Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 21:07:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080711.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_SRR3080711 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080711.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 21:07:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080711.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,113,520
Mapped reads	1,940,655 / 91.82%
Unmapped reads	172,865 / 8.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,080 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	102,062 / 4.83%
Duplication rate	4.61%
Clipped reads	737,478 / 34.89%

2.2. ACGT Content

Number/percentage of A's	37,403,691 / 28.24%
Number/percentage of C's	24,487,744 / 18.49%
Number/percentage of T's	42,143,138 / 31.82%
Number/percentage of G's	28,409,413 / 21.45%
Number/percentage of N's	1,950 / 0%
GC Percentage	39.94%

2.3. Coverage

Mean	0.0428

Standard Deviation	0.3106

2.4. Mapping Quality

Mean Mapping Quality	46.58

2.5. Mismatches and indels

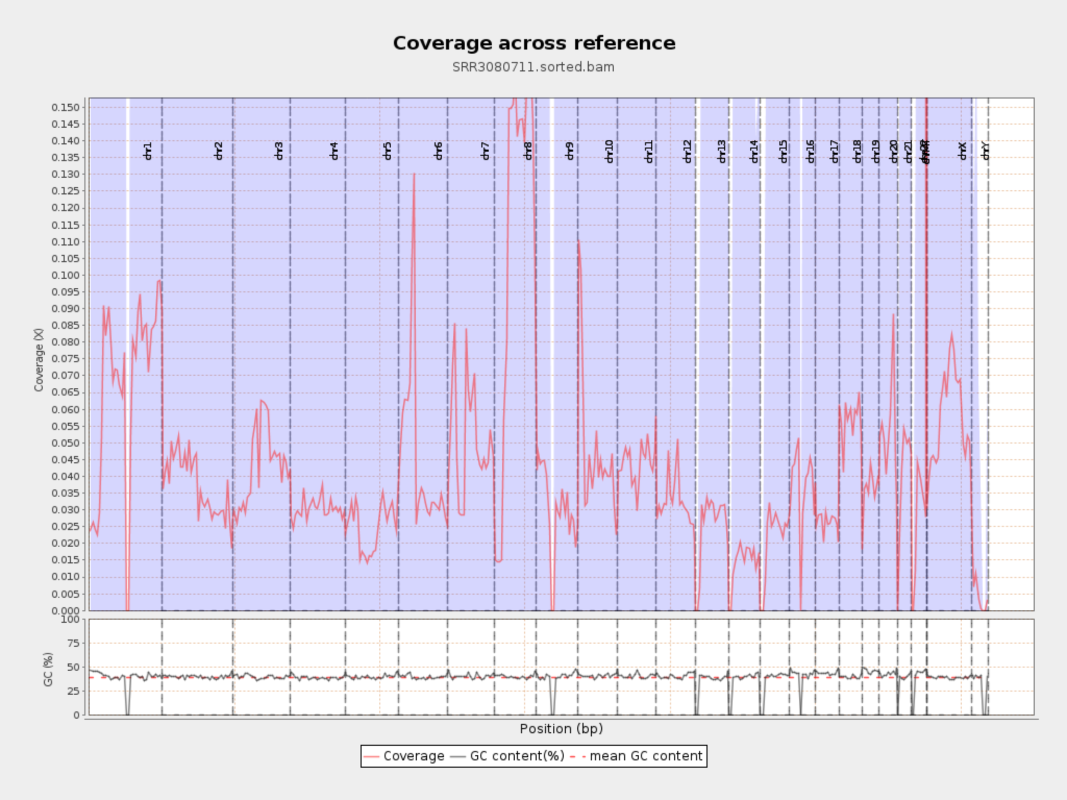
General error rate	0.78%
Mismatches	1,019,969
Insertions	9,252
Mapped reads with at least one insertion	0.47%
Deletions	27,561
Mapped reads with at least one deletion	1.41%
Homopolymer indels	48.23%

2.6. Chromosome stats

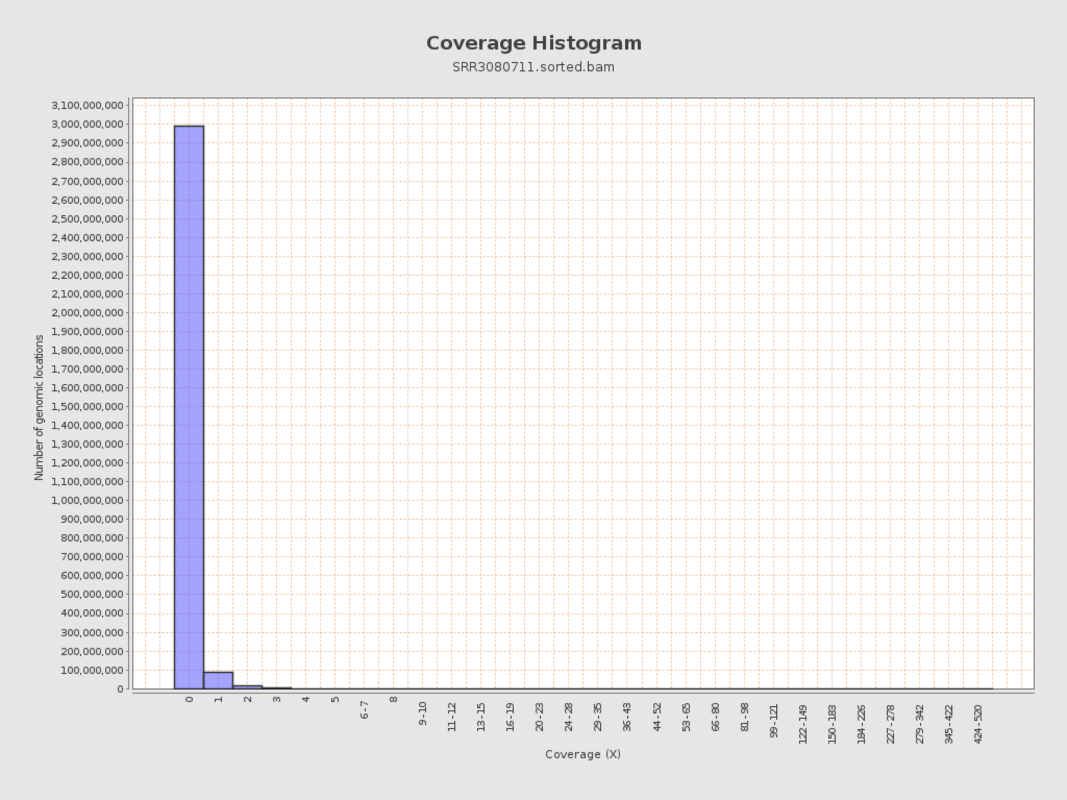
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16445828	0.066	0.4242
chr2	243199373	9062732	0.0373	0.3298
chr3	198022430	8619382	0.0435	0.2476
chr4	191154276	5778092	0.0302	0.2099
chr5	180915260	4508361	0.0249	0.1861
chr6	171115067	7836872	0.0458	0.3065
chr7	159138663	8345862	0.0524	0.6007

chr8	146364022	16215168	0.1108	0.4648
chr9	141213431	4189562	0.0297	0.2434
chr10	135534747	6569331	0.0485	0.3037
chr11	135006516	5892473	0.0436	0.2631
chr12	133851895	4377293	0.0327	0.2161
chr13	115169878	2883667	0.025	0.1881
chr14	107349540	1532954	0.0143	0.1477
chr15	102531392	2181191	0.0213	0.1726
chr16	90354753	3361651	0.0372	0.236
chr17	81195210	2125591	0.0262	0.1976
chr18	78077248	4436419	0.0568	0.3692
chr19	59128983	2186457	0.037	0.3055
chr20	63025520	3401532	0.054	0.2801
chr21	48129895	1943336	0.0404	0.244
chr22	51304566	1308046	0.0255	0.189
chrMT	16571	29742	1.7948	1.7567
chrX	155270560	8980178	0.0578	0.2951
chrY	59373566	282729	0.0048	0.0924

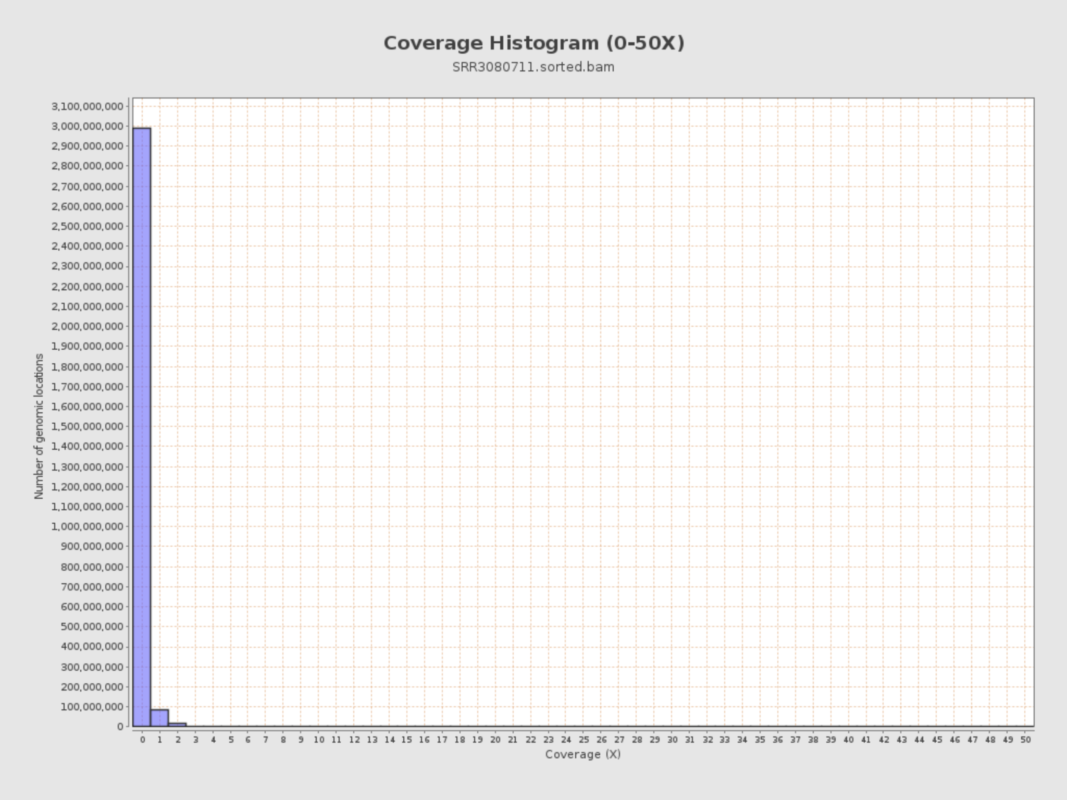
3. Results : Coverage across reference



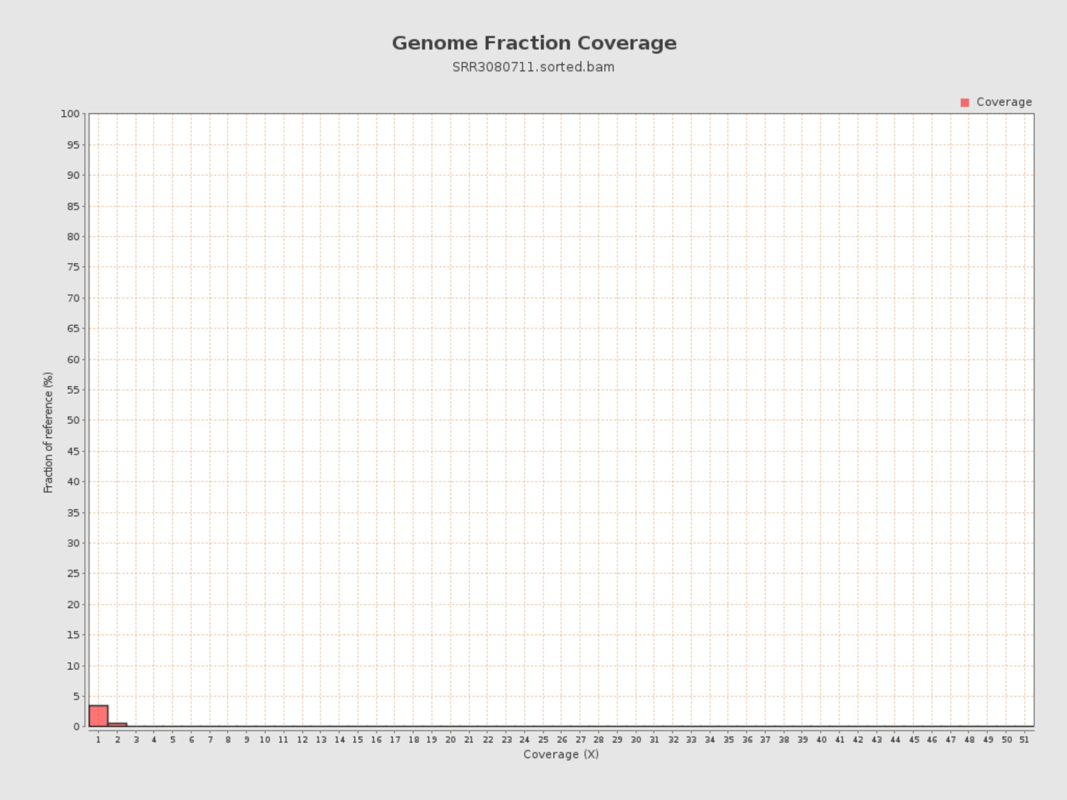
4. Results : Coverage Histogram



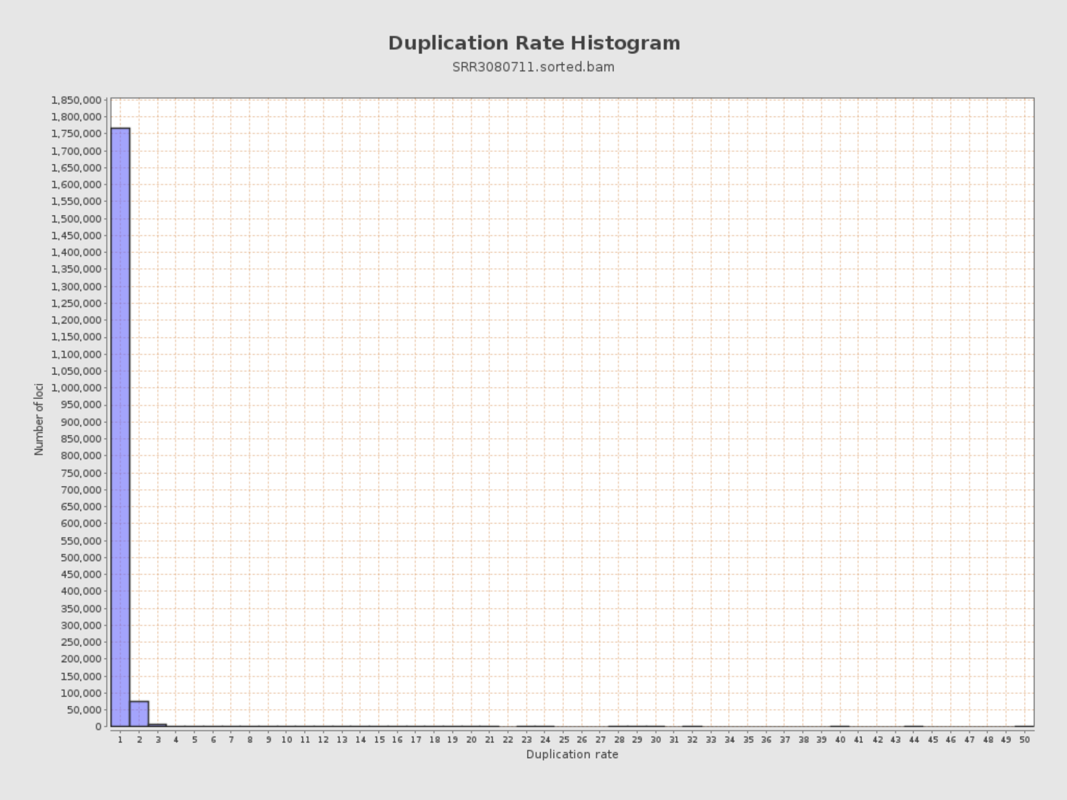
5. Results : Coverage Histogram (0-50X)



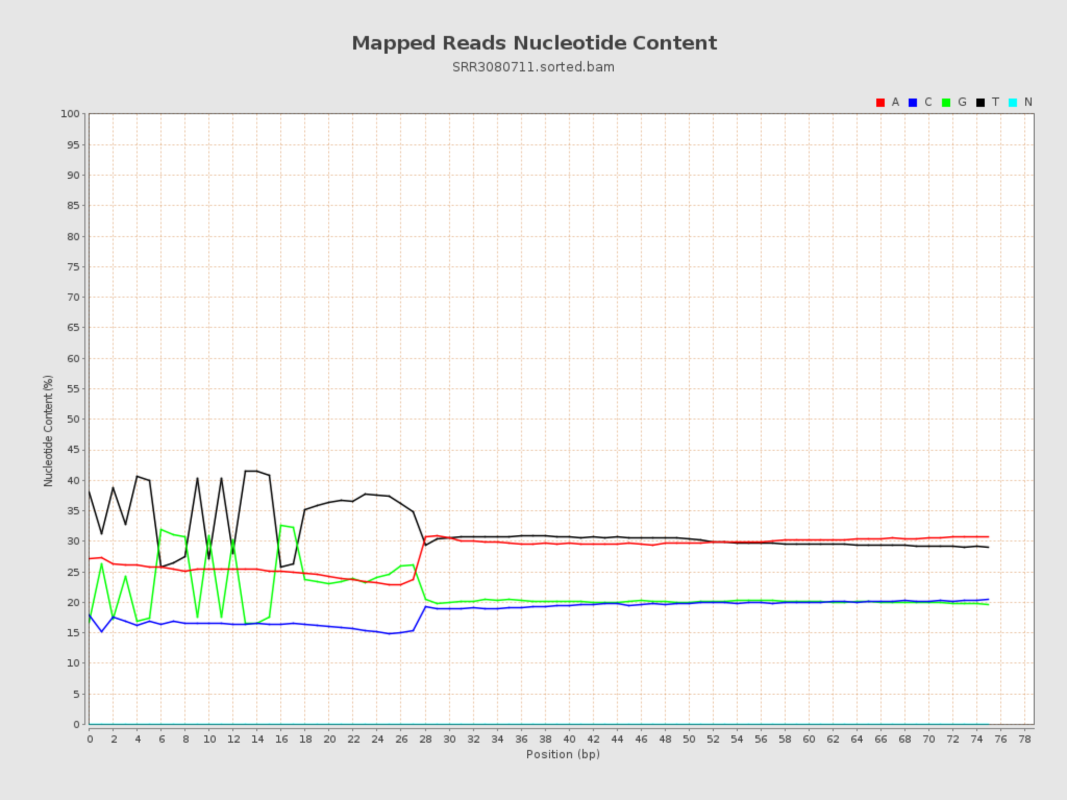
6. Results : Genome Fraction Coverage



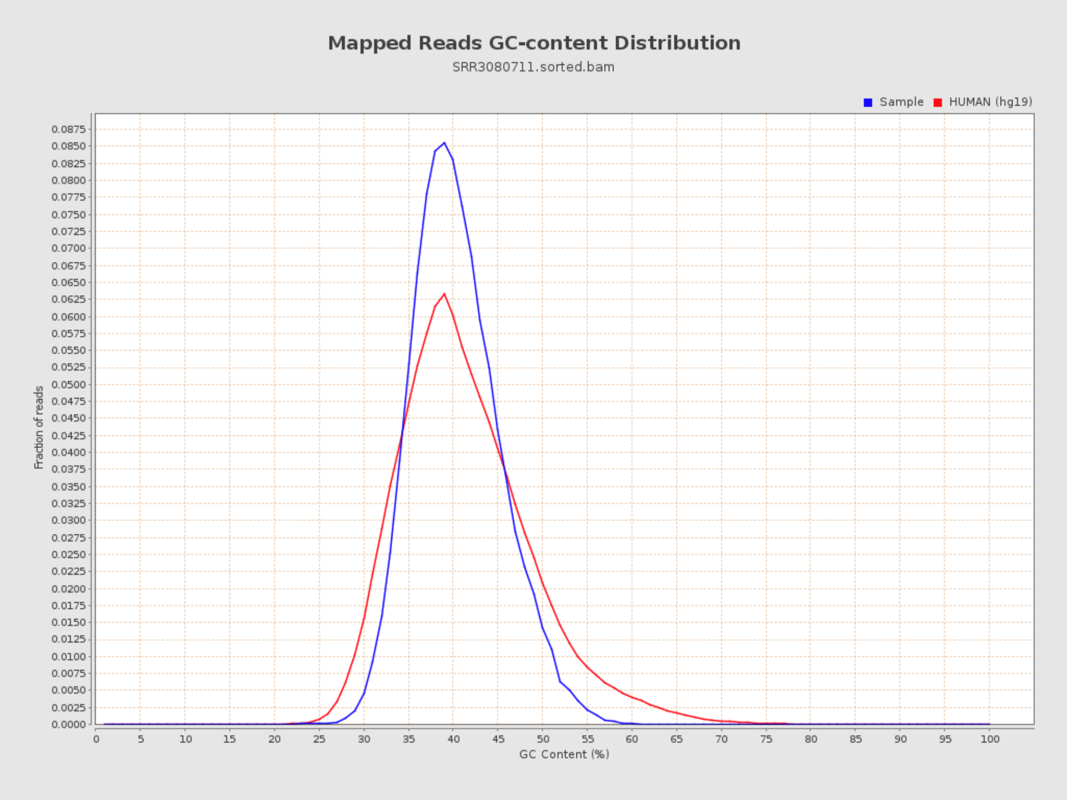
7. Results : Duplication Rate Histogram



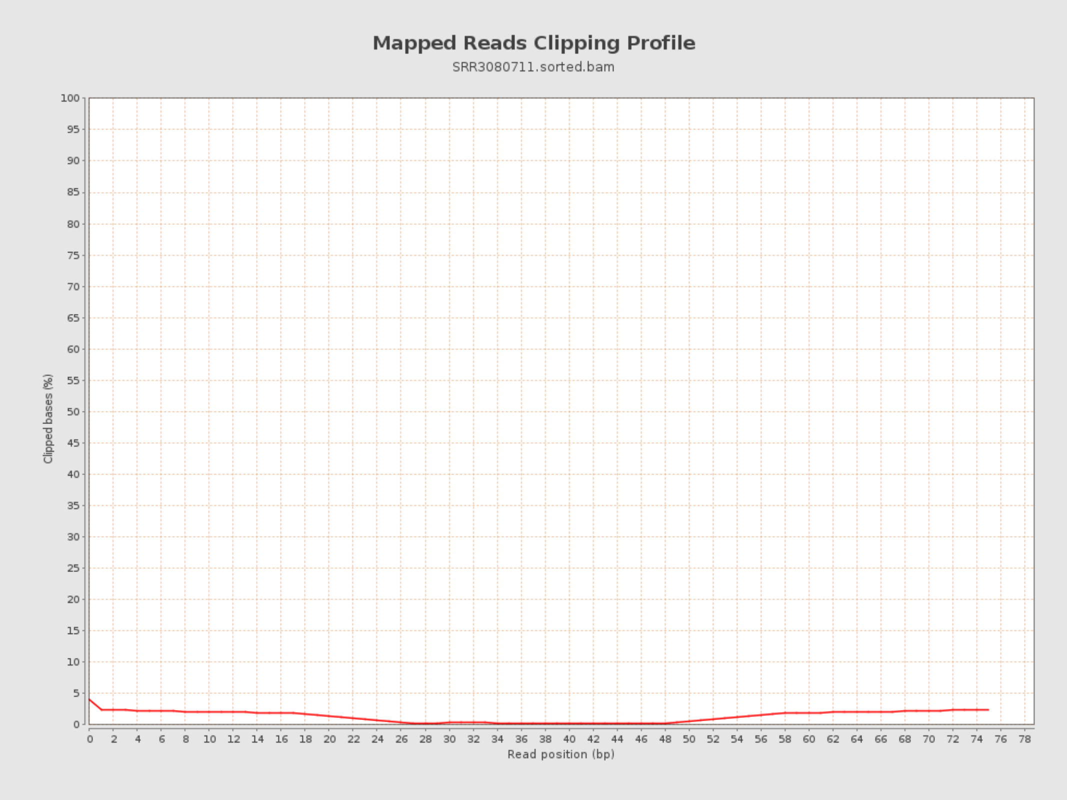
8. Results : Mapped Reads Nucleotide Content



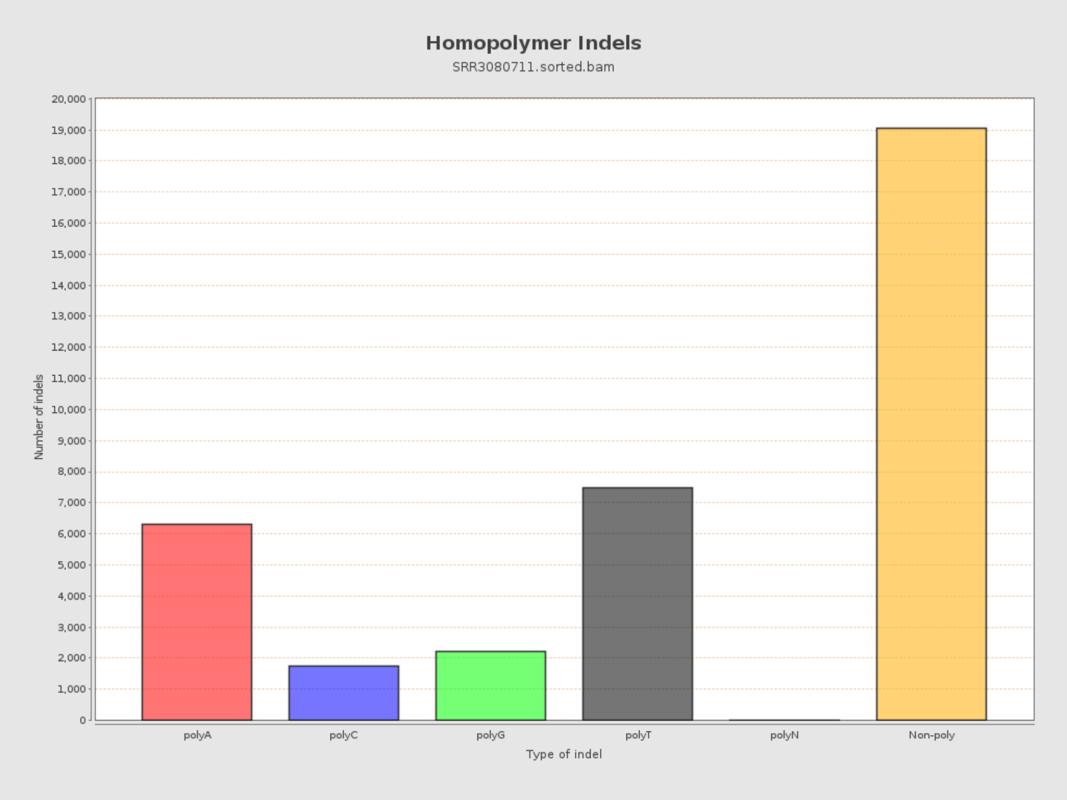
9. Results : Mapped Reads GC-content Distribution



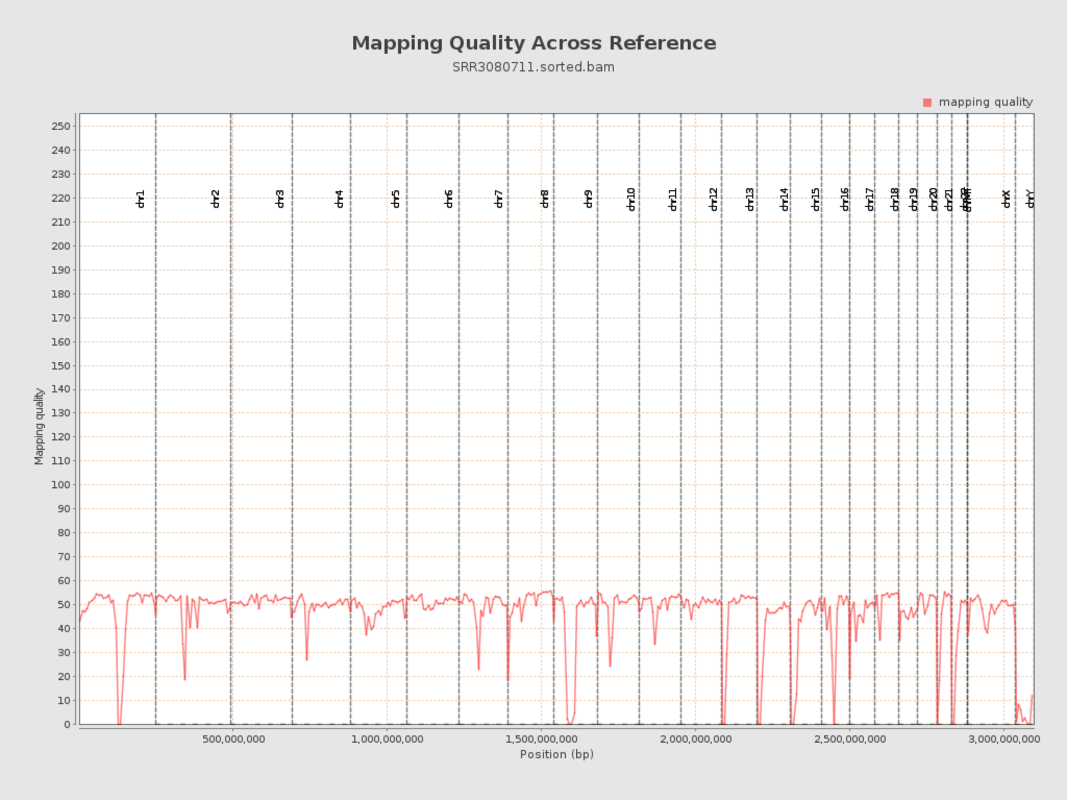
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram