Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:56:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751212.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_SRR8751212 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751212.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:56:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751212.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,613,075
Mapped reads	3,772,429 / 81.78%
Unmapped reads	840,646 / 18.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	211,482 / 4.58%
Read min/max/mean length	30 / 101 / 102.89
Duplicated reads (estimated)	99,921 / 2.17%
Duplication rate	1.42%
Clipped reads	873,083 / 18.93%

2.2. ACGT Content

Number/percentage of A's	109,592,773 / 29.49%
Number/percentage of C's	76,143,933 / 20.49%
Number/percentage of T's	110,261,665 / 29.67%
Number/percentage of G's	75,681,032 / 20.36%
Number/percentage of N's	2,722 / 0%
GC Percentage	40.85%

2.3. Coverage

Mean	0.1201

Standard Deviation	1.0415

2.4. Mapping Quality

Mean Mapping Quality	51.13

2.5. Mismatches and indels

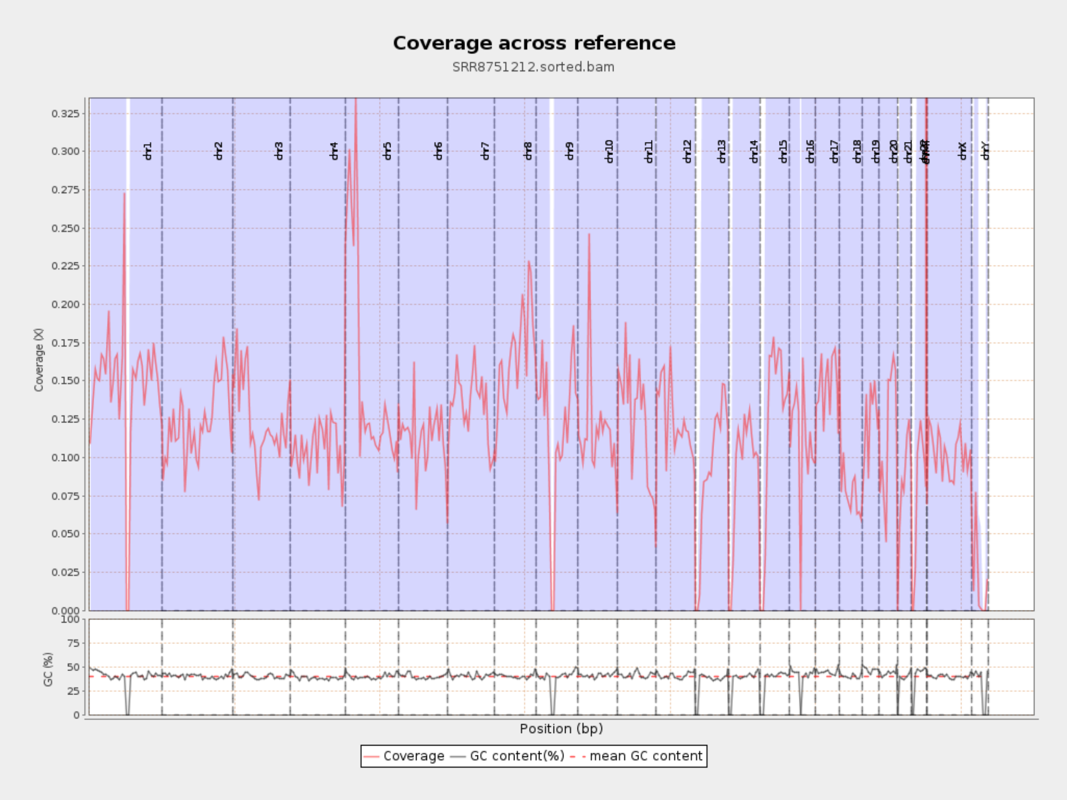
General error rate	0.44%
Mismatches	1,334,993
Insertions	227,389
Mapped reads with at least one insertion	5.8%
Deletions	56,498
Mapped reads with at least one deletion	1.46%
Homopolymer indels	52.6%

2.6. Chromosome stats

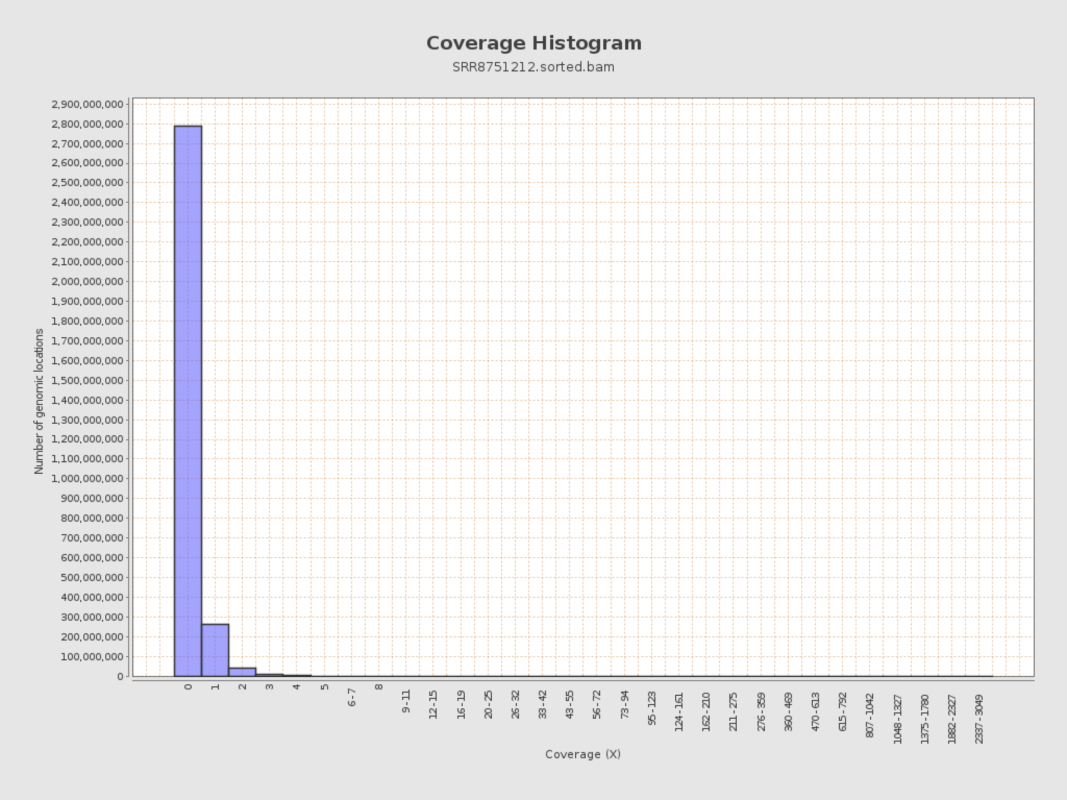
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	36679817	0.1472	2.8451
chr2	243199373	30097199	0.1238	0.5182
chr3	198022430	24666184	0.1246	0.4702
chr4	191154276	20058184	0.1049	0.402
chr5	180915260	28282316	0.1563	0.461
chr6	171115067	19426276	0.1135	0.6082
chr7	159138663	21567741	0.1355	0.6751

chr8	146364022	24389811	0.1666	0.6681
chr9	141213431	16567654	0.1173	0.6211
chr10	135534747	15989369	0.118	1.4773
chr11	135006516	16916221	0.1253	0.5117
chr12	133851895	16836029	0.1258	0.4041
chr13	115169878	10537010	0.0915	0.3379
chr14	107349540	9761318	0.0909	0.3555
chr15	102531392	12538194	0.1223	0.3954
chr16	90354753	9983849	0.1105	0.6641
chr17	81195210	11910717	0.1467	0.5737
chr18	78077248	6280659	0.0804	1.344
chr19	59128983	7282150	0.1232	1.9096
chr20	63025520	7294340	0.1157	0.392
chr21	48129895	4019276	0.0835	0.3591
chr22	51304566	3729356	0.0727	0.3065
chrMT	16571	157254	9.4897	7.9272
chrX	155270560	15805303	0.1018	0.3977
chrY	59373566	1031785	0.0174	0.7976

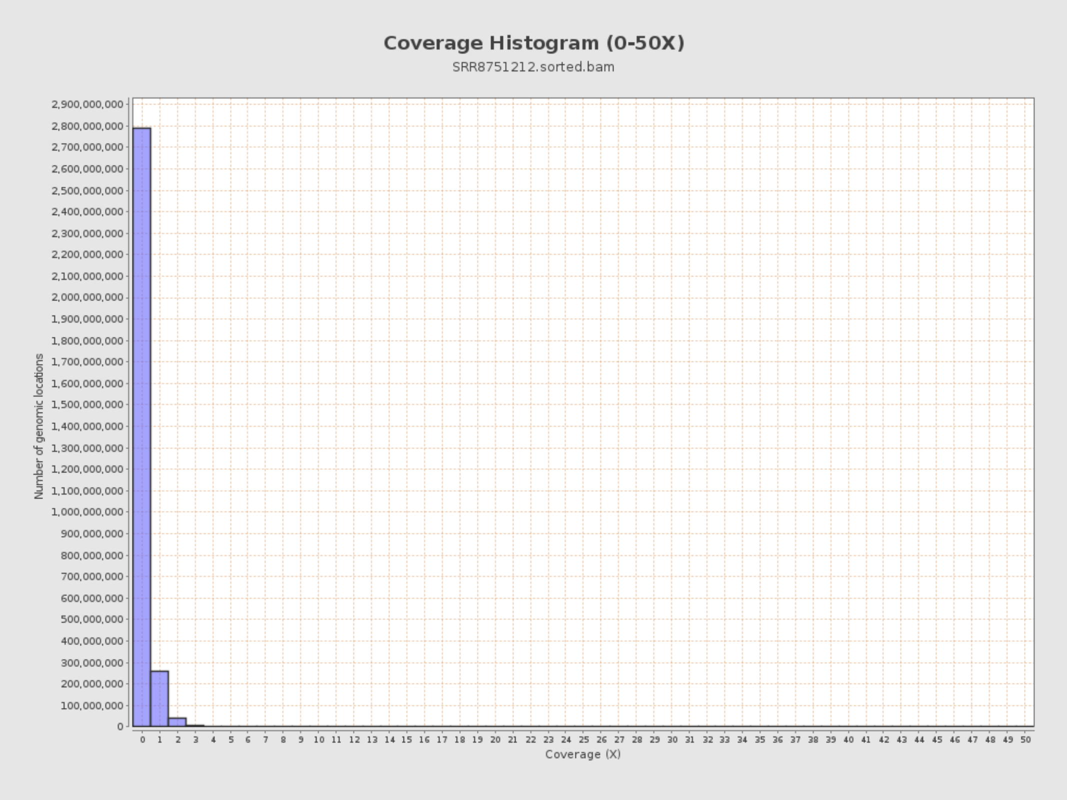
3. Results : Coverage across reference



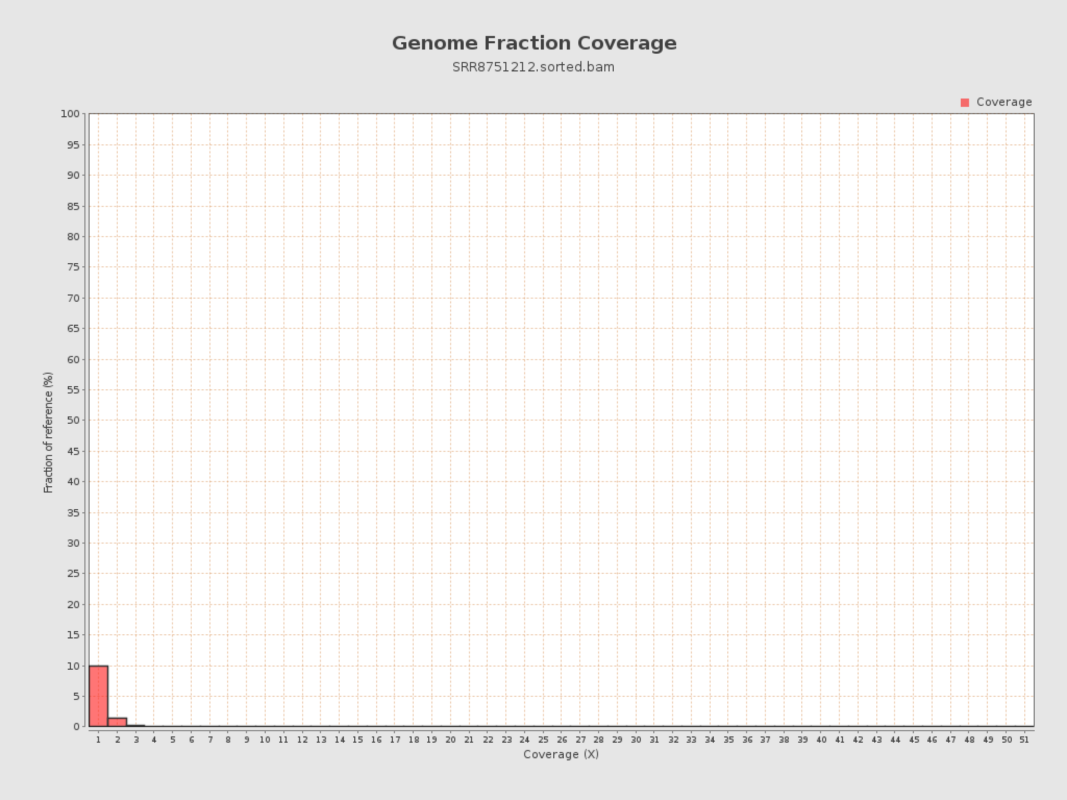
4. Results : Coverage Histogram



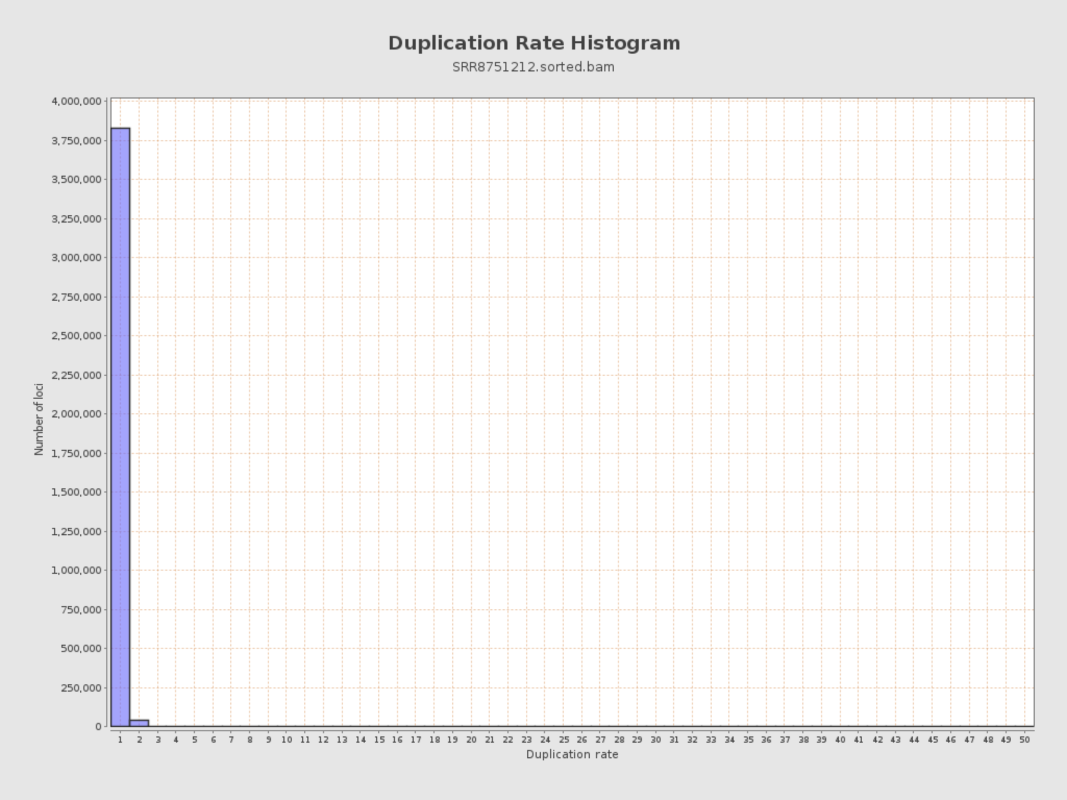
5. Results : Coverage Histogram (0-50X)



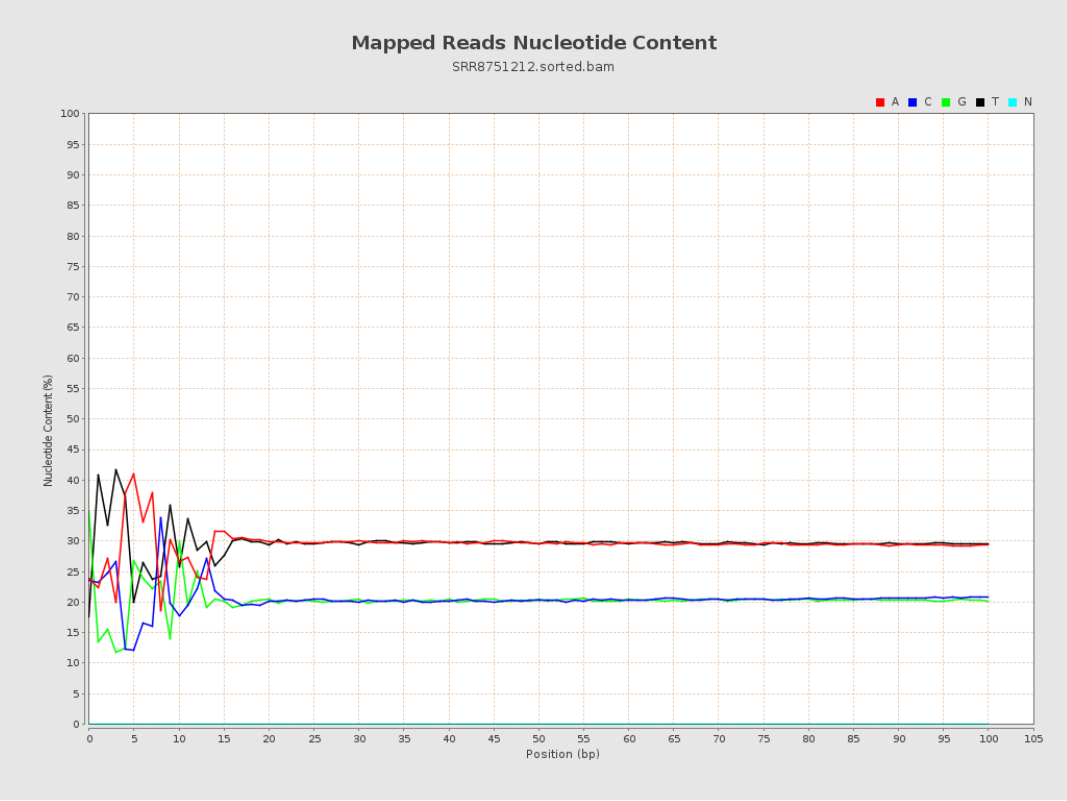
6. Results : Genome Fraction Coverage



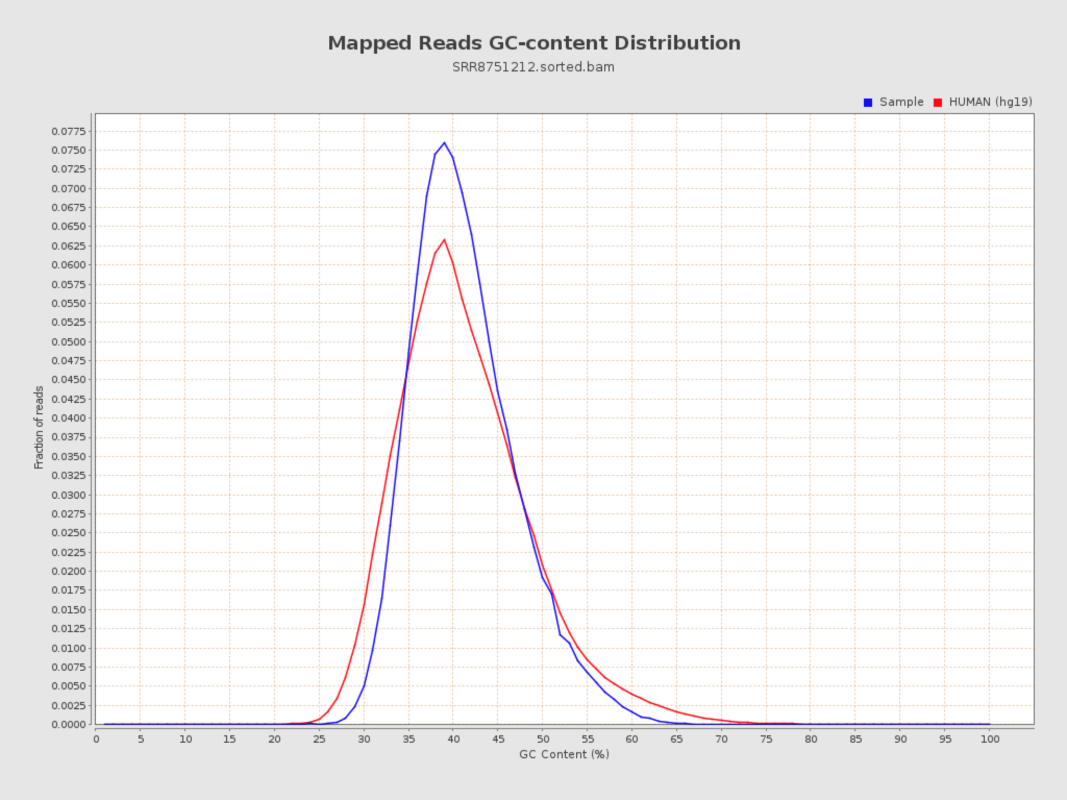
7. Results : Duplication Rate Histogram



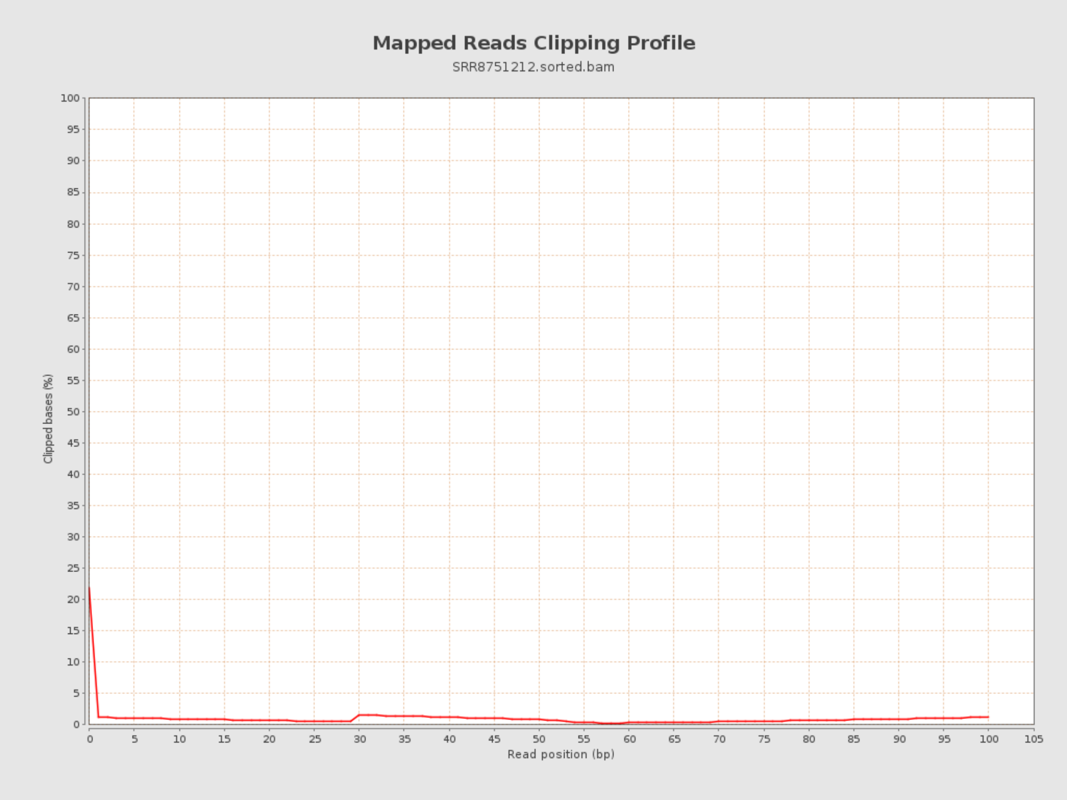
8. Results : Mapped Reads Nucleotide Content



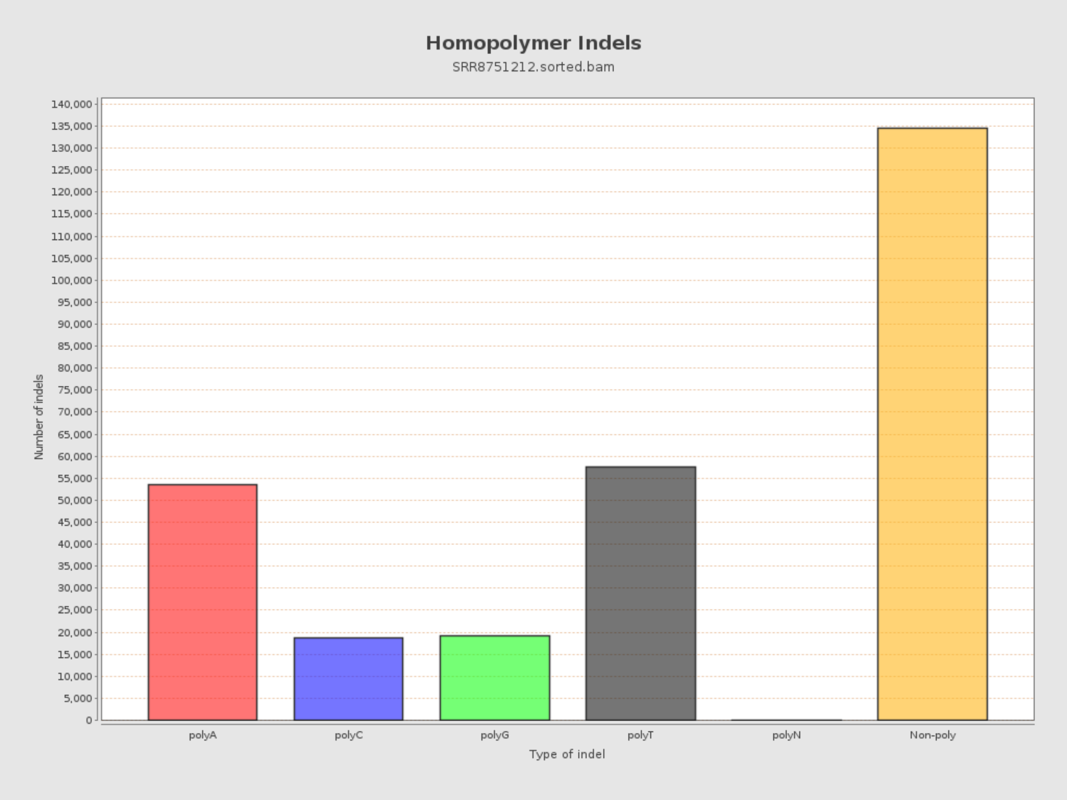
9. Results : Mapped Reads GC-content Distribution



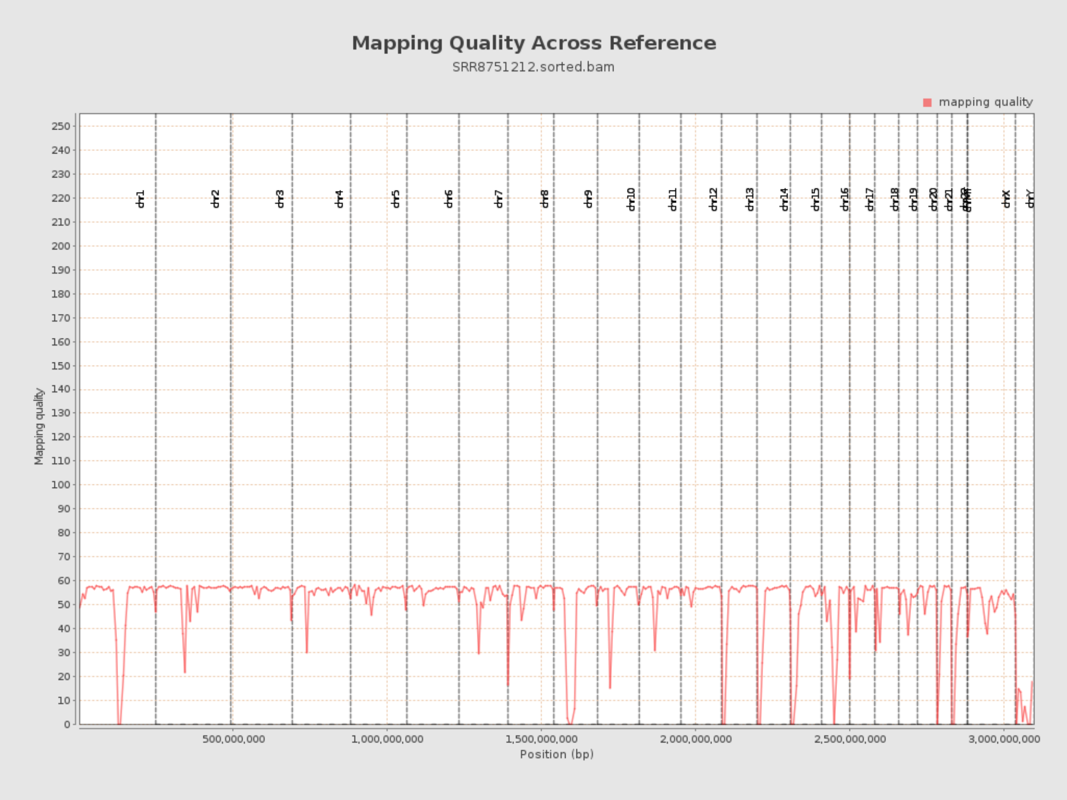
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram