Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 03:34:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063580.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_SRR6063580 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063580.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 03:34:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063580.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,728,387
Mapped reads	2,402,664 / 88.06%
Unmapped reads	325,723 / 11.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,911 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	326,364 / 11.96%
Duplication rate	10.35%
Clipped reads	1,109,695 / 40.67%

2.2. ACGT Content

Number/percentage of A's	44,468,406 / 27.96%
Number/percentage of C's	29,313,139 / 18.43%
Number/percentage of T's	50,586,493 / 31.81%
Number/percentage of G's	34,670,163 / 21.8%
Number/percentage of N's	4,445 / 0%
GC Percentage	40.23%

2.3. Coverage

Mean	0.0514

Standard Deviation	0.5632

2.4. Mapping Quality

Mean Mapping Quality	45.43

2.5. Mismatches and indels

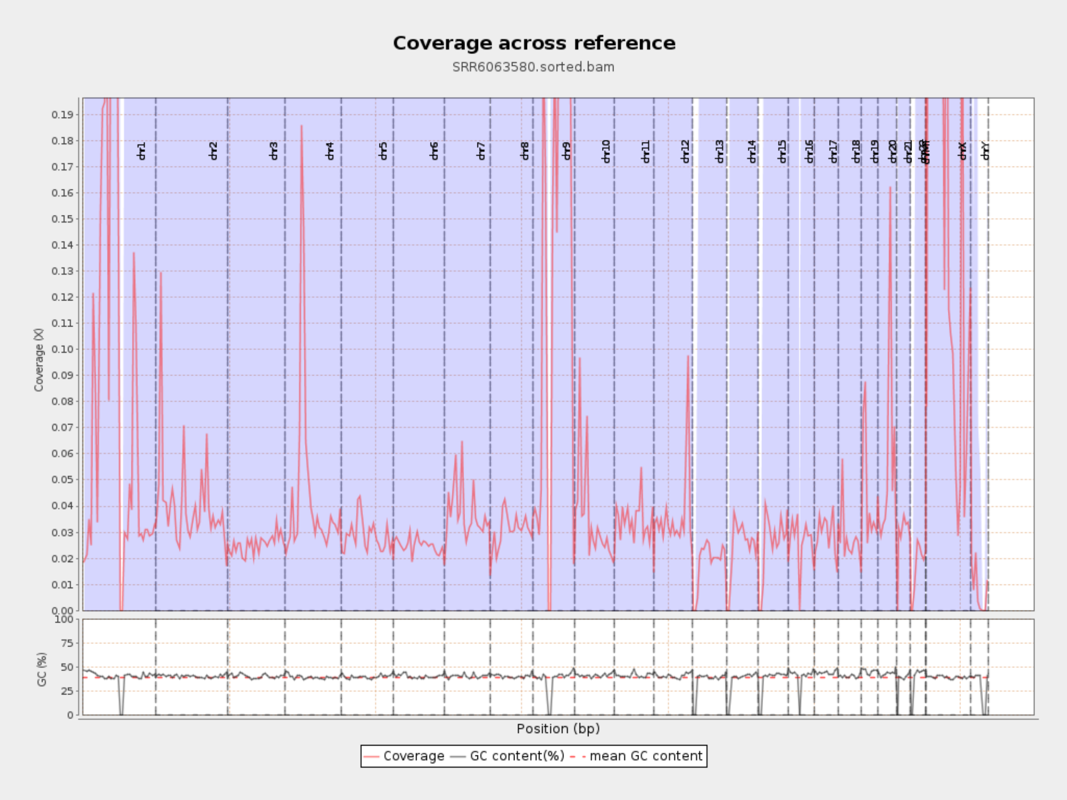
General error rate	0.77%
Mismatches	1,195,898
Insertions	11,933
Mapped reads with at least one insertion	0.49%
Deletions	41,101
Mapped reads with at least one deletion	1.69%
Homopolymer indels	47.9%

2.6. Chromosome stats

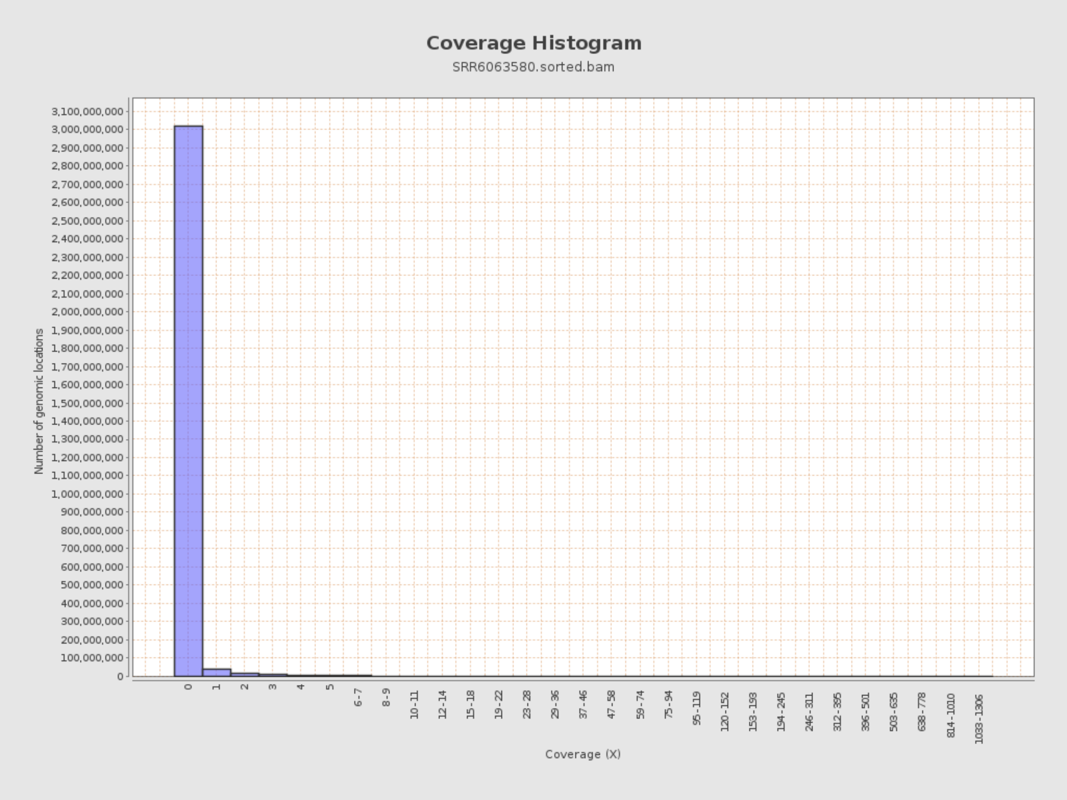
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21588624	0.0866	0.6643
chr2	243199373	10005260	0.0411	0.5686
chr3	198022430	5059898	0.0256	0.2907
chr4	191154276	8874702	0.0464	0.4489
chr5	180915260	5128039	0.0283	0.333
chr6	171115067	4289187	0.0251	0.2908
chr7	159138663	5927494	0.0372	0.5991

chr8	146364022	4511276	0.0308	0.4097
chr9	141213431	21522656	0.1524	0.9912
chr10	135534747	4771300	0.0352	0.5273
chr11	135006516	4660997	0.0345	0.4362
chr12	133851895	5009427	0.0374	0.4165
chr13	115169878	2135205	0.0185	0.2401
chr14	107349540	2653403	0.0247	0.4726
chr15	102531392	2570552	0.0251	0.2816
chr16	90354753	2353421	0.026	0.445
chr17	81195210	2403992	0.0296	0.3172
chr18	78077248	2216605	0.0284	1.3447
chr19	59128983	2619225	0.0443	0.4916
chr20	63025520	3572579	0.0567	0.4507
chr21	48129895	1399053	0.0291	0.5146
chr22	51304566	827812	0.0161	0.2232
chrMT	16571	184730	11.1478	8.7663
chrX	155270560	34380639	0.2214	0.929
chrY	59373566	449564	0.0076	0.2445

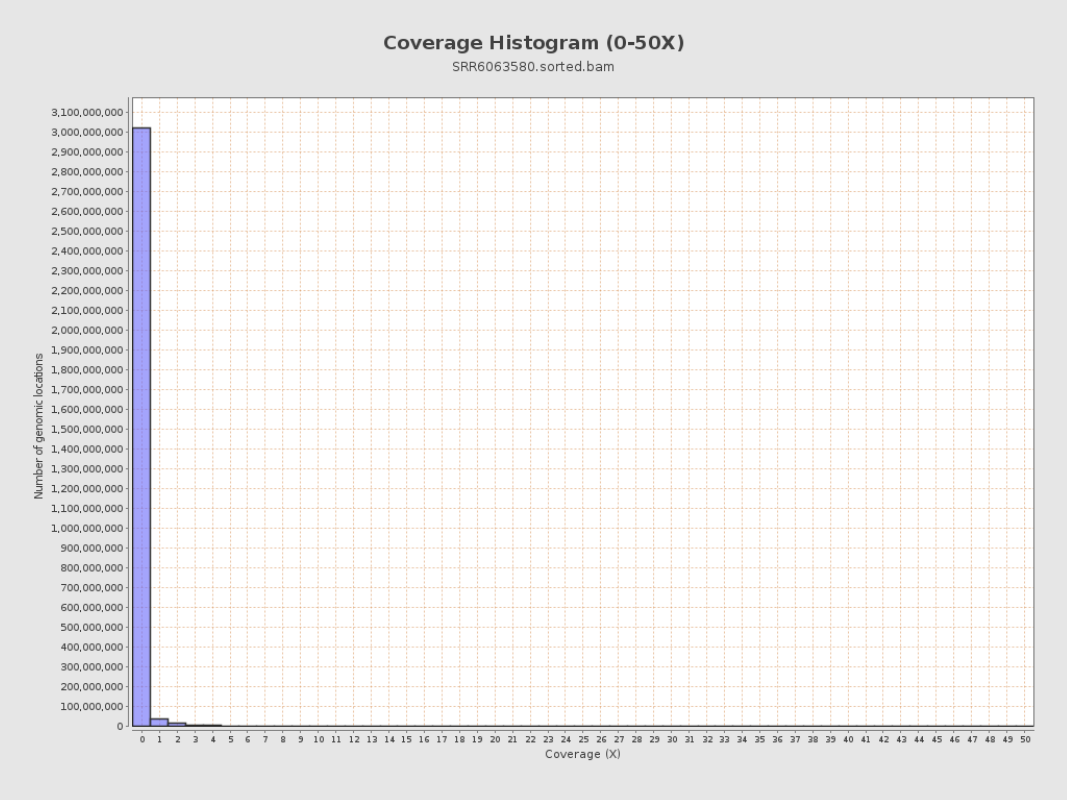
3. Results : Coverage across reference



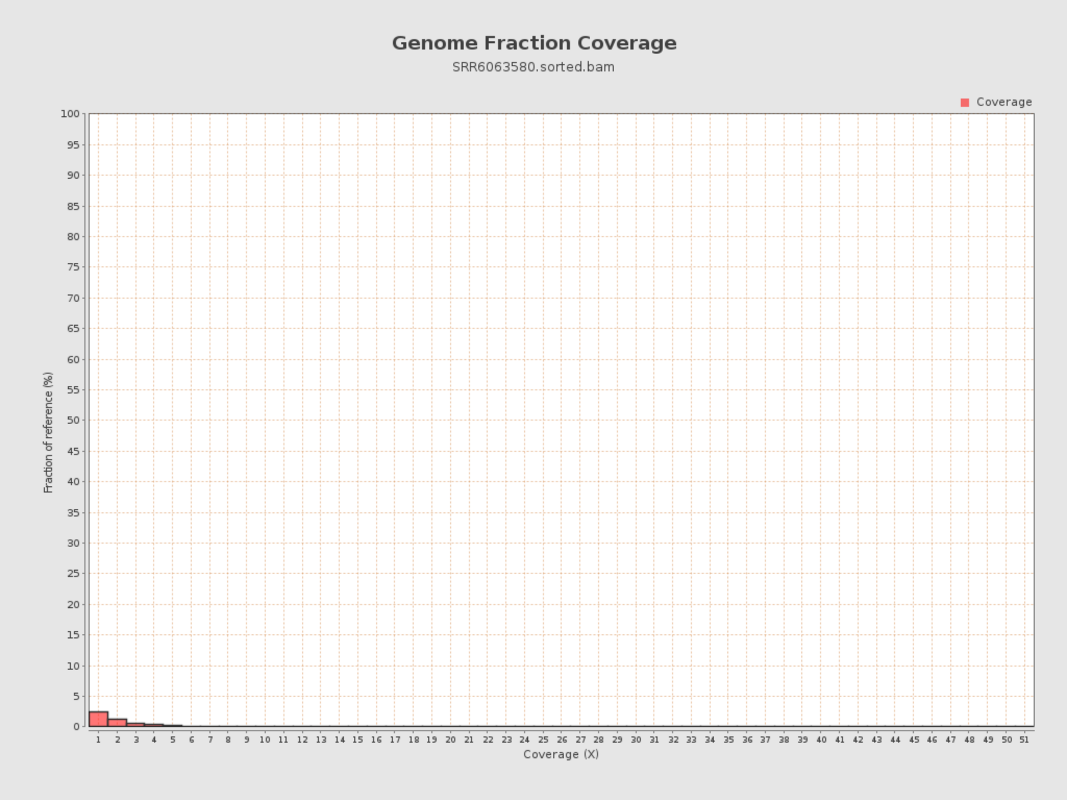
4. Results : Coverage Histogram



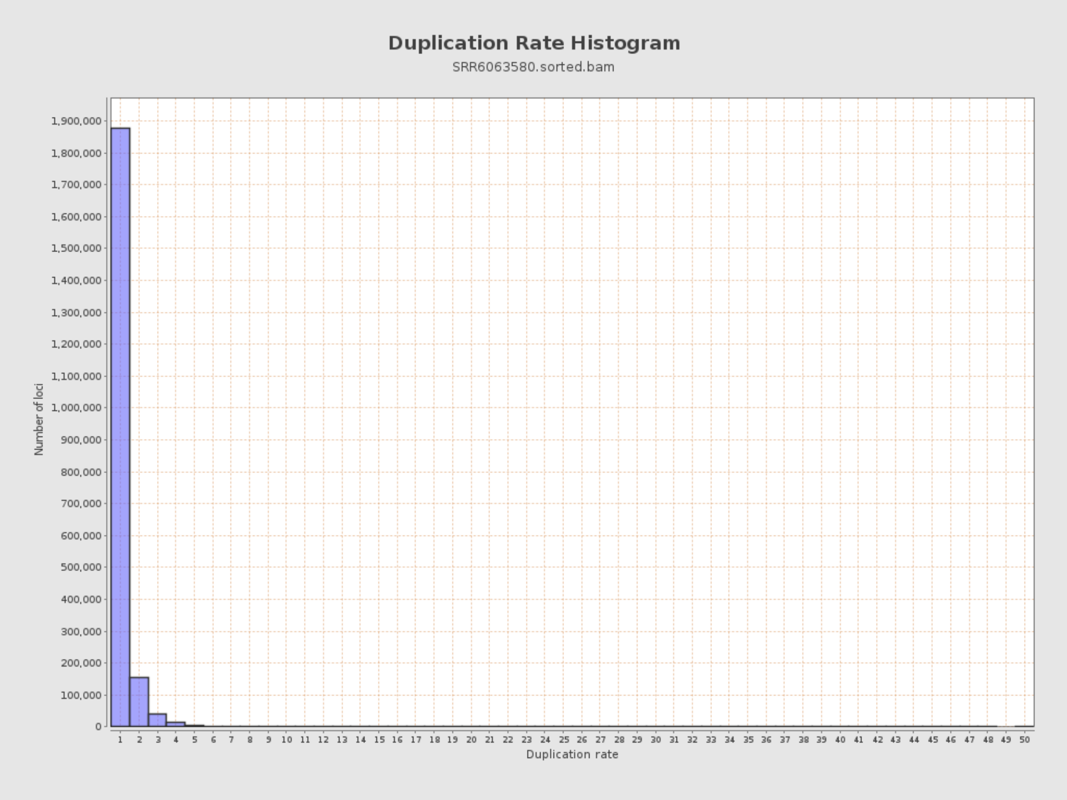
5. Results : Coverage Histogram (0-50X)



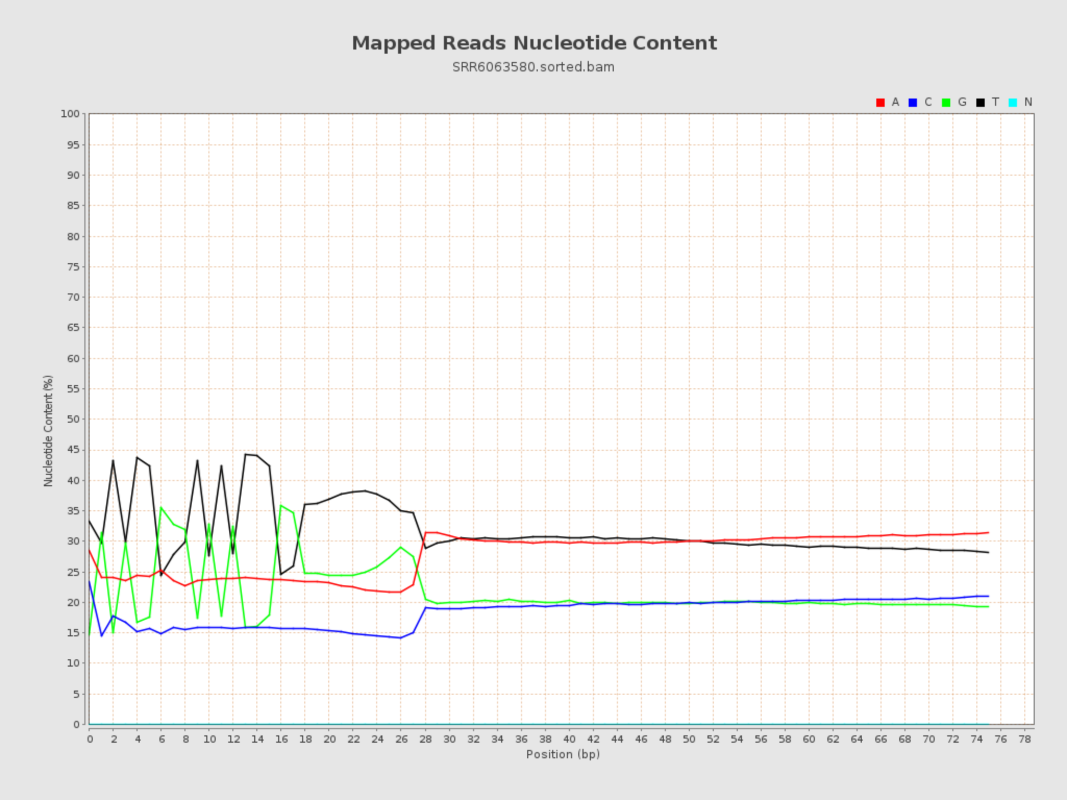
6. Results : Genome Fraction Coverage



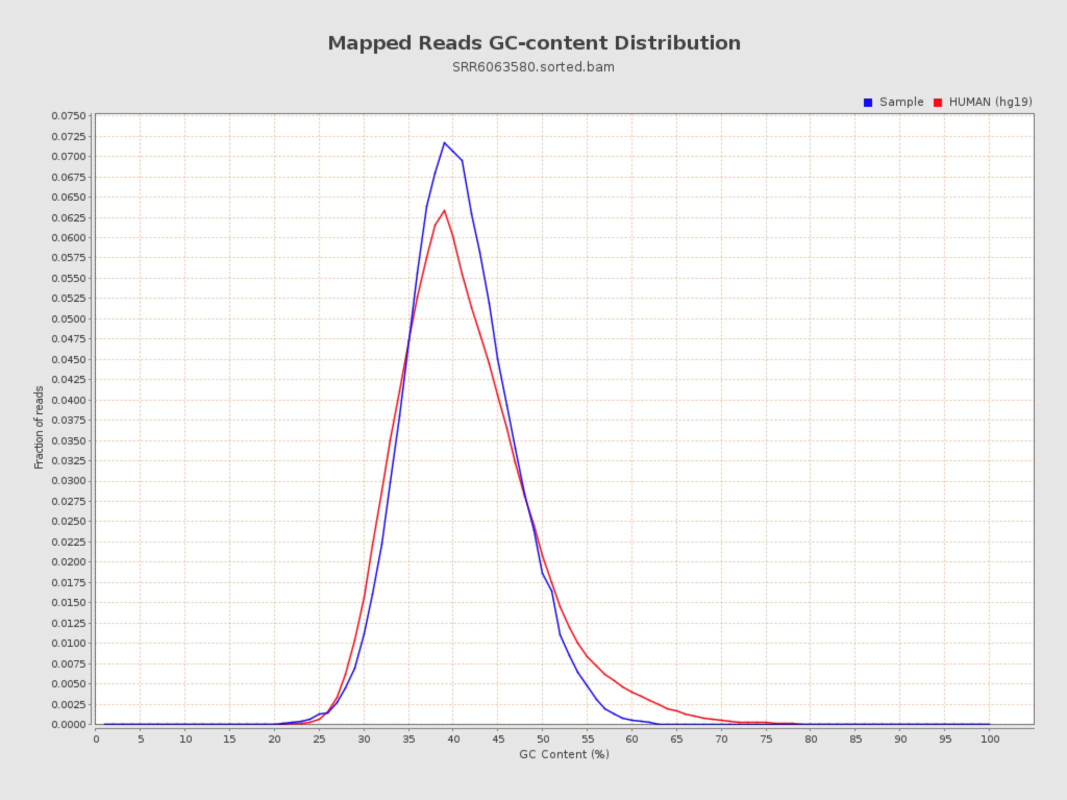
7. Results : Duplication Rate Histogram



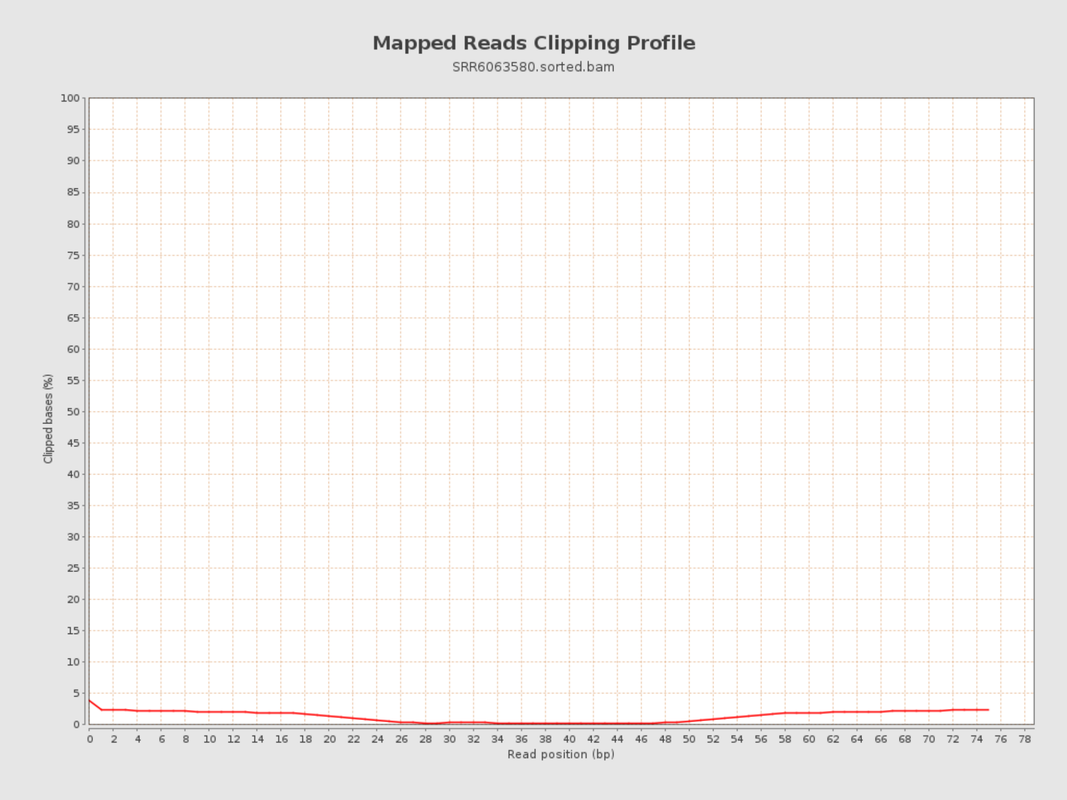
8. Results : Mapped Reads Nucleotide Content



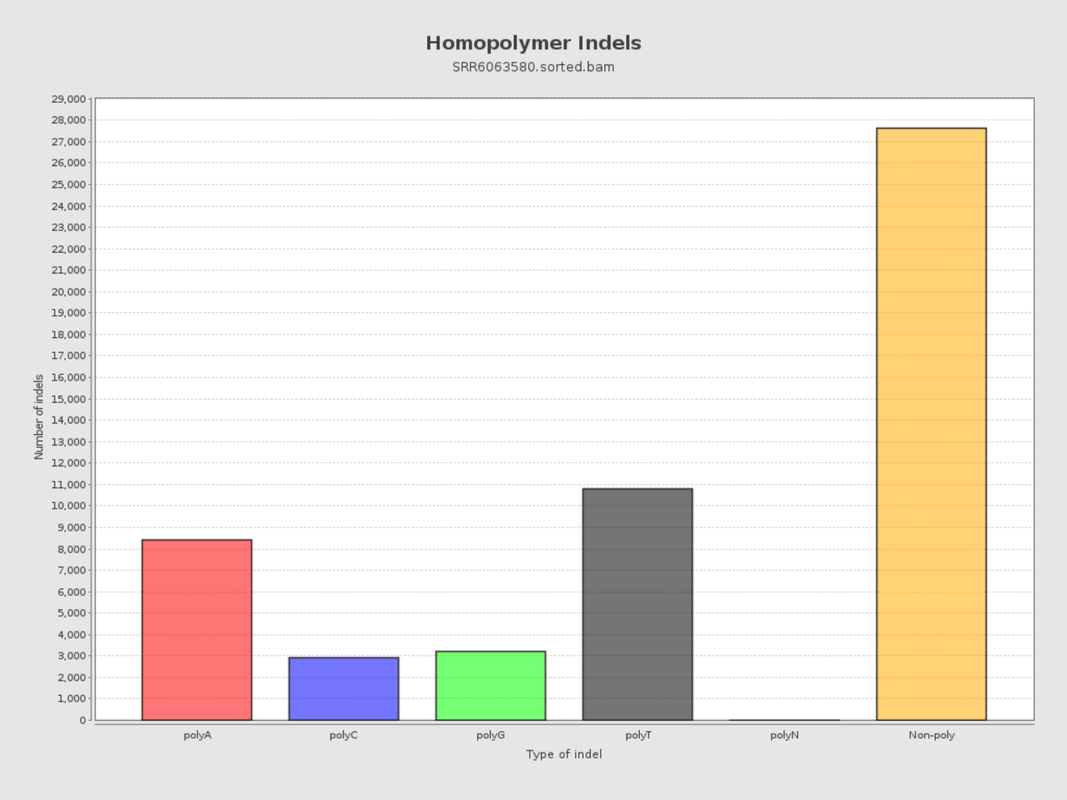
9. Results : Mapped Reads GC-content Distribution



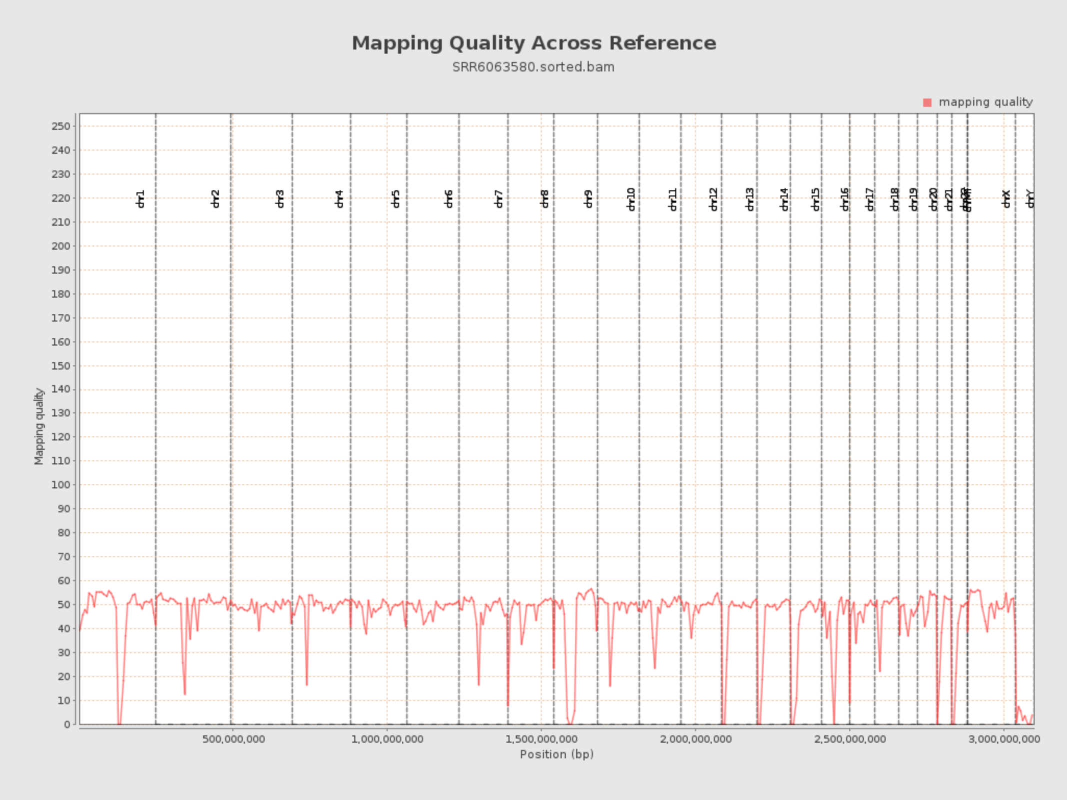
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram