Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 16:59:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751187.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_SRR8751187 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751187.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 16:59:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751187.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,091,818
Mapped reads	4,885,633 / 95.95%
Unmapped reads	206,185 / 4.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	159,571 / 3.13%
Read min/max/mean length	30 / 101 / 102.3
Duplicated reads (estimated)	139,237 / 2.73%
Duplication rate	1.47%
Clipped reads	1,000,802 / 19.66%

2.2. ACGT Content

Number/percentage of A's	139,778,791 / 29.24%
Number/percentage of C's	99,375,978 / 20.79%
Number/percentage of T's	140,525,168 / 29.4%
Number/percentage of G's	98,311,904 / 20.57%
Number/percentage of N's	2,507 / 0%
GC Percentage	41.36%

2.3. Coverage

Mean	0.1545

Standard Deviation	1.4785

2.4. Mapping Quality

Mean Mapping Quality	51.26

2.5. Mismatches and indels

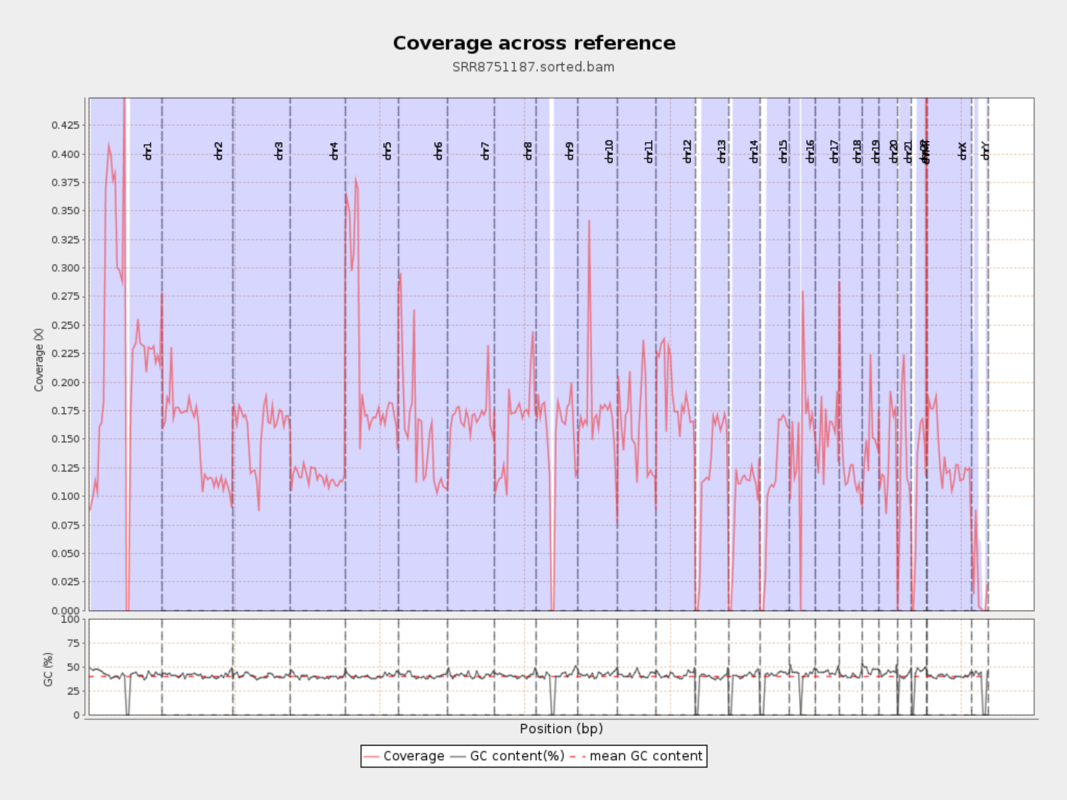
General error rate	0.41%
Mismatches	1,785,799
Insertions	129,184
Mapped reads with at least one insertion	2.58%
Deletions	63,593
Mapped reads with at least one deletion	1.27%
Homopolymer indels	48.69%

2.6. Chromosome stats

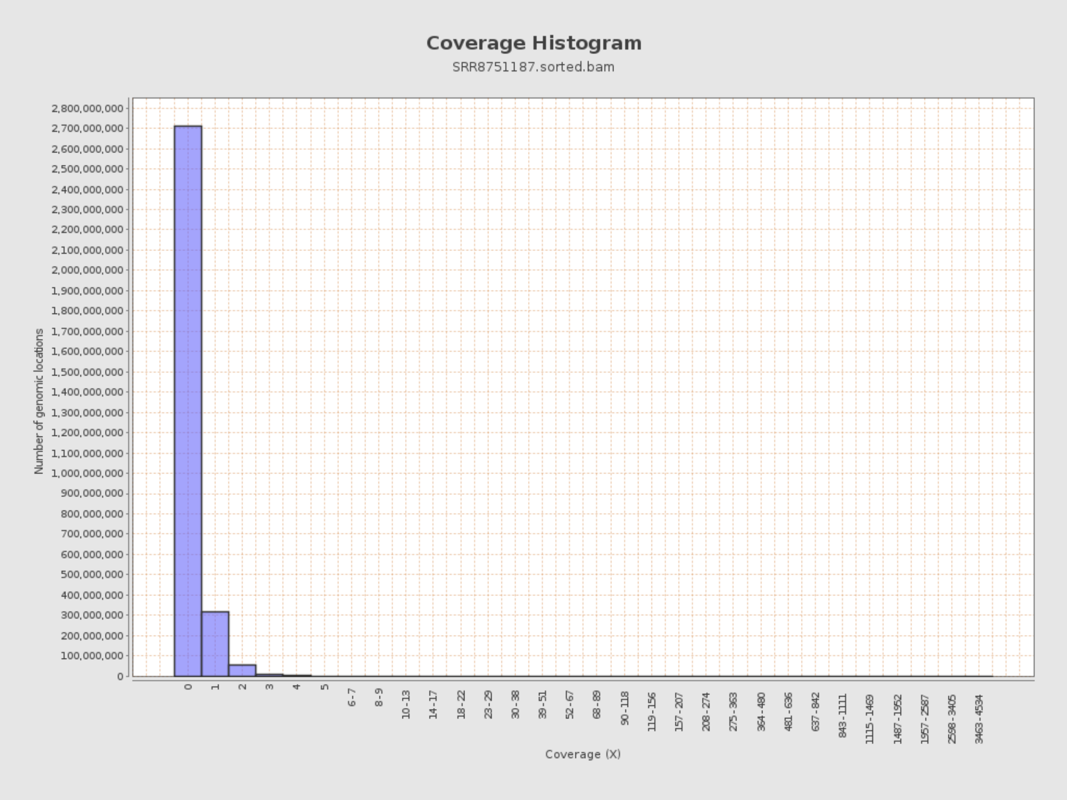
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	57365487	0.2302	4.2287
chr2	243199373	35817277	0.1473	0.6141
chr3	198022430	31512256	0.1591	0.4929
chr4	191154276	22323262	0.1168	0.4414
chr5	180915260	38864145	0.2148	0.5378
chr6	171115067	26909925	0.1573	1.1246
chr7	159138663	27060963	0.17	0.7748

chr8	146364022	23710422	0.162	0.5821
chr9	141213431	21058976	0.1491	0.7308
chr10	135534747	23732568	0.1751	1.8402
chr11	135006516	21577800	0.1598	0.728
chr12	133851895	25605661	0.1913	0.507
chr13	115169878	13912586	0.1208	0.3924
chr14	107349540	10203607	0.0951	0.3794
chr15	102531392	11325395	0.1105	0.3772
chr16	90354753	13657633	0.1512	1.0684
chr17	81195210	12542256	0.1545	0.7348
chr18	78077248	9976972	0.1278	1.6908
chr19	59128983	8898293	0.1505	3.0175
chr20	63025520	8523206	0.1352	0.4333
chr21	48129895	5986743	0.1244	0.4466
chr22	51304566	5358444	0.1044	0.3752
chrMT	16571	271783	16.4011	8.376
chrX	155270560	20739886	0.1336	0.4855
chrY	59373566	1198830	0.0202	0.8927

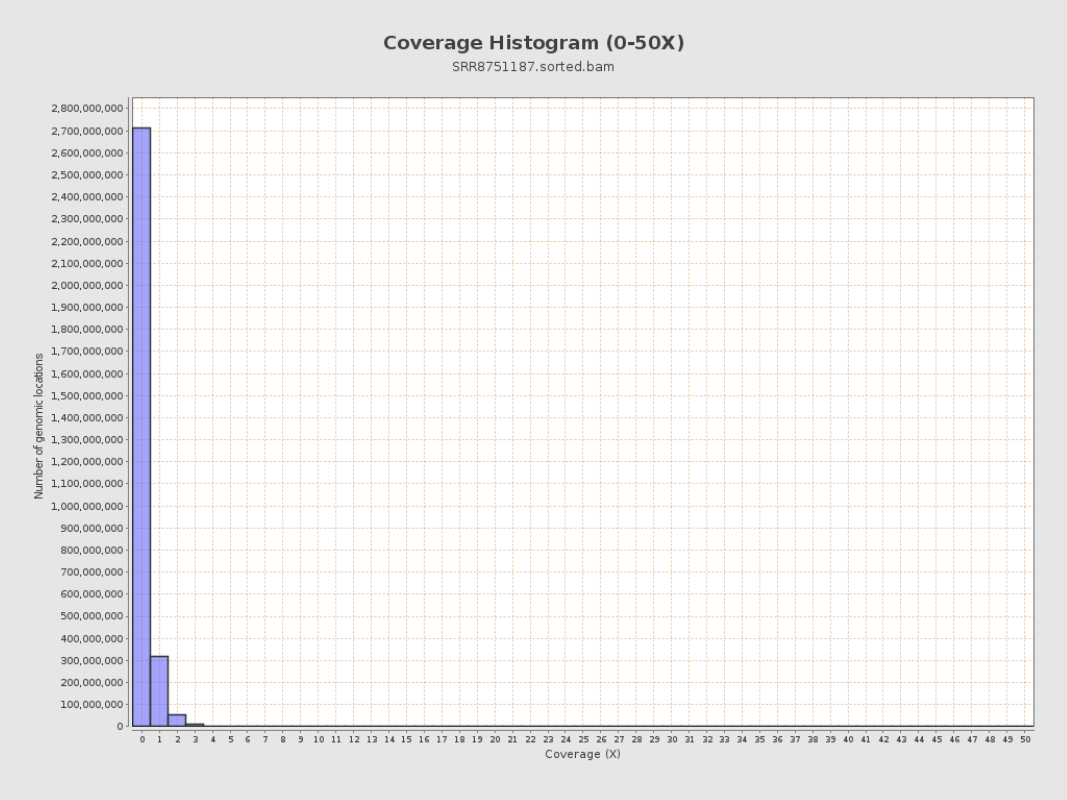
3. Results : Coverage across reference



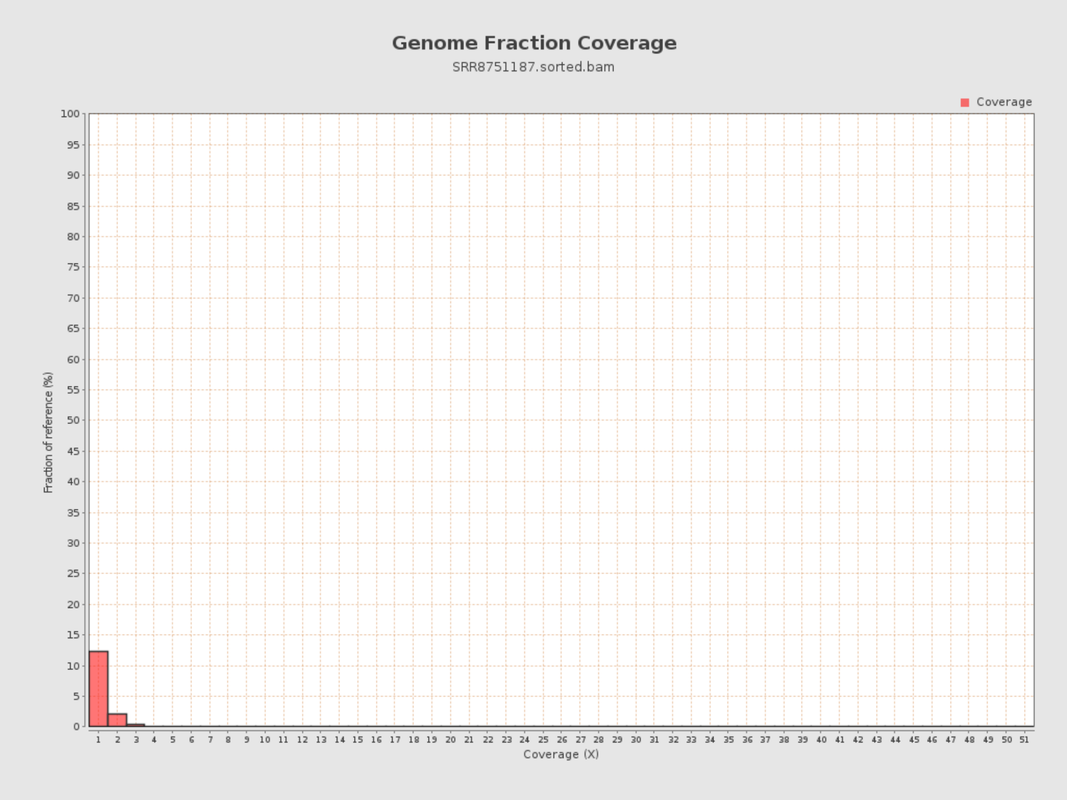
4. Results : Coverage Histogram



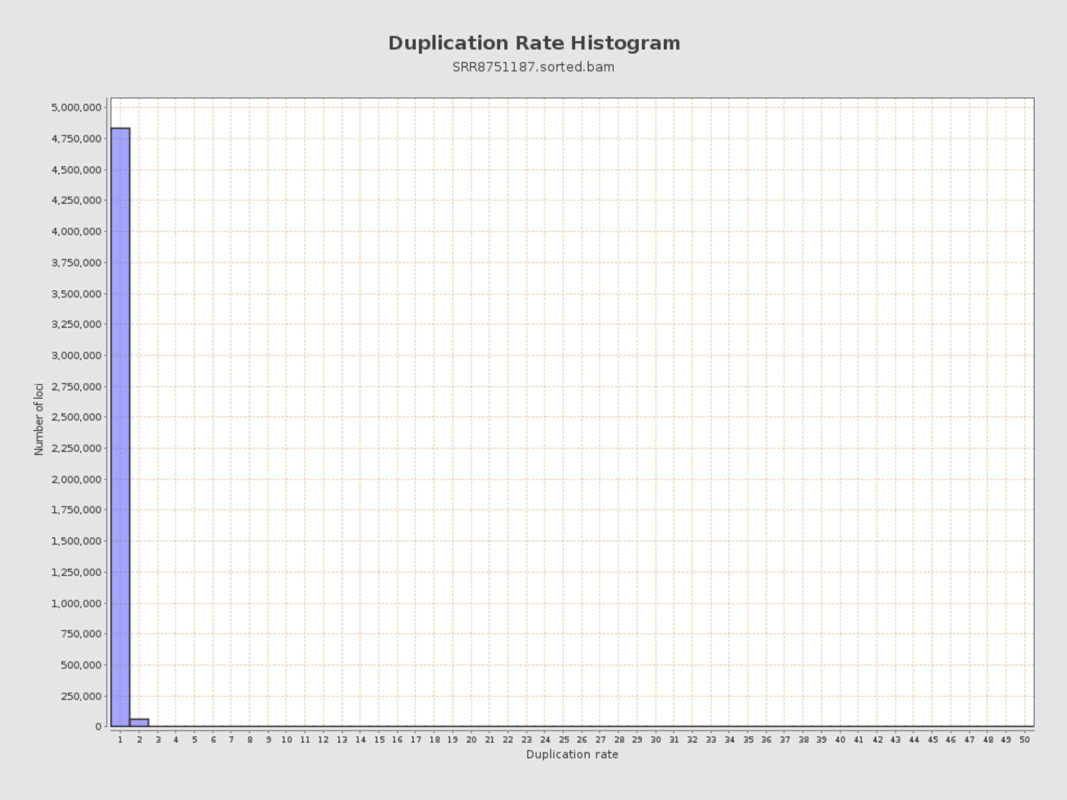
5. Results : Coverage Histogram (0-50X)



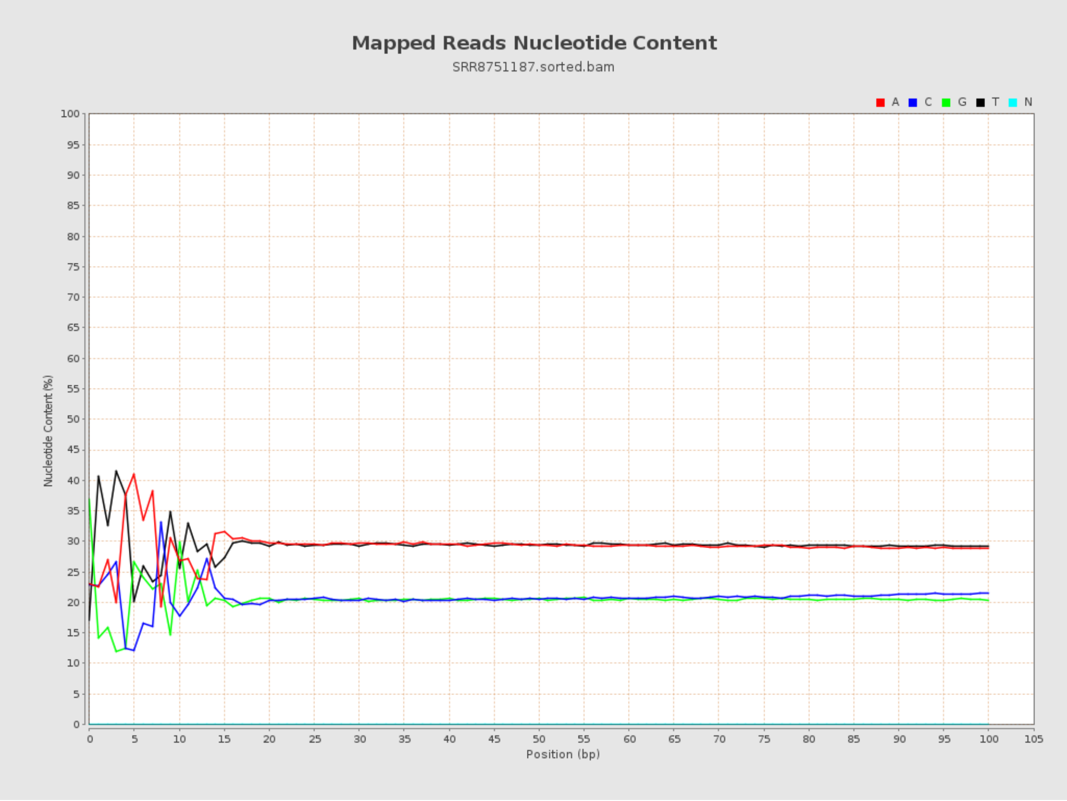
6. Results : Genome Fraction Coverage



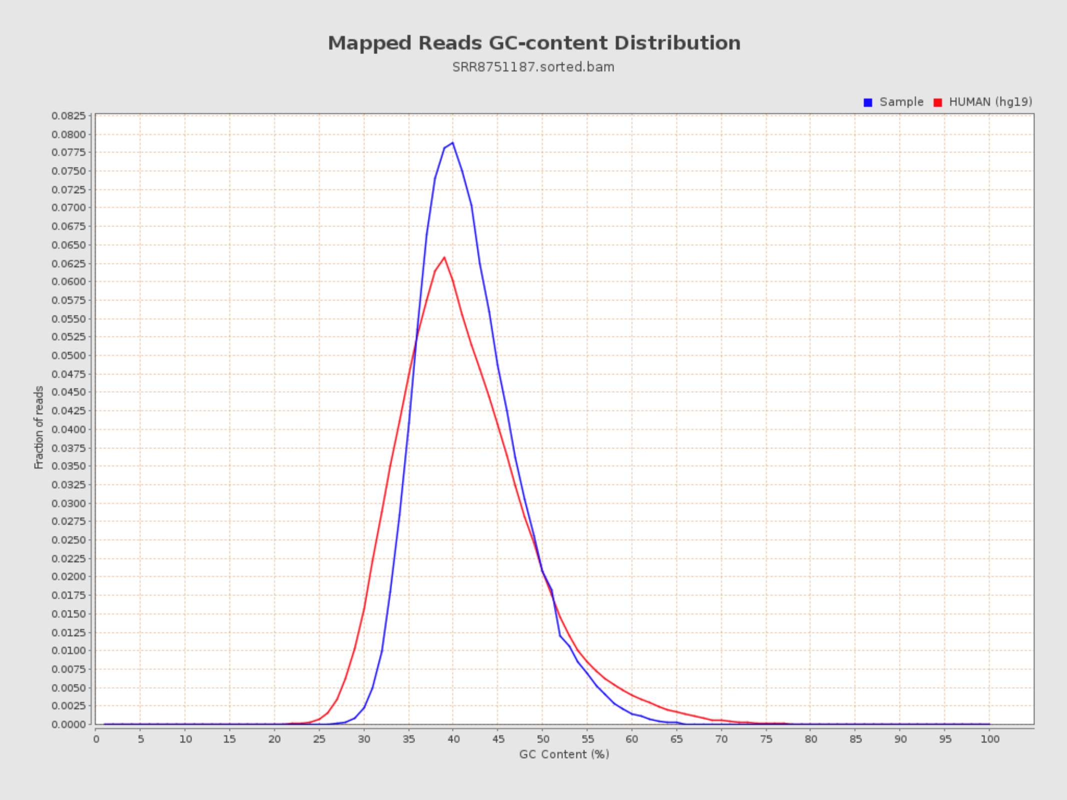
7. Results : Duplication Rate Histogram



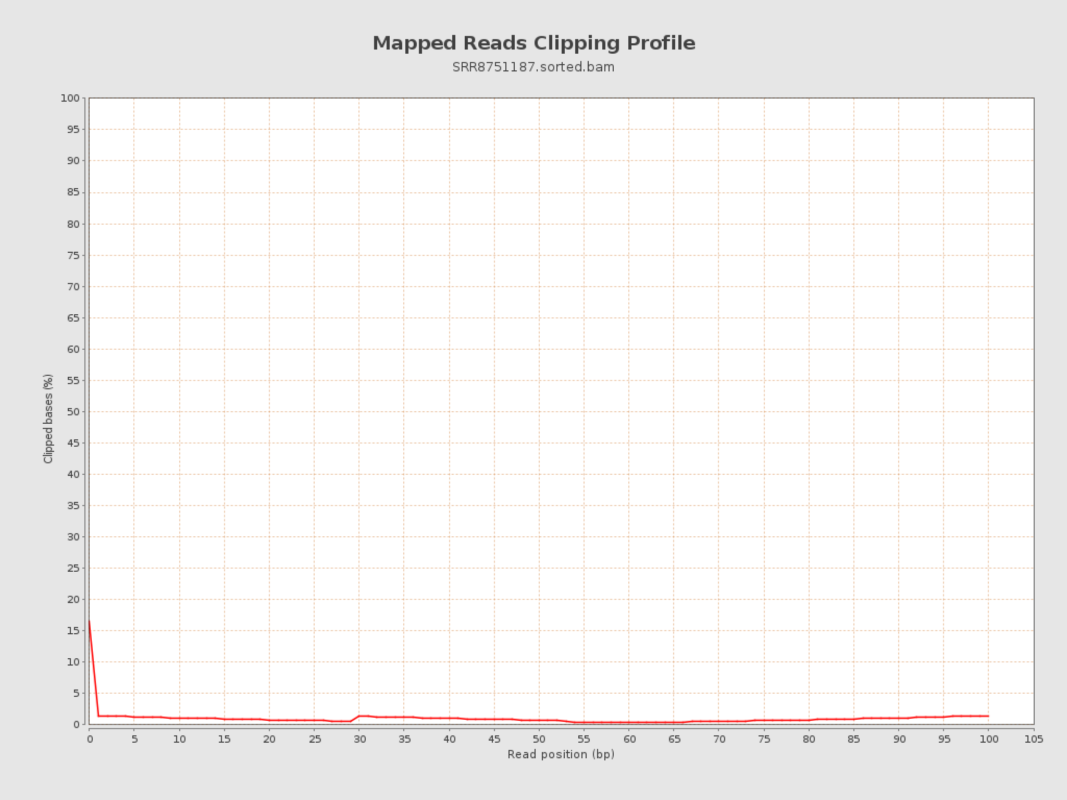
8. Results : Mapped Reads Nucleotide Content



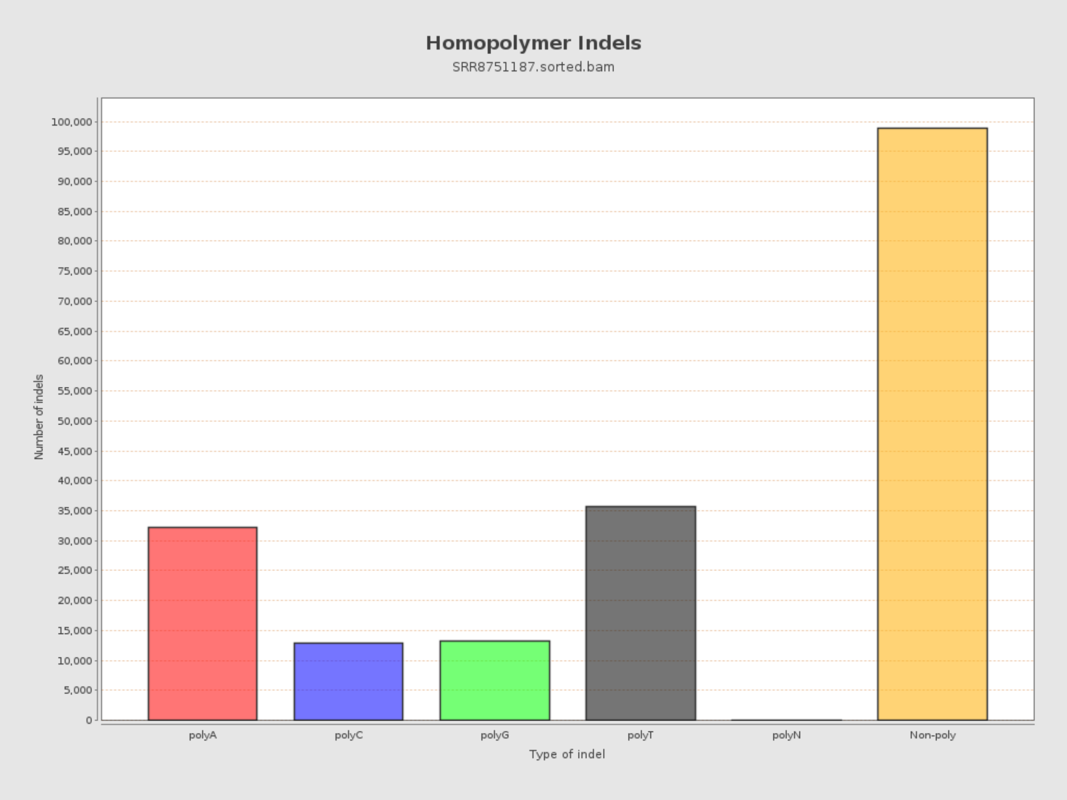
9. Results : Mapped Reads GC-content Distribution



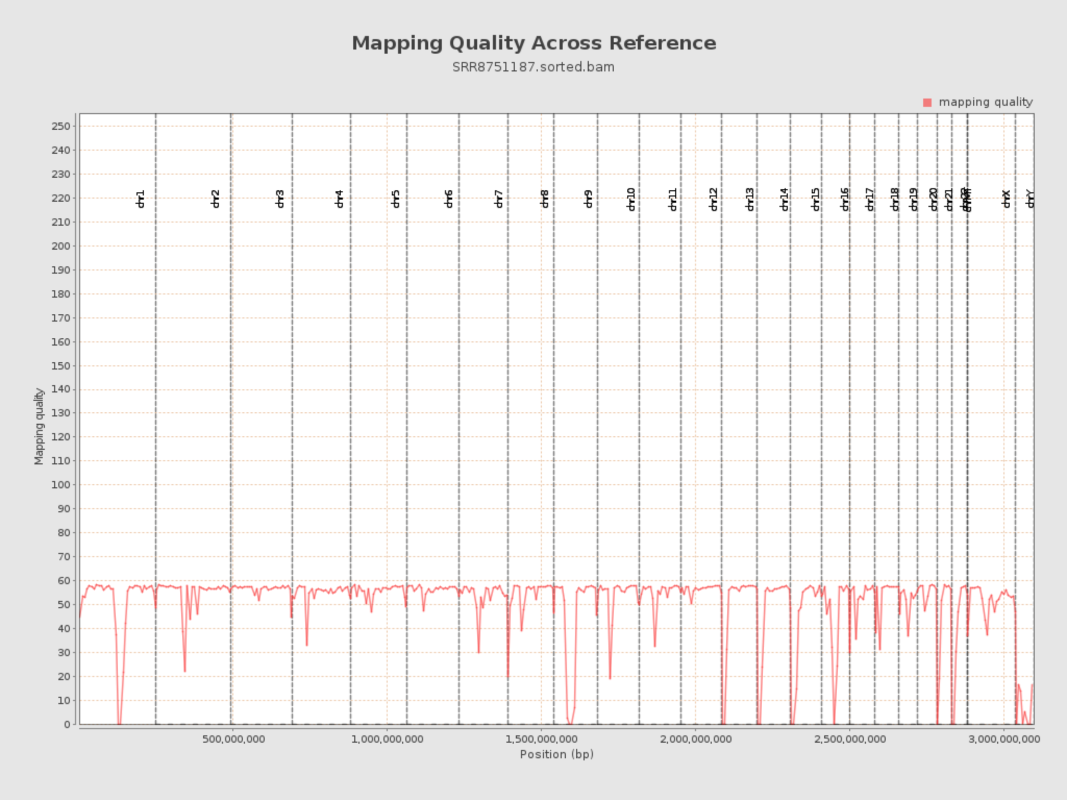
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram