Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 04:03:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818747.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_SRR1818747 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818747.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 04:03:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818747.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	270,672
Mapped reads	251,312 / 92.85%
Unmapped reads	19,360 / 7.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,819 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	33,172 / 12.26%
Duplication rate	11.83%
Clipped reads	252,035 / 93.11%

2.2. ACGT Content

Number/percentage of A's	4,875,259 / 28.54%
Number/percentage of C's	3,830,510 / 22.43%
Number/percentage of T's	4,858,990 / 28.45%
Number/percentage of G's	3,514,406 / 20.58%
Number/percentage of N's	1,279 / 0.01%
GC Percentage	43%

2.3. Coverage

Mean	0.0055

Standard Deviation	0.1003

2.4. Mapping Quality

Mean Mapping Quality	47.29

2.5. Mismatches and indels

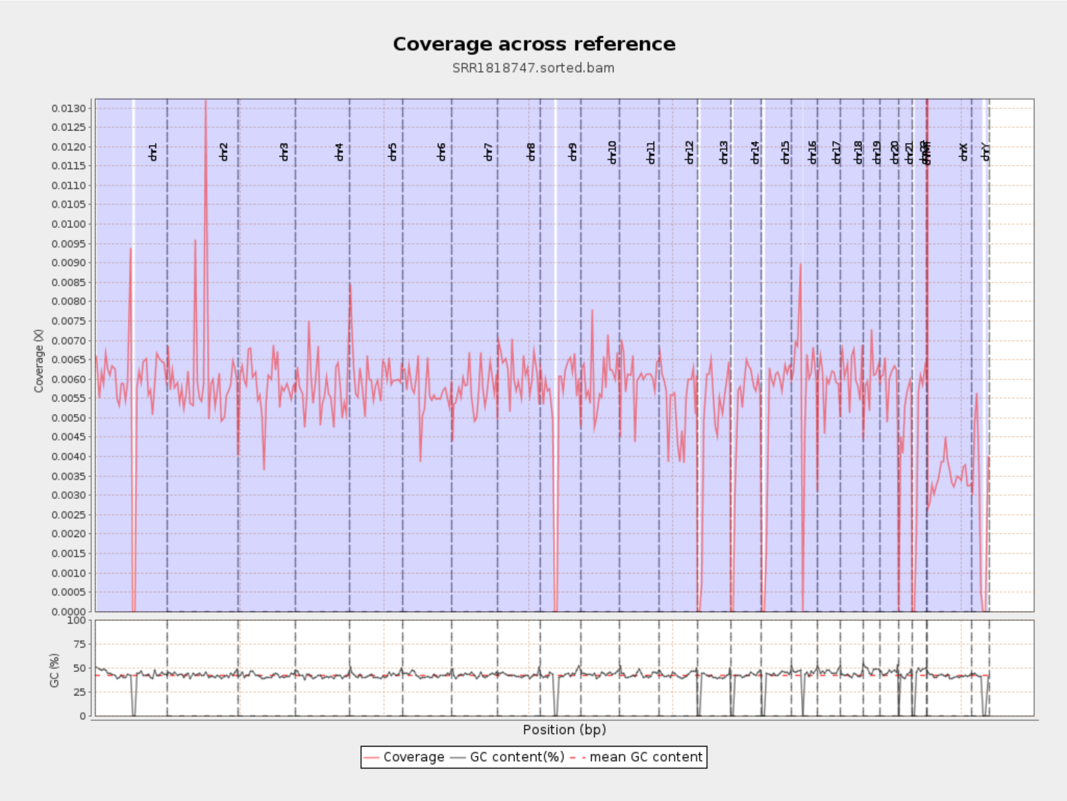
General error rate	0.53%
Mismatches	86,571
Insertions	1,857
Mapped reads with at least one insertion	0.73%
Deletions	4,256
Mapped reads with at least one deletion	1.68%
Homopolymer indels	40.73%

2.6. Chromosome stats

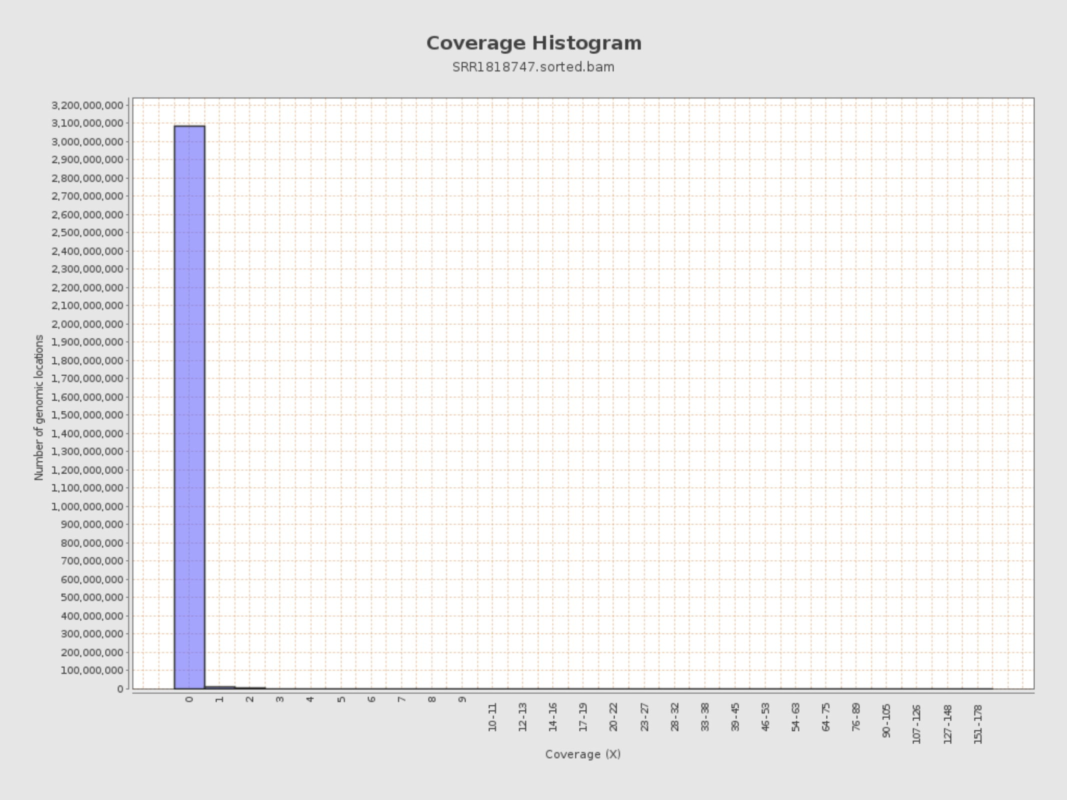
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1435981	0.0058	0.1258
chr2	243199373	1479031	0.0061	0.1438
chr3	198022430	1157190	0.0058	0.0887
chr4	191154276	1101759	0.0058	0.0916
chr5	180915260	1091323	0.006	0.0918
chr6	171115067	969293	0.0057	0.0907
chr7	159138663	910300	0.0057	0.0957

chr8	146364022	901537	0.0062	0.095
chr9	141213431	749276	0.0053	0.0928
chr10	135534747	816808	0.006	0.1039
chr11	135006516	816069	0.006	0.0947
chr12	133851895	715922	0.0053	0.0866
chr13	115169878	537627	0.0047	0.0797
chr14	107349540	531547	0.005	0.087
chr15	102531392	502925	0.0049	0.0838
chr16	90354753	534925	0.0059	0.114
chr17	81195210	479600	0.0059	0.091
chr18	78077248	482661	0.0062	0.1039
chr19	59128983	356785	0.006	0.1122
chr20	63025520	377130	0.006	0.0926
chr21	48129895	225558	0.0047	0.0807
chr22	51304566	213424	0.0042	0.078
chrMT	16571	1943	0.1173	0.4123
chrX	155270560	537645	0.0035	0.0712
chrY	59373566	161226	0.0027	0.112

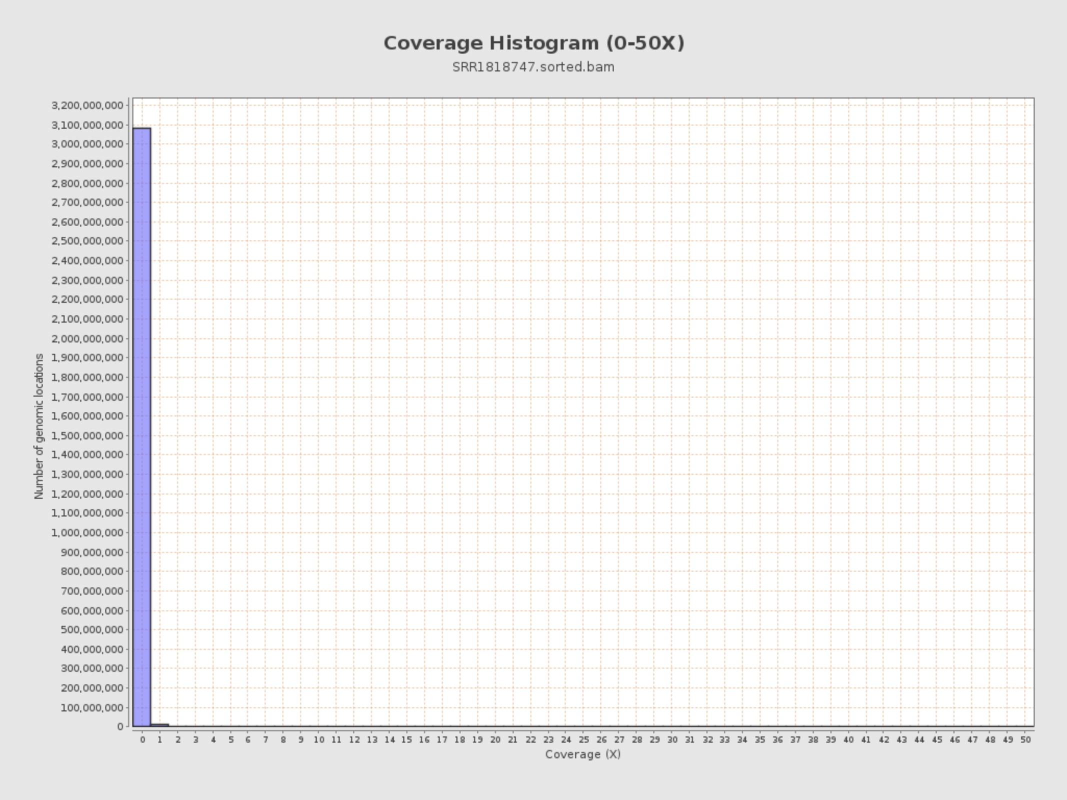
3. Results : Coverage across reference



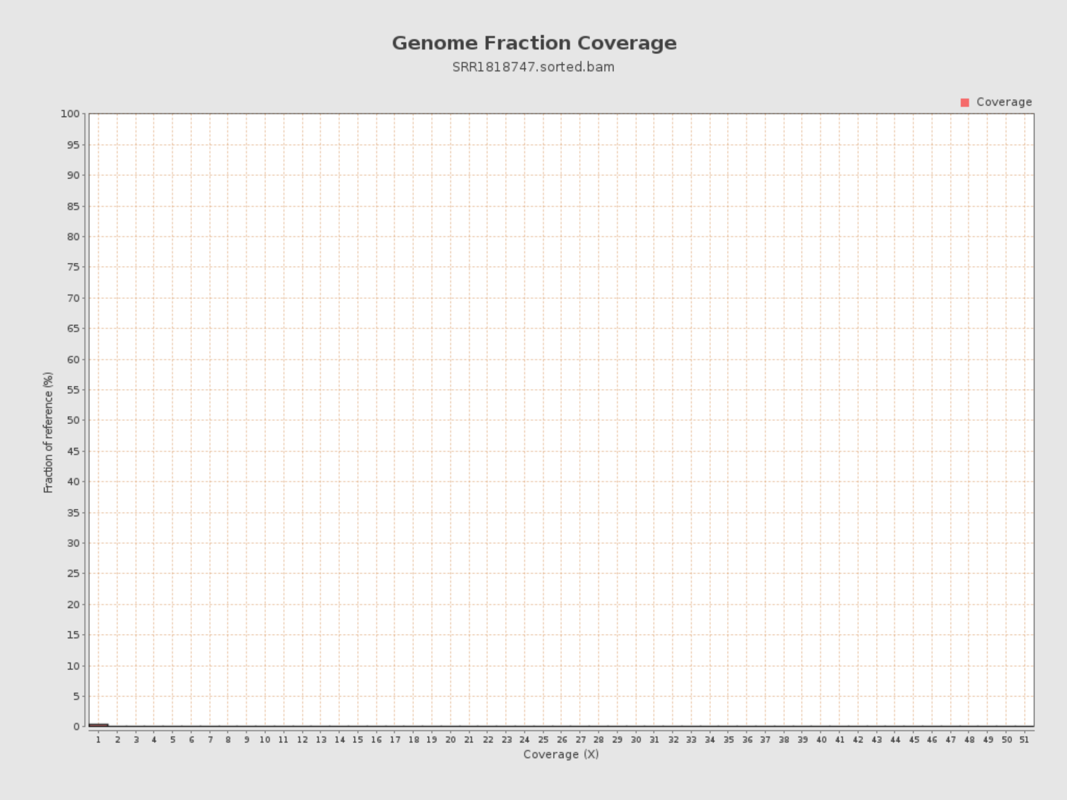
4. Results : Coverage Histogram



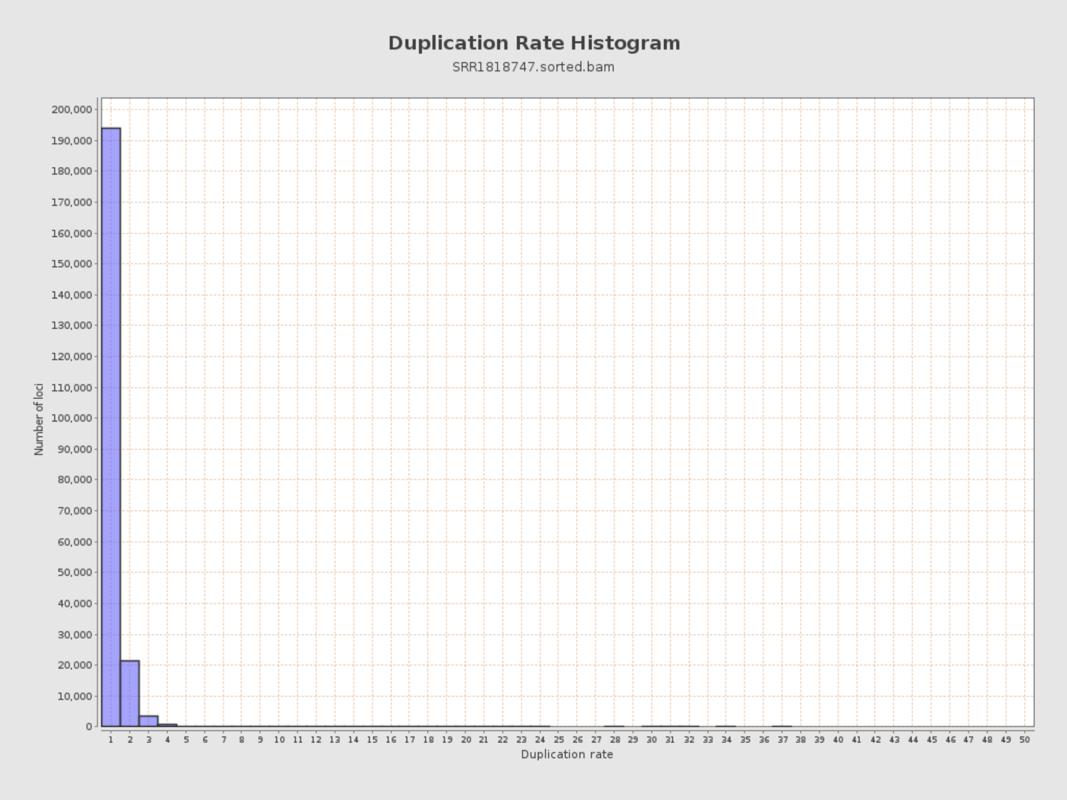
5. Results : Coverage Histogram (0-50X)



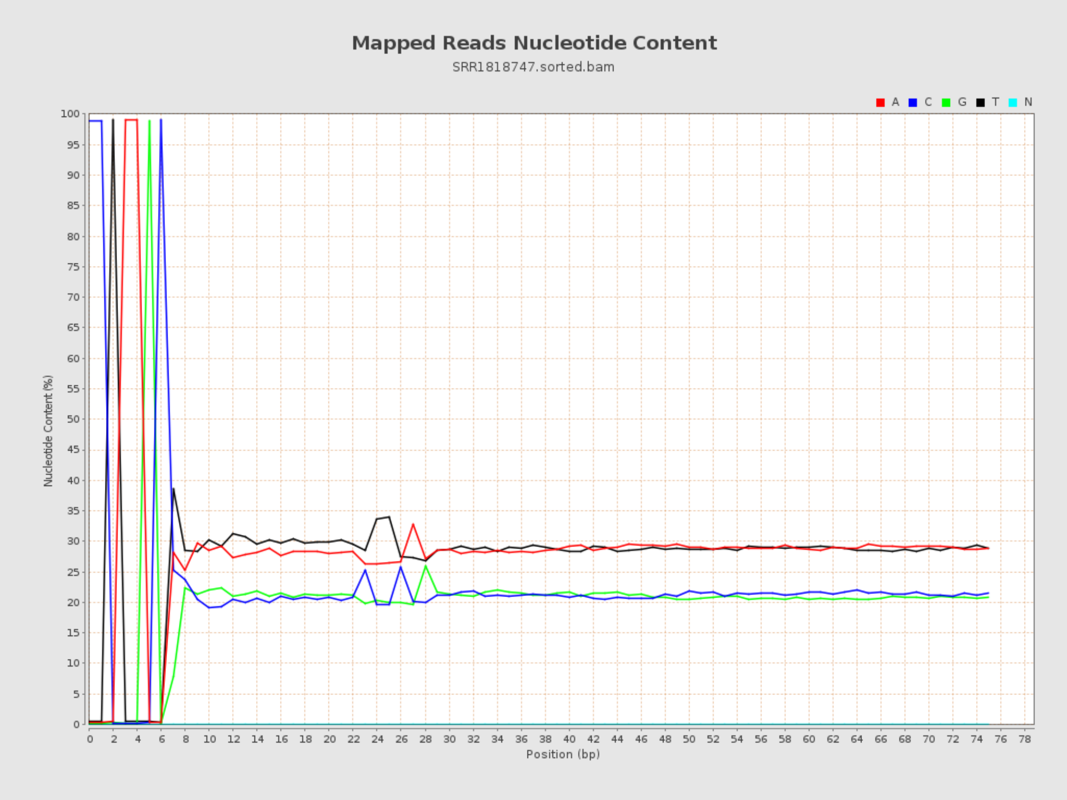
6. Results : Genome Fraction Coverage



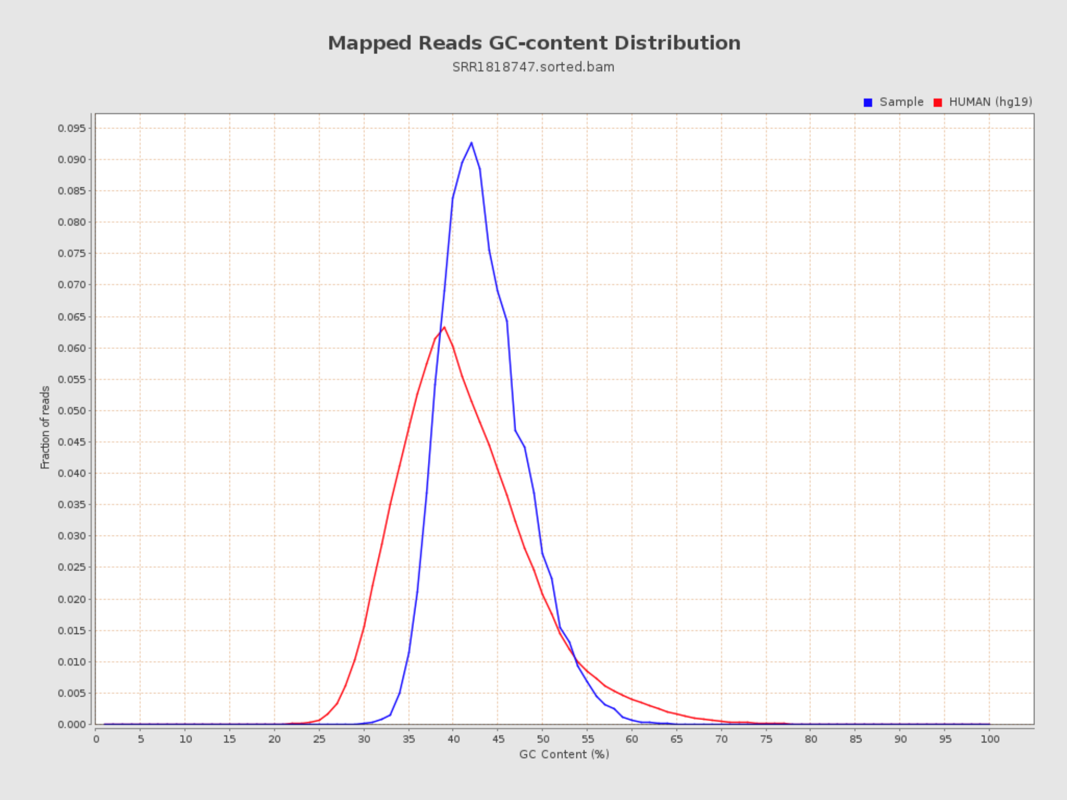
7. Results : Duplication Rate Histogram



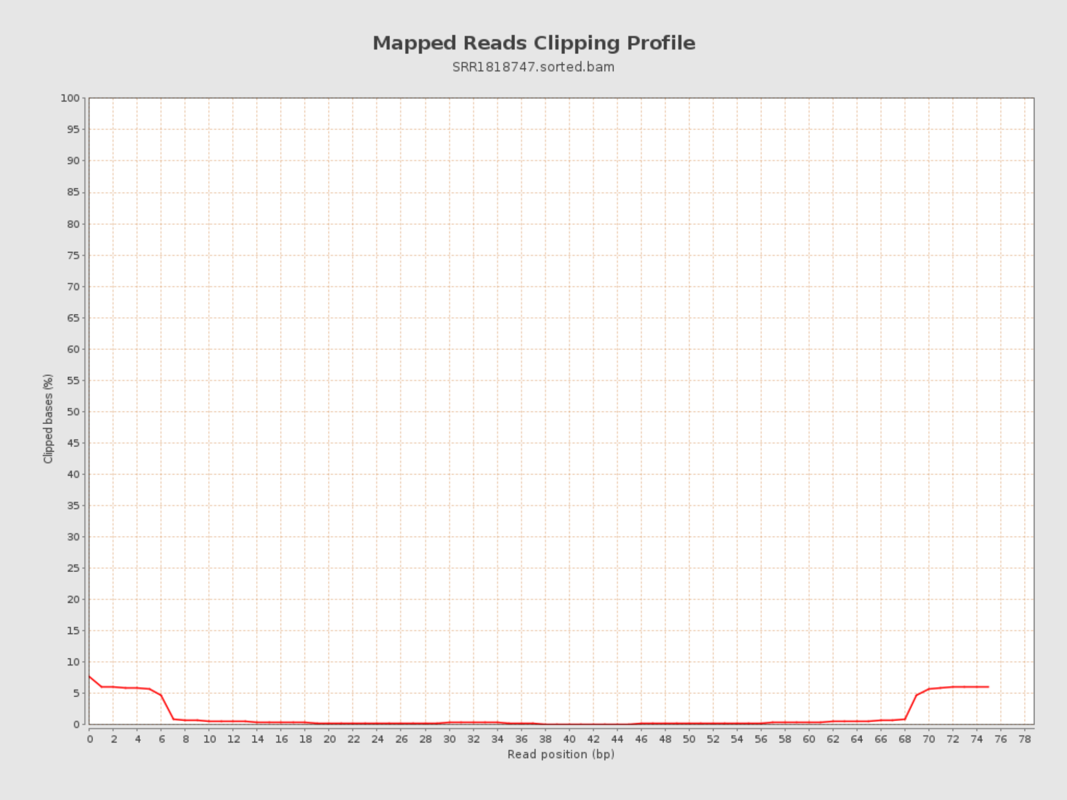
8. Results : Mapped Reads Nucleotide Content



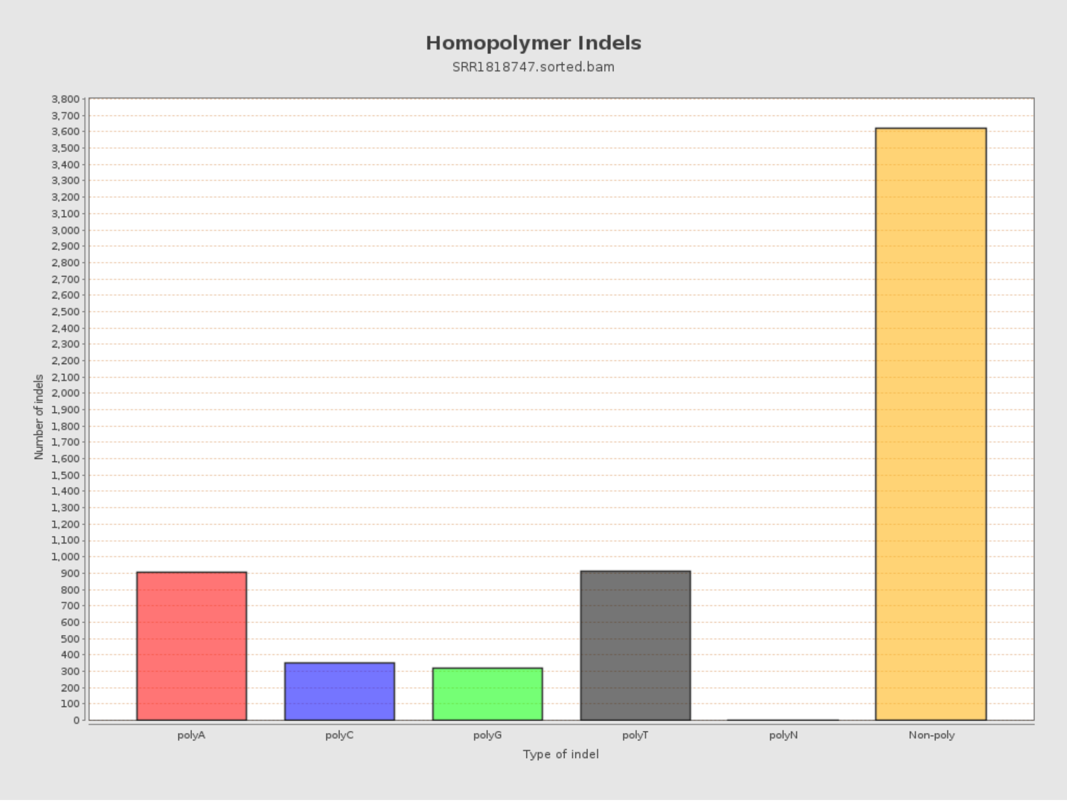
9. Results : Mapped Reads GC-content Distribution



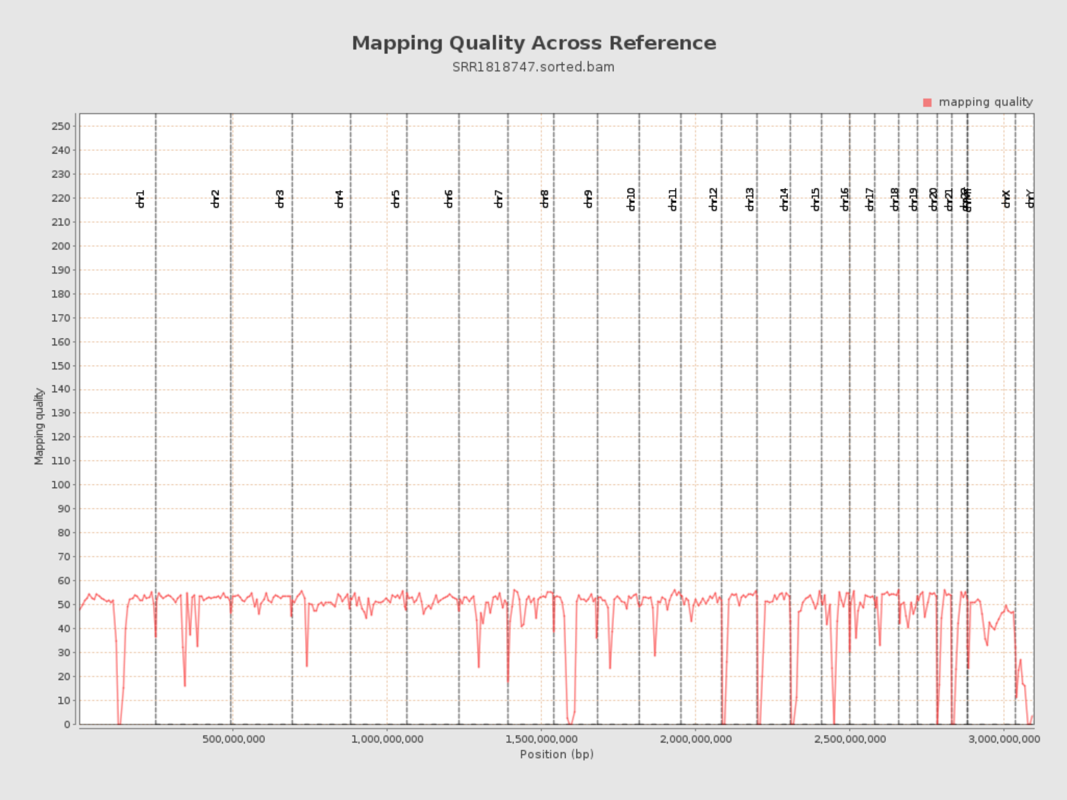
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram