Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 10:03:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068101.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_SRR6068101 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068101.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 10:03:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068101.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,415,681
Mapped reads	2,073,936 / 85.85%
Unmapped reads	341,745 / 14.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,529 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	210,556 / 8.72%
Duplication rate	8.33%
Clipped reads	1,138,429 / 47.13%

2.2. ACGT Content

Number/percentage of A's	35,024,440 / 26.35%
Number/percentage of C's	24,034,425 / 18.08%
Number/percentage of T's	42,745,650 / 32.15%
Number/percentage of G's	31,130,082 / 23.42%
Number/percentage of N's	2,412 / 0%
GC Percentage	41.5%

2.3. Coverage

Mean	0.043

Standard Deviation	0.4018

2.4. Mapping Quality

Mean Mapping Quality	42.62

2.5. Mismatches and indels

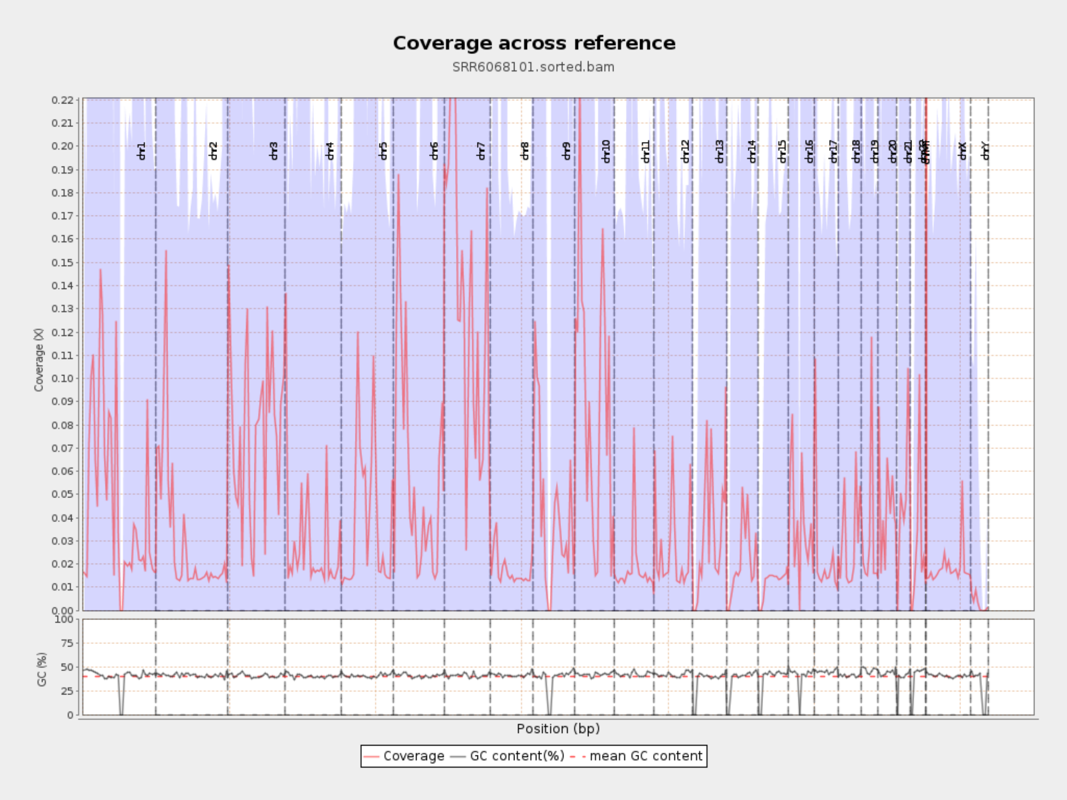
General error rate	0.76%
Mismatches	990,182
Insertions	9,180
Mapped reads with at least one insertion	0.44%
Deletions	33,352
Mapped reads with at least one deletion	1.59%
Homopolymer indels	46.24%

2.6. Chromosome stats

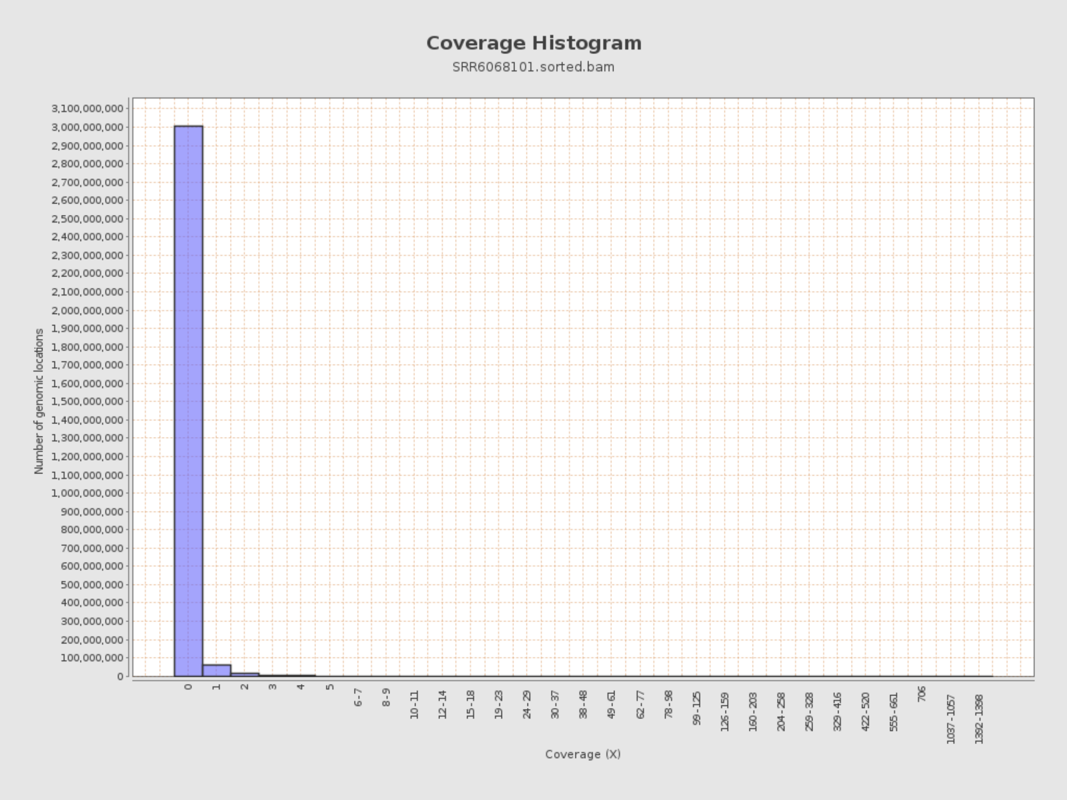
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11949628	0.0479	0.4147
chr2	243199373	7415166	0.0305	0.6691
chr3	198022430	15289693	0.0772	0.3922
chr4	191154276	5415085	0.0283	0.24
chr5	180915260	7087220	0.0392	0.2756
chr6	171115067	10042118	0.0587	0.4263
chr7	159138663	21966439	0.138	0.8945

chr8	146364022	2508756	0.0171	0.2429
chr9	141213431	5967650	0.0423	0.3347
chr10	135534747	12576822	0.0928	0.4458
chr11	135006516	2496084	0.0185	0.2106
chr12	133851895	3704484	0.0277	0.2348
chr13	115169878	3791621	0.0329	0.2592
chr14	107349540	2287831	0.0213	0.209
chr15	102531392	1213905	0.0118	0.1579
chr16	90354753	3291678	0.0364	0.2779
chr17	81195210	1949870	0.024	0.2134
chr18	78077248	2358443	0.0302	0.386
chr19	59128983	1938719	0.0328	0.3631
chr20	63025520	2772611	0.044	0.3034
chr21	48129895	2304671	0.0479	0.3085
chr22	51304566	1459760	0.0285	0.2375
chrMT	16571	119789	7.2288	5.5809
chrX	155270560	2905052	0.0187	0.21
chrY	59373566	177000	0.003	0.0787

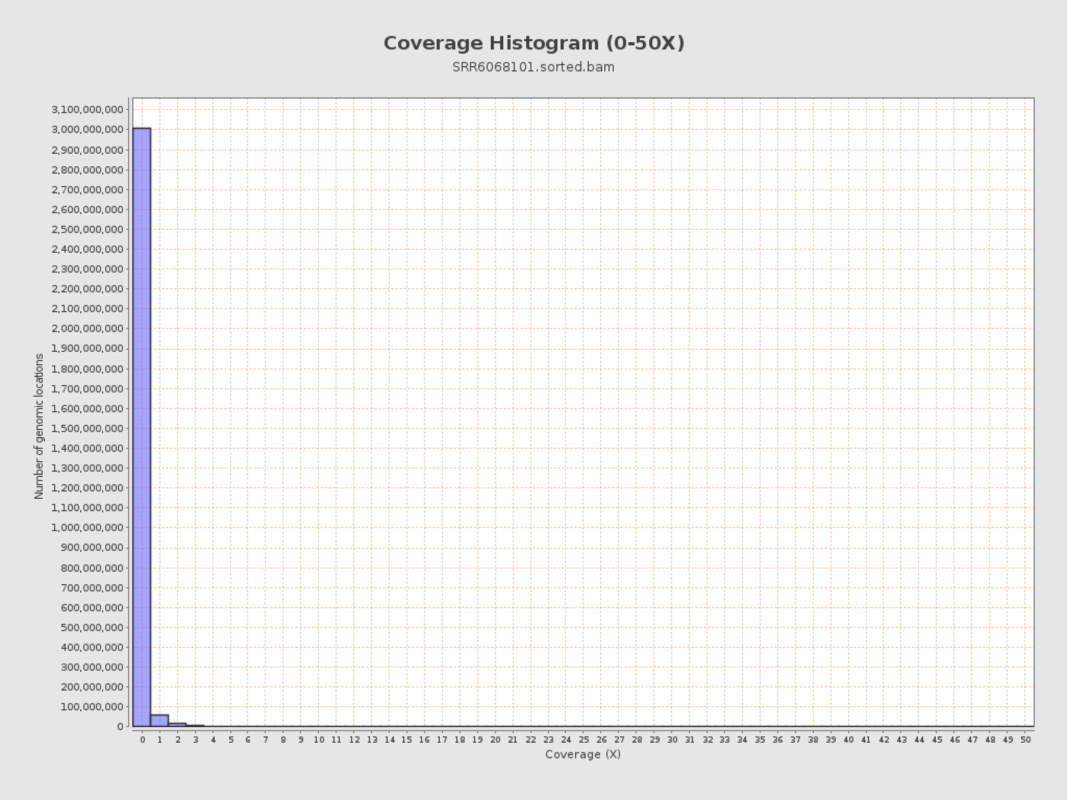
3. Results : Coverage across reference



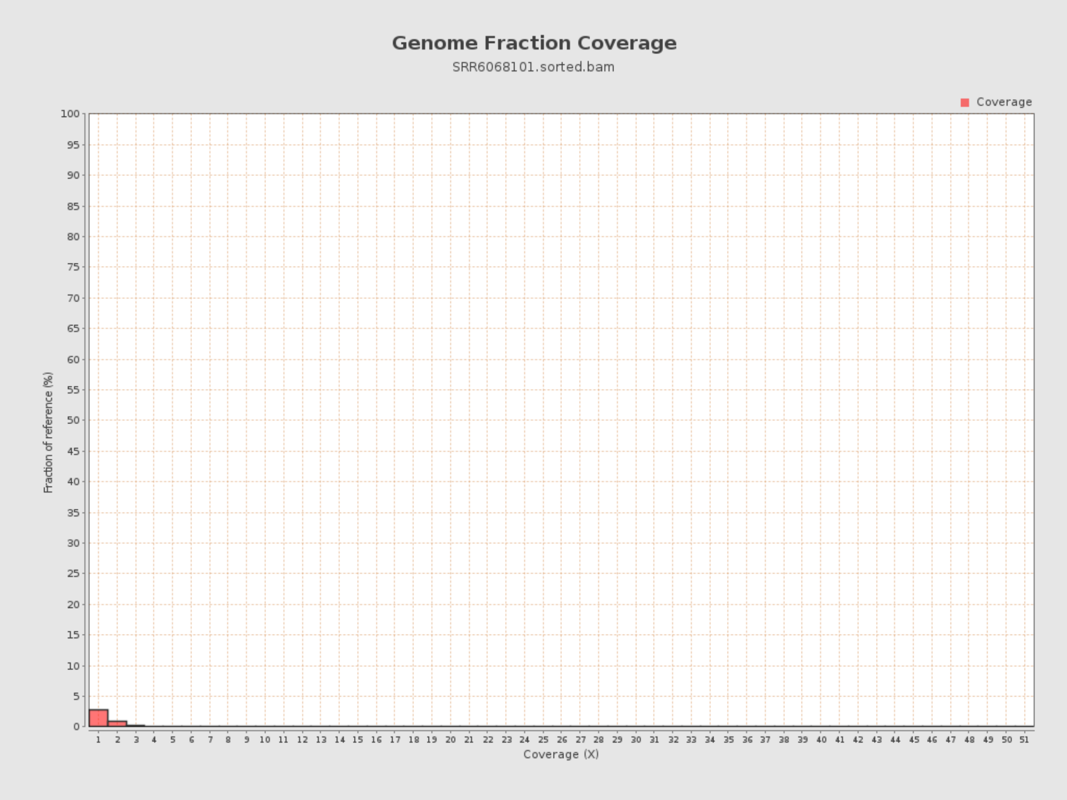
4. Results : Coverage Histogram



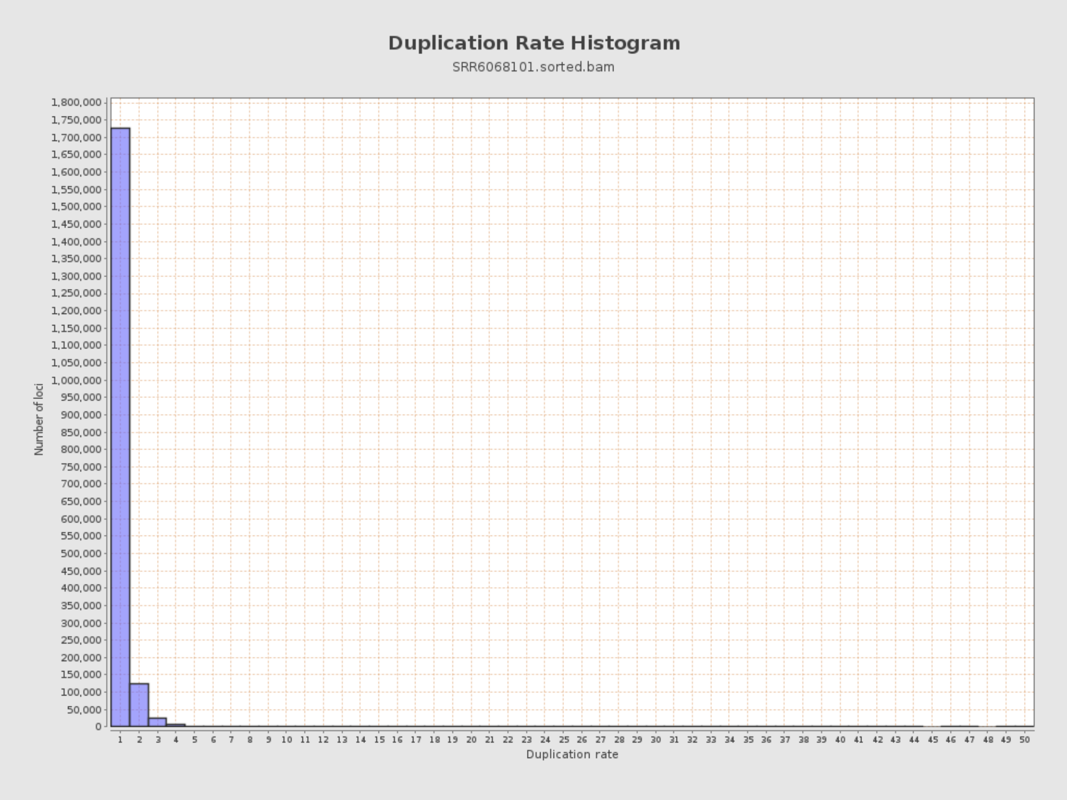
5. Results : Coverage Histogram (0-50X)



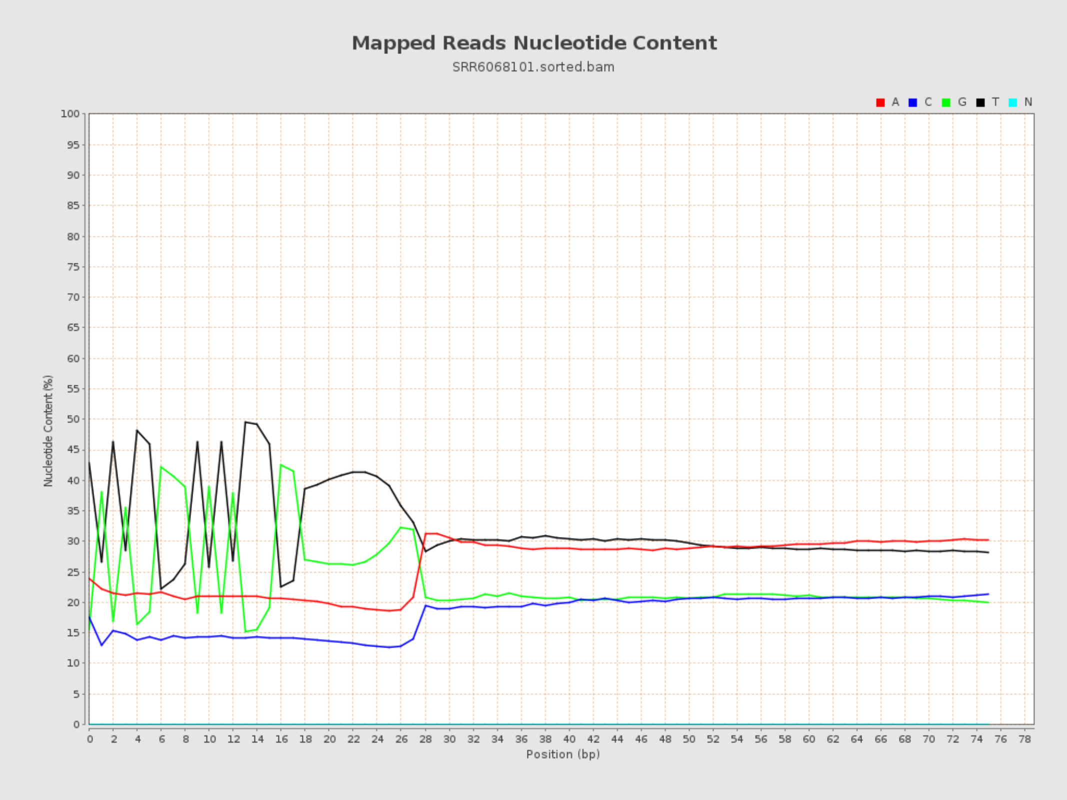
6. Results : Genome Fraction Coverage



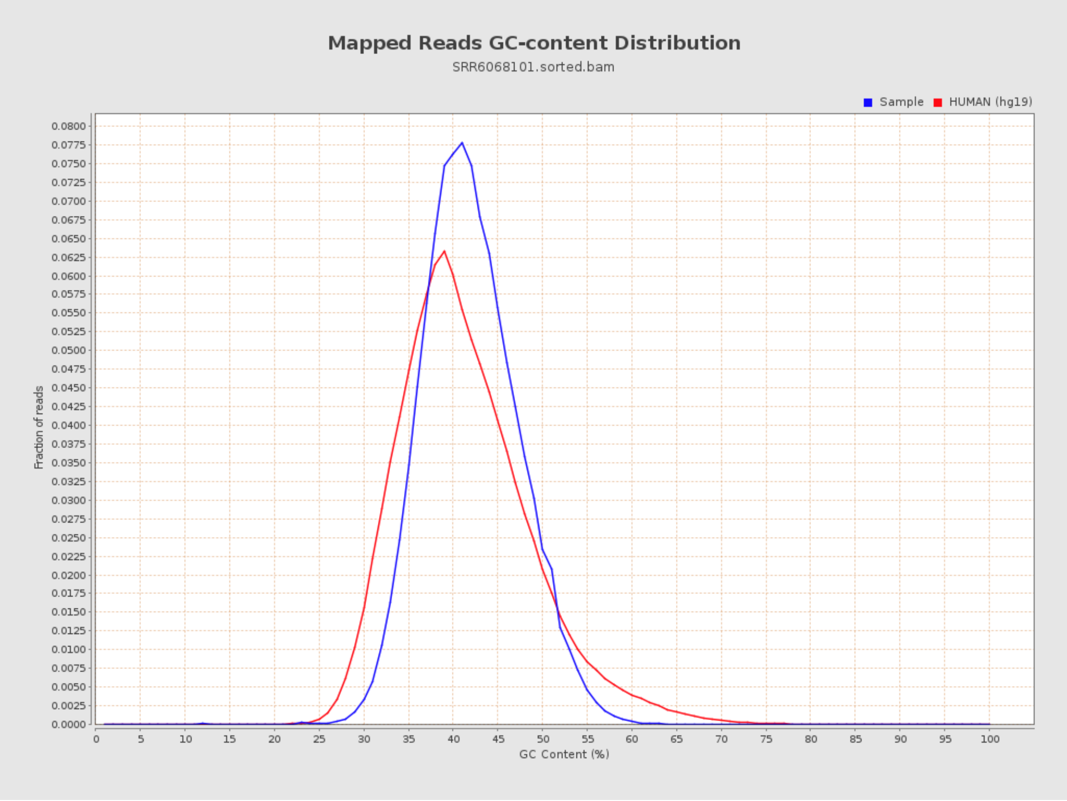
7. Results : Duplication Rate Histogram



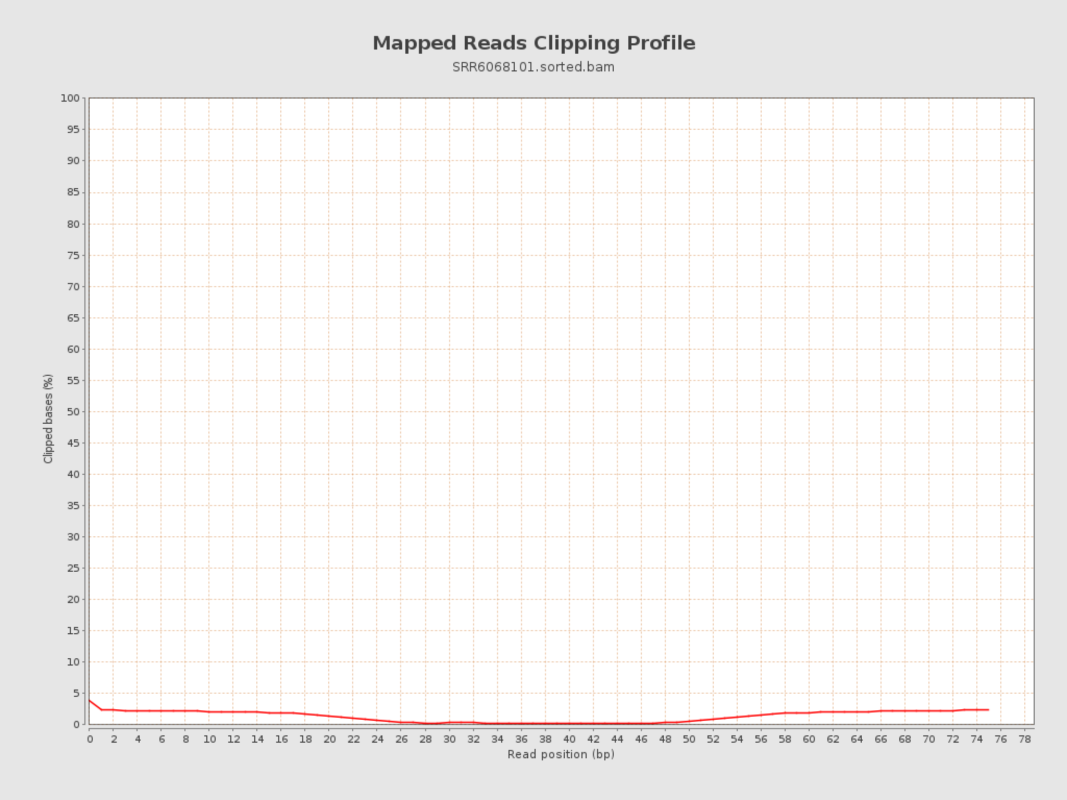
8. Results : Mapped Reads Nucleotide Content



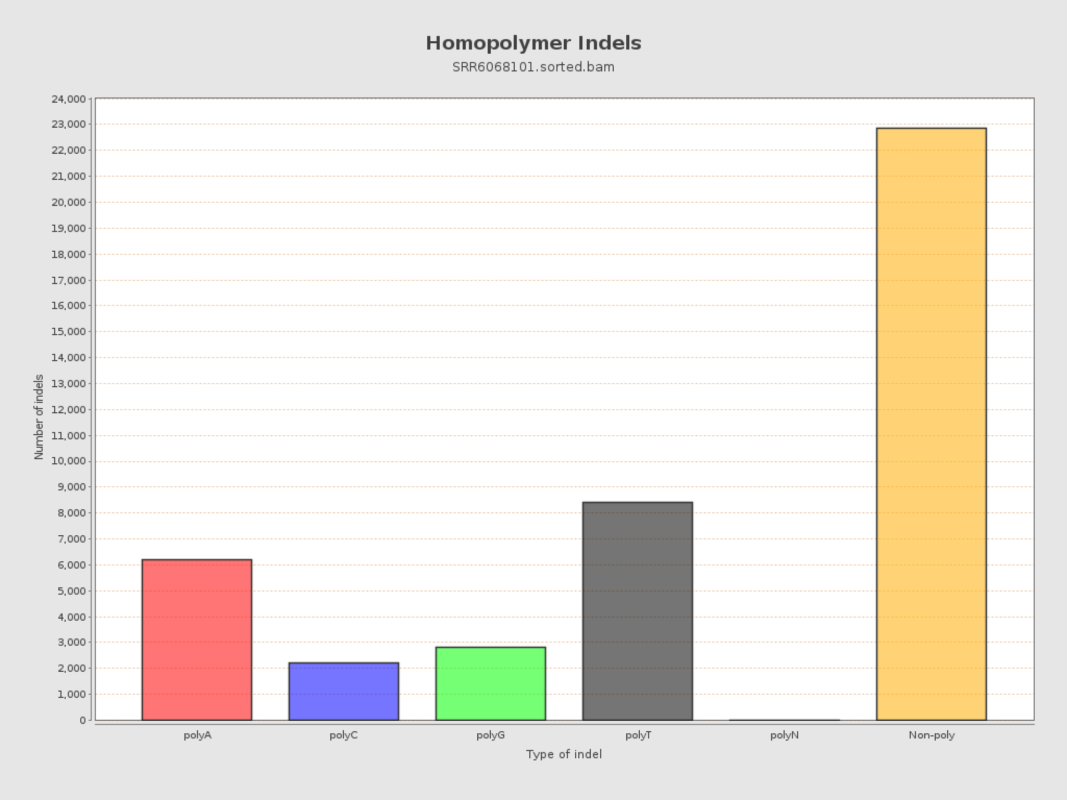
9. Results : Mapped Reads GC-content Distribution



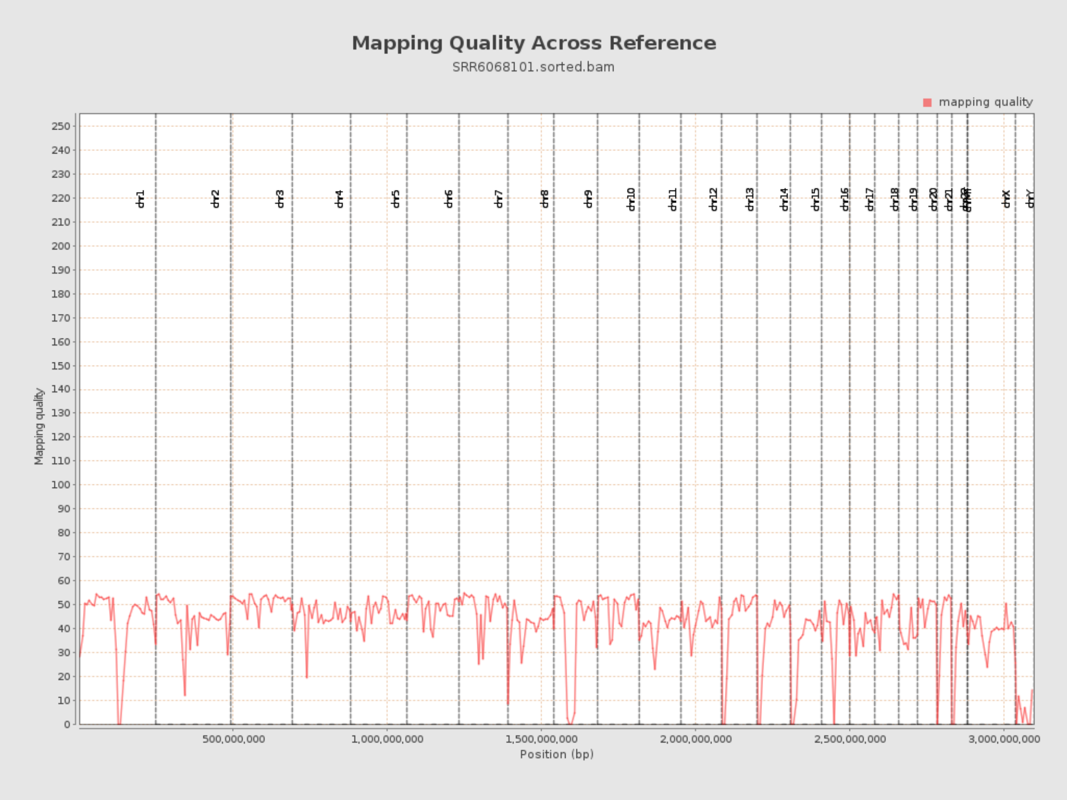
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram