Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:06:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751205.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_SRR8751205 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751205.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:06:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751205.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,778,421
Mapped reads	4,502,156 / 94.22%
Unmapped reads	276,265 / 5.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	170,846 / 3.58%
Read min/max/mean length	30 / 101 / 102.48
Duplicated reads (estimated)	138,199 / 2.89%
Duplication rate	1.61%
Clipped reads	905,967 / 18.96%

2.2. ACGT Content

Number/percentage of A's	129,716,532 / 29.35%
Number/percentage of C's	91,351,922 / 20.67%
Number/percentage of T's	130,363,818 / 29.49%
Number/percentage of G's	90,596,867 / 20.5%
Number/percentage of N's	2,338 / 0%
GC Percentage	41.16%

2.3. Coverage

Mean	0.1428

Standard Deviation	1.3525

2.4. Mapping Quality

Mean Mapping Quality	51.2

2.5. Mismatches and indels

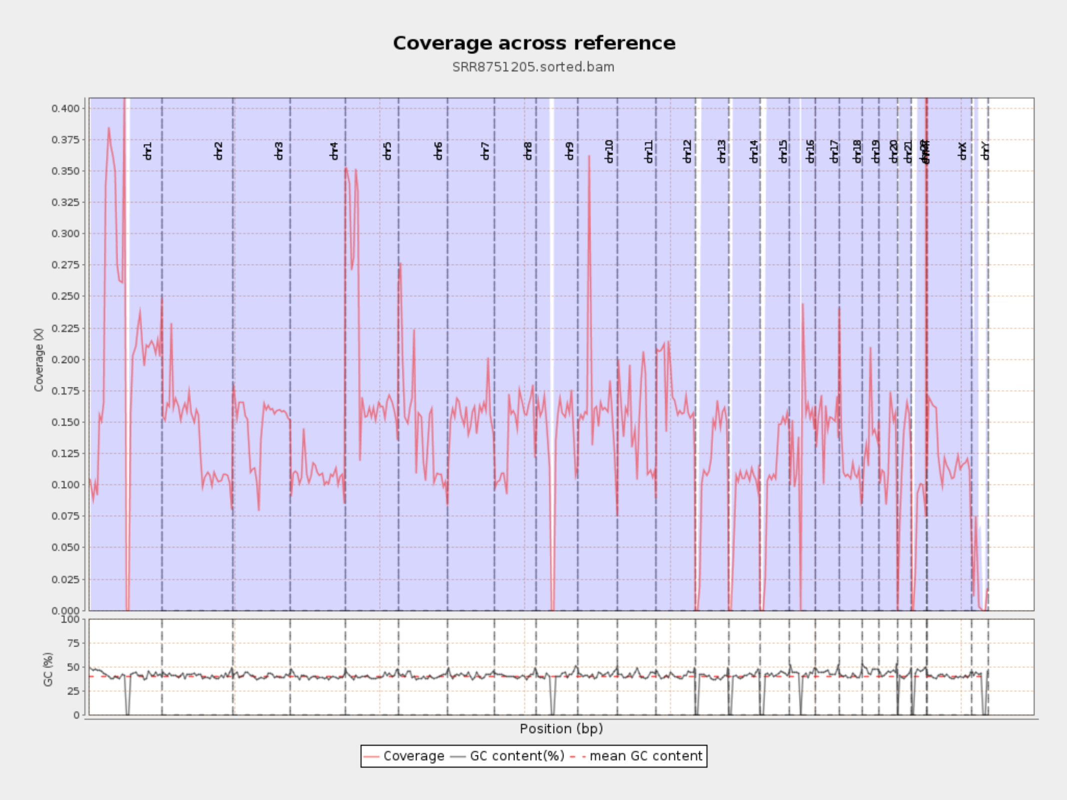
General error rate	0.44%
Mismatches	1,701,436
Insertions	177,791
Mapped reads with at least one insertion	3.83%
Deletions	61,903
Mapped reads with at least one deletion	1.35%
Homopolymer indels	51.16%

2.6. Chromosome stats

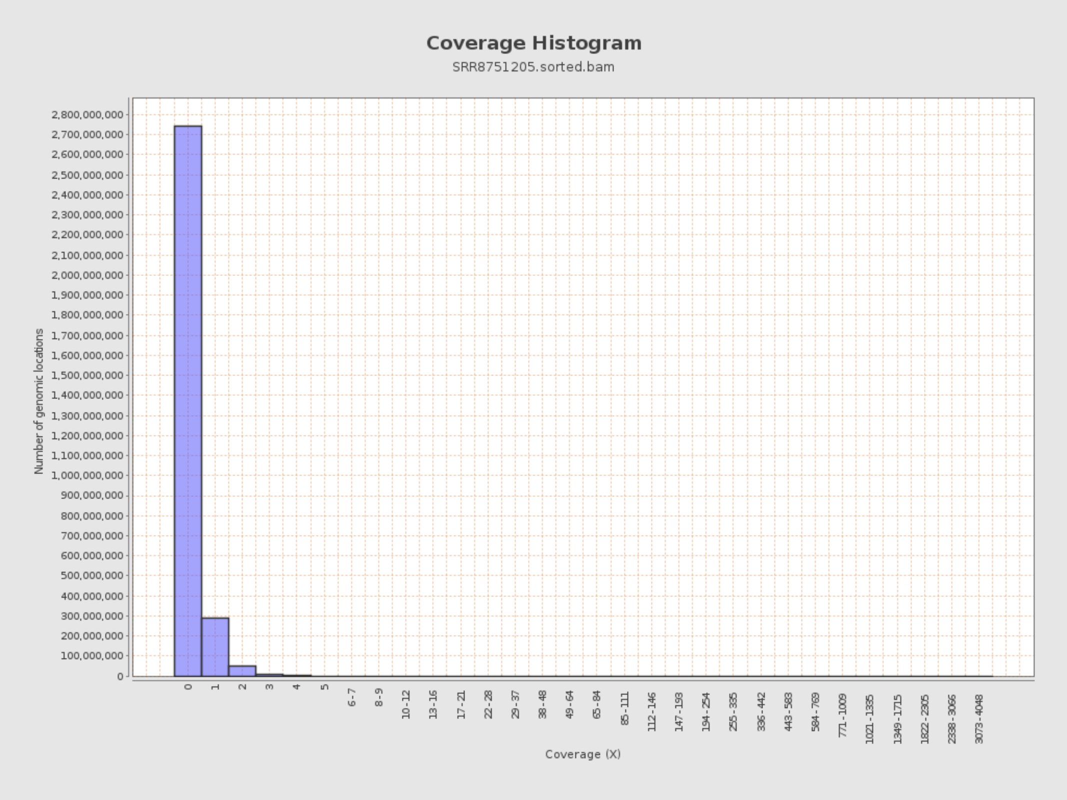
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	52955505	0.2125	3.7747
chr2	243199373	33270946	0.1368	0.573
chr3	198022430	29411983	0.1485	0.4952
chr4	191154276	20566577	0.1076	0.504
chr5	180915260	36234632	0.2003	0.5197
chr6	171115067	25316401	0.1479	0.7877
chr7	159138663	24955820	0.1568	0.787

chr8	146364022	20769570	0.1419	0.5328
chr9	141213431	19131139	0.1355	0.6326
chr10	135534747	22405699	0.1653	1.9481
chr11	135006516	20084851	0.1488	0.6592
chr12	133851895	23416269	0.1749	0.4831
chr13	115169878	13006817	0.1129	0.3862
chr14	107349540	9426082	0.0878	0.3627
chr15	102531392	10586955	0.1033	0.3678
chr16	90354753	12307720	0.1362	0.8953
chr17	81195210	12074405	0.1487	0.6408
chr18	78077248	9136933	0.117	1.2191
chr19	59128983	8286655	0.1401	2.5583
chr20	63025520	7851214	0.1246	0.4242
chr21	48129895	5589770	0.1161	0.4635
chr22	51304566	3325333	0.0648	0.2924
chrMT	16571	1838728	110.9606	43.1312
chrX	155270560	19190957	0.1236	0.4533
chrY	59373566	1027422	0.0173	0.687

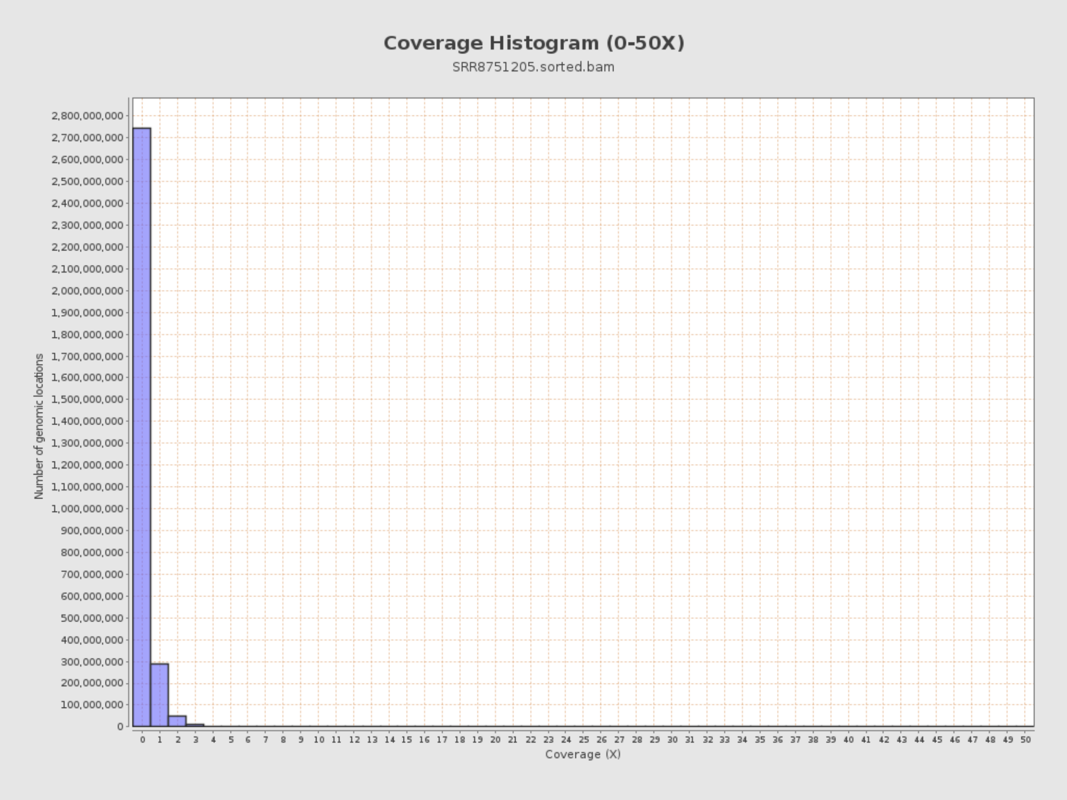
3. Results : Coverage across reference



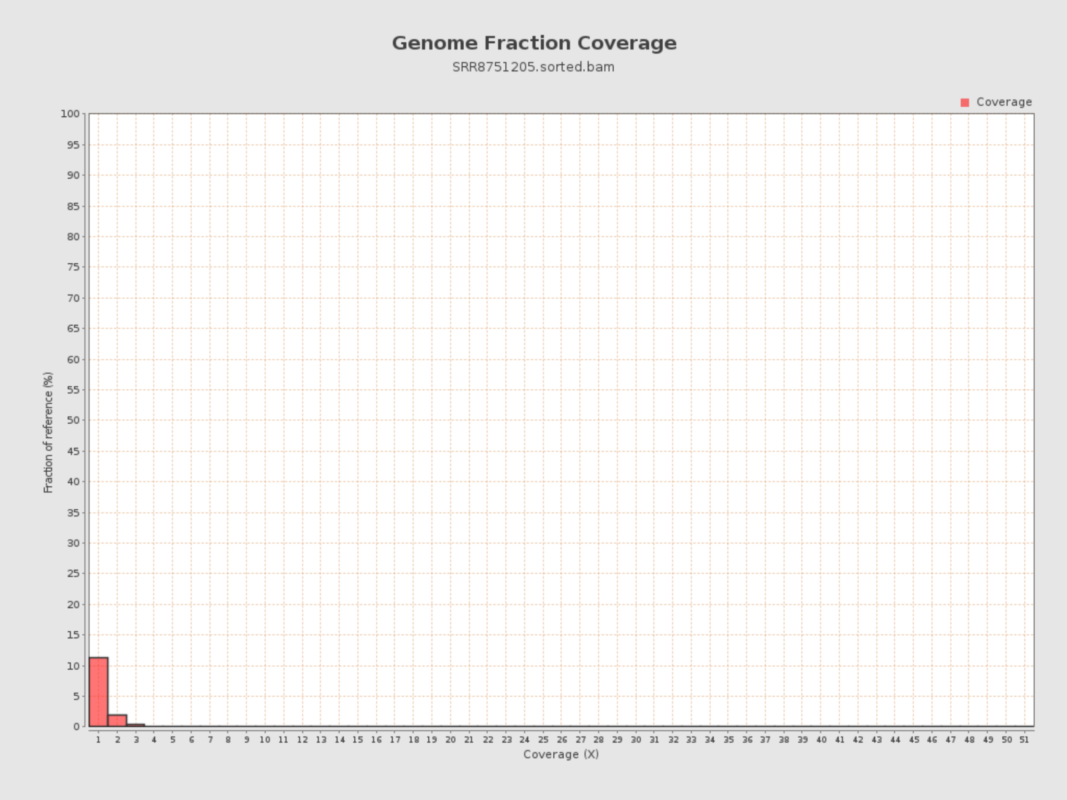
4. Results : Coverage Histogram



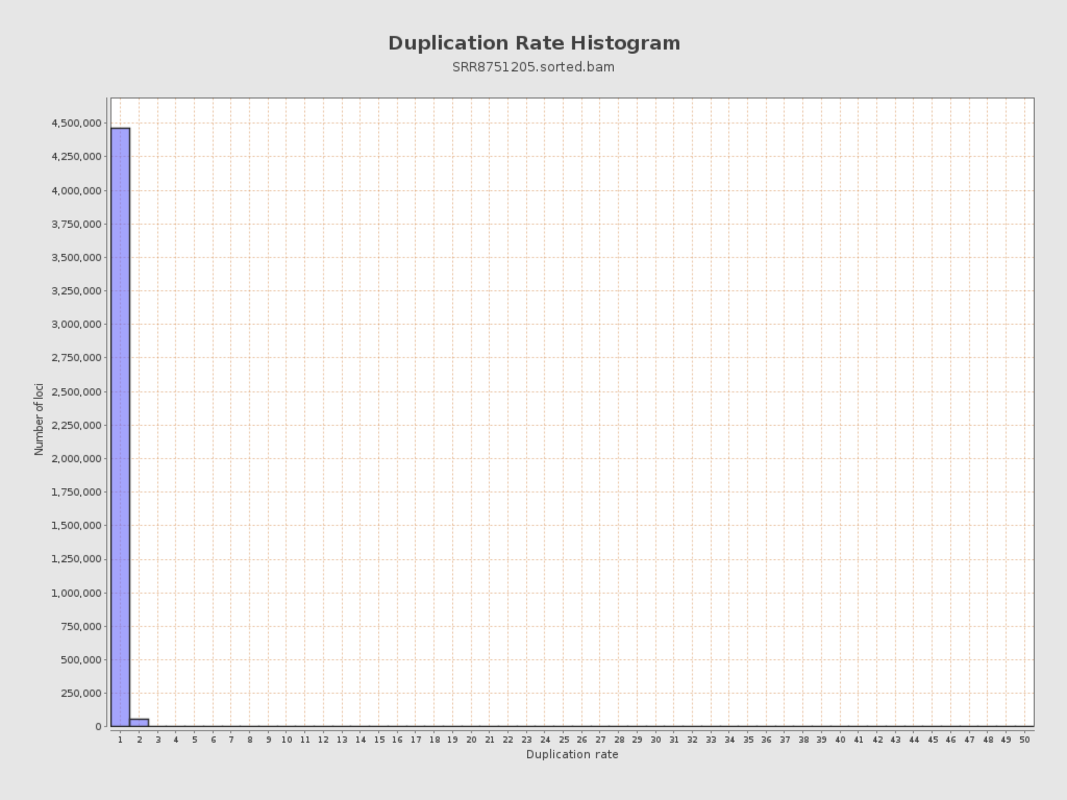
5. Results : Coverage Histogram (0-50X)



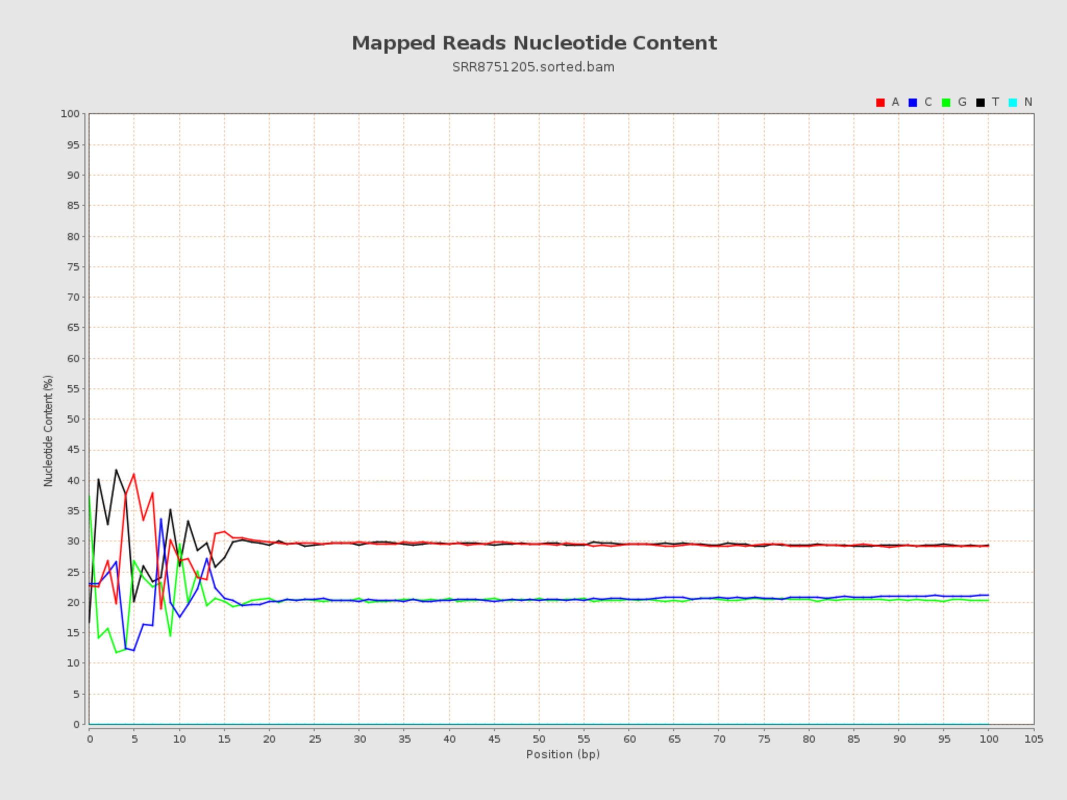
6. Results : Genome Fraction Coverage



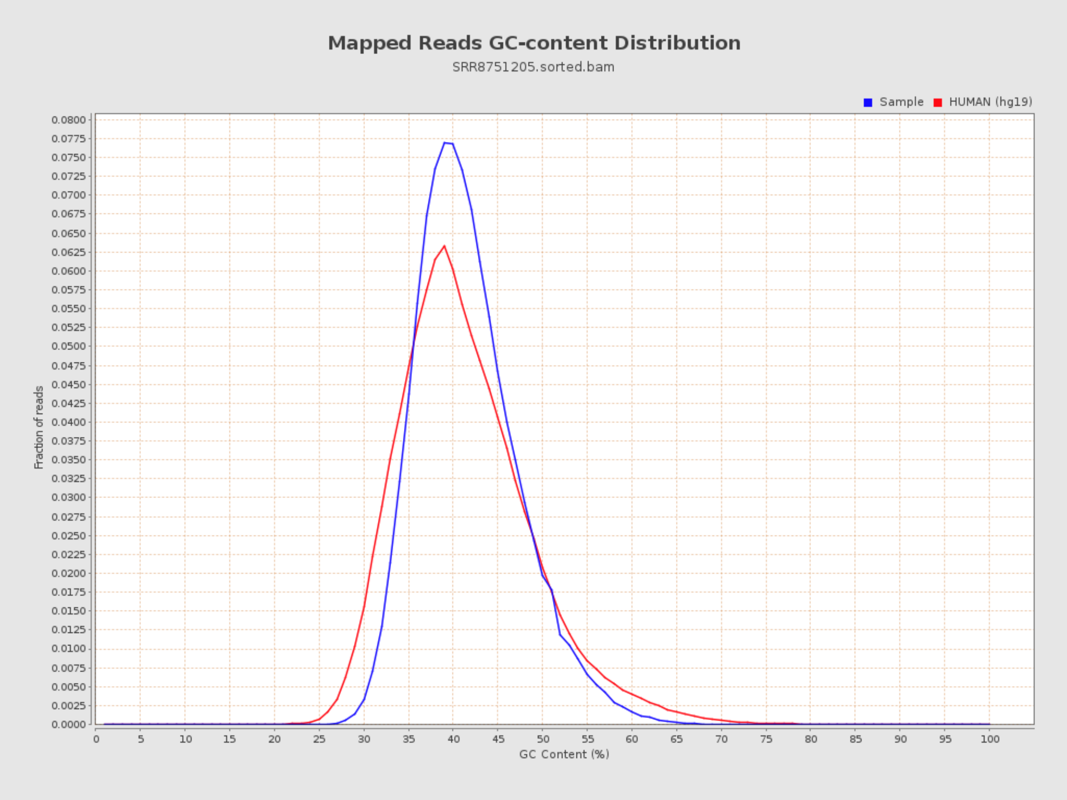
7. Results : Duplication Rate Histogram



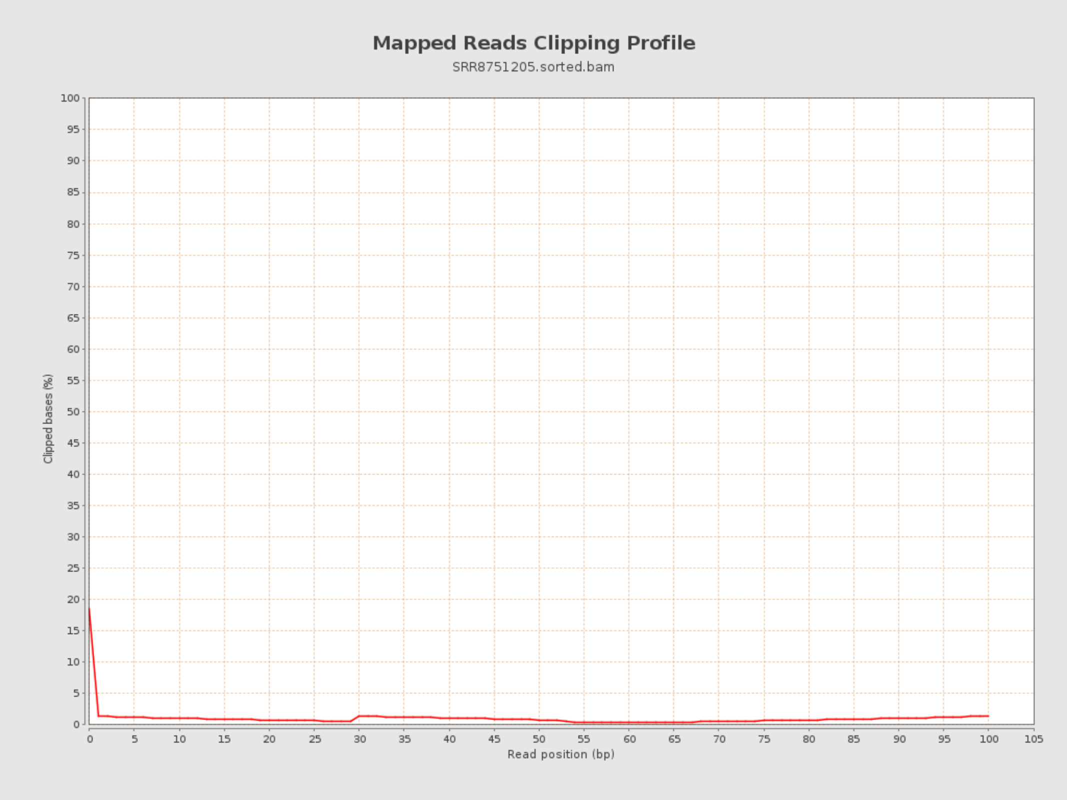
8. Results : Mapped Reads Nucleotide Content



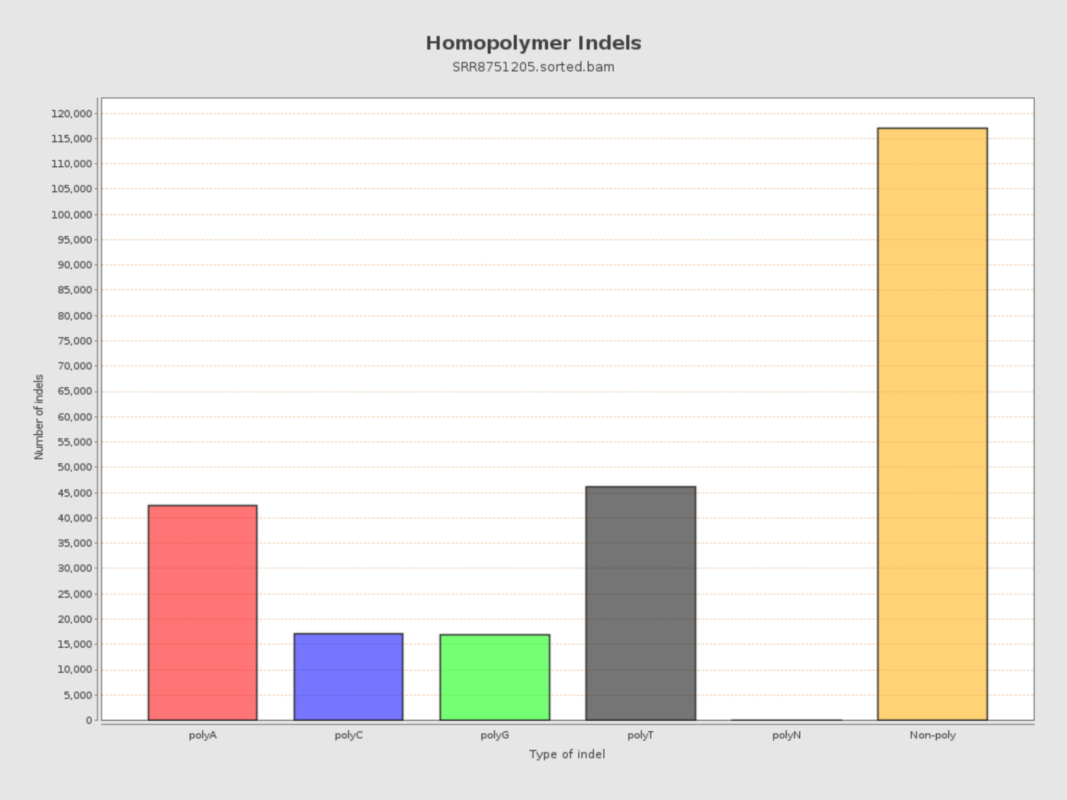
9. Results : Mapped Reads GC-content Distribution



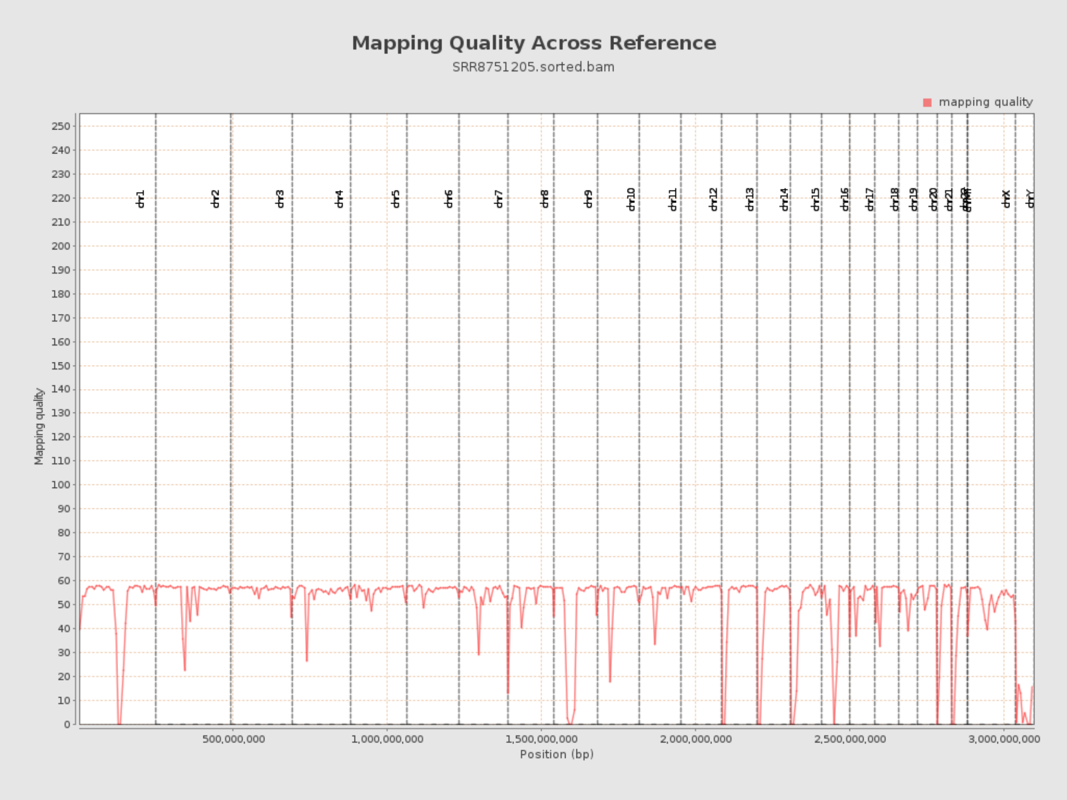
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram