Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:38:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080819.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_SRR3080819 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080819.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:38:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080819.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,441,129
Mapped reads	2,212,428 / 90.63%
Unmapped reads	228,701 / 9.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,749 / 0.93%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	128,108 / 5.25%
Duplication rate	4.97%
Clipped reads	931,916 / 38.18%

2.2. ACGT Content

Number/percentage of A's	42,366,189 / 28.37%
Number/percentage of C's	27,790,900 / 18.61%
Number/percentage of T's	47,227,154 / 31.63%
Number/percentage of G's	31,909,290 / 21.37%
Number/percentage of N's	21,577 / 0.01%
GC Percentage	39.98%

2.3. Coverage

Mean	0.0483

Standard Deviation	0.3551

2.4. Mapping Quality

Mean Mapping Quality	46.25

2.5. Mismatches and indels

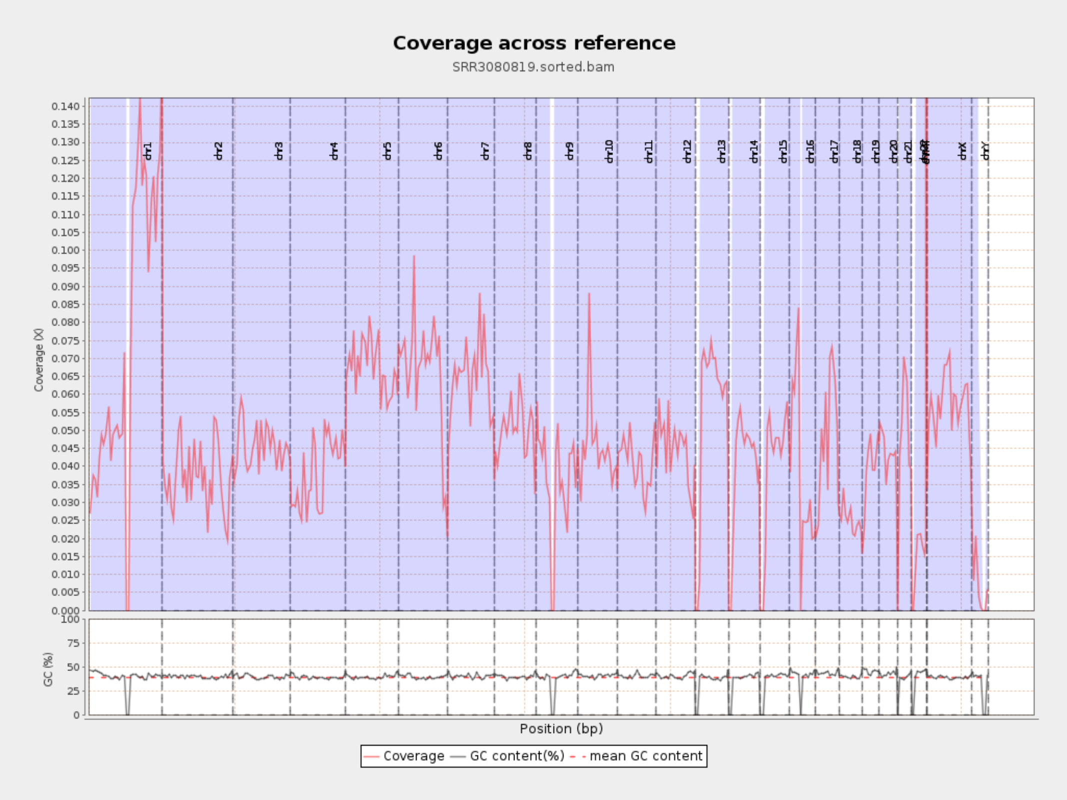
General error rate	0.83%
Mismatches	1,215,378
Insertions	10,754
Mapped reads with at least one insertion	0.48%
Deletions	32,250
Mapped reads with at least one deletion	1.44%
Homopolymer indels	47.32%

2.6. Chromosome stats

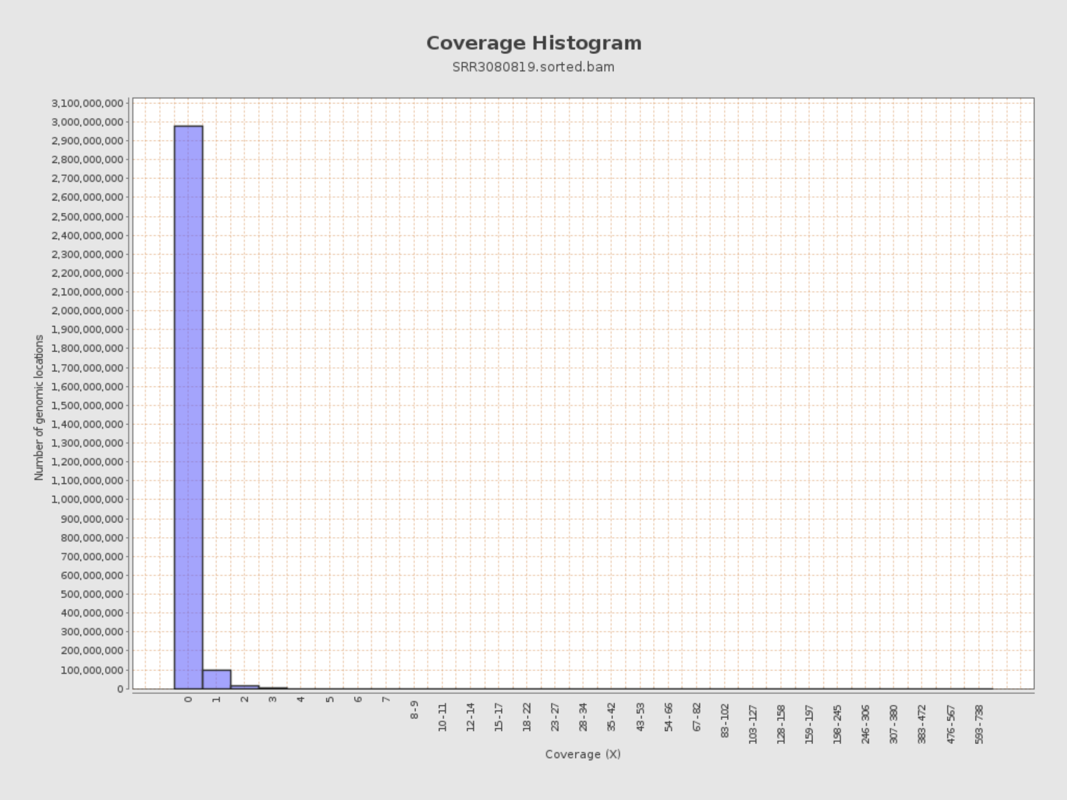
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18449690	0.074	0.5707
chr2	243199373	8973529	0.0369	0.3334
chr3	198022430	9084594	0.0459	0.2628
chr4	191154276	7339128	0.0384	0.245
chr5	180915260	12222366	0.0676	0.3102
chr6	171115067	11430301	0.0668	0.3879
chr7	159138663	10375466	0.0652	0.4714

chr8	146364022	7311220	0.05	0.524
chr9	141213431	5025191	0.0356	0.2668
chr10	135534747	6130459	0.0452	0.4568
chr11	135006516	5570506	0.0413	0.2649
chr12	133851895	5938690	0.0444	0.2521
chr13	115169878	6388214	0.0555	0.2813
chr14	107349540	4208270	0.0392	0.2458
chr15	102531392	4060615	0.0396	0.2372
chr16	90354753	3512451	0.0389	0.2548
chr17	81195210	3903574	0.0481	0.2741
chr18	78077248	1978103	0.0253	0.3866
chr19	59128983	2321847	0.0393	0.4248
chr20	63025520	2757636	0.0438	0.2531
chr21	48129895	2278966	0.0474	0.2695
chr22	51304566	705089	0.0137	0.1355
chrMT	16571	168617	10.1754	5.9535
chrX	155270560	8843519	0.057	0.2937
chrY	59373566	393873	0.0066	0.1622

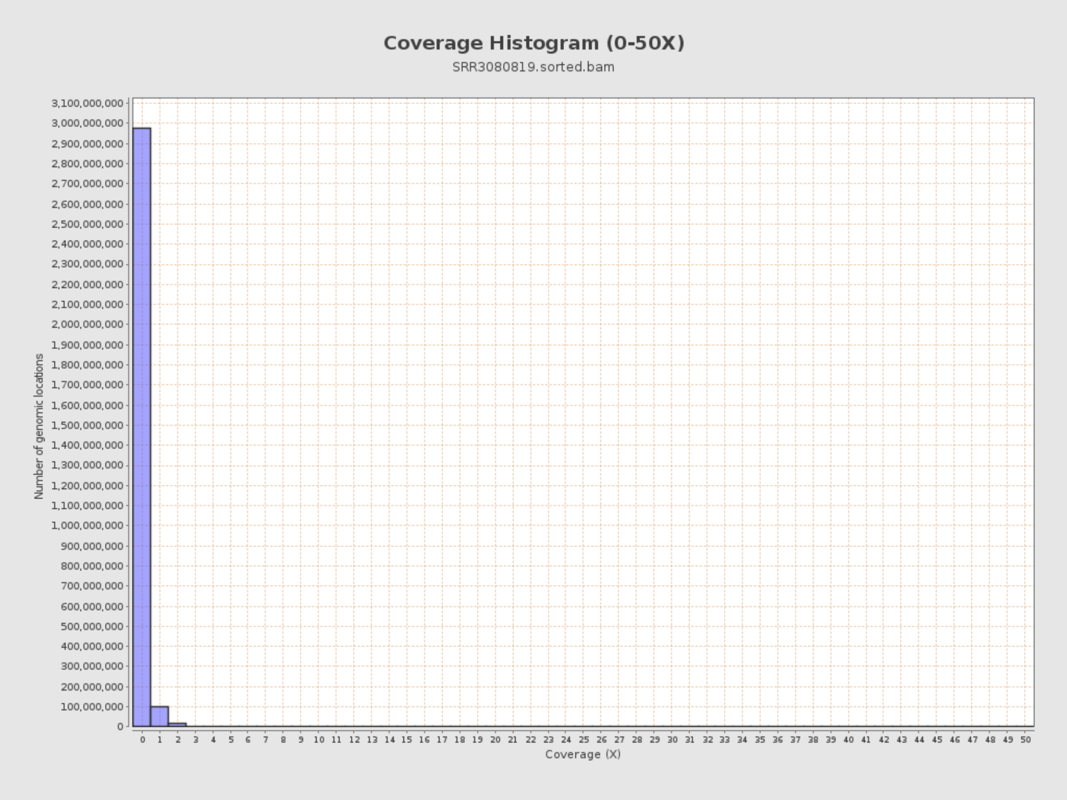
3. Results : Coverage across reference



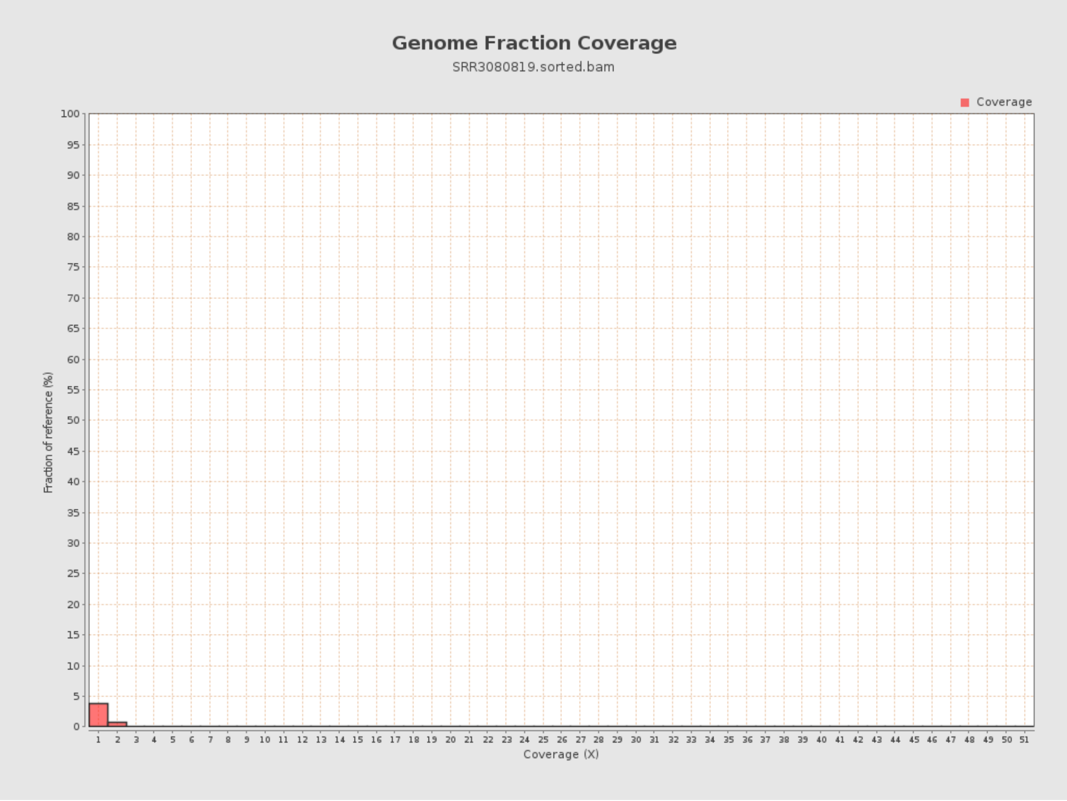
4. Results : Coverage Histogram



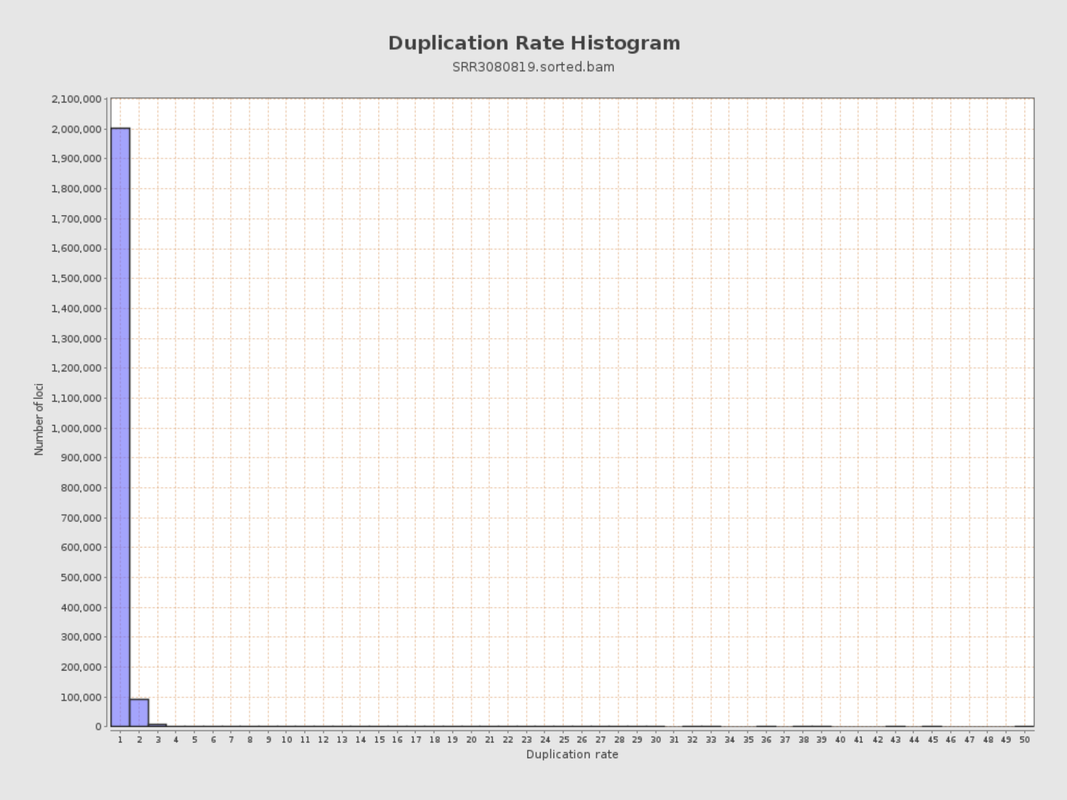
5. Results : Coverage Histogram (0-50X)



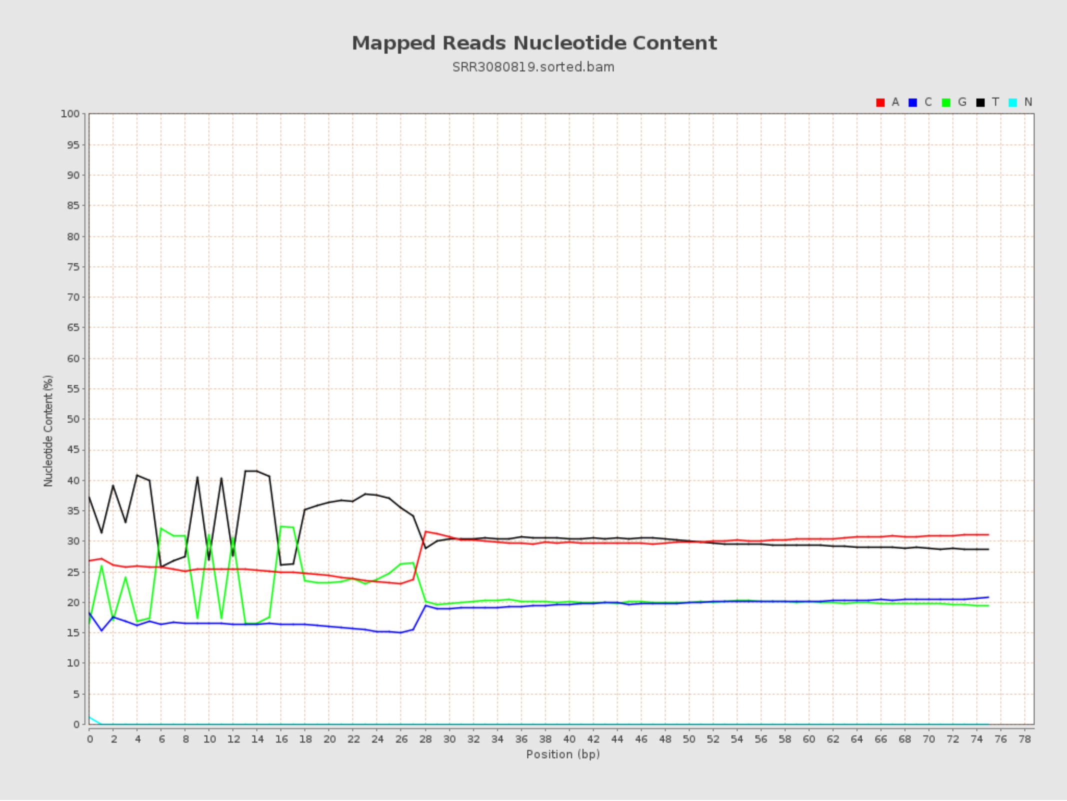
6. Results : Genome Fraction Coverage



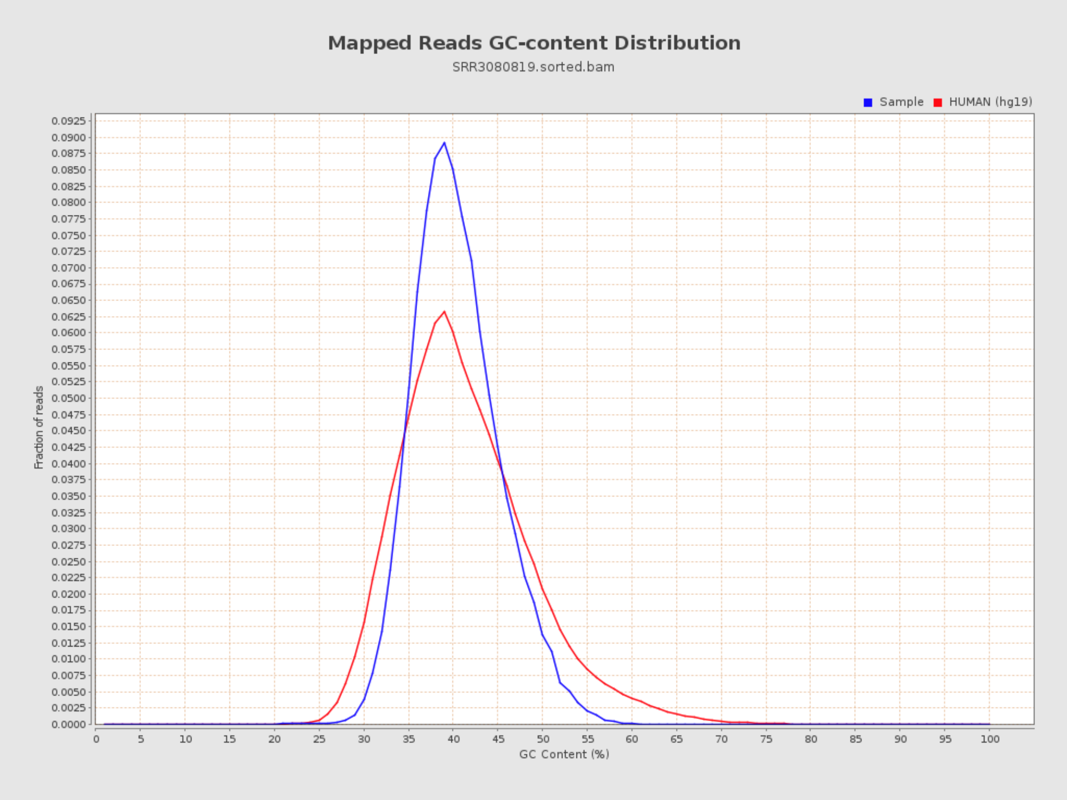
7. Results : Duplication Rate Histogram



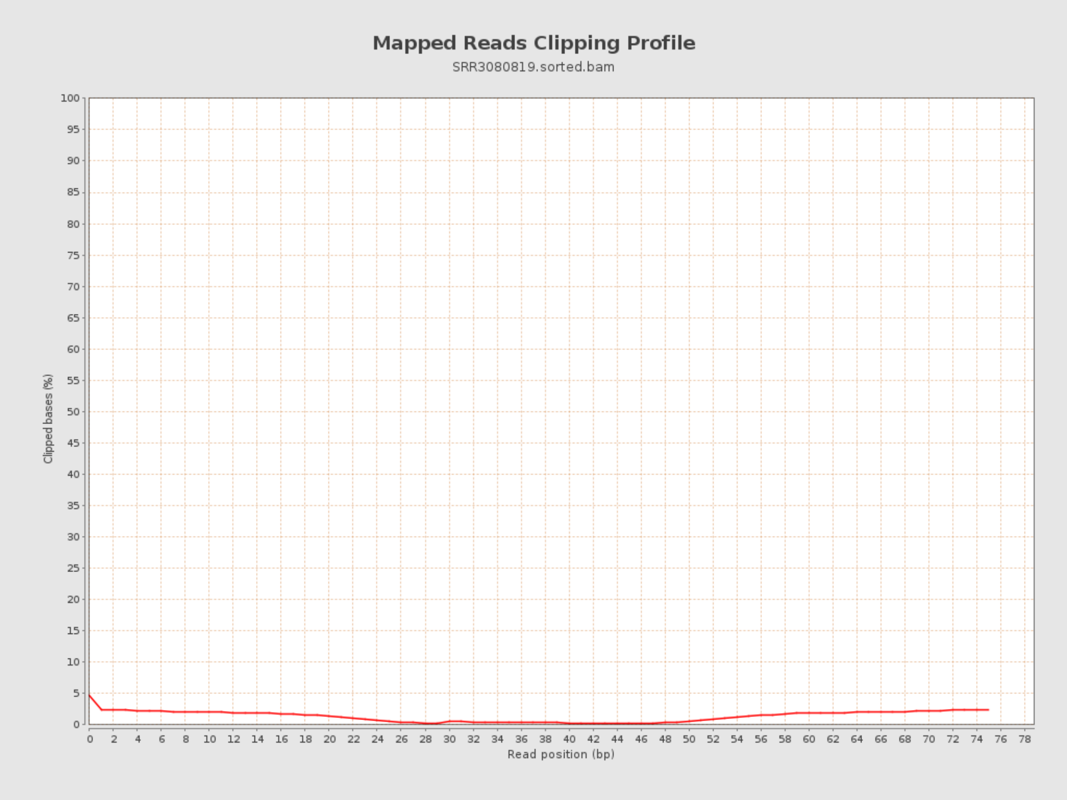
8. Results : Mapped Reads Nucleotide Content



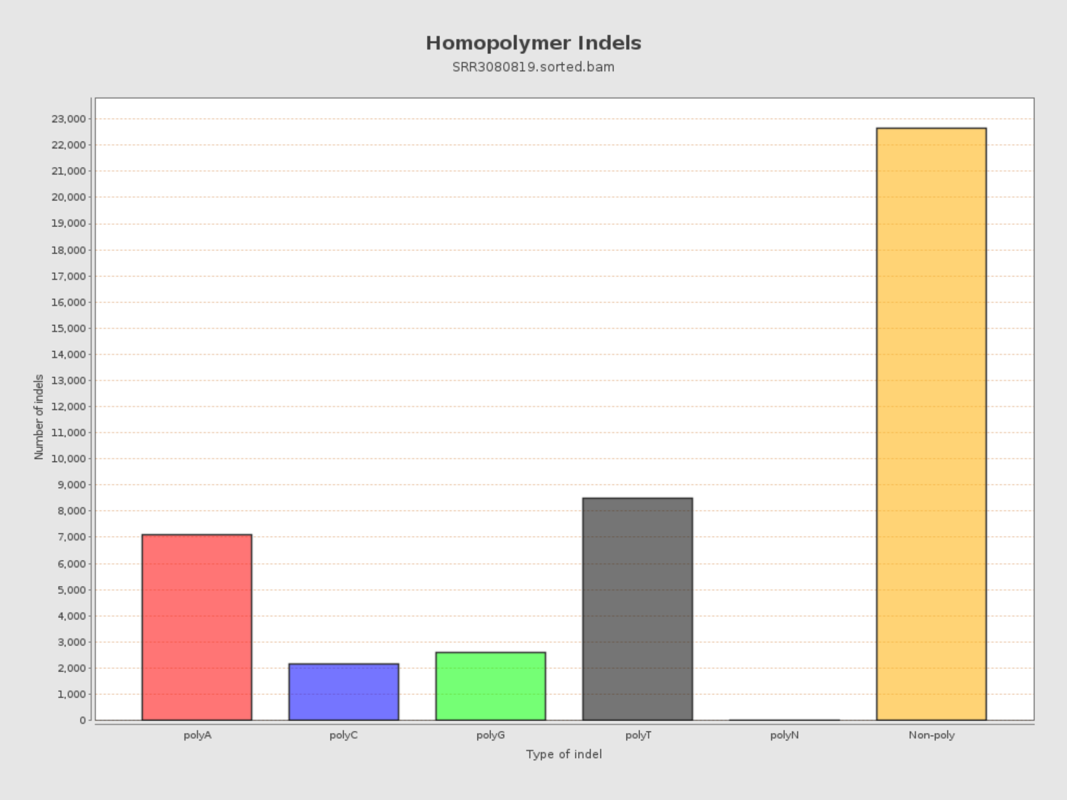
9. Results : Mapped Reads GC-content Distribution



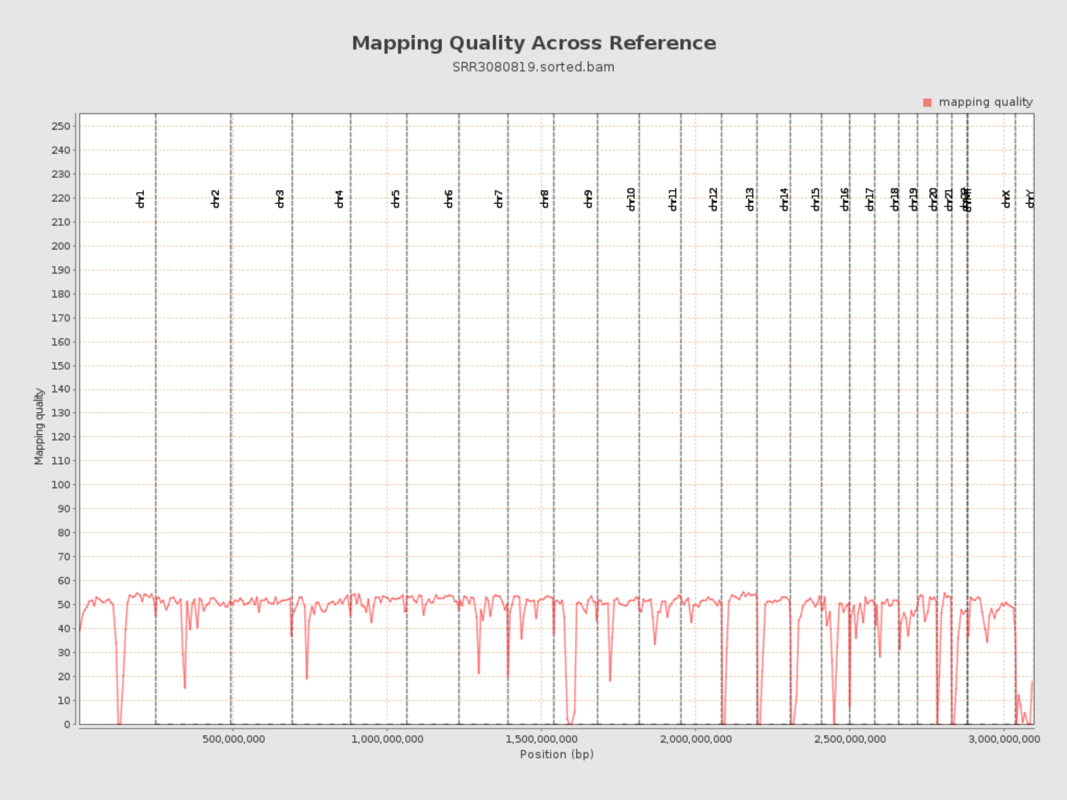
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram