Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/18 22:55:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR536757.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_SRR536757 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536757.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Mar 18 22:55:12 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR536757.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,993,248
Mapped reads	20,519,507 / 97.74%
Unmapped reads	473,741 / 2.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	551 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	216,578 / 1.03%
Duplication rate	1.04%
Clipped reads	258,605 / 1.23%

2.2. ACGT Content

Number/percentage of A's	315,248,370 / 30.8%
Number/percentage of C's	194,988,686 / 19.05%
Number/percentage of T's	315,241,704 / 30.8%
Number/percentage of G's	197,959,209 / 19.34%
Number/percentage of N's	35,699 / 0%
GC Percentage	38.39%

2.3. Coverage

Mean	0.3306

Standard Deviation	0.6785

2.4. Mapping Quality

Mean Mapping Quality	46.4

2.5. Mismatches and indels

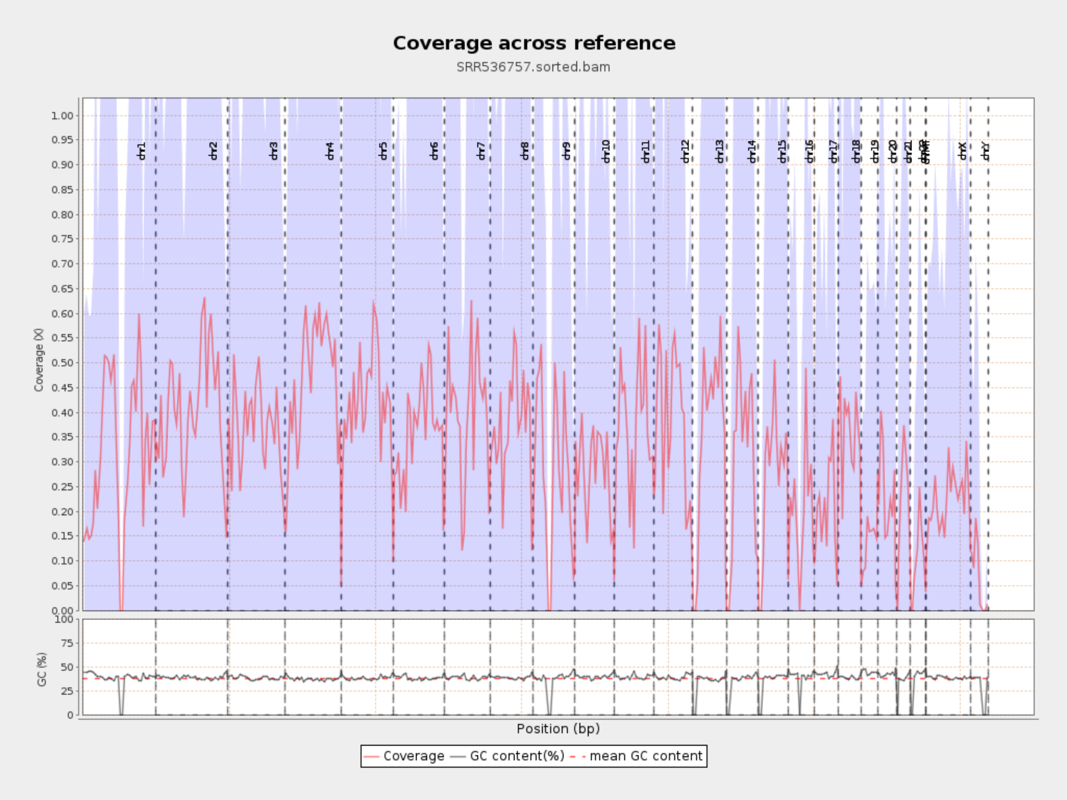
General error rate	0.2%
Mismatches	1,930,096
Insertions	58,467
Mapped reads with at least one insertion	0.28%
Deletions	53,530
Mapped reads with at least one deletion	0.26%
Homopolymer indels	48.8%

2.6. Chromosome stats

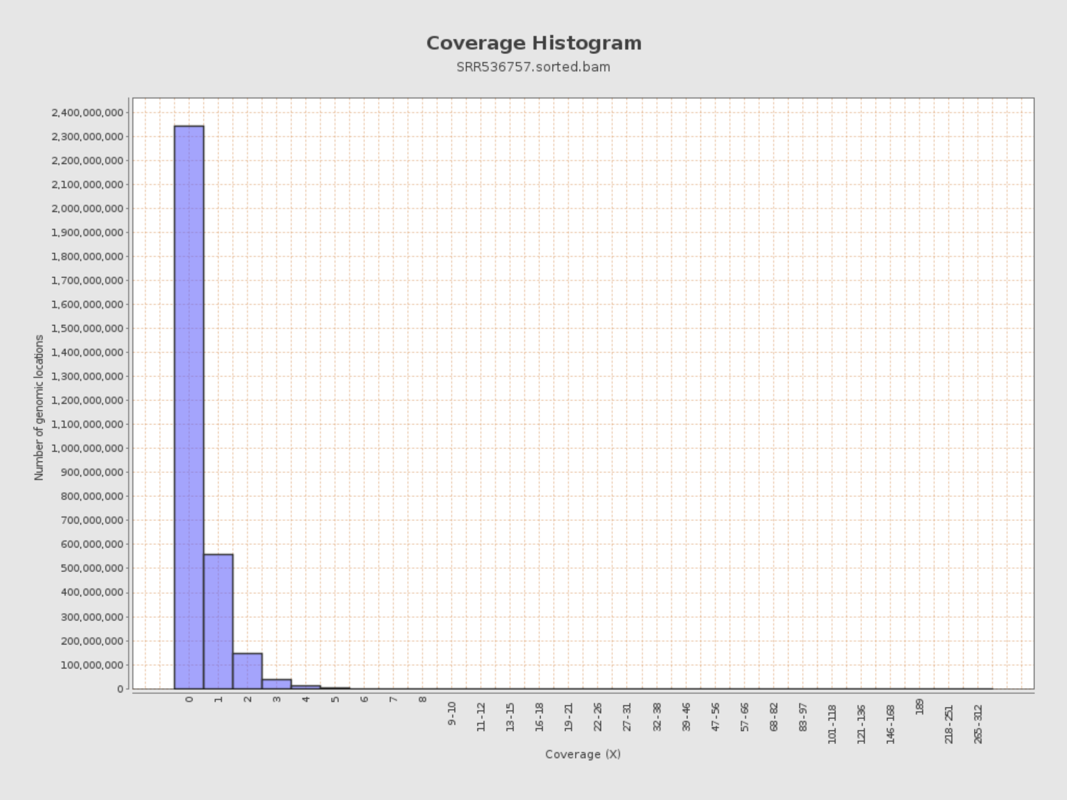
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	79238839	0.3179	0.6773
chr2	243199373	98293419	0.4042	0.7415
chr3	198022430	72725719	0.3673	0.6983
chr4	191154276	90671807	0.4743	0.7994
chr5	180915260	75600308	0.4179	0.7481
chr6	171115067	62675131	0.3663	0.7081
chr7	159138663	63055212	0.3962	0.7415

chr8	146364022	55410379	0.3786	0.7097
chr9	141213431	41390102	0.2931	0.6451
chr10	135534747	38795893	0.2862	0.6136
chr11	135006516	49966974	0.3701	0.7187
chr12	133851895	51192789	0.3825	0.7302
chr13	115169878	41003594	0.356	0.7014
chr14	107349540	33576900	0.3128	0.6632
chr15	102531392	28384686	0.2768	0.6291
chr16	90354753	17786857	0.1969	0.5177
chr17	81195210	17189149	0.2117	0.5446
chr18	78077248	28527151	0.3654	0.6963
chr19	59128983	8371273	0.1416	0.431
chr20	63025520	14873335	0.236	0.5644
chr21	48129895	10556543	0.2193	0.5545
chr22	51304566	5629774	0.1097	0.3819
chrMT	16571	1288	0.0777	0.297
chrX	155270560	34658628	0.2232	0.5422
chrY	59373566	3987100	0.0672	0.3031

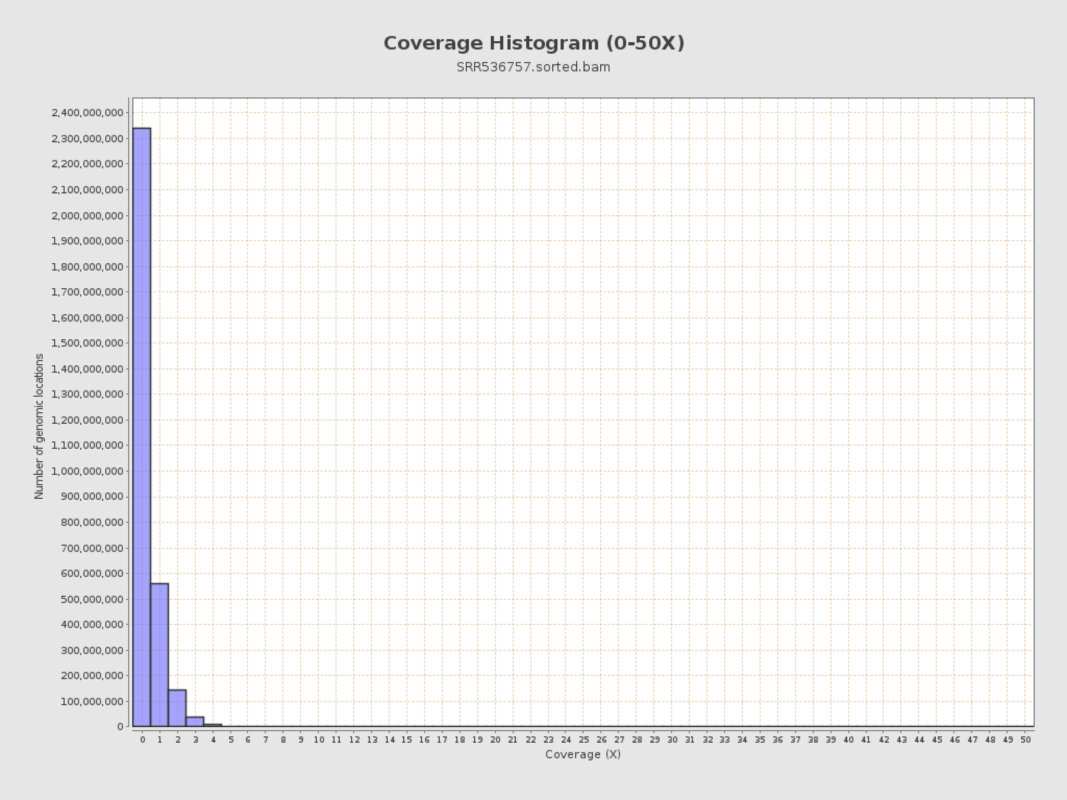
3. Results : Coverage across reference



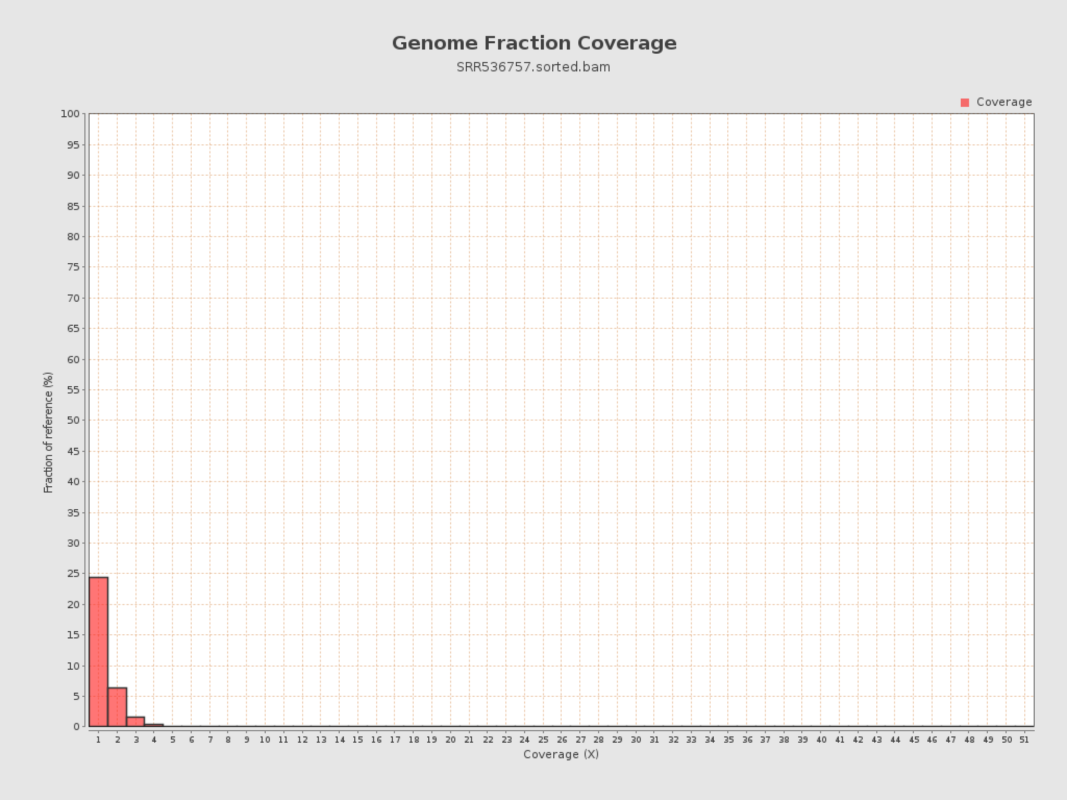
4. Results : Coverage Histogram



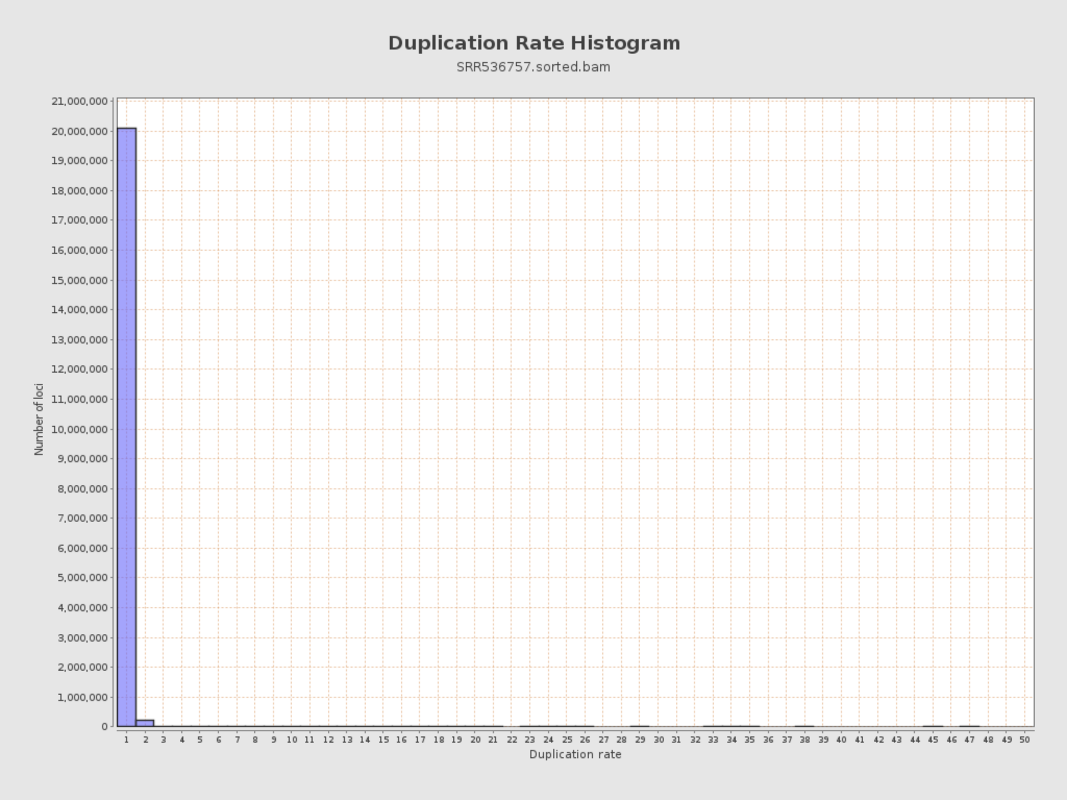
5. Results : Coverage Histogram (0-50X)



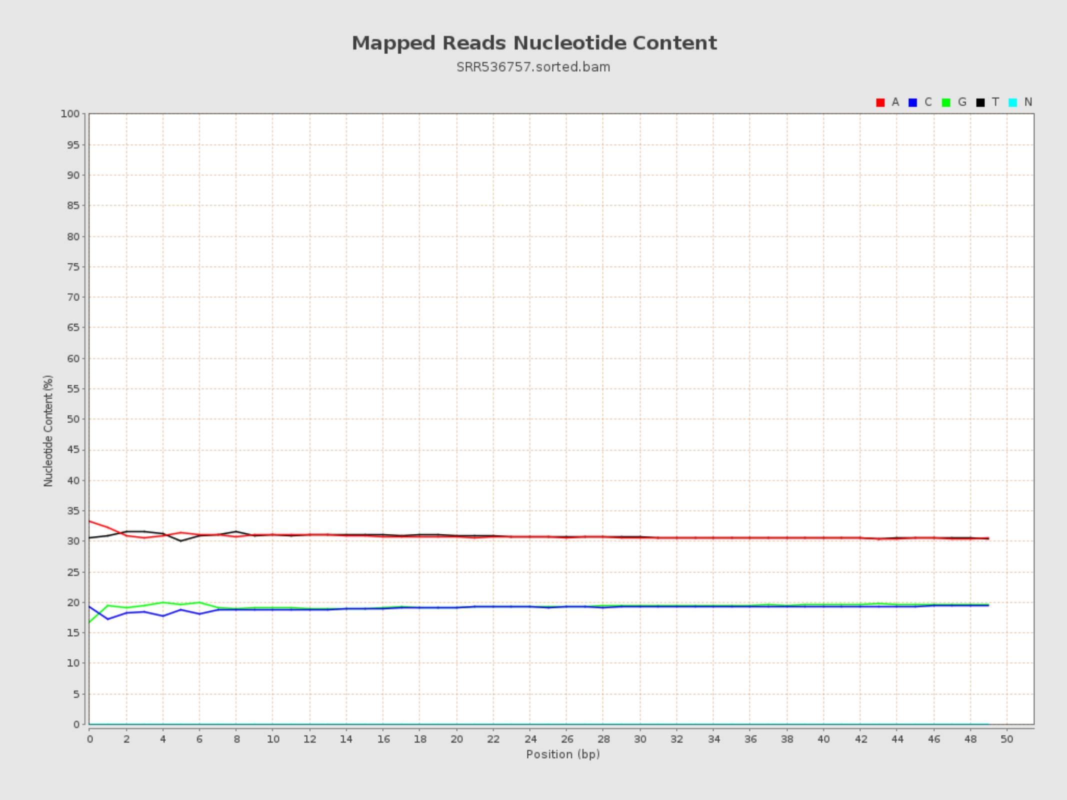
6. Results : Genome Fraction Coverage



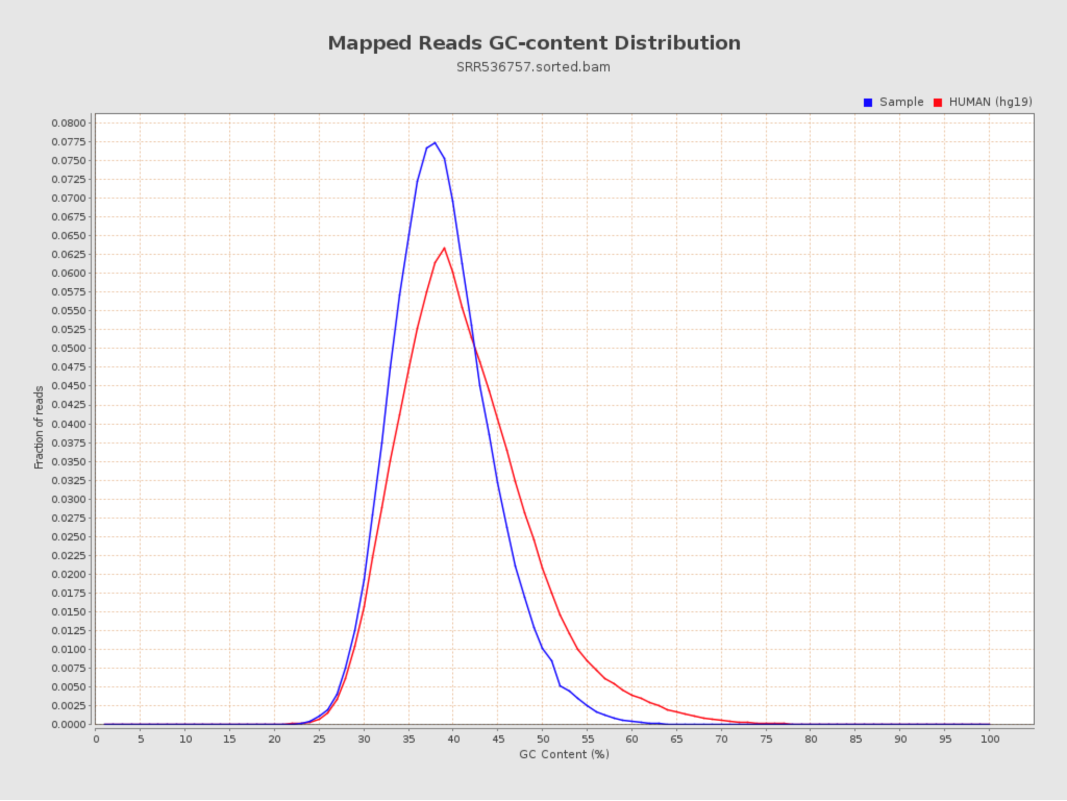
7. Results : Duplication Rate Histogram



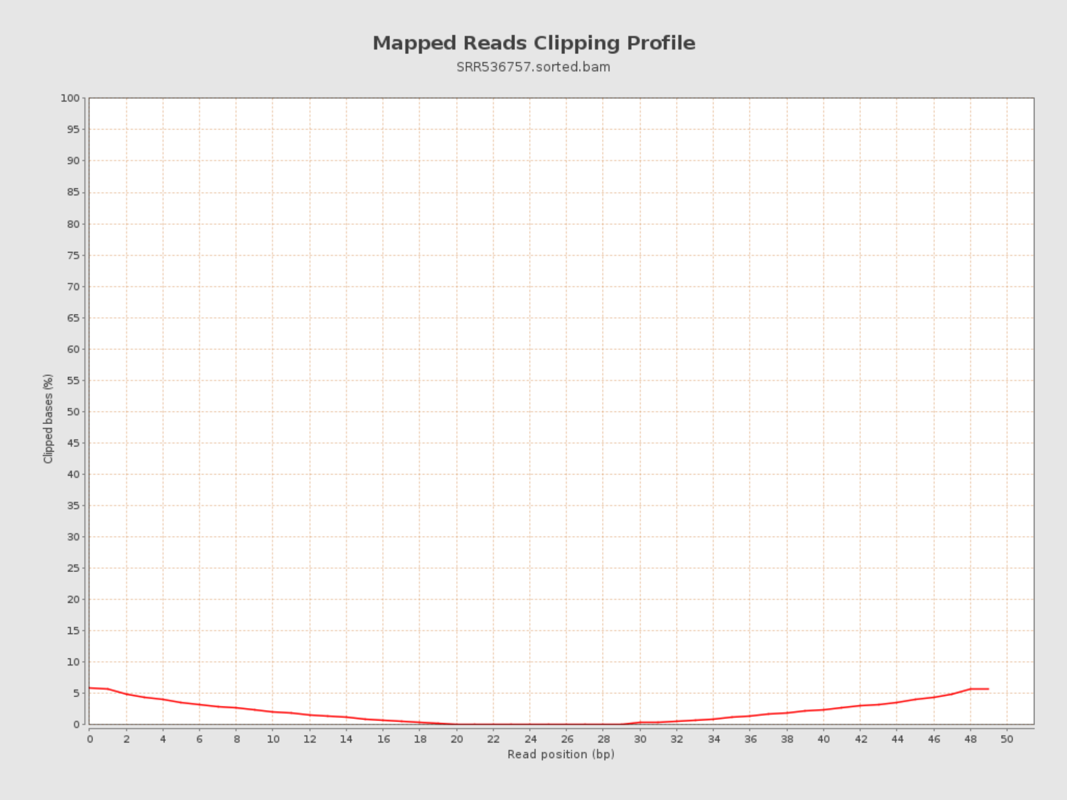
8. Results : Mapped Reads Nucleotide Content



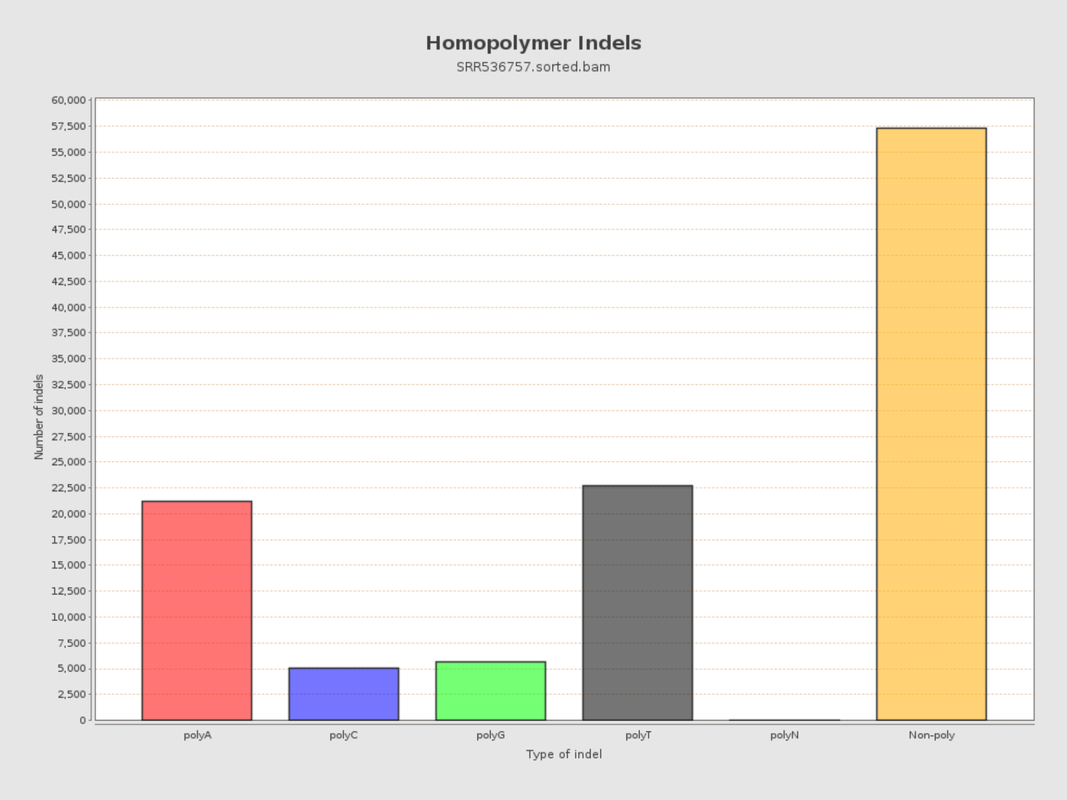
9. Results : Mapped Reads GC-content Distribution



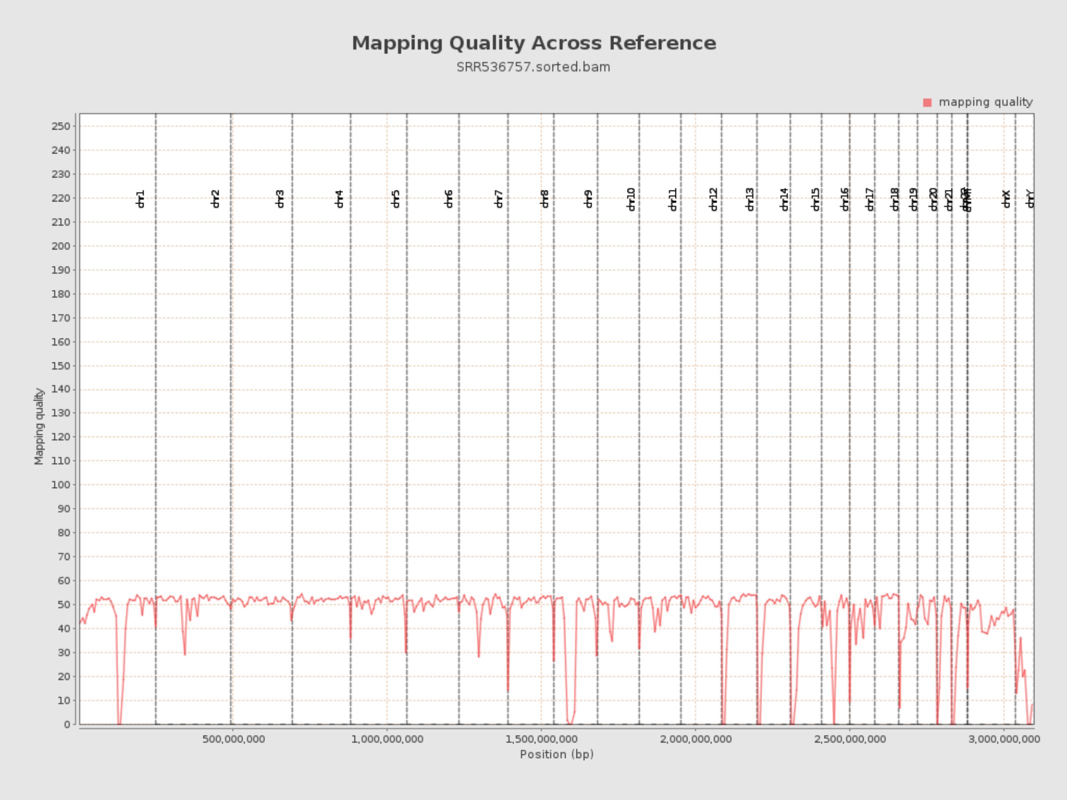
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram