Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 20:49:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236105.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_SRR6236105 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236105.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 20:49:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236105.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,449,790
Mapped reads	1,153,398 / 79.56%
Unmapped reads	296,392 / 20.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,855 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	30,230 / 2.09%
Duplication rate	1.71%
Clipped reads	597,938 / 41.24%

2.2. ACGT Content

Number/percentage of A's	20,990,038 / 28.24%
Number/percentage of C's	13,524,195 / 18.2%
Number/percentage of T's	22,875,783 / 30.78%
Number/percentage of G's	16,934,803 / 22.78%
Number/percentage of N's	650 / 0%
GC Percentage	40.98%

2.3. Coverage

Mean	0.024

Standard Deviation	0.2594

2.4. Mapping Quality

Mean Mapping Quality	43.2

2.5. Mismatches and indels

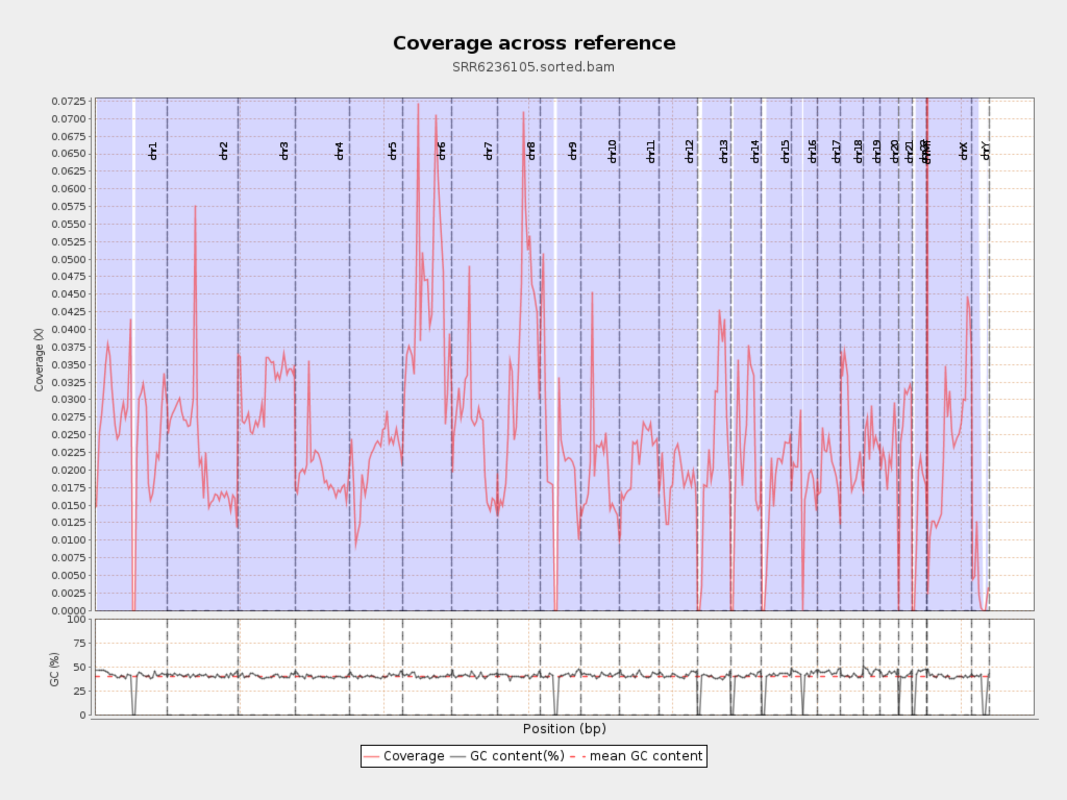
General error rate	0.88%
Mismatches	640,317
Insertions	6,353
Mapped reads with at least one insertion	0.55%
Deletions	21,840
Mapped reads with at least one deletion	1.87%
Homopolymer indels	45.84%

2.6. Chromosome stats

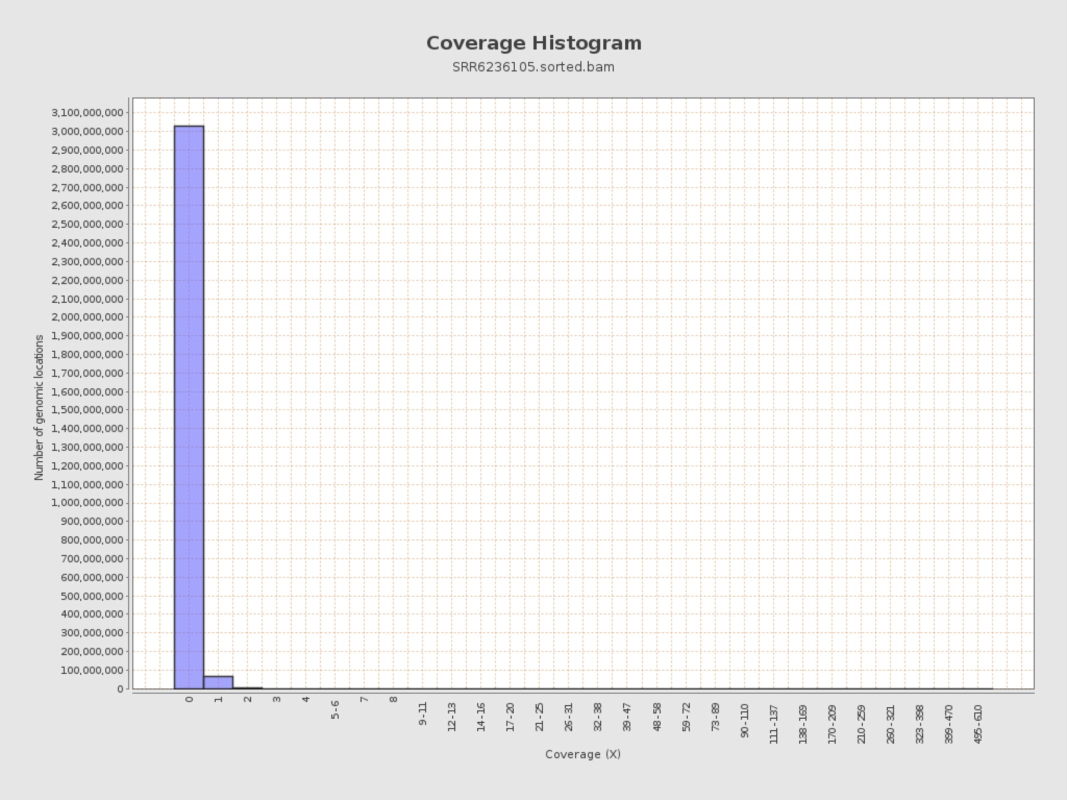
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6421990	0.0258	0.3894
chr2	243199373	5484077	0.0225	0.3023
chr3	198022430	6206878	0.0313	0.1863
chr4	191154276	3736278	0.0195	0.1632
chr5	180915260	3874138	0.0214	0.1542
chr6	171115067	7584961	0.0443	0.3181
chr7	159138663	4065839	0.0255	0.3439

chr8	146364022	5273344	0.036	0.4426
chr9	141213431	3063400	0.0217	0.2493
chr10	135534747	2689072	0.0198	0.2361
chr11	135006516	2956748	0.0219	0.2161
chr12	133851895	2476451	0.0185	0.1466
chr13	115169878	2622587	0.0228	0.1584
chr14	107349540	2290443	0.0213	0.17
chr15	102531392	1708539	0.0167	0.1403
chr16	90354753	1609527	0.0178	0.173
chr17	81195210	1649658	0.0203	0.1746
chr18	78077248	1939552	0.0248	0.4175
chr19	59128983	1453089	0.0246	0.2876
chr20	63025520	1360794	0.0216	0.1581
chr21	48129895	1274200	0.0265	0.1918
chr22	51304566	706735	0.0138	0.1222
chrMT	16571	29178	1.7608	1.7249
chrX	155270560	3680516	0.0237	0.1791
chrY	59373566	205600	0.0035	0.109

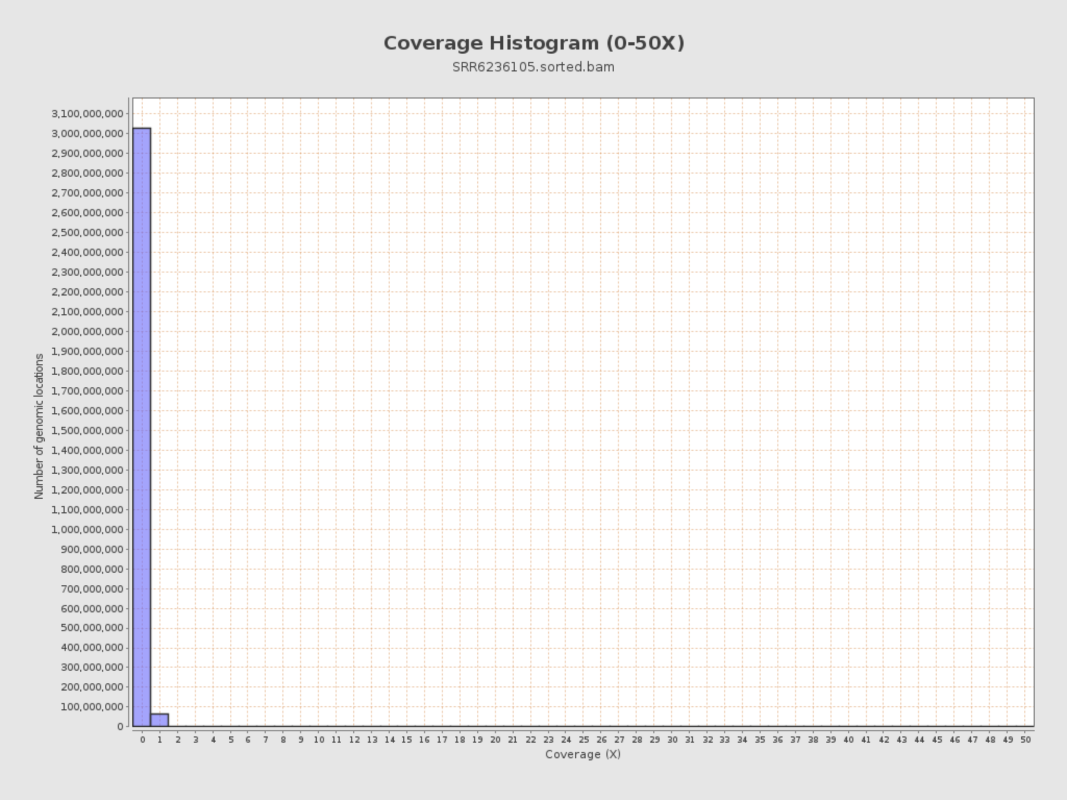
3. Results : Coverage across reference



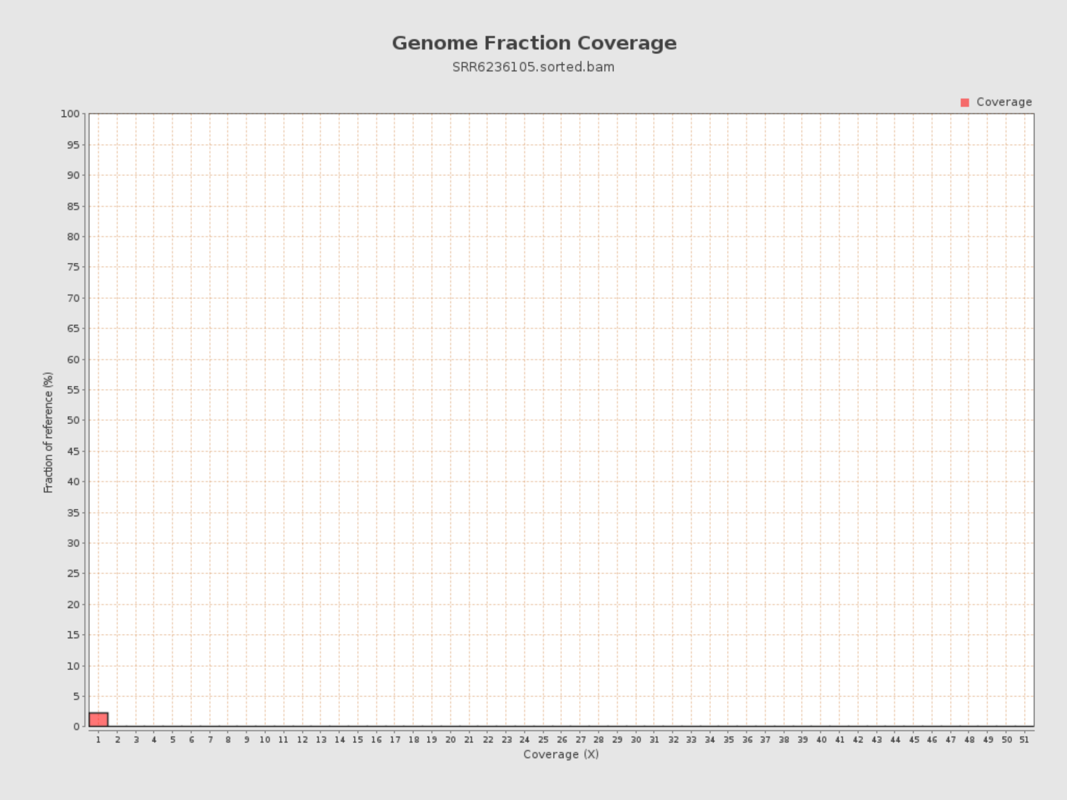
4. Results : Coverage Histogram



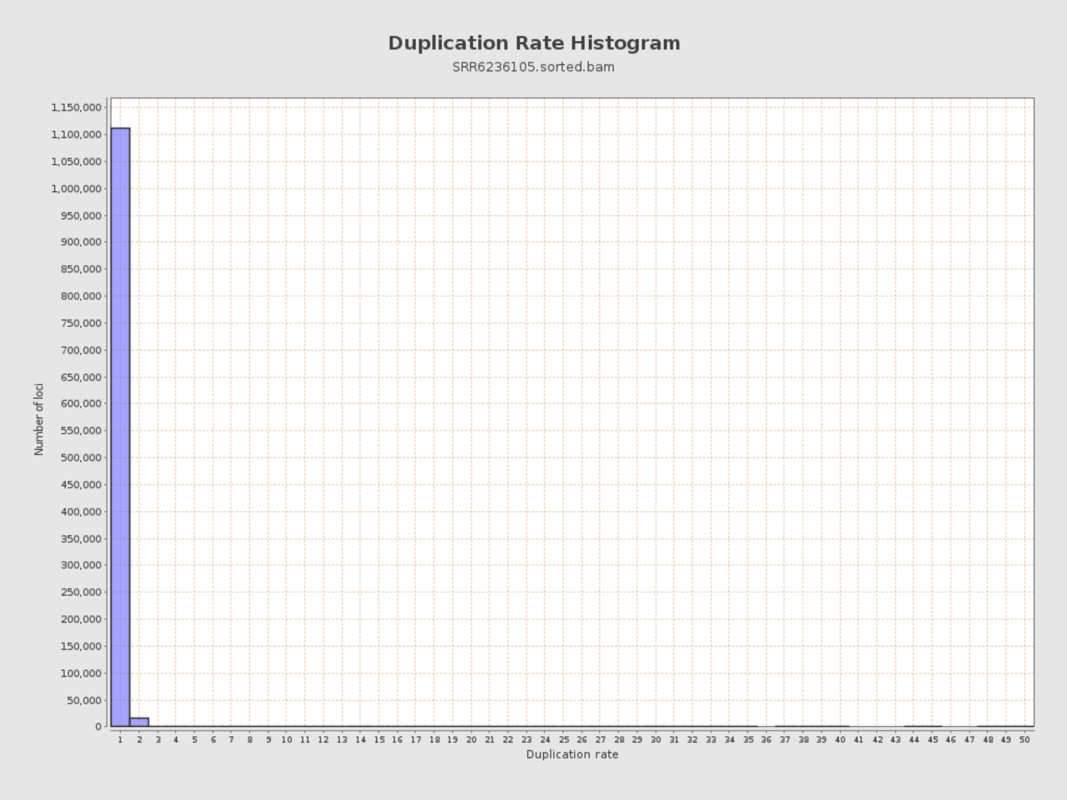
5. Results : Coverage Histogram (0-50X)



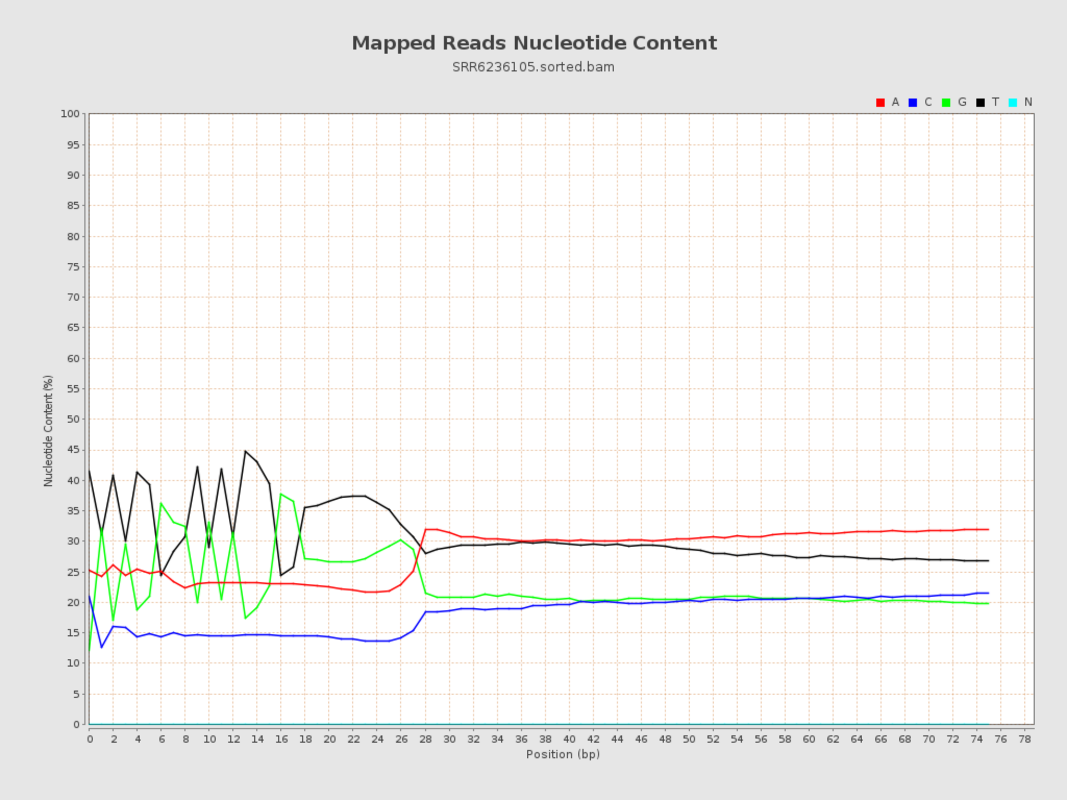
6. Results : Genome Fraction Coverage



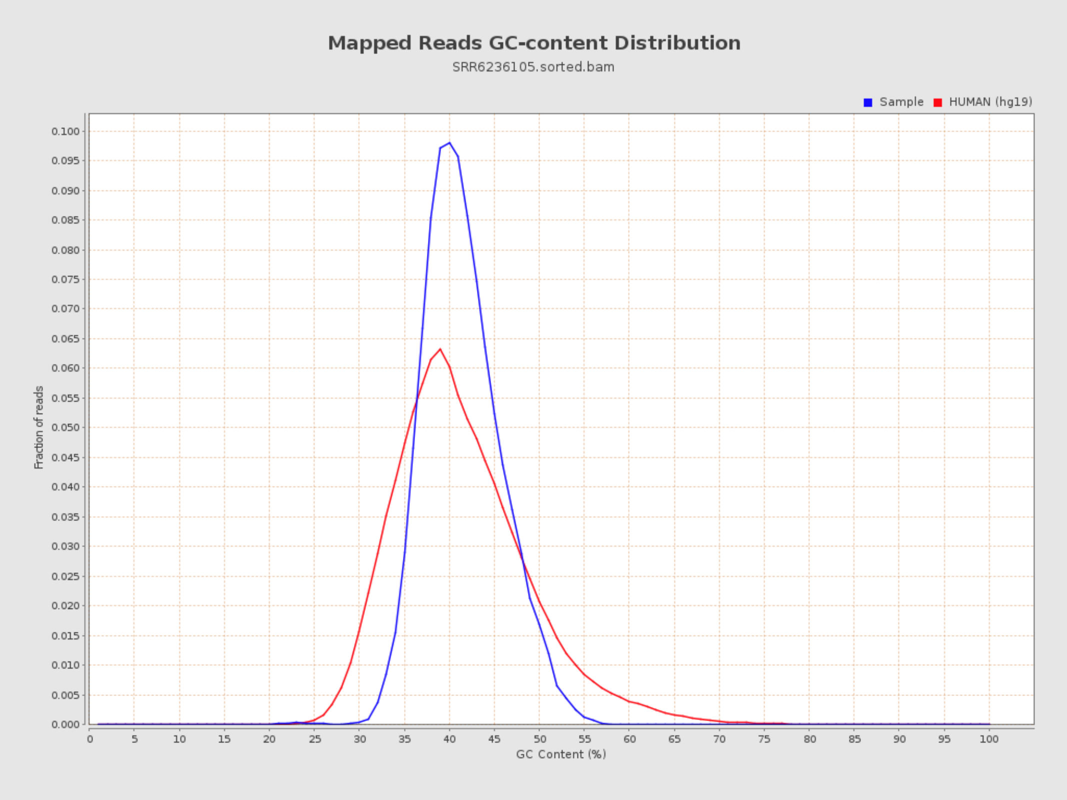
7. Results : Duplication Rate Histogram



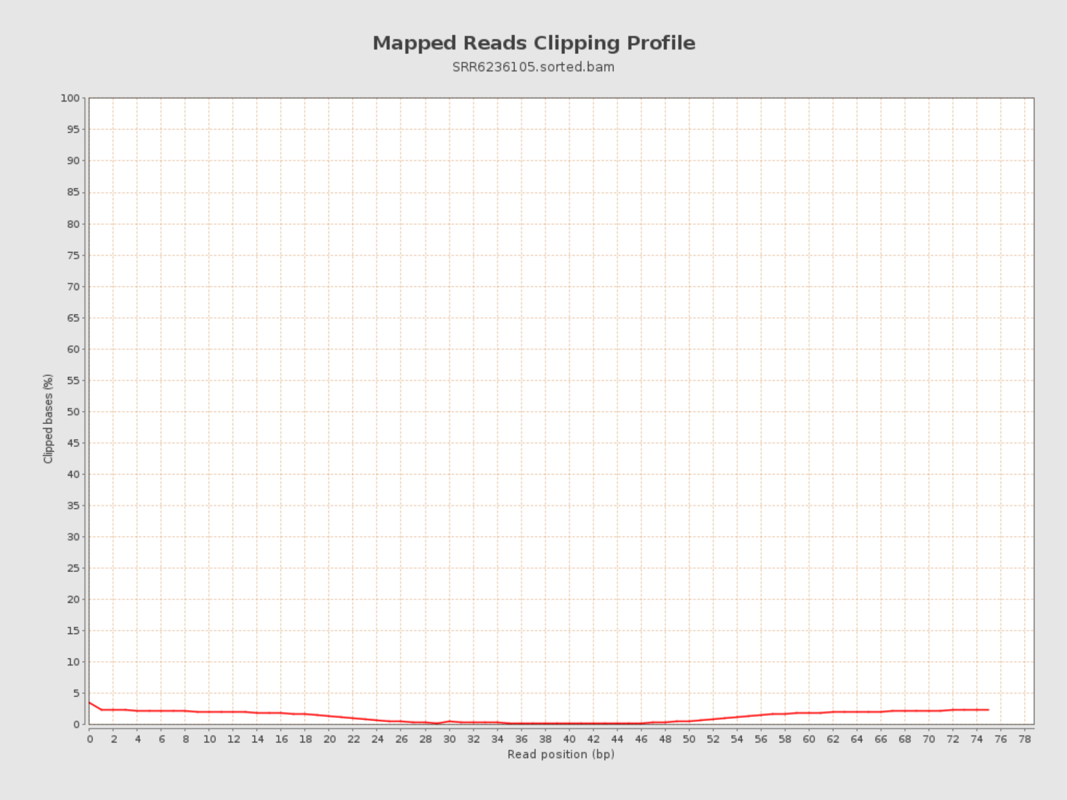
8. Results : Mapped Reads Nucleotide Content



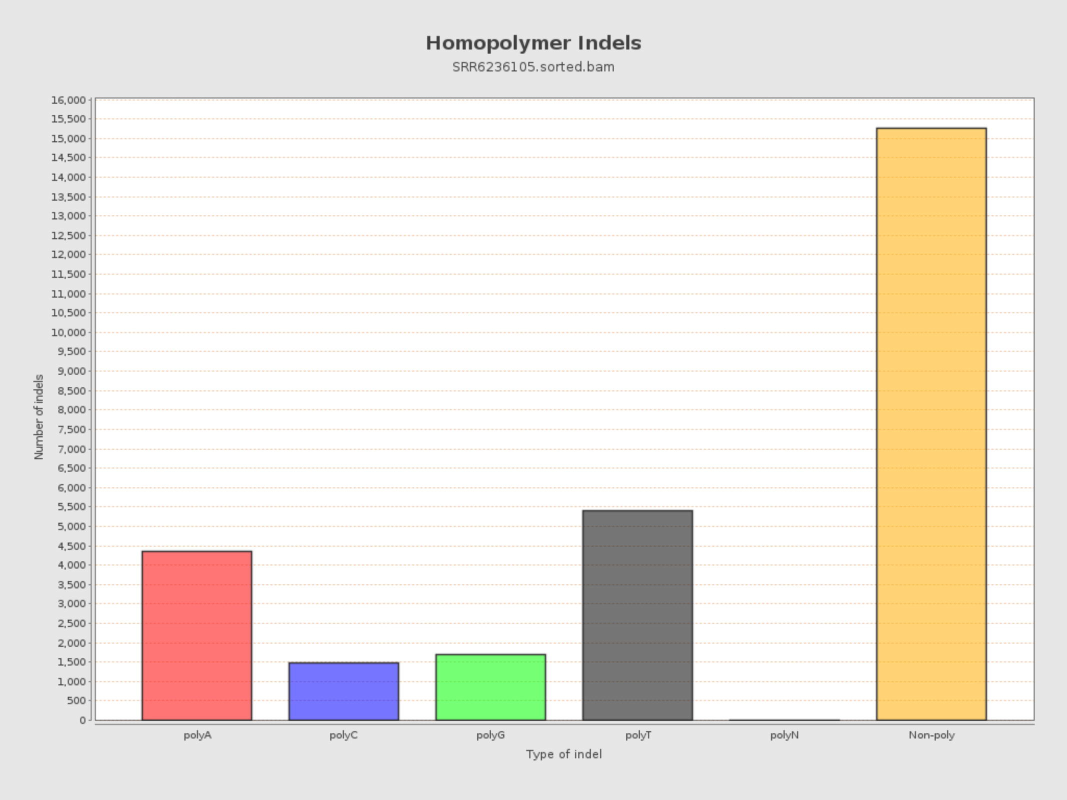
9. Results : Mapped Reads GC-content Distribution



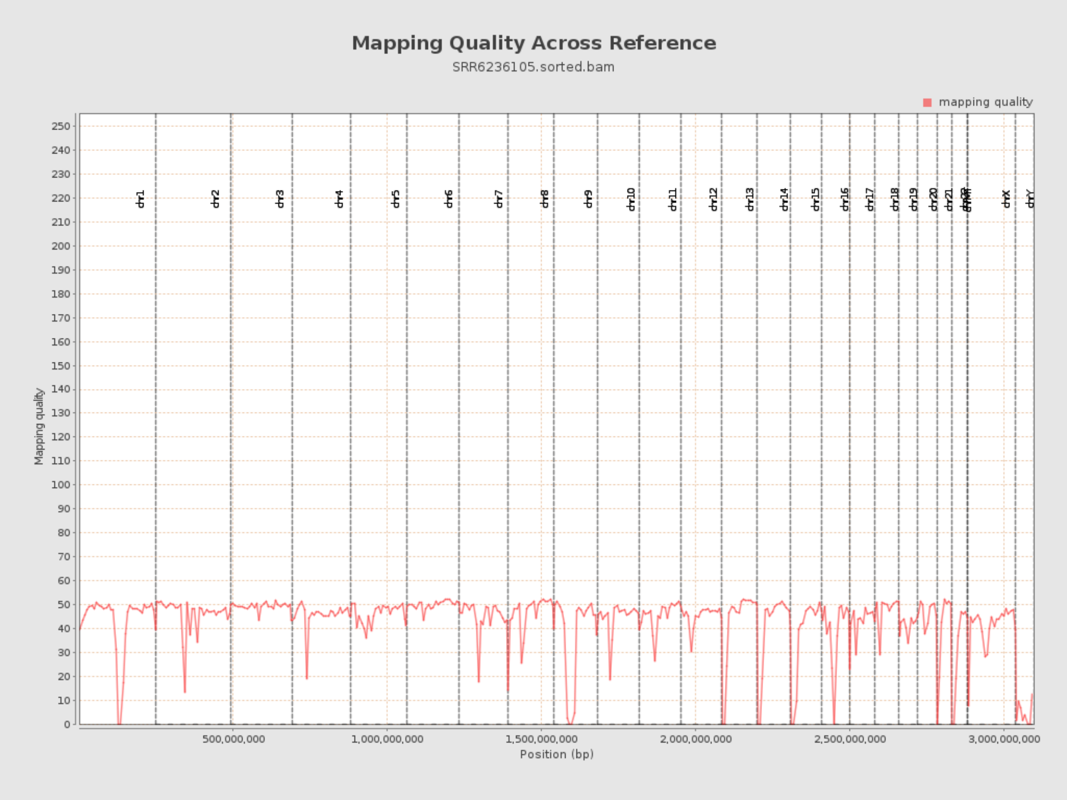
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram