Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/19 00:53:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR536762.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_SRR536762 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536762.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Mar 19 00:53:15 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR536762.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,168,003
Mapped reads	20,678,312 / 97.69%
Unmapped reads	489,691 / 2.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	566 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	219,140 / 1.04%
Duplication rate	1.05%
Clipped reads	288,467 / 1.36%

2.2. ACGT Content

Number/percentage of A's	321,054,771 / 31.13%
Number/percentage of C's	193,107,618 / 18.73%
Number/percentage of T's	319,451,182 / 30.98%
Number/percentage of G's	197,561,748 / 19.16%
Number/percentage of N's	36,643 / 0%
GC Percentage	37.88%

2.3. Coverage

Mean	0.3331

Standard Deviation	0.6637

2.4. Mapping Quality

Mean Mapping Quality	46.68

2.5. Mismatches and indels

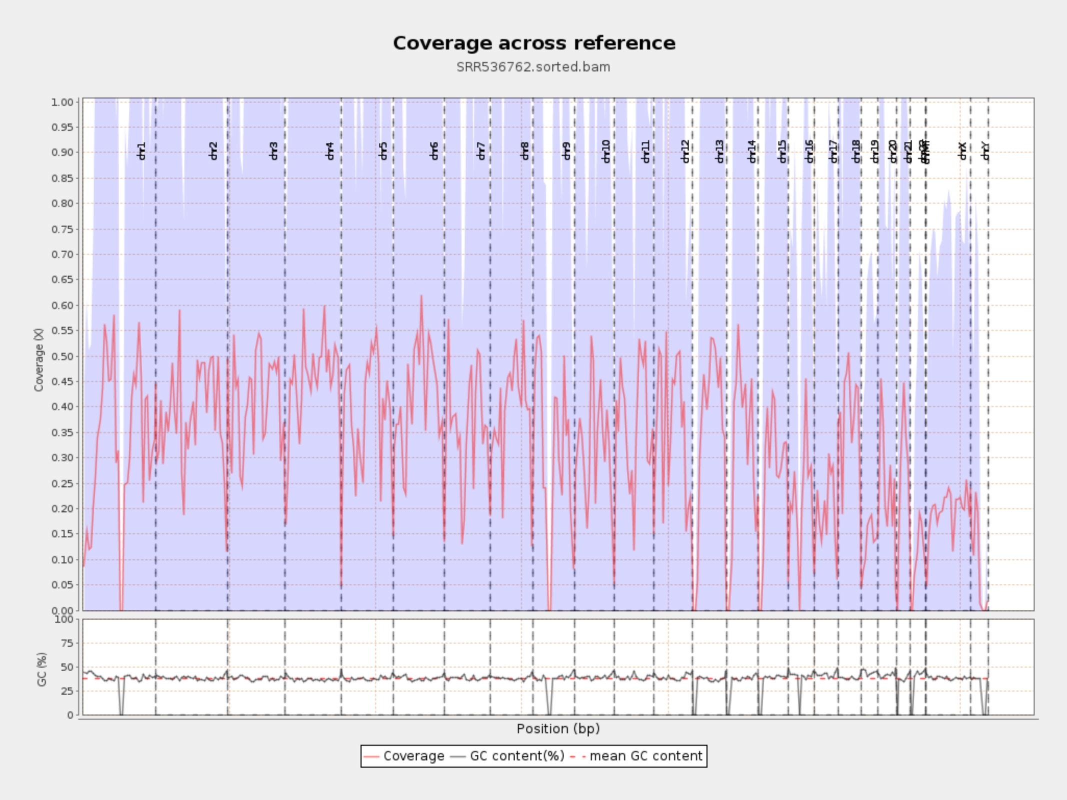
General error rate	0.21%
Mismatches	2,033,903
Insertions	62,322
Mapped reads with at least one insertion	0.3%
Deletions	56,832
Mapped reads with at least one deletion	0.27%
Homopolymer indels	49.2%

2.6. Chromosome stats

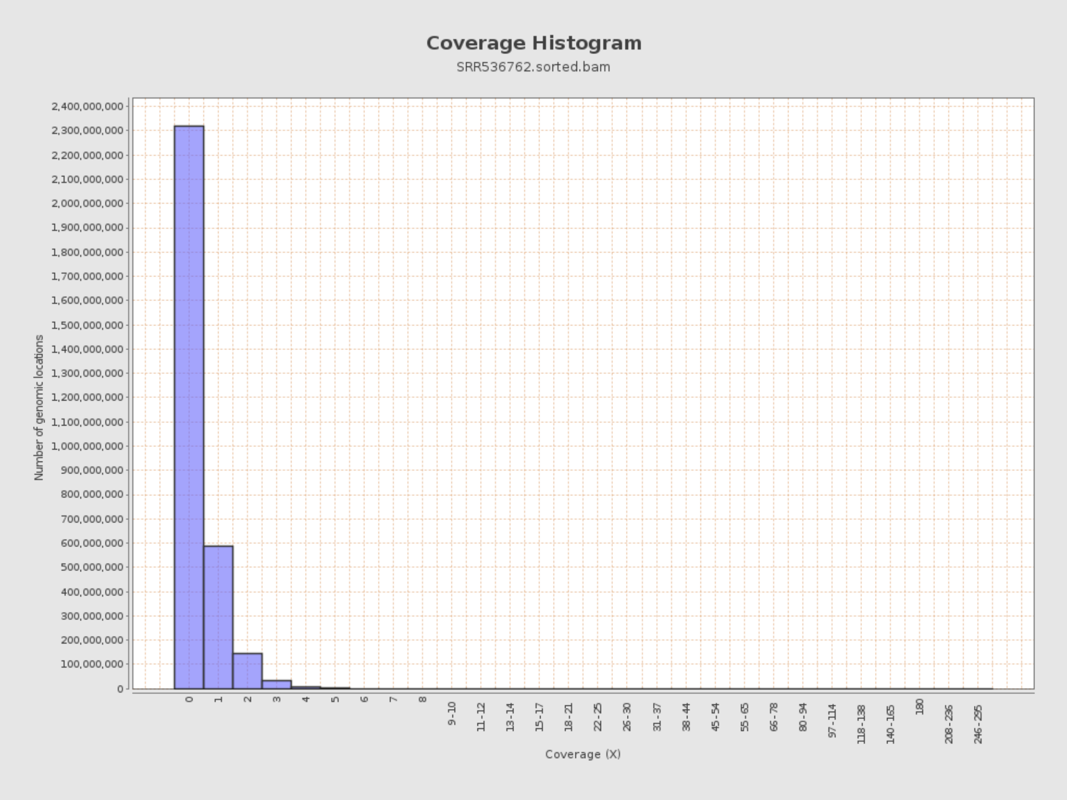
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	81203434	0.3258	0.6733
chr2	243199373	93666421	0.3851	0.7014
chr3	198022430	81950269	0.4138	0.7249
chr4	191154276	86116976	0.4505	0.7533
chr5	180915260	69876123	0.3862	0.7034
chr6	171115067	72841654	0.4257	0.7373
chr7	159138663	56929094	0.3577	0.6824

chr8	146364022	57775280	0.3947	0.7103
chr9	141213431	43940566	0.3112	0.6505
chr10	135534747	44108351	0.3254	0.6433
chr11	135006516	49382499	0.3658	0.6995
chr12	133851895	48176528	0.3599	0.6826
chr13	115169878	40888617	0.355	0.6829
chr14	107349540	33995250	0.3167	0.6549
chr15	102531392	27174291	0.265	0.5976
chr16	90354753	19199742	0.2125	0.5289
chr17	81195210	16122156	0.1986	0.5068
chr18	78077248	30277739	0.3878	0.7029
chr19	59128983	8128625	0.1375	0.4126
chr20	63025520	16166116	0.2565	0.5843
chr21	48129895	12227452	0.2541	0.5917
chr22	51304566	5343419	0.1042	0.3637
chrMT	16571	1169	0.0705	0.2918
chrX	155270560	30678629	0.1976	0.4902
chrY	59373566	5136670	0.0865	0.3392

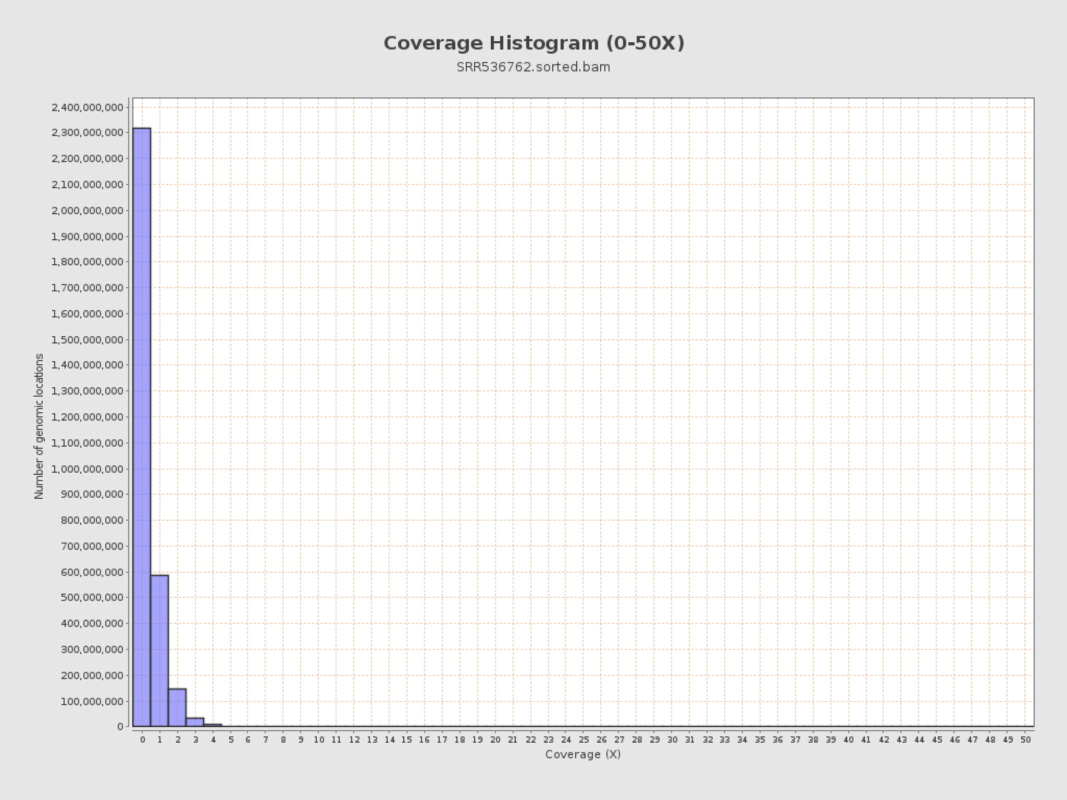
3. Results : Coverage across reference



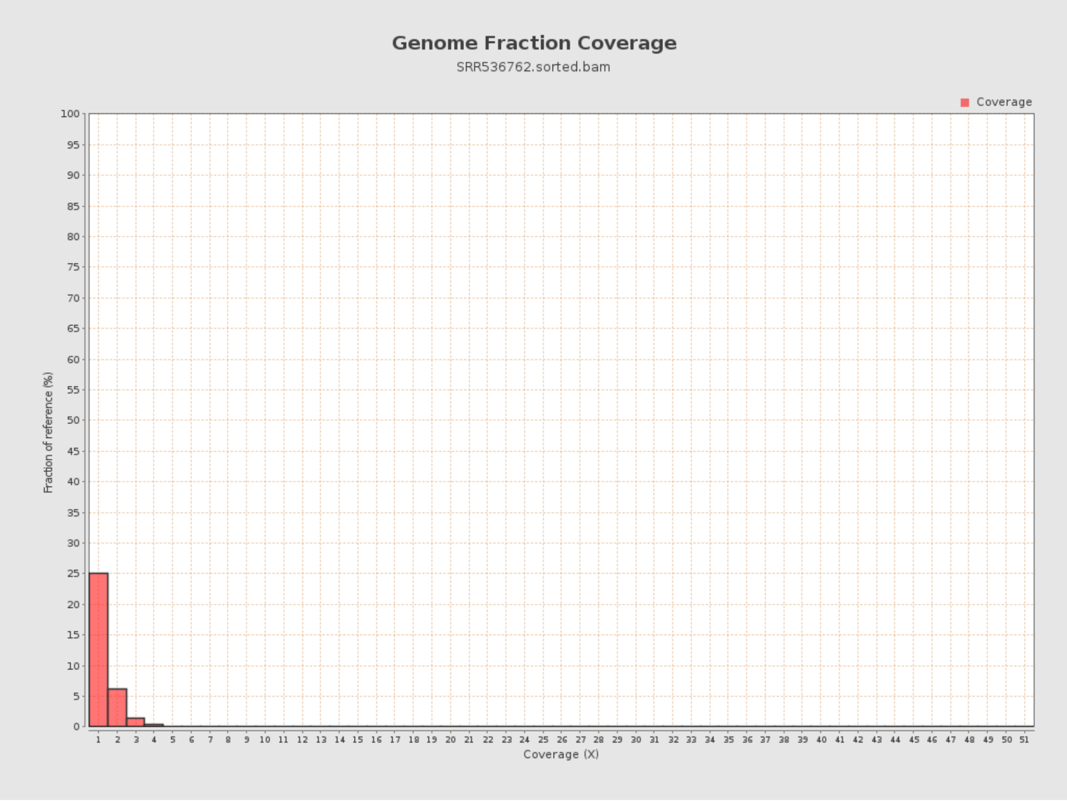
4. Results : Coverage Histogram



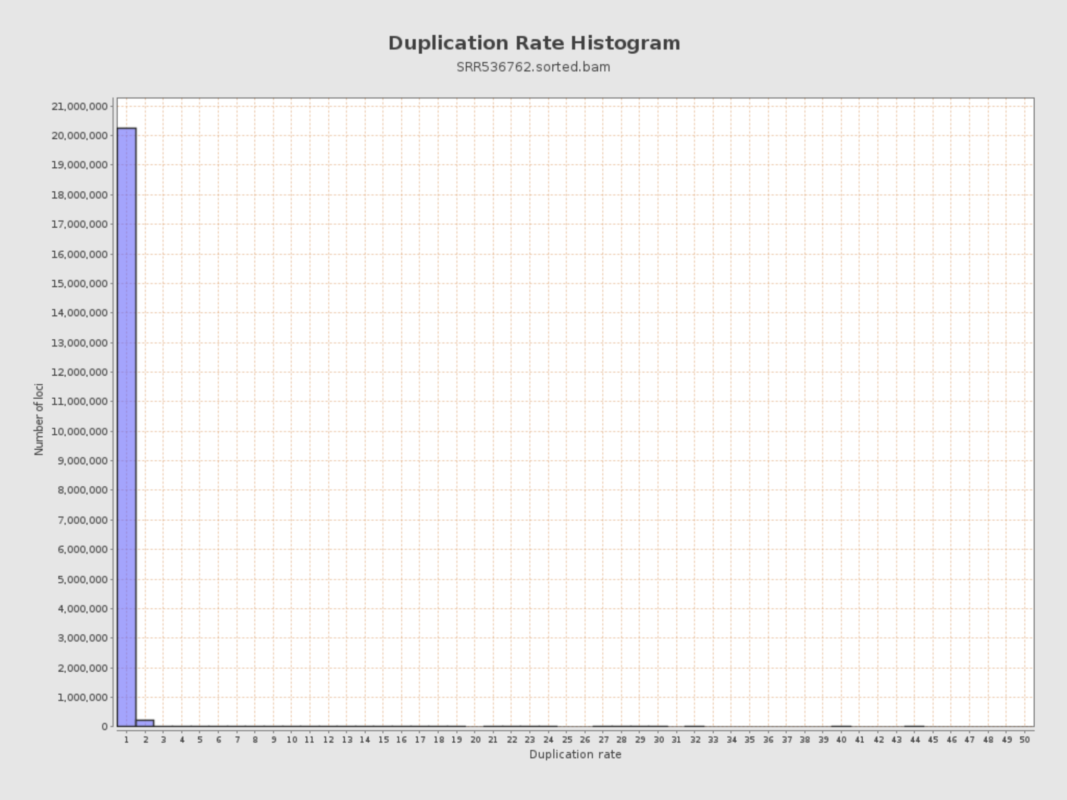
5. Results : Coverage Histogram (0-50X)



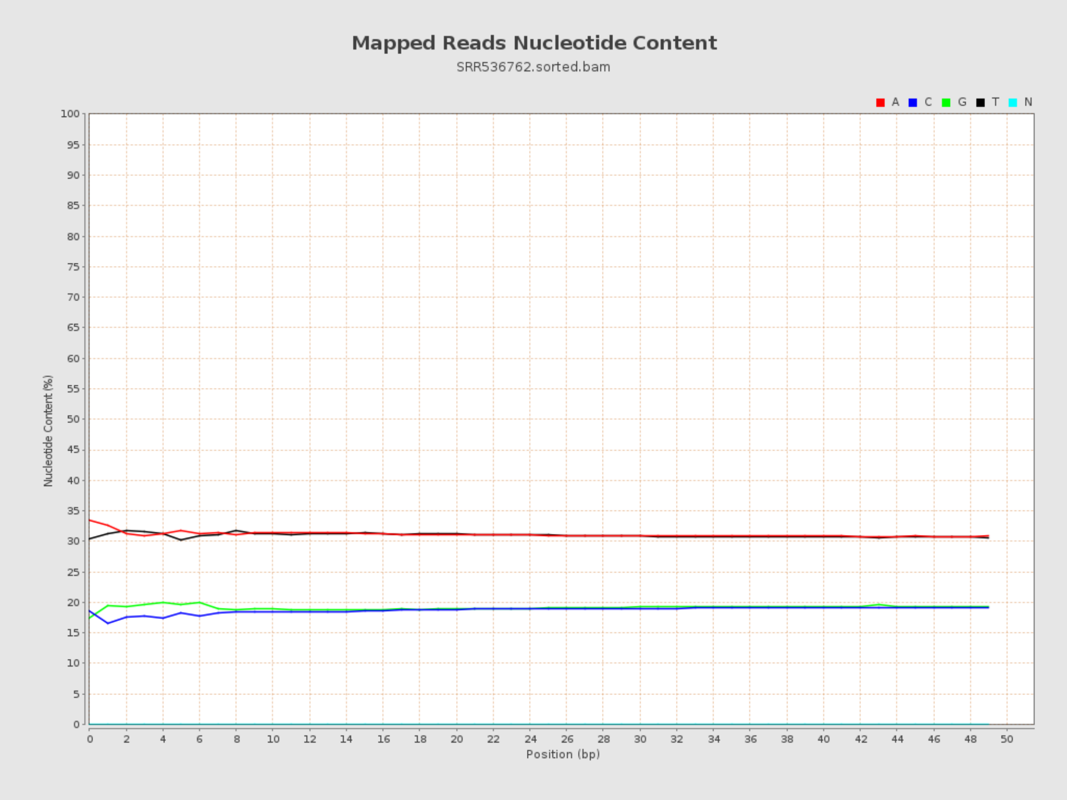
6. Results : Genome Fraction Coverage



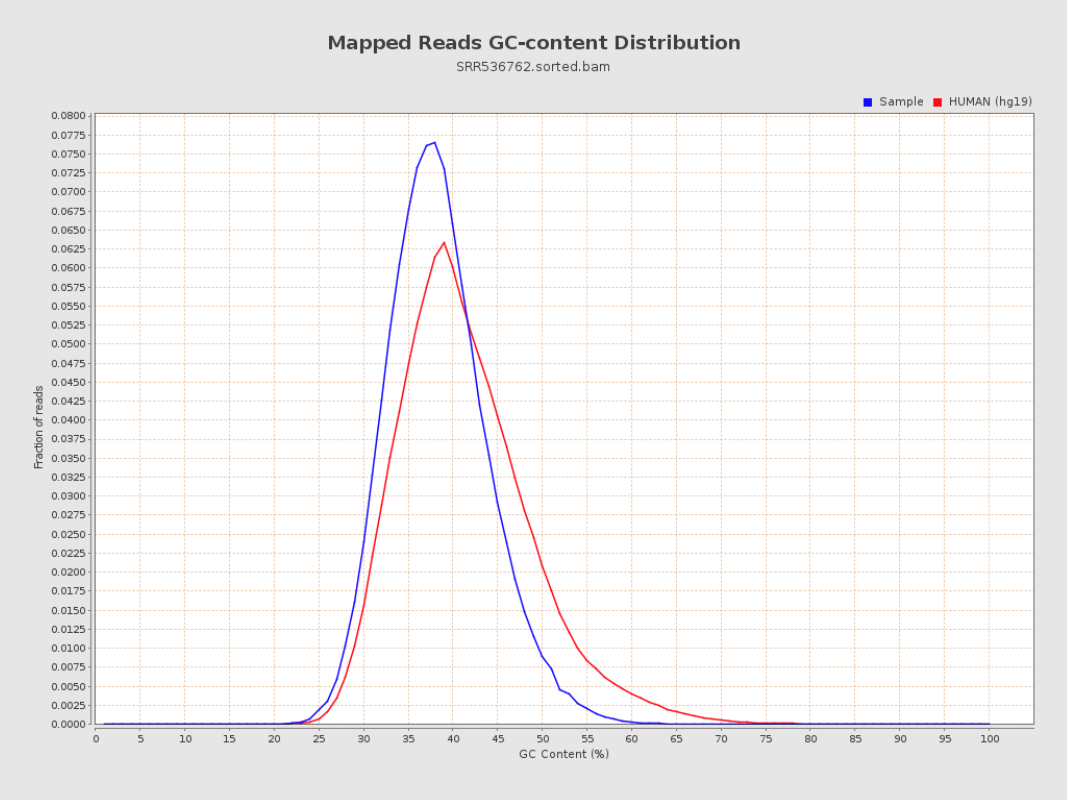
7. Results : Duplication Rate Histogram



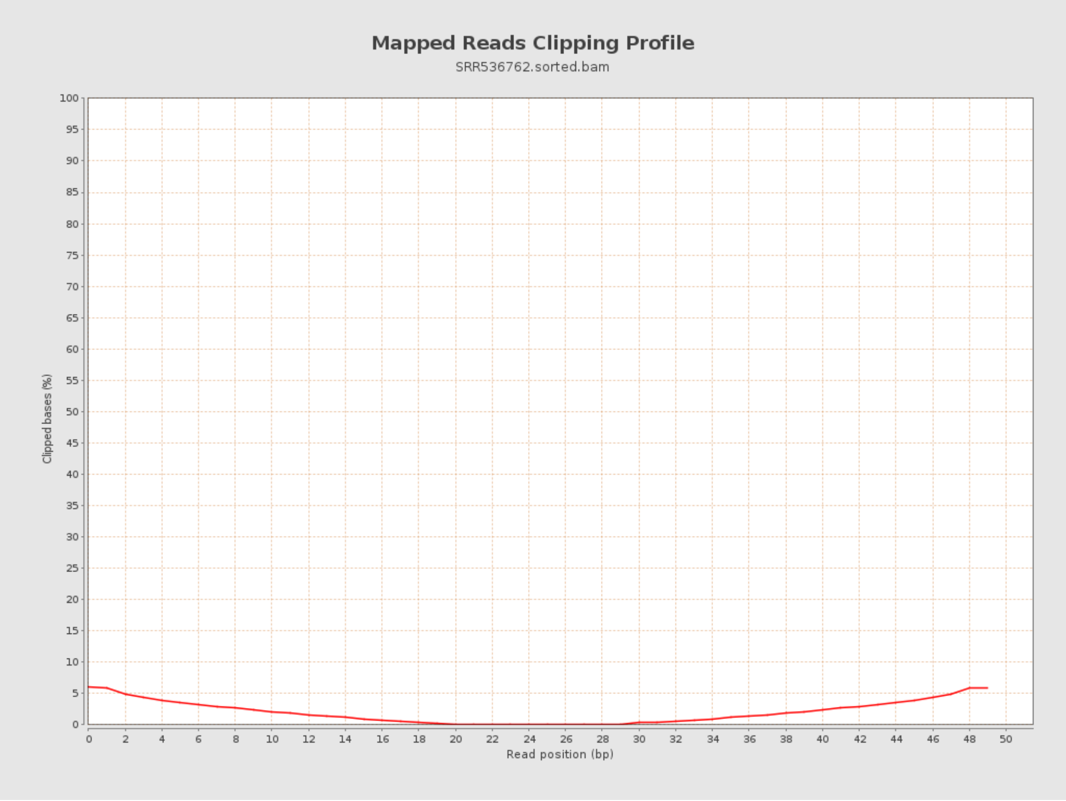
8. Results : Mapped Reads Nucleotide Content



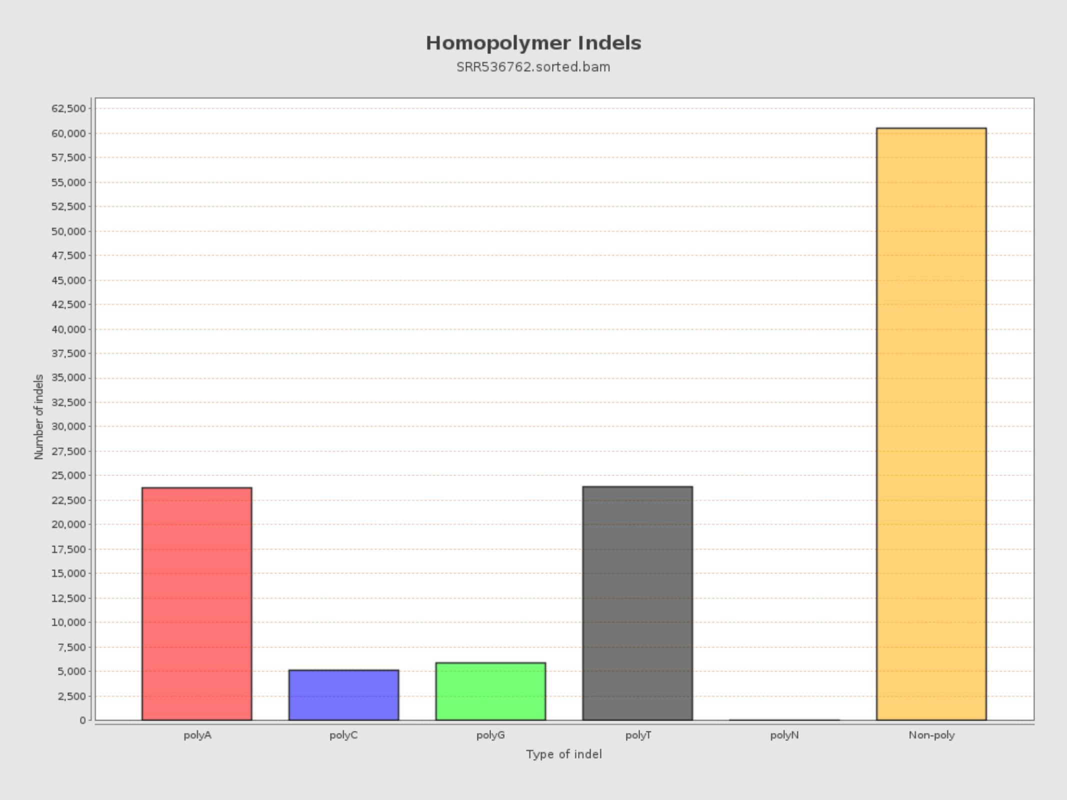
9. Results : Mapped Reads GC-content Distribution



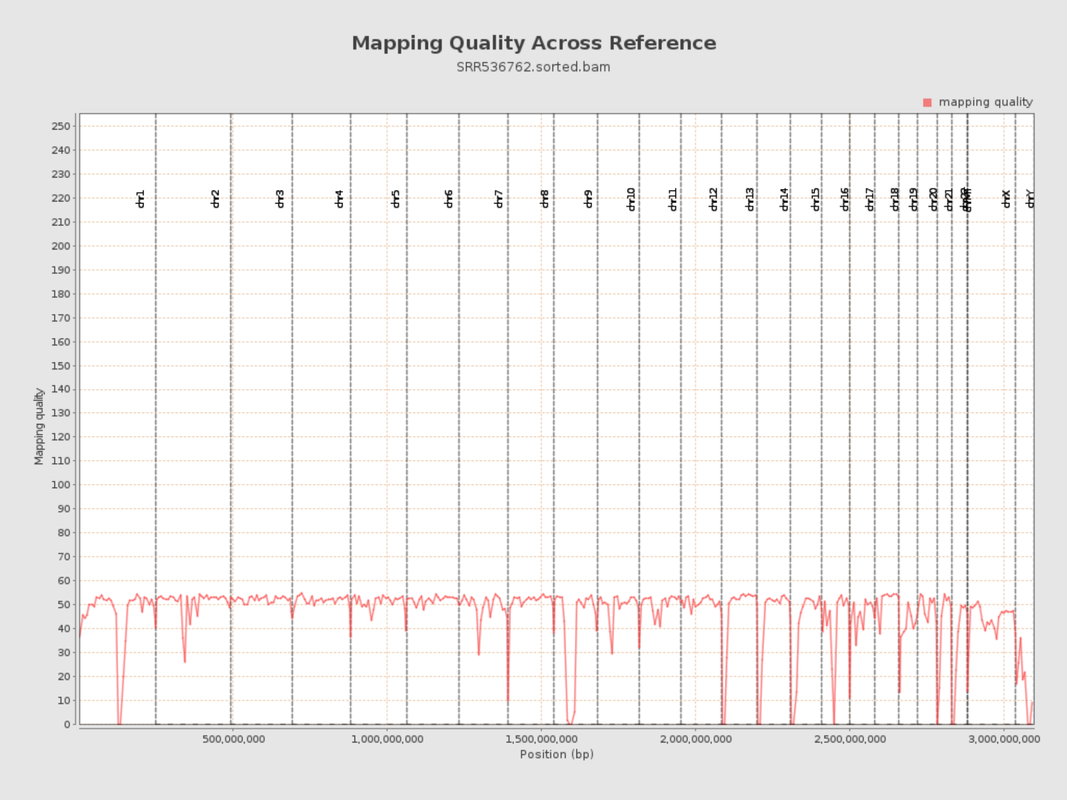
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram