Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 06:25:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063597.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_SRR6063597 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063597.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 06:25:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063597.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,710,194
Mapped reads	893,703 / 52.26%
Unmapped reads	816,491 / 47.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,439 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	161,366 / 9.44%
Duplication rate	12.33%
Clipped reads	484,807 / 28.35%

2.2. ACGT Content

Number/percentage of A's	16,025,602 / 27.94%
Number/percentage of C's	10,660,311 / 18.59%
Number/percentage of T's	18,096,429 / 31.55%
Number/percentage of G's	12,566,831 / 21.91%
Number/percentage of N's	1,338 / 0%
GC Percentage	40.5%

2.3. Coverage

Mean	0.0185

Standard Deviation	0.3669

2.4. Mapping Quality

Mean Mapping Quality	45.64

2.5. Mismatches and indels

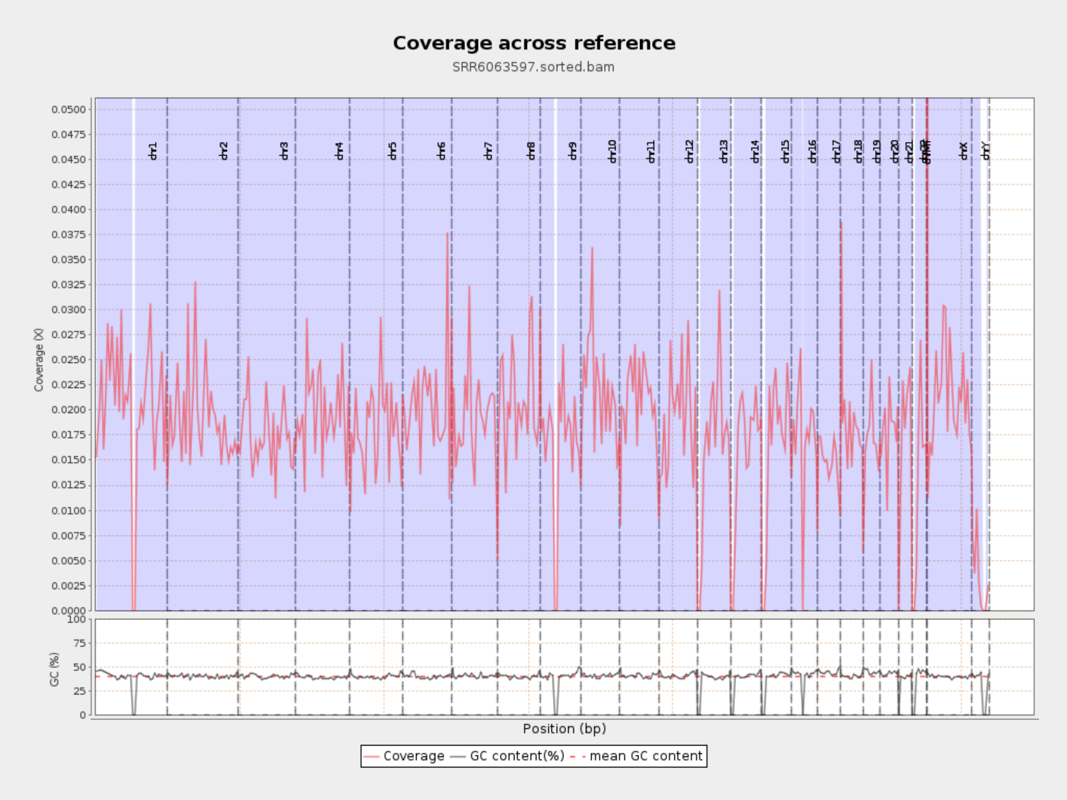
General error rate	0.82%
Mismatches	464,574
Insertions	4,619
Mapped reads with at least one insertion	0.51%
Deletions	13,977
Mapped reads with at least one deletion	1.55%
Homopolymer indels	46.39%

2.6. Chromosome stats

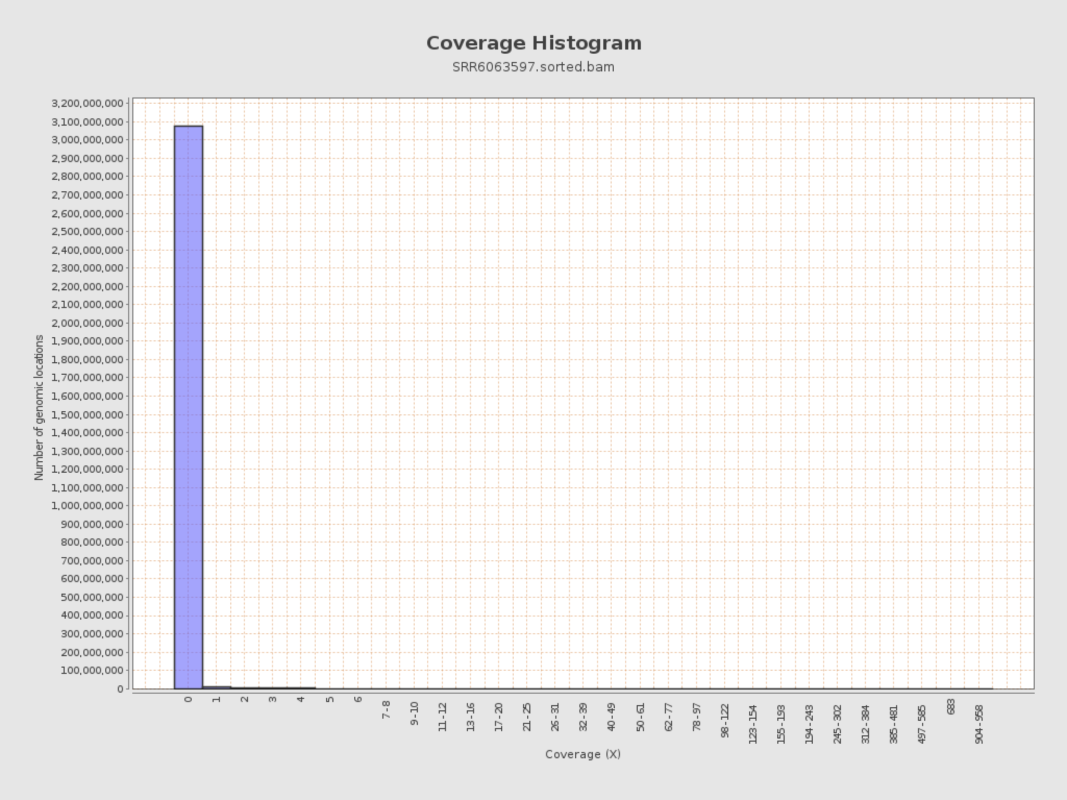
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5101096	0.0205	0.4145
chr2	243199373	4683376	0.0193	0.4175
chr3	198022430	3479383	0.0176	0.297
chr4	191154276	3805034	0.0199	0.5095
chr5	180915260	3329240	0.0184	0.3228
chr6	171115067	3505353	0.0205	0.3662
chr7	159138663	3068340	0.0193	0.3362

chr8	146364022	3081591	0.0211	0.3808
chr9	141213431	2350251	0.0166	0.2978
chr10	135534747	3001824	0.0221	0.3513
chr11	135006516	2848800	0.0211	0.3529
chr12	133851895	2560660	0.0191	0.324
chr13	115169878	1859393	0.0161	0.3209
chr14	107349540	1664538	0.0155	0.3753
chr15	102531392	1661790	0.0162	0.5481
chr16	90354753	1525570	0.0169	0.2909
chr17	81195210	1217911	0.015	0.2636
chr18	78077248	1470523	0.0188	0.3622
chr19	59128983	1013969	0.0171	0.3101
chr20	63025520	1128922	0.0179	0.3208
chr21	48129895	836748	0.0174	0.2986
chr22	51304566	653393	0.0127	0.2479
chrMT	16571	11051	0.6669	1.8214
chrX	155270560	3325396	0.0214	0.3582
chrY	59373566	189026	0.0032	0.1987

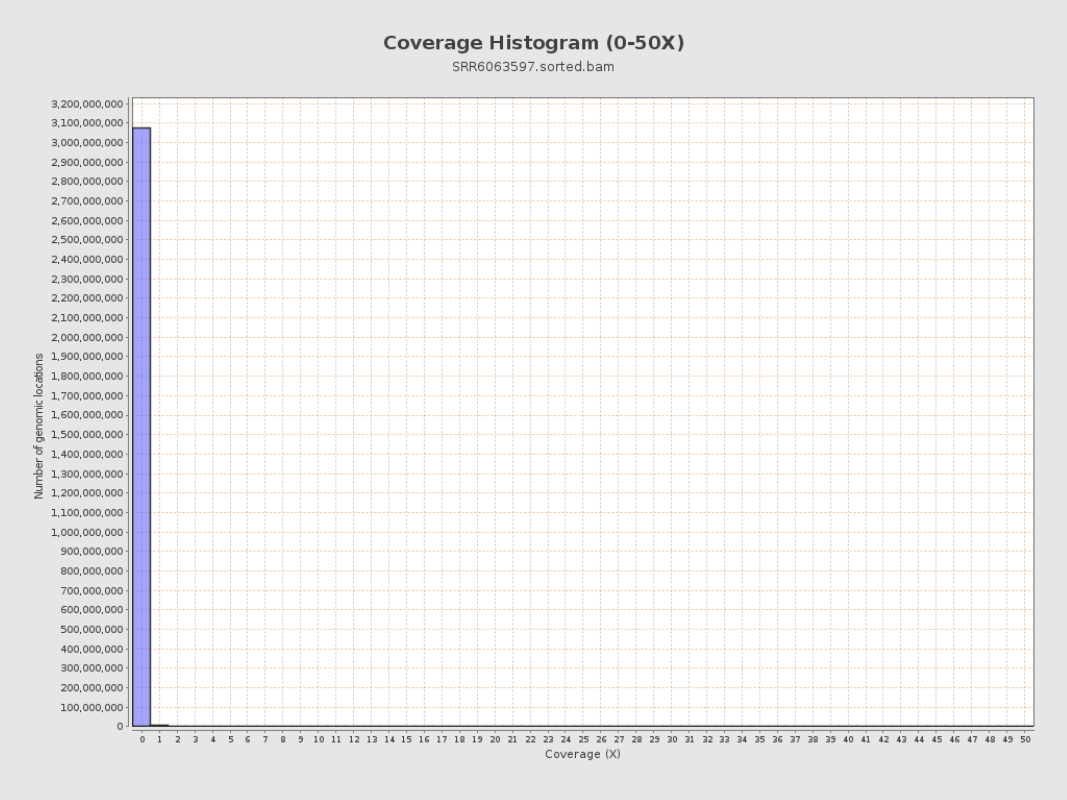
3. Results : Coverage across reference



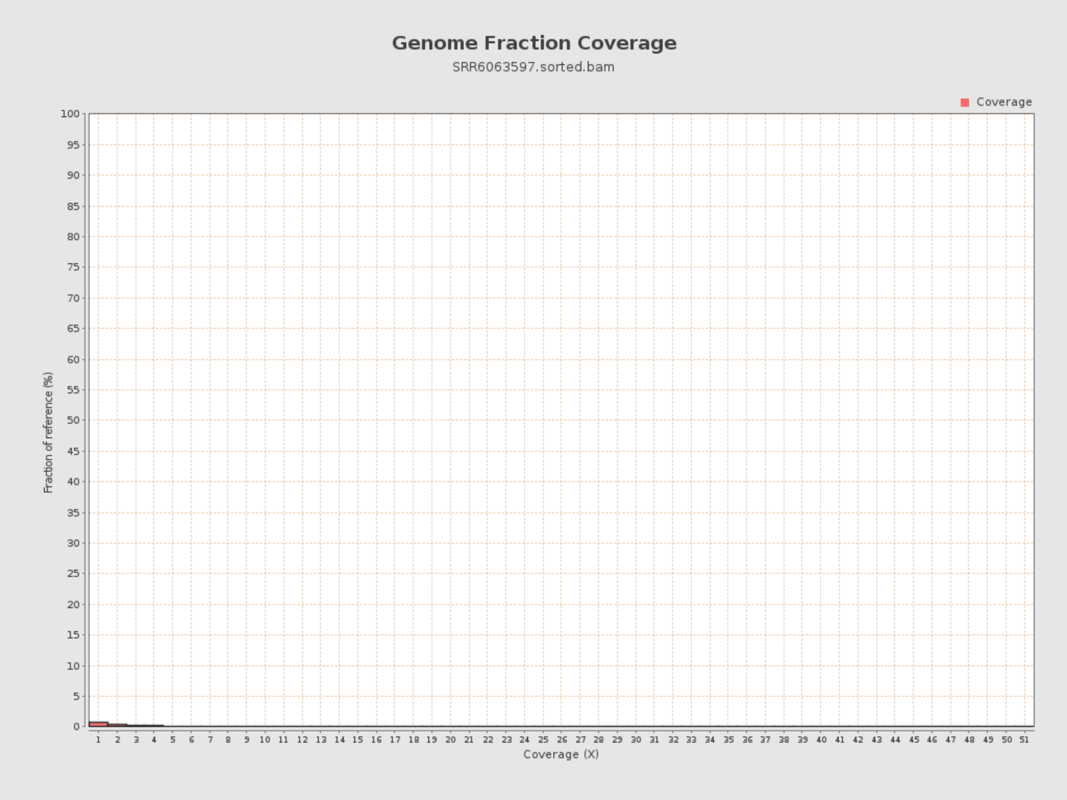
4. Results : Coverage Histogram



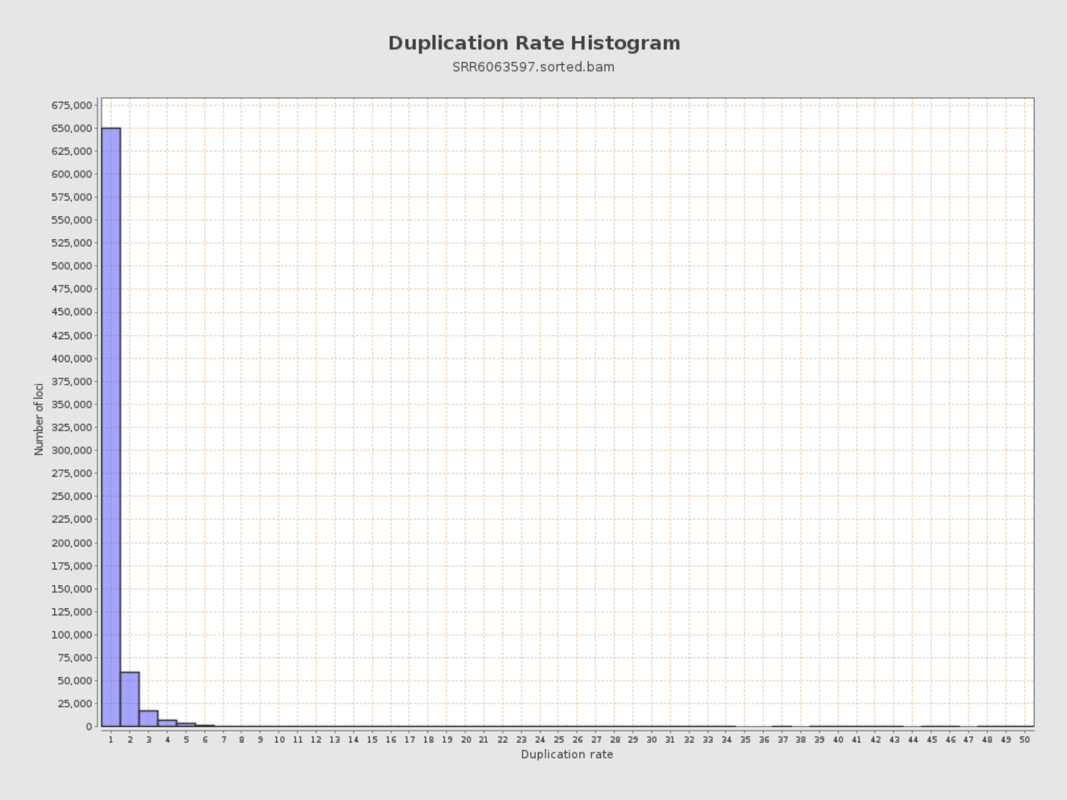
5. Results : Coverage Histogram (0-50X)



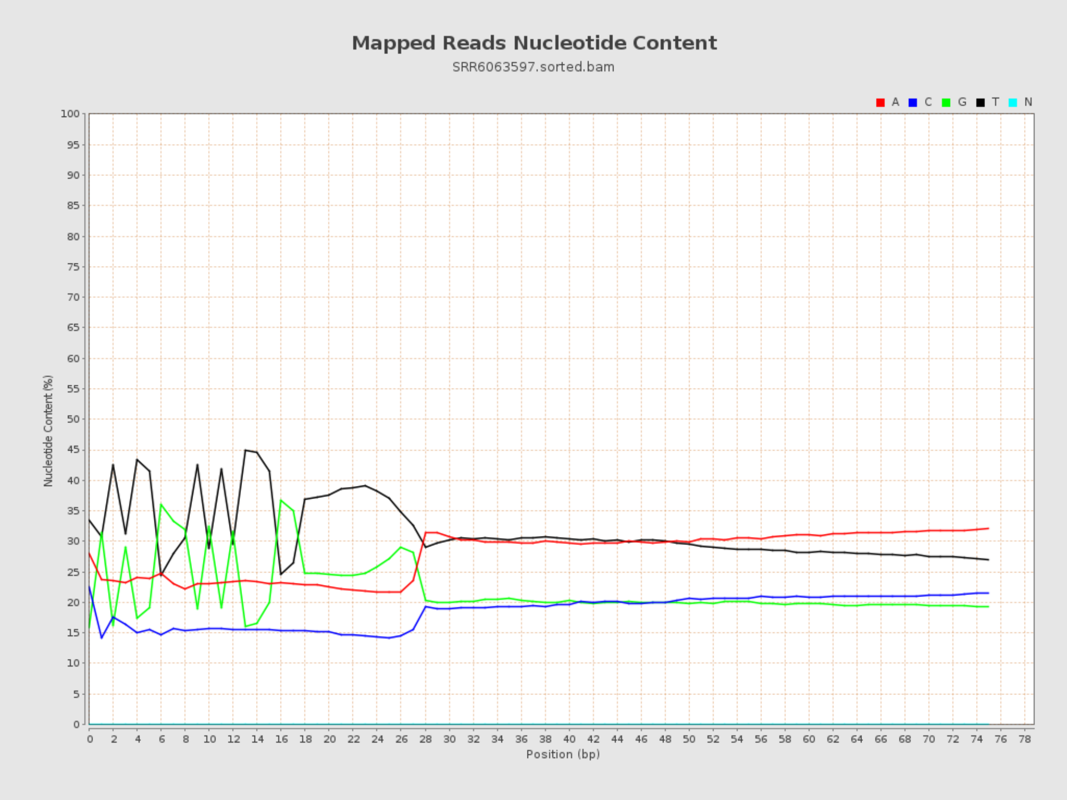
6. Results : Genome Fraction Coverage



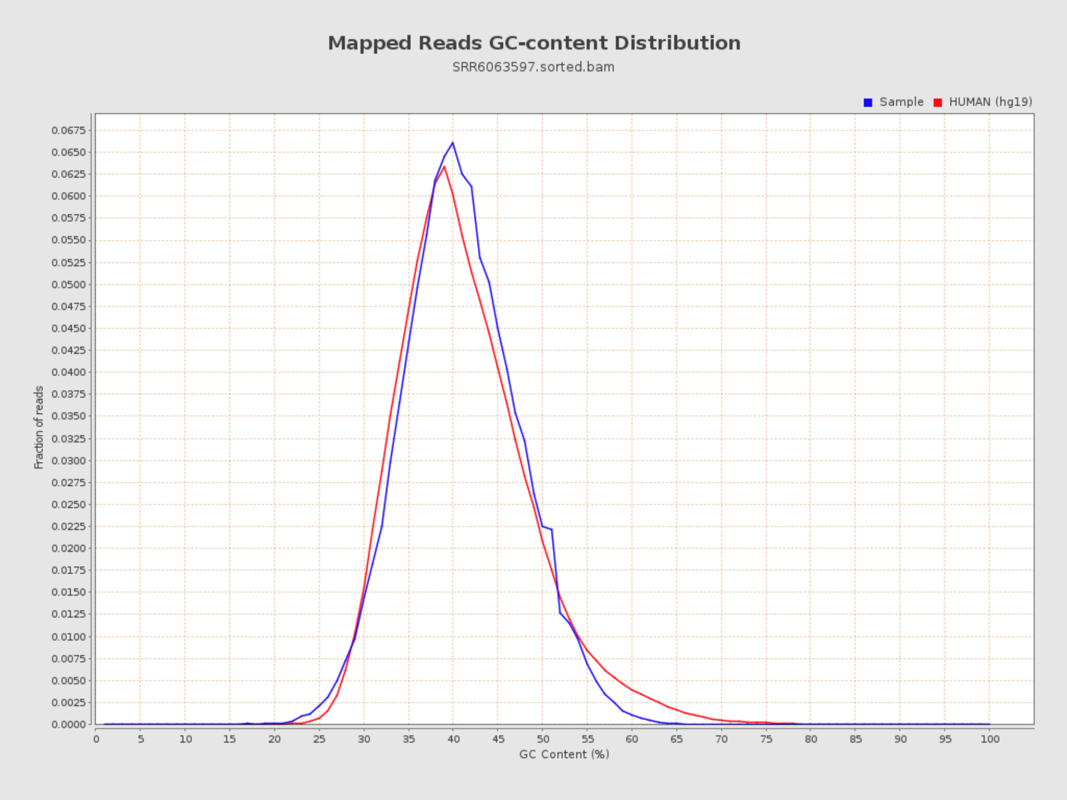
7. Results : Duplication Rate Histogram



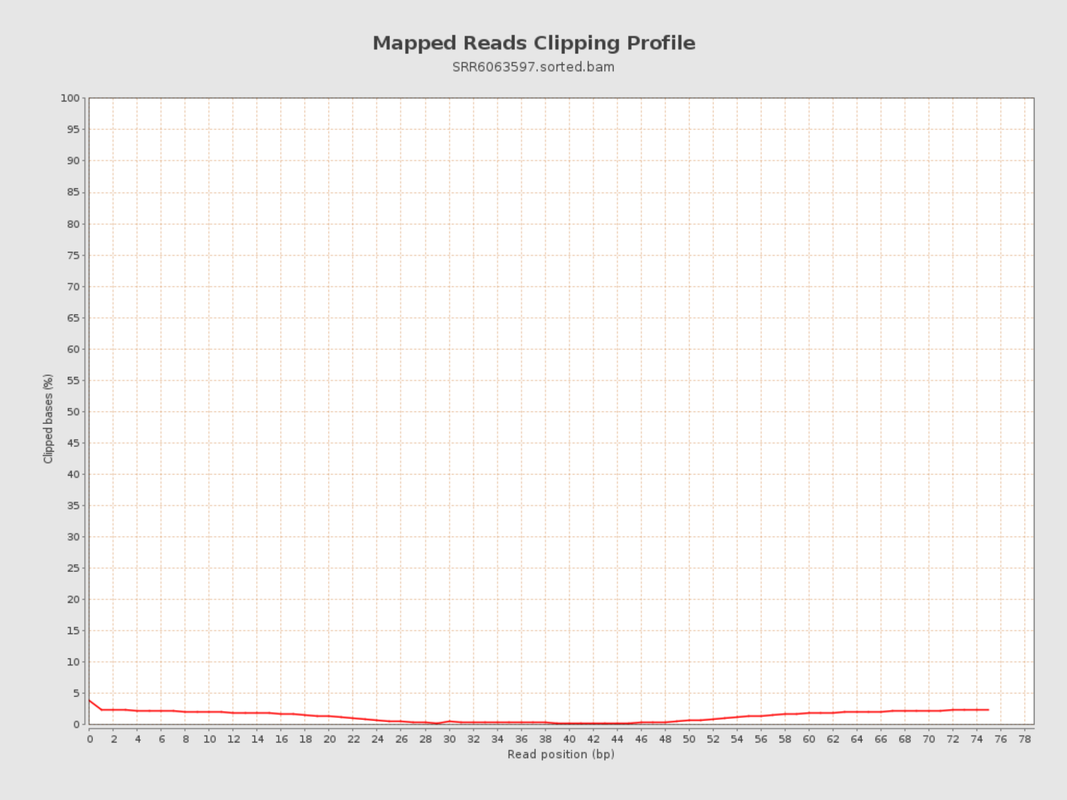
8. Results : Mapped Reads Nucleotide Content



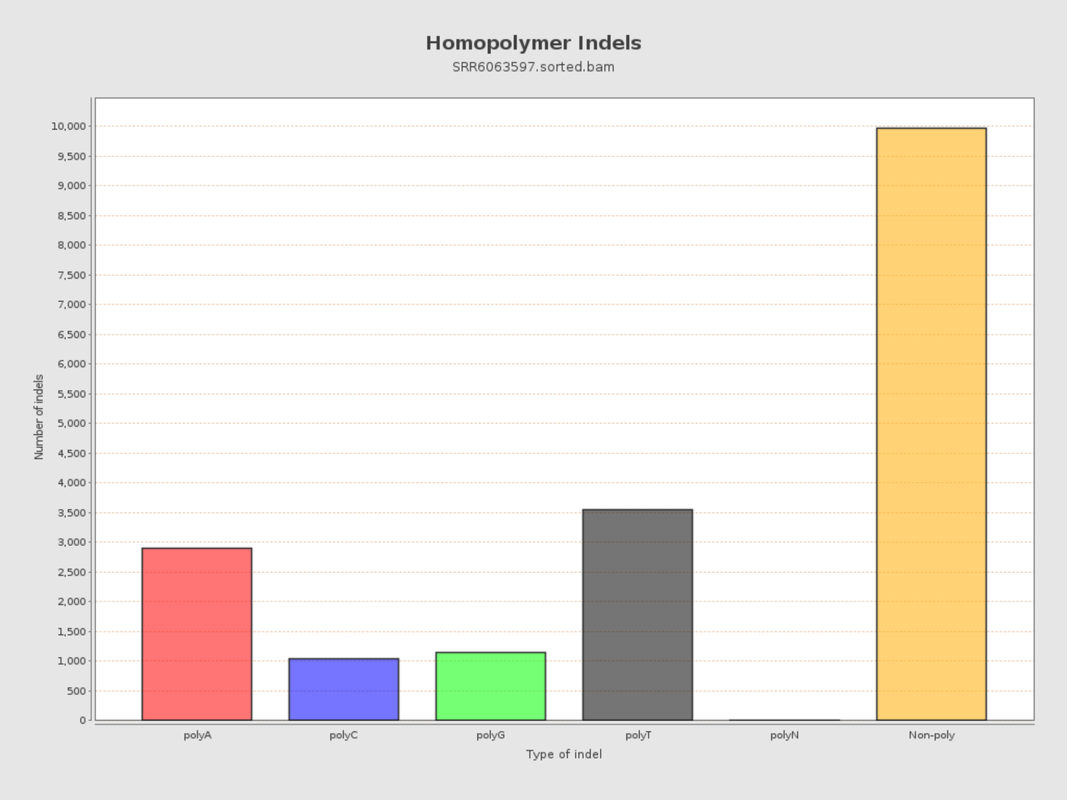
9. Results : Mapped Reads GC-content Distribution



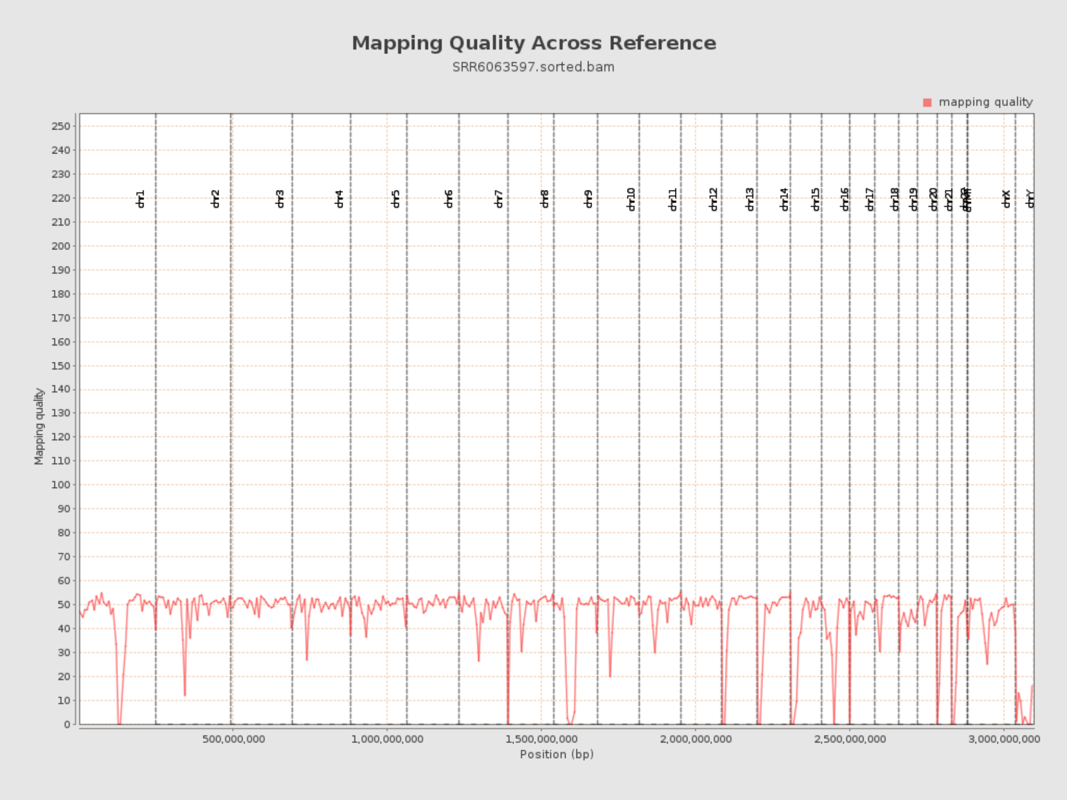
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram