Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 02:53:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063568.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_SRR6063568 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063568.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 02:53:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063568.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,600,928
Mapped reads	2,319,585 / 89.18%
Unmapped reads	281,343 / 10.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,556 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	112,084 / 4.31%
Duplication rate	3.8%
Clipped reads	1,179,180 / 45.34%

2.2. ACGT Content

Number/percentage of A's	42,354,332 / 27.95%
Number/percentage of C's	27,789,667 / 18.34%
Number/percentage of T's	48,070,328 / 31.72%
Number/percentage of G's	33,339,714 / 22%
Number/percentage of N's	3,067 / 0%
GC Percentage	40.33%

2.3. Coverage

Mean	0.049

Standard Deviation	0.4791

2.4. Mapping Quality

Mean Mapping Quality	43.34

2.5. Mismatches and indels

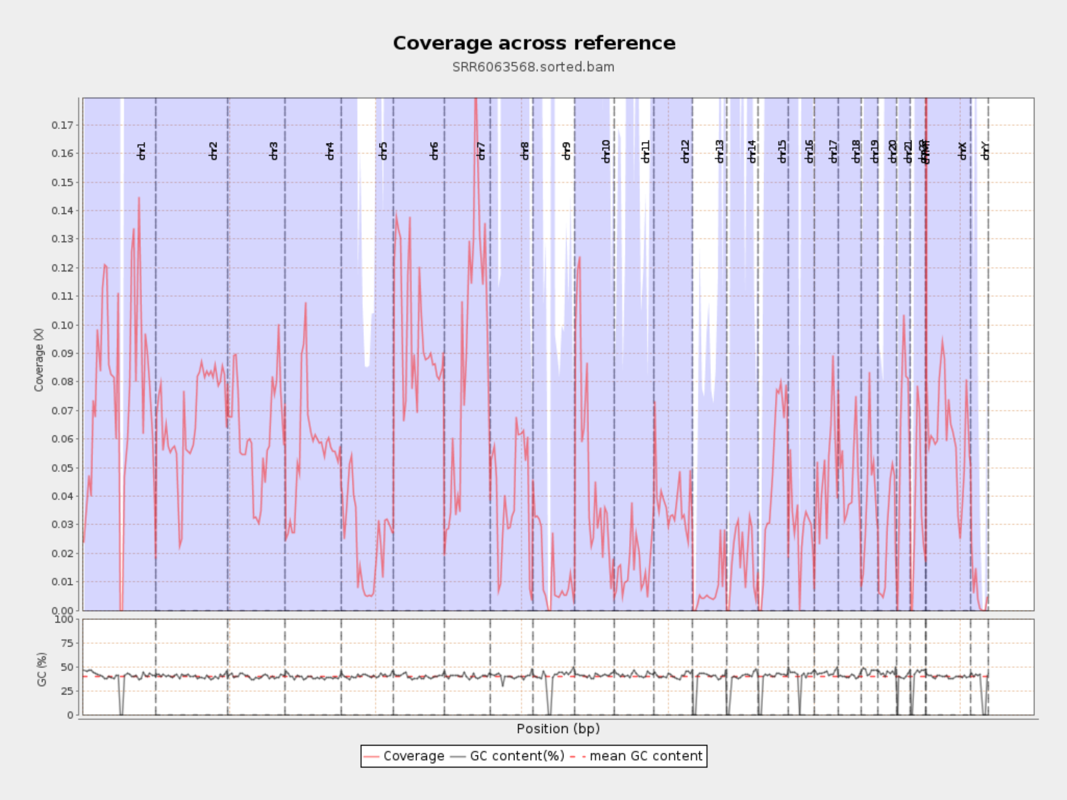
General error rate	0.8%
Mismatches	1,186,068
Insertions	11,133
Mapped reads with at least one insertion	0.48%
Deletions	40,688
Mapped reads with at least one deletion	1.74%
Homopolymer indels	46.22%

2.6. Chromosome stats

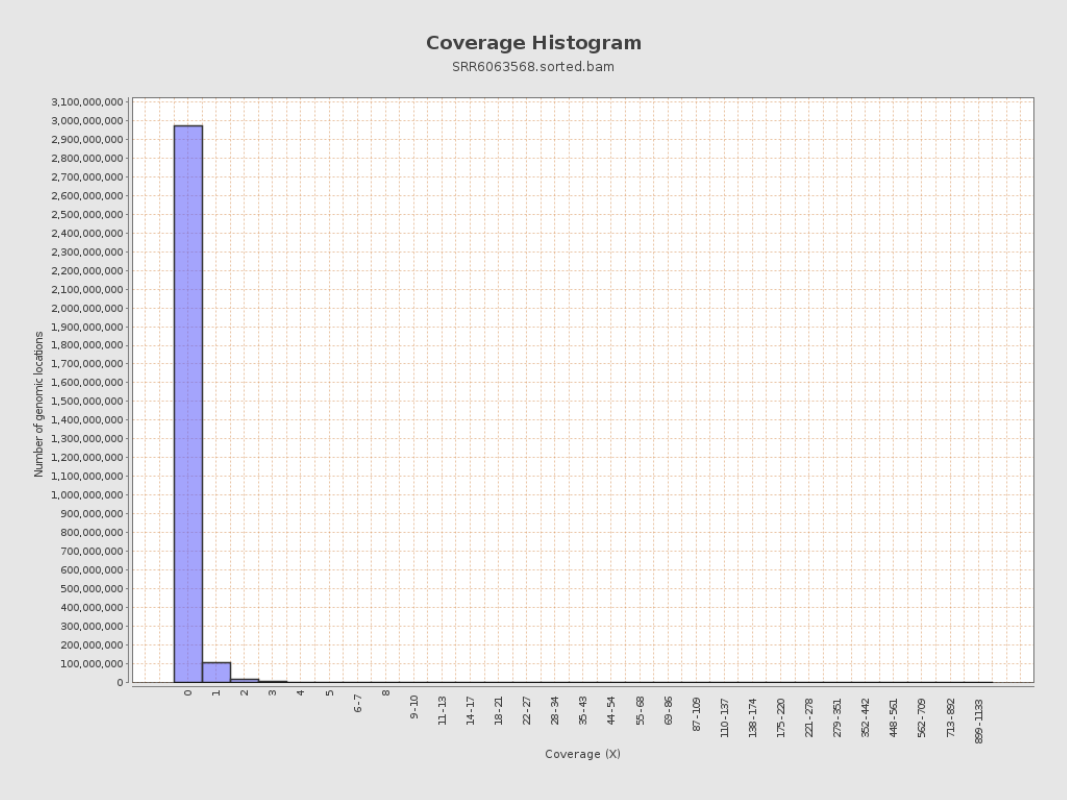
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19006717	0.0763	1.0166
chr2	243199373	16606496	0.0683	0.5115
chr3	198022430	12340195	0.0623	0.3014
chr4	191154276	10824086	0.0566	0.2812
chr5	180915260	4318797	0.0239	0.1829
chr6	171115067	16692896	0.0976	0.4704
chr7	159138663	14008103	0.088	0.7611

chr8	146364022	5767752	0.0394	0.6806
chr9	141213431	1786851	0.0127	0.2615
chr10	135534747	6650935	0.0491	0.4723
chr11	135006516	2069329	0.0153	0.1865
chr12	133851895	5031095	0.0376	0.2339
chr13	115169878	897676	0.0078	0.1065
chr14	107349540	1932355	0.018	0.1814
chr15	102531392	4768328	0.0465	0.2605
chr16	90354753	2600473	0.0288	0.2175
chr17	81195210	3942387	0.0486	0.27
chr18	78077248	3722443	0.0477	0.5847
chr19	59128983	2390808	0.0404	0.6225
chr20	63025520	1583223	0.0251	0.2033
chr21	48129895	2956822	0.0614	0.2956
chr22	51304566	1792705	0.0349	0.2174
chrMT	16571	42327	2.5543	2.3739
chrX	155270560	9537559	0.0614	0.3273
chrY	59373566	352818	0.0059	0.1085

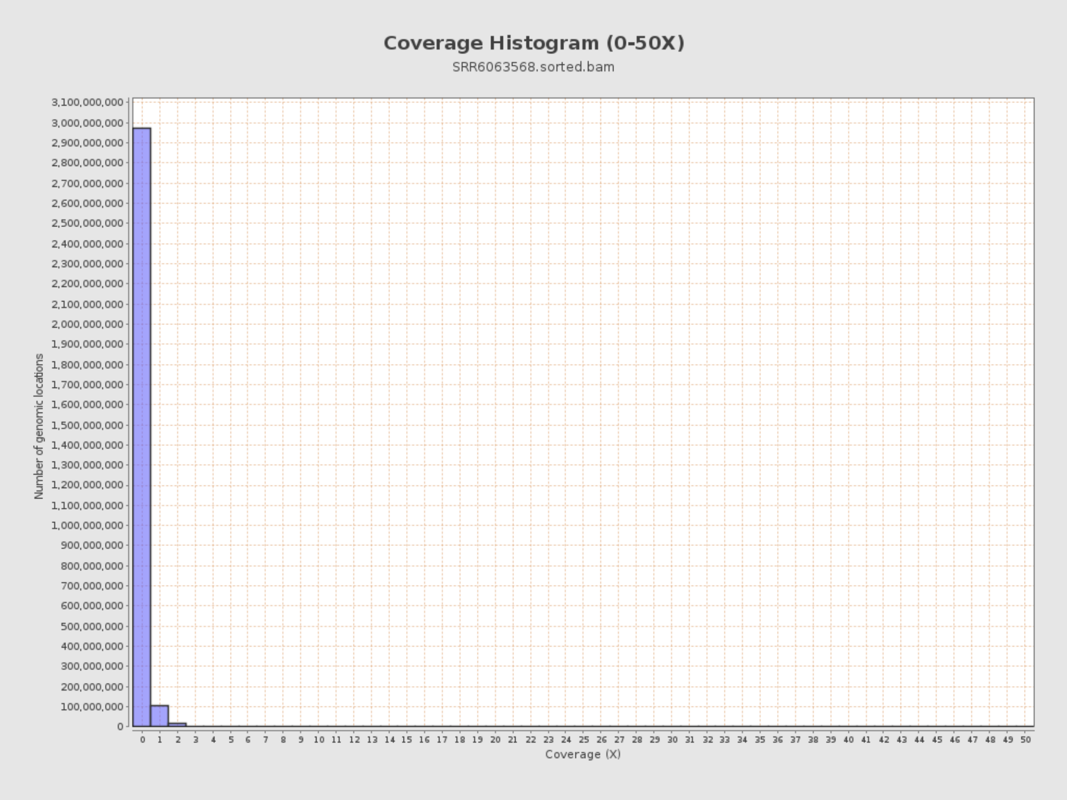
3. Results : Coverage across reference



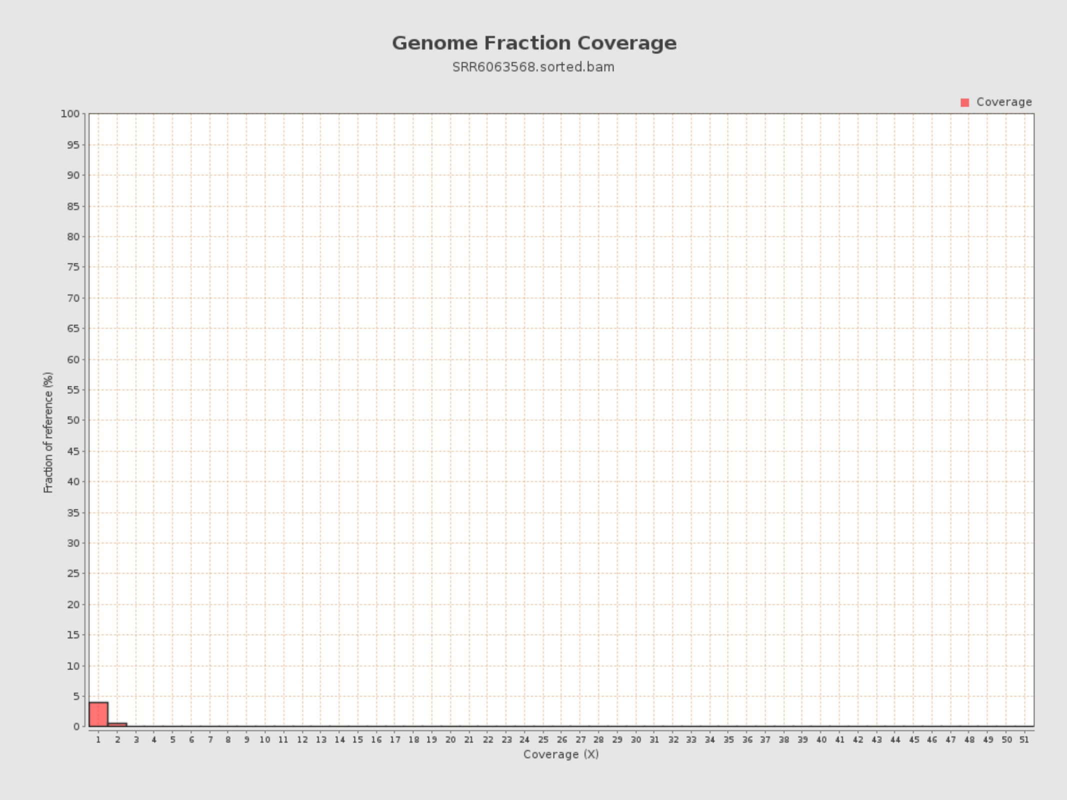
4. Results : Coverage Histogram



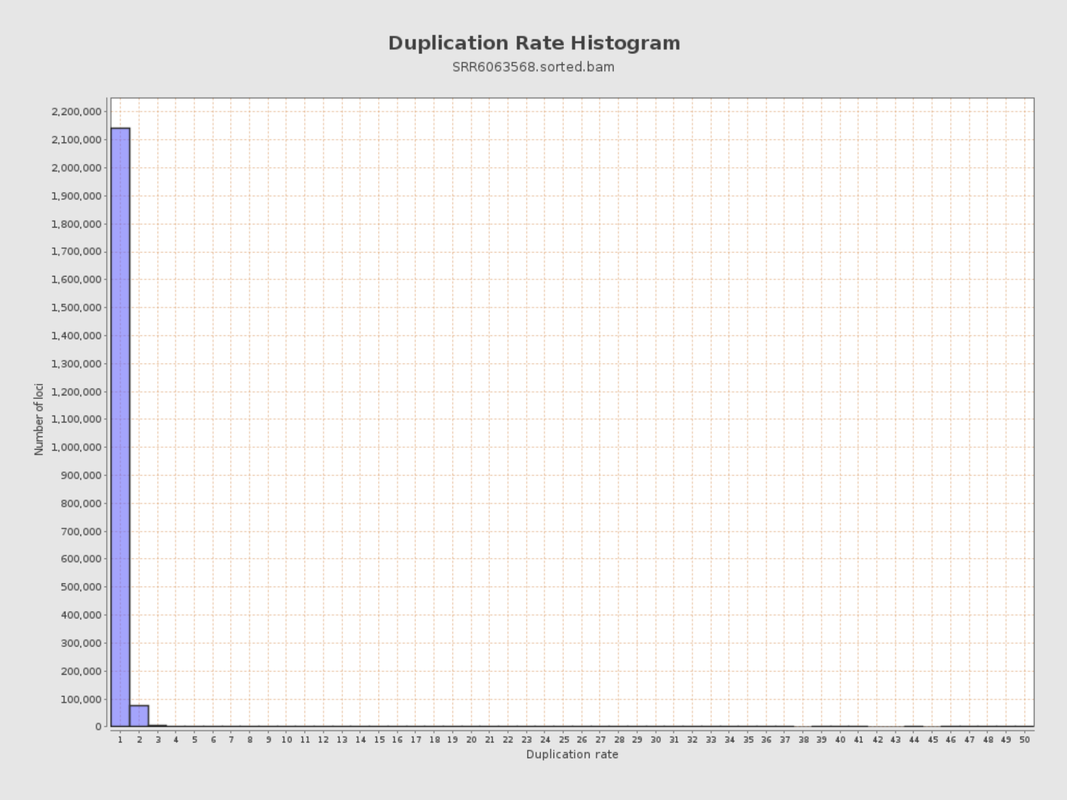
5. Results : Coverage Histogram (0-50X)



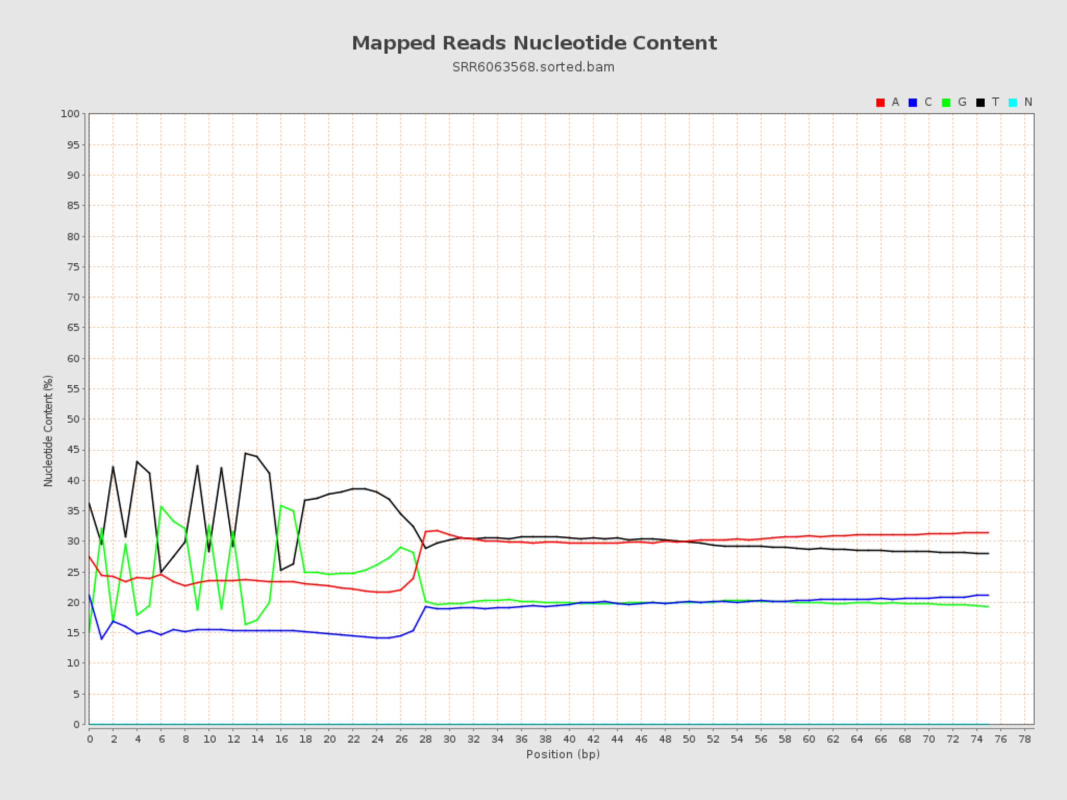
6. Results : Genome Fraction Coverage



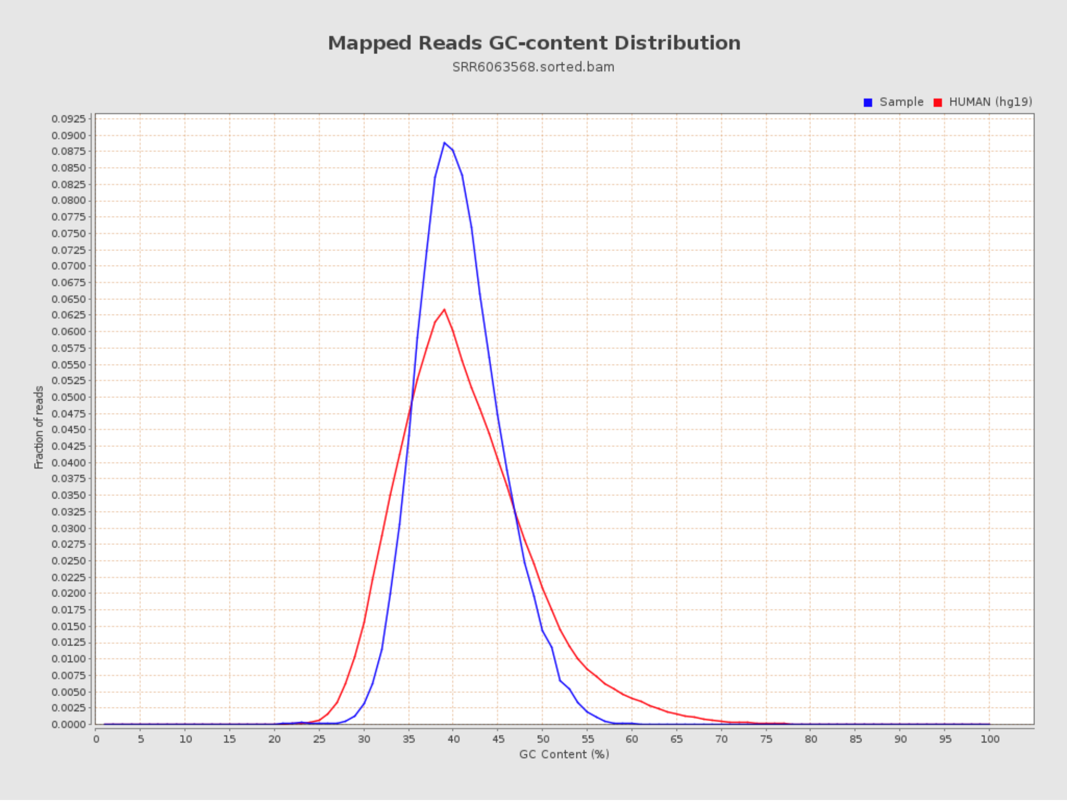
7. Results : Duplication Rate Histogram



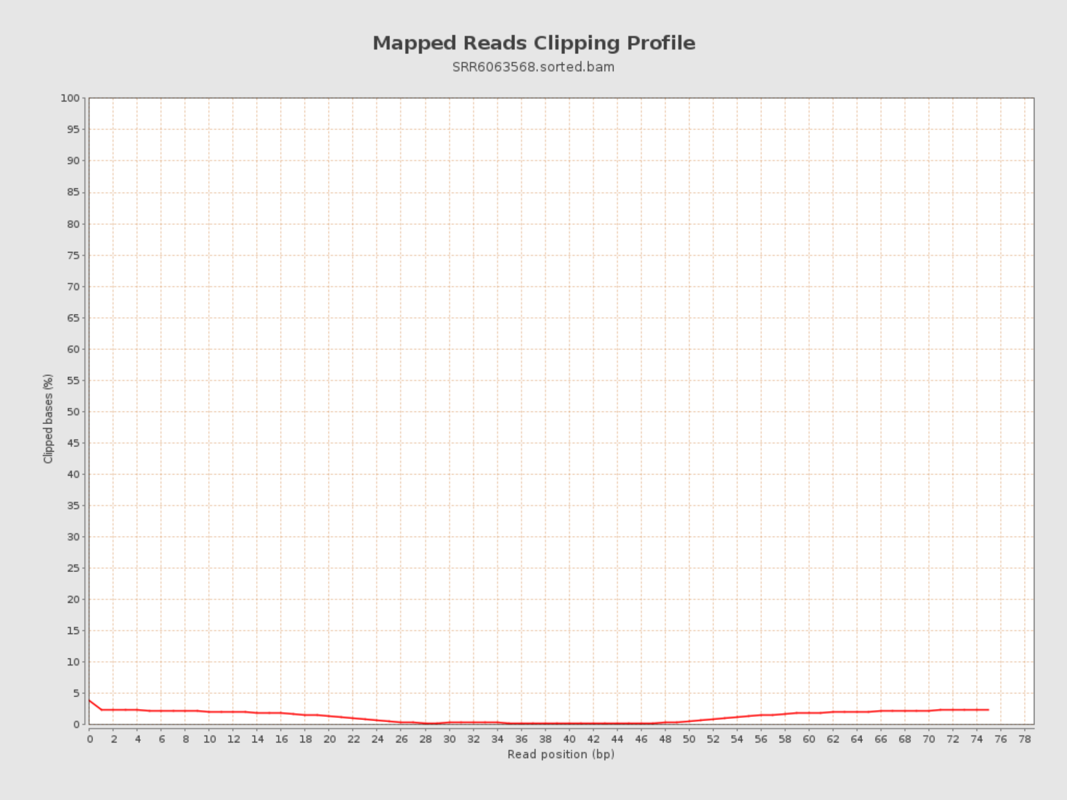
8. Results : Mapped Reads Nucleotide Content



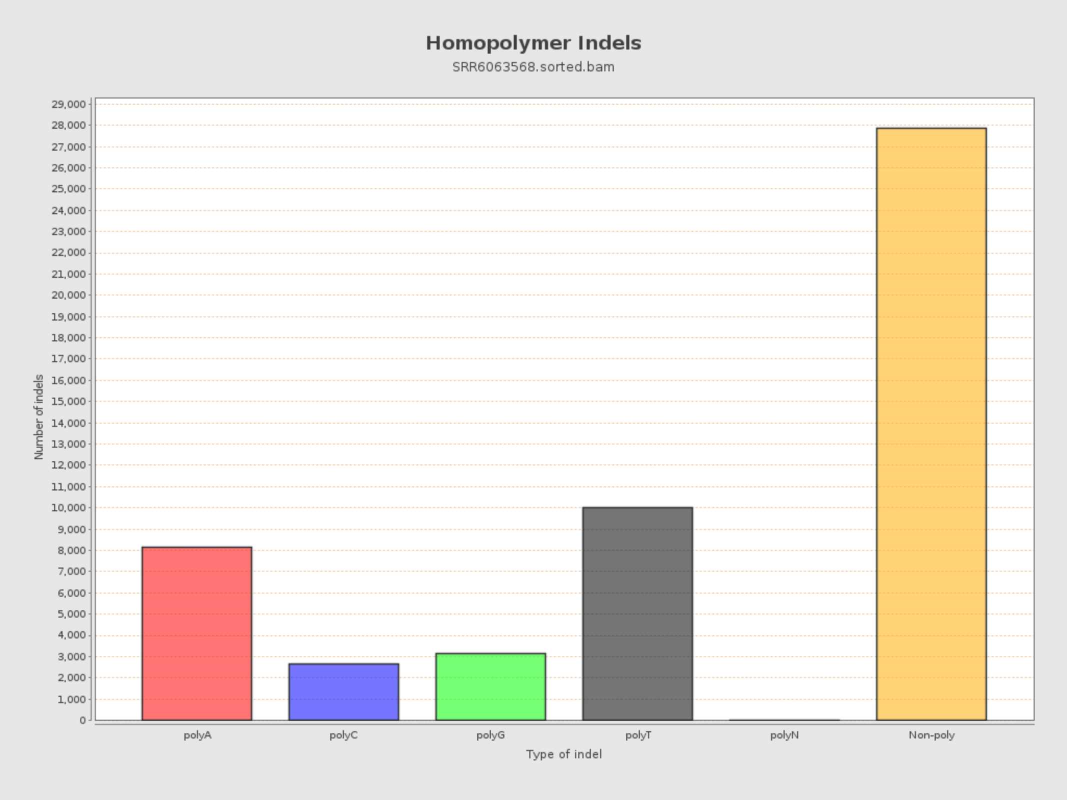
9. Results : Mapped Reads GC-content Distribution



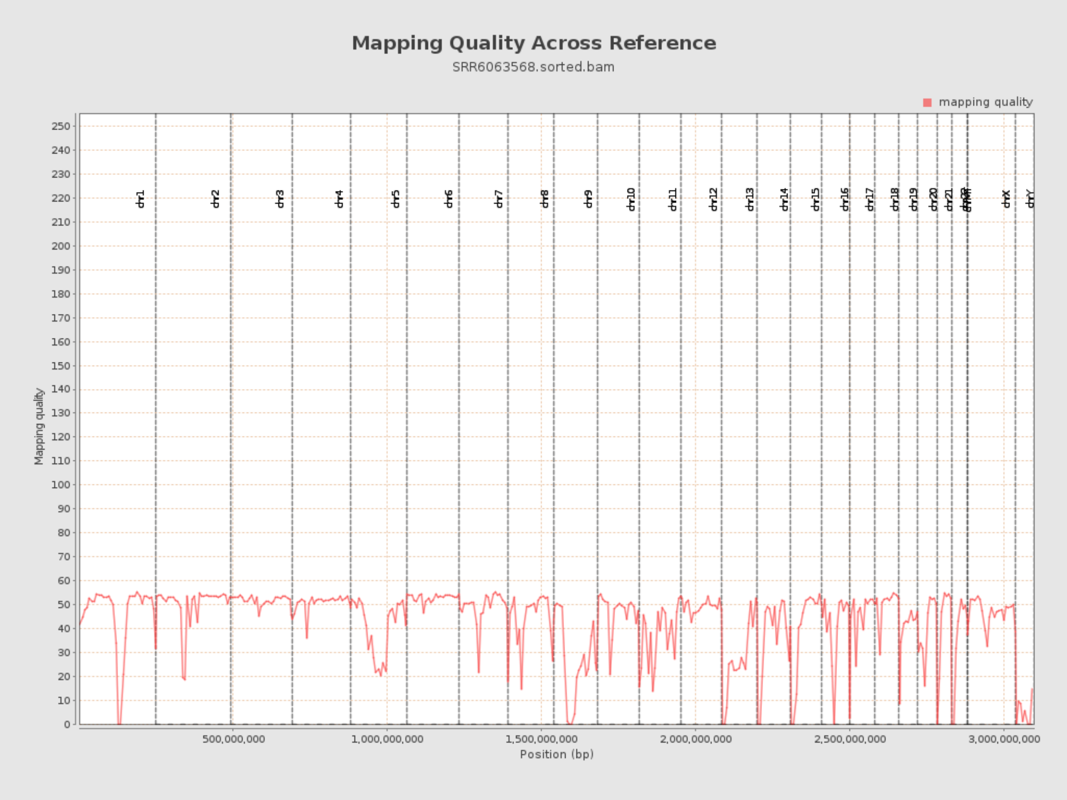
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram