Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 09:35:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818777.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_SRR1818777 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818777.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 09:35:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818777.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,719,639
Mapped reads	1,675,766 / 97.45%
Unmapped reads	43,873 / 2.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,228 / 0.94%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	889,962 / 51.75%
Duplication rate	44.55%
Clipped reads	1,680,615 / 97.73%

2.2. ACGT Content

Number/percentage of A's	32,172,444 / 28.33%
Number/percentage of C's	25,123,517 / 22.12%
Number/percentage of T's	32,149,745 / 28.31%
Number/percentage of G's	24,113,802 / 21.23%
Number/percentage of N's	6,839 / 0.01%
GC Percentage	43.36%

2.3. Coverage

Mean	0.0367

Standard Deviation	0.5205

2.4. Mapping Quality

Mean Mapping Quality	47.87

2.5. Mismatches and indels

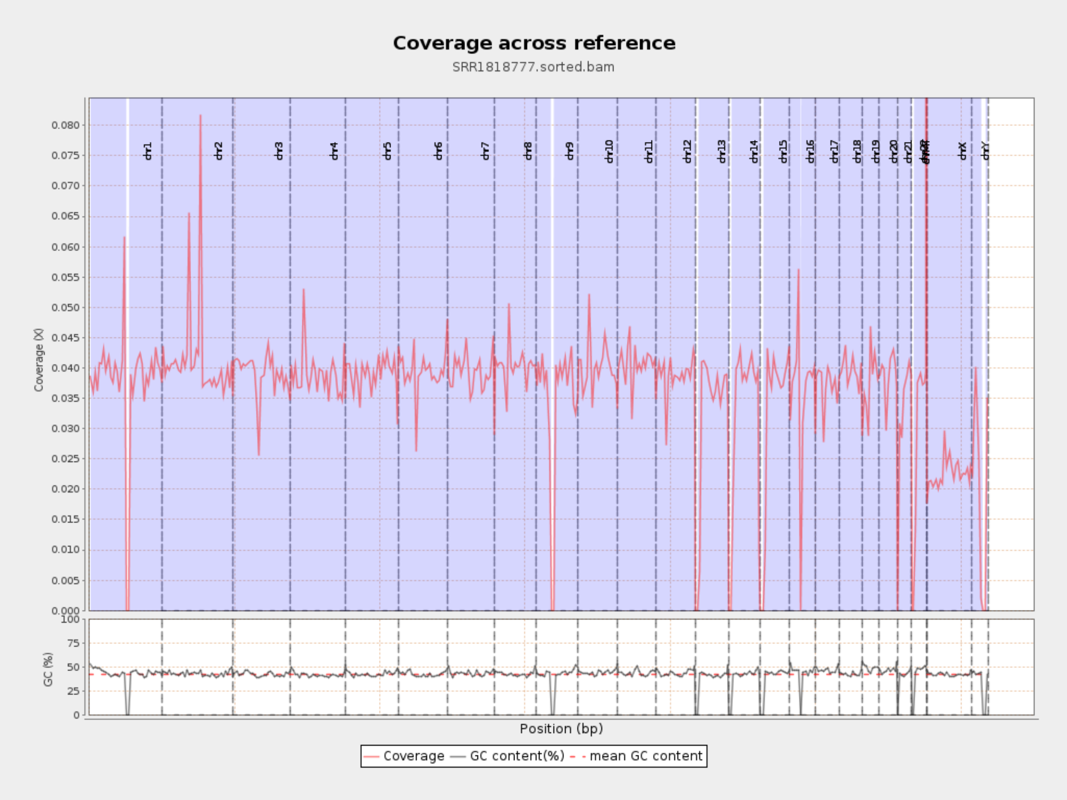
General error rate	0.54%
Mismatches	586,932
Insertions	13,834
Mapped reads with at least one insertion	0.82%
Deletions	29,570
Mapped reads with at least one deletion	1.75%
Homopolymer indels	39.81%

2.6. Chromosome stats

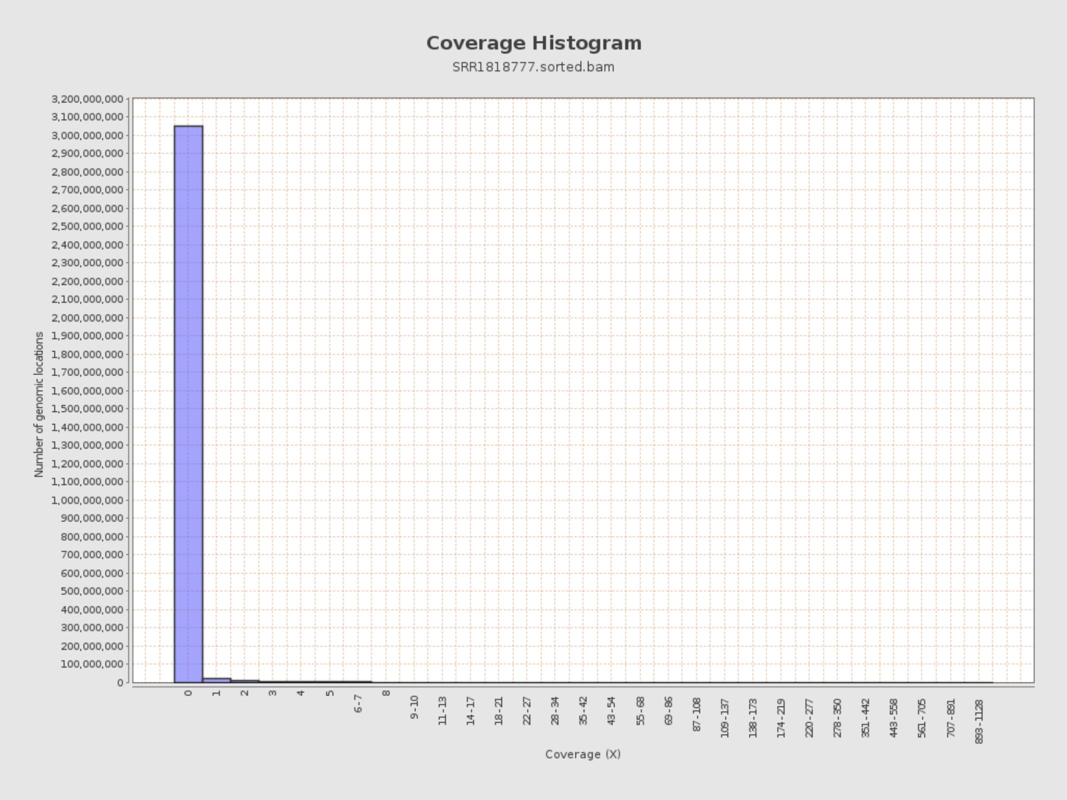
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9376396	0.0376	0.6796
chr2	243199373	10119412	0.0416	0.8417
chr3	198022430	7729610	0.039	0.4011
chr4	191154276	7426573	0.0389	0.4376
chr5	180915260	7069229	0.0391	0.4162
chr6	171115067	6739111	0.0394	0.4329
chr7	159138663	6262615	0.0394	0.4768

chr8	146364022	5926850	0.0405	0.4499
chr9	141213431	4814593	0.0341	0.4352
chr10	135534747	5451605	0.0402	0.5335
chr11	135006516	5479097	0.0406	0.4603
chr12	133851895	5177893	0.0387	0.4304
chr13	115169878	3627144	0.0315	0.3638
chr14	107349540	3546276	0.033	0.4066
chr15	102531392	3244746	0.0316	0.3607
chr16	90354753	3266432	0.0362	0.5638
chr17	81195210	2997786	0.0369	0.4093
chr18	78077248	3095775	0.0397	0.5831
chr19	59128983	2213825	0.0374	0.604
chr20	63025520	2446226	0.0388	0.4361
chr21	48129895	1552136	0.0322	0.39
chr22	51304566	1352637	0.0264	0.3729
chrMT	16571	53394	3.2221	4.2801
chrX	155270560	3508111	0.0226	0.3212
chrY	59373566	1136014	0.0191	0.9631

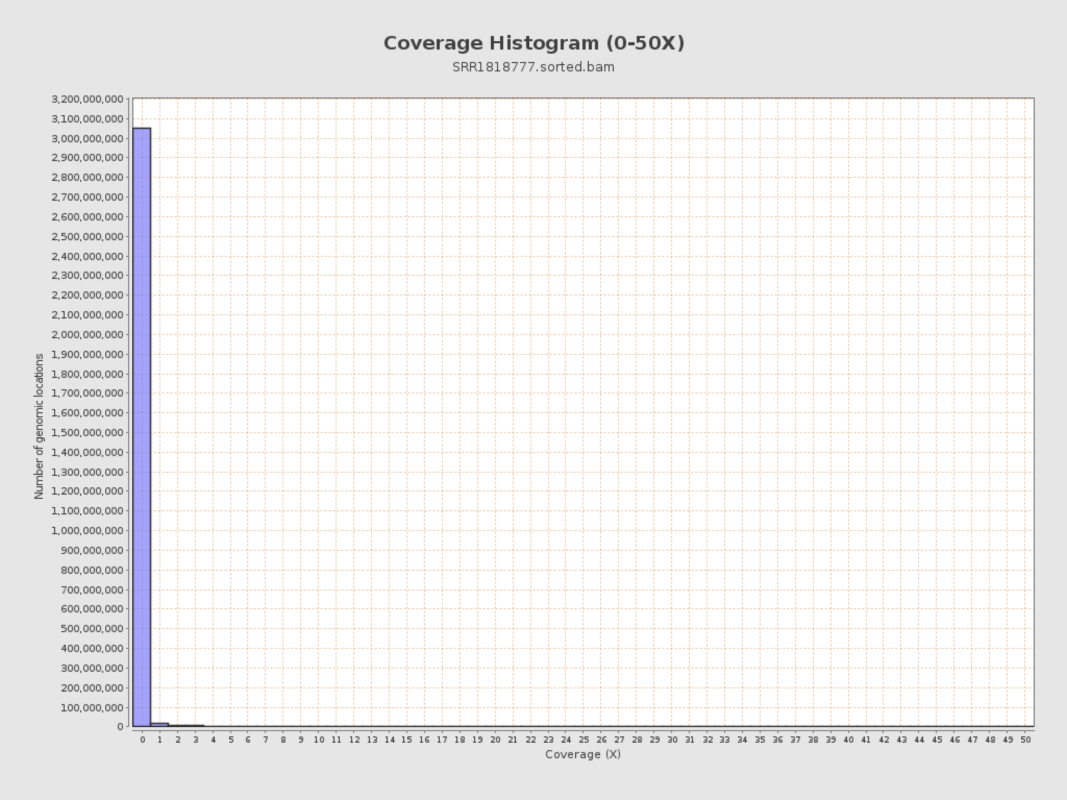
3. Results : Coverage across reference



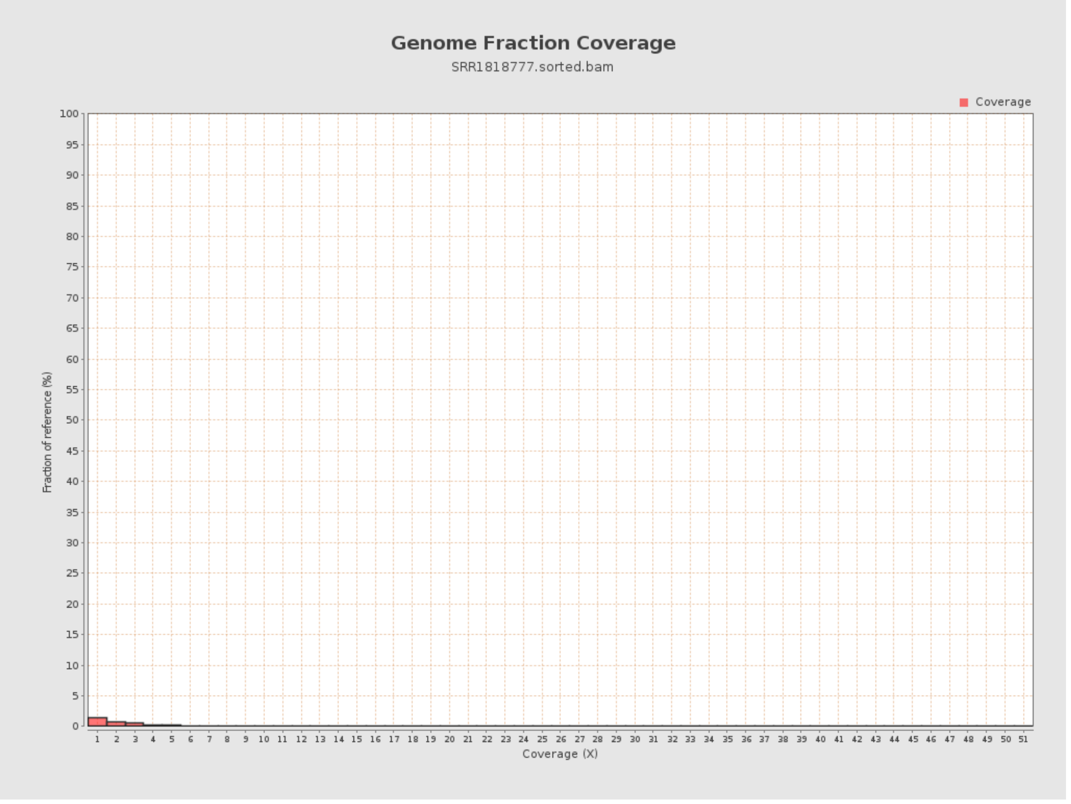
4. Results : Coverage Histogram



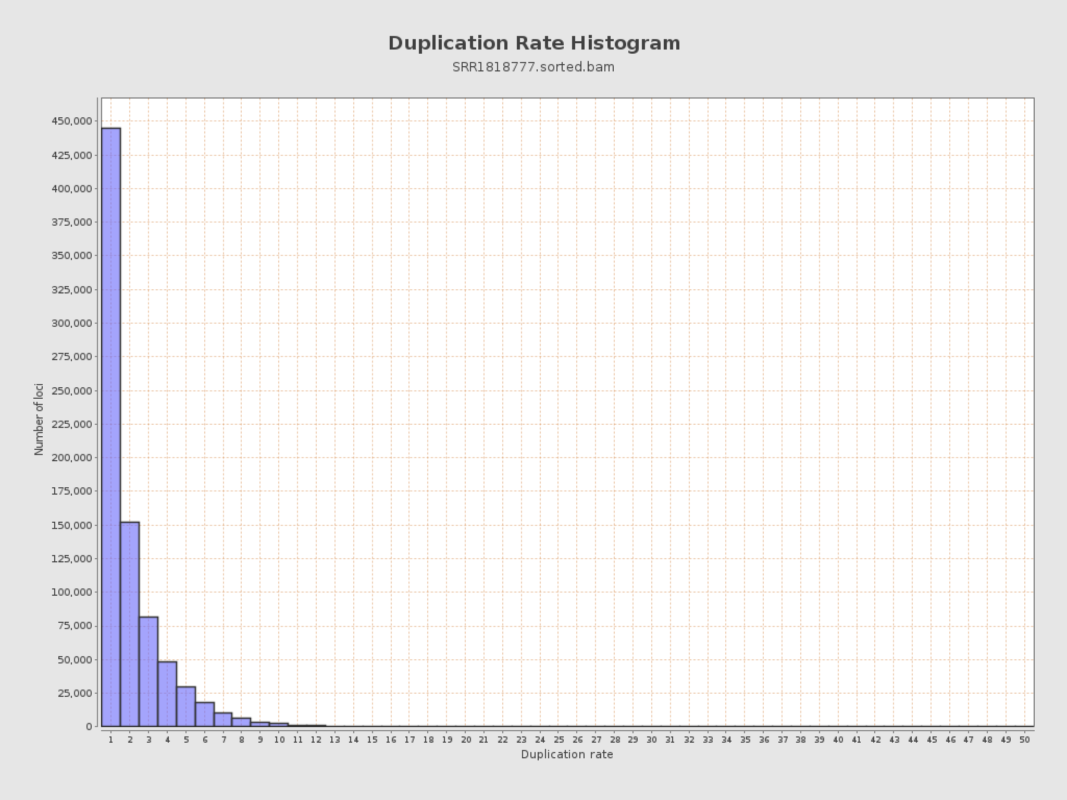
5. Results : Coverage Histogram (0-50X)



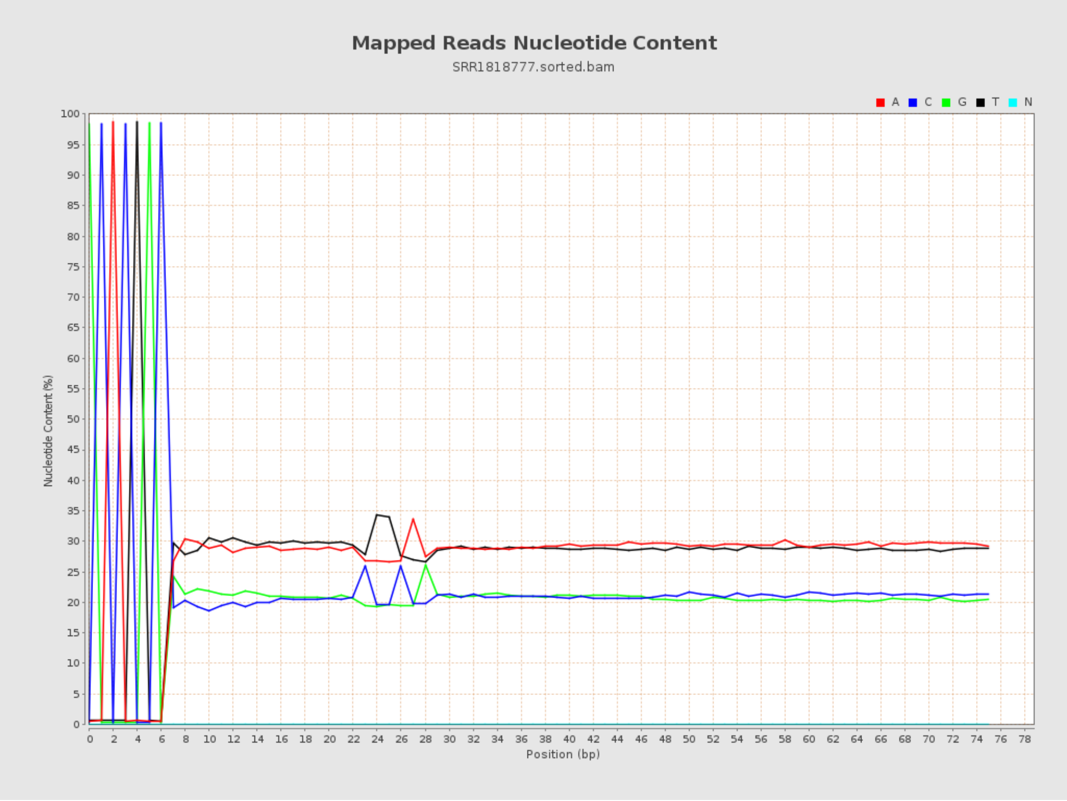
6. Results : Genome Fraction Coverage



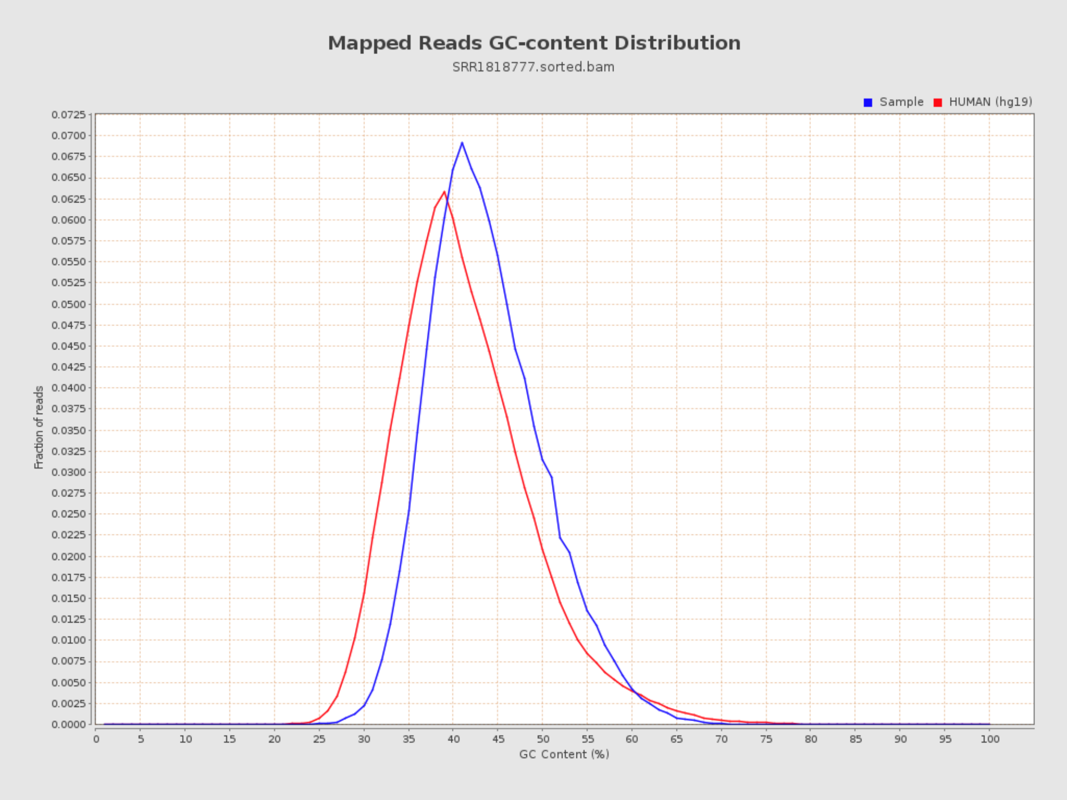
7. Results : Duplication Rate Histogram



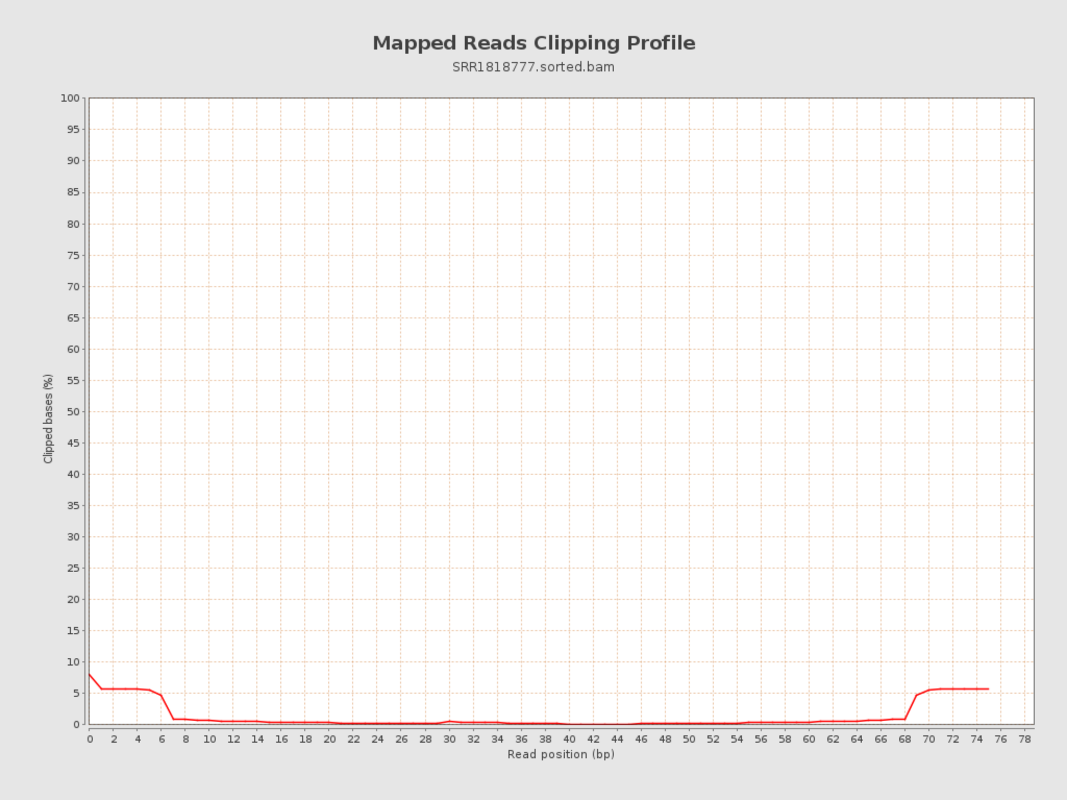
8. Results : Mapped Reads Nucleotide Content



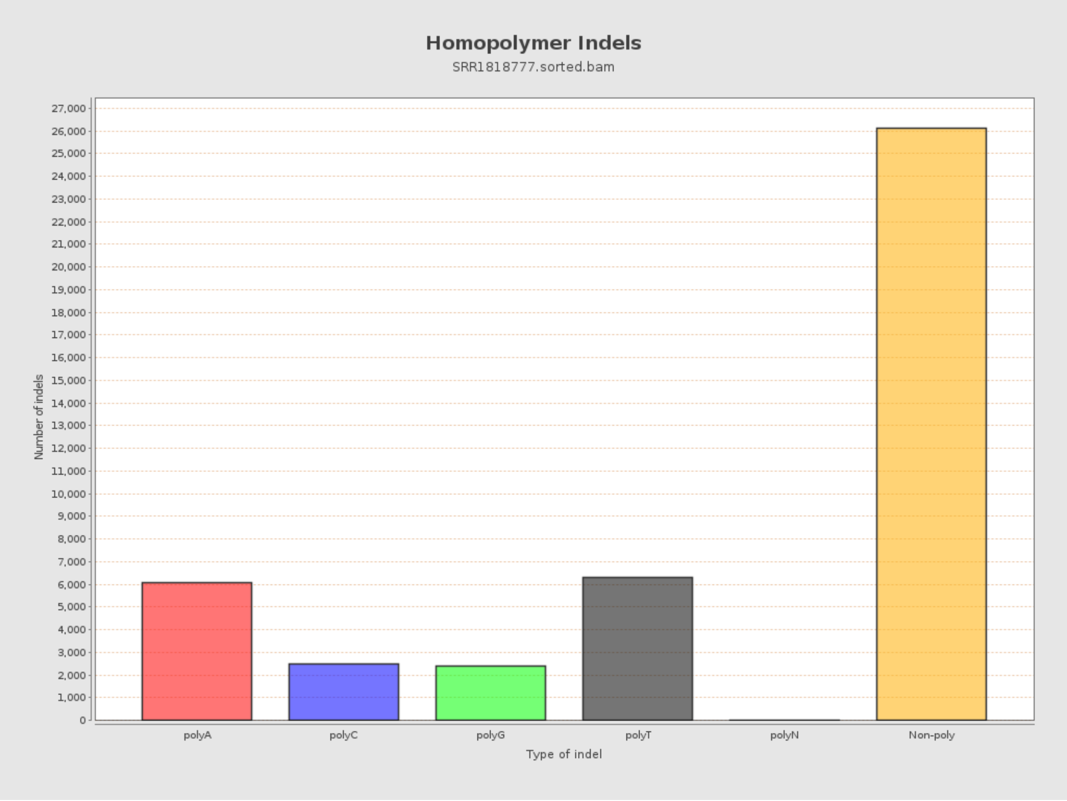
9. Results : Mapped Reads GC-content Distribution



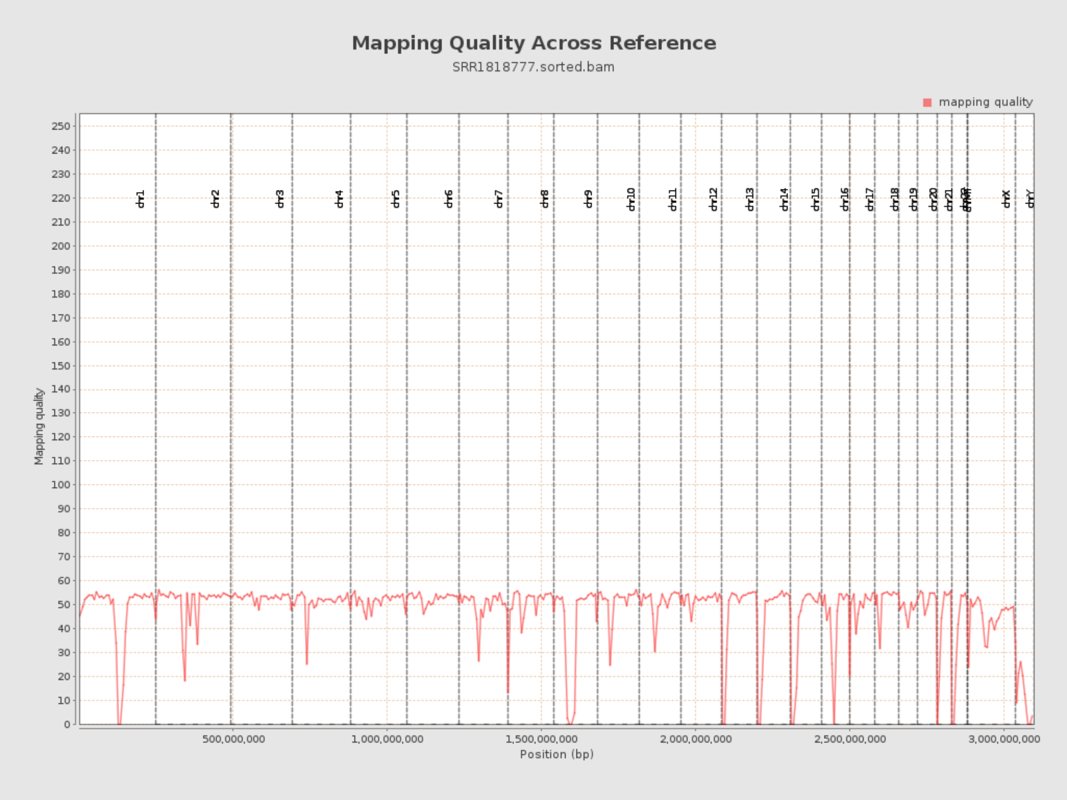
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram