Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 19:55:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163158.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_SRR1163158 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163158.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 19:55:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163158.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	94,184,514
Mapped reads	90,926,518 / 96.54%
Unmapped reads	3,257,996 / 3.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,042,250 / 1.11%
Read min/max/mean length	30 / 100 / 100.46
Duplicated reads (estimated)	54,481,183 / 57.85%
Duplication rate	53.2%
Clipped reads	5,377,395 / 5.71%

2.2. ACGT Content

Number/percentage of A's	2,401,780,069 / 26.56%
Number/percentage of C's	2,118,235,769 / 23.43%
Number/percentage of T's	2,437,126,919 / 26.96%
Number/percentage of G's	2,080,186,486 / 23.01%
Number/percentage of N's	3,972,083 / 0.04%
GC Percentage	46.44%

2.3. Coverage

Mean	2.9211

Standard Deviation	28.5749

2.4. Mapping Quality

Mean Mapping Quality	49.36

2.5. Mismatches and indels

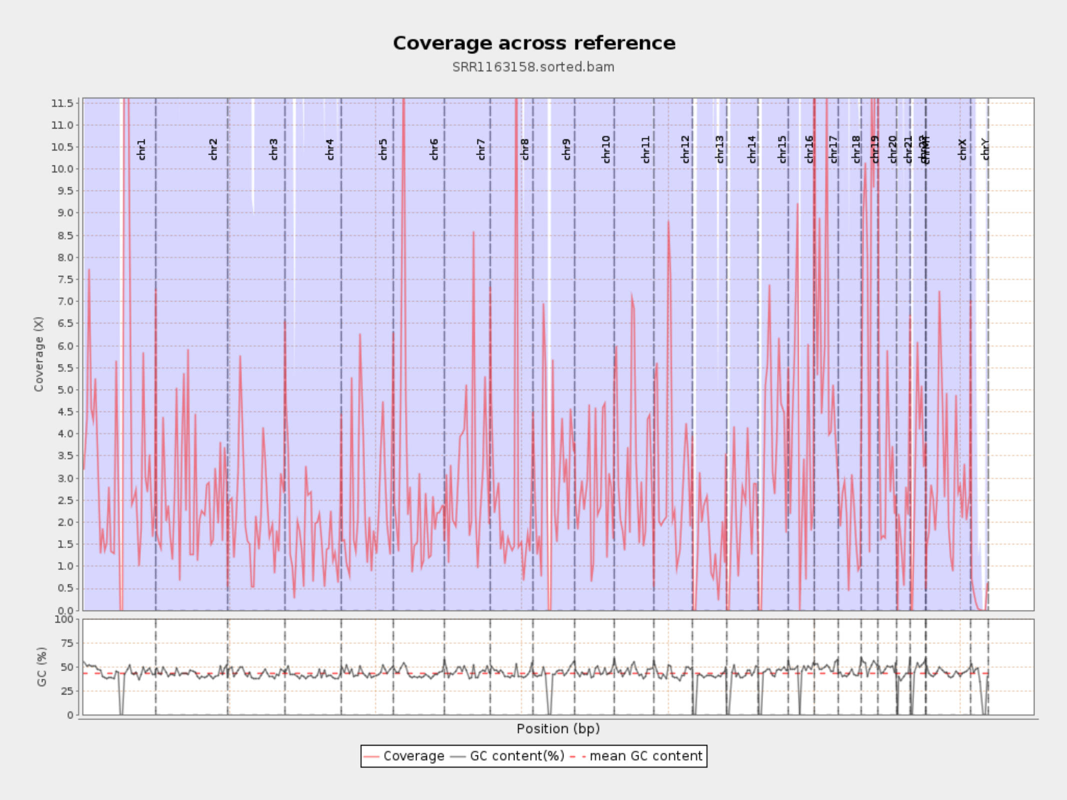
General error rate	0.83%
Mismatches	74,351,441
Insertions	686,693
Mapped reads with at least one insertion	0.75%
Deletions	768,543
Mapped reads with at least one deletion	0.83%
Homopolymer indels	46.36%

2.6. Chromosome stats

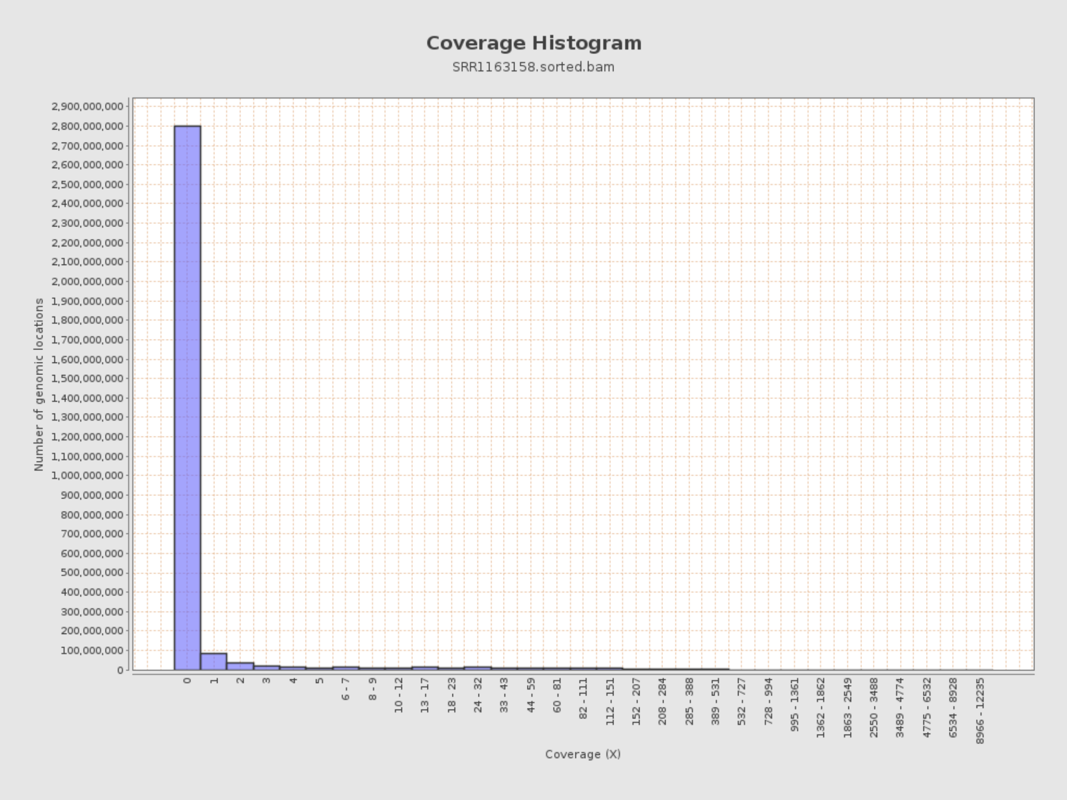
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	947983135	3.8033	33.5713
chr2	243199373	627216952	2.579	25.6876
chr3	198022430	450159058	2.2733	20.6717
chr4	191154276	336666192	1.7612	20.1865
chr5	180915260	455033596	2.5152	34.2444
chr6	171115067	455116289	2.6597	24.5922
chr7	159138663	492361064	3.0939	28.4144

chr8	146364022	374545107	2.559	41.2448
chr9	141213431	408400837	2.8921	25.9825
chr10	135534747	367751941	2.7133	24.8258
chr11	135006516	442776665	3.2797	26.0867
chr12	133851895	451103322	3.3702	25.8627
chr13	115169878	165579916	1.4377	16.3467
chr14	107349540	234534800	2.1848	20.0453
chr15	102531392	376344859	3.6705	28.7705
chr16	90354753	326877074	3.6177	27.7017
chr17	81195210	491602950	6.0546	41.7365
chr18	78077248	155370271	1.99	24.474
chr19	59128983	555388549	9.3928	56.9171
chr20	63025520	185779586	2.9477	24.6792
chr21	48129895	105301191	2.1879	30.7526
chr22	51304566	167278738	3.2605	26.7545
chrMT	16571	8203	0.495	0.8452
chrX	155270560	456001454	2.9368	27.6729
chrY	59373566	13679494	0.2304	17.4746

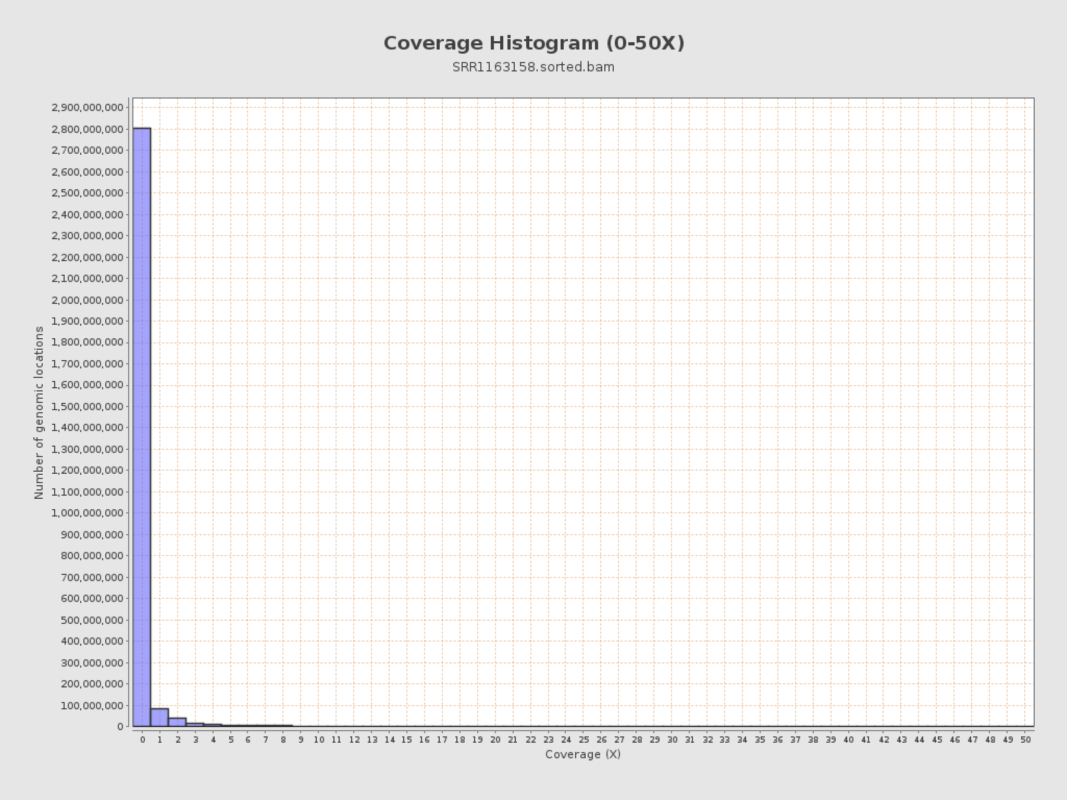
3. Results : Coverage across reference



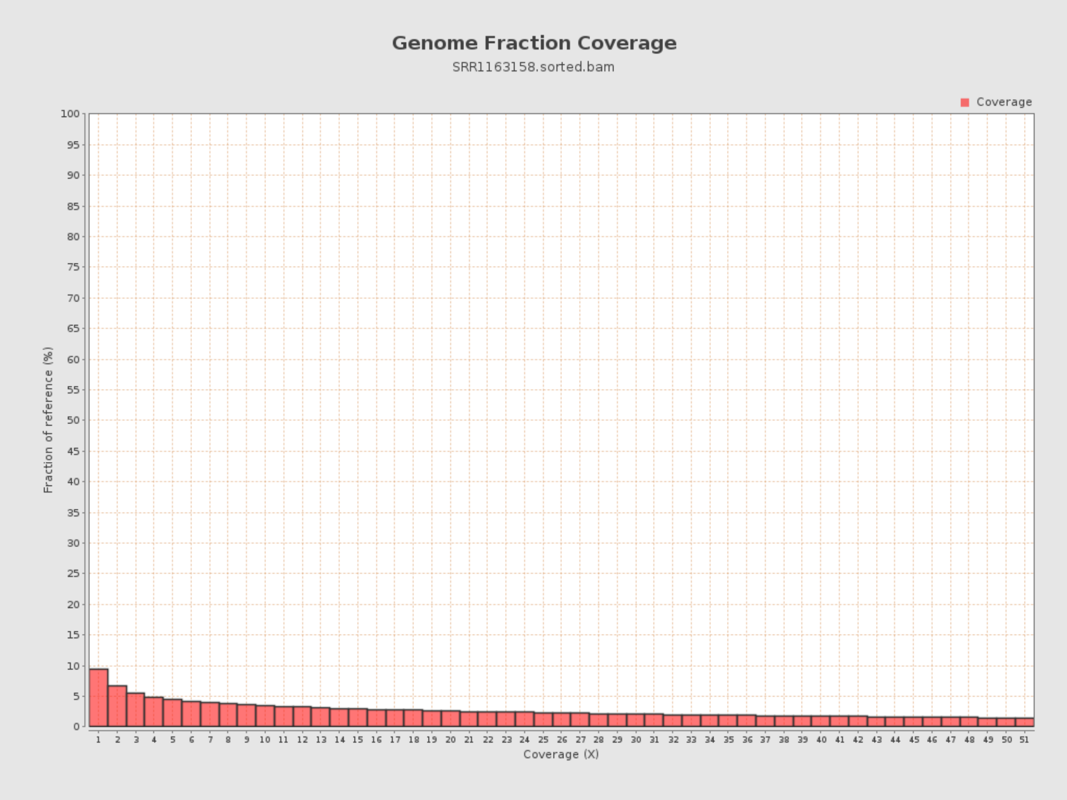
4. Results : Coverage Histogram



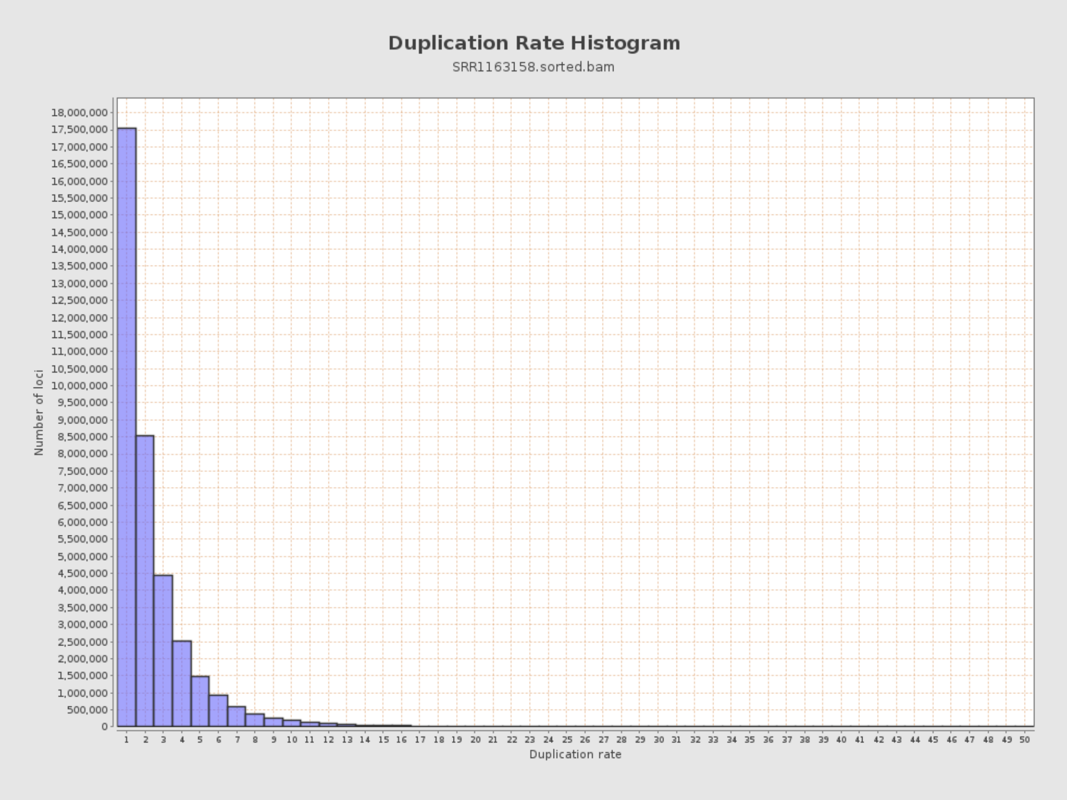
5. Results : Coverage Histogram (0-50X)



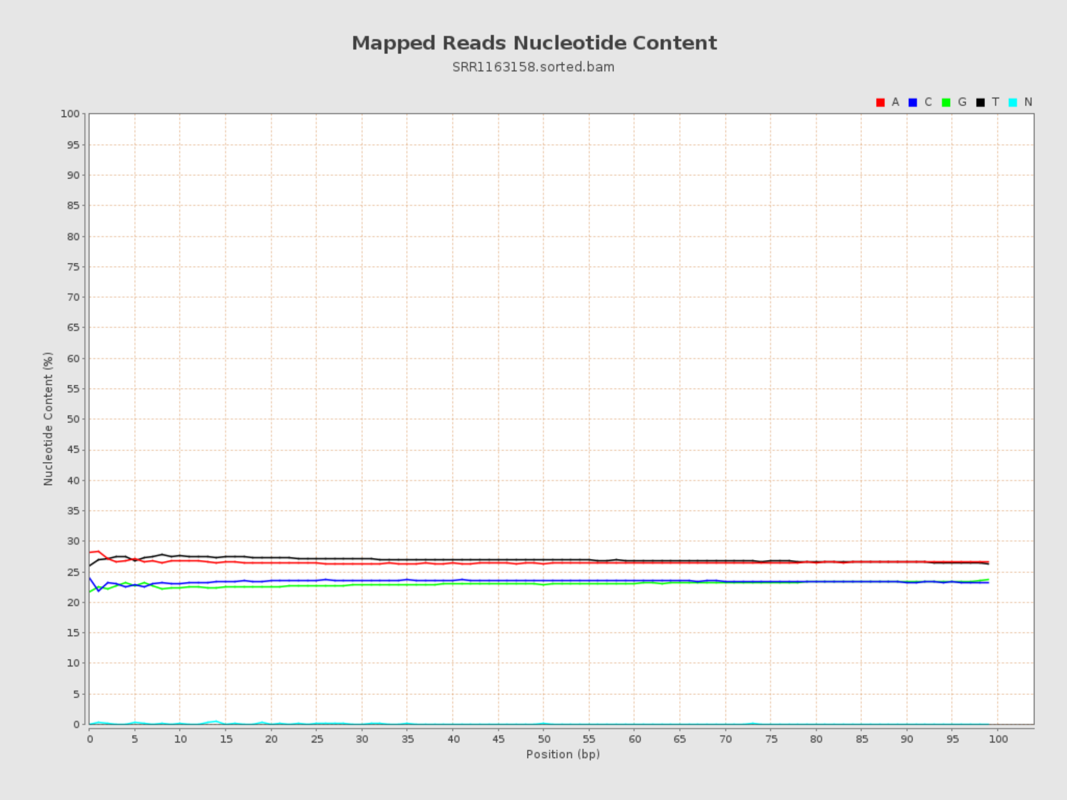
6. Results : Genome Fraction Coverage



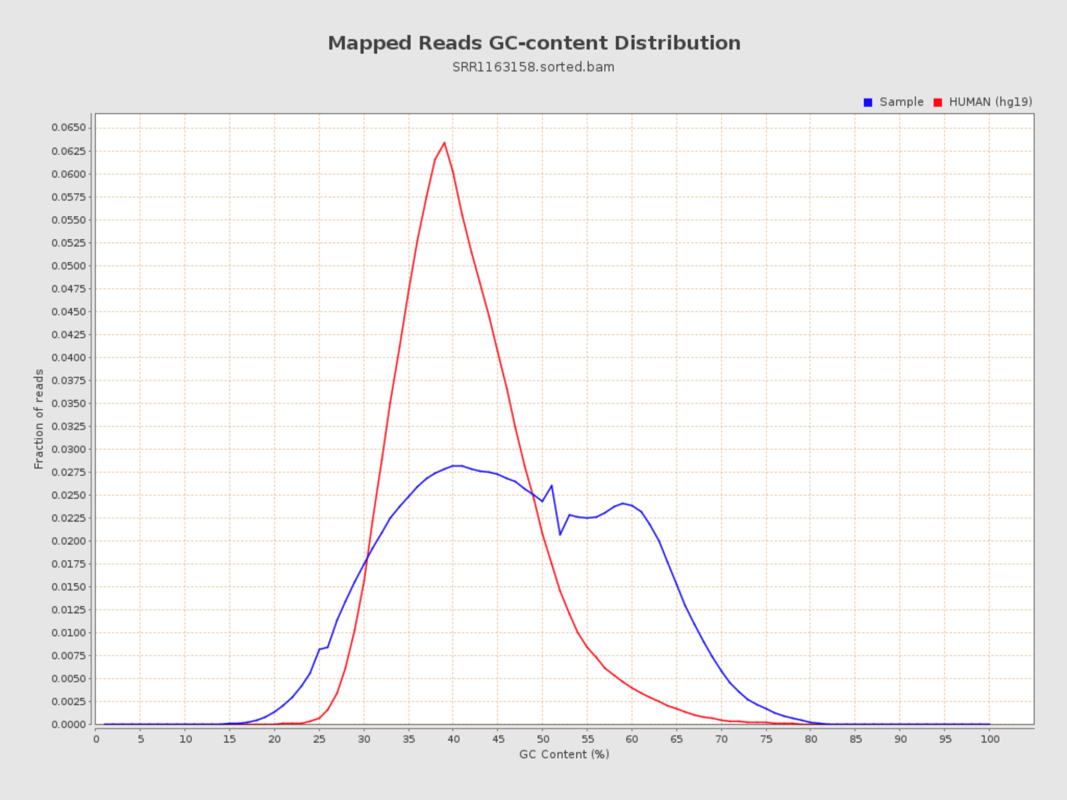
7. Results : Duplication Rate Histogram



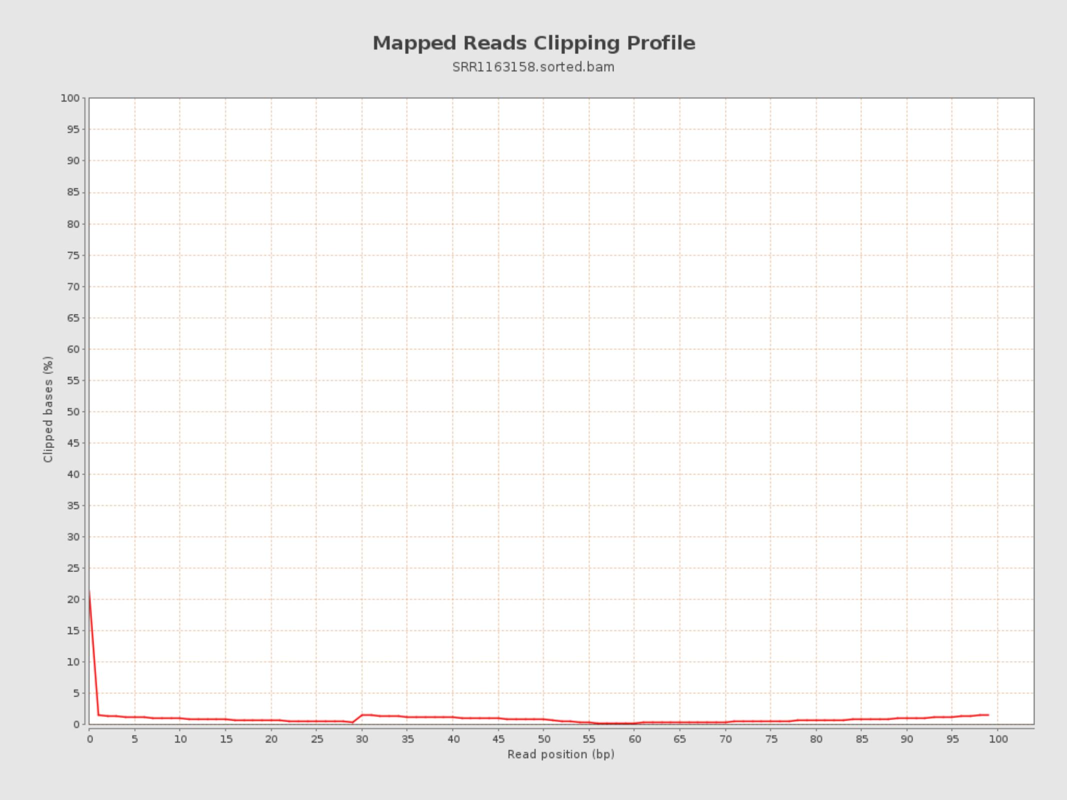
8. Results : Mapped Reads Nucleotide Content



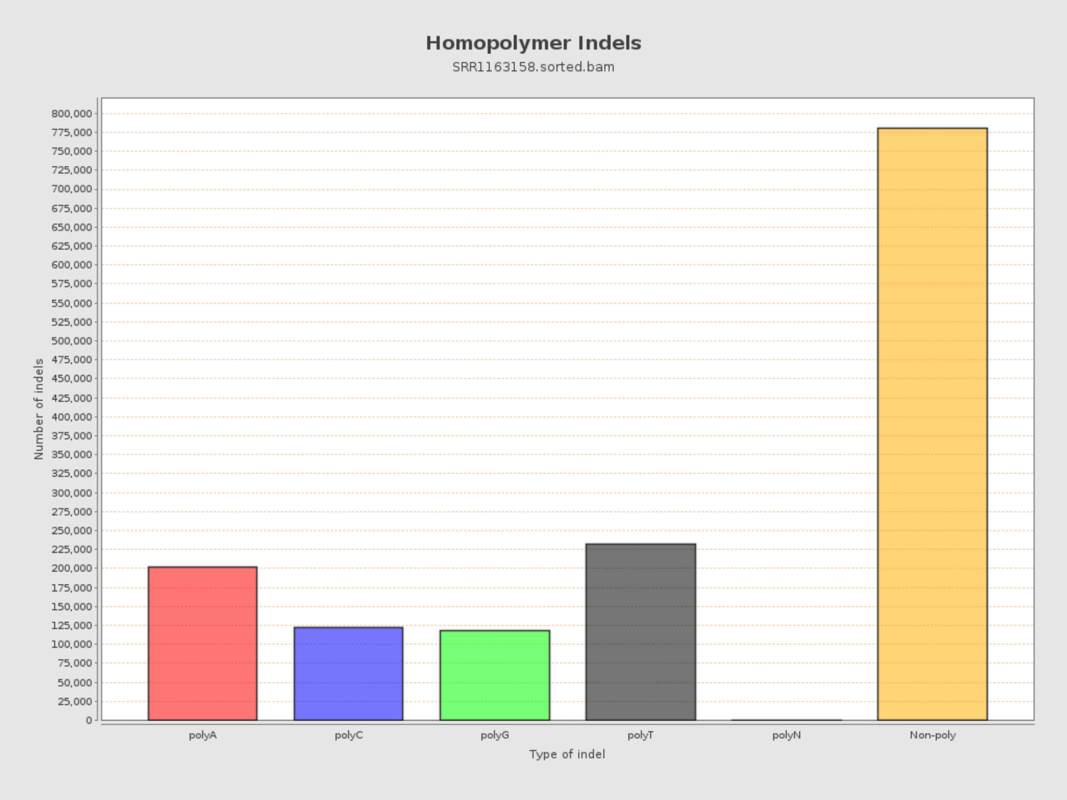
9. Results : Mapped Reads GC-content Distribution



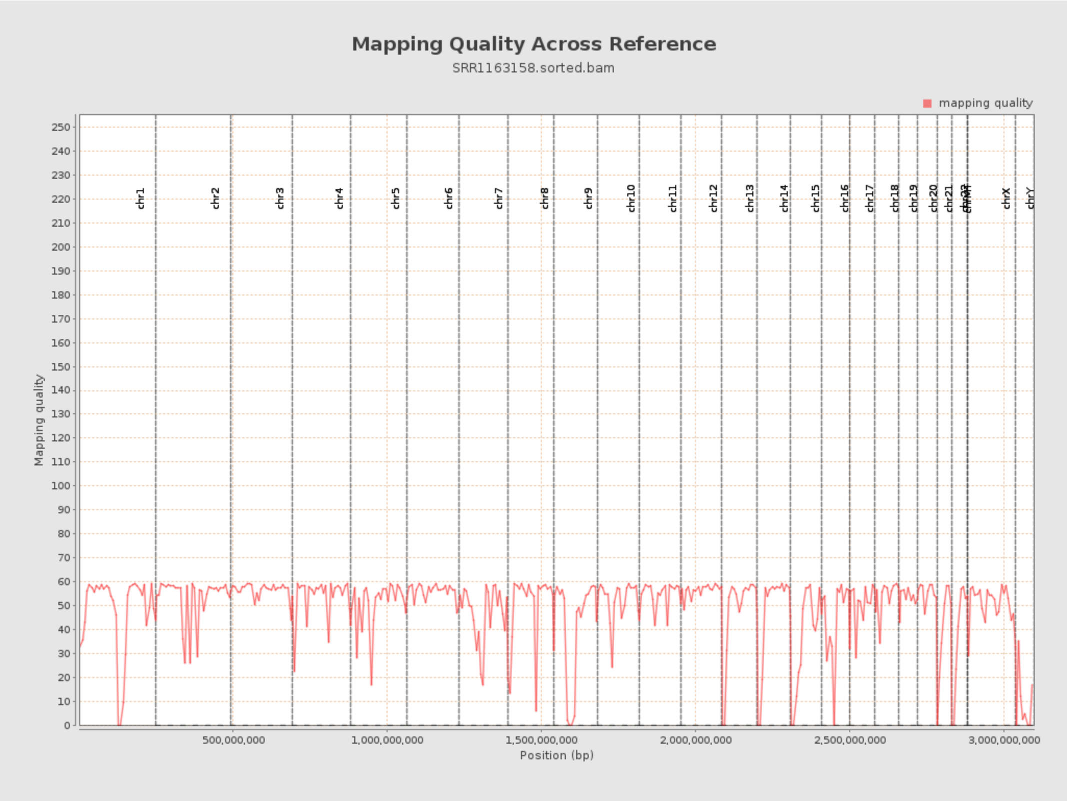
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram