Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 16:16:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068937.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_SRR6068937 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068937.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 16:16:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068937.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,285,766
Mapped reads	854,149 / 66.43%
Unmapped reads	431,617 / 33.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,083 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	59,043 / 4.59%
Duplication rate	5.93%
Clipped reads	445,394 / 34.64%

2.2. ACGT Content

Number/percentage of A's	14,940,879 / 27.08%
Number/percentage of C's	9,371,722 / 16.98%
Number/percentage of T's	18,485,093 / 33.5%
Number/percentage of G's	12,260,385 / 22.22%
Number/percentage of N's	125,136 / 0.23%
GC Percentage	39.2%

2.3. Coverage

Mean	0.0178

Standard Deviation	0.19

2.4. Mapping Quality

Mean Mapping Quality	45.37

2.5. Mismatches and indels

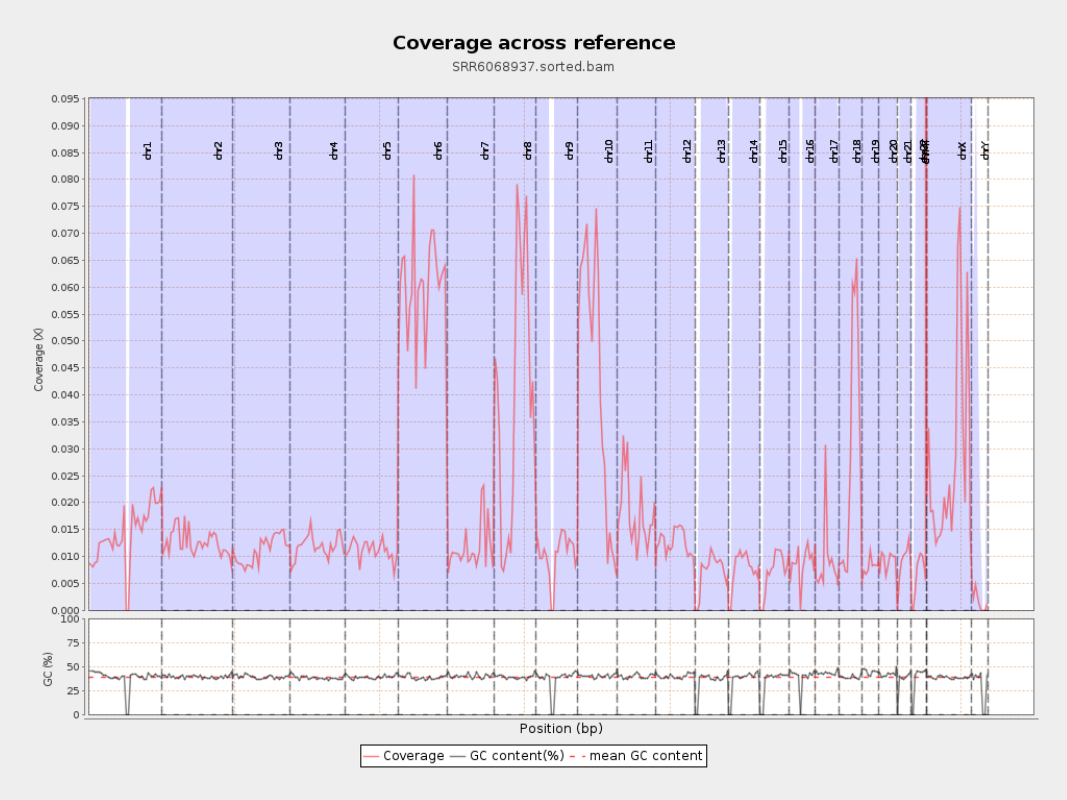
General error rate	1.04%
Mismatches	565,079
Insertions	4,719
Mapped reads with at least one insertion	0.55%
Deletions	17,287
Mapped reads with at least one deletion	2%
Homopolymer indels	48.82%

2.6. Chromosome stats

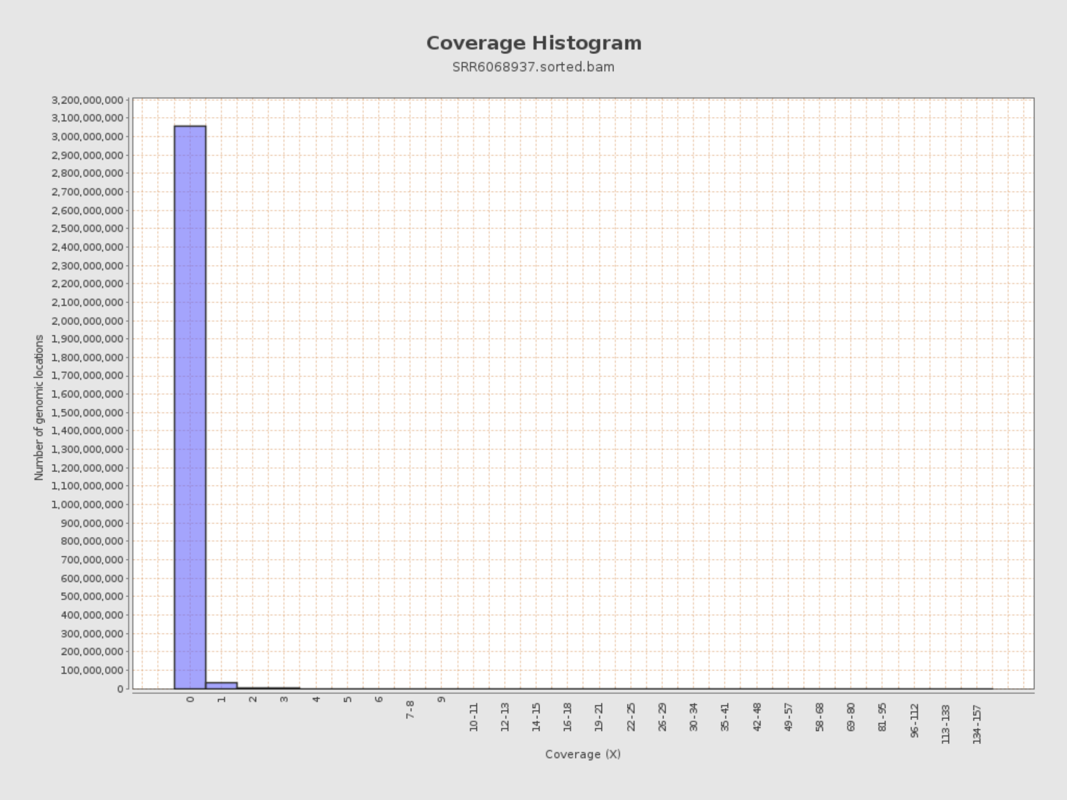
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3478000	0.014	0.1995
chr2	243199373	3062092	0.0126	0.1638
chr3	198022430	2218824	0.0112	0.1356
chr4	191154276	2264799	0.0118	0.1414
chr5	180915260	2023419	0.0112	0.1363
chr6	171115067	10226739	0.0598	0.3658
chr7	159138663	1882418	0.0118	0.1577

chr8	146364022	5885026	0.0402	0.2729
chr9	141213431	1431059	0.0101	0.1381
chr10	135534747	5945556	0.0439	0.2995
chr11	135006516	2428476	0.018	0.1922
chr12	133851895	1685366	0.0126	0.1448
chr13	115169878	818703	0.0071	0.1072
chr14	107349540	812775	0.0076	0.1133
chr15	102531392	729376	0.0071	0.107
chr16	90354753	774257	0.0086	0.1192
chr17	81195210	754668	0.0093	0.1259
chr18	78077248	2381335	0.0305	0.2538
chr19	59128983	483987	0.0082	0.1477
chr20	63025520	570873	0.0091	0.1223
chr21	48129895	426859	0.0089	0.1199
chr22	51304566	325615	0.0063	0.0991
chrMT	16571	91872	5.5441	3.8434
chrX	155270560	4411977	0.0284	0.2222
chrY	59373566	96934	0.0016	0.05

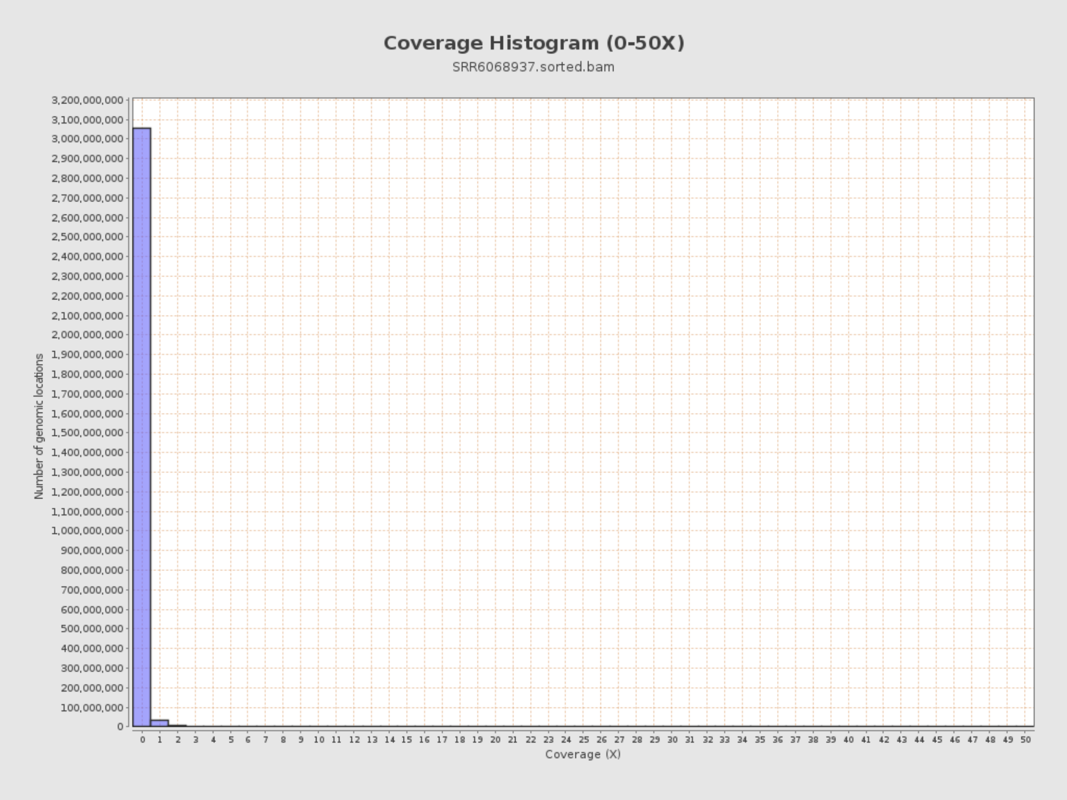
3. Results : Coverage across reference



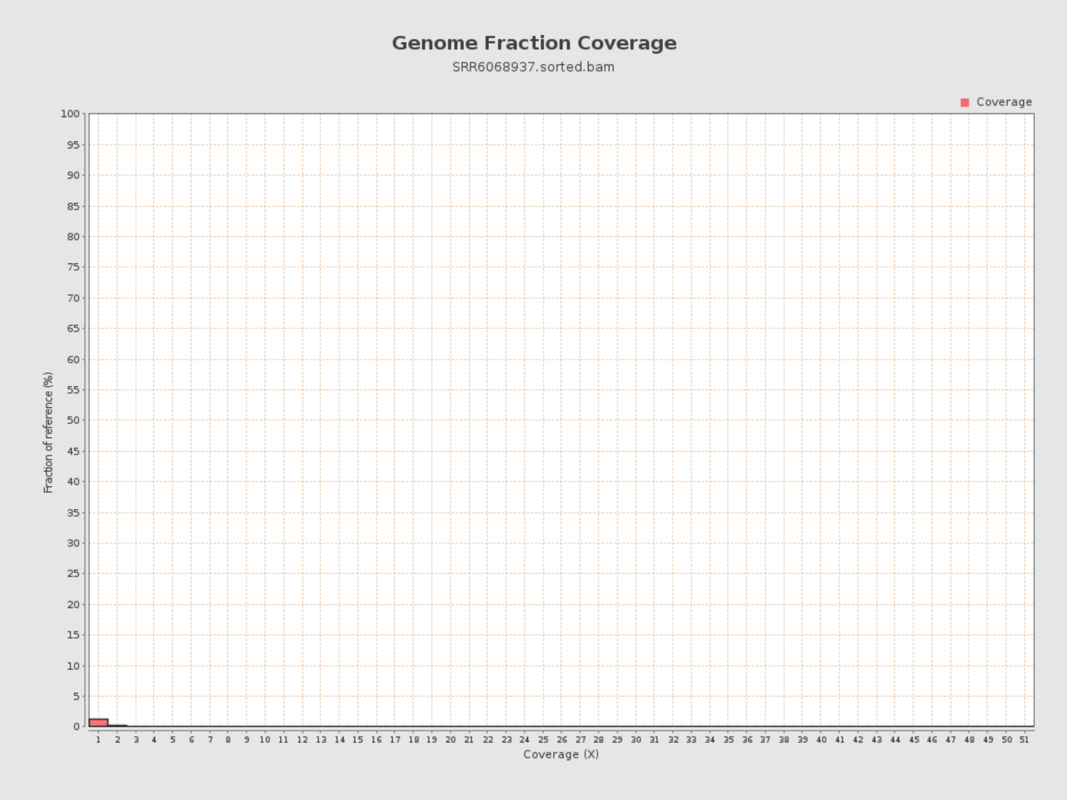
4. Results : Coverage Histogram



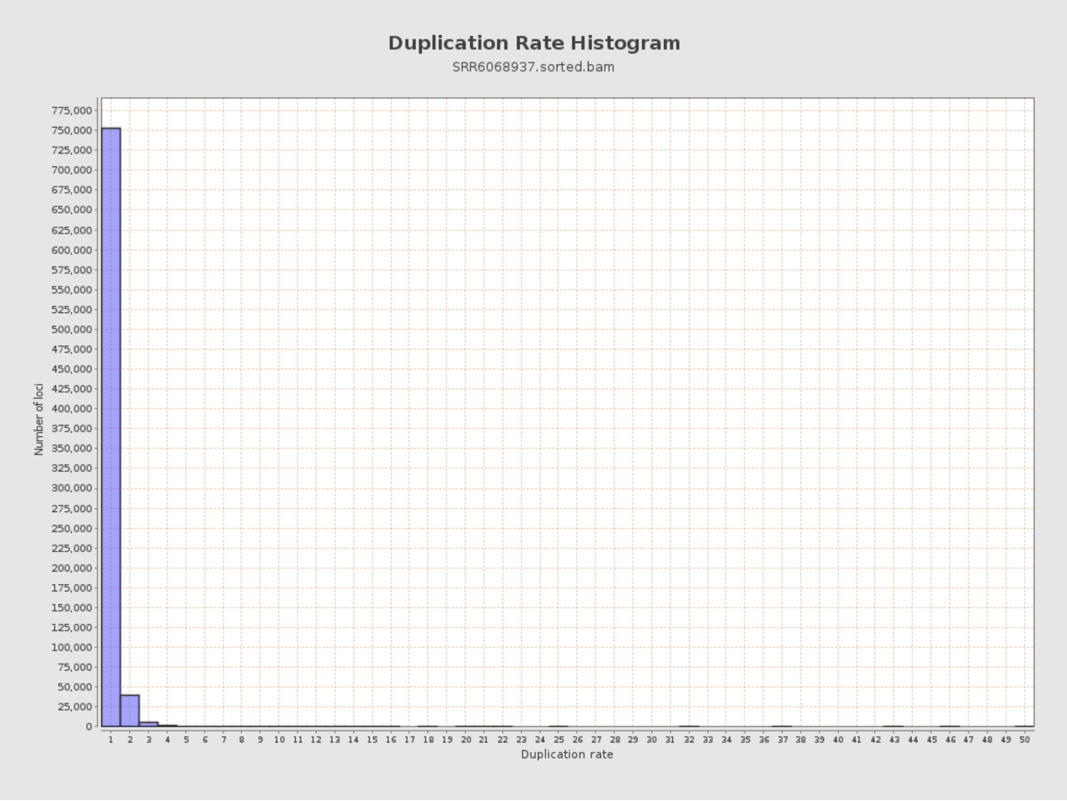
5. Results : Coverage Histogram (0-50X)



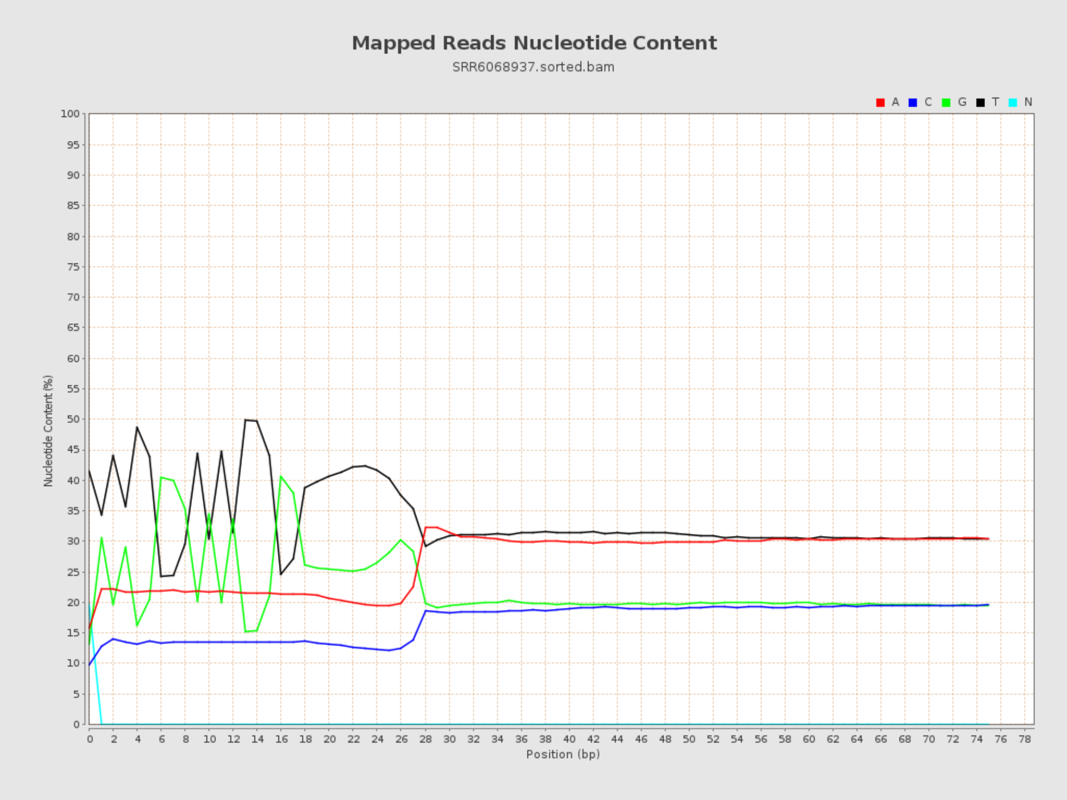
6. Results : Genome Fraction Coverage



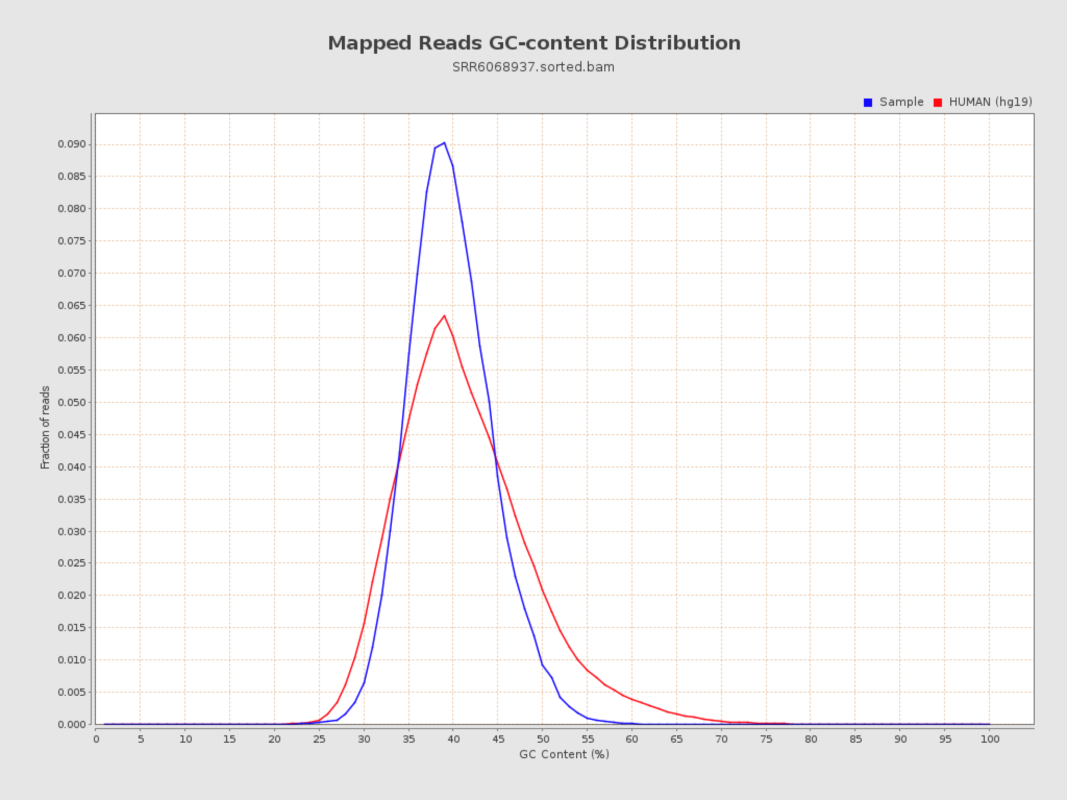
7. Results : Duplication Rate Histogram



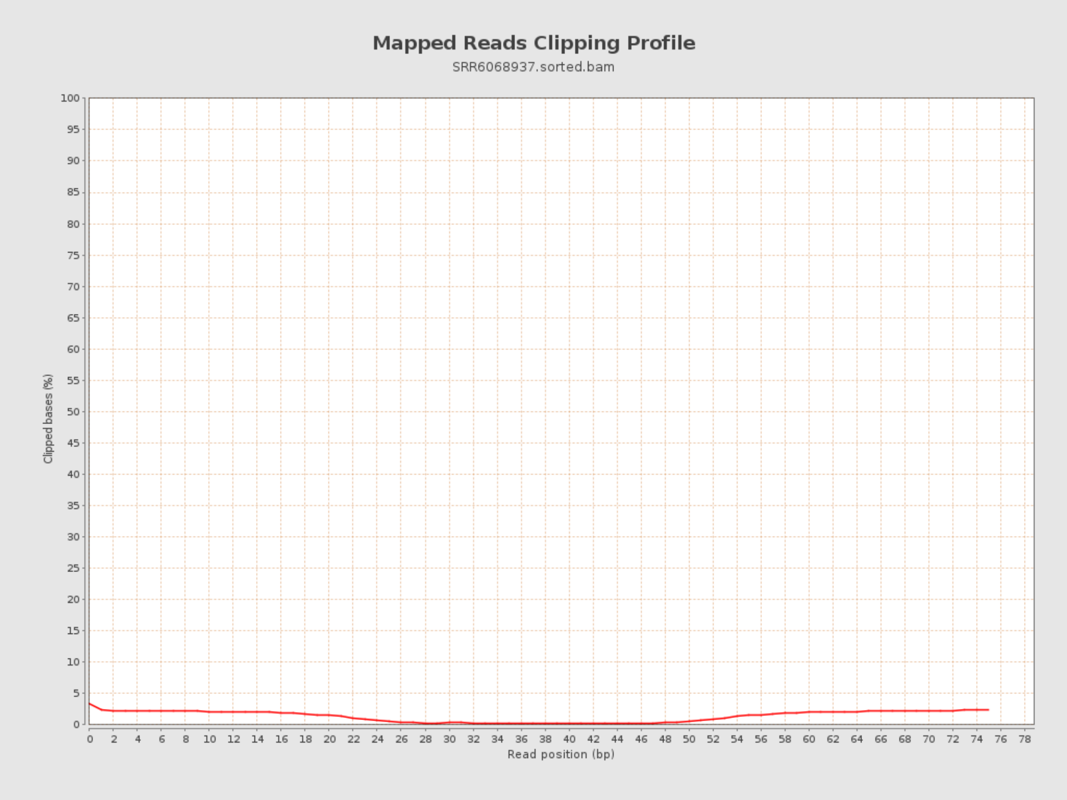
8. Results : Mapped Reads Nucleotide Content



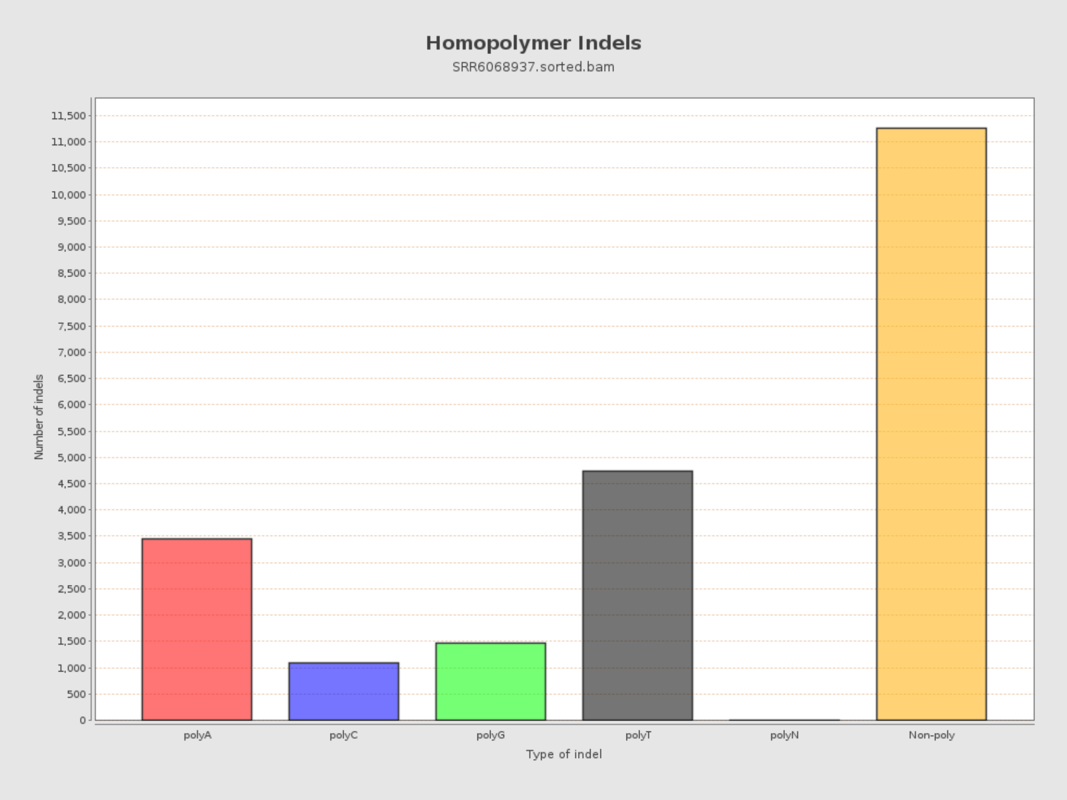
9. Results : Mapped Reads GC-content Distribution



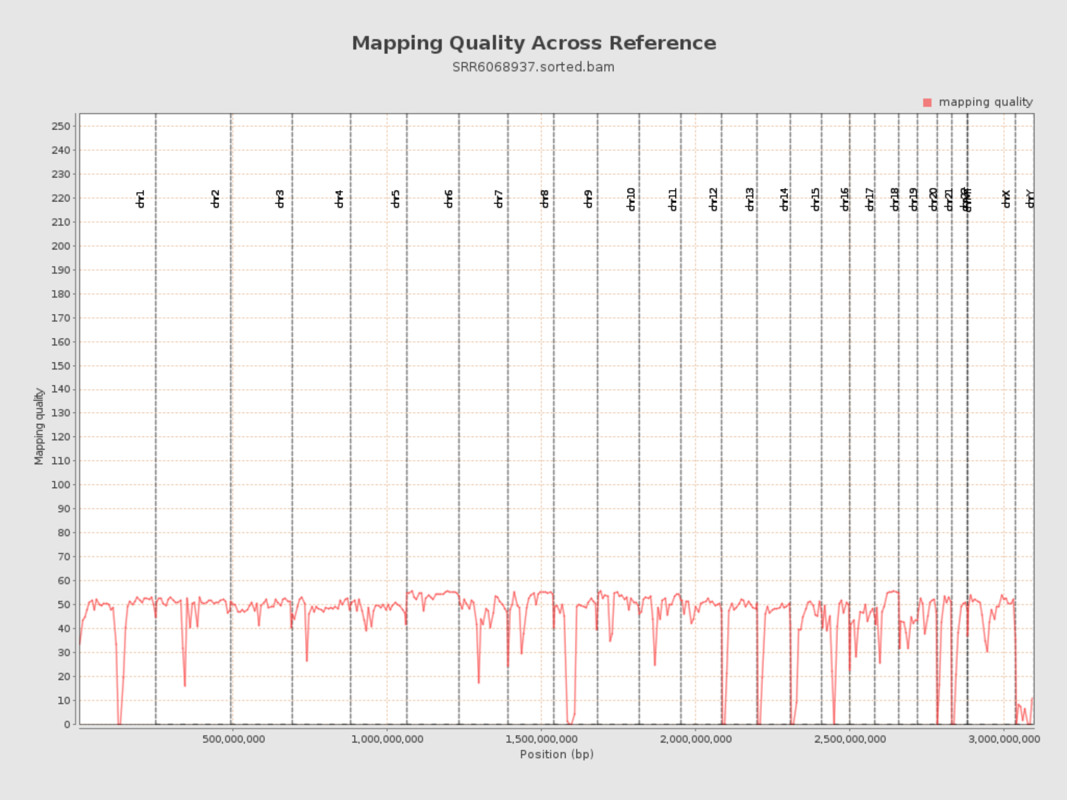
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram