Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:38:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818977.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_SRR1818977 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818977.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:38:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818977.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	966,172
Mapped reads	939,509 / 97.24%
Unmapped reads	26,663 / 2.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,294 / 1.58%
Read min/max/mean length	30 / 101 / 101.61
Duplicated reads (estimated)	309,455 / 32.03%
Duplication rate	28.07%
Clipped reads	946,800 / 97.99%

2.2. ACGT Content

Number/percentage of A's	25,411,440 / 29.29%
Number/percentage of C's	18,384,817 / 21.19%
Number/percentage of T's	25,134,980 / 28.97%
Number/percentage of G's	17,832,071 / 20.55%
Number/percentage of N's	4,680 / 0.01%
GC Percentage	41.74%

2.3. Coverage

Mean	0.028

Standard Deviation	0.382

2.4. Mapping Quality

Mean Mapping Quality	48.75

2.5. Mismatches and indels

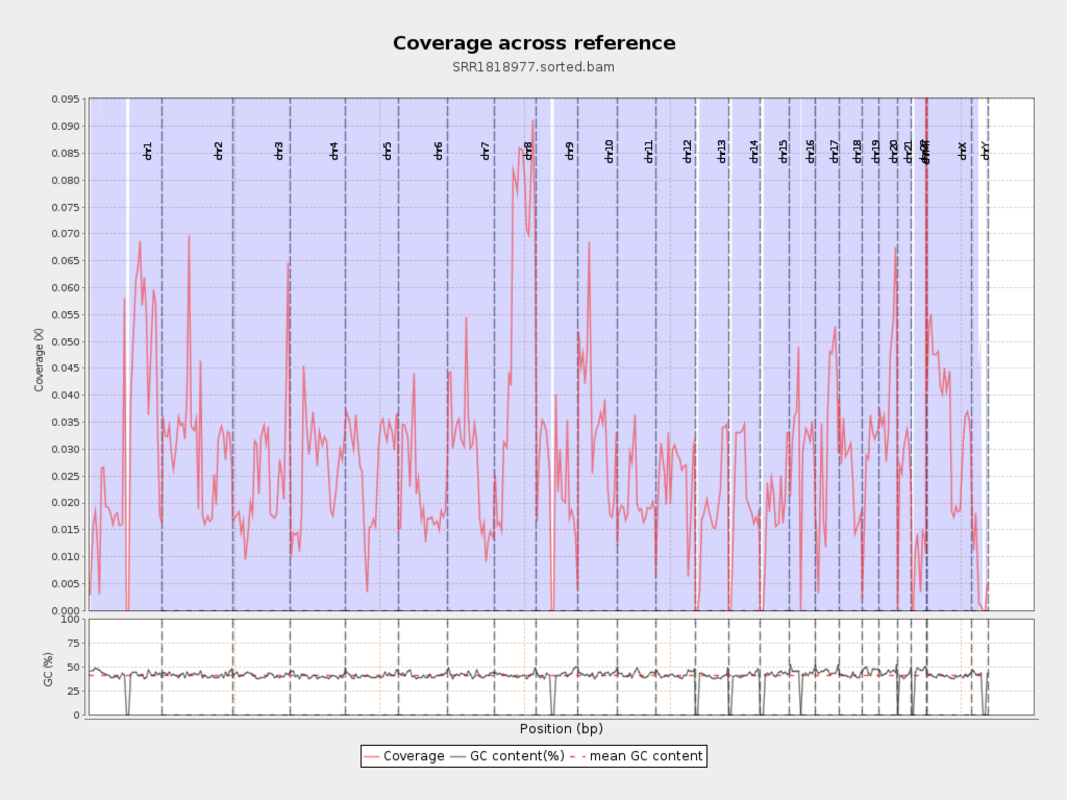
General error rate	0.69%
Mismatches	568,777
Insertions	15,019
Mapped reads with at least one insertion	1.56%
Deletions	28,416
Mapped reads with at least one deletion	2.96%
Homopolymer indels	40.2%

2.6. Chromosome stats

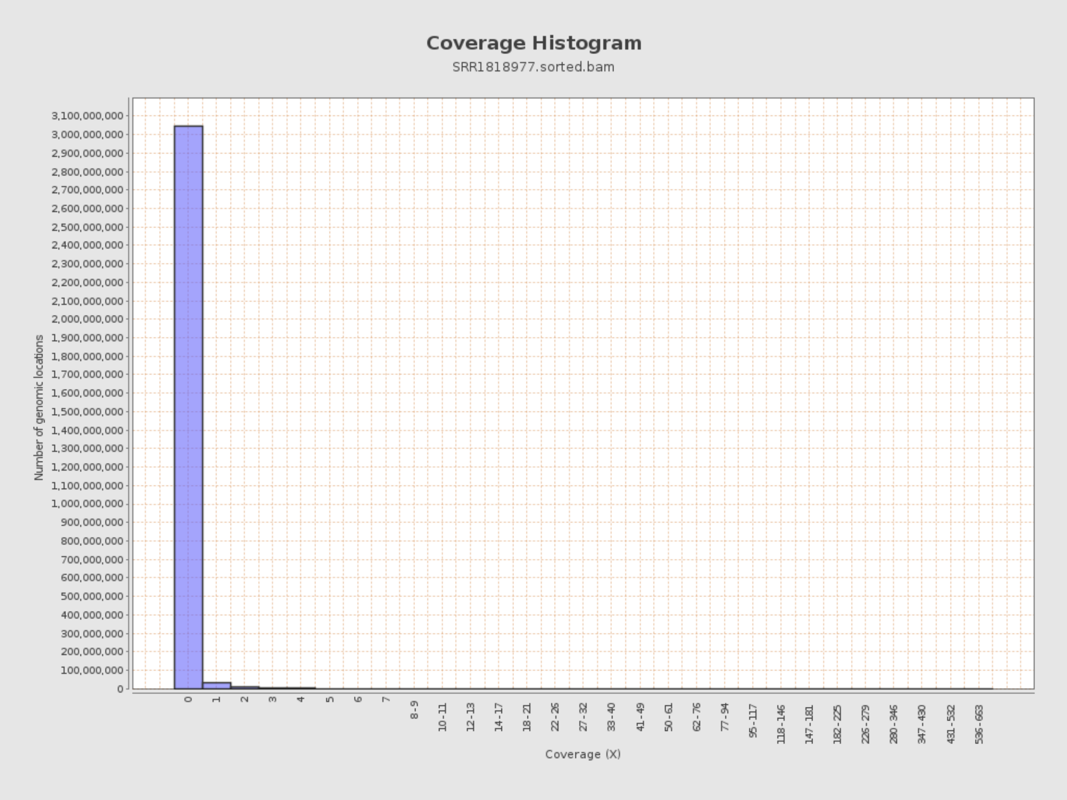
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7873839	0.0316	0.6205
chr2	243199373	7492818	0.0308	0.5443
chr3	198022430	4813884	0.0243	0.237
chr4	191154276	4974303	0.026	0.2816
chr5	180915260	5005850	0.0277	0.2607
chr6	171115067	3782200	0.0221	0.2609
chr7	159138663	4499658	0.0283	0.4696

chr8	146364022	8419524	0.0575	0.3959
chr9	141213431	3275873	0.0232	0.3405
chr10	135534747	4899893	0.0362	0.4833
chr11	135006516	2761734	0.0205	0.2536
chr12	133851895	3323699	0.0248	0.2427
chr13	115169878	2140486	0.0186	0.2065
chr14	107349540	2244040	0.0209	0.2328
chr15	102531392	1837614	0.0179	0.2041
chr16	90354753	2777590	0.0307	0.4605
chr17	81195210	2521011	0.031	0.3049
chr18	78077248	1955682	0.025	0.4001
chr19	59128983	1682500	0.0285	0.5686
chr20	63025520	2725887	0.0433	0.3387
chr21	48129895	1246385	0.0259	0.2643
chr22	51304566	463306	0.009	0.1594
chrMT	16571	47303	2.8546	3.1674
chrX	155270560	5701183	0.0367	0.331
chrY	59373566	355026	0.006	0.3673

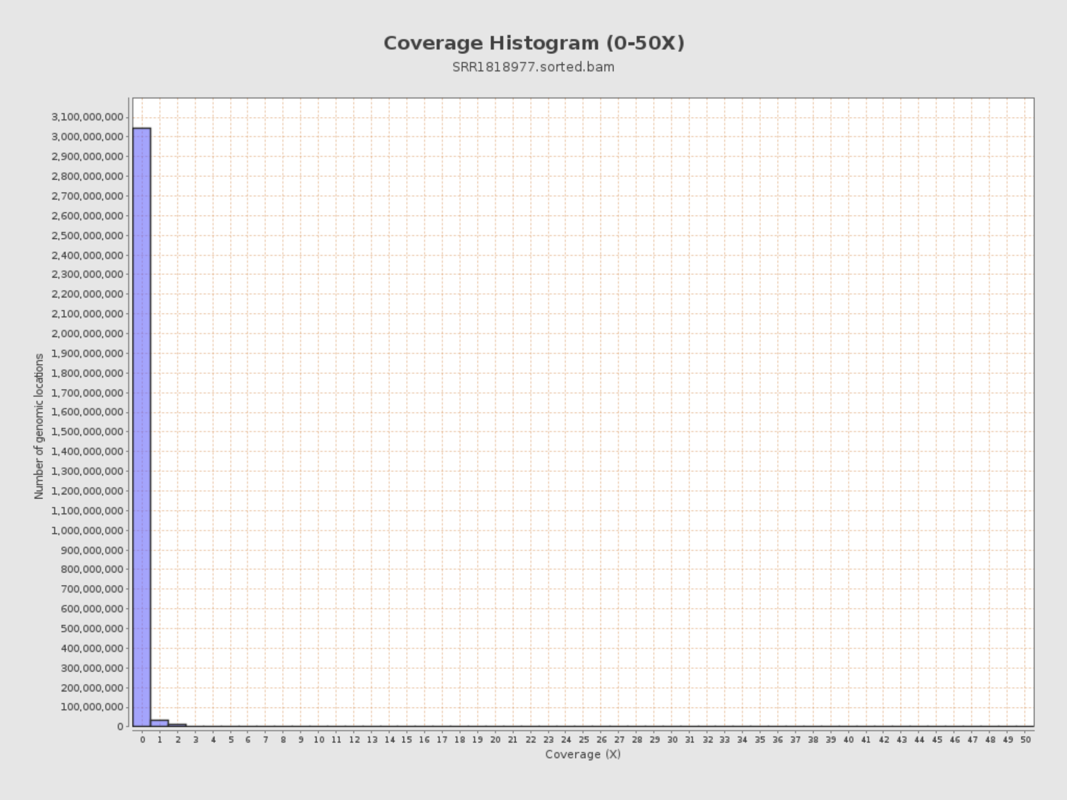
3. Results : Coverage across reference



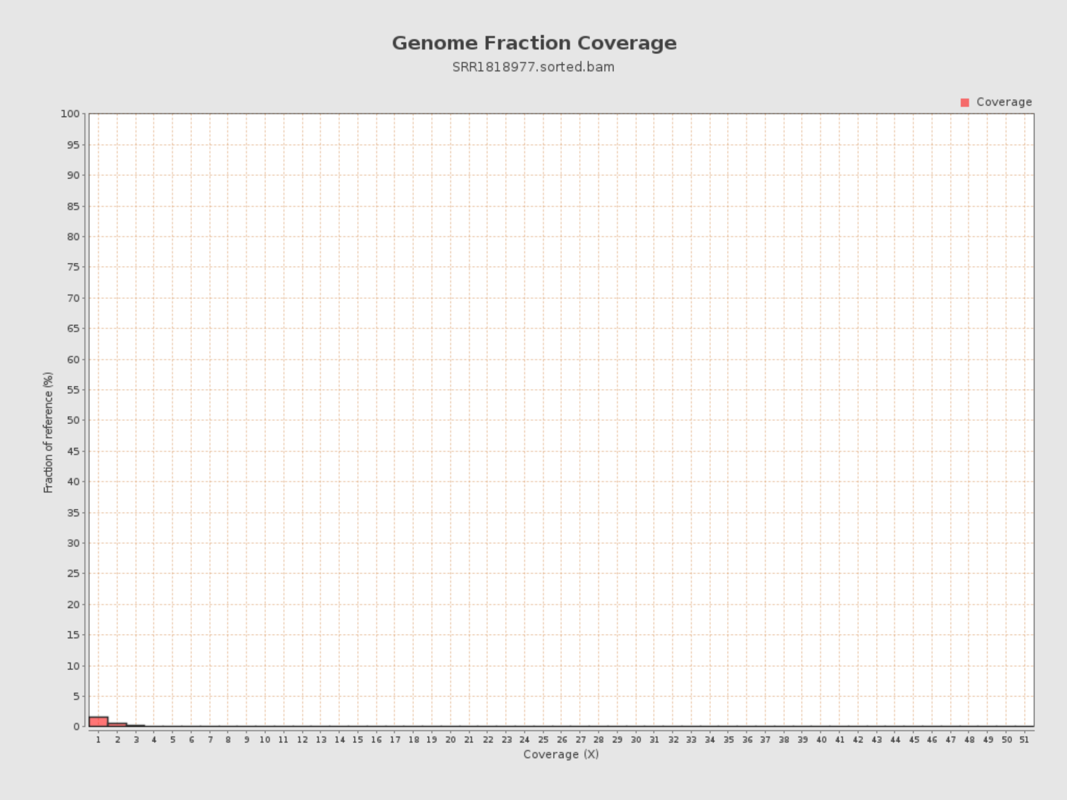
4. Results : Coverage Histogram



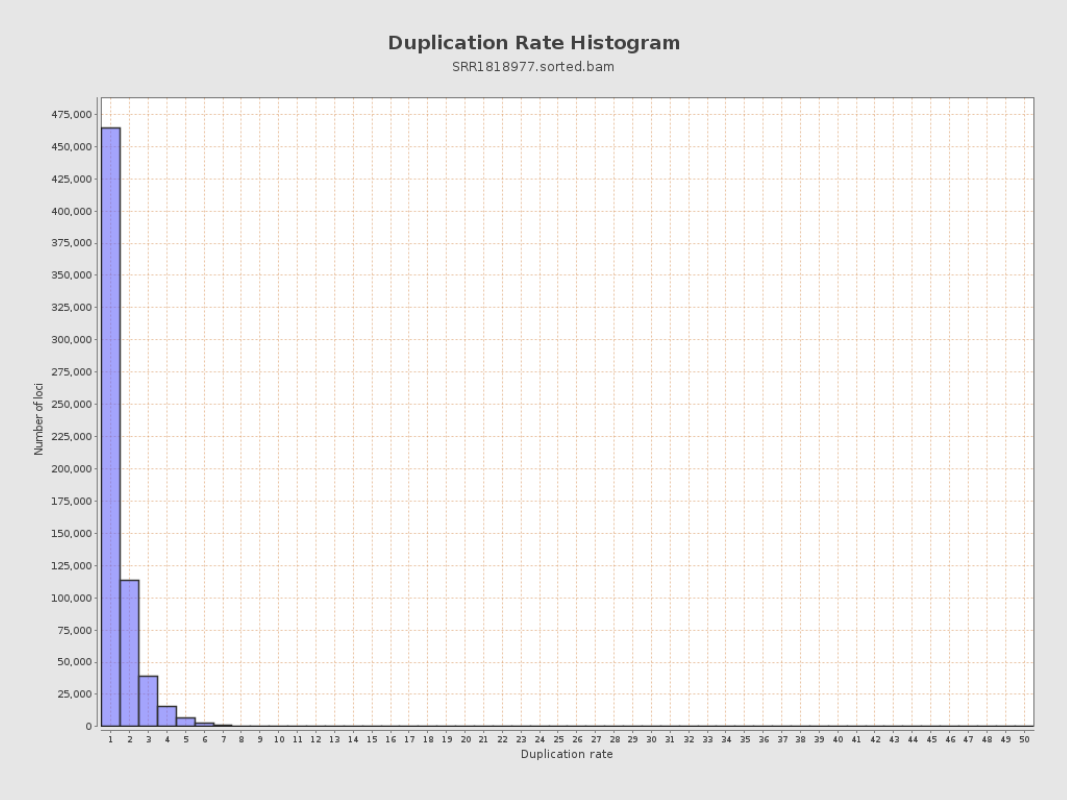
5. Results : Coverage Histogram (0-50X)



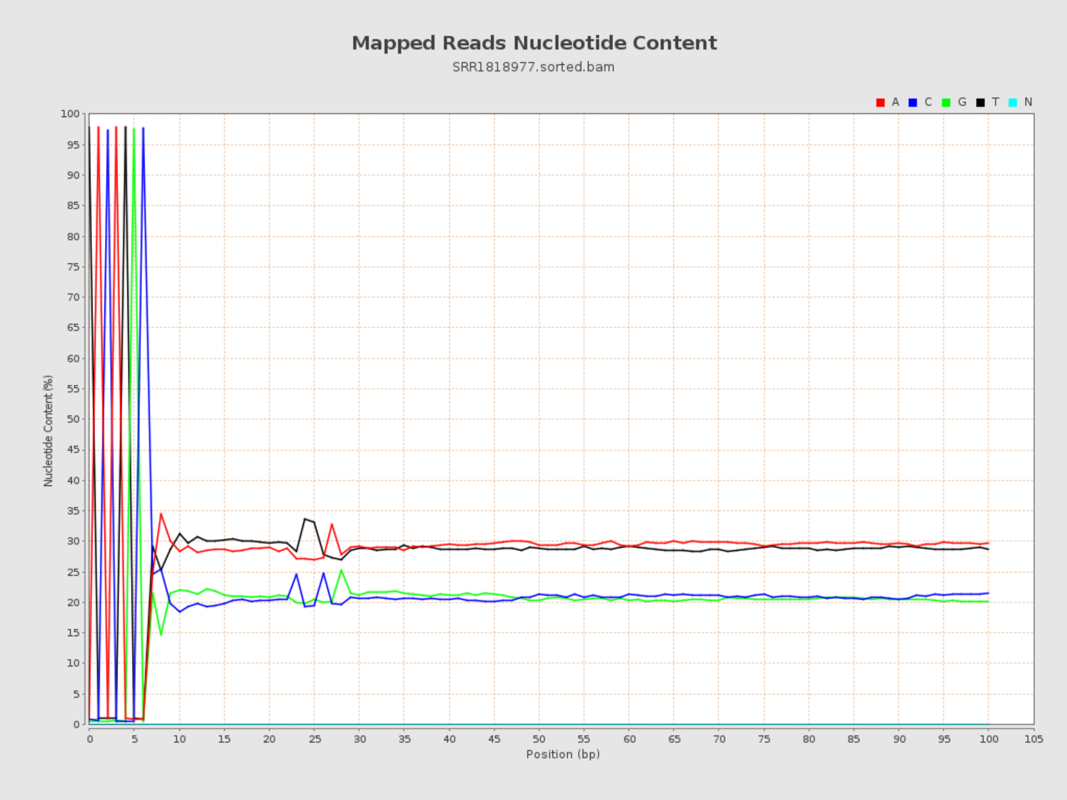
6. Results : Genome Fraction Coverage



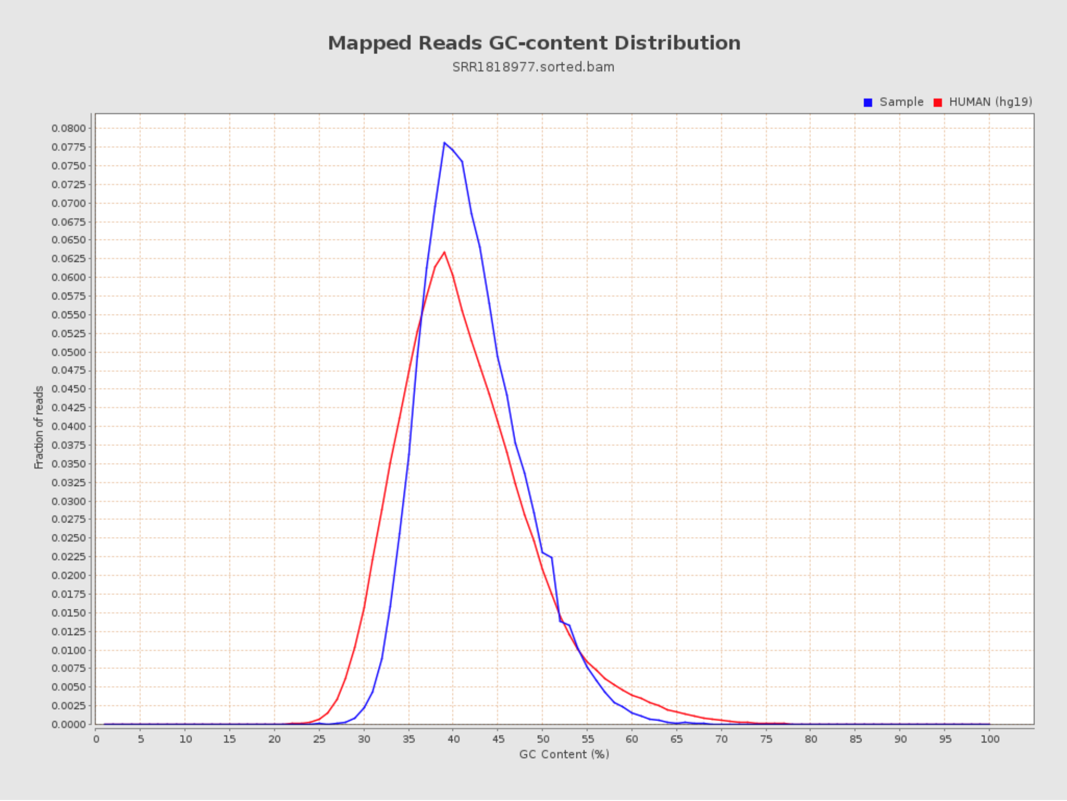
7. Results : Duplication Rate Histogram



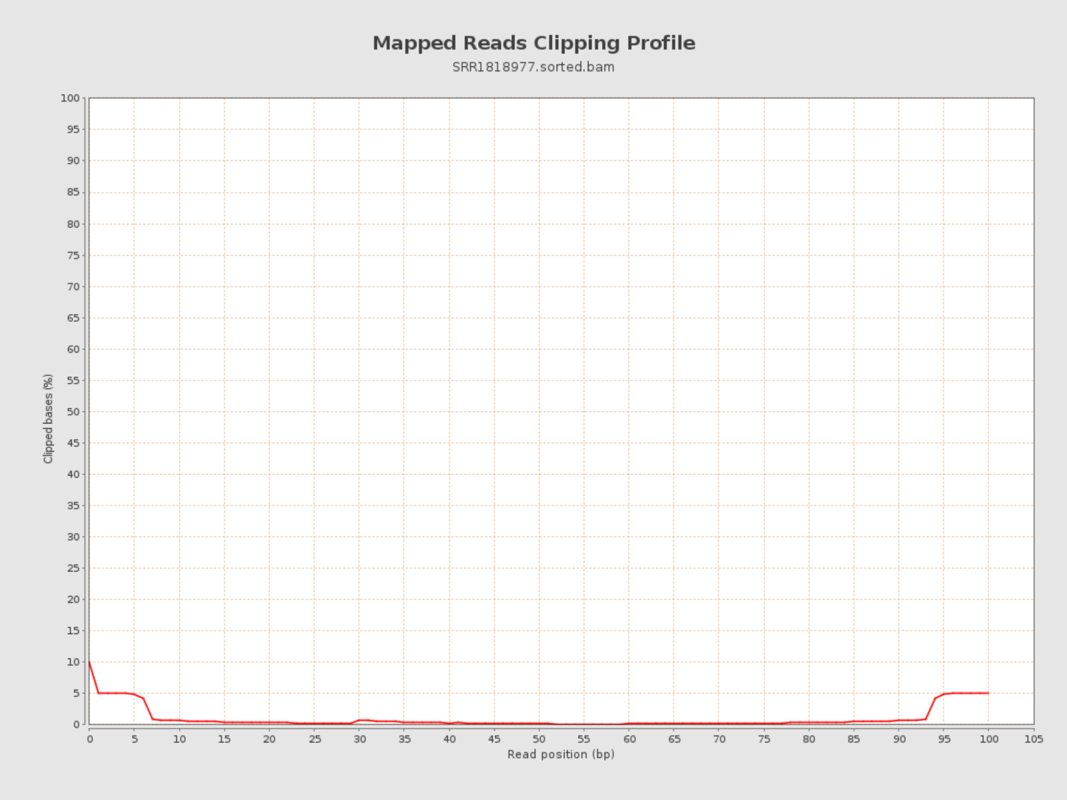
8. Results : Mapped Reads Nucleotide Content



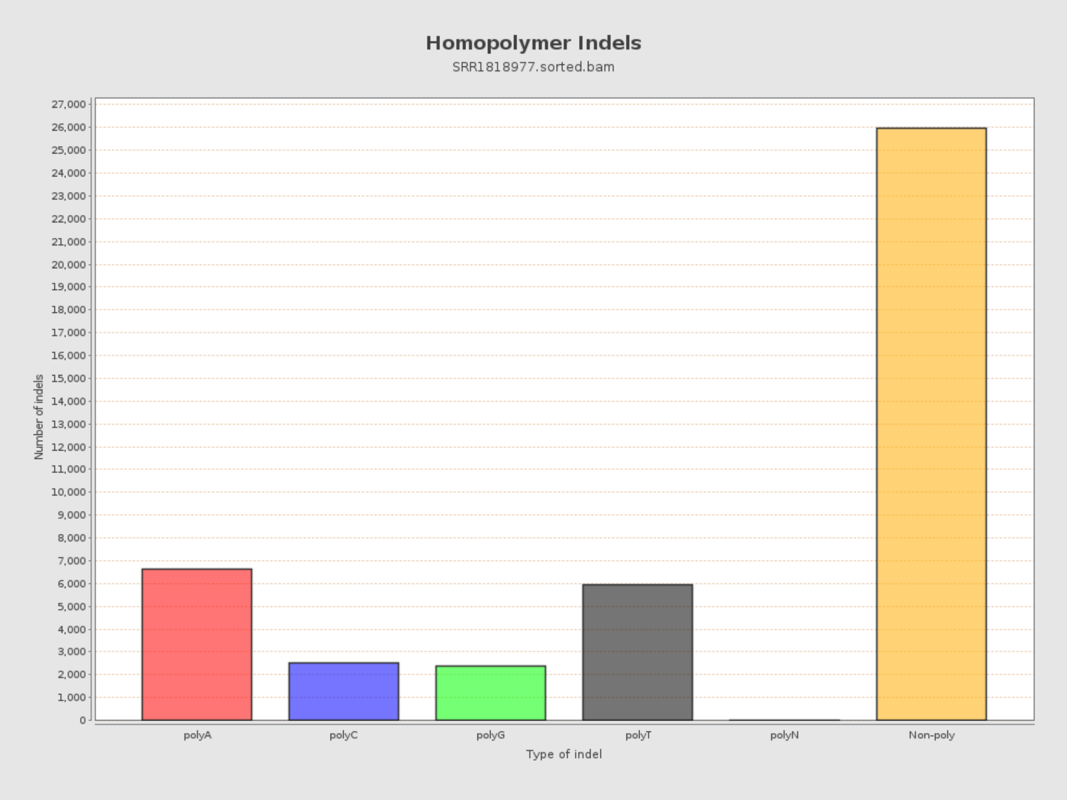
9. Results : Mapped Reads GC-content Distribution



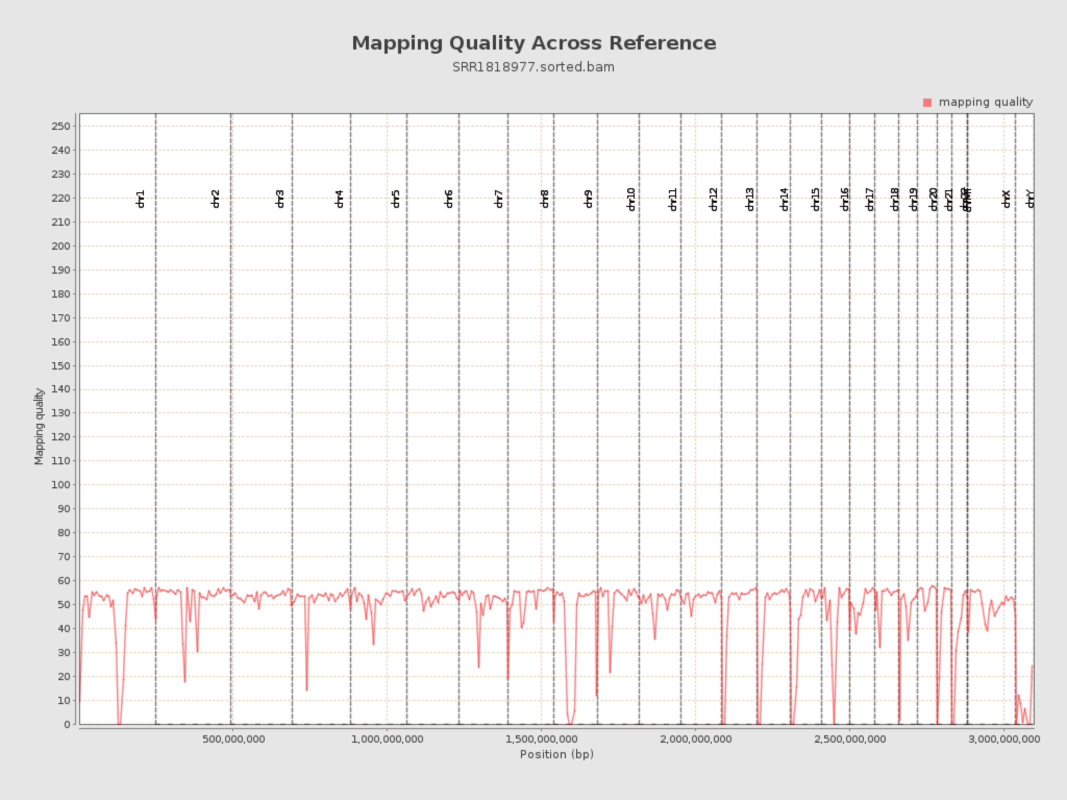
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram