Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:13:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751206.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_SRR8751206 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751206.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:13:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751206.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,937,462
Mapped reads	2,992,899 / 60.62%
Unmapped reads	1,944,563 / 39.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	207,040 / 4.19%
Read min/max/mean length	30 / 101 / 102.73
Duplicated reads (estimated)	127,749 / 2.59%
Duplication rate	1.89%
Clipped reads	938,077 / 19%

2.2. ACGT Content

Number/percentage of A's	85,032,236 / 29.34%
Number/percentage of C's	59,923,796 / 20.68%
Number/percentage of T's	85,586,557 / 29.53%
Number/percentage of G's	59,247,736 / 20.44%
Number/percentage of N's	2,081 / 0%
GC Percentage	41.12%

2.3. Coverage

Mean	0.0936

Standard Deviation	1.4133

2.4. Mapping Quality

Mean Mapping Quality	50.66

2.5. Mismatches and indels

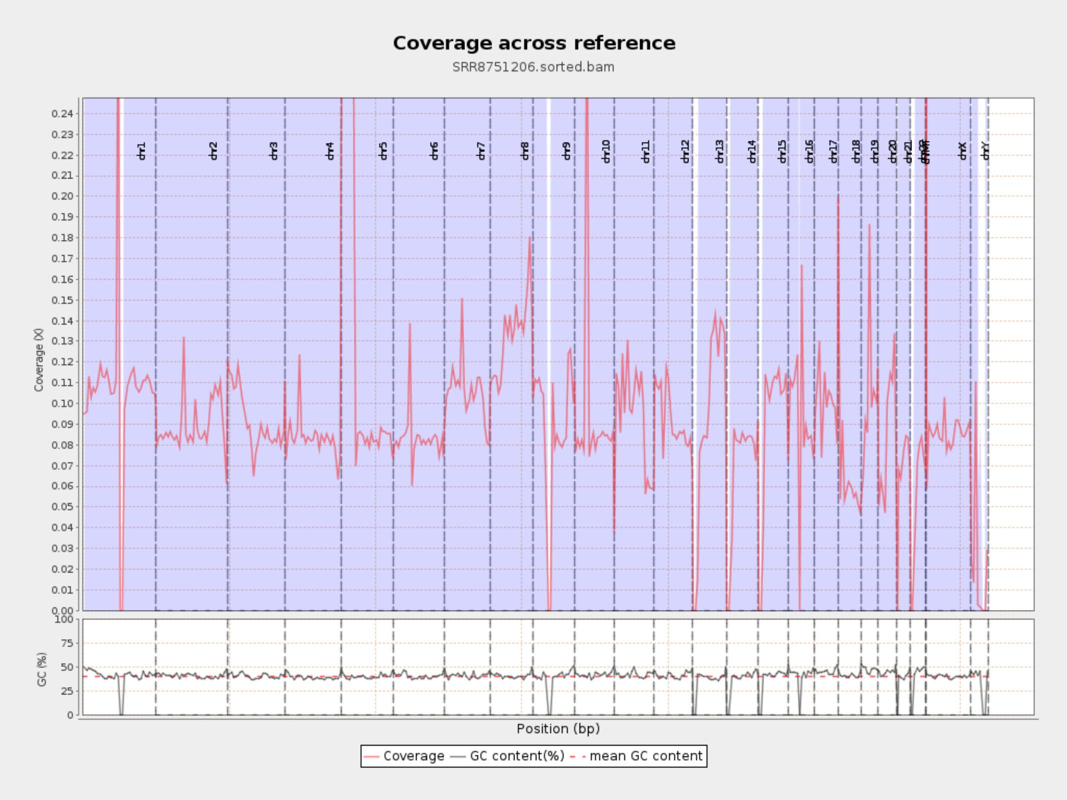
General error rate	0.54%
Mismatches	1,306,787
Insertions	188,123
Mapped reads with at least one insertion	6.04%
Deletions	48,508
Mapped reads with at least one deletion	1.58%
Homopolymer indels	51.24%

2.6. Chromosome stats

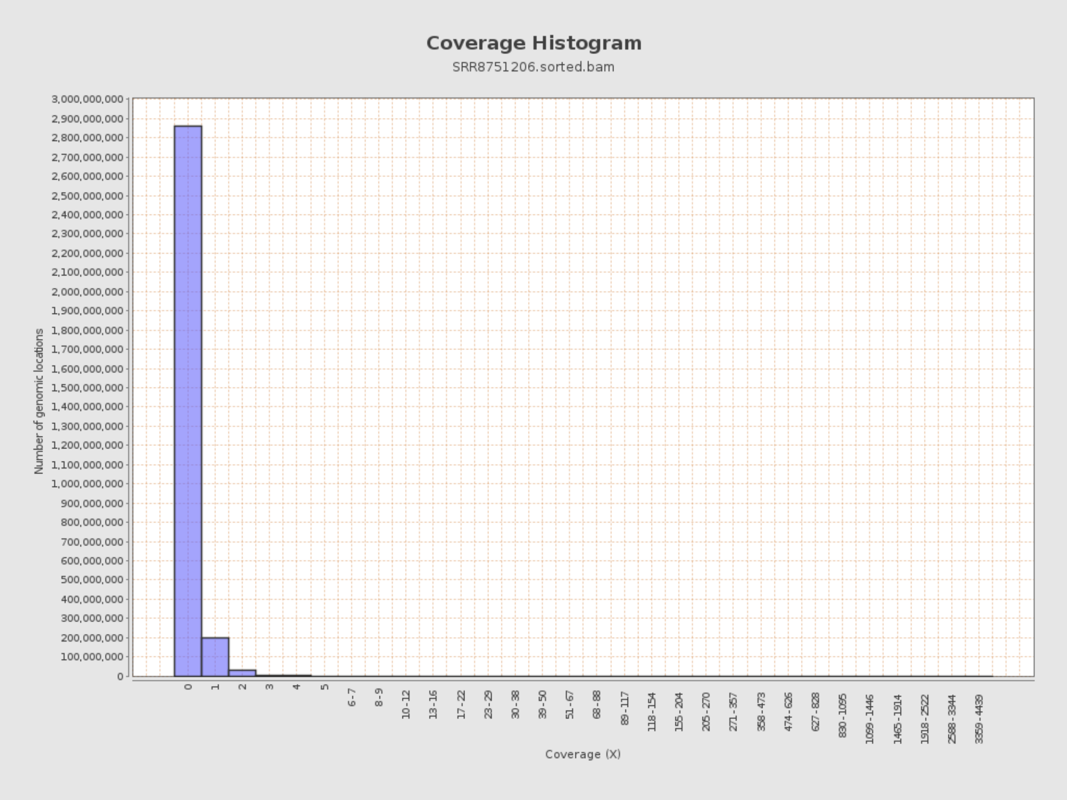
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27014105	0.1084	4.0776
chr2	243199373	21816548	0.0897	0.6001
chr3	198022430	18180442	0.0918	0.4369
chr4	191154276	15987484	0.0836	0.4286
chr5	180915260	24419997	0.135	0.5033
chr6	171115067	14345689	0.0838	0.6458
chr7	159138663	16741719	0.1052	0.8076

chr8	146364022	19591519	0.1339	1.006
chr9	141213431	12328759	0.0873	0.6767
chr10	135534747	12834690	0.0947	1.8118
chr11	135006516	12767556	0.0946	0.6045
chr12	133851895	12477201	0.0932	0.3828
chr13	115169878	10912257	0.0947	0.3544
chr14	107349540	7368579	0.0686	0.337
chr15	102531392	9118612	0.0889	0.3442
chr16	90354753	8368542	0.0926	0.7527
chr17	81195210	8279561	0.102	0.5849
chr18	78077248	5121124	0.0656	1.7346
chr19	59128983	6087433	0.103	2.7732
chr20	63025520	5448530	0.0864	0.3576
chr21	48129895	3258683	0.0677	0.3713
chr22	51304566	2748375	0.0536	0.2712
chrMT	16571	151305	9.1307	15.3456
chrX	155270560	13197049	0.085	0.3978
chrY	59373566	1339723	0.0226	1.113

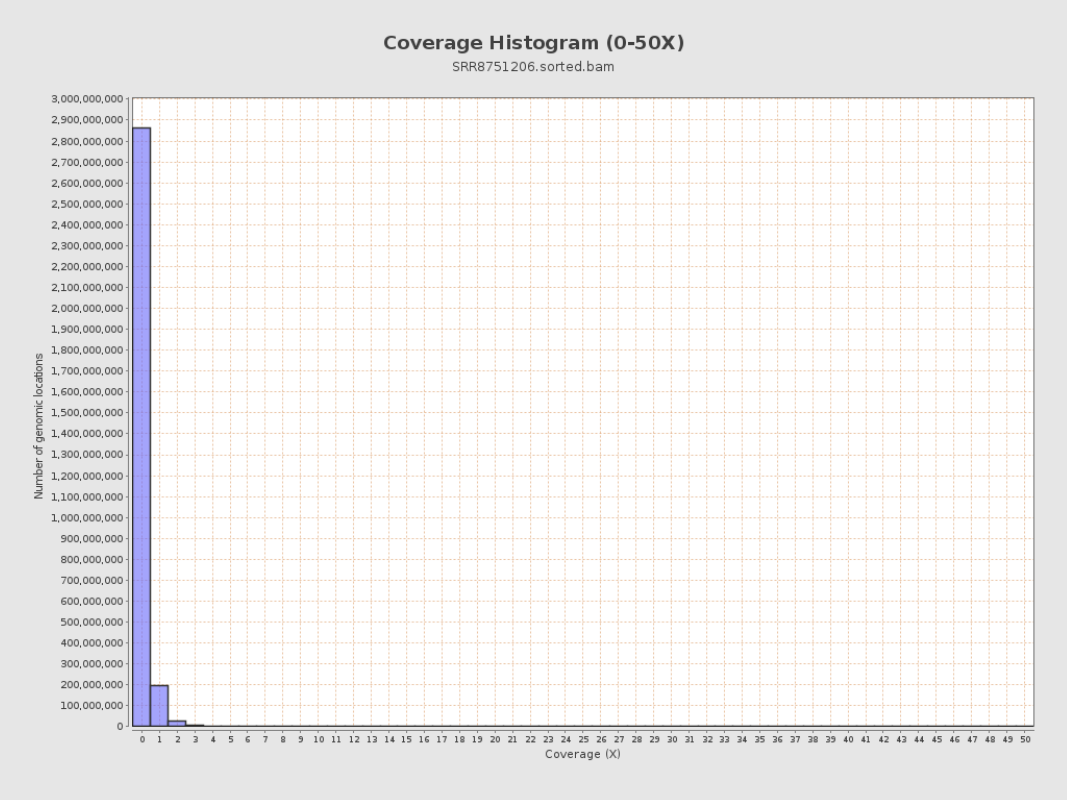
3. Results : Coverage across reference



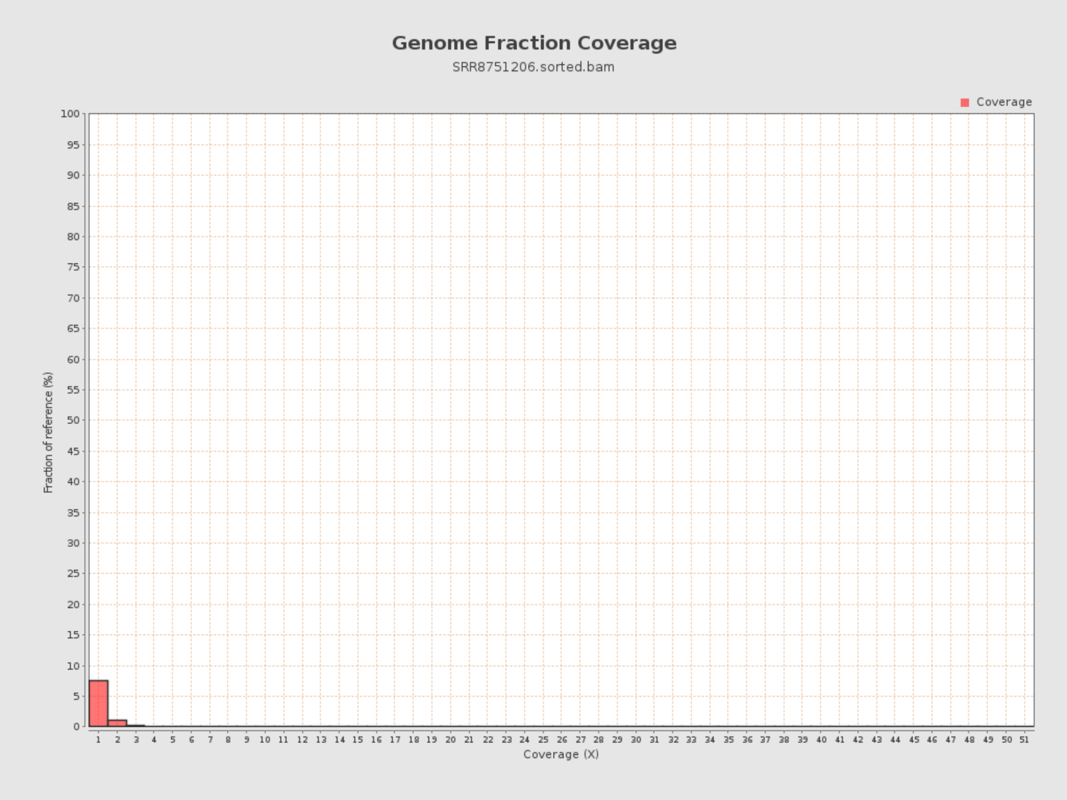
4. Results : Coverage Histogram



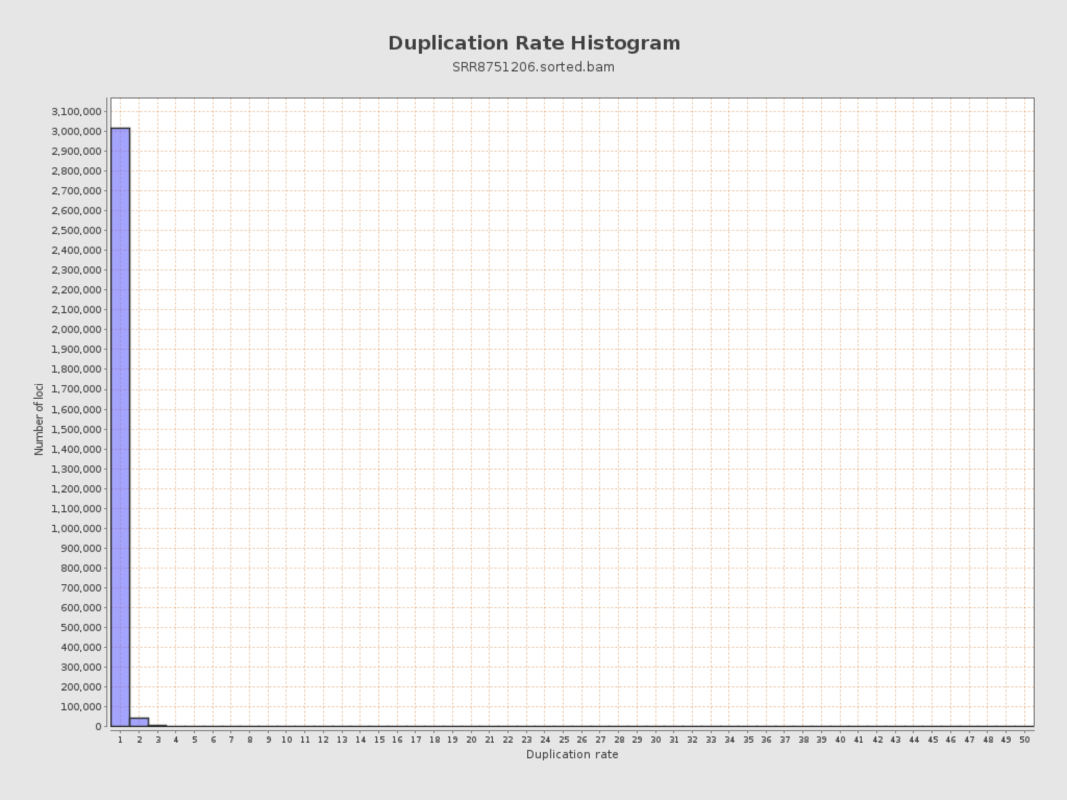
5. Results : Coverage Histogram (0-50X)



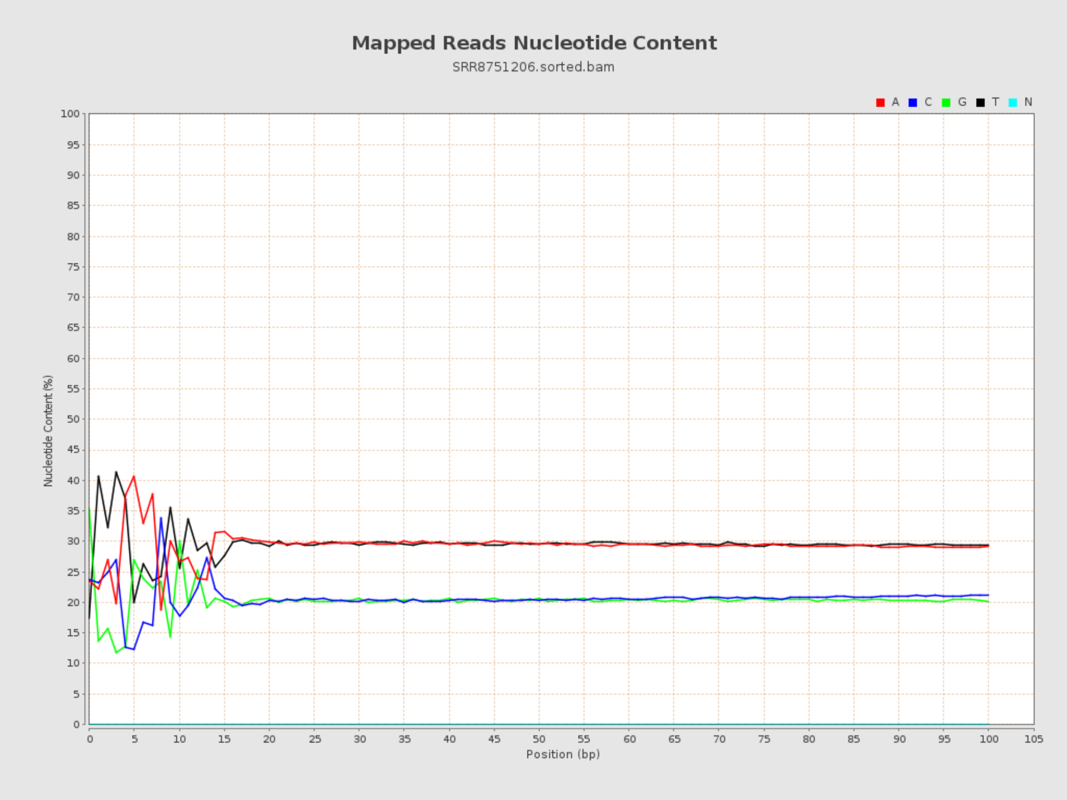
6. Results : Genome Fraction Coverage



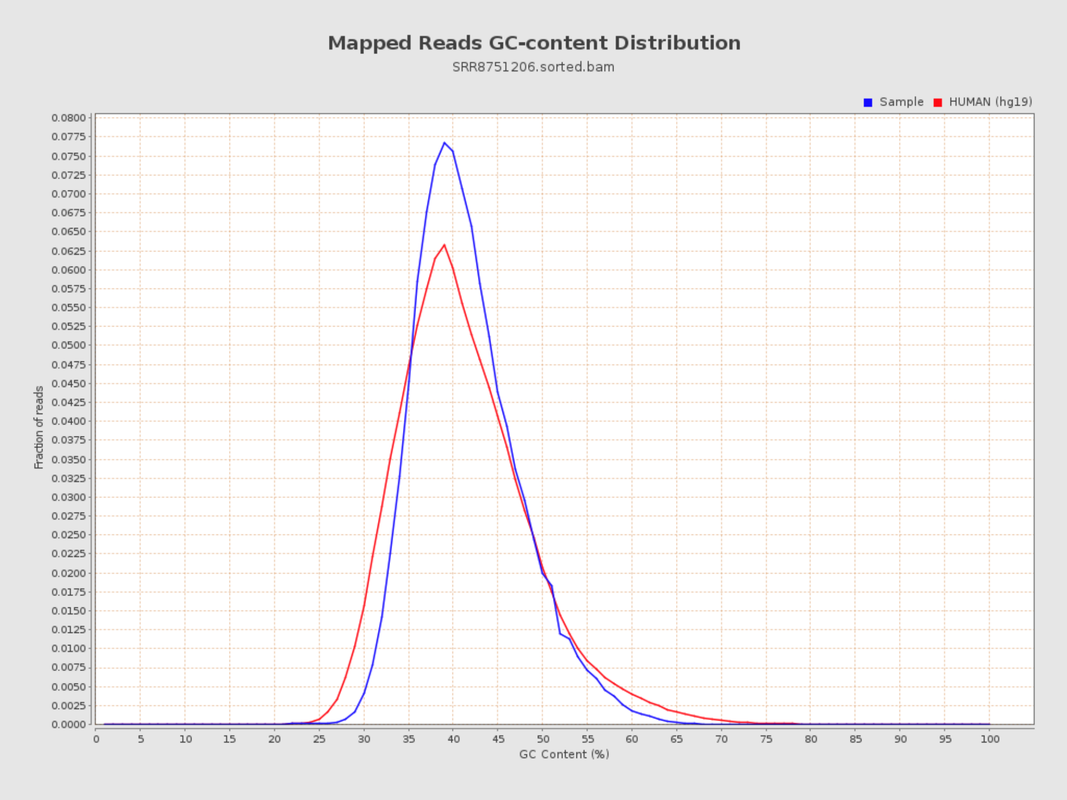
7. Results : Duplication Rate Histogram



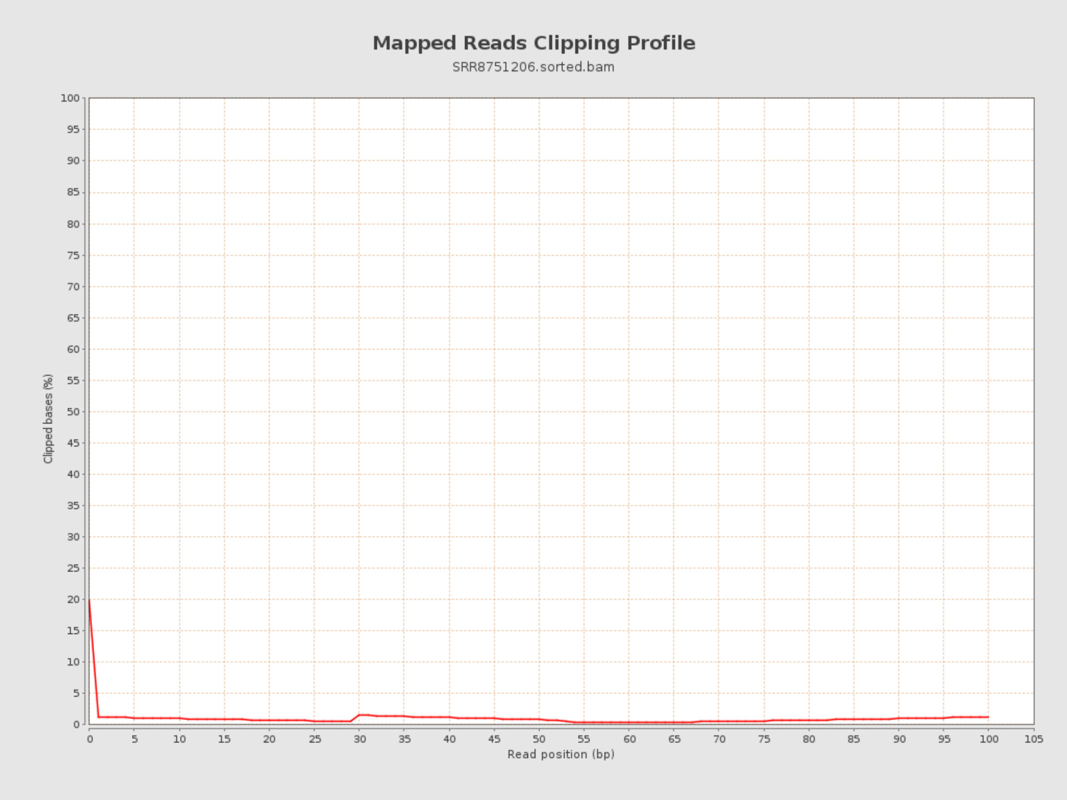
8. Results : Mapped Reads Nucleotide Content



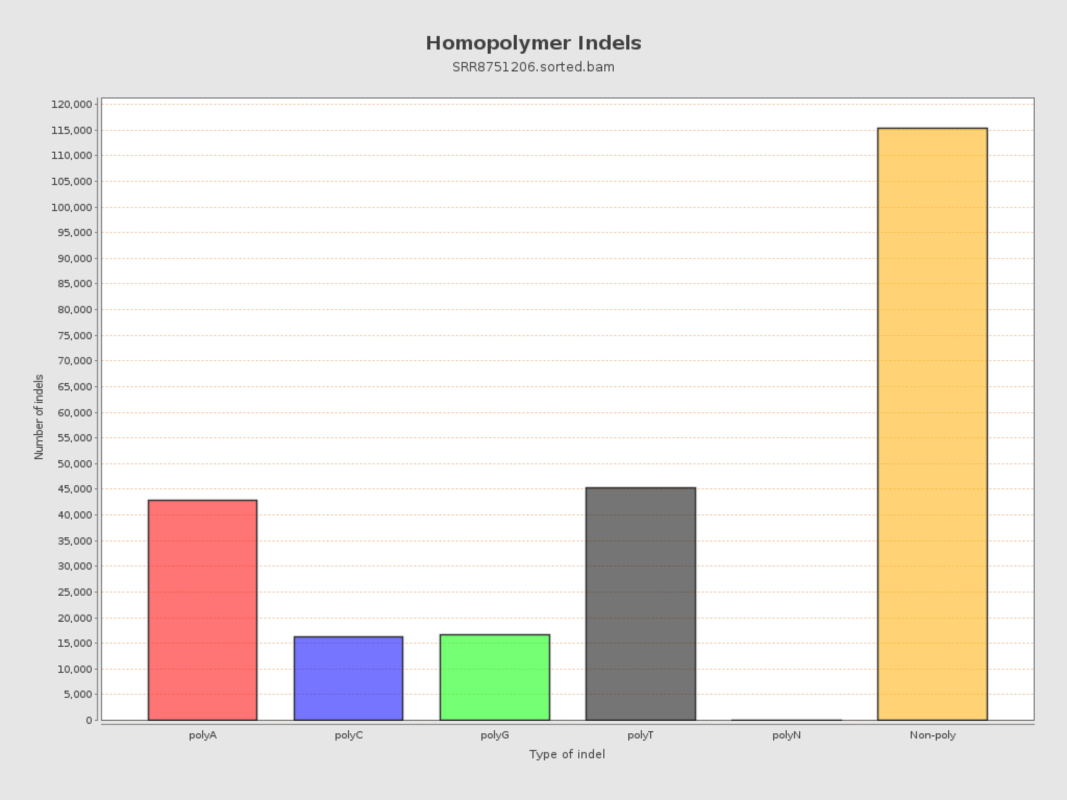
9. Results : Mapped Reads GC-content Distribution



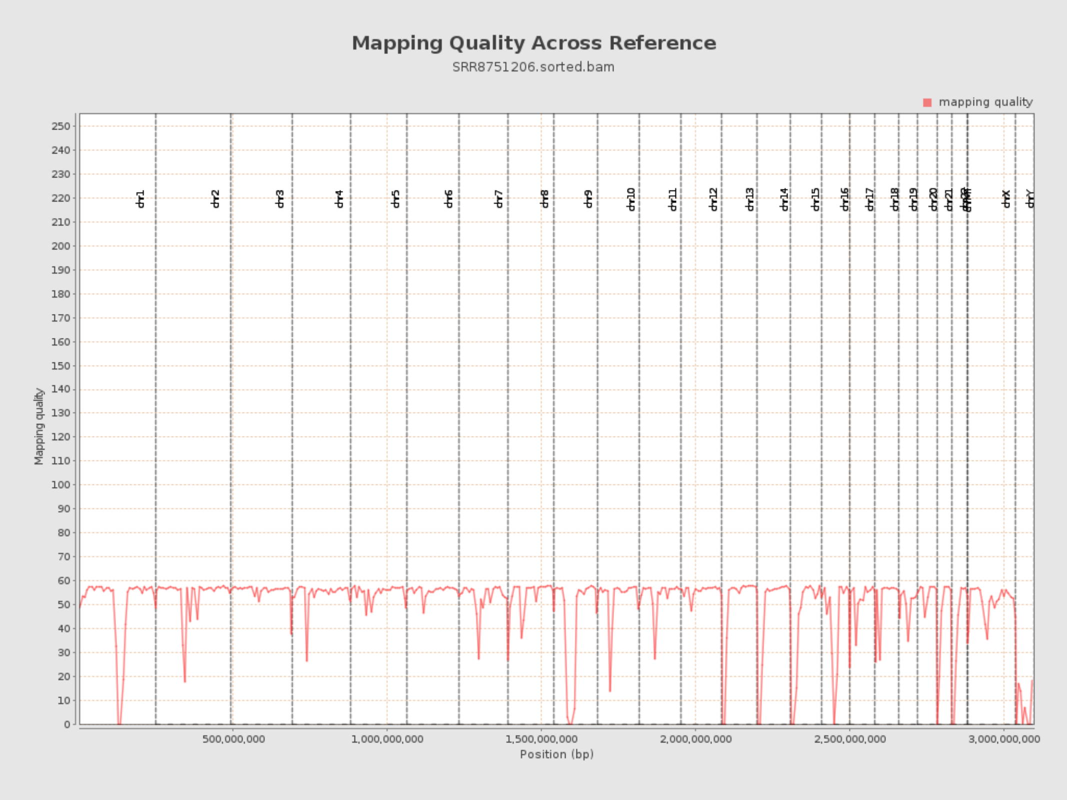
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram