Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 23:49:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083613.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_SRR3083613 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083613.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 23:49:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083613.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,444,341
Mapped reads	1,327,303 / 91.9%
Unmapped reads	117,038 / 8.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,204 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	46,314 / 3.21%
Duplication rate	2.97%
Clipped reads	555,050 / 38.43%

2.2. ACGT Content

Number/percentage of A's	24,647,856 / 27.67%
Number/percentage of C's	16,240,650 / 18.23%
Number/percentage of T's	28,463,893 / 31.96%
Number/percentage of G's	19,708,780 / 22.13%
Number/percentage of N's	4,298 / 0%
GC Percentage	40.36%

2.3. Coverage

Mean	0.0288

Standard Deviation	0.2451

2.4. Mapping Quality

Mean Mapping Quality	46.25

2.5. Mismatches and indels

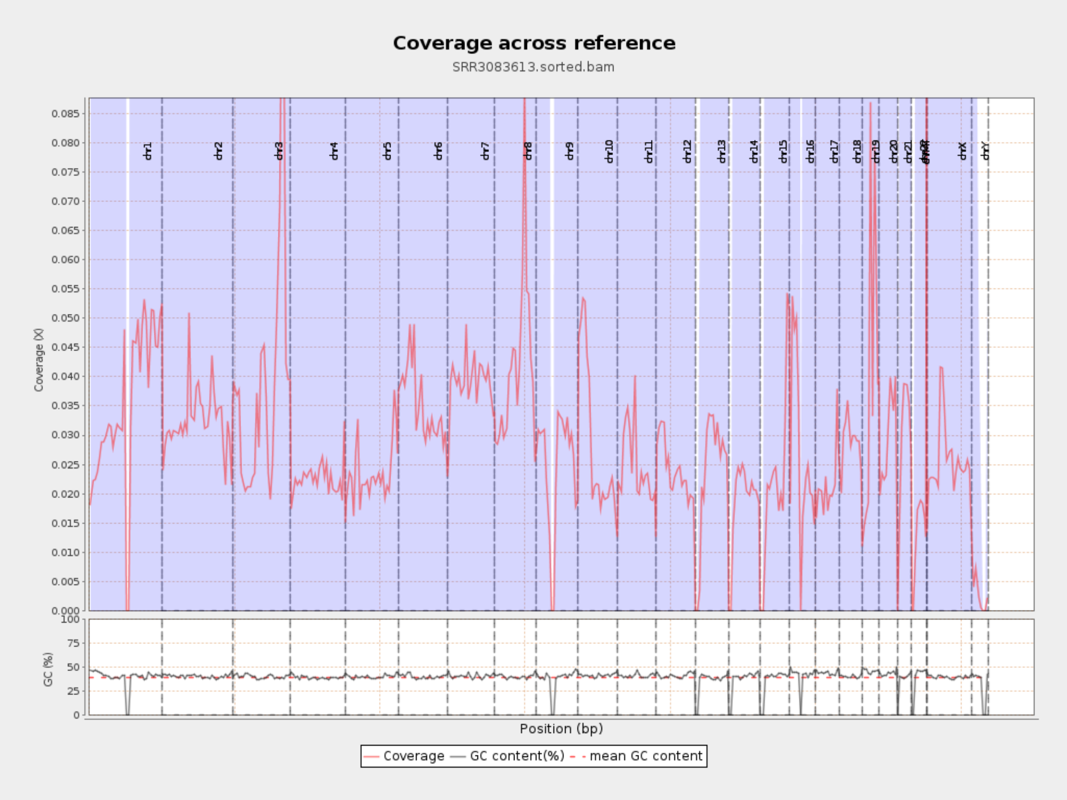
General error rate	0.7%
Mismatches	608,878
Insertions	6,885
Mapped reads with at least one insertion	0.51%
Deletions	20,172
Mapped reads with at least one deletion	1.51%
Homopolymer indels	49.27%

2.6. Chromosome stats

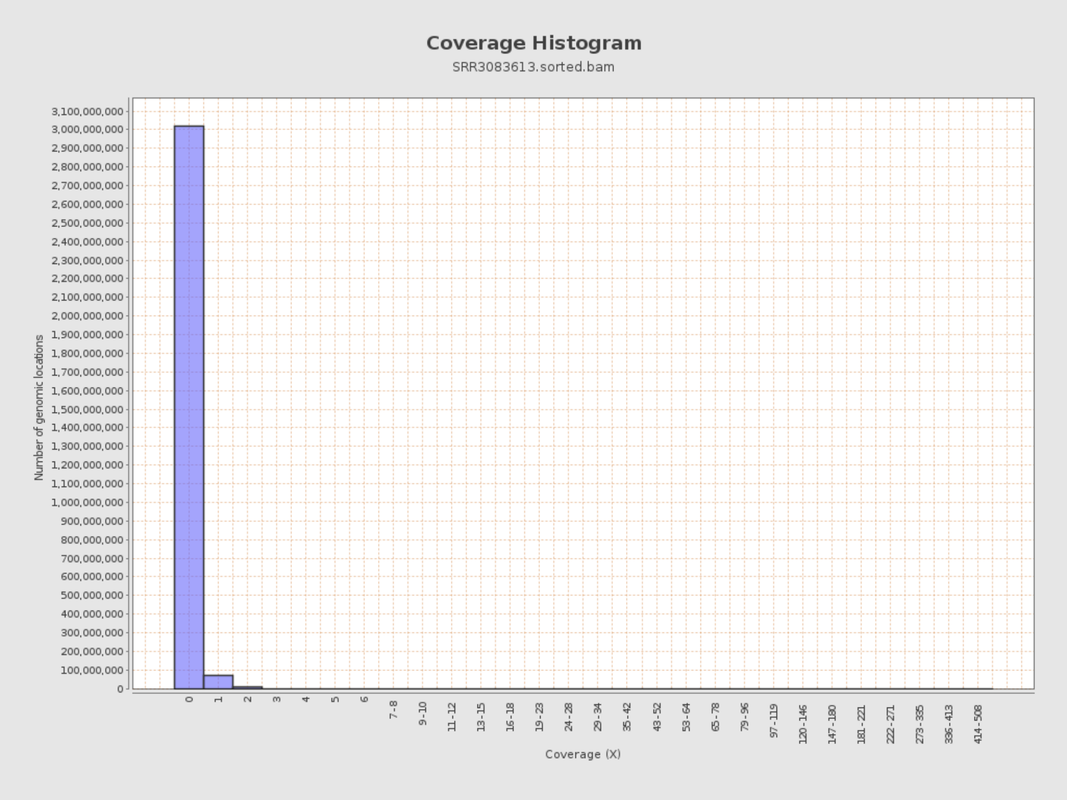
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8680244	0.0348	0.4158
chr2	243199373	7931044	0.0326	0.3077
chr3	198022430	7718181	0.039	0.2208
chr4	191154276	4314849	0.0226	0.1685
chr5	180915260	4257568	0.0235	0.1693
chr6	171115067	6039476	0.0353	0.2354
chr7	159138663	6280592	0.0395	0.3309

chr8	146364022	6132204	0.0419	0.3193
chr9	141213431	3489928	0.0247	0.1968
chr10	135534747	3966976	0.0293	0.2156
chr11	135006516	3334411	0.0247	0.1928
chr12	133851895	3196170	0.0239	0.1715
chr13	115169878	2711658	0.0235	0.1698
chr14	107349540	1997433	0.0186	0.153
chr15	102531392	2198907	0.0214	0.1675
chr16	90354753	2460424	0.0272	0.1879
chr17	81195210	1752097	0.0216	0.1668
chr18	78077248	2254480	0.0289	0.299
chr19	59128983	2345292	0.0397	0.3018
chr20	63025520	1844295	0.0293	0.1923
chr21	48129895	1378052	0.0286	0.1902
chr22	51304566	641826	0.0125	0.1222
chrMT	16571	2152	0.1299	0.4087
chrX	155270560	4005616	0.0258	0.1837
chrY	59373566	164592	0.0028	0.0645

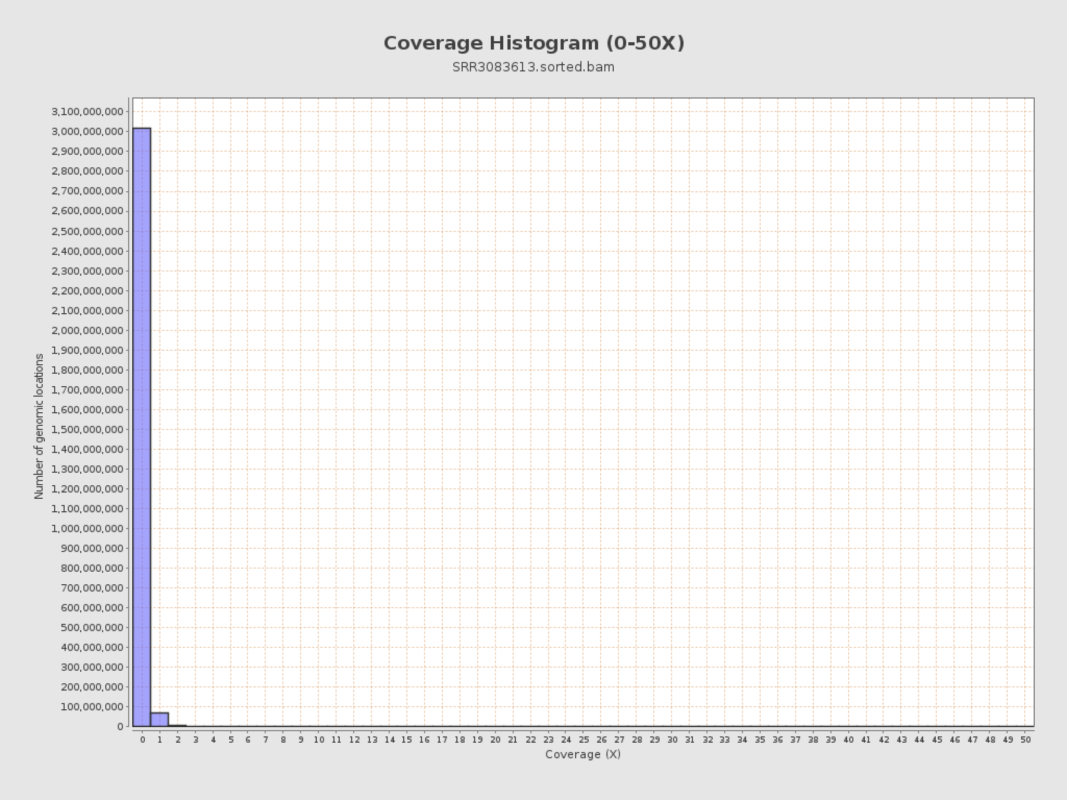
3. Results : Coverage across reference



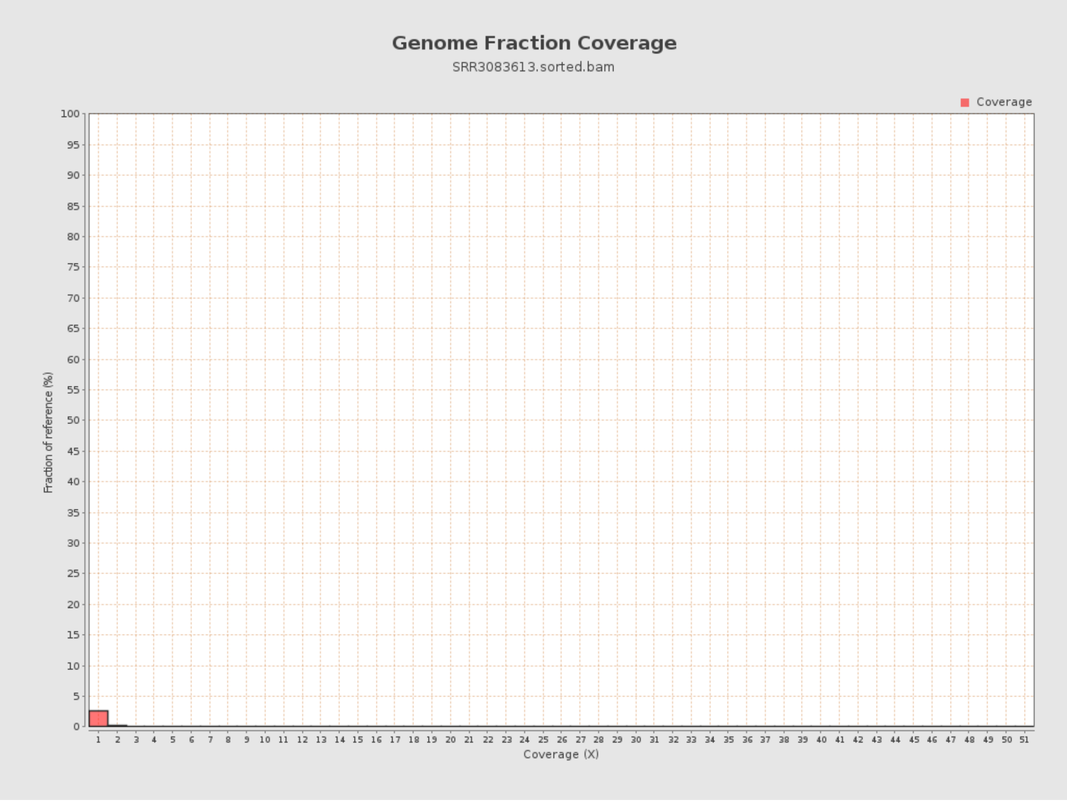
4. Results : Coverage Histogram



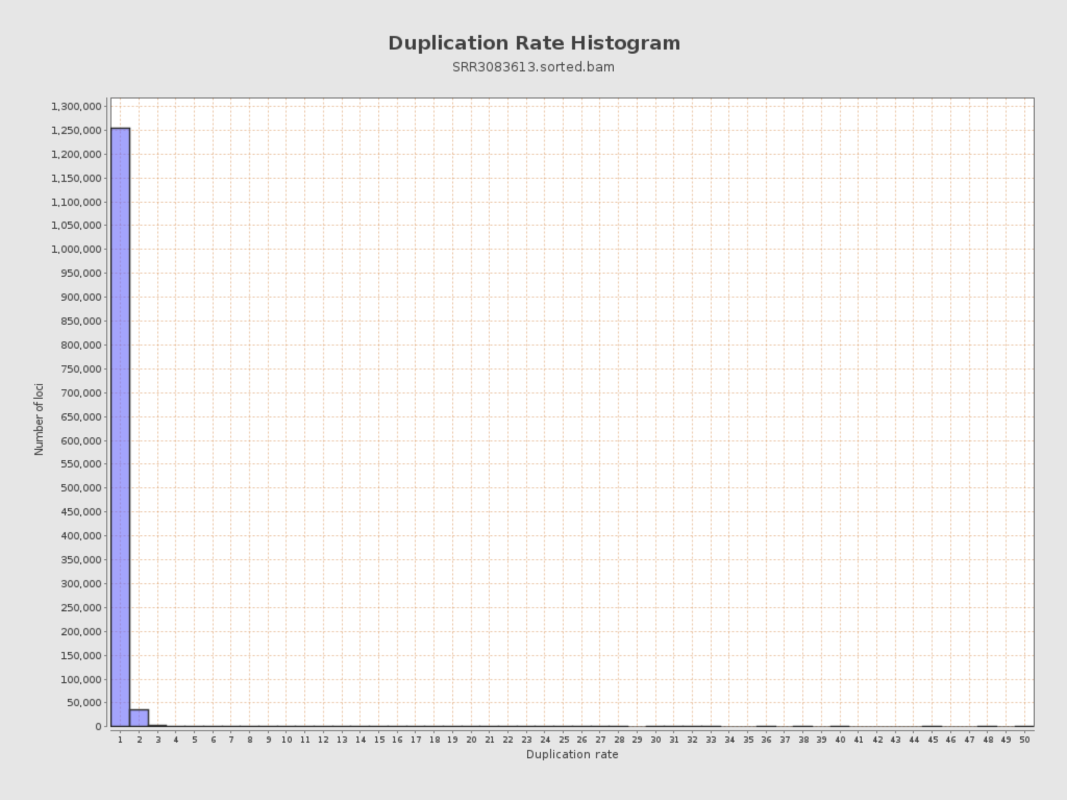
5. Results : Coverage Histogram (0-50X)



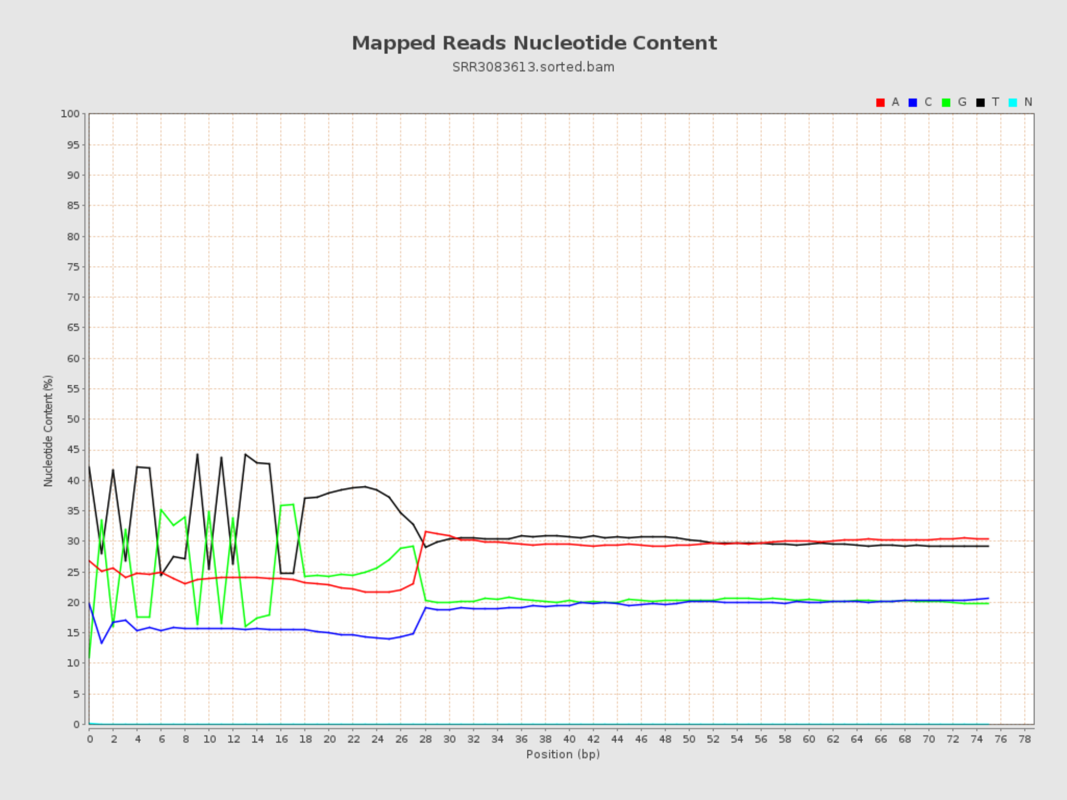
6. Results : Genome Fraction Coverage



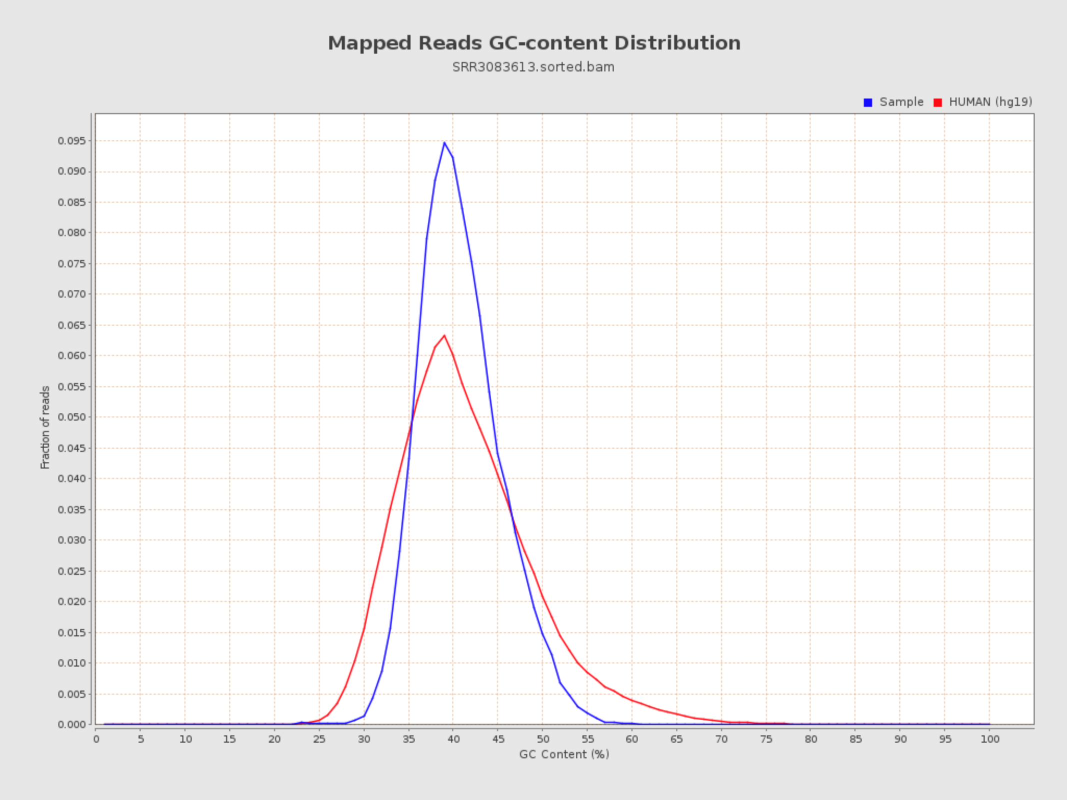
7. Results : Duplication Rate Histogram



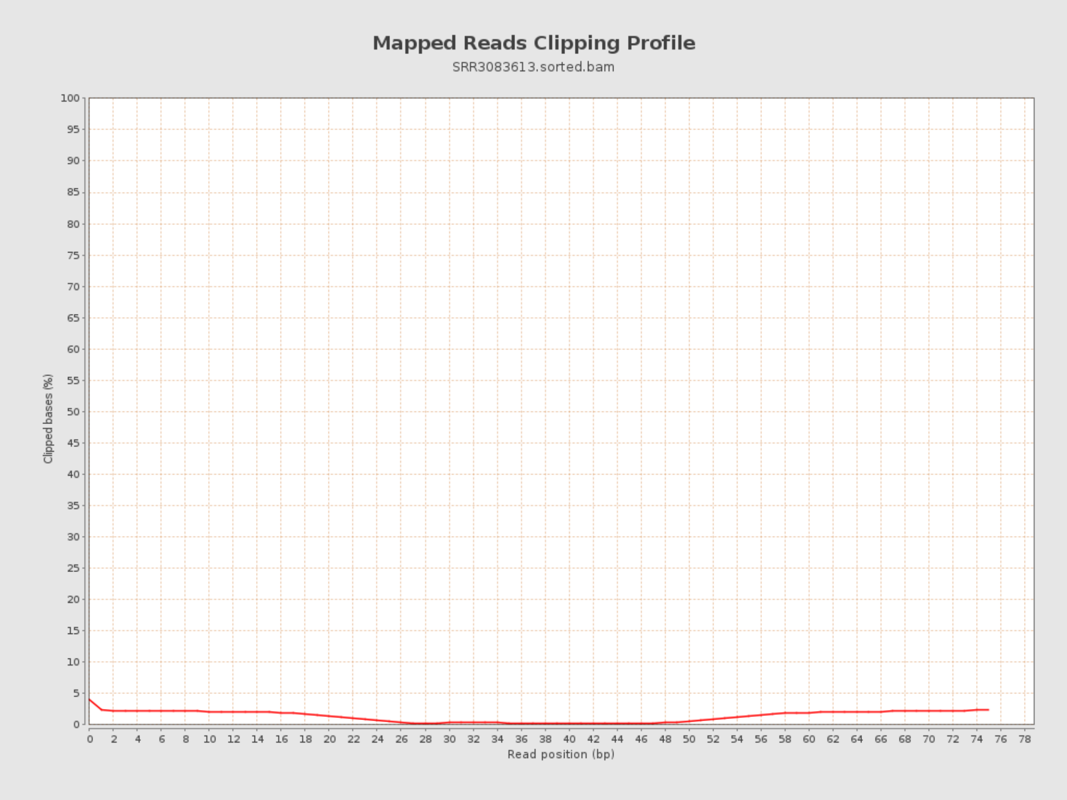
8. Results : Mapped Reads Nucleotide Content



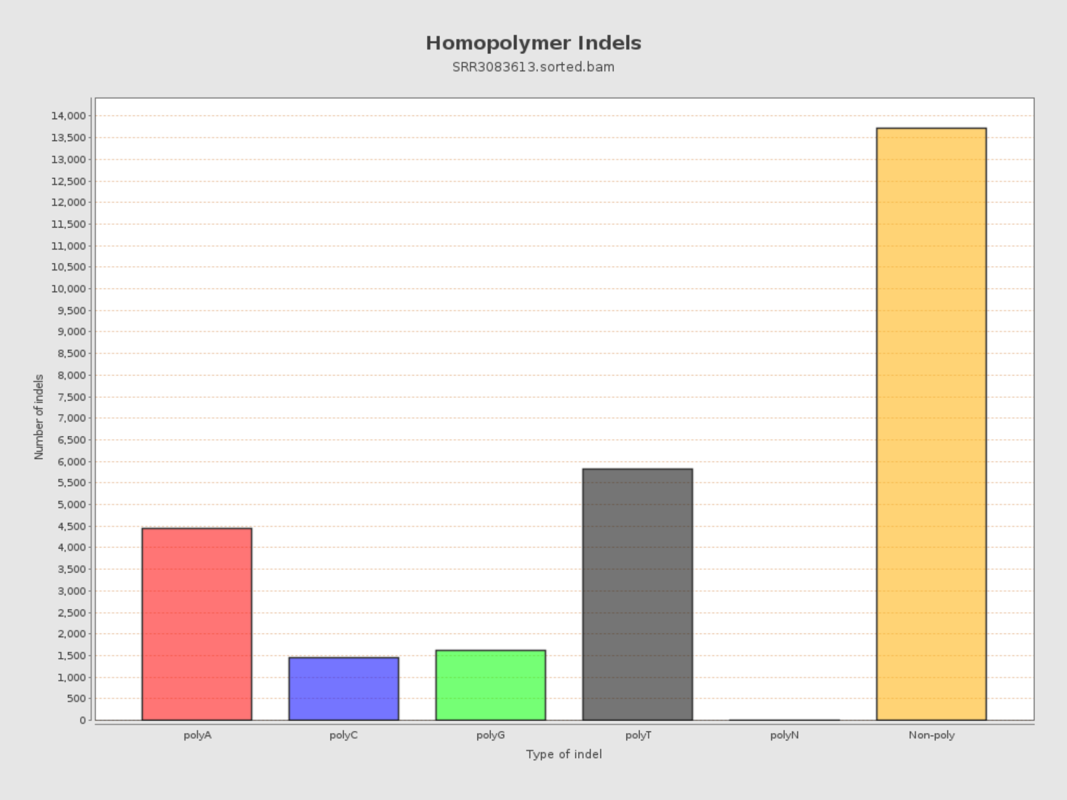
9. Results : Mapped Reads GC-content Distribution



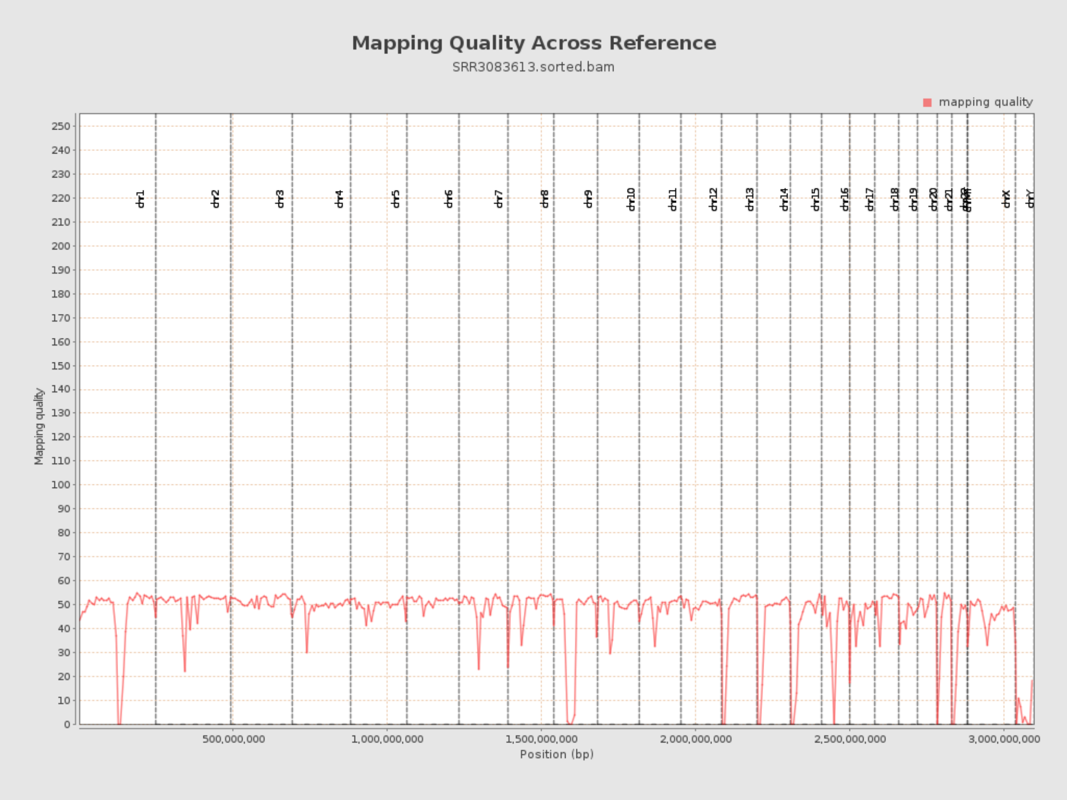
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram