Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 12:50:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068146.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_SRR6068146 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068146.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 12:50:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068146.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,789,609
Mapped reads	4,346,209 / 90.74%
Unmapped reads	443,400 / 9.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,620 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	596,891 / 12.46%
Duplication rate	11.5%
Clipped reads	2,272,735 / 47.45%

2.2. ACGT Content

Number/percentage of A's	74,176,902 / 26.44%
Number/percentage of C's	50,202,790 / 17.89%
Number/percentage of T's	91,584,419 / 32.64%
Number/percentage of G's	64,578,211 / 23.02%
Number/percentage of N's	32,608 / 0.01%
GC Percentage	40.91%

2.3. Coverage

Mean	0.0907

Standard Deviation	0.8631

2.4. Mapping Quality

Mean Mapping Quality	46.49

2.5. Mismatches and indels

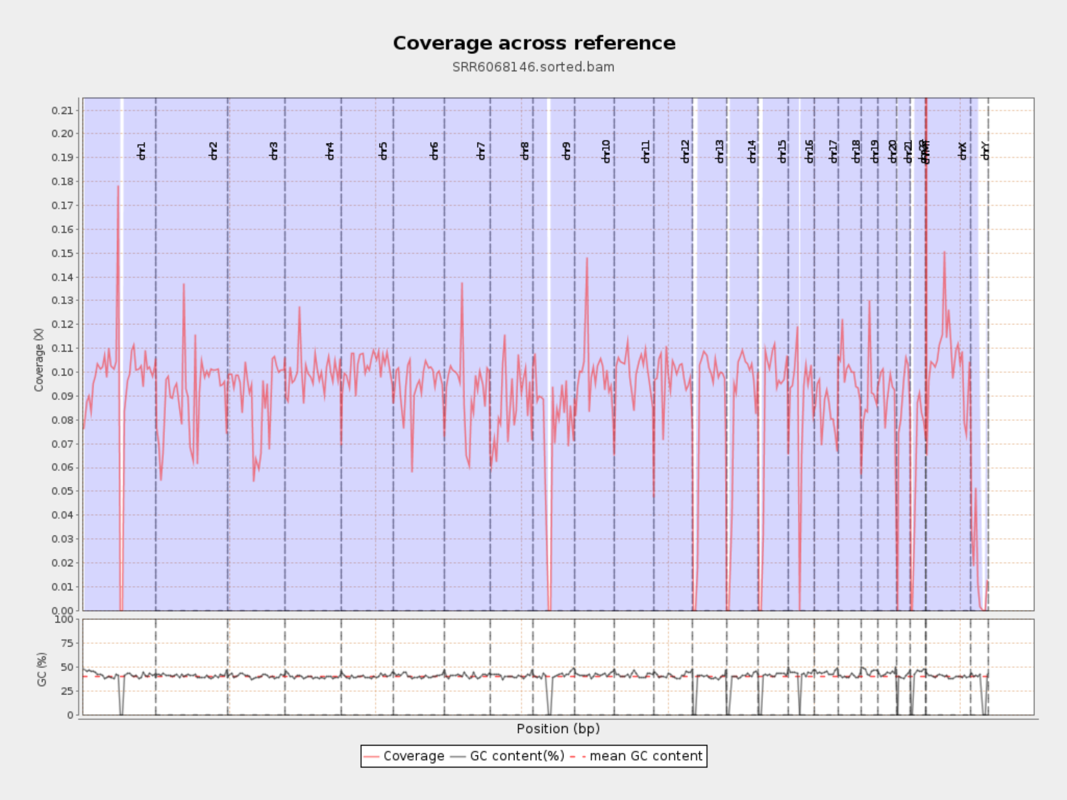
General error rate	0.58%
Mismatches	1,583,039
Insertions	18,494
Mapped reads with at least one insertion	0.42%
Deletions	64,317
Mapped reads with at least one deletion	1.47%
Homopolymer indels	45.09%

2.6. Chromosome stats

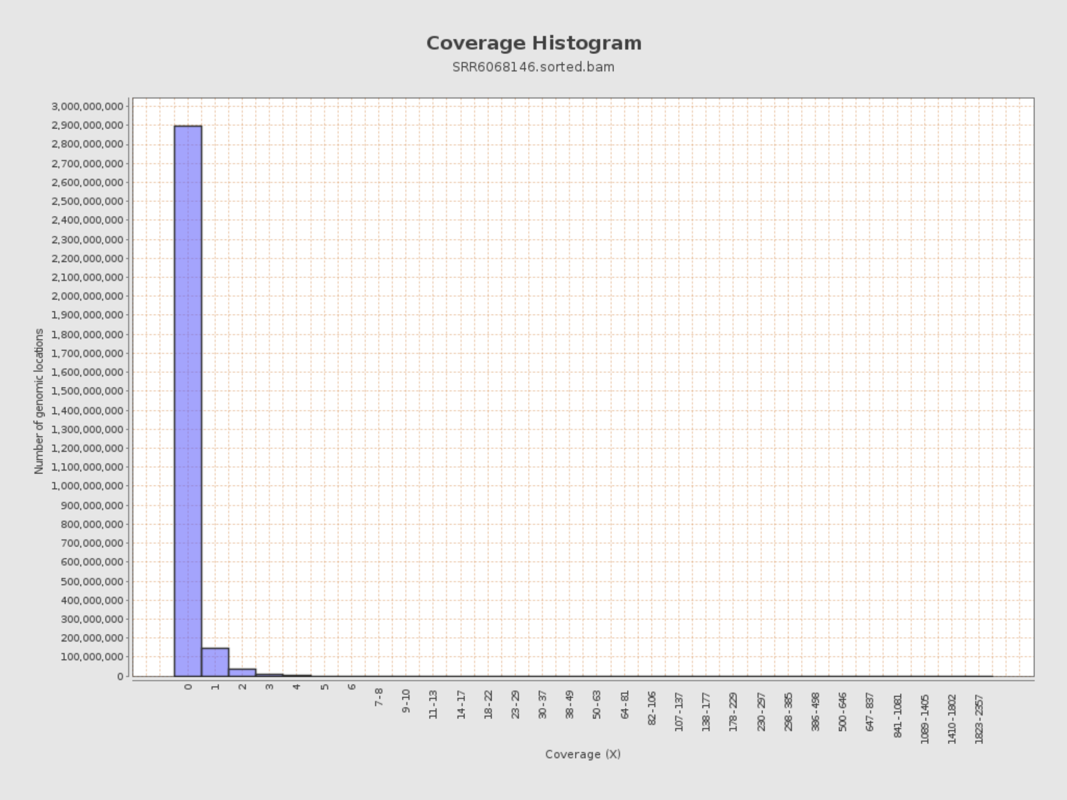
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23785395	0.0954	1.895
chr2	243199373	21929465	0.0902	1.2176
chr3	198022430	17933858	0.0906	0.4048
chr4	191154276	19067042	0.0997	0.4616
chr5	180915260	18439654	0.1019	0.4306
chr6	171115067	16252852	0.095	0.5215
chr7	159138663	14918577	0.0937	0.8311

chr8	146364022	12607160	0.0861	1.0008
chr9	141213431	10578923	0.0749	0.6505
chr10	135534747	13445411	0.0992	0.71
chr11	135006516	13461197	0.0997	0.6485
chr12	133851895	13141149	0.0982	0.4418
chr13	115169878	9739208	0.0846	0.4049
chr14	107349540	8898507	0.0829	0.4225
chr15	102531392	8463864	0.0825	0.4153
chr16	90354753	7708156	0.0853	0.4614
chr17	81195210	6837282	0.0842	0.4528
chr18	78077248	7887574	0.101	1.4457
chr19	59128983	5357744	0.0906	1.2342
chr20	63025520	5759774	0.0914	0.4443
chr21	48129895	3978303	0.0827	0.4212
chr22	51304566	3019021	0.0588	0.3173
chrMT	16571	247860	14.9575	9.1586
chrX	155270560	16313463	0.1051	0.5225
chrY	59373566	917449	0.0155	0.4269

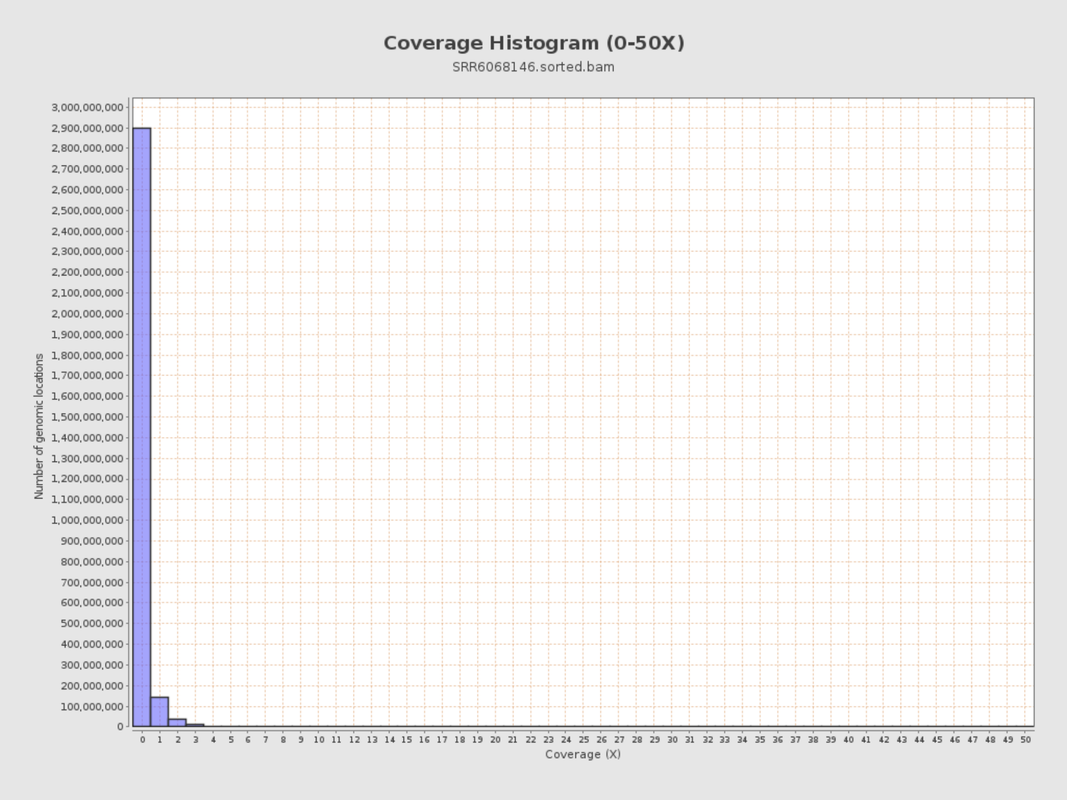
3. Results : Coverage across reference



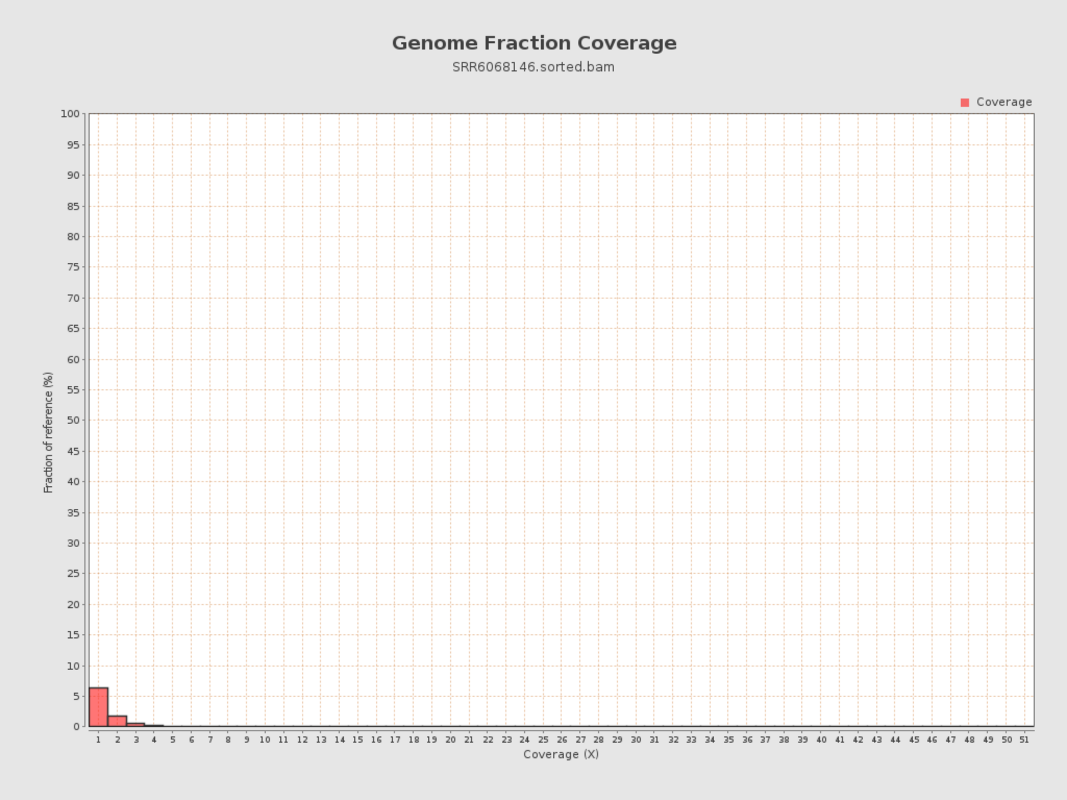
4. Results : Coverage Histogram



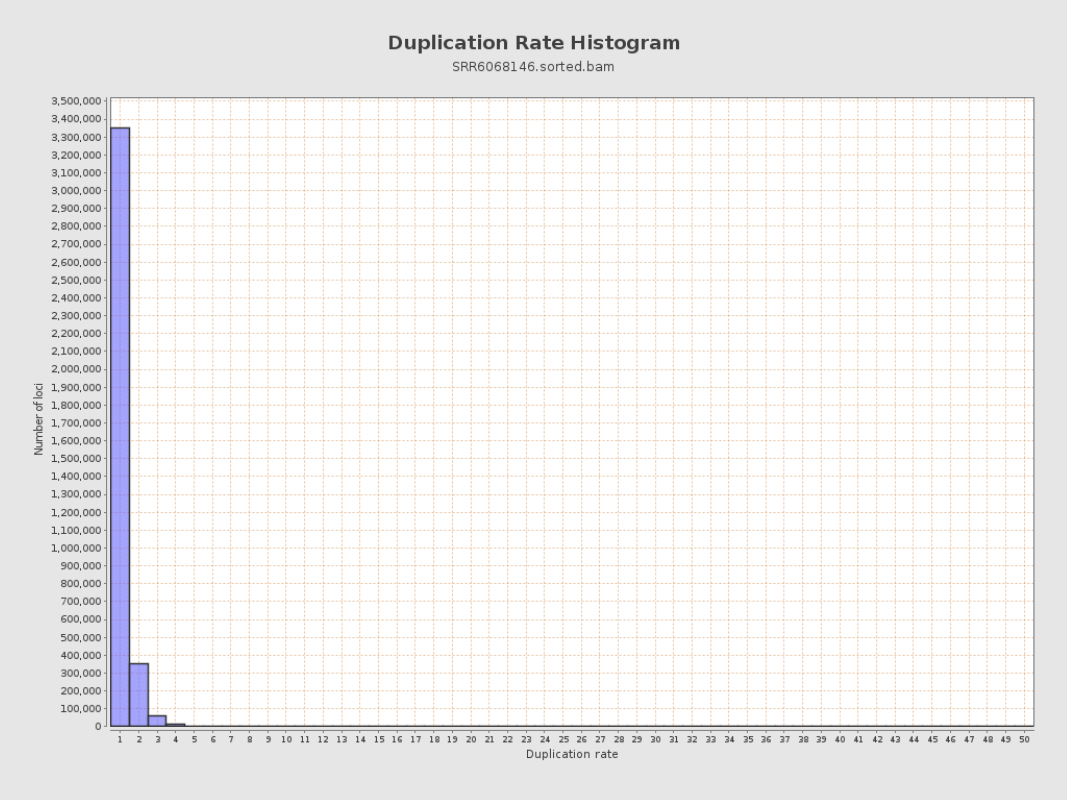
5. Results : Coverage Histogram (0-50X)



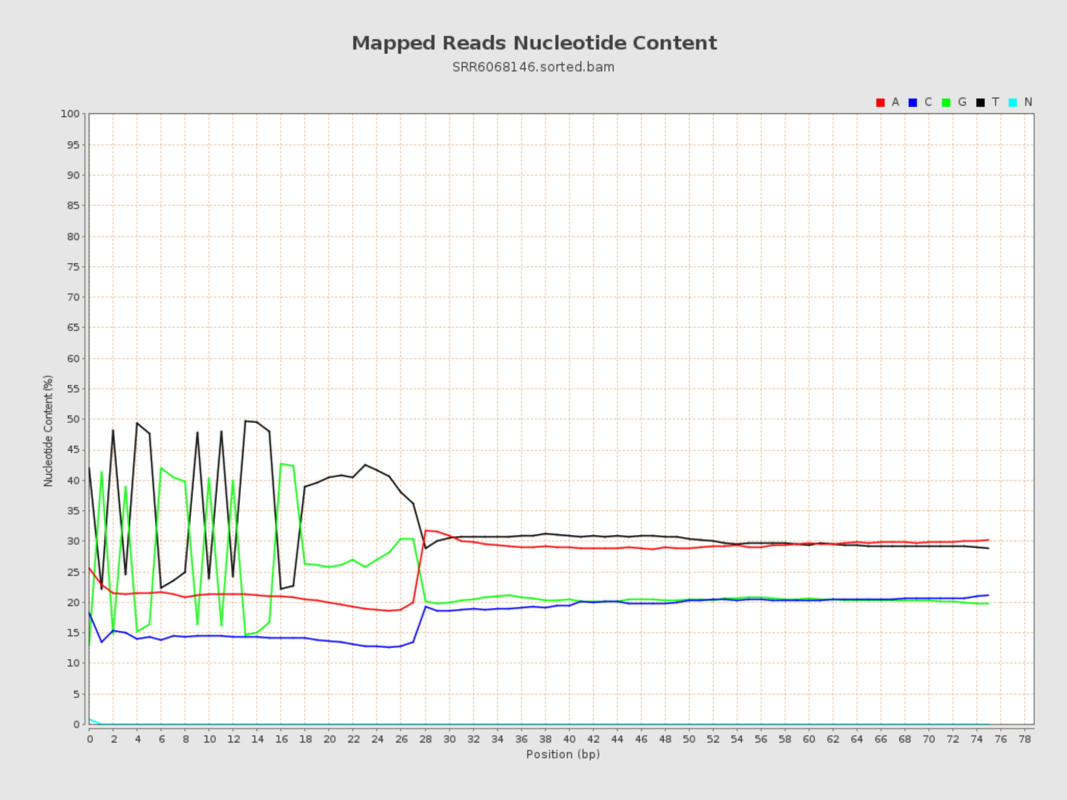
6. Results : Genome Fraction Coverage



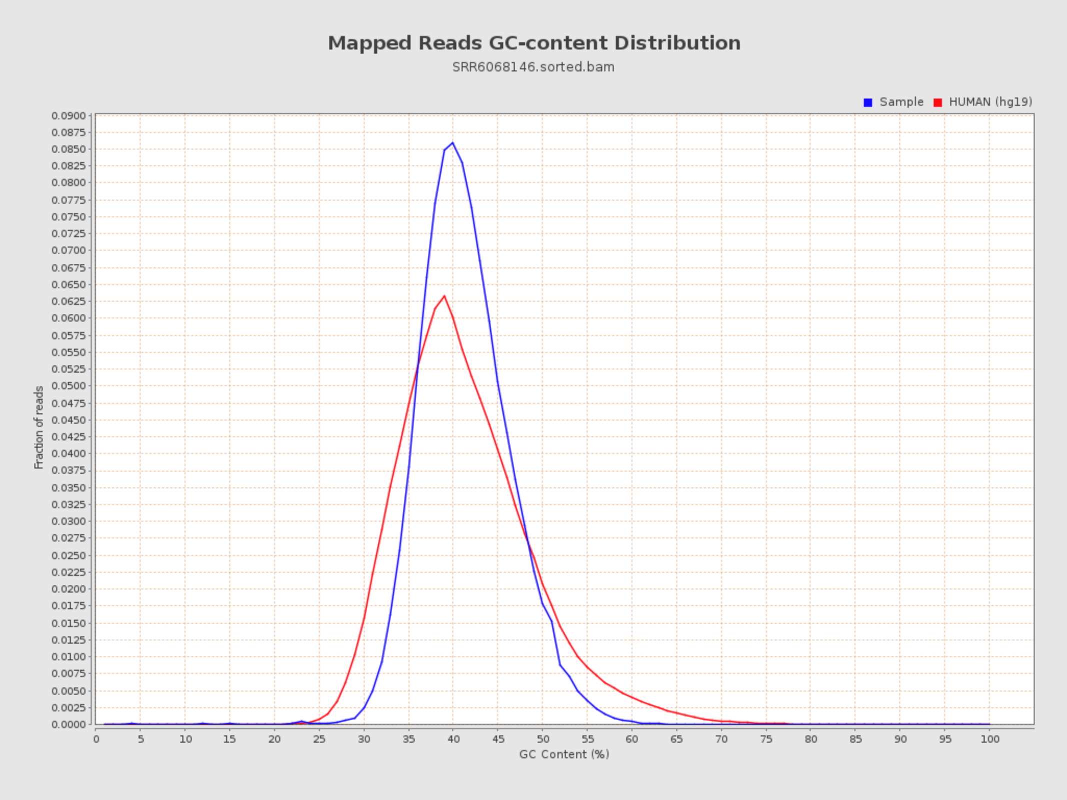
7. Results : Duplication Rate Histogram



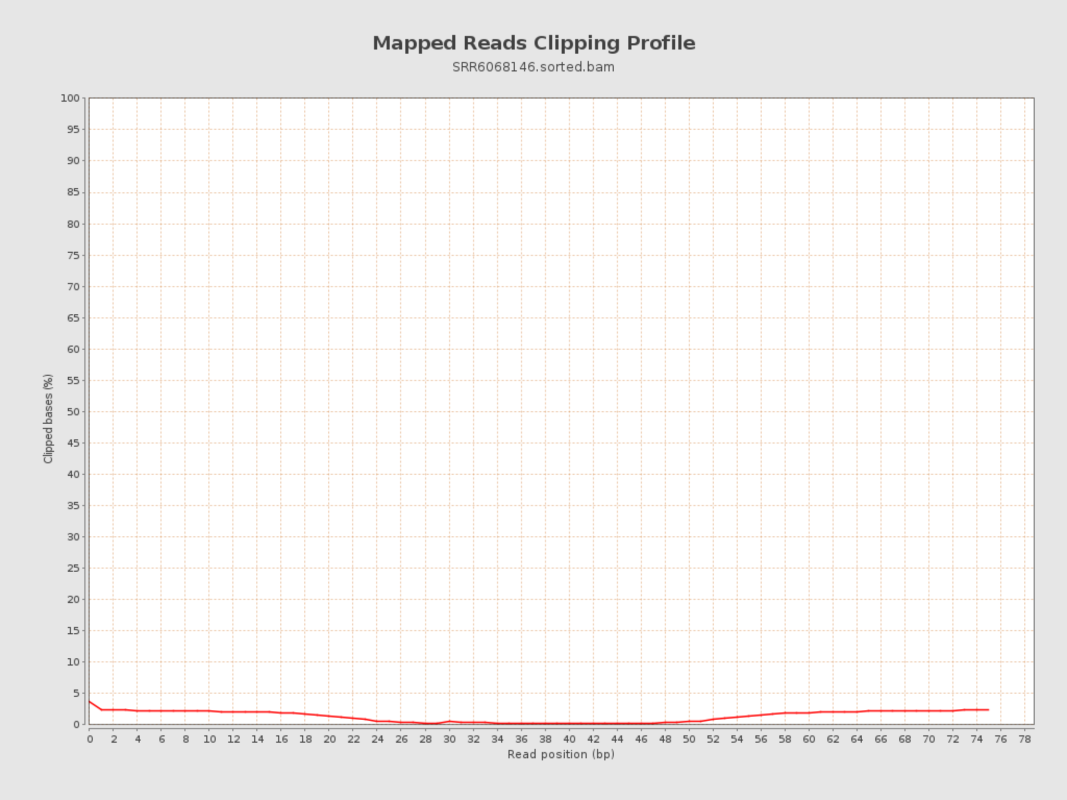
8. Results : Mapped Reads Nucleotide Content



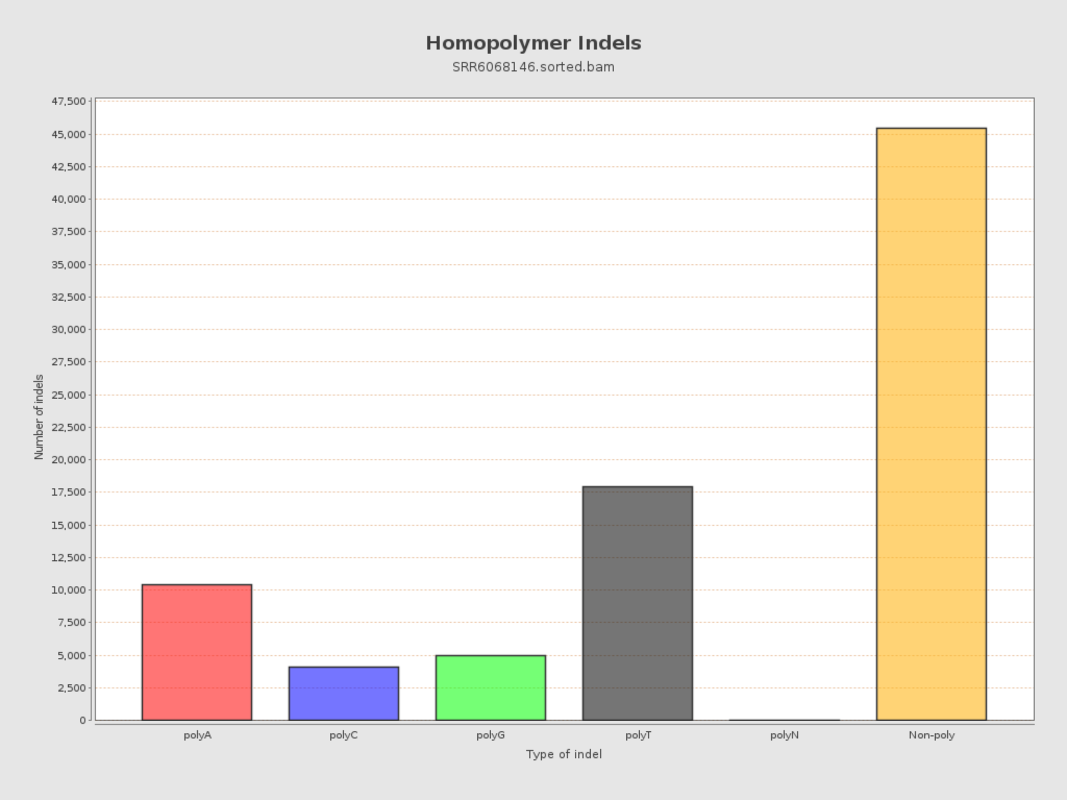
9. Results : Mapped Reads GC-content Distribution



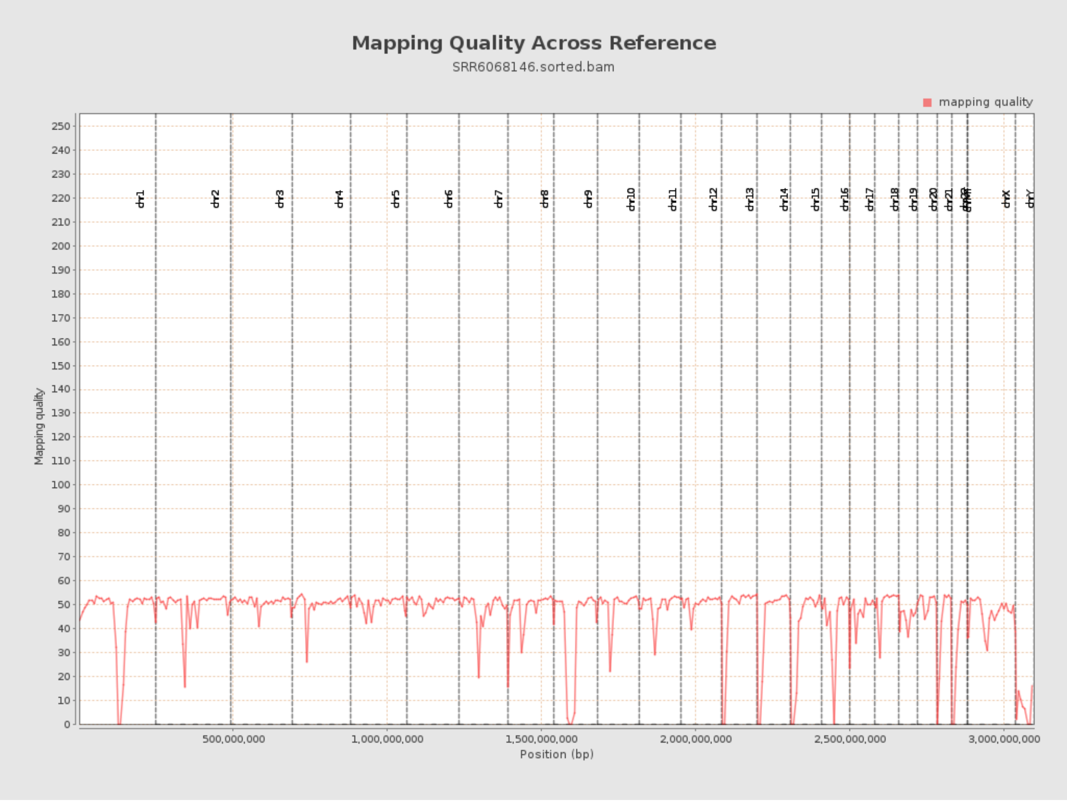
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram