Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 23:36:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083609.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_SRR3083609 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083609.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 23:36:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083609.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,978,361
Mapped reads	1,783,843 / 90.17%
Unmapped reads	194,518 / 9.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,149 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	87,416 / 4.42%
Duplication rate	4.2%
Clipped reads	816,501 / 41.27%

2.2. ACGT Content

Number/percentage of A's	31,775,466 / 26.86%
Number/percentage of C's	22,242,955 / 18.8%
Number/percentage of T's	37,033,576 / 31.31%
Number/percentage of G's	27,226,397 / 23.02%
Number/percentage of N's	5,664 / 0%
GC Percentage	41.82%

2.3. Coverage

Mean	0.0382

Standard Deviation	0.3007

2.4. Mapping Quality

Mean Mapping Quality	45.43

2.5. Mismatches and indels

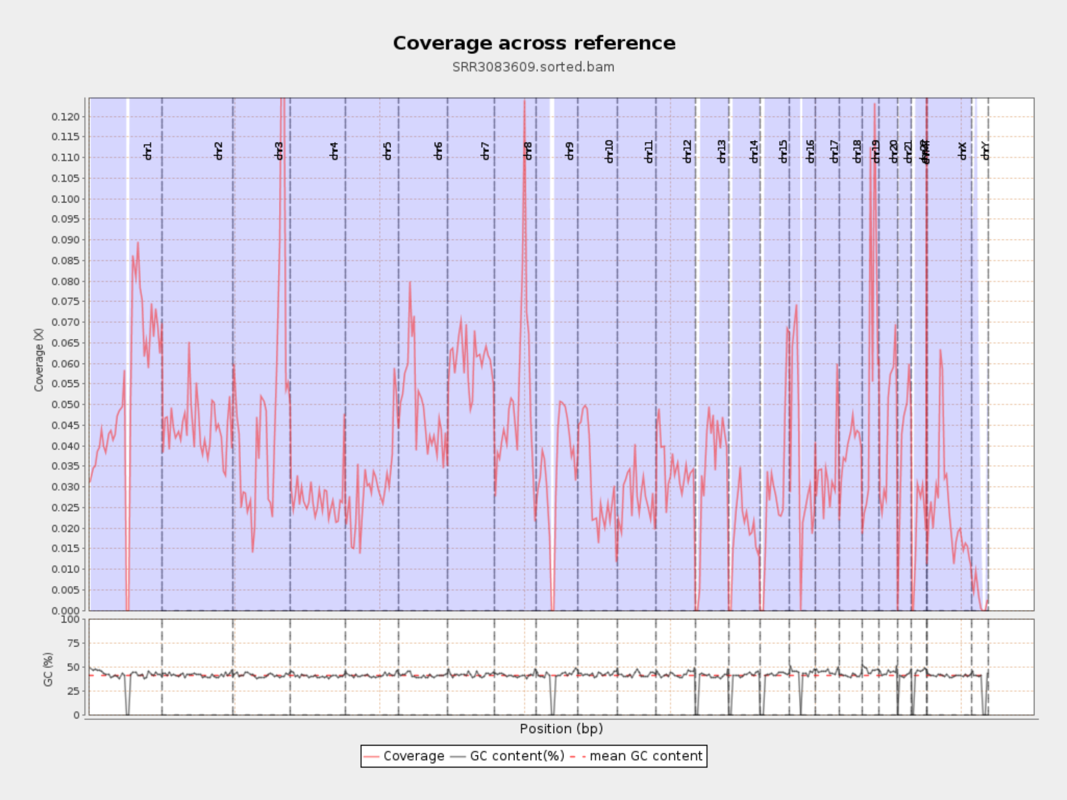
General error rate	0.69%
Mismatches	804,355
Insertions	8,711
Mapped reads with at least one insertion	0.48%
Deletions	27,043
Mapped reads with at least one deletion	1.5%
Homopolymer indels	47.98%

2.6. Chromosome stats

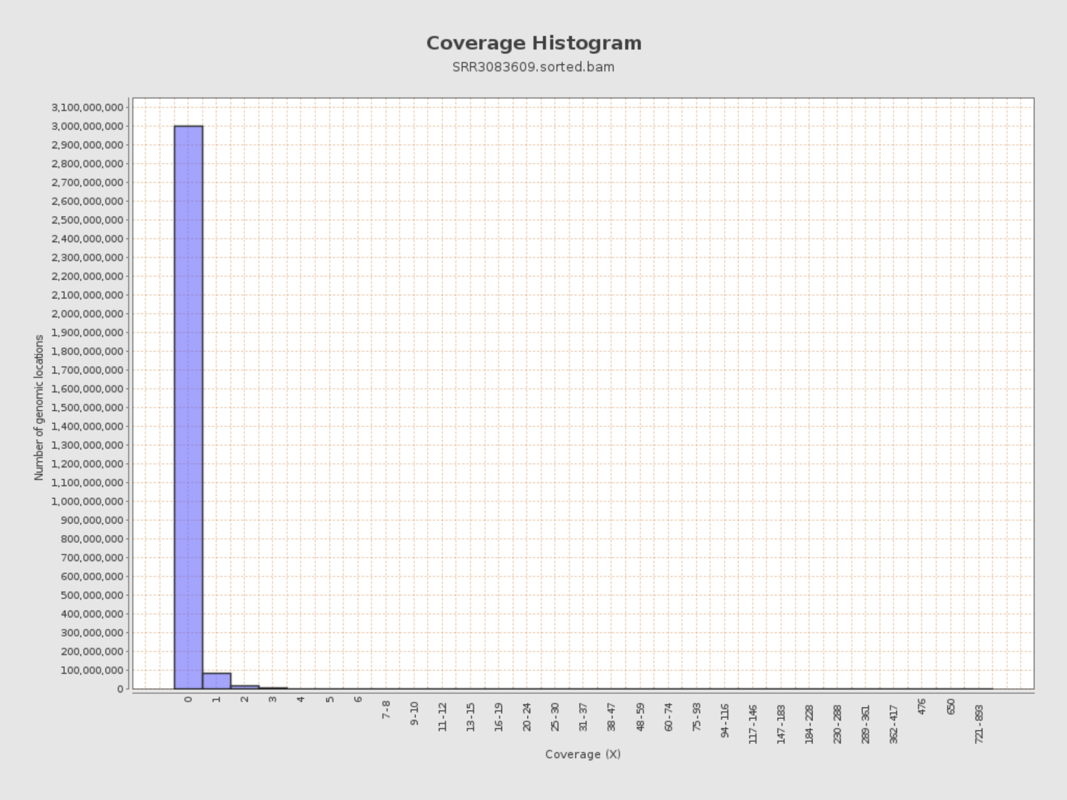
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13040349	0.0523	0.4622
chr2	243199373	10833471	0.0445	0.4565
chr3	198022430	9588649	0.0484	0.2627
chr4	191154276	5200471	0.0272	0.1993
chr5	180915260	5448578	0.0301	0.2035
chr6	171115067	8442852	0.0493	0.304
chr7	159138663	9699122	0.0609	0.4822

chr8	146364022	7508516	0.0513	0.3111
chr9	141213431	4769433	0.0338	0.2363
chr10	135534747	4175679	0.0308	0.2283
chr11	135006516	3699826	0.0274	0.2057
chr12	133851895	4615970	0.0345	0.2183
chr13	115169878	3909591	0.0339	0.2177
chr14	107349540	2037730	0.019	0.1621
chr15	102531392	2941679	0.0287	0.2082
chr16	90354753	3301296	0.0365	0.2324
chr17	81195210	2753141	0.0339	0.2209
chr18	78077248	3101158	0.0397	0.316
chr19	59128983	3512860	0.0594	0.3956
chr20	63025520	2787961	0.0442	0.2514
chr21	48129895	1961463	0.0408	0.2444
chr22	51304566	1003801	0.0196	0.1625
chrMT	16571	2285	0.1379	0.4102
chrX	155270560	3806822	0.0245	0.1892
chrY	59373566	184895	0.0031	0.0745

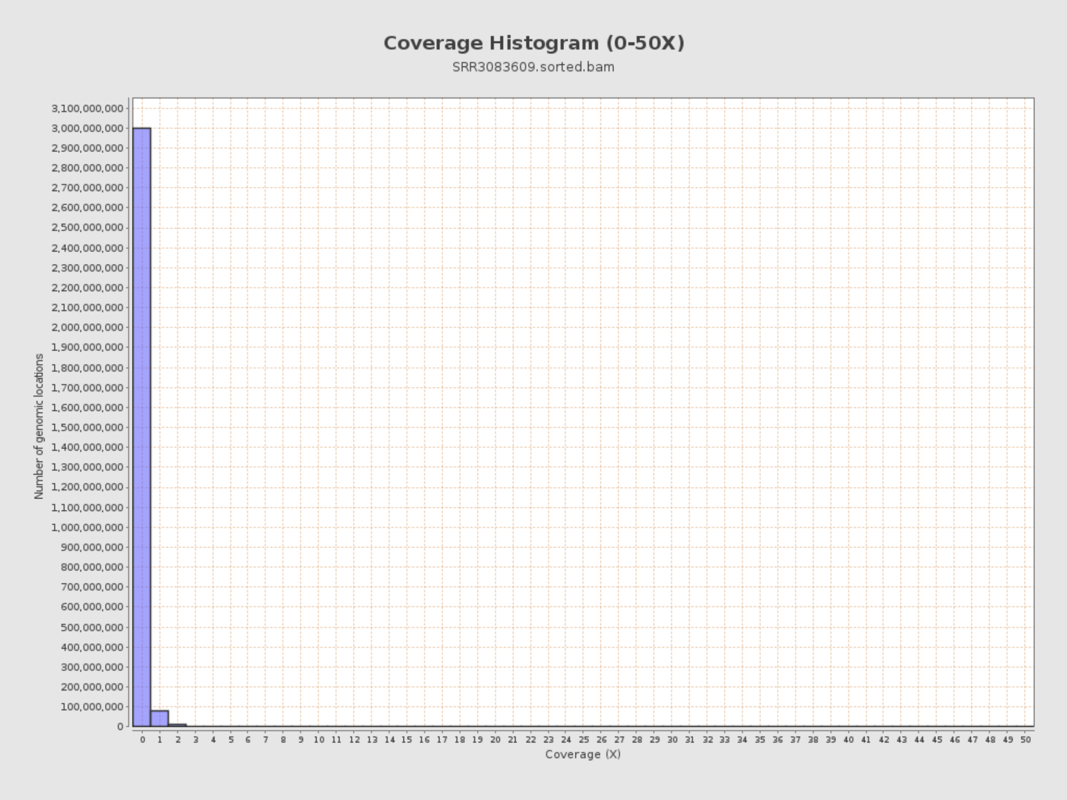
3. Results : Coverage across reference



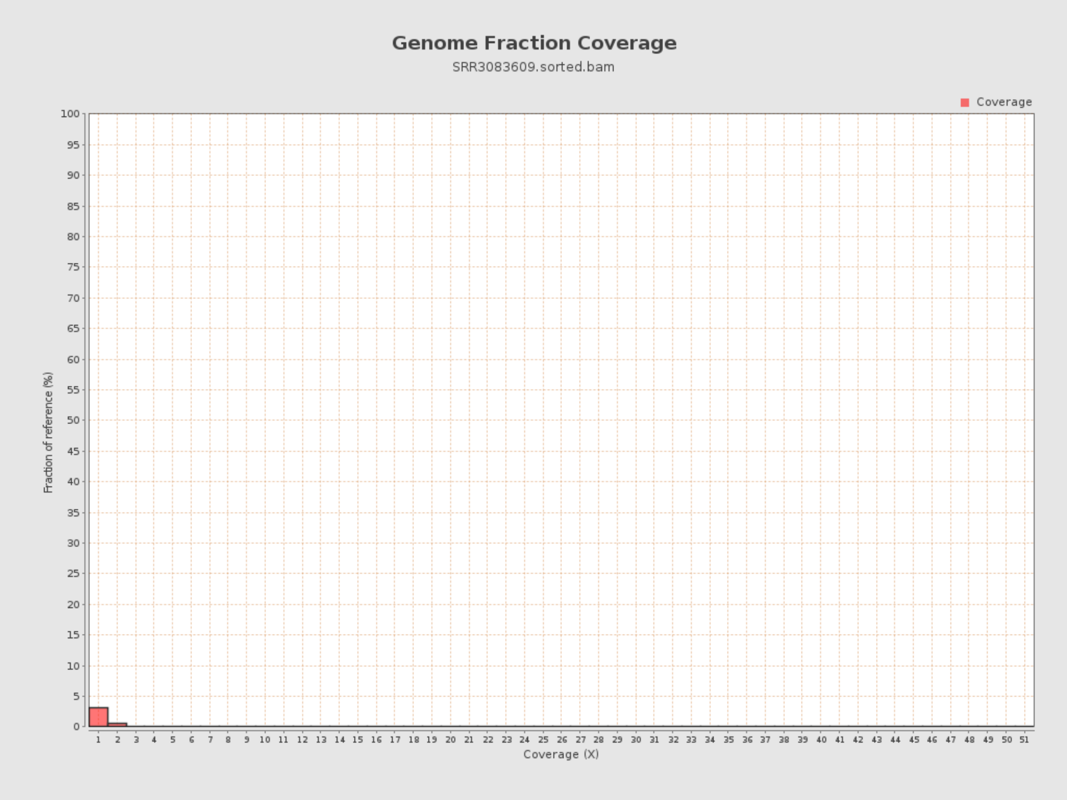
4. Results : Coverage Histogram



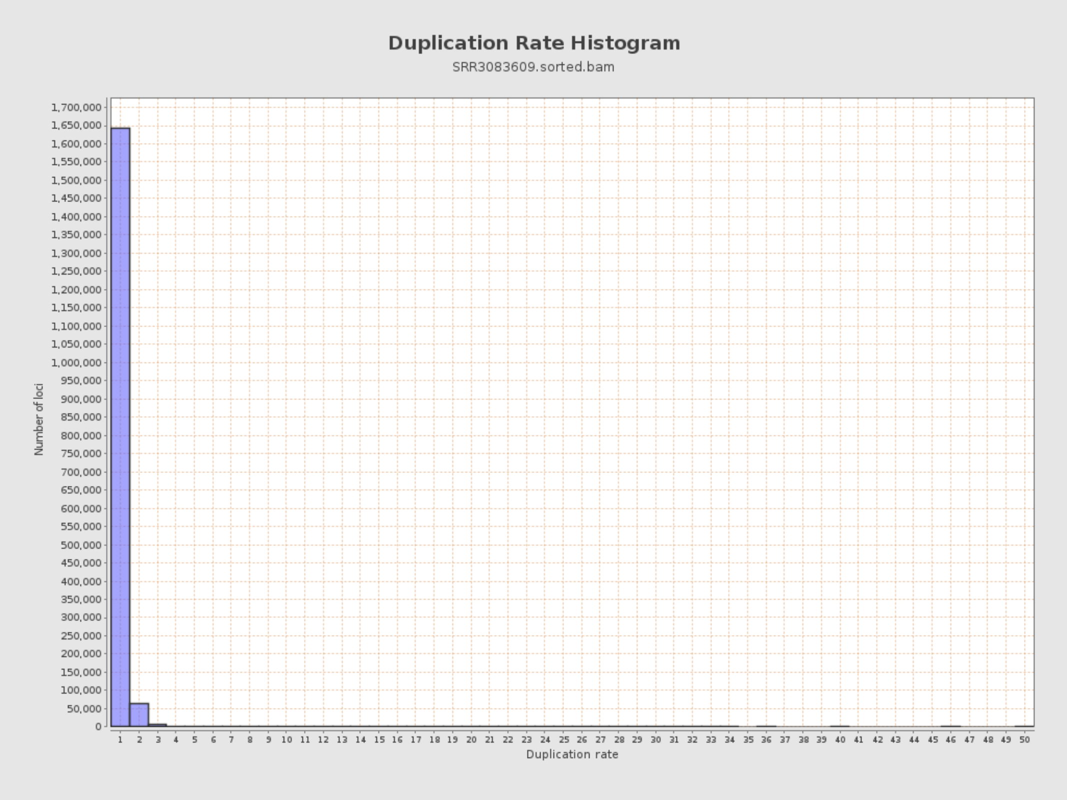
5. Results : Coverage Histogram (0-50X)



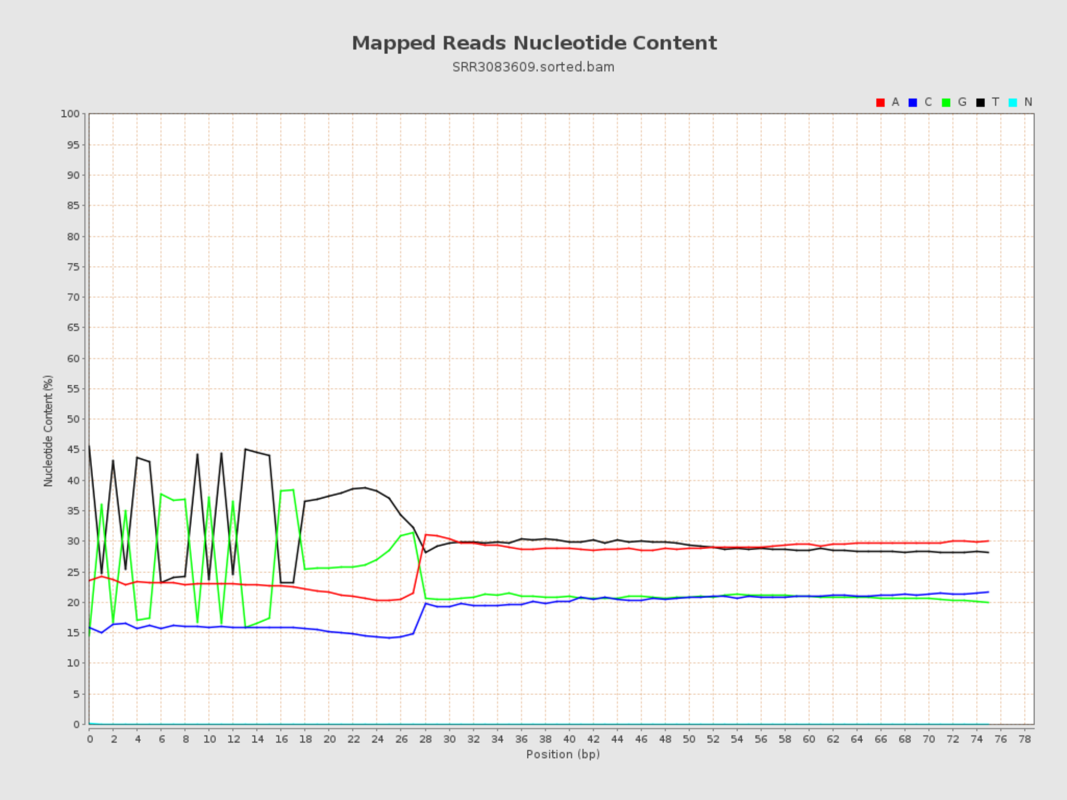
6. Results : Genome Fraction Coverage



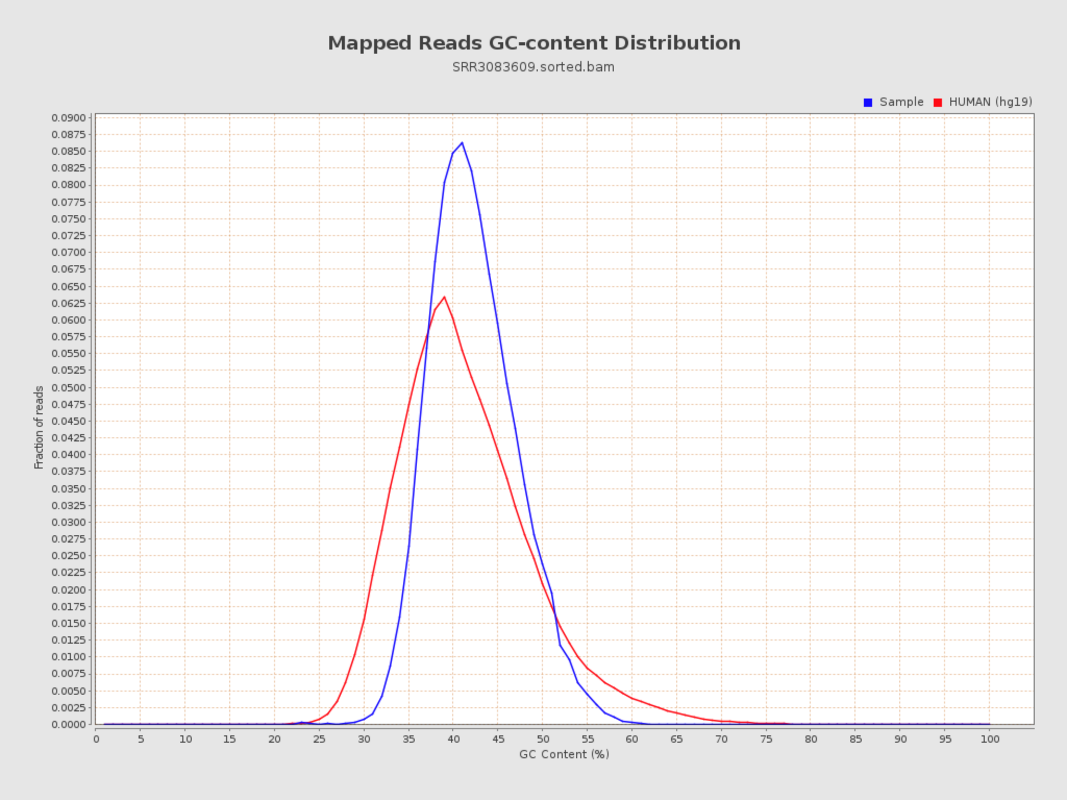
7. Results : Duplication Rate Histogram



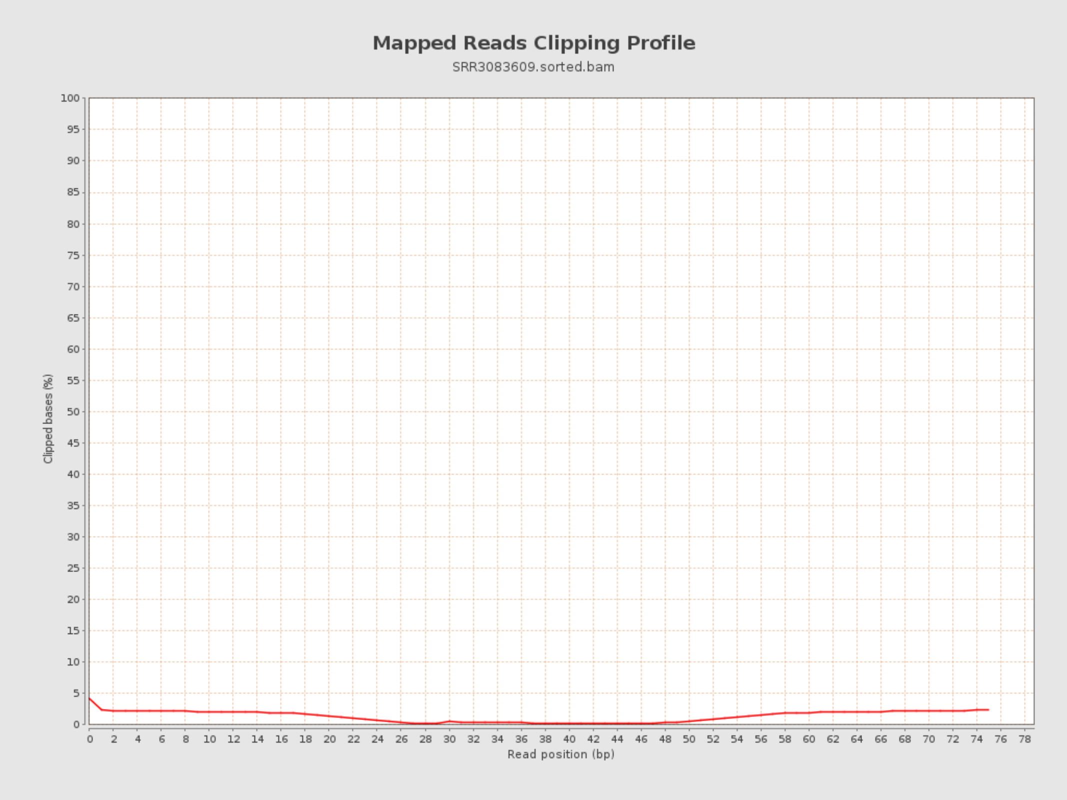
8. Results : Mapped Reads Nucleotide Content



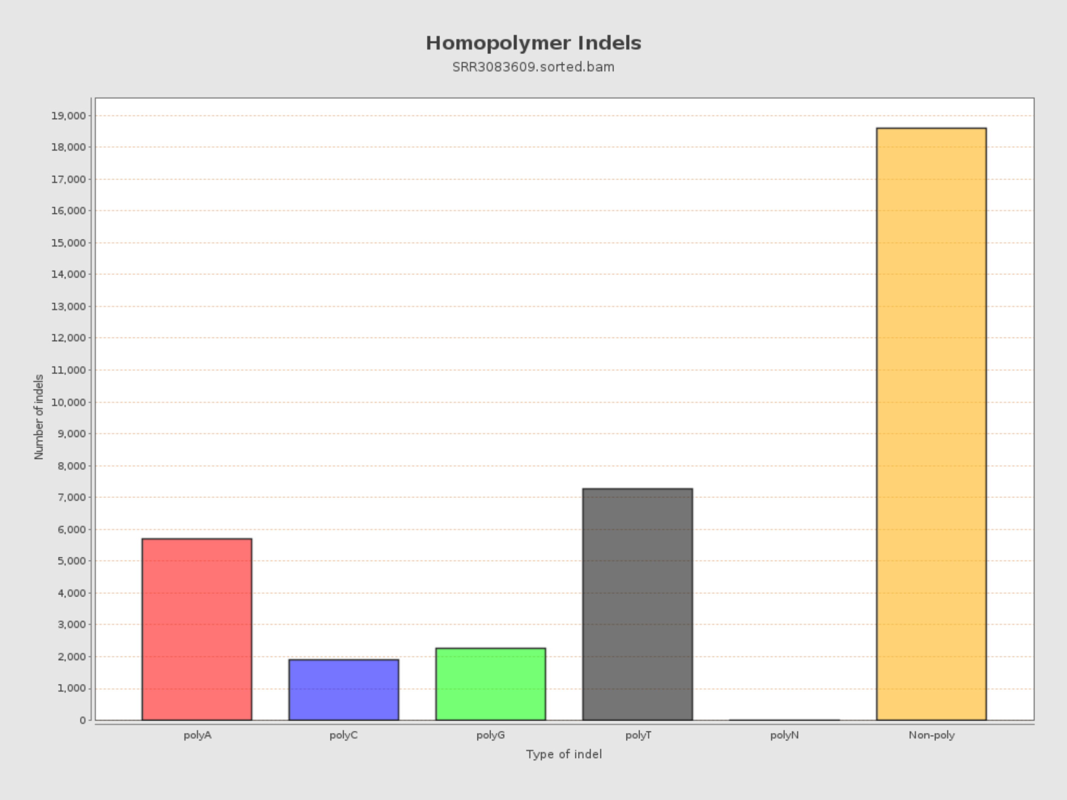
9. Results : Mapped Reads GC-content Distribution



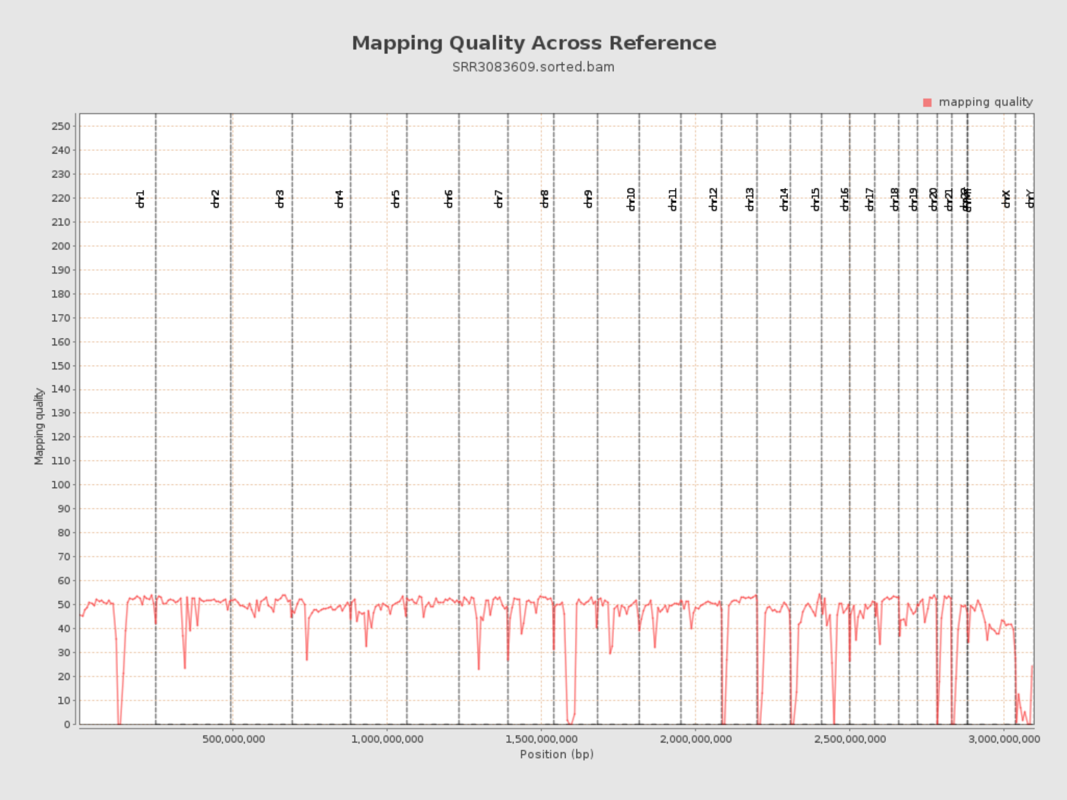
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram