Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 15:13:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068180.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_SRR6068180 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068180.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 15:13:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068180.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,087,565
Mapped reads	4,669,882 / 91.79%
Unmapped reads	417,683 / 8.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,967 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	631,465 / 12.41%
Duplication rate	11.06%
Clipped reads	2,603,032 / 51.16%

2.2. ACGT Content

Number/percentage of A's	77,327,803 / 26.02%
Number/percentage of C's	52,991,360 / 17.83%
Number/percentage of T's	97,147,649 / 32.69%
Number/percentage of G's	69,657,155 / 23.44%
Number/percentage of N's	33,731 / 0.01%
GC Percentage	41.27%

2.3. Coverage

Mean	0.096

Standard Deviation	1.0152

2.4. Mapping Quality

Mean Mapping Quality	45.68

2.5. Mismatches and indels

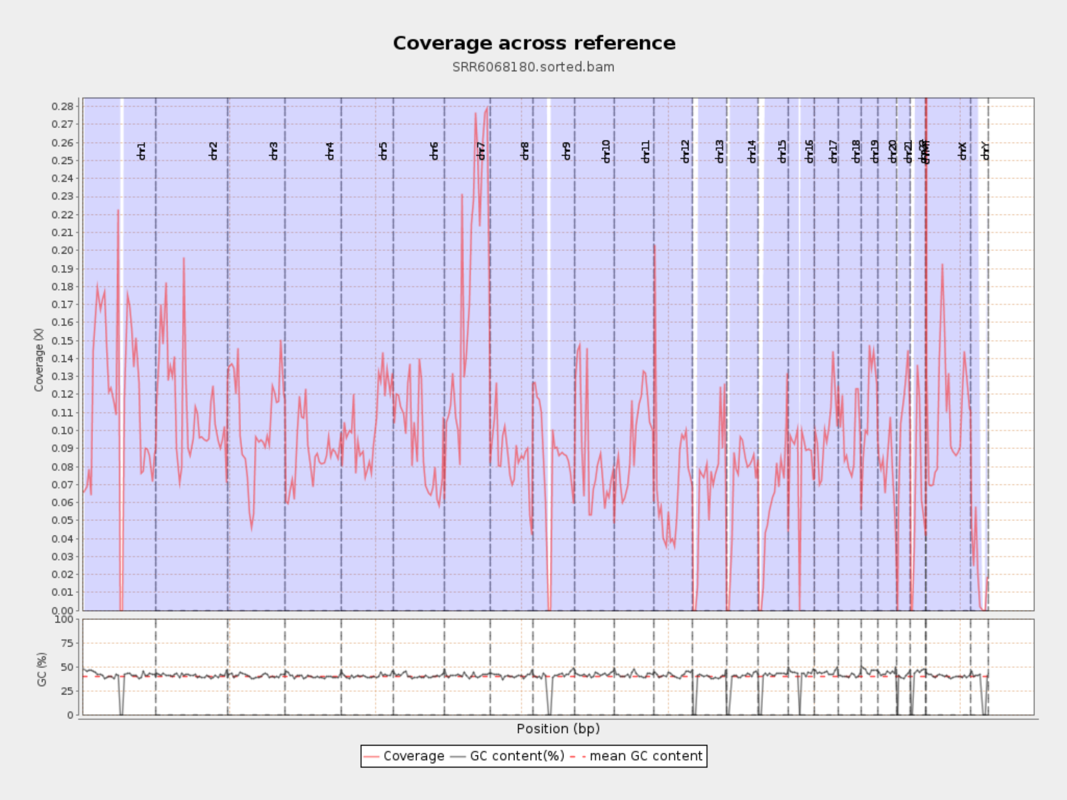
General error rate	0.61%
Mismatches	1,771,668
Insertions	18,884
Mapped reads with at least one insertion	0.4%
Deletions	74,331
Mapped reads with at least one deletion	1.58%
Homopolymer indels	45.31%

2.6. Chromosome stats

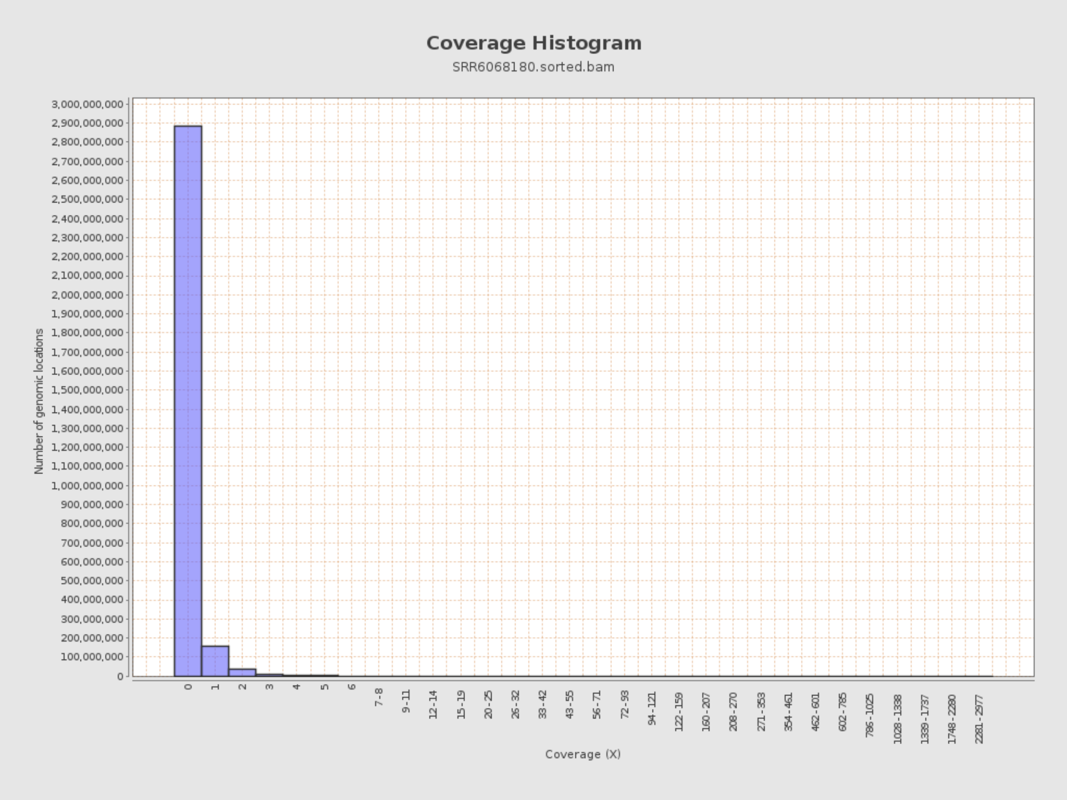
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29025244	0.1165	2.3233
chr2	243199373	27653084	0.1137	1.3064
chr3	198022430	20501563	0.1035	0.439
chr4	191154276	16561618	0.0866	0.4368
chr5	180915260	18625839	0.103	0.4391
chr6	171115067	16254269	0.095	0.5622
chr7	159138663	28153361	0.1769	1.7228

chr8	146364022	12415026	0.0848	1.0742
chr9	141213431	11561167	0.0819	0.6974
chr10	135534747	11604490	0.0856	0.6552
chr11	135006516	12794911	0.0948	0.5689
chr12	133851895	9453059	0.0706	0.4127
chr13	115169878	8015135	0.0696	0.3797
chr14	107349540	7510479	0.07	0.4406
chr15	102531392	5788171	0.0565	0.3776
chr16	90354753	7364099	0.0815	0.4404
chr17	81195210	8201214	0.101	0.4674
chr18	78077248	7663306	0.0982	1.2712
chr19	59128983	6819585	0.1153	1.4584
chr20	63025520	4917279	0.078	0.4164
chr21	48129895	4832190	0.1004	0.4575
chr22	51304566	3194436	0.0623	0.3319
chrMT	16571	305342	18.4263	11.5638
chrX	155270560	16869147	0.1086	0.5484
chrY	59373566	1205018	0.0203	0.3923

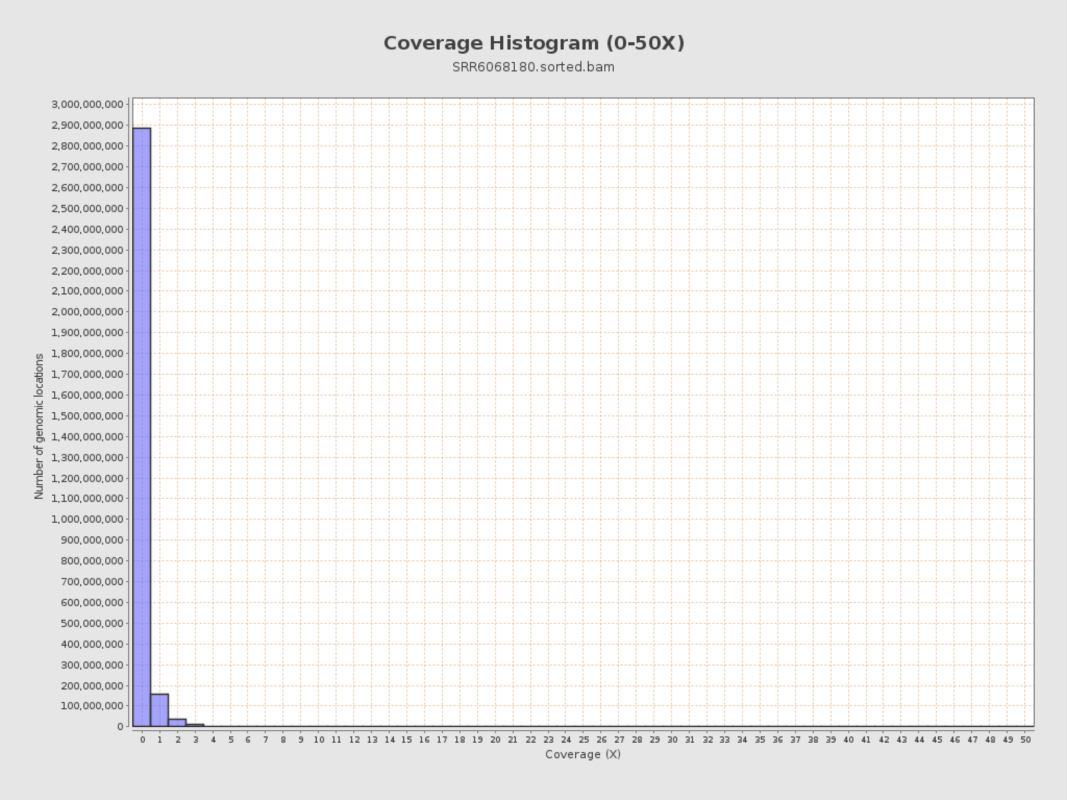
3. Results : Coverage across reference



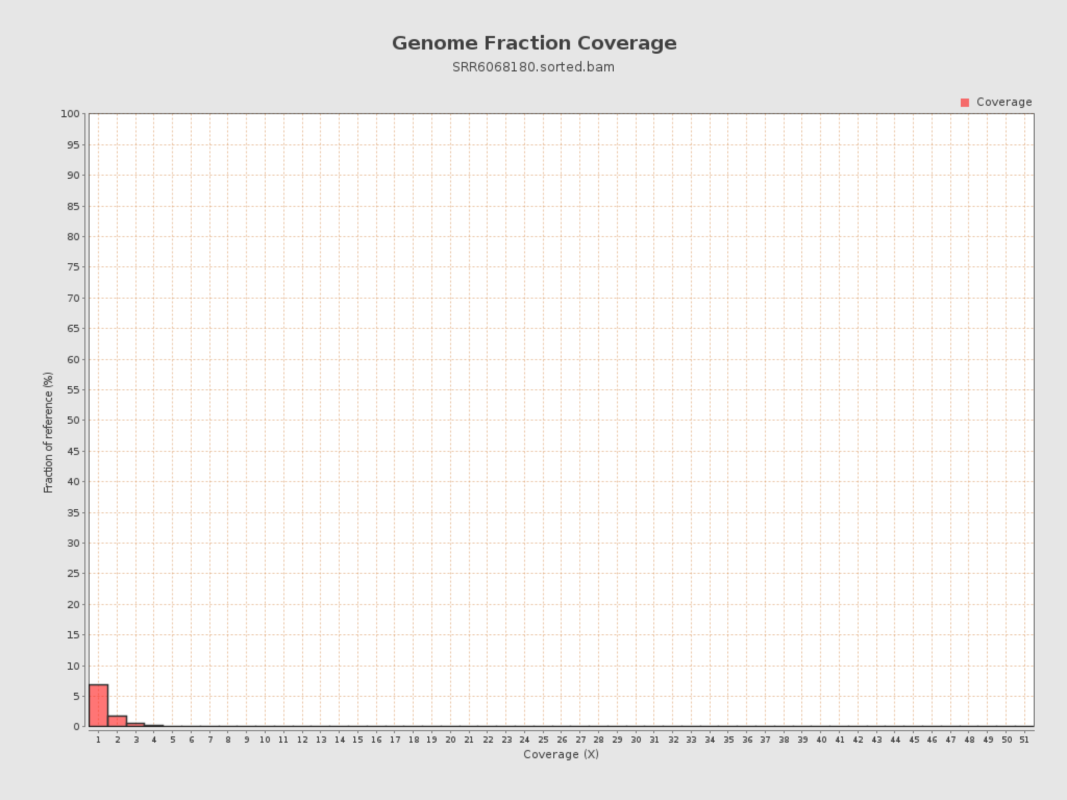
4. Results : Coverage Histogram



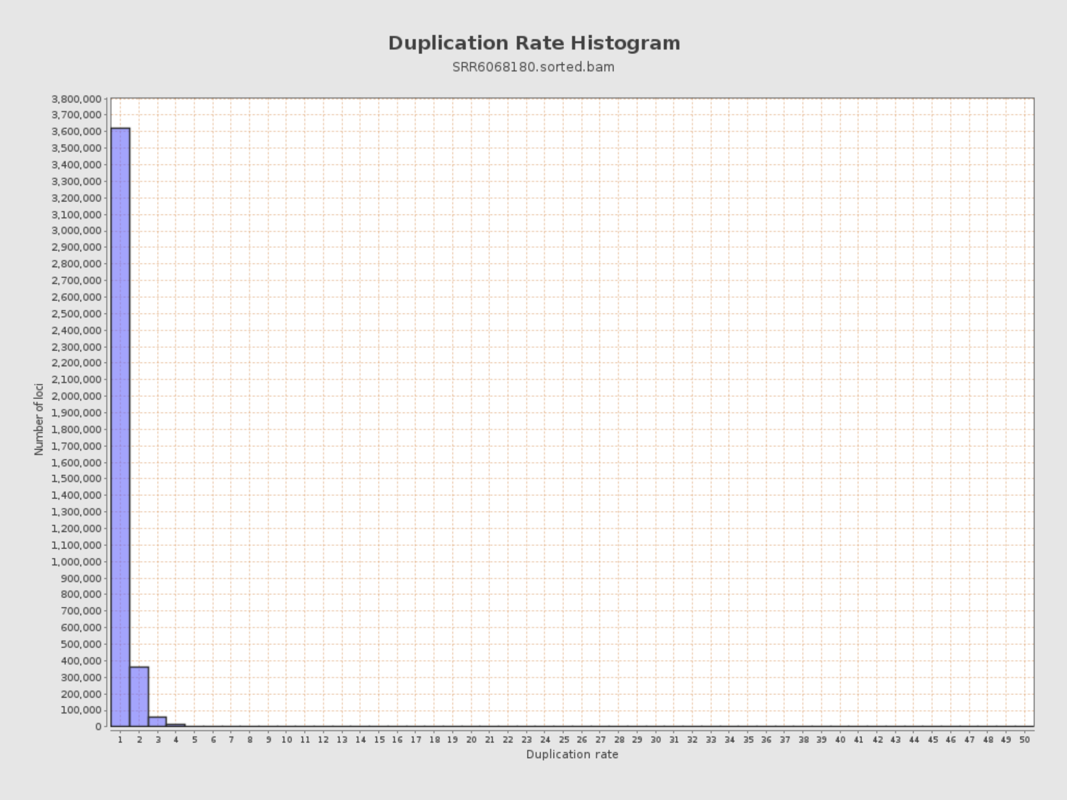
5. Results : Coverage Histogram (0-50X)



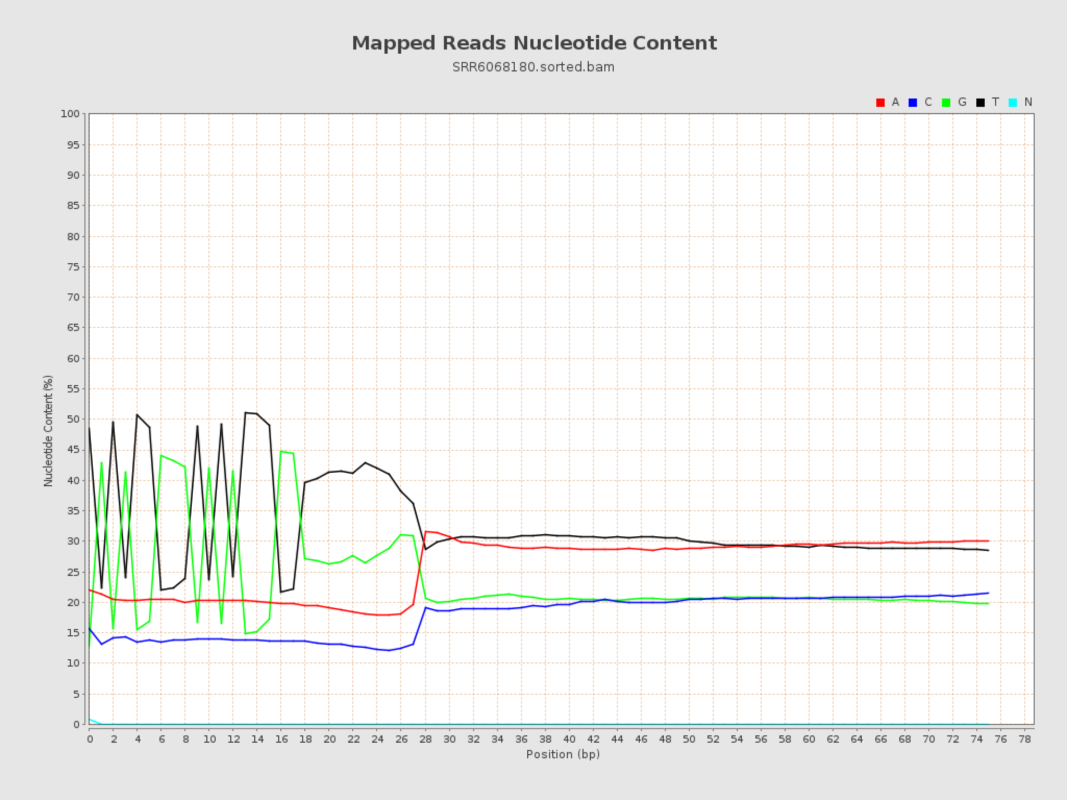
6. Results : Genome Fraction Coverage



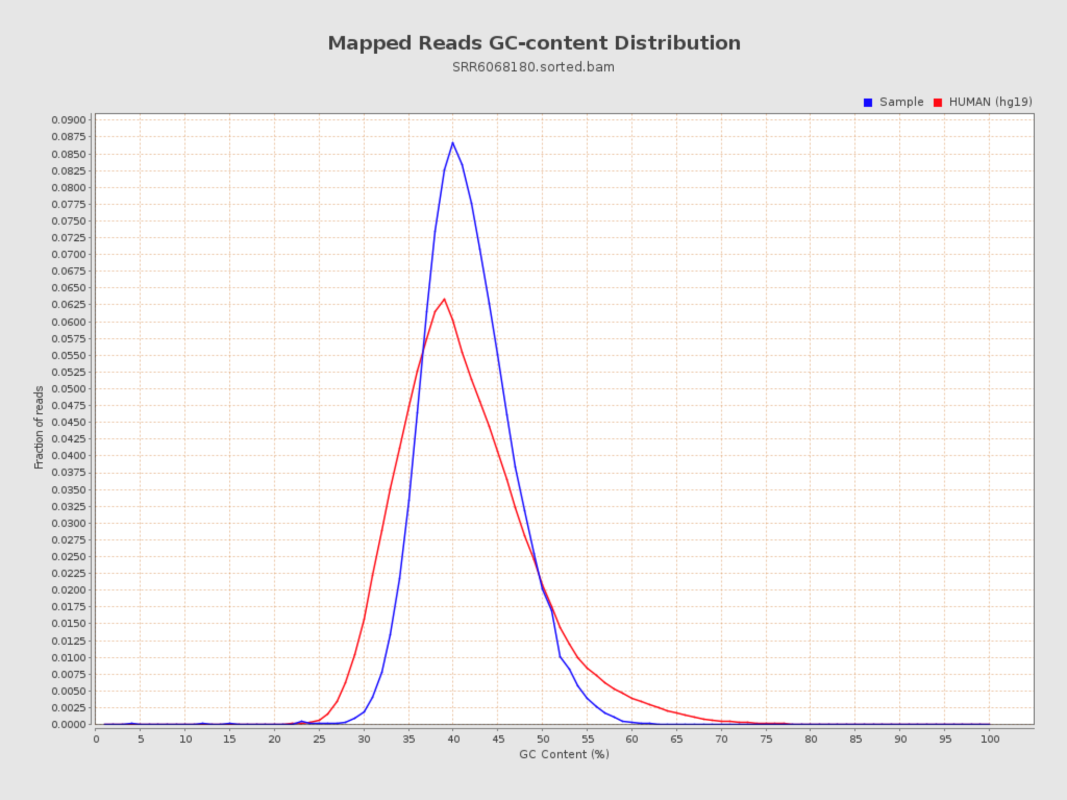
7. Results : Duplication Rate Histogram



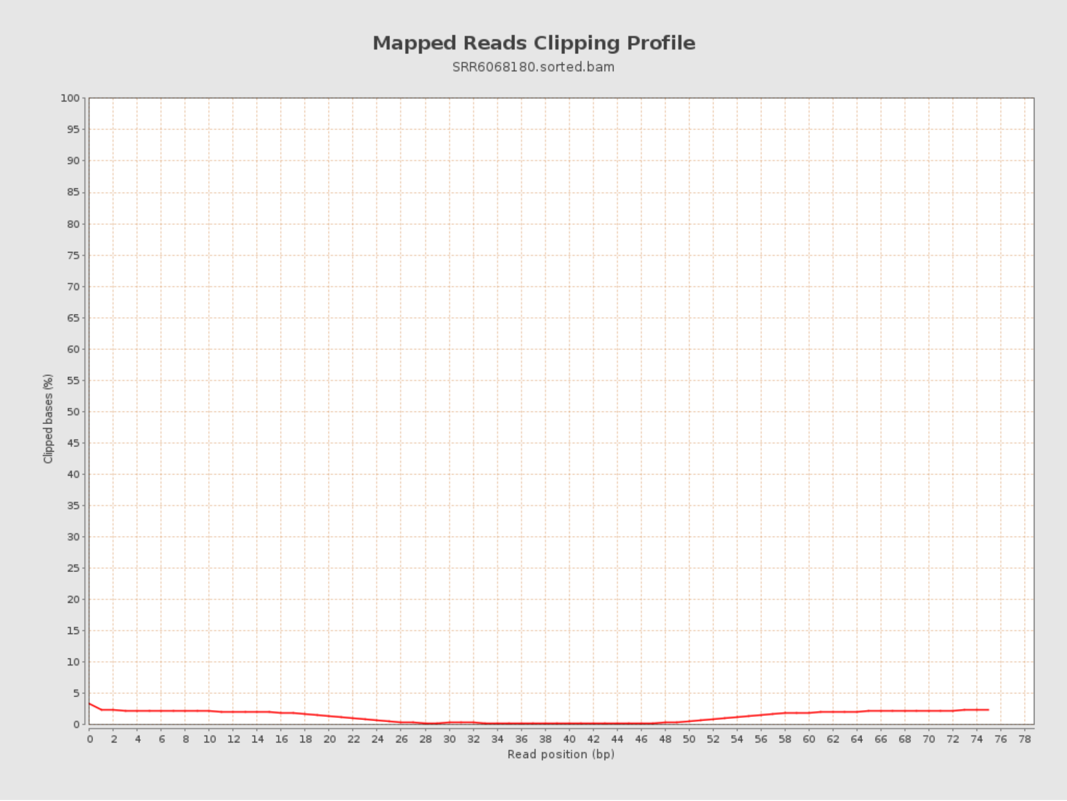
8. Results : Mapped Reads Nucleotide Content



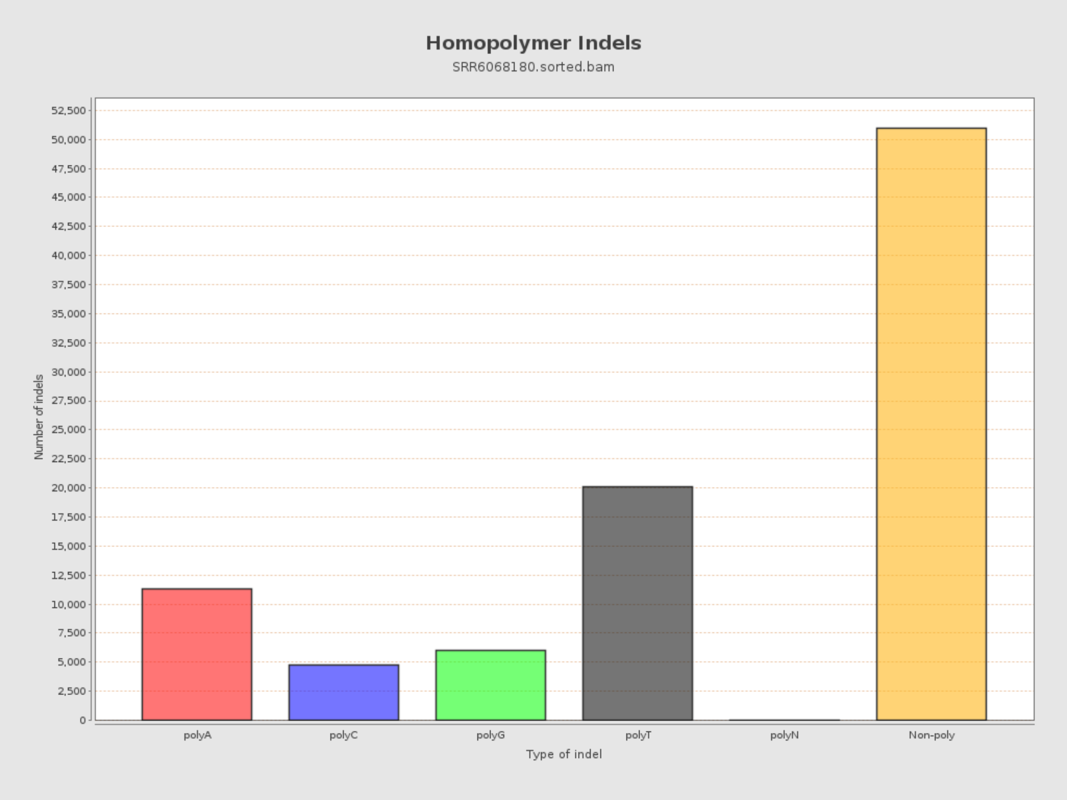
9. Results : Mapped Reads GC-content Distribution



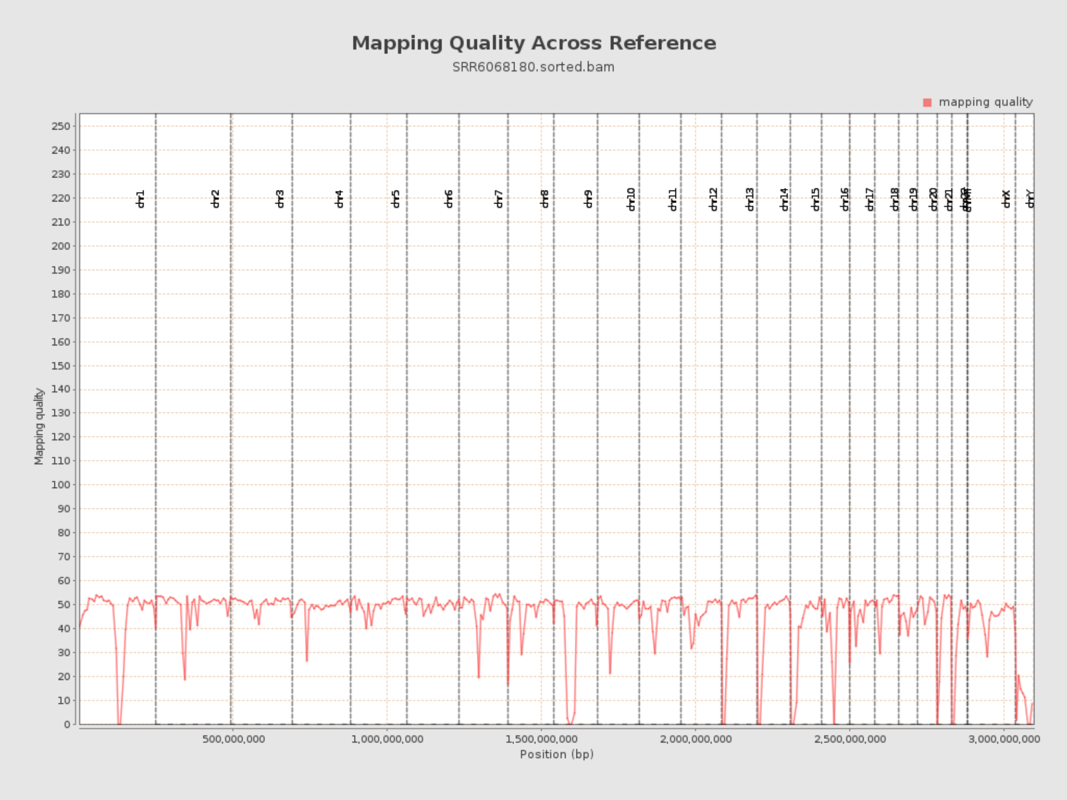
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram