Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 08:33:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084262.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_SRR3084262 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084262.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 08:33:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084262.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,919,108
Mapped reads	1,649,667 / 85.96%
Unmapped reads	269,441 / 14.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,125 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	51,521 / 2.68%
Duplication rate	2.54%
Clipped reads	870,637 / 45.37%

2.2. ACGT Content

Number/percentage of A's	30,597,688 / 28.69%
Number/percentage of C's	20,116,736 / 18.86%
Number/percentage of T's	32,531,315 / 30.51%
Number/percentage of G's	23,389,364 / 21.93%
Number/percentage of N's	1,264 / 0%
GC Percentage	40.8%

2.3. Coverage

Mean	0.0345

Standard Deviation	0.2677

2.4. Mapping Quality

Mean Mapping Quality	45.96

2.5. Mismatches and indels

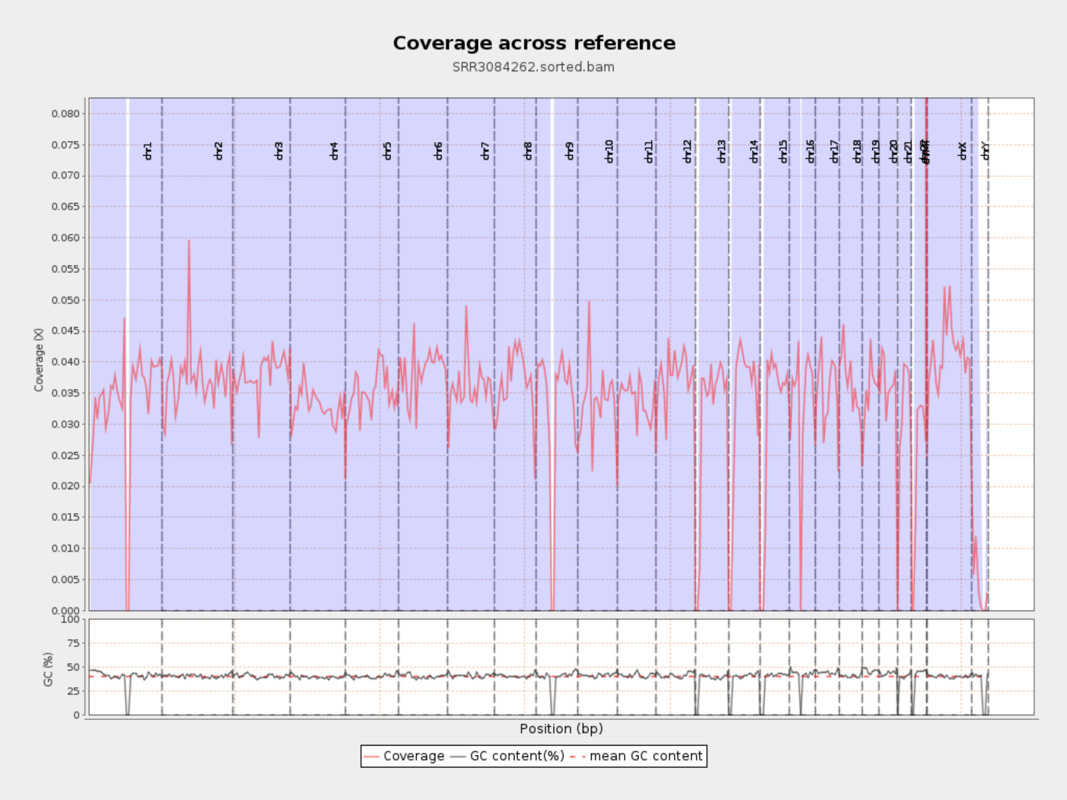
General error rate	0.87%
Mismatches	911,805
Insertions	8,402
Mapped reads with at least one insertion	0.51%
Deletions	23,797
Mapped reads with at least one deletion	1.43%
Homopolymer indels	46.27%

2.6. Chromosome stats

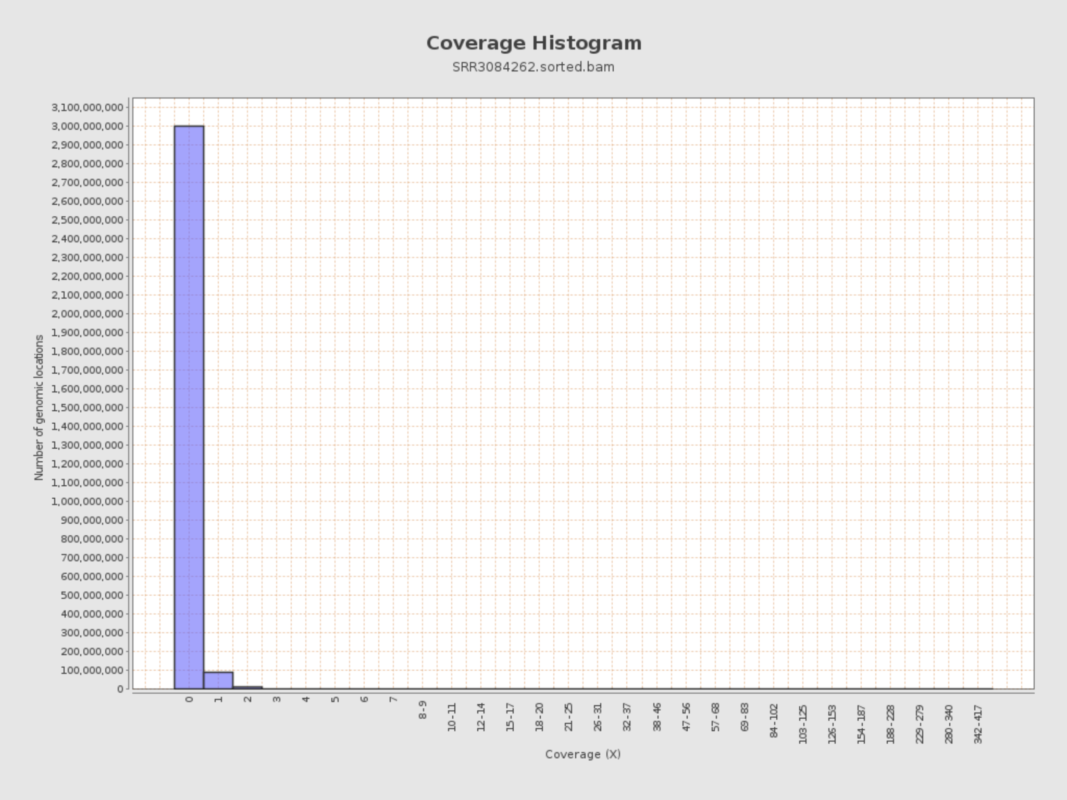
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8363121	0.0336	0.3928
chr2	243199373	9081936	0.0373	0.3384
chr3	198022430	7585173	0.0383	0.2127
chr4	191154276	6310868	0.033	0.2036
chr5	180915260	6369402	0.0352	0.2058
chr6	171115067	6600694	0.0386	0.2416
chr7	159138663	5745428	0.0361	0.316

chr8	146364022	5355036	0.0366	0.2758
chr9	141213431	4603353	0.0326	0.2547
chr10	135534747	4579145	0.0338	0.2704
chr11	135006516	4577048	0.0339	0.2435
chr12	133851895	5052541	0.0377	0.2125
chr13	115169878	3512567	0.0305	0.1899
chr14	107349540	3448487	0.0321	0.2047
chr15	102531392	3139011	0.0306	0.1941
chr16	90354753	3017694	0.0334	0.2161
chr17	81195210	2837861	0.035	0.2281
chr18	78077248	2874039	0.0368	0.488
chr19	59128983	2101657	0.0355	0.3142
chr20	63025520	2261214	0.0359	0.2119
chr21	48129895	1468714	0.0305	0.1965
chr22	51304566	1147048	0.0224	0.1615
chrMT	16571	9912	0.5982	0.9045
chrX	155270560	6376971	0.0411	0.2392
chrY	59373566	255561	0.0043	0.0899

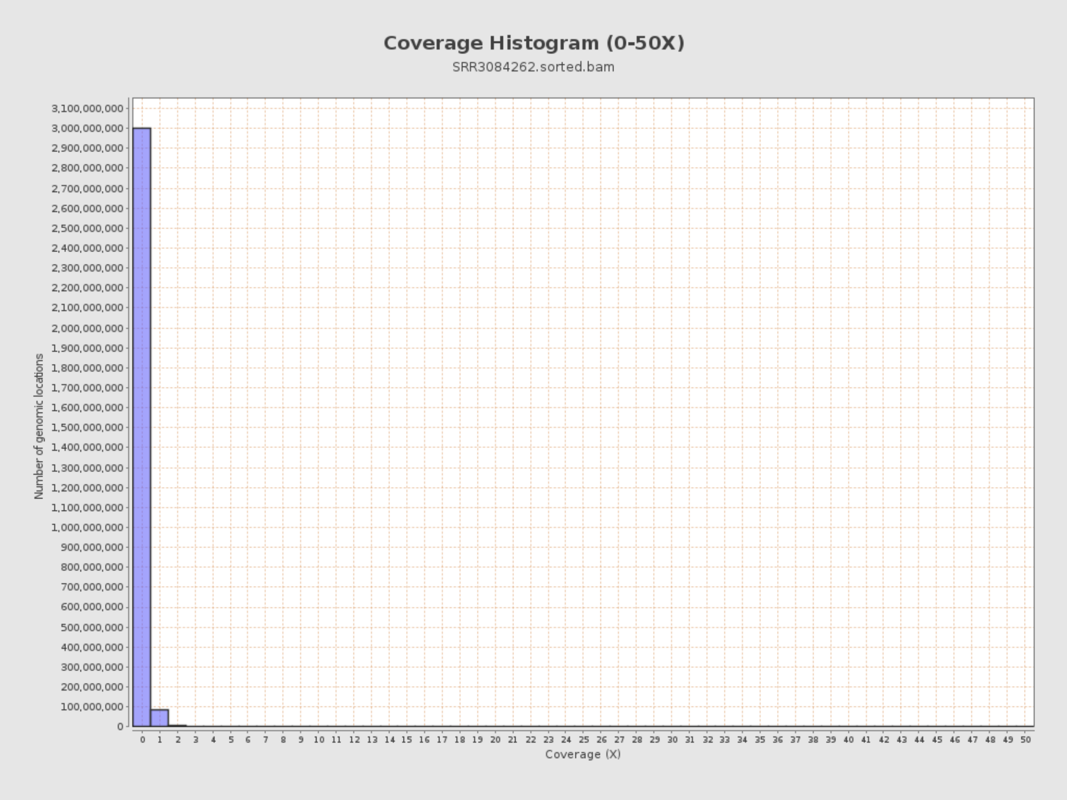
3. Results : Coverage across reference



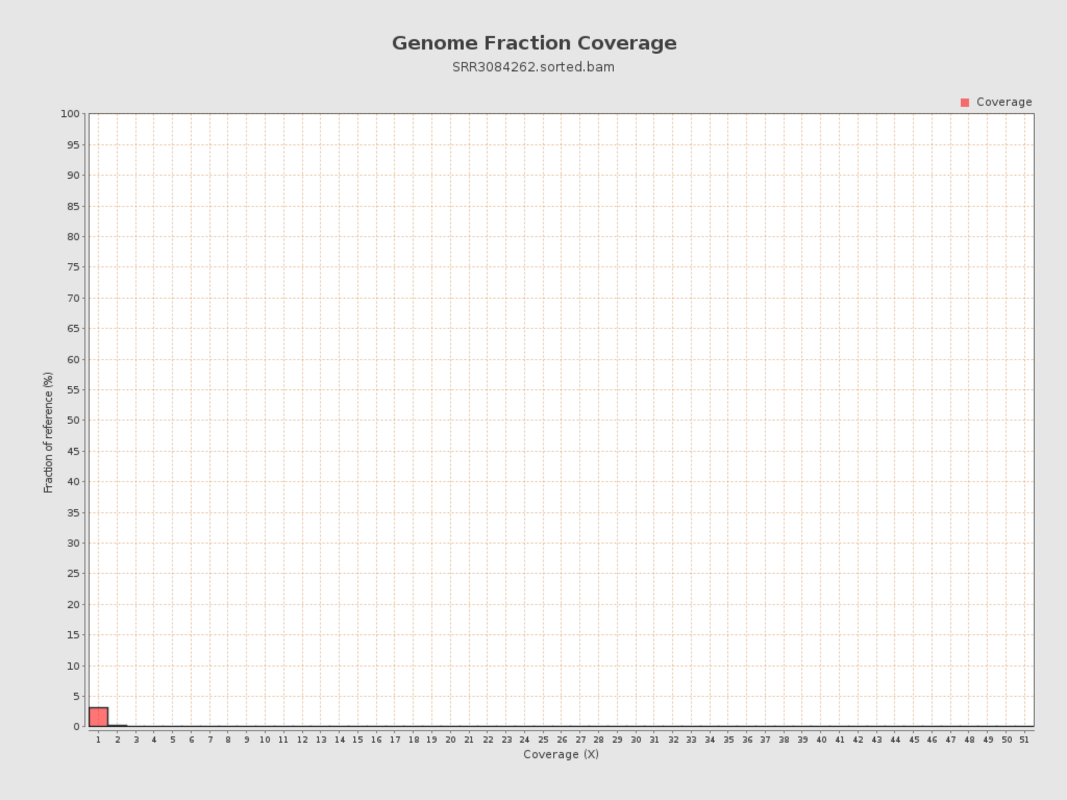
4. Results : Coverage Histogram



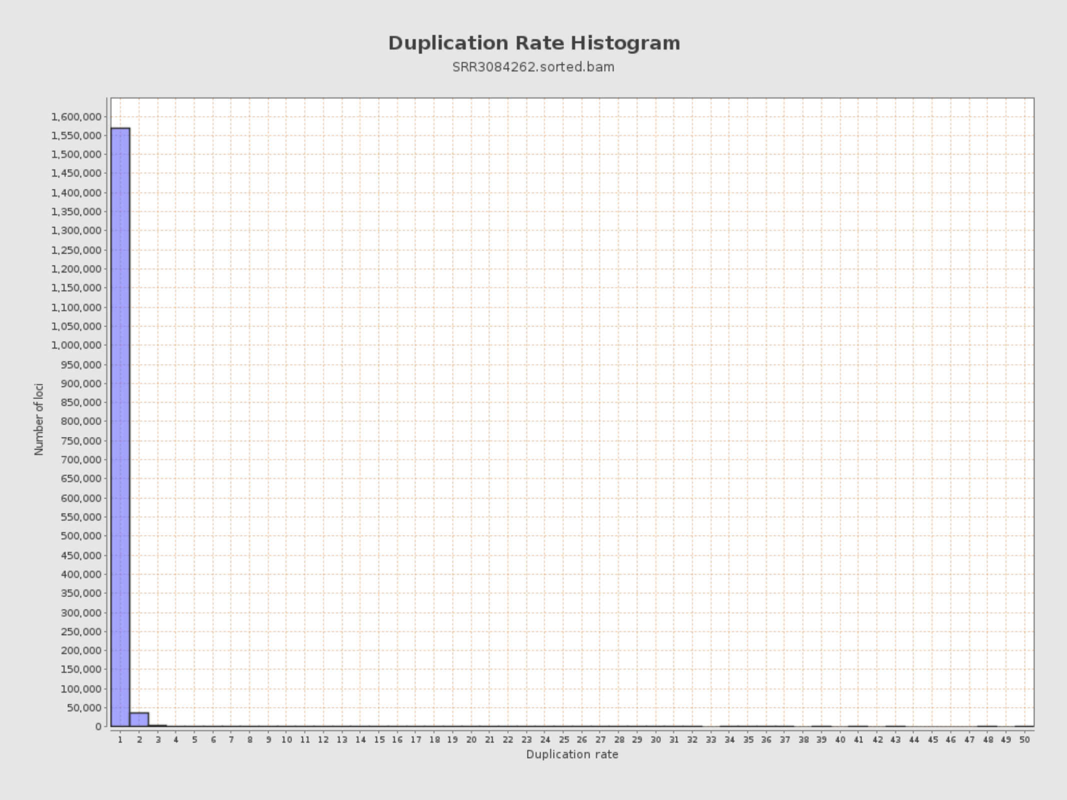
5. Results : Coverage Histogram (0-50X)



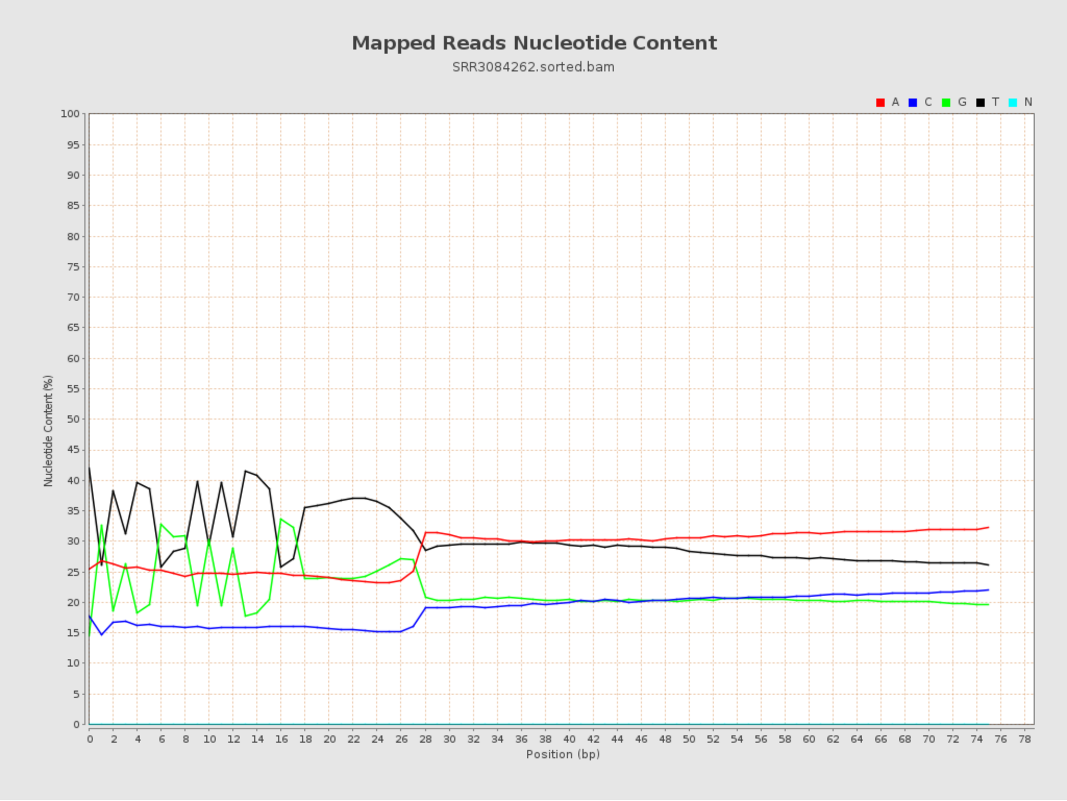
6. Results : Genome Fraction Coverage



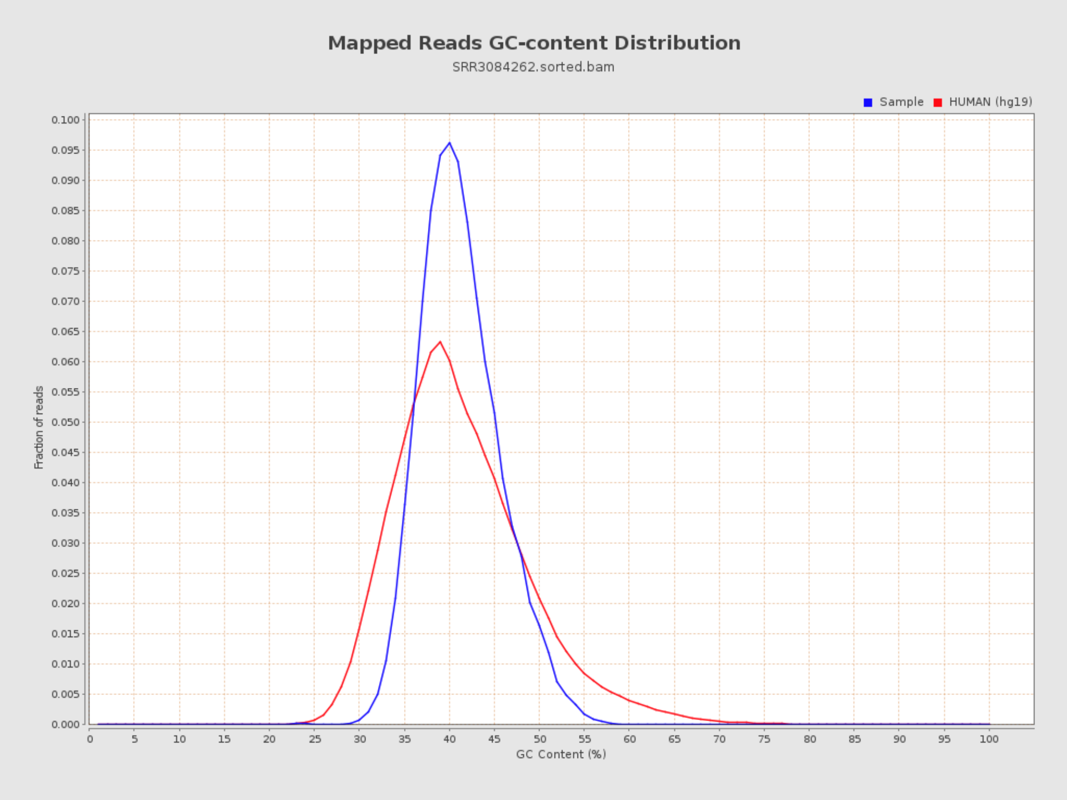
7. Results : Duplication Rate Histogram



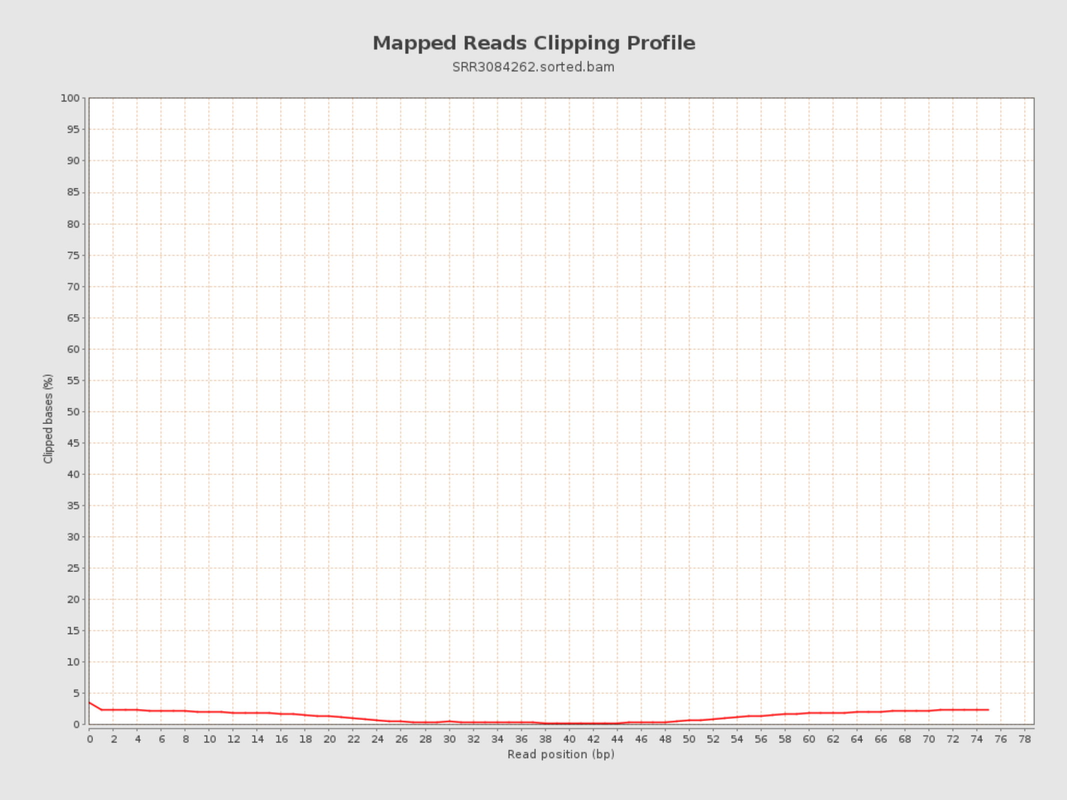
8. Results : Mapped Reads Nucleotide Content



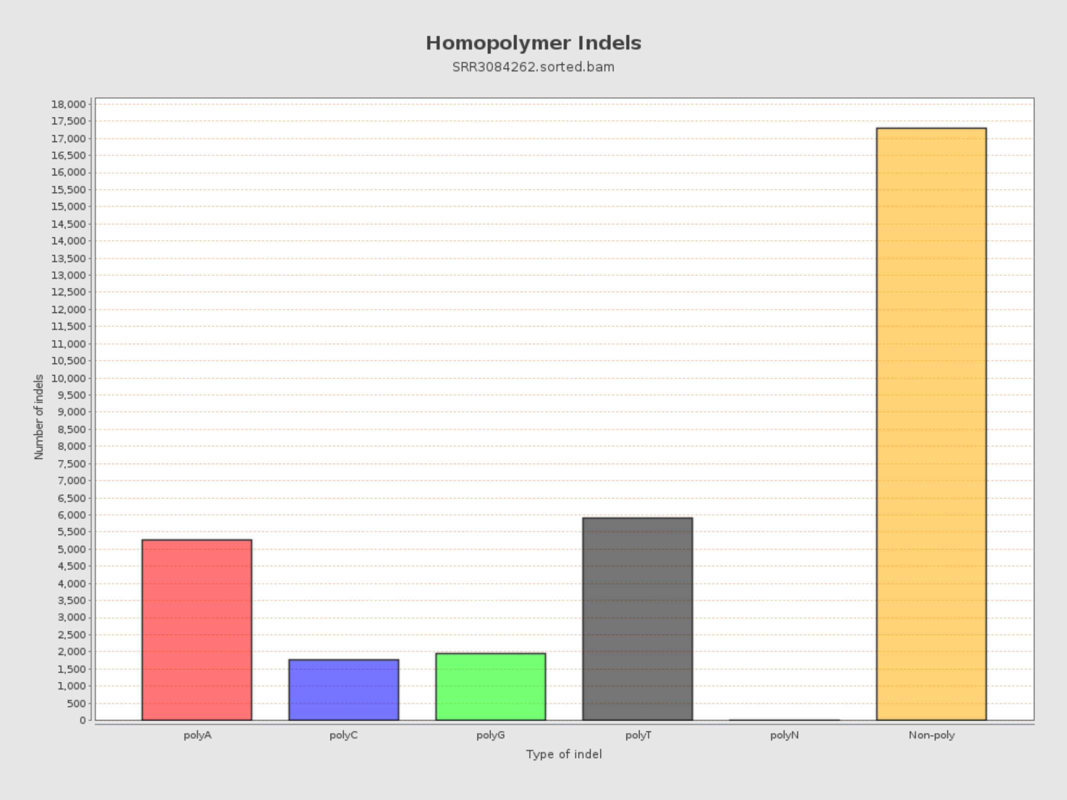
9. Results : Mapped Reads GC-content Distribution



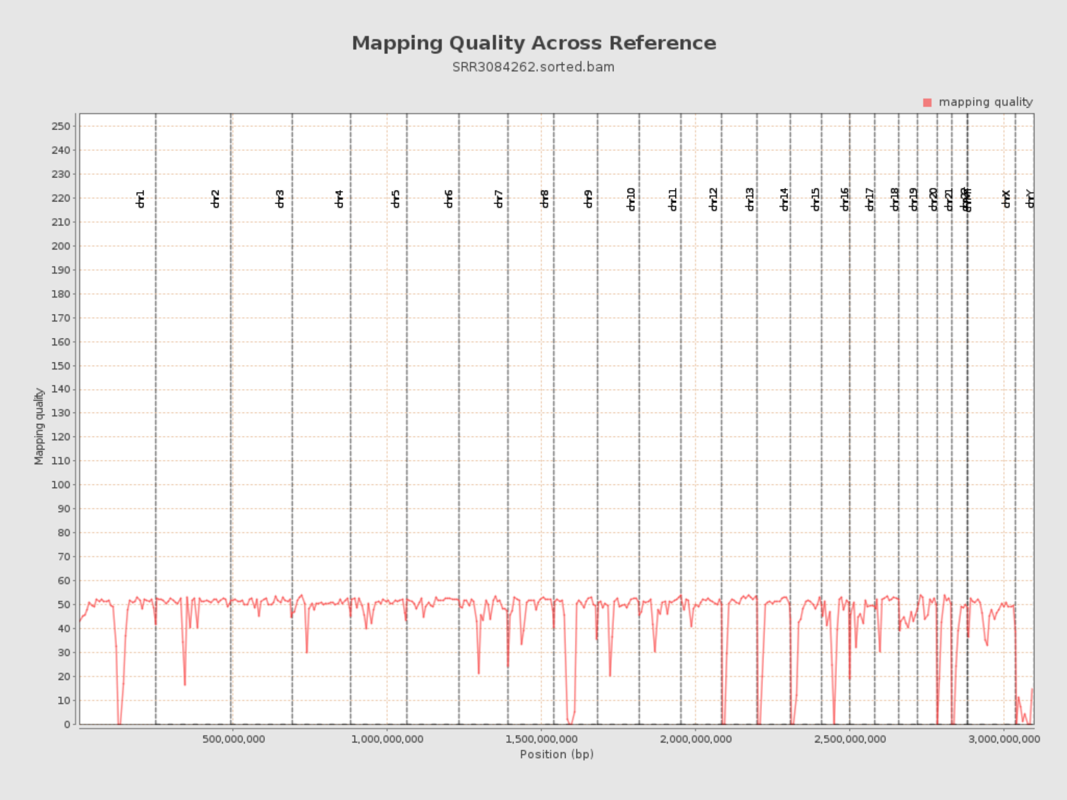
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram