Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 19:00:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751199.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_SRR8751199 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751199.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 19:00:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751199.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,335,726
Mapped reads	7,269,128 / 99.09%
Unmapped reads	66,598 / 0.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	195,389 / 2.66%
Read min/max/mean length	30 / 151 / 152.4
Duplicated reads (estimated)	1,161,673 / 15.84%
Duplication rate	15.33%
Clipped reads	1,790,659 / 24.41%

2.2. ACGT Content

Number/percentage of A's	297,203,034 / 28.31%
Number/percentage of C's	228,184,960 / 21.74%
Number/percentage of T's	299,730,483 / 28.55%
Number/percentage of G's	224,586,604 / 21.4%
Number/percentage of N's	10,072 / 0%
GC Percentage	43.13%

2.3. Coverage

Mean	0.3392

Standard Deviation	1.3051

2.4. Mapping Quality

Mean Mapping Quality	52.76

2.5. Mismatches and indels

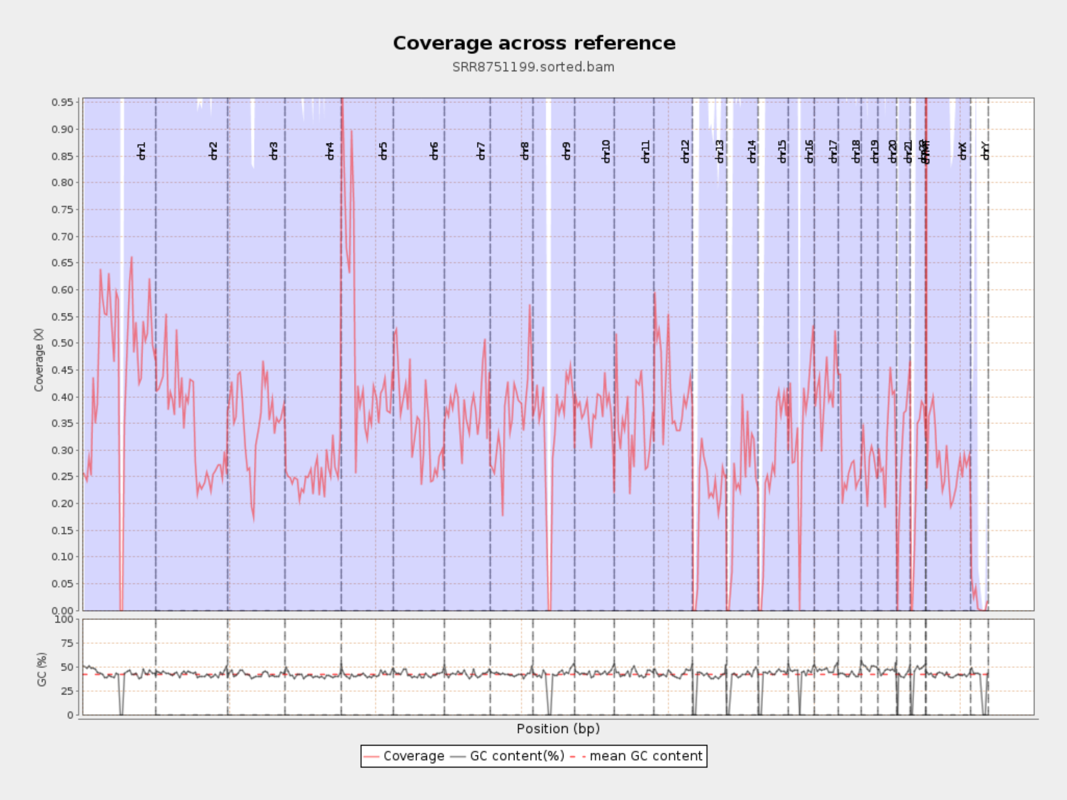
General error rate	0.73%
Mismatches	7,333,170
Insertions	210,582
Mapped reads with at least one insertion	2.81%
Deletions	123,677
Mapped reads with at least one deletion	1.66%
Homopolymer indels	49.29%

2.6. Chromosome stats

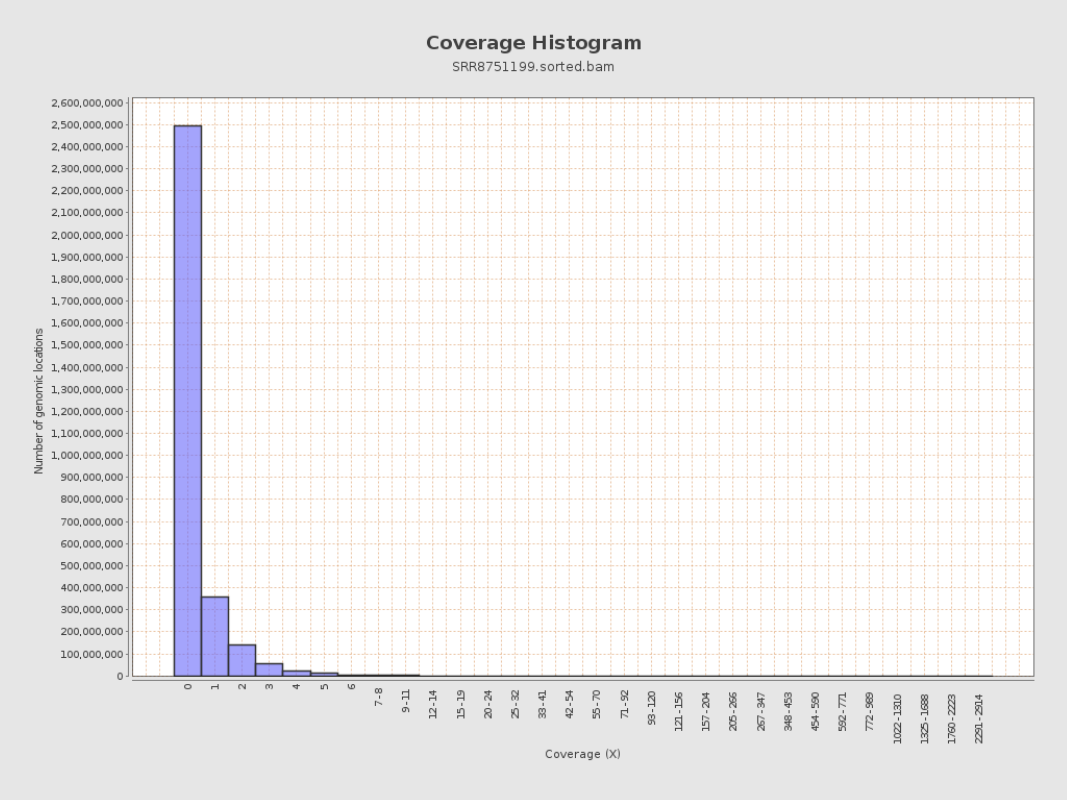
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	113450526	0.4552	2.8024
chr2	243199373	83032740	0.3414	1.0295
chr3	198022430	70601129	0.3565	0.9104
chr4	191154276	48662305	0.2546	0.7973
chr5	180915260	88490669	0.4891	1.0917
chr6	171115067	59631917	0.3485	1.1287
chr7	159138663	60527606	0.3803	1.1359

chr8	146364022	53253386	0.3638	0.9759
chr9	141213431	47628500	0.3373	1.1045
chr10	135534747	50870473	0.3753	1.9185
chr11	135006516	46905654	0.3474	1.1467
chr12	133851895	56501258	0.4221	0.9894
chr13	115169878	23568756	0.2046	0.6653
chr14	107349540	25242935	0.2351	0.8906
chr15	102531392	26343249	0.2569	0.773
chr16	90354753	31187967	0.3452	0.9523
chr17	81195210	33647806	0.4144	1.1821
chr18	78077248	21260678	0.2723	1.2723
chr19	59128983	16327089	0.2761	1.9146
chr20	63025520	20696429	0.3284	0.8869
chr21	48129895	14375389	0.2987	0.8778
chr22	51304566	12916249	0.2518	0.7726
chrMT	16571	561143	33.863	14.8294
chrX	155270560	43323704	0.279	0.823
chrY	59373566	1021533	0.0172	0.4213

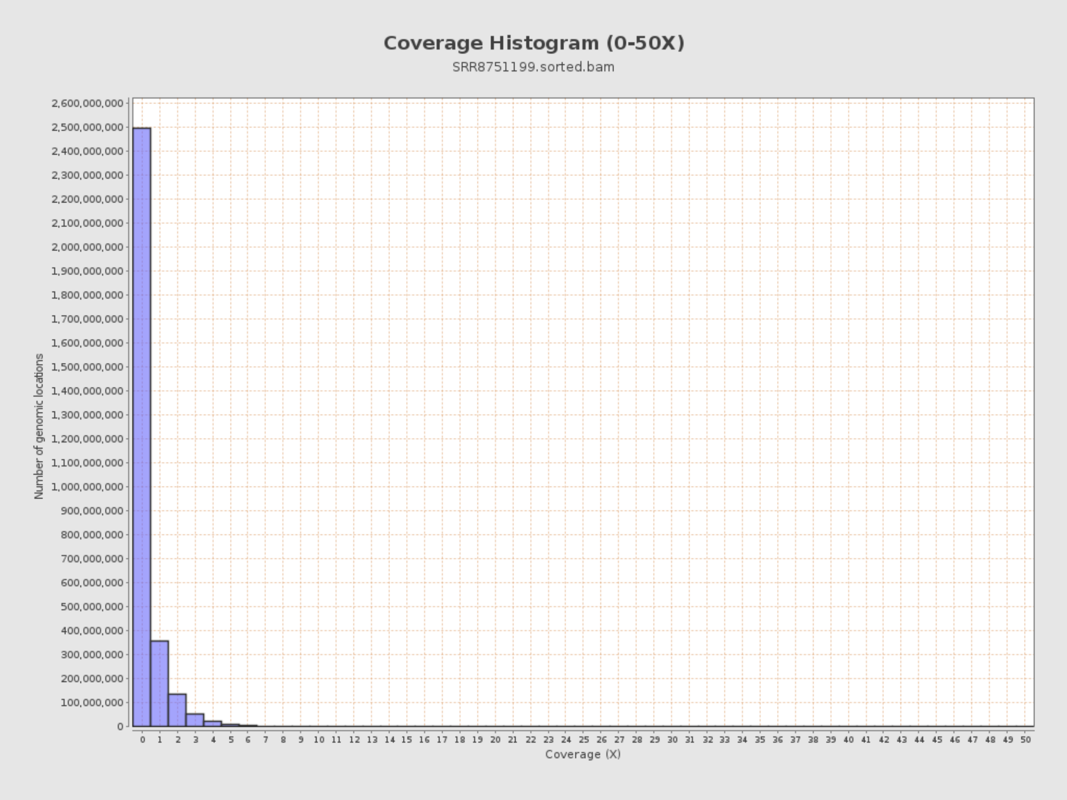
3. Results : Coverage across reference



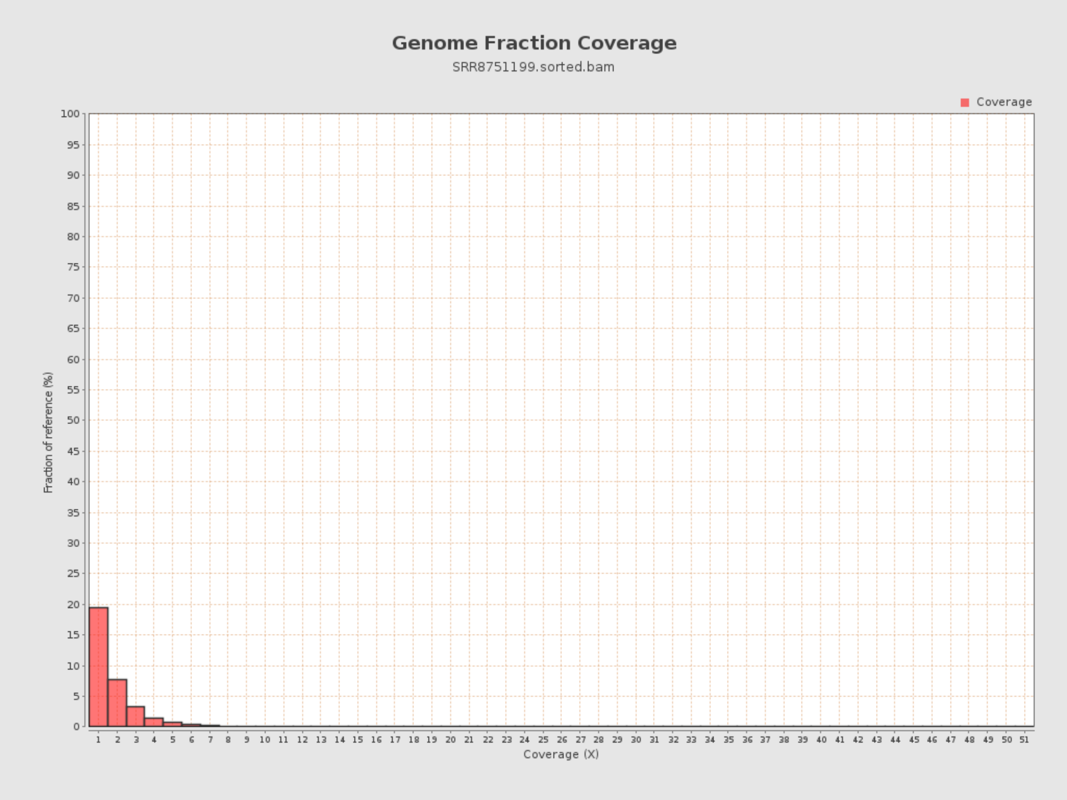
4. Results : Coverage Histogram



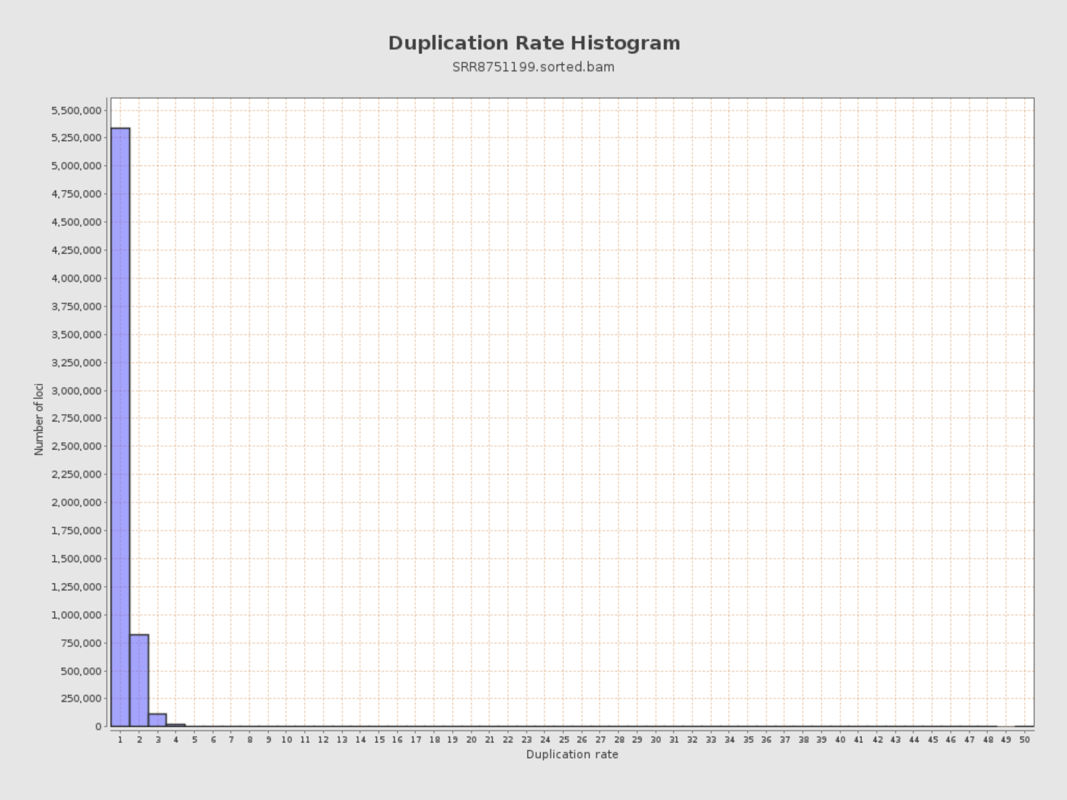
5. Results : Coverage Histogram (0-50X)



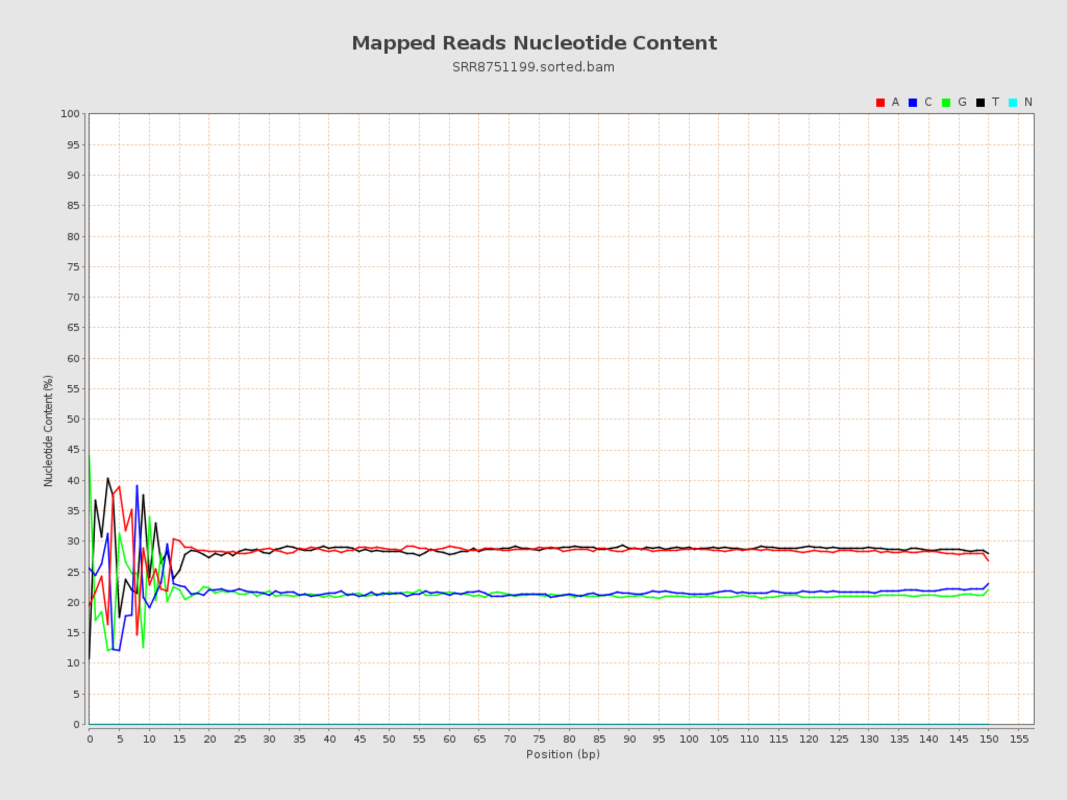
6. Results : Genome Fraction Coverage



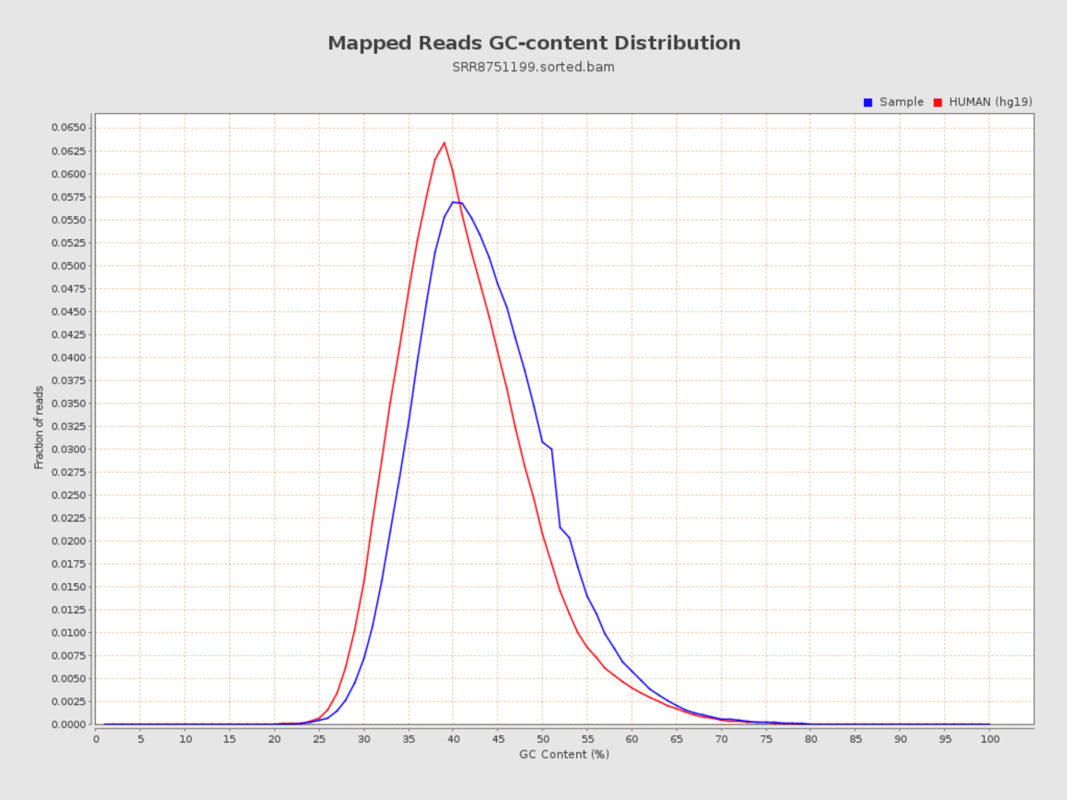
7. Results : Duplication Rate Histogram



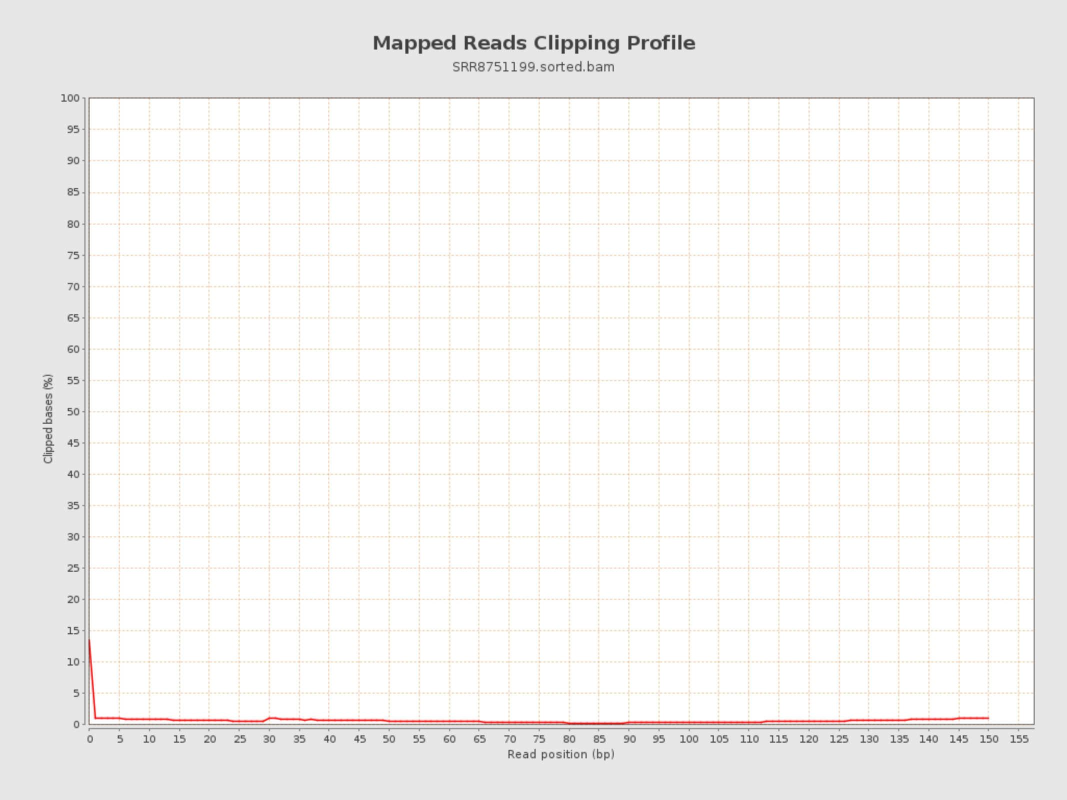
8. Results : Mapped Reads Nucleotide Content



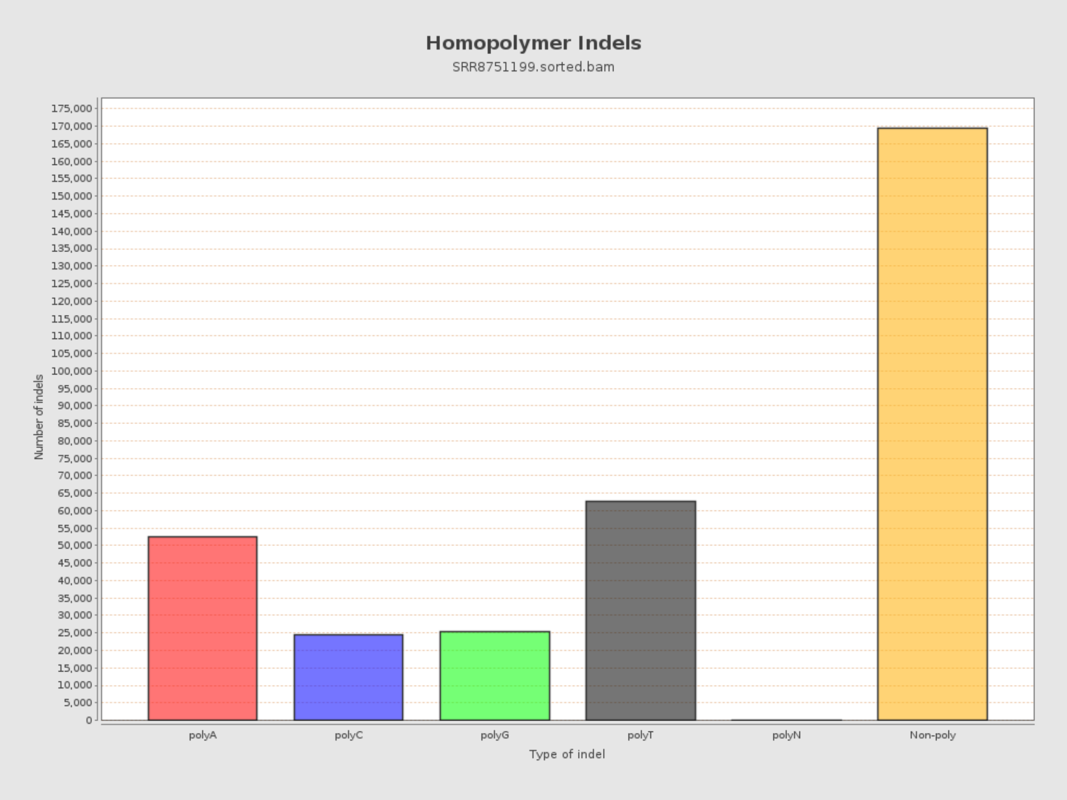
9. Results : Mapped Reads GC-content Distribution



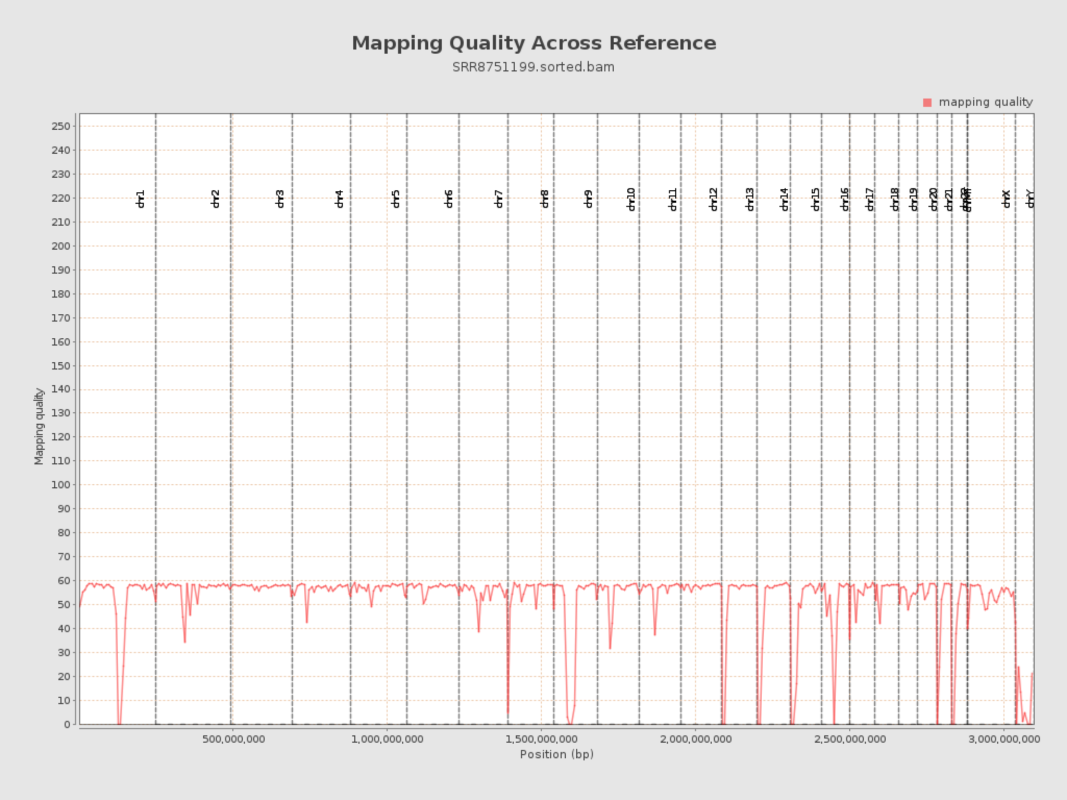
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram