Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 18:26:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818829.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_SRR1818829 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818829.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 18:26:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818829.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	923,848
Mapped reads	899,118 / 97.32%
Unmapped reads	24,730 / 2.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,603 / 0.71%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	300,003 / 32.47%
Duplication rate	28.56%
Clipped reads	903,523 / 97.8%

2.2. ACGT Content

Number/percentage of A's	17,464,766 / 28.66%
Number/percentage of C's	14,106,631 / 23.15%
Number/percentage of T's	16,528,276 / 27.13%
Number/percentage of G's	12,824,601 / 21.05%
Number/percentage of N's	3,949 / 0.01%
GC Percentage	44.2%

2.3. Coverage

Mean	0.0197

Standard Deviation	0.2884

2.4. Mapping Quality

Mean Mapping Quality	47.78

2.5. Mismatches and indels

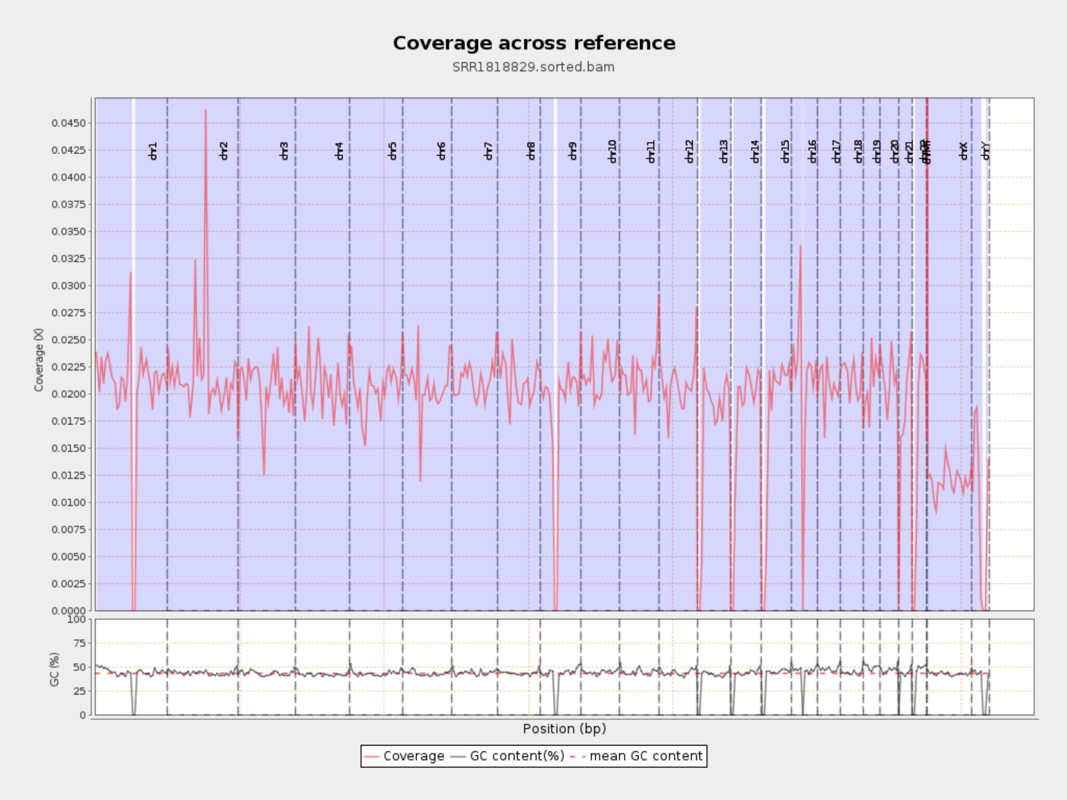
General error rate	0.54%
Mismatches	315,805
Insertions	6,311
Mapped reads with at least one insertion	0.69%
Deletions	15,187
Mapped reads with at least one deletion	1.67%
Homopolymer indels	41.57%

2.6. Chromosome stats

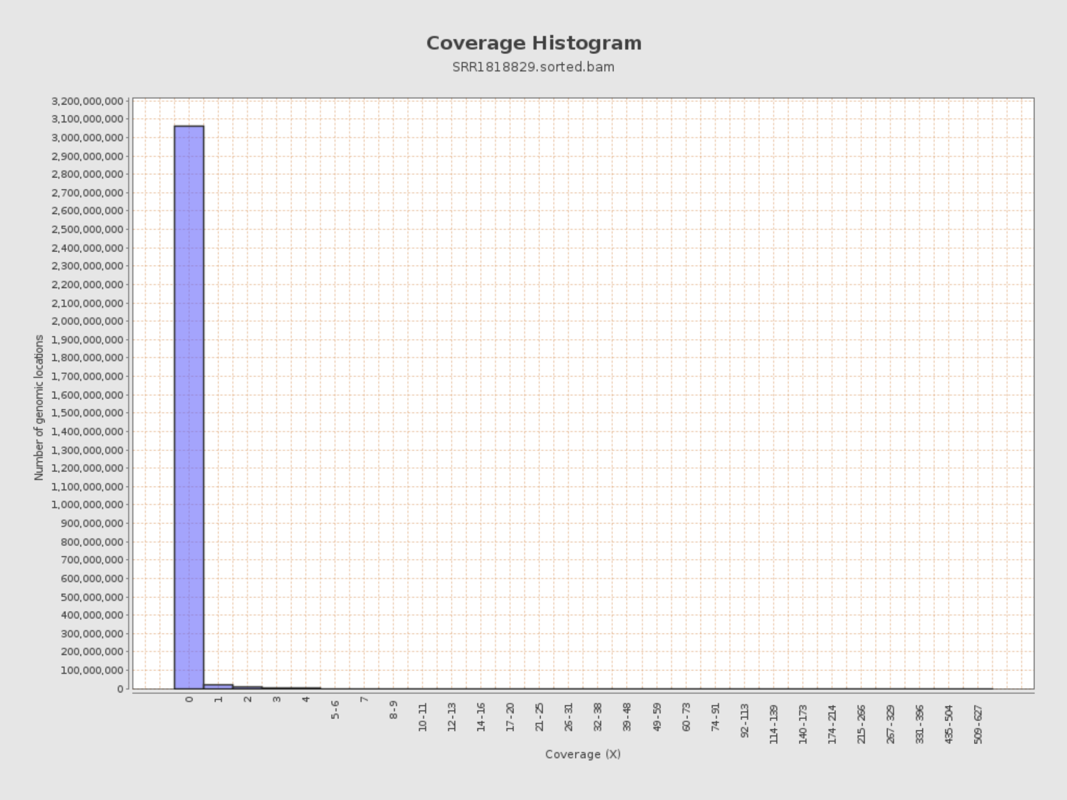
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5102803	0.0205	0.3519
chr2	243199373	5382108	0.0221	0.4823
chr3	198022430	4072666	0.0206	0.2231
chr4	191154276	4000877	0.0209	0.2566
chr5	180915260	3704577	0.0205	0.2317
chr6	171115067	3553095	0.0208	0.2463
chr7	159138663	3386092	0.0213	0.2571

chr8	146364022	3098067	0.0212	0.2361
chr9	141213431	2557508	0.0181	0.2322
chr10	135534747	2971417	0.0219	0.3051
chr11	135006516	2889090	0.0214	0.2508
chr12	133851895	2785206	0.0208	0.2372
chr13	115169878	1892610	0.0164	0.1983
chr14	107349540	1855553	0.0173	0.2271
chr15	102531392	1763691	0.0172	0.2058
chr16	90354753	1892555	0.0209	0.3562
chr17	81195210	1689418	0.0208	0.238
chr18	78077248	1680828	0.0215	0.3001
chr19	59128983	1238484	0.0209	0.2957
chr20	63025520	1333918	0.0212	0.2333
chr21	48129895	866427	0.018	0.2234
chr22	51304566	776188	0.0151	0.2133
chrMT	16571	50293	3.035	3.9625
chrX	155270560	1853801	0.0119	0.1788
chrY	59373566	555450	0.0094	0.5245

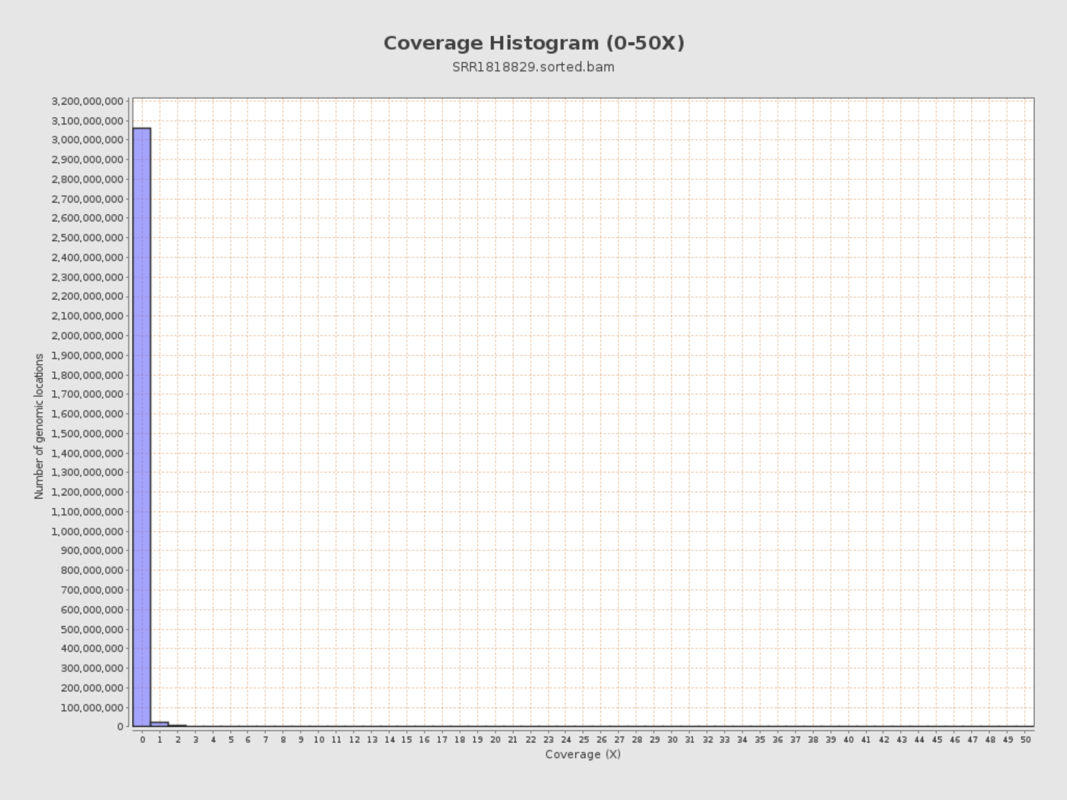
3. Results : Coverage across reference



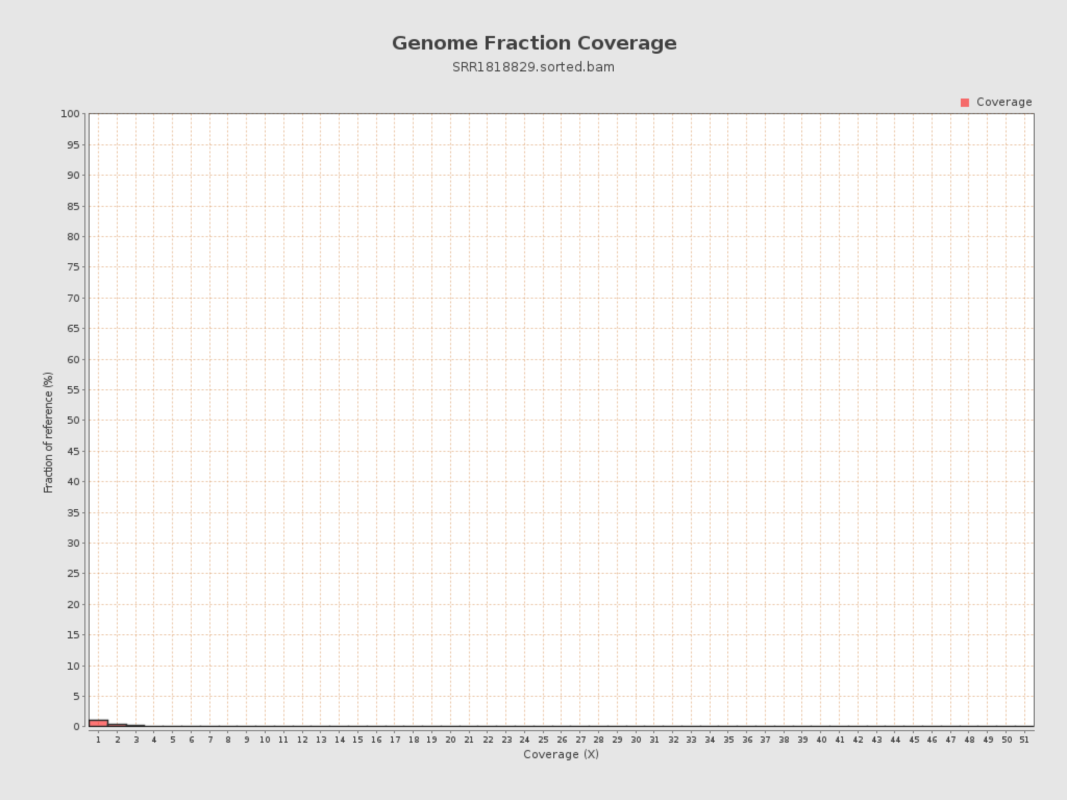
4. Results : Coverage Histogram



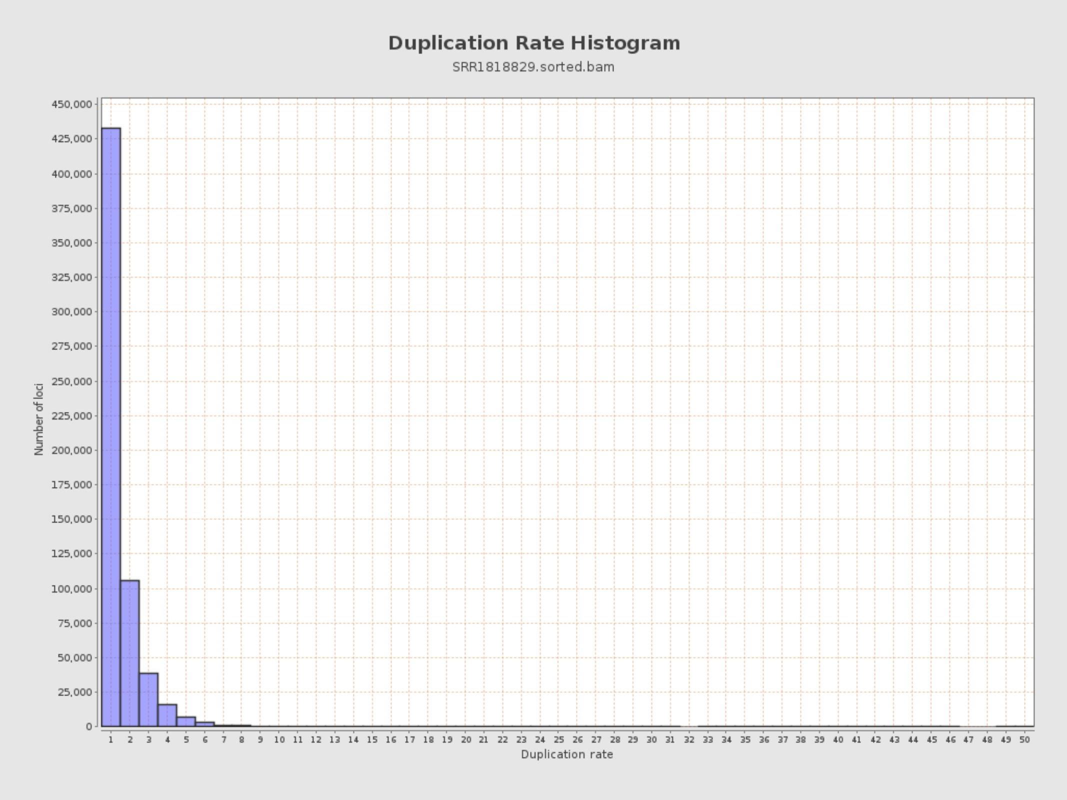
5. Results : Coverage Histogram (0-50X)



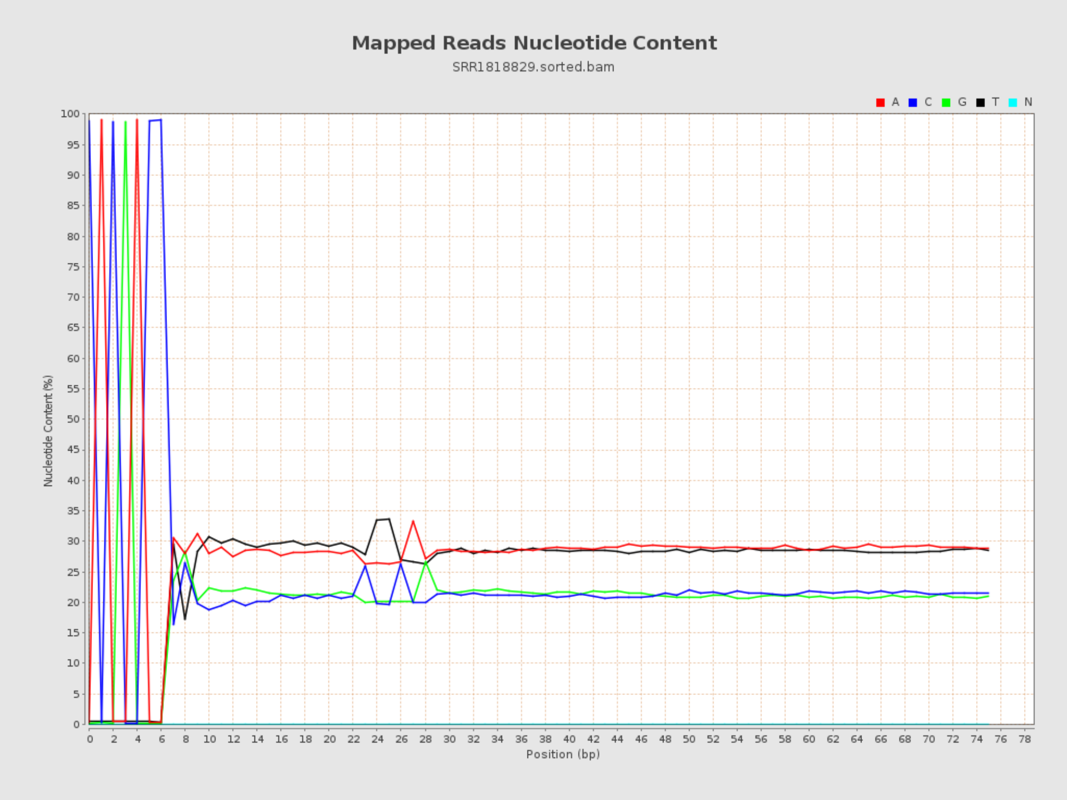
6. Results : Genome Fraction Coverage



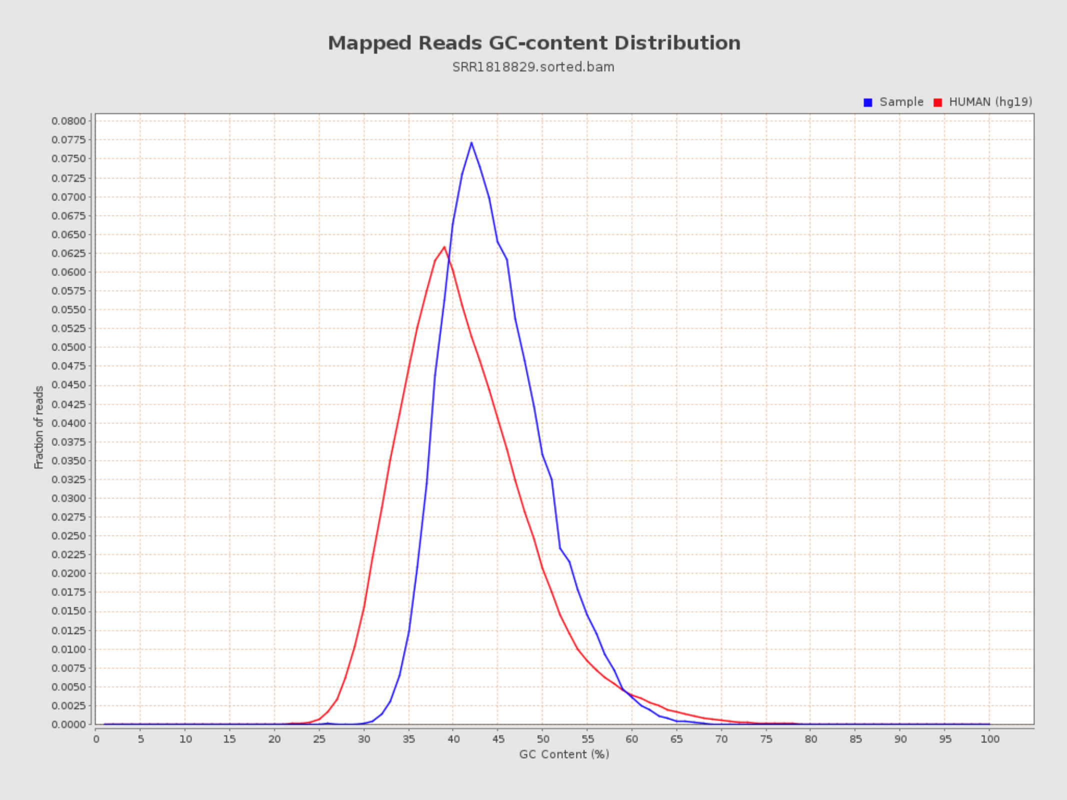
7. Results : Duplication Rate Histogram



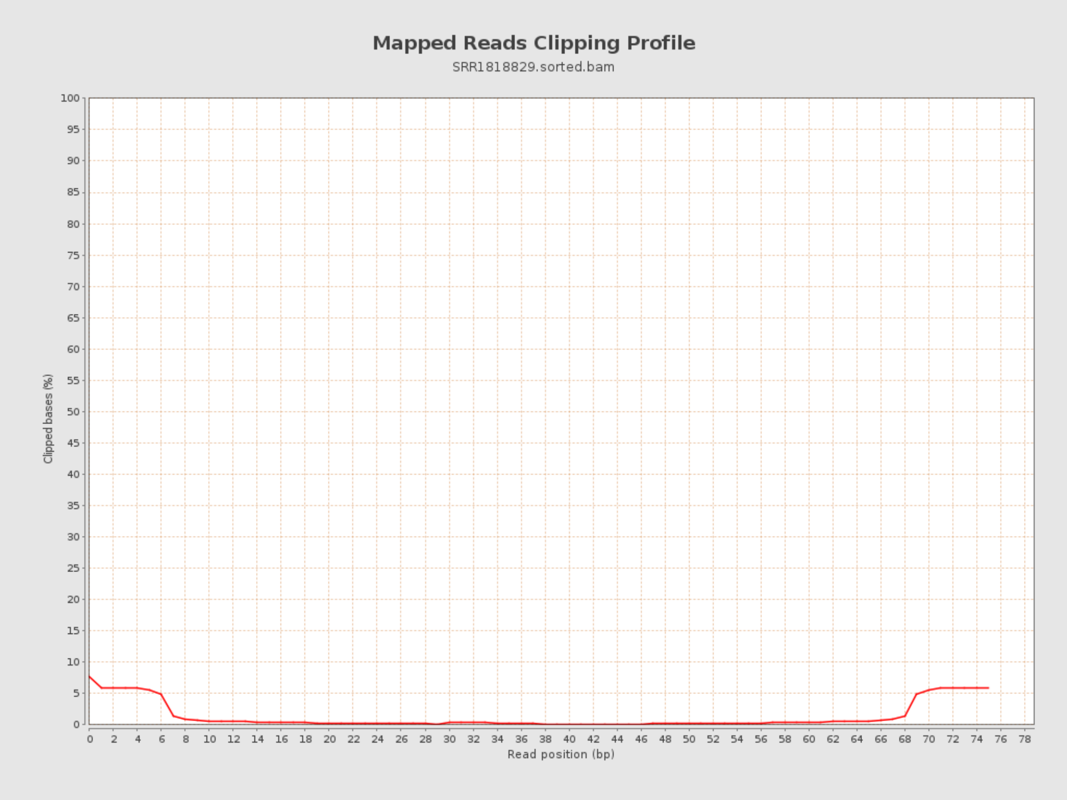
8. Results : Mapped Reads Nucleotide Content



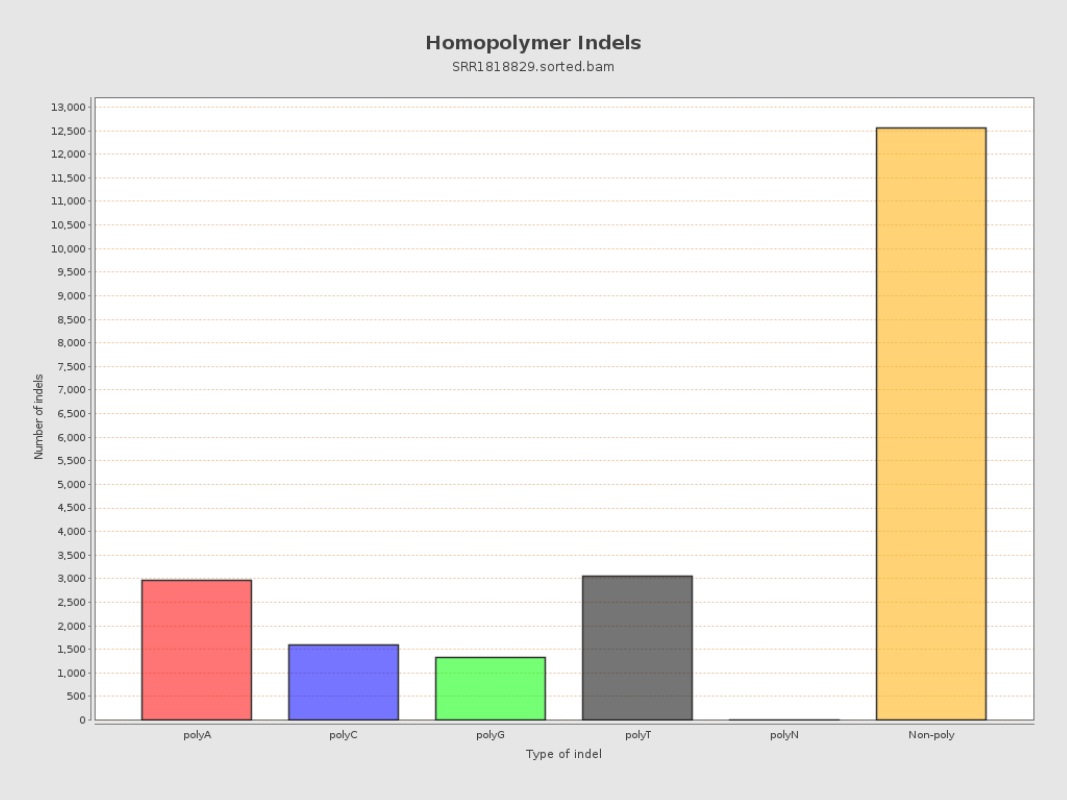
9. Results : Mapped Reads GC-content Distribution



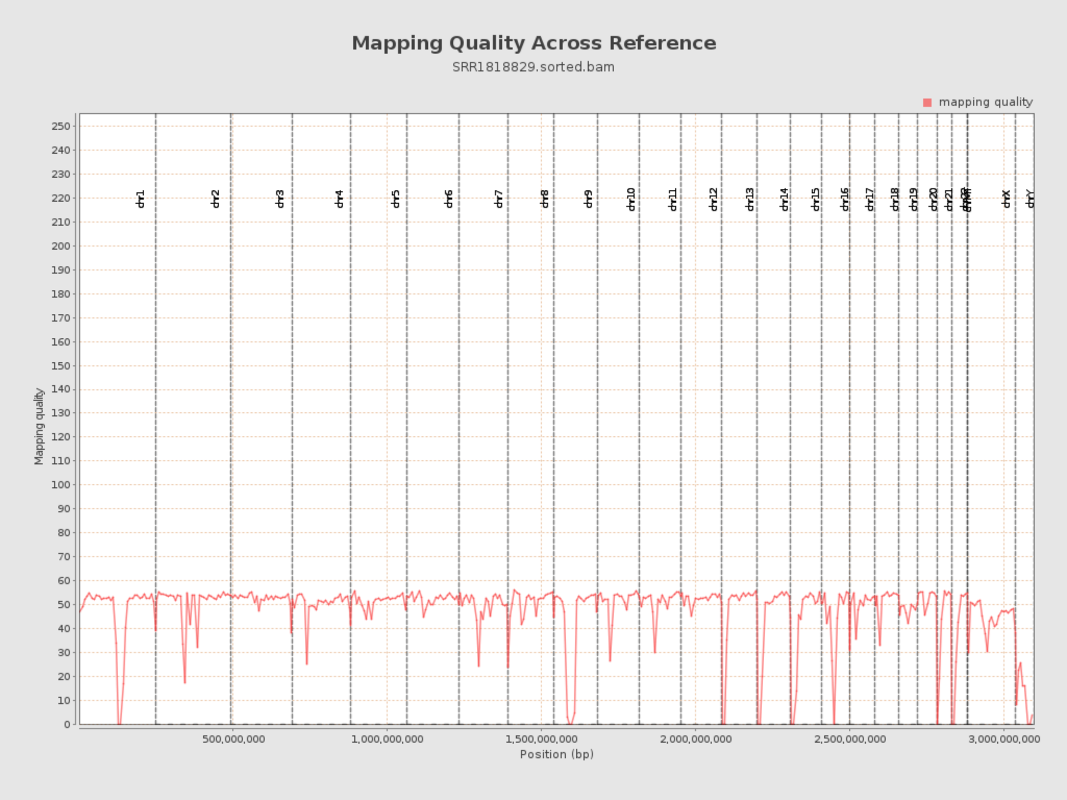
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram