Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 12:20:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084412.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_SRR3084412 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084412.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 12:20:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084412.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,631,632
Mapped reads	1,460,260 / 89.5%
Unmapped reads	171,372 / 10.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,424 / 1.25%
Read min/max/mean length	30 / 76 / 76.44
Duplicated reads (estimated)	46,980 / 2.88%
Duplication rate	1.94%
Clipped reads	668,023 / 40.94%

2.2. ACGT Content

Number/percentage of A's	27,937,636 / 28.56%
Number/percentage of C's	18,977,678 / 19.4%
Number/percentage of T's	28,820,424 / 29.46%
Number/percentage of G's	21,957,112 / 22.45%
Number/percentage of N's	122,758 / 0.13%
GC Percentage	41.85%

2.3. Coverage

Mean	0.0316

Standard Deviation	0.4127

2.4. Mapping Quality

Mean Mapping Quality	42.39

2.5. Mismatches and indels

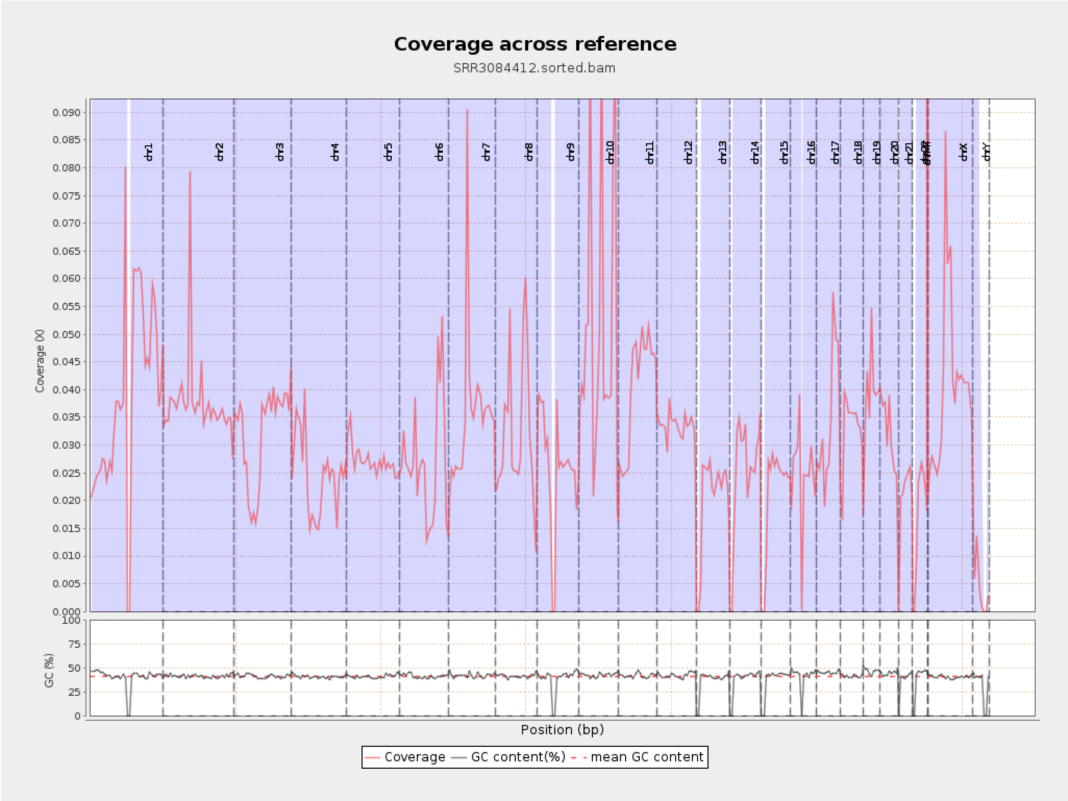
General error rate	1.05%
Mismatches	1,010,152
Insertions	8,470
Mapped reads with at least one insertion	0.57%
Deletions	18,766
Mapped reads with at least one deletion	1.27%
Homopolymer indels	43.27%

2.6. Chromosome stats

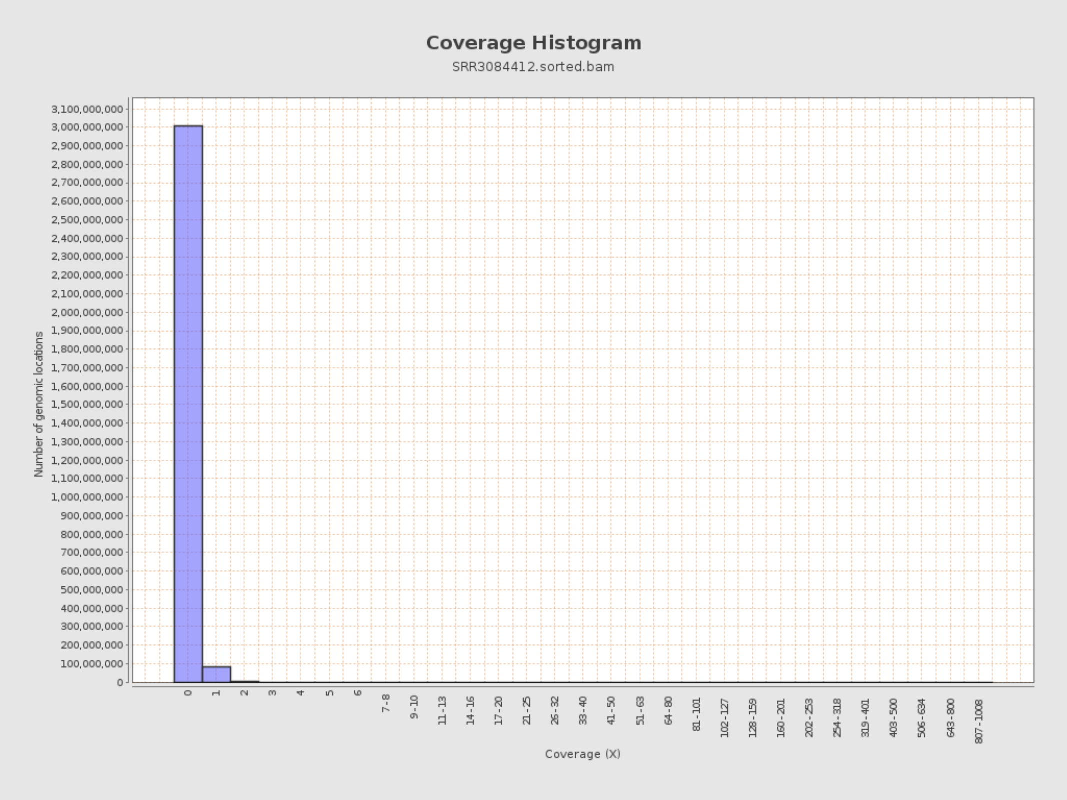
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9569014	0.0384	0.889
chr2	243199373	9193836	0.0378	0.3686
chr3	198022430	6353788	0.0321	0.2102
chr4	191154276	4687410	0.0245	0.1842
chr5	180915260	4921329	0.0272	0.177
chr6	171115067	4624913	0.027	0.214
chr7	159138663	5683997	0.0357	0.7159

chr8	146364022	4668487	0.0319	0.3357
chr9	141213431	3625961	0.0257	0.3012
chr10	135534747	7083360	0.0523	0.6157
chr11	135006516	5390409	0.0399	0.3453
chr12	133851895	4480881	0.0335	0.1973
chr13	115169878	2326752	0.0202	0.1482
chr14	107349540	2635127	0.0245	0.1934
chr15	102531392	2150439	0.021	0.1596
chr16	90354753	2223660	0.0246	0.2205
chr17	81195210	2814522	0.0347	0.2421
chr18	78077248	2582045	0.0331	0.609
chr19	59128983	2353882	0.0398	0.5822
chr20	63025520	1994461	0.0316	0.199
chr21	48129895	999913	0.0208	0.173
chr22	51304566	854504	0.0167	0.135
chrMT	16571	45233	2.7296	2.2758
chrX	155270560	6318013	0.0407	0.2715
chrY	59373566	266023	0.0045	0.1152

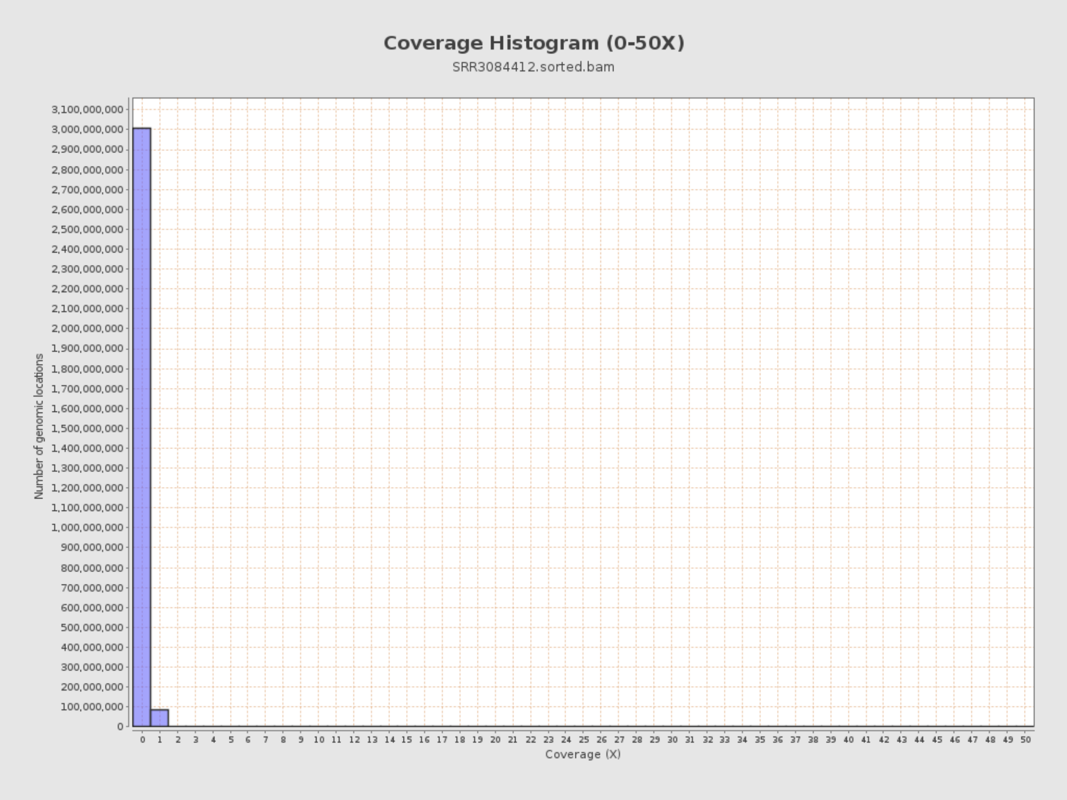
3. Results : Coverage across reference



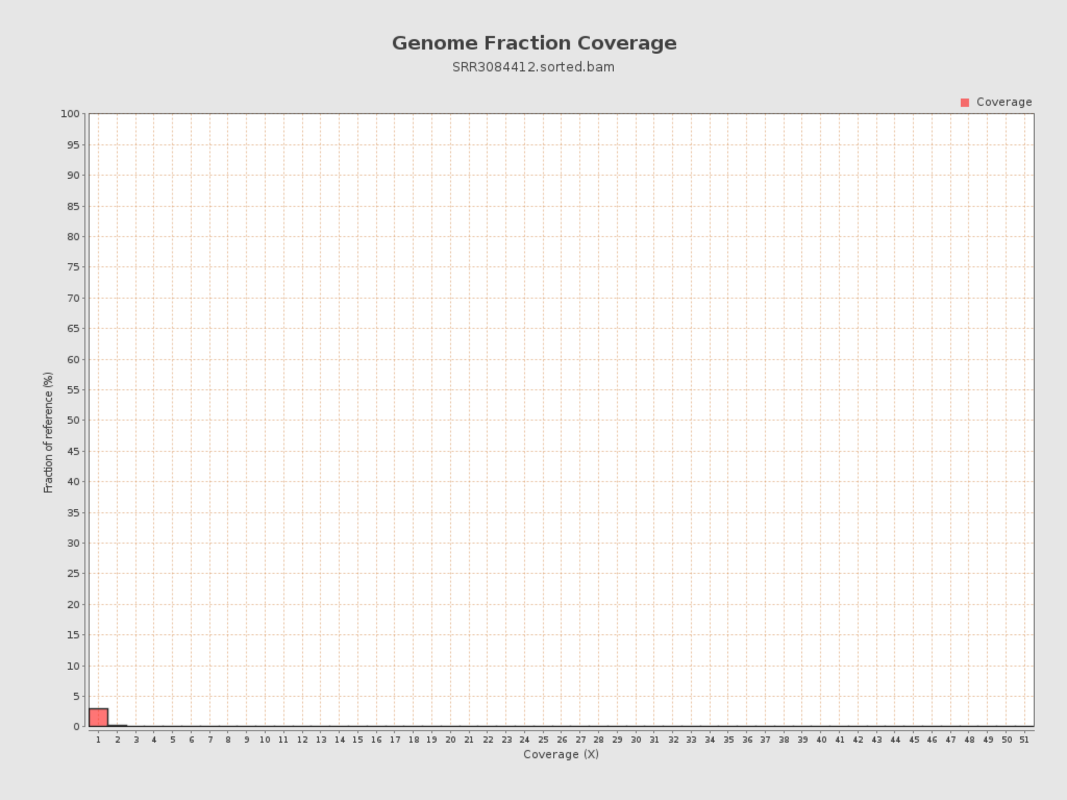
4. Results : Coverage Histogram



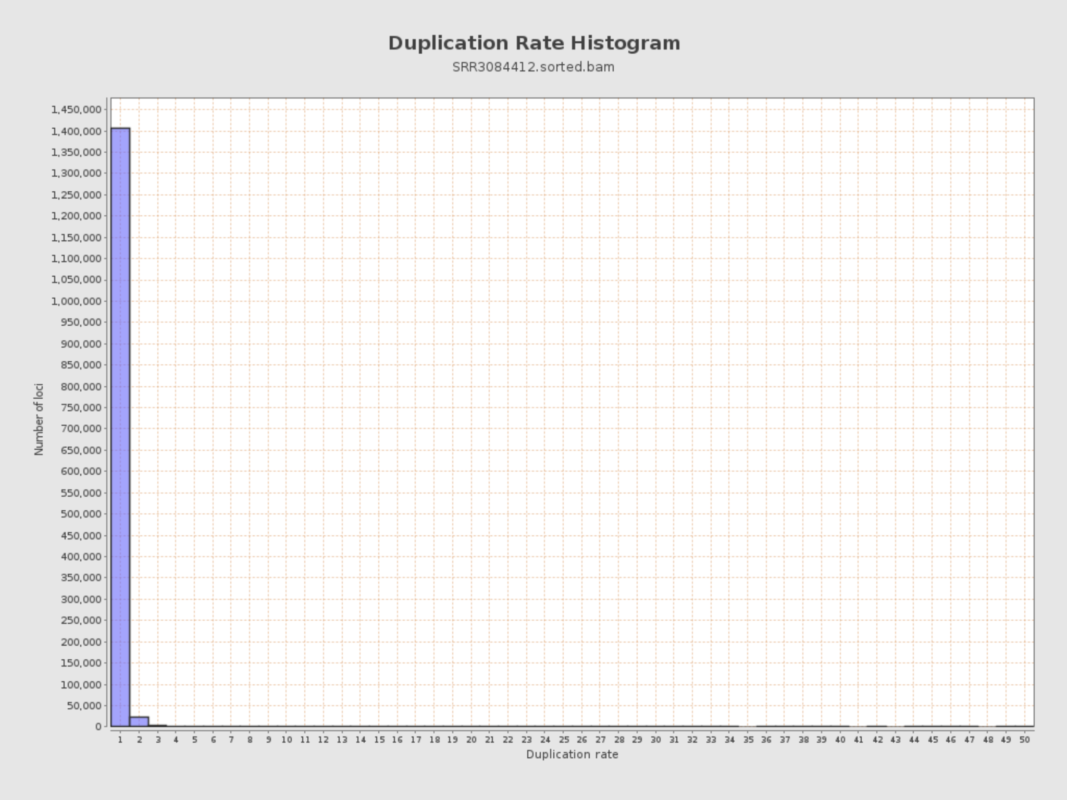
5. Results : Coverage Histogram (0-50X)



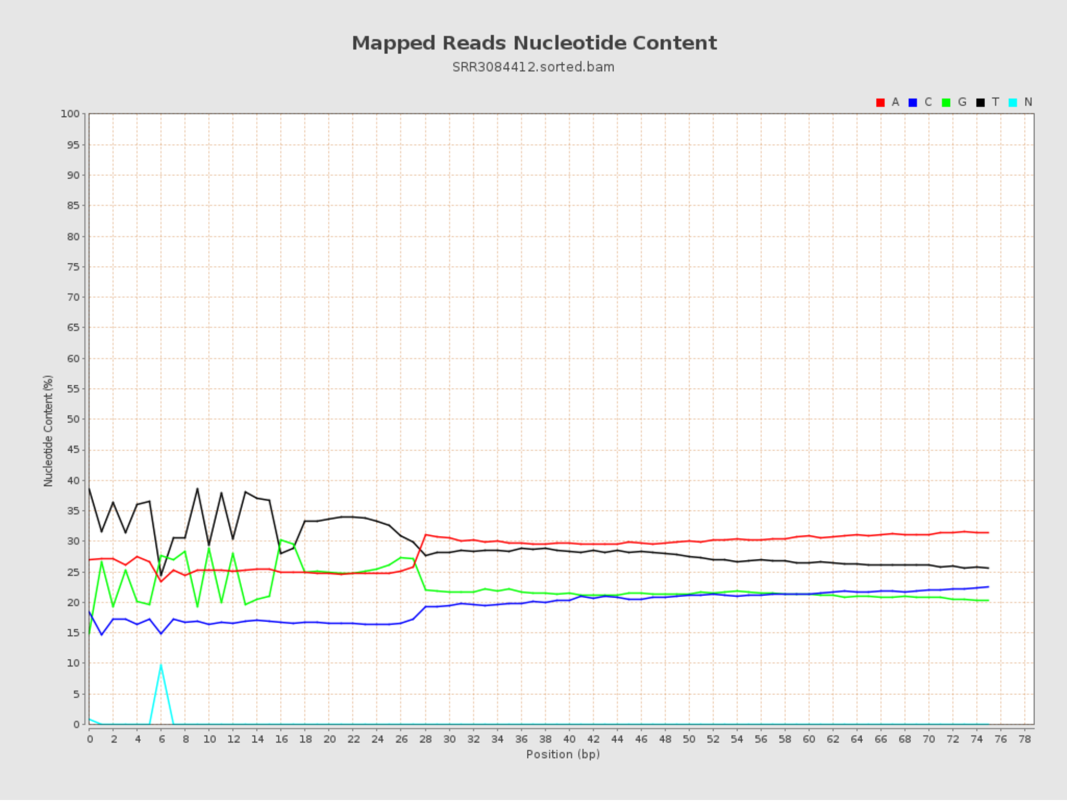
6. Results : Genome Fraction Coverage



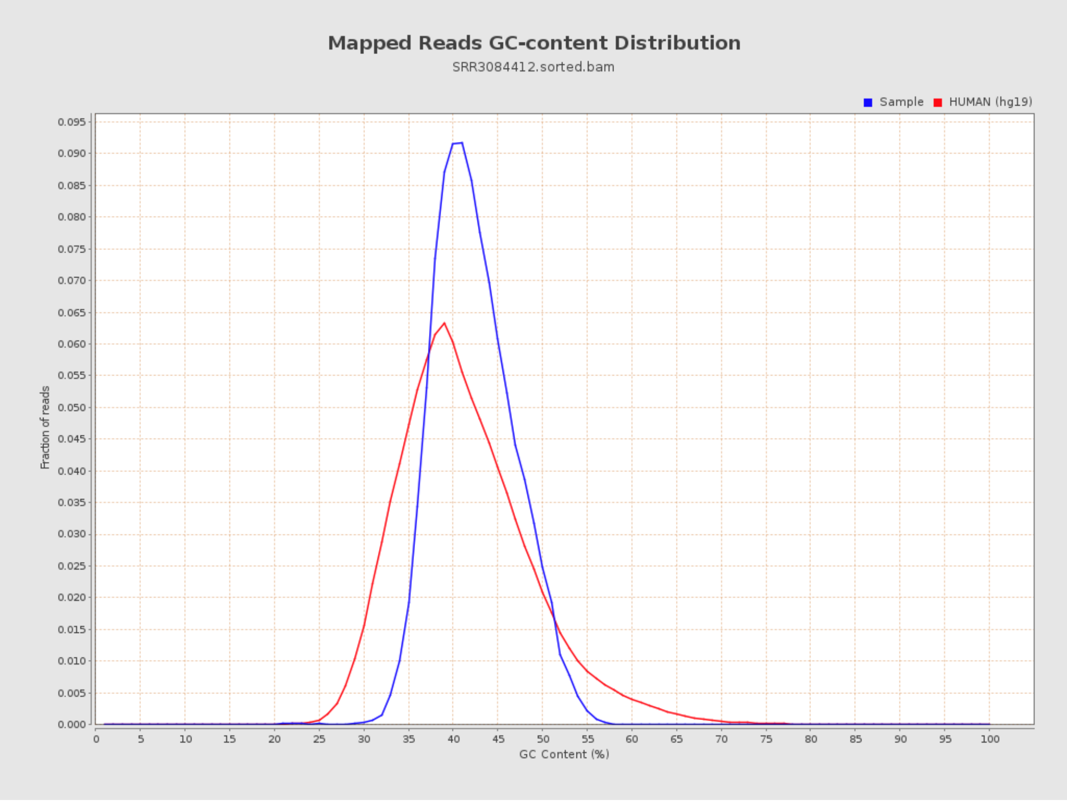
7. Results : Duplication Rate Histogram



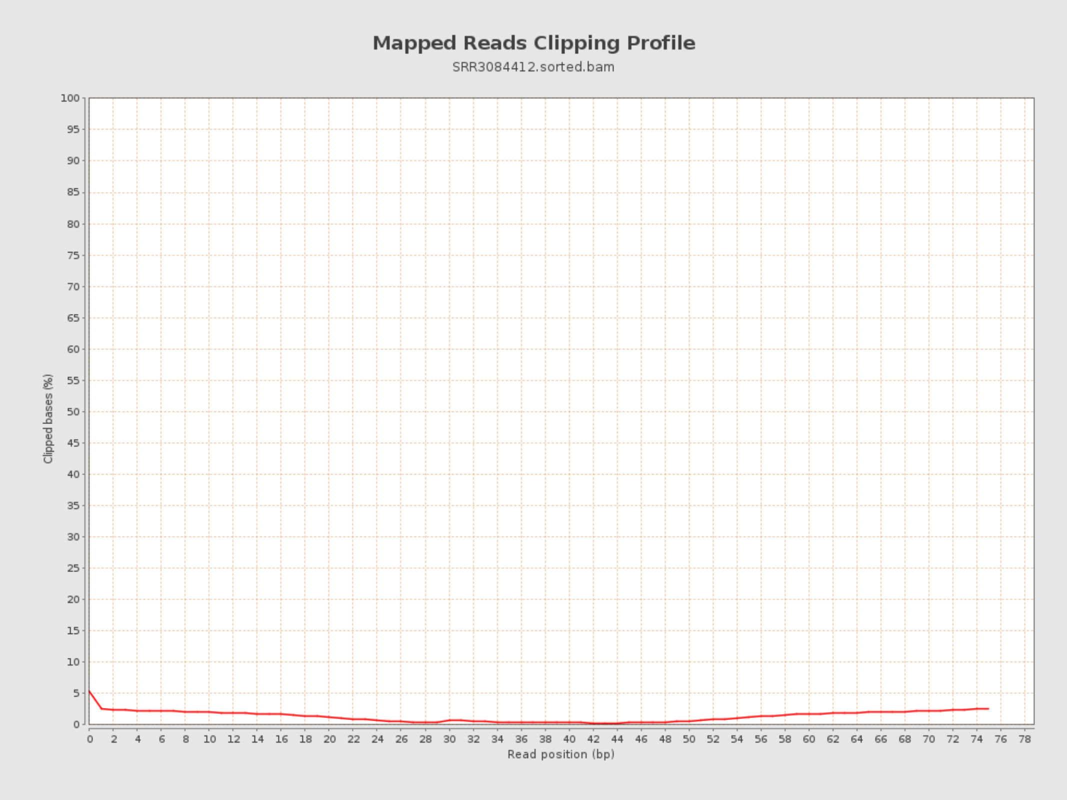
8. Results : Mapped Reads Nucleotide Content



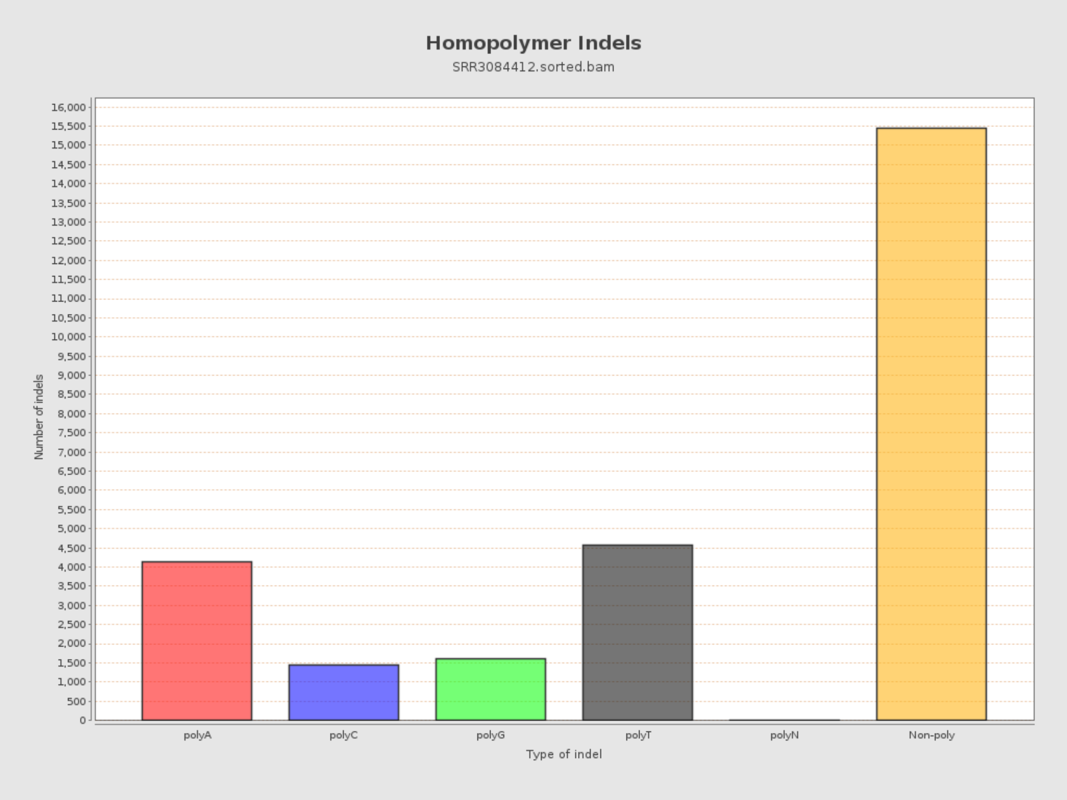
9. Results : Mapped Reads GC-content Distribution



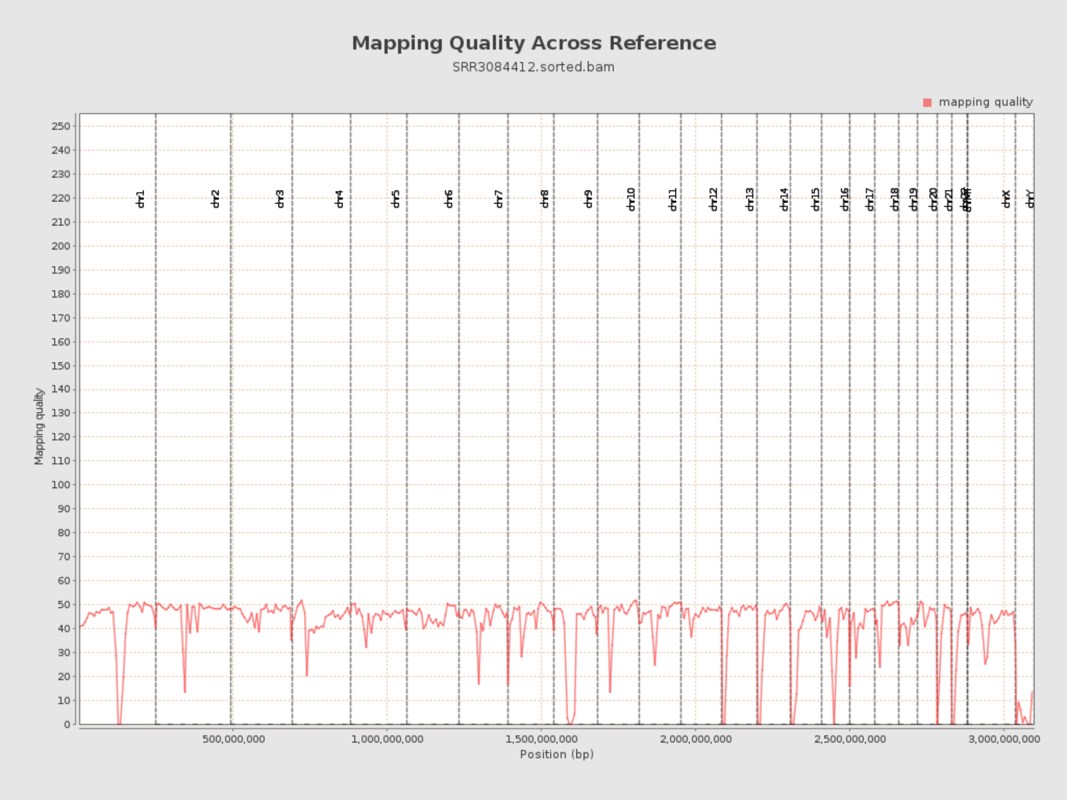
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram