Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:51:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549034.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_SRR1549034 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549034.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:51:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549034.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,693,973
Mapped reads	6,492,364 / 84.38%
Unmapped reads	1,201,609 / 15.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	341,493 / 4.44%
Duplication rate	4.32%
Clipped reads	405,727 / 5.27%

2.2. ACGT Content

Number/percentage of A's	74,586,091 / 28.98%
Number/percentage of C's	53,849,614 / 20.92%
Number/percentage of T's	75,057,140 / 29.16%
Number/percentage of G's	53,861,779 / 20.93%
Number/percentage of N's	187 / 0%
GC Percentage	41.85%

2.3. Coverage

Mean	0.0831
Standard Deviation	0.5924

2.4. Mapping Quality

Mean Mapping Quality	42.1

2.5. Mismatches and indels

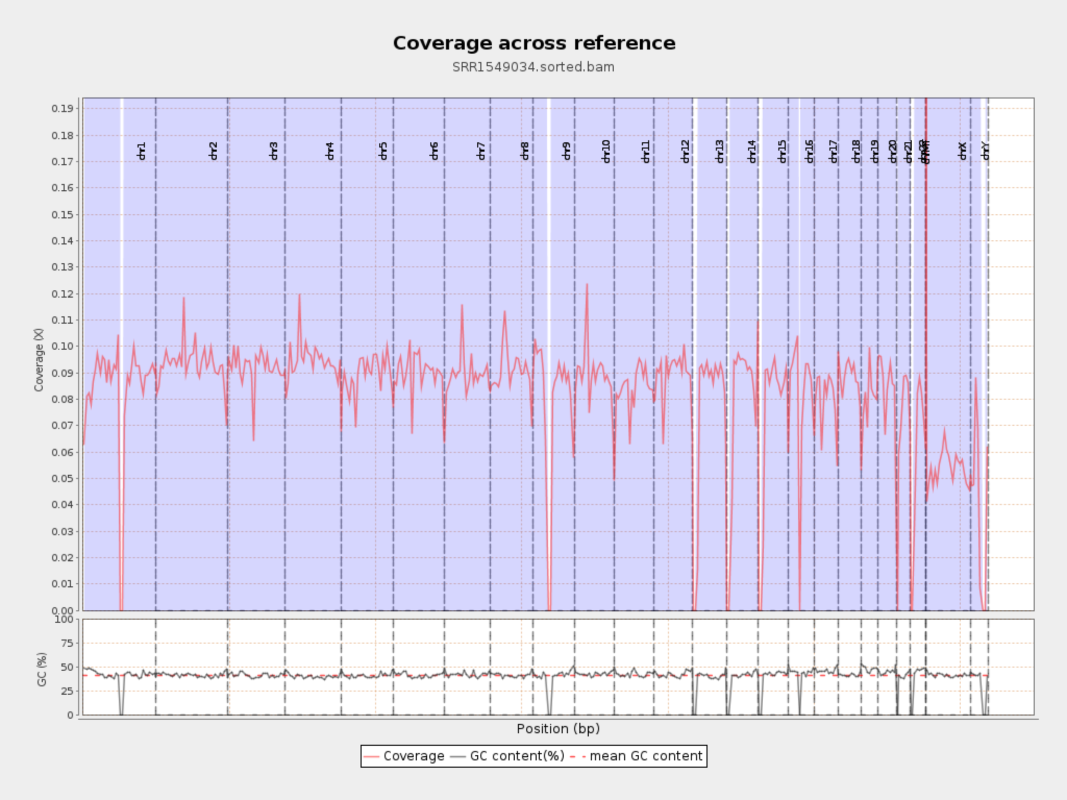
General error rate	0.26%
Mismatches	652,136
Insertions	6,794
Mapped reads with at least one insertion	0.1%
Deletions	18,134
Mapped reads with at least one deletion	0.28%
Homopolymer indels	43.3%

2.6. Chromosome stats

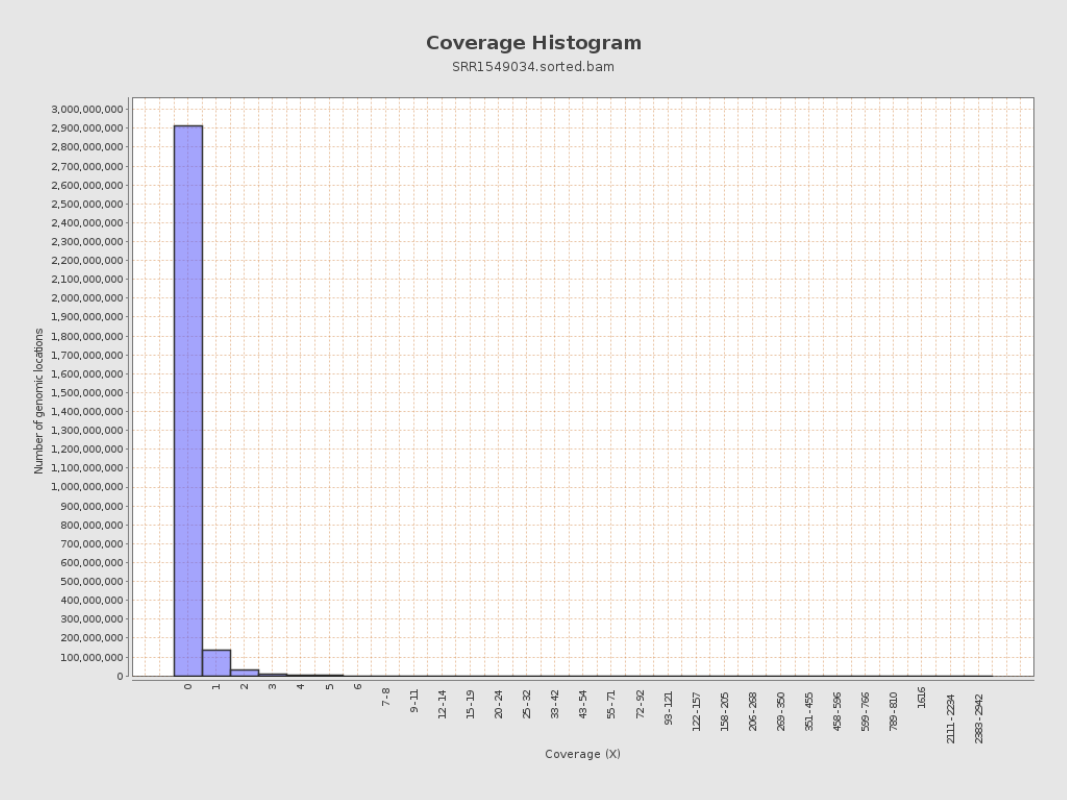
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20784502	0.0834	0.7385
chr2	243199373	22747096	0.0935	0.5566
chr3	198022430	18257575	0.0922	0.4117
chr4	191154276	18149729	0.0949	0.4465
chr5	180915260	16137857	0.0892	0.4092
chr6	171115067	15445304	0.0903	0.4357
chr7	159138663	14201716	0.0892	0.6691
chr8	146364022	13277455	0.0907	1.4955

chr9	141213431	11001119	0.0779	0.512
chr10	135534747	12158585	0.0897	0.5264
chr11	135006516	11340129	0.084	0.4555
chr12	133851895	12018490	0.0898	0.412
chr13	115169878	8617795	0.0748	0.3716
chr14	107349540	8136277	0.0758	0.435
chr15	102531392	7326385	0.0715	0.3631
chr16	90354753	7164579	0.0793	0.4156
chr17	81195210	6562975	0.0808	0.4001
chr18	78077248	6935539	0.0888	0.806
chr19	59128983	4776491	0.0808	0.6927
chr20	63025520	5357652	0.085	0.4135
chr21	48129895	3366803	0.07	0.4394
chr22	51304566	2877410	0.0561	0.4665
chrMT	16571	10877	0.6564	1.0238
chrX	155270560	8349384	0.0538	0.345
chrY	59373566	2376992	0.04	0.3929

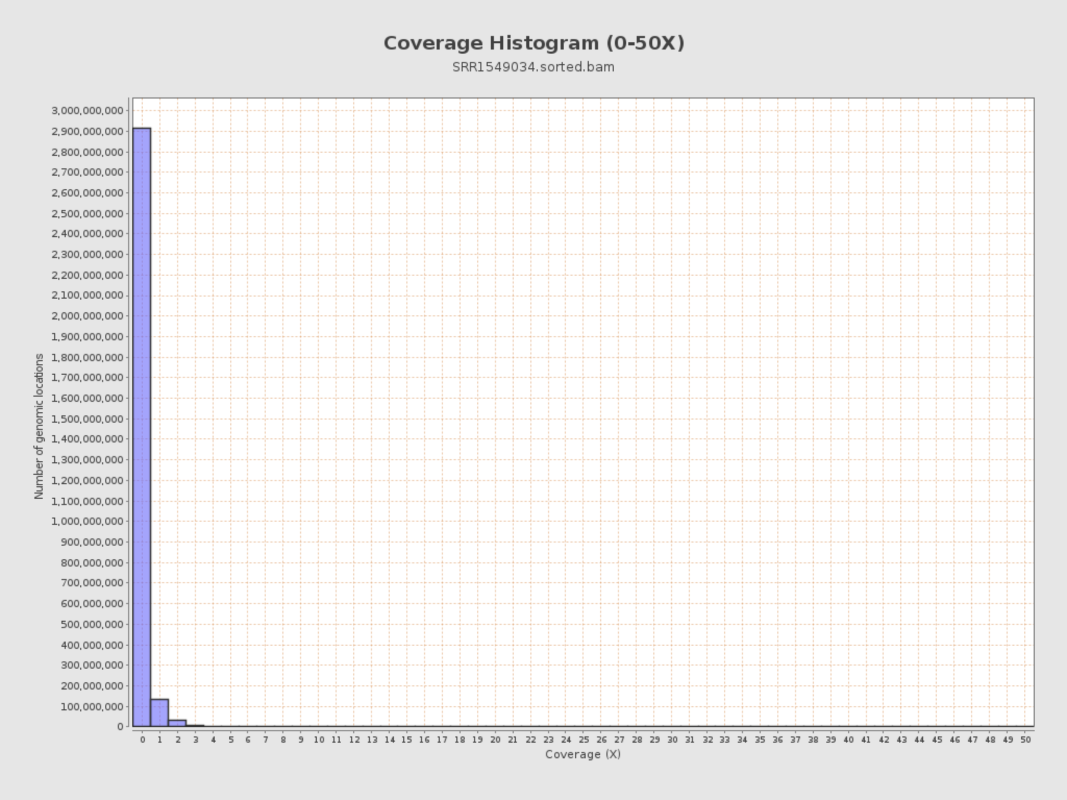
3. Results : Coverage across reference



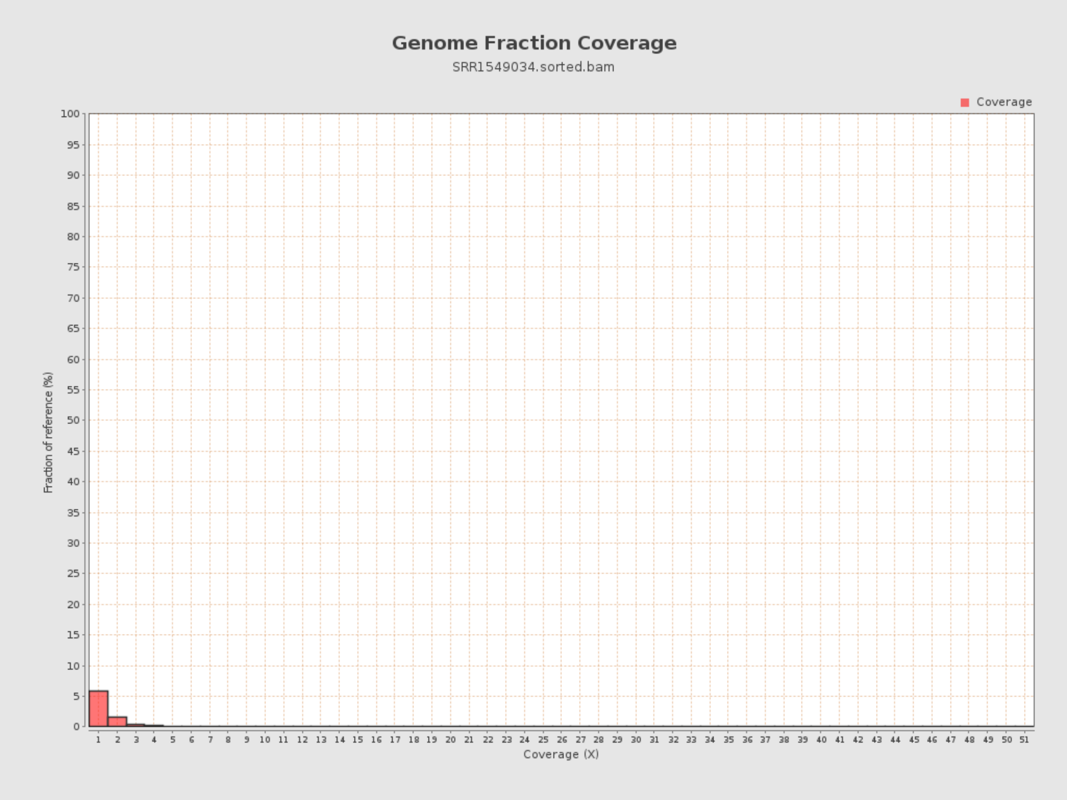
4. Results : Coverage Histogram



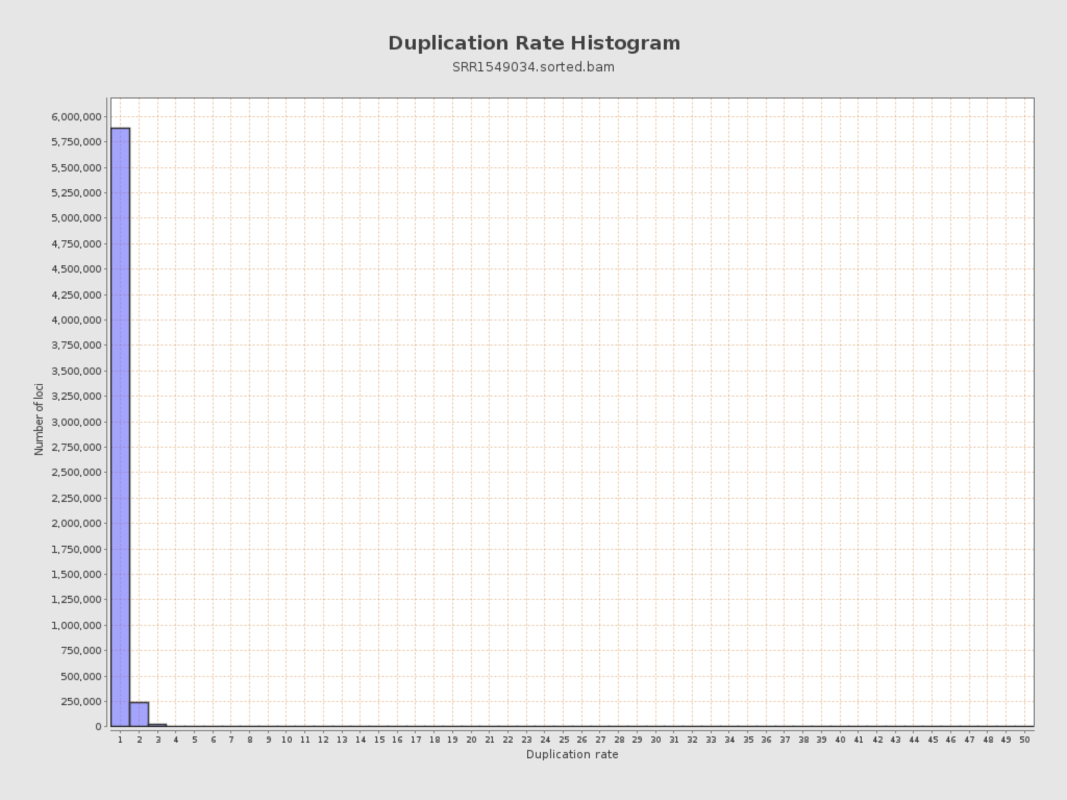
5. Results : Coverage Histogram (0-50X)



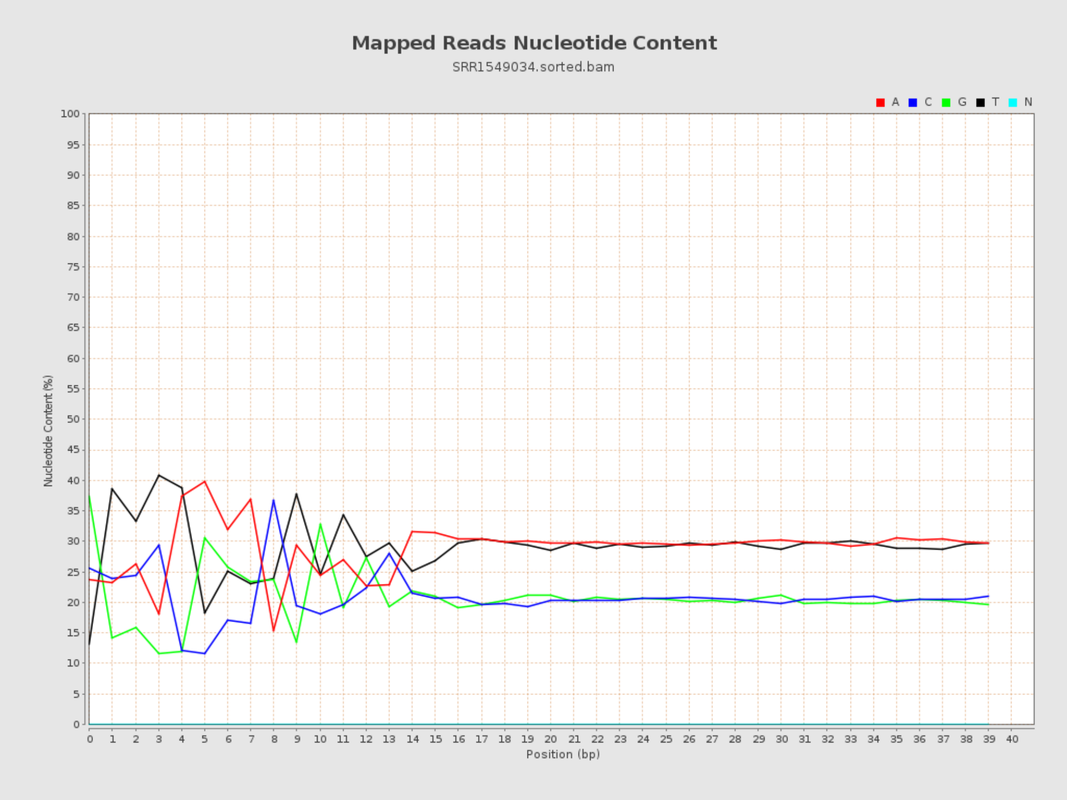
6. Results : Genome Fraction Coverage



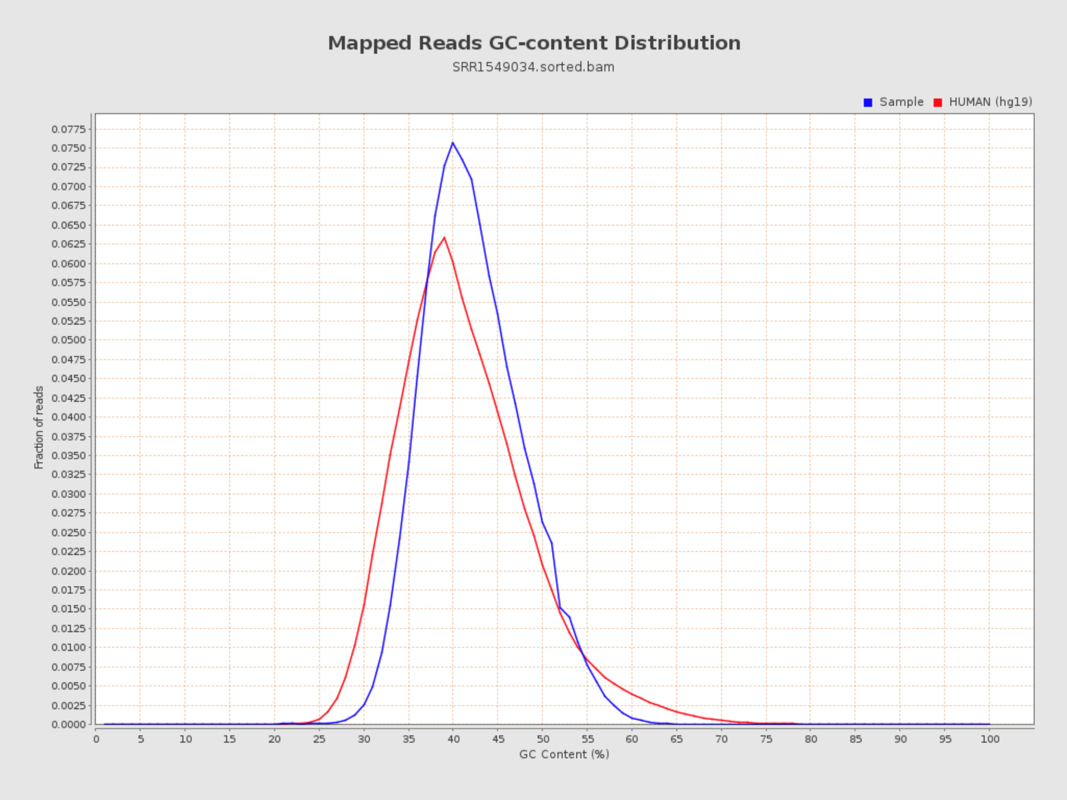
7. Results : Duplication Rate Histogram



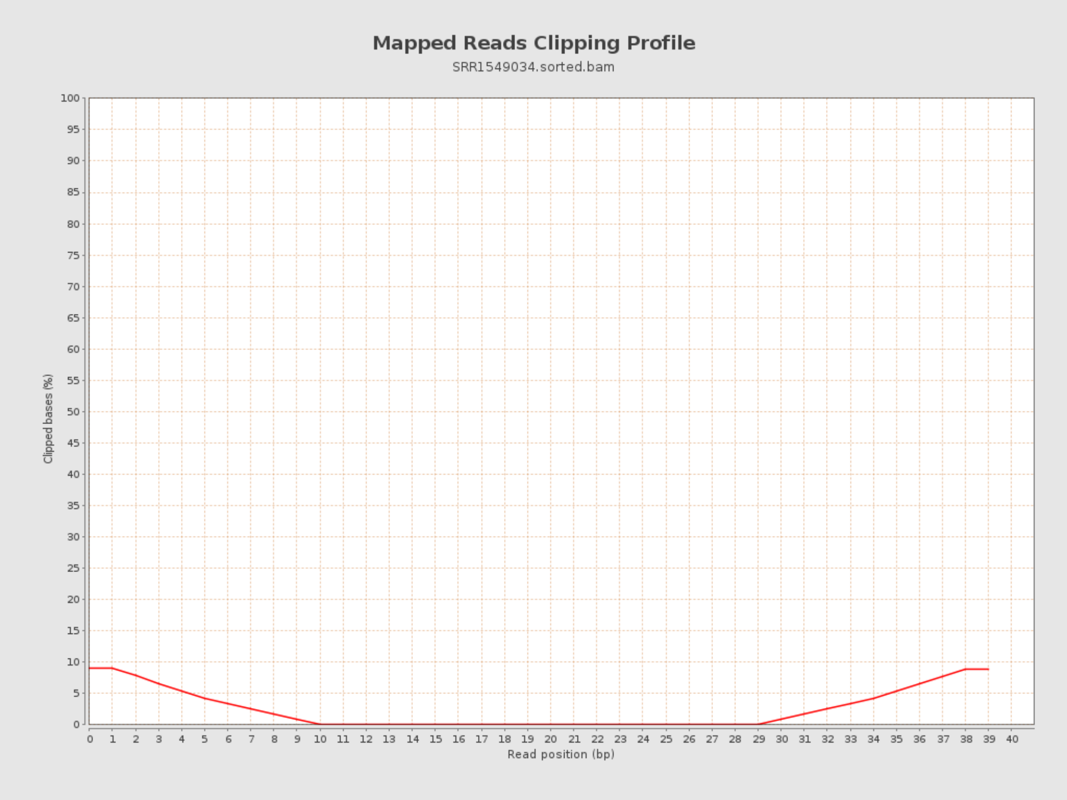
8. Results : Mapped Reads Nucleotide Content



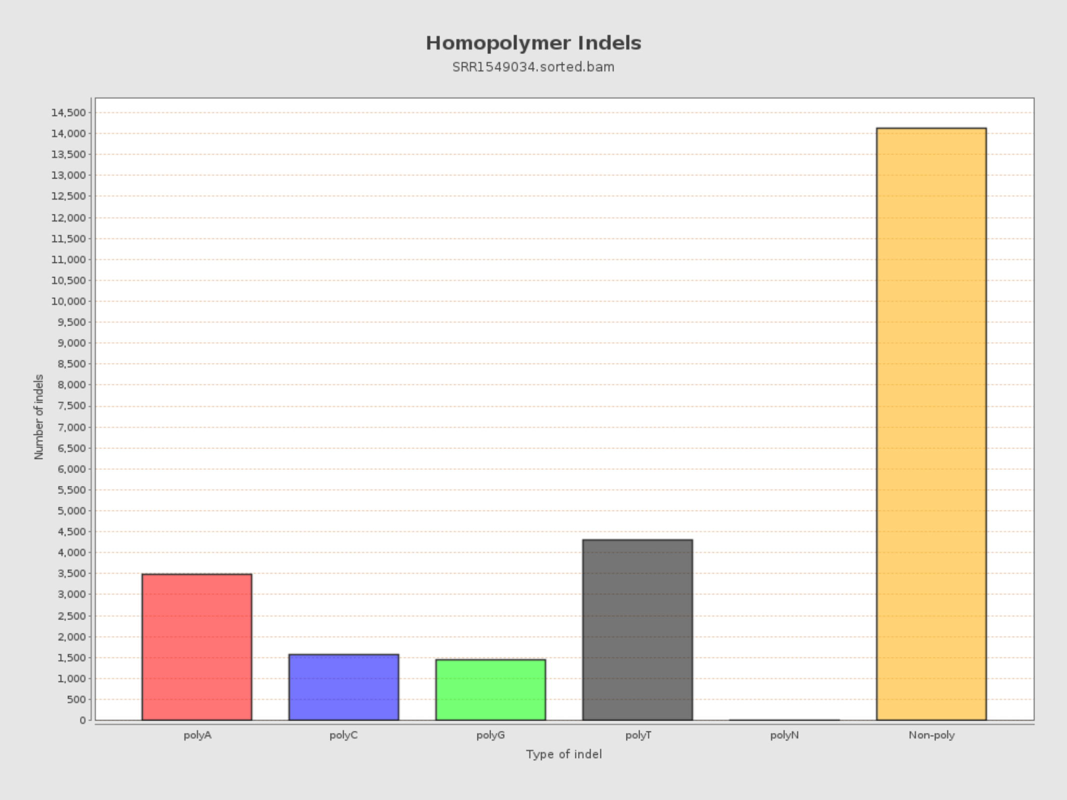
9. Results : Mapped Reads GC-content Distribution



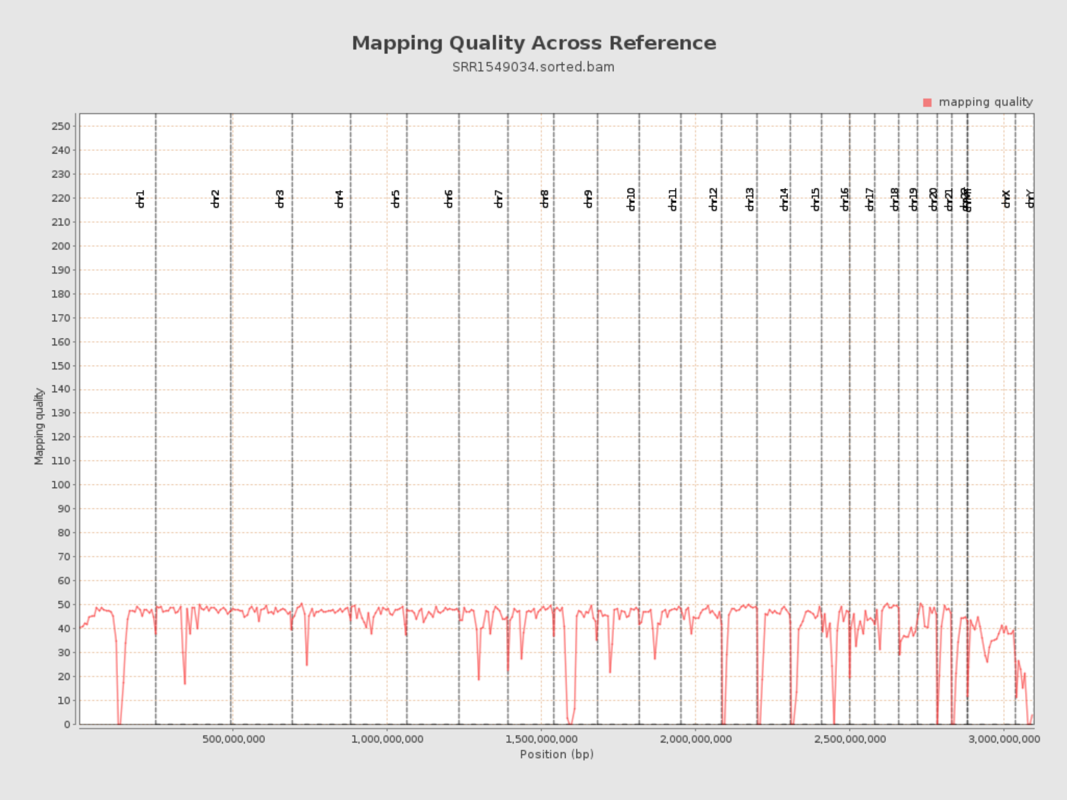
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram