Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 12:32:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818796.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_SRR1818796 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818796.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 12:32:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818796.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,607,862
Mapped reads	1,569,480 / 97.61%
Unmapped reads	38,382 / 2.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,925 / 0.68%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	726,994 / 45.21%
Duplication rate	37.86%
Clipped reads	1,565,050 / 97.34%

2.2. ACGT Content

Number/percentage of A's	29,988,003 / 28.11%
Number/percentage of C's	24,514,142 / 22.98%
Number/percentage of T's	28,717,165 / 26.92%
Number/percentage of G's	23,445,306 / 21.98%
Number/percentage of N's	6,080 / 0.01%
GC Percentage	44.96%

2.3. Coverage

Mean	0.0345

Standard Deviation	0.4862

2.4. Mapping Quality

Mean Mapping Quality	47.61

2.5. Mismatches and indels

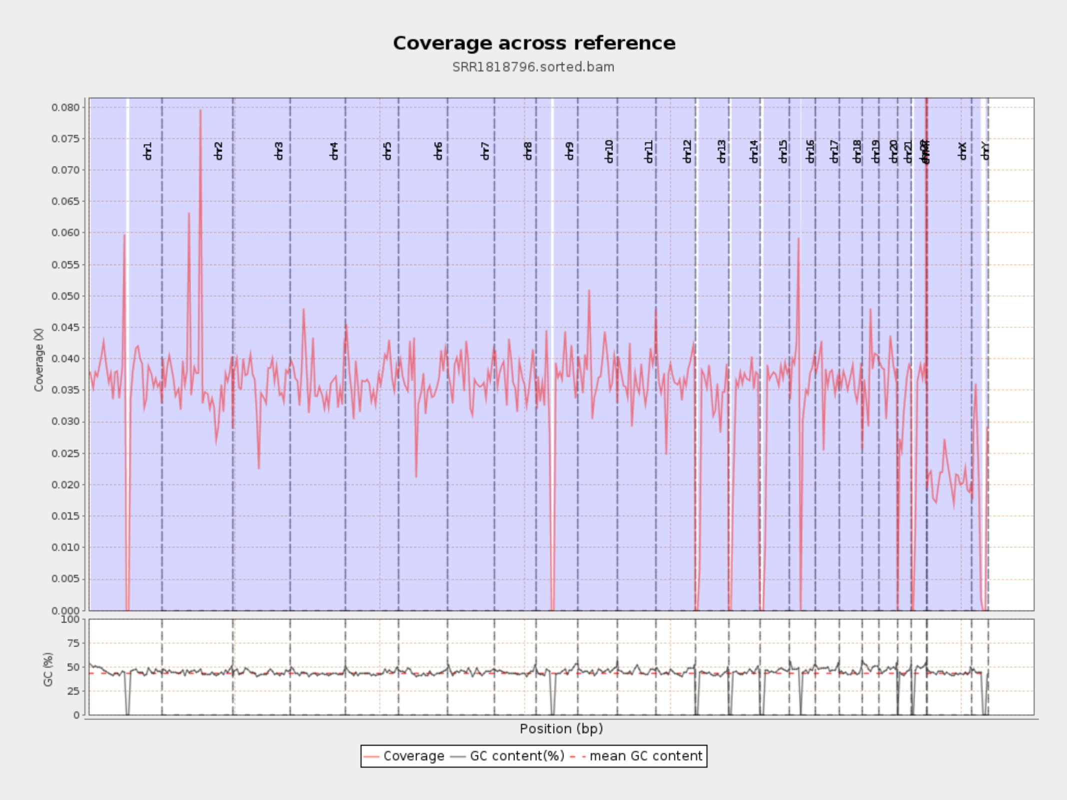
General error rate	0.54%
Mismatches	556,602
Insertions	11,753
Mapped reads with at least one insertion	0.74%
Deletions	27,478
Mapped reads with at least one deletion	1.73%
Homopolymer indels	41.68%

2.6. Chromosome stats

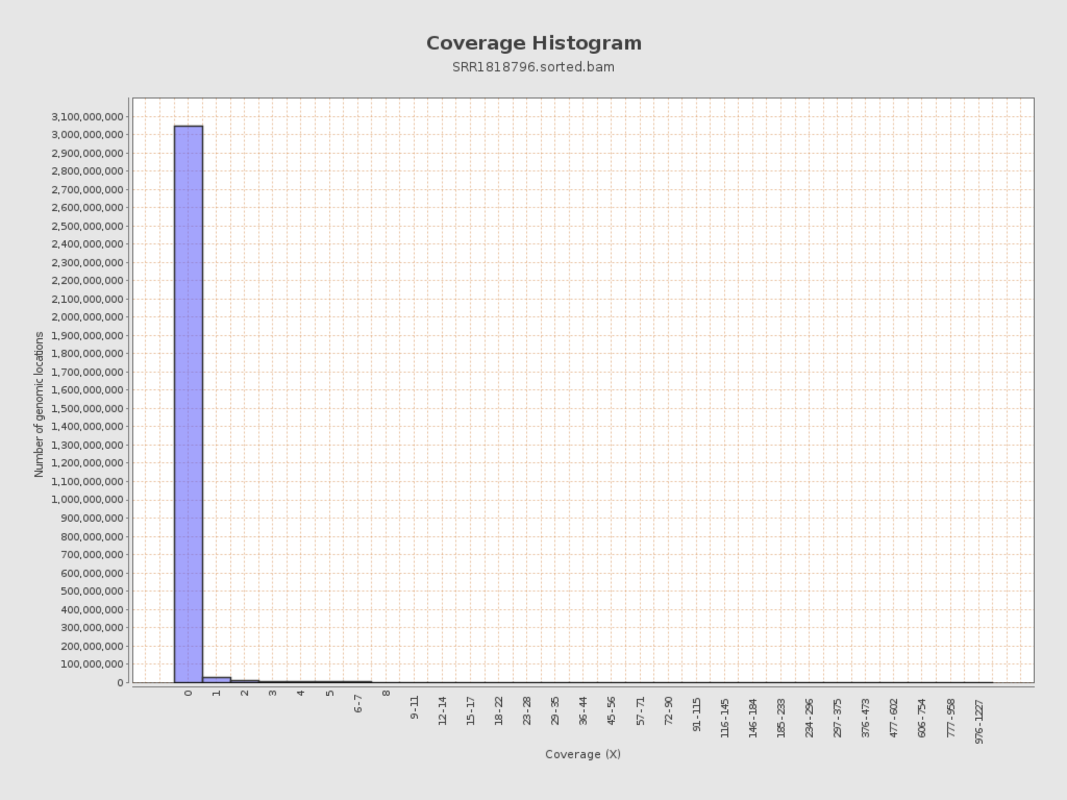
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8928806	0.0358	0.6407
chr2	243199373	9205352	0.0379	0.8497
chr3	198022430	7142689	0.0361	0.3602
chr4	191154276	6939617	0.0363	0.4145
chr5	180915260	6672244	0.0369	0.3767
chr6	171115067	6215615	0.0363	0.4003
chr7	159138663	5873283	0.0369	0.4225

chr8	146364022	5460063	0.0373	0.3906
chr9	141213431	4675653	0.0331	0.4073
chr10	135534747	5195822	0.0383	0.512
chr11	135006516	4973050	0.0368	0.403
chr12	133851895	4918758	0.0367	0.3942
chr13	115169878	3379224	0.0293	0.3229
chr14	107349540	3311126	0.0308	0.3621
chr15	102531392	3111199	0.0303	0.3307
chr16	90354753	3253887	0.036	0.5413
chr17	81195210	2974101	0.0366	0.3873
chr18	78077248	2844290	0.0364	0.4776
chr19	59128983	2221698	0.0376	0.5429
chr20	63025520	2385352	0.0378	0.3946
chr21	48129895	1431720	0.0297	0.3361
chr22	51304566	1346300	0.0262	0.3443
chrMT	16571	32530	1.9631	3.1526
chrX	155270560	3227358	0.0208	0.3083
chrY	59373566	995364	0.0168	0.8428

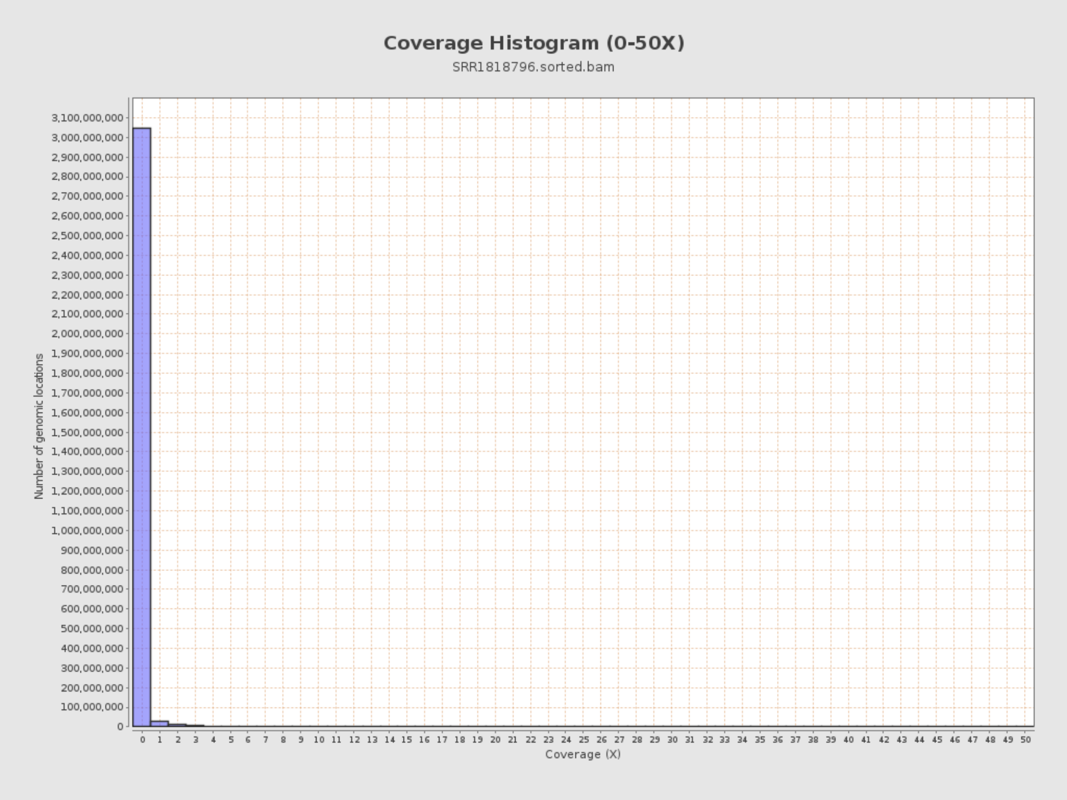
3. Results : Coverage across reference



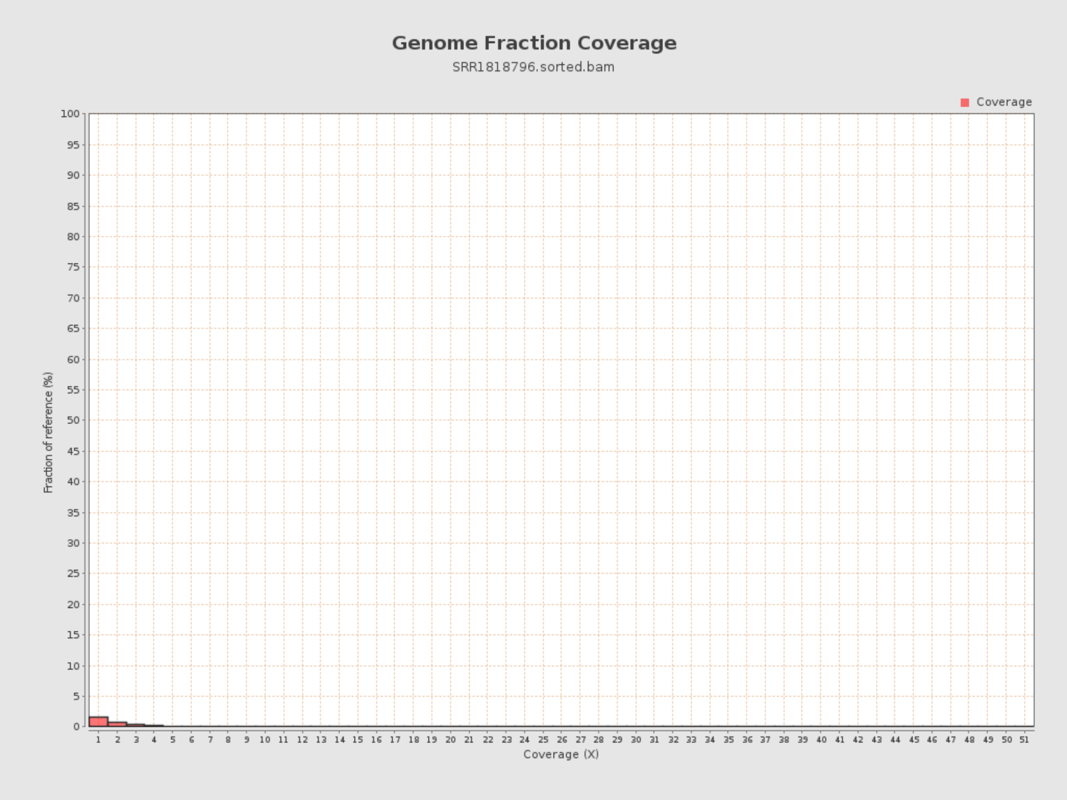
4. Results : Coverage Histogram



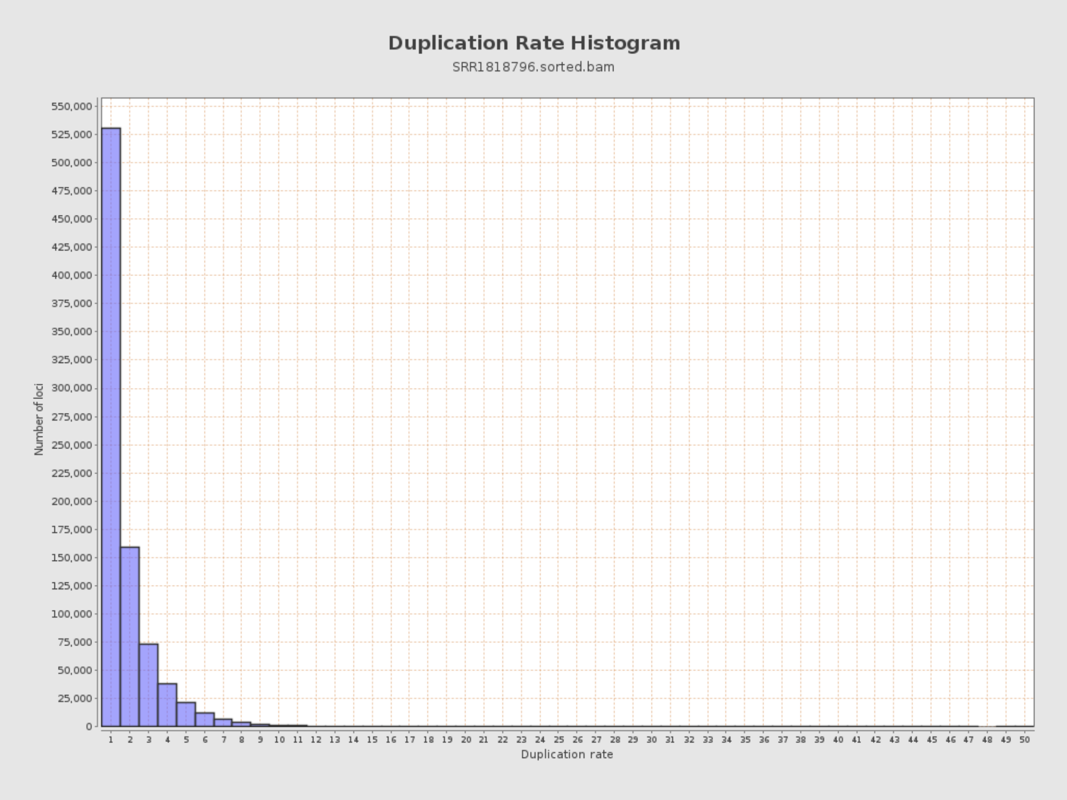
5. Results : Coverage Histogram (0-50X)



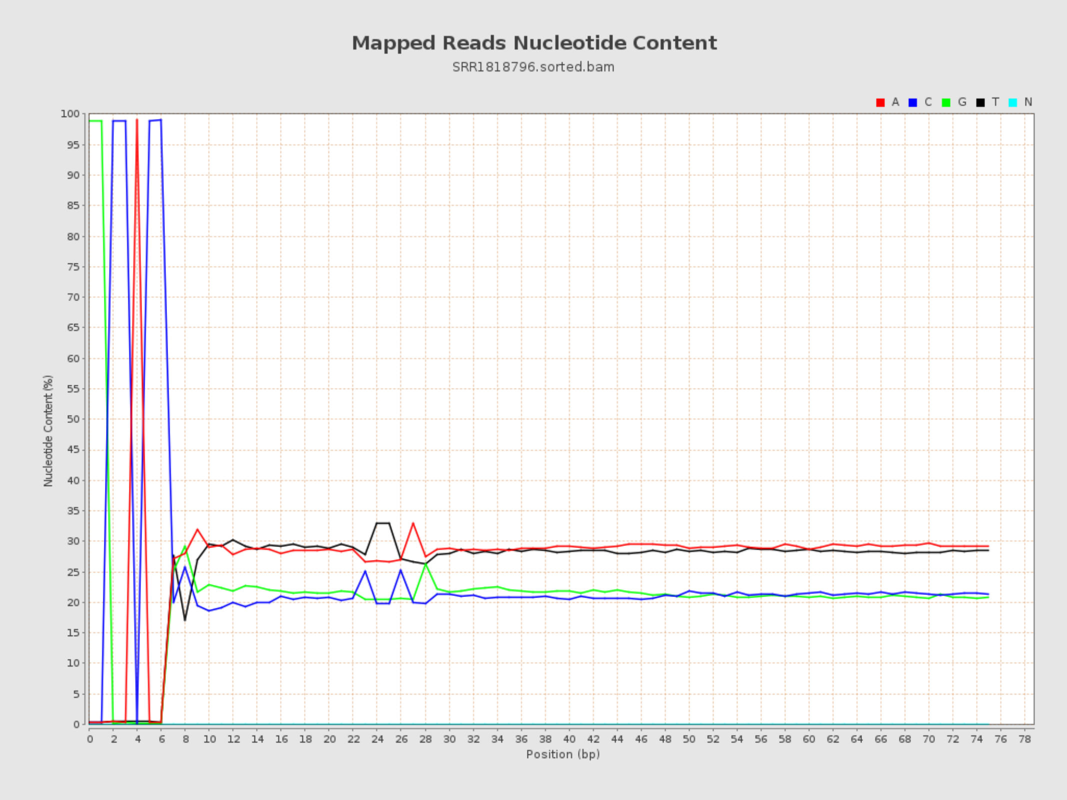
6. Results : Genome Fraction Coverage



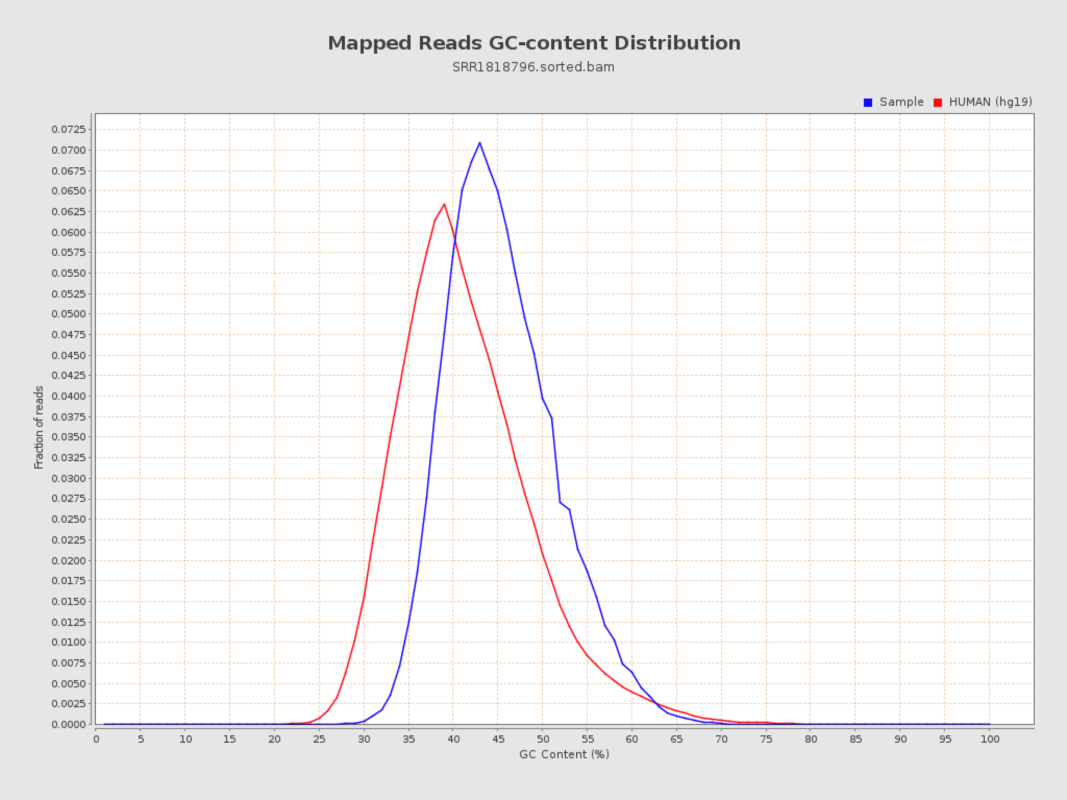
7. Results : Duplication Rate Histogram



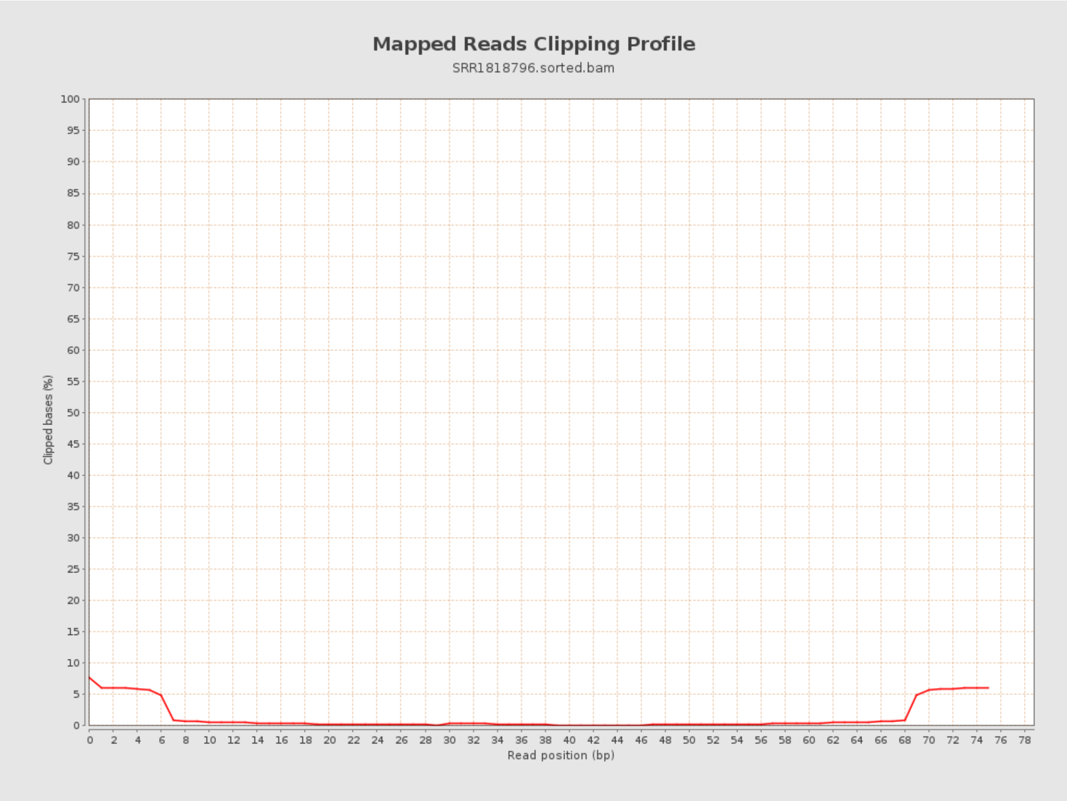
8. Results : Mapped Reads Nucleotide Content



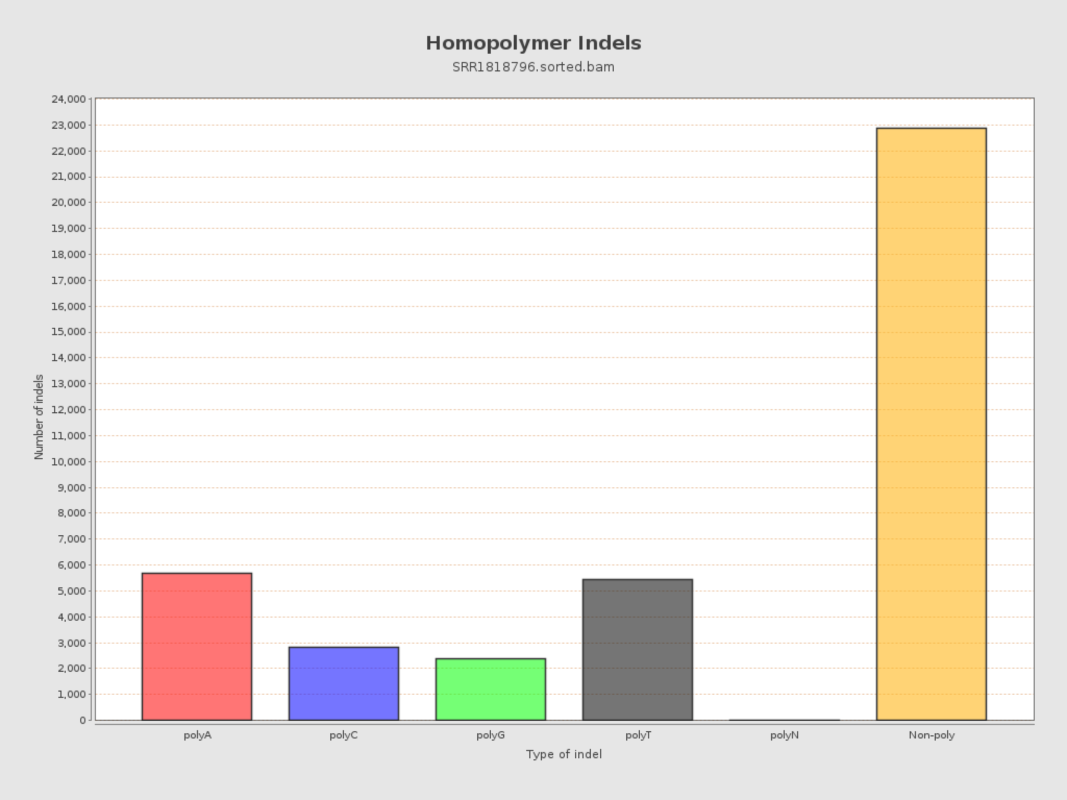
9. Results : Mapped Reads GC-content Distribution



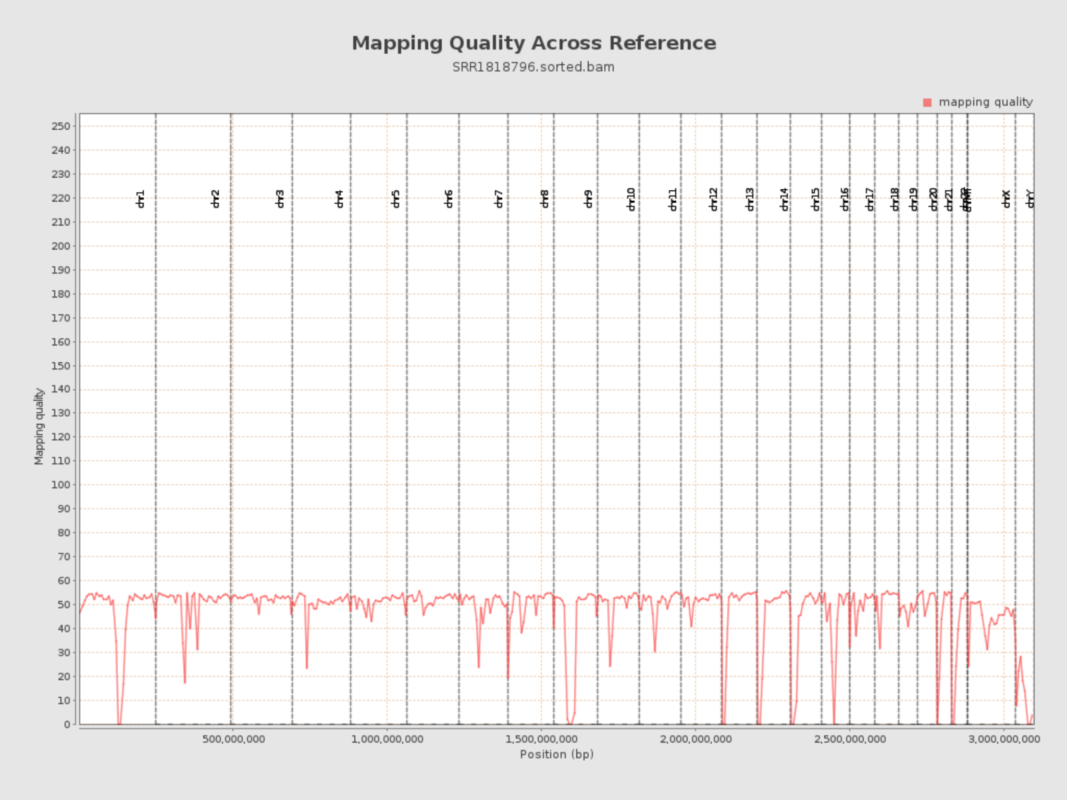
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram