Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 17:36:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751190.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_SRR8751190 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751190.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 17:36:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751190.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,577,191
Mapped reads	4,407,633 / 96.3%
Unmapped reads	169,558 / 3.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	104,398 / 2.28%
Read min/max/mean length	30 / 101 / 101.95
Duplicated reads (estimated)	82,125 / 1.79%
Duplication rate	1.25%
Clipped reads	640,624 / 14%

2.2. ACGT Content

Number/percentage of A's	126,211,006 / 29.01%
Number/percentage of C's	91,365,257 / 21%
Number/percentage of T's	126,630,879 / 29.11%
Number/percentage of G's	90,810,631 / 20.88%
Number/percentage of N's	2,368 / 0%
GC Percentage	41.88%

2.3. Coverage

Mean	0.1406

Standard Deviation	0.8628

2.4. Mapping Quality

Mean Mapping Quality	51.54

2.5. Mismatches and indels

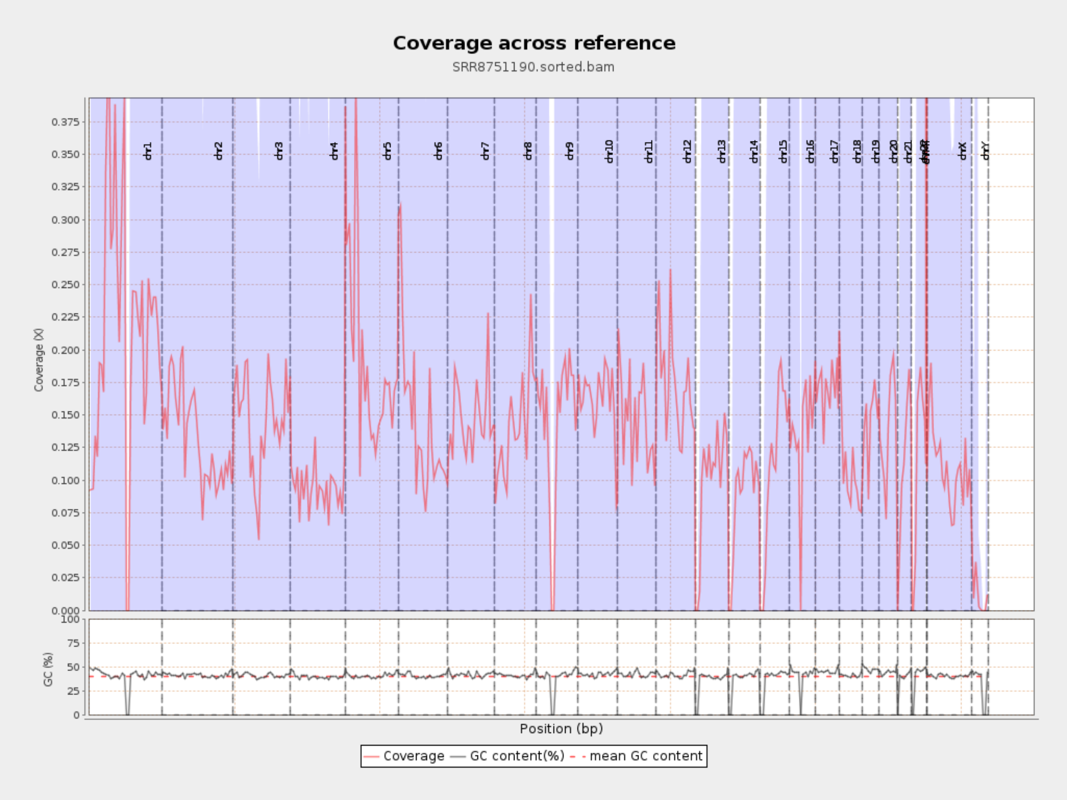
General error rate	0.34%
Mismatches	1,358,936
Insertions	67,051
Mapped reads with at least one insertion	1.5%
Deletions	53,951
Mapped reads with at least one deletion	1.2%
Homopolymer indels	47.78%

2.6. Chromosome stats

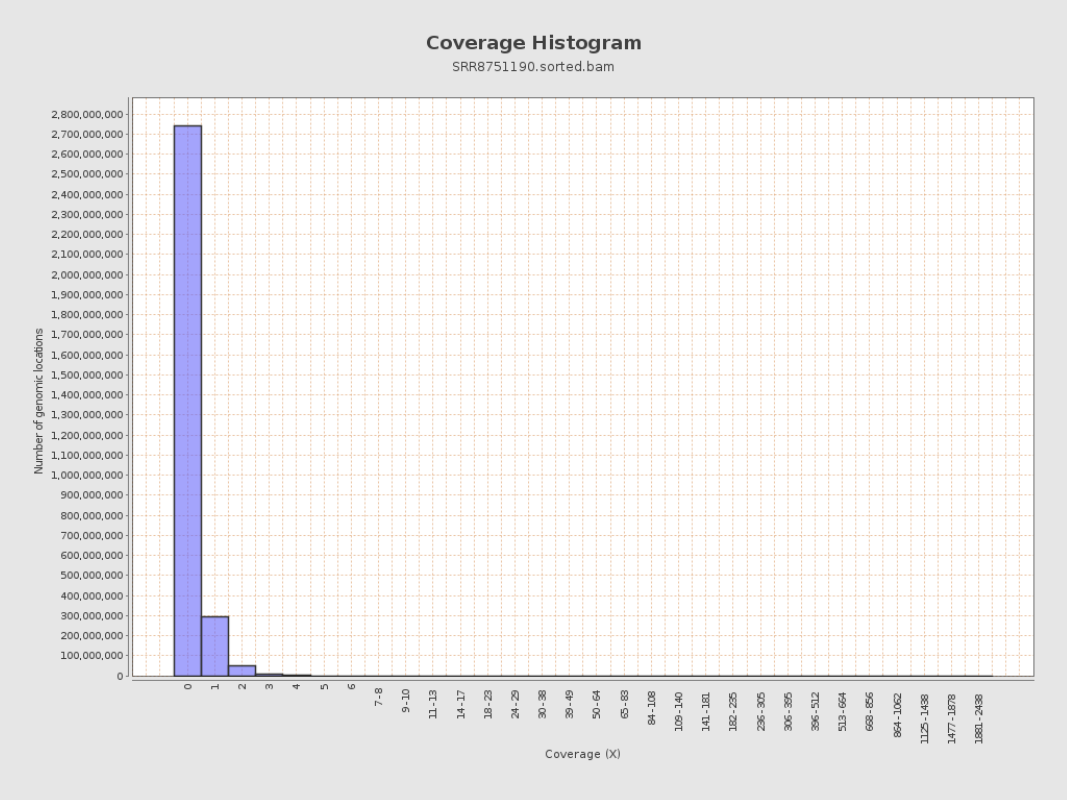
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	54117378	0.2171	2.3527
chr2	243199373	32293454	0.1328	0.4587
chr3	198022430	28596041	0.1444	0.4297
chr4	191154276	17877608	0.0935	0.3591
chr5	180915260	34290270	0.1895	0.4988
chr6	171115067	24863621	0.1453	0.6851
chr7	159138663	23566274	0.1481	0.5018

chr8	146364022	20767141	0.1419	0.4509
chr9	141213431	20064316	0.1421	0.5263
chr10	135534747	22161071	0.1635	0.8396
chr11	135006516	19726216	0.1461	0.5305
chr12	133851895	23503332	0.1756	0.4767
chr13	115169878	11380553	0.0988	0.3551
chr14	107349540	9545053	0.0889	0.3434
chr15	102531392	11491003	0.1121	0.3799
chr16	90354753	12107851	0.134	0.5132
chr17	81195210	13719309	0.169	0.6196
chr18	78077248	8483388	0.1087	0.8532
chr19	59128983	8528768	0.1442	1.6289
chr20	63025520	8541099	0.1355	0.4203
chr21	48129895	5403012	0.1123	0.3974
chr22	51304566	5586429	0.1089	0.382
chrMT	16571	762625	46.0217	17.8751
chrX	155270560	17103746	0.1102	0.3988
chrY	59373566	657619	0.0111	0.3679

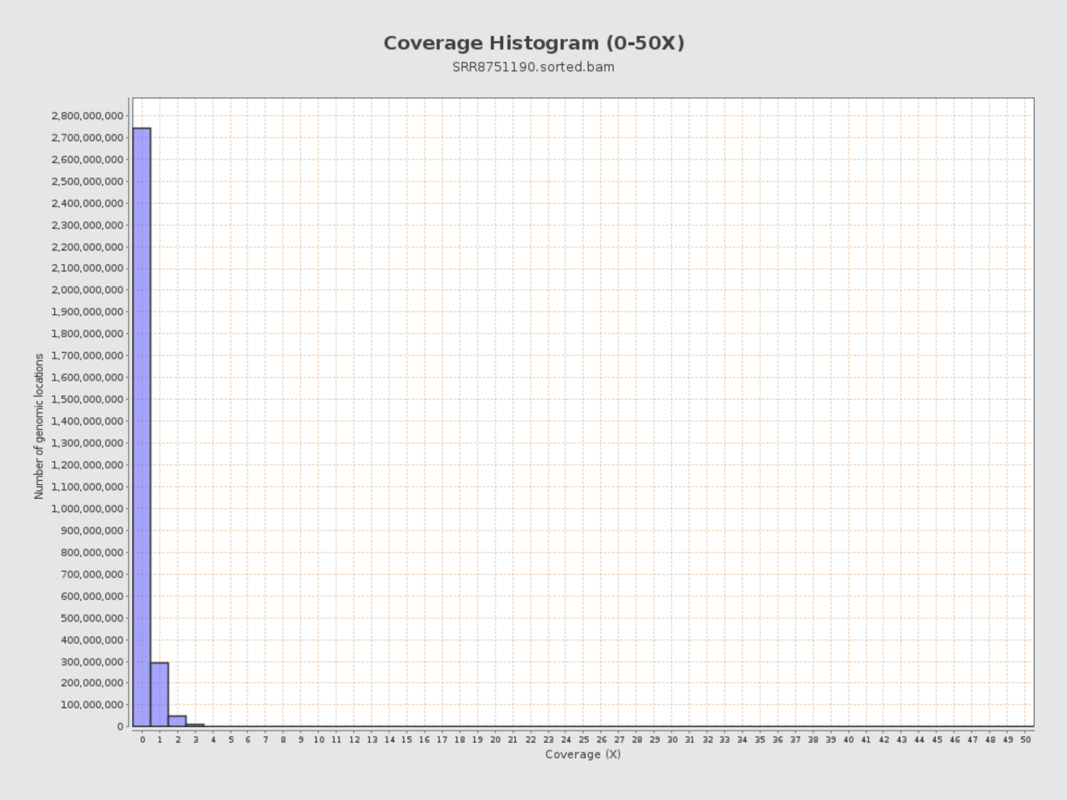
3. Results : Coverage across reference



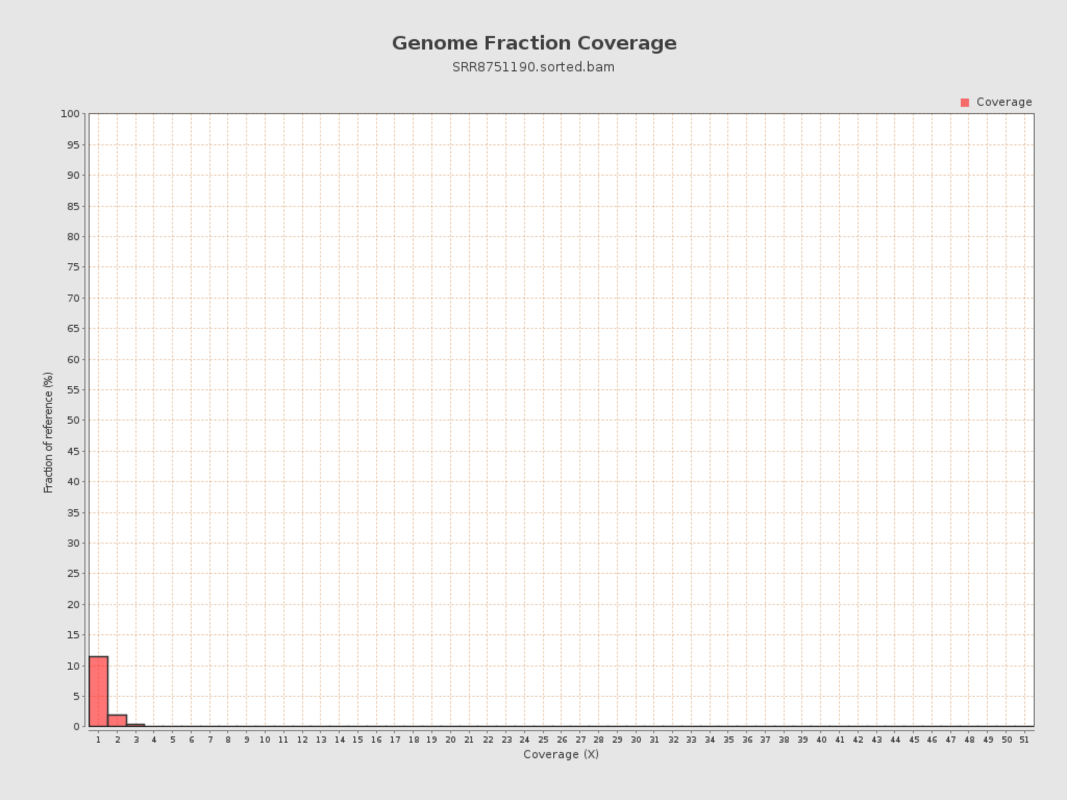
4. Results : Coverage Histogram



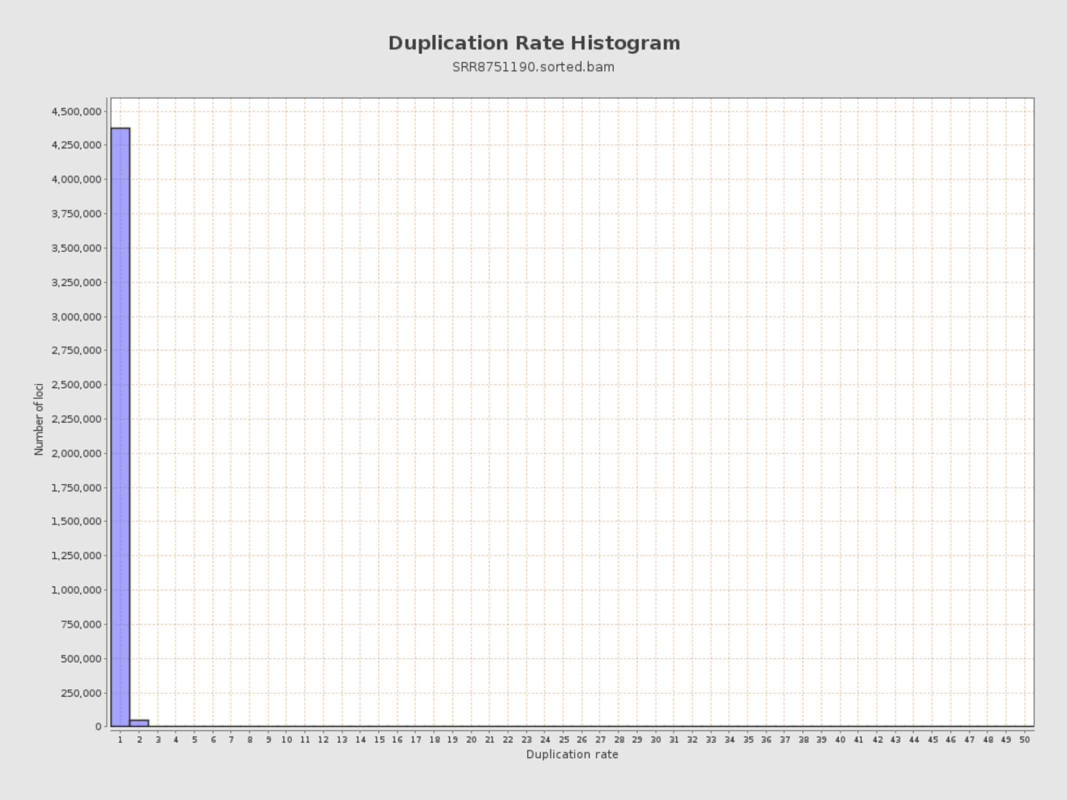
5. Results : Coverage Histogram (0-50X)



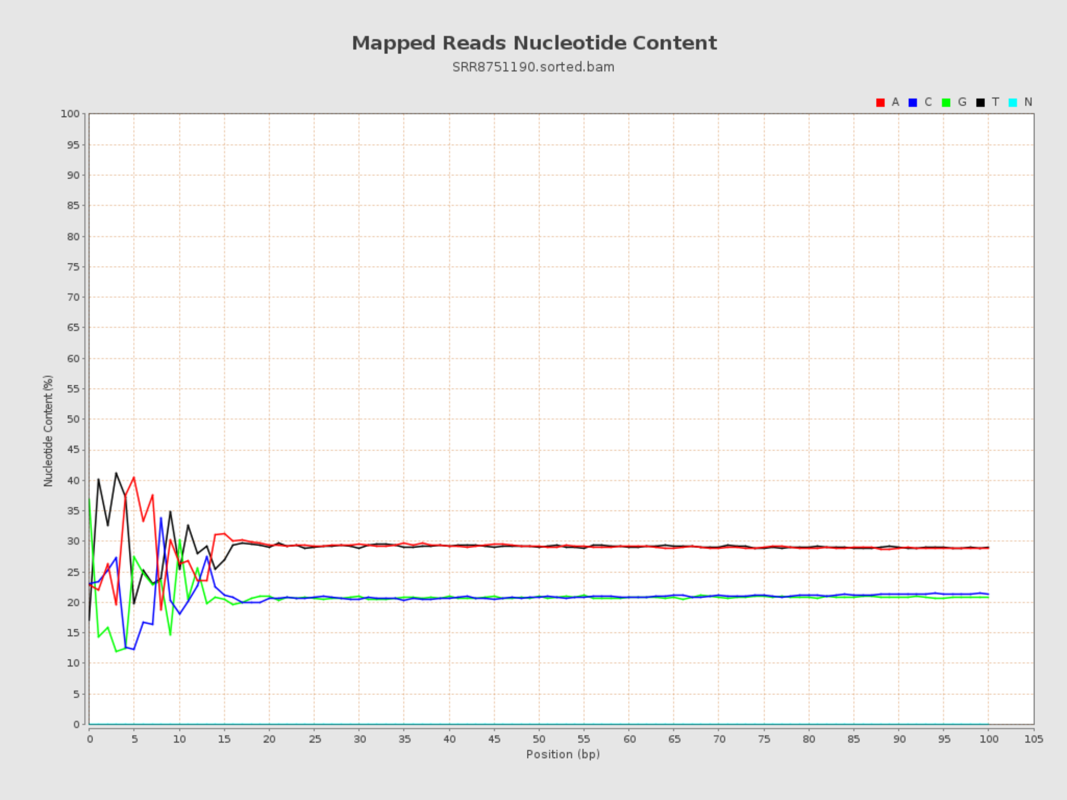
6. Results : Genome Fraction Coverage



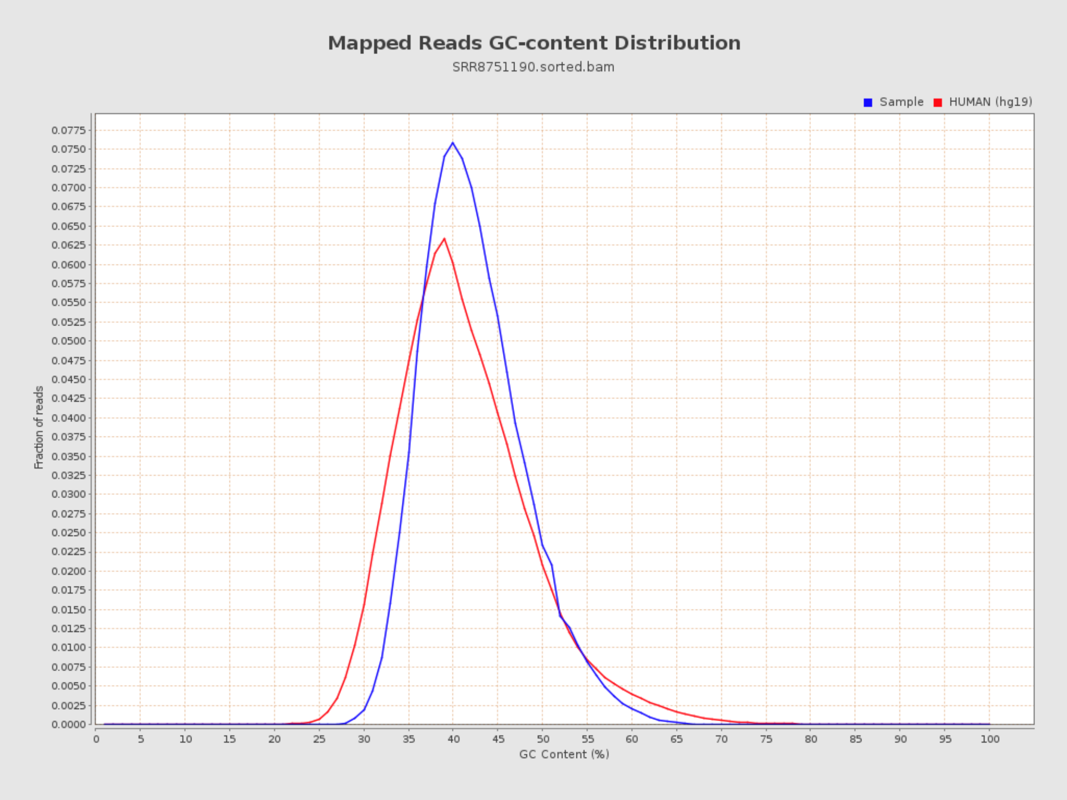
7. Results : Duplication Rate Histogram



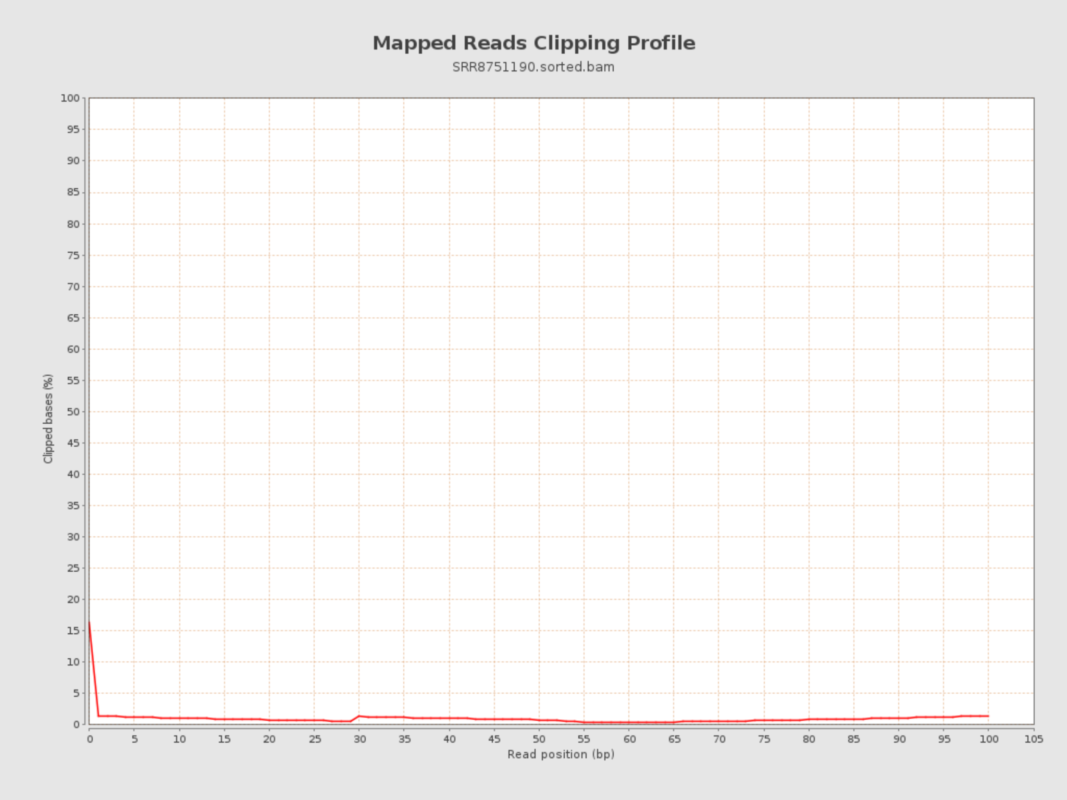
8. Results : Mapped Reads Nucleotide Content



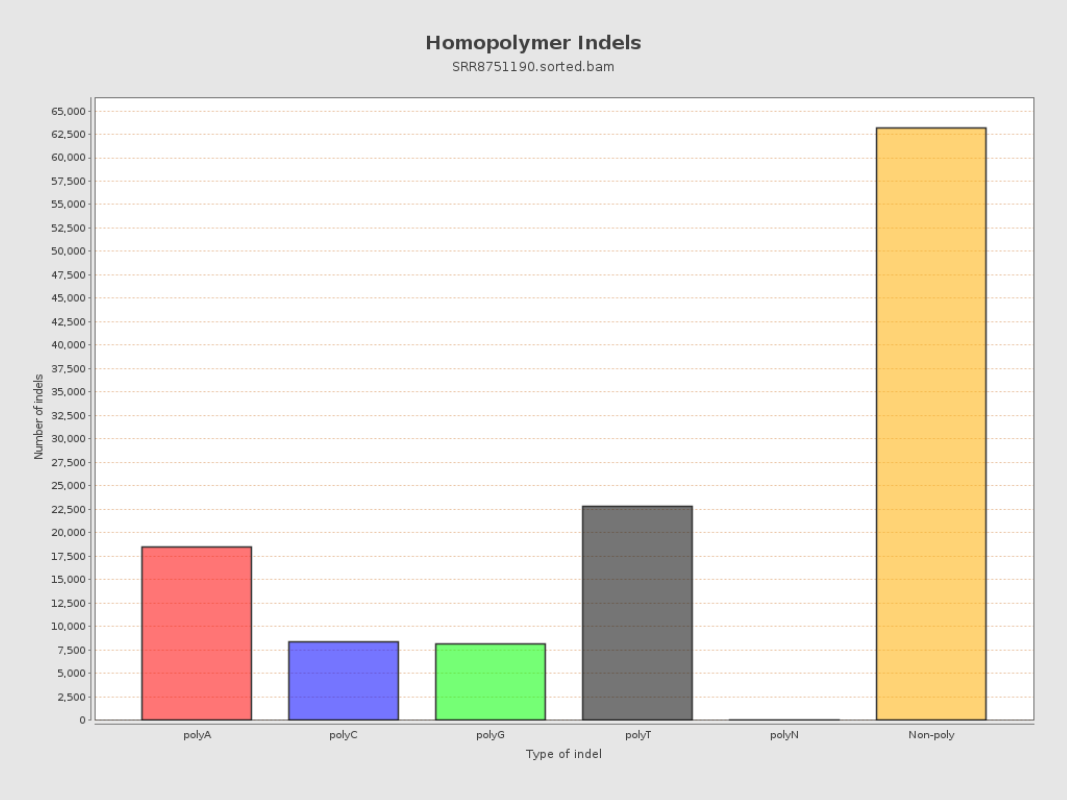
9. Results : Mapped Reads GC-content Distribution



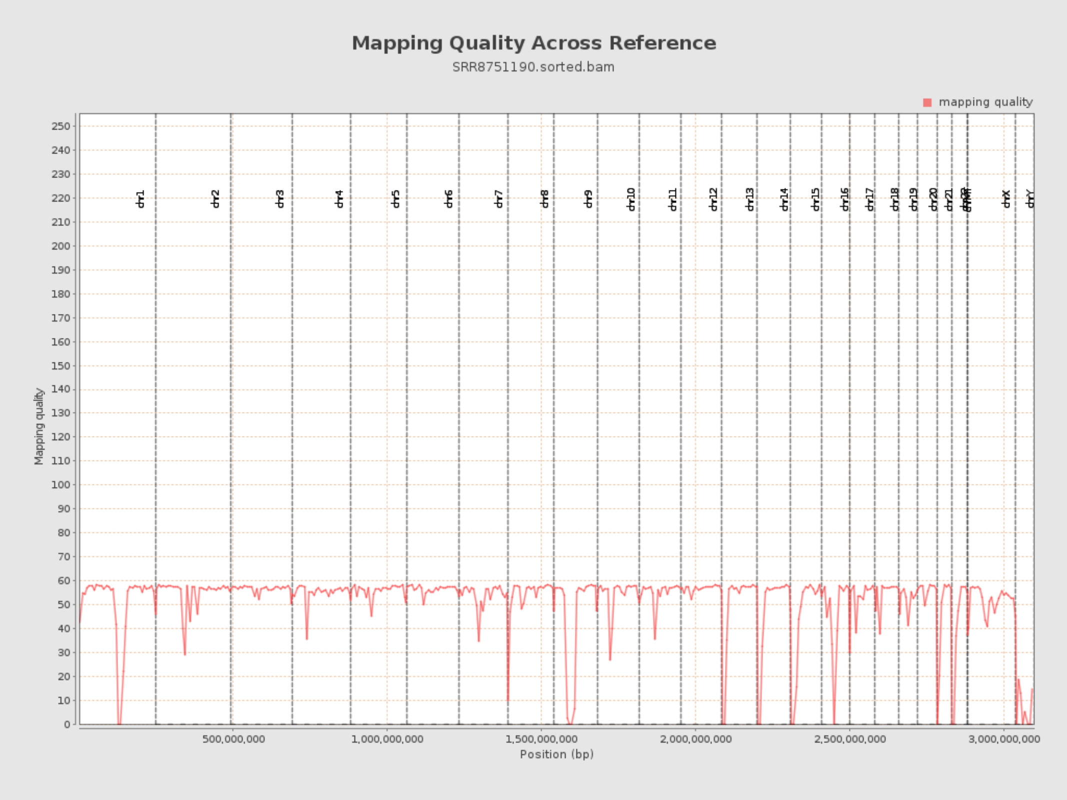
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram