Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 01:07:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063537.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_SRR6063537 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063537.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 01:07:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063537.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,706,434
Mapped reads	4,409,319 / 93.69%
Unmapped reads	297,115 / 6.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	44,614 / 0.95%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	1,331,400 / 28.29%
Duplication rate	17.48%
Clipped reads	2,157,476 / 45.84%

2.2. ACGT Content

Number/percentage of A's	75,413,004 / 26.12%
Number/percentage of C's	52,624,883 / 18.23%
Number/percentage of T's	93,122,026 / 32.25%
Number/percentage of G's	67,520,755 / 23.39%
Number/percentage of N's	33,255 / 0.01%
GC Percentage	41.61%

2.3. Coverage

Mean	0.0933

Standard Deviation	1.0422

2.4. Mapping Quality

Mean Mapping Quality	45.73

2.5. Mismatches and indels

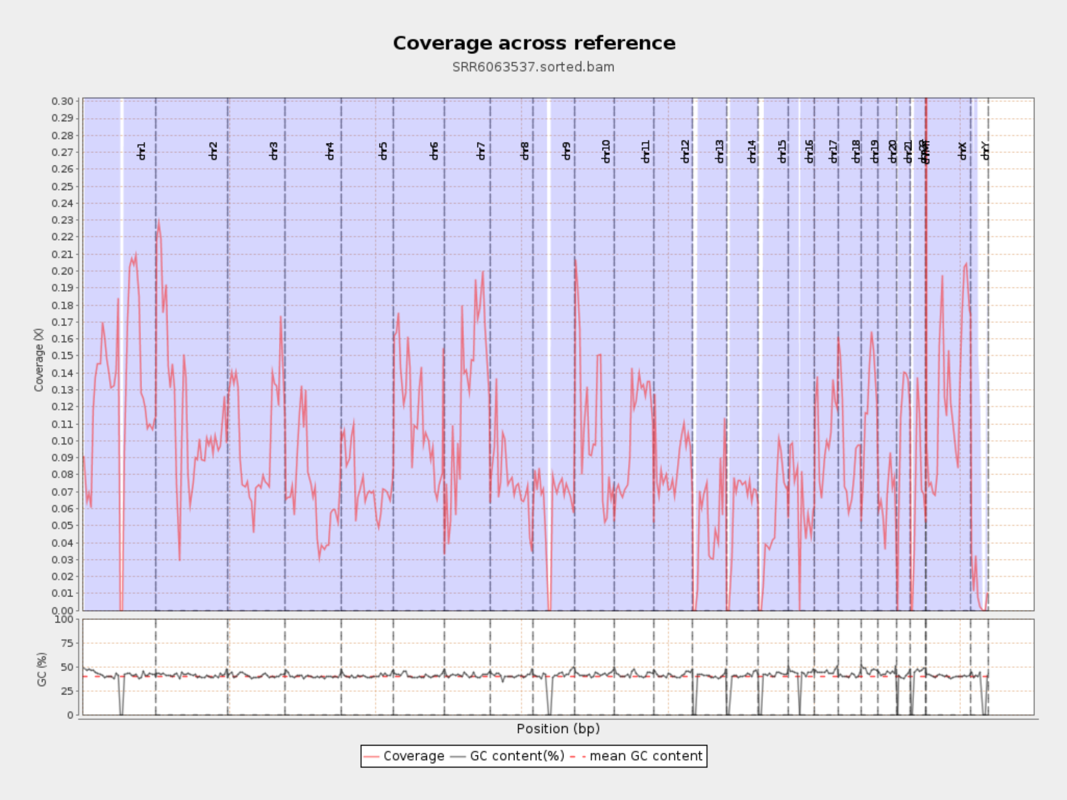
General error rate	0.5%
Mismatches	1,413,444
Insertions	19,282
Mapped reads with at least one insertion	0.43%
Deletions	58,164
Mapped reads with at least one deletion	1.3%
Homopolymer indels	45.75%

2.6. Chromosome stats

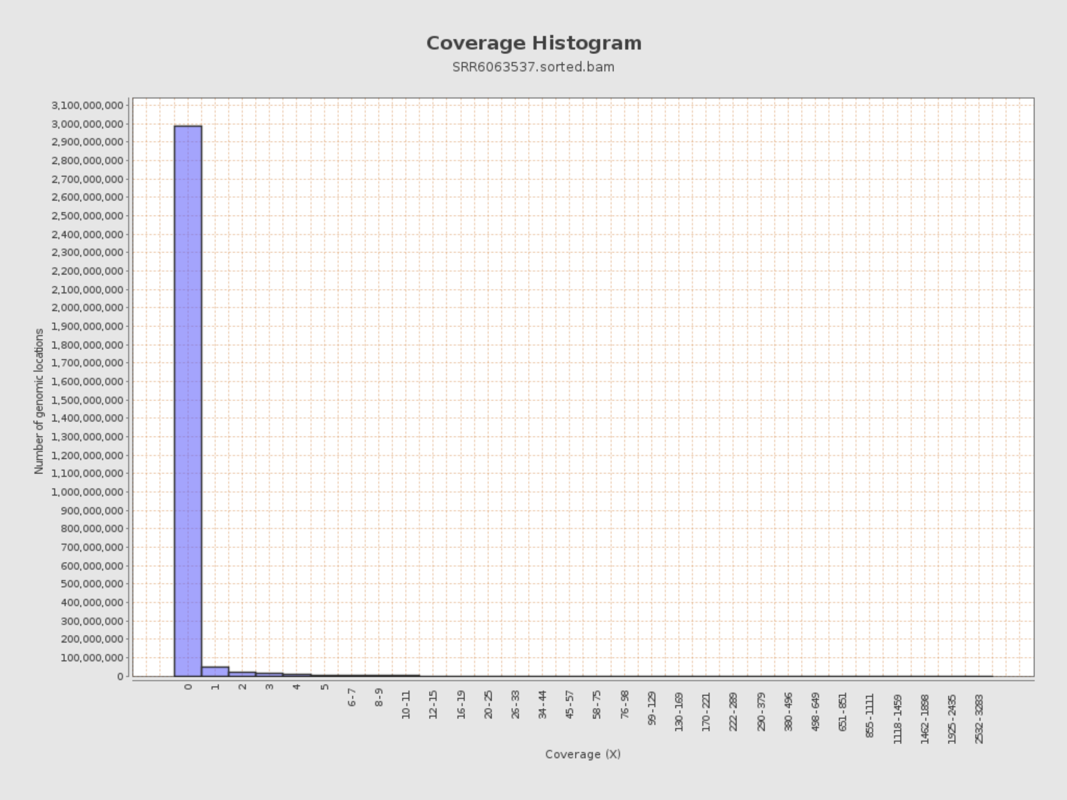
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	32094967	0.1288	1.6151
chr2	243199373	28593514	0.1176	1.6616
chr3	198022430	19995964	0.101	0.6844
chr4	191154276	13277859	0.0695	0.5927
chr5	180915260	13570455	0.075	0.5867
chr6	171115067	19865838	0.1161	0.8495
chr7	159138663	20066978	0.1261	1.3214

chr8	146364022	11242212	0.0768	1.754
chr9	141213431	8958121	0.0634	0.6986
chr10	135534747	14695508	0.1084	0.8338
chr11	135006516	14212957	0.1053	0.7661
chr12	133851895	11593150	0.0866	0.639
chr13	115169878	5830053	0.0506	0.5331
chr14	107349540	6526320	0.0608	0.5567
chr15	102531392	5099366	0.0497	0.484
chr16	90354753	5689457	0.063	0.5578
chr17	81195210	8593862	0.1058	0.725
chr18	78077248	7327342	0.0938	1.2232
chr19	59128983	7268652	0.1229	1.1594
chr20	63025520	4149322	0.0658	0.5675
chr21	48129895	5100484	0.106	0.7099
chr22	51304566	3421286	0.0667	0.5458
chrMT	16571	1215219	73.3341	55.1166
chrX	155270560	19764891	0.1273	0.8288
chrY	59373566	662780	0.0112	0.279

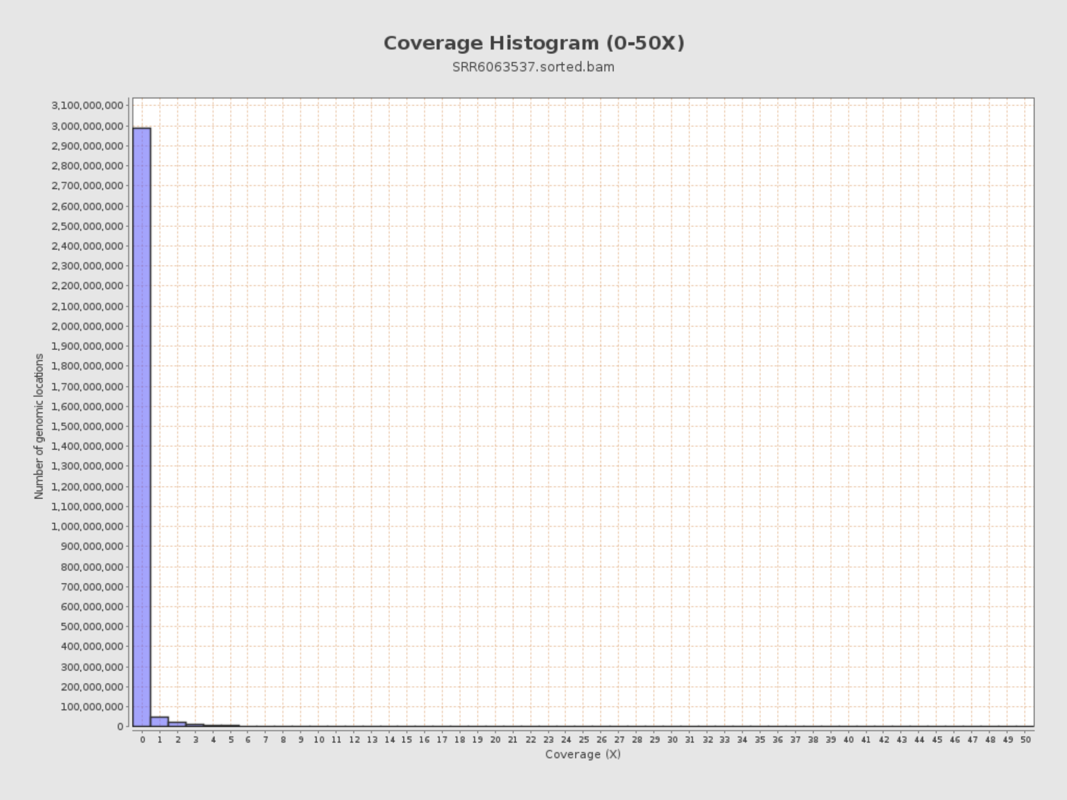
3. Results : Coverage across reference



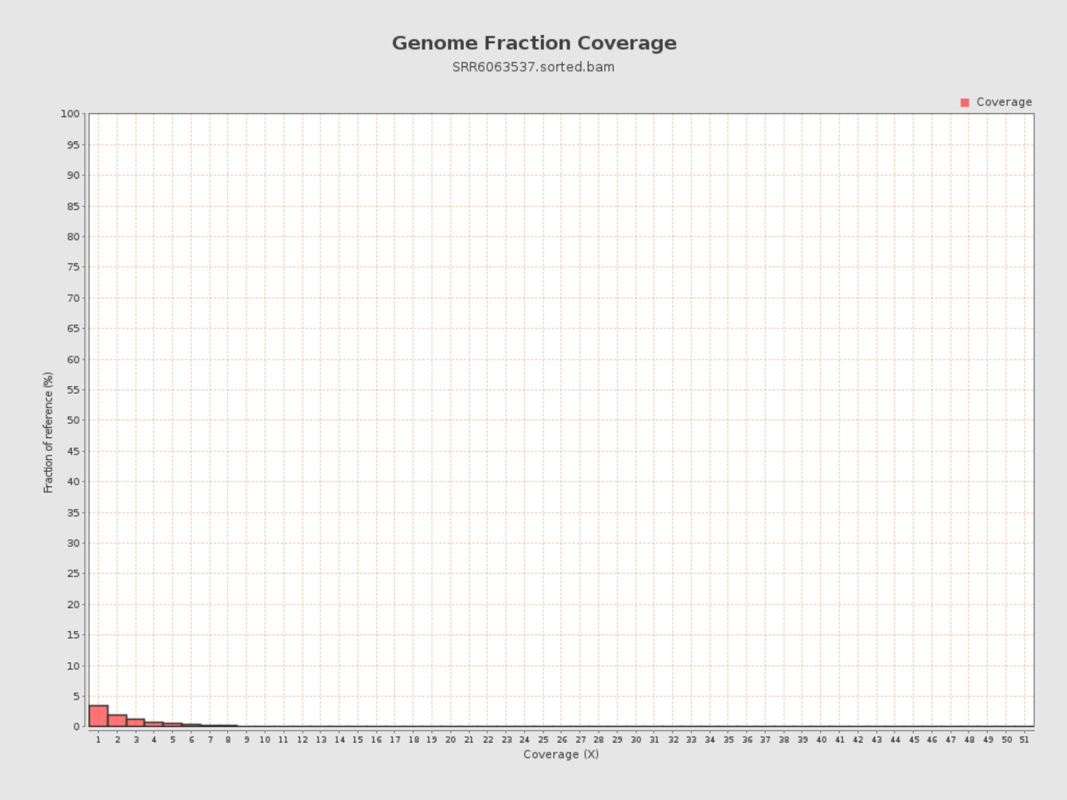
4. Results : Coverage Histogram



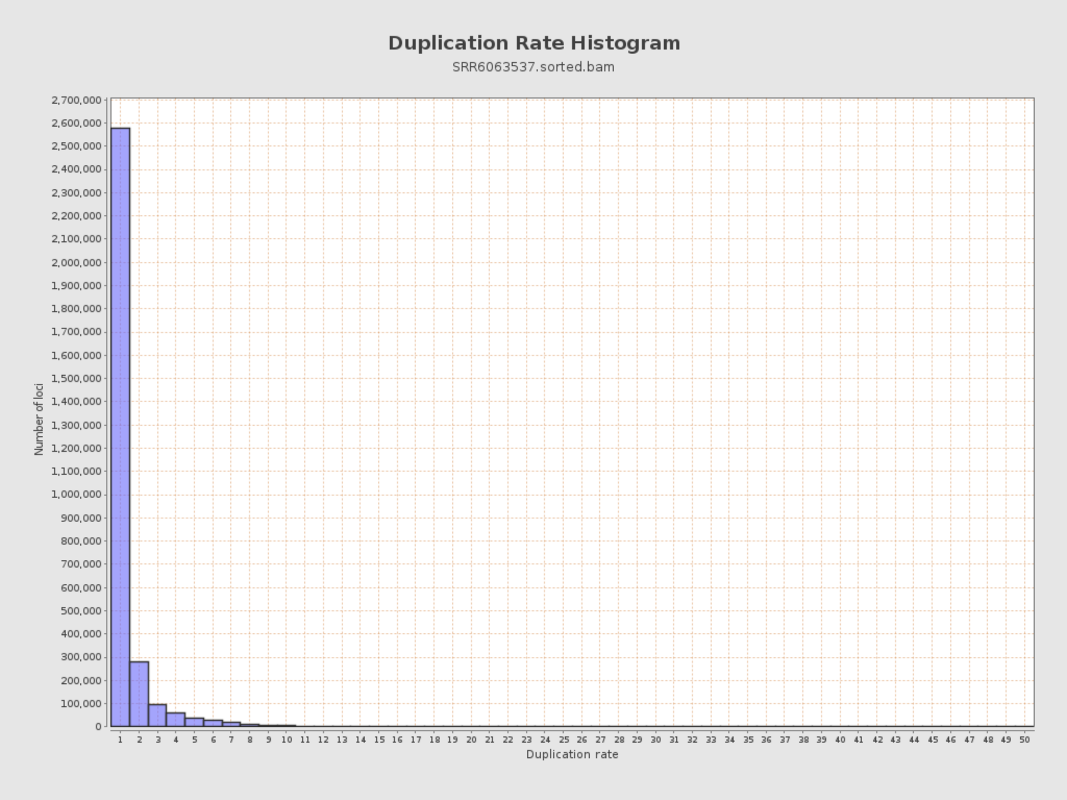
5. Results : Coverage Histogram (0-50X)



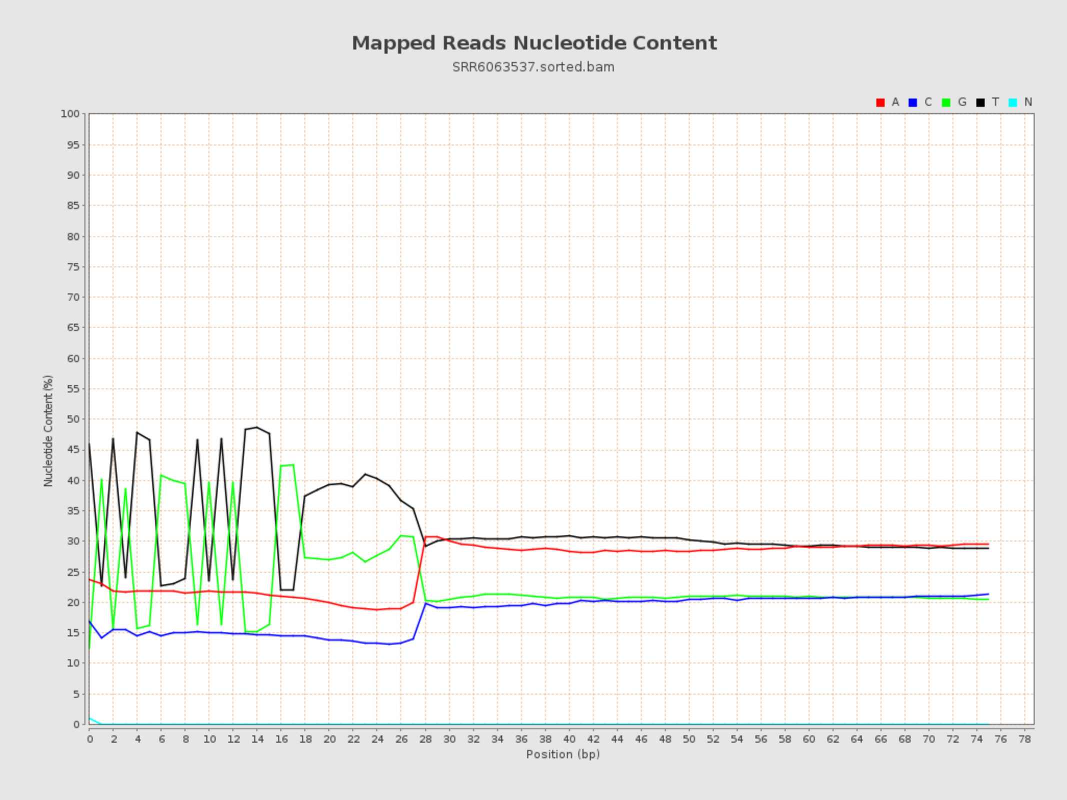
6. Results : Genome Fraction Coverage



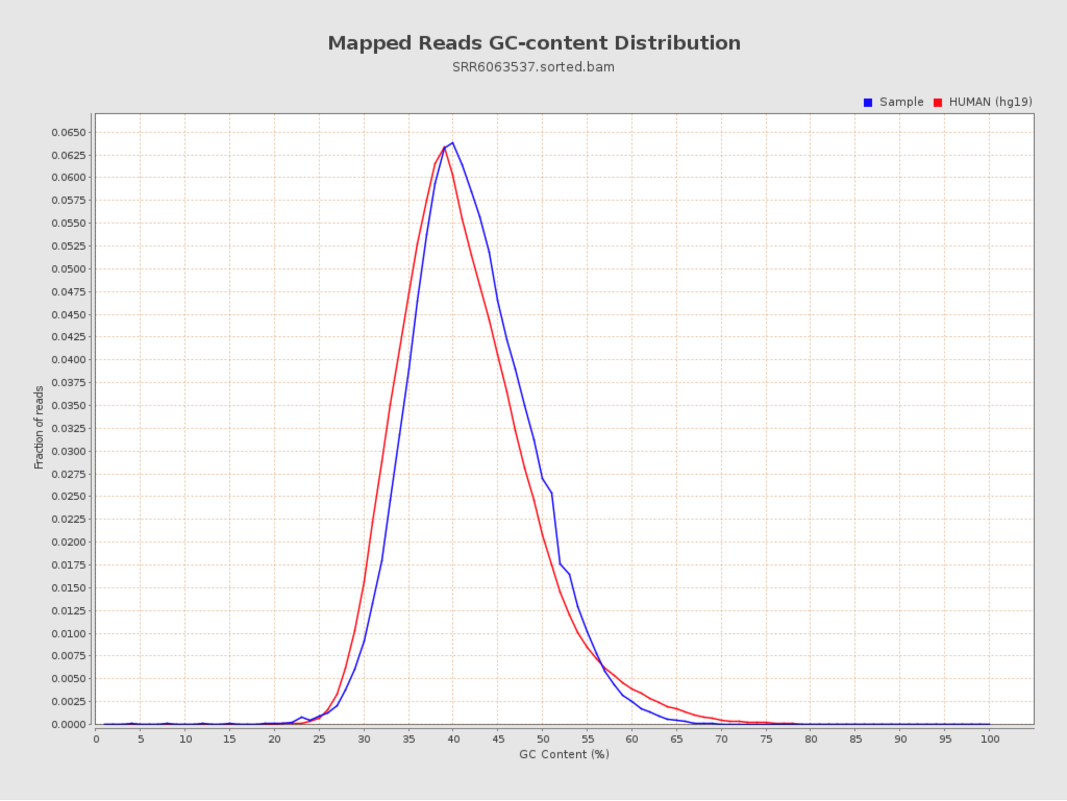
7. Results : Duplication Rate Histogram



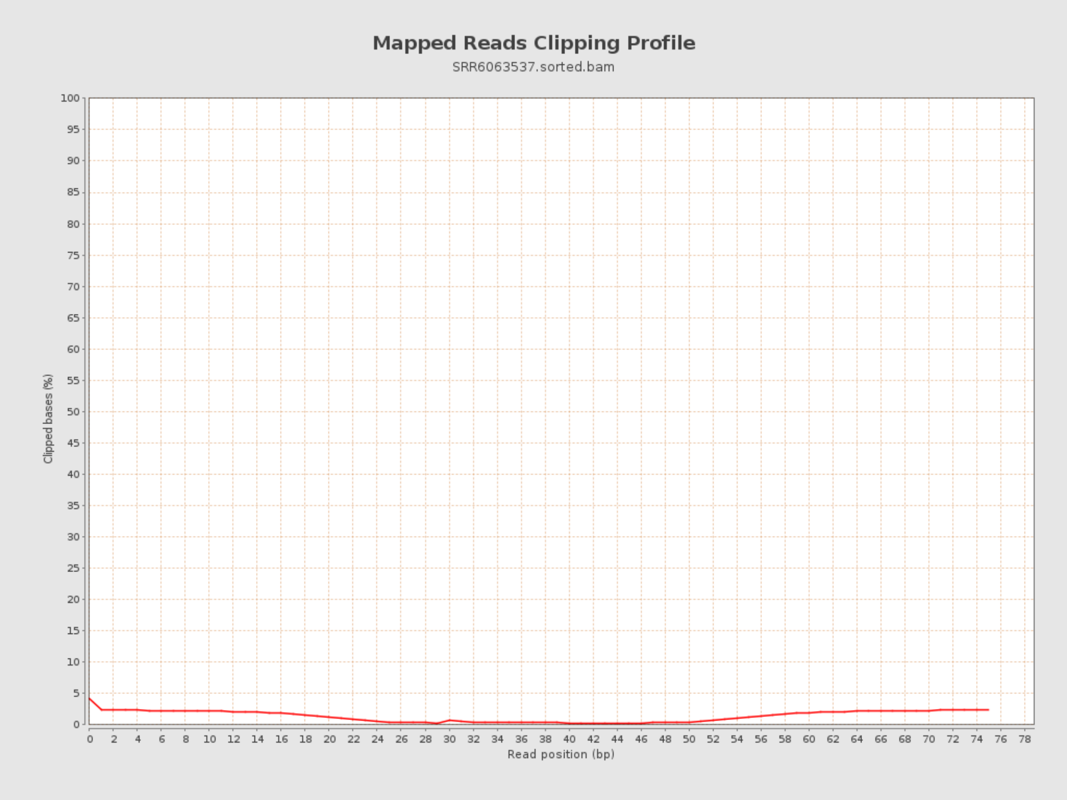
8. Results : Mapped Reads Nucleotide Content



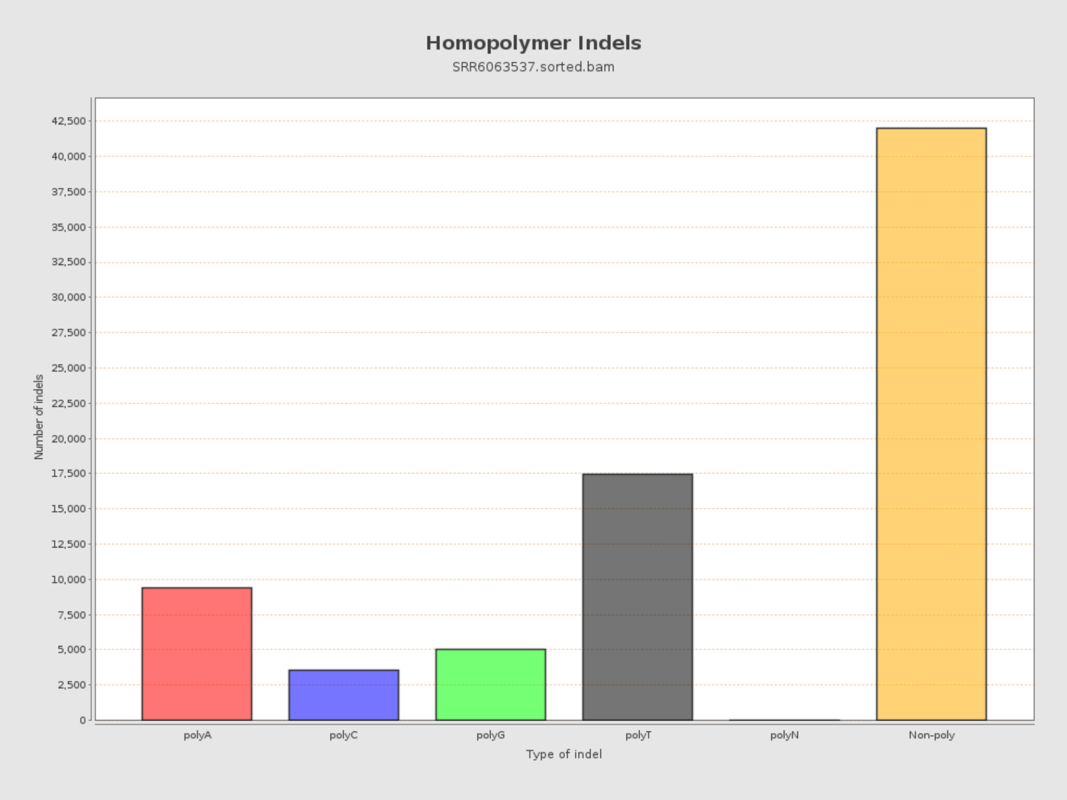
9. Results : Mapped Reads GC-content Distribution



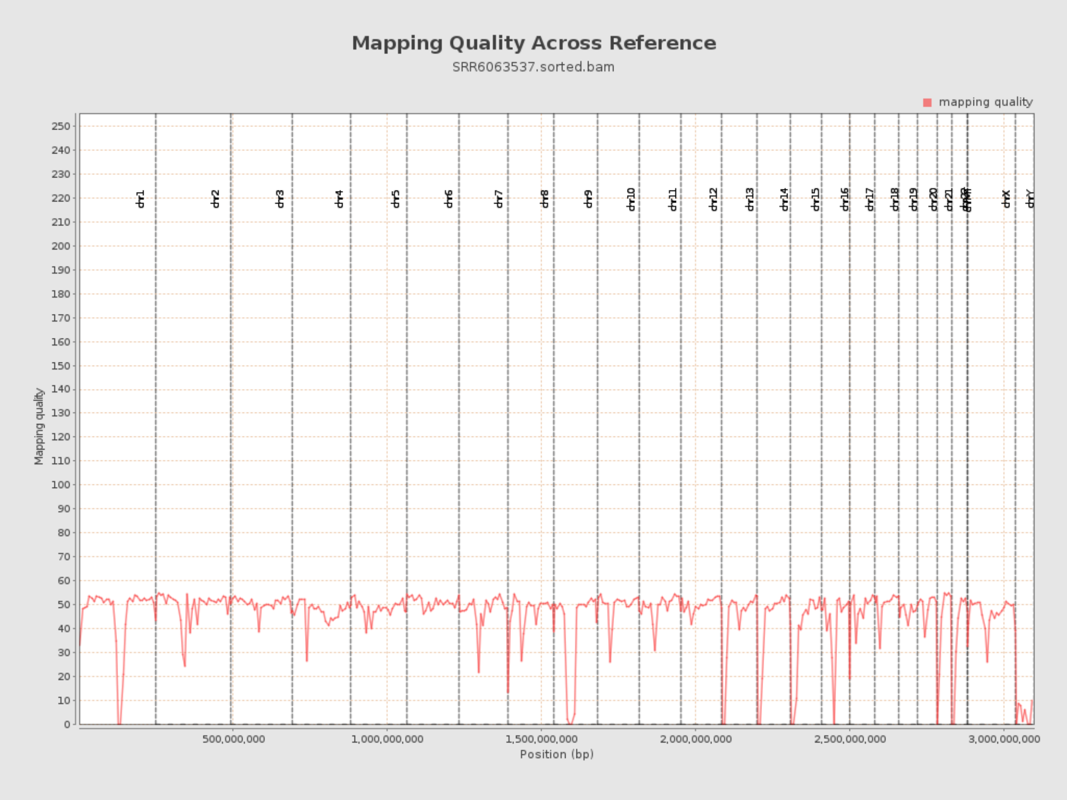
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram