Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 07:38:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818765.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_SRR1818765 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818765.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 07:38:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818765.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	839,637
Mapped reads	798,501 / 95.1%
Unmapped reads	41,136 / 4.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,223 / 0.86%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	268,789 / 32.01%
Duplication rate	28.26%
Clipped reads	799,106 / 95.17%

2.2. ACGT Content

Number/percentage of A's	15,439,021 / 28.55%
Number/percentage of C's	10,783,653 / 19.94%
Number/percentage of T's	15,878,237 / 29.37%
Number/percentage of G's	11,963,605 / 22.13%
Number/percentage of N's	3,283 / 0.01%
GC Percentage	42.07%

2.3. Coverage

Mean	0.0175

Standard Deviation	0.2585

2.4. Mapping Quality

Mean Mapping Quality	47.59

2.5. Mismatches and indels

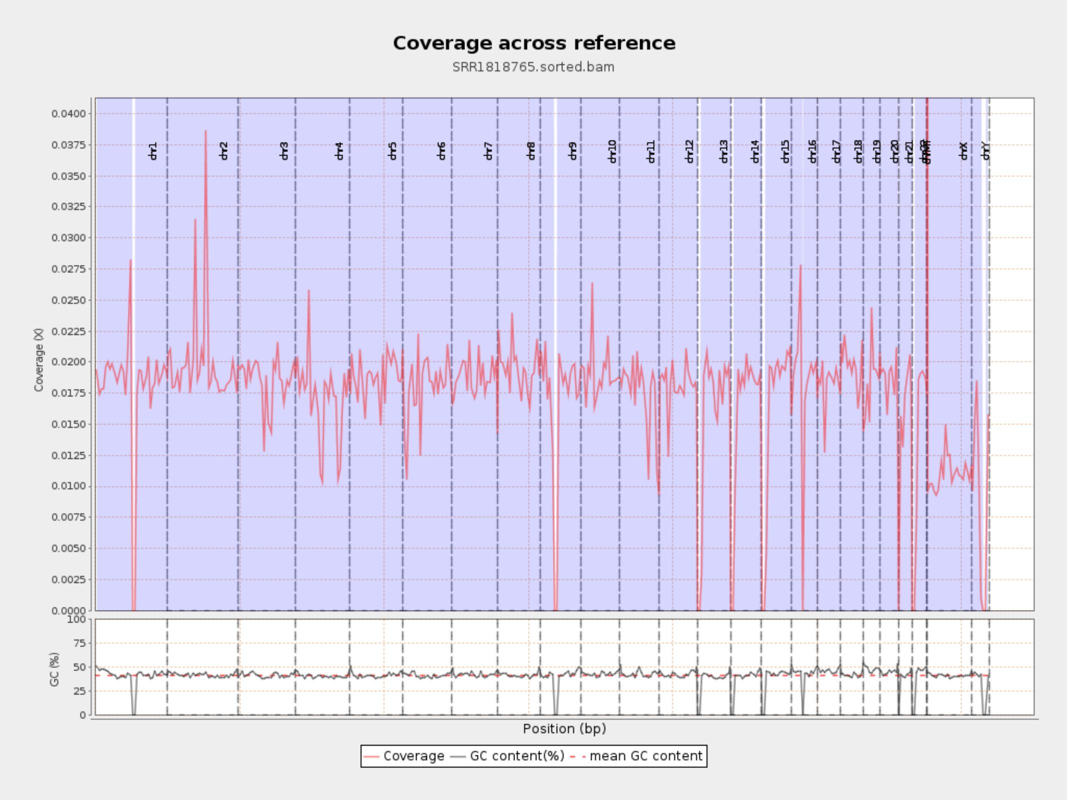
General error rate	0.54%
Mismatches	276,308
Insertions	6,893
Mapped reads with at least one insertion	0.85%
Deletions	14,160
Mapped reads with at least one deletion	1.75%
Homopolymer indels	41.15%

2.6. Chromosome stats

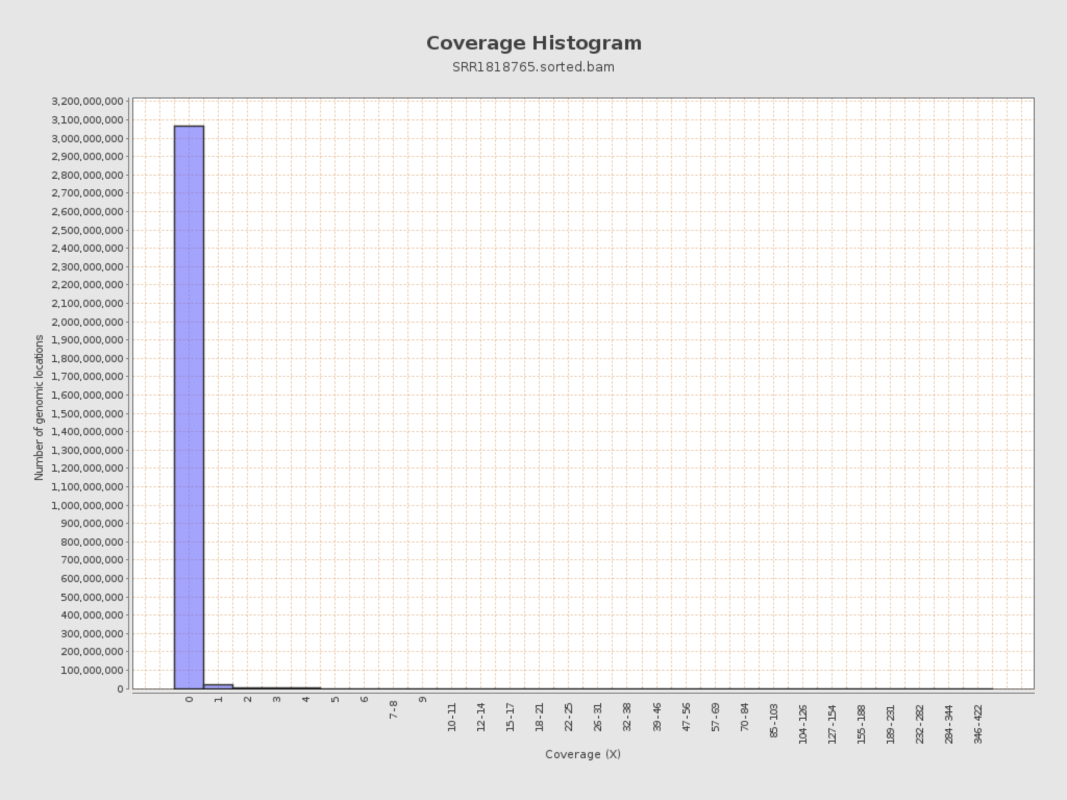
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4484577	0.018	0.3269
chr2	243199373	4864772	0.02	0.3727
chr3	198022430	3675129	0.0186	0.2133
chr4	191154276	3260568	0.0171	0.2229
chr5	180915260	3418801	0.0189	0.2176
chr6	171115067	3084876	0.018	0.2285
chr7	159138663	3005991	0.0189	0.2309

chr8	146364022	2857551	0.0195	0.2422
chr9	141213431	2342924	0.0166	0.2301
chr10	135534747	2595689	0.0192	0.2895
chr11	135006516	2374879	0.0176	0.23
chr12	133851895	2438238	0.0182	0.2211
chr13	115169878	1775641	0.0154	0.1933
chr14	107349540	1694918	0.0158	0.2183
chr15	102531392	1615920	0.0158	0.197
chr16	90354753	1637216	0.0181	0.2794
chr17	81195210	1479892	0.0182	0.2205
chr18	78077248	1535128	0.0197	0.3123
chr19	59128983	1096827	0.0185	0.3103
chr20	63025520	1174154	0.0186	0.2234
chr21	48129895	747516	0.0155	0.2062
chr22	51304566	674021	0.0131	0.1926
chrMT	16571	21757	1.313	2.0074
chrX	155270560	1710143	0.011	0.174
chrY	59373566	523123	0.0088	0.4336

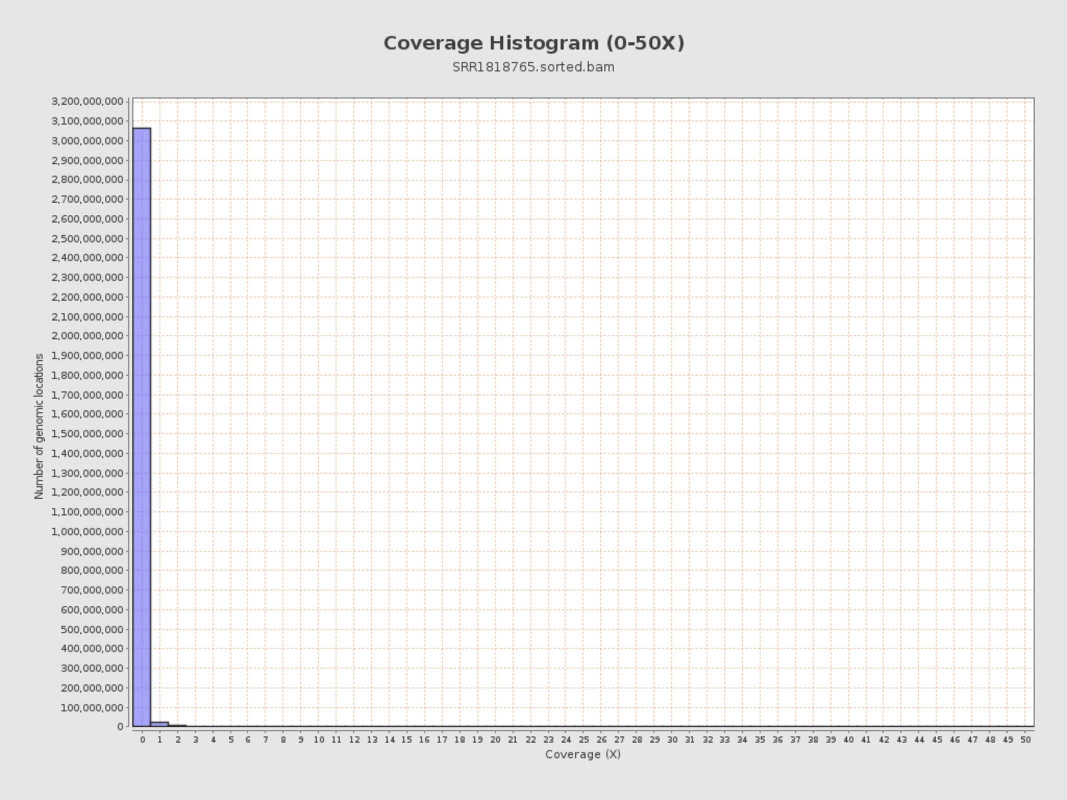
3. Results : Coverage across reference



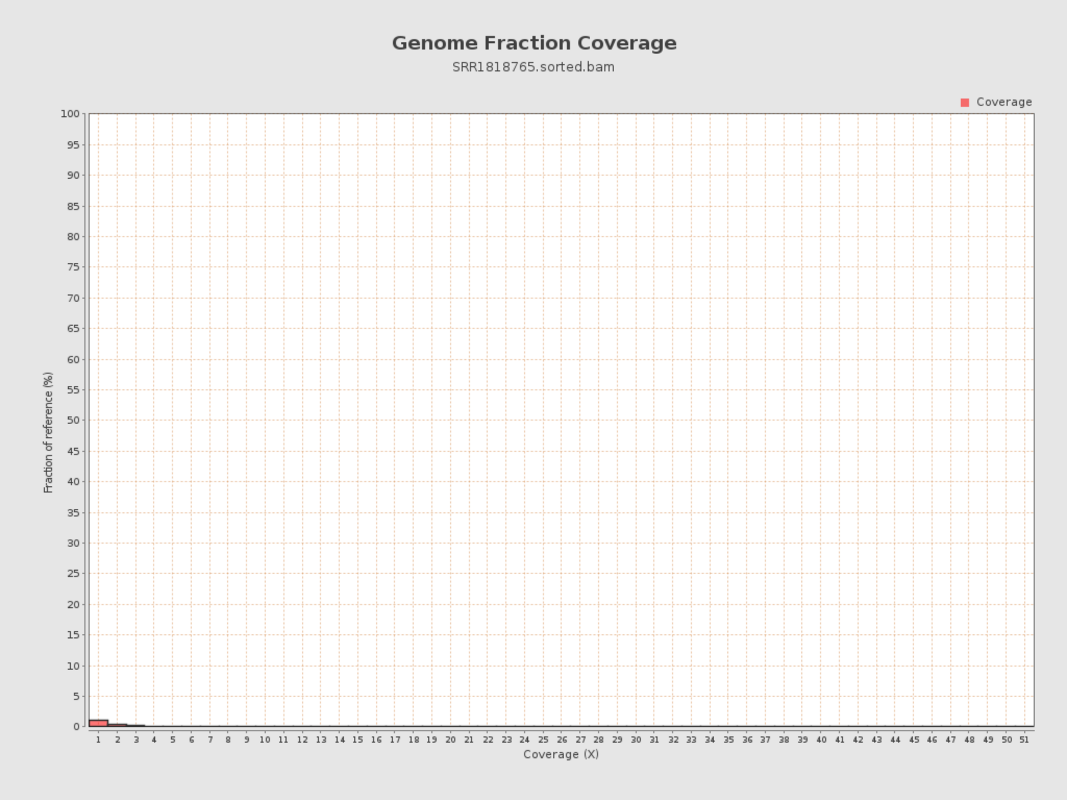
4. Results : Coverage Histogram



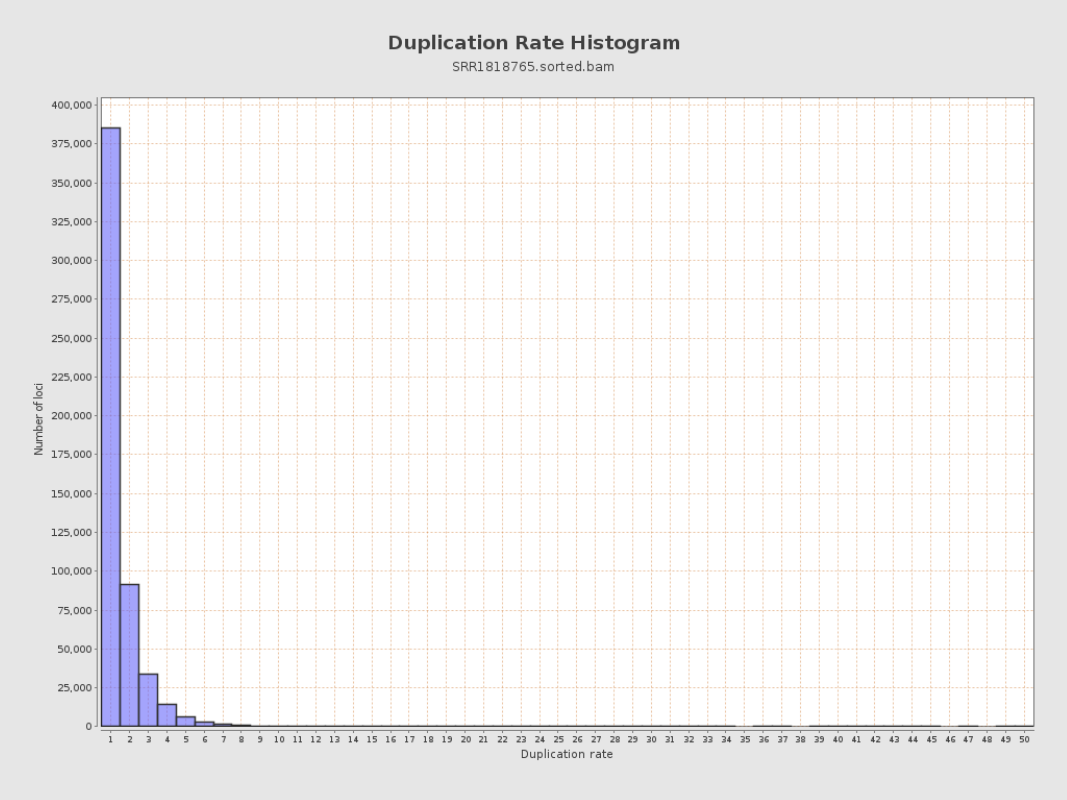
5. Results : Coverage Histogram (0-50X)



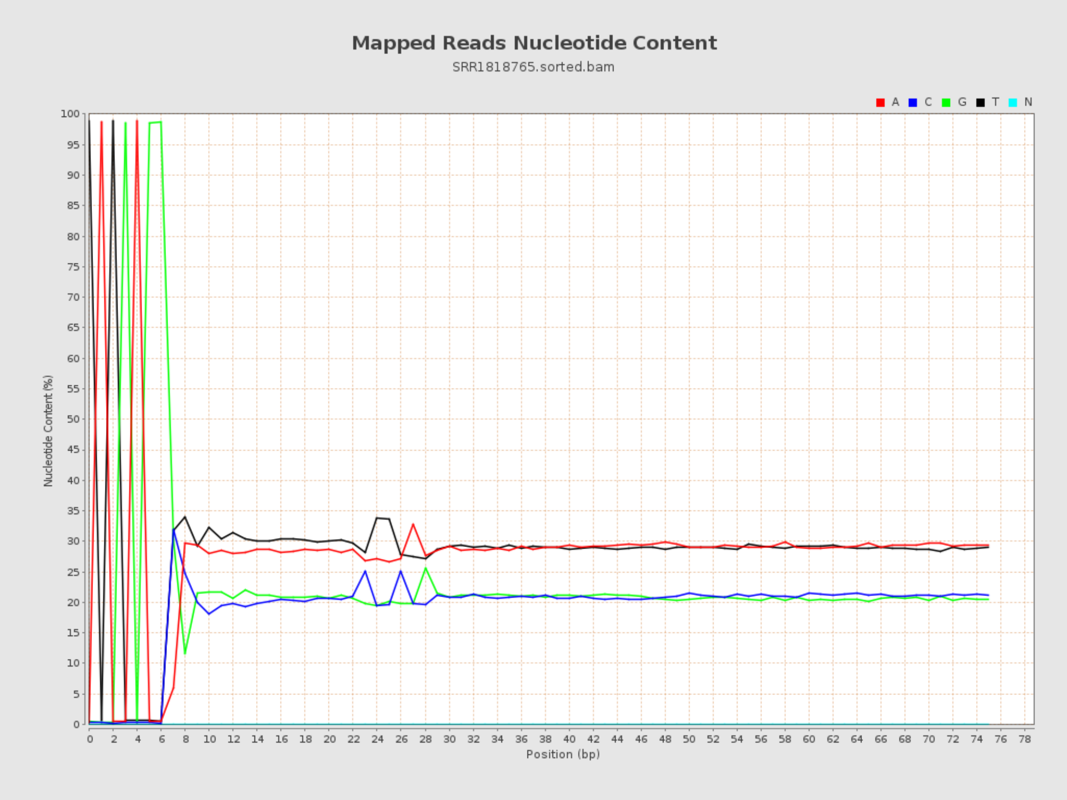
6. Results : Genome Fraction Coverage



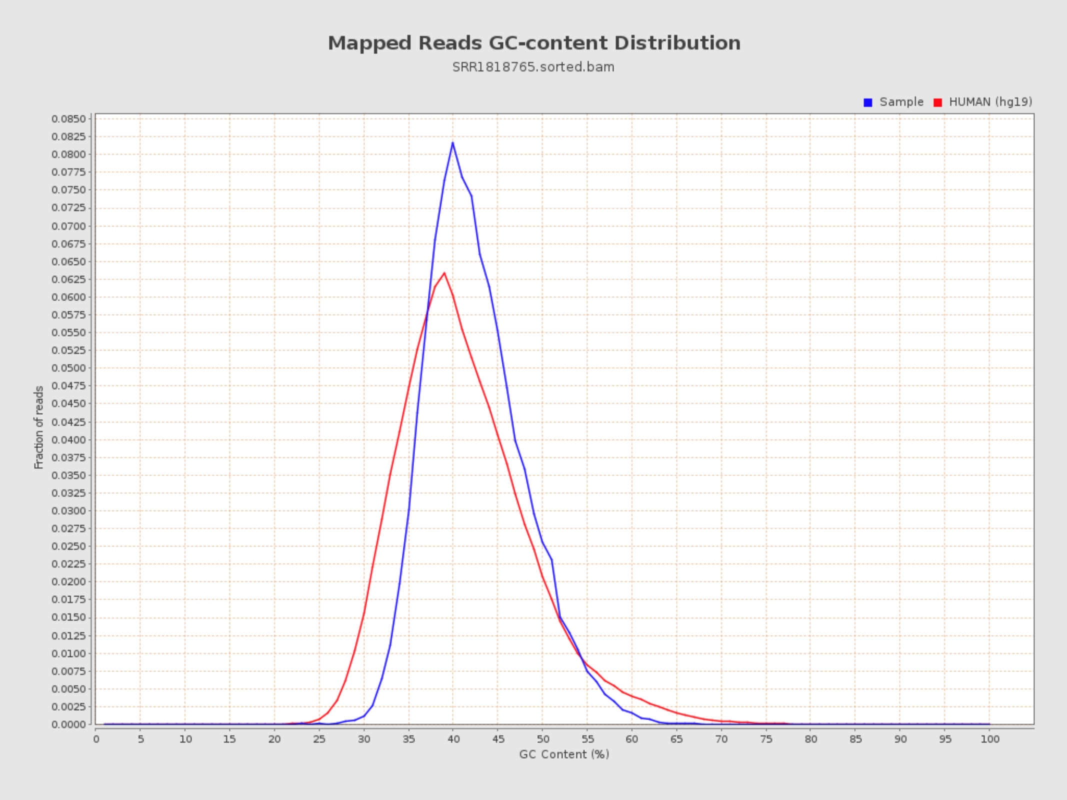
7. Results : Duplication Rate Histogram



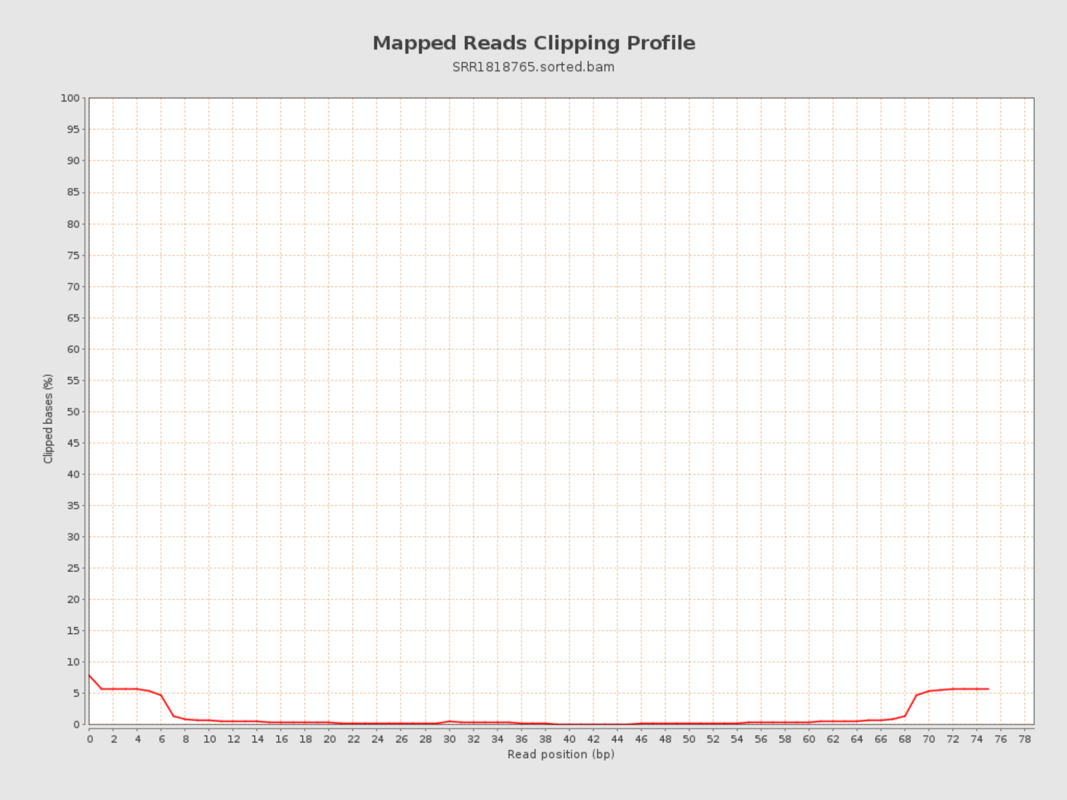
8. Results : Mapped Reads Nucleotide Content



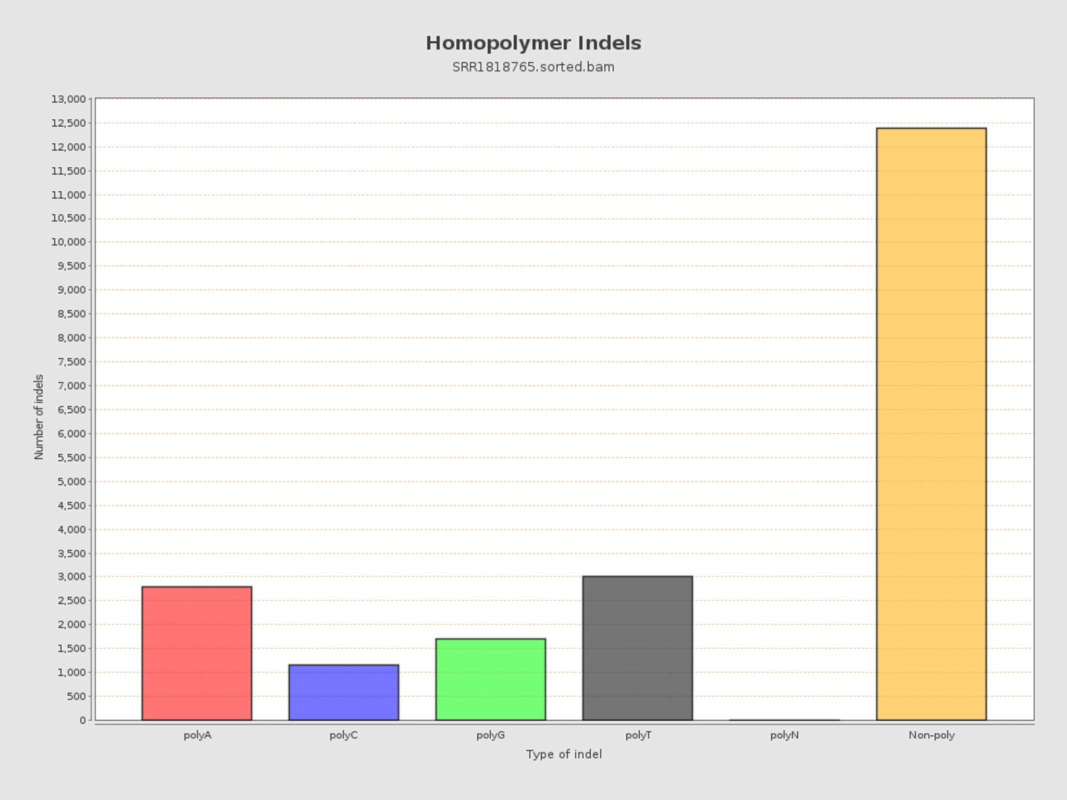
9. Results : Mapped Reads GC-content Distribution



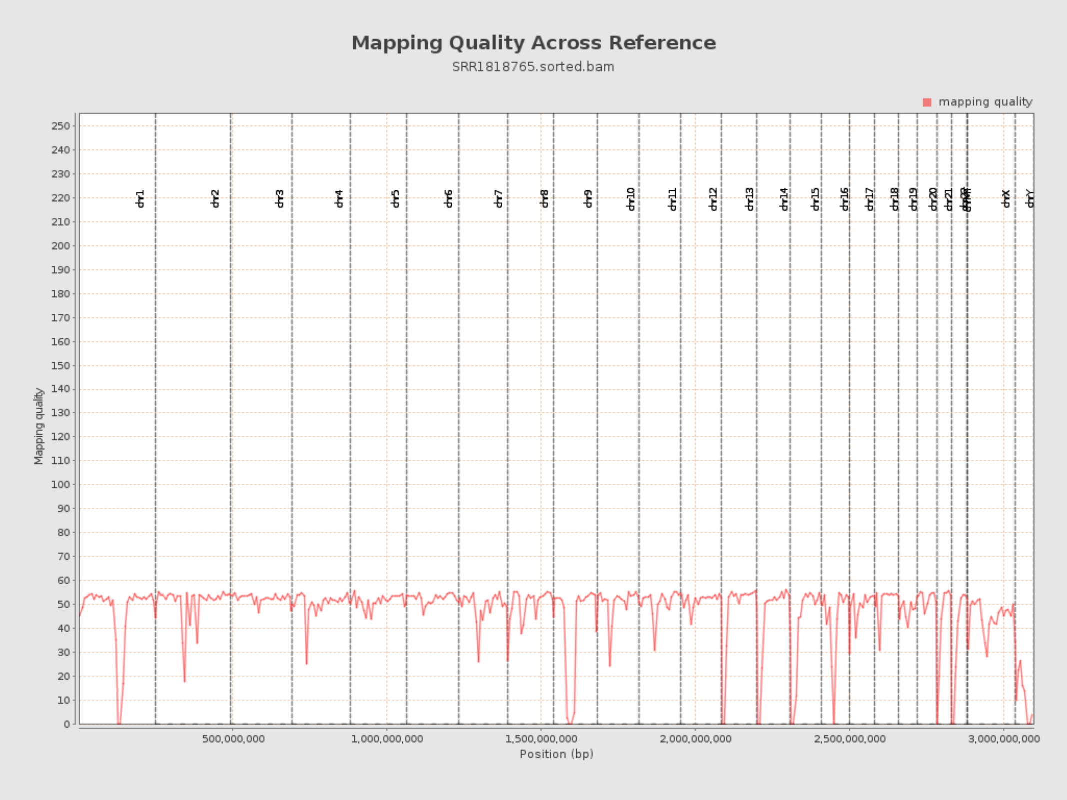
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram