Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 02:25:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063559.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_SRR6063559 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063559.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 02:25:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063559.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,091,022
Mapped reads	2,781,475 / 89.99%
Unmapped reads	309,547 / 10.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,481 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	165,122 / 5.34%
Duplication rate	4.65%
Clipped reads	1,417,790 / 45.87%

2.2. ACGT Content

Number/percentage of A's	50,105,903 / 27.6%
Number/percentage of C's	32,774,393 / 18.05%
Number/percentage of T's	58,201,330 / 32.06%
Number/percentage of G's	40,479,044 / 22.29%
Number/percentage of N's	4,797 / 0%
GC Percentage	40.35%

2.3. Coverage

Mean	0.0587

Standard Deviation	0.5549

2.4. Mapping Quality

Mean Mapping Quality	45.87

2.5. Mismatches and indels

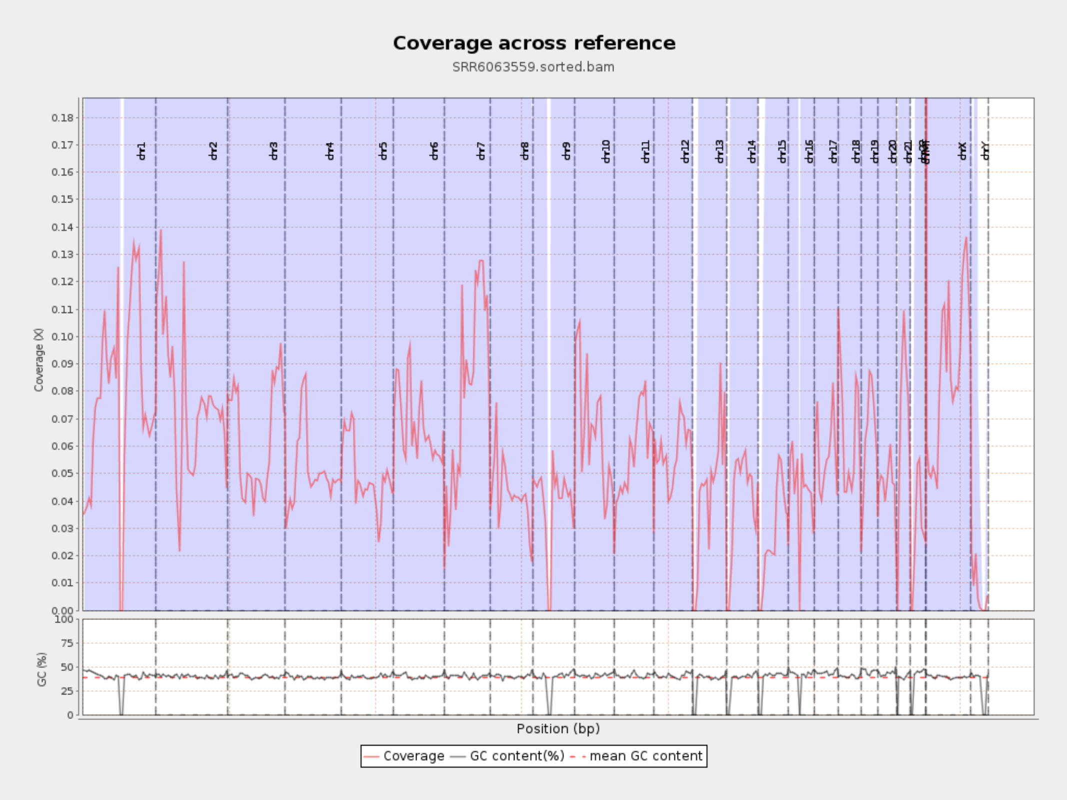
General error rate	0.83%
Mismatches	1,480,932
Insertions	13,762
Mapped reads with at least one insertion	0.49%
Deletions	49,195
Mapped reads with at least one deletion	1.75%
Homopolymer indels	46.32%

2.6. Chromosome stats

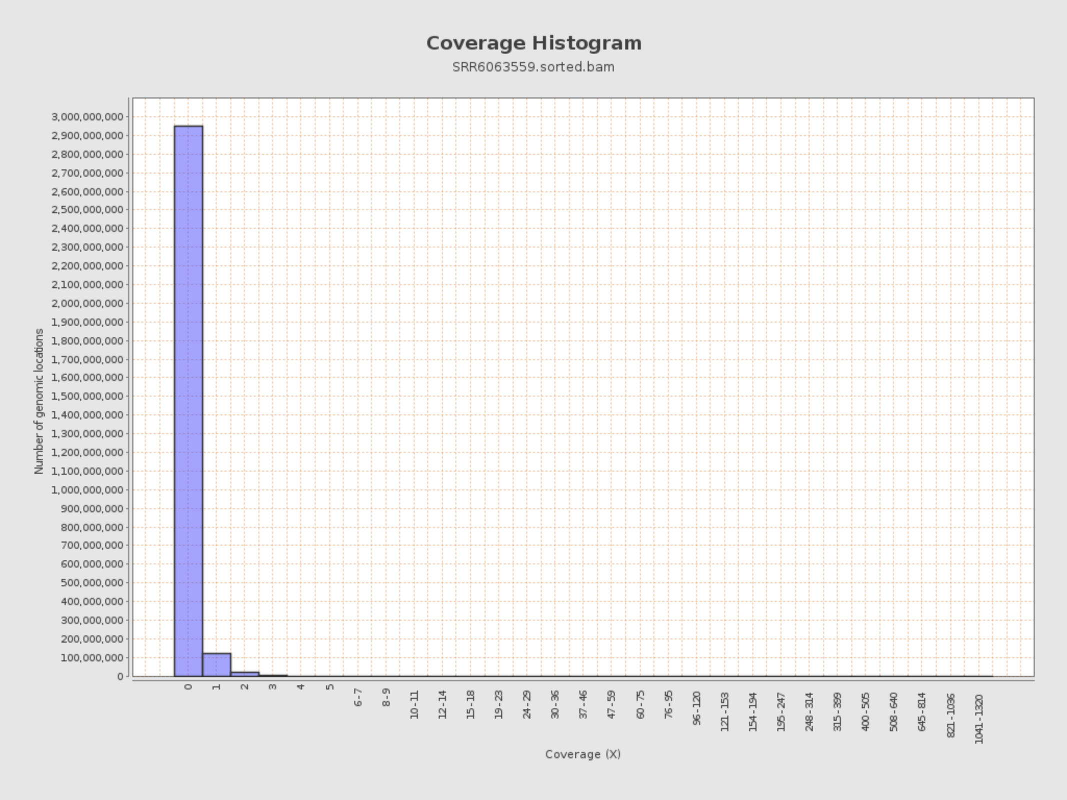
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19525700	0.0783	1.1437
chr2	243199373	18867501	0.0776	0.7239
chr3	198022430	12387222	0.0626	0.3033
chr4	191154276	9784150	0.0512	0.2885
chr5	180915260	8907297	0.0492	0.2676
chr6	171115067	11696446	0.0684	0.3835
chr7	159138663	12791819	0.0804	0.8004

chr8	146364022	6226593	0.0425	0.7798
chr9	141213431	5537162	0.0392	0.4176
chr10	135534747	8969736	0.0662	0.462
chr11	135006516	7877141	0.0583	0.3933
chr12	133851895	7749675	0.0579	0.3039
chr13	115169878	5069773	0.044	0.2573
chr14	107349540	4312784	0.0402	0.2818
chr15	102531392	2794722	0.0273	0.2149
chr16	90354753	3850579	0.0426	0.2749
chr17	81195210	4749446	0.0585	0.3229
chr18	78077248	5050695	0.0647	0.6891
chr19	59128983	3828075	0.0647	0.7708
chr20	63025520	2963938	0.047	0.2781
chr21	48129895	3277170	0.0681	0.3267
chr22	51304566	1476979	0.0288	0.198
chrMT	16571	44924	2.711	2.5846
chrX	155270560	13481004	0.0868	0.4112
chrY	59373566	424793	0.0072	0.1838

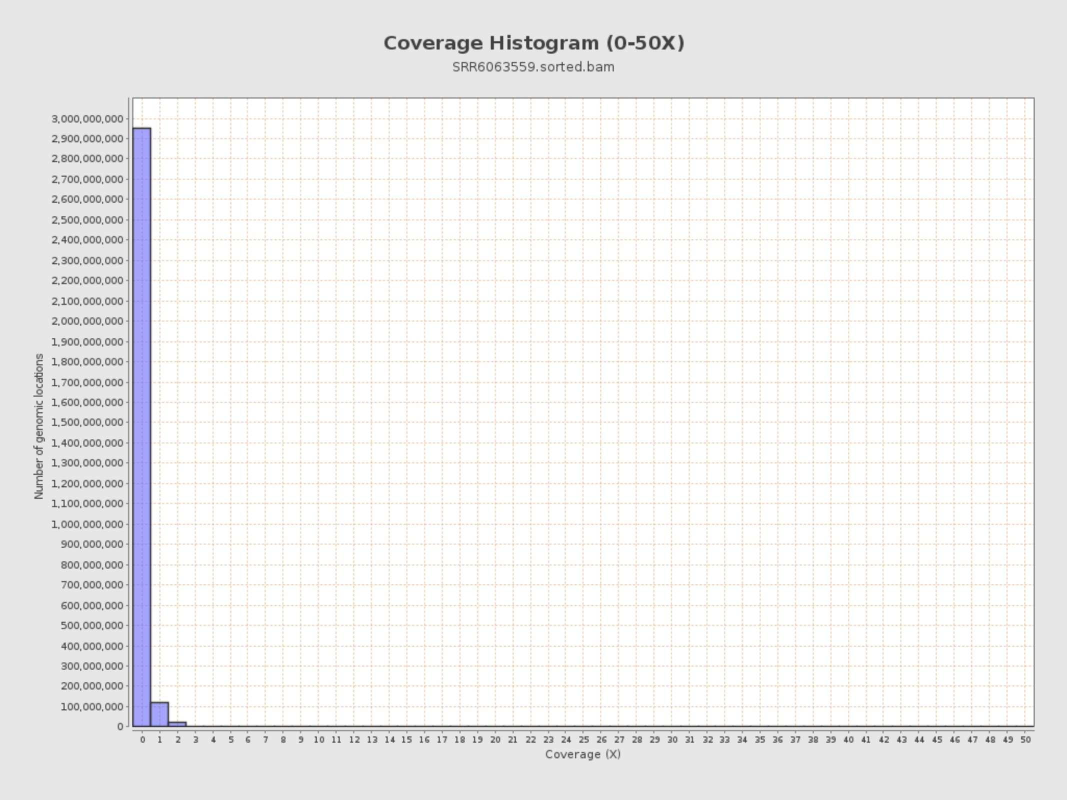
3. Results : Coverage across reference



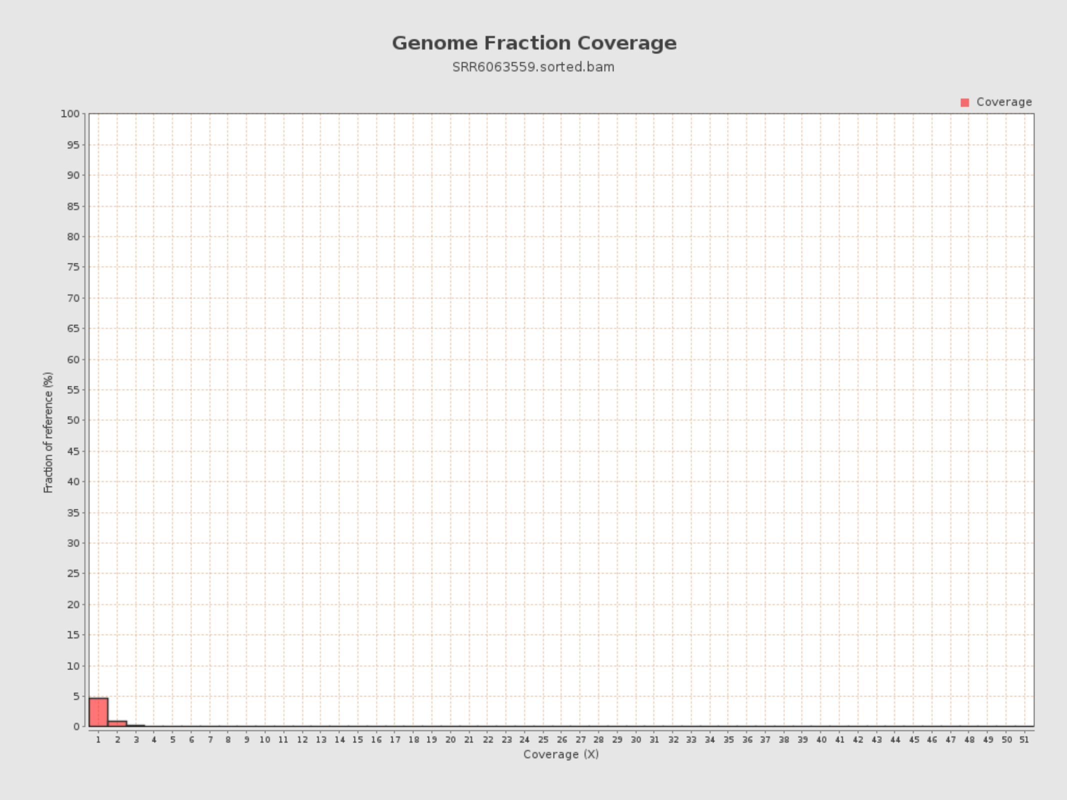
4. Results : Coverage Histogram



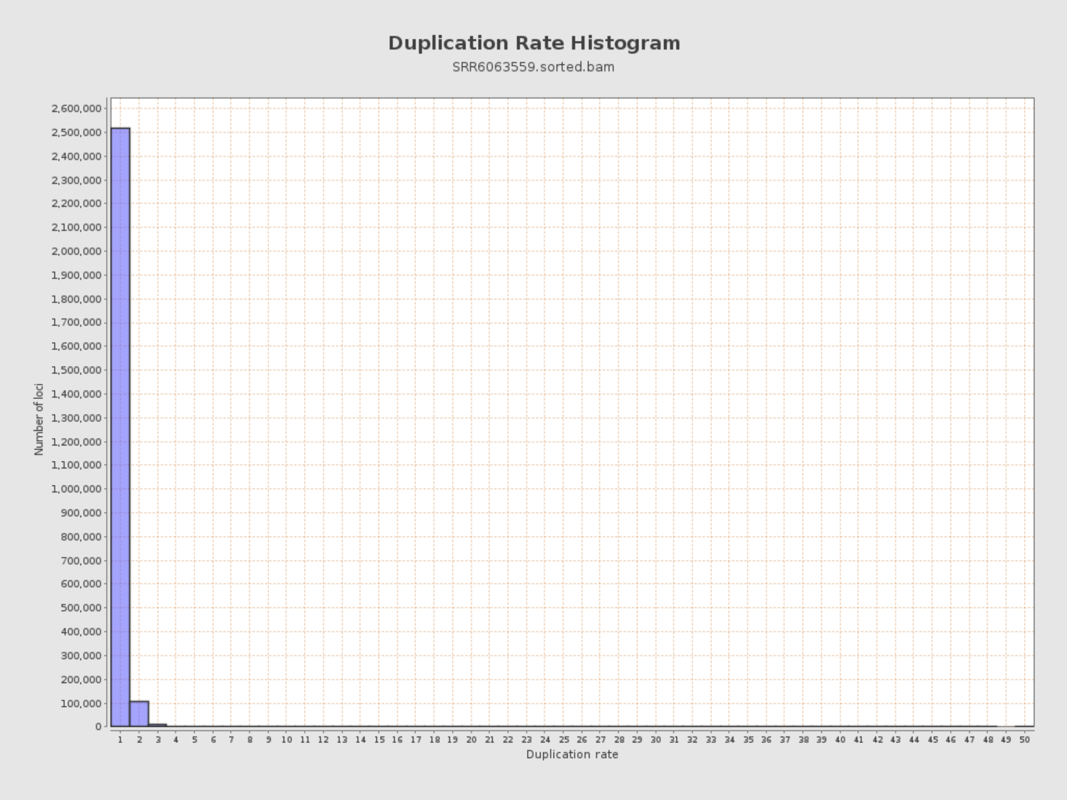
5. Results : Coverage Histogram (0-50X)



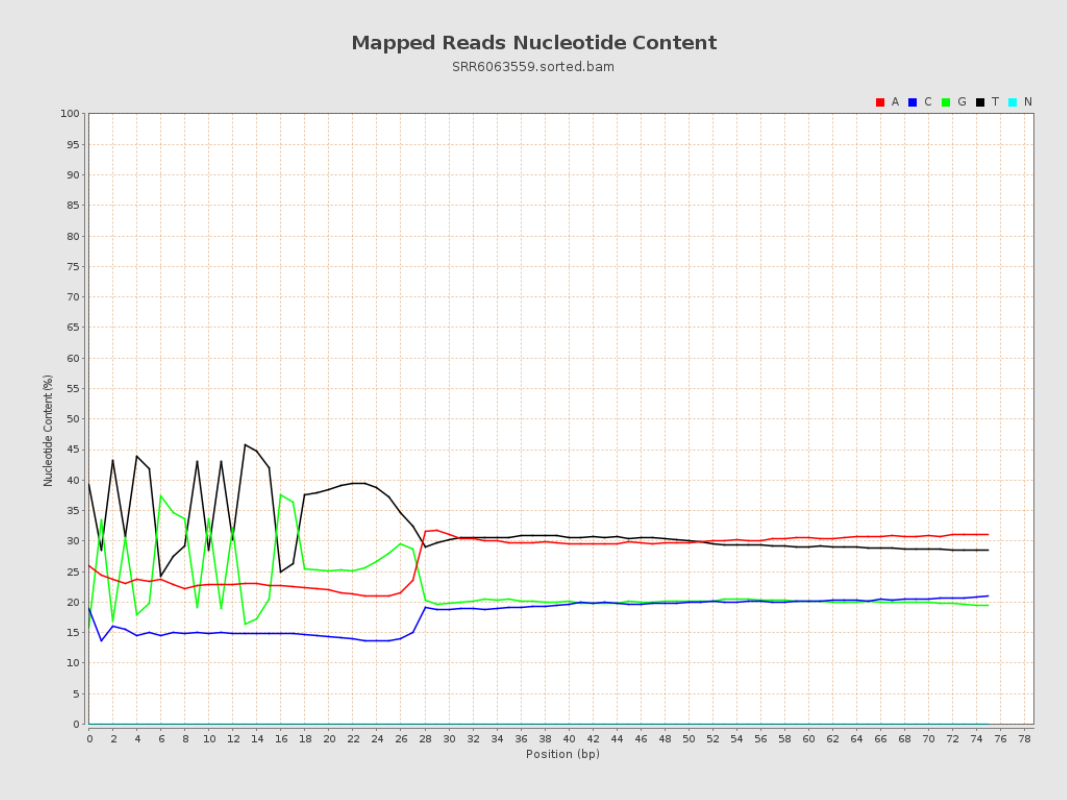
6. Results : Genome Fraction Coverage



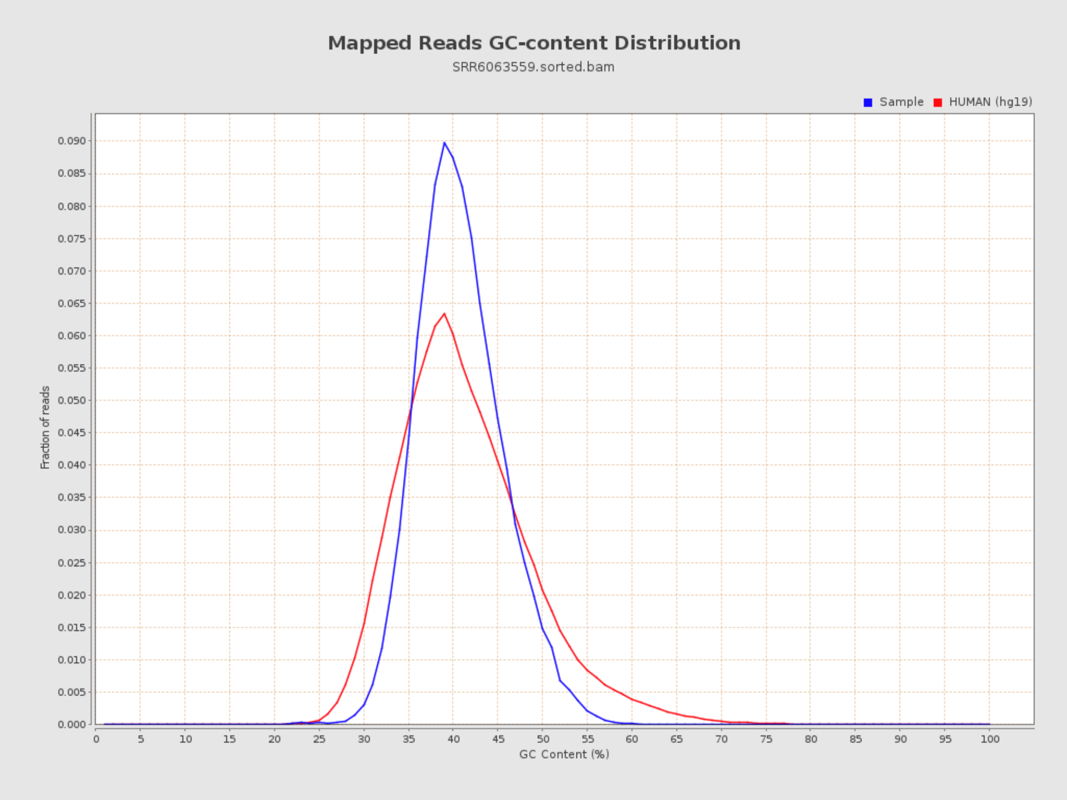
7. Results : Duplication Rate Histogram



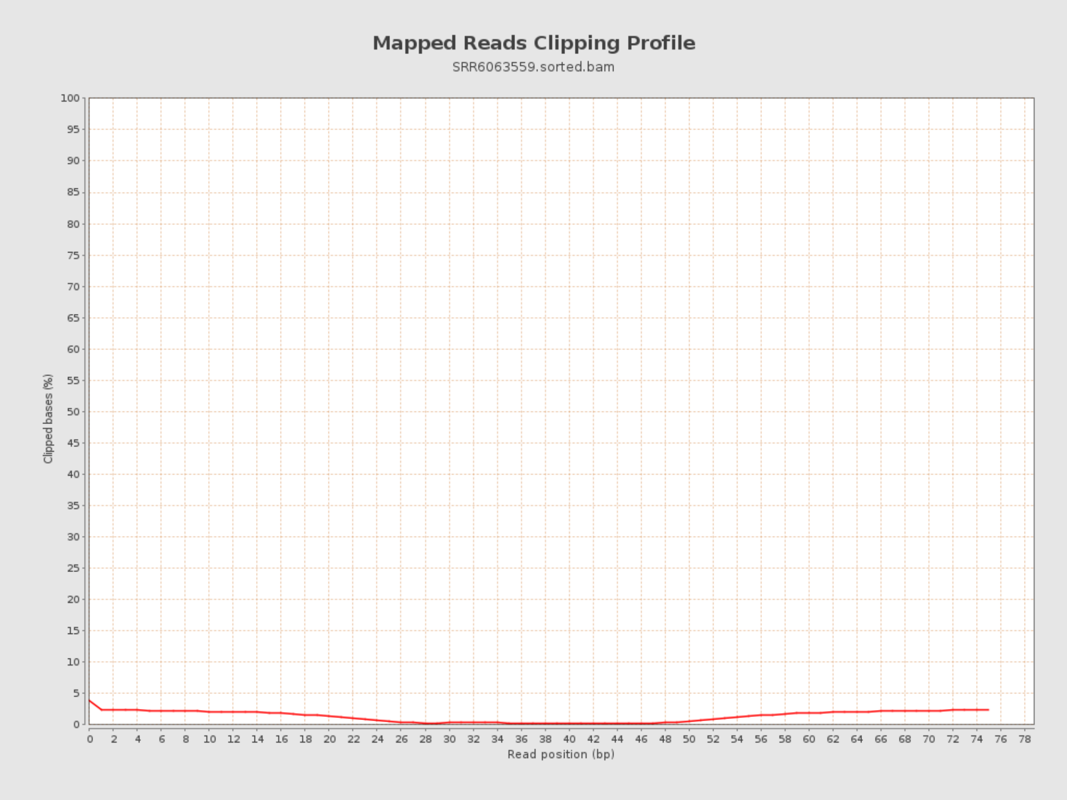
8. Results : Mapped Reads Nucleotide Content



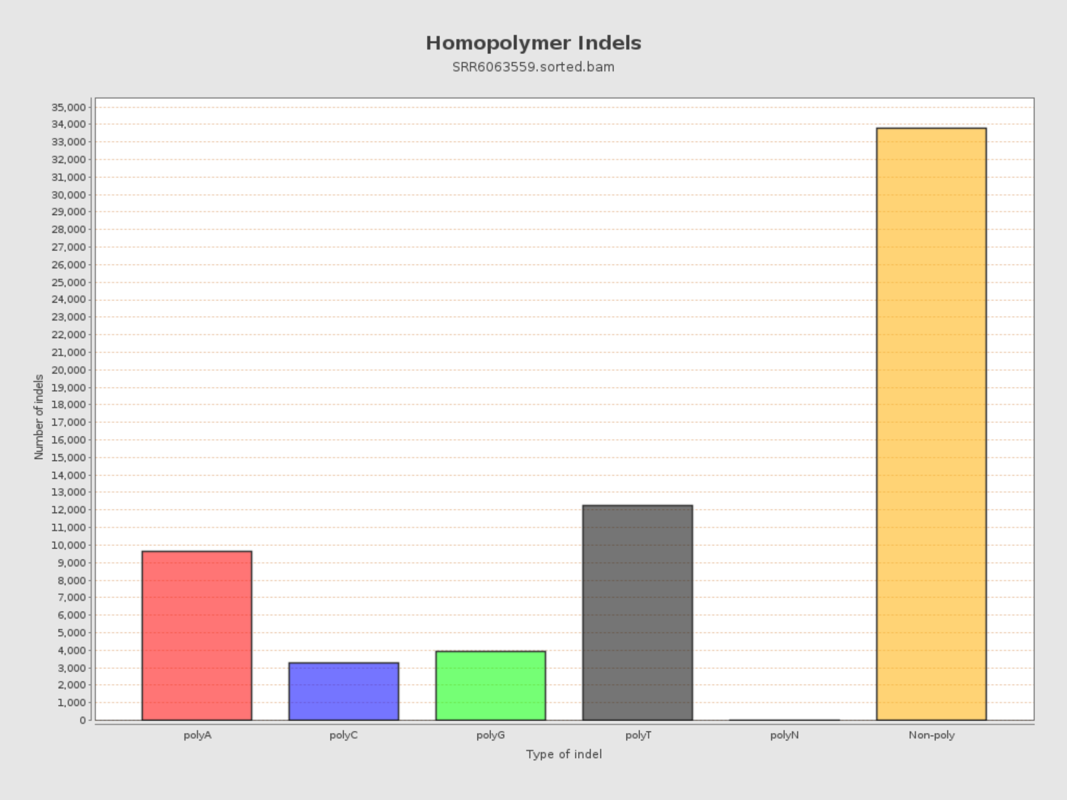
9. Results : Mapped Reads GC-content Distribution



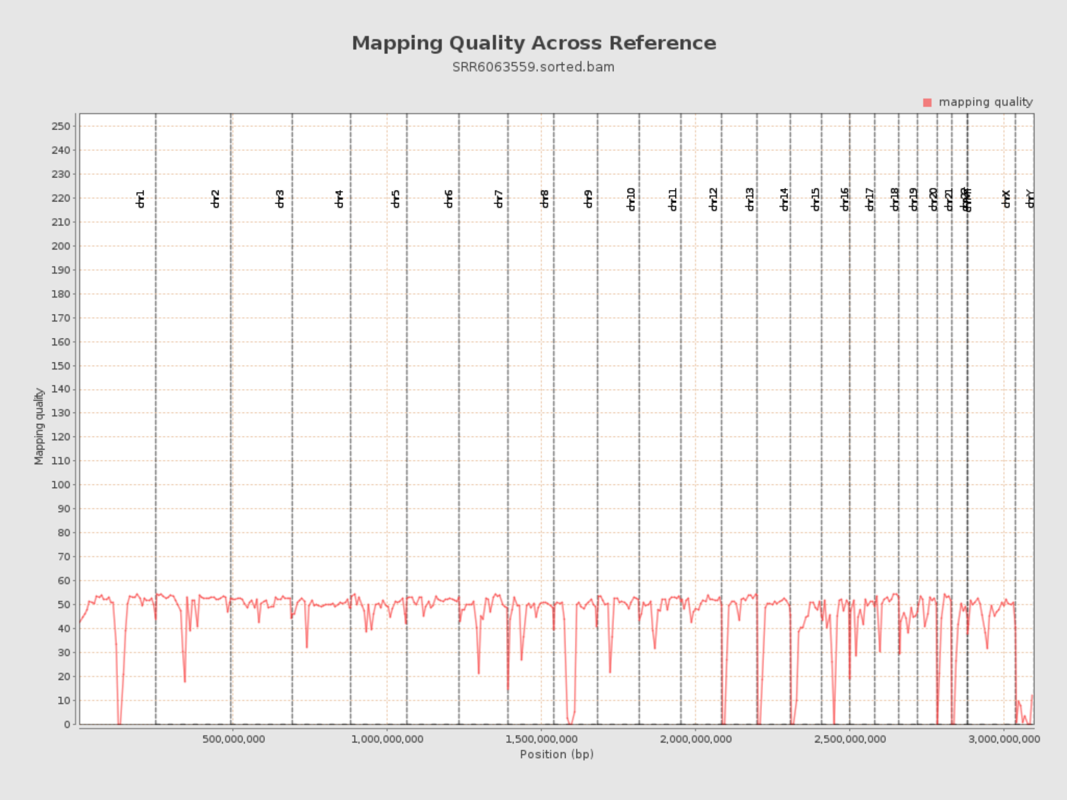
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram