Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 16:16:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751182.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_SRR8751182 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751182.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 16:16:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751182.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,238,140
Mapped reads	4,059,552 / 77.5%
Unmapped reads	1,178,588 / 22.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	220,874 / 4.22%
Read min/max/mean length	30 / 101 / 102.74
Duplicated reads (estimated)	145,526 / 2.78%
Duplication rate	1.69%
Clipped reads	963,881 / 18.4%

2.2. ACGT Content

Number/percentage of A's	117,547,966 / 29.47%
Number/percentage of C's	81,930,909 / 20.54%
Number/percentage of T's	118,455,325 / 29.69%
Number/percentage of G's	80,997,684 / 20.3%
Number/percentage of N's	2,886 / 0%
GC Percentage	40.84%

2.3. Coverage

Mean	0.1289

Standard Deviation	1.7175

2.4. Mapping Quality

Mean Mapping Quality	51.02

2.5. Mismatches and indels

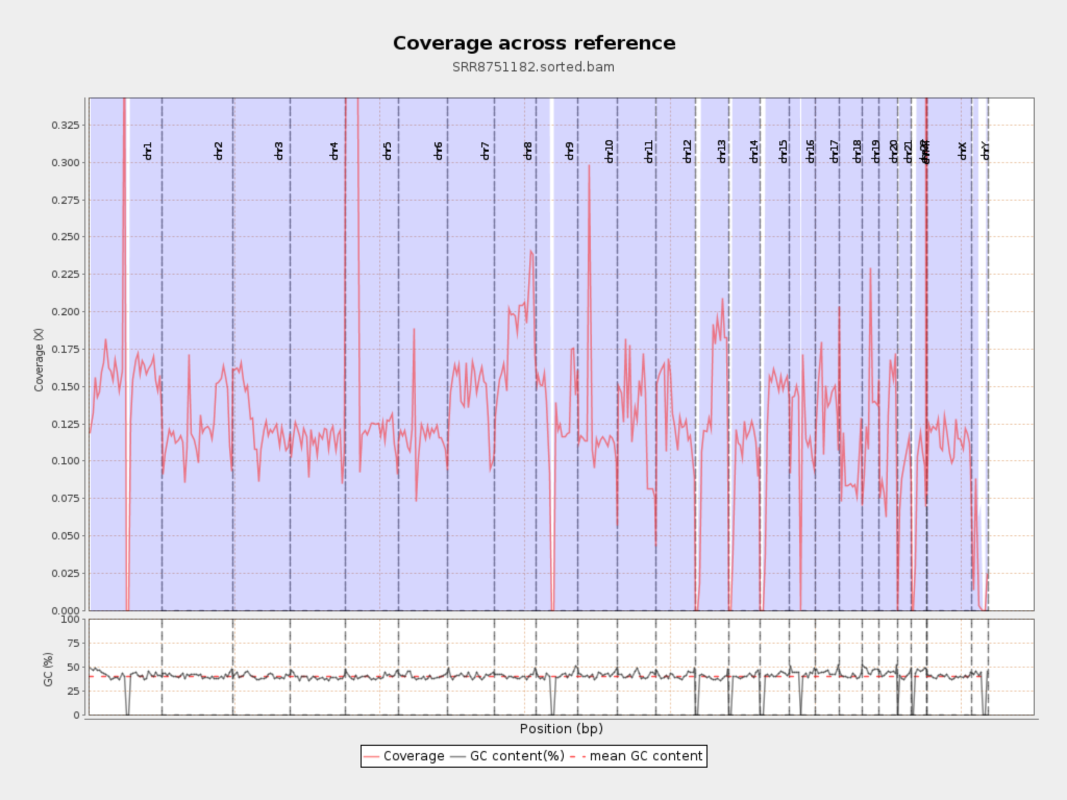
General error rate	0.47%
Mismatches	1,563,558
Insertions	234,279
Mapped reads with at least one insertion	5.56%
Deletions	61,167
Mapped reads with at least one deletion	1.47%
Homopolymer indels	51.85%

2.6. Chromosome stats

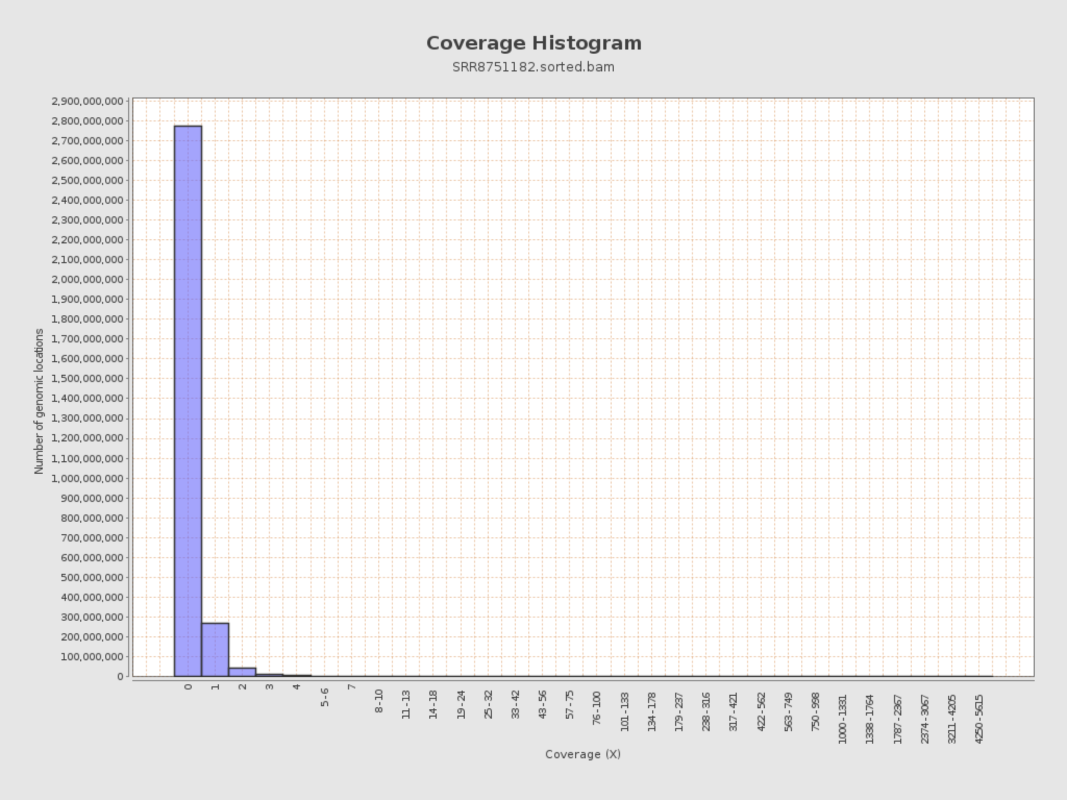
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	38541117	0.1546	5.1565
chr2	243199373	29918914	0.123	0.6479
chr3	198022430	25317752	0.1279	0.4582
chr4	191154276	21703655	0.1135	0.4373
chr5	180915260	34483753	0.1906	0.5387
chr6	171115067	20074458	0.1173	0.8369
chr7	159138663	23289689	0.1463	1.0139

chr8	146364022	27380922	0.1871	1.0186
chr9	141213431	17327582	0.1227	0.8153
chr10	135534747	16617565	0.1226	1.688
chr11	135006516	17392617	0.1288	0.6942
chr12	133851895	17675277	0.1321	0.4299
chr13	115169878	15205562	0.132	0.4194
chr14	107349540	10166120	0.0947	0.3909
chr15	102531392	12414136	0.1211	0.4025
chr16	90354753	10468796	0.1159	0.7033
chr17	81195210	11364295	0.14	0.7579
chr18	78077248	7461538	0.0956	1.8366
chr19	59128983	8014458	0.1355	3.5518
chr20	63025520	7360481	0.1168	0.4135
chr21	48129895	4109949	0.0854	0.3843
chr22	51304566	3660361	0.0713	0.3117
chrMT	16571	164042	9.8993	8.1813
chrX	155270560	17776518	0.1145	0.4744
chrY	59373566	1182962	0.0199	0.9129

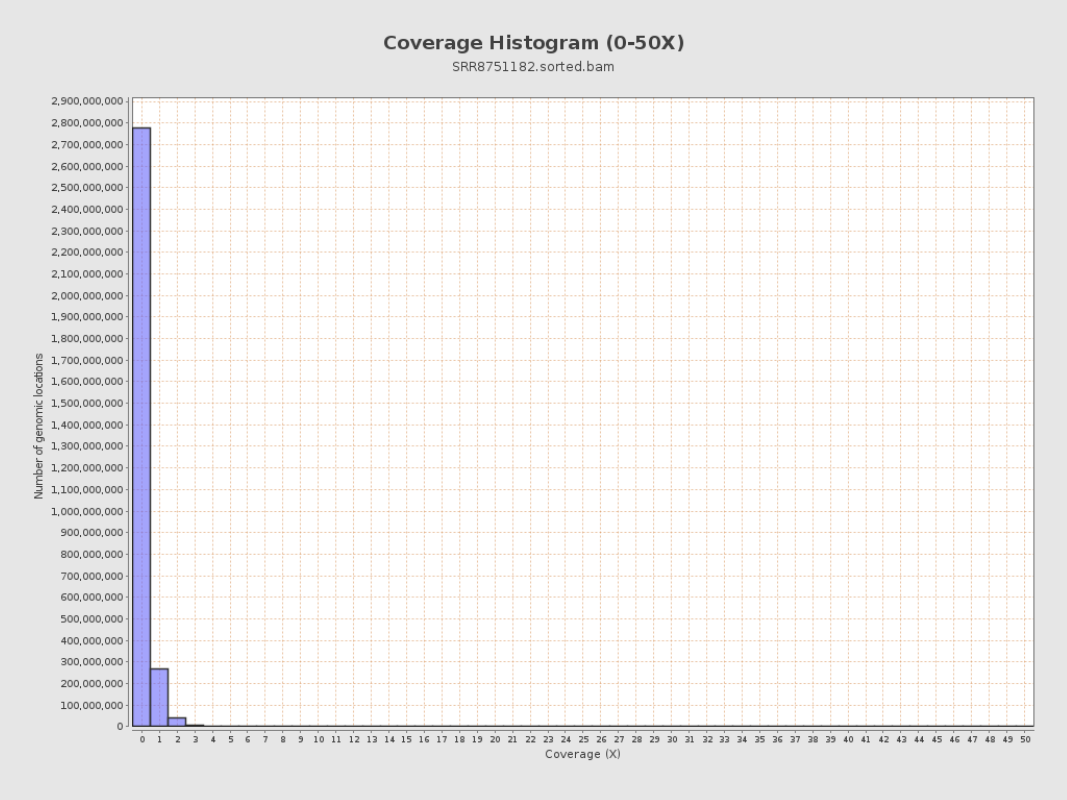
3. Results : Coverage across reference



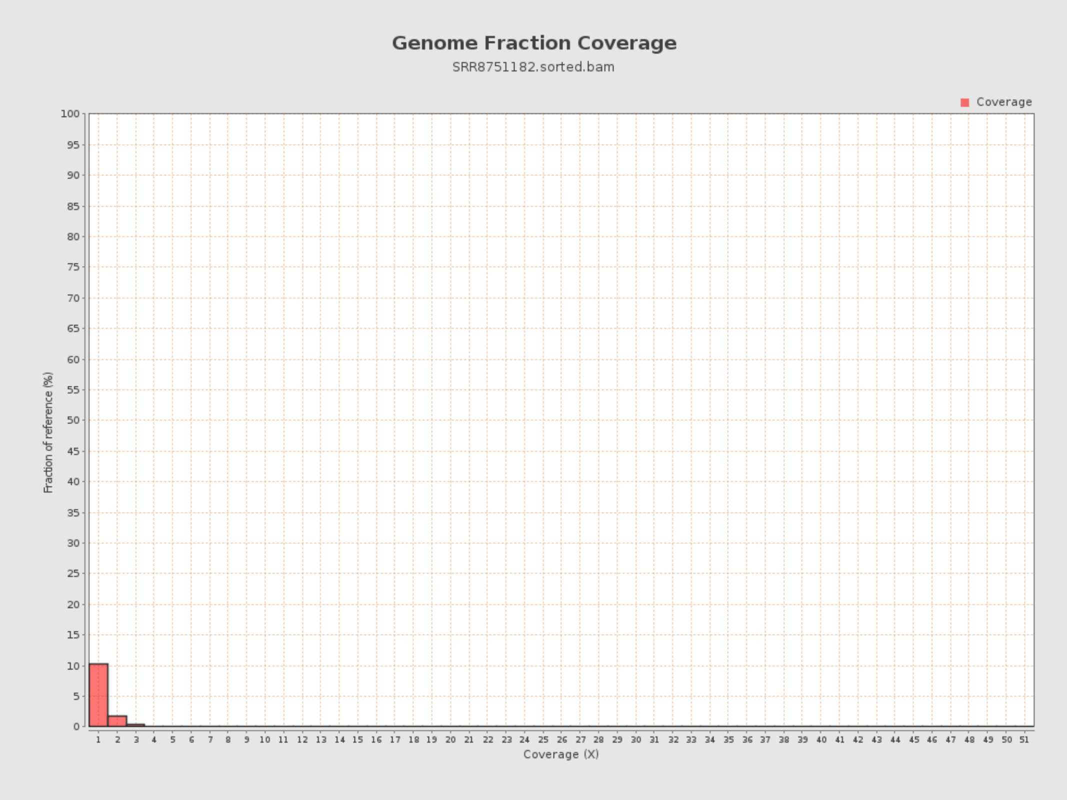
4. Results : Coverage Histogram



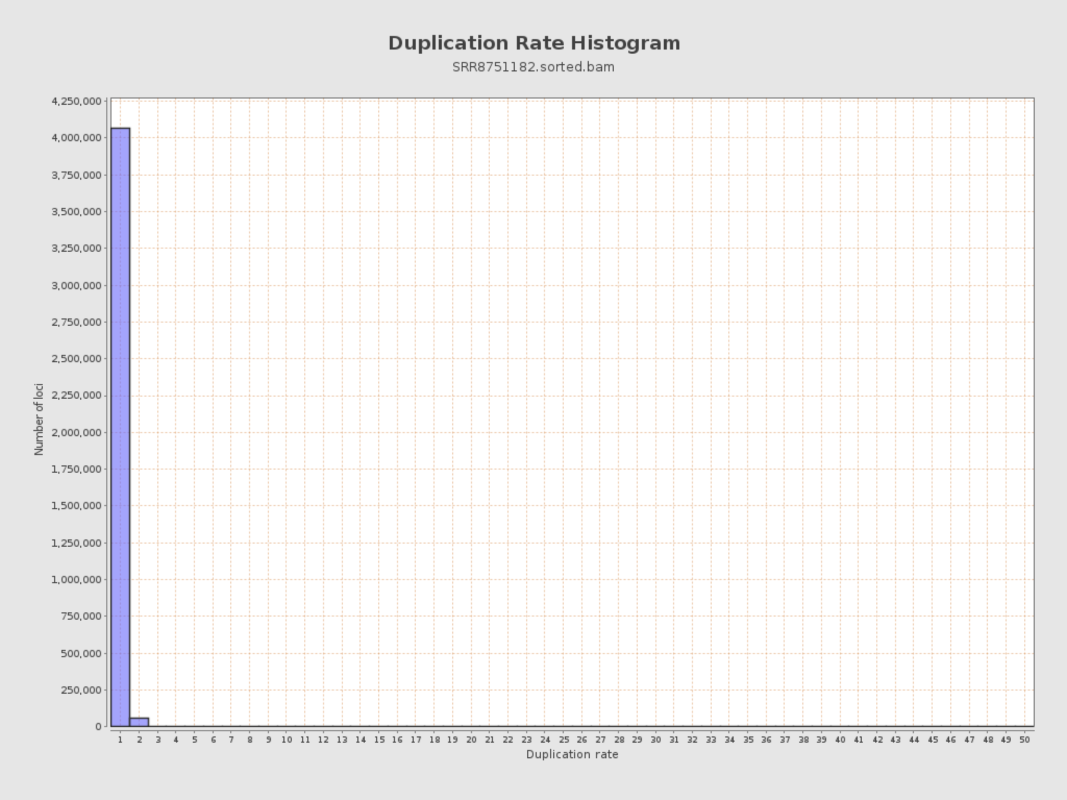
5. Results : Coverage Histogram (0-50X)



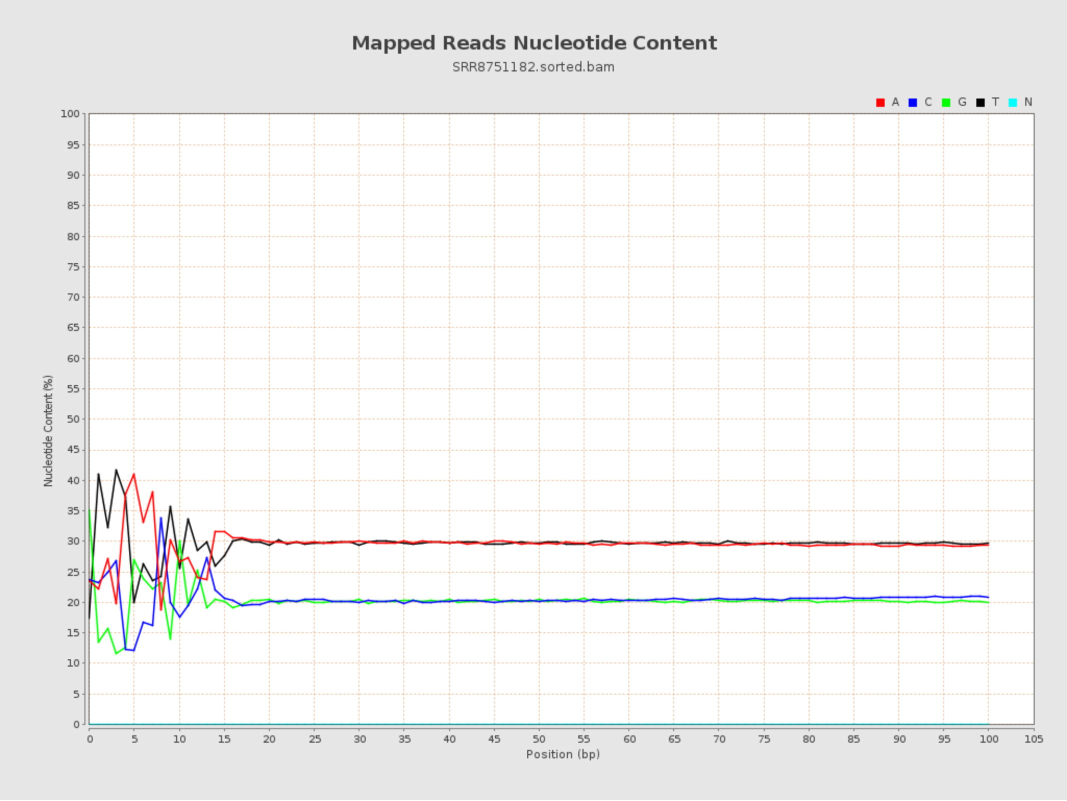
6. Results : Genome Fraction Coverage



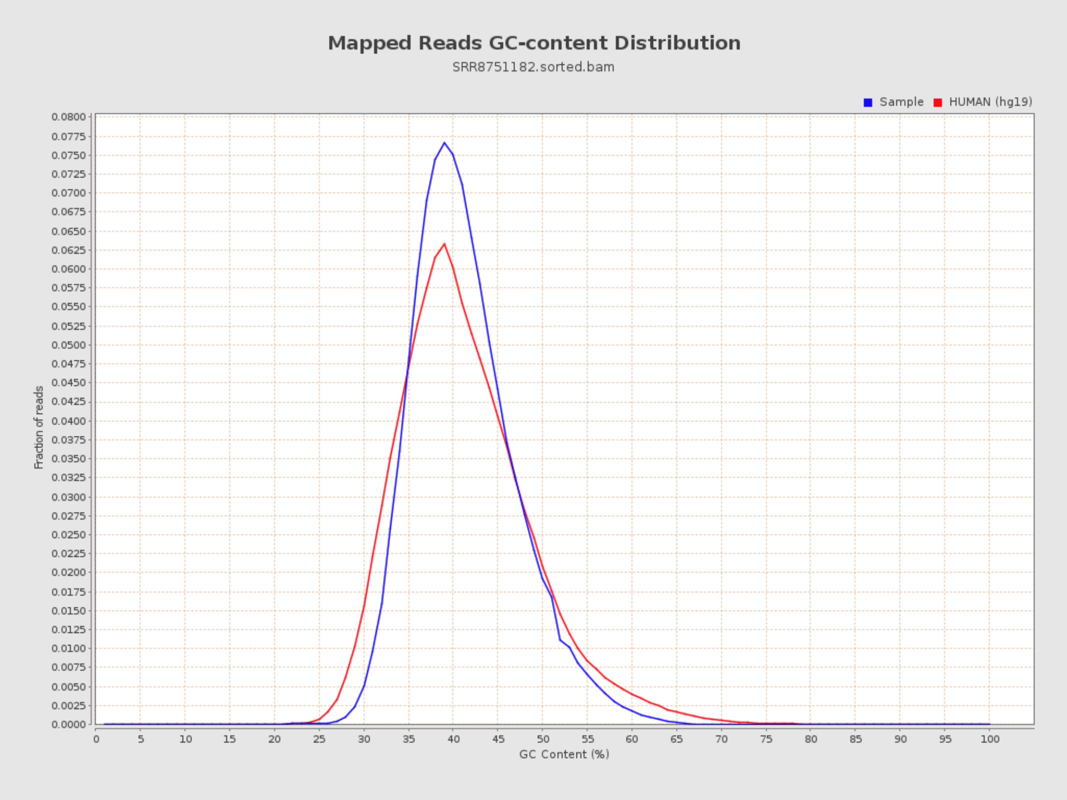
7. Results : Duplication Rate Histogram



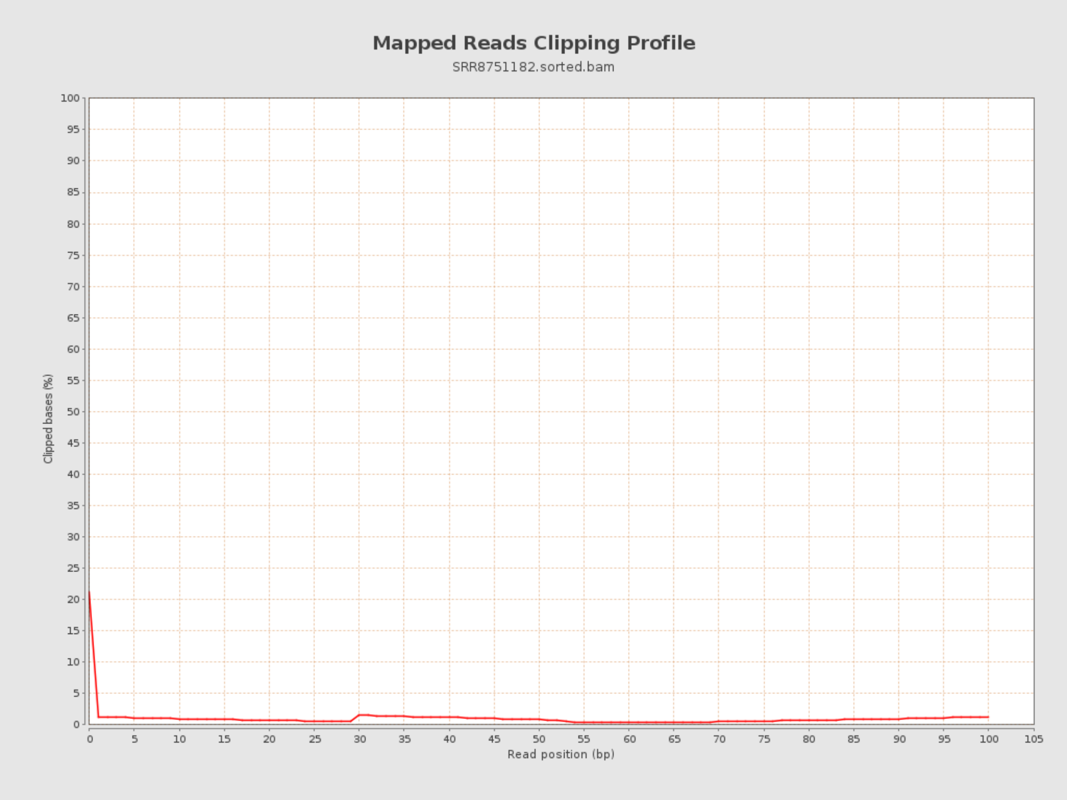
8. Results : Mapped Reads Nucleotide Content



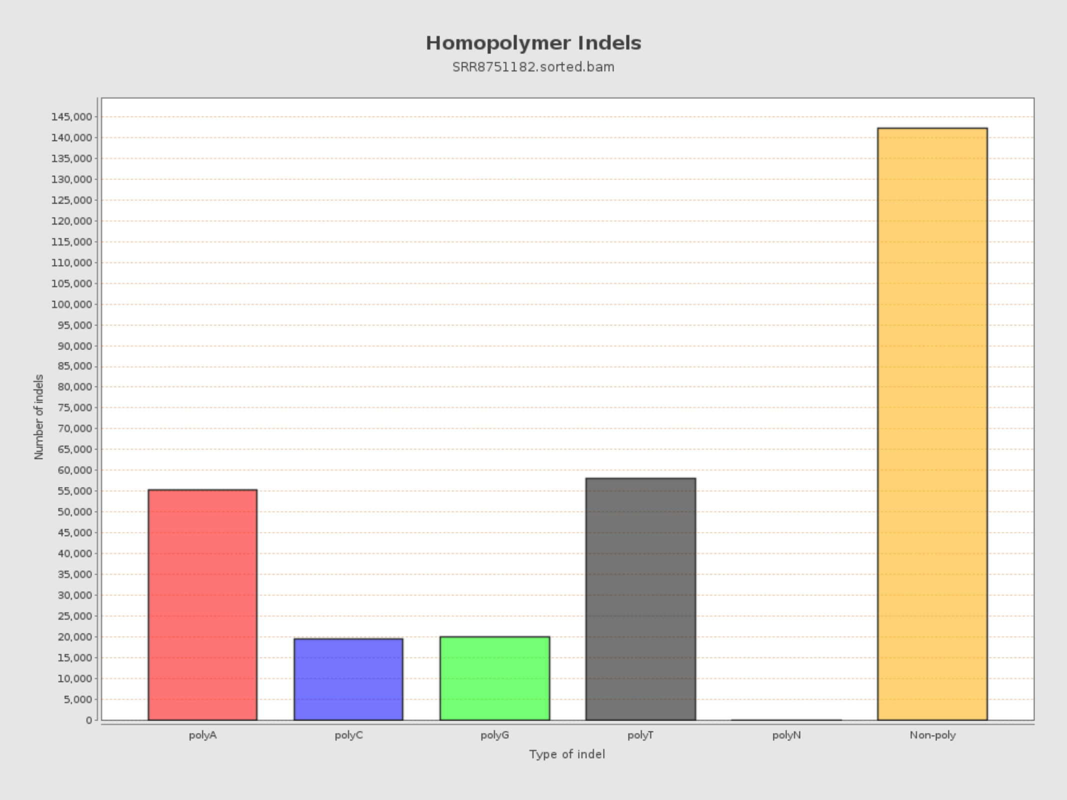
9. Results : Mapped Reads GC-content Distribution



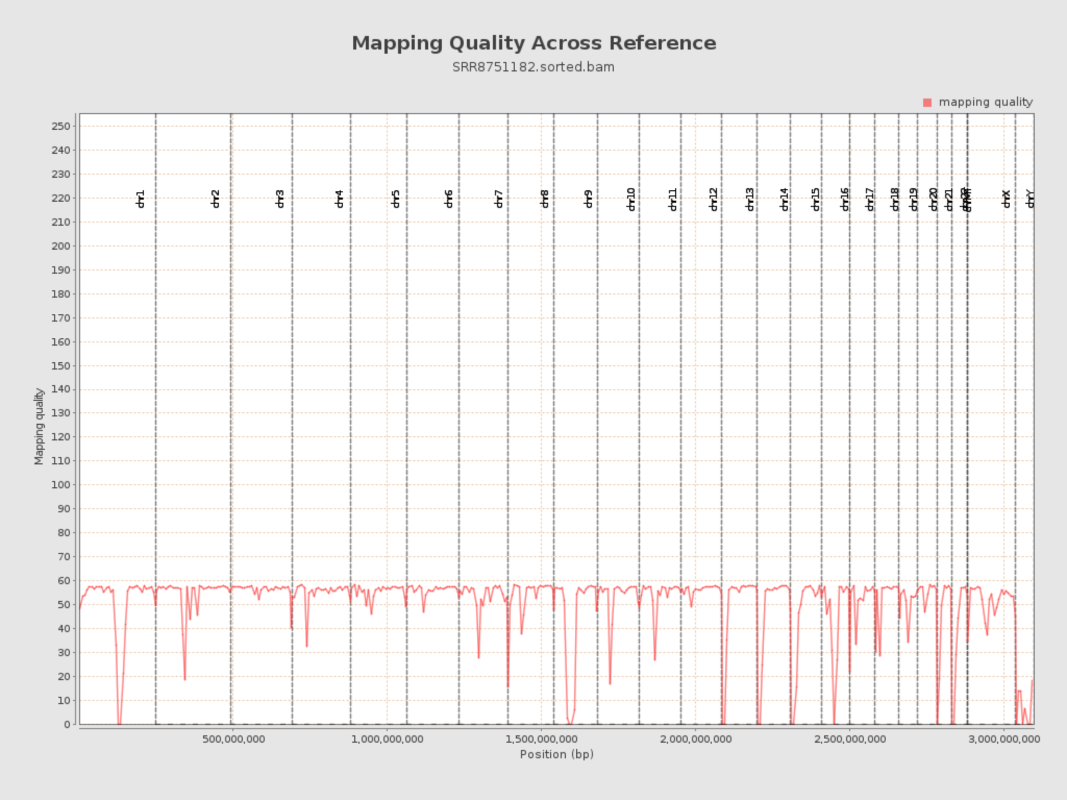
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram