Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 15:53:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068929.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_SRR6068929 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068929.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 15:53:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068929.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,555,572
Mapped reads	1,053,549 / 67.73%
Unmapped reads	502,023 / 32.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,196 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	66,528 / 4.28%
Duplication rate	5.28%
Clipped reads	601,006 / 38.64%

2.2. ACGT Content

Number/percentage of A's	17,644,469 / 26.42%
Number/percentage of C's	11,288,168 / 16.9%
Number/percentage of T's	22,608,483 / 33.85%
Number/percentage of G's	15,089,305 / 22.6%
Number/percentage of N's	150,572 / 0.23%
GC Percentage	39.5%

2.3. Coverage

Mean	0.0216

Standard Deviation	0.2542

2.4. Mapping Quality

Mean Mapping Quality	45.9

2.5. Mismatches and indels

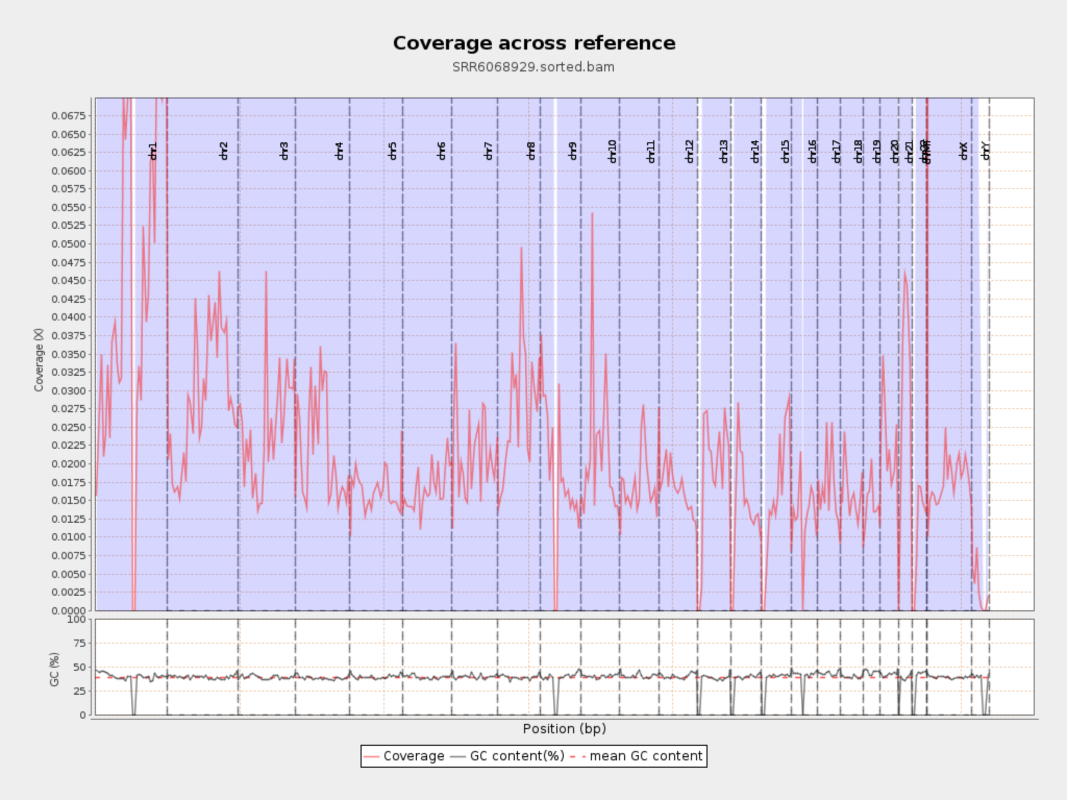
General error rate	1.06%
Mismatches	698,527
Insertions	5,747
Mapped reads with at least one insertion	0.54%
Deletions	19,203
Mapped reads with at least one deletion	1.8%
Homopolymer indels	48.36%

2.6. Chromosome stats

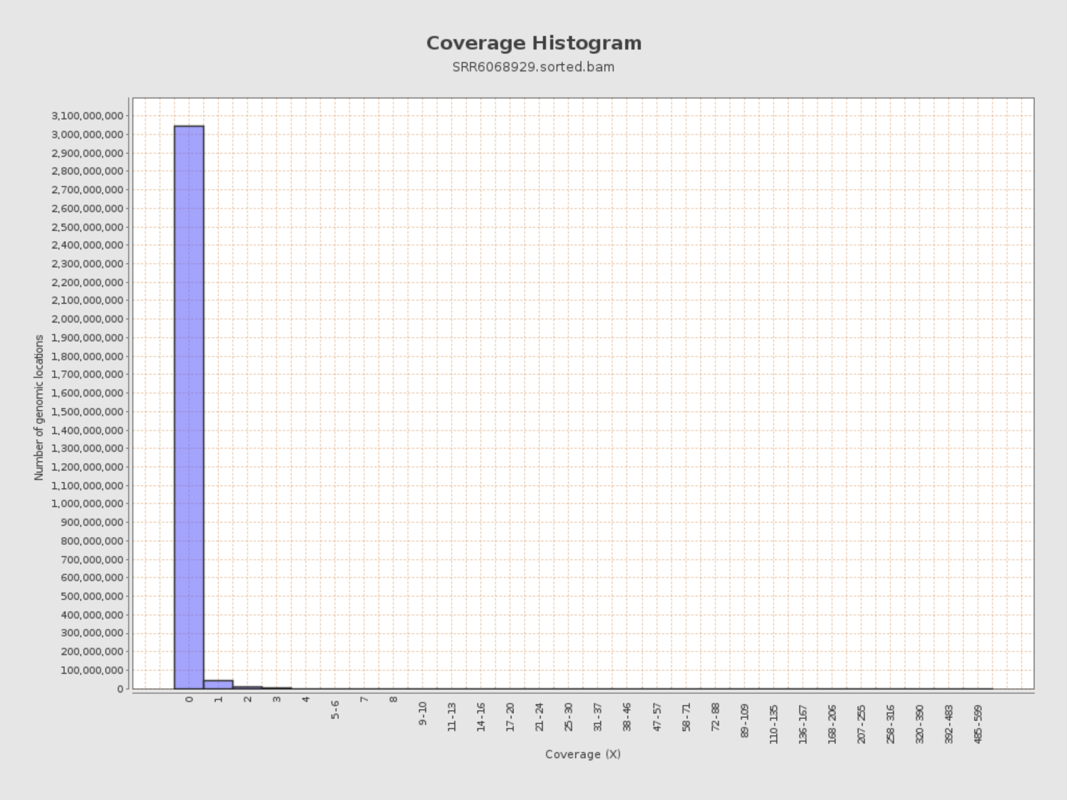
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11053988	0.0443	0.5261
chr2	243199373	7091558	0.0292	0.262
chr3	198022430	4887716	0.0247	0.1998
chr4	191154276	4211497	0.022	0.1875
chr5	180915260	2943479	0.0163	0.1557
chr6	171115067	2853422	0.0167	0.1749
chr7	159138663	3398873	0.0214	0.222

chr8	146364022	4021015	0.0275	0.3438
chr9	141213431	2619164	0.0185	0.2178
chr10	135534747	2917090	0.0215	0.323
chr11	135006516	2324494	0.0172	0.1937
chr12	133851895	2217816	0.0166	0.1592
chr13	115169878	2141075	0.0186	0.1674
chr14	107349540	1469853	0.0137	0.1457
chr15	102531392	1594208	0.0155	0.1531
chr16	90354753	1143753	0.0127	0.1478
chr17	81195210	1354435	0.0167	0.1671
chr18	78077248	1239362	0.0159	0.3127
chr19	59128983	866703	0.0147	0.2853
chr20	63025520	1452802	0.0231	0.1903
chr21	48129895	1465529	0.0304	0.223
chr22	51304566	557678	0.0109	0.1243
chrMT	16571	63524	3.8334	3.0545
chrX	155270560	2761292	0.0178	0.1723
chrY	59373566	161529	0.0027	0.0752

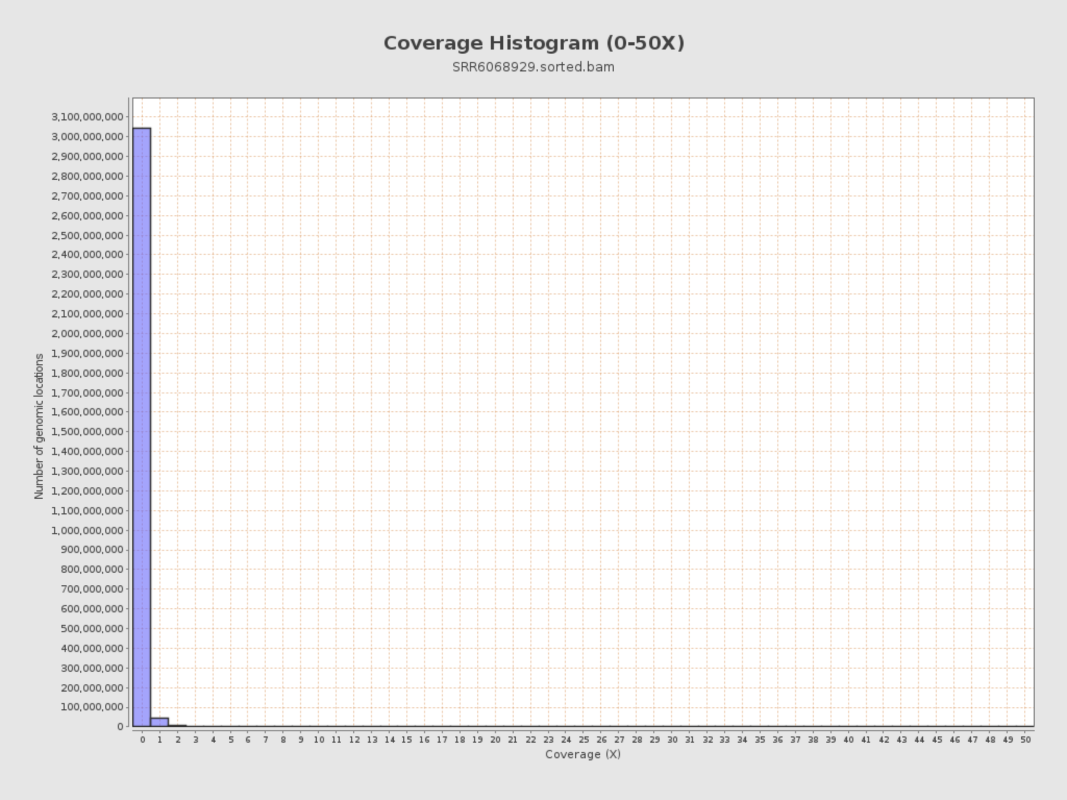
3. Results : Coverage across reference



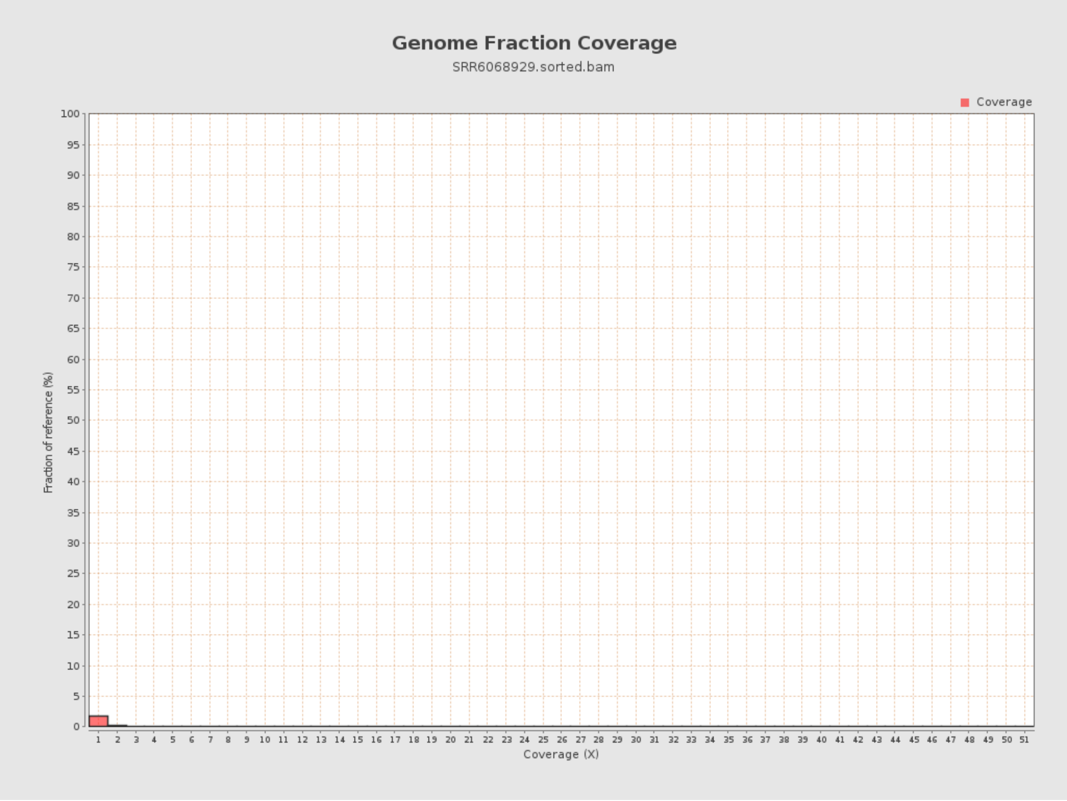
4. Results : Coverage Histogram



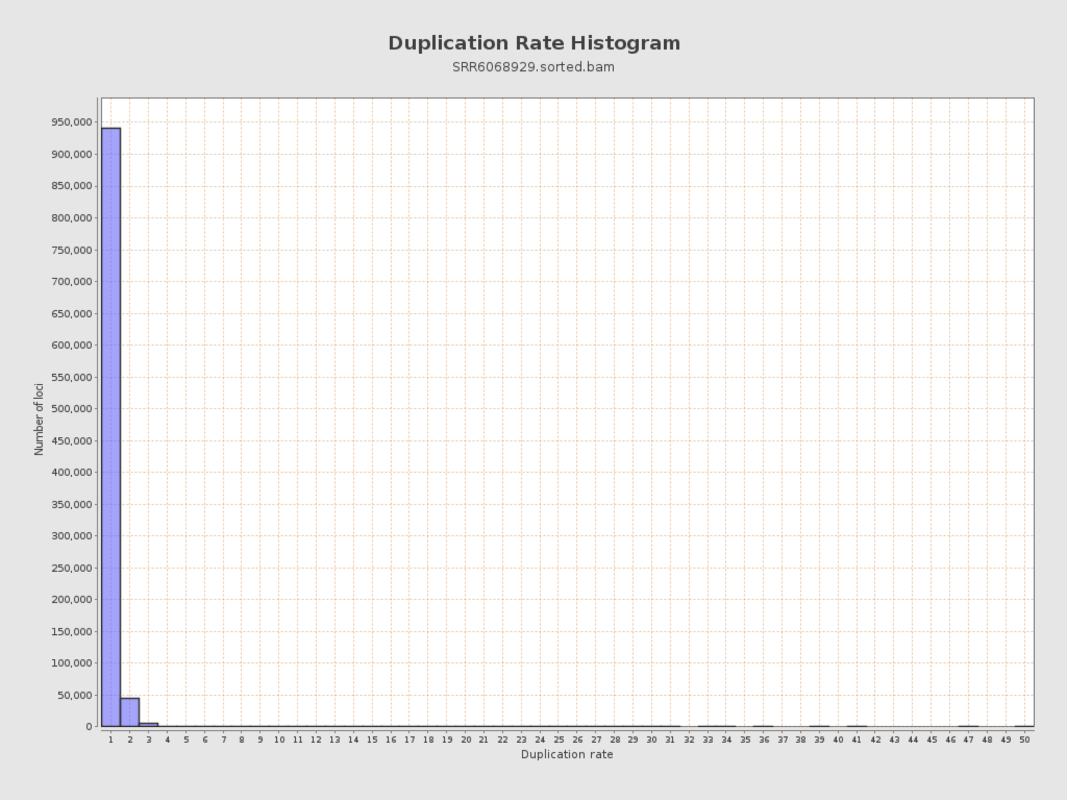
5. Results : Coverage Histogram (0-50X)



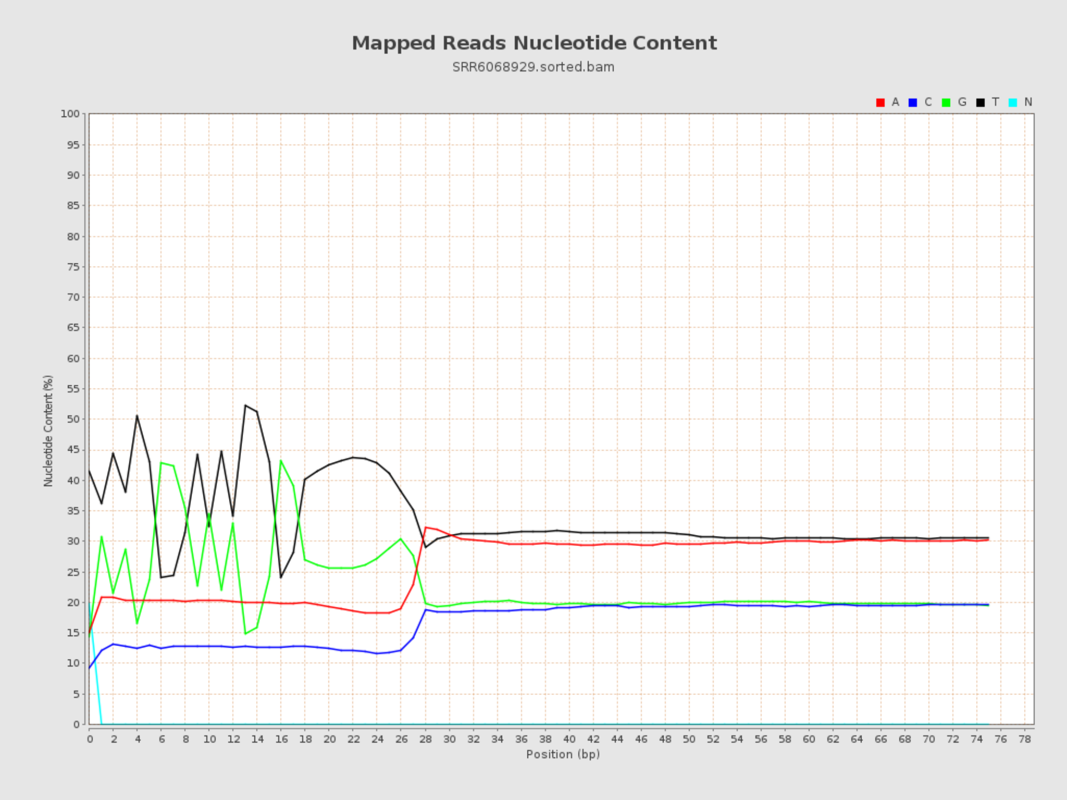
6. Results : Genome Fraction Coverage



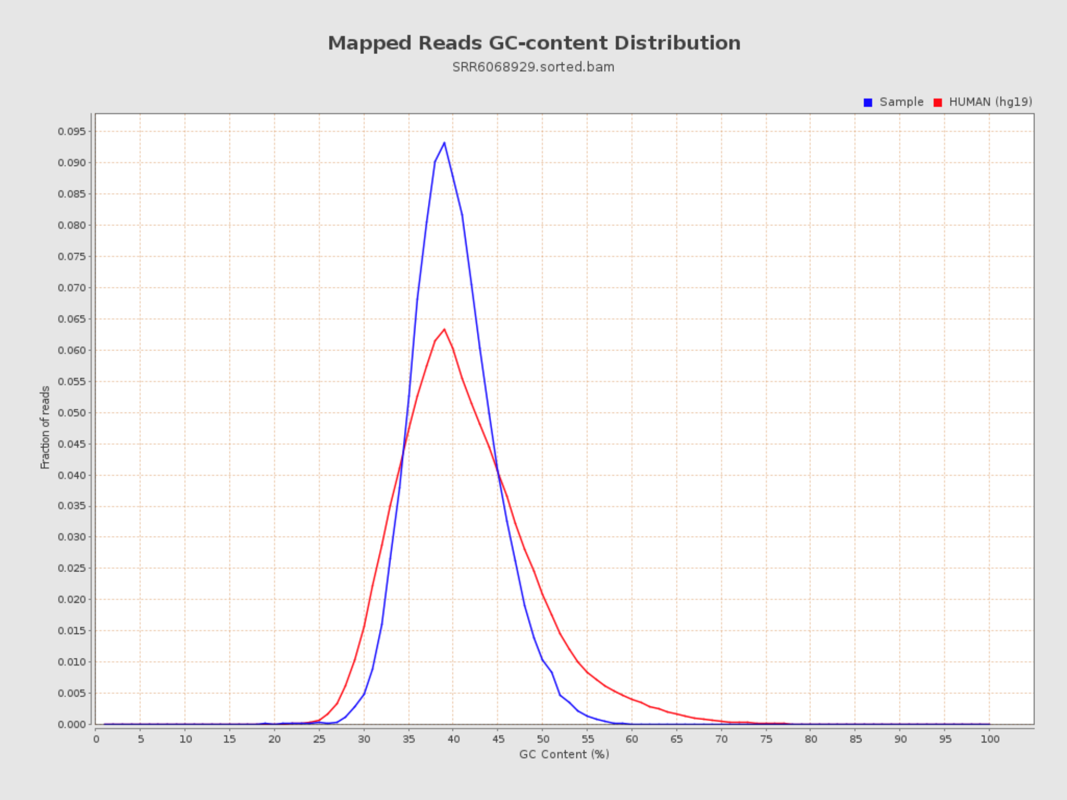
7. Results : Duplication Rate Histogram



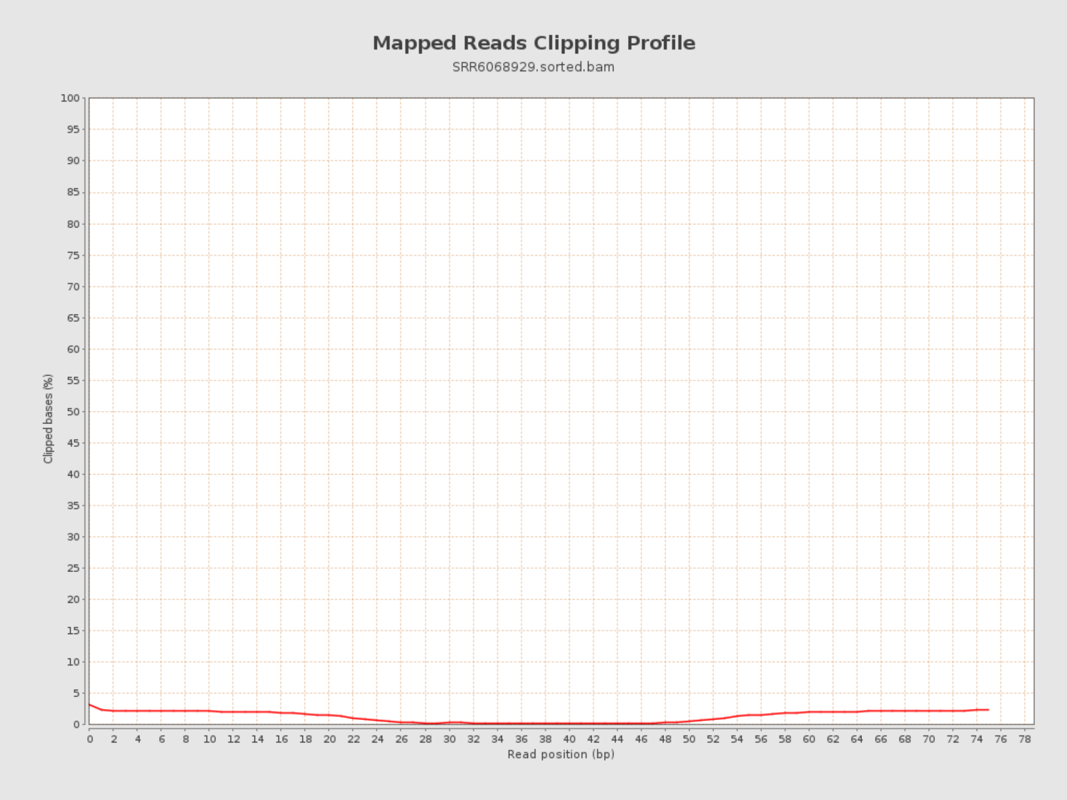
8. Results : Mapped Reads Nucleotide Content



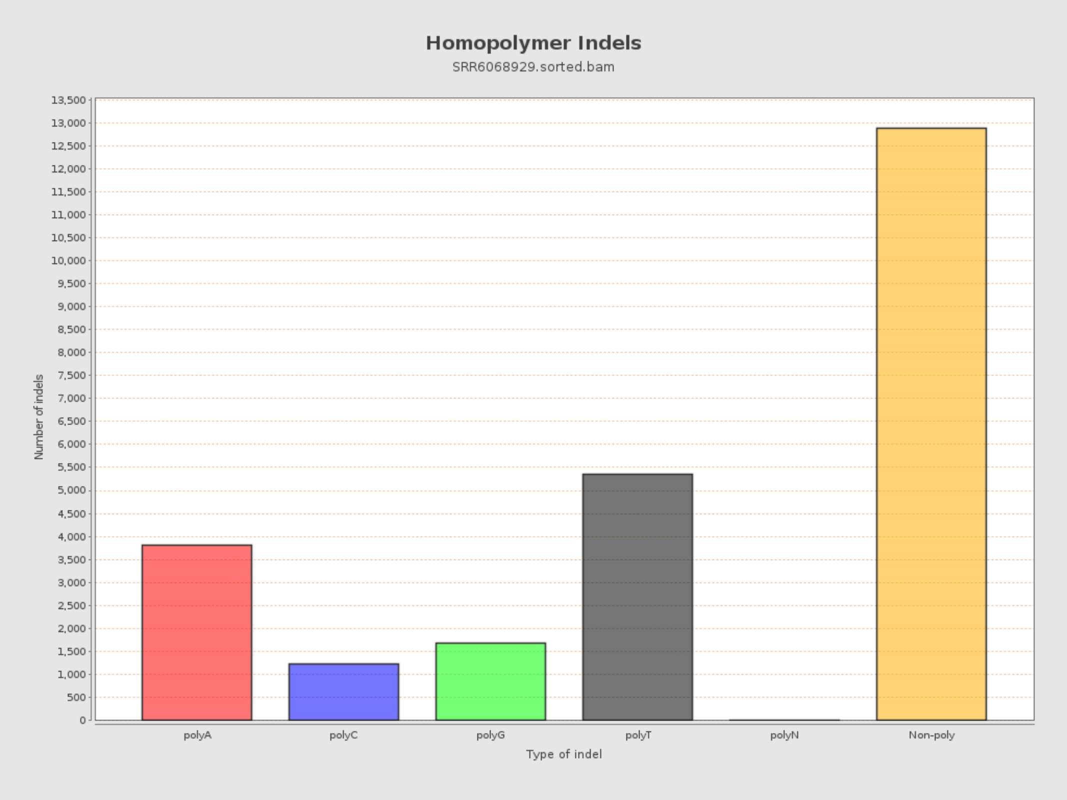
9. Results : Mapped Reads GC-content Distribution



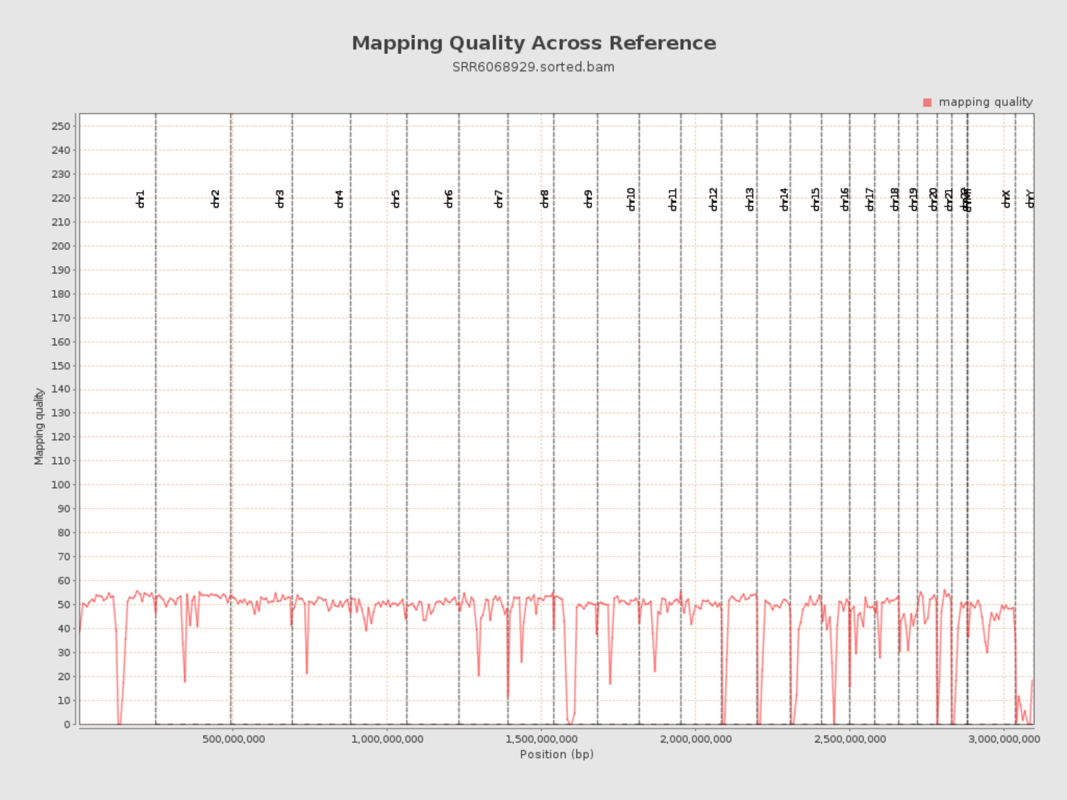
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram