Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 12:25:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084413.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_SRR3084413 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084413.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 12:25:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084413.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,590,819
Mapped reads	2,285,888 / 88.23%
Unmapped reads	304,931 / 11.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,086 / 1.05%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	67,435 / 2.6%
Duplication rate	1.9%
Clipped reads	1,097,640 / 42.37%

2.2. ACGT Content

Number/percentage of A's	42,011,404 / 27.61%
Number/percentage of C's	30,693,920 / 20.17%
Number/percentage of T's	43,902,523 / 28.85%
Number/percentage of G's	35,370,453 / 23.24%
Number/percentage of N's	196,102 / 0.13%
GC Percentage	43.41%

2.3. Coverage

Mean	0.0492

Standard Deviation	0.4752

2.4. Mapping Quality

Mean Mapping Quality	41.91

2.5. Mismatches and indels

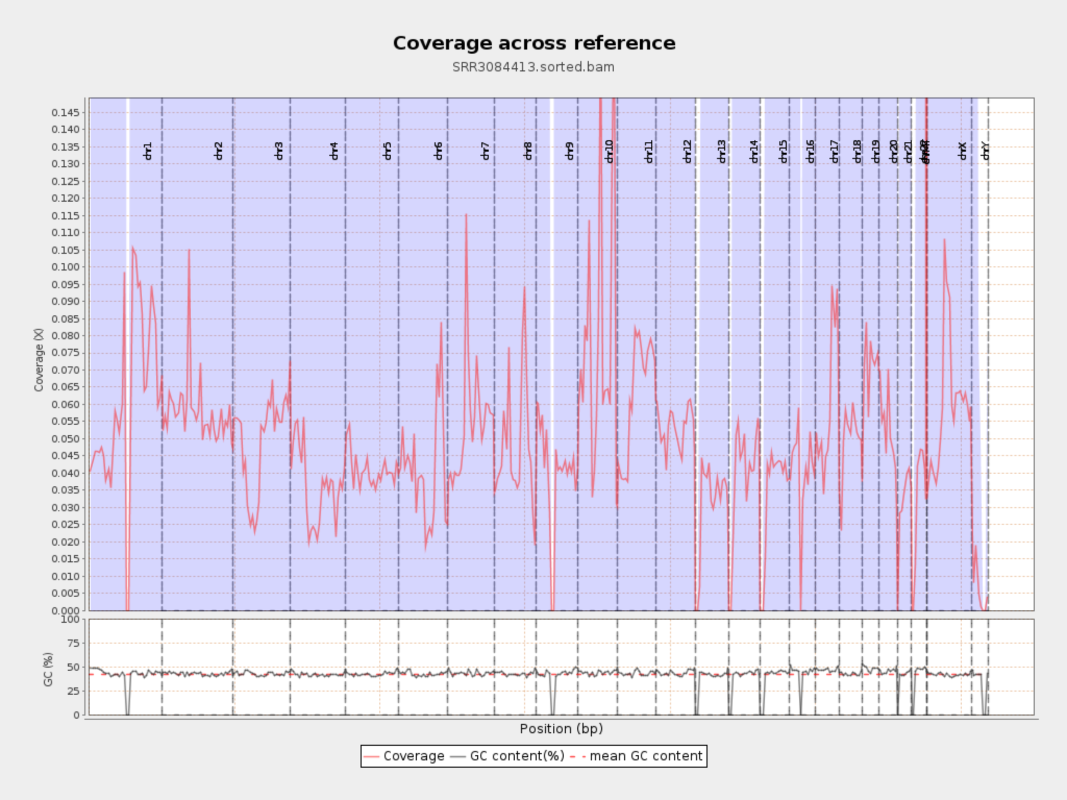
General error rate	1.04%
Mismatches	1,555,321
Insertions	12,761
Mapped reads with at least one insertion	0.55%
Deletions	28,557
Mapped reads with at least one deletion	1.23%
Homopolymer indels	42.54%

2.6. Chromosome stats

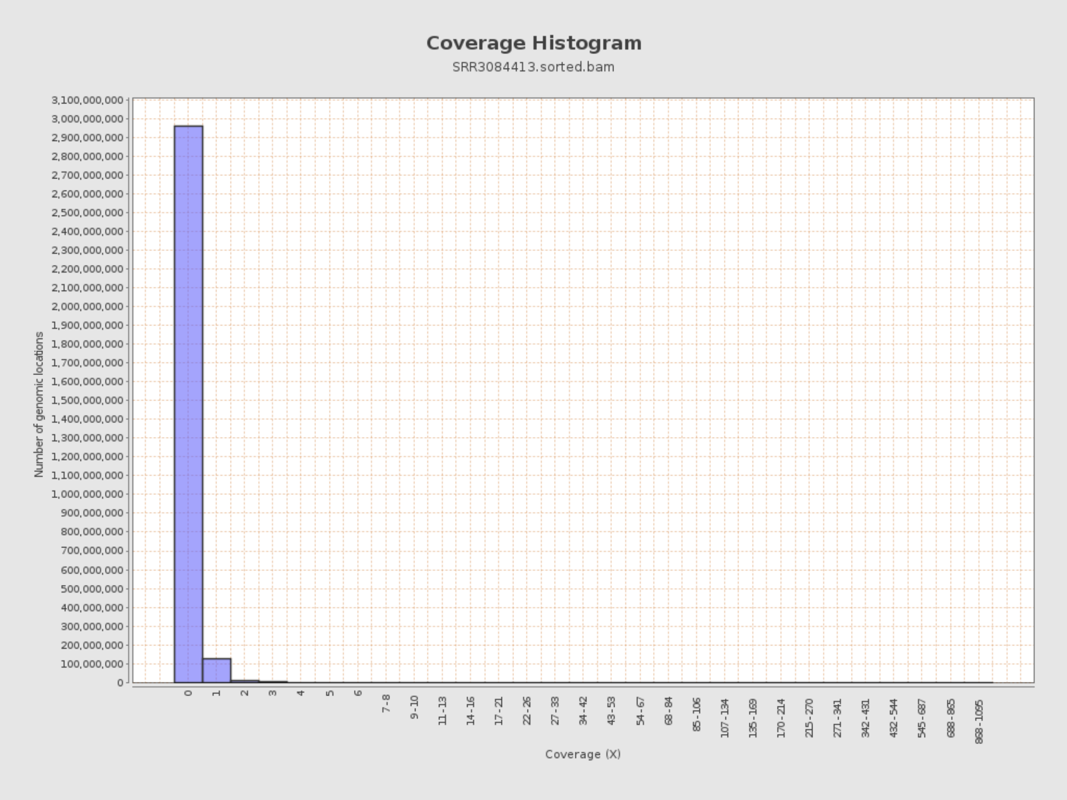
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15082133	0.0605	0.9749
chr2	243199373	14130699	0.0581	0.4784
chr3	198022430	9704402	0.049	0.2483
chr4	191154276	6905709	0.0361	0.2319
chr5	180915260	7407594	0.0409	0.2192
chr6	171115067	7047188	0.0412	0.2627
chr7	159138663	8771310	0.0551	0.8539

chr8	146364022	7017607	0.0479	0.3533
chr9	141213431	5583068	0.0395	0.3563
chr10	135534747	11047398	0.0815	0.649
chr11	135006516	8458072	0.0626	0.4087
chr12	133851895	7123341	0.0532	0.2519
chr13	115169878	3545574	0.0308	0.1878
chr14	107349540	4160711	0.0388	0.2392
chr15	102531392	3488598	0.034	0.2183
chr16	90354753	3666400	0.0406	0.2724
chr17	81195210	4916307	0.0605	0.2995
chr18	78077248	3888005	0.0498	0.7018
chr19	59128983	4198039	0.071	0.6973
chr20	63025520	3329333	0.0528	0.2555
chr21	48129895	1516069	0.0315	0.2176
chr22	51304566	1537036	0.03	0.1849
chrMT	16571	88849	5.3617	4.0597
chrX	155270560	9228539	0.0594	0.3218
chrY	59373566	382160	0.0064	0.1494

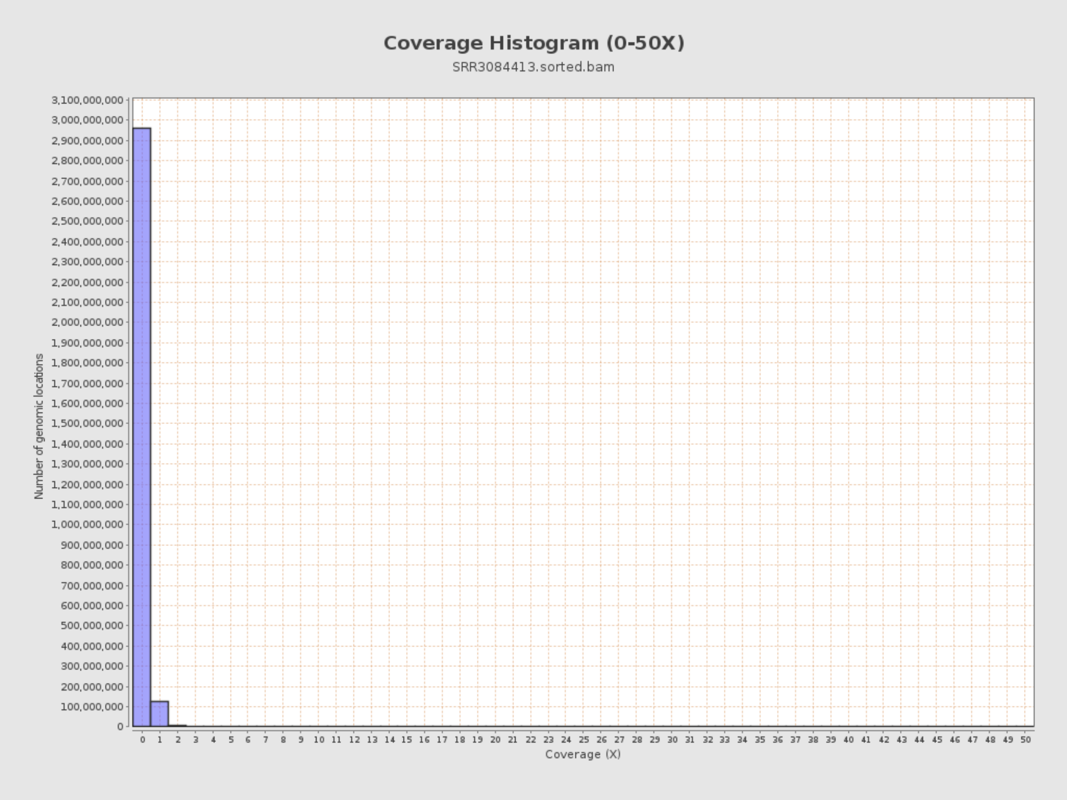
3. Results : Coverage across reference



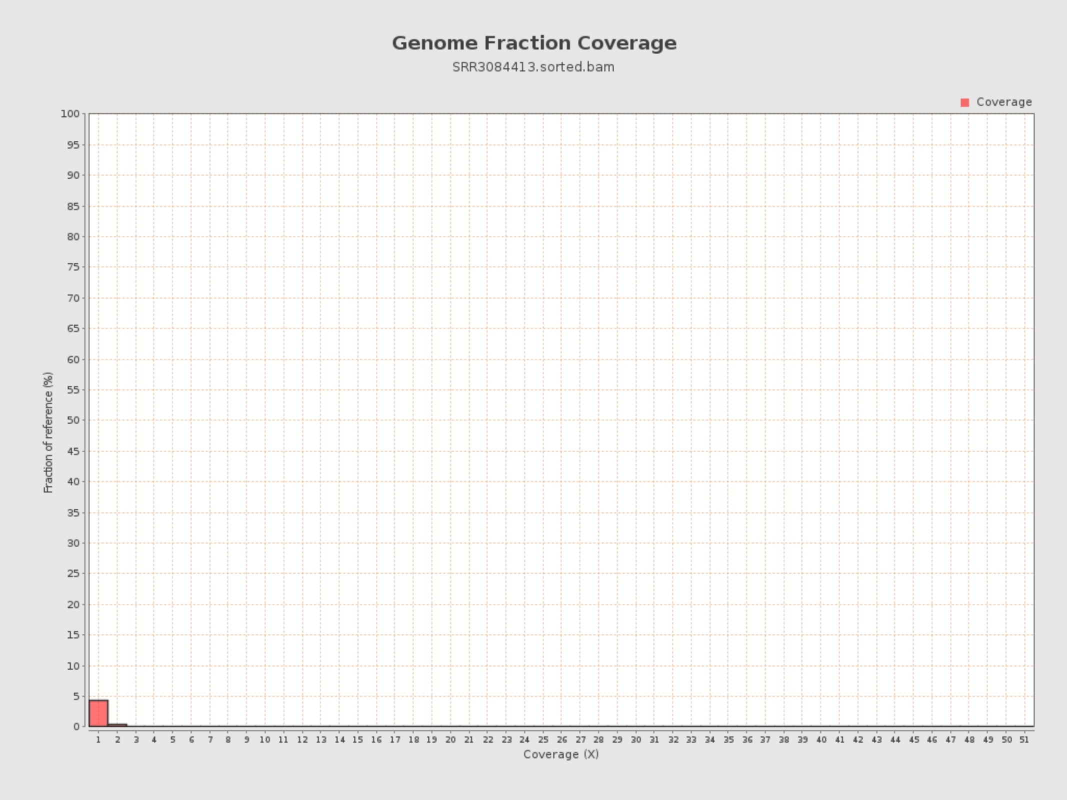
4. Results : Coverage Histogram



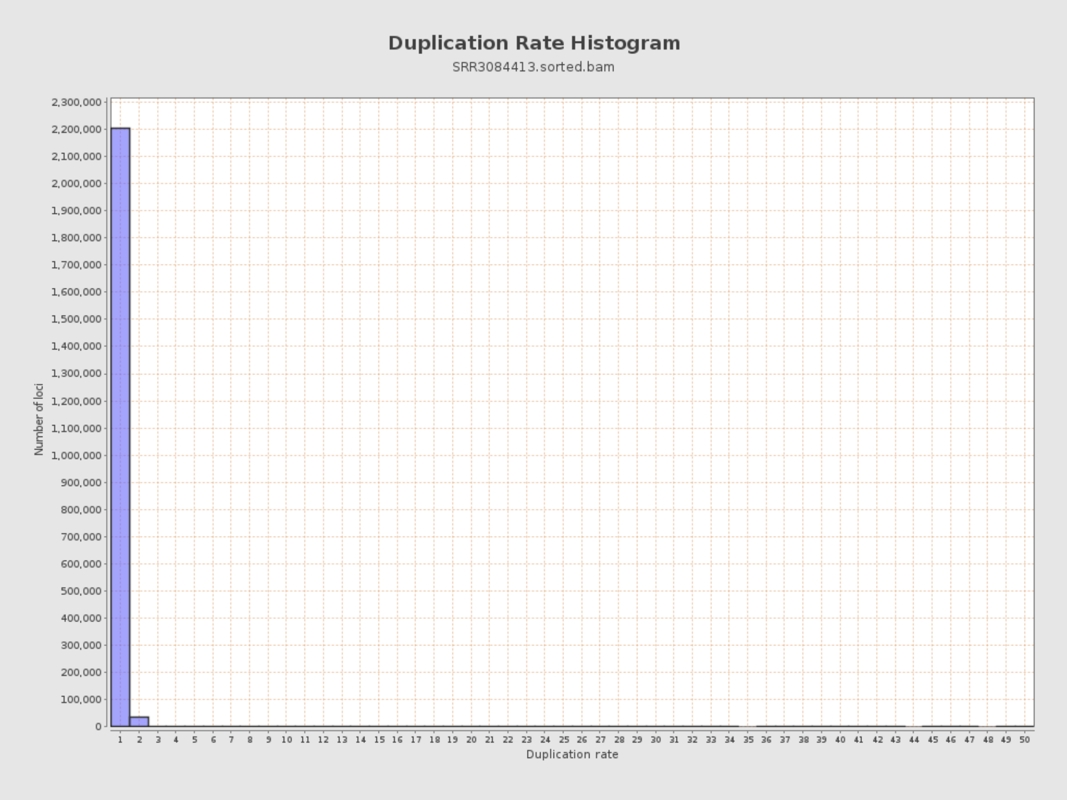
5. Results : Coverage Histogram (0-50X)



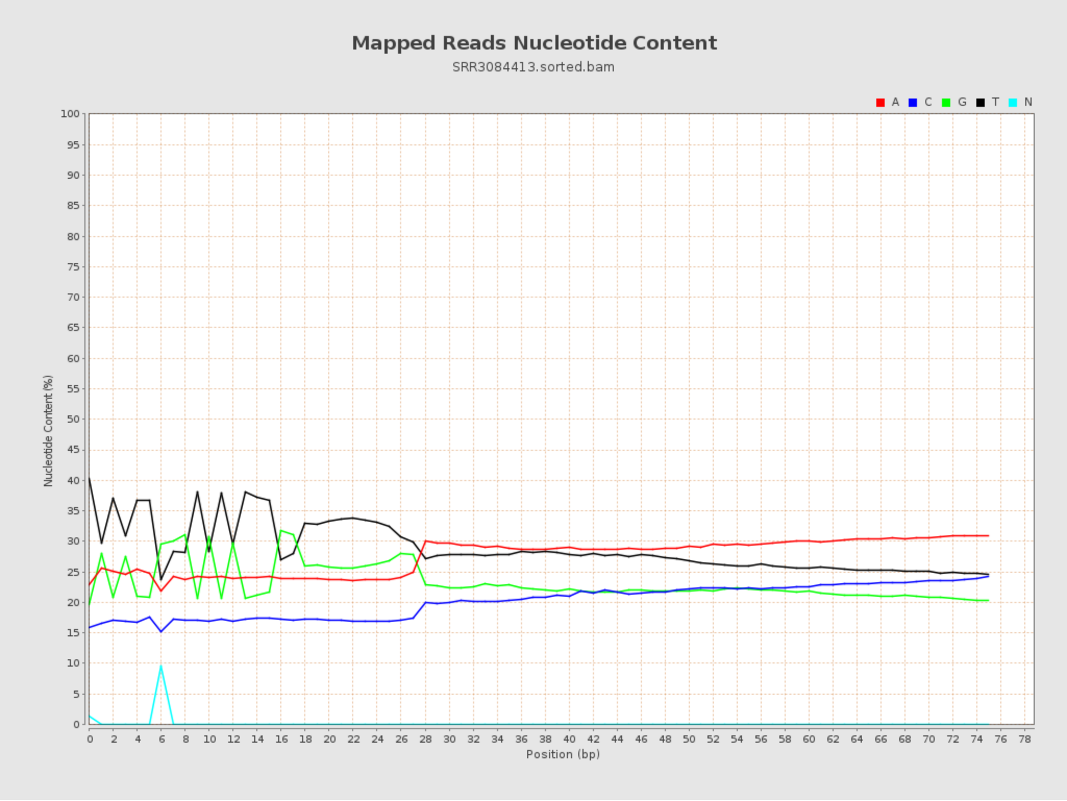
6. Results : Genome Fraction Coverage



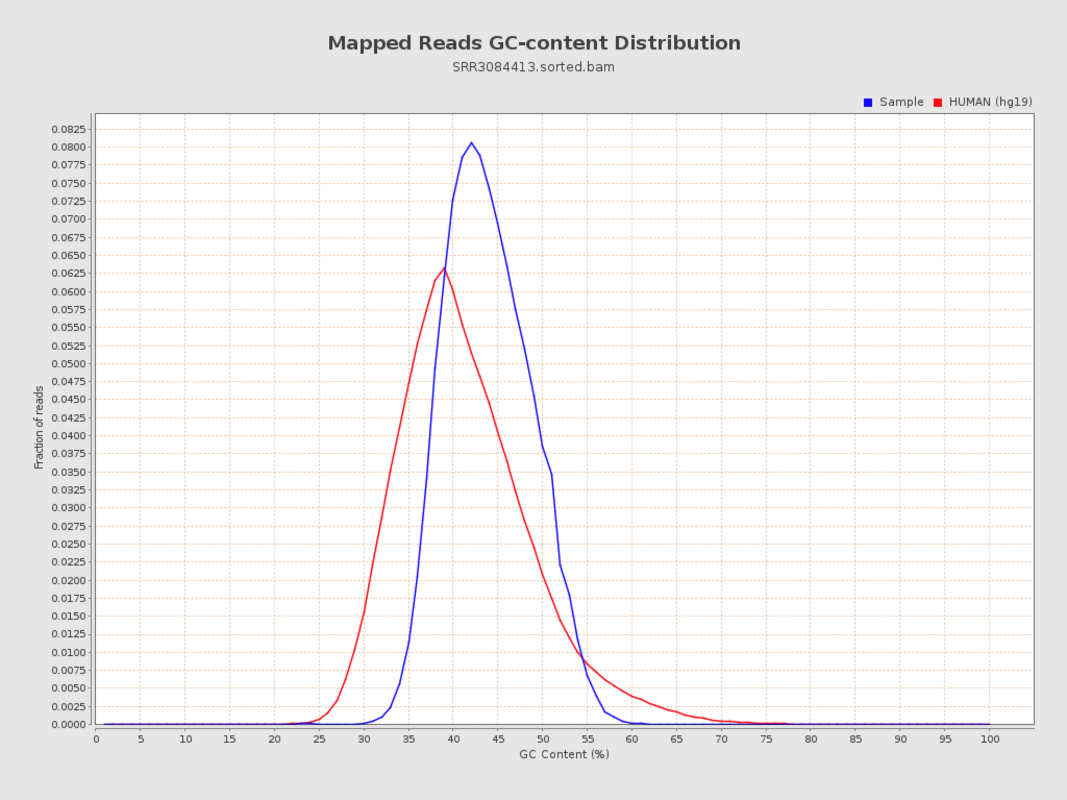
7. Results : Duplication Rate Histogram



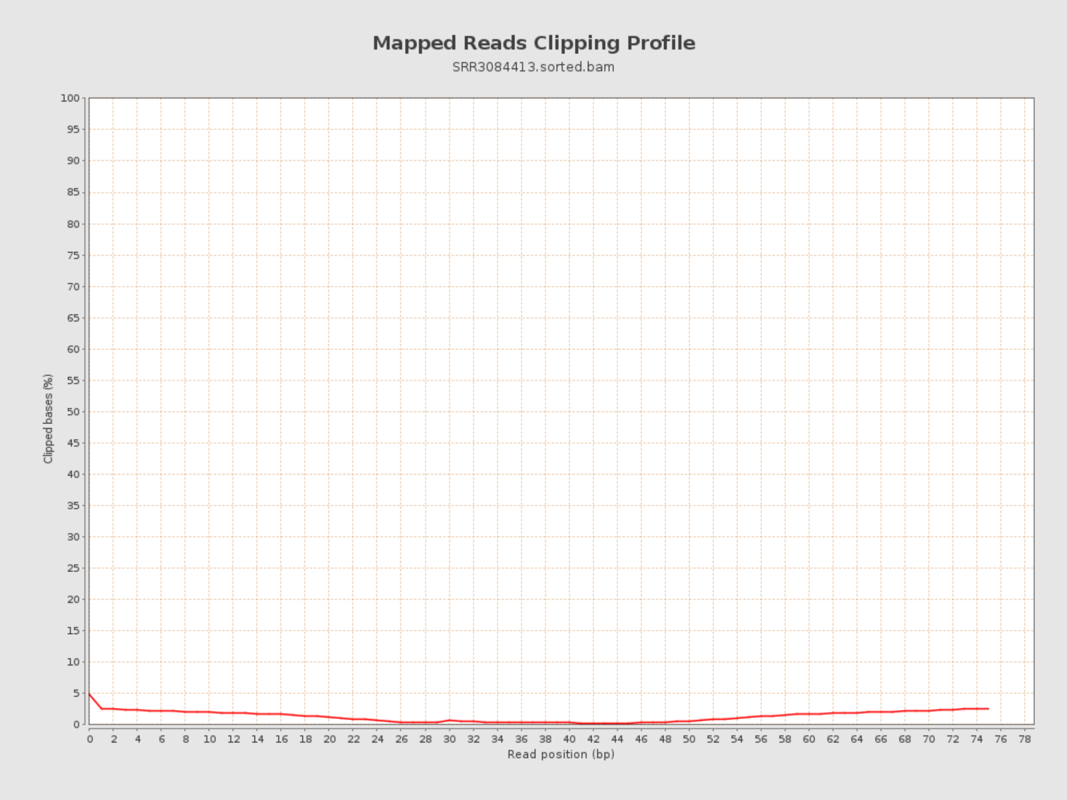
8. Results : Mapped Reads Nucleotide Content



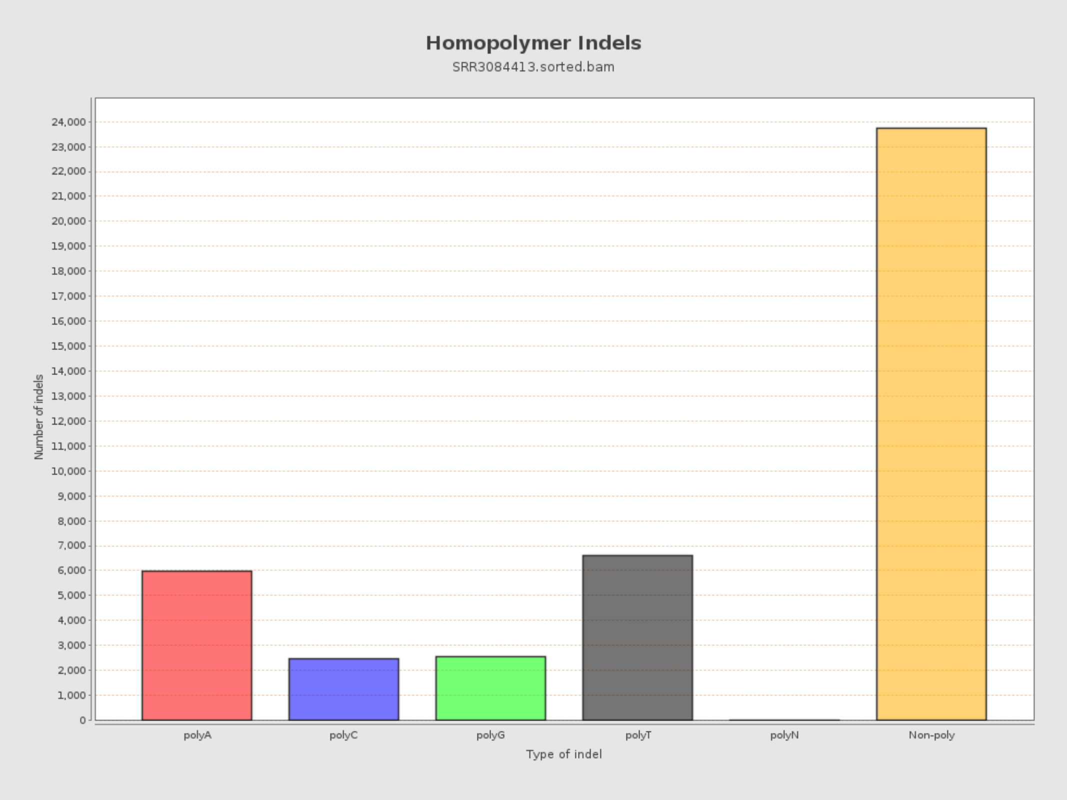
9. Results : Mapped Reads GC-content Distribution



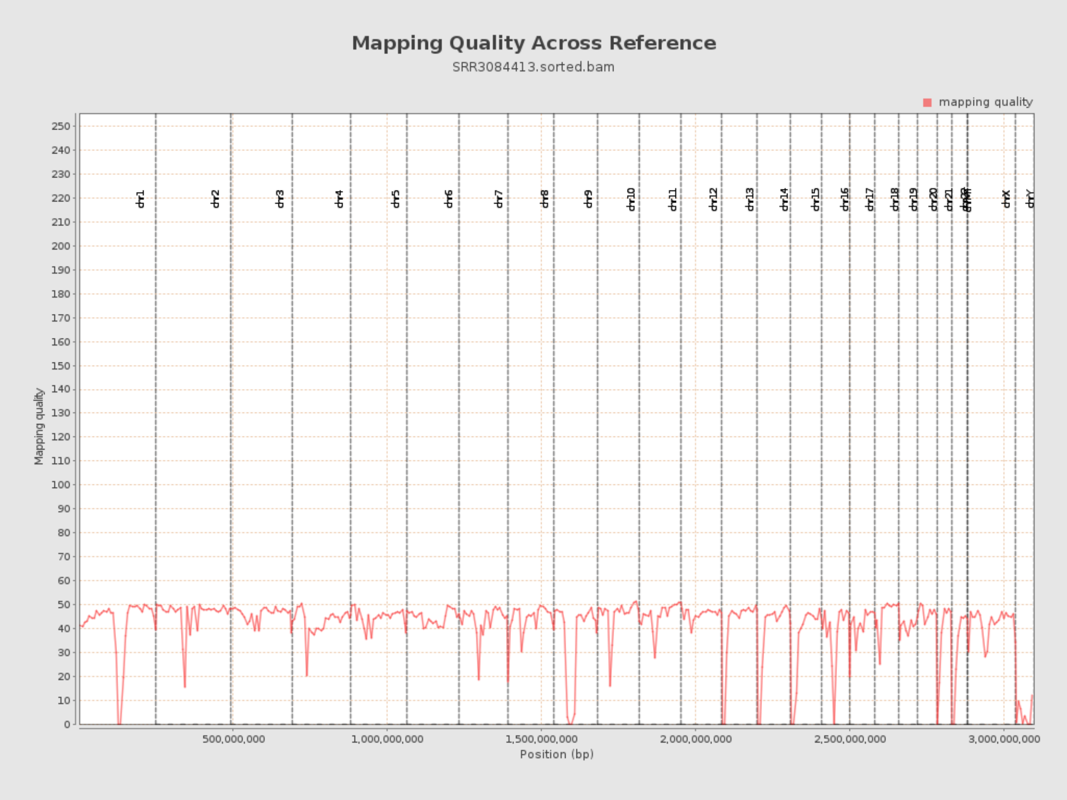
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram