Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 01:12:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548965.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_SRR1548965 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548965.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 01:12:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548965.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,772,065
Mapped reads	4,982,951 / 86.33%
Unmapped reads	789,114 / 13.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	282,586 / 4.9%
Duplication rate	2.95%
Clipped reads	455,654 / 7.89%

2.2. ACGT Content

Number/percentage of A's	55,828,367 / 28.39%
Number/percentage of C's	42,091,112 / 21.4%
Number/percentage of T's	56,927,362 / 28.95%
Number/percentage of G's	41,808,682 / 21.26%
Number/percentage of N's	257 / 0%
GC Percentage	42.66%

2.3. Coverage

Mean	0.0635
Standard Deviation	0.8965

2.4. Mapping Quality

Mean Mapping Quality	34.44

2.5. Mismatches and indels

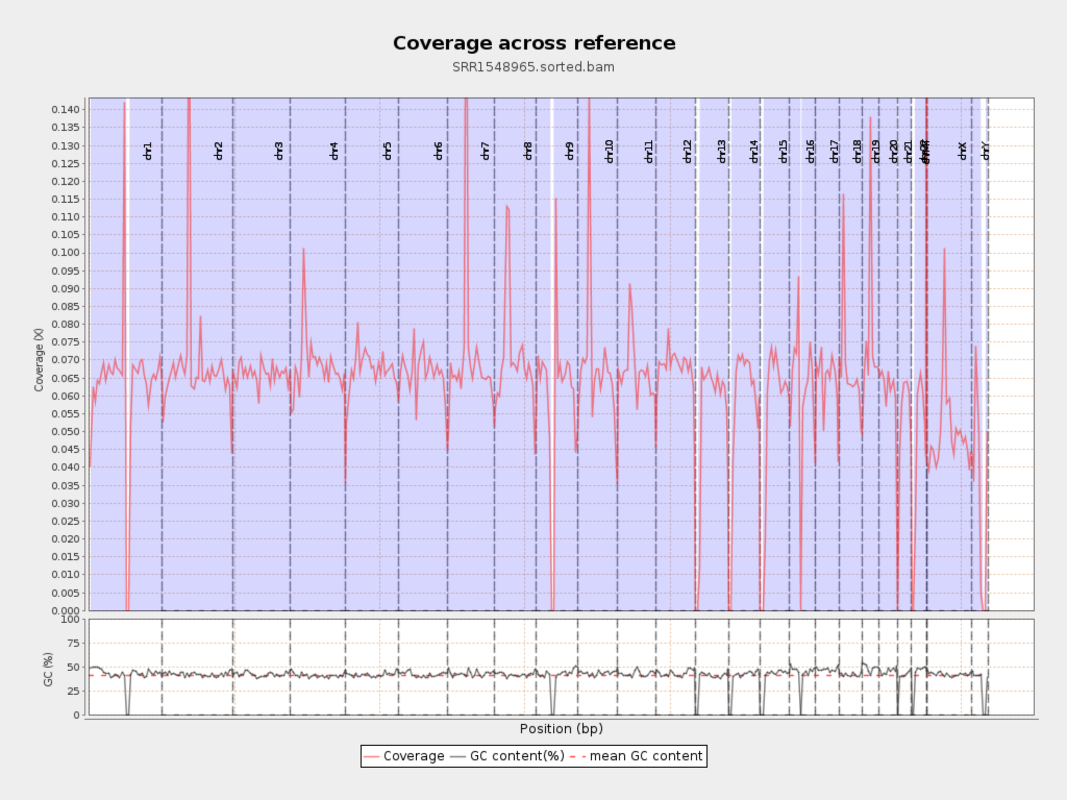
General error rate	0.37%
Mismatches	723,583
Insertions	7,336
Mapped reads with at least one insertion	0.15%
Deletions	15,928
Mapped reads with at least one deletion	0.32%
Homopolymer indels	38.69%

2.6. Chromosome stats

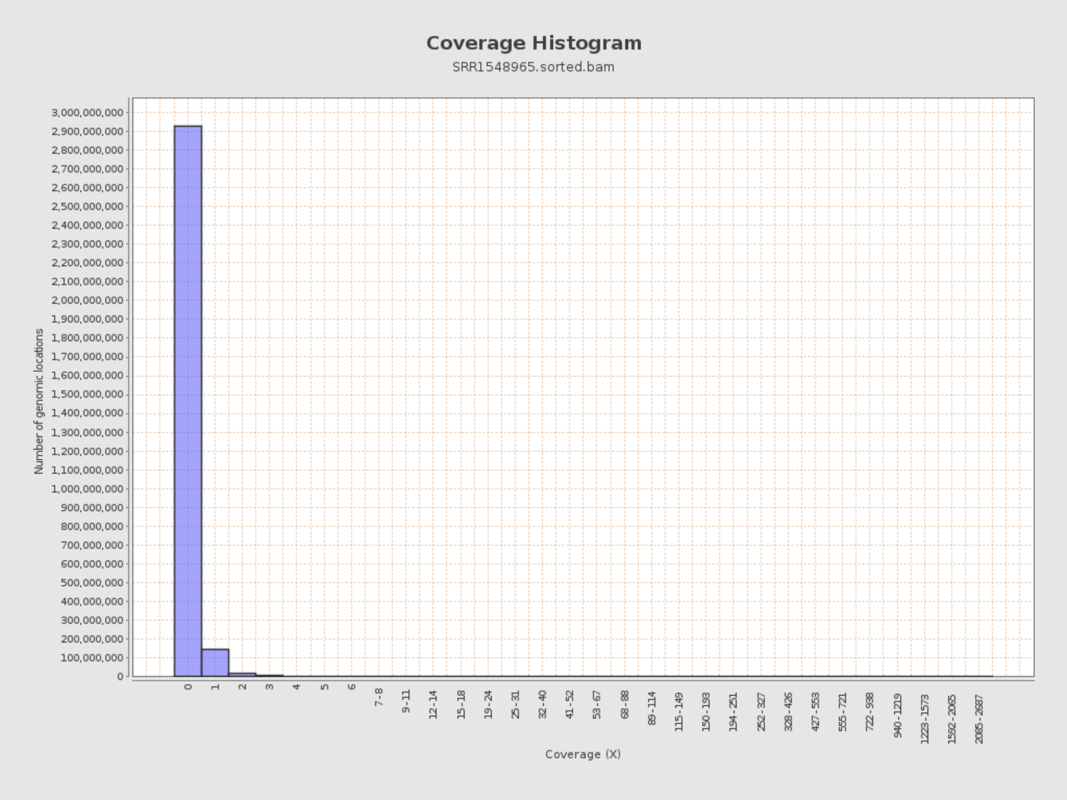
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15717226	0.0631	1.6645
chr2	243199373	16923923	0.0696	0.9444
chr3	198022430	13116210	0.0662	0.3053
chr4	191154276	13053885	0.0683	0.3407
chr5	180915260	12202775	0.0675	0.3375
chr6	171115067	11373687	0.0665	0.3473
chr7	159138663	11633081	0.0731	1.3913
chr8	146364022	10296461	0.0703	1.3869

chr9	141213431	8436400	0.0597	0.9233
chr10	135534747	9350505	0.069	0.7096
chr11	135006516	9007798	0.0667	0.6061
chr12	133851895	9141341	0.0683	0.3682
chr13	115169878	6095391	0.0529	0.2555
chr14	107349540	5986666	0.0558	0.4587
chr15	102531392	5448668	0.0531	0.2712
chr16	90354753	5536476	0.0613	0.4647
chr17	81195210	5212917	0.0642	0.3262
chr18	78077248	5362754	0.0687	2.0686
chr19	59128983	4561014	0.0771	1.7214
chr20	63025520	3886147	0.0617	0.3514
chr21	48129895	2480947	0.0515	0.4361
chr22	51304566	2132395	0.0416	0.2904
chrMT	16571	6403	0.3864	0.7779
chrX	155270560	7827066	0.0504	0.5687
chrY	59373566	1885904	0.0318	0.3184

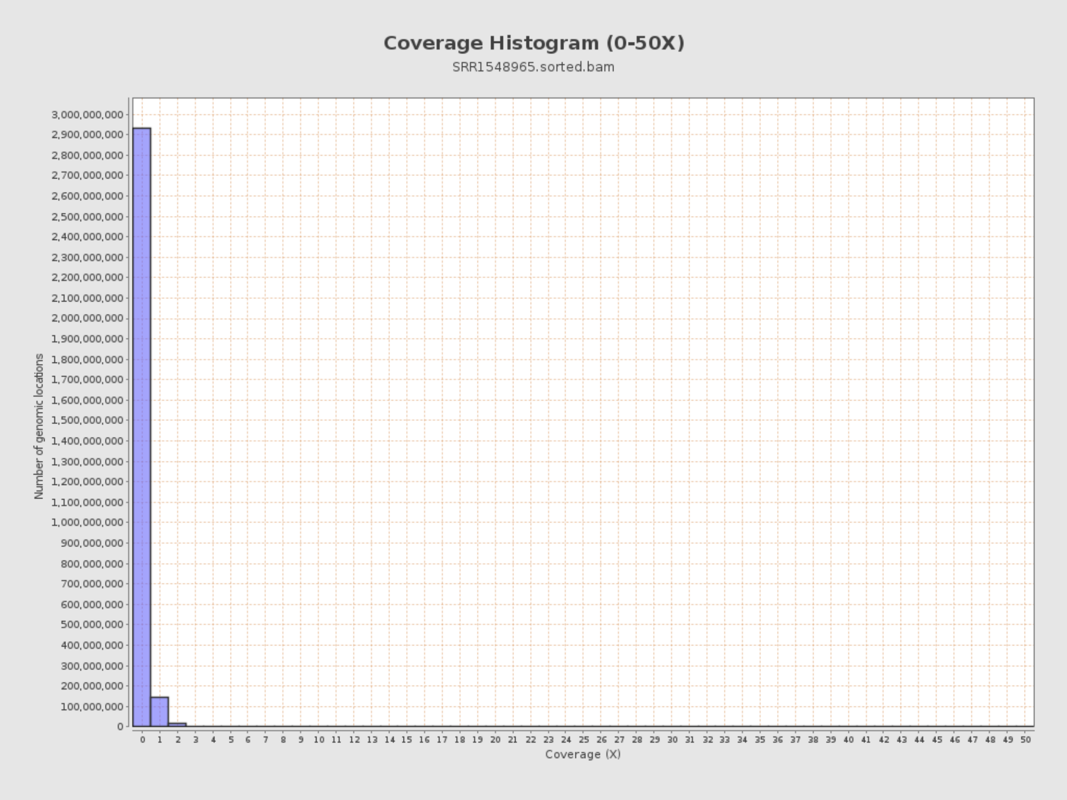
3. Results : Coverage across reference



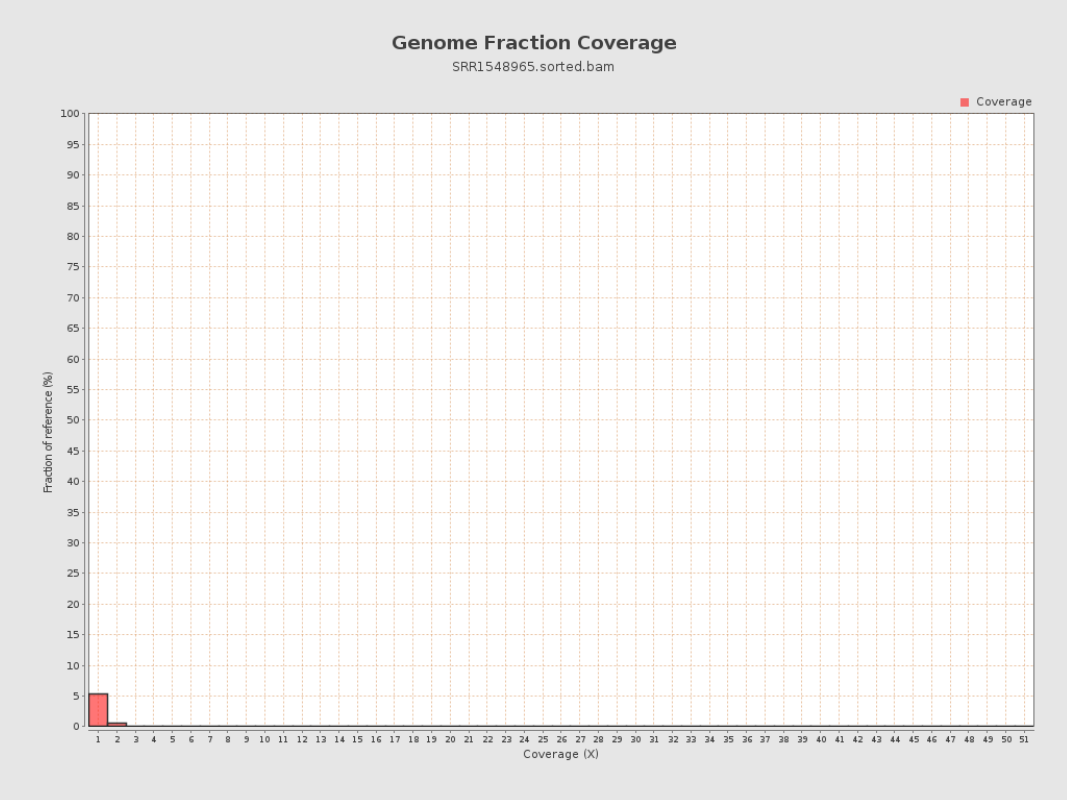
4. Results : Coverage Histogram



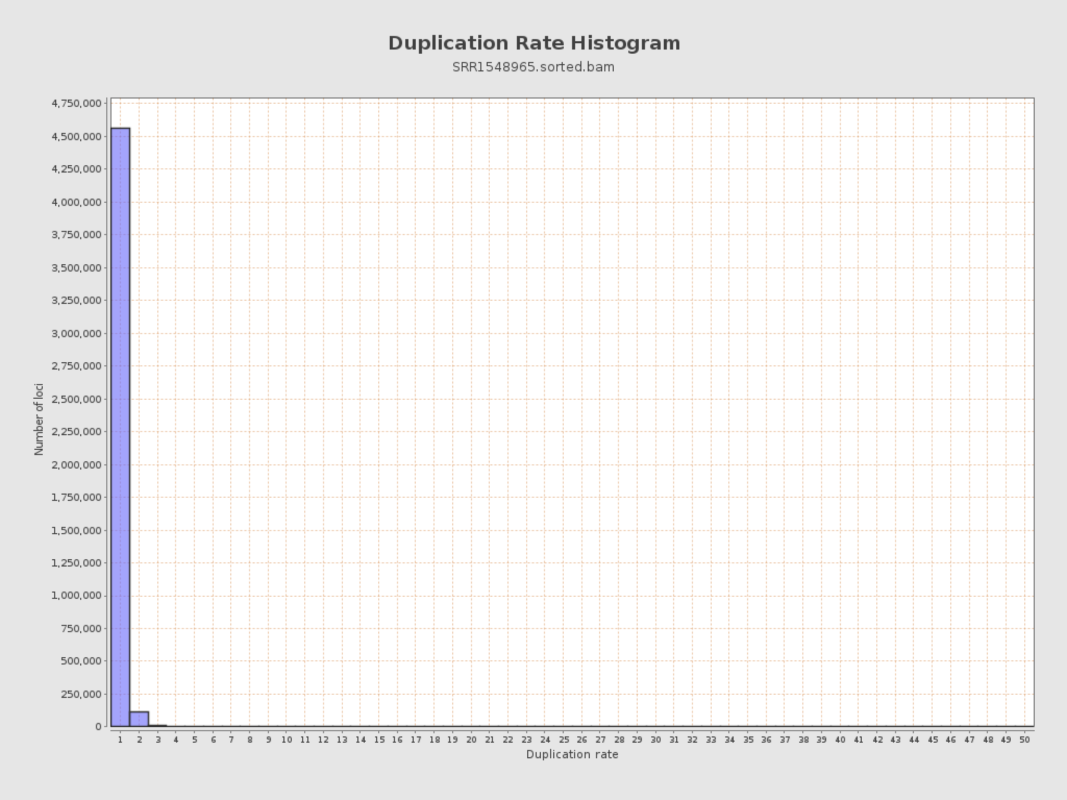
5. Results : Coverage Histogram (0-50X)



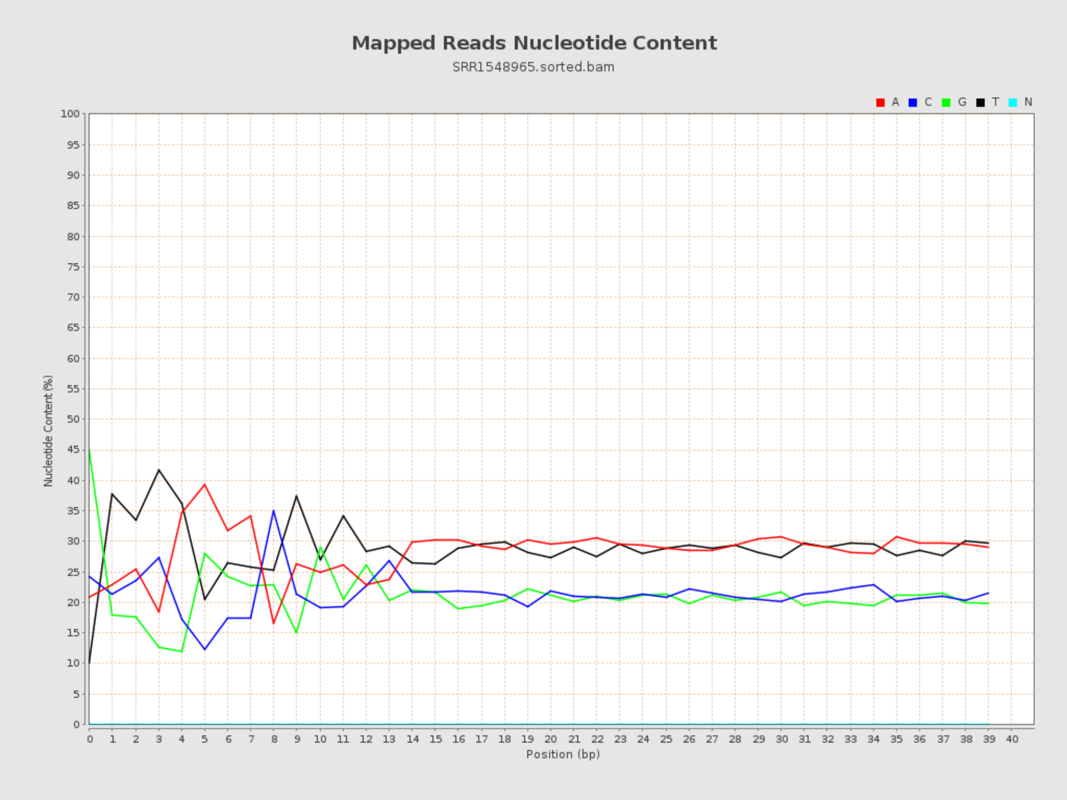
6. Results : Genome Fraction Coverage



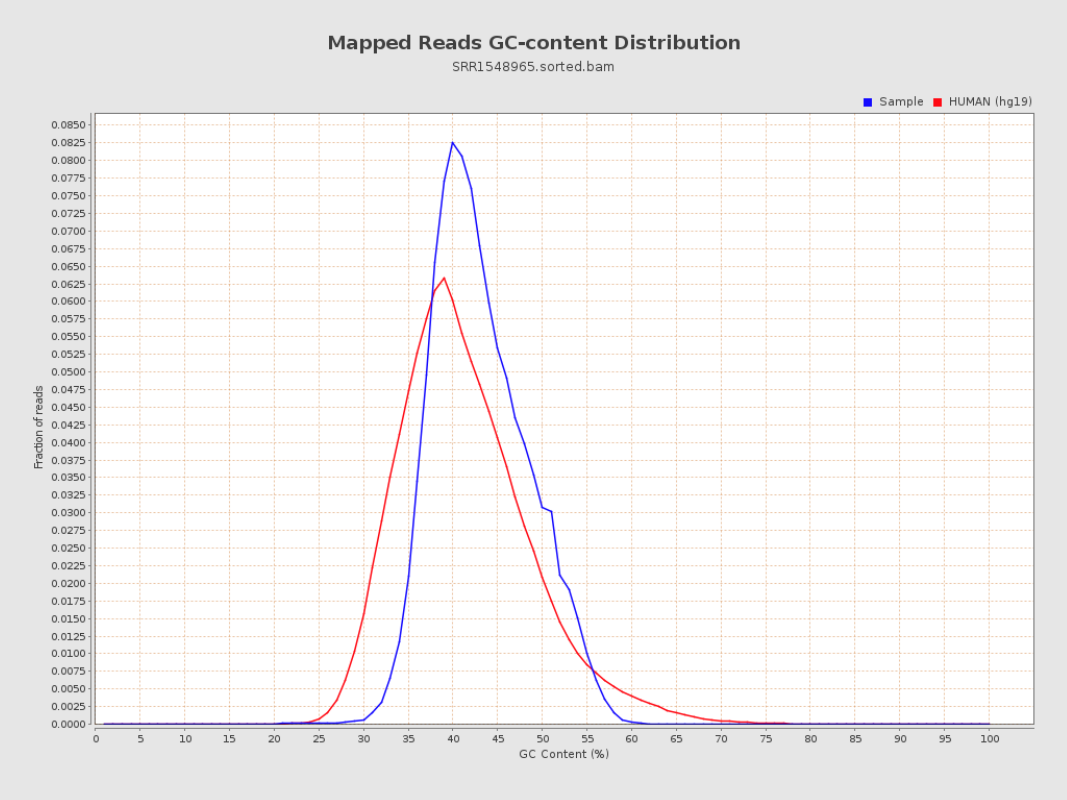
7. Results : Duplication Rate Histogram



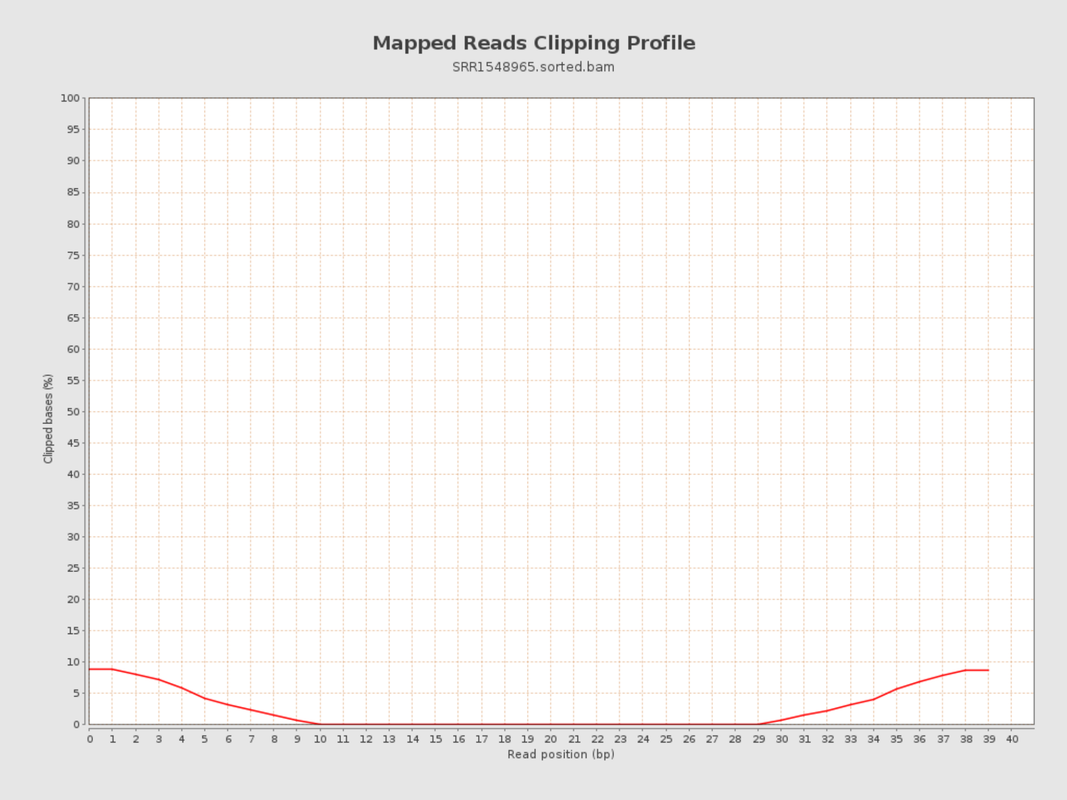
8. Results : Mapped Reads Nucleotide Content



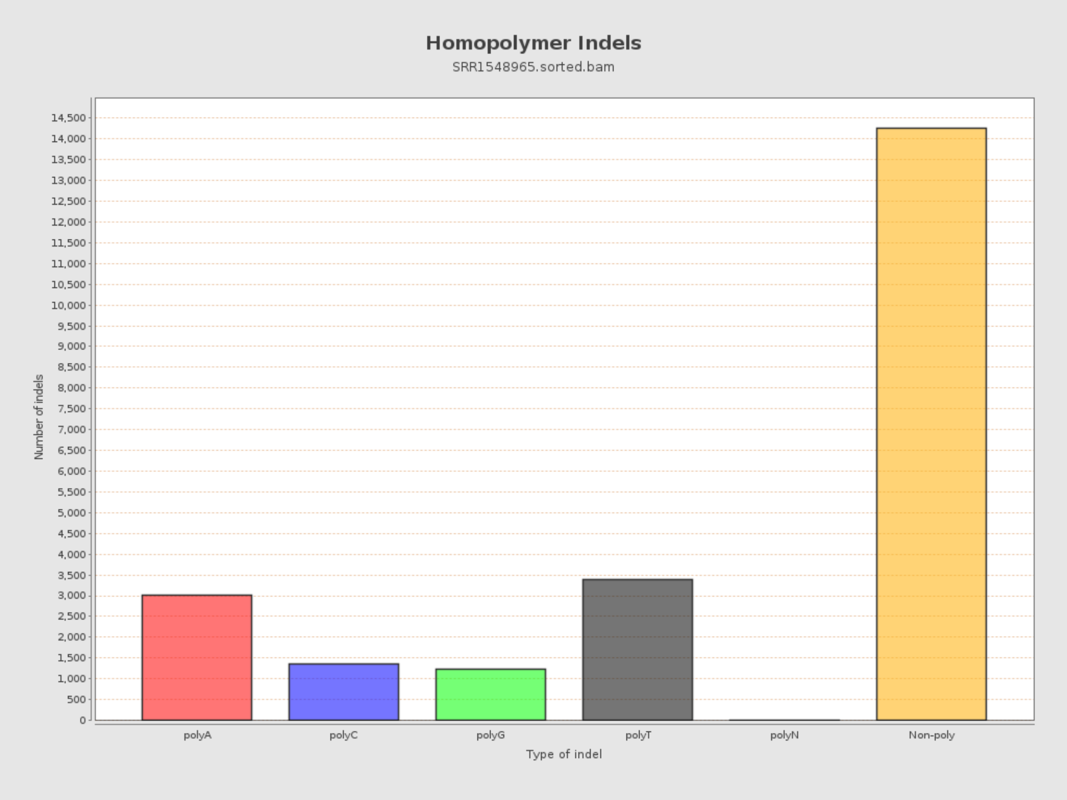
9. Results : Mapped Reads GC-content Distribution



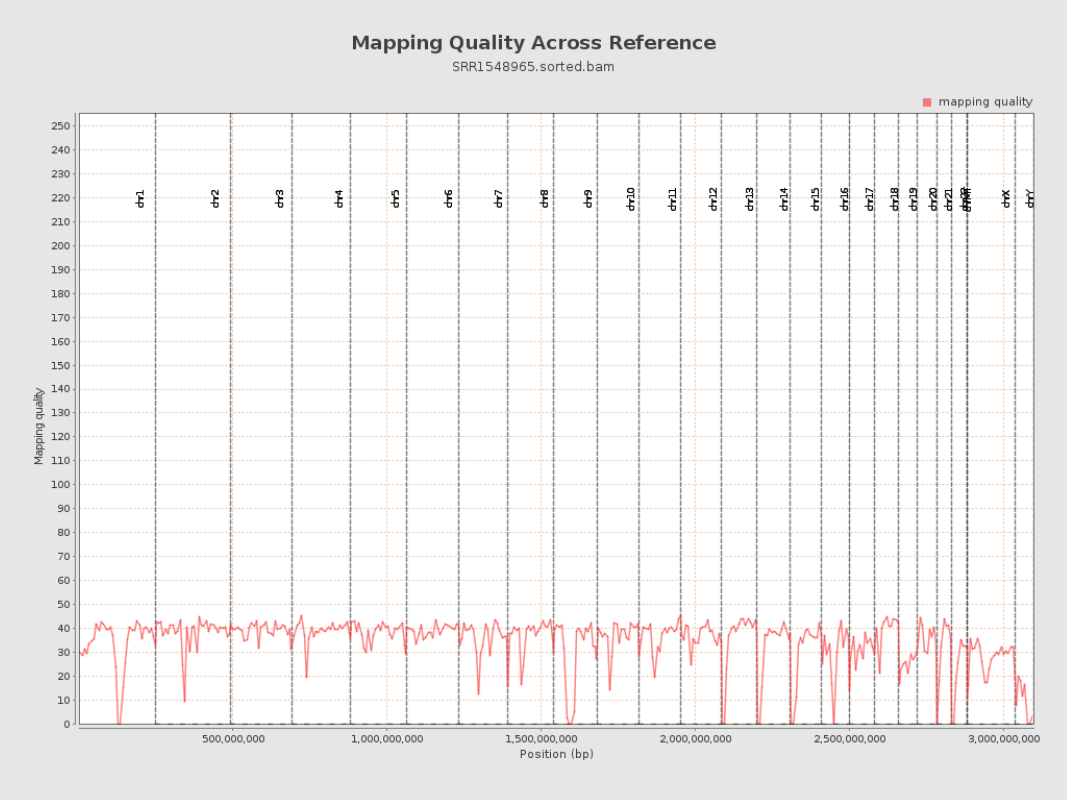
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram