Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 08:40:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818772.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_SRR1818772 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818772.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 08:40:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818772.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,440,836
Mapped reads	1,398,506 / 97.06%
Unmapped reads	42,330 / 2.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,717 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	611,769 / 42.46%
Duplication rate	37.79%
Clipped reads	1,401,075 / 97.24%

2.2. ACGT Content

Number/percentage of A's	27,045,172 / 28.44%
Number/percentage of C's	19,828,233 / 20.85%
Number/percentage of T's	26,210,791 / 27.57%
Number/percentage of G's	21,992,406 / 23.13%
Number/percentage of N's	5,724 / 0.01%
GC Percentage	43.98%

2.3. Coverage

Mean	0.0307

Standard Deviation	0.4027

2.4. Mapping Quality

Mean Mapping Quality	47.8

2.5. Mismatches and indels

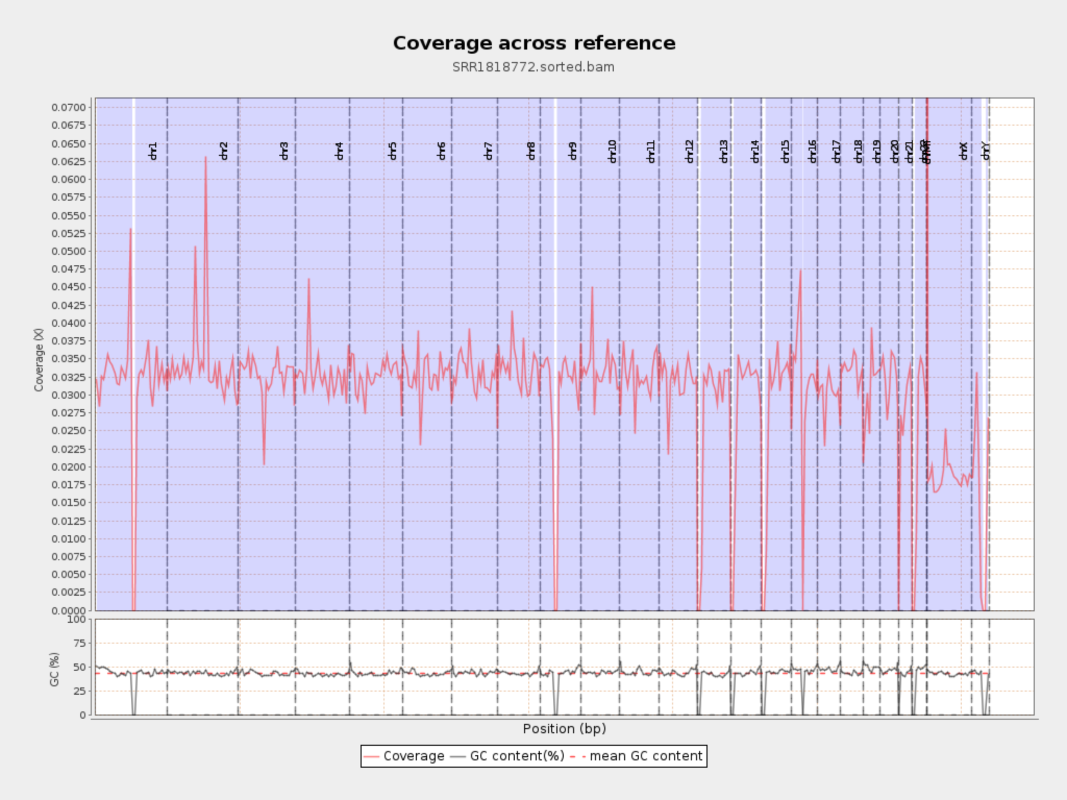
General error rate	0.52%
Mismatches	473,241
Insertions	8,494
Mapped reads with at least one insertion	0.6%
Deletions	24,408
Mapped reads with at least one deletion	1.73%
Homopolymer indels	44.23%

2.6. Chromosome stats

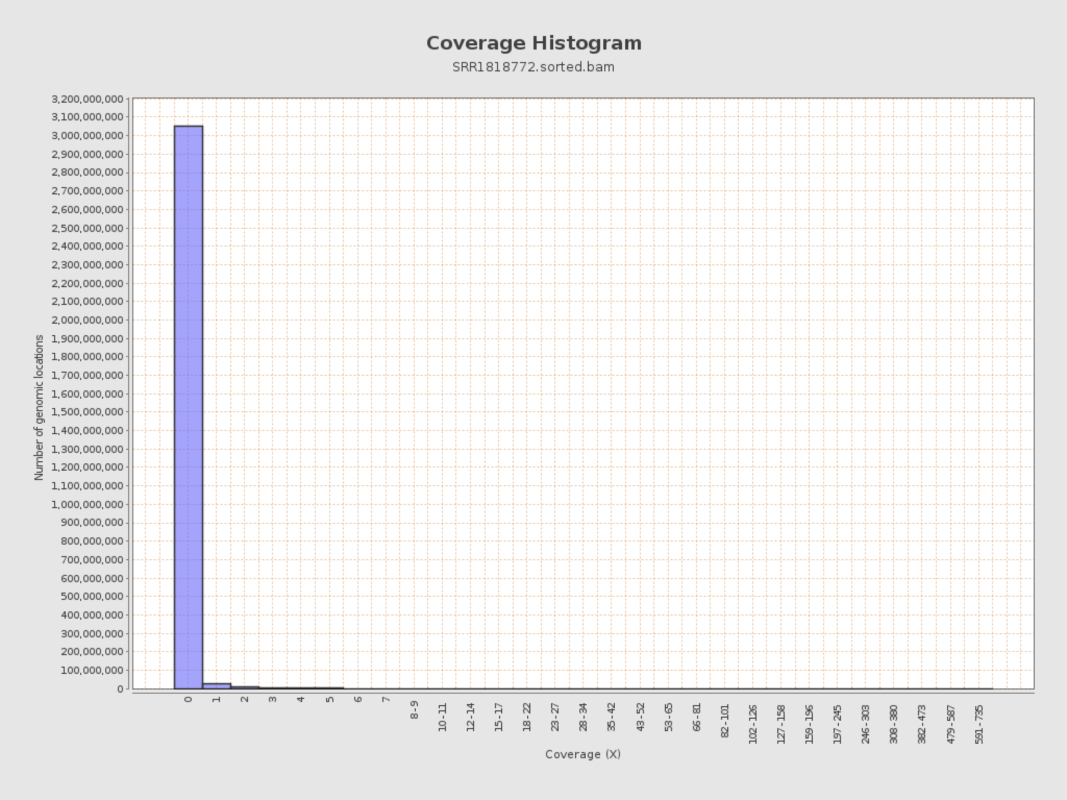
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7851167	0.0315	0.5846
chr2	243199373	8401686	0.0345	0.593
chr3	198022430	6484943	0.0327	0.3259
chr4	191154276	6298889	0.033	0.3522
chr5	180915260	5928198	0.0328	0.3273
chr6	171115067	5605430	0.0328	0.3458
chr7	159138663	5279432	0.0332	0.3714

chr8	146364022	4958570	0.0339	0.3702
chr9	141213431	4101446	0.029	0.3401
chr10	135534747	4565441	0.0337	0.4129
chr11	135006516	4411075	0.0327	0.3532
chr12	133851895	4294479	0.0321	0.3339
chr13	115169878	3083983	0.0268	0.2883
chr14	107349540	2961605	0.0276	0.3209
chr15	102531392	2760319	0.0269	0.2941
chr16	90354753	2795276	0.0309	0.4283
chr17	81195210	2429891	0.0299	0.3228
chr18	78077248	2630245	0.0337	0.4576
chr19	59128983	1827813	0.0309	0.4619
chr20	63025520	2050057	0.0325	0.3393
chr21	48129895	1275636	0.0265	0.3071
chr22	51304566	1156220	0.0225	0.2947
chrMT	16571	139912	8.4432	7.9854
chrX	155270560	2914220	0.0188	0.2649
chrY	59373566	915268	0.0154	0.589

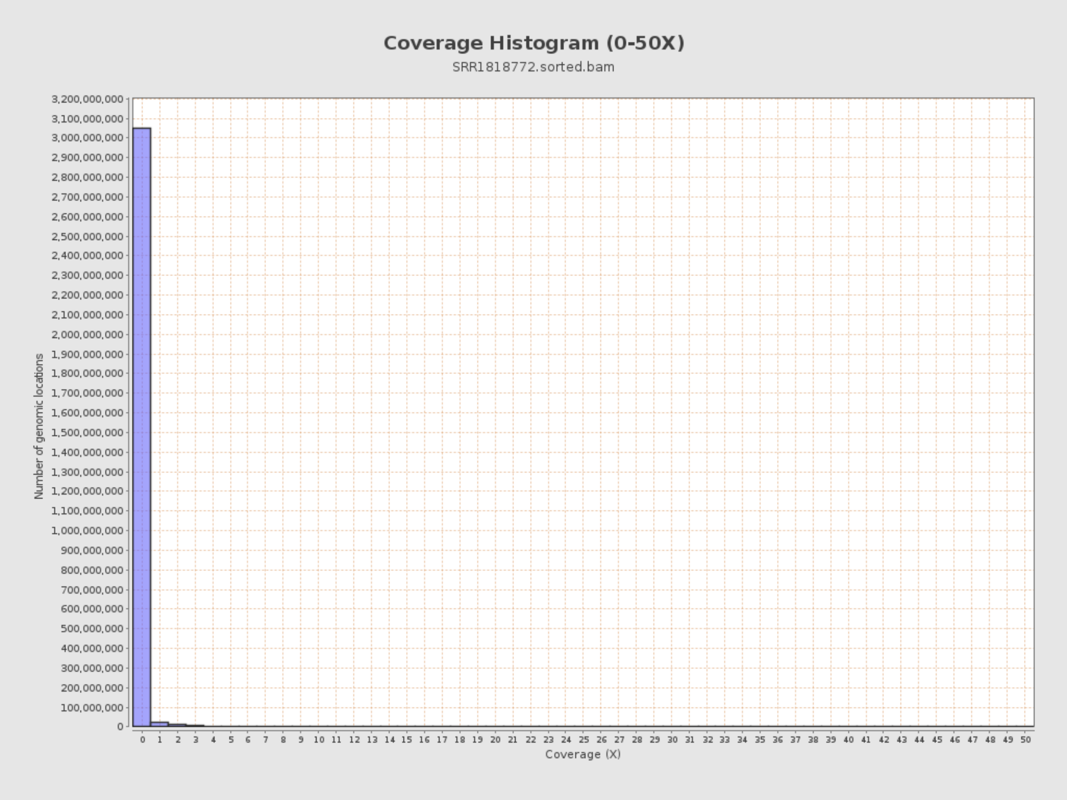
3. Results : Coverage across reference



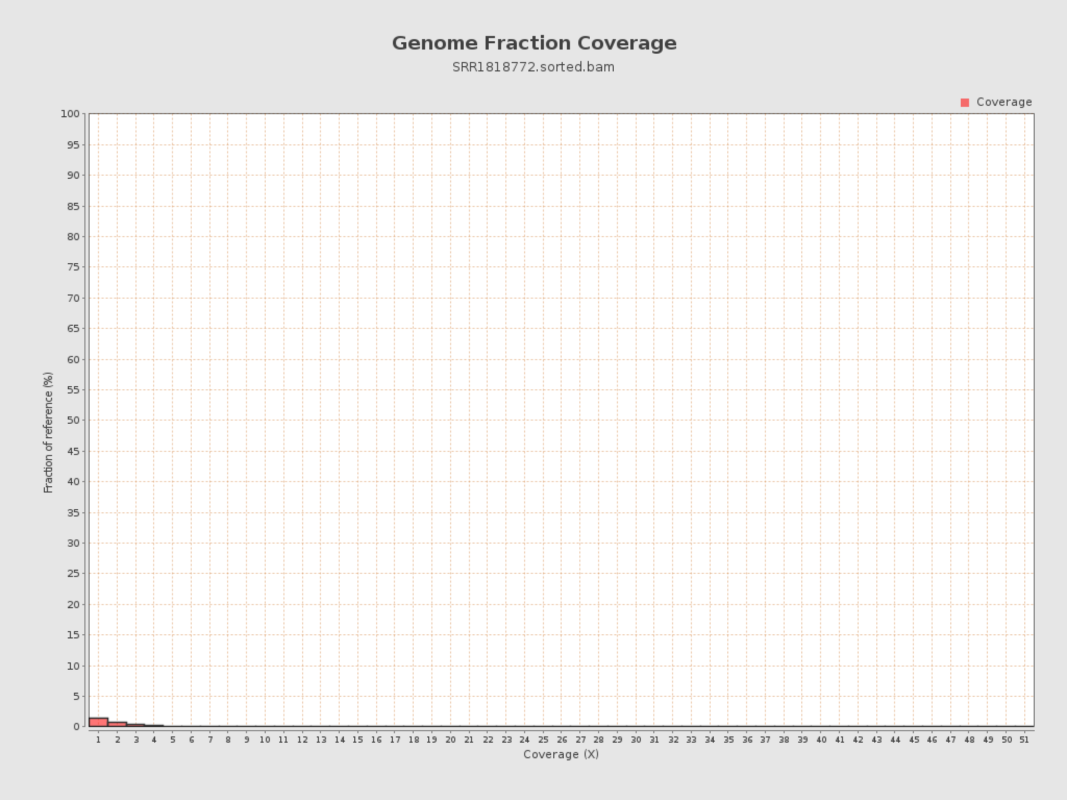
4. Results : Coverage Histogram



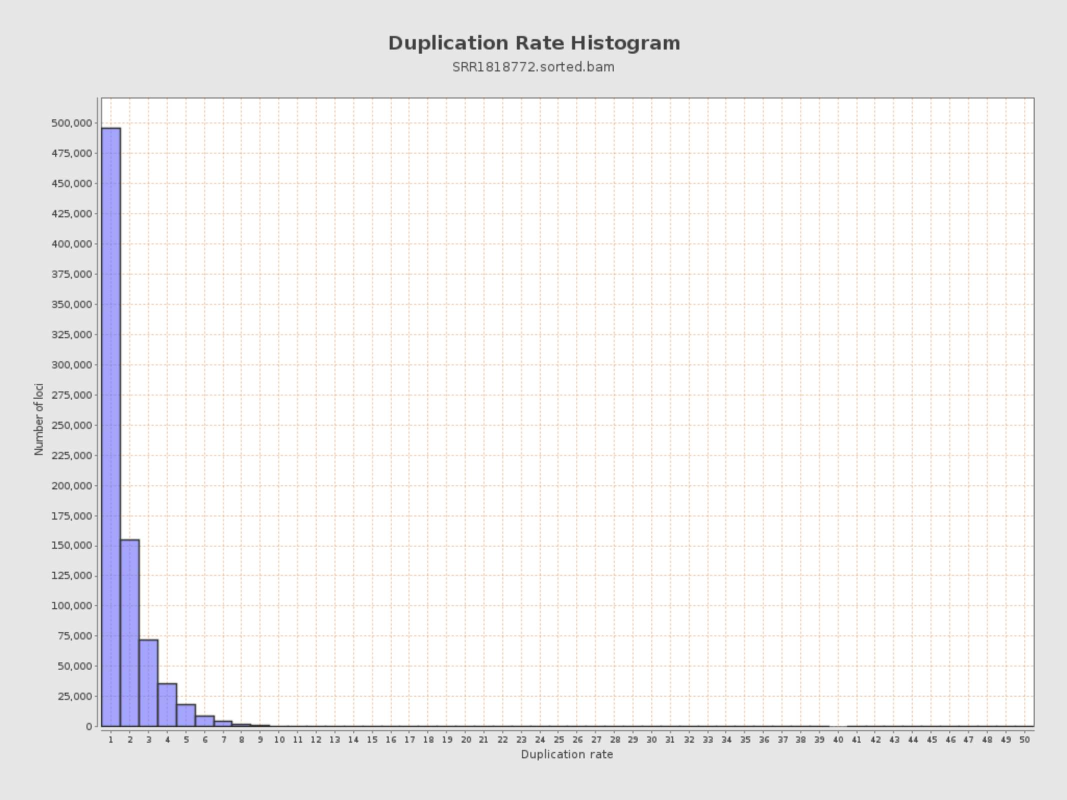
5. Results : Coverage Histogram (0-50X)



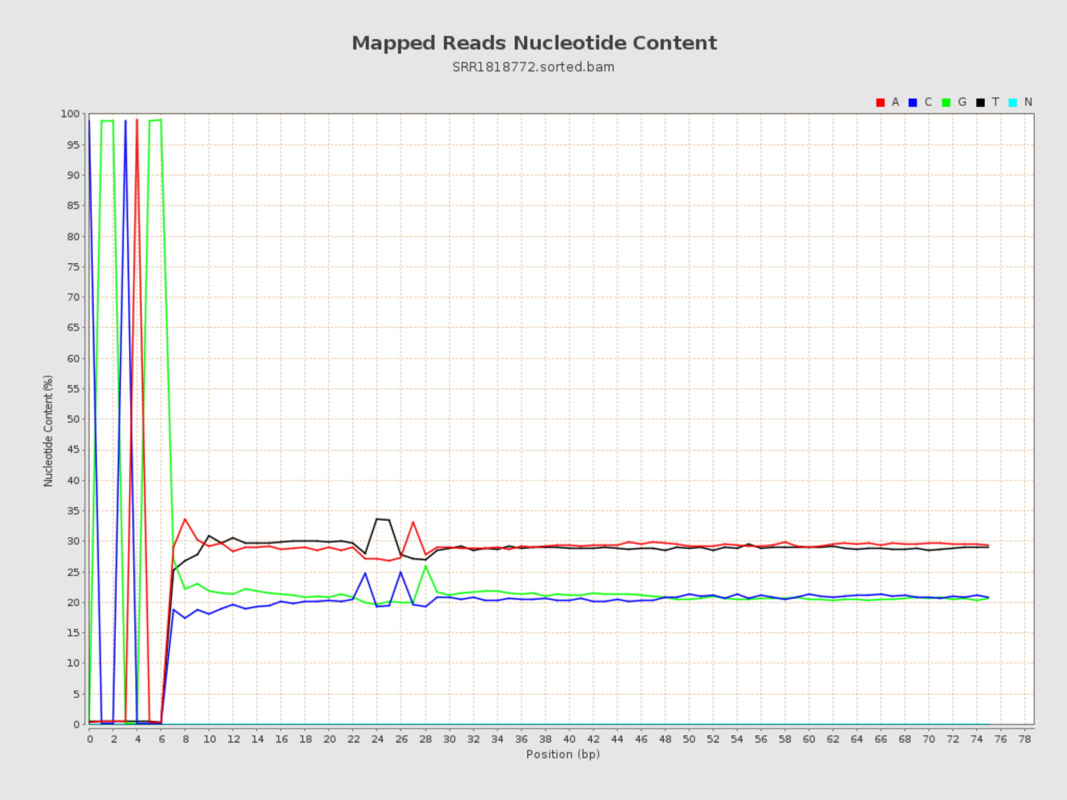
6. Results : Genome Fraction Coverage



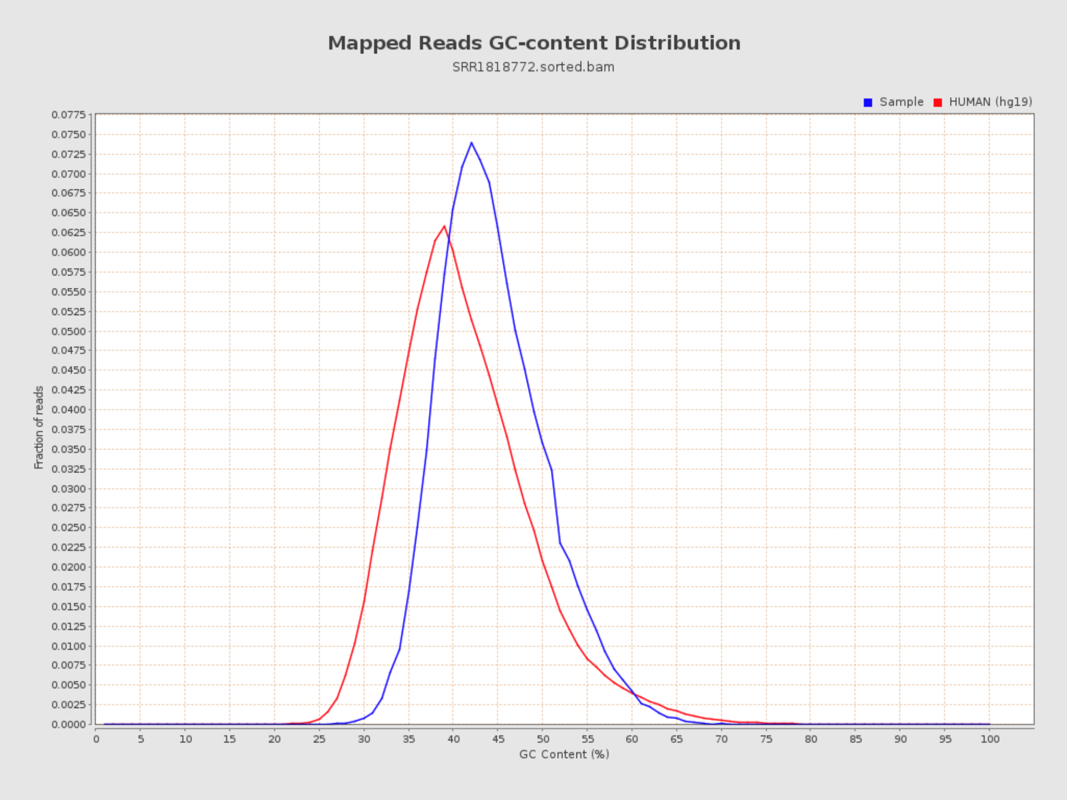
7. Results : Duplication Rate Histogram



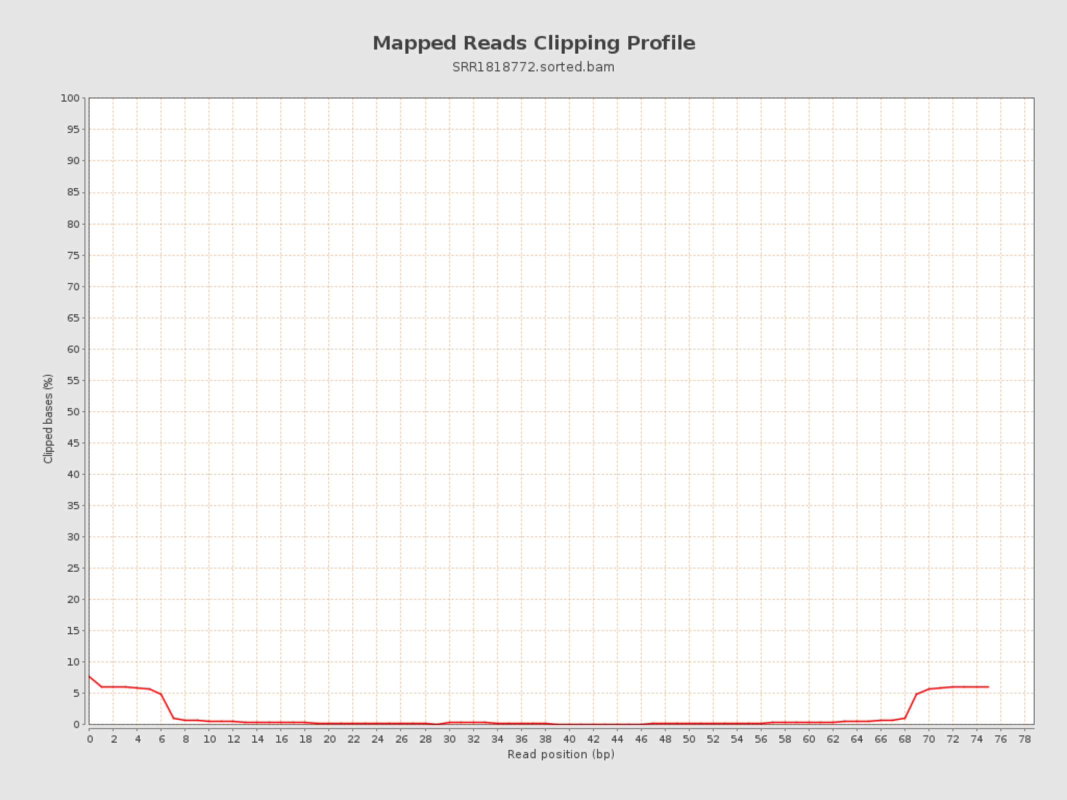
8. Results : Mapped Reads Nucleotide Content



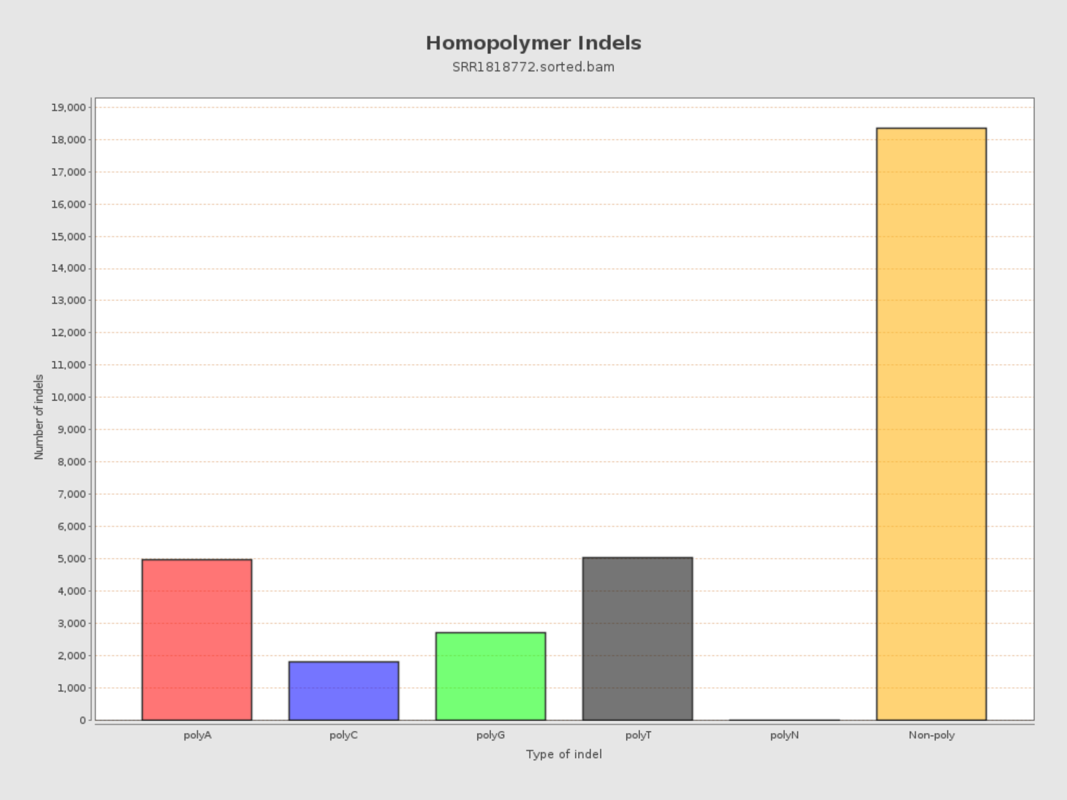
9. Results : Mapped Reads GC-content Distribution



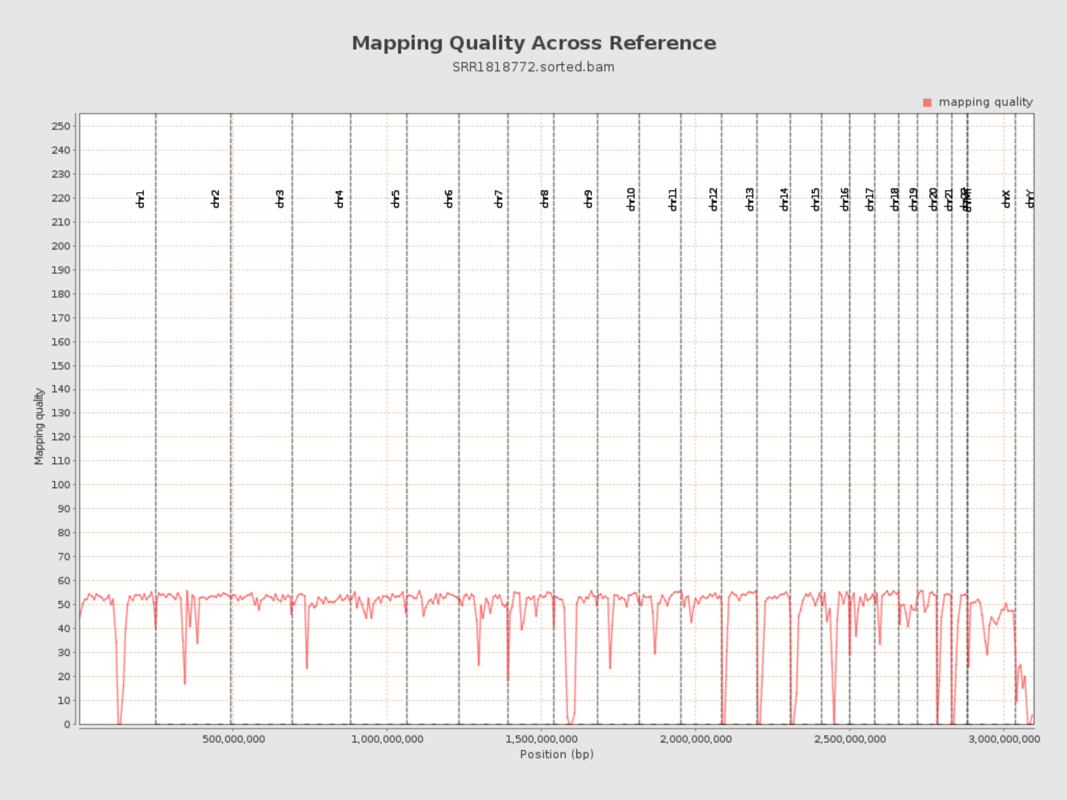
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram