Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 07:43:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068065.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_SRR6068065 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068065.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 07:43:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068065.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,441,964
Mapped reads	3,228,609 / 93.8%
Unmapped reads	213,355 / 6.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,493 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	469,571 / 13.64%
Duplication rate	11.96%
Clipped reads	1,725,712 / 50.14%

2.2. ACGT Content

Number/percentage of A's	54,433,187 / 26.27%
Number/percentage of C's	36,566,574 / 17.65%
Number/percentage of T's	68,447,425 / 33.04%
Number/percentage of G's	47,716,062 / 23.03%
Number/percentage of N's	23,629 / 0.01%
GC Percentage	40.68%

2.3. Coverage

Mean	0.067

Standard Deviation	0.8277

2.4. Mapping Quality

Mean Mapping Quality	45.34

2.5. Mismatches and indels

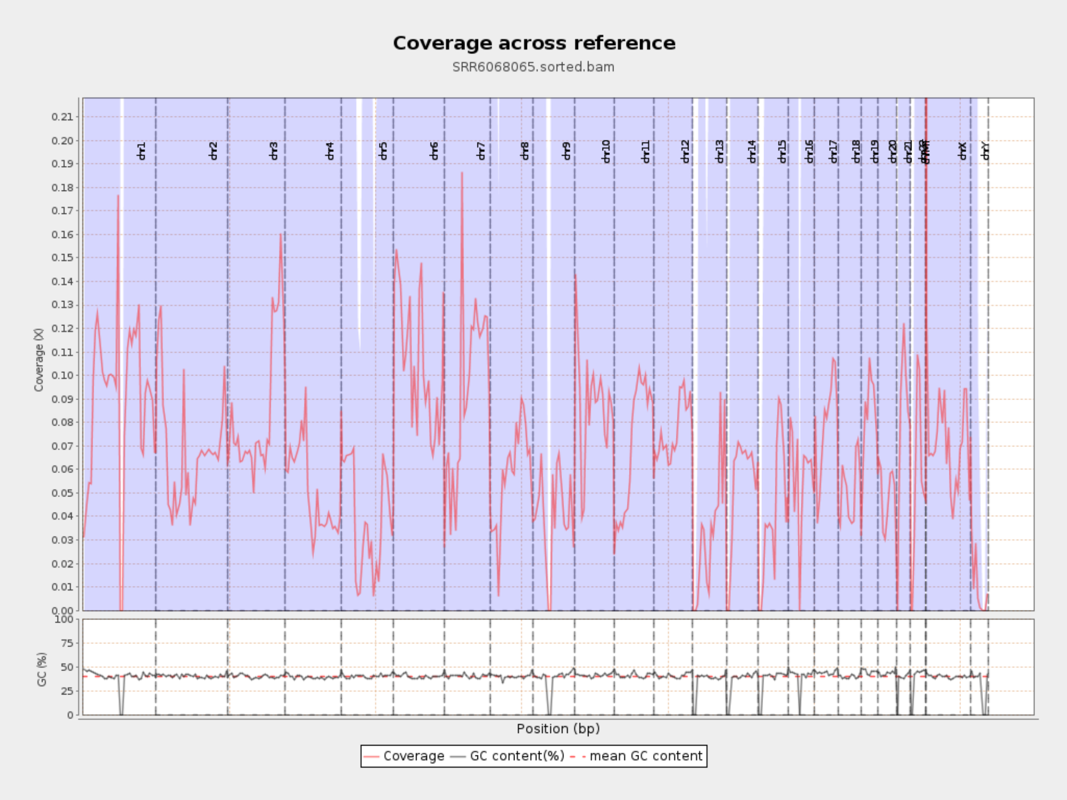
General error rate	0.55%
Mismatches	1,120,335
Insertions	13,241
Mapped reads with at least one insertion	0.41%
Deletions	45,530
Mapped reads with at least one deletion	1.4%
Homopolymer indels	44.93%

2.6. Chromosome stats

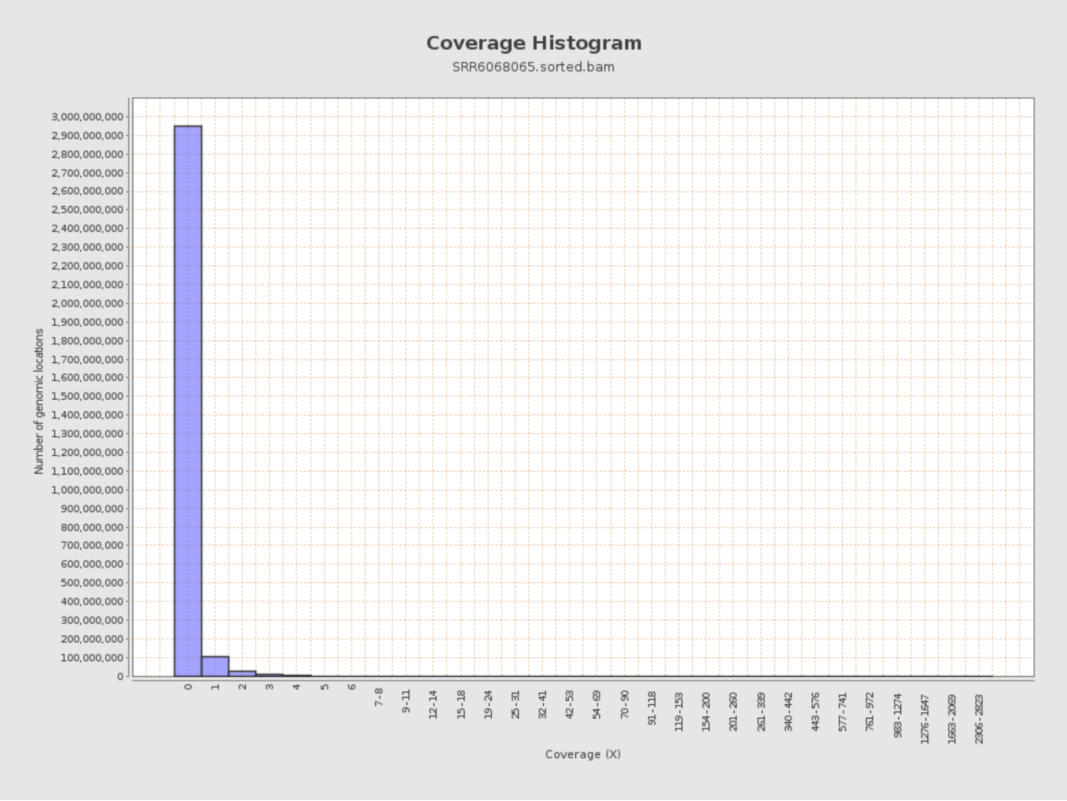
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22321924	0.0896	1.734
chr2	243199373	16501730	0.0679	1.3201
chr3	198022430	16576497	0.0837	0.394
chr4	191154276	9691998	0.0507	0.3261
chr5	180915260	7125213	0.0394	0.2745
chr6	171115067	18198896	0.1064	0.6212
chr7	159138663	14915867	0.0937	1.3454

chr8	146364022	8476563	0.0579	1.0091
chr9	141213431	5759042	0.0408	0.4685
chr10	135534747	11998403	0.0885	0.5424
chr11	135006516	9487777	0.0703	0.452
chr12	133851895	10263665	0.0767	0.3879
chr13	115169878	3939060	0.0342	0.309
chr14	107349540	5825669	0.0543	0.3465
chr15	102531392	4178013	0.0407	0.3162
chr16	90354753	5034915	0.0557	0.341
chr17	81195210	6463670	0.0796	0.3997
chr18	78077248	4027164	0.0516	1.0206
chr19	59128983	4931476	0.0834	1.078
chr20	63025520	3081129	0.0489	0.3068
chr21	48129895	3782762	0.0786	0.3883
chr22	51304566	2780064	0.0542	0.3062
chrMT	16571	231857	13.9917	8.4691
chrX	155270560	11094231	0.0715	0.4046
chrY	59373566	577852	0.0097	0.2605

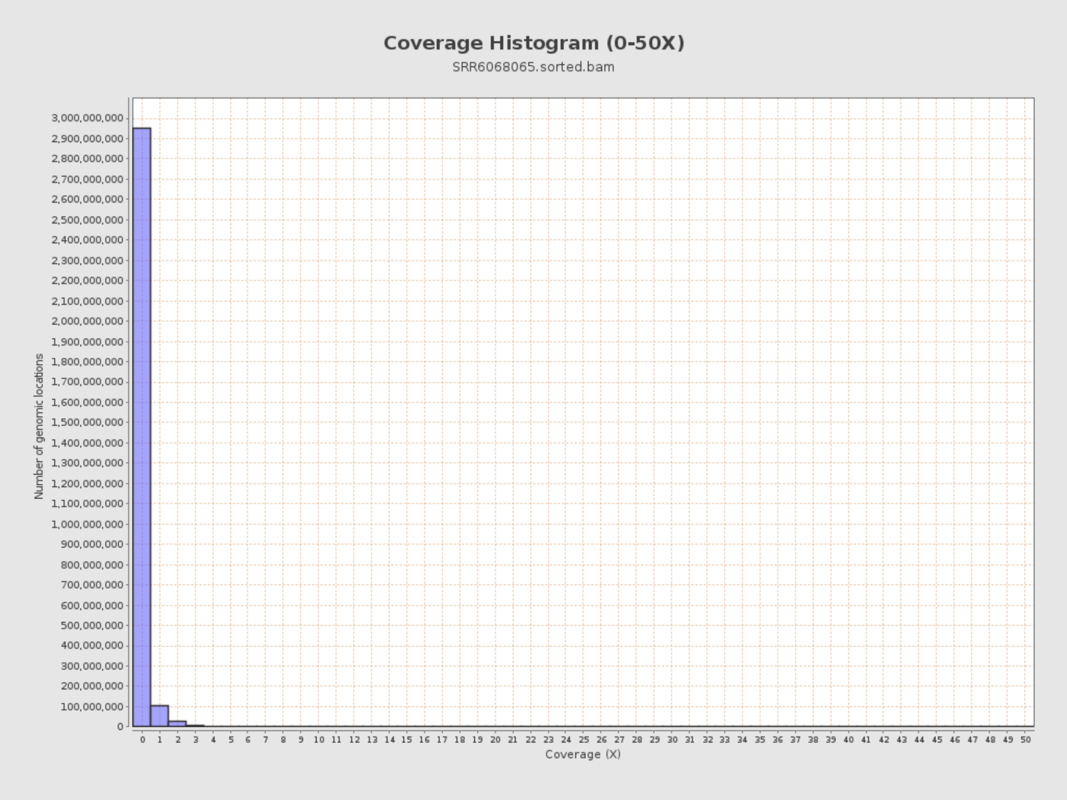
3. Results : Coverage across reference



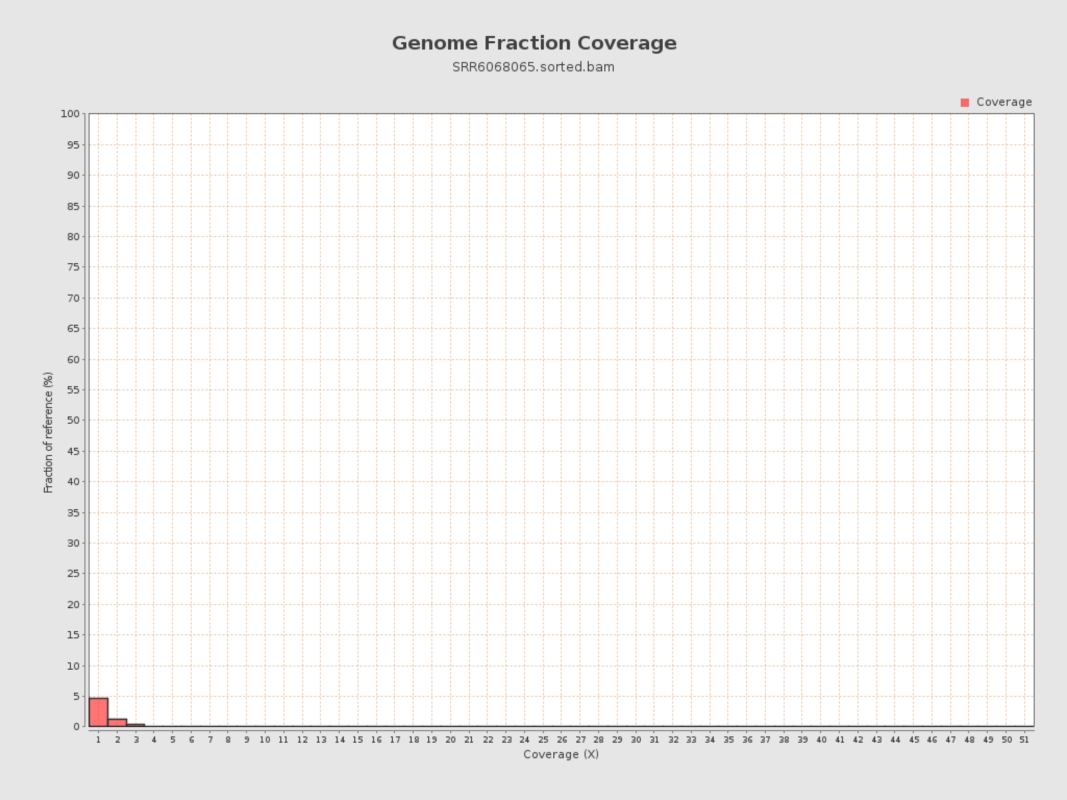
4. Results : Coverage Histogram



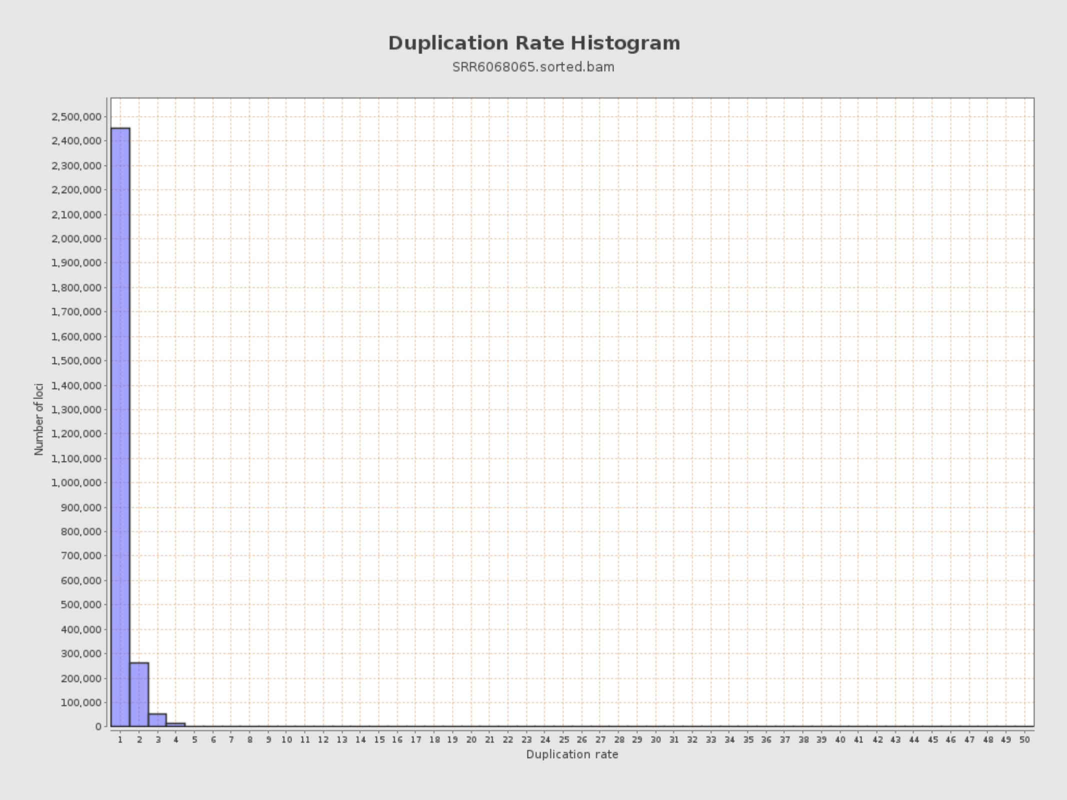
5. Results : Coverage Histogram (0-50X)



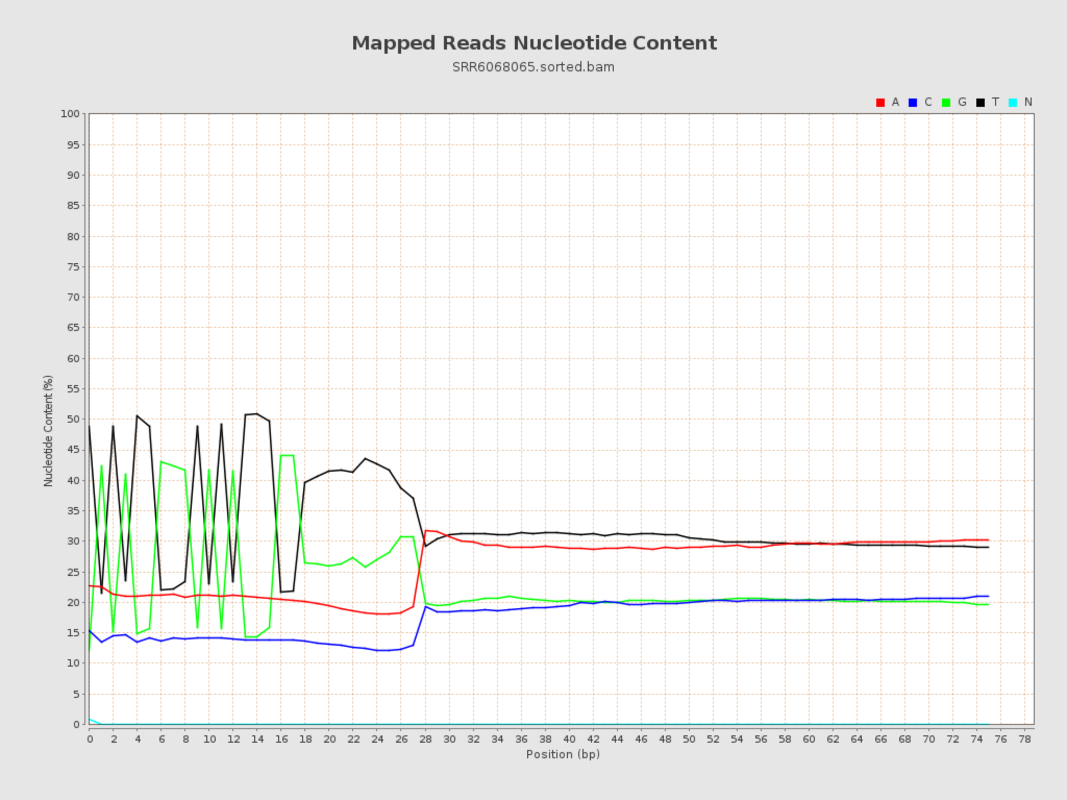
6. Results : Genome Fraction Coverage



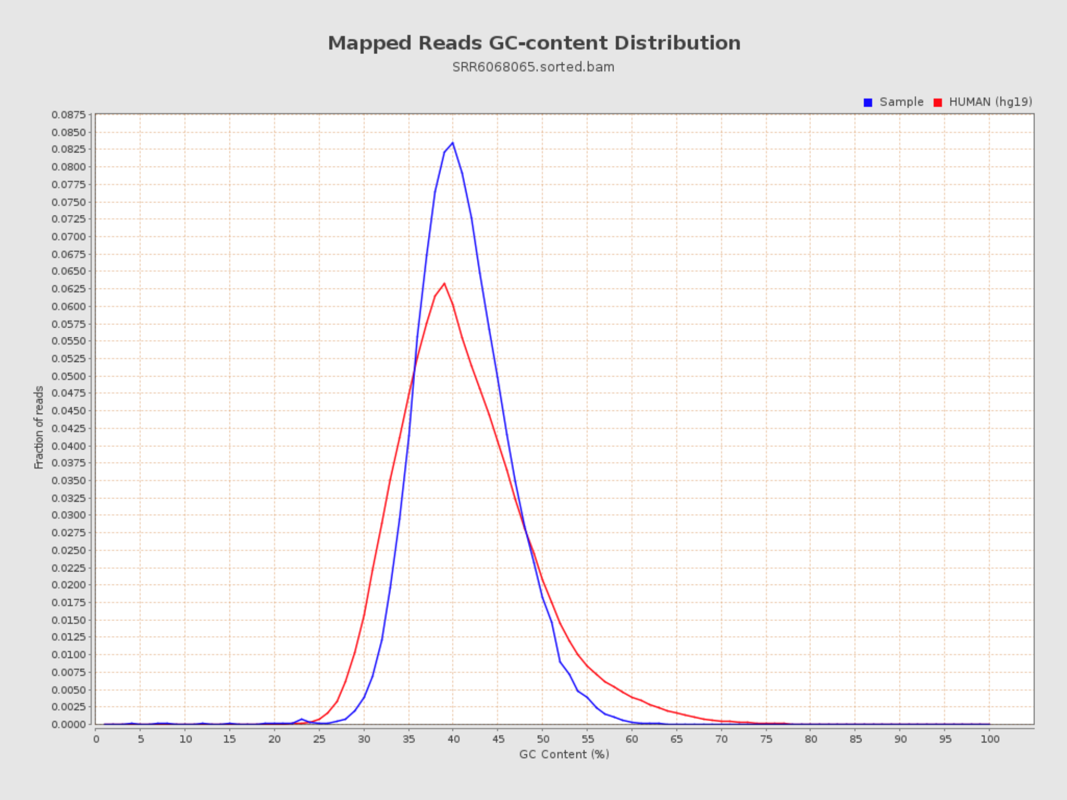
7. Results : Duplication Rate Histogram



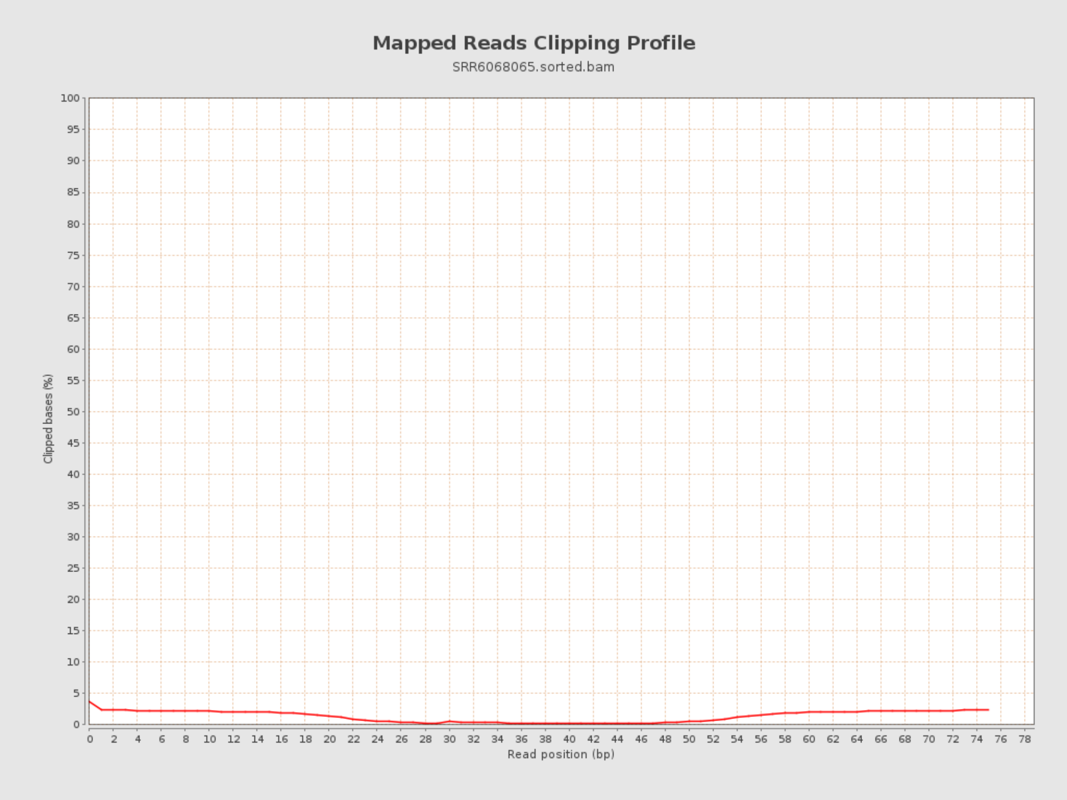
8. Results : Mapped Reads Nucleotide Content



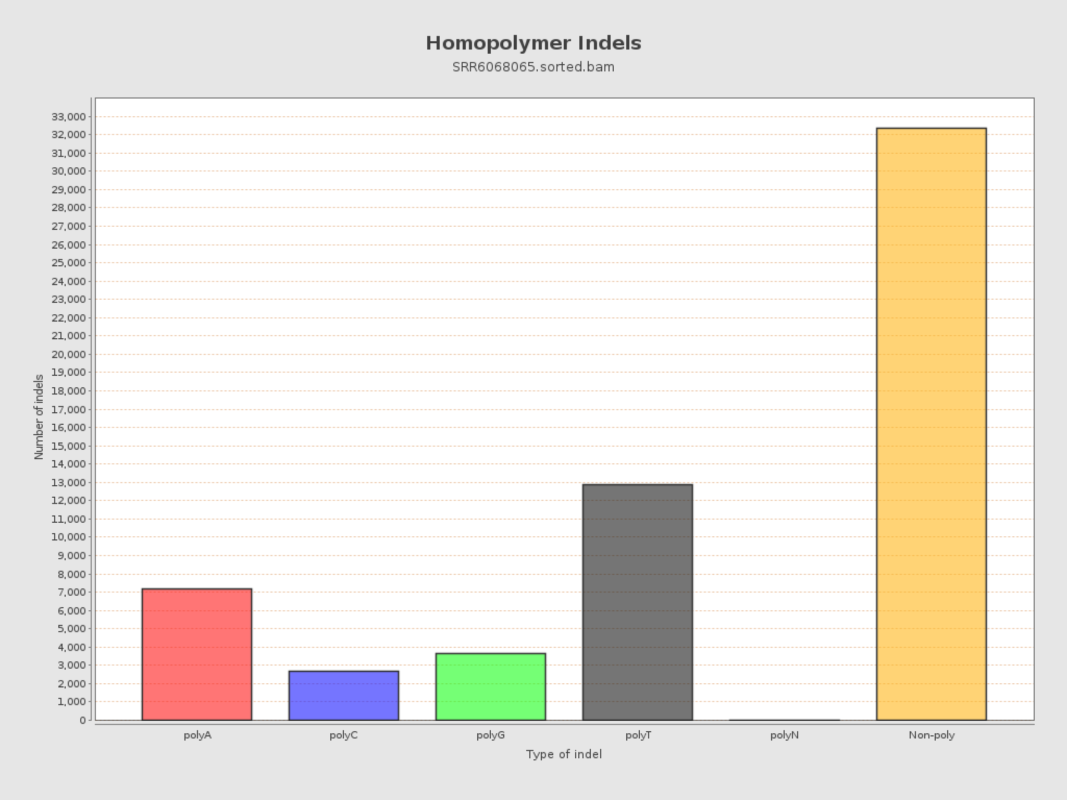
9. Results : Mapped Reads GC-content Distribution



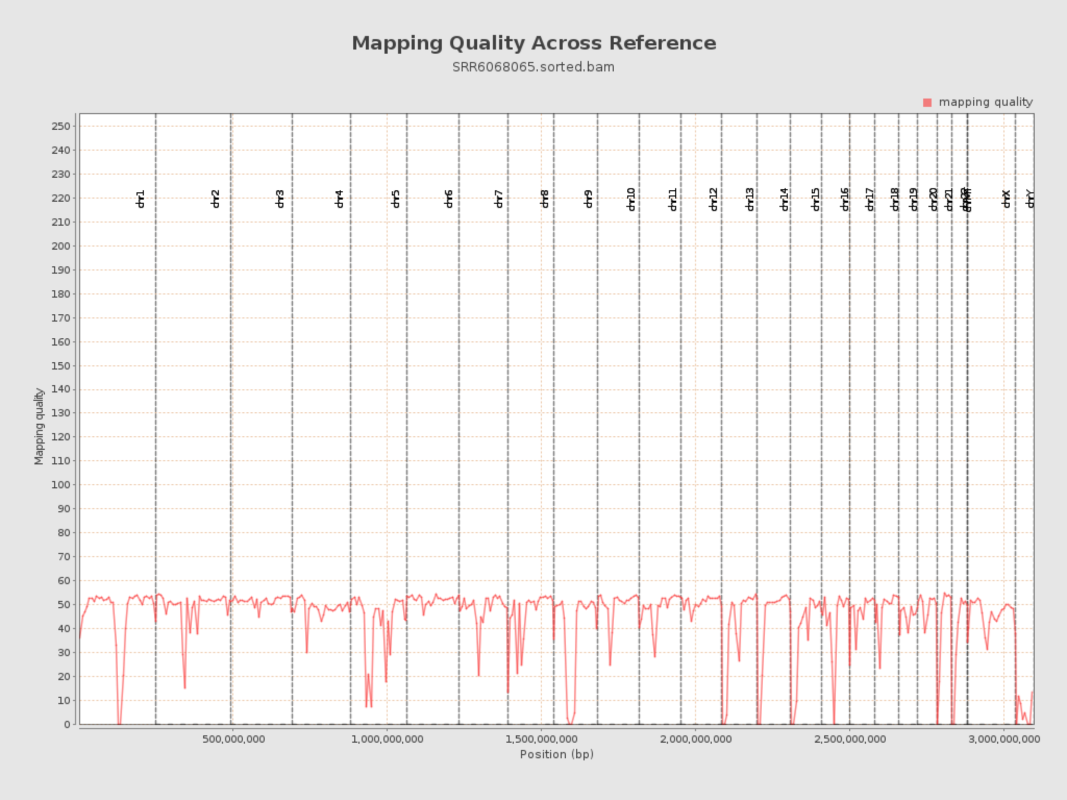
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram