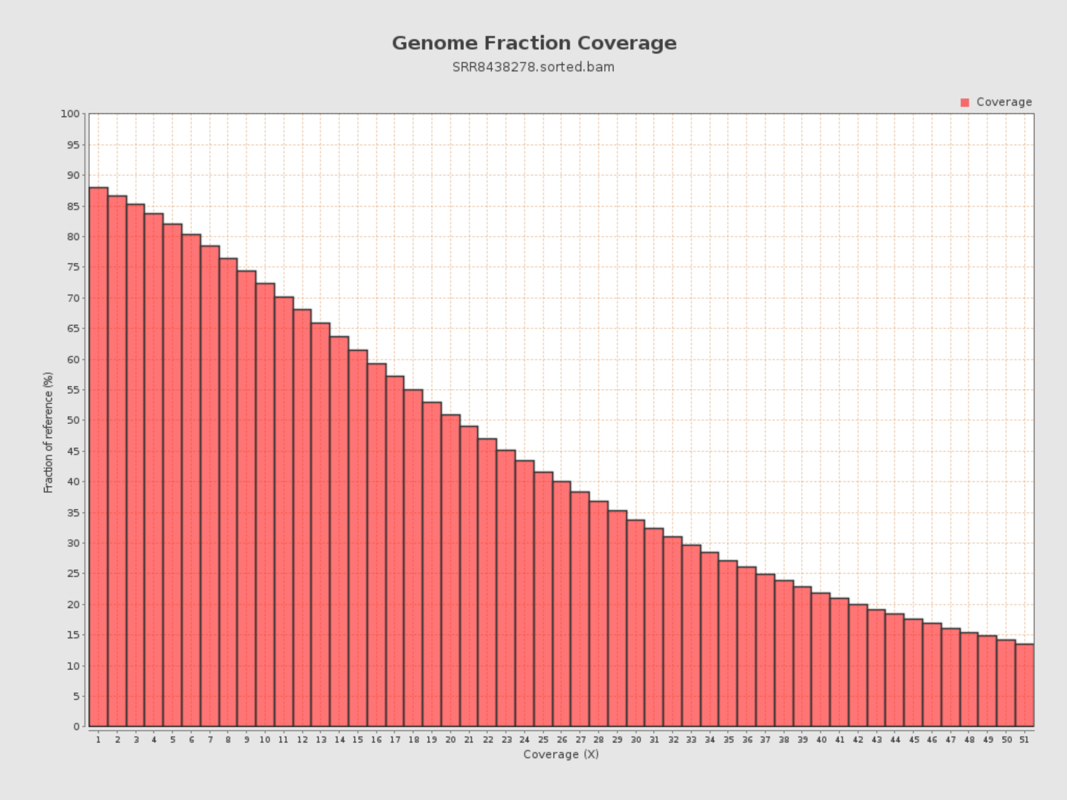
4. Results : Coverage Histogram



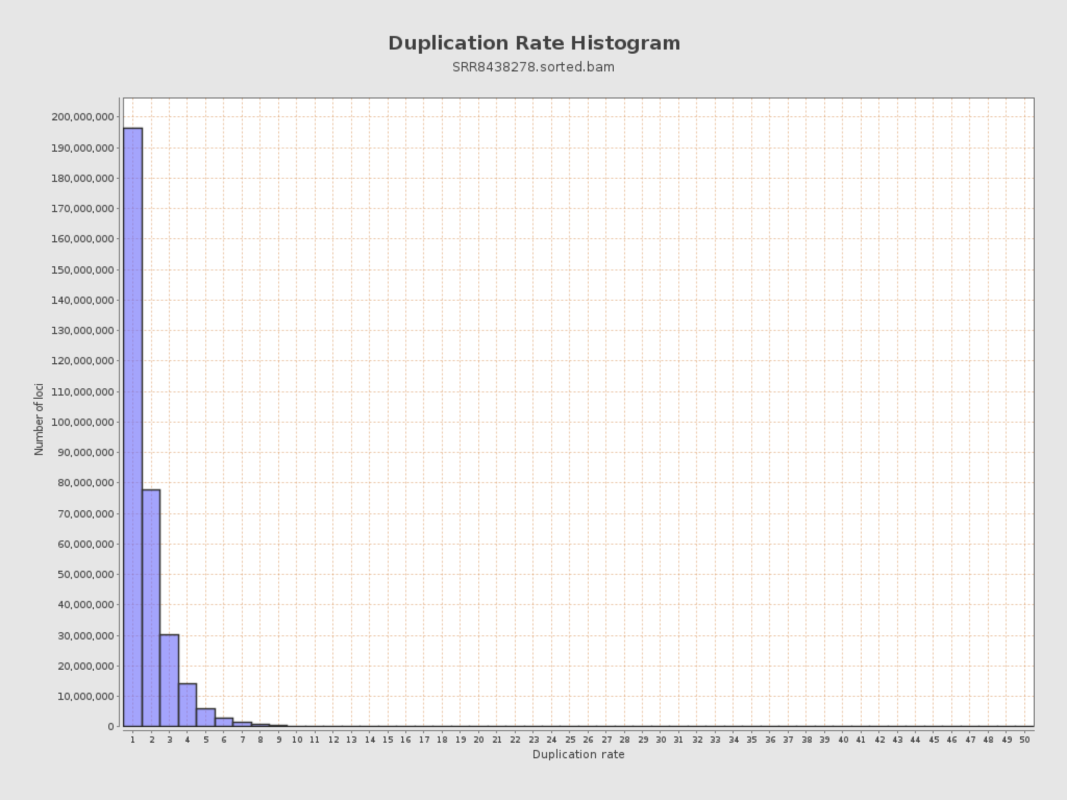
5. Results : Coverage Histogram (0-50X)



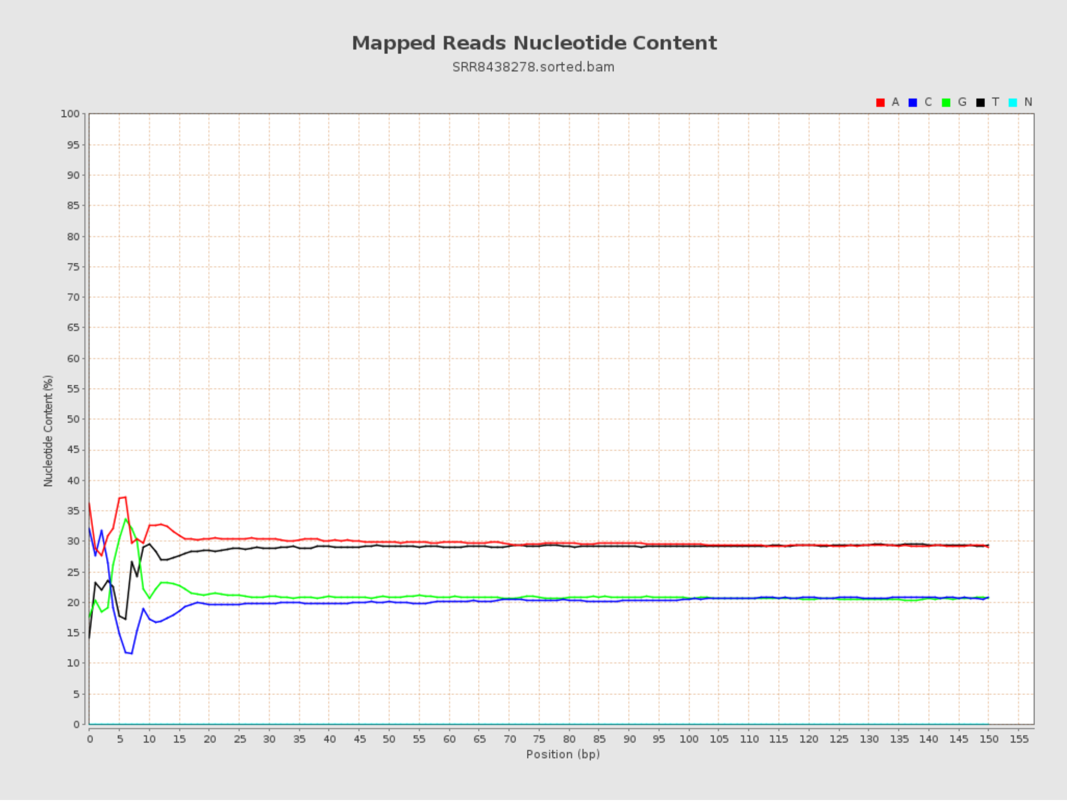
6. Results : Genome Fraction Coverage



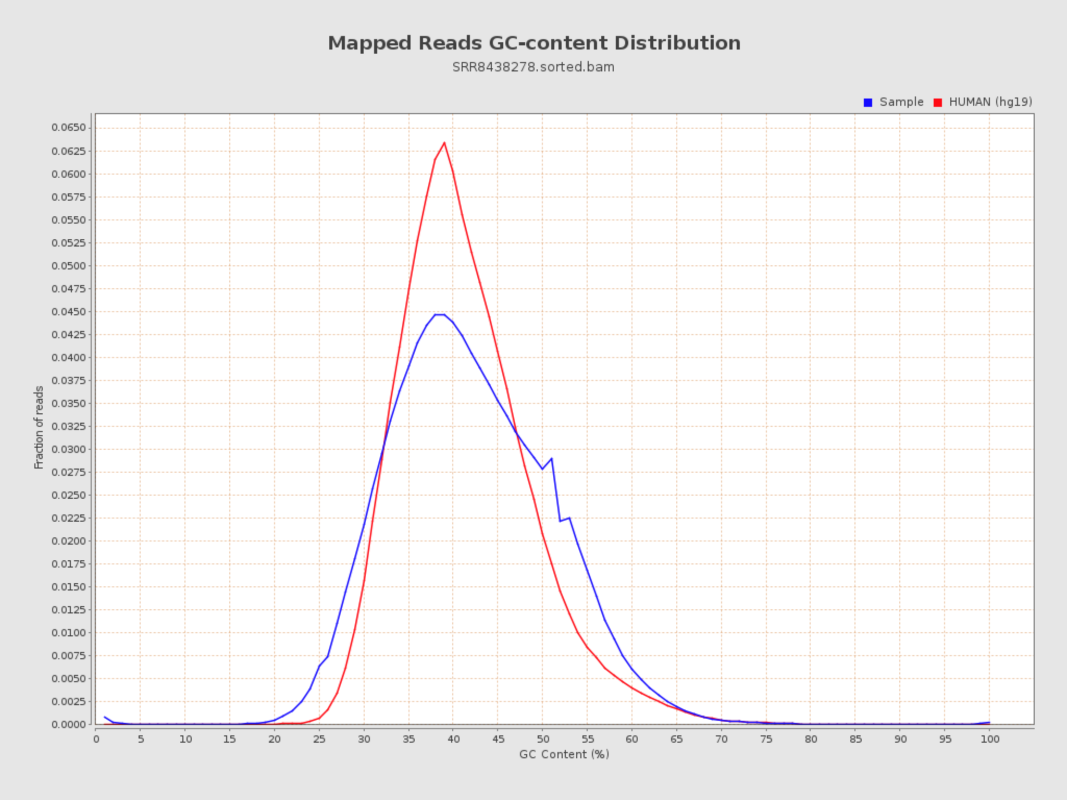
7. Results : Duplication Rate Histogram



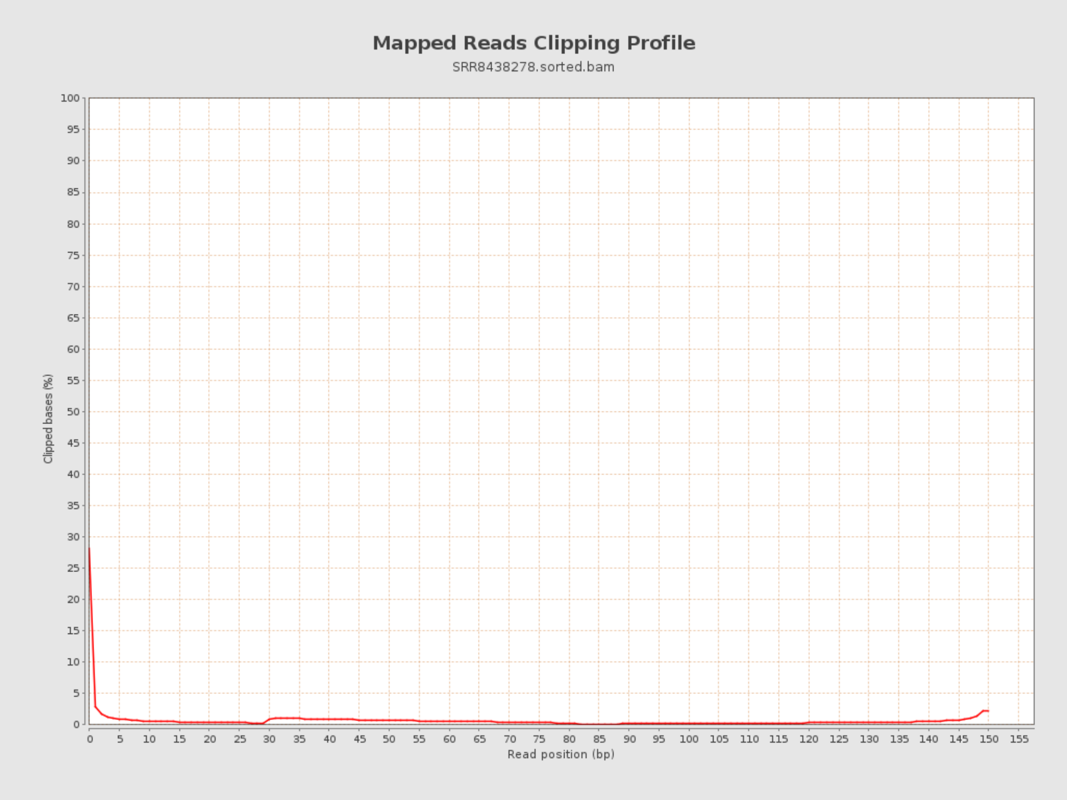
8. Results : Mapped Reads Nucleotide Content



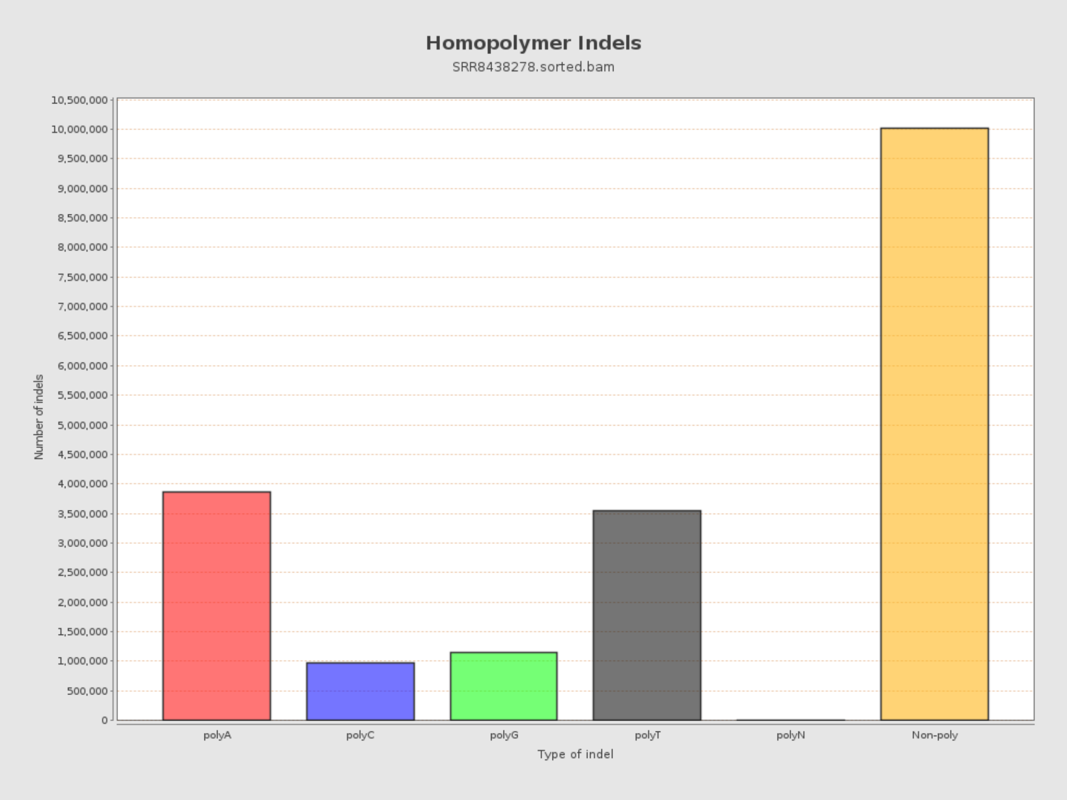
9. Results : Mapped Reads GC-content Distribution



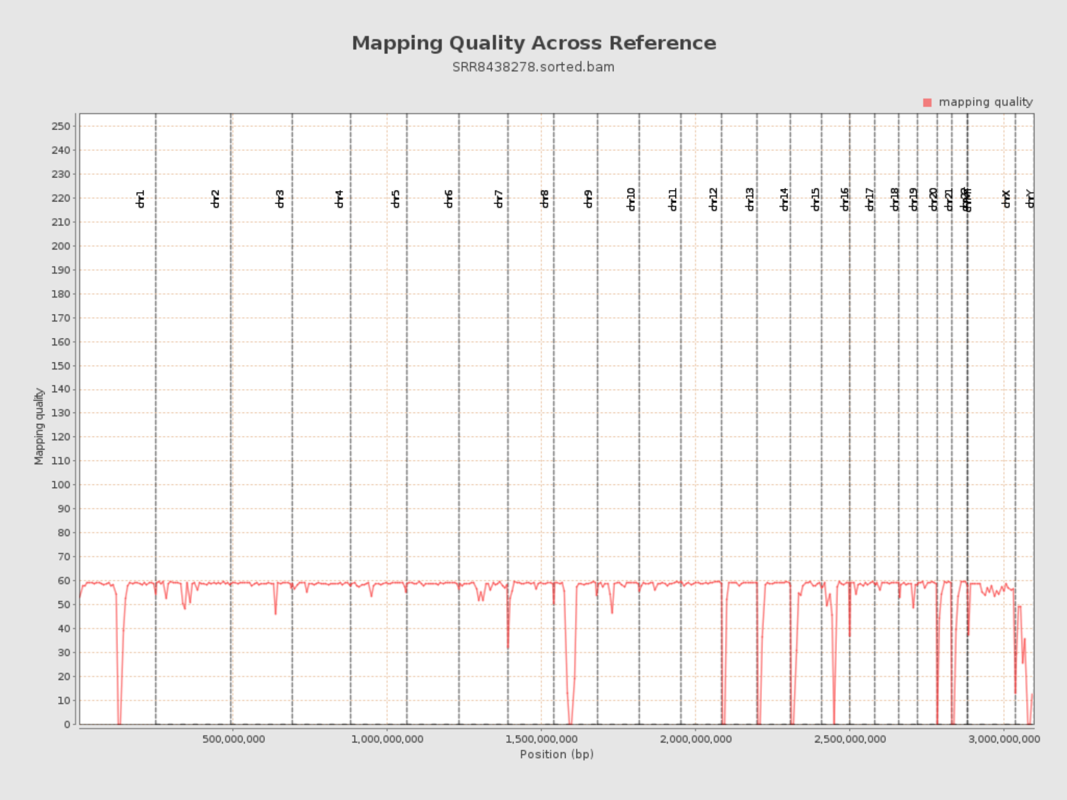
10. Results : Mapped Reads Clipping Profile



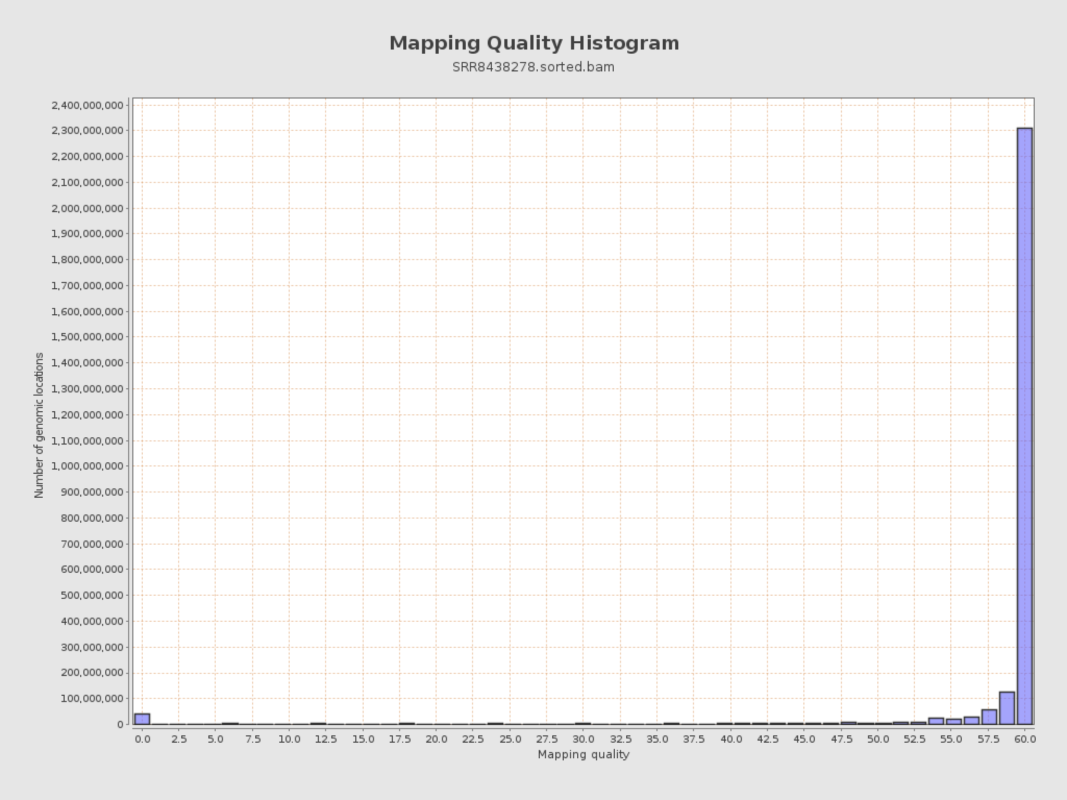
11. Results : Homopolymer Indels



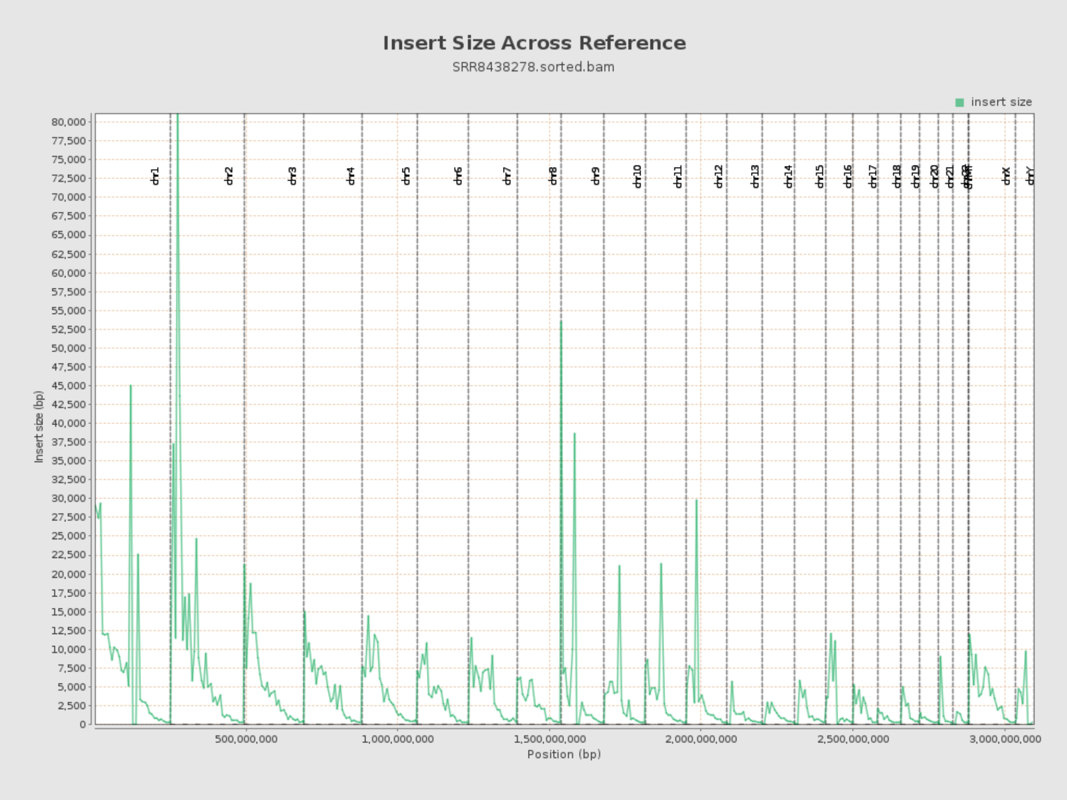
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram