Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 12:26:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068140.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_SRR6068140 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068140.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 12:26:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068140.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,389,333
Mapped reads	2,193,395 / 91.8%
Unmapped reads	195,938 / 8.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,728 / 0.91%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	94,323 / 3.95%
Duplication rate	3.36%
Clipped reads	942,998 / 39.47%

2.2. ACGT Content

Number/percentage of A's	41,315,542 / 28.06%
Number/percentage of C's	27,102,577 / 18.41%
Number/percentage of T's	46,805,404 / 31.79%
Number/percentage of G's	32,021,249 / 21.75%
Number/percentage of N's	3,093 / 0%
GC Percentage	40.15%

2.3. Coverage

Mean	0.0476

Standard Deviation	0.6211

2.4. Mapping Quality

Mean Mapping Quality	42.46

2.5. Mismatches and indels

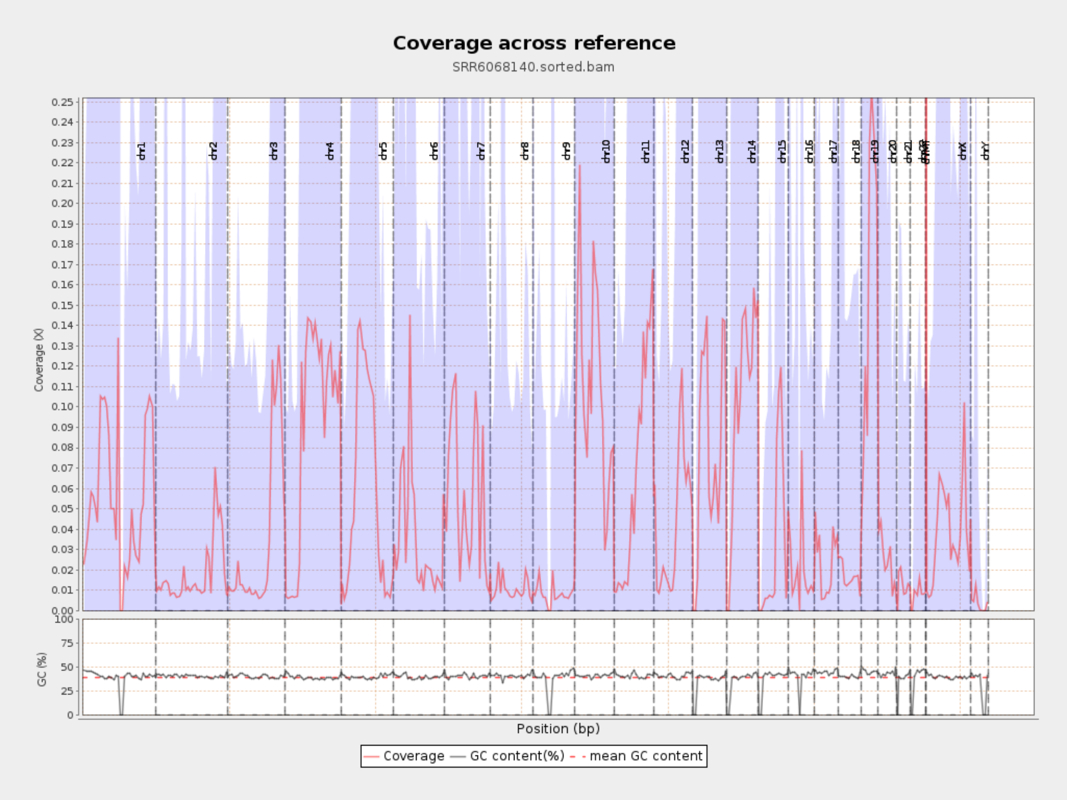
General error rate	0.78%
Mismatches	1,123,316
Insertions	11,015
Mapped reads with at least one insertion	0.5%
Deletions	44,513
Mapped reads with at least one deletion	2.01%
Homopolymer indels	46.82%

2.6. Chromosome stats

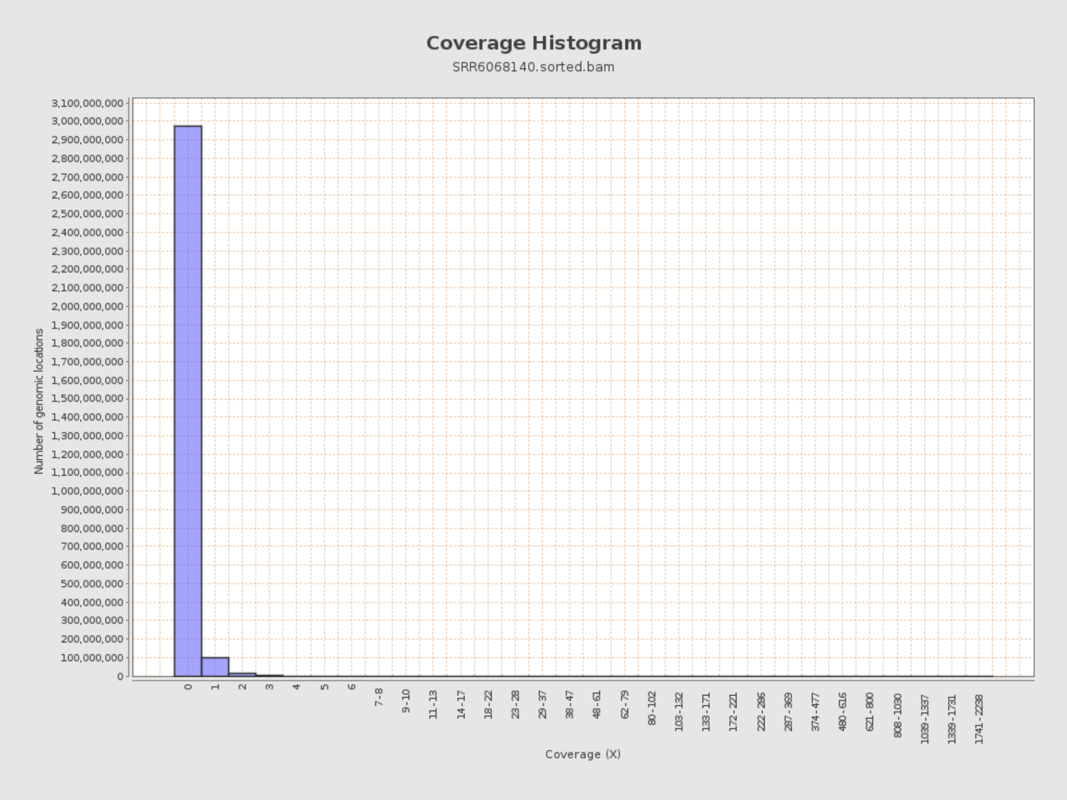
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14097678	0.0566	1.8725
chr2	243199373	4410793	0.0181	0.3593
chr3	198022430	6743640	0.0341	0.216
chr4	191154276	17296562	0.0905	0.3531
chr5	180915260	10504430	0.0581	0.2856
chr6	171115067	5978393	0.0349	0.3411
chr7	159138663	8878873	0.0558	0.3115

chr8	146364022	1544587	0.0106	0.3636
chr9	141213431	1147007	0.0081	0.1938
chr10	135534747	15023159	0.1108	0.46
chr11	135006516	9016810	0.0668	0.3207
chr12	133851895	5760017	0.043	0.2466
chr13	115169878	9061189	0.0787	0.327
chr14	107349540	10923424	0.1018	0.3756
chr15	102531392	3166010	0.0309	0.212
chr16	90354753	1914660	0.0212	0.1824
chr17	81195210	1915005	0.0236	0.178
chr18	78077248	1335590	0.0171	0.3432
chr19	59128983	9726235	0.1645	1.0556
chr20	63025520	1556889	0.0247	0.1901
chr21	48129895	600449	0.0125	0.1295
chr22	51304566	401374	0.0078	0.1
chrMT	16571	20785	1.2543	1.5385
chrX	155270560	6076091	0.0391	0.2488
chrY	59373566	220639	0.0037	0.117

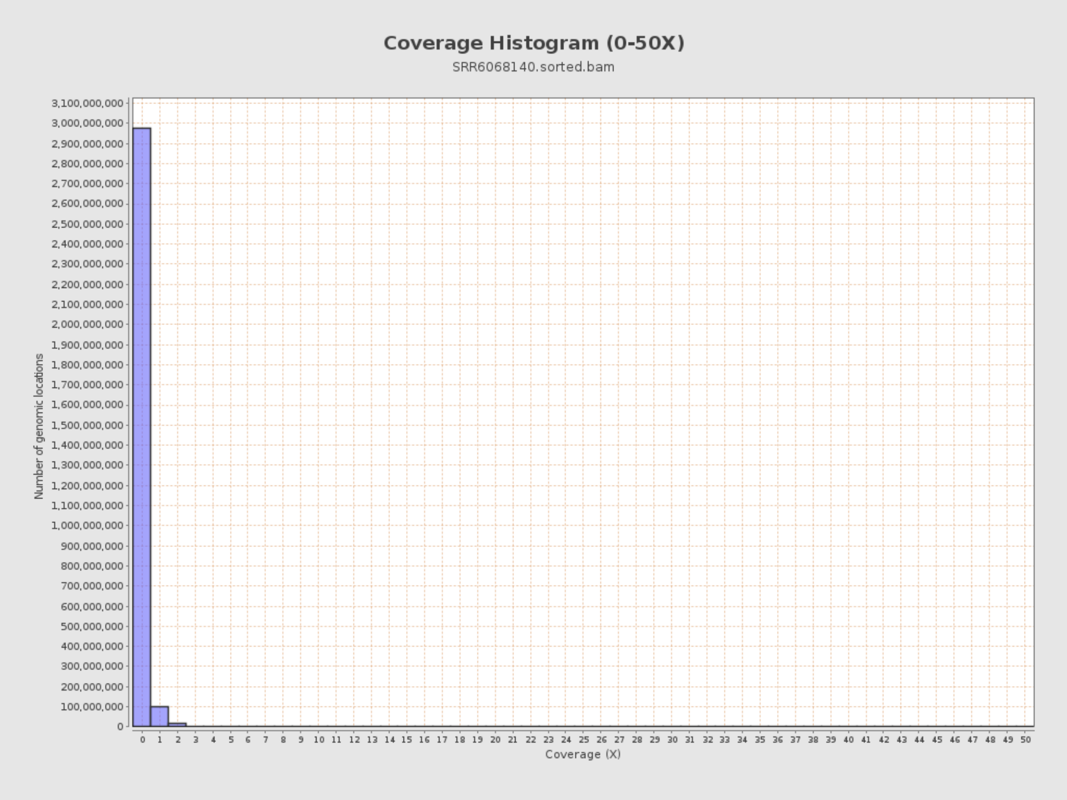
3. Results : Coverage across reference



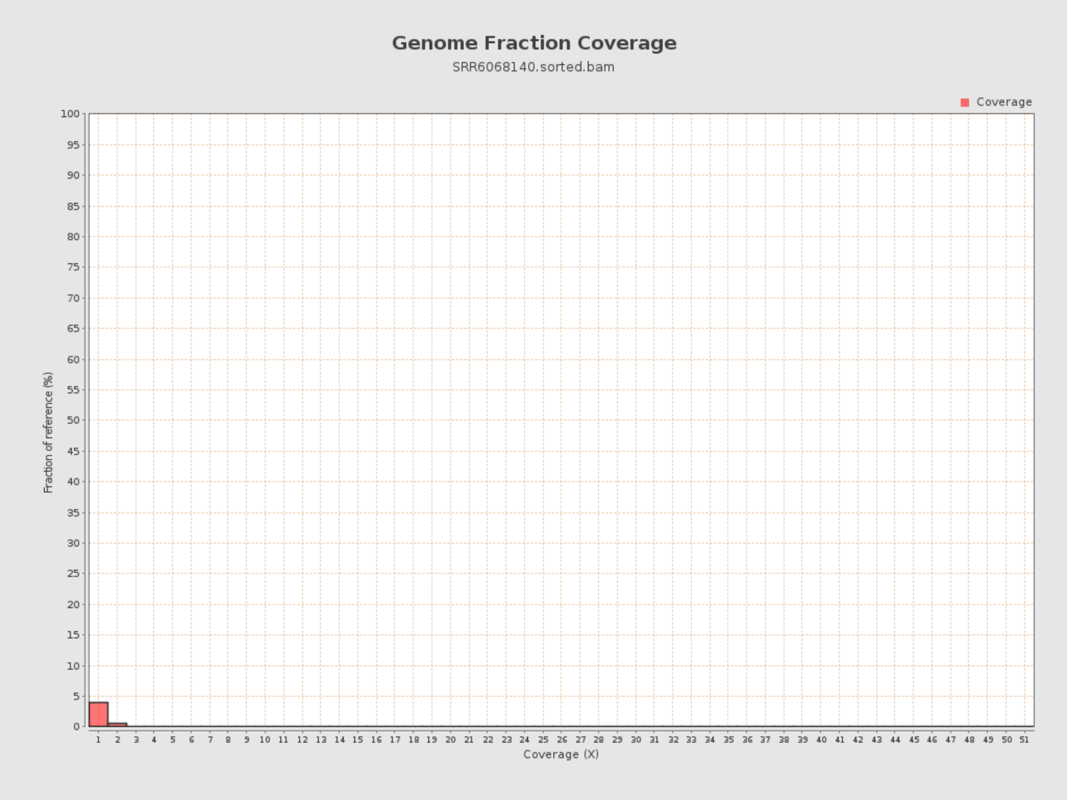
4. Results : Coverage Histogram



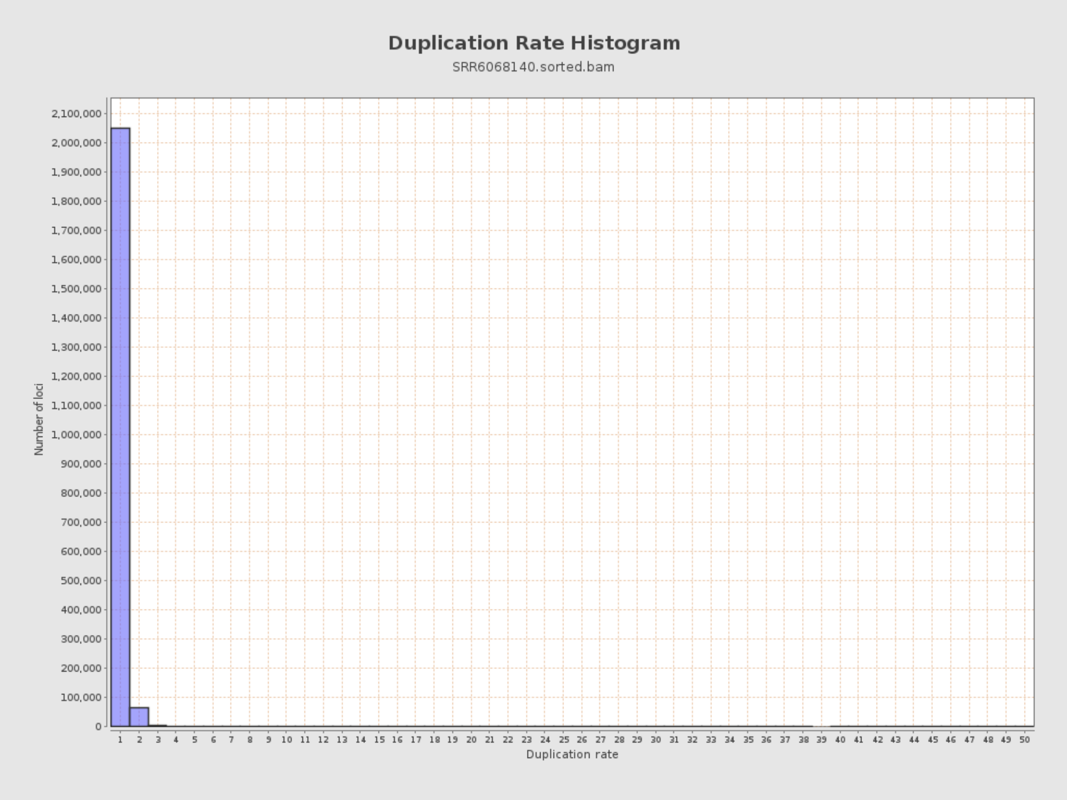
5. Results : Coverage Histogram (0-50X)



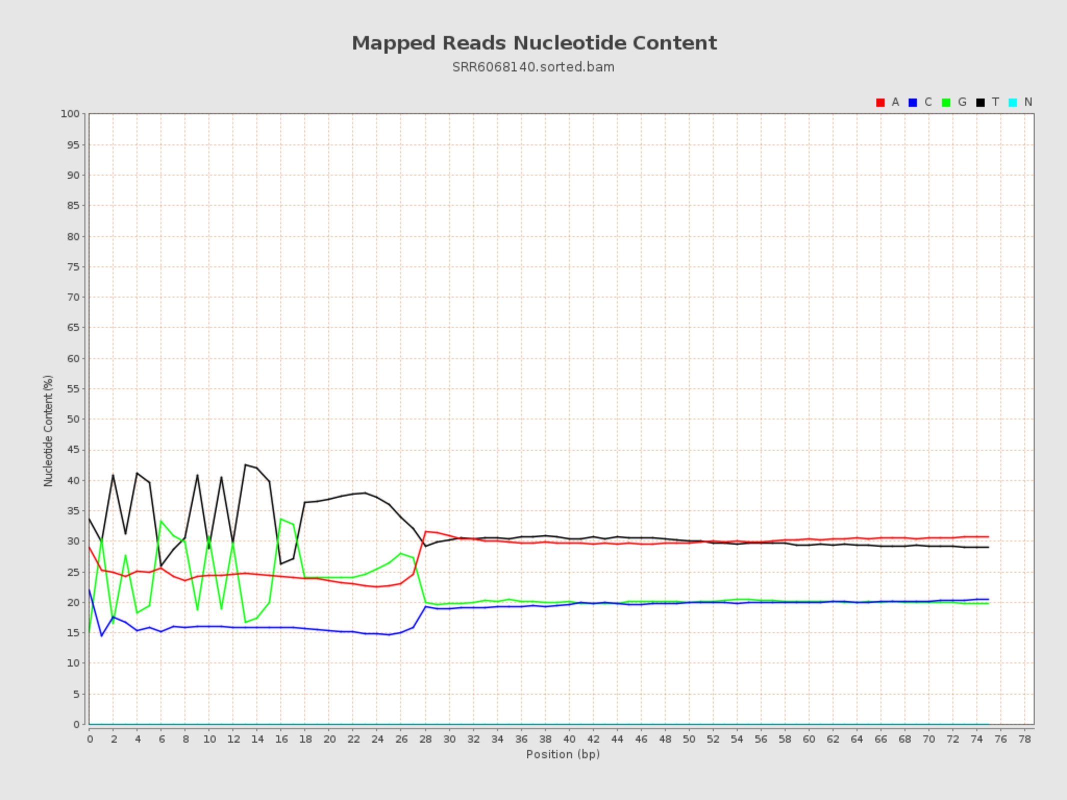
6. Results : Genome Fraction Coverage



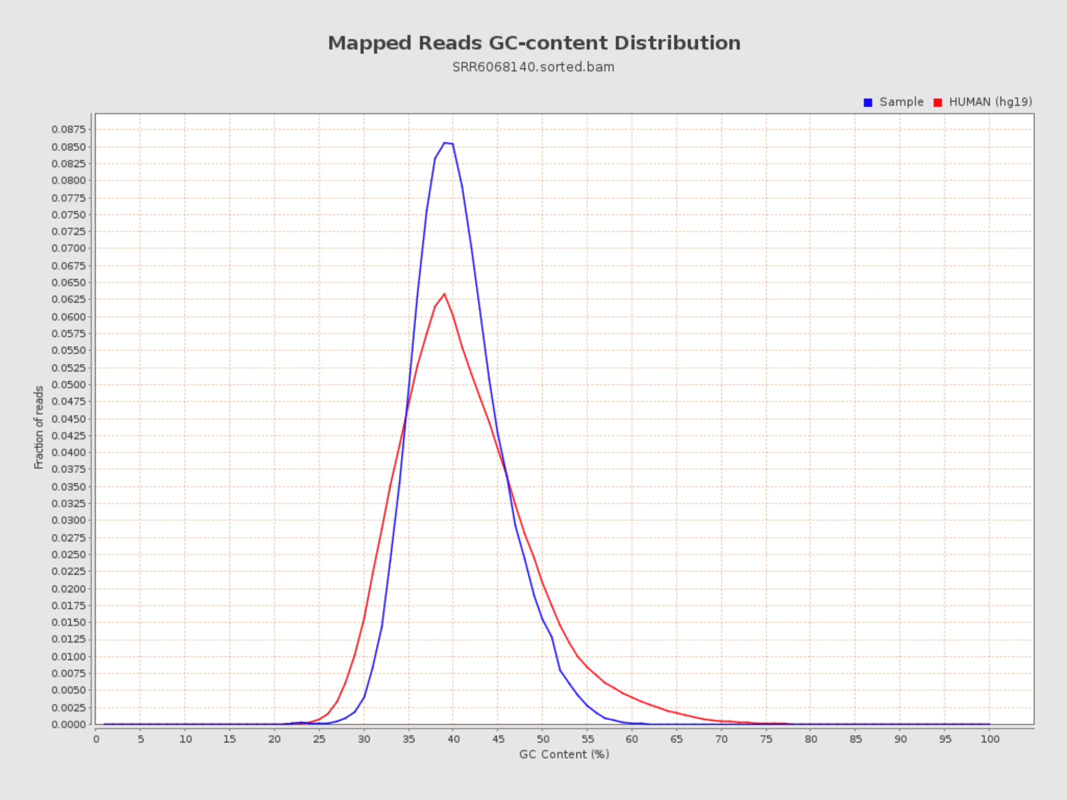
7. Results : Duplication Rate Histogram



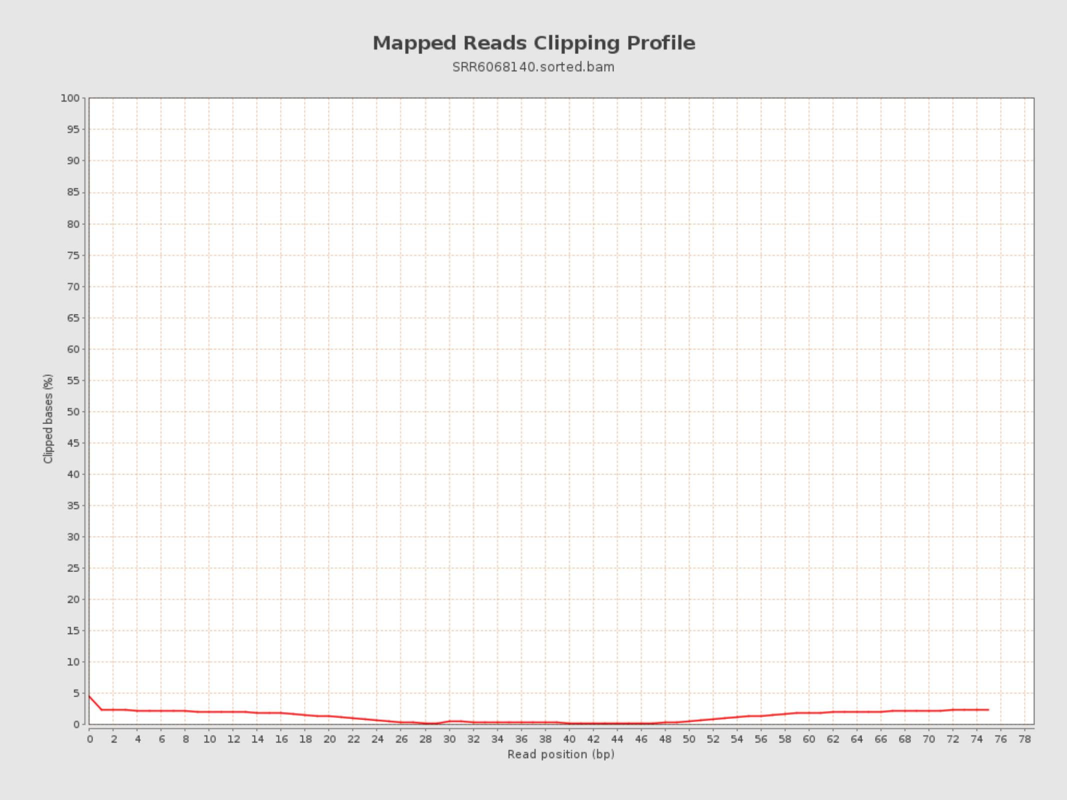
8. Results : Mapped Reads Nucleotide Content



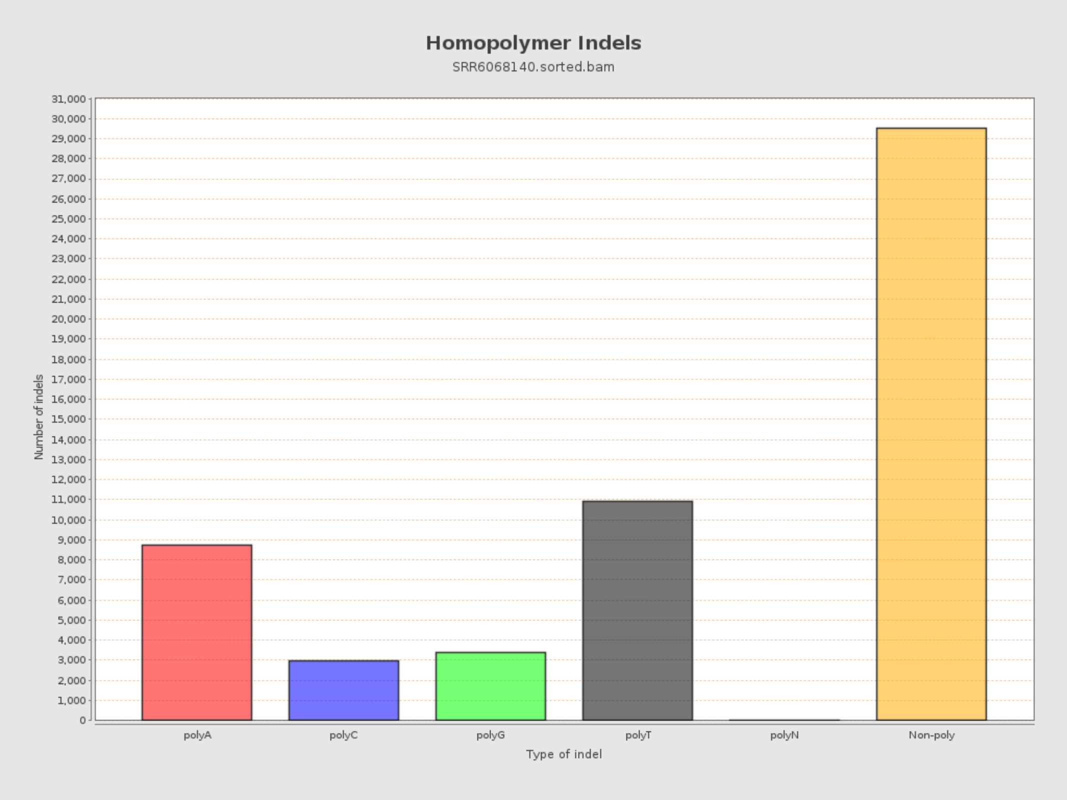
9. Results : Mapped Reads GC-content Distribution



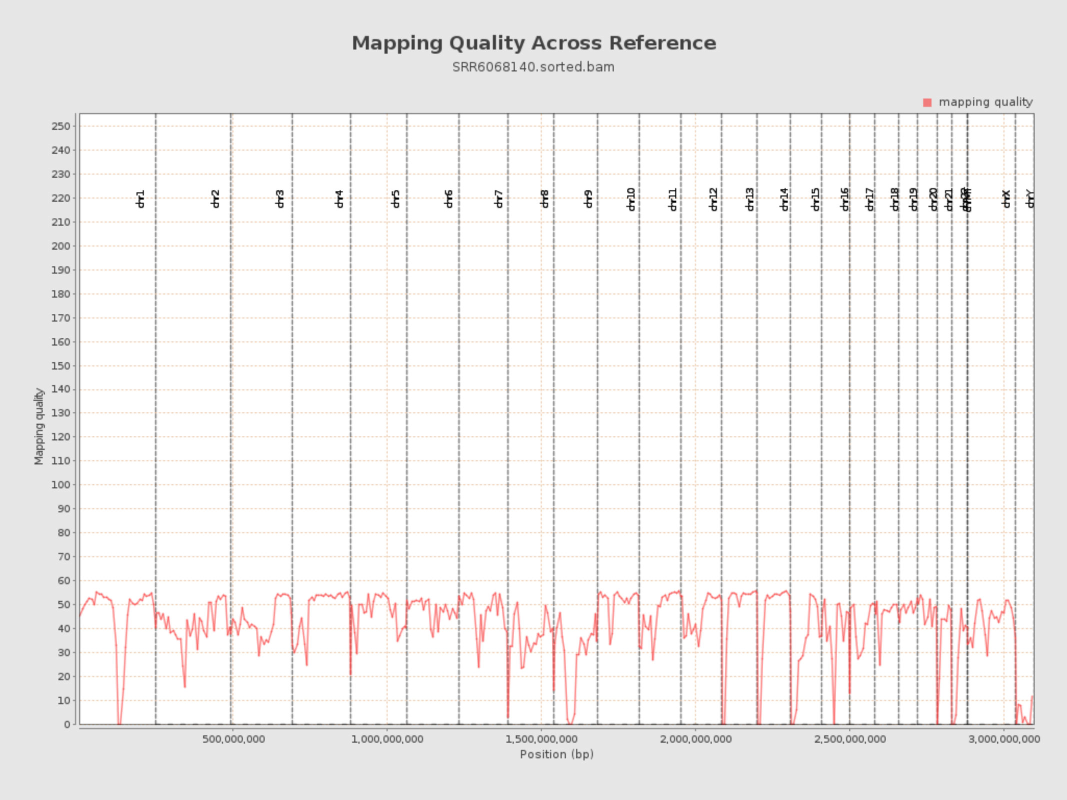
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram