Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:53:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080804.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_SRR3080804 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080804.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:53:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080804.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,493,755
Mapped reads	2,266,086 / 90.87%
Unmapped reads	227,669 / 9.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,314 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	144,140 / 5.78%
Duplication rate	5.42%
Clipped reads	896,392 / 35.95%

2.2. ACGT Content

Number/percentage of A's	43,990,094 / 28.5%
Number/percentage of C's	28,735,749 / 18.62%
Number/percentage of T's	48,846,744 / 31.64%
Number/percentage of G's	32,773,169 / 21.23%
Number/percentage of N's	21,896 / 0.01%
GC Percentage	39.85%

2.3. Coverage

Mean	0.0499

Standard Deviation	0.3595

2.4. Mapping Quality

Mean Mapping Quality	46.81

2.5. Mismatches and indels

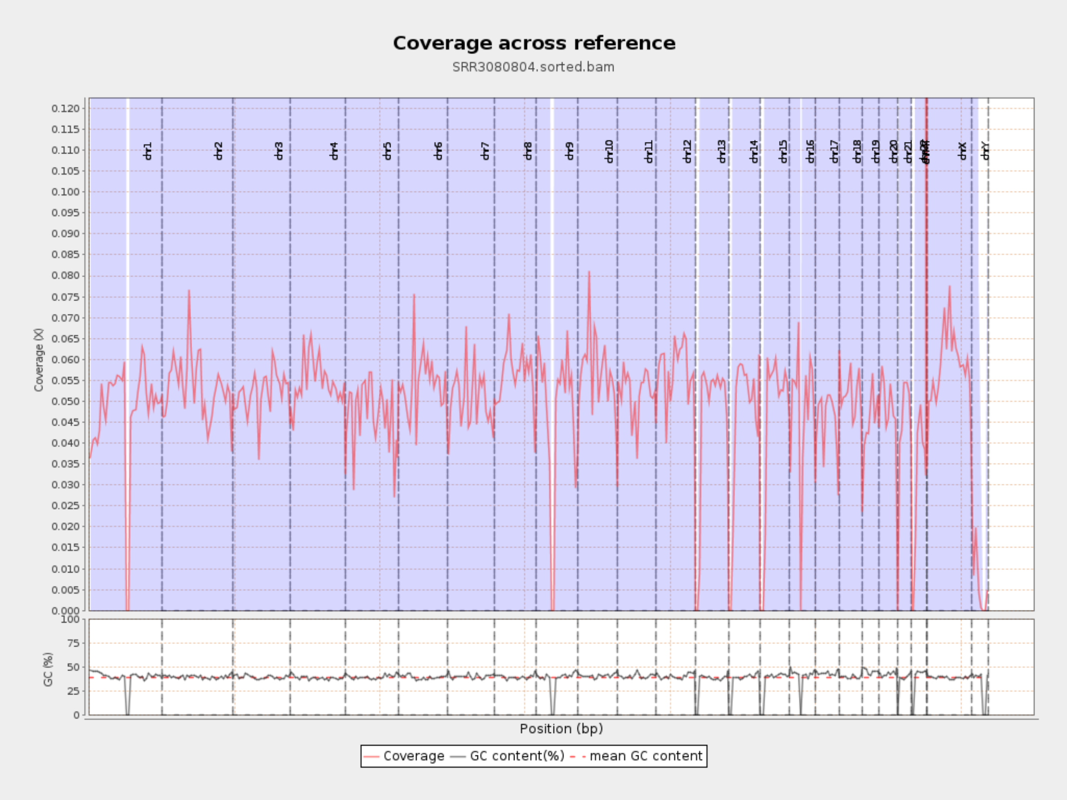
General error rate	0.82%
Mismatches	1,249,403
Insertions	11,589
Mapped reads with at least one insertion	0.51%
Deletions	31,907
Mapped reads with at least one deletion	1.39%
Homopolymer indels	48.29%

2.6. Chromosome stats

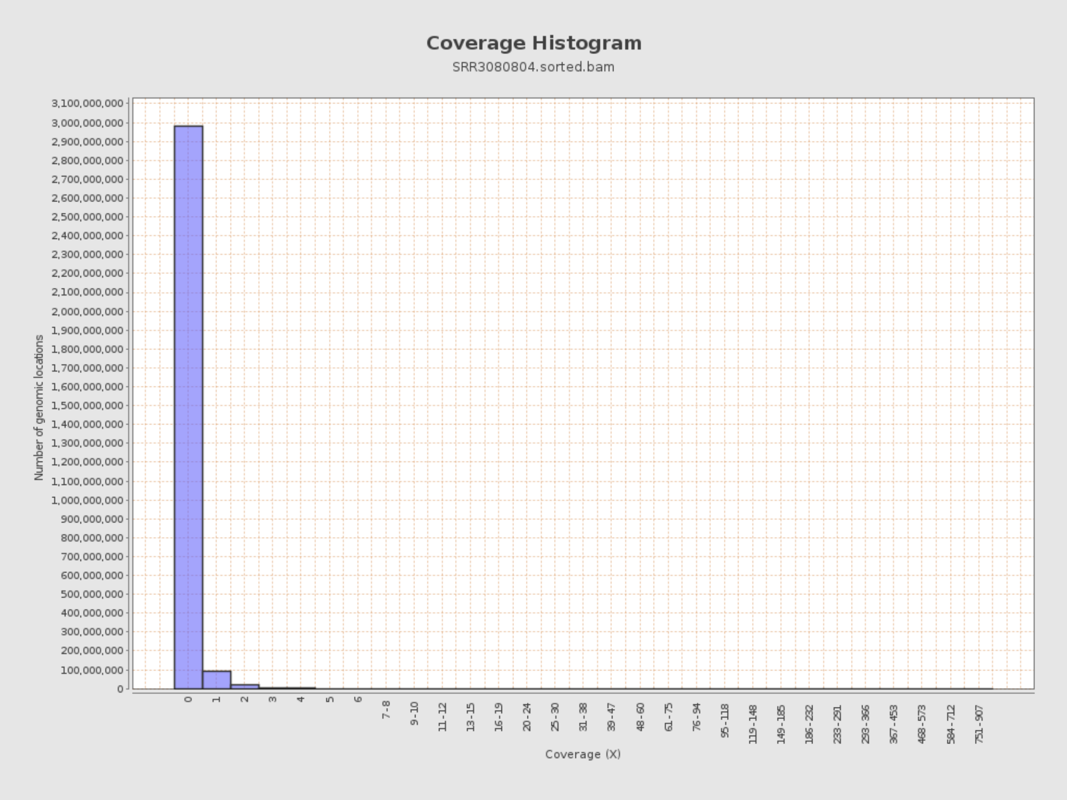
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11850833	0.0475	0.4334
chr2	243199373	13048290	0.0537	0.4132
chr3	198022430	10357883	0.0523	0.2877
chr4	191154276	10469743	0.0548	0.309
chr5	180915260	8475810	0.0468	0.2729
chr6	171115067	9299781	0.0543	0.3616
chr7	159138663	8129482	0.0511	0.3817

chr8	146364022	8254735	0.0564	0.6304
chr9	141213431	6641657	0.047	0.323
chr10	135534747	7827813	0.0578	0.4332
chr11	135006516	6984704	0.0517	0.3134
chr12	133851895	7658055	0.0572	0.3036
chr13	115169878	5142801	0.0447	0.2679
chr14	107349540	4731064	0.0441	0.2702
chr15	102531392	4594766	0.0448	0.2671
chr16	90354753	4304853	0.0476	0.2908
chr17	81195210	3660444	0.0451	0.2733
chr18	78077248	4052175	0.0519	0.5054
chr19	59128983	2688358	0.0455	0.3634
chr20	63025520	3077017	0.0488	0.2833
chr21	48129895	2084267	0.0433	0.2752
chr22	51304566	1507342	0.0294	0.2136
chrMT	16571	101400	6.1191	4.363
chrX	155270560	9094060	0.0586	0.3184
chrY	59373566	387067	0.0065	0.1559

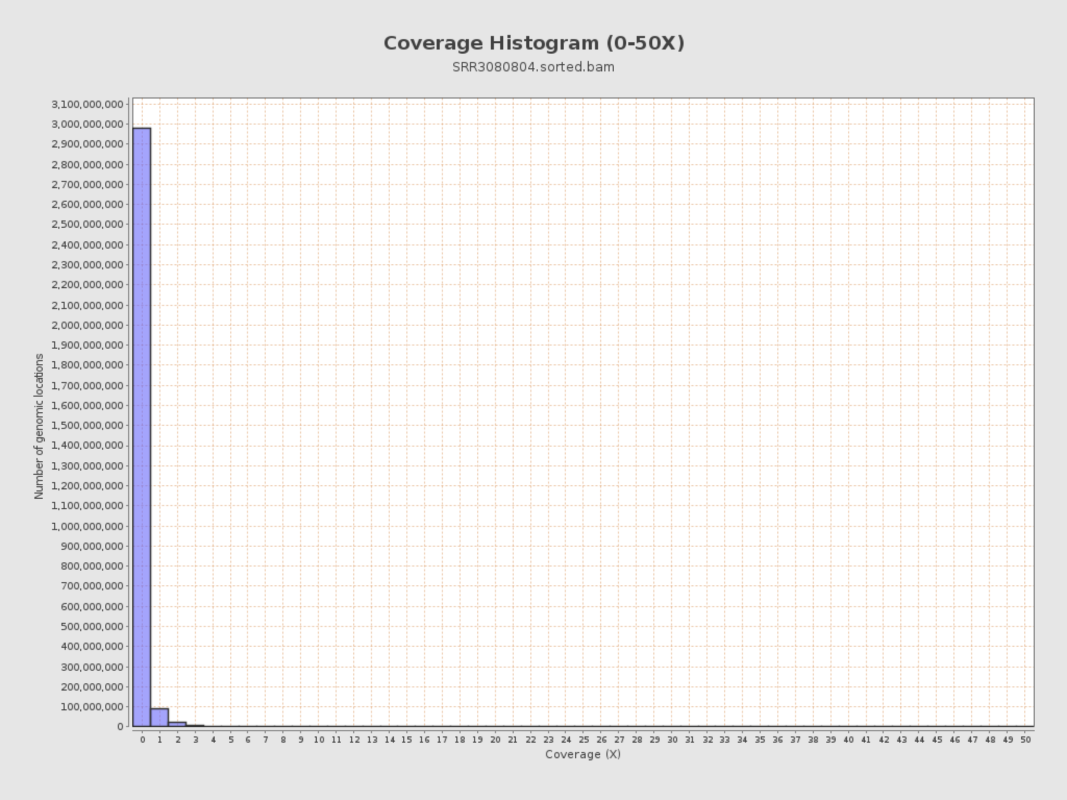
3. Results : Coverage across reference



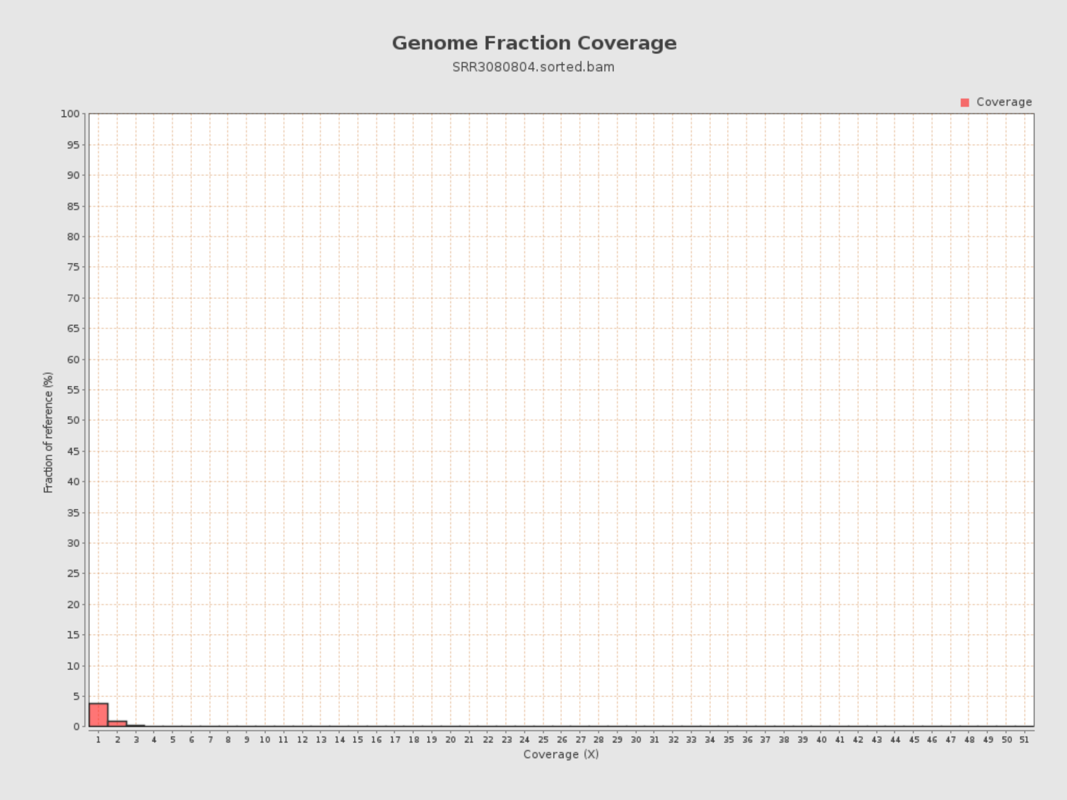
4. Results : Coverage Histogram



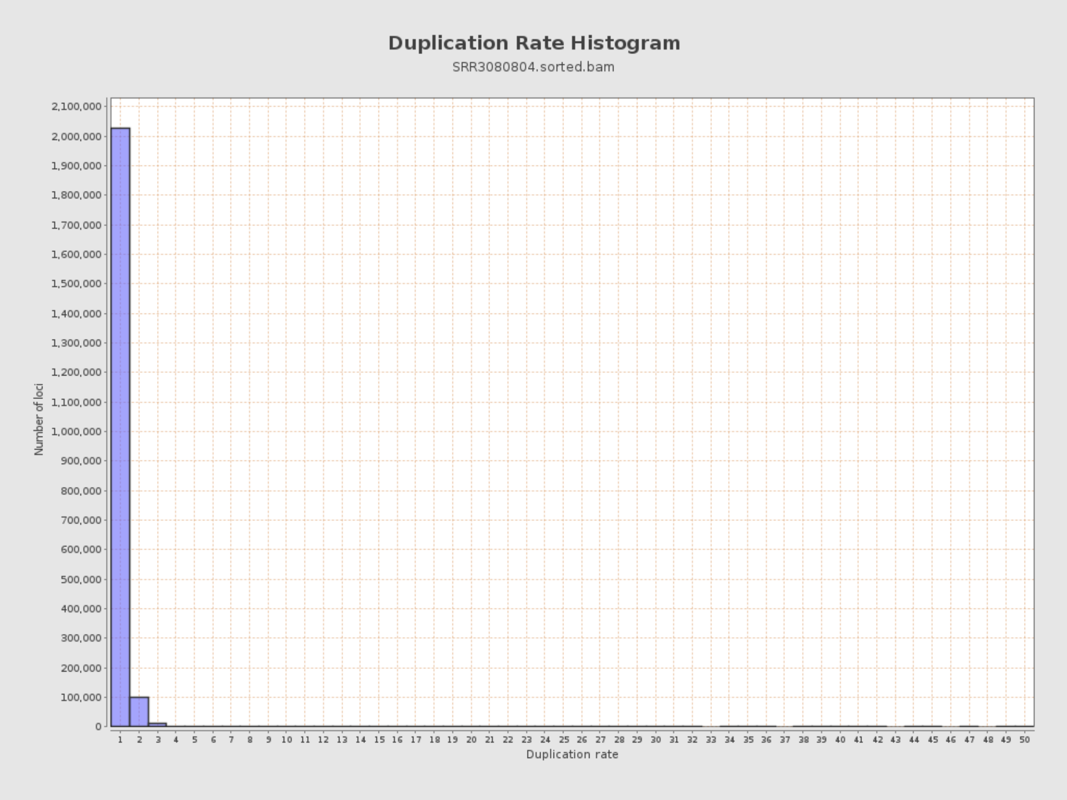
5. Results : Coverage Histogram (0-50X)



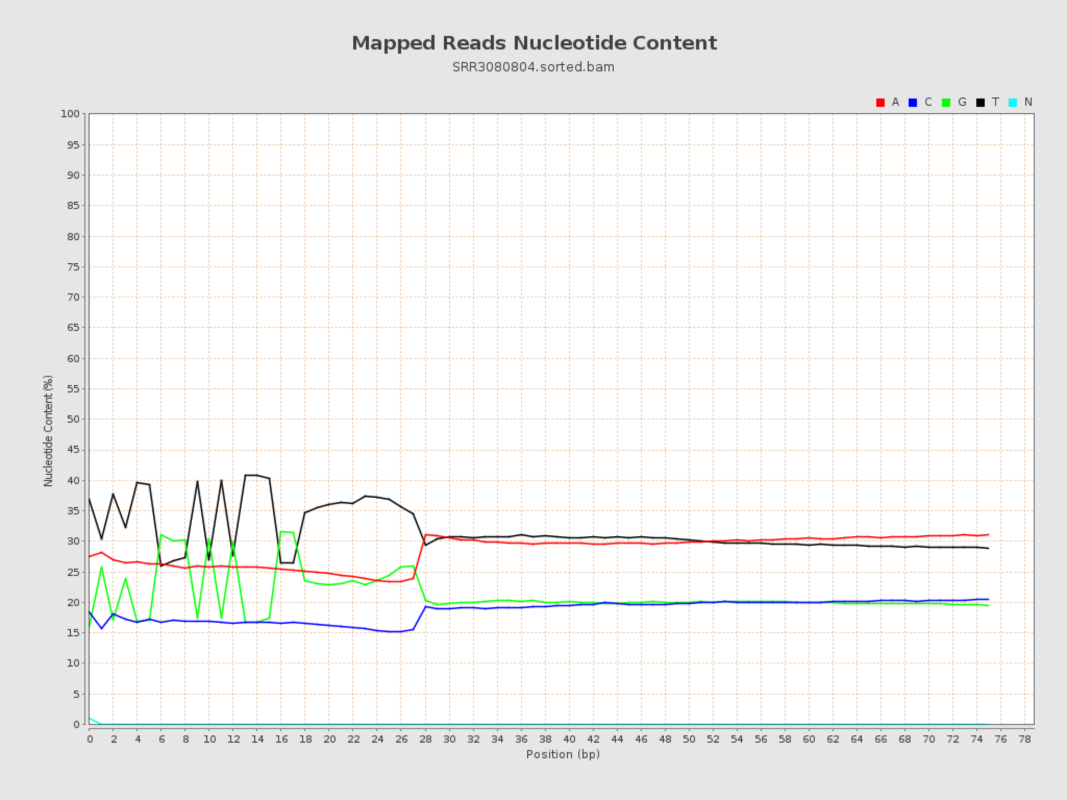
6. Results : Genome Fraction Coverage


Genome Fraction Coverage
SRR3080804.sorted.bam

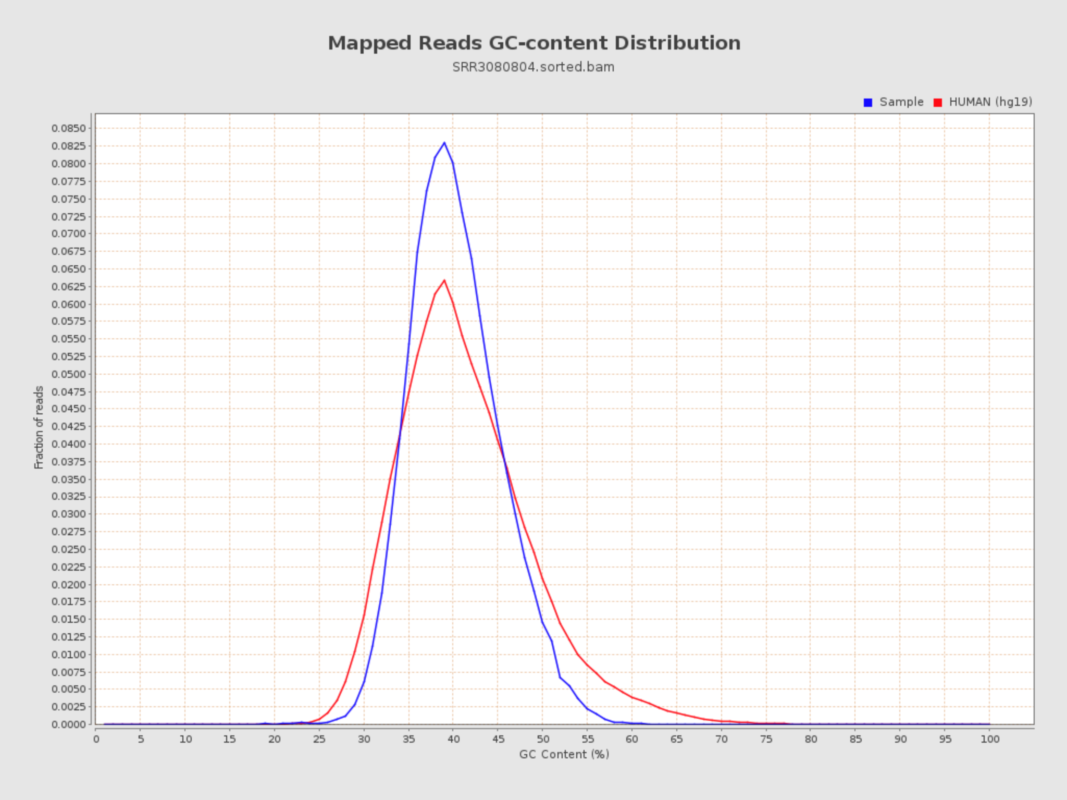
7. Results : Duplication Rate Histogram



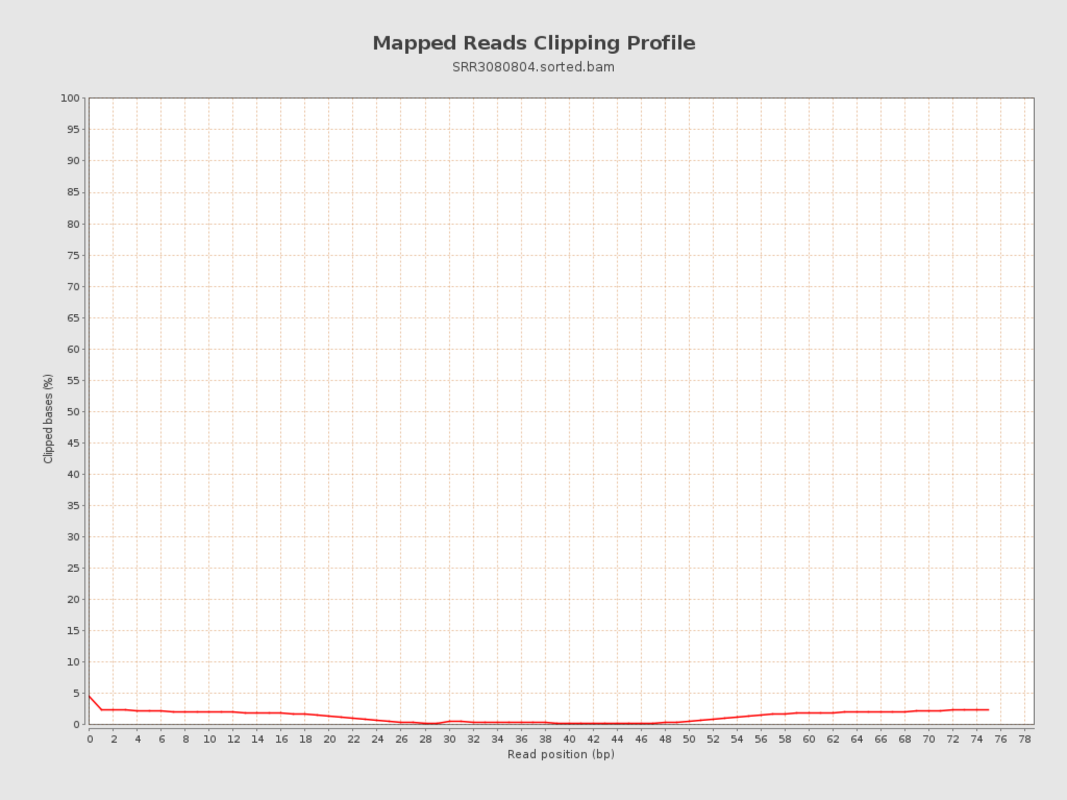
8. Results : Mapped Reads Nucleotide Content



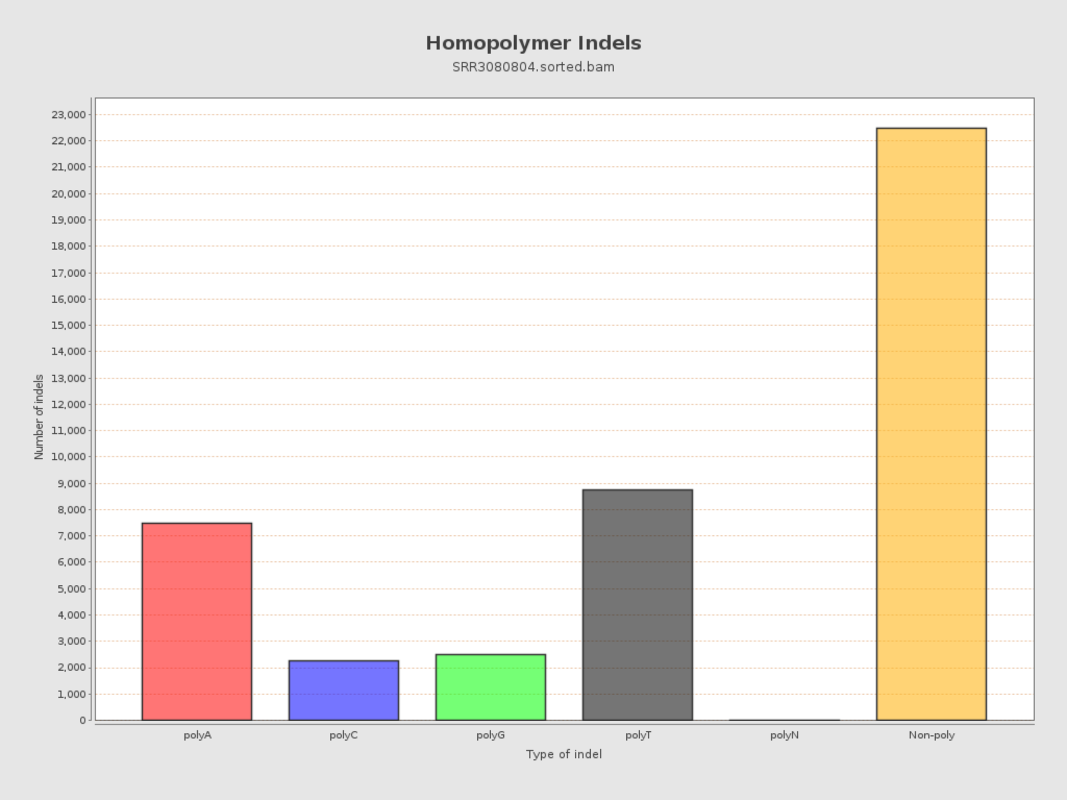
9. Results : Mapped Reads GC-content Distribution



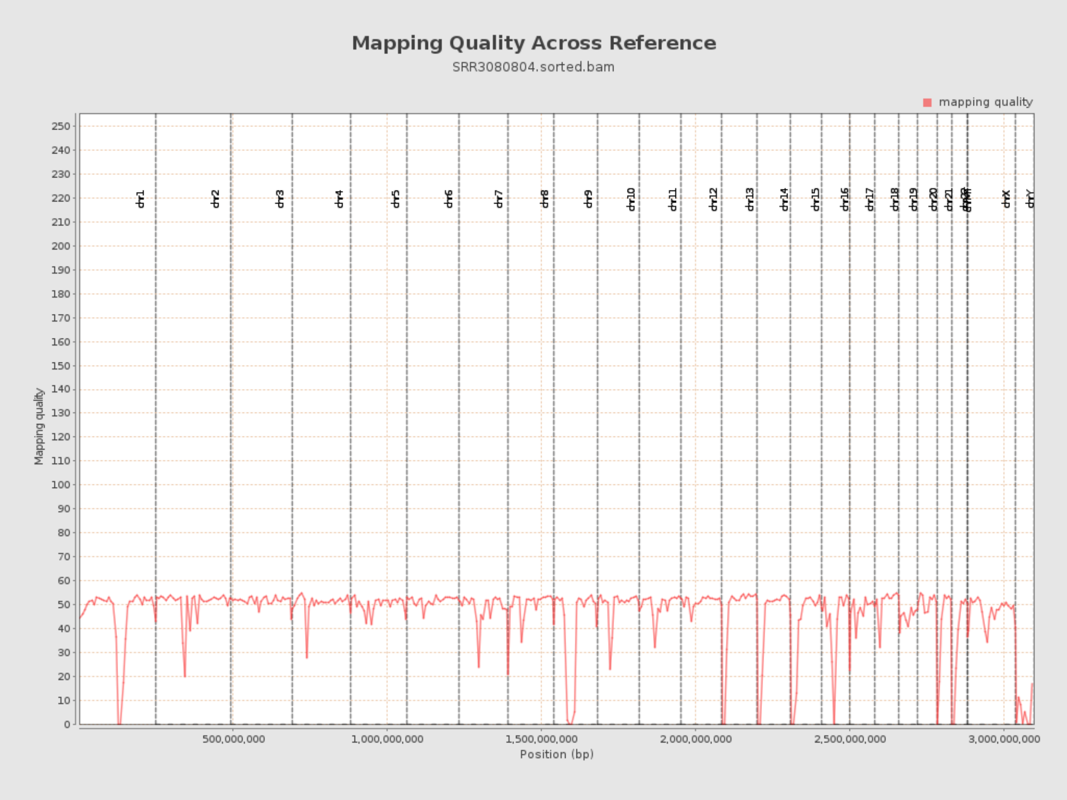
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram