Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 09:11:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008736.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_SRR6008736 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008736.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 09:10:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008736.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,415,379
Mapped reads	1,035,254 / 73.14%
Unmapped reads	380,125 / 26.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,014 / 0.28%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	55,249 / 3.9%
Duplication rate	3.76%
Clipped reads	673,252 / 47.57%

2.2. ACGT Content

Number/percentage of A's	17,040,692 / 26.62%
Number/percentage of C's	10,962,015 / 17.13%
Number/percentage of T's	19,951,259 / 31.17%
Number/percentage of G's	16,050,223 / 25.08%
Number/percentage of N's	3,002 / 0%
GC Percentage	42.2%

2.3. Coverage

Mean	0.0207

Standard Deviation	0.2266

2.4. Mapping Quality

Mean Mapping Quality	43.16

2.5. Mismatches and indels

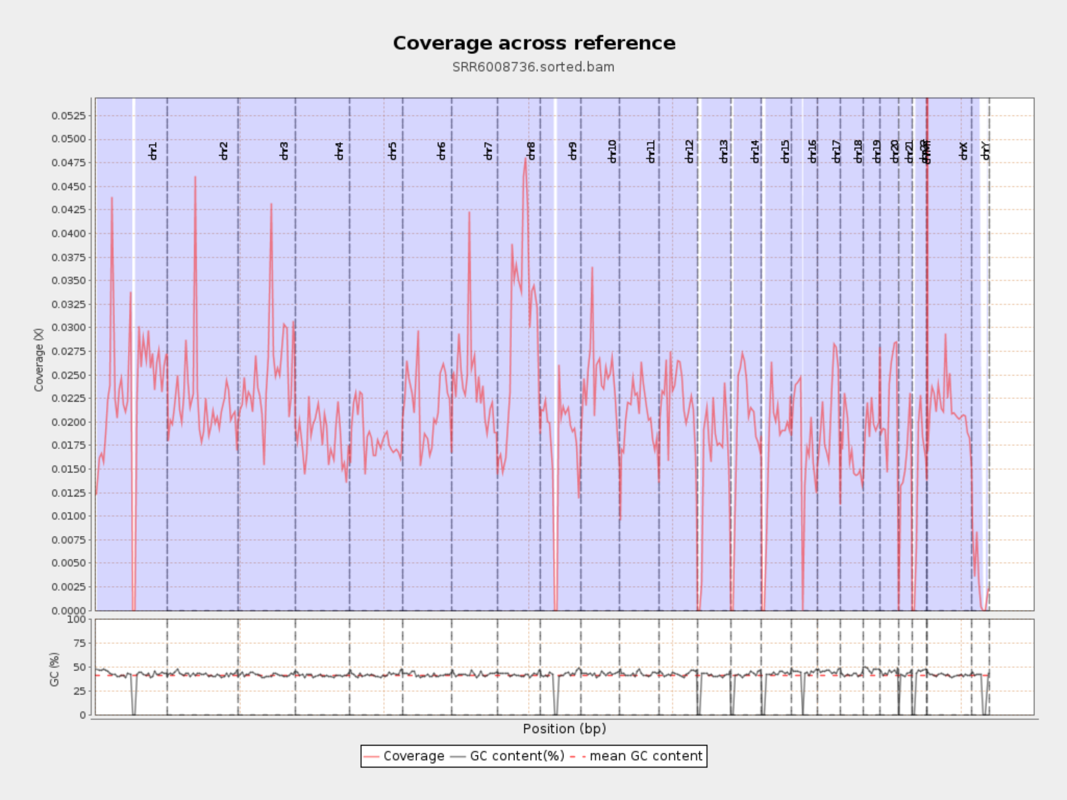
General error rate	0.99%
Mismatches	621,561
Insertions	5,464
Mapped reads with at least one insertion	0.52%
Deletions	25,890
Mapped reads with at least one deletion	2.47%
Homopolymer indels	48.45%

2.6. Chromosome stats

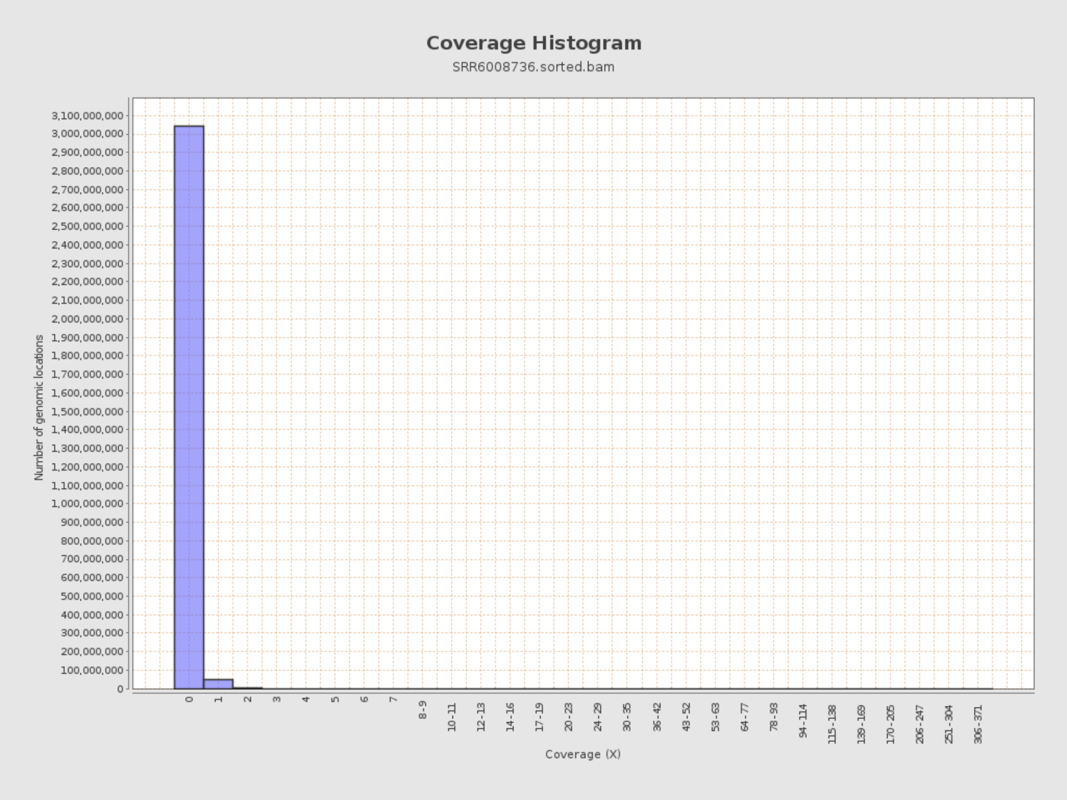
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5691034	0.0228	0.3011
chr2	243199373	5365911	0.0221	0.3044
chr3	198022430	4937766	0.0249	0.1888
chr4	191154276	3504793	0.0183	0.1643
chr5	180915260	3354089	0.0185	0.1603
chr6	171115067	3715967	0.0217	0.197
chr7	159138663	3841668	0.0241	0.372

chr8	146364022	4434910	0.0303	0.2536
chr9	141213431	2492991	0.0177	0.2216
chr10	135534747	3317397	0.0245	0.2156
chr11	135006516	2787015	0.0206	0.2352
chr12	133851895	2993611	0.0224	0.1835
chr13	115169878	1806136	0.0157	0.1535
chr14	107349540	1997822	0.0186	0.165
chr15	102531392	1709162	0.0167	0.158
chr16	90354753	1573690	0.0174	0.1644
chr17	81195210	1690842	0.0208	0.1874
chr18	78077248	1304557	0.0167	0.3088
chr19	59128983	1191245	0.0201	0.2137
chr20	63025520	1395965	0.0221	0.1781
chr21	48129895	713113	0.0148	0.1495
chr22	51304566	676083	0.0132	0.1341
chrMT	16571	27677	1.6702	1.8009
chrX	155270560	3343082	0.0215	0.1884
chrY	59373566	181769	0.0031	0.0755

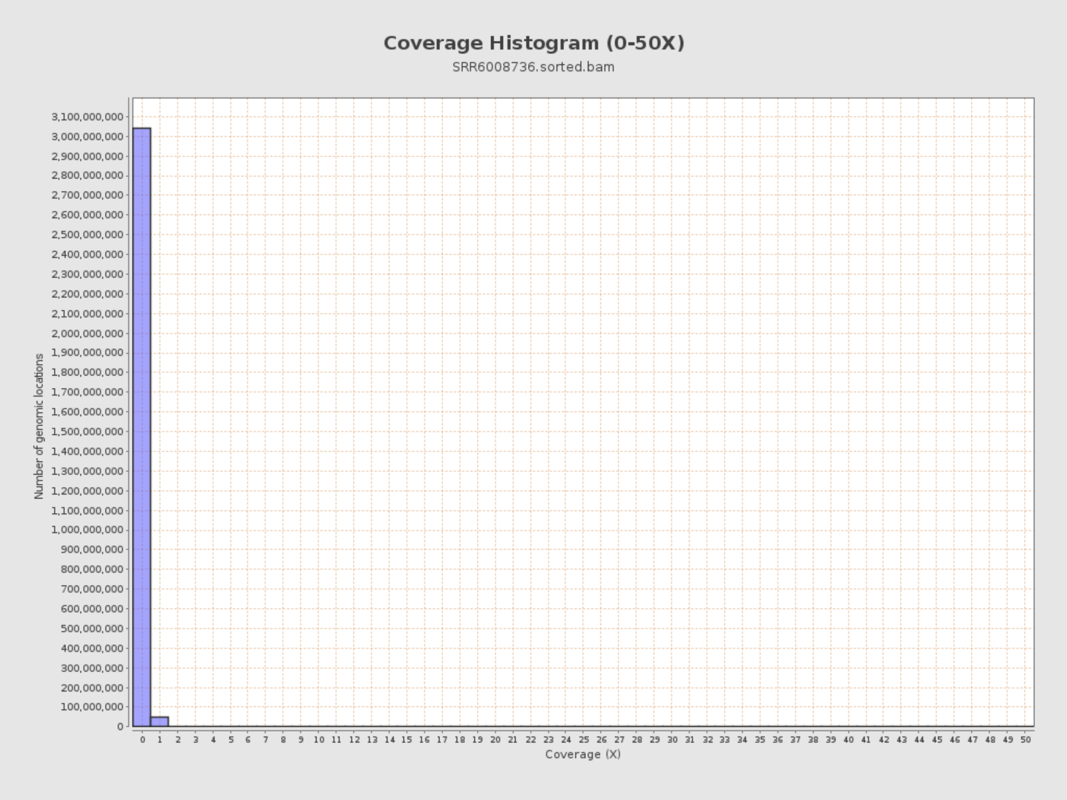
3. Results : Coverage across reference



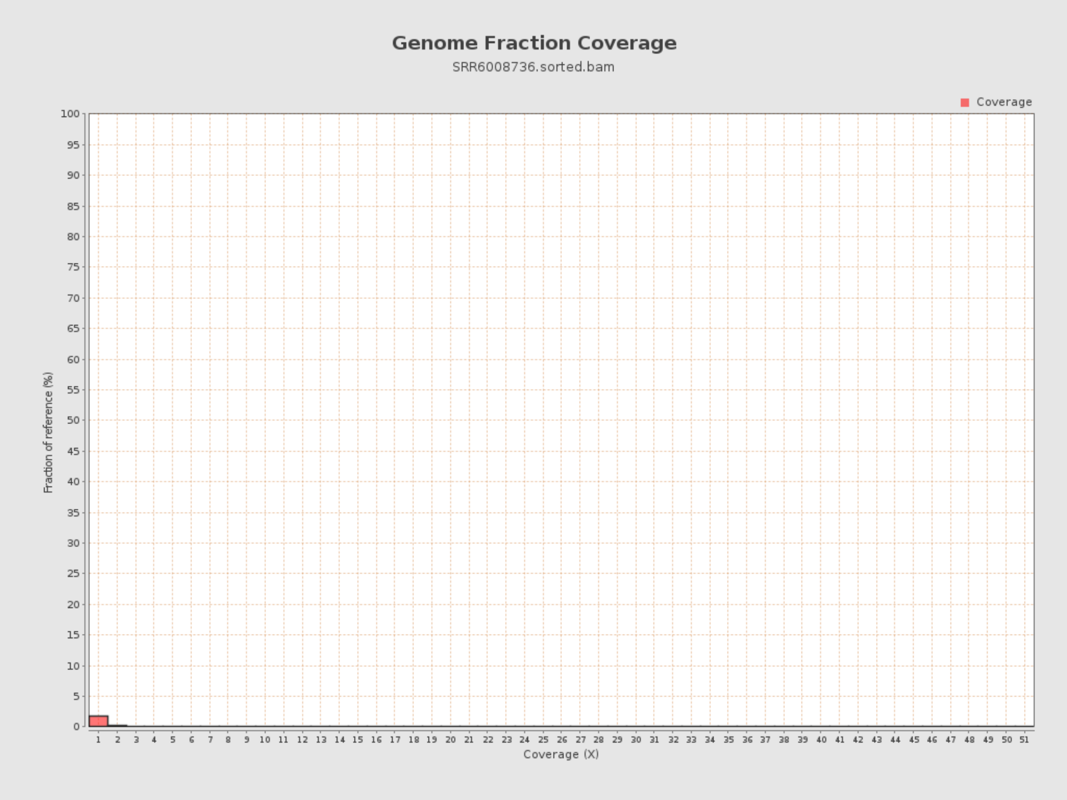
4. Results : Coverage Histogram



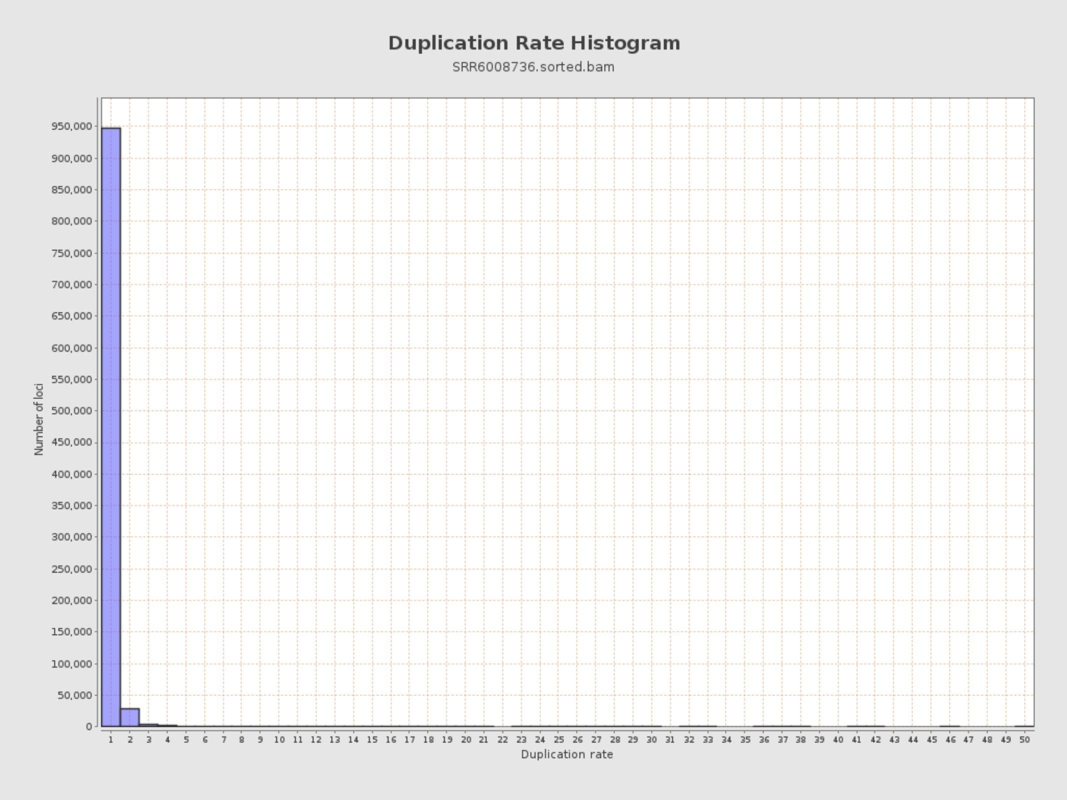
5. Results : Coverage Histogram (0-50X)



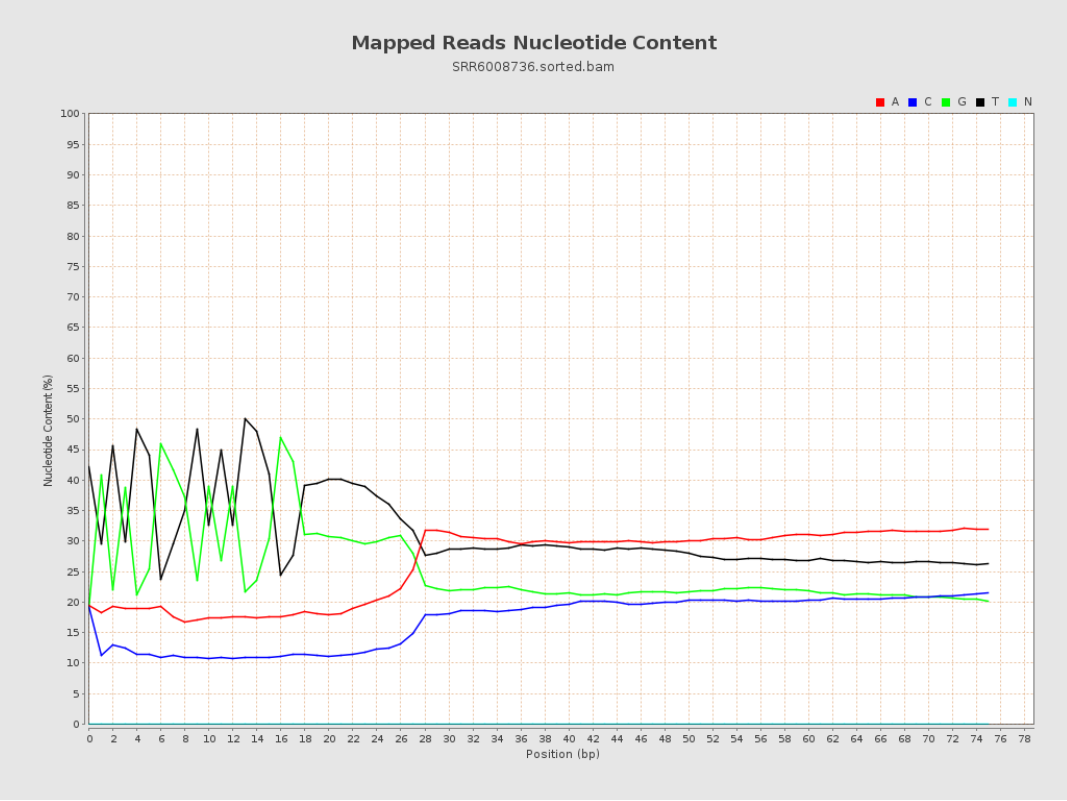
6. Results : Genome Fraction Coverage



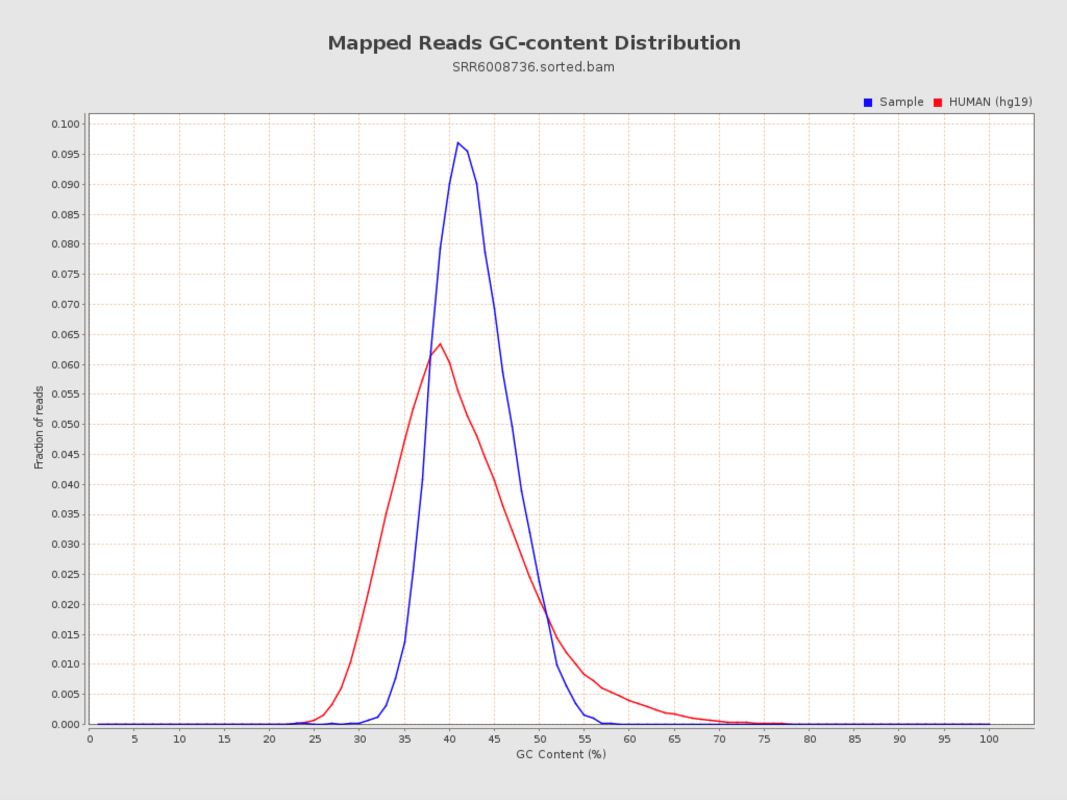
7. Results : Duplication Rate Histogram



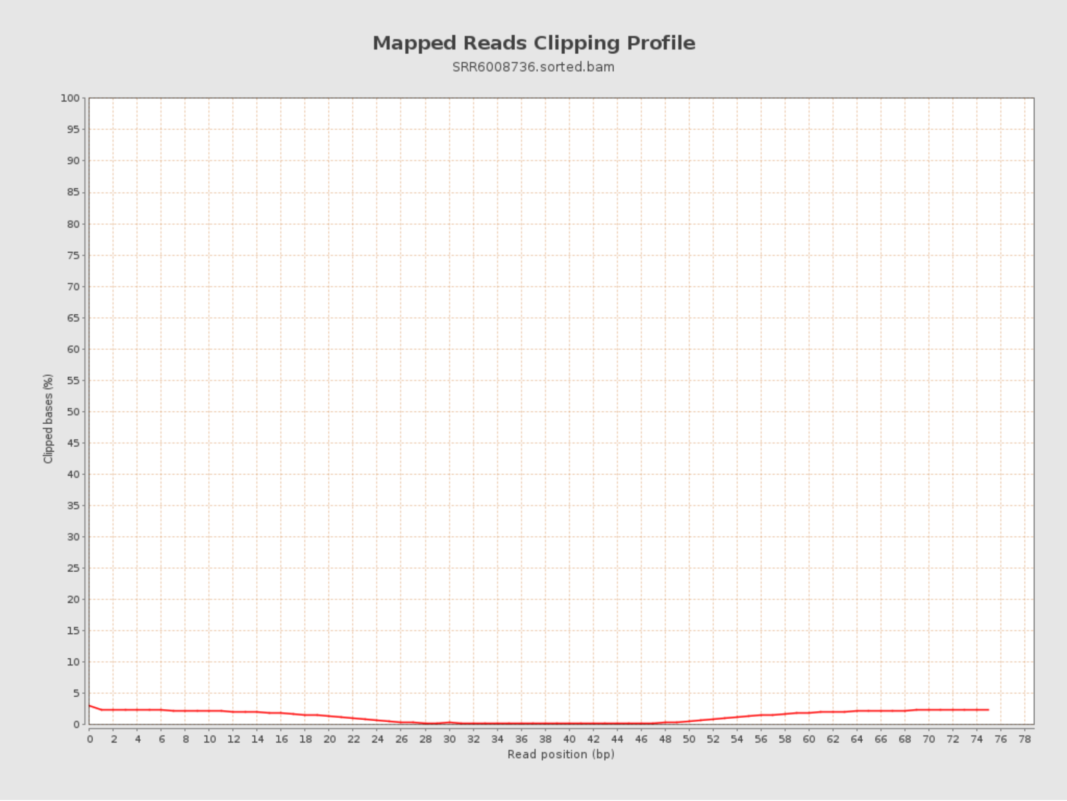
8. Results : Mapped Reads Nucleotide Content



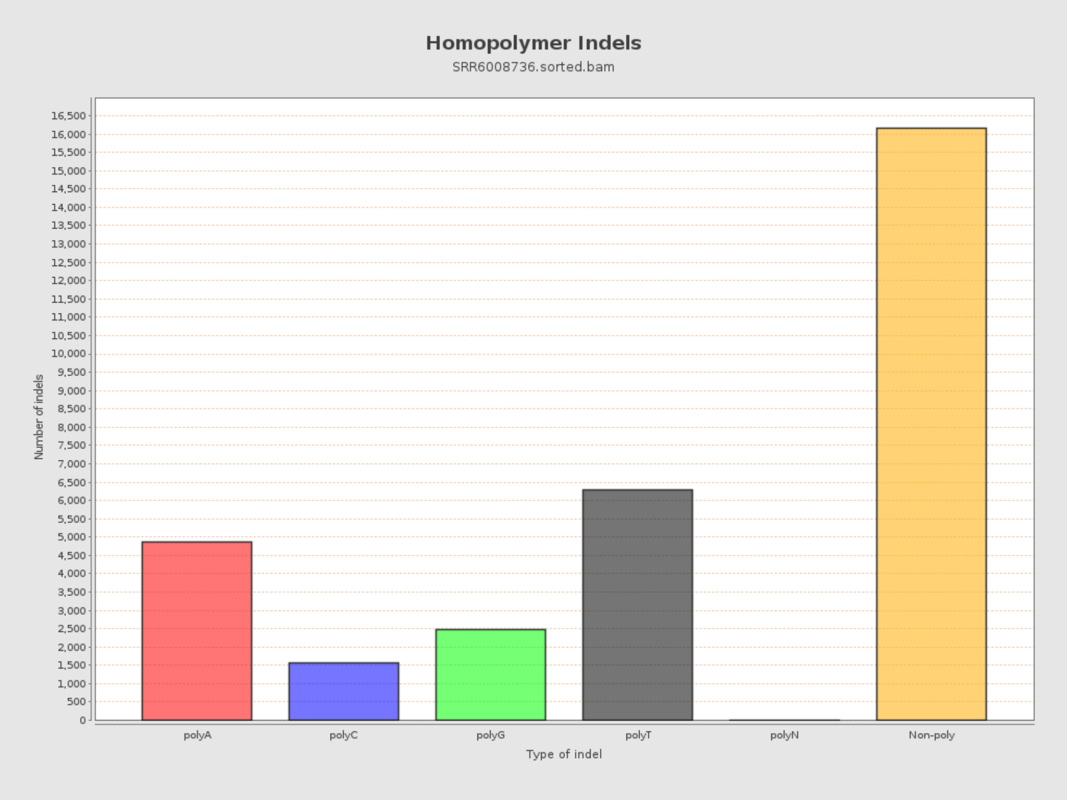
9. Results : Mapped Reads GC-content Distribution



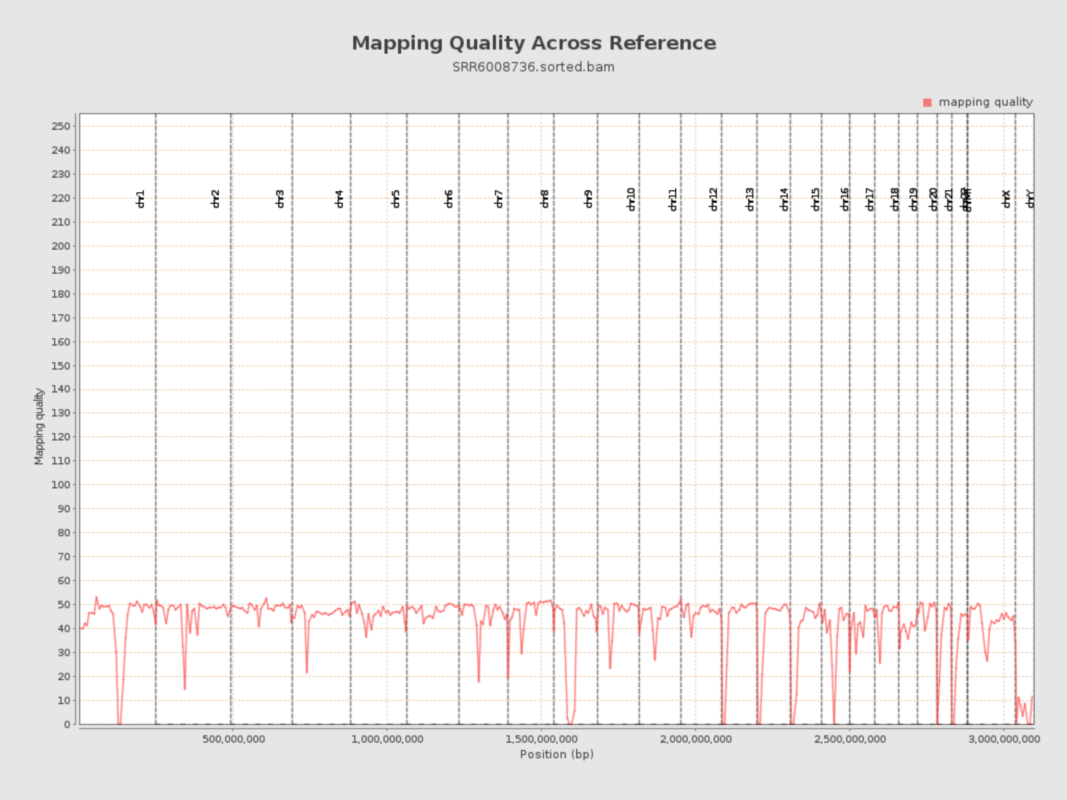
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram