Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 21:13:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549083.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_SRR1549083 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549083.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 21:13:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549083.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,790,583
Mapped reads	6,779,953 / 87.03%
Unmapped reads	1,010,630 / 12.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	210,480 / 2.7%
Duplication rate	2.05%
Clipped reads	321,269 / 4.12%

2.2. ACGT Content

Number/percentage of A's	79,793,915 / 29.63%
Number/percentage of C's	54,922,536 / 20.4%
Number/percentage of T's	80,955,572 / 30.06%
Number/percentage of G's	53,550,002 / 19.89%
Number/percentage of N's	64,003 / 0.02%
GC Percentage	40.28%

2.3. Coverage

Mean	0.087
Standard Deviation	0.6665

2.4. Mapping Quality

Mean Mapping Quality	44.1

2.5. Mismatches and indels

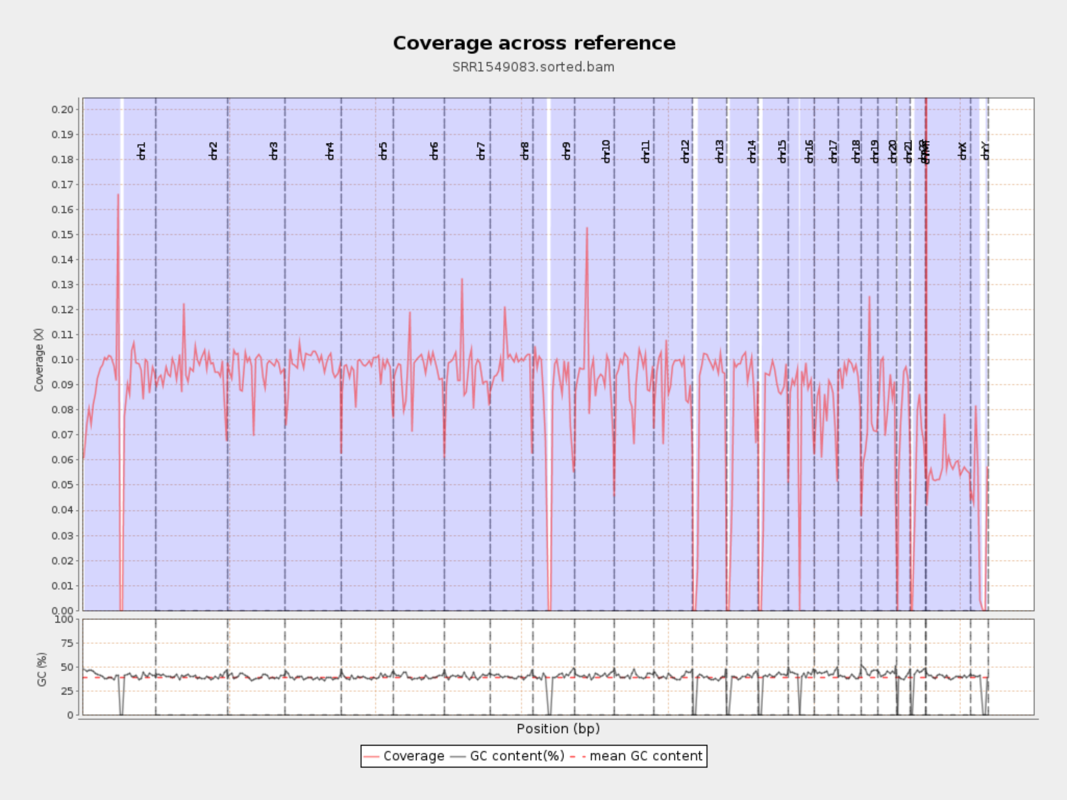
General error rate	0.39%
Mismatches	1,047,526
Insertions	6,193
Mapped reads with at least one insertion	0.09%
Deletions	19,077
Mapped reads with at least one deletion	0.28%
Homopolymer indels	45.61%

2.6. Chromosome stats

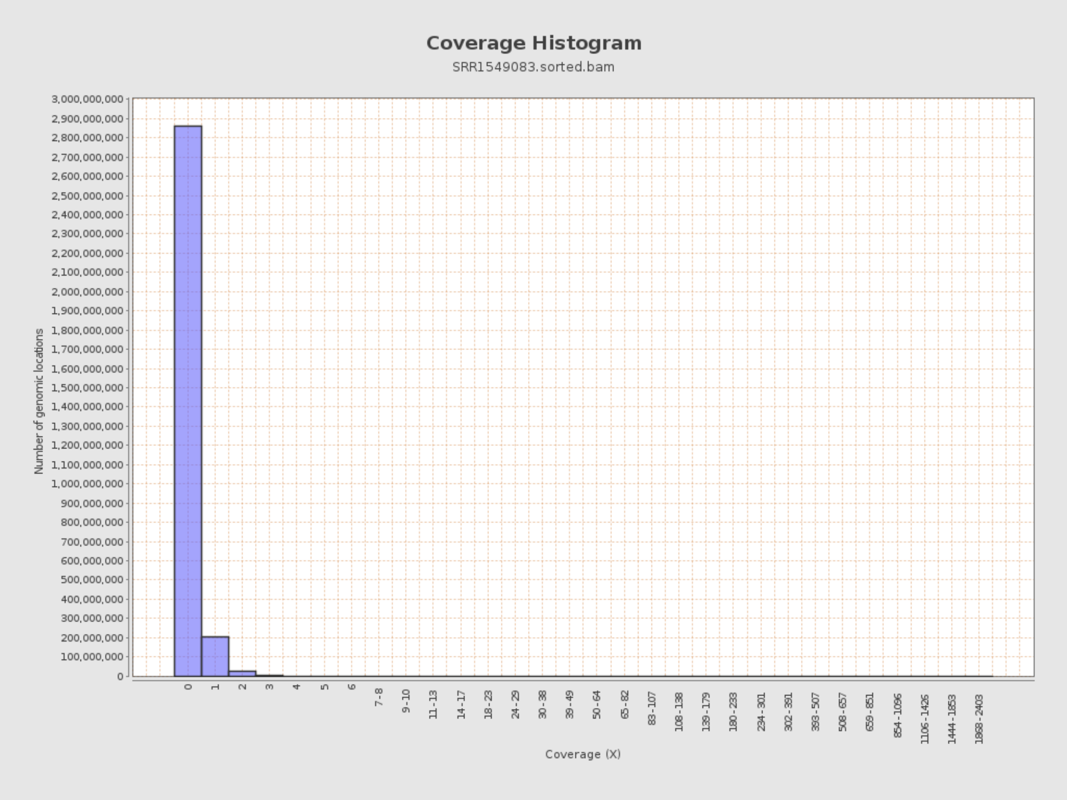
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22015093	0.0883	1.6436
chr2	243199373	23415591	0.0963	0.4918
chr3	198022430	19115164	0.0965	0.3527
chr4	191154276	18810018	0.0984	0.3591
chr5	180915260	17312957	0.0957	0.3509
chr6	171115067	16452663	0.0961	0.4295
chr7	159138663	15094051	0.0948	0.6558
chr8	146364022	14340723	0.098	0.617

chr9	141213431	11325305	0.0802	0.4825
chr10	135534747	12935231	0.0954	0.6769
chr11	135006516	12492178	0.0925	0.4874
chr12	133851895	12404081	0.0927	0.3551
chr13	115169878	9363588	0.0813	0.3105
chr14	107349540	8470081	0.0789	0.3613
chr15	102531392	7695630	0.0751	0.3007
chr16	90354753	7242025	0.0802	0.4134
chr17	81195210	6466944	0.0796	0.3594
chr18	78077248	7416583	0.095	0.9673
chr19	59128983	4429429	0.0749	1.2825
chr20	63025520	5405139	0.0858	0.3332
chr21	48129895	3521238	0.0732	0.35
chr22	51304566	2706933	0.0528	0.2889
chrMT	16571	16098	0.9715	1.3585
chrX	155270560	8732645	0.0562	0.3346
chrY	59373566	2130516	0.0359	0.3166

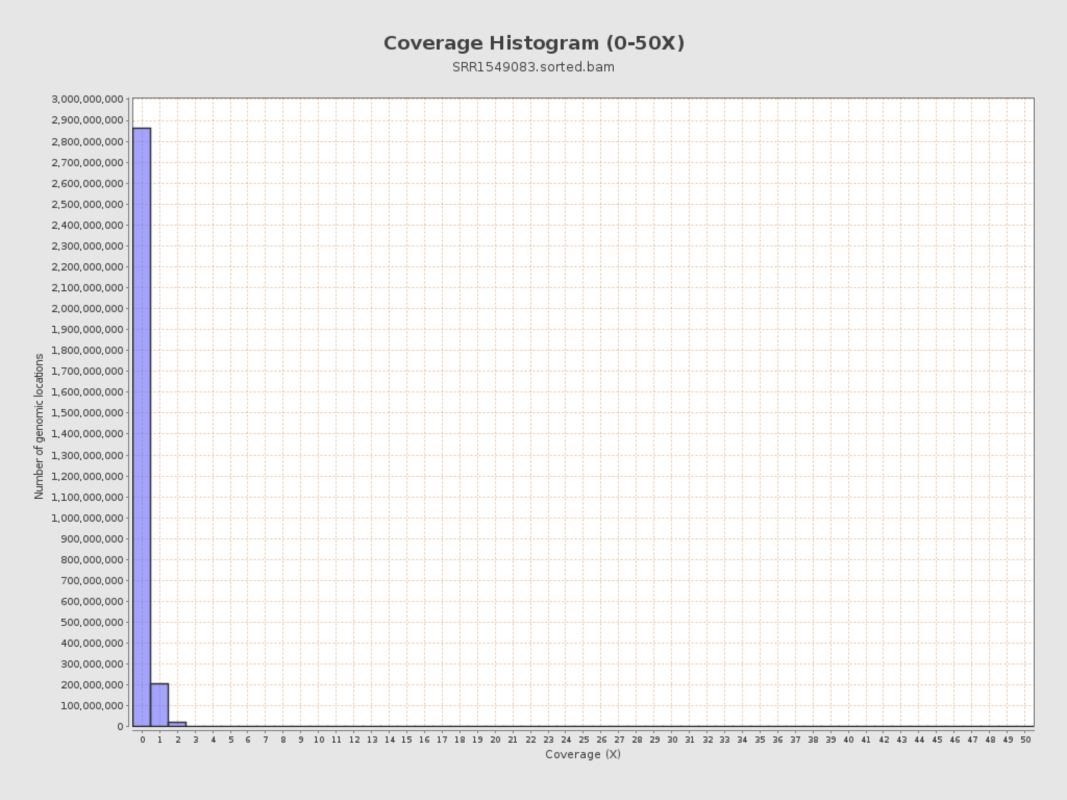
3. Results : Coverage across reference



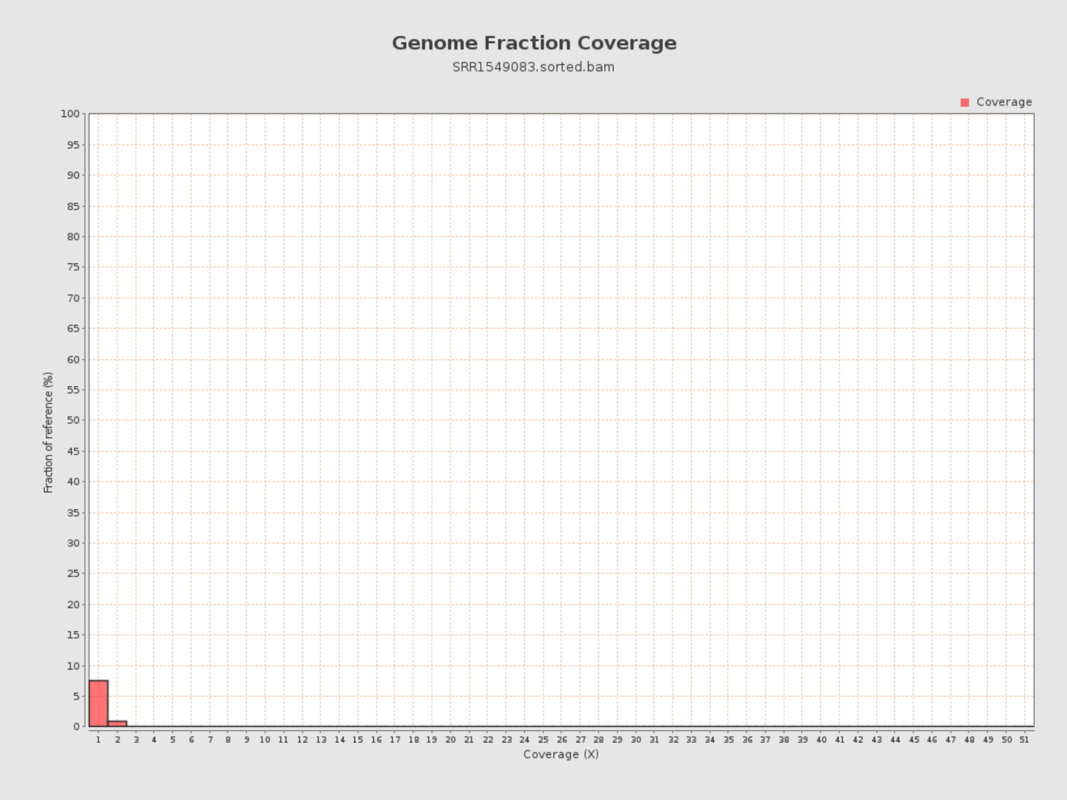
4. Results : Coverage Histogram



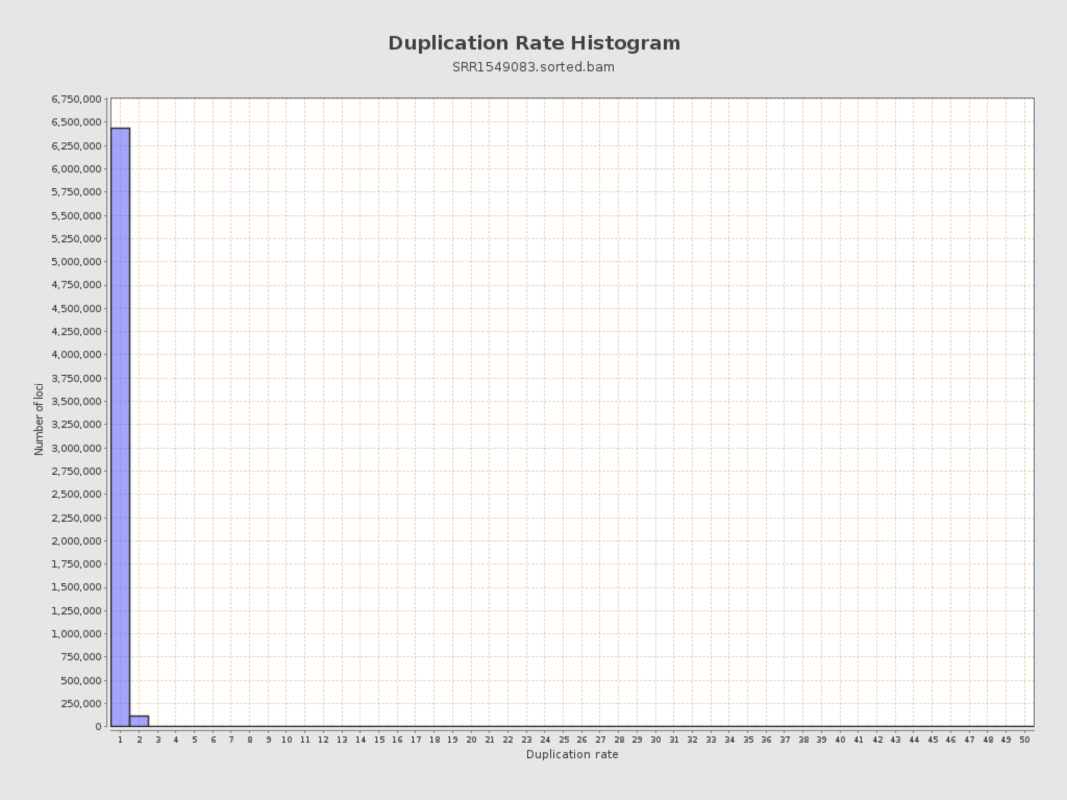
5. Results : Coverage Histogram (0-50X)



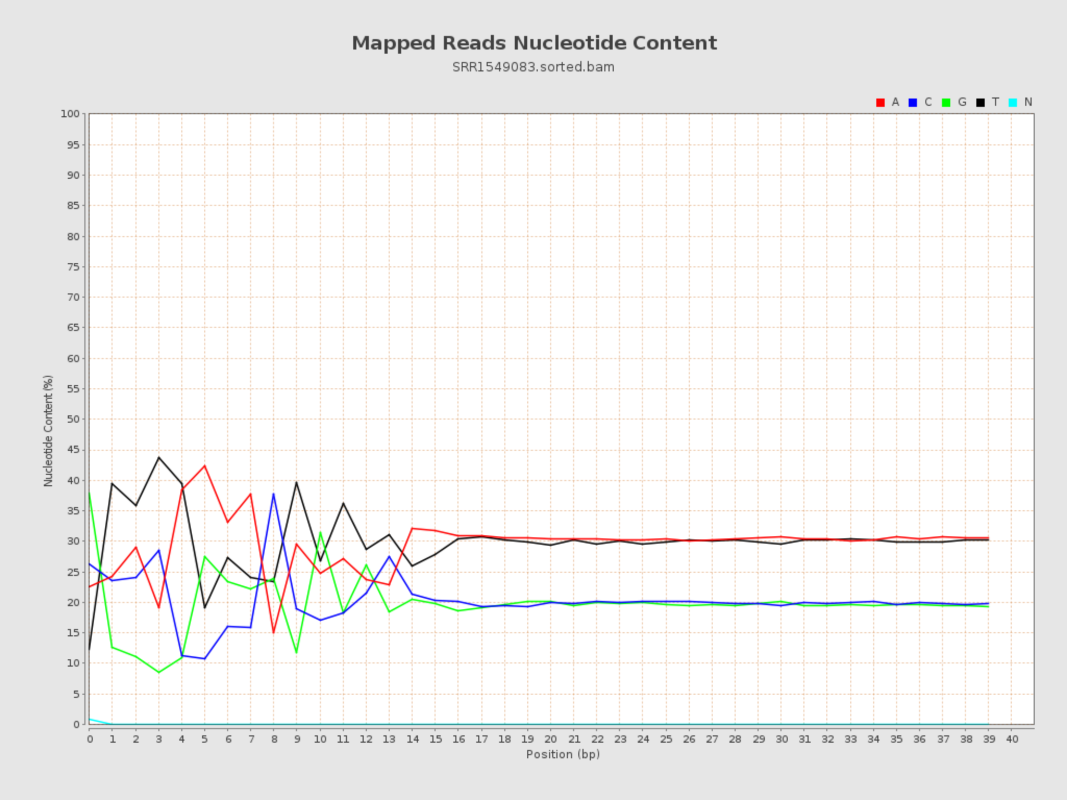
6. Results : Genome Fraction Coverage



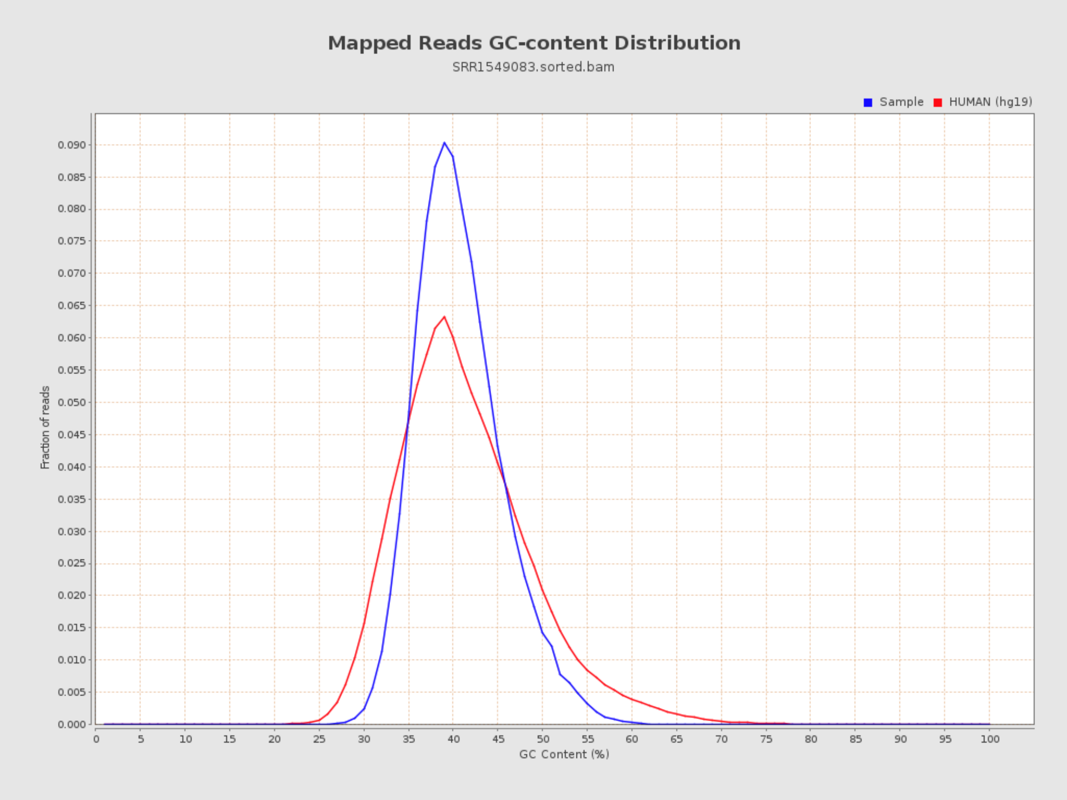
7. Results : Duplication Rate Histogram



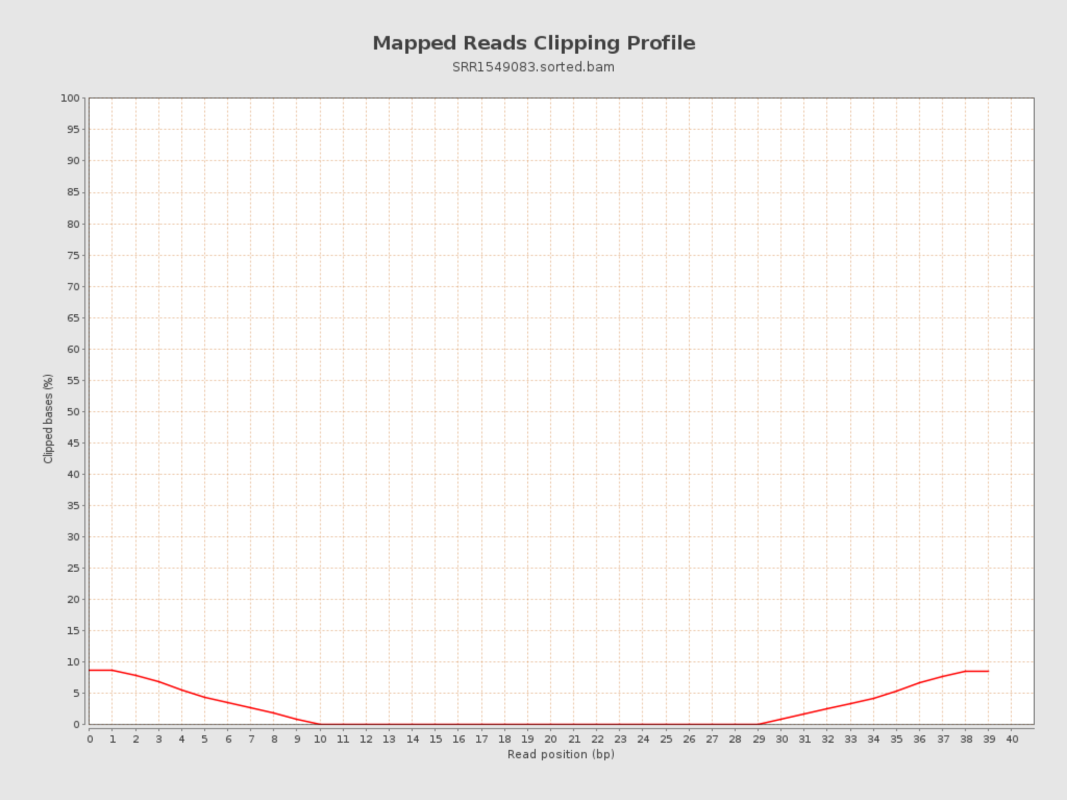
8. Results : Mapped Reads Nucleotide Content



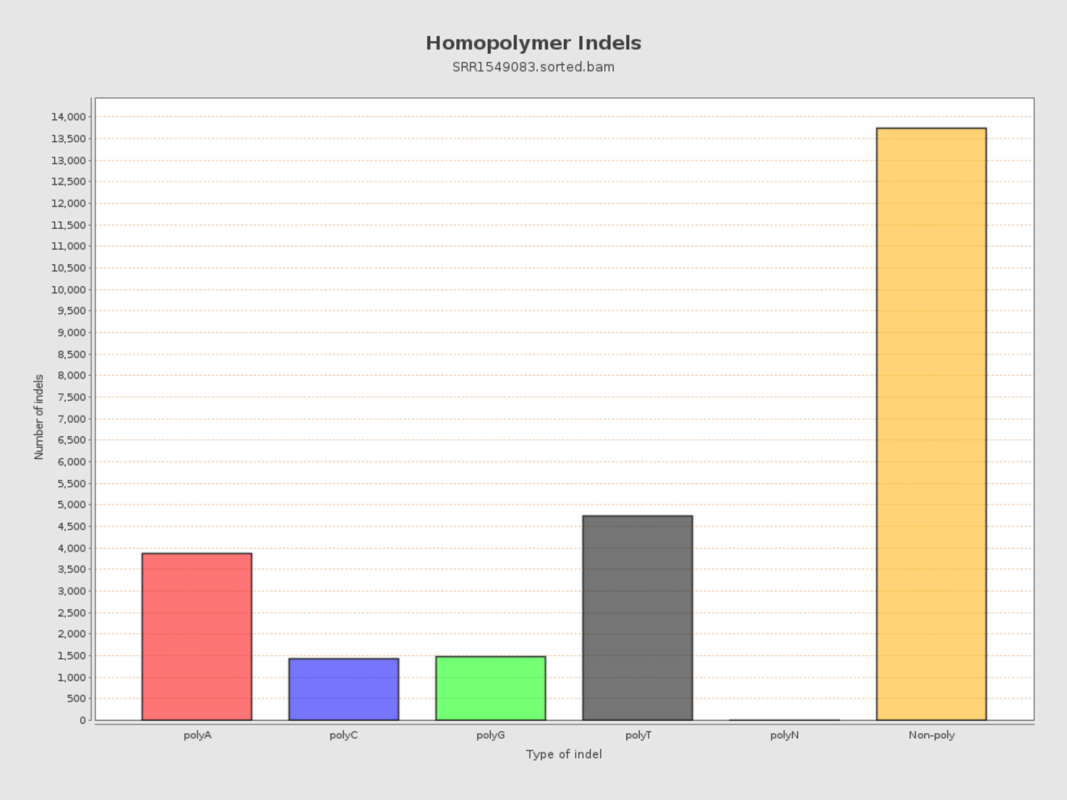
9. Results : Mapped Reads GC-content Distribution



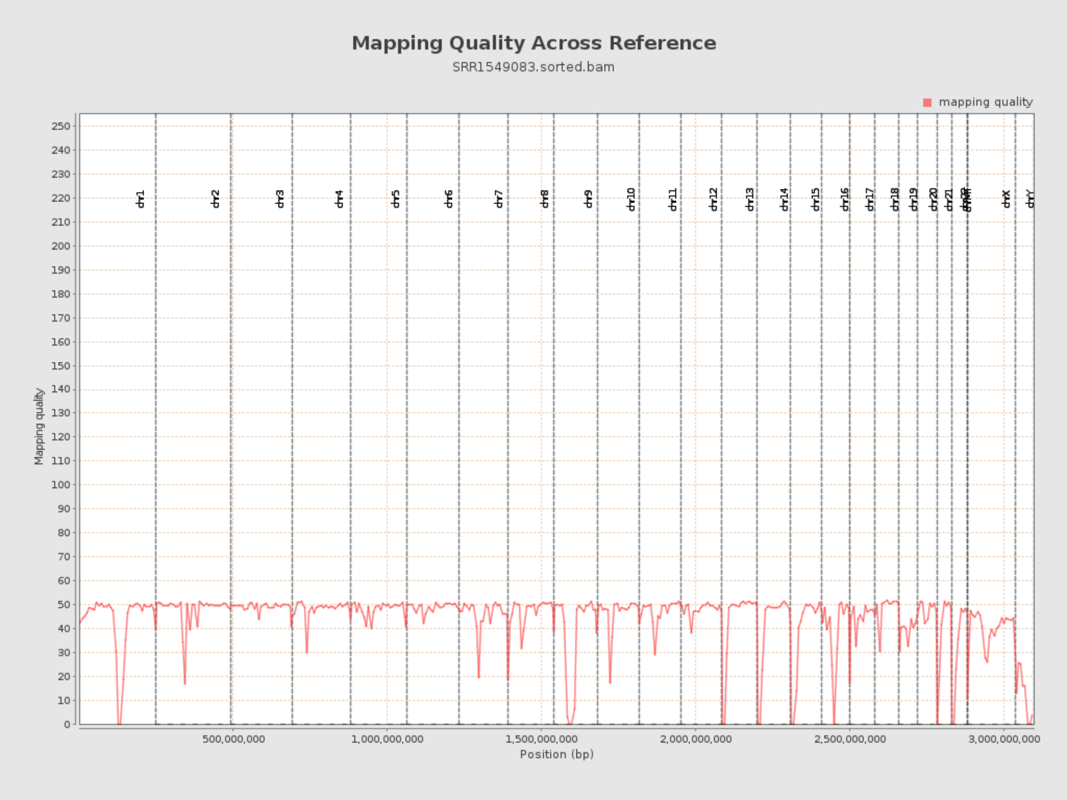
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram