Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 07:36:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068063.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_SRR6068063 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068063.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 07:36:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068063.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,736,501
Mapped reads	1,463,714 / 84.29%
Unmapped reads	272,787 / 15.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,838 / 0.91%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	134,357 / 7.74%
Duplication rate	7.43%
Clipped reads	849,998 / 48.95%

2.2. ACGT Content

Number/percentage of A's	24,900,075 / 26.76%
Number/percentage of C's	16,946,387 / 18.22%
Number/percentage of T's	29,729,894 / 31.96%
Number/percentage of G's	21,456,637 / 23.06%
Number/percentage of N's	1,733 / 0%
GC Percentage	41.28%

2.3. Coverage

Mean	0.0301

Standard Deviation	0.3682

2.4. Mapping Quality

Mean Mapping Quality	43.16

2.5. Mismatches and indels

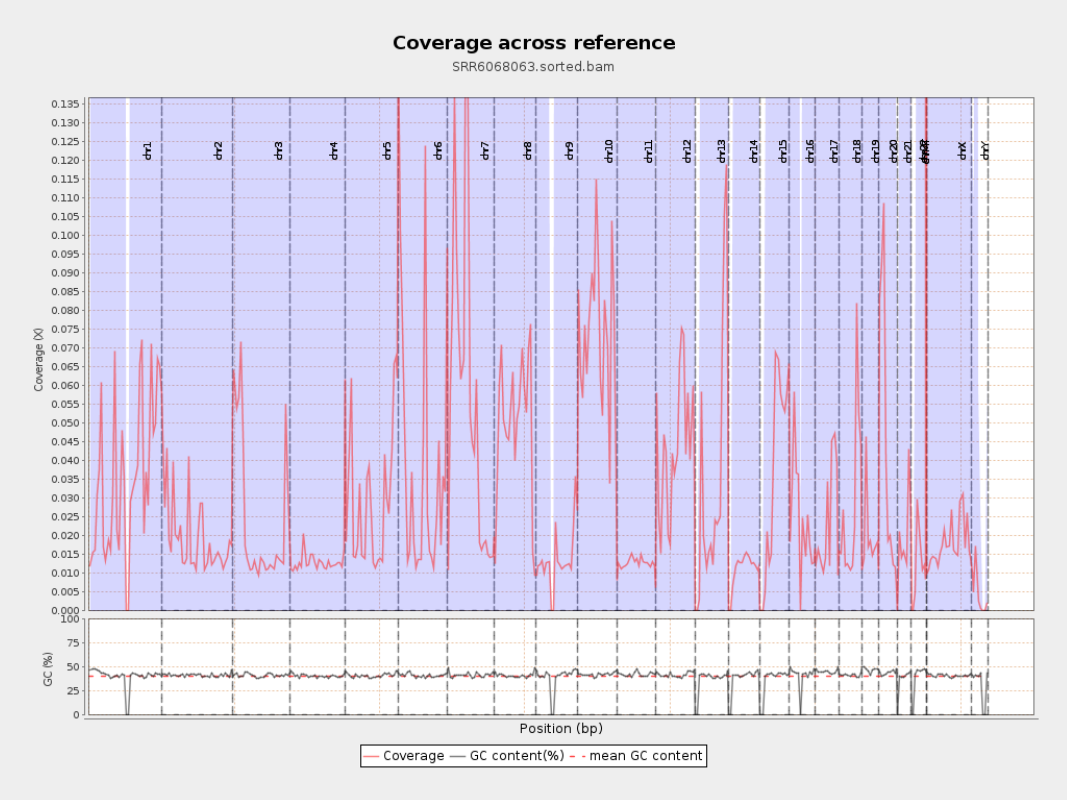
General error rate	0.79%
Mismatches	719,405
Insertions	6,795
Mapped reads with at least one insertion	0.46%
Deletions	23,322
Mapped reads with at least one deletion	1.58%
Homopolymer indels	45.56%

2.6. Chromosome stats

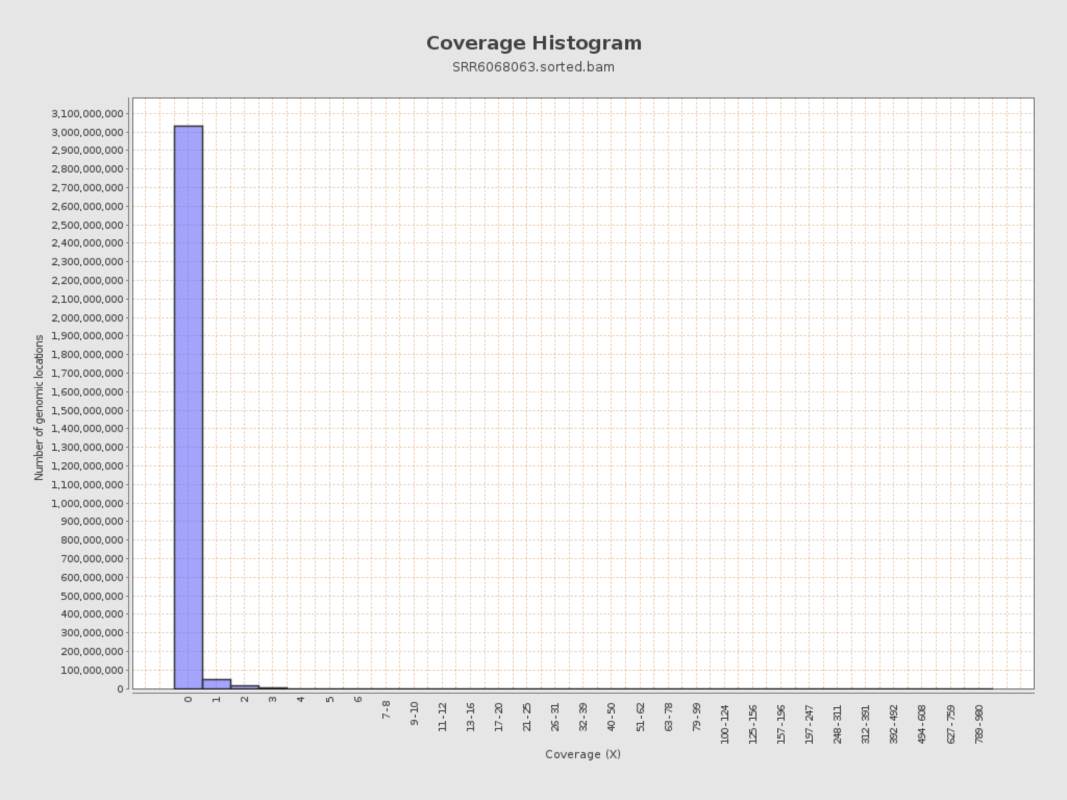
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8723654	0.035	0.2979
chr2	243199373	4750126	0.0195	0.4461
chr3	198022430	4858794	0.0245	0.2096
chr4	191154276	2422491	0.0127	0.1619
chr5	180915260	5350863	0.0296	0.2318
chr6	171115067	6865053	0.0401	0.2926
chr7	159138663	9360596	0.0588	1.1109

chr8	146364022	7249409	0.0495	0.3642
chr9	141213431	1868556	0.0132	0.1922
chr10	135534747	10082741	0.0744	0.4284
chr11	135006516	1705204	0.0126	0.1584
chr12	133851895	5964044	0.0446	0.2848
chr13	115169878	4091394	0.0355	0.256
chr14	107349540	1164978	0.0109	0.1457
chr15	102531392	3694149	0.036	0.2654
chr16	90354753	2194875	0.0243	0.2123
chr17	81195210	1917531	0.0236	0.203
chr18	78077248	2166865	0.0278	0.258
chr19	59128983	1174305	0.0199	0.2279
chr20	63025520	2843194	0.0451	0.2901
chr21	48129895	951512	0.0198	0.1944
chr22	51304566	597886	0.0117	0.1426
chrMT	16571	70485	4.2535	3.4613
chrX	155270560	2742151	0.0177	0.1872
chrY	59373566	261120	0.0044	0.2367

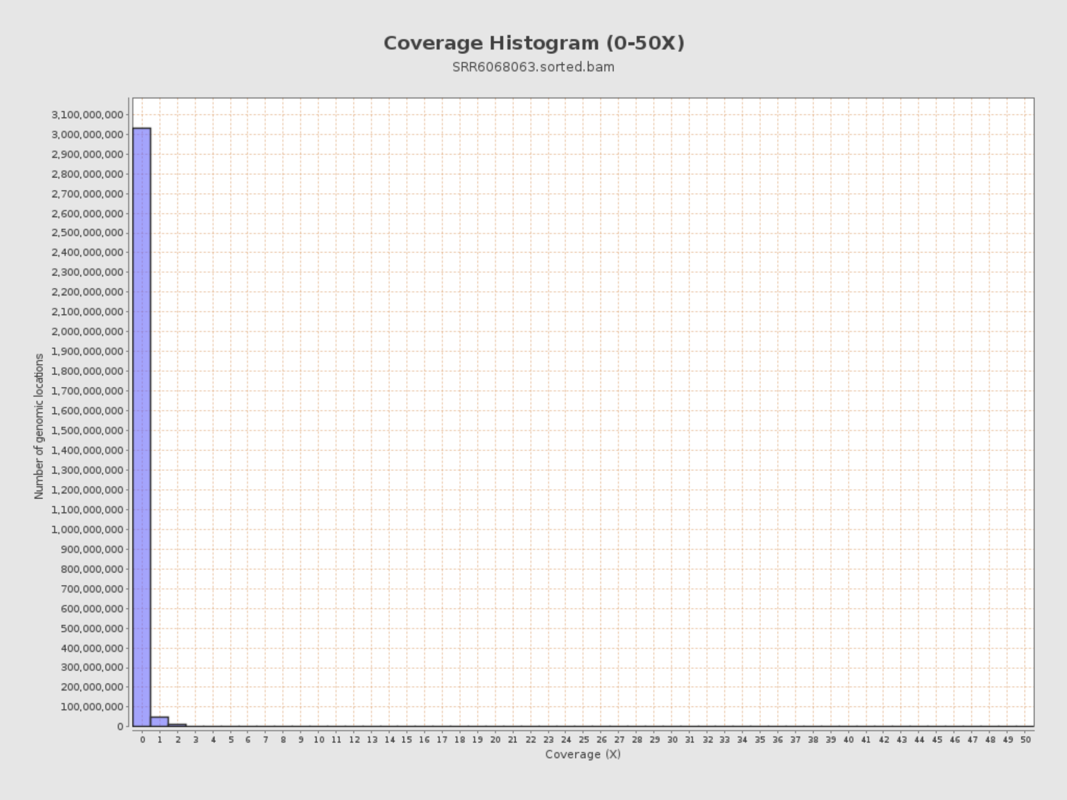
3. Results : Coverage across reference



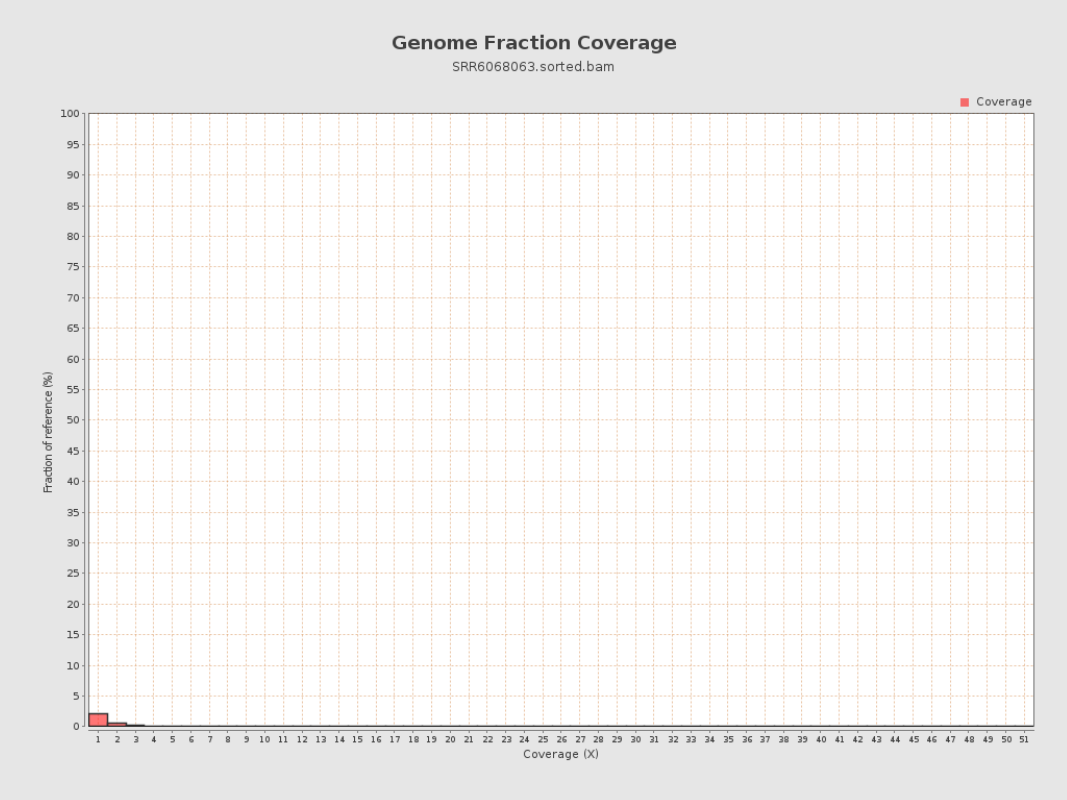
4. Results : Coverage Histogram



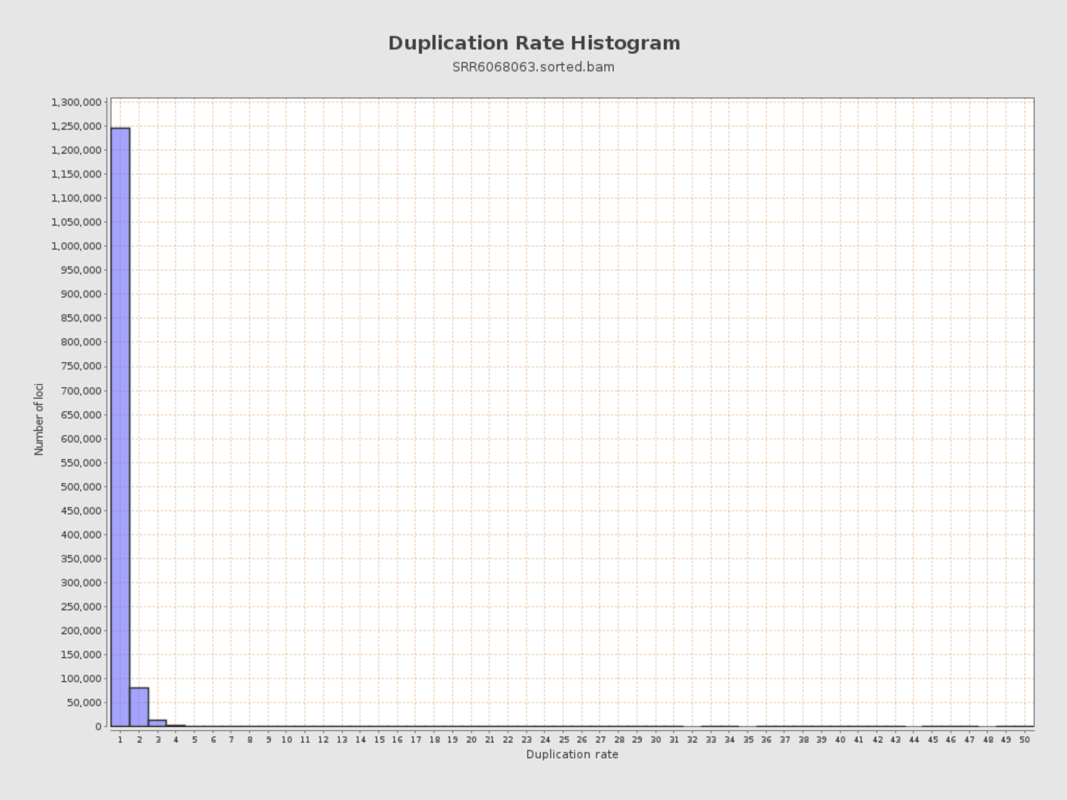
5. Results : Coverage Histogram (0-50X)



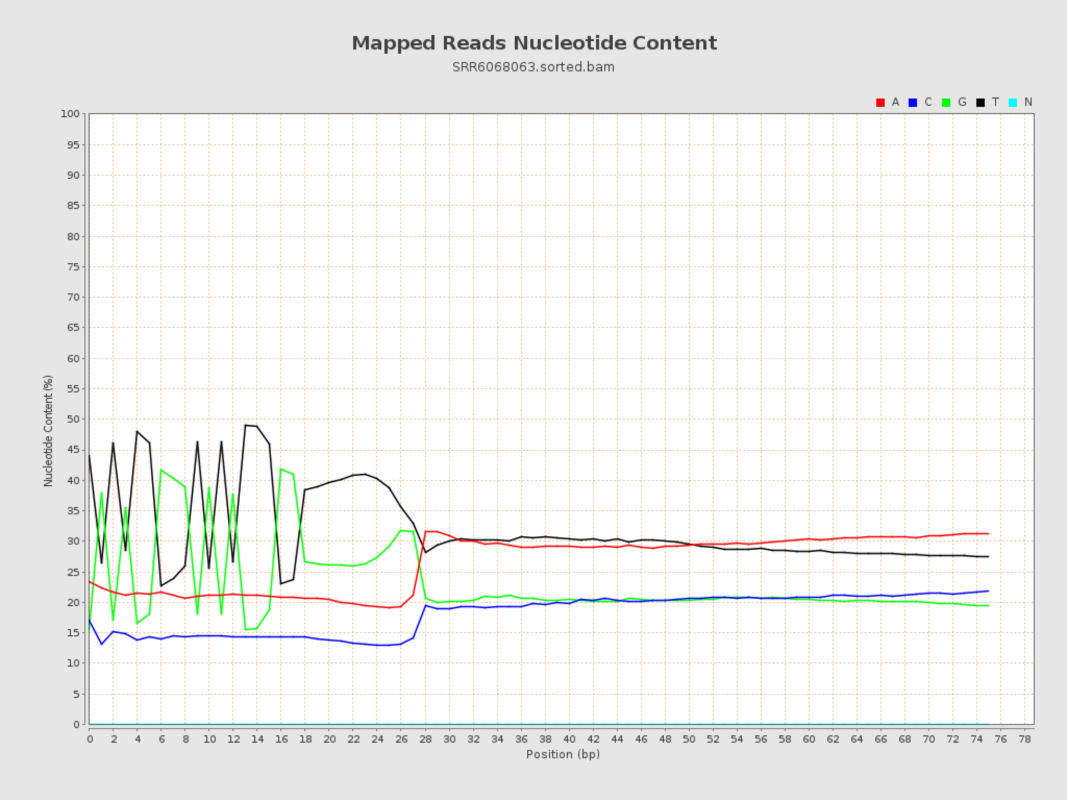
6. Results : Genome Fraction Coverage



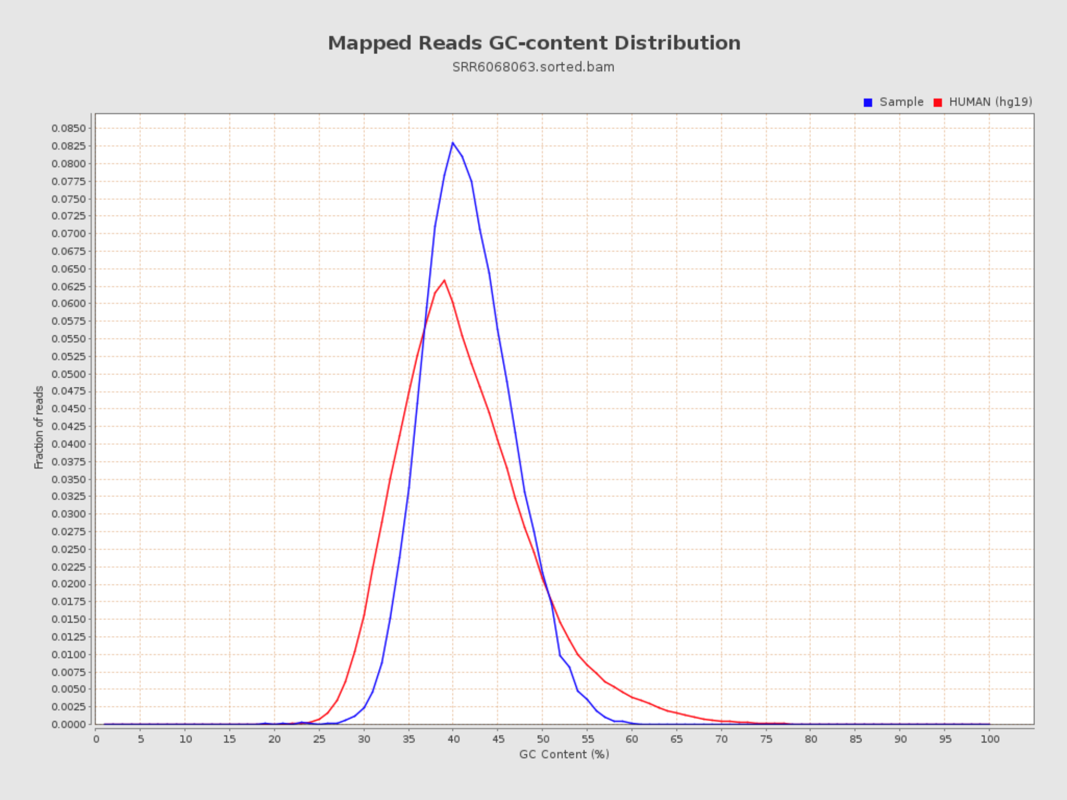
7. Results : Duplication Rate Histogram



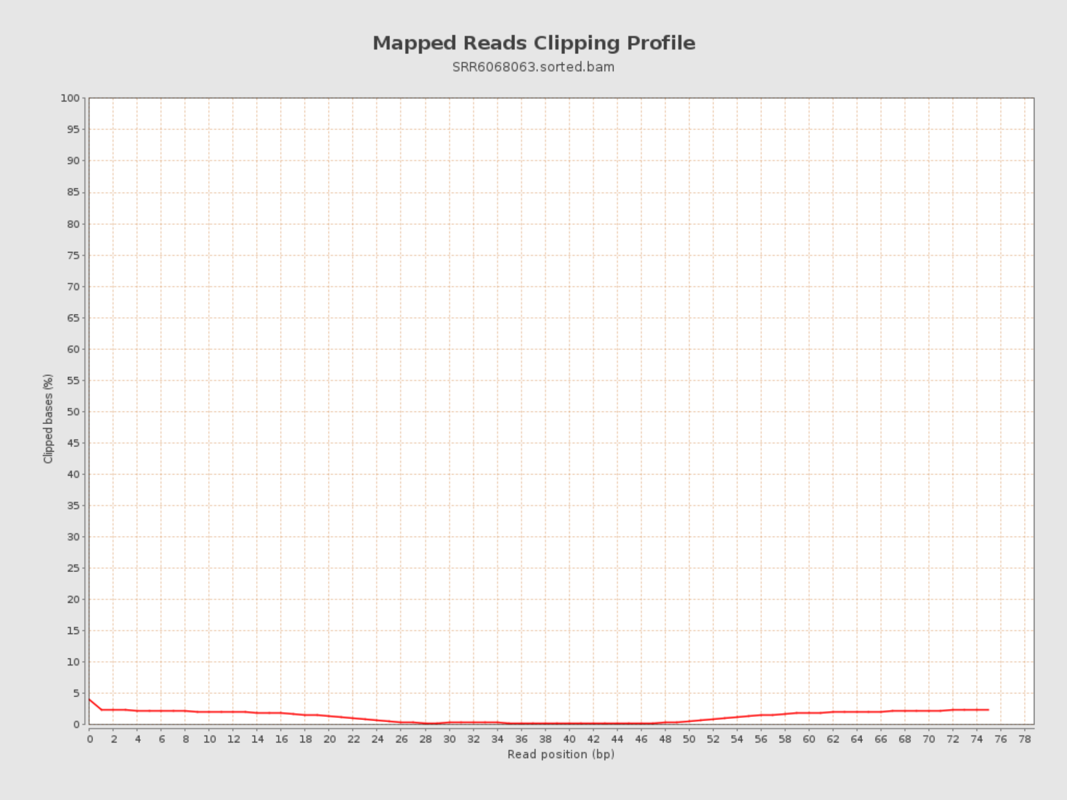
8. Results : Mapped Reads Nucleotide Content



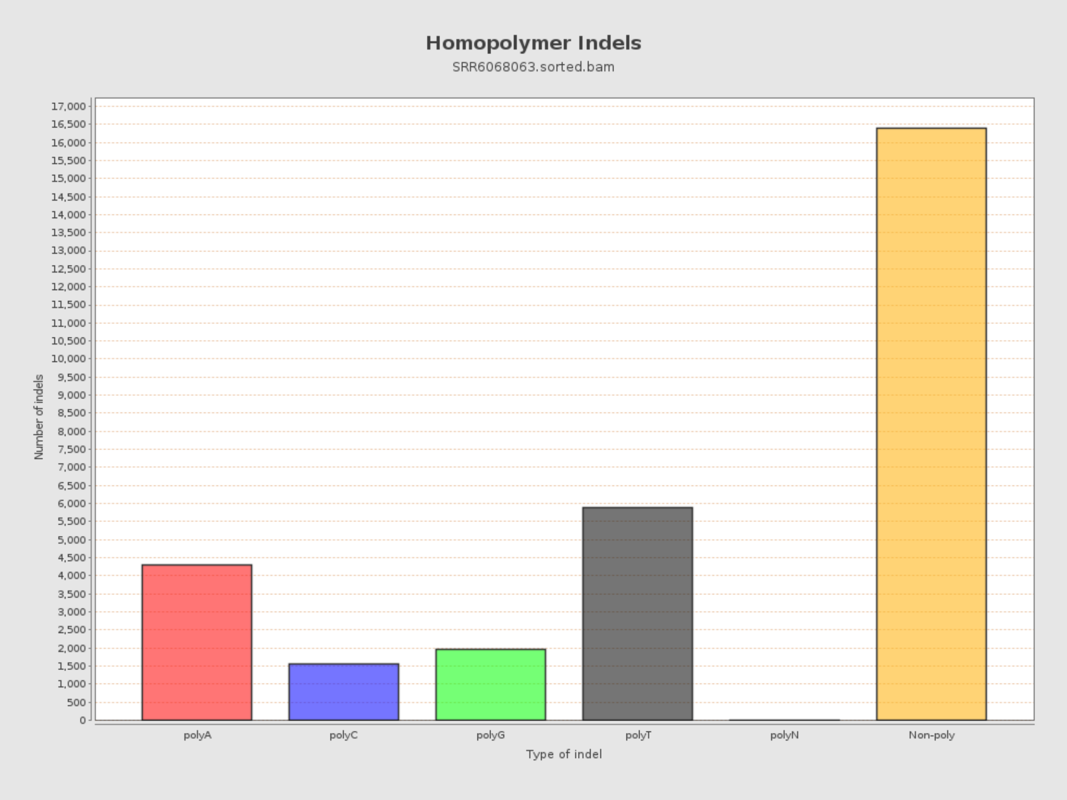
9. Results : Mapped Reads GC-content Distribution



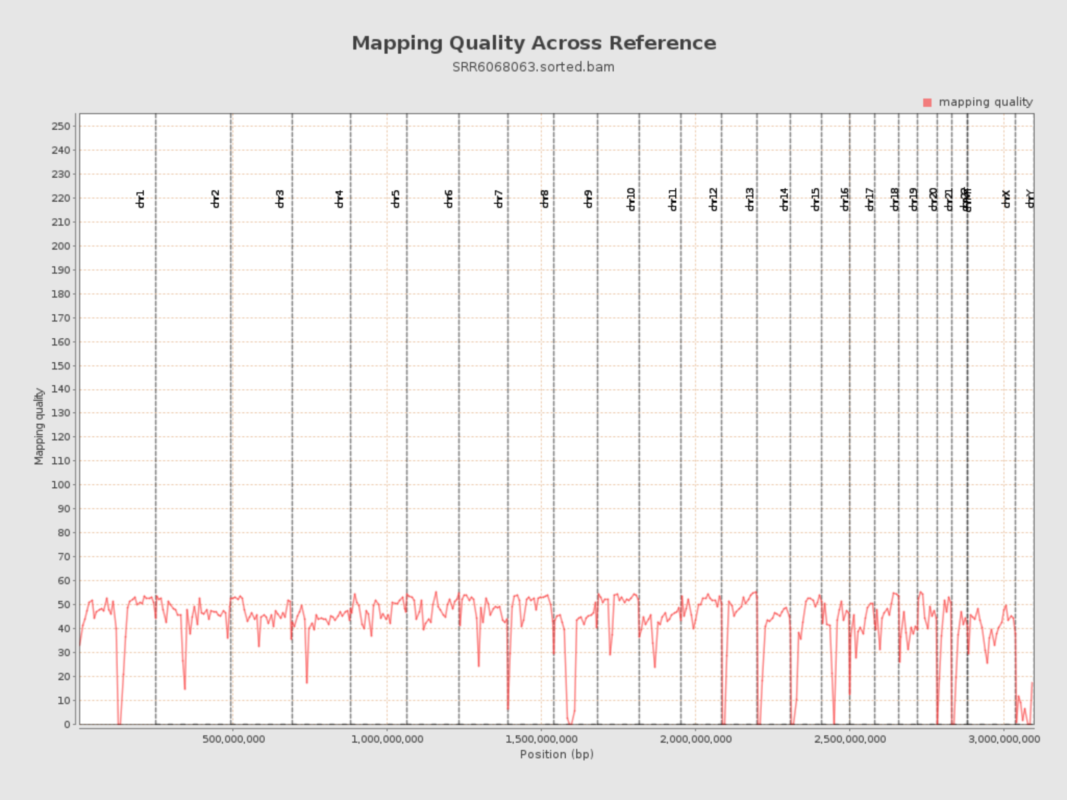
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram