Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 13:38:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818803.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_SRR1818803 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818803.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 13:38:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818803.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	891,929
Mapped reads	868,847 / 97.41%
Unmapped reads	23,082 / 2.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,683 / 0.75%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	524,136 / 58.76%
Duplication rate	47.53%
Clipped reads	867,845 / 97.3%

2.2. ACGT Content

Number/percentage of A's	17,175,539 / 29.11%
Number/percentage of C's	13,483,594 / 22.85%
Number/percentage of T's	16,214,816 / 27.48%
Number/percentage of G's	12,128,816 / 20.56%
Number/percentage of N's	3,541 / 0.01%
GC Percentage	43.41%

2.3. Coverage

Mean	0.0191

Standard Deviation	0.3807

2.4. Mapping Quality

Mean Mapping Quality	47.79

2.5. Mismatches and indels

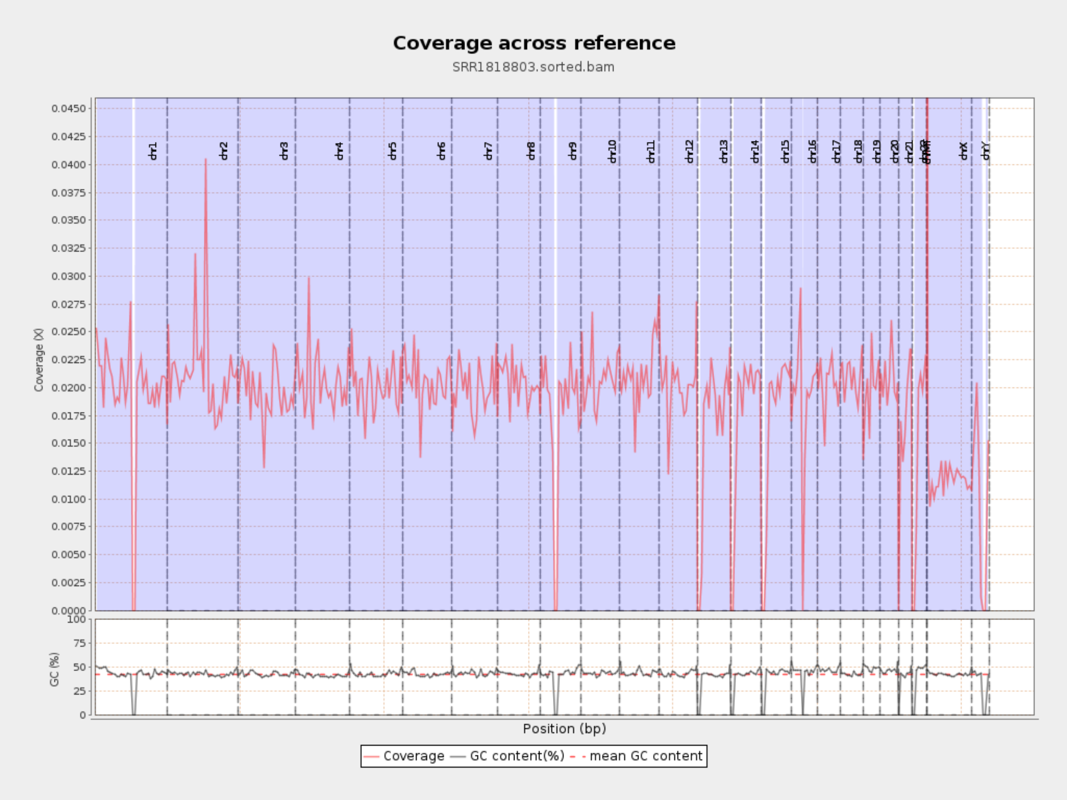
General error rate	0.54%
Mismatches	303,296
Insertions	8,028
Mapped reads with at least one insertion	0.91%
Deletions	15,006
Mapped reads with at least one deletion	1.71%
Homopolymer indels	40.63%

2.6. Chromosome stats

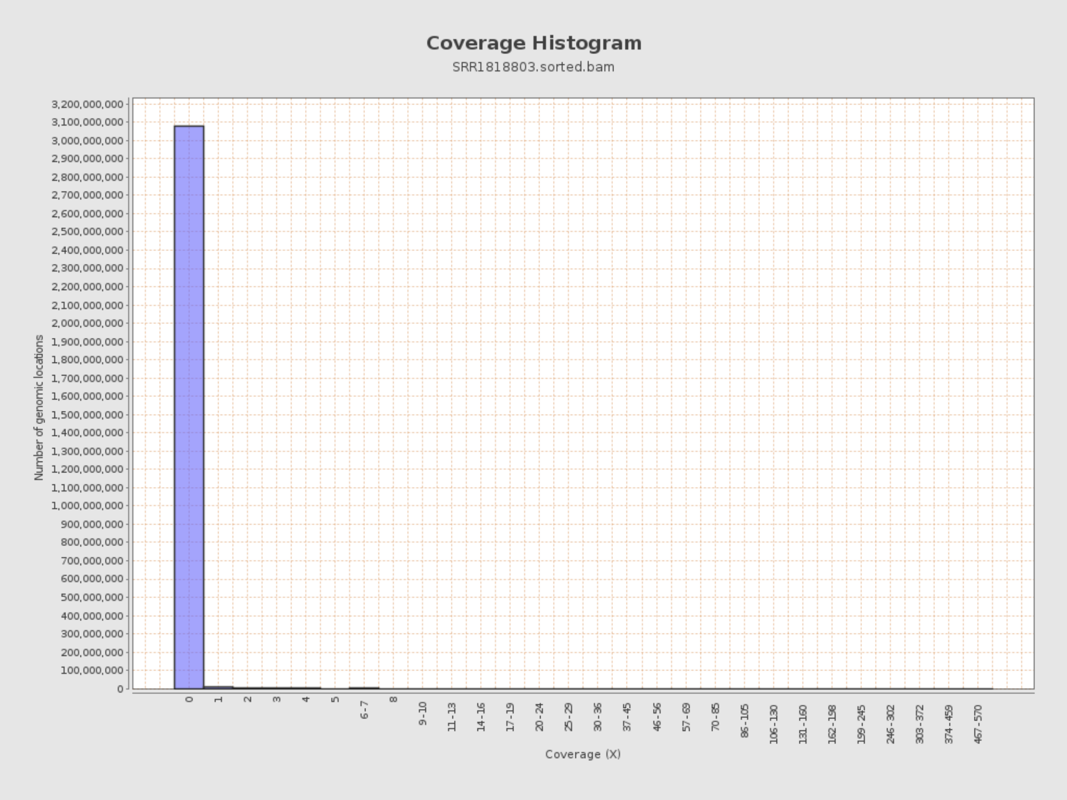
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4882143	0.0196	0.4048
chr2	243199373	5216103	0.0214	0.5411
chr3	198022430	3869140	0.0195	0.336
chr4	191154276	3929093	0.0206	0.3562
chr5	180915260	3645362	0.0201	0.3501
chr6	171115067	3517536	0.0206	0.3672
chr7	159138663	3175207	0.02	0.3559

chr8	146364022	3005905	0.0205	0.3625
chr9	141213431	2495235	0.0177	0.3288
chr10	135534747	2845901	0.021	0.4329
chr11	135006516	2838128	0.021	0.3651
chr12	133851895	2680370	0.02	0.3611
chr13	115169878	1862138	0.0162	0.3044
chr14	107349540	1840717	0.0171	0.3351
chr15	102531392	1701851	0.0166	0.3181
chr16	90354753	1678263	0.0186	0.3981
chr17	81195210	1636439	0.0202	0.3743
chr18	78077248	1633575	0.0209	0.3772
chr19	59128983	1178012	0.0199	0.4222
chr20	63025520	1308974	0.0208	0.3707
chr21	48129895	806125	0.0167	0.331
chr22	51304566	744067	0.0145	0.3324
chrMT	16571	132003	7.9659	10.7112
chrX	155270560	1822290	0.0117	0.2585
chrY	59373566	585021	0.0099	0.5188

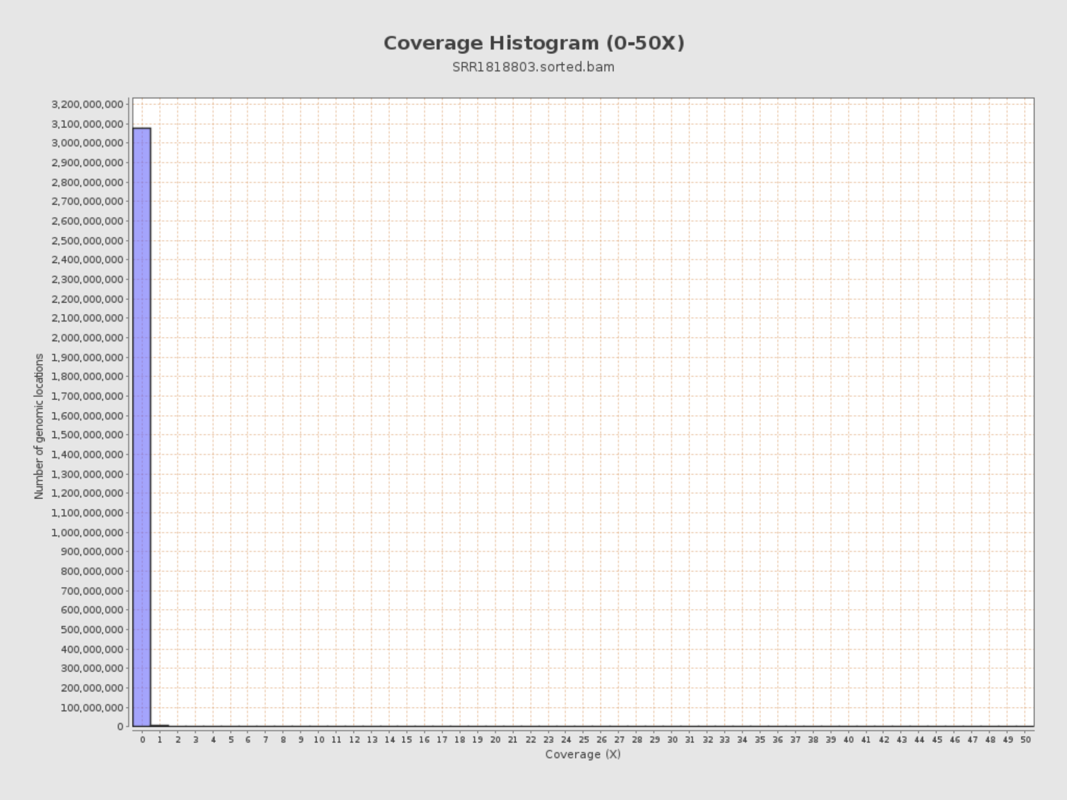
3. Results : Coverage across reference



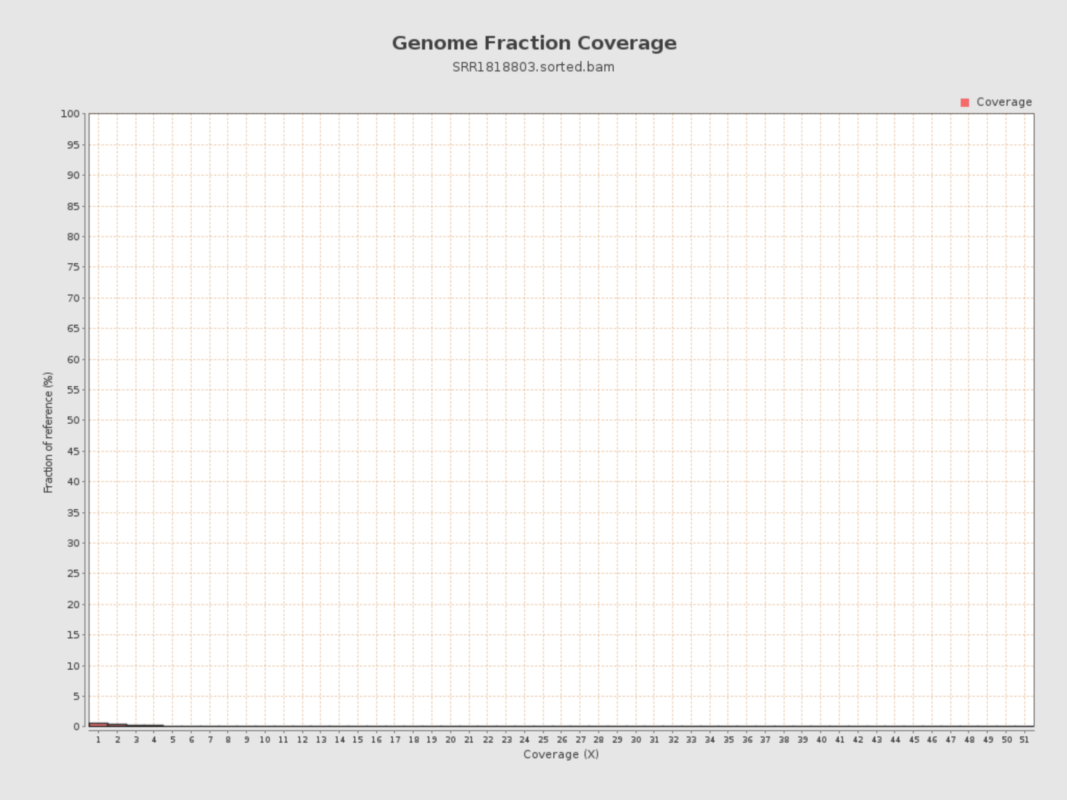
4. Results : Coverage Histogram



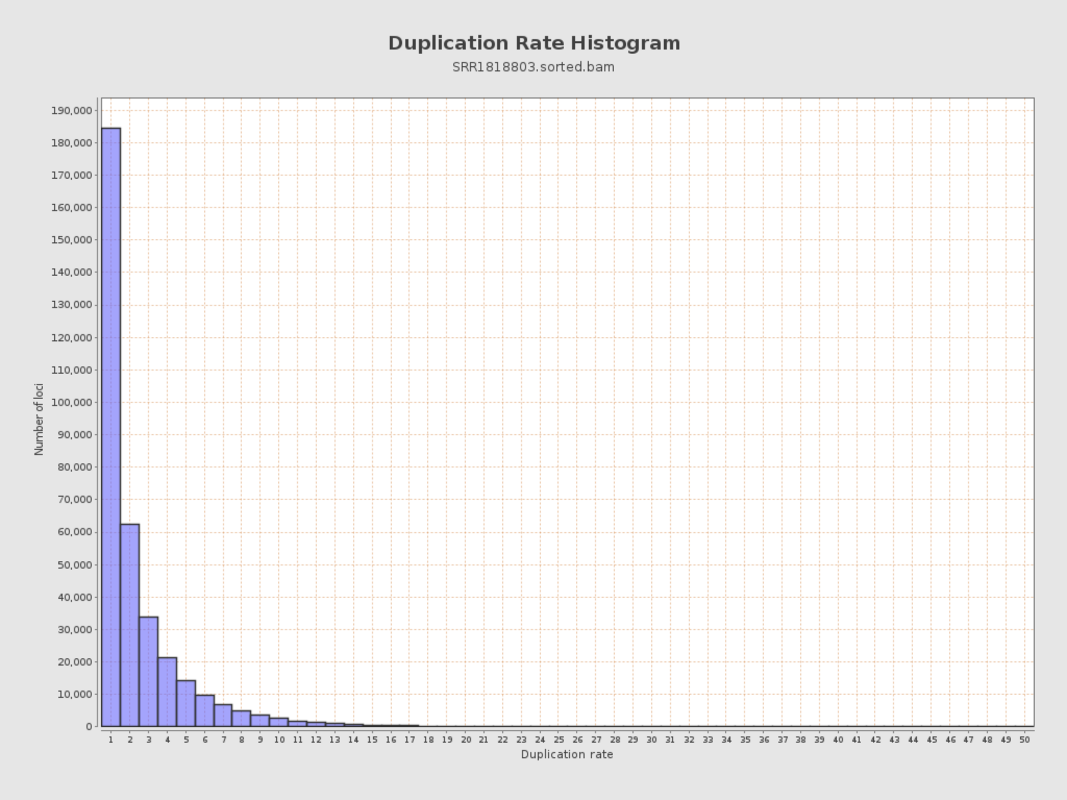
5. Results : Coverage Histogram (0-50X)



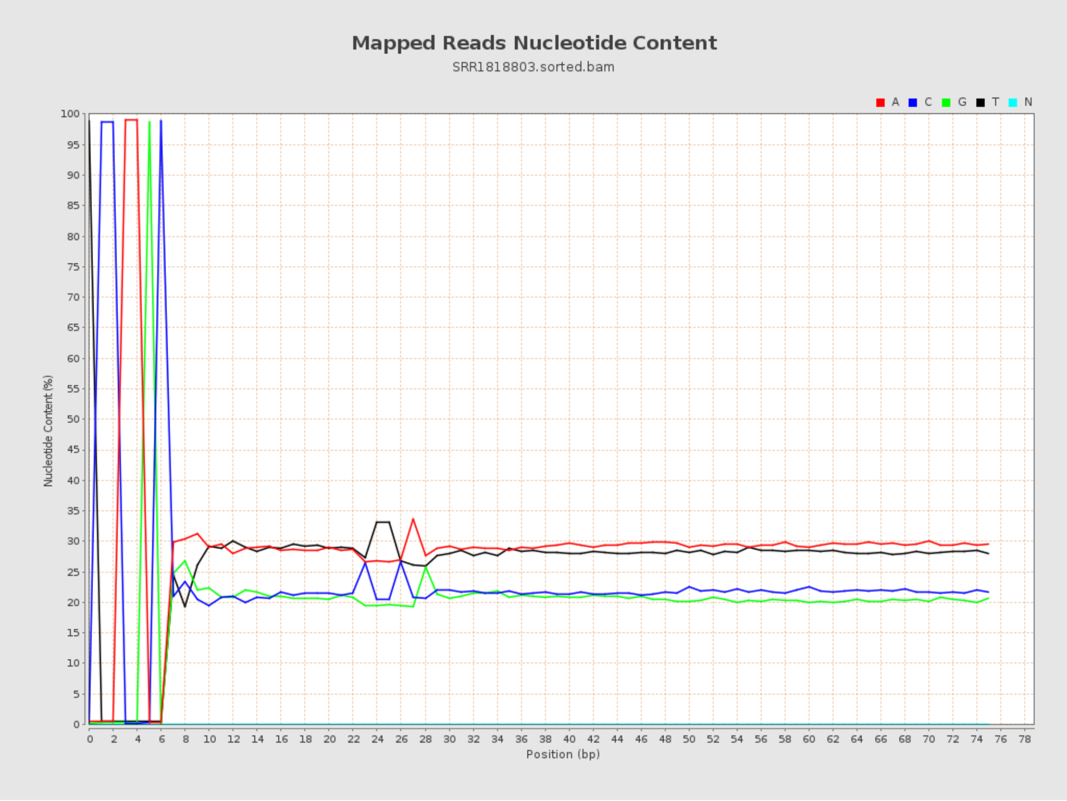
6. Results : Genome Fraction Coverage



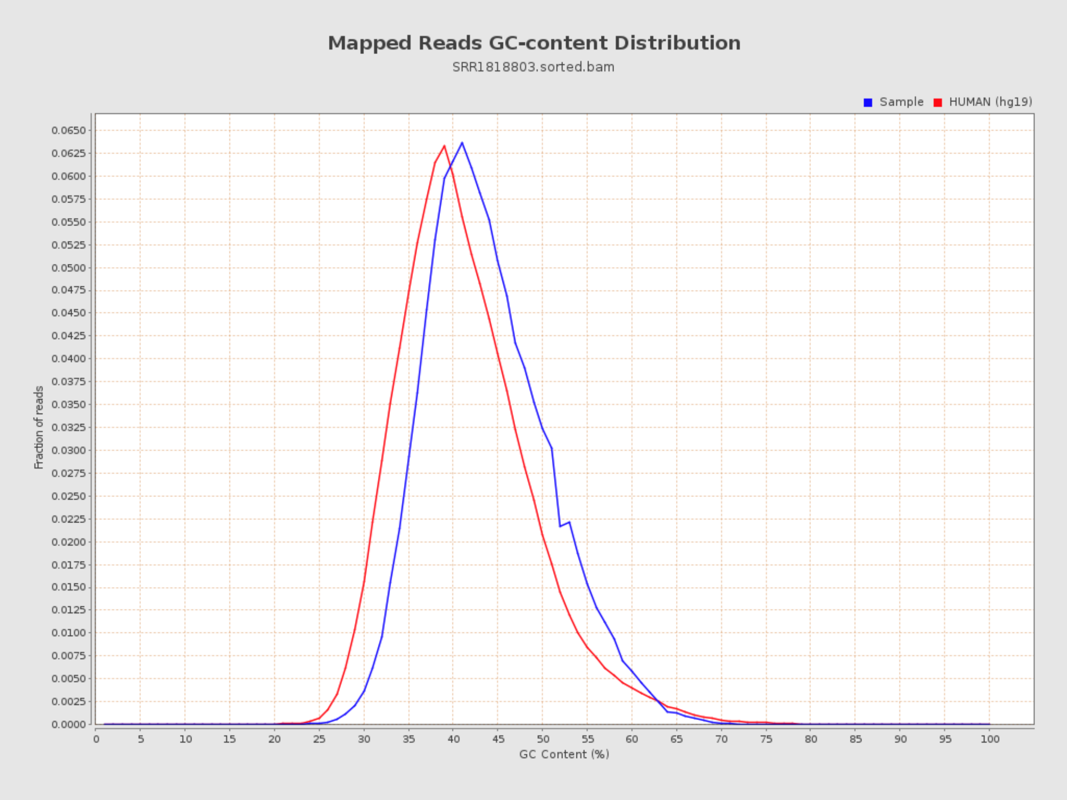
7. Results : Duplication Rate Histogram



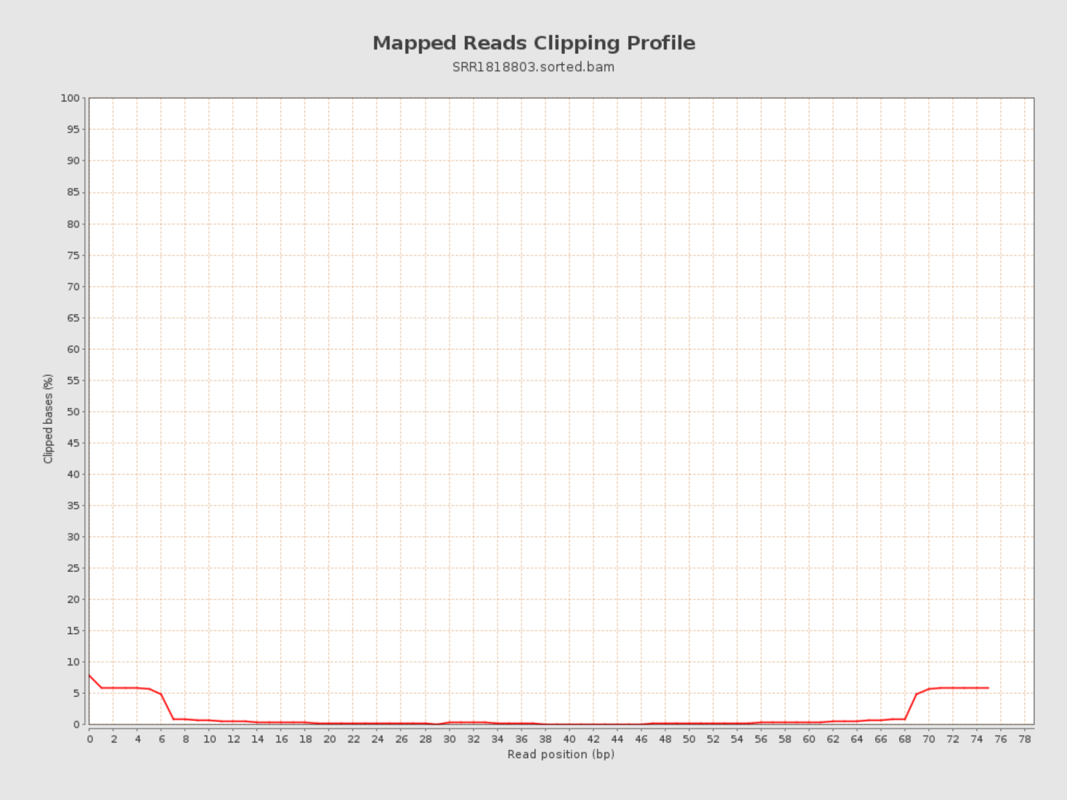
8. Results : Mapped Reads Nucleotide Content



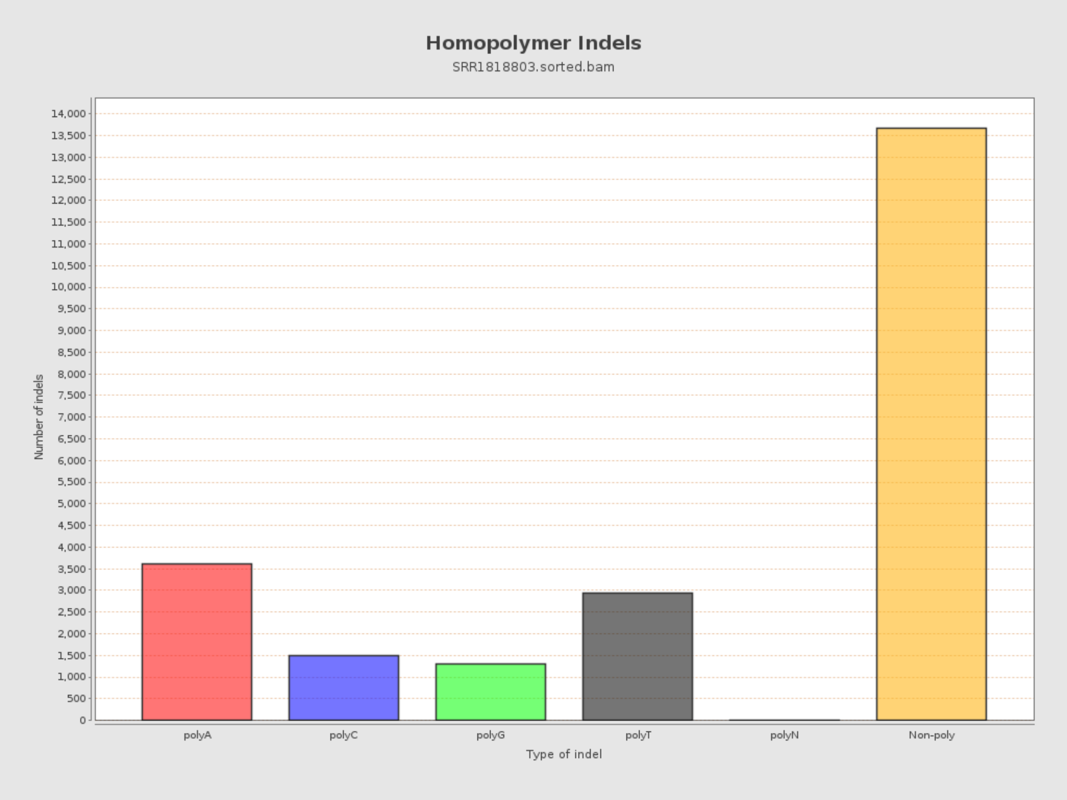
9. Results : Mapped Reads GC-content Distribution



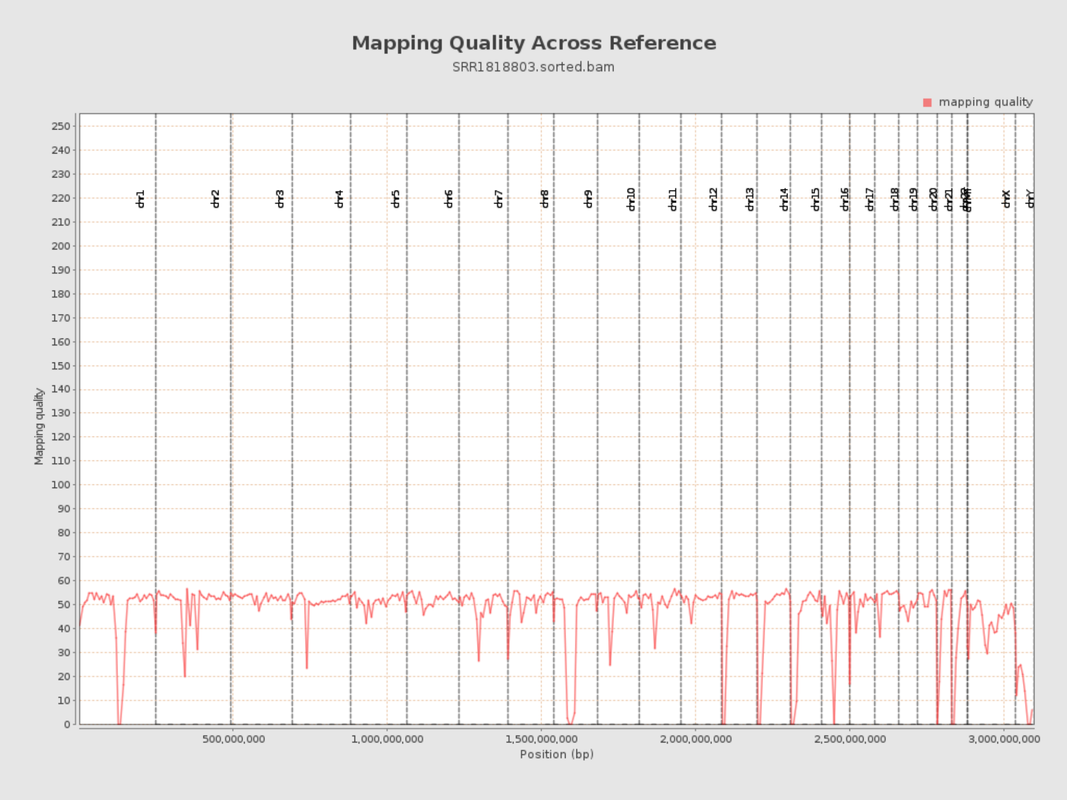
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram