Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 00:18:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506088.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_SRR1506088 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506088.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 00:18:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506088.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,647,978
Mapped reads	12,035,141 / 82.16%
Unmapped reads	2,612,837 / 17.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	194,283 / 1.33%
Read min/max/mean length	30 / 94 / 94.48
Duplicated reads (estimated)	2,390,671 / 16.32%
Duplication rate	13.58%
Clipped reads	7,586,832 / 51.79%

2.2. ACGT Content

Number/percentage of A's	253,314,808 / 26.84%
Number/percentage of C's	179,196,973 / 18.99%
Number/percentage of T's	275,005,281 / 29.14%
Number/percentage of G's	236,156,379 / 25.02%
Number/percentage of N's	138,257 / 0.01%
GC Percentage	44.01%

2.3. Coverage

Mean	0.305

Standard Deviation	1.8813

2.4. Mapping Quality

Mean Mapping Quality	47.57

2.5. Mismatches and indels

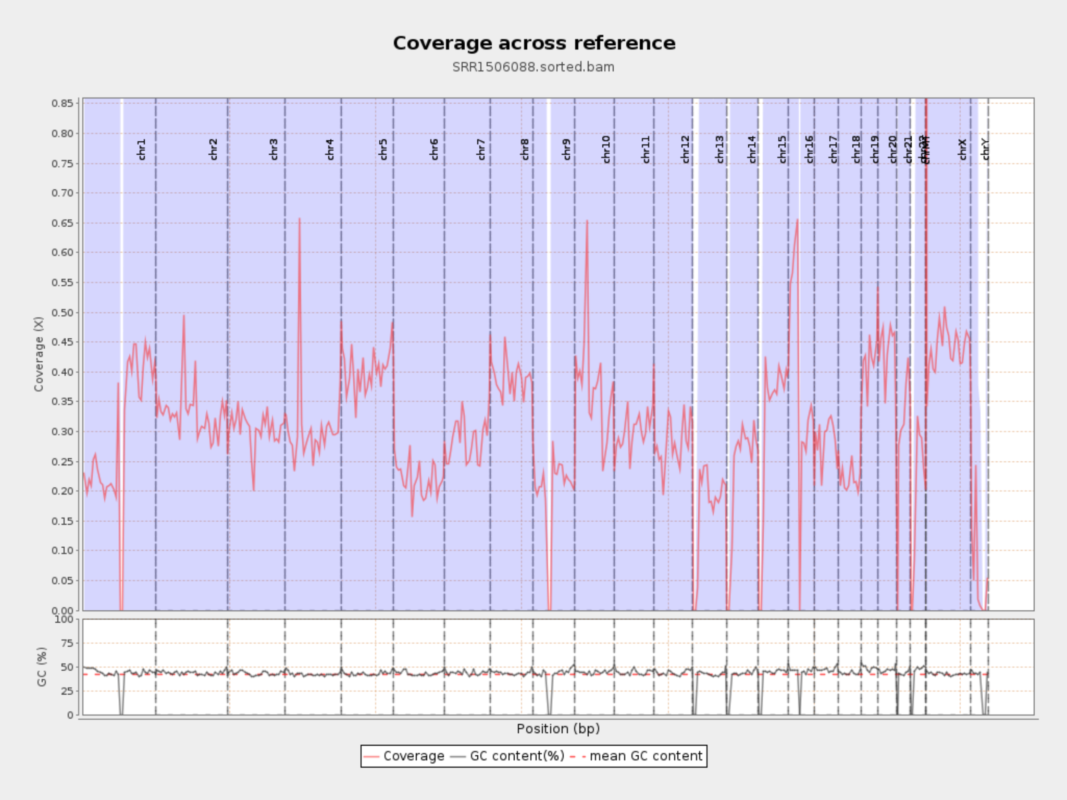
General error rate	0.8%
Mismatches	7,350,762
Insertions	75,349
Mapped reads with at least one insertion	0.61%
Deletions	185,796
Mapped reads with at least one deletion	1.51%
Homopolymer indels	42.3%

2.6. Chromosome stats

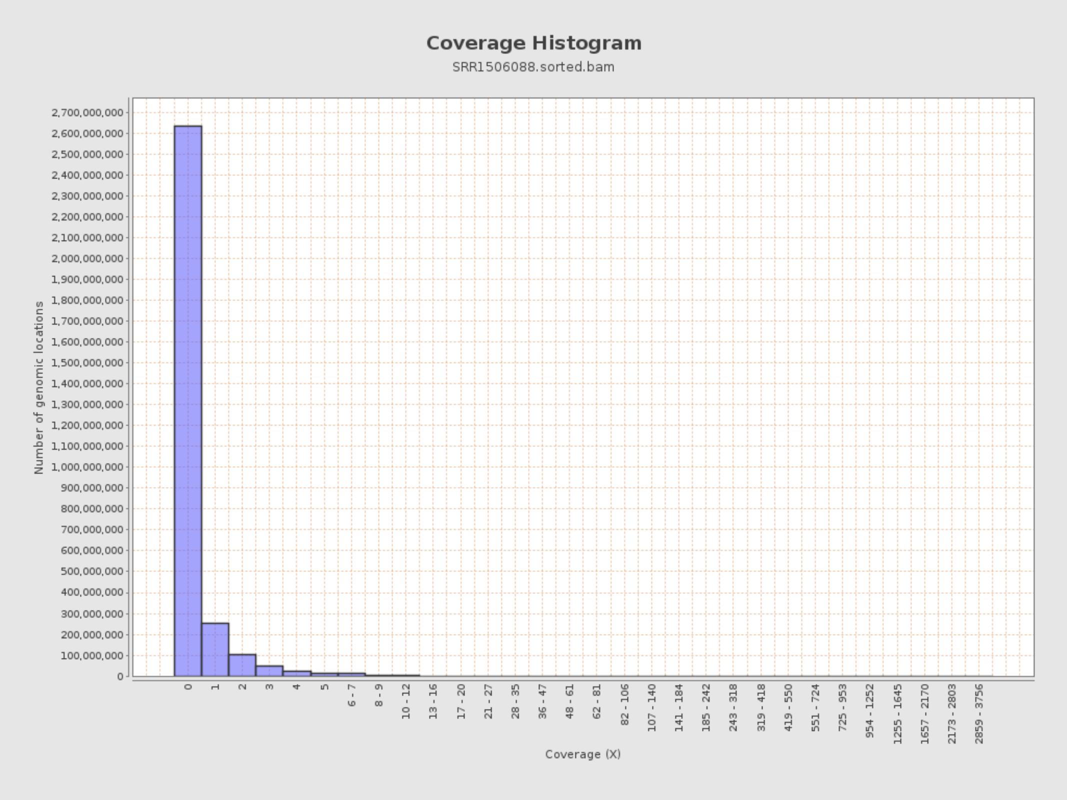
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	72855958	0.2923	3.4778
chr2	243199373	80788713	0.3322	2.115
chr3	198022430	60122482	0.3036	0.9851
chr4	191154276	58667564	0.3069	1.7383
chr5	180915260	72879085	0.4028	1.1989
chr6	171115067	37599799	0.2197	0.993
chr7	159138663	45901322	0.2884	1.9295

chr8	146364022	56801306	0.3881	2.1361
chr9	141213431	27944609	0.1979	1.7586
chr10	135534747	50686627	0.374	2.4463
chr11	135006516	40538219	0.3003	1.6997
chr12	133851895	37640388	0.2812	1.0008
chr13	115169878	19781989	0.1718	0.724
chr14	107349540	25148481	0.2343	1.1114
chr15	102531392	31937049	0.3115	1.0641
chr16	90354753	34484915	0.3817	1.5098
chr17	81195210	23578773	0.2904	1.2658
chr18	78077248	17206248	0.2204	2.7473
chr19	59128983	24852365	0.4203	2.7243
chr20	63025520	27600641	0.4379	1.3718
chr21	48129895	14877183	0.3091	1.6119
chr22	51304566	9928873	0.1935	0.966
chrMT	16571	406941	24.5574	15.6484
chrX	155270560	68339907	0.4401	1.46
chrY	59373566	3622012	0.061	2.2263

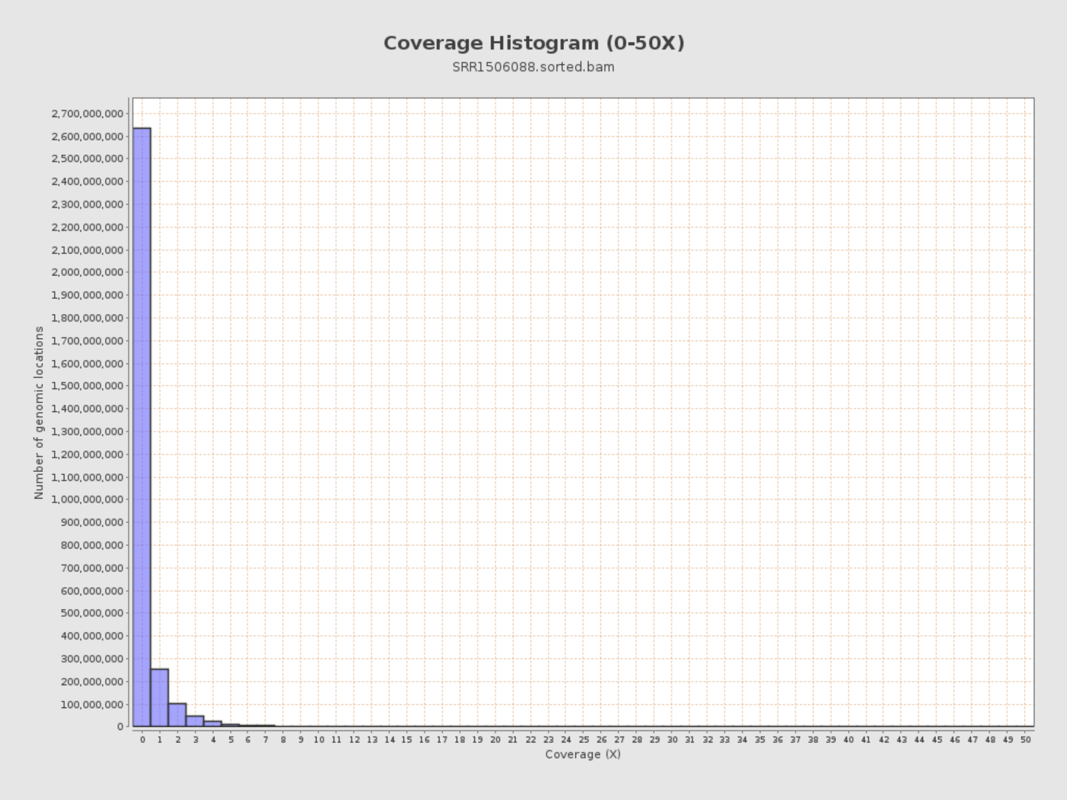
3. Results : Coverage across reference



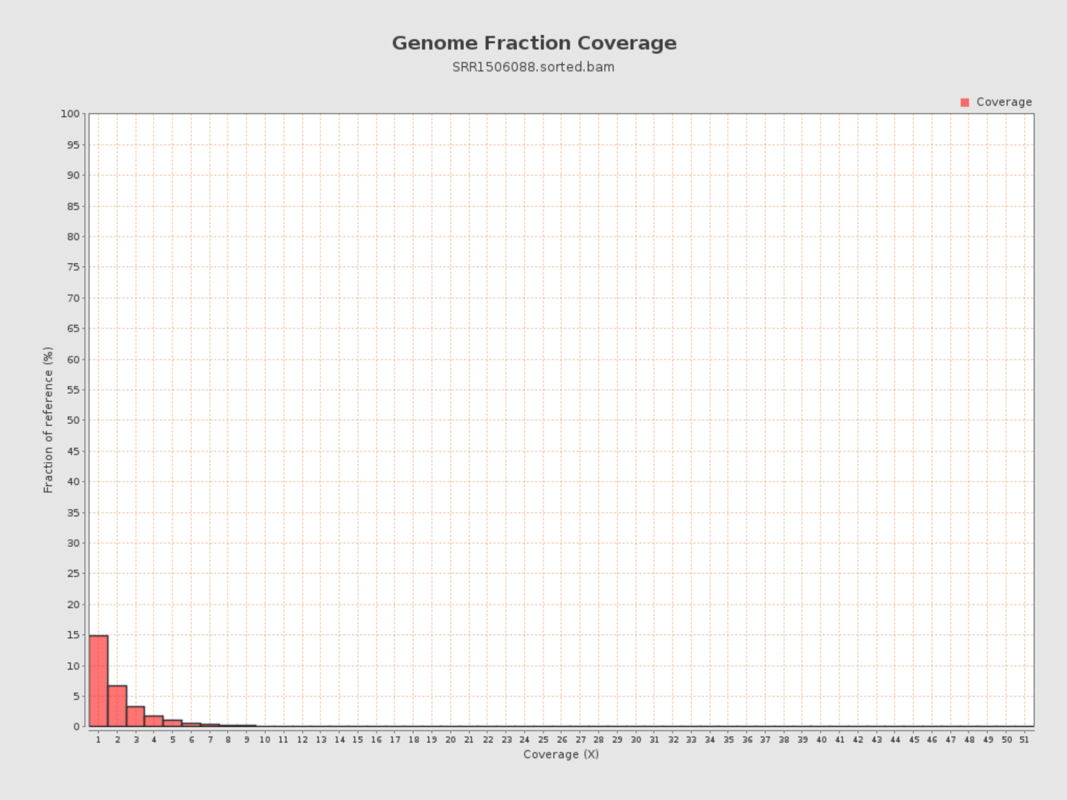
4. Results : Coverage Histogram



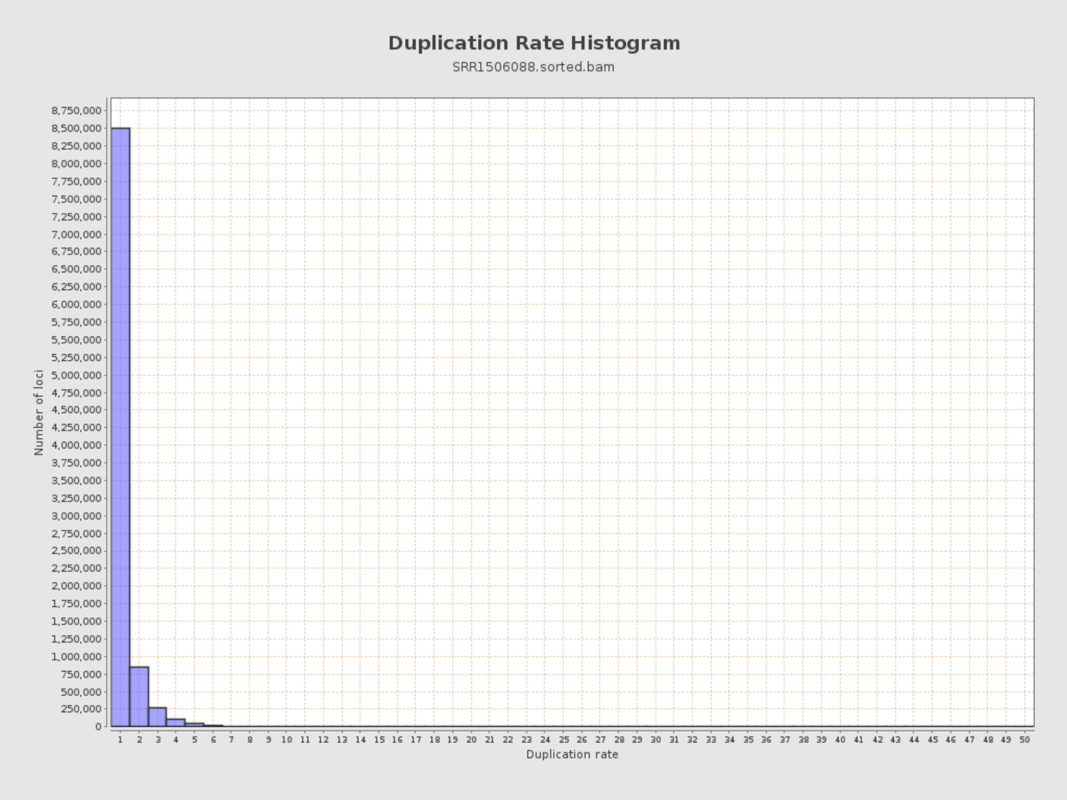
5. Results : Coverage Histogram (0-50X)



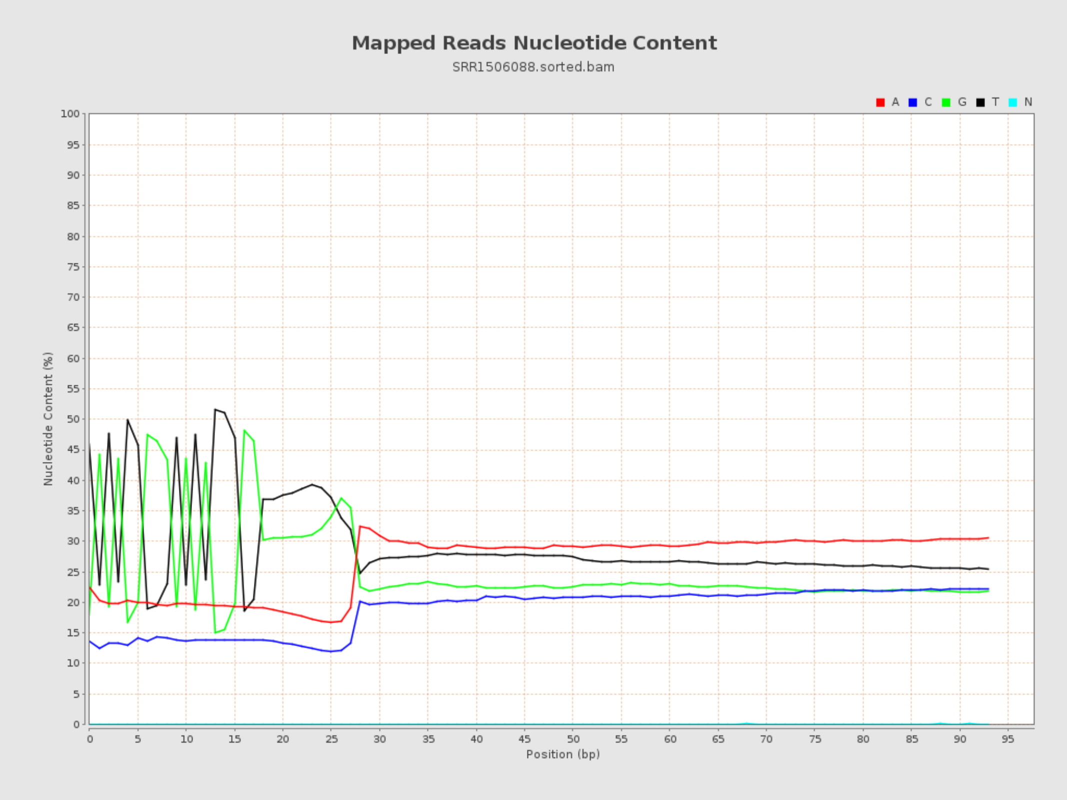
6. Results : Genome Fraction Coverage



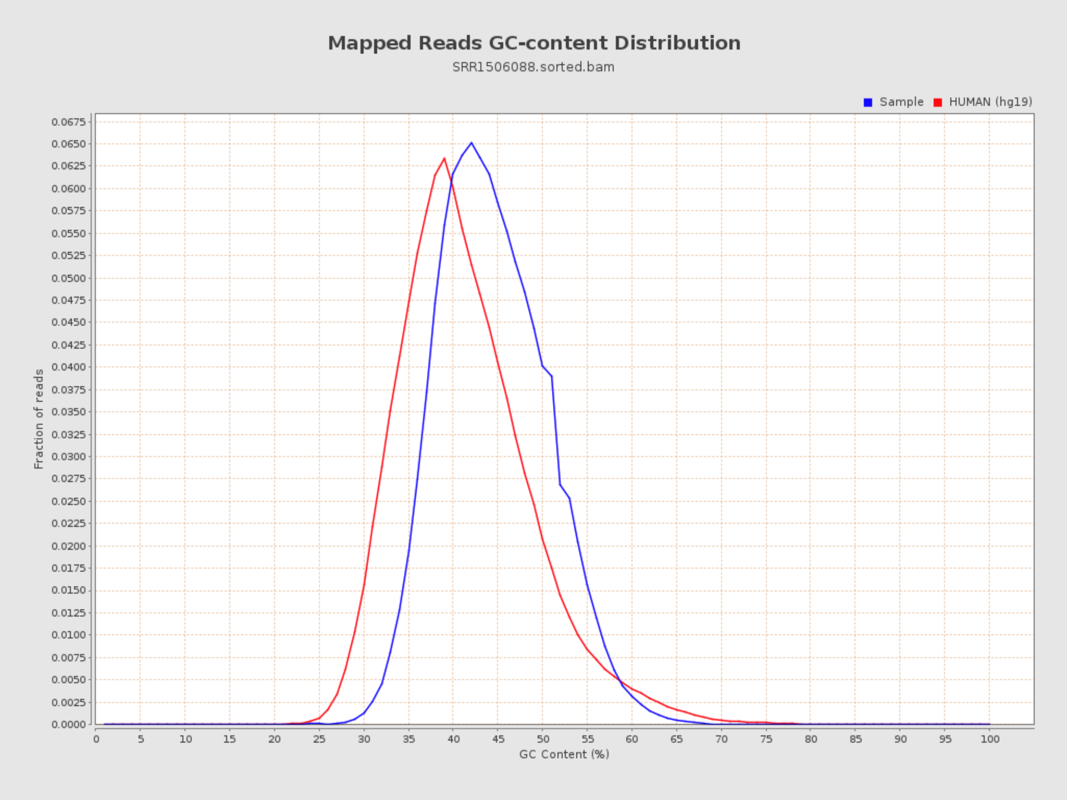
7. Results : Duplication Rate Histogram



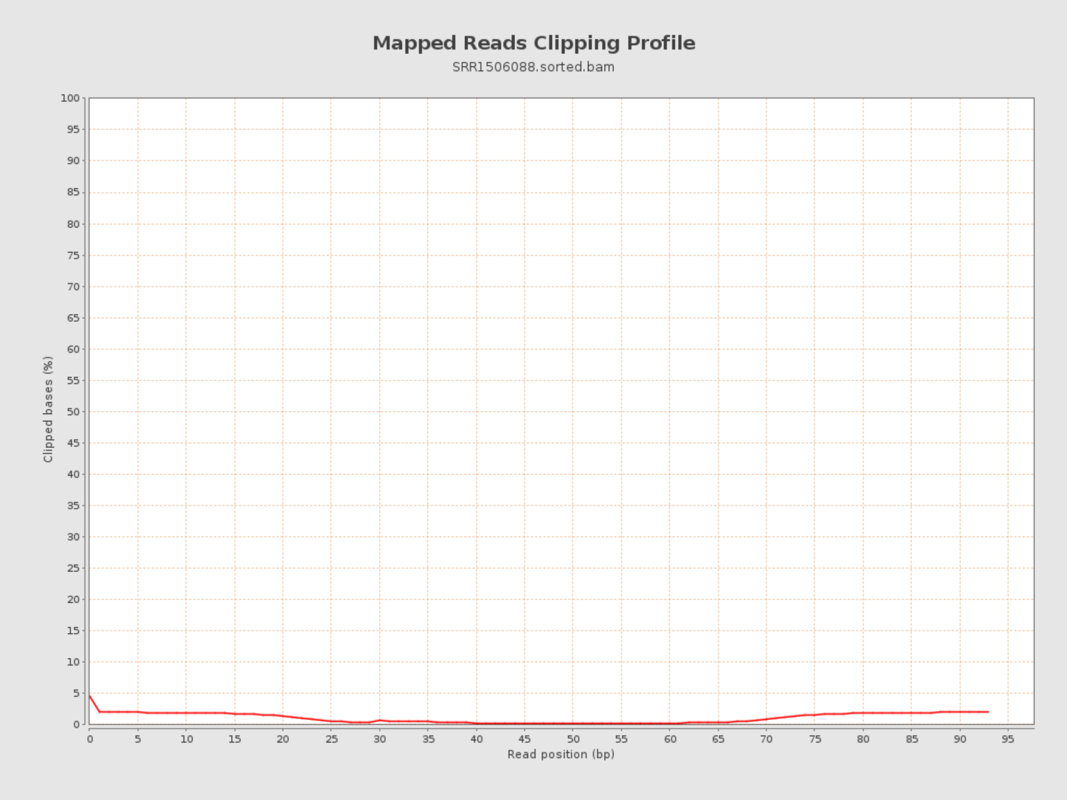
8. Results : Mapped Reads Nucleotide Content



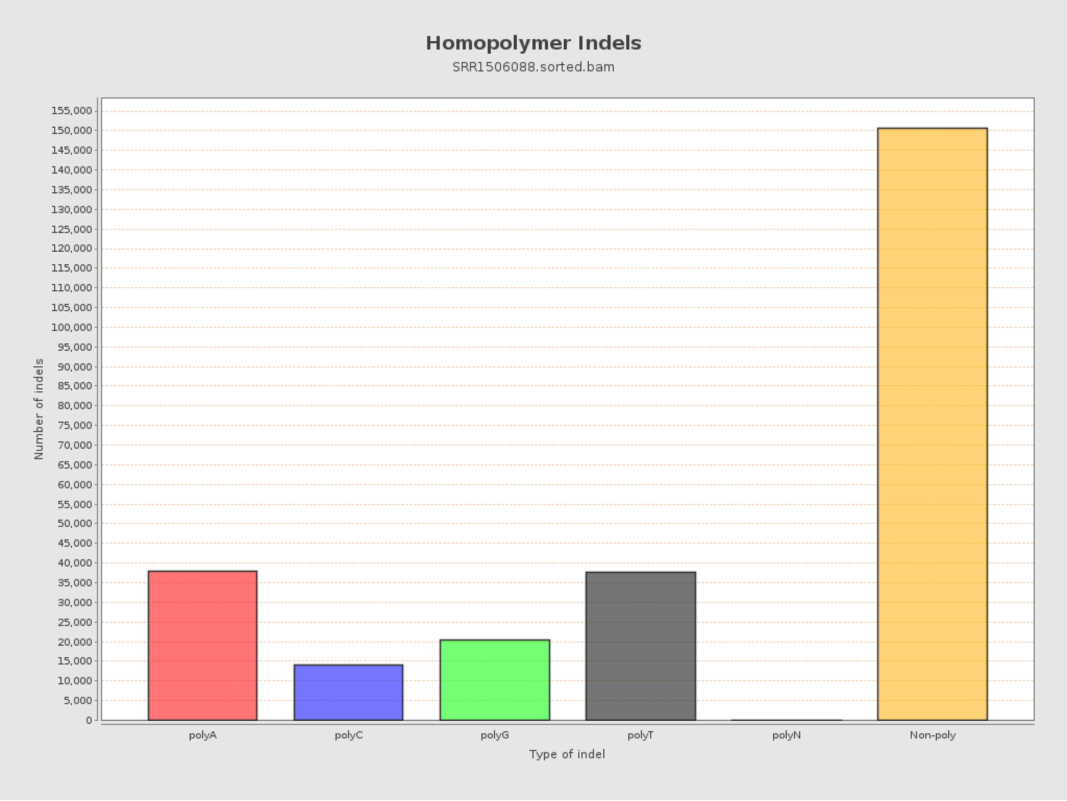
9. Results : Mapped Reads GC-content Distribution



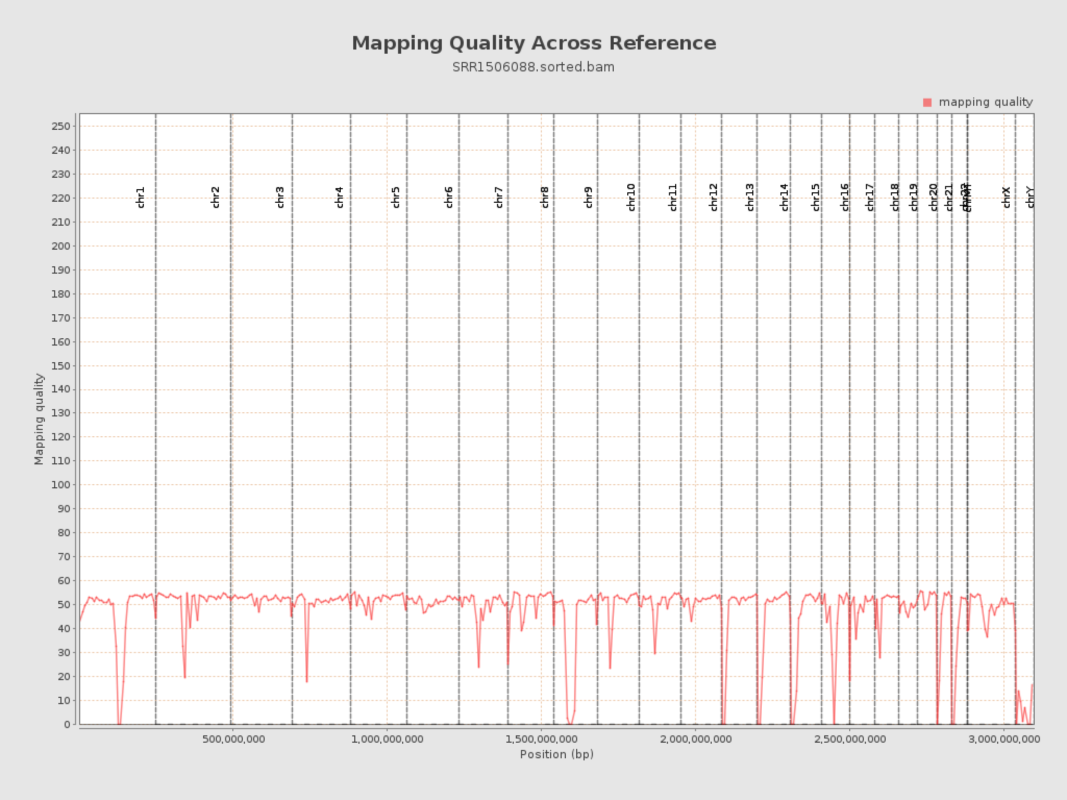
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram