Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 18:03:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751193.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_SRR8751193 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751193.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 18:03:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751193.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,382,545
Mapped reads	6,134,601 / 96.12%
Unmapped reads	247,944 / 3.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	144,869 / 2.27%
Read min/max/mean length	30 / 101 / 101.94
Duplicated reads (estimated)	132,702 / 2.08%
Duplication rate	1.49%
Clipped reads	954,702 / 14.96%

2.2. ACGT Content

Number/percentage of A's	175,616,367 / 29.07%
Number/percentage of C's	126,555,889 / 20.95%
Number/percentage of T's	176,502,142 / 29.21%
Number/percentage of G's	125,525,308 / 20.78%
Number/percentage of N's	3,174 / 0%
GC Percentage	41.72%

2.3. Coverage

Mean	0.1952

Standard Deviation	1.0954

2.4. Mapping Quality

Mean Mapping Quality	51.55

2.5. Mismatches and indels

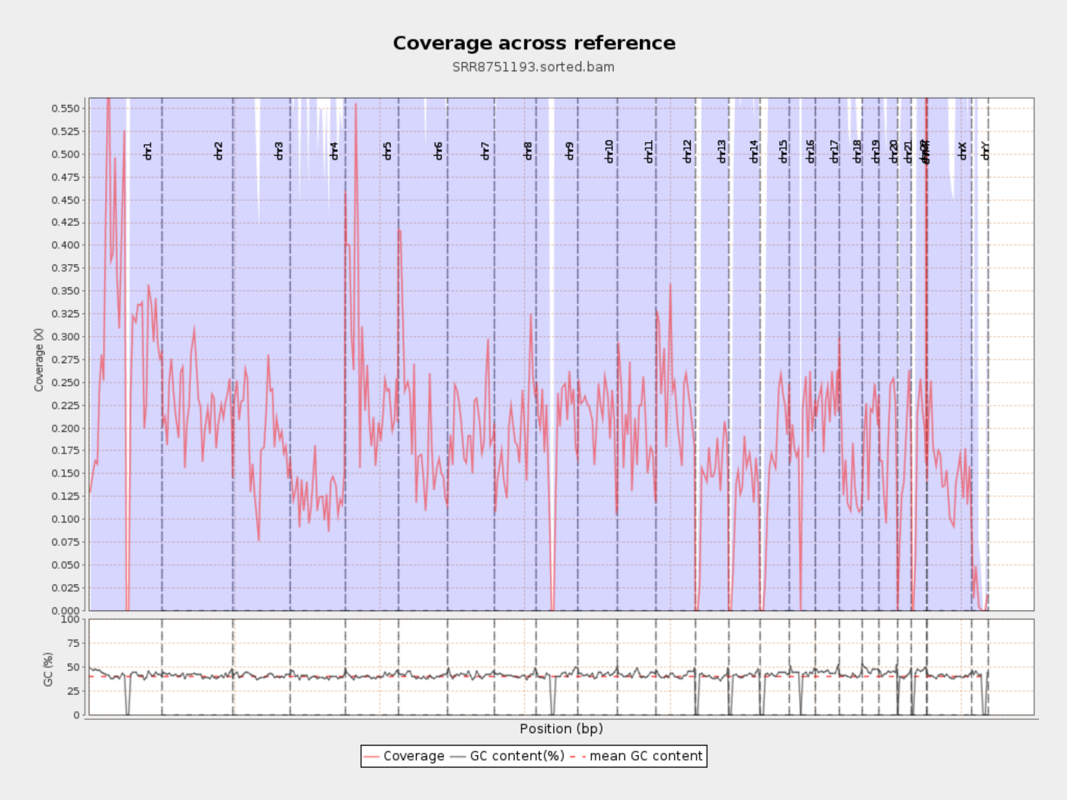
General error rate	0.34%
Mismatches	1,886,406
Insertions	97,151
Mapped reads with at least one insertion	1.56%
Deletions	75,330
Mapped reads with at least one deletion	1.21%
Homopolymer indels	47.66%

2.6. Chromosome stats

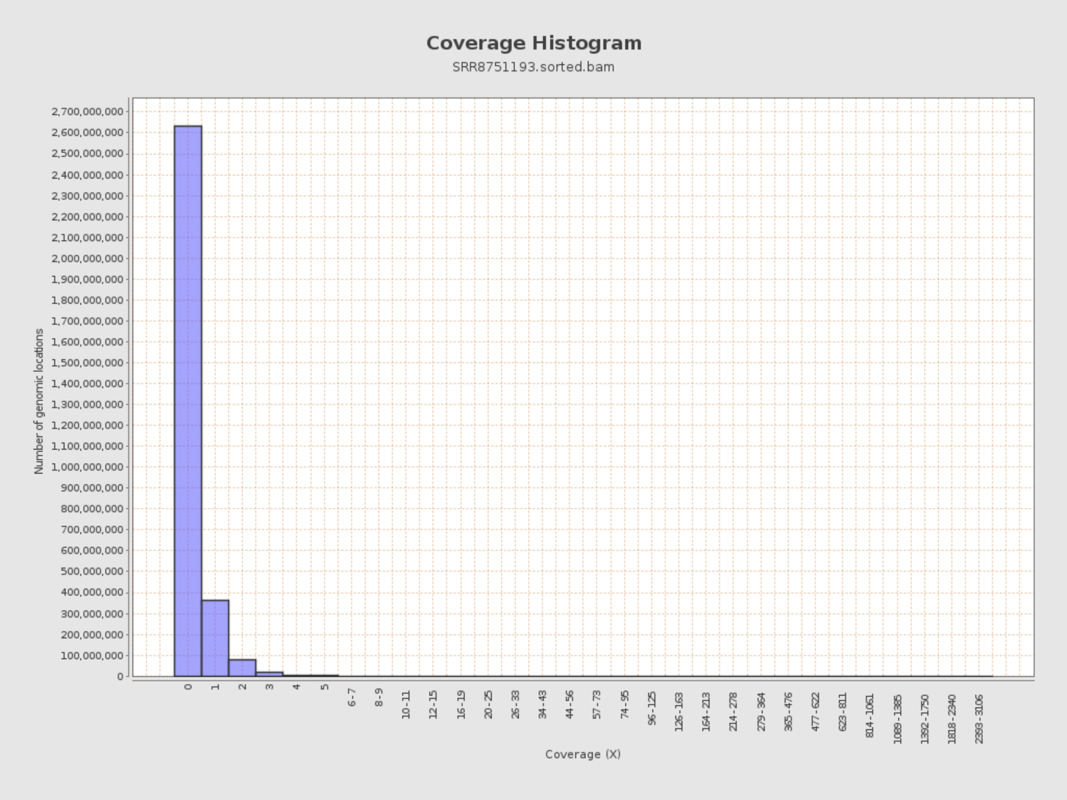
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	74449418	0.2987	2.9372
chr2	243199373	54683716	0.2249	0.6213
chr3	198022430	38346545	0.1936	0.5219
chr4	191154276	24104855	0.1261	0.4381
chr5	180915260	47669743	0.2635	0.6132
chr6	171115067	34272219	0.2003	0.9656
chr7	159138663	32342156	0.2032	0.6433

chr8	146364022	28064632	0.1917	0.5686
chr9	141213431	26246988	0.1859	0.6529
chr10	135534747	29530767	0.2179	1.2201
chr11	135006516	26875516	0.1991	0.6615
chr12	133851895	32533624	0.2431	0.5845
chr13	115169878	15771719	0.1369	0.435
chr14	107349540	13223677	0.1232	0.4225
chr15	102531392	15807373	0.1542	0.4643
chr16	90354753	16751888	0.1854	0.6437
chr17	81195210	18505687	0.2279	0.7519
chr18	78077248	11441888	0.1465	1.0473
chr19	59128983	11955601	0.2022	2.1613
chr20	63025520	11454089	0.1817	0.5082
chr21	48129895	7234633	0.1503	0.4792
chr22	51304566	7593839	0.148	0.4647
chrMT	16571	960947	57.9897	23.6053
chrX	155270560	23635811	0.1522	0.4997
chrY	59373566	909529	0.0153	0.4711

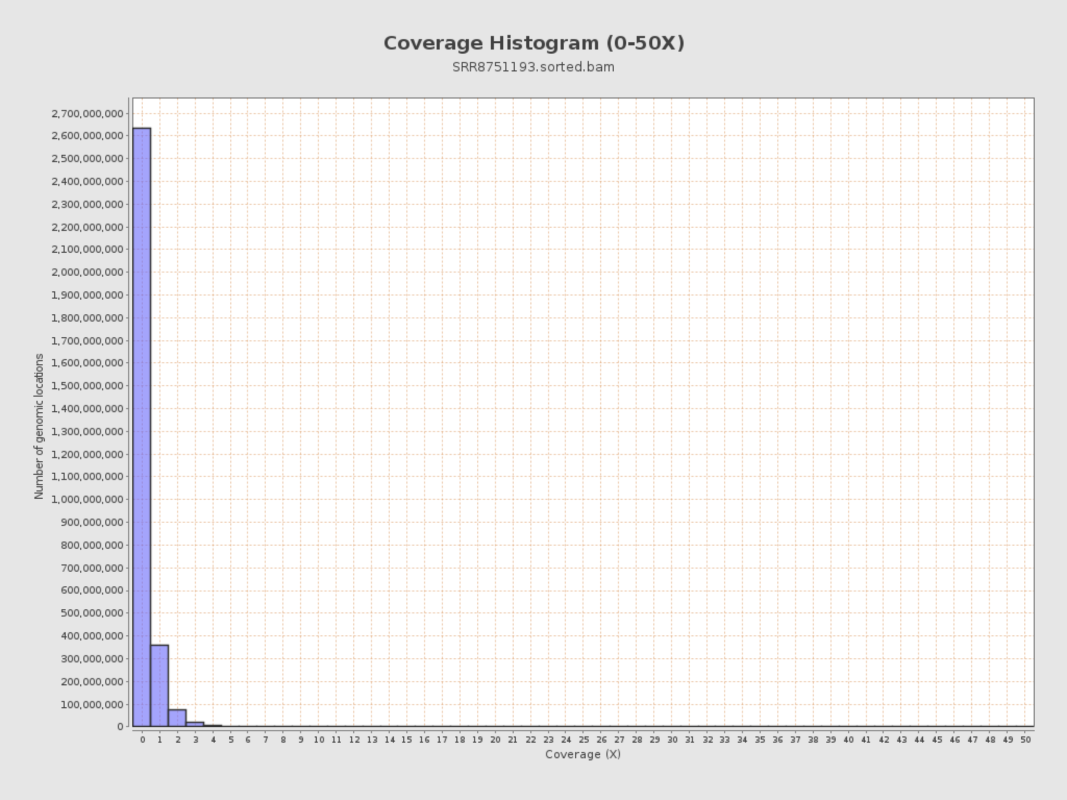
3. Results : Coverage across reference



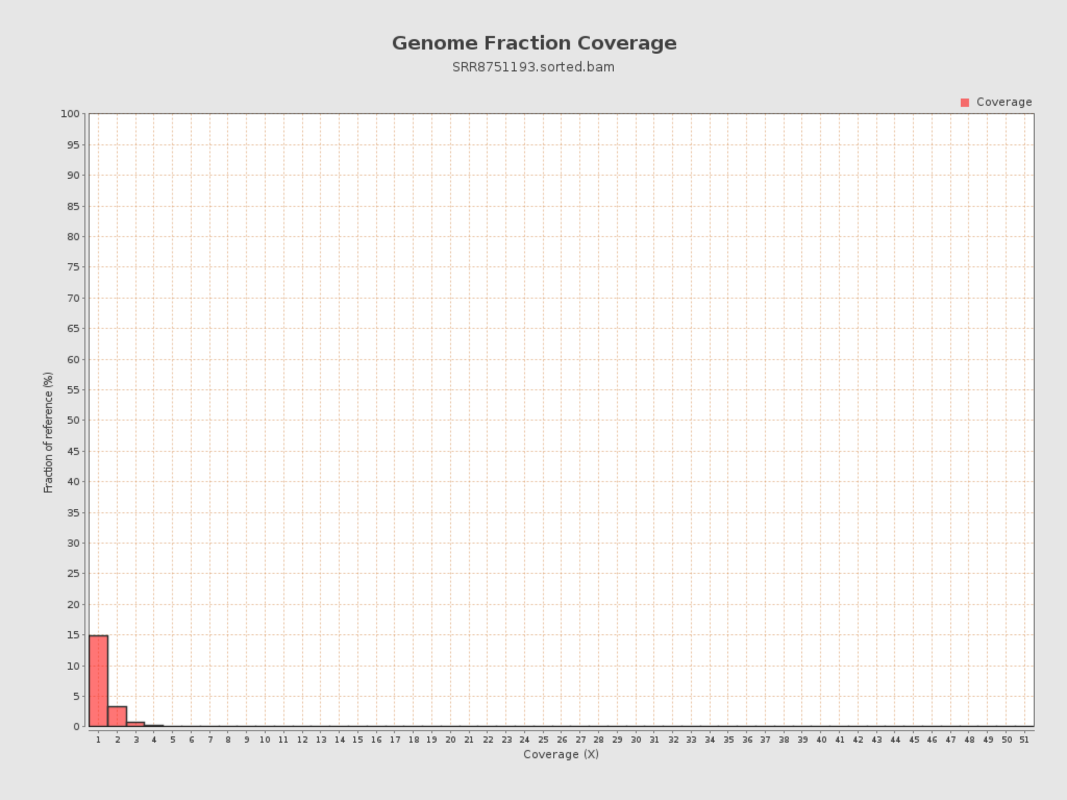
4. Results : Coverage Histogram



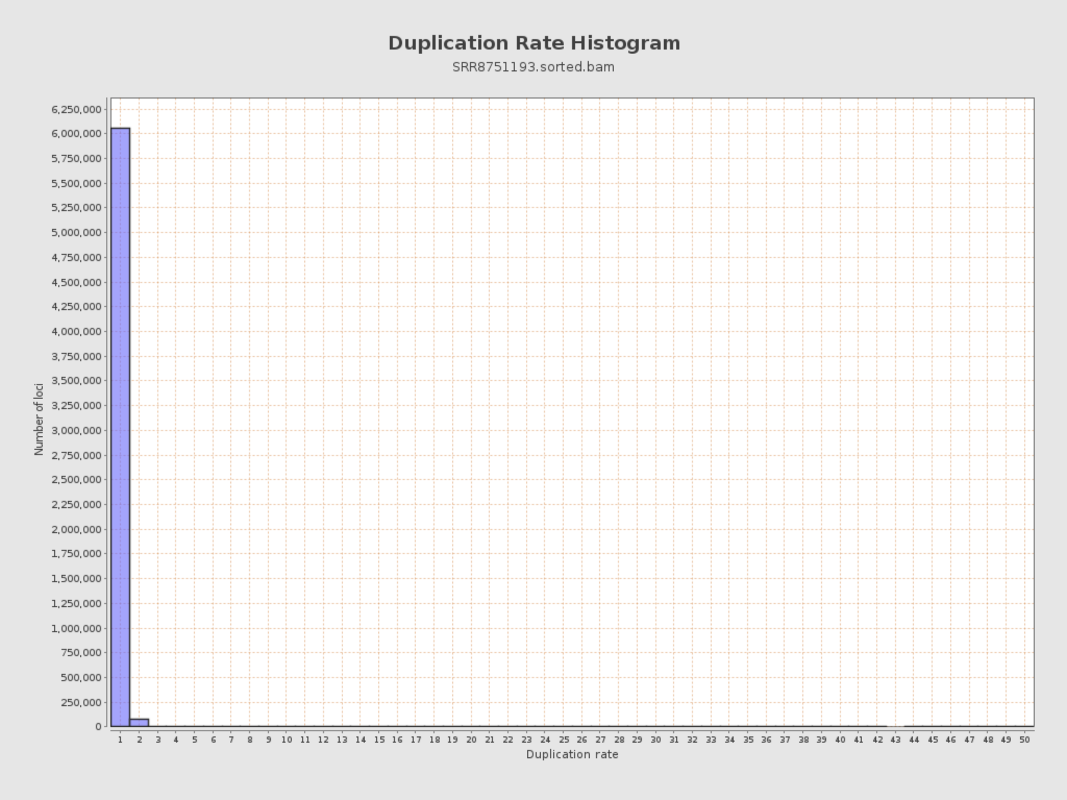
5. Results : Coverage Histogram (0-50X)



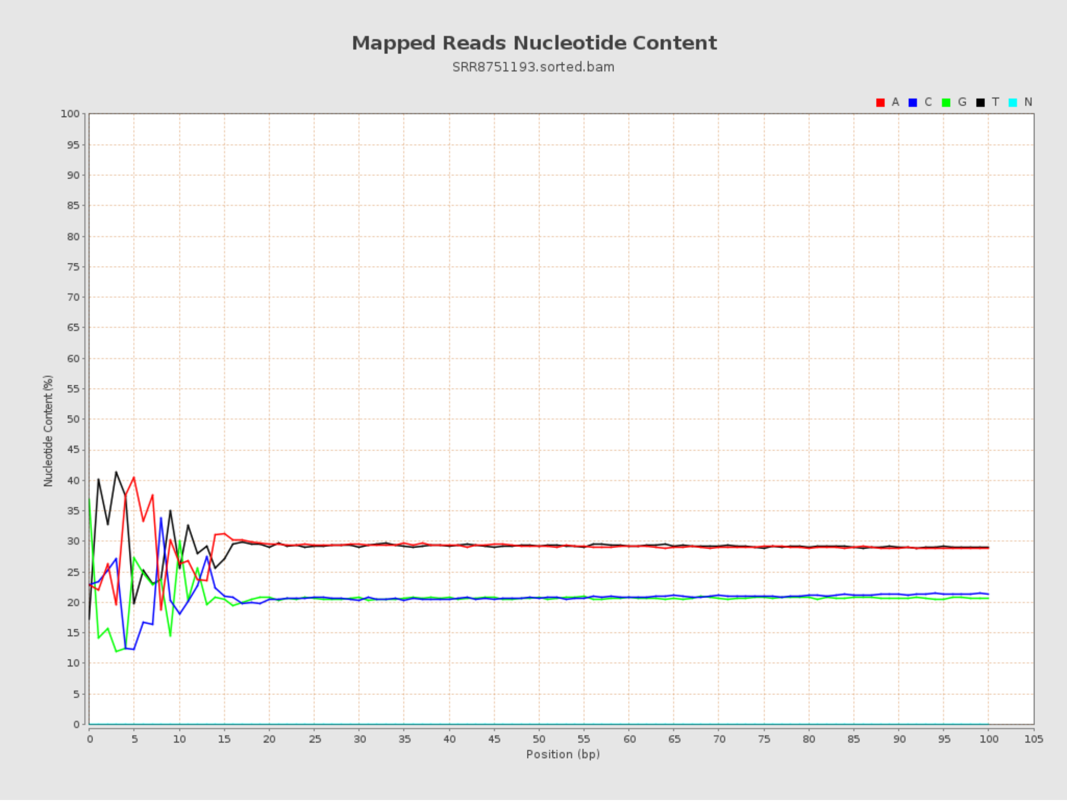
6. Results : Genome Fraction Coverage



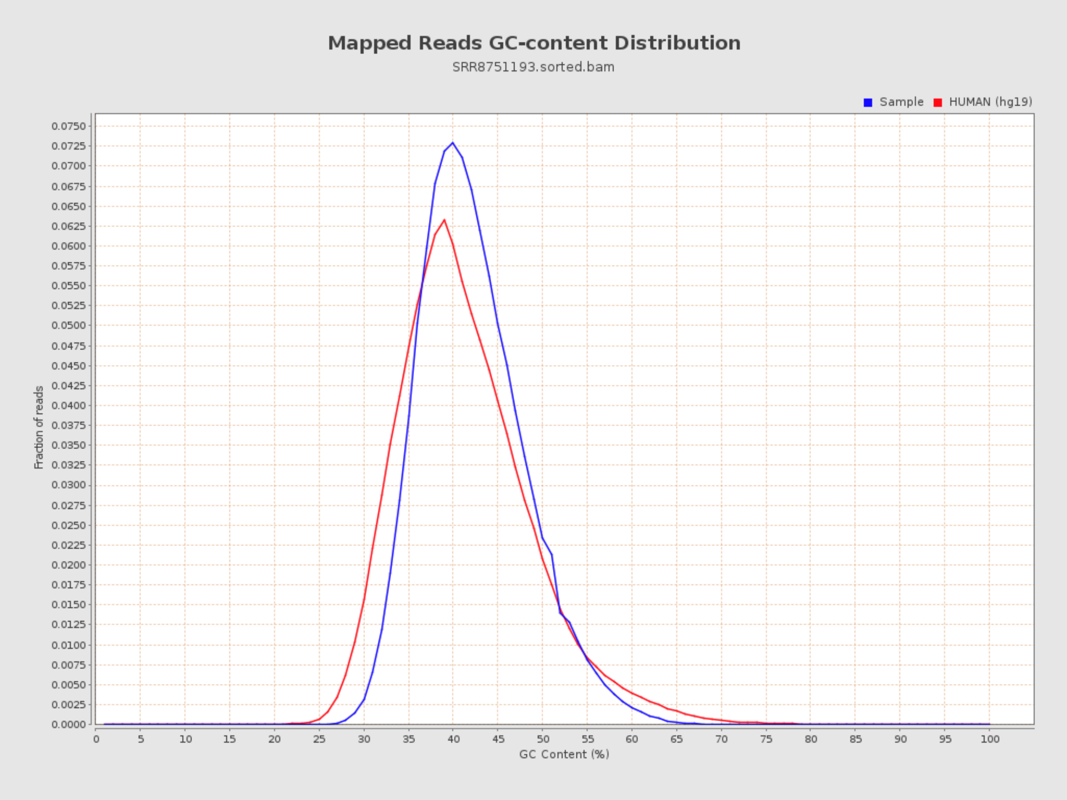
7. Results : Duplication Rate Histogram



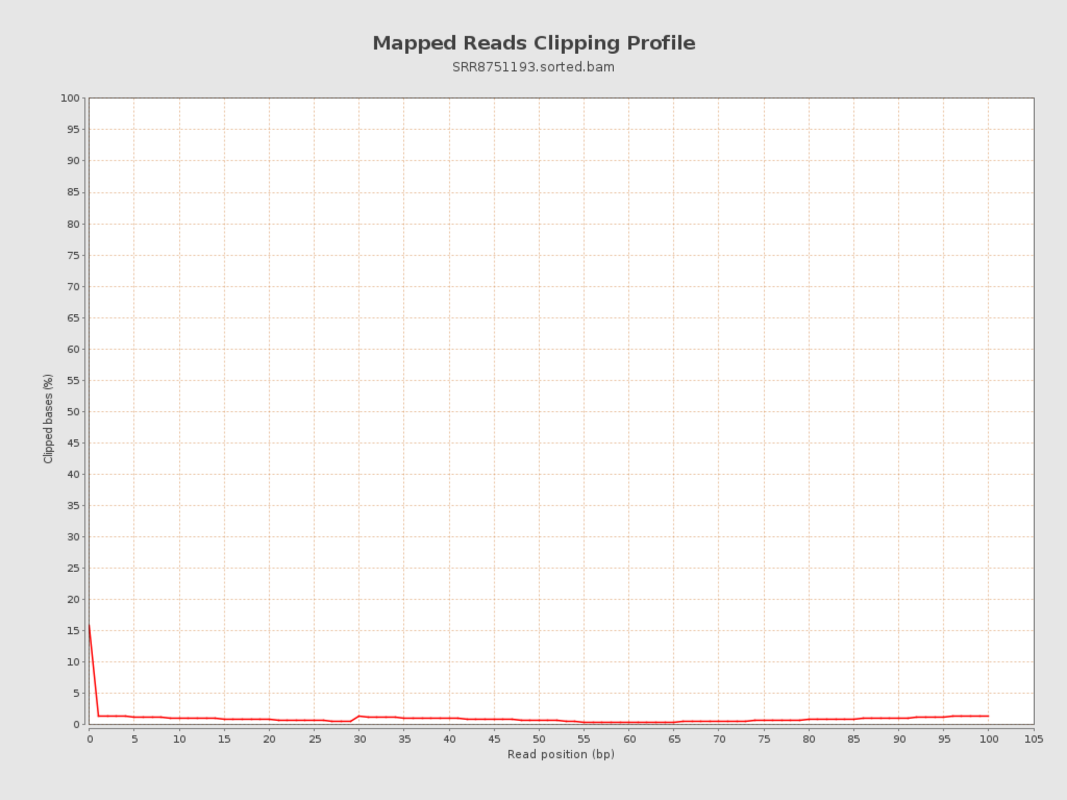
8. Results : Mapped Reads Nucleotide Content



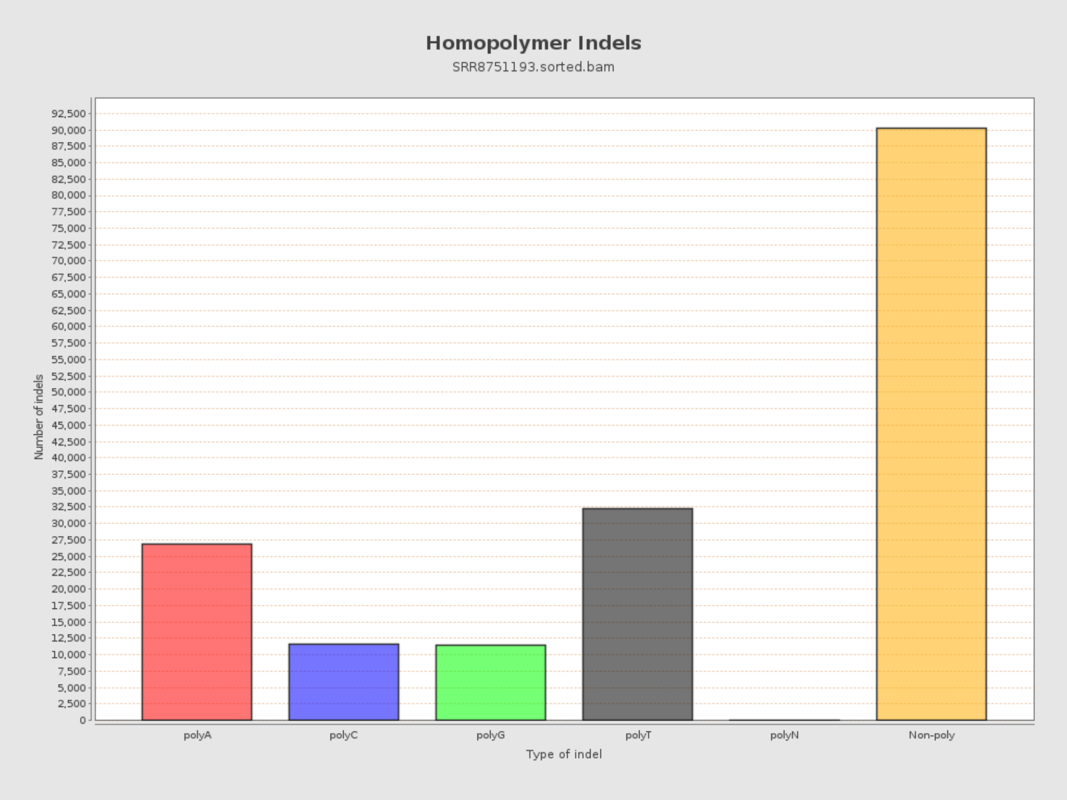
9. Results : Mapped Reads GC-content Distribution



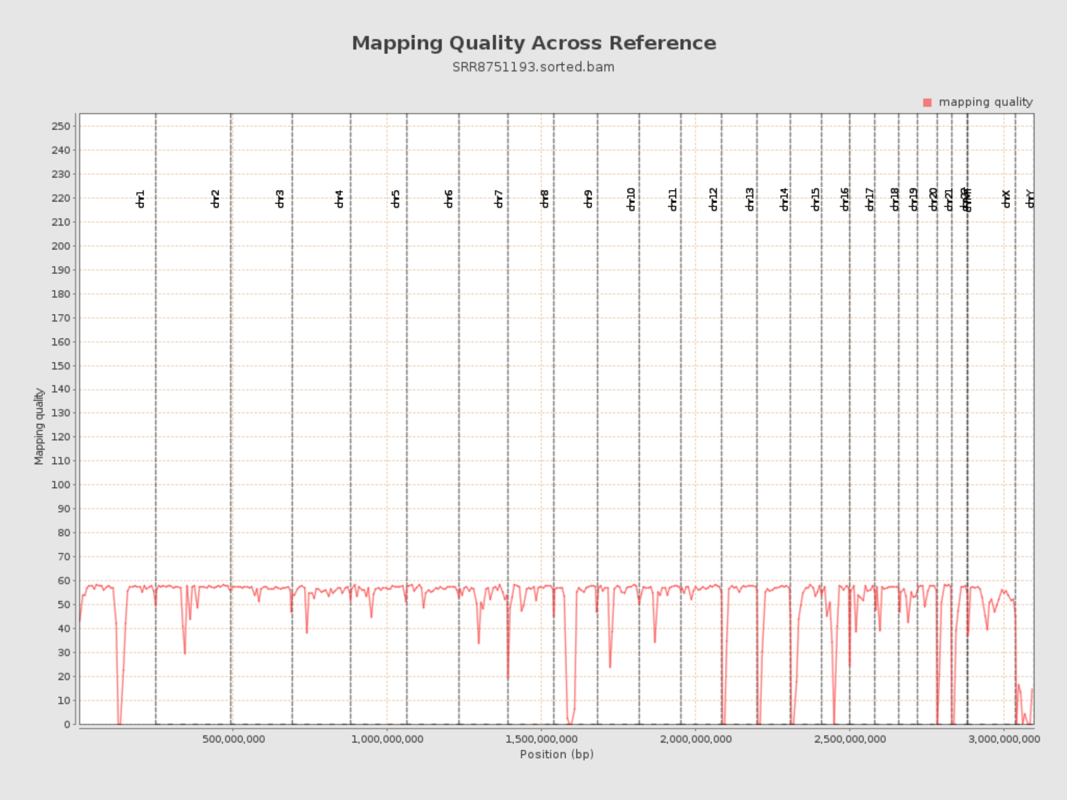
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram