Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 21:56:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080715.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_SRR3080715 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080715.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 21:56:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080715.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,931,626
Mapped reads	1,721,959 / 89.15%
Unmapped reads	209,667 / 10.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,590 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	91,715 / 4.75%
Duplication rate	4.56%
Clipped reads	716,137 / 37.07%

2.2. ACGT Content

Number/percentage of A's	32,330,155 / 27.89%
Number/percentage of C's	21,267,241 / 18.35%
Number/percentage of T's	37,104,434 / 32.01%
Number/percentage of G's	25,202,925 / 21.74%
Number/percentage of N's	1,820 / 0%
GC Percentage	40.09%

2.3. Coverage

Mean	0.0375

Standard Deviation	0.3239

2.4. Mapping Quality

Mean Mapping Quality	46.09

2.5. Mismatches and indels

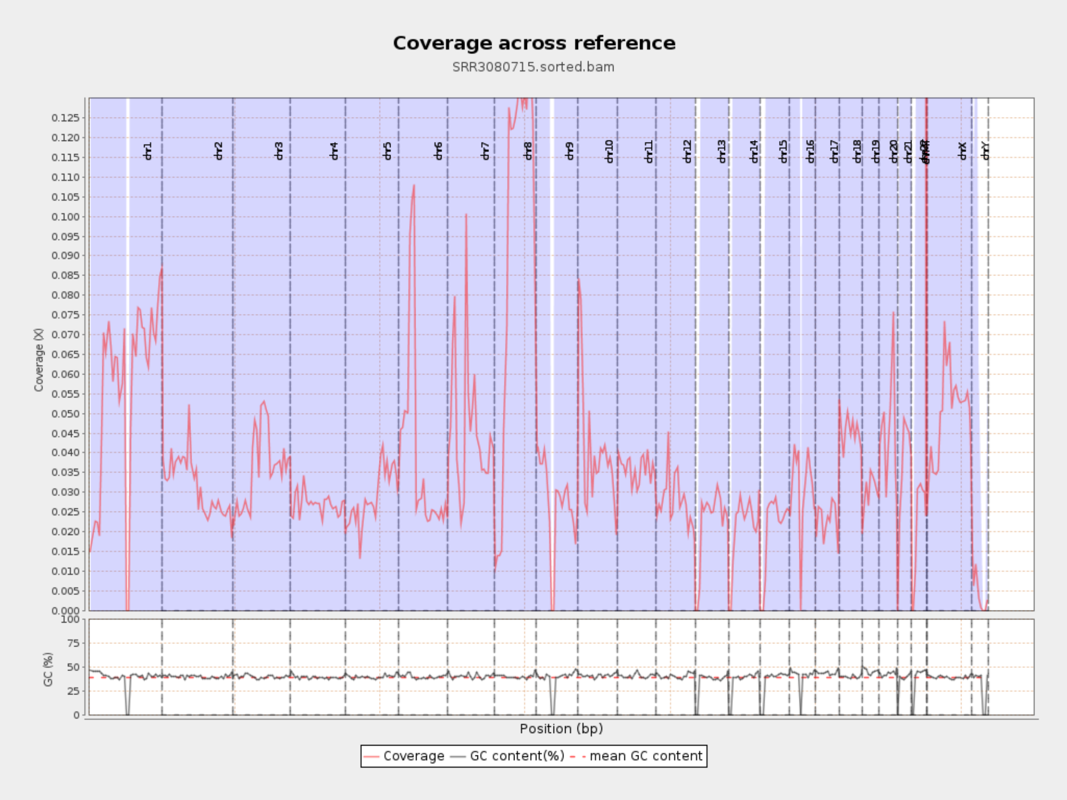
General error rate	0.82%
Mismatches	932,786
Insertions	8,084
Mapped reads with at least one insertion	0.47%
Deletions	24,372
Mapped reads with at least one deletion	1.4%
Homopolymer indels	47.8%

2.6. Chromosome stats

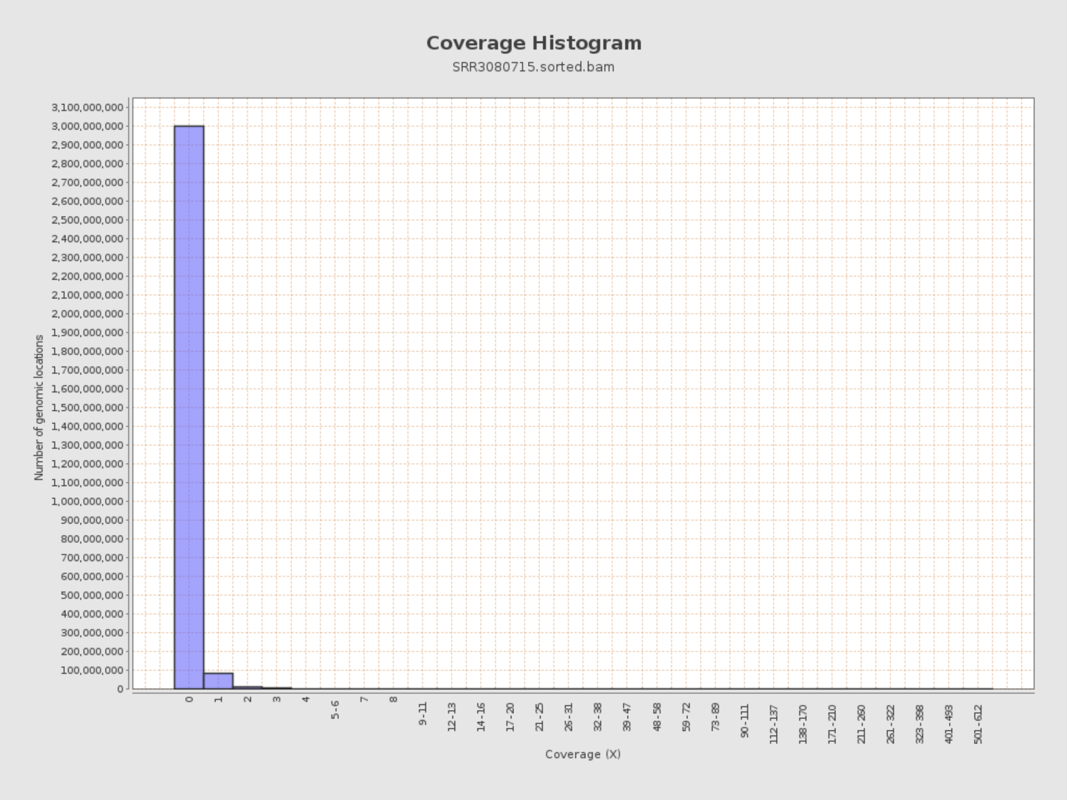
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13838025	0.0555	0.4396
chr2	243199373	7687179	0.0316	0.3301
chr3	198022430	7154836	0.0361	0.2184
chr4	191154276	5173802	0.0271	0.1922
chr5	180915260	5254090	0.029	0.1948
chr6	171115067	6913021	0.0404	0.2863
chr7	159138663	7433150	0.0467	0.7884

chr8	146364022	13883239	0.0949	0.4633
chr9	141213431	3815871	0.027	0.2247
chr10	135534747	5608469	0.0414	0.3145
chr11	135006516	4830828	0.0358	0.2361
chr12	133851895	3725107	0.0278	0.1926
chr13	115169878	2542713	0.0221	0.1694
chr14	107349540	2217618	0.0207	0.1712
chr15	102531392	2109092	0.0206	0.1642
chr16	90354753	2836471	0.0314	0.2082
chr17	81195210	1826501	0.0225	0.1816
chr18	78077248	3566610	0.0457	0.3201
chr19	59128983	1805091	0.0305	0.2958
chr20	63025520	2886020	0.0458	0.2467
chr21	48129895	1722117	0.0358	0.2235
chr22	51304566	1082307	0.0211	0.1645
chrMT	16571	25366	1.5307	1.5339
chrX	155270560	7752622	0.0499	0.2697
chrY	59373566	259297	0.0044	0.0922

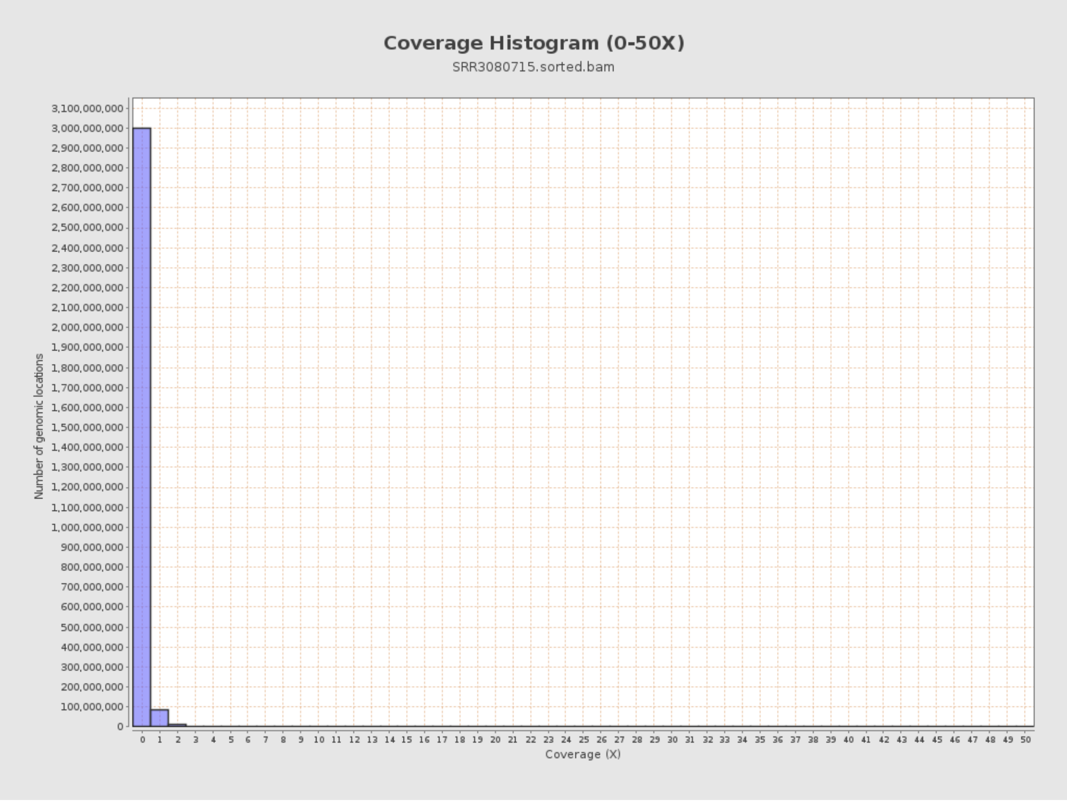
3. Results : Coverage across reference



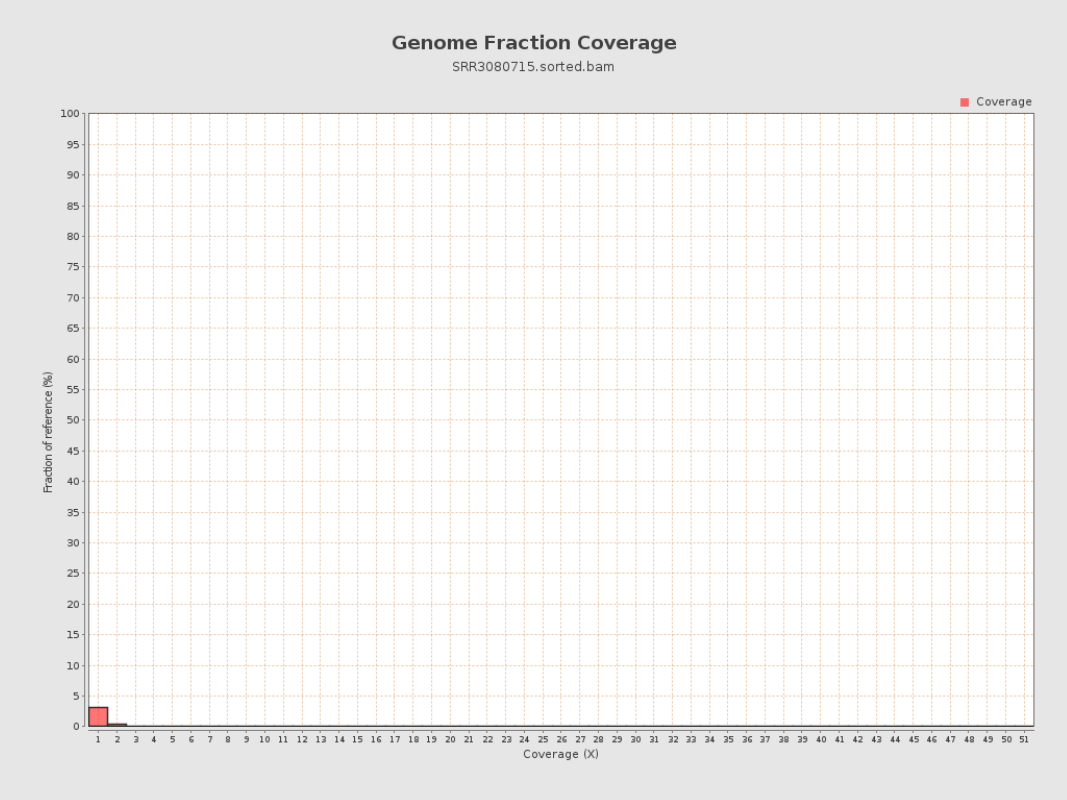
4. Results : Coverage Histogram



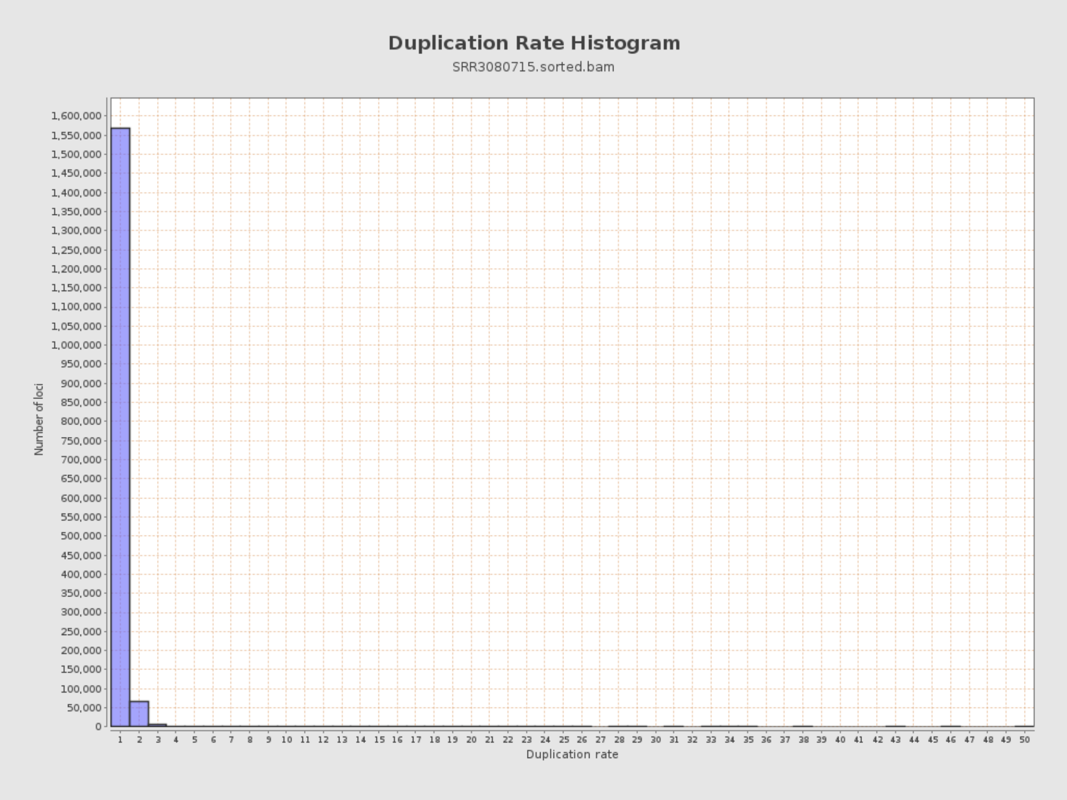
5. Results : Coverage Histogram (0-50X)



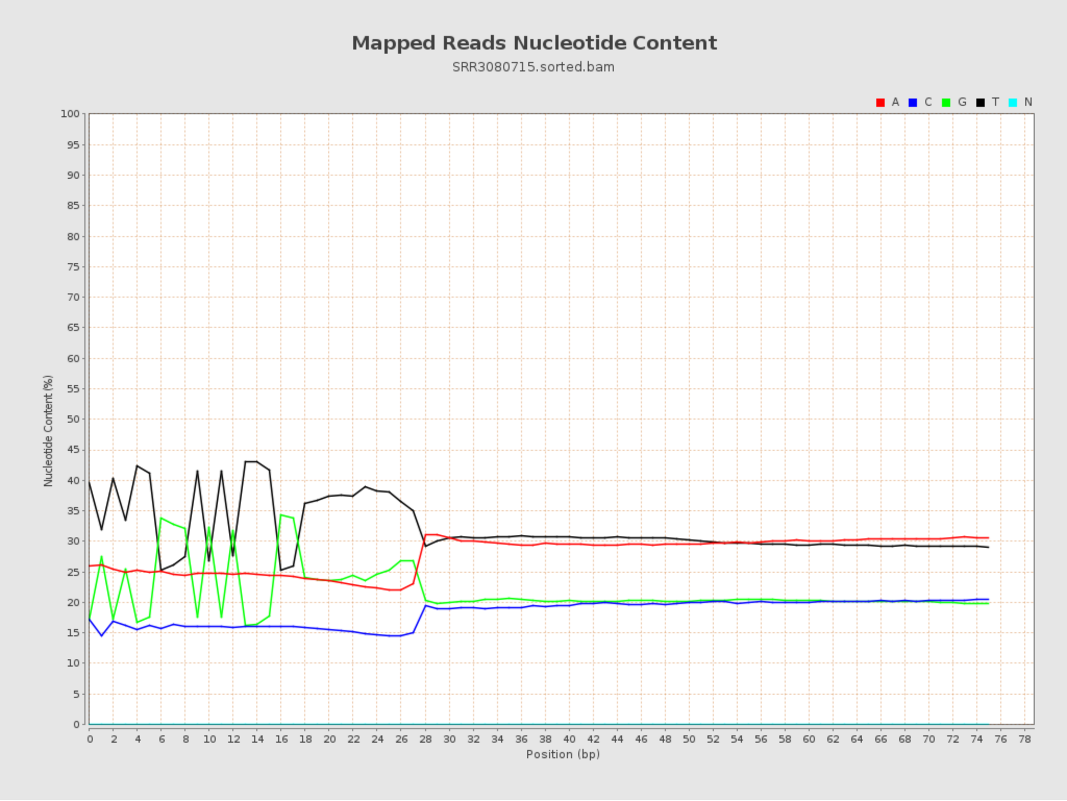
6. Results : Genome Fraction Coverage



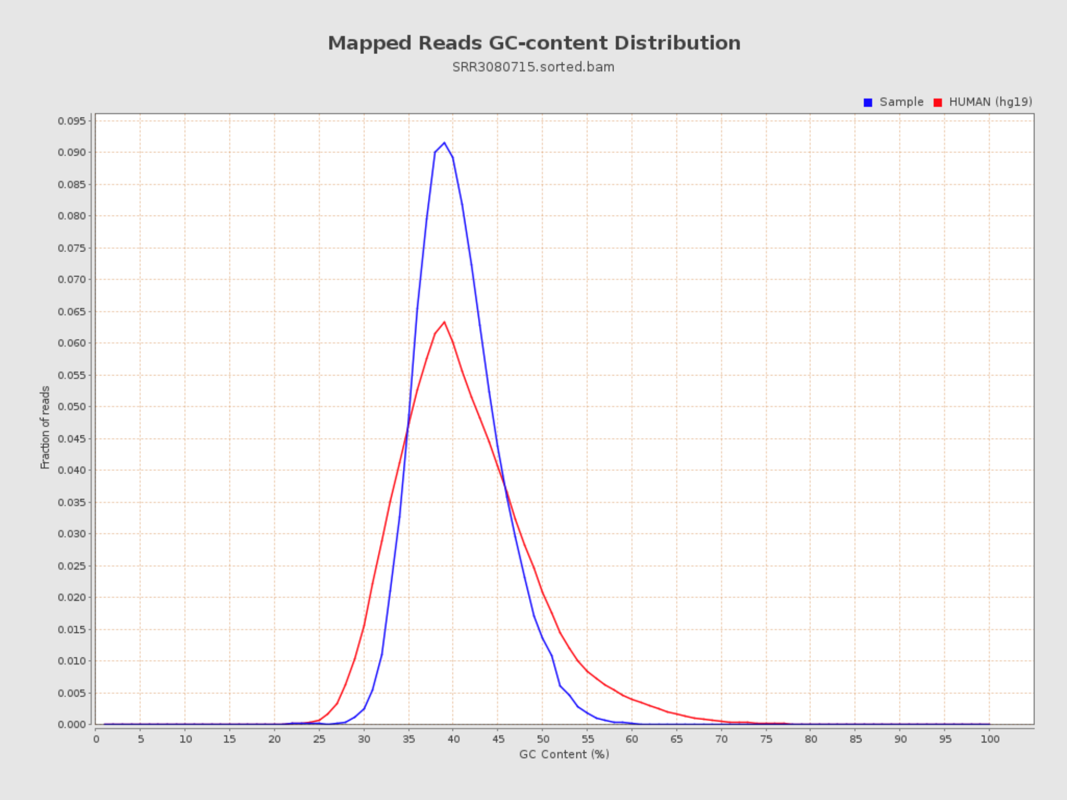
7. Results : Duplication Rate Histogram



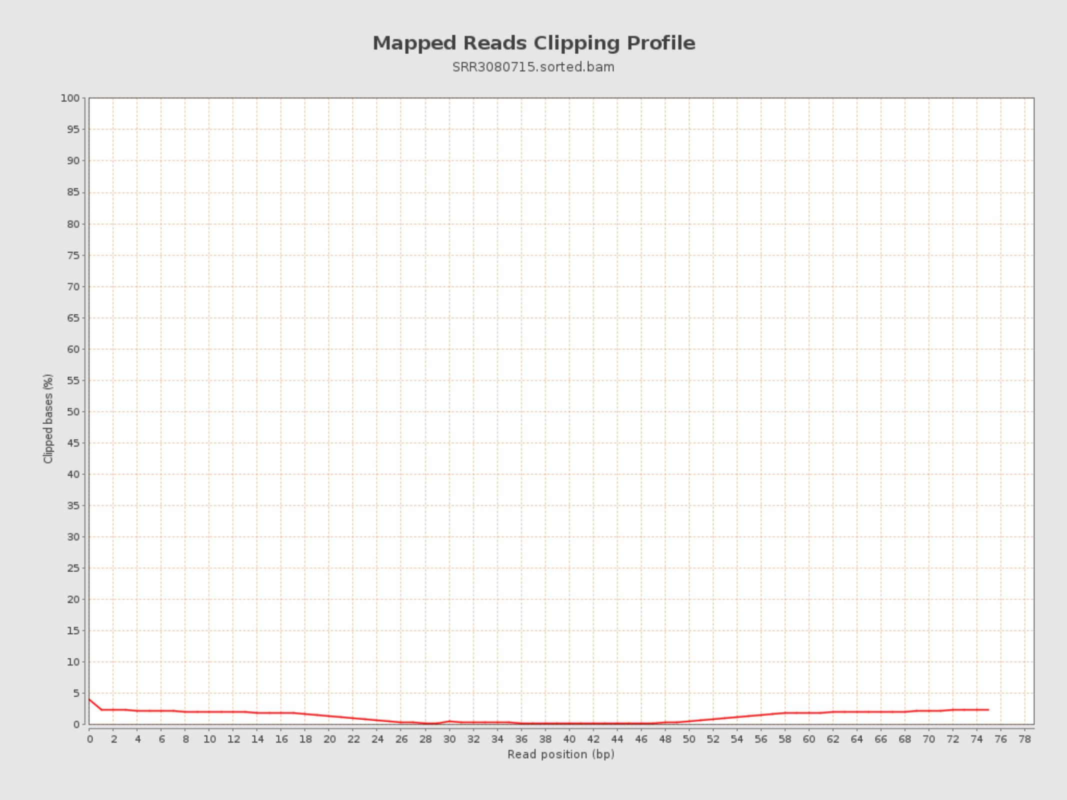
8. Results : Mapped Reads Nucleotide Content



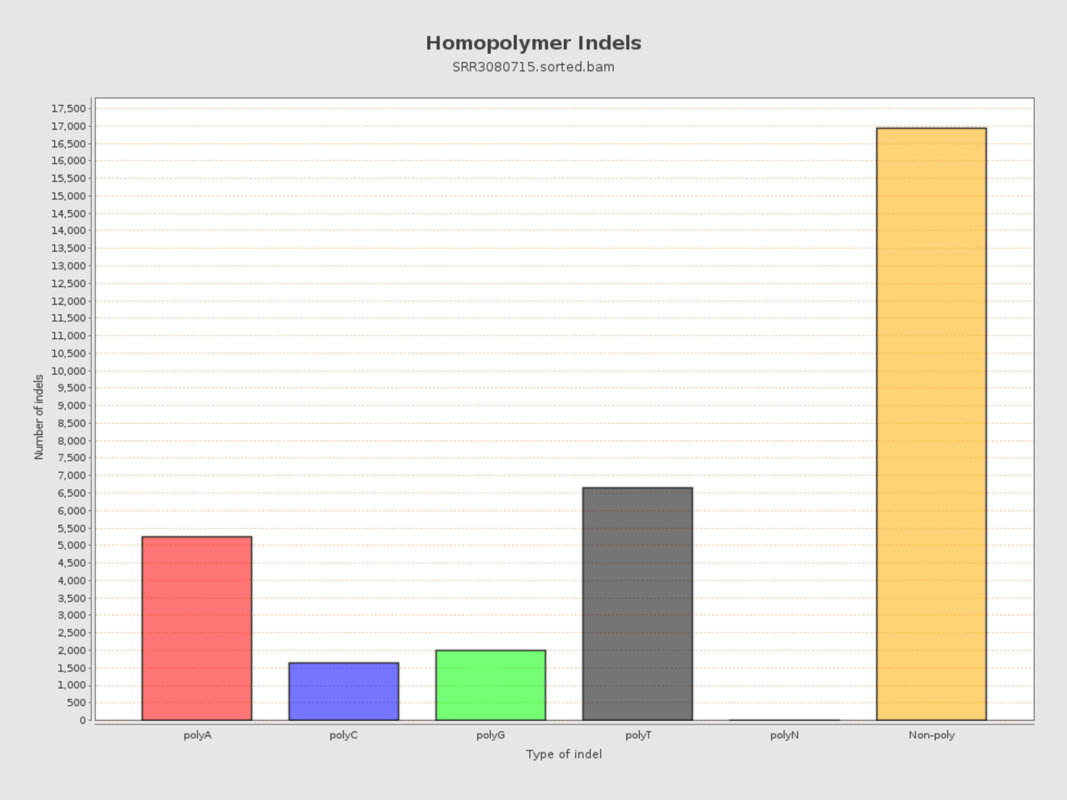
9. Results : Mapped Reads GC-content Distribution



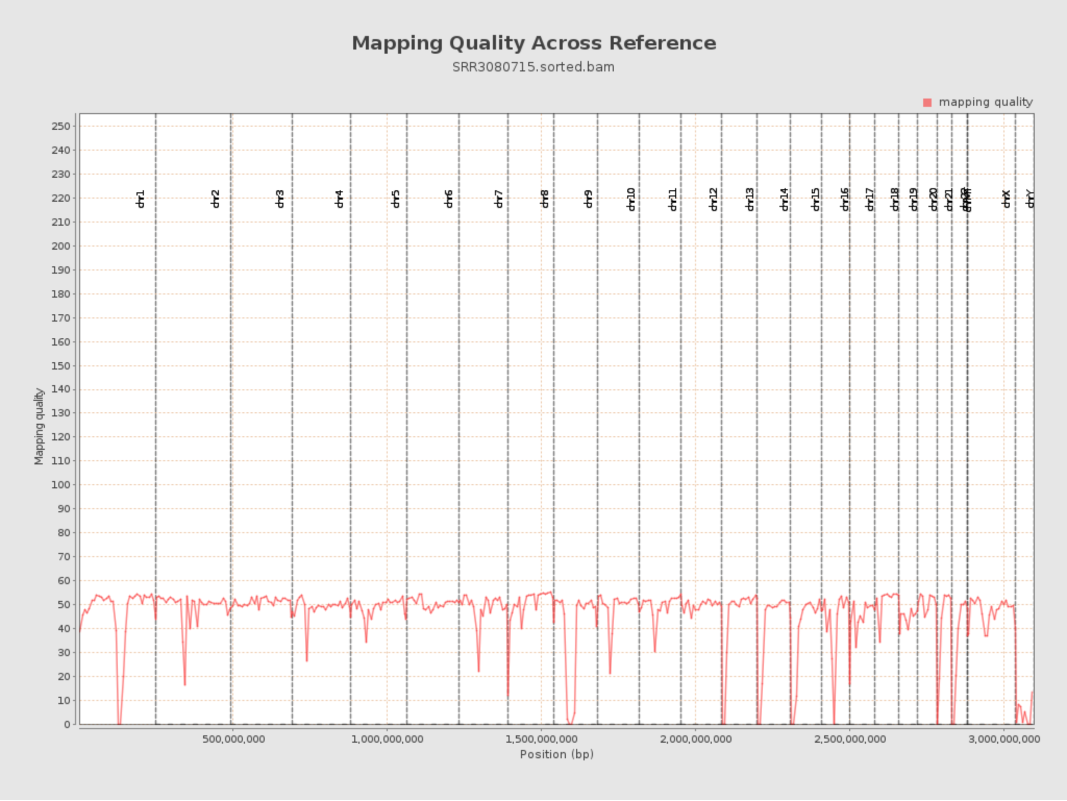
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram