Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/18 20:09:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR536750.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_SRR536750 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536750.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Mar 18 20:09:45 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR536750.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,228,568
Mapped reads	24,342,989 / 96.49%
Unmapped reads	885,579 / 3.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	530 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	232,862 / 0.92%
Duplication rate	0.94%
Clipped reads	388,043 / 1.54%

2.2. ACGT Content

Number/percentage of A's	378,515,050 / 31.18%
Number/percentage of C's	226,852,409 / 18.69%
Number/percentage of T's	376,970,123 / 31.06%
Number/percentage of G's	231,011,261 / 19.03%
Number/percentage of N's	486,122 / 0.04%
GC Percentage	37.72%

2.3. Coverage

Mean	0.3921

Standard Deviation	0.7034

2.4. Mapping Quality

Mean Mapping Quality	46.56

2.5. Mismatches and indels

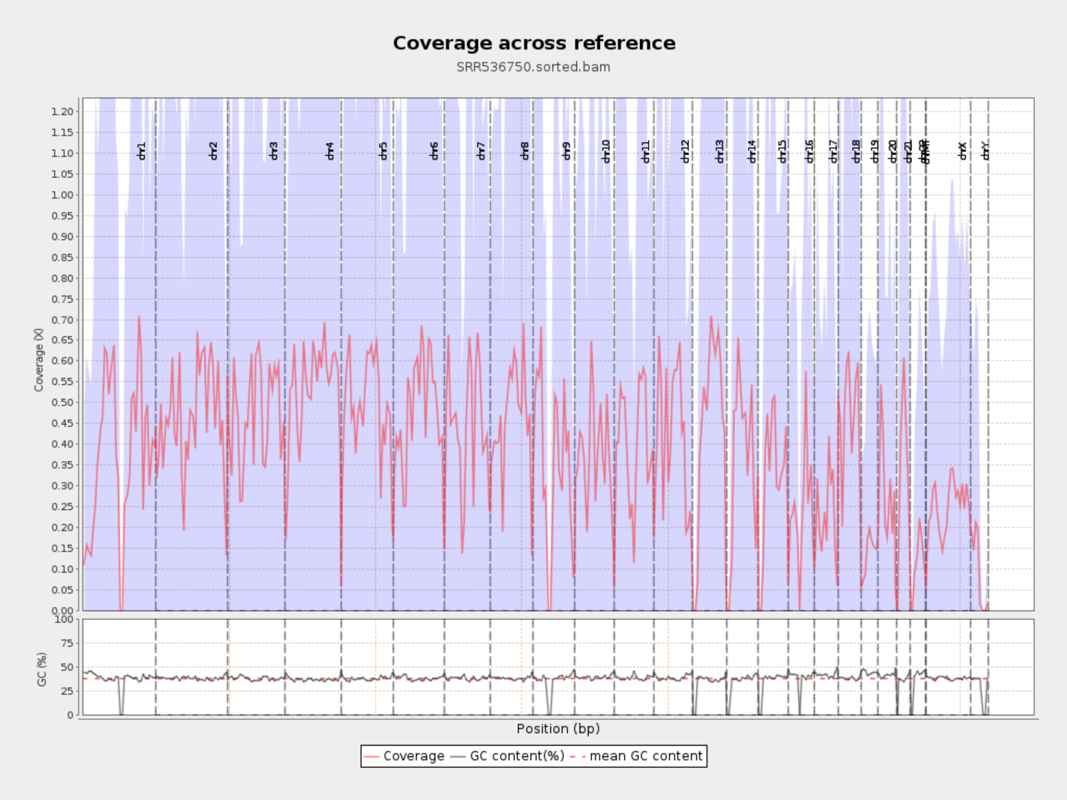
General error rate	0.35%
Mismatches	4,199,653
Insertions	66,050
Mapped reads with at least one insertion	0.27%
Deletions	63,694
Mapped reads with at least one deletion	0.26%
Homopolymer indels	48.33%

2.6. Chromosome stats

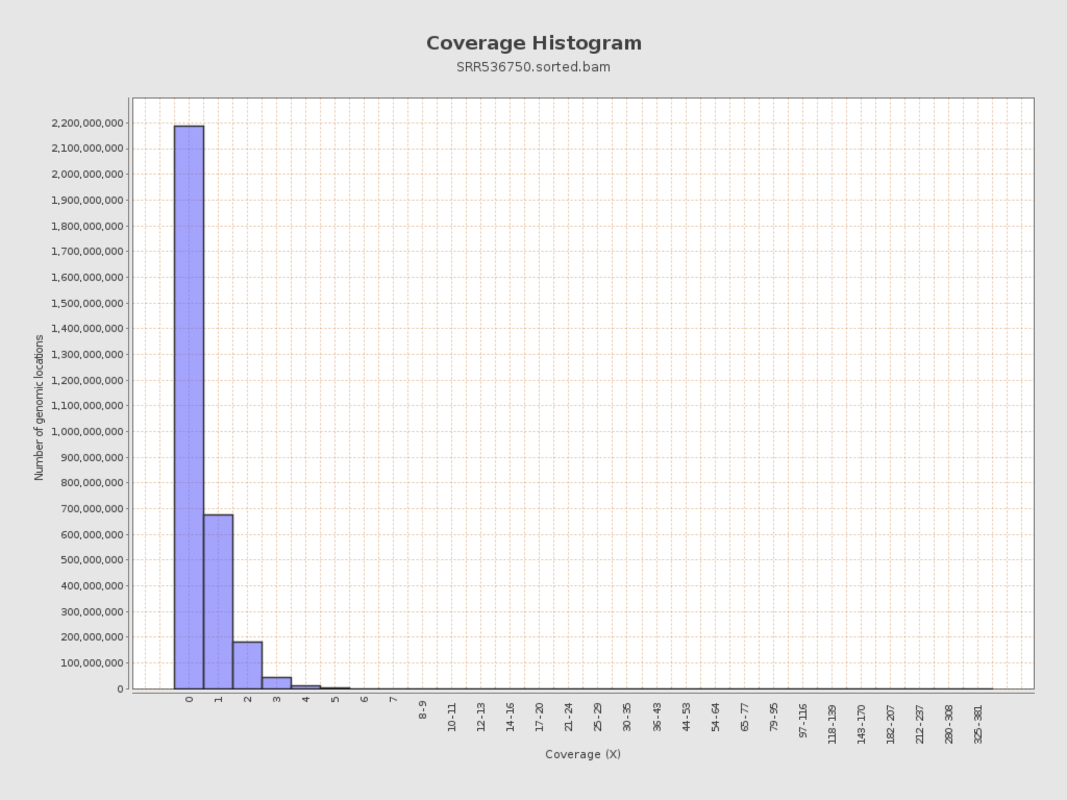
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	92735703	0.3721	0.7036
chr2	243199373	112452481	0.4624	0.7474
chr3	198022430	94198335	0.4757	0.7521
chr4	191154276	102412466	0.5358	0.7958
chr5	180915260	87595502	0.4842	0.7602
chr6	171115067	82910068	0.4845	0.7641
chr7	159138663	69833317	0.4388	0.7401

chr8	146364022	67784661	0.4631	0.746
chr9	141213431	50464635	0.3574	0.679
chr10	135534747	51550925	0.3804	0.6761
chr11	135006516	53894402	0.3992	0.717
chr12	133851895	56107472	0.4192	0.7239
chr13	115169878	51720400	0.4491	0.7533
chr14	107349540	38735688	0.3608	0.6821
chr15	102531392	32228674	0.3143	0.641
chr16	90354753	21389022	0.2367	0.5455
chr17	81195210	18873038	0.2324	0.5494
chr18	78077248	36820442	0.4716	0.7536
chr19	59128983	8240440	0.1394	0.4098
chr20	63025520	18167845	0.2883	0.6042
chr21	48129895	15712705	0.3265	0.6736
chr22	51304566	5921115	0.1154	0.3786
chrMT	16571	863	0.0521	0.2222
chrX	155270560	38687688	0.2492	0.5278
chrY	59373566	5502069	0.0927	0.3438

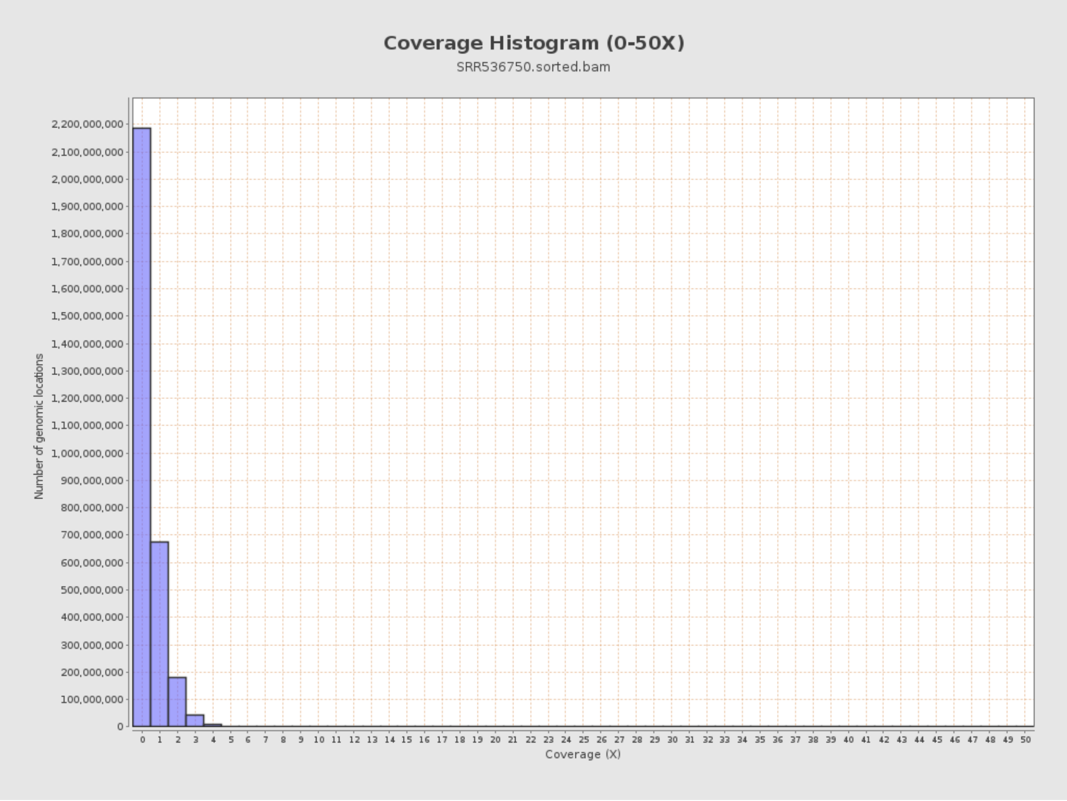
3. Results : Coverage across reference



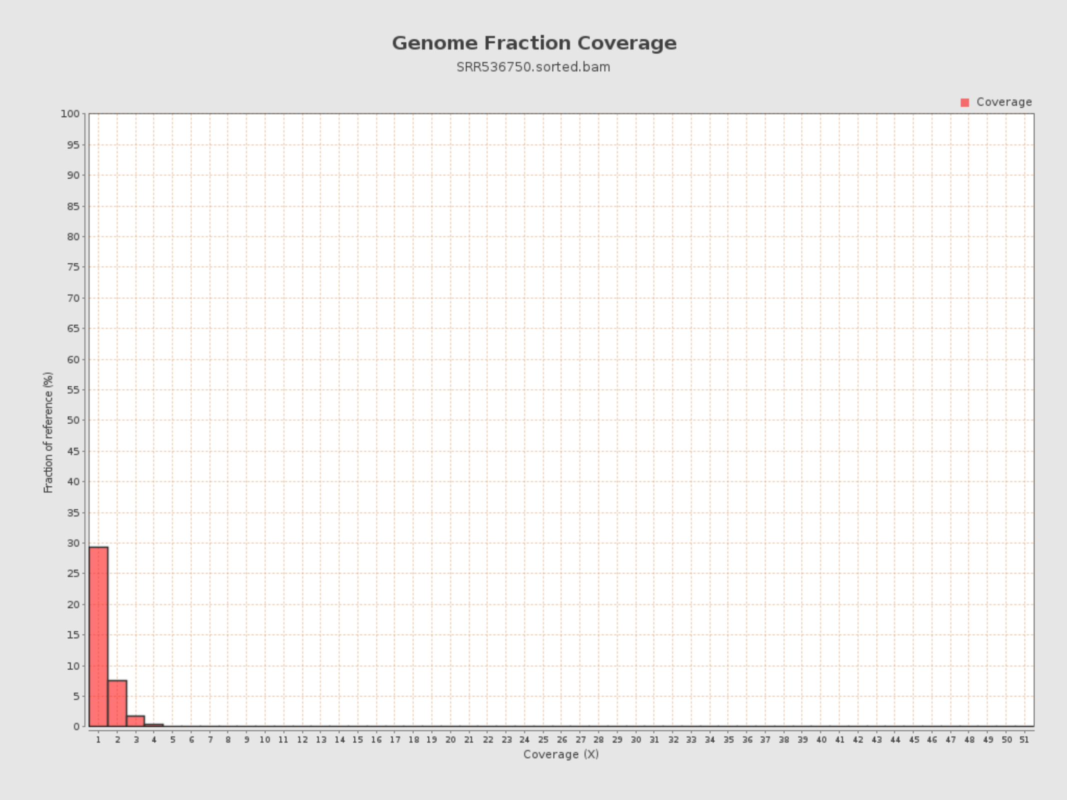
4. Results : Coverage Histogram



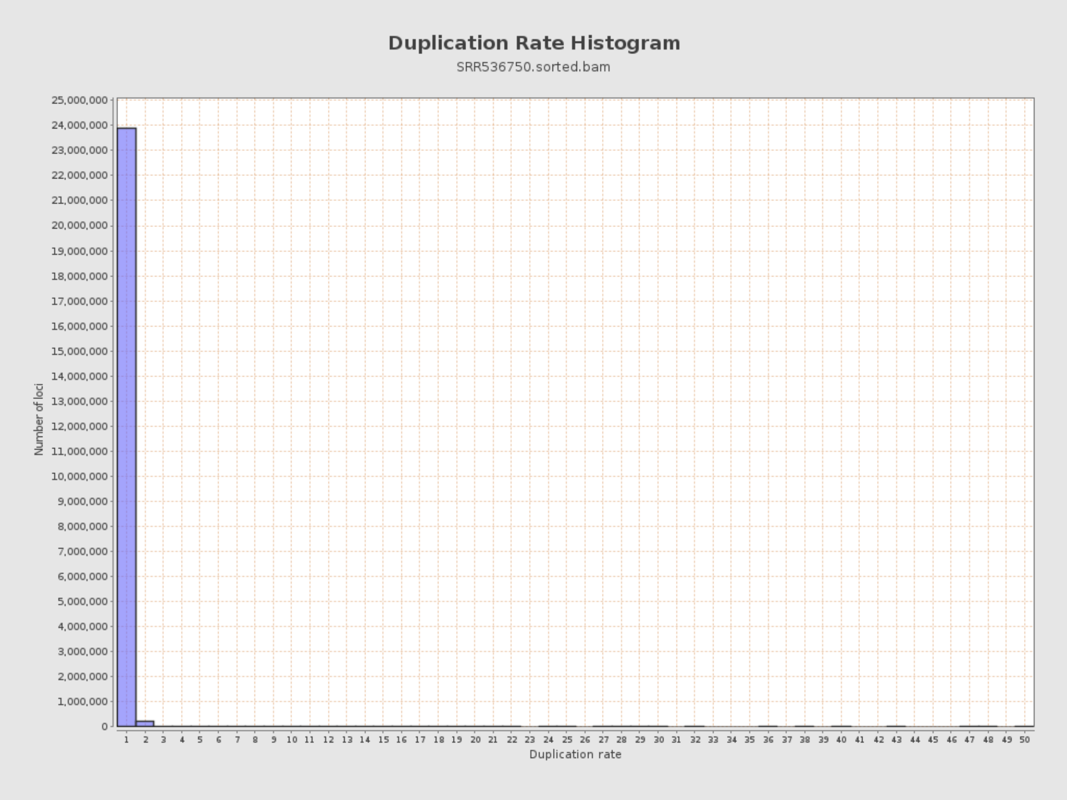
5. Results : Coverage Histogram (0-50X)



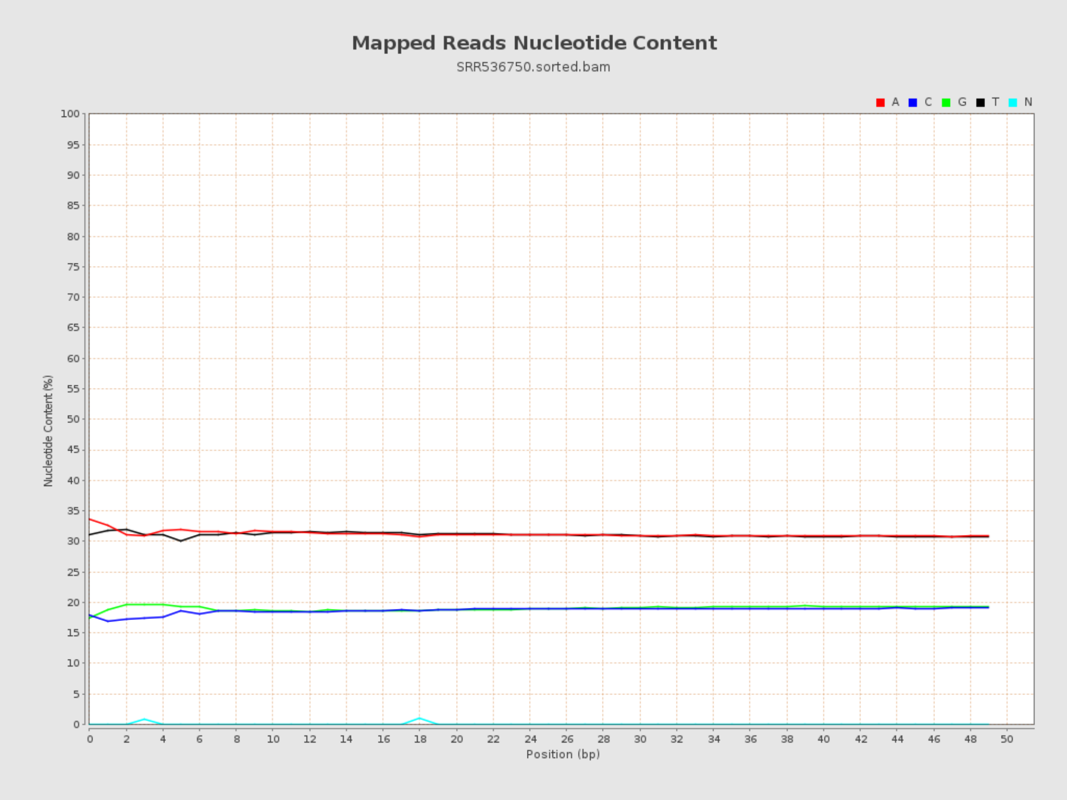
6. Results : Genome Fraction Coverage



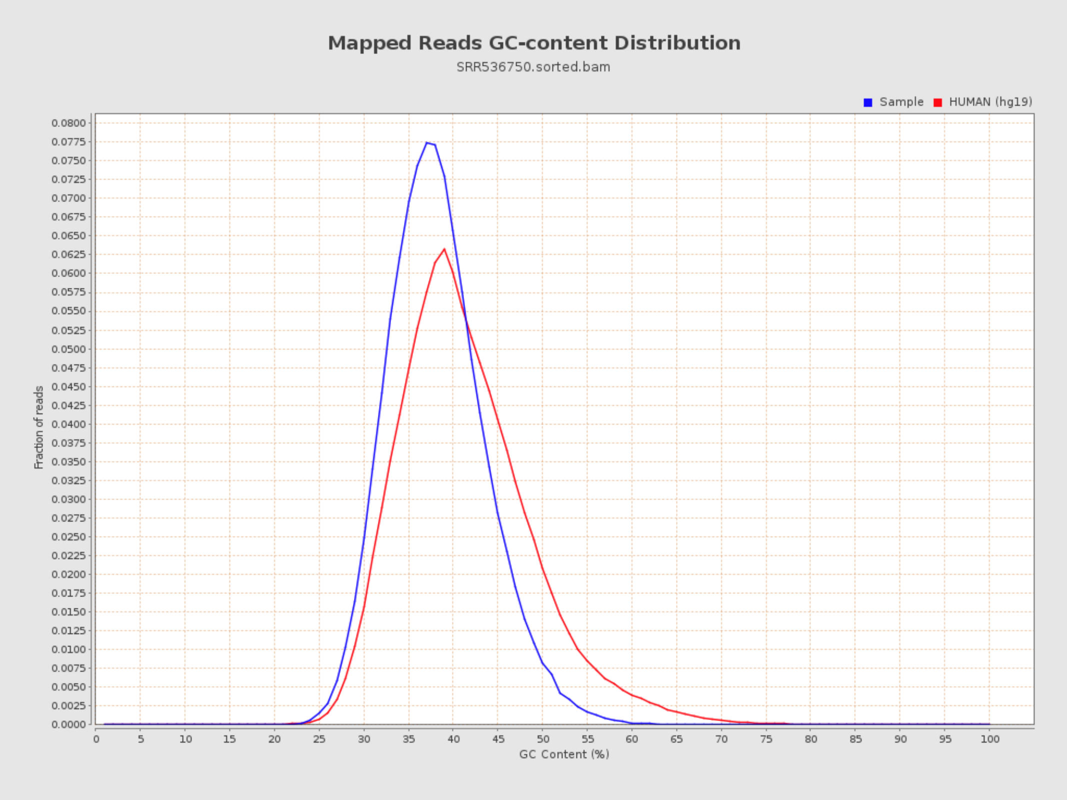
7. Results : Duplication Rate Histogram



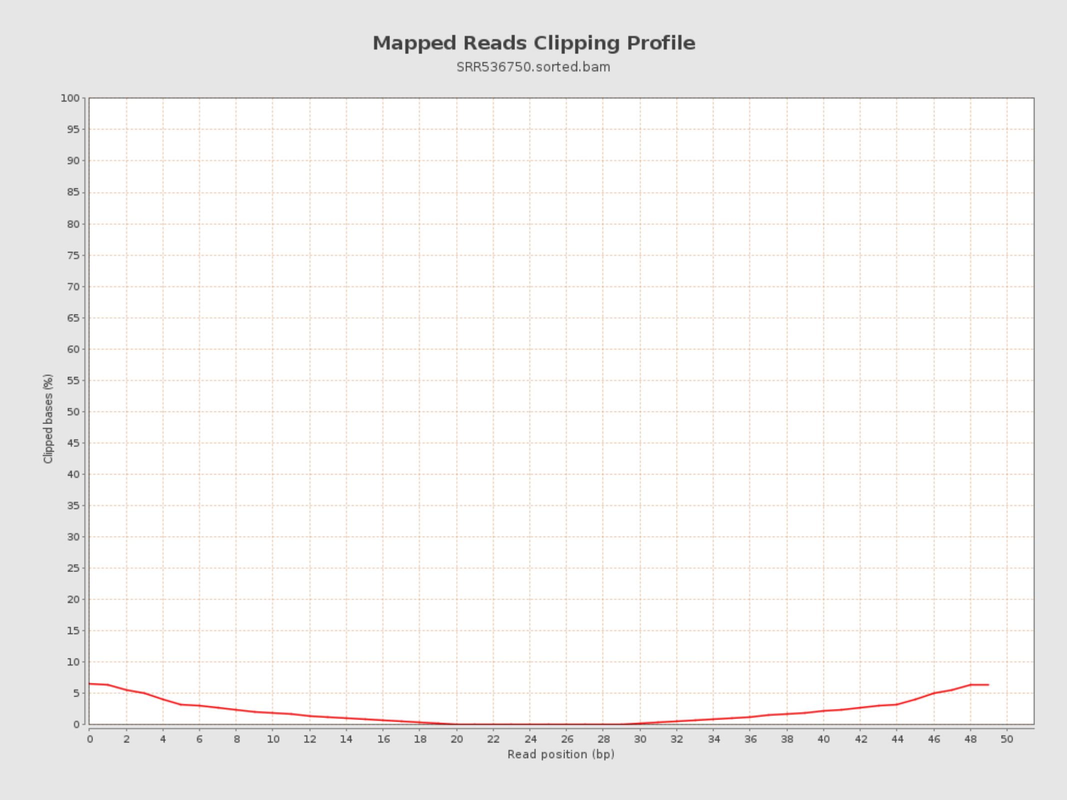
8. Results : Mapped Reads Nucleotide Content



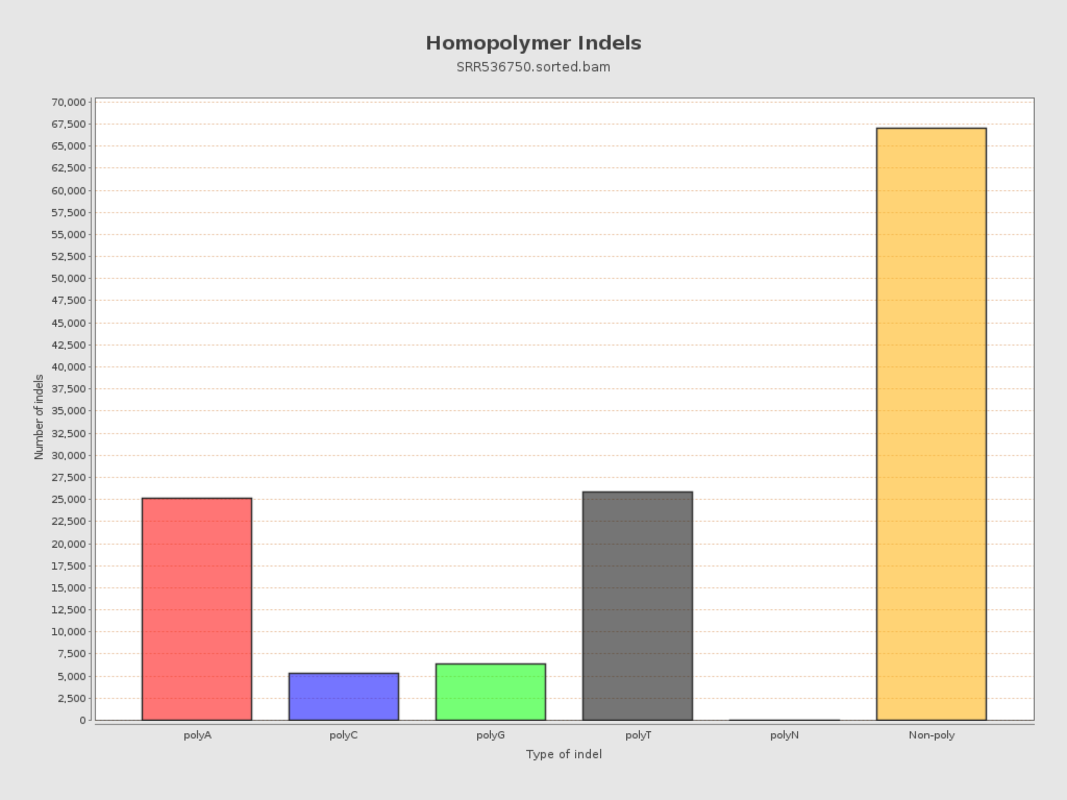
9. Results : Mapped Reads GC-content Distribution



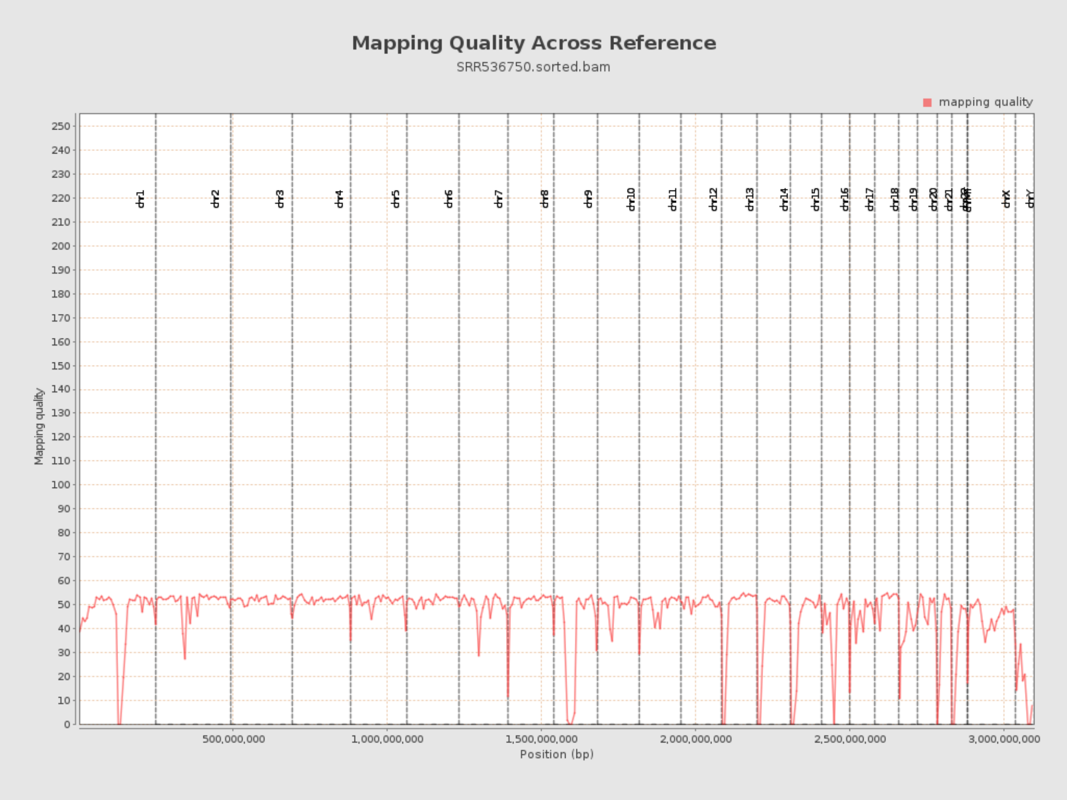
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram