Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 17:04:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068952.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_SRR6068952 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068952.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 17:04:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068952.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,681,143
Mapped reads	1,107,702 / 65.89%
Unmapped reads	573,441 / 34.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,150 / 0.25%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	75,155 / 4.47%
Duplication rate	5.84%
Clipped reads	659,639 / 39.24%

2.2. ACGT Content

Number/percentage of A's	18,237,591 / 26.19%
Number/percentage of C's	11,610,804 / 16.67%
Number/percentage of T's	23,684,569 / 34.01%
Number/percentage of G's	15,951,146 / 22.9%
Number/percentage of N's	156,493 / 0.22%
GC Percentage	39.58%

2.3. Coverage

Mean	0.0225

Standard Deviation	0.2283

2.4. Mapping Quality

Mean Mapping Quality	46.52

2.5. Mismatches and indels

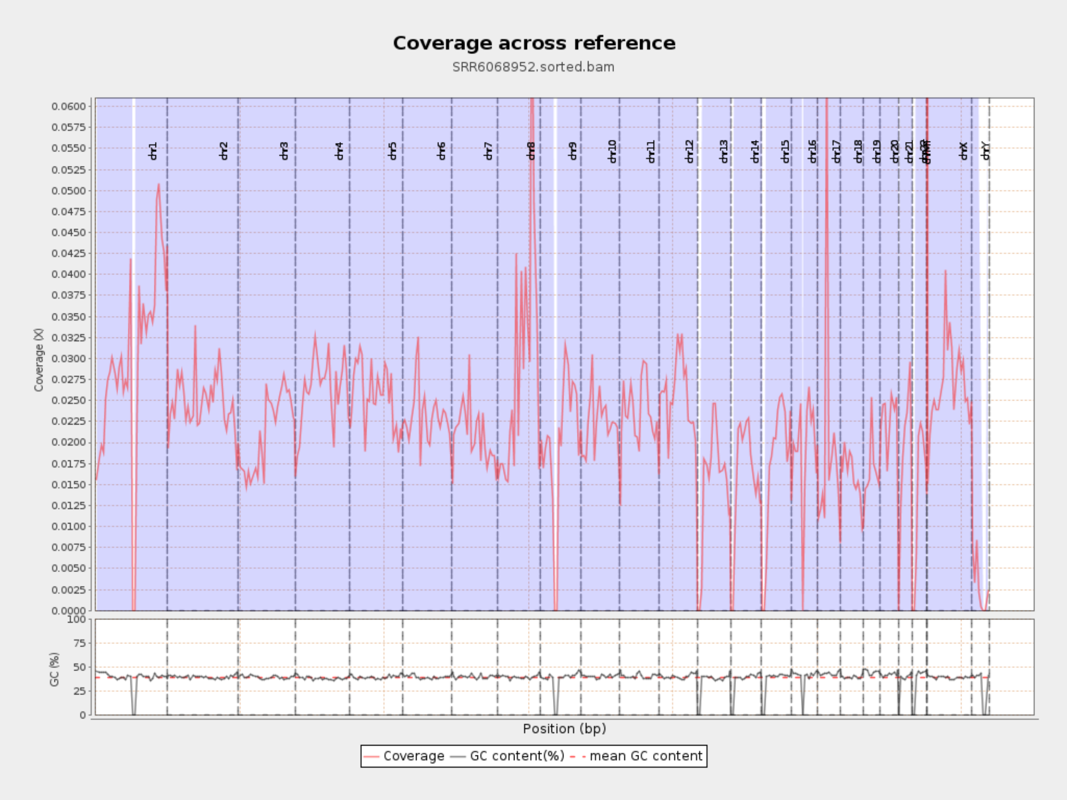
General error rate	1.12%
Mismatches	773,172
Insertions	5,967
Mapped reads with at least one insertion	0.53%
Deletions	25,439
Mapped reads with at least one deletion	2.27%
Homopolymer indels	49.81%

2.6. Chromosome stats

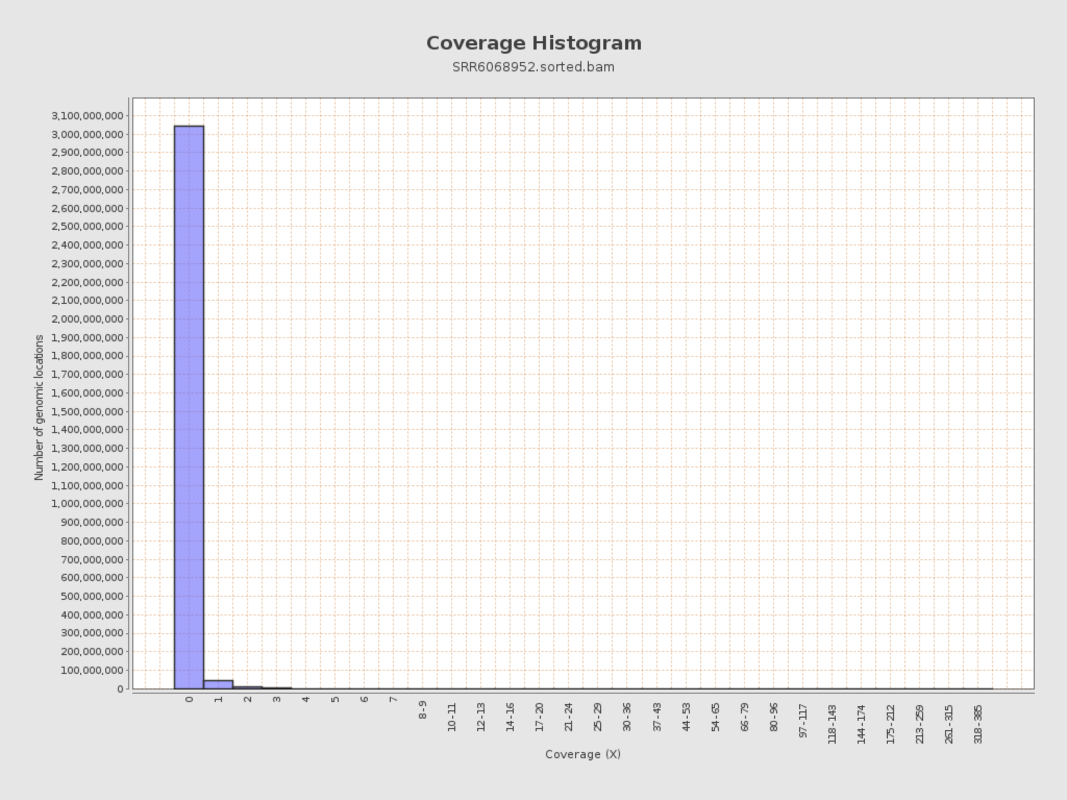
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7408654	0.0297	0.3692
chr2	243199373	6063774	0.0249	0.2355
chr3	198022430	4184950	0.0211	0.1802
chr4	191154276	5037070	0.0264	0.2061
chr5	180915260	4661605	0.0258	0.2006
chr6	171115067	3965951	0.0232	0.2139
chr7	159138663	3342812	0.021	0.2575

chr8	146364022	4304036	0.0294	0.2927
chr9	141213431	2836612	0.0201	0.214
chr10	135534747	3006251	0.0222	0.2144
chr11	135006516	3180410	0.0236	0.217
chr12	133851895	3439085	0.0257	0.2017
chr13	115169878	1722079	0.015	0.1521
chr14	107349540	1697538	0.0158	0.1622
chr15	102531392	1756120	0.0171	0.1649
chr16	90354753	1706172	0.0189	0.1741
chr17	81195210	1605846	0.0198	0.1851
chr18	78077248	1267008	0.0162	0.2733
chr19	59128983	990385	0.0167	0.254
chr20	63025520	1425697	0.0226	0.1885
chr21	48129895	916043	0.019	0.1752
chr22	51304566	710345	0.0138	0.1433
chrMT	16571	85597	5.1655	4.1782
chrX	155270560	4196828	0.027	0.2165
chrY	59373566	169314	0.0029	0.078

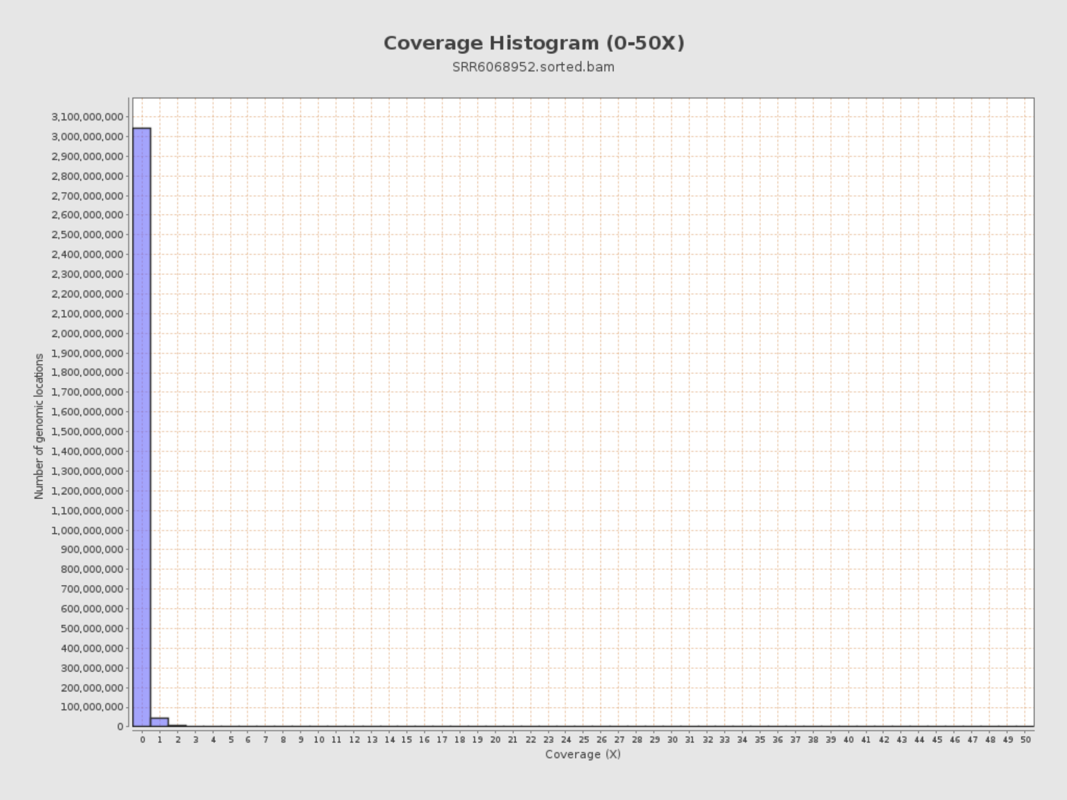
3. Results : Coverage across reference



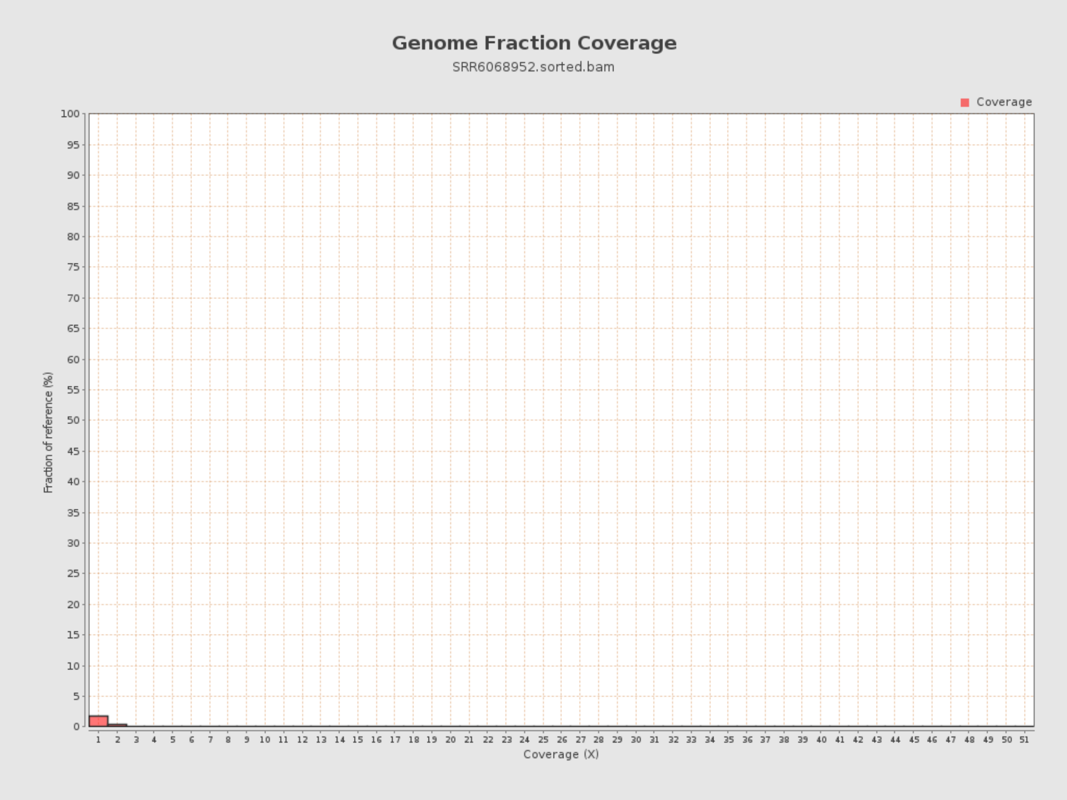
4. Results : Coverage Histogram



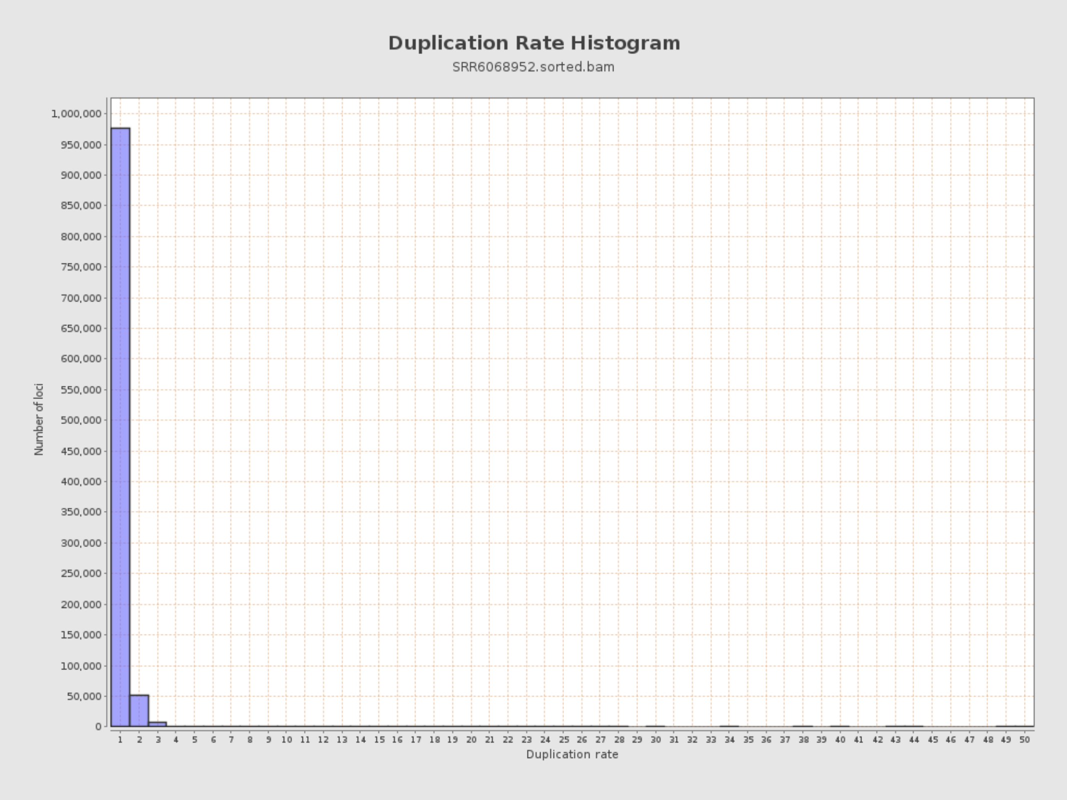
5. Results : Coverage Histogram (0-50X)



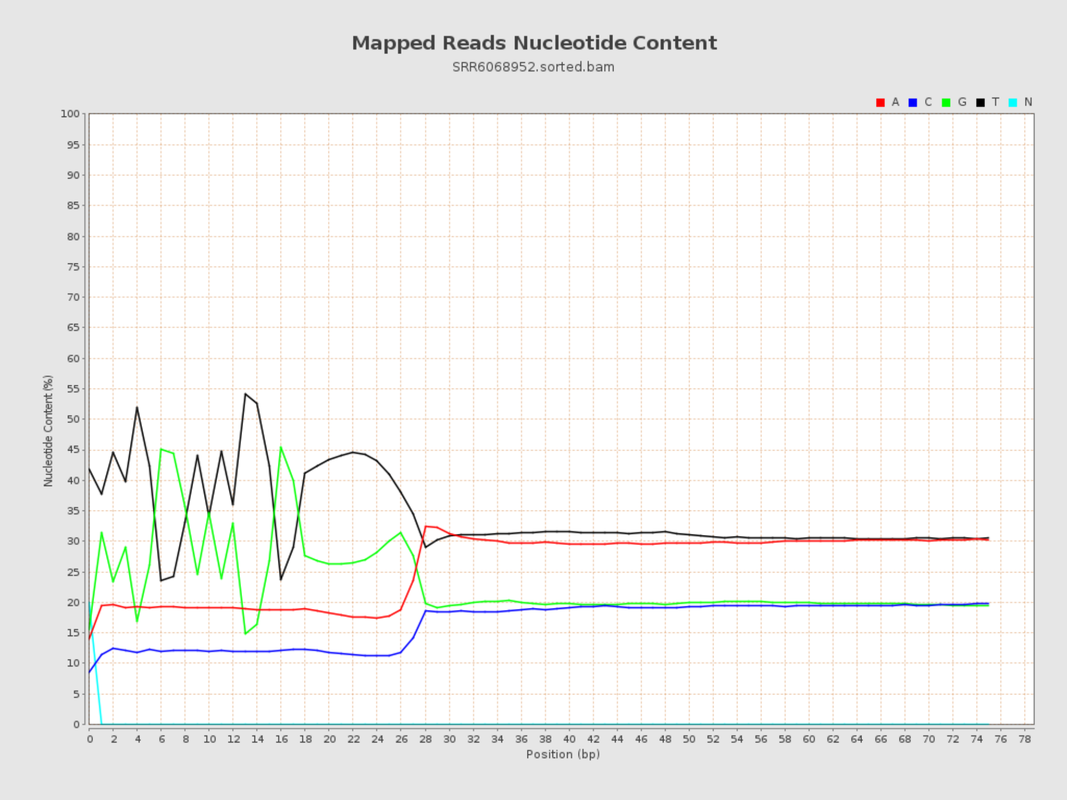
6. Results : Genome Fraction Coverage



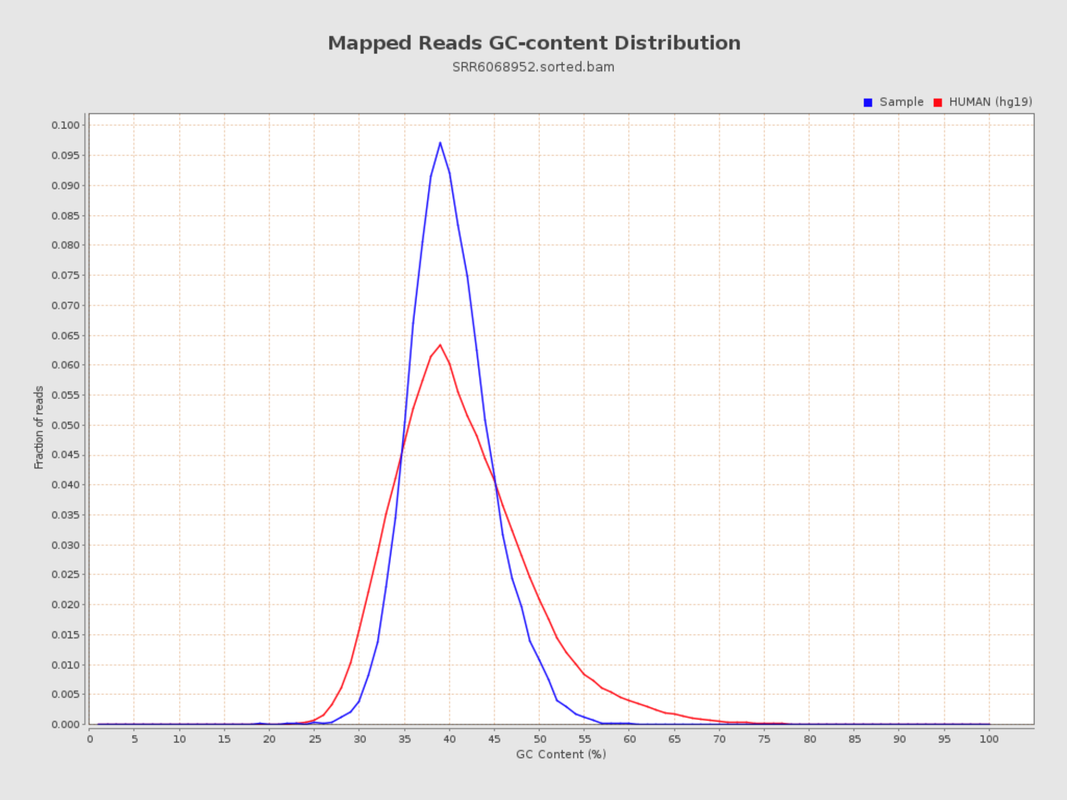
7. Results : Duplication Rate Histogram



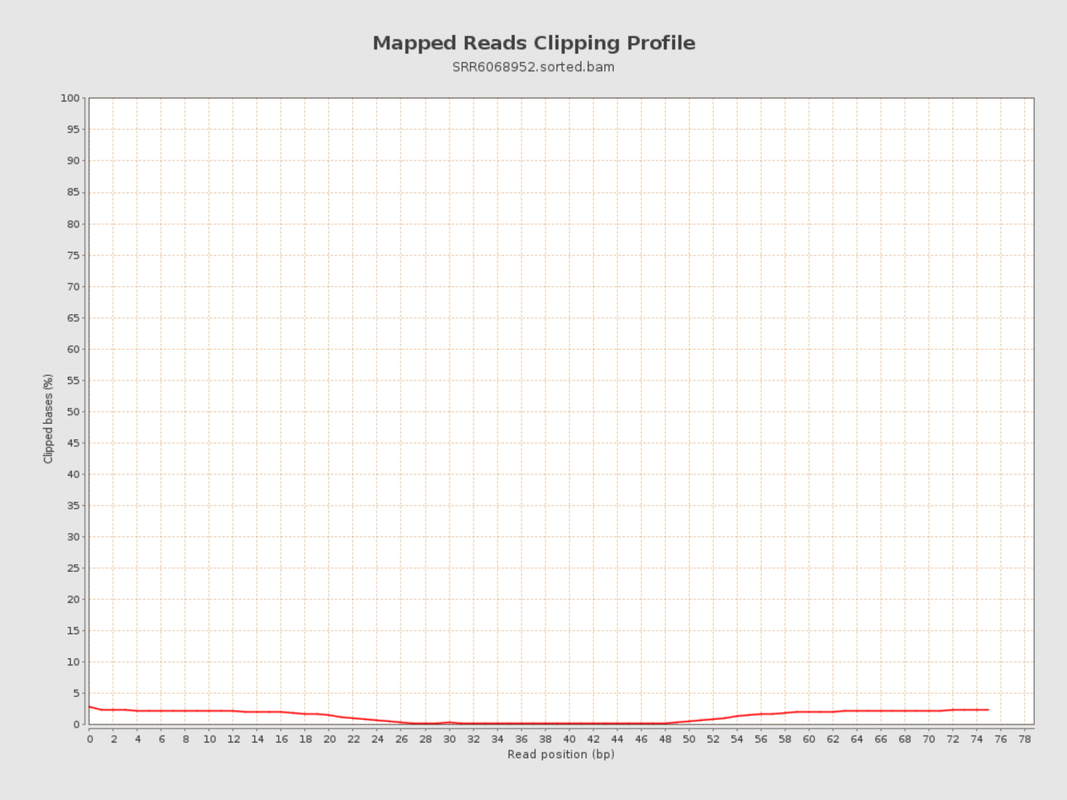
8. Results : Mapped Reads Nucleotide Content



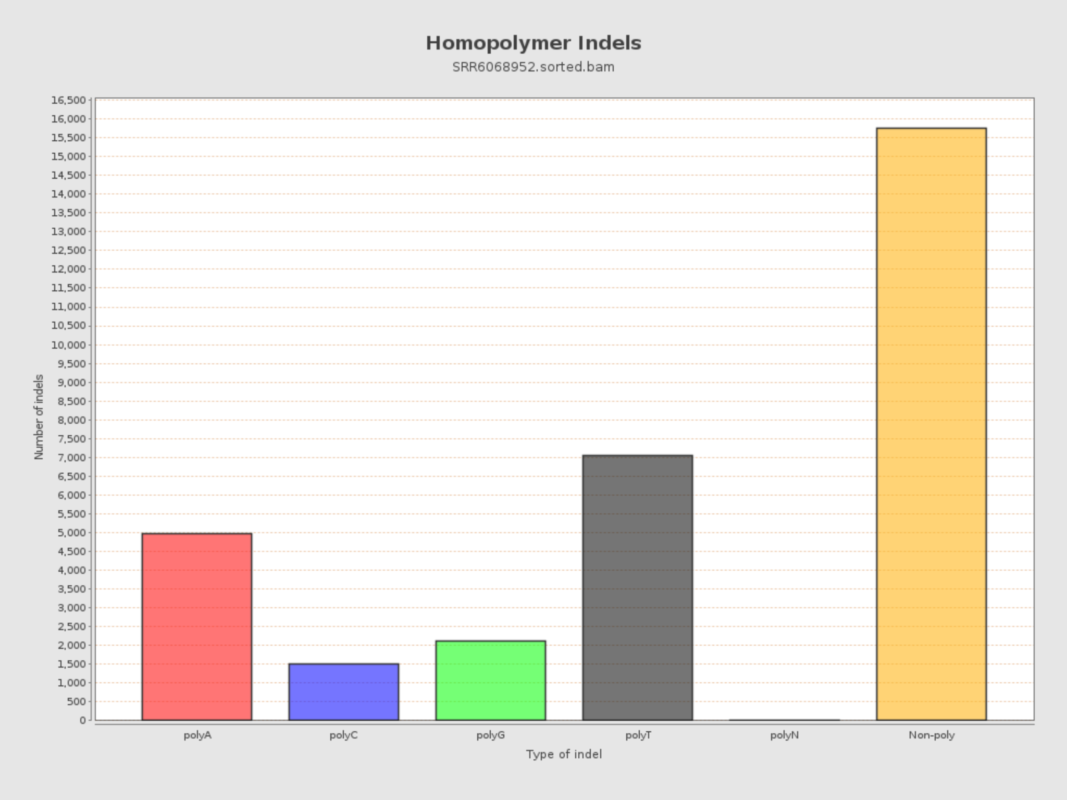
9. Results : Mapped Reads GC-content Distribution



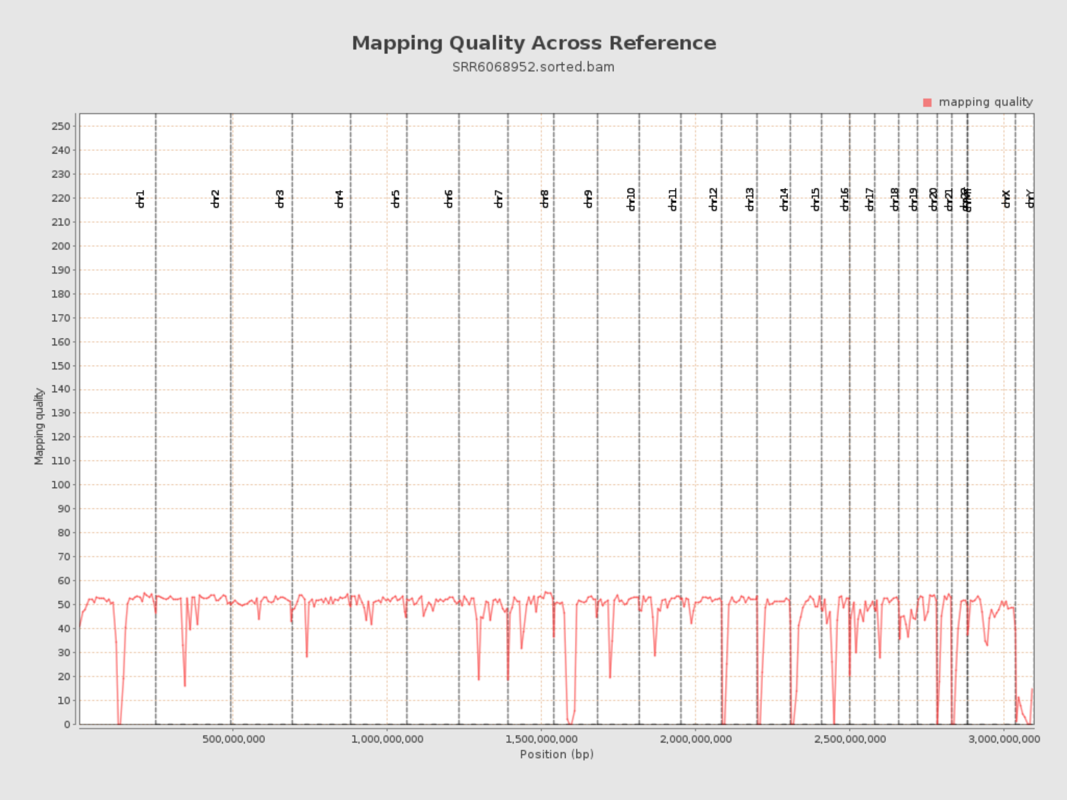
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram