Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 10:29:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068106.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_SRR6068106 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068106.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 10:28:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068106.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,916,590
Mapped reads	4,657,207 / 94.72%
Unmapped reads	259,383 / 5.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,602 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	607,838 / 12.36%
Duplication rate	10.96%
Clipped reads	2,200,382 / 44.75%

2.2. ACGT Content

Number/percentage of A's	83,463,721 / 27.33%
Number/percentage of C's	54,454,856 / 17.83%
Number/percentage of T's	99,907,919 / 32.71%
Number/percentage of G's	67,536,158 / 22.11%
Number/percentage of N's	36,178 / 0.01%
GC Percentage	39.94%

2.3. Coverage

Mean	0.0987

Standard Deviation	1.0715

2.4. Mapping Quality

Mean Mapping Quality	46.39

2.5. Mismatches and indels

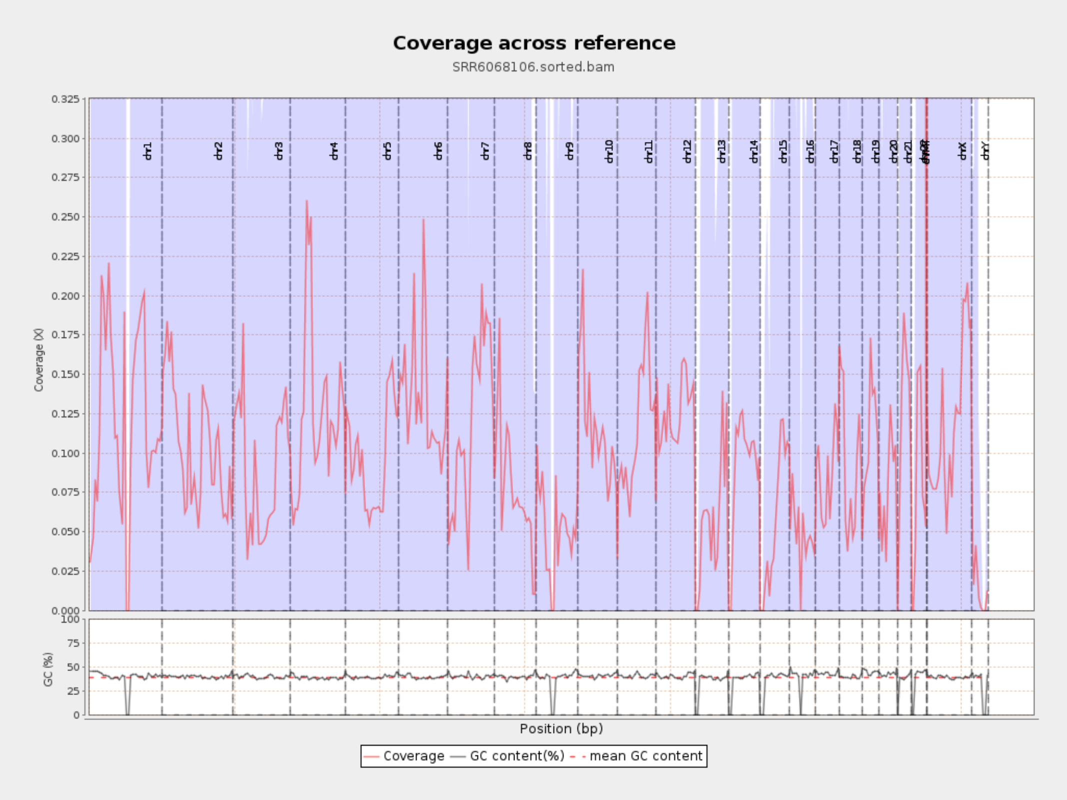
General error rate	0.57%
Mismatches	1,708,068
Insertions	20,216
Mapped reads with at least one insertion	0.43%
Deletions	80,890
Mapped reads with at least one deletion	1.72%
Homopolymer indels	45.67%

2.6. Chromosome stats

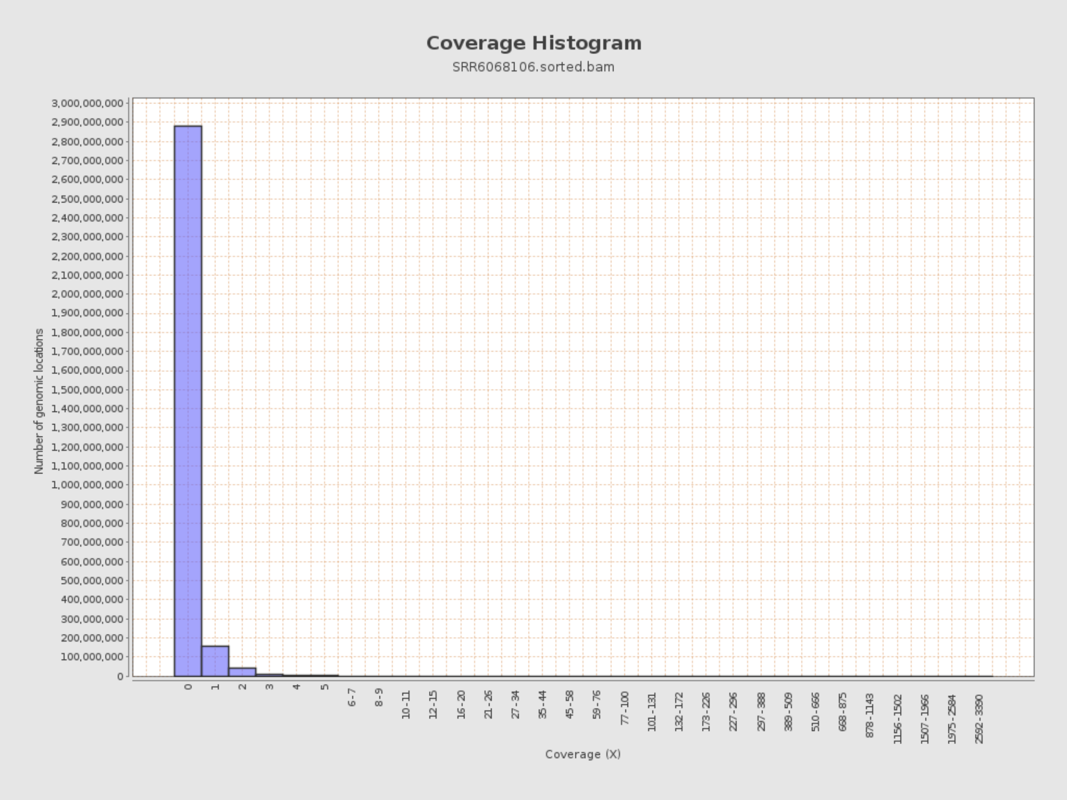
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30265777	0.1214	2.7542
chr2	243199373	25325003	0.1041	1.0553
chr3	198022430	17914342	0.0905	0.4038
chr4	191154276	24057350	0.1259	0.4919
chr5	180915260	17325396	0.0958	0.4193
chr6	171115067	23151672	0.1353	0.6399
chr7	159138663	19057038	0.1198	0.5489

chr8	146364022	11235782	0.0768	1.7809
chr9	141213431	6935889	0.0491	0.727
chr10	135534747	16062673	0.1185	0.7086
chr11	135006516	15569367	0.1153	0.5639
chr12	133851895	17070133	0.1275	0.516
chr13	115169878	6679763	0.058	0.3467
chr14	107349540	9671790	0.0901	0.4644
chr15	102531392	5860721	0.0572	0.3481
chr16	90354753	4346225	0.0481	0.3681
chr17	81195210	6975362	0.0859	0.4084
chr18	78077248	7184410	0.092	1.4199
chr19	59128983	6558314	0.1109	1.6267
chr20	63025520	4878540	0.0774	0.4423
chr21	48129895	5915055	0.1229	0.4853
chr22	51304566	3835681	0.0748	0.3574
chrMT	16571	263911	15.9261	10.0036
chrX	155270560	18578596	0.1197	0.5266
chrY	59373566	823059	0.0139	0.3746

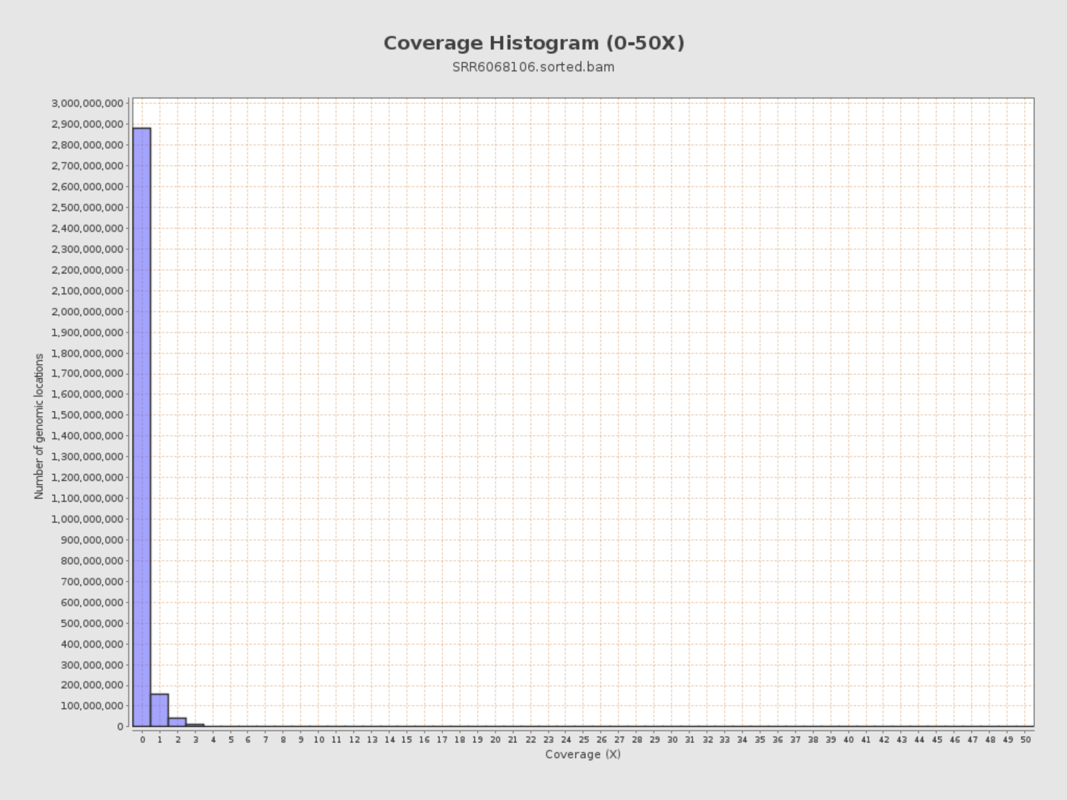
3. Results : Coverage across reference



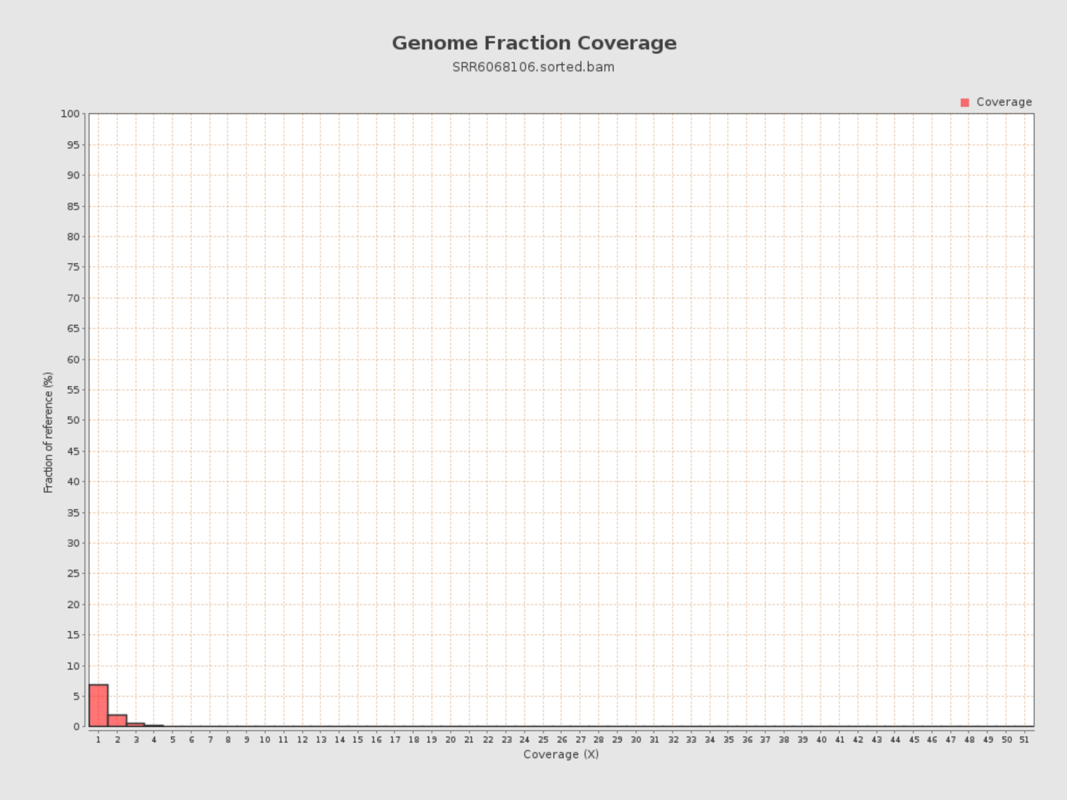
4. Results : Coverage Histogram



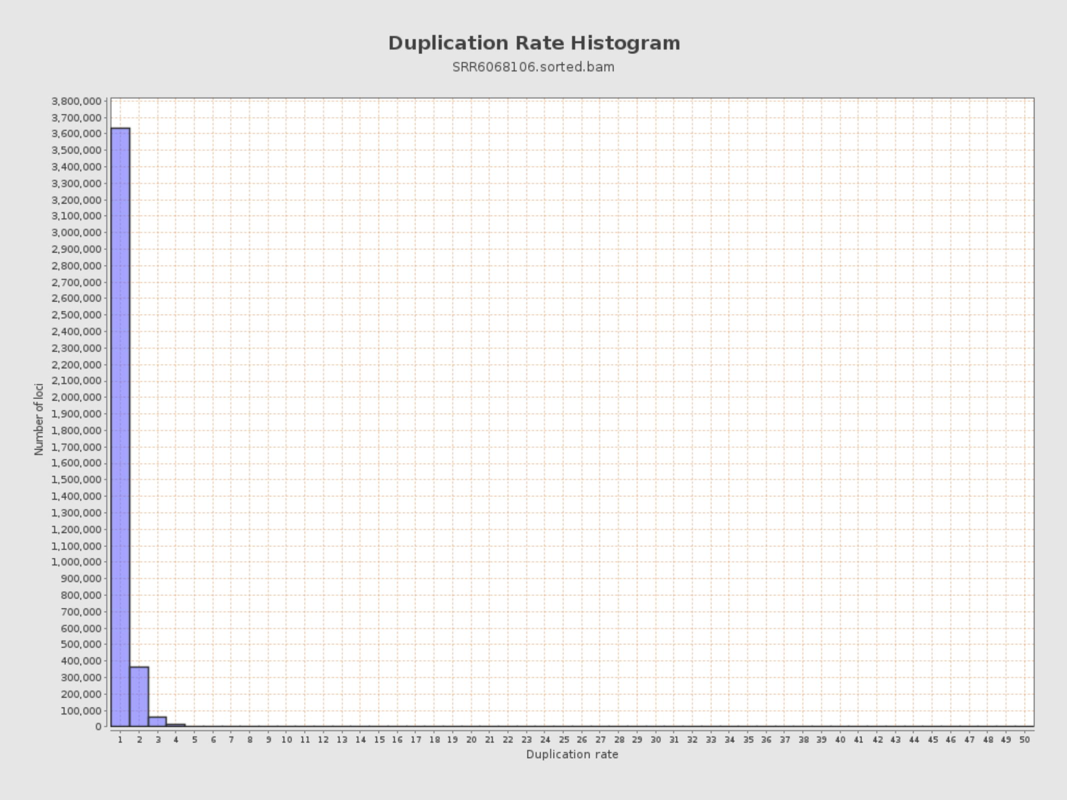
5. Results : Coverage Histogram (0-50X)



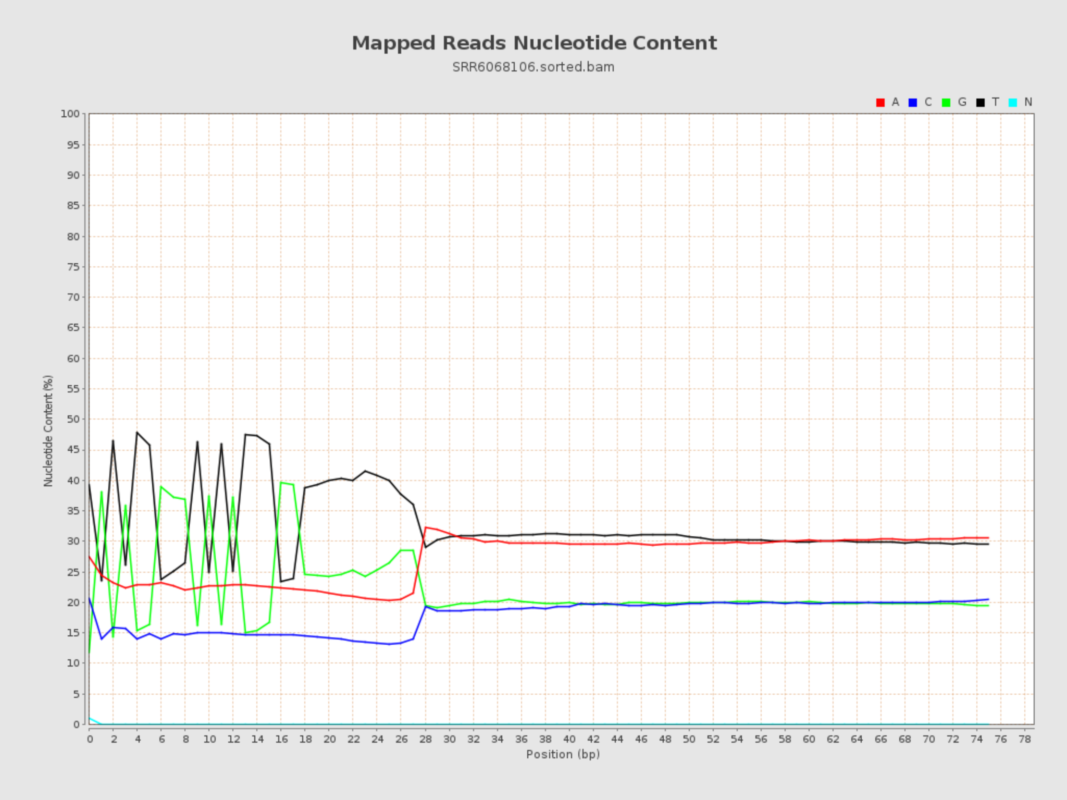
6. Results : Genome Fraction Coverage



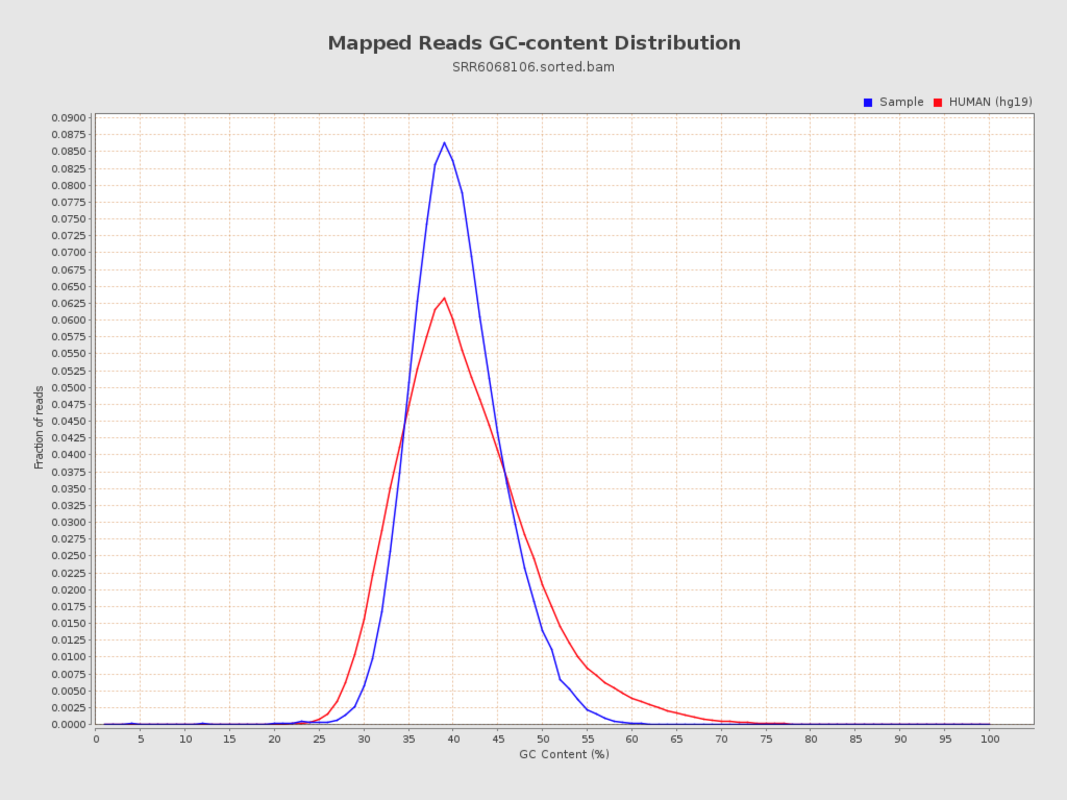
7. Results : Duplication Rate Histogram



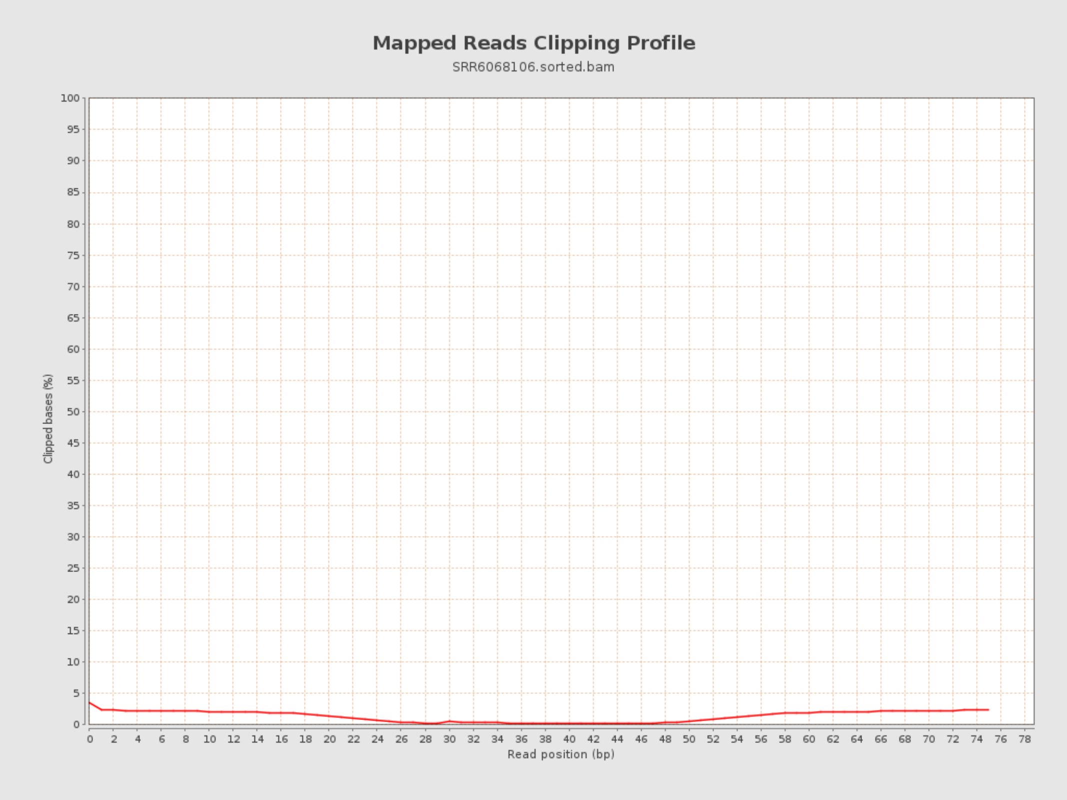
8. Results : Mapped Reads Nucleotide Content



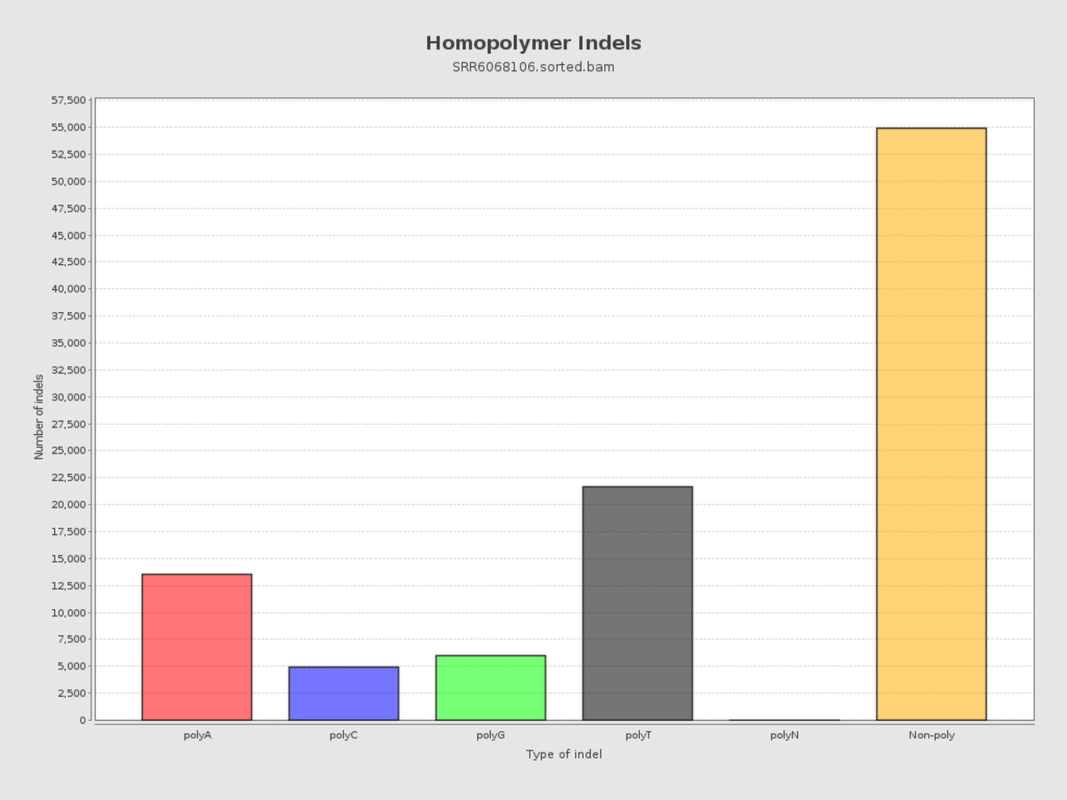
9. Results : Mapped Reads GC-content Distribution



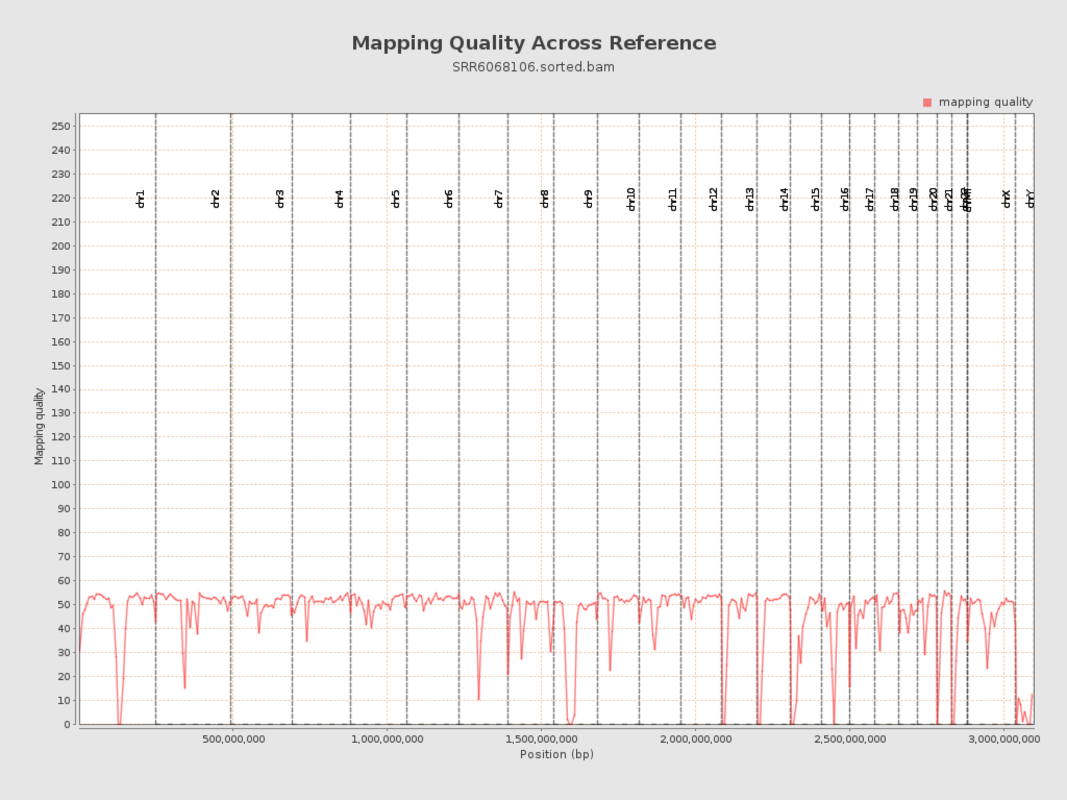
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram