Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 10:44:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867848.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_SRR9867848 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867848.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 10:44:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867848.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,561,264
Mapped reads	1,441,302 / 92.32%
Unmapped reads	119,962 / 7.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,195 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	59,308 / 3.8%
Duplication rate	3.06%
Clipped reads	1,444,343 / 92.51%

2.2. ACGT Content

Number/percentage of A's	21,316,487 / 25.07%
Number/percentage of C's	16,681,931 / 19.62%
Number/percentage of T's	26,513,758 / 31.18%
Number/percentage of G's	20,516,397 / 24.13%
Number/percentage of N's	11,640 / 0.01%
GC Percentage	43.74%

2.3. Coverage

Mean	0.0275

Standard Deviation	0.2666

2.4. Mapping Quality

Mean Mapping Quality	45.9

2.5. Mismatches and indels

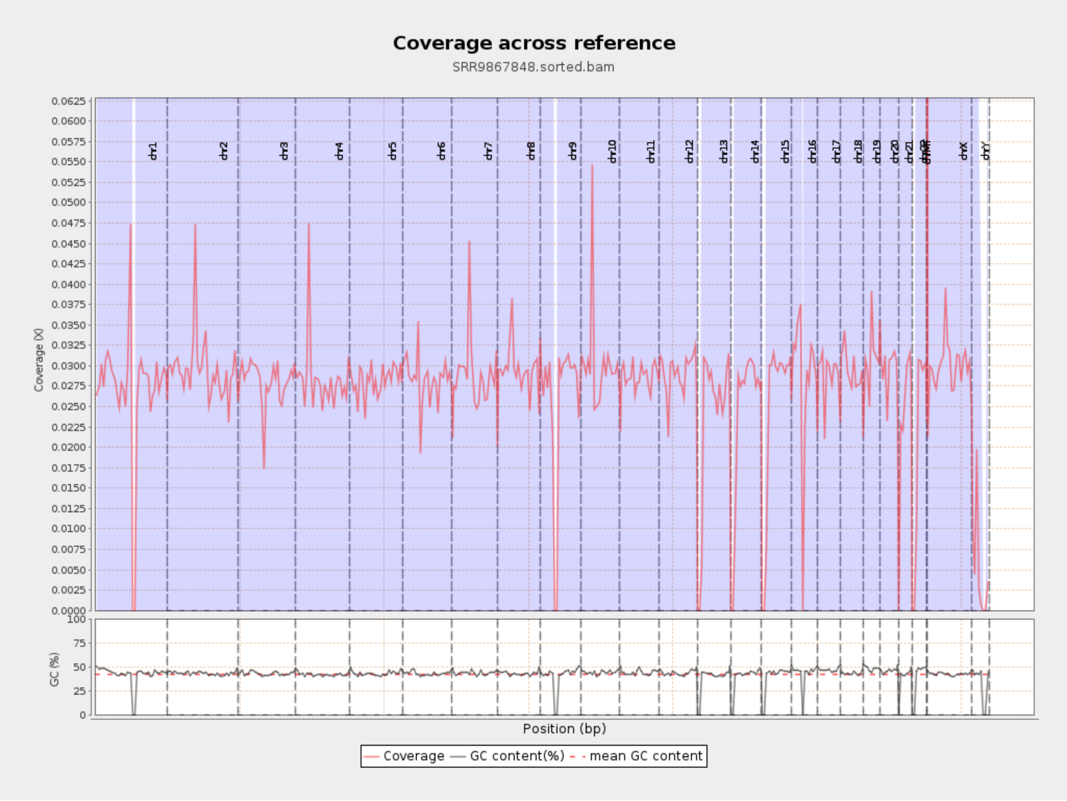
General error rate	0.51%
Mismatches	425,839
Insertions	5,797
Mapped reads with at least one insertion	0.4%
Deletions	15,978
Mapped reads with at least one deletion	1.1%
Homopolymer indels	44.16%

2.6. Chromosome stats

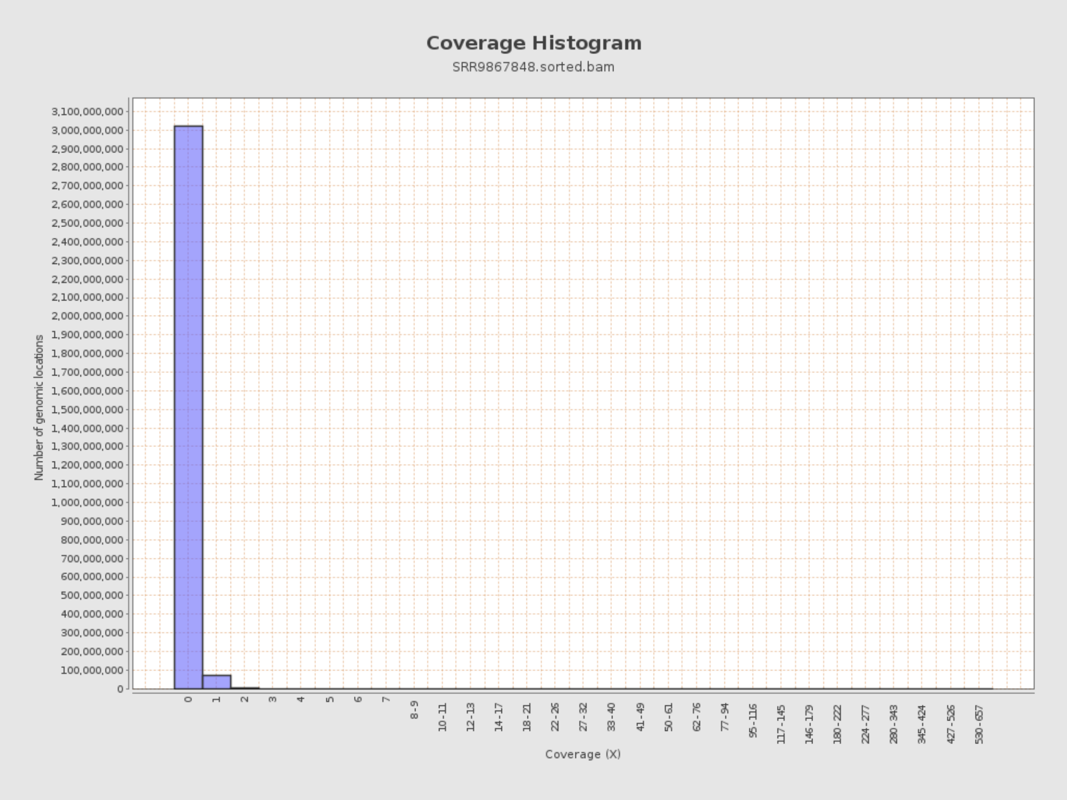
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6742223	0.027	0.4678
chr2	243199373	7203054	0.0296	0.3529
chr3	198022430	5557631	0.0281	0.18
chr4	191154276	5420200	0.0284	0.2066
chr5	180915260	5101013	0.0282	0.1823
chr6	171115067	4840050	0.0283	0.2055
chr7	159138663	4600630	0.0289	0.2999

chr8	146364022	4331484	0.0296	0.2927
chr9	141213431	3615738	0.0256	0.2262
chr10	135534747	4117702	0.0304	0.2807
chr11	135006516	3872517	0.0287	0.2324
chr12	133851895	3897029	0.0291	0.1878
chr13	115169878	2681853	0.0233	0.1673
chr14	107349540	2558290	0.0238	0.1703
chr15	102531392	2479061	0.0242	0.1688
chr16	90354753	2531370	0.028	0.1934
chr17	81195210	2338936	0.0288	0.1951
chr18	78077248	2307494	0.0296	0.4081
chr19	59128983	1823292	0.0308	0.3645
chr20	63025520	1851677	0.0294	0.1883
chr21	48129895	1167778	0.0243	0.196
chr22	51304566	1057341	0.0206	0.155
chrMT	16571	21420	1.2926	1.3163
chrX	155270560	4652644	0.03	0.2024
chrY	59373566	295124	0.005	0.1985

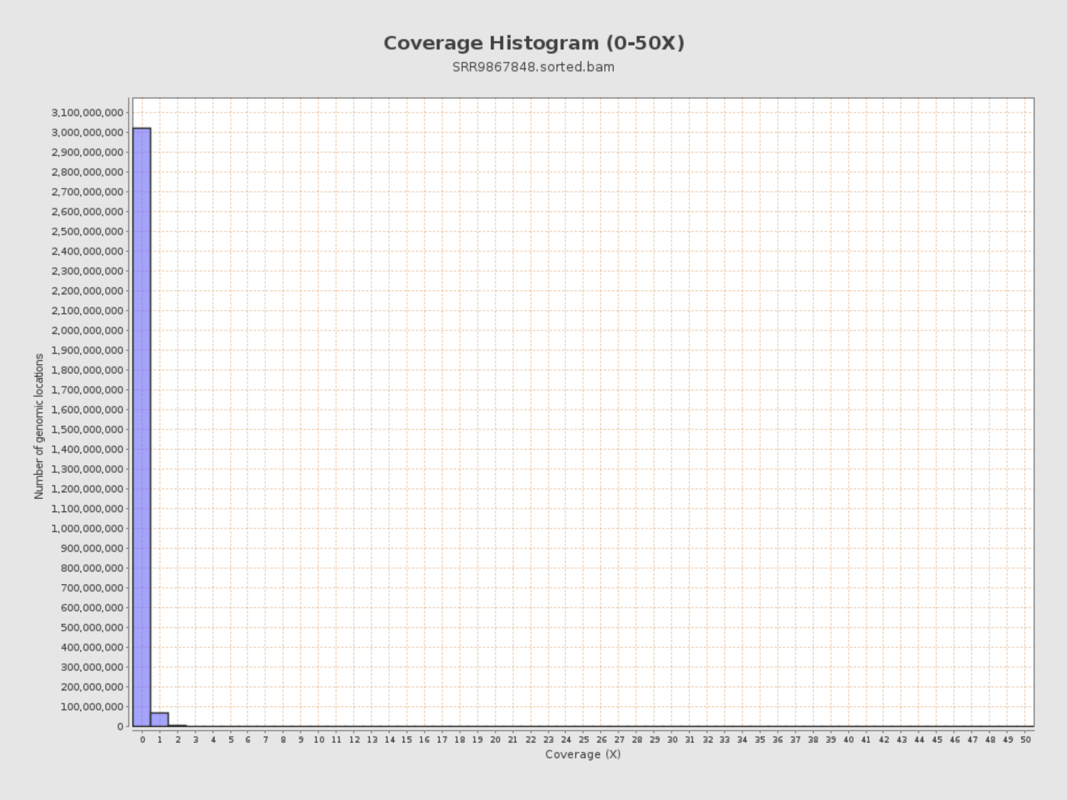
3. Results : Coverage across reference



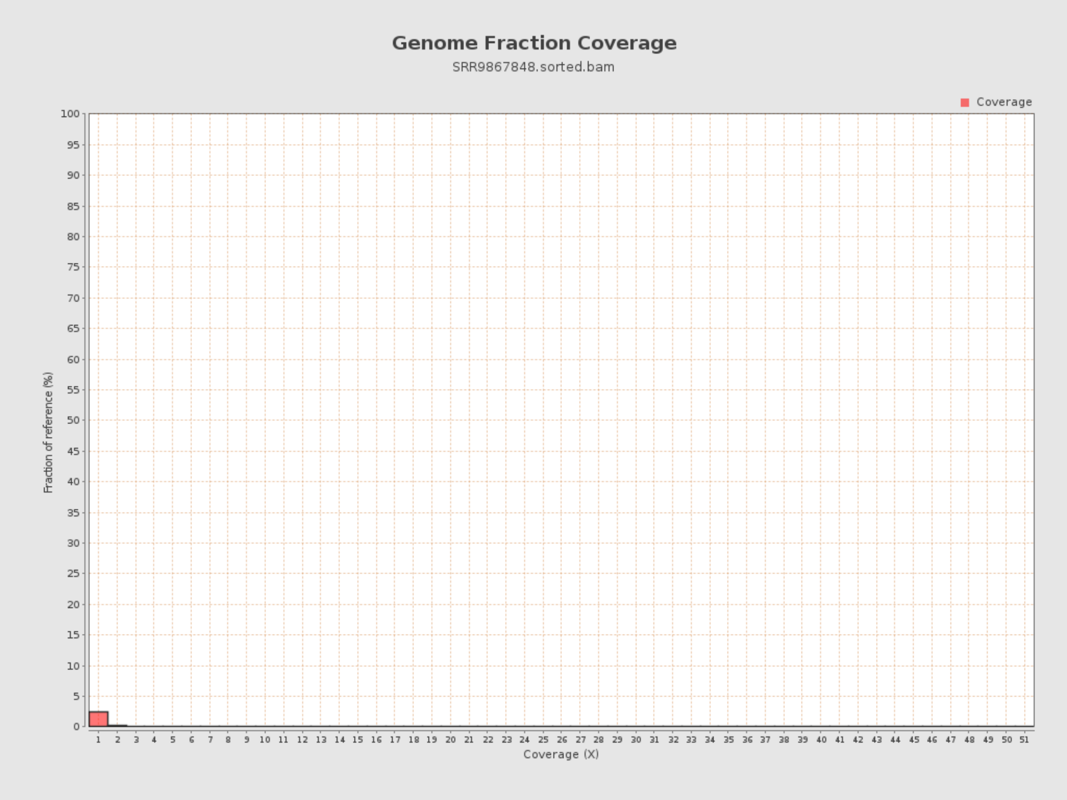
4. Results : Coverage Histogram



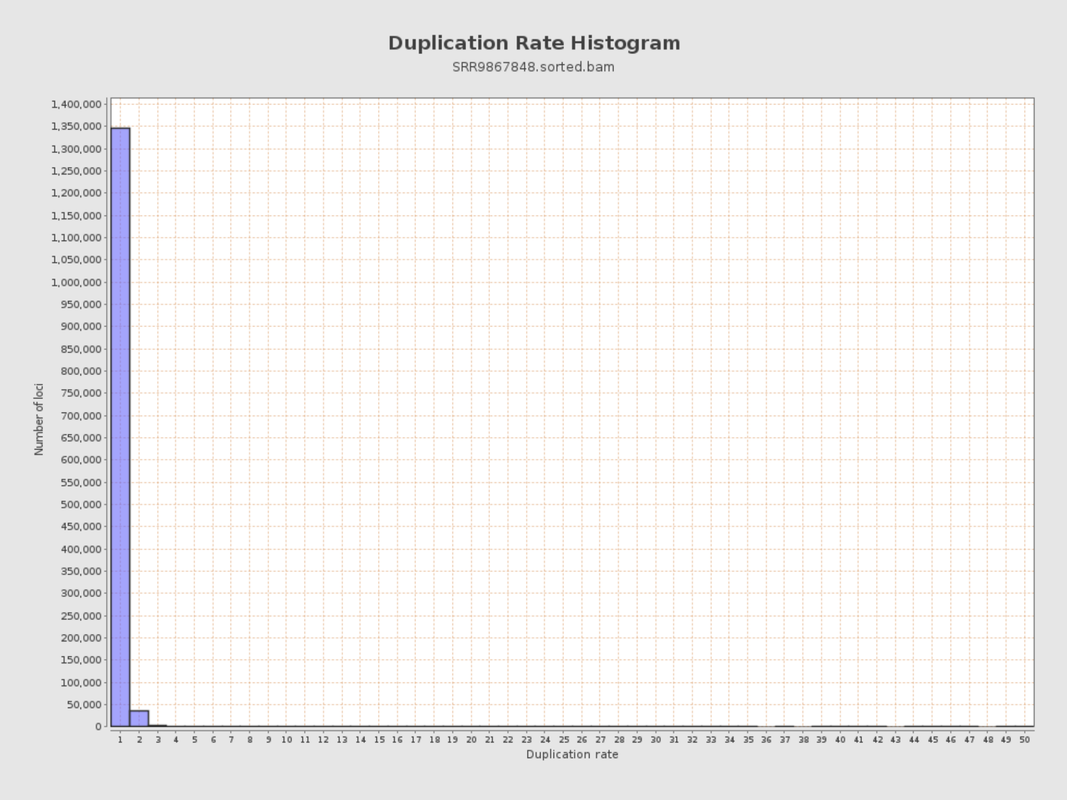
5. Results : Coverage Histogram (0-50X)



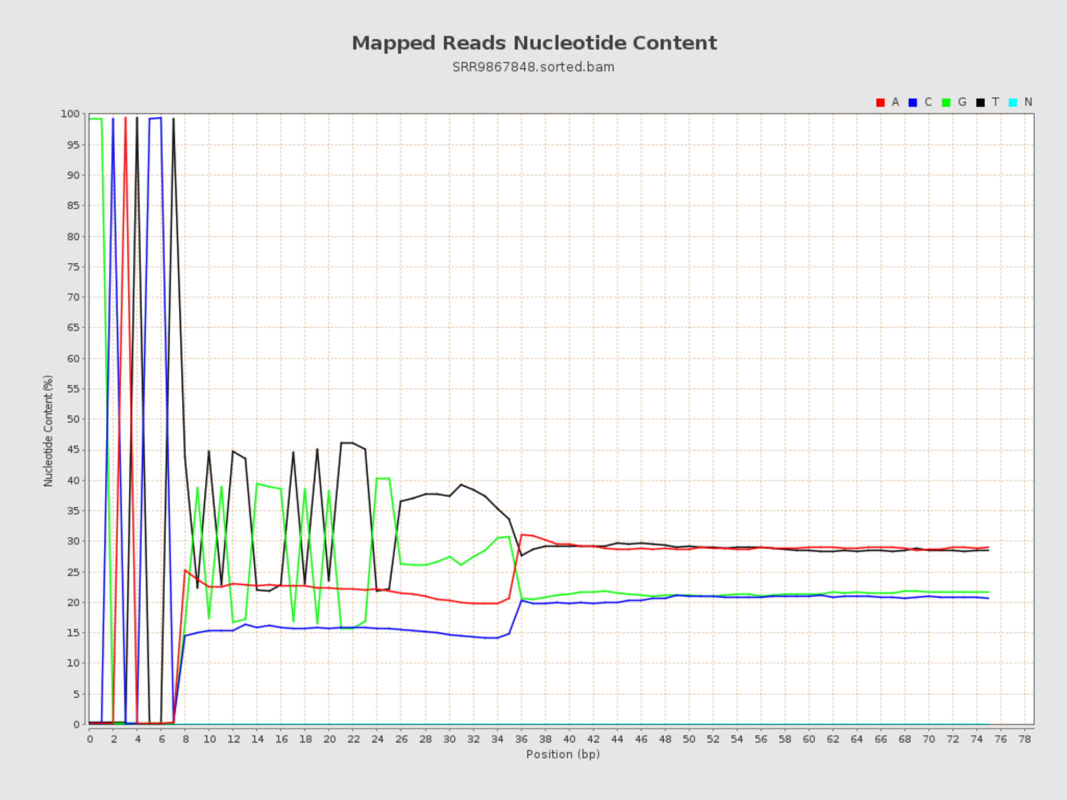
6. Results : Genome Fraction Coverage



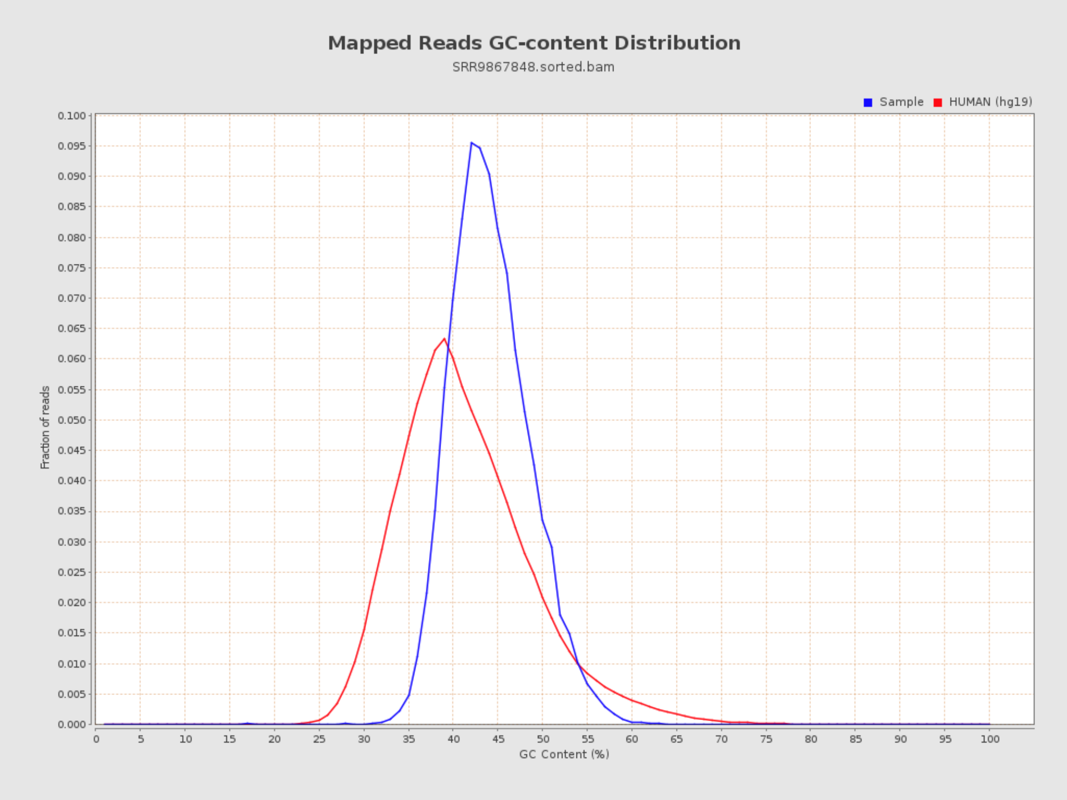
7. Results : Duplication Rate Histogram



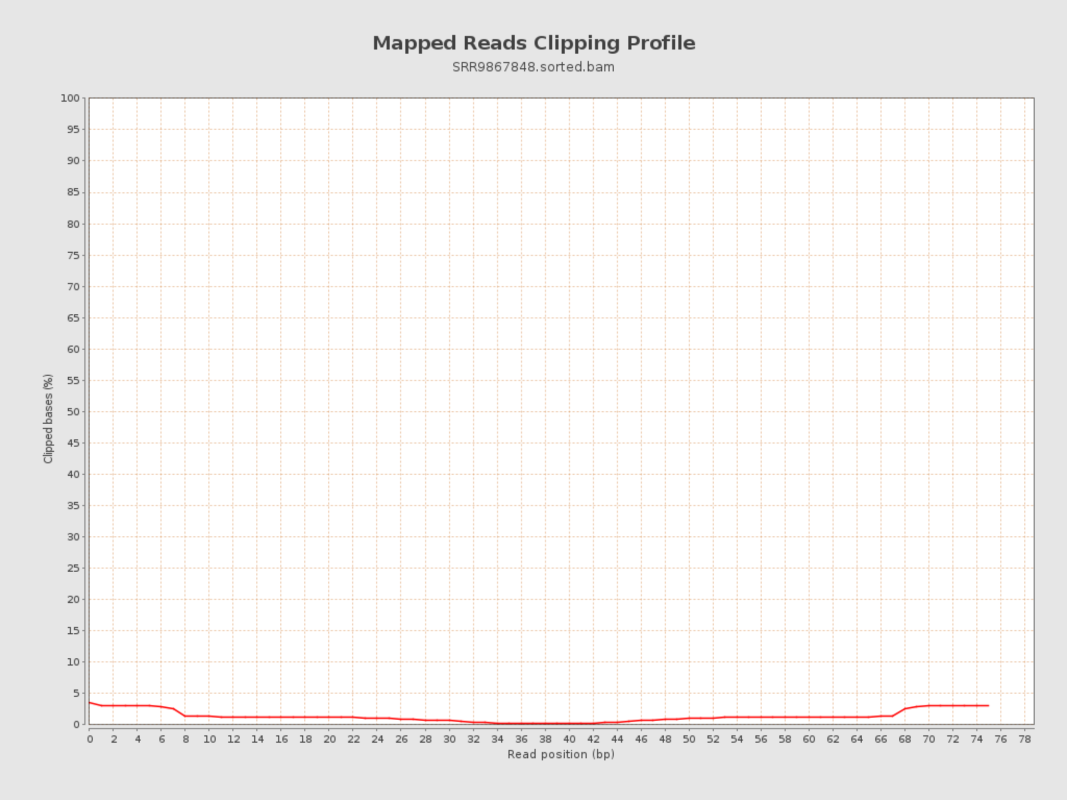
8. Results : Mapped Reads Nucleotide Content



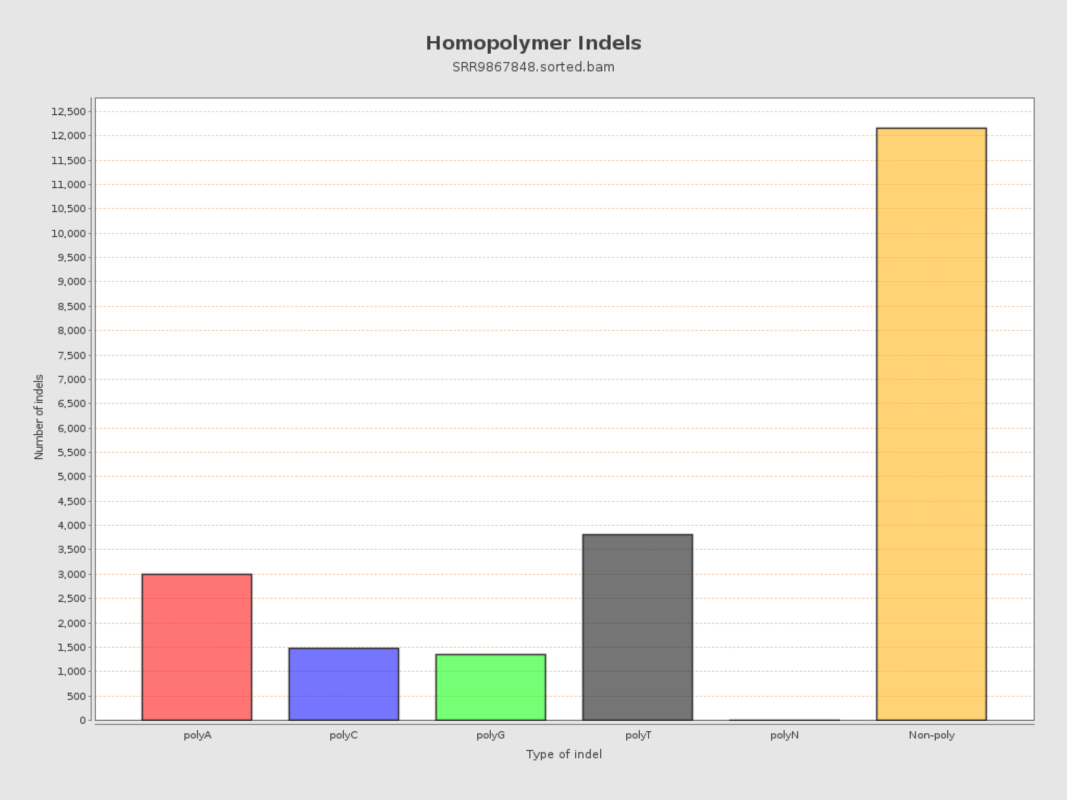
9. Results : Mapped Reads GC-content Distribution



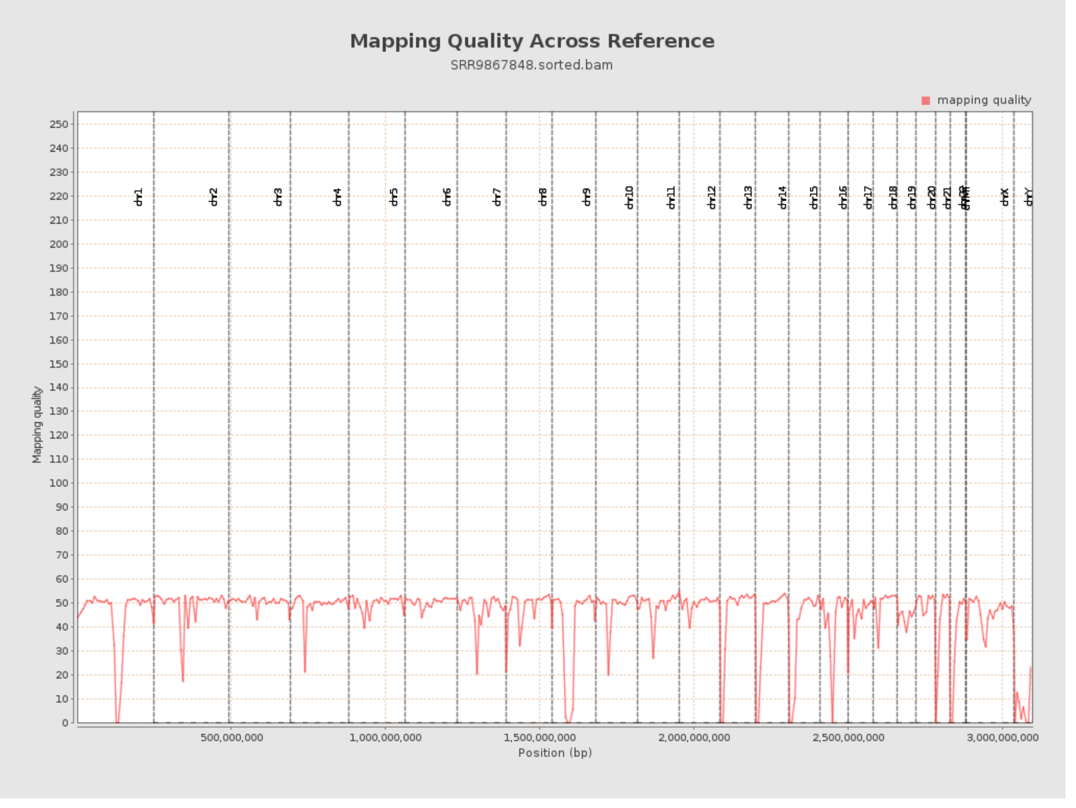
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram