Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 09:02:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818774.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_SRR1818774 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818774.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 09:02:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818774.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	357,827
Mapped reads	312,189 / 87.25%
Unmapped reads	45,638 / 12.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,429 / 0.68%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	85,480 / 23.89%
Duplication rate	23.57%
Clipped reads	312,972 / 87.46%

2.2. ACGT Content

Number/percentage of A's	5,991,714 / 28.28%
Number/percentage of C's	4,840,248 / 22.84%
Number/percentage of T's	5,919,118 / 27.94%
Number/percentage of G's	4,435,467 / 20.93%
Number/percentage of N's	1,323 / 0.01%
GC Percentage	43.78%

2.3. Coverage

Mean	0.0068

Standard Deviation	0.1322

2.4. Mapping Quality

Mean Mapping Quality	47.29

2.5. Mismatches and indels

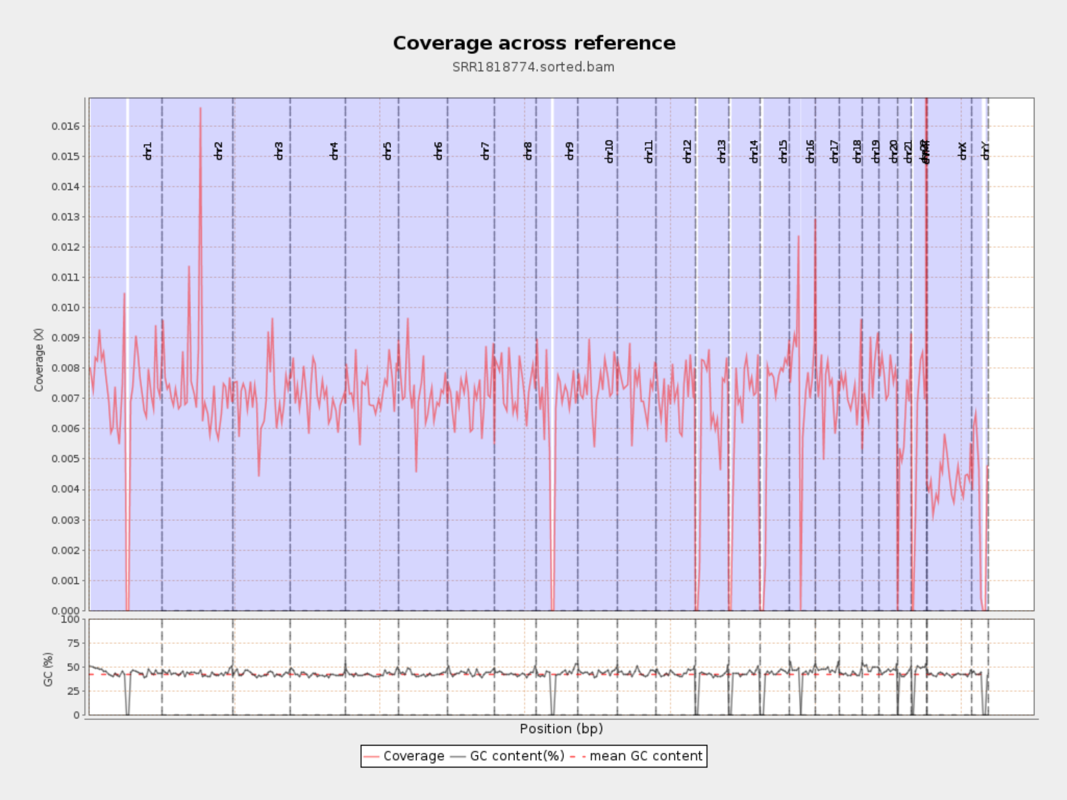
General error rate	0.52%
Mismatches	105,957
Insertions	2,490
Mapped reads with at least one insertion	0.79%
Deletions	5,343
Mapped reads with at least one deletion	1.69%
Homopolymer indels	41.95%

2.6. Chromosome stats

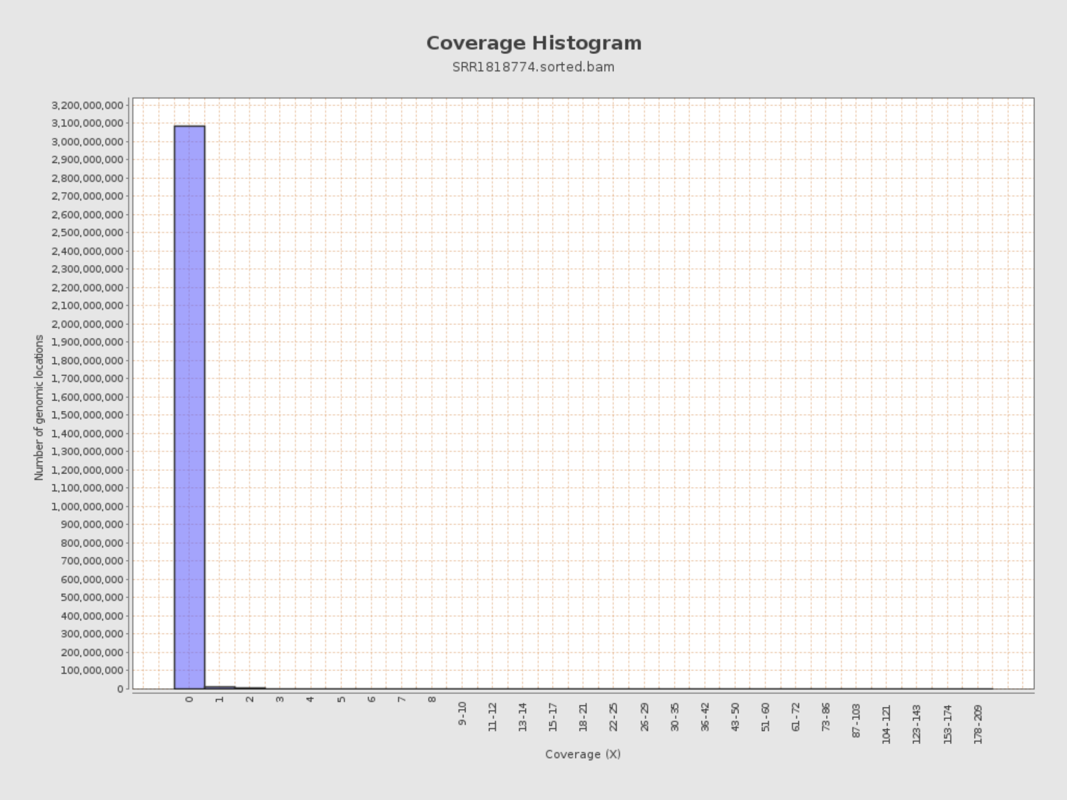
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1767904	0.0071	0.146
chr2	243199373	1825821	0.0075	0.1851
chr3	198022430	1400345	0.0071	0.1198
chr4	191154276	1358837	0.0071	0.1239
chr5	180915260	1314933	0.0073	0.1219
chr6	171115067	1227753	0.0072	0.1259
chr7	159138663	1126516	0.0071	0.1231

chr8	146364022	1093773	0.0075	0.1253
chr9	141213431	895448	0.0063	0.116
chr10	135534747	1005971	0.0074	0.1382
chr11	135006516	994693	0.0074	0.1273
chr12	133851895	954915	0.0071	0.1229
chr13	115169878	693083	0.006	0.1118
chr14	107349540	669209	0.0062	0.1157
chr15	102531392	646011	0.0063	0.1126
chr16	90354753	684059	0.0076	0.1594
chr17	81195210	586890	0.0072	0.1236
chr18	78077248	571120	0.0073	0.1432
chr19	59128983	447728	0.0076	0.1365
chr20	63025520	488622	0.0078	0.1314
chr21	48129895	278969	0.0058	0.1089
chr22	51304566	275710	0.0054	0.1113
chrMT	16571	26801	1.6173	2.5245
chrX	155270560	666982	0.0043	0.0955
chrY	59373566	194418	0.0033	0.164

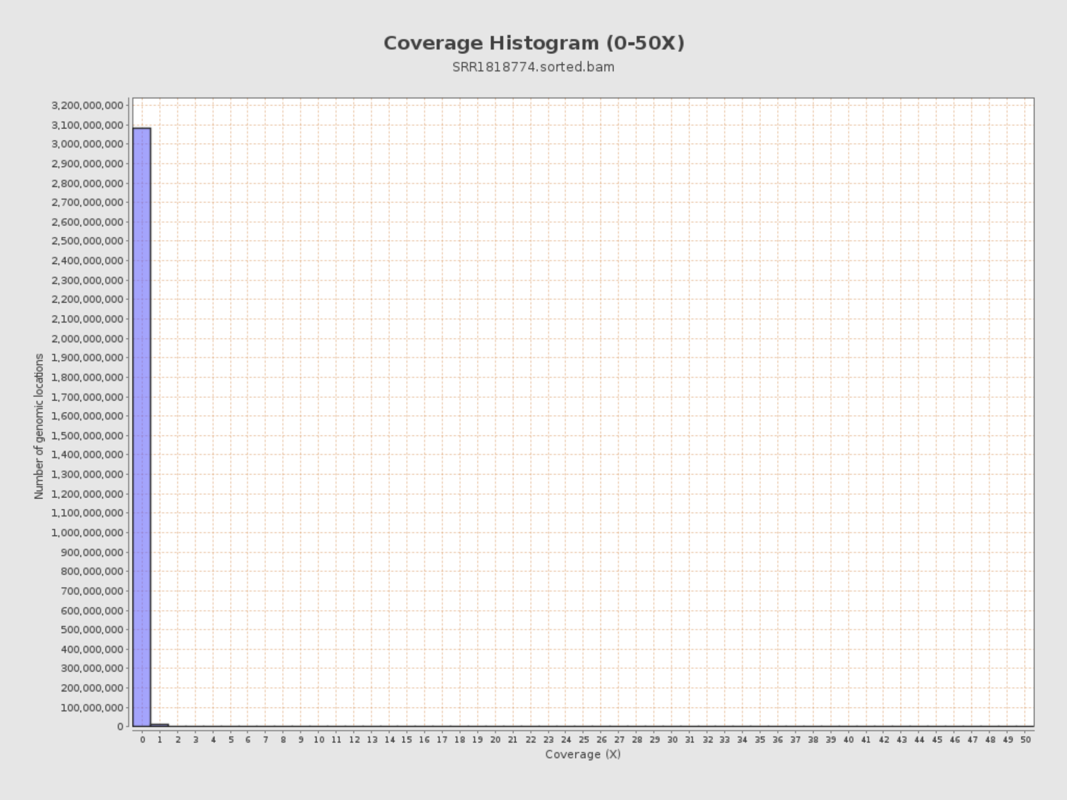
3. Results : Coverage across reference



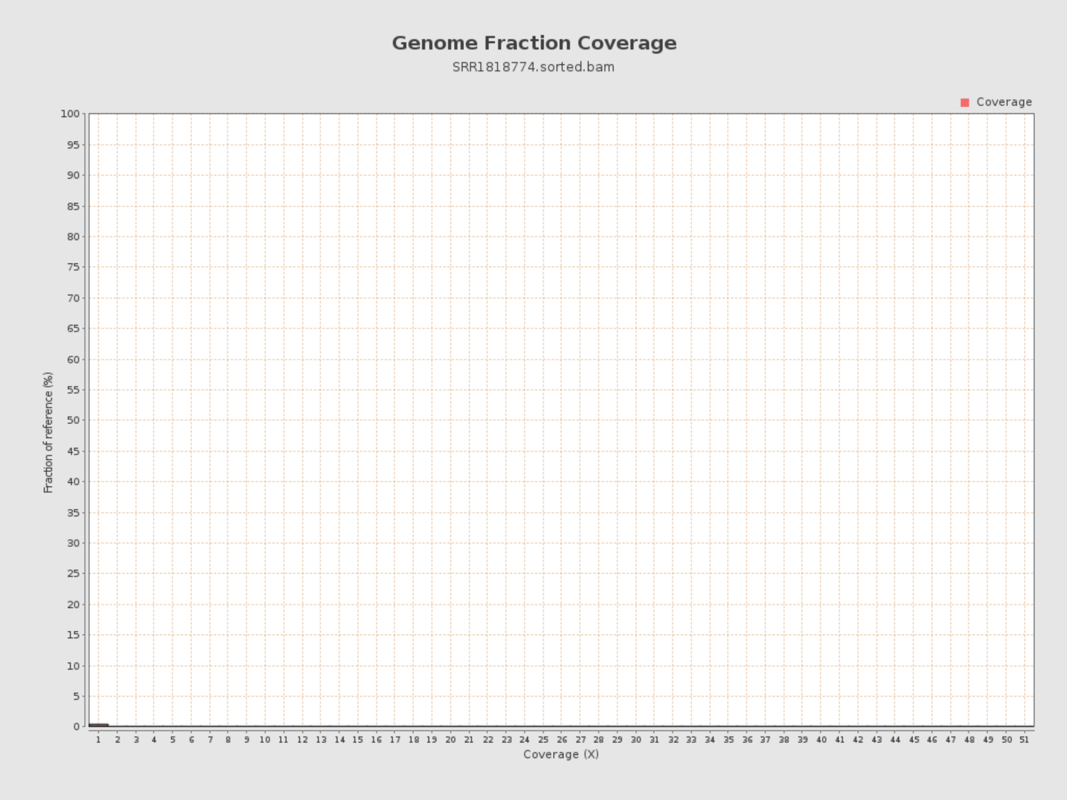
4. Results : Coverage Histogram



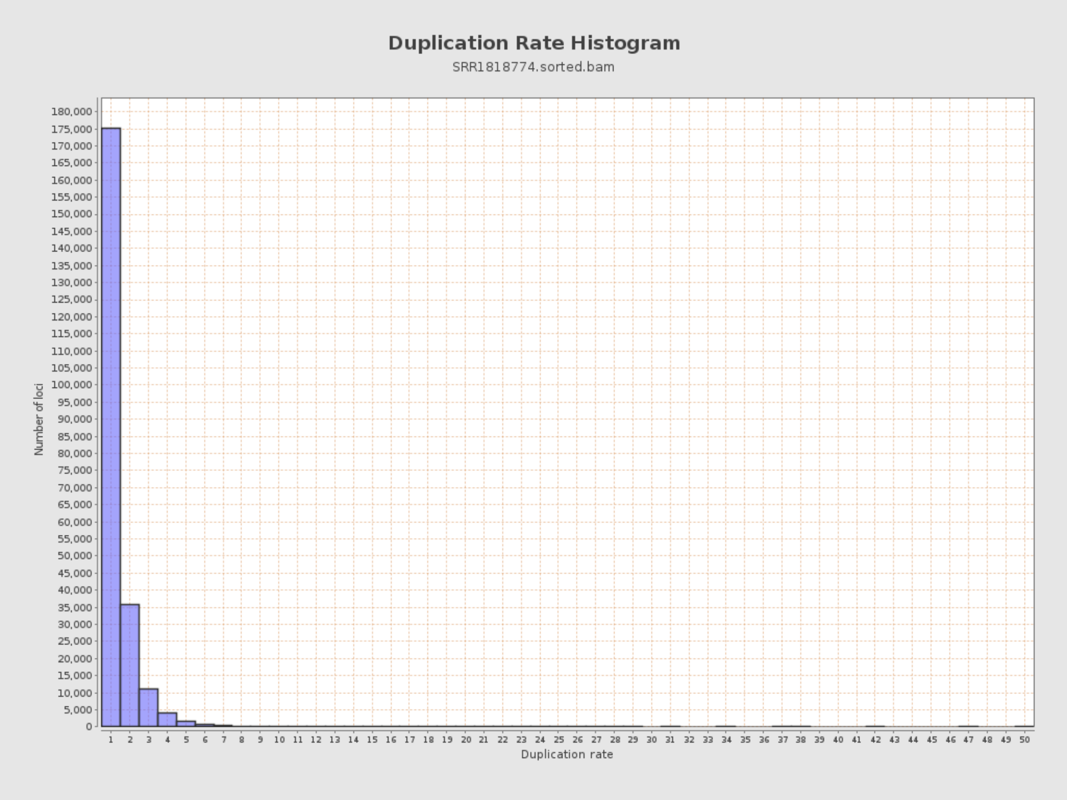
5. Results : Coverage Histogram (0-50X)



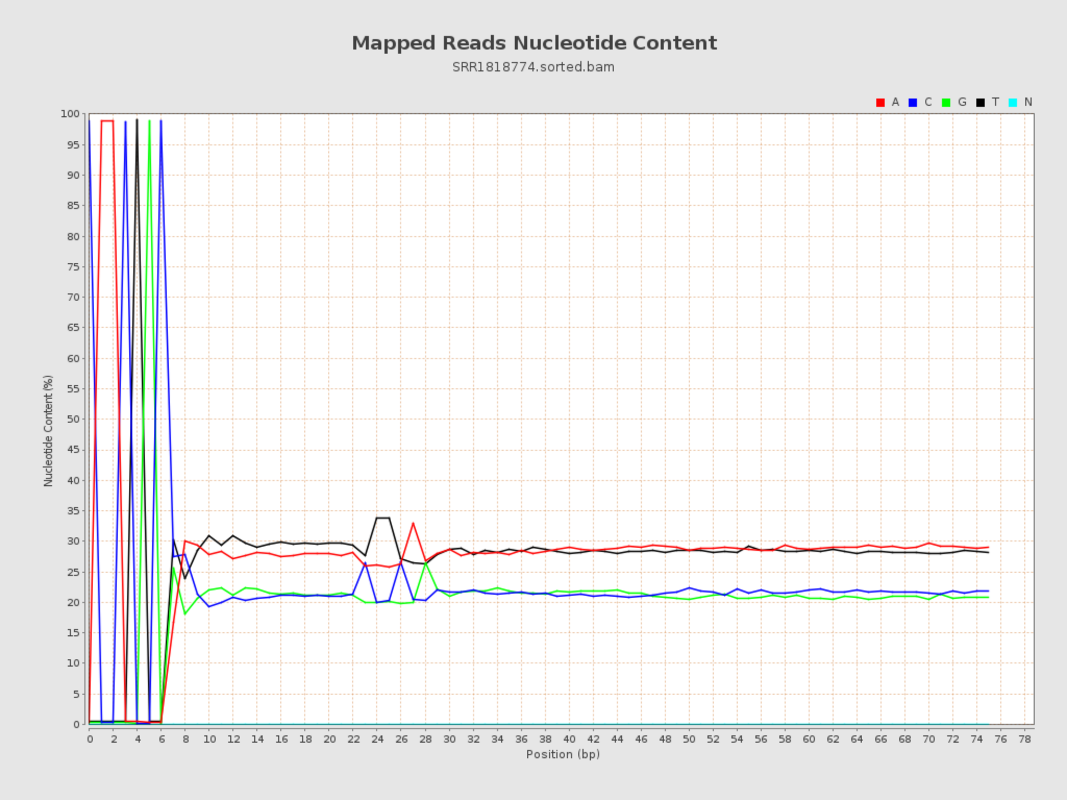
6. Results : Genome Fraction Coverage



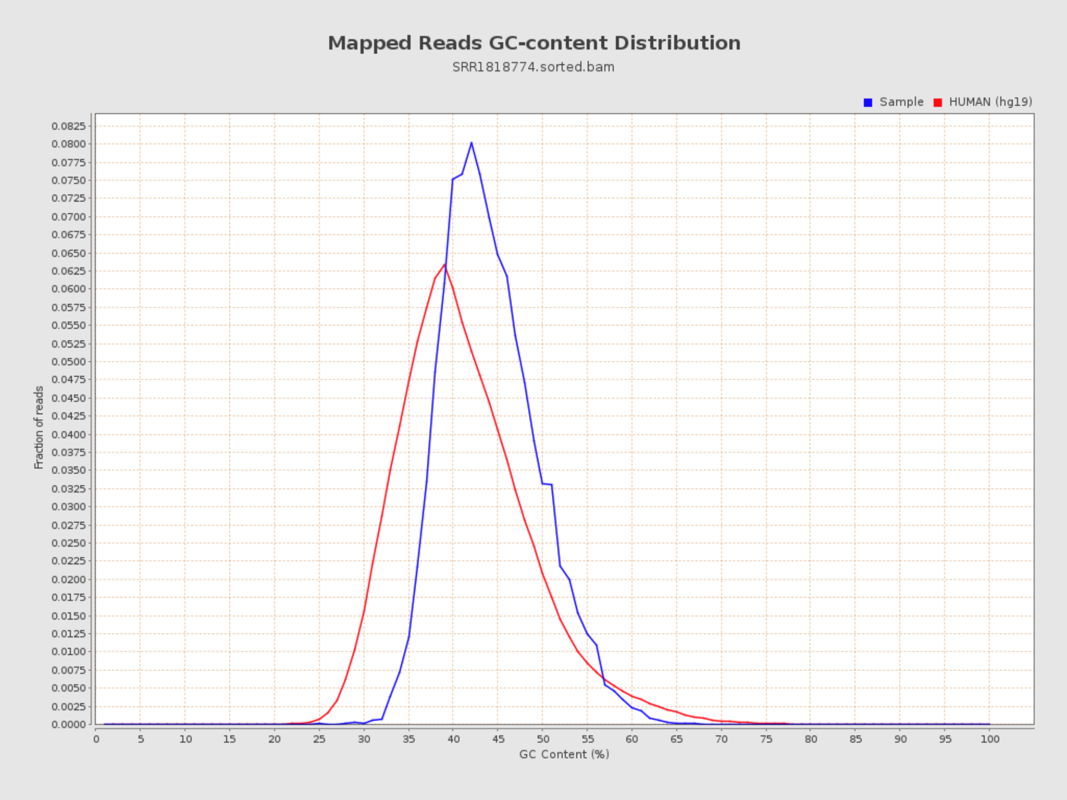
7. Results : Duplication Rate Histogram



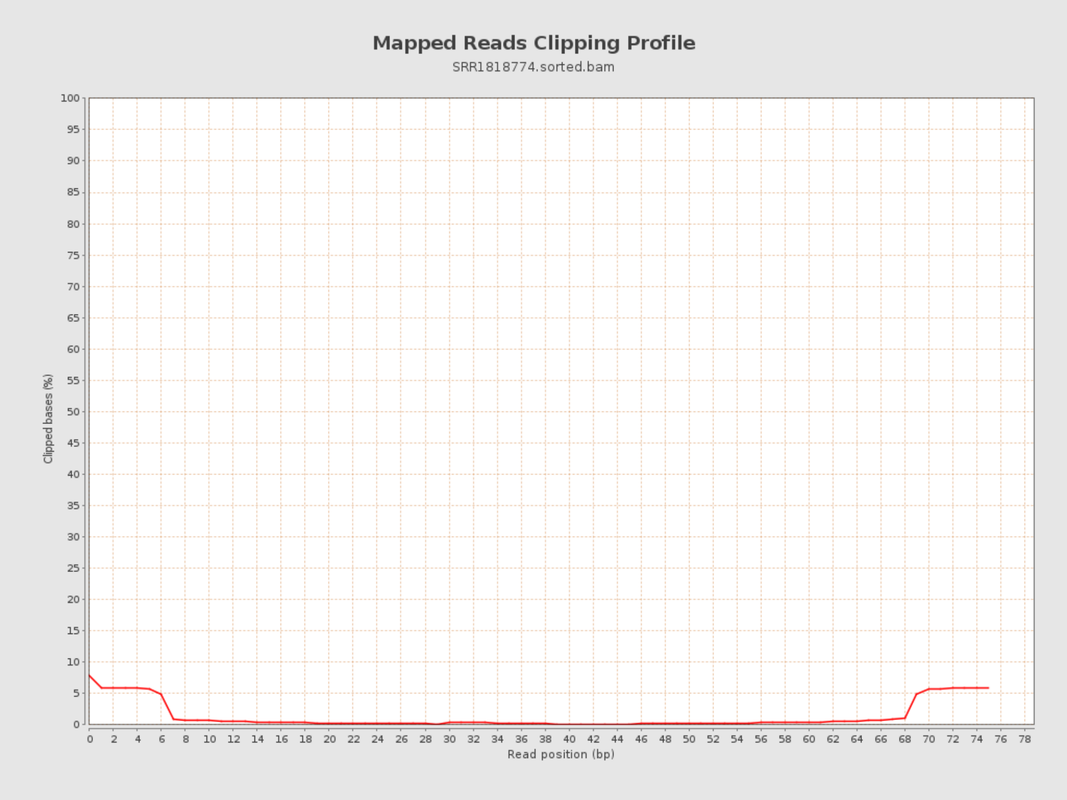
8. Results : Mapped Reads Nucleotide Content



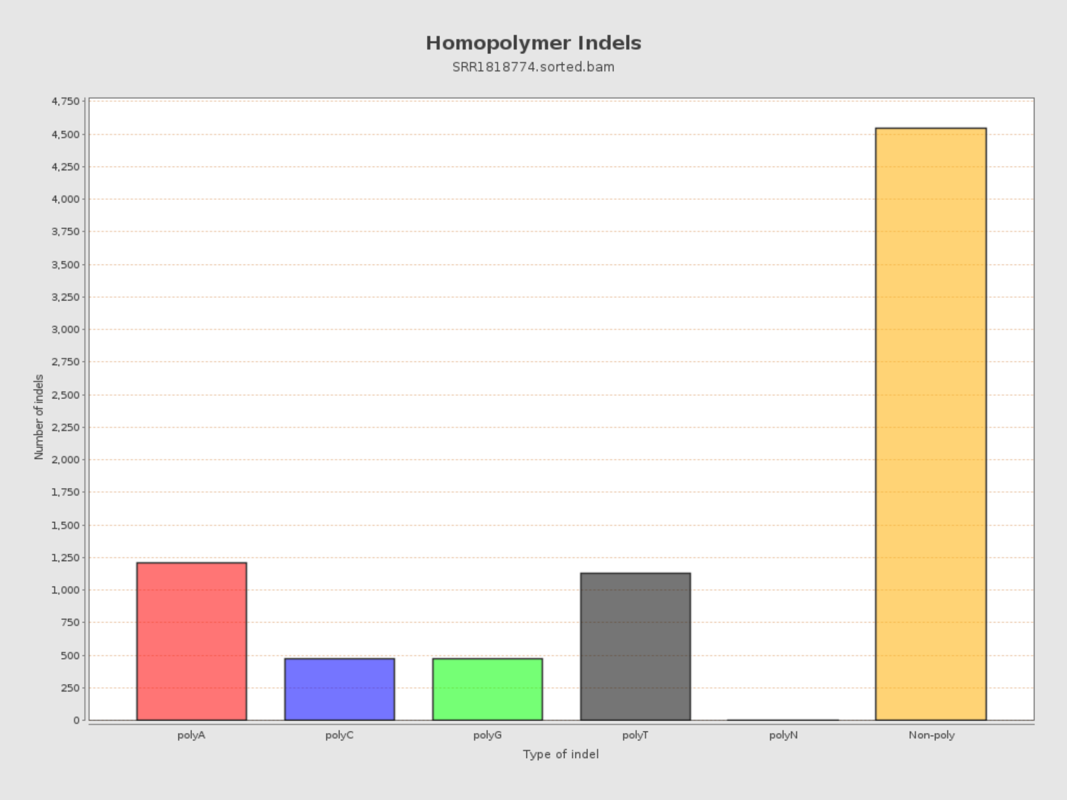
9. Results : Mapped Reads GC-content Distribution



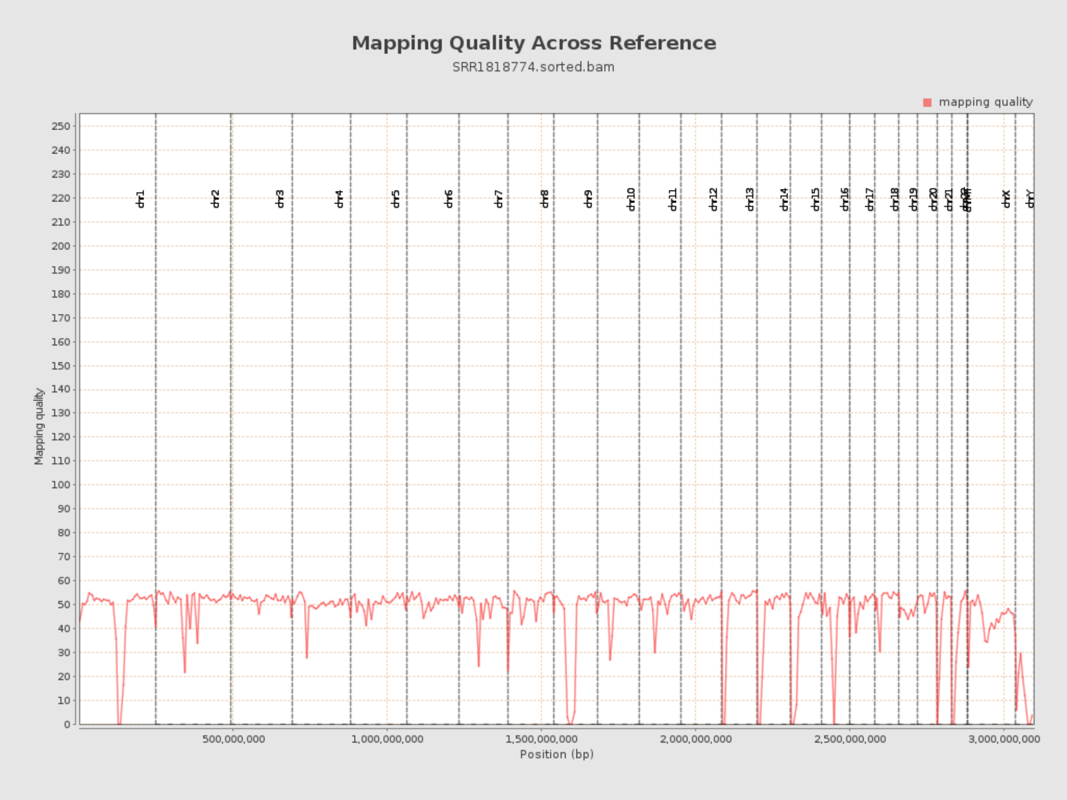
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram