Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 08:46:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068079.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_SRR6068079 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068079.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 08:46:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068079.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,752,461
Mapped reads	2,355,773 / 85.59%
Unmapped reads	396,688 / 14.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,385 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	175,787 / 6.39%
Duplication rate	6.07%
Clipped reads	1,291,277 / 46.91%

2.2. ACGT Content

Number/percentage of A's	39,435,152 / 26.04%
Number/percentage of C's	28,059,800 / 18.53%
Number/percentage of T's	47,969,263 / 31.67%
Number/percentage of G's	35,989,518 / 23.76%
Number/percentage of N's	2,919 / 0%
GC Percentage	42.29%

2.3. Coverage

Mean	0.0489

Standard Deviation	0.4806

2.4. Mapping Quality

Mean Mapping Quality	43.28

2.5. Mismatches and indels

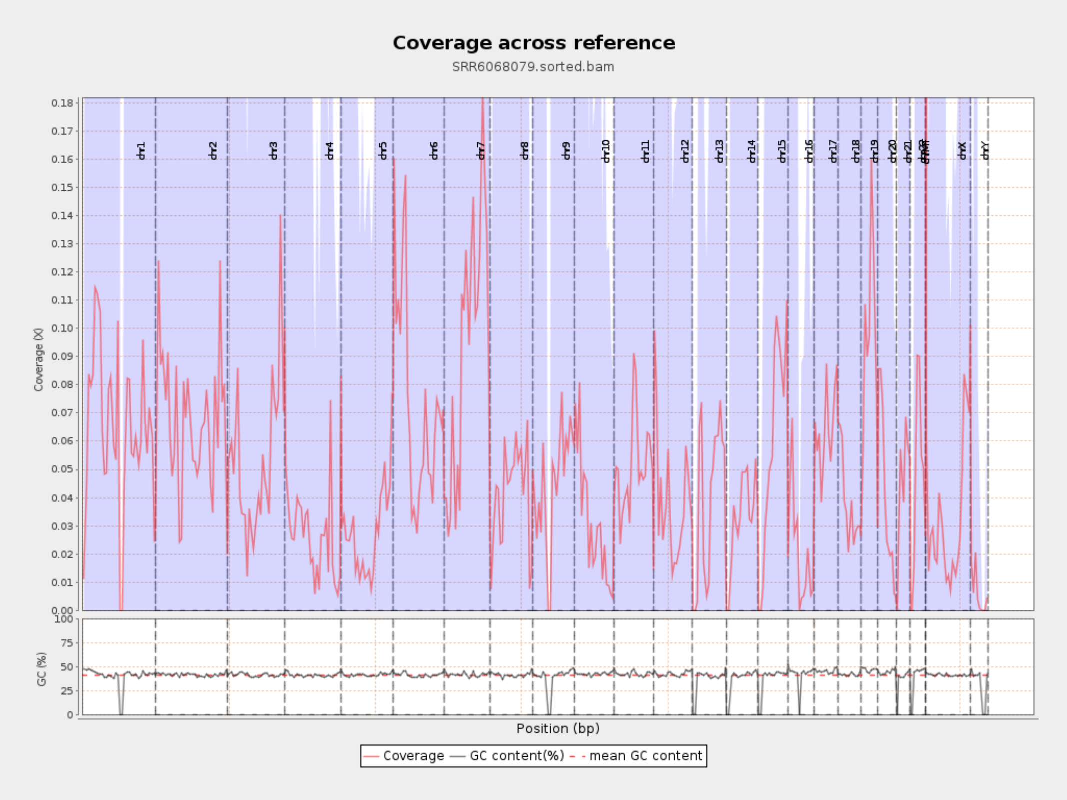
General error rate	0.82%
Mismatches	1,222,721
Insertions	11,111
Mapped reads with at least one insertion	0.47%
Deletions	41,102
Mapped reads with at least one deletion	1.73%
Homopolymer indels	45.96%

2.6. Chromosome stats

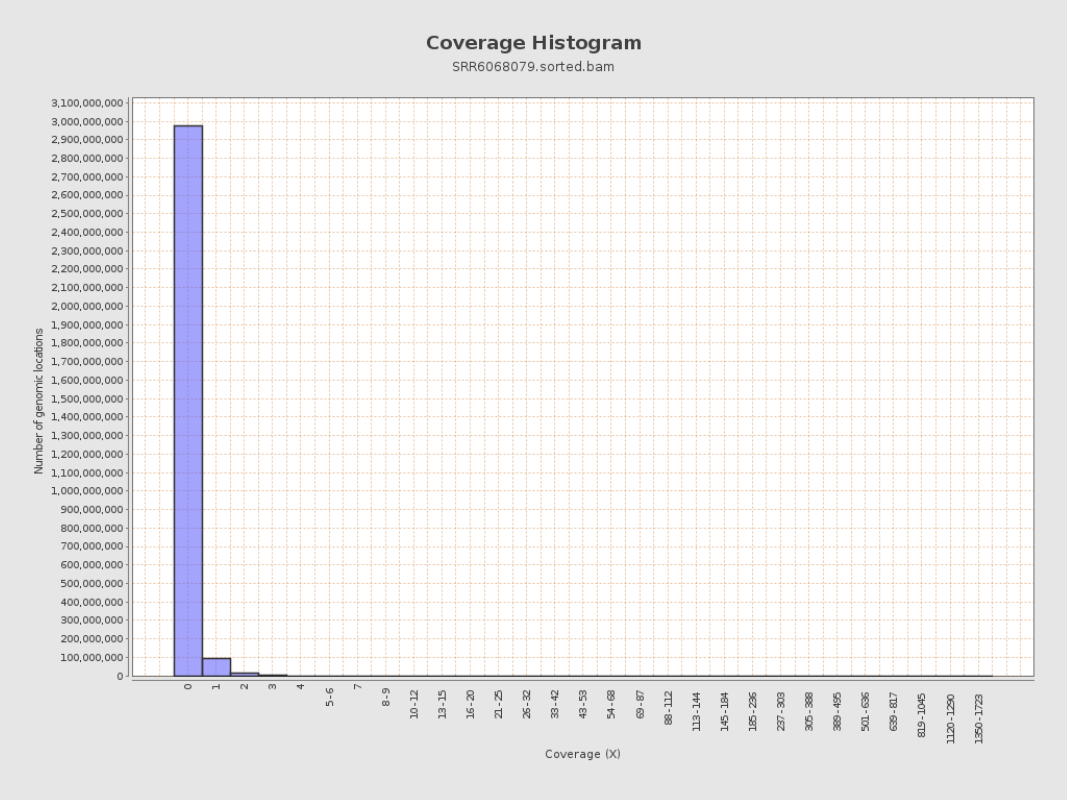
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15858555	0.0636	1.0207
chr2	243199373	16468501	0.0677	0.8009
chr3	198022430	10430653	0.0527	0.2804
chr4	191154276	5039870	0.0264	0.2213
chr5	180915260	5228228	0.0289	0.2088
chr6	171115067	12464569	0.0728	0.3728
chr7	159138663	14845285	0.0933	0.6188

chr8	146364022	6076031	0.0415	0.3546
chr9	141213431	6239438	0.0442	0.3806
chr10	135534747	4107440	0.0303	0.2616
chr11	135006516	6852685	0.0508	0.3196
chr12	133851895	5261534	0.0393	0.2508
chr13	115169878	4573365	0.0397	0.2463
chr14	107349540	3523310	0.0328	0.2413
chr15	102531392	6036135	0.0589	0.3038
chr16	90354753	1870545	0.0207	0.1962
chr17	81195210	5242570	0.0646	0.3219
chr18	78077248	3032029	0.0388	0.5607
chr19	59128983	5707469	0.0965	0.6765
chr20	63025520	2578176	0.0409	0.2525
chr21	48129895	2163027	0.0449	0.2708
chr22	51304566	2394445	0.0467	0.2614
chrMT	16571	78067	4.7111	4.2054
chrX	155270560	5086005	0.0328	0.24
chrY	59373566	363952	0.0061	0.2353

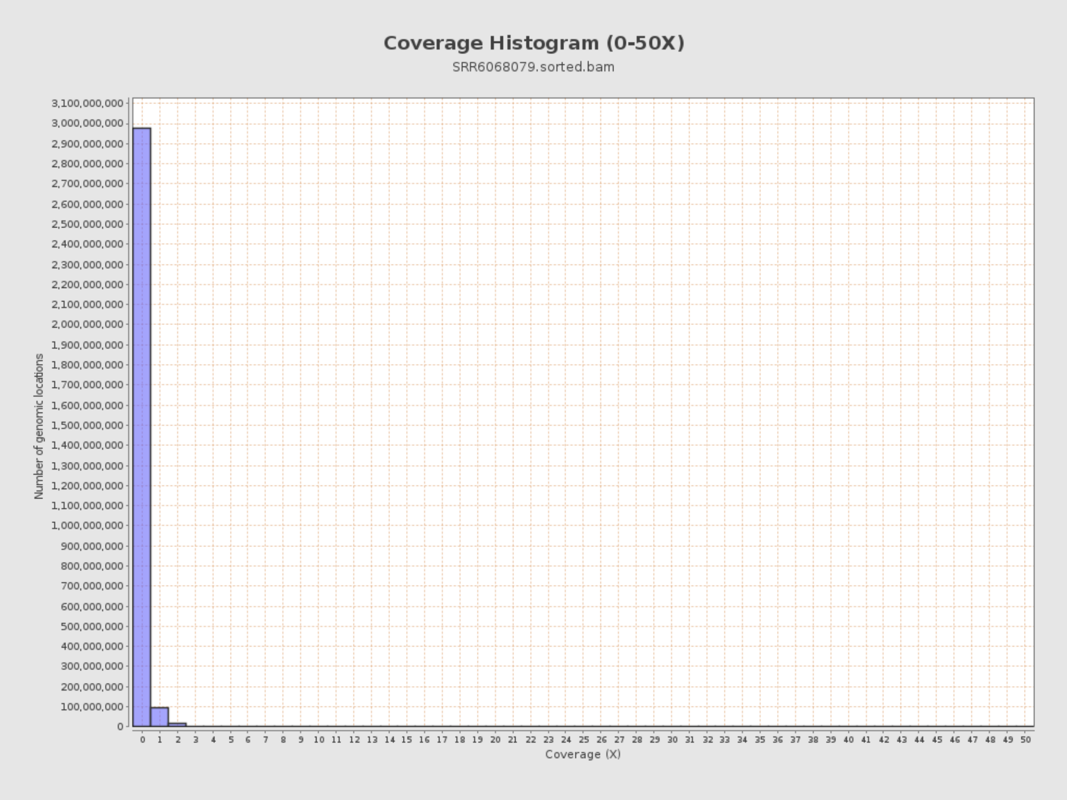
3. Results : Coverage across reference



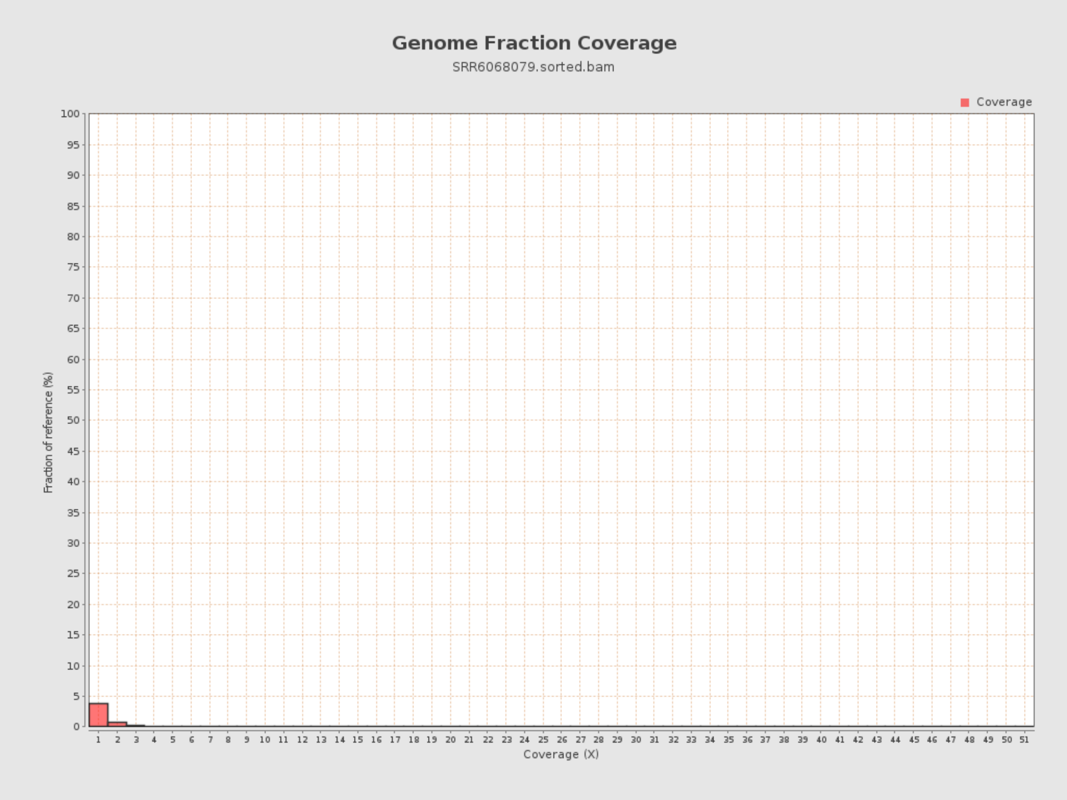
4. Results : Coverage Histogram



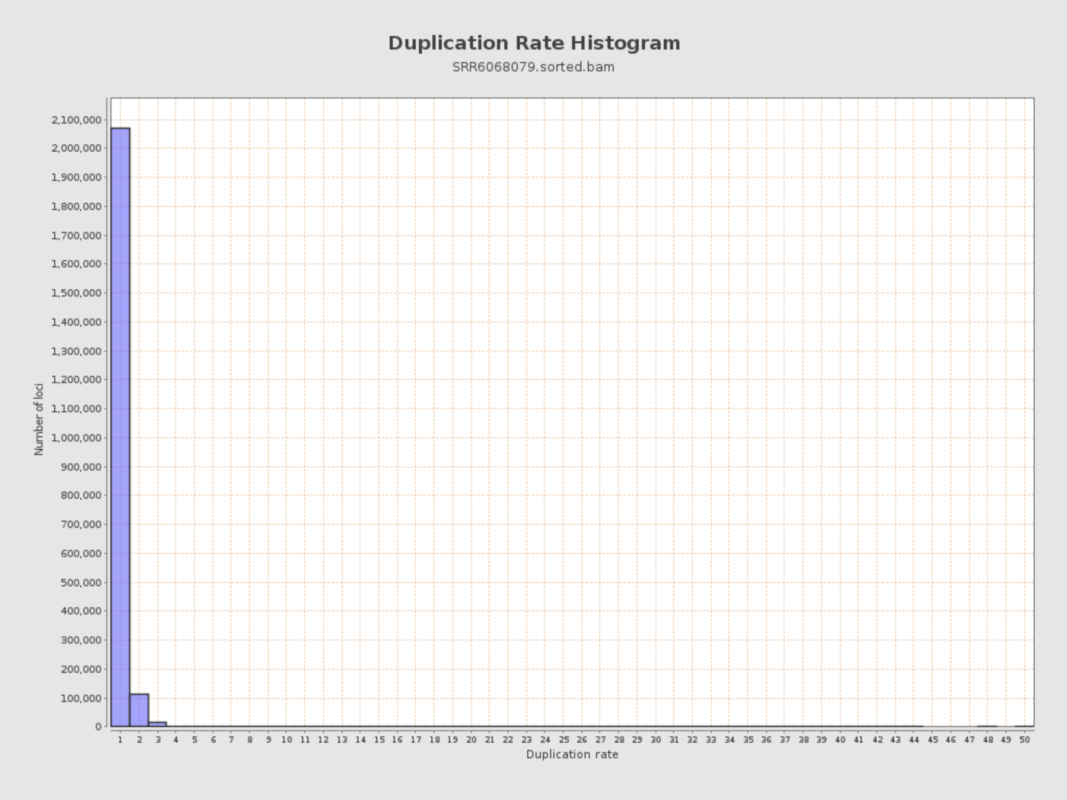
5. Results : Coverage Histogram (0-50X)



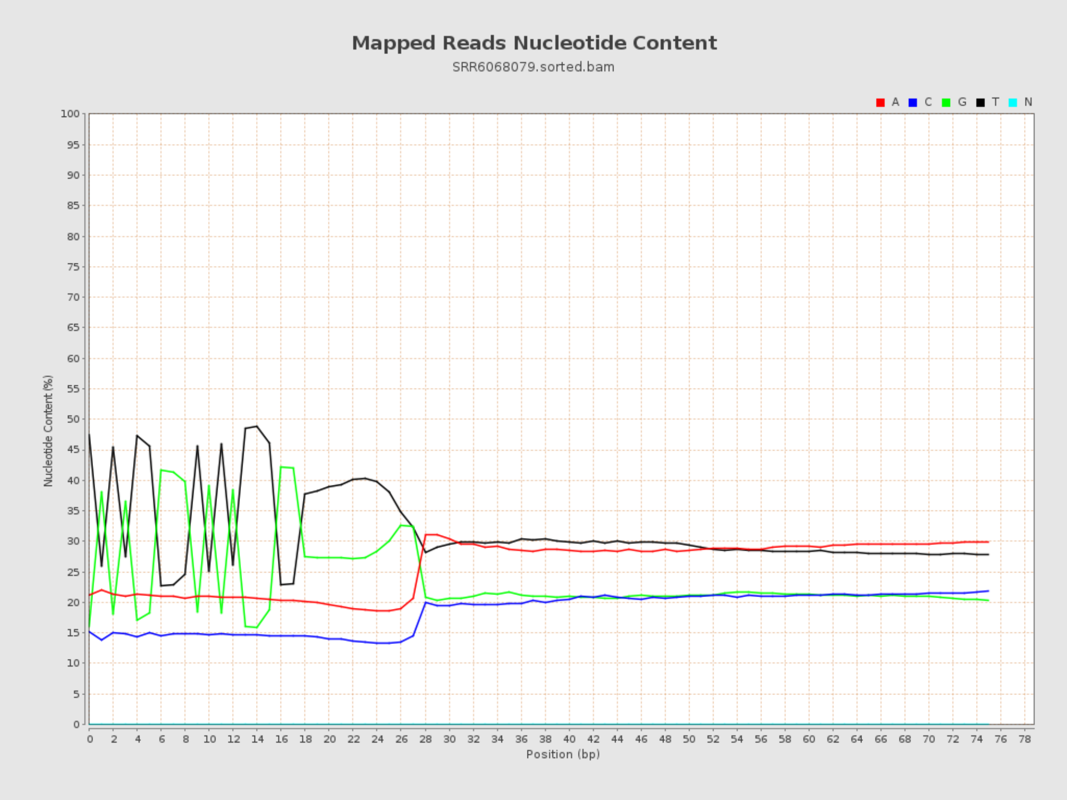
6. Results : Genome Fraction Coverage



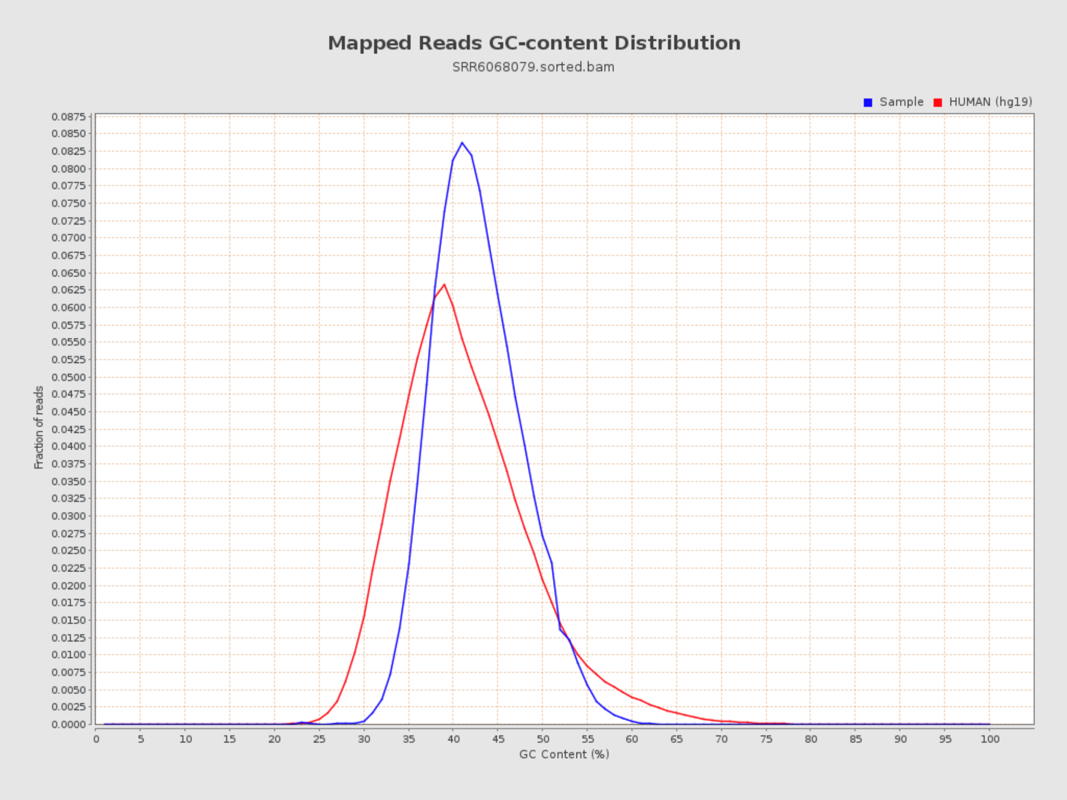
7. Results : Duplication Rate Histogram



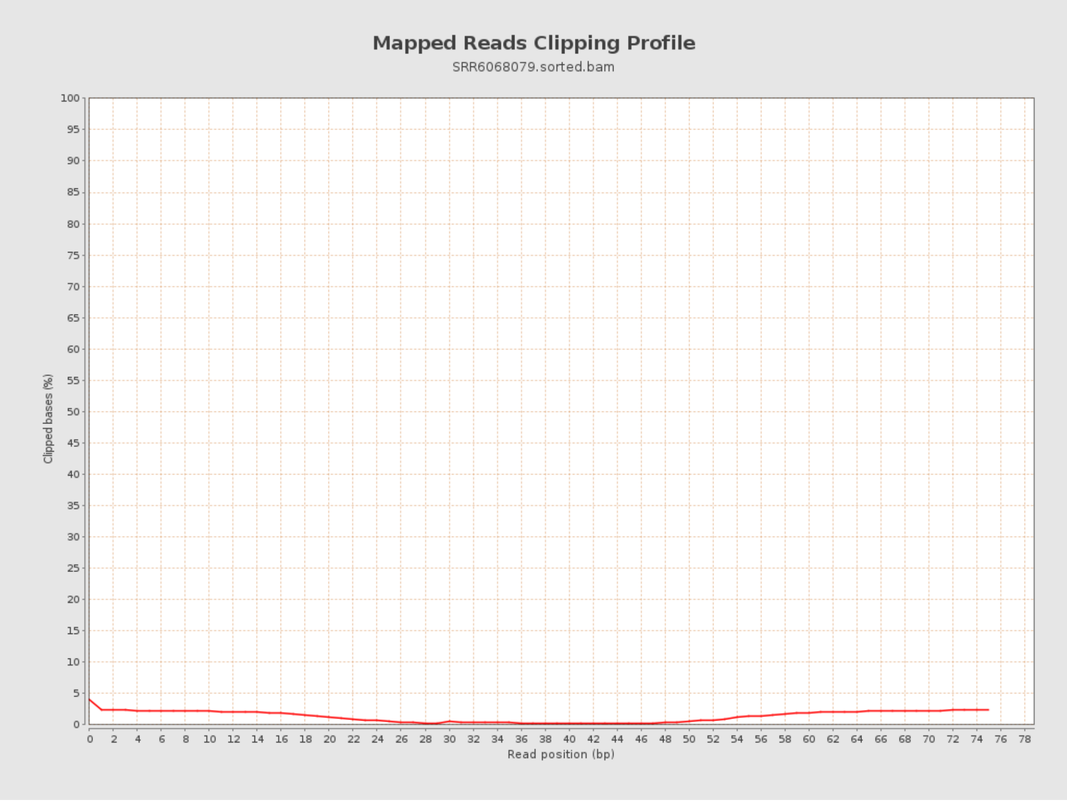
8. Results : Mapped Reads Nucleotide Content



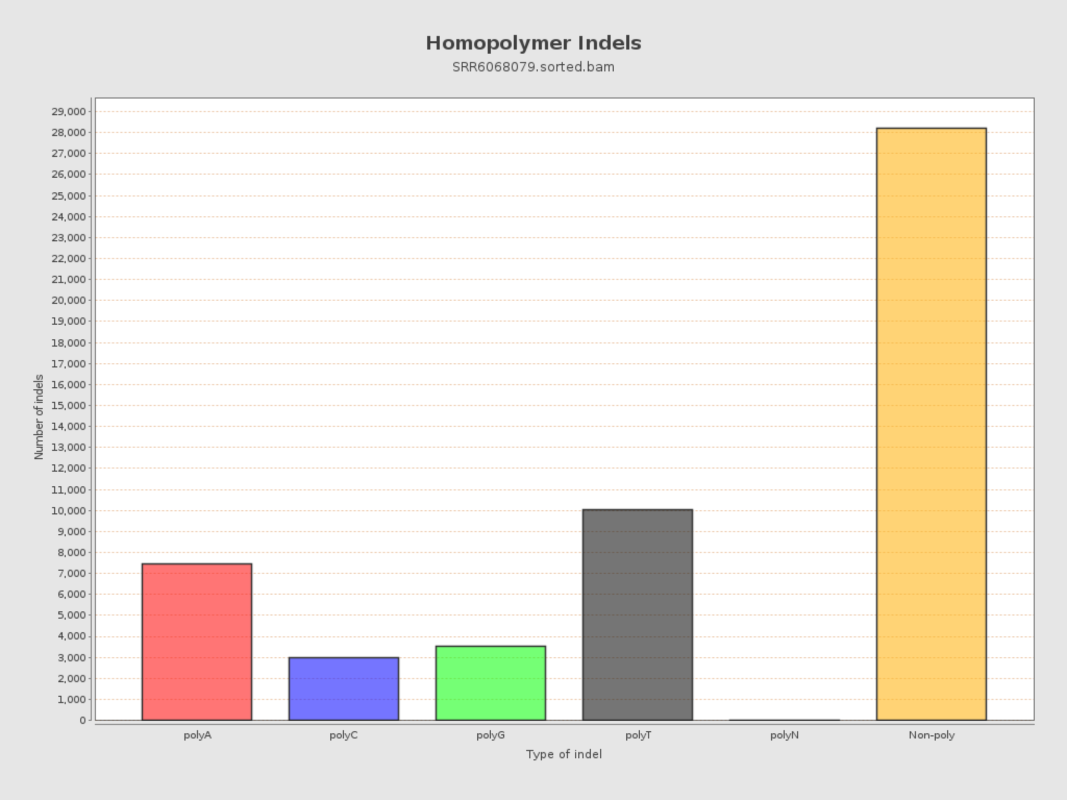
9. Results : Mapped Reads GC-content Distribution



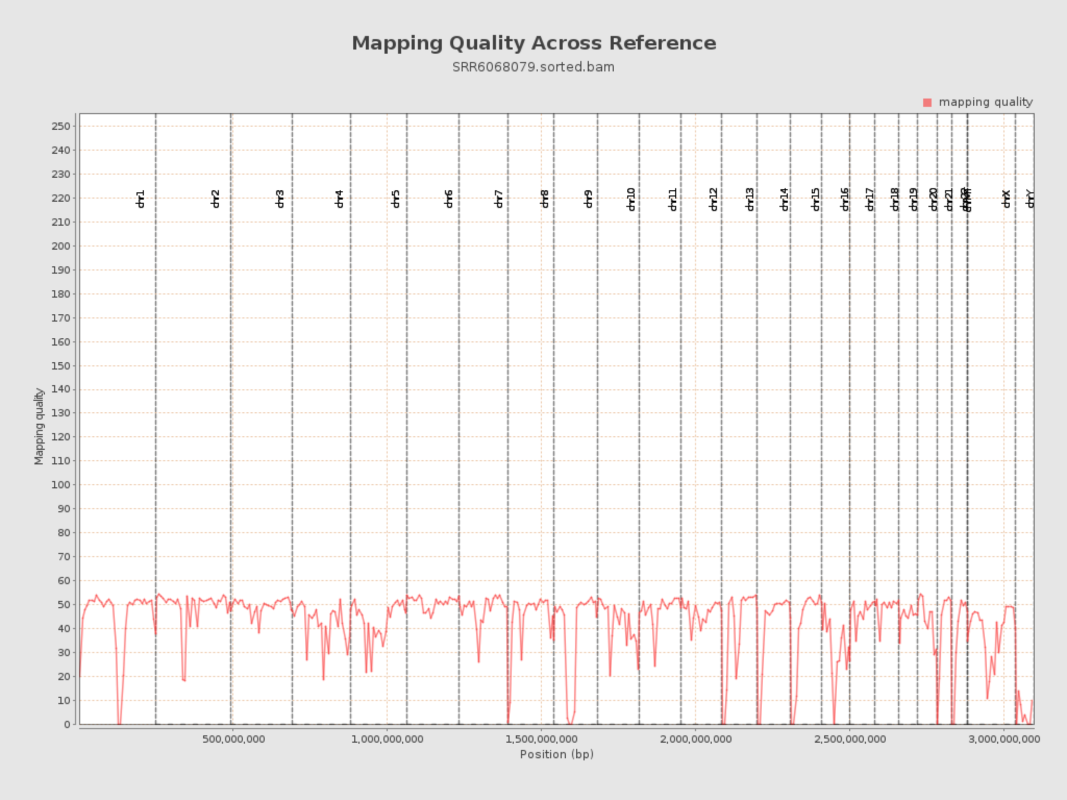
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram