Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 11:10:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068118.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_SRR6068118 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068118.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 11:10:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068118.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,551,633
Mapped reads	1,060,596 / 68.35%
Unmapped reads	491,037 / 31.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,600 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	216,289 / 13.94%
Duplication rate	13.09%
Clipped reads	501,540 / 32.32%

2.2. ACGT Content

Number/percentage of A's	19,319,316 / 27.74%
Number/percentage of C's	12,347,910 / 17.73%
Number/percentage of T's	22,642,628 / 32.51%
Number/percentage of G's	15,262,403 / 21.91%
Number/percentage of N's	73,211 / 0.11%
GC Percentage	39.64%

2.3. Coverage

Mean	0.0225

Standard Deviation	0.4034

2.4. Mapping Quality

Mean Mapping Quality	46.74

2.5. Mismatches and indels

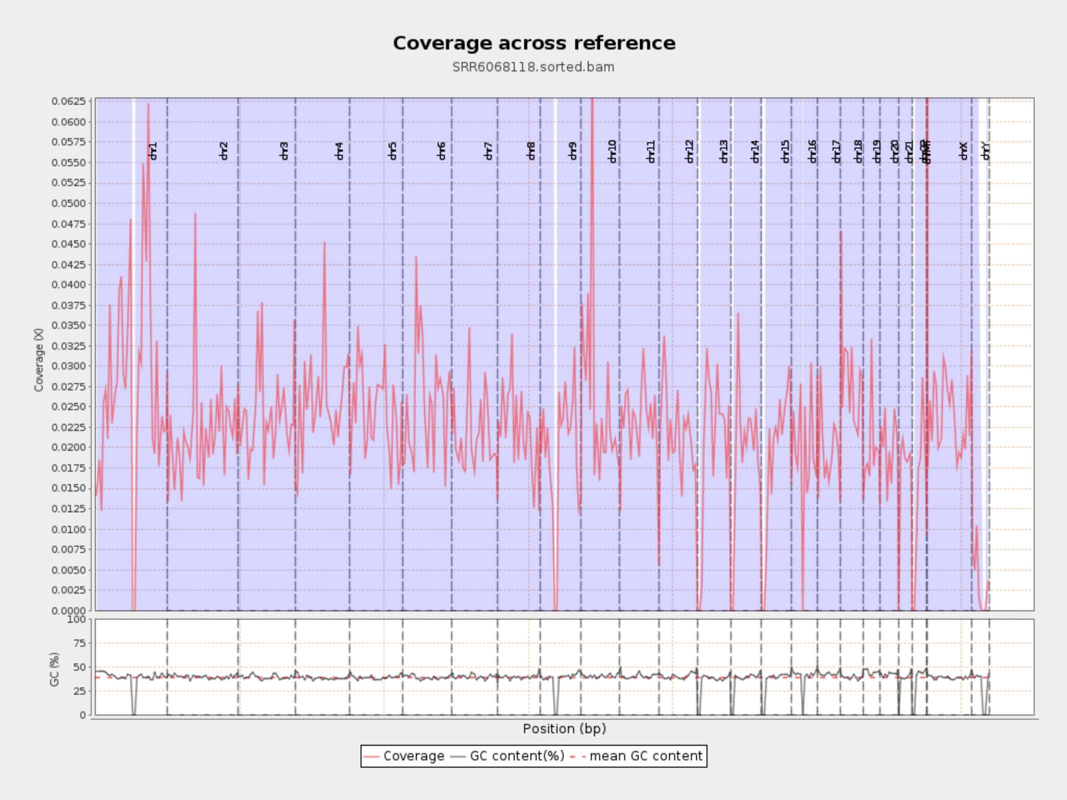
General error rate	0.9%
Mismatches	618,486
Insertions	5,515
Mapped reads with at least one insertion	0.52%
Deletions	16,267
Mapped reads with at least one deletion	1.52%
Homopolymer indels	47.4%

2.6. Chromosome stats

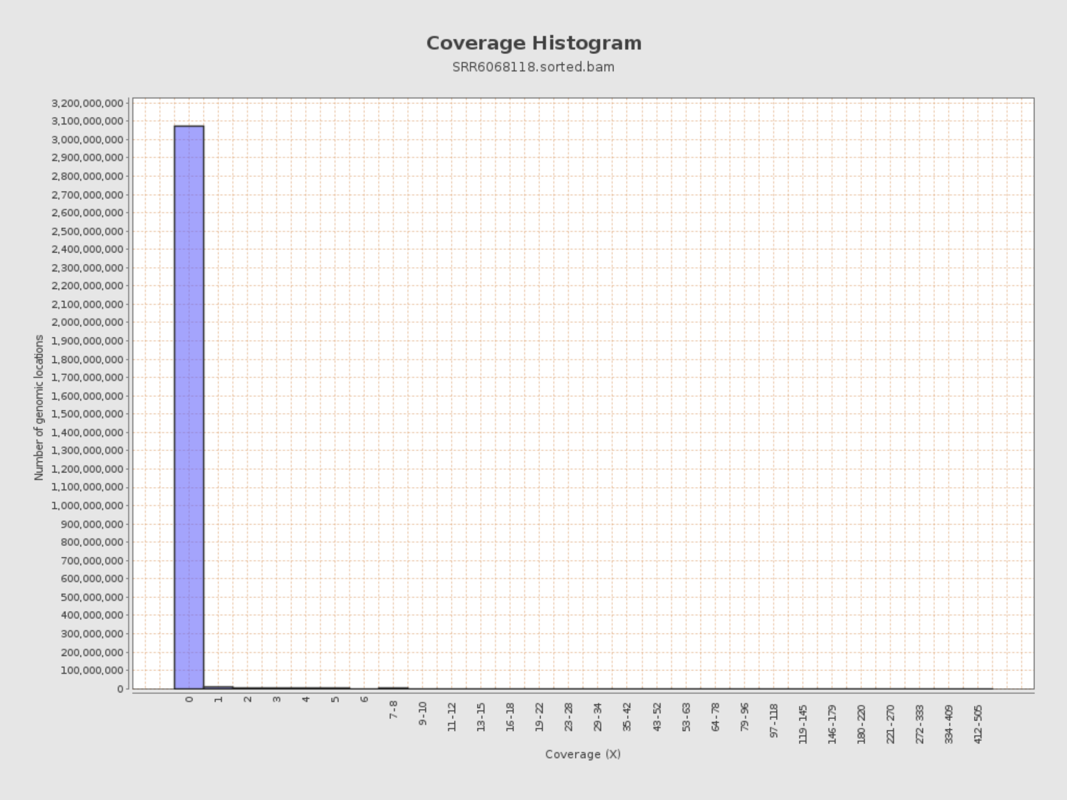
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6958195	0.0279	0.5361
chr2	243199373	5297184	0.0218	0.4099
chr3	198022430	4718430	0.0238	0.3812
chr4	191154276	4917195	0.0257	0.3955
chr5	180915260	4413540	0.0244	0.377
chr6	171115067	4386664	0.0256	0.3968
chr7	159138663	3475106	0.0218	0.387

chr8	146364022	3276015	0.0224	0.4326
chr9	141213431	2737231	0.0194	0.3604
chr10	135534747	3646931	0.0269	0.5969
chr11	135006516	3194003	0.0237	0.3778
chr12	133851895	2927640	0.0219	0.3521
chr13	115169878	2296072	0.0199	0.3468
chr14	107349540	2017369	0.0188	0.3372
chr15	102531392	1919224	0.0187	0.3532
chr16	90354753	1715708	0.019	0.3266
chr17	81195210	1590566	0.0196	0.3264
chr18	78077248	2180174	0.0279	0.5218
chr19	59128983	1168712	0.0198	0.4055
chr20	63025520	1276755	0.0203	0.3242
chr21	48129895	829586	0.0172	0.2953
chr22	51304566	711055	0.0139	0.2569
chrMT	16571	89748	5.416	4.8342
chrX	155270560	3730159	0.024	0.3761
chrY	59373566	198709	0.0033	0.1322

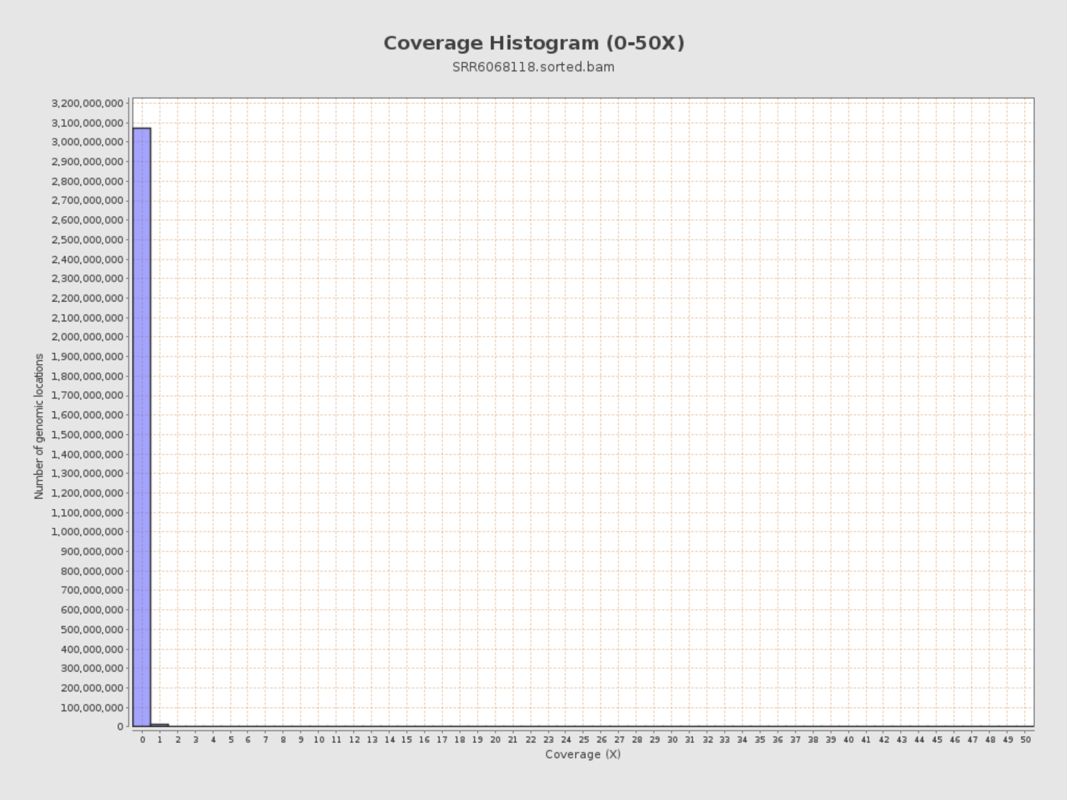
3. Results : Coverage across reference



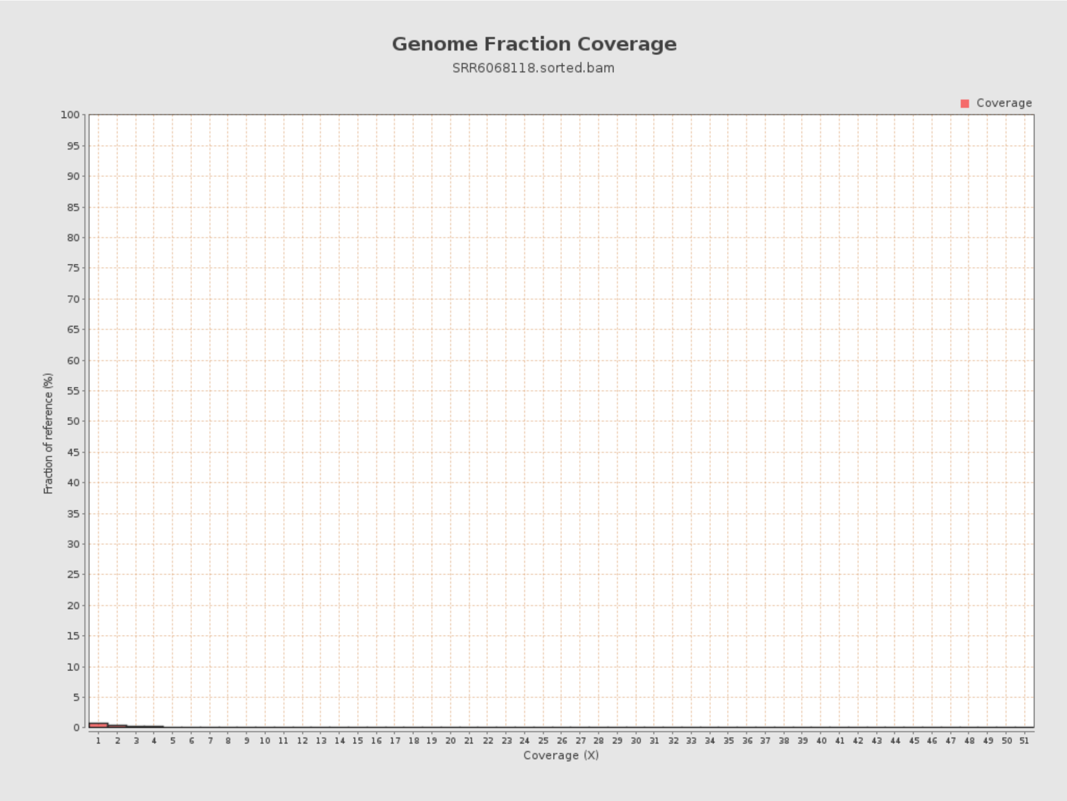
4. Results : Coverage Histogram



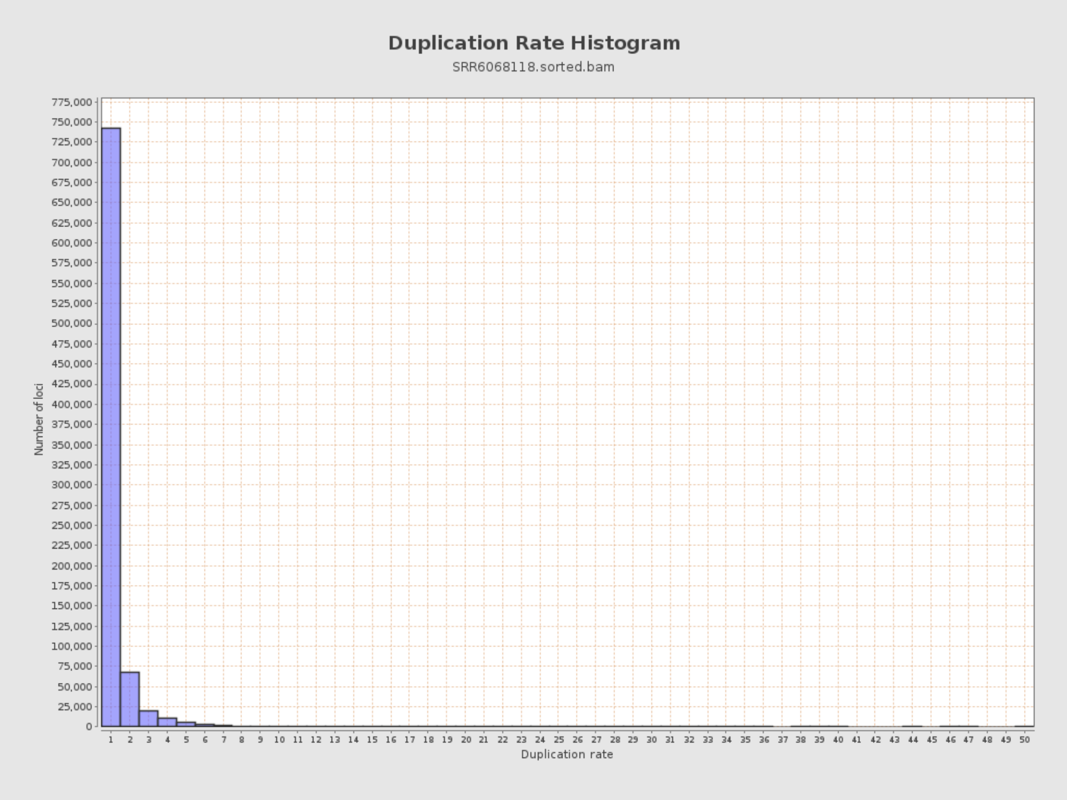
5. Results : Coverage Histogram (0-50X)



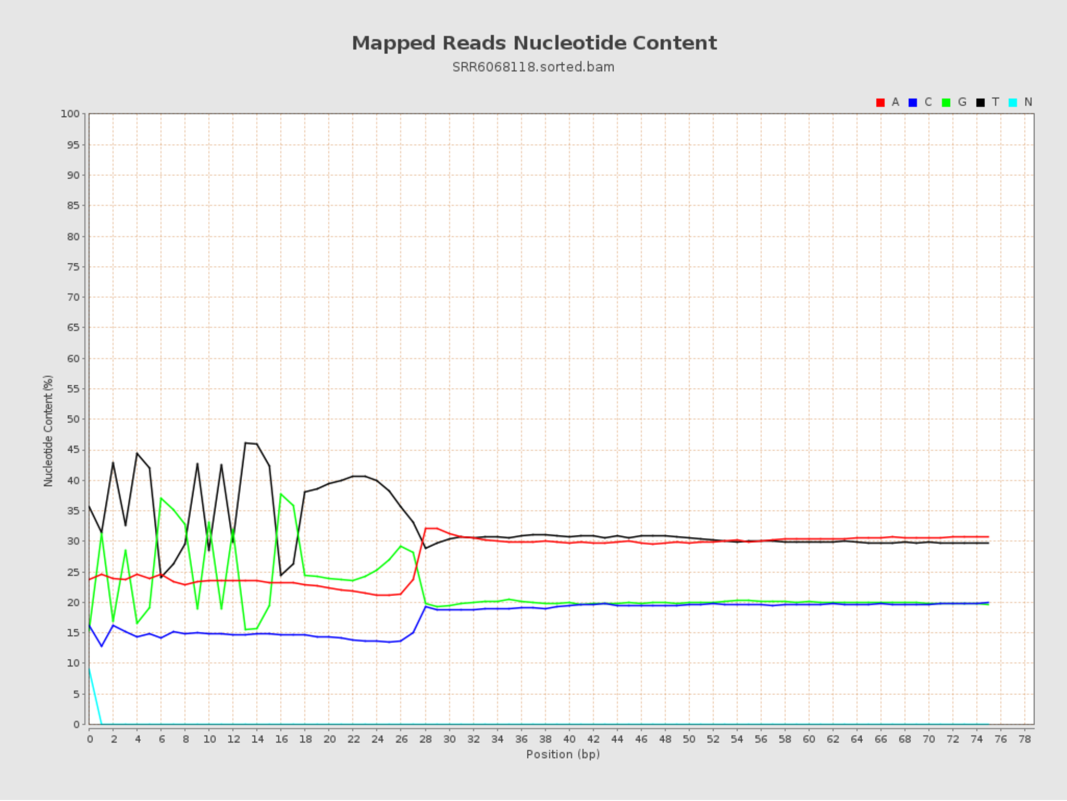
6. Results : Genome Fraction Coverage



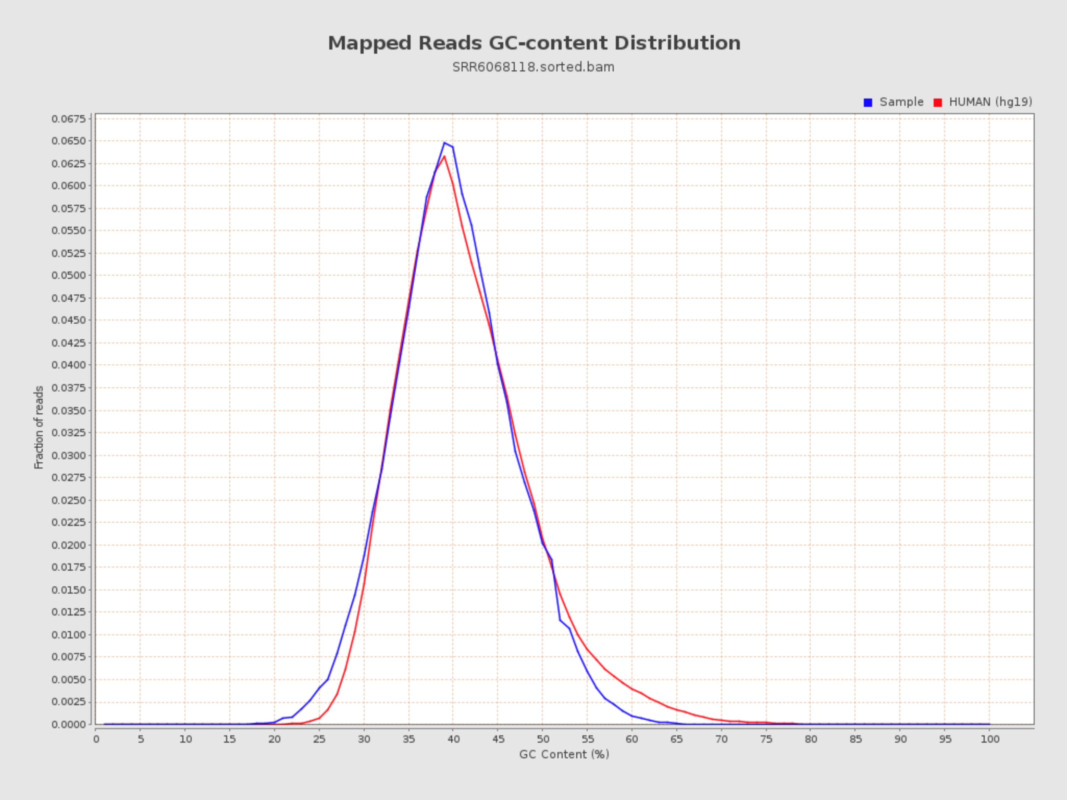
7. Results : Duplication Rate Histogram



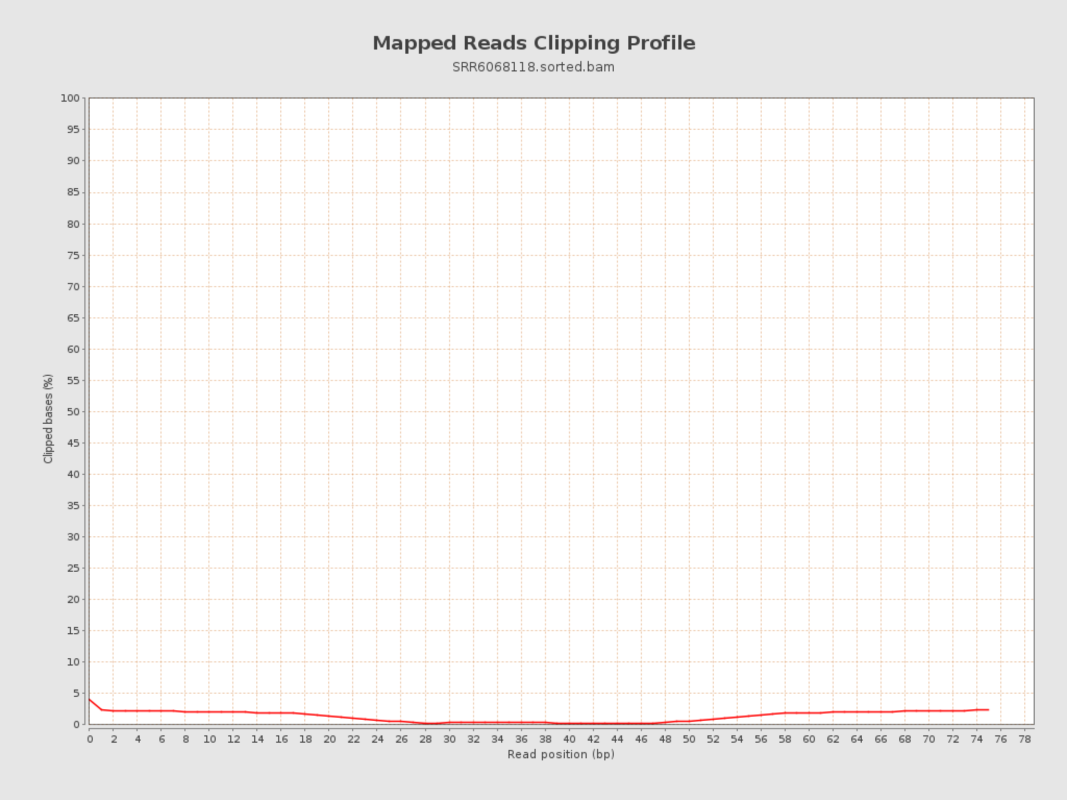
8. Results : Mapped Reads Nucleotide Content



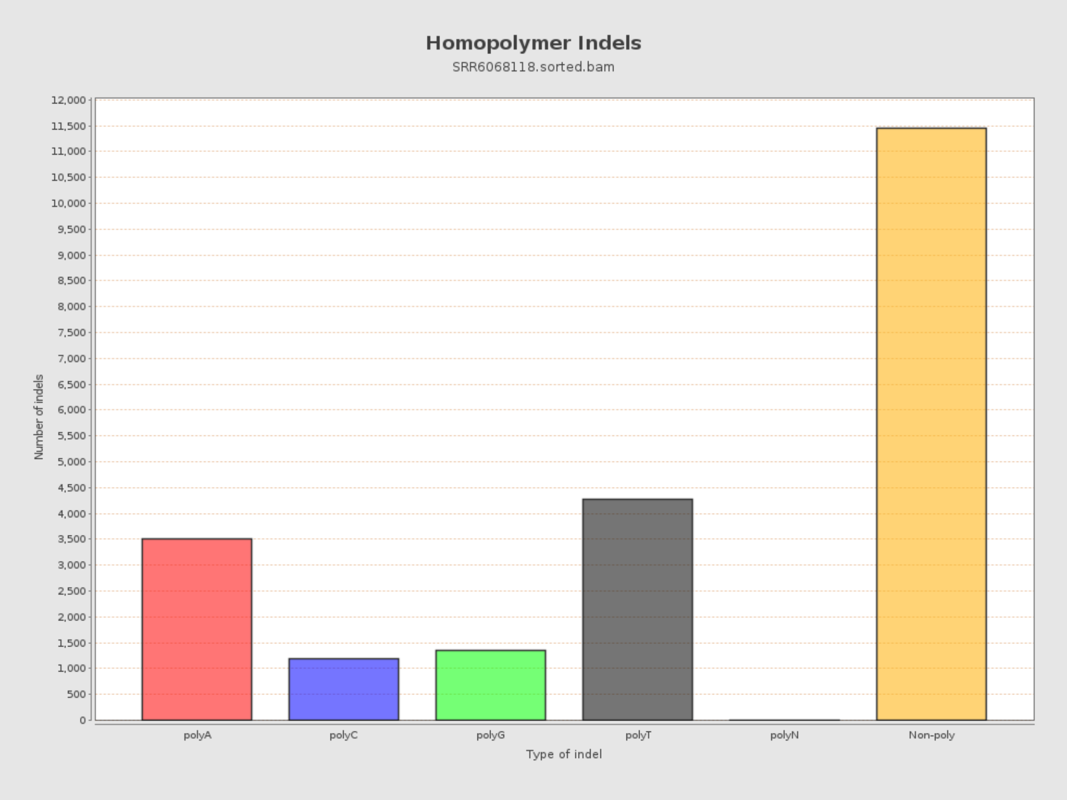
9. Results : Mapped Reads GC-content Distribution



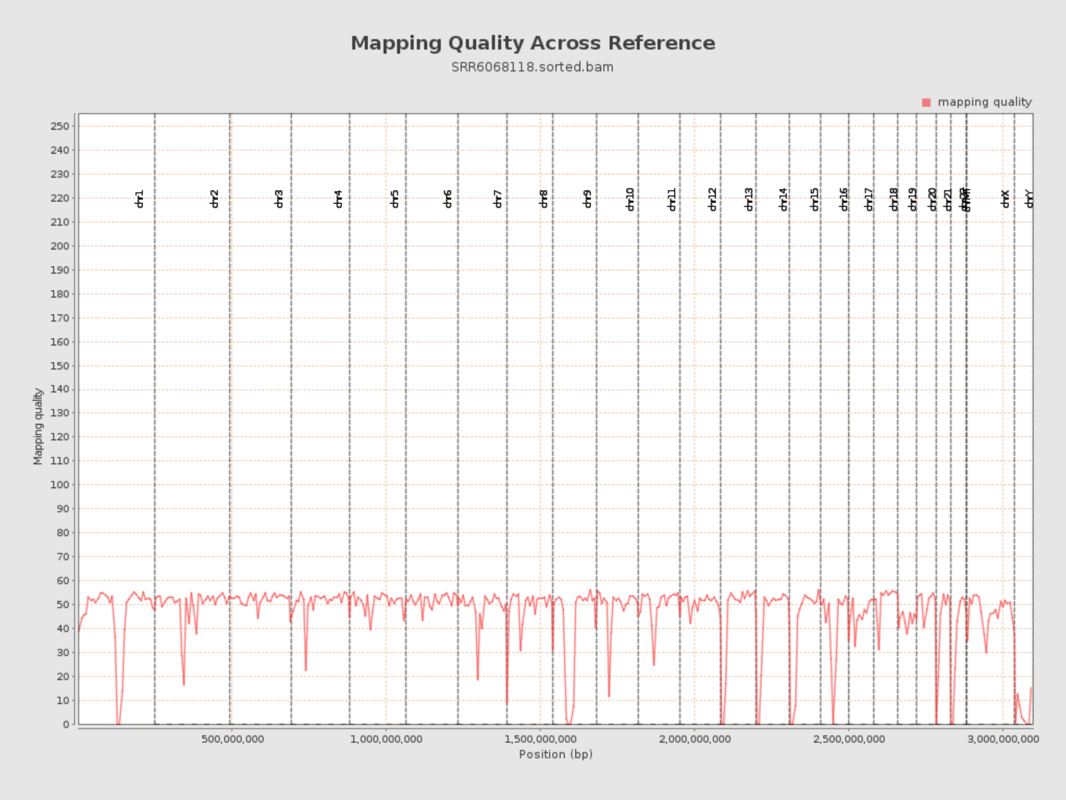
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram