Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 08:09:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818770.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_SRR1818770 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818770.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 08:09:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818770.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,053,901
Mapped reads	1,027,811 / 97.52%
Unmapped reads	26,090 / 2.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,807 / 0.74%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	495,930 / 47.06%
Duplication rate	40.44%
Clipped reads	1,028,710 / 97.61%

2.2. ACGT Content

Number/percentage of A's	20,132,801 / 28.84%
Number/percentage of C's	16,488,313 / 23.62%
Number/percentage of T's	18,842,965 / 26.99%
Number/percentage of G's	14,344,465 / 20.55%
Number/percentage of N's	4,406 / 0.01%
GC Percentage	44.16%

2.3. Coverage

Mean	0.0226

Standard Deviation	0.3342

2.4. Mapping Quality

Mean Mapping Quality	48.01

2.5. Mismatches and indels

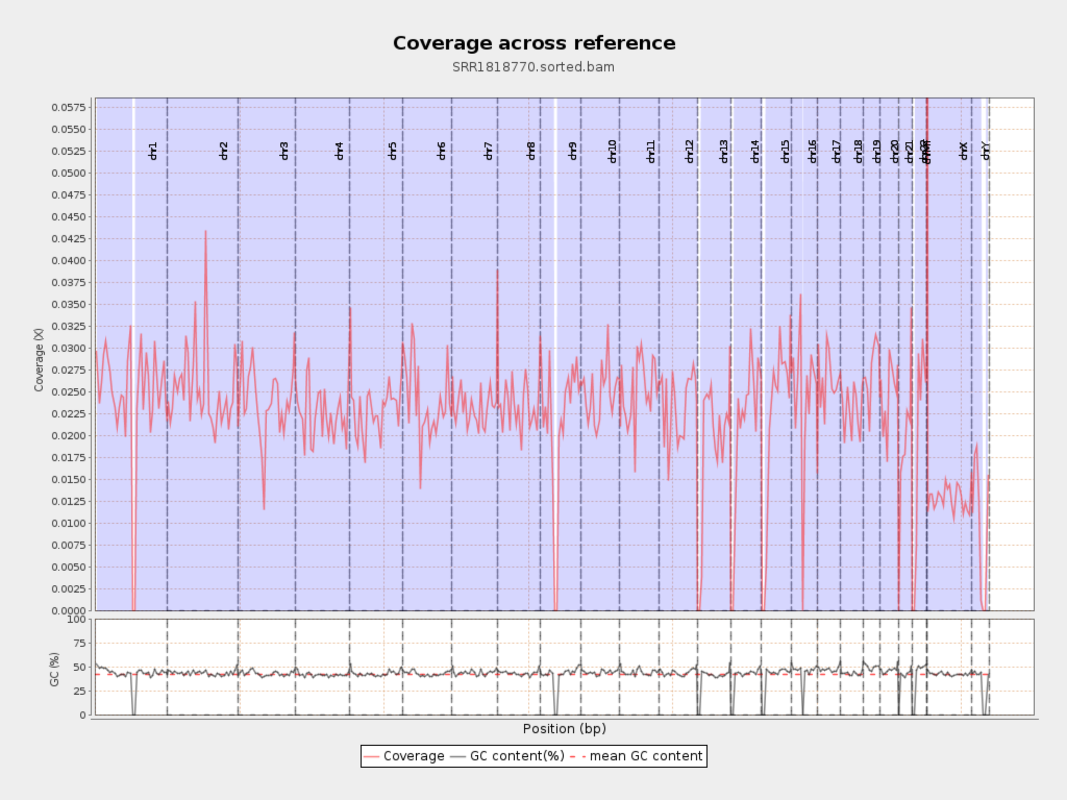
General error rate	0.54%
Mismatches	358,586
Insertions	7,917
Mapped reads with at least one insertion	0.76%
Deletions	17,967
Mapped reads with at least one deletion	1.73%
Homopolymer indels	41.44%

2.6. Chromosome stats

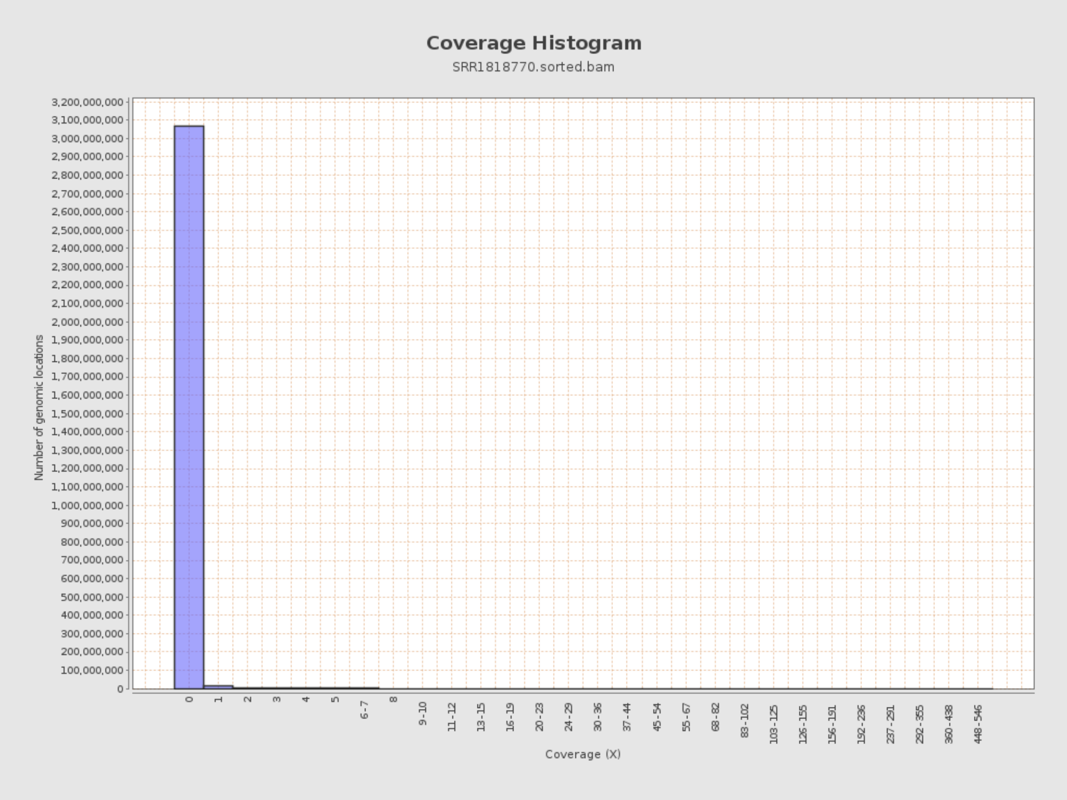
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6088578	0.0244	0.3807
chr2	243199373	6144684	0.0253	0.4844
chr3	198022430	4713048	0.0238	0.2956
chr4	191154276	4298695	0.0225	0.3081
chr5	180915260	4140680	0.0229	0.2923
chr6	171115067	4086551	0.0239	0.3032
chr7	159138663	3684076	0.0232	0.3134

chr8	146364022	3420891	0.0234	0.3006
chr9	141213431	3026270	0.0214	0.2897
chr10	135534747	3382805	0.025	0.3597
chr11	135006516	3415347	0.0253	0.3183
chr12	133851895	3121203	0.0233	0.3125
chr13	115169878	2098270	0.0182	0.263
chr14	107349540	2224791	0.0207	0.2953
chr15	102531392	2178576	0.0212	0.2839
chr16	90354753	2179897	0.0241	0.3906
chr17	81195210	2151121	0.0265	0.3302
chr18	78077248	1781657	0.0228	0.3319
chr19	59128983	1618067	0.0274	0.3767
chr20	63025520	1542461	0.0245	0.3162
chr21	48129895	910765	0.0189	0.2725
chr22	51304566	969975	0.0189	0.2931
chrMT	16571	113292	6.8368	8.1234
chrX	155270560	1981546	0.0128	0.2205
chrY	59373566	568616	0.0096	0.4501

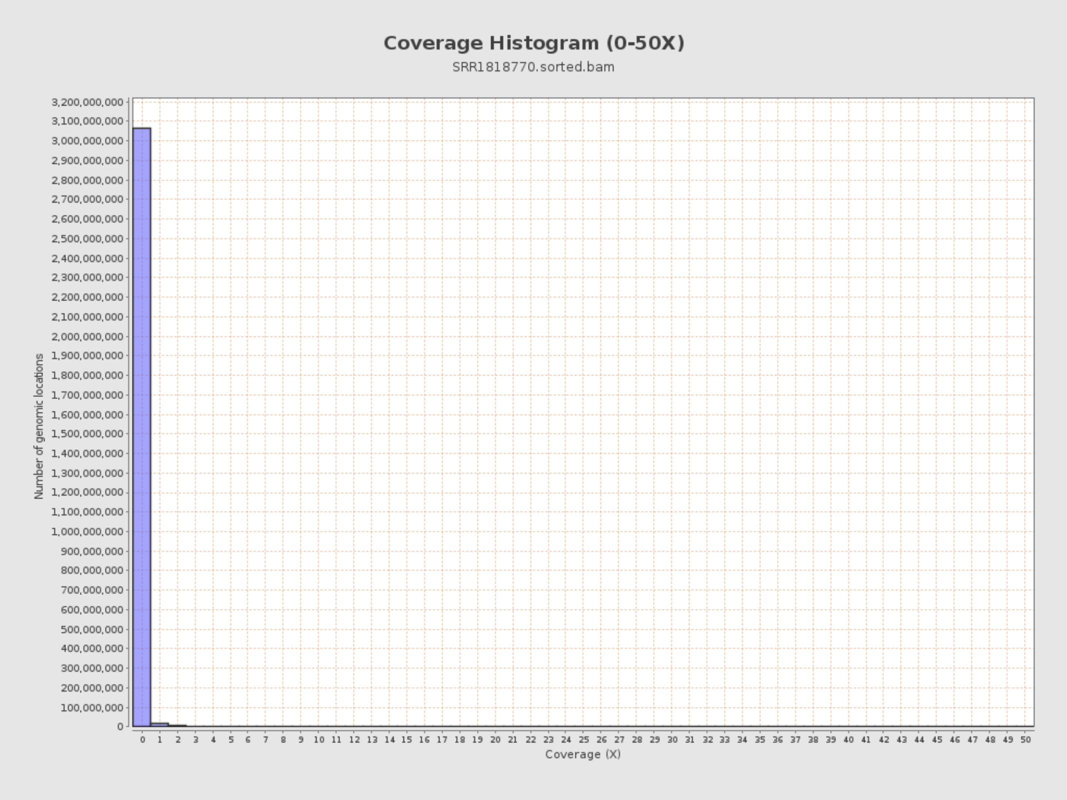
3. Results : Coverage across reference



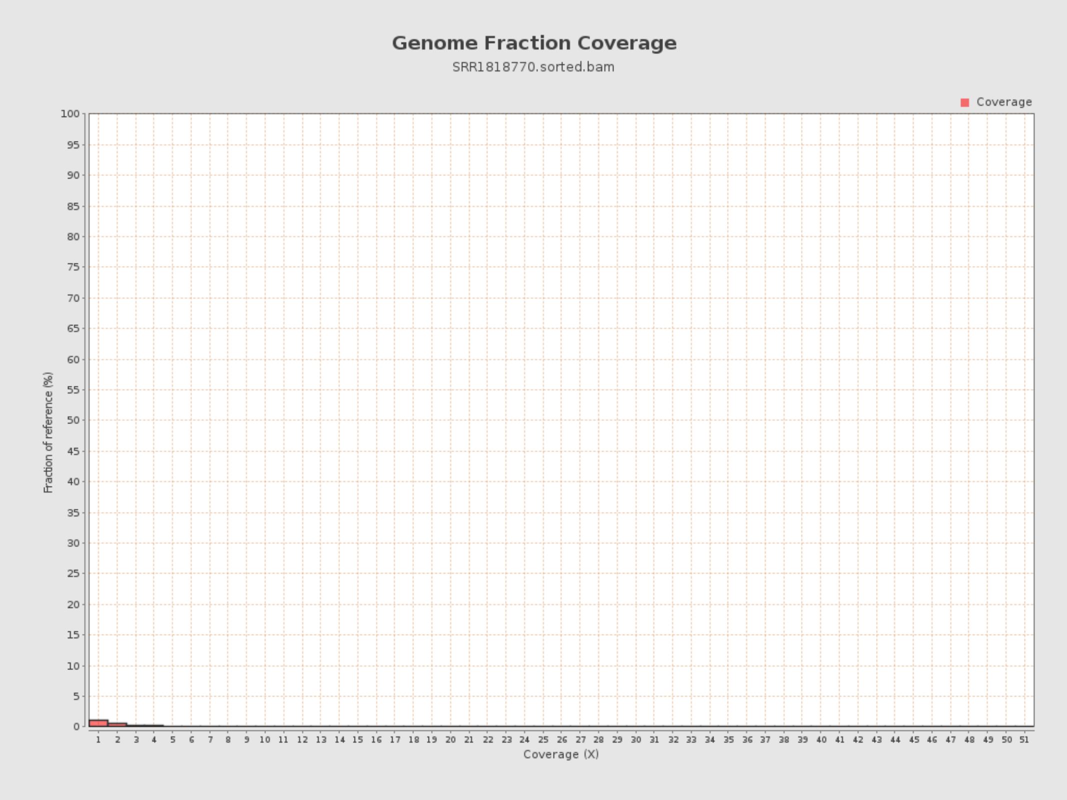
4. Results : Coverage Histogram



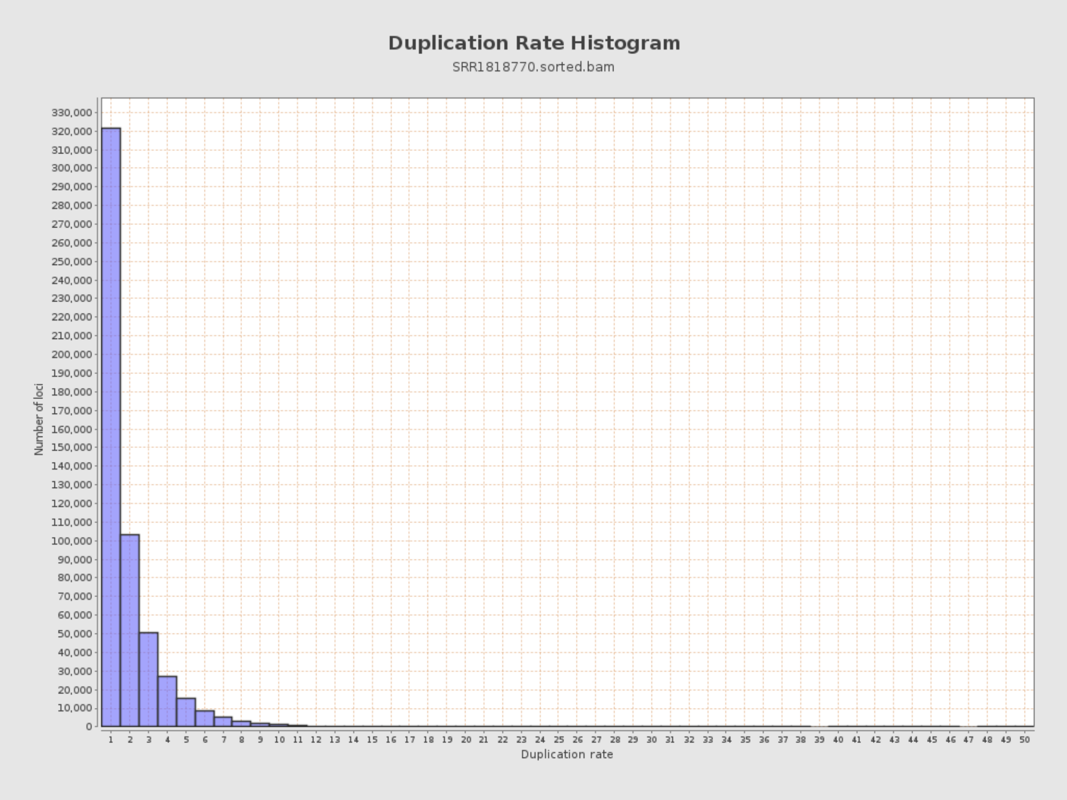
5. Results : Coverage Histogram (0-50X)



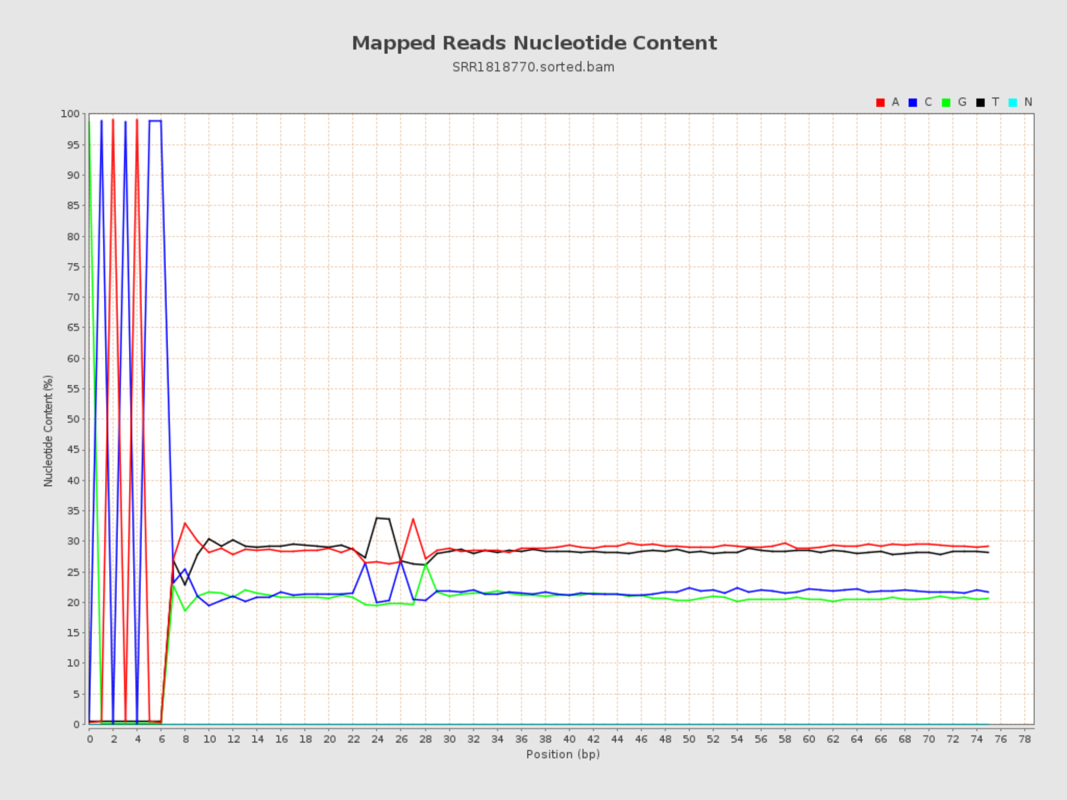
6. Results : Genome Fraction Coverage



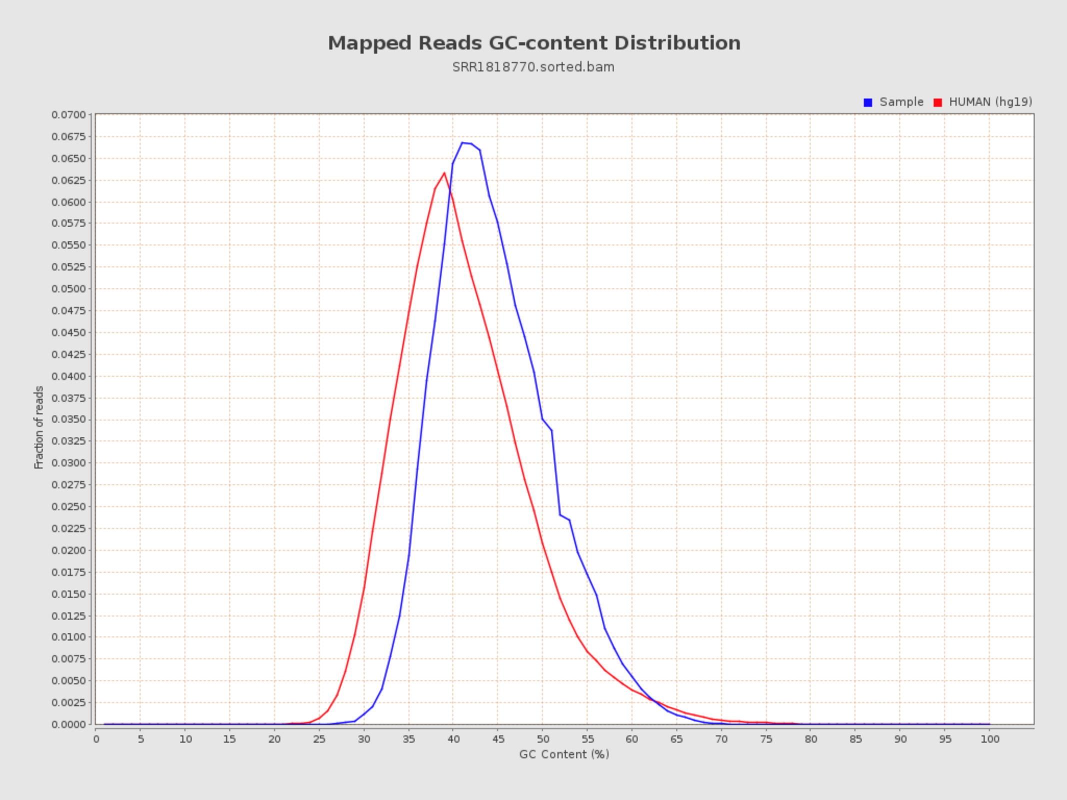
7. Results : Duplication Rate Histogram



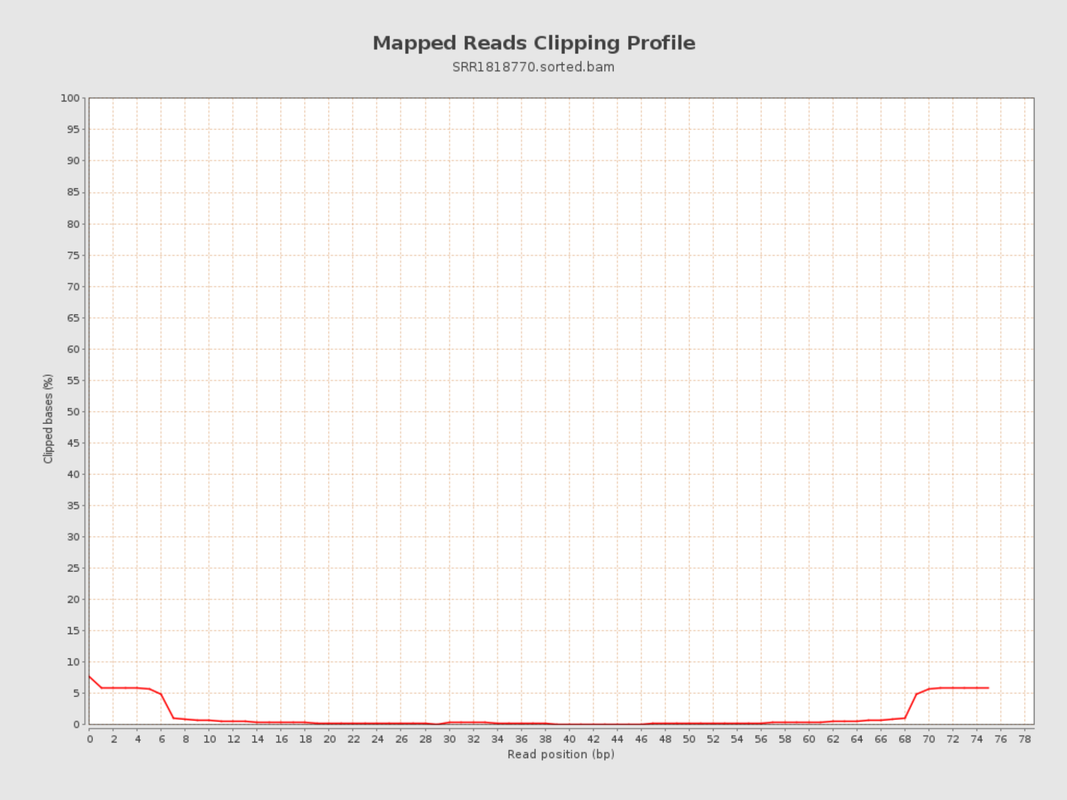
8. Results : Mapped Reads Nucleotide Content



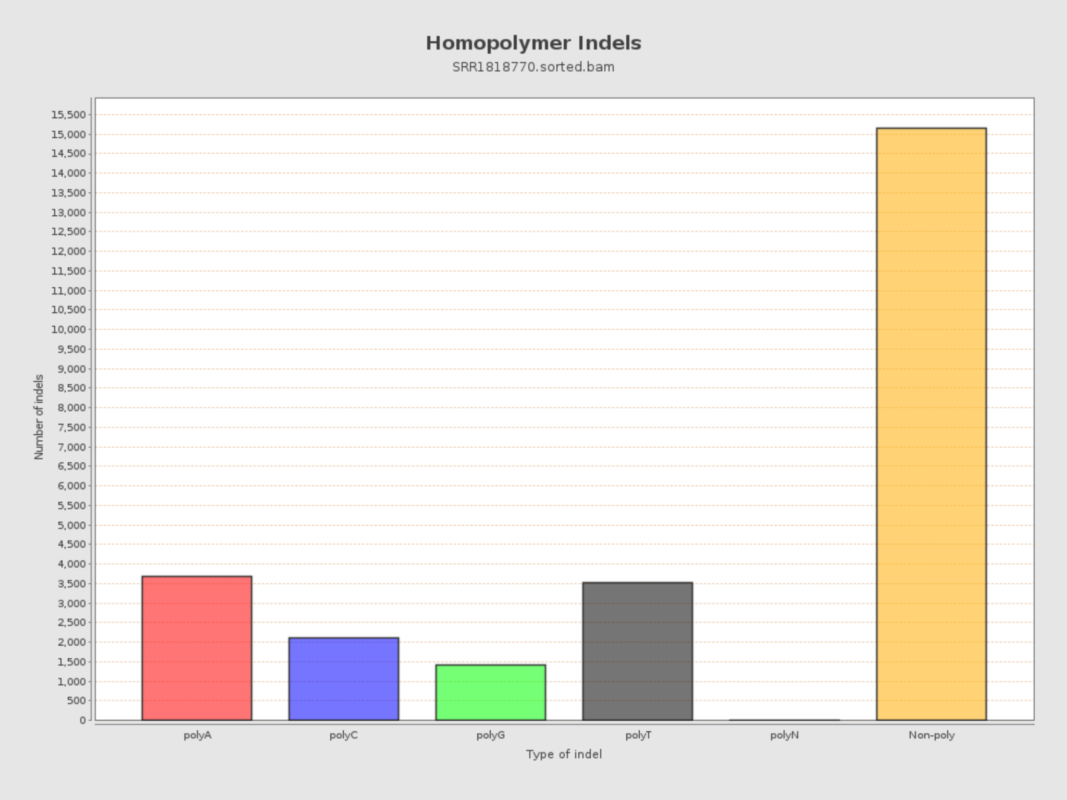
9. Results : Mapped Reads GC-content Distribution



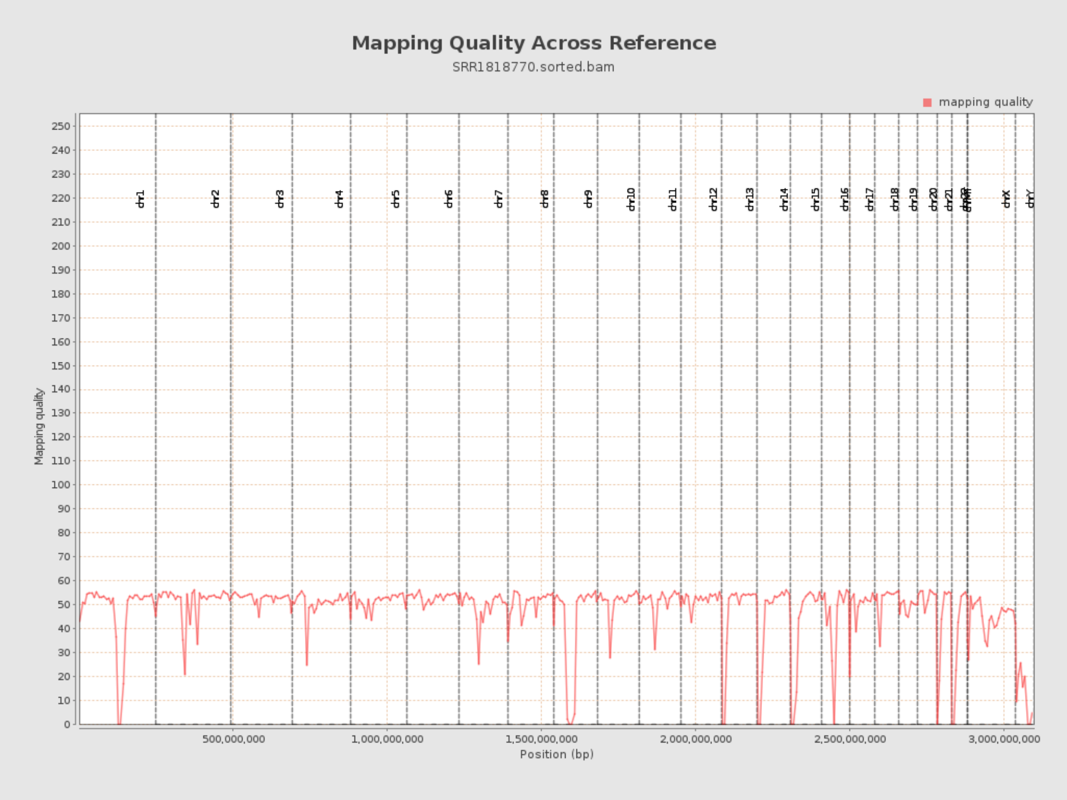
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram