Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:53:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819117.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_SRR1819117 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819117.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:53:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819117.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,976,775
Mapped reads	1,801,111 / 91.11%
Unmapped reads	175,664 / 8.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,506 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	83,838 / 4.24%
Duplication rate	3.48%
Clipped reads	1,800,784 / 91.1%

2.2. ACGT Content

Number/percentage of A's	27,134,472 / 26%
Number/percentage of C's	19,457,487 / 18.65%
Number/percentage of T's	31,918,081 / 30.59%
Number/percentage of G's	25,837,495 / 24.76%
Number/percentage of N's	1,489 / 0%
GC Percentage	43.41%

2.3. Coverage

Mean	0.0337

Standard Deviation	0.3094

2.4. Mapping Quality

Mean Mapping Quality	44.79

2.5. Mismatches and indels

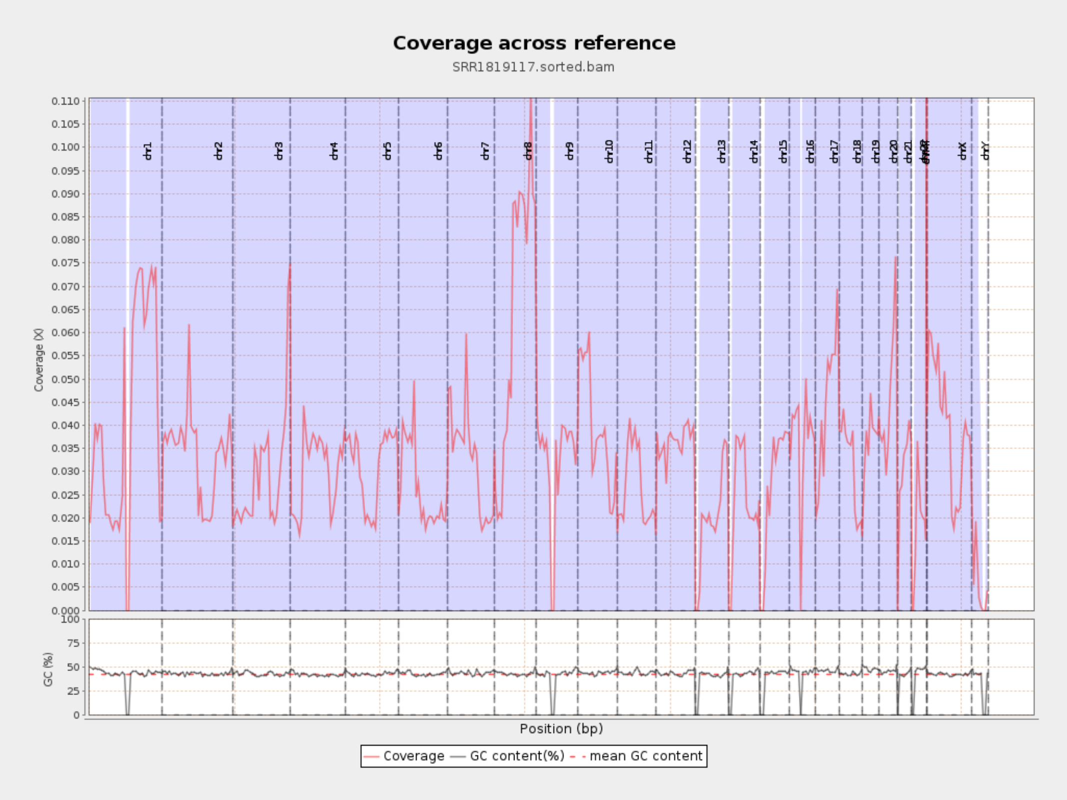
General error rate	0.53%
Mismatches	538,583
Insertions	7,941
Mapped reads with at least one insertion	0.44%
Deletions	19,661
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.33%

2.6. Chromosome stats

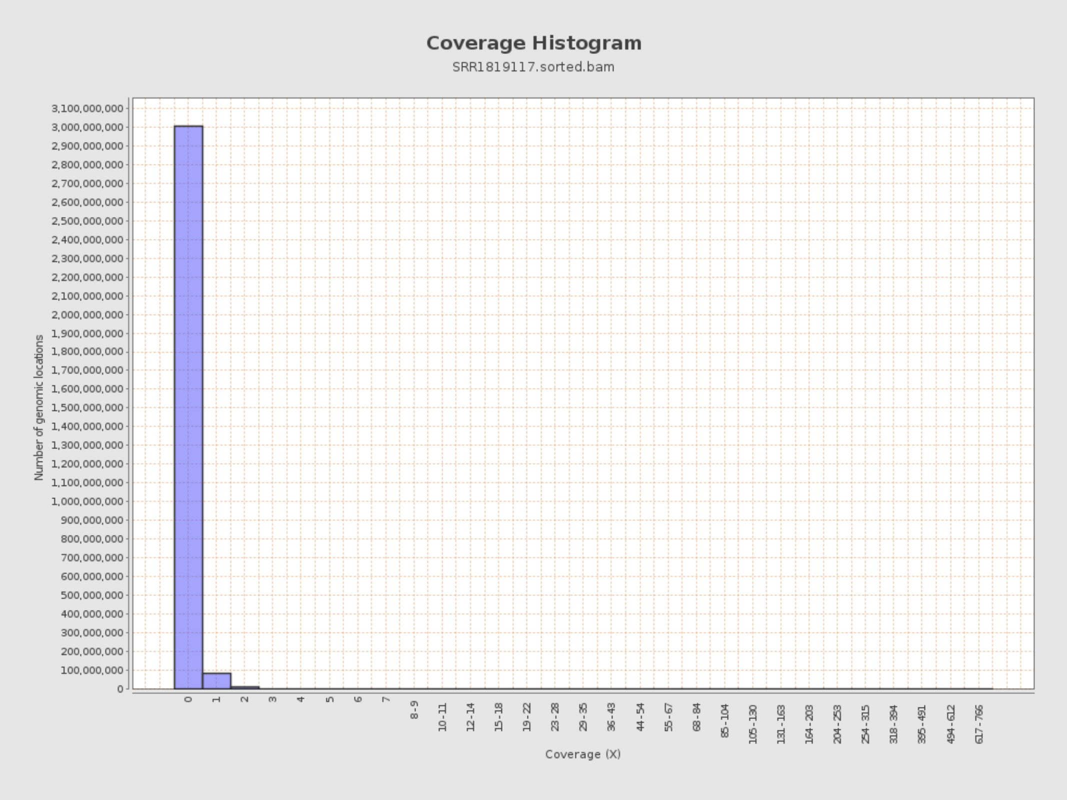
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10258244	0.0412	0.5683
chr2	243199373	8263258	0.034	0.3823
chr3	198022430	5736076	0.029	0.1925
chr4	191154276	5760886	0.0301	0.2182
chr5	180915260	5666507	0.0313	0.1983
chr6	171115067	4519471	0.0264	0.2378
chr7	159138663	5186968	0.0326	0.401

chr8	146364022	9557254	0.0653	0.34
chr9	141213431	4457957	0.0316	0.2584
chr10	135534747	5419068	0.04	0.3
chr11	135006516	3611409	0.0267	0.2872
chr12	133851895	4888147	0.0365	0.2144
chr13	115169878	2298130	0.02	0.1567
chr14	107349540	2503663	0.0233	0.1747
chr15	102531392	2772820	0.027	0.1973
chr16	90354753	3298065	0.0365	0.2279
chr17	81195210	3686107	0.0454	0.2537
chr18	78077248	2465793	0.0316	0.4877
chr19	59128983	2188646	0.037	0.3805
chr20	63025520	2930835	0.0465	0.2424
chr21	48129895	1445800	0.03	0.2144
chr22	51304566	877488	0.0171	0.1443
chrMT	16571	3782	0.2282	0.5658
chrX	155270560	6247518	0.0402	0.2502
chrY	59373566	337952	0.0057	0.156

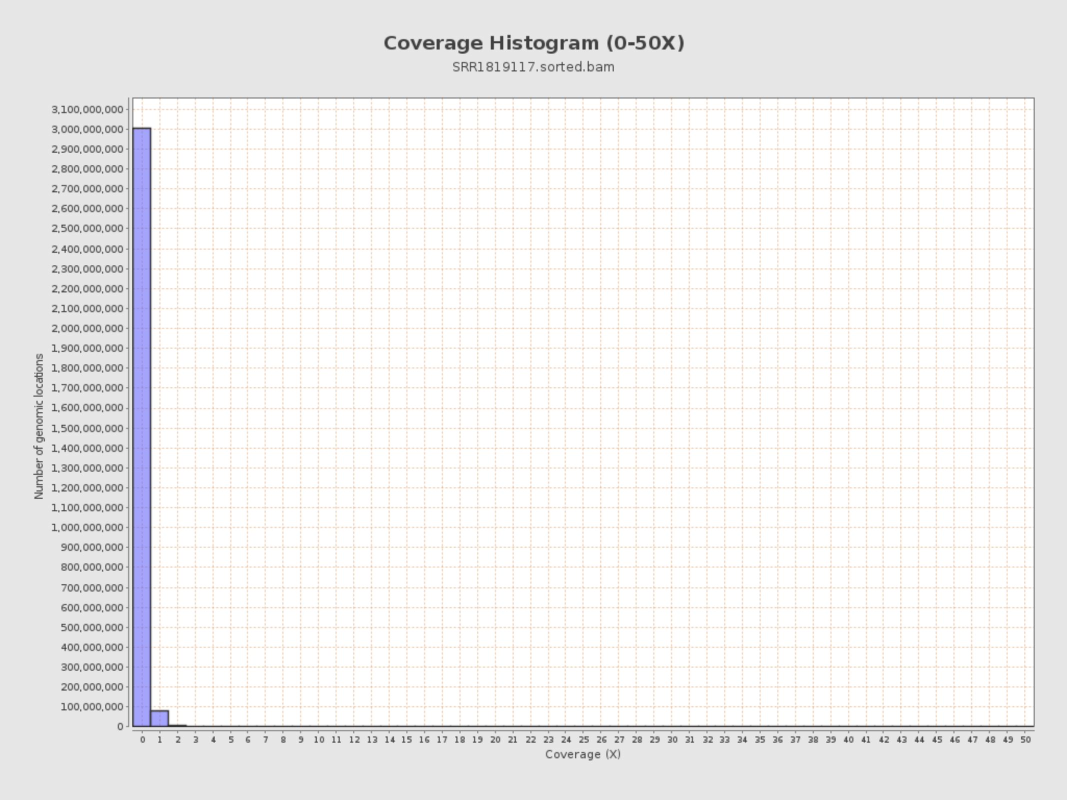
3. Results : Coverage across reference



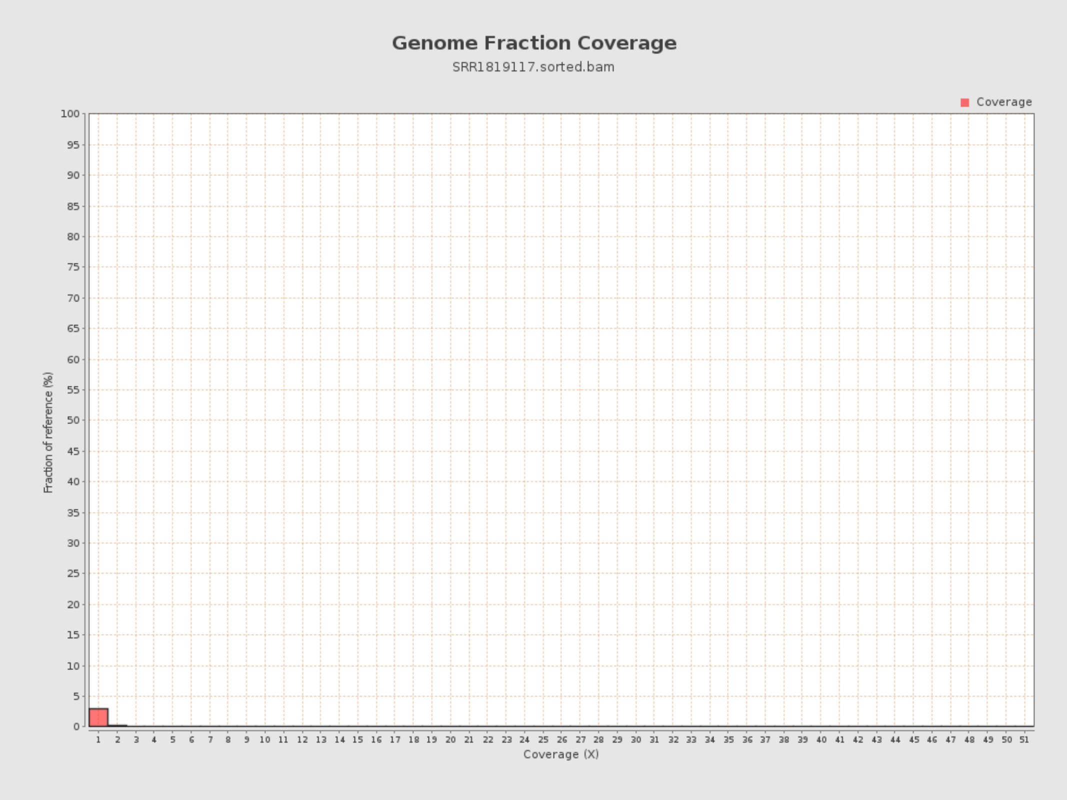
4. Results : Coverage Histogram



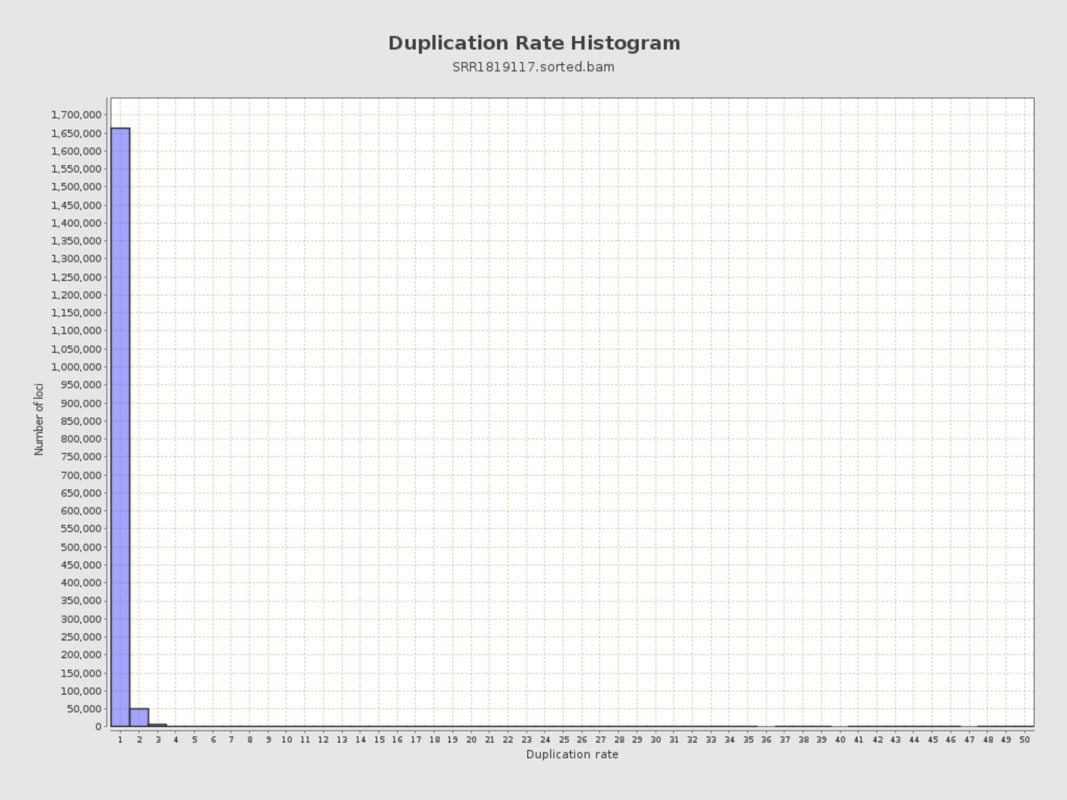
5. Results : Coverage Histogram (0-50X)



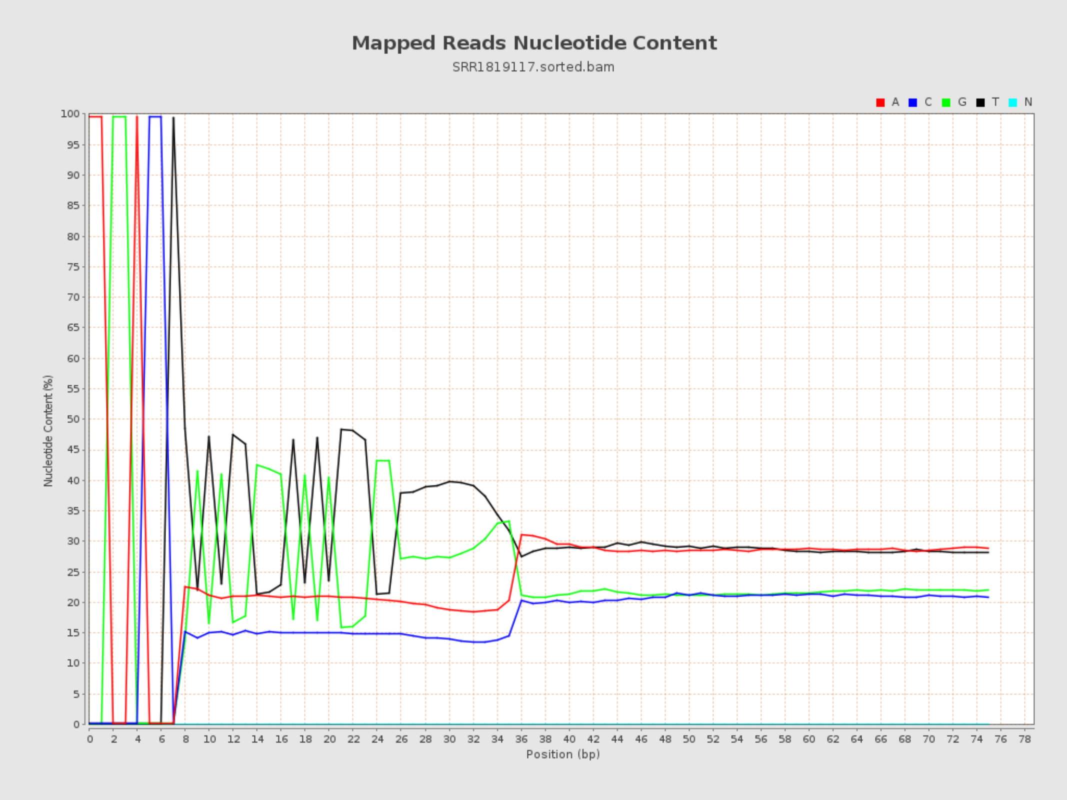
6. Results : Genome Fraction Coverage



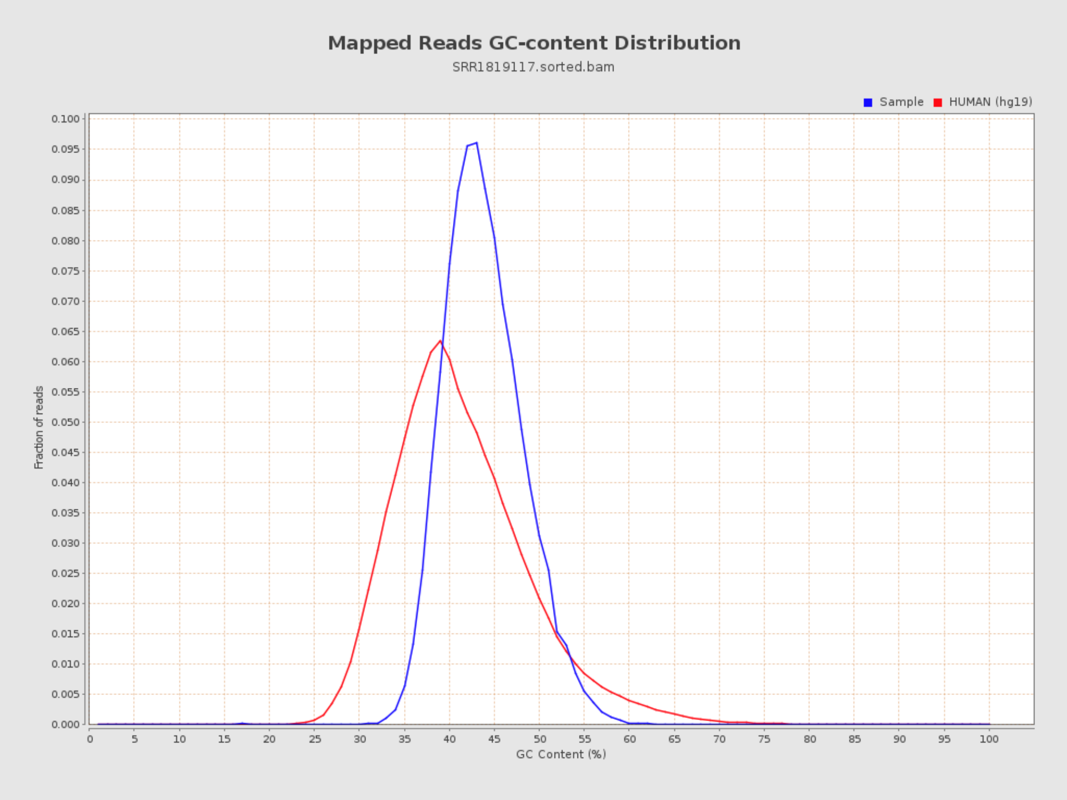
7. Results : Duplication Rate Histogram



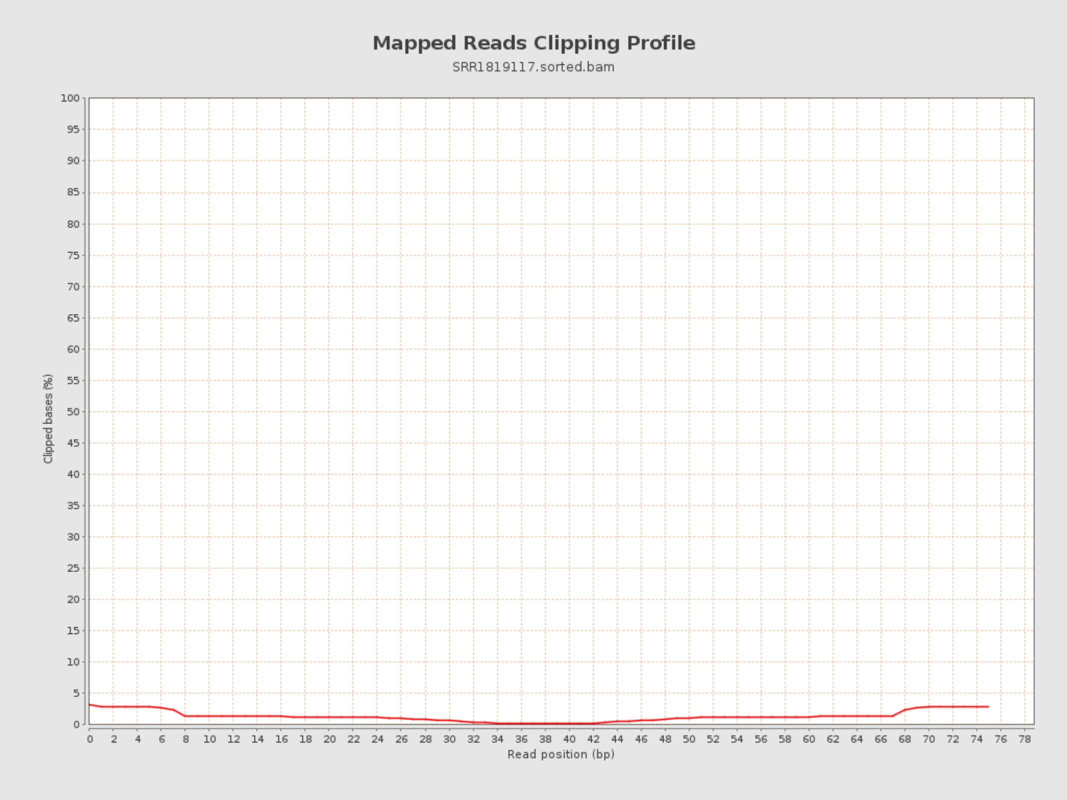
8. Results : Mapped Reads Nucleotide Content



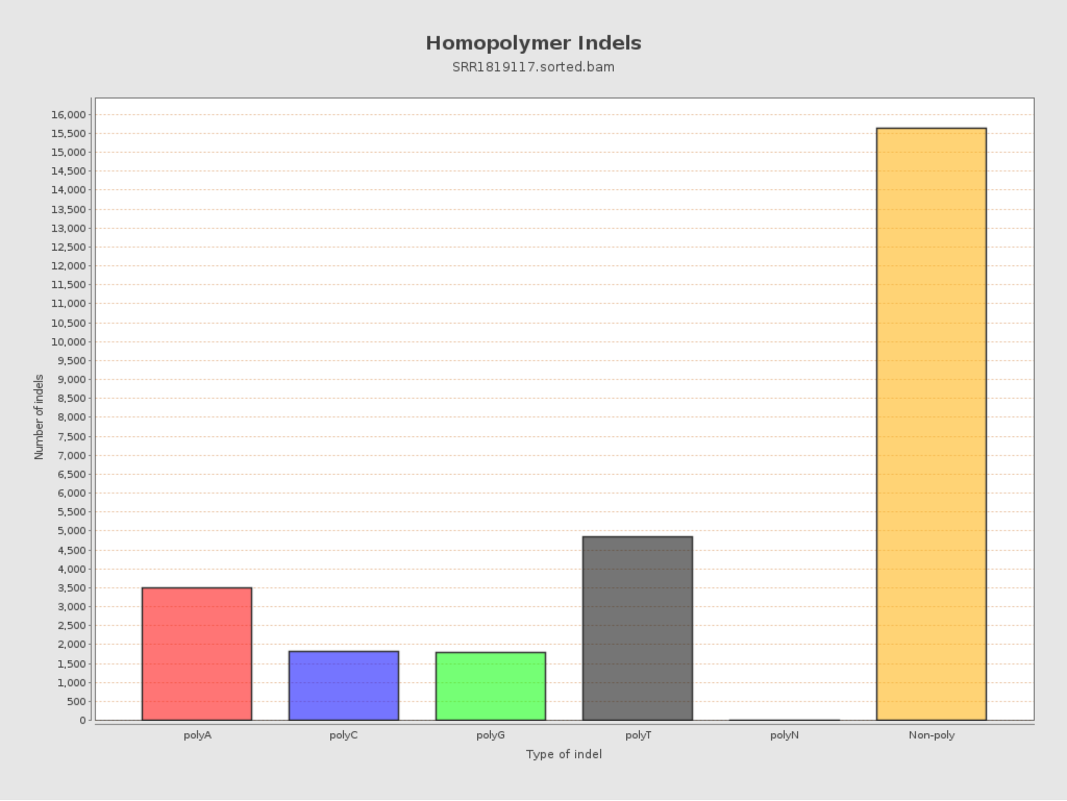
9. Results : Mapped Reads GC-content Distribution



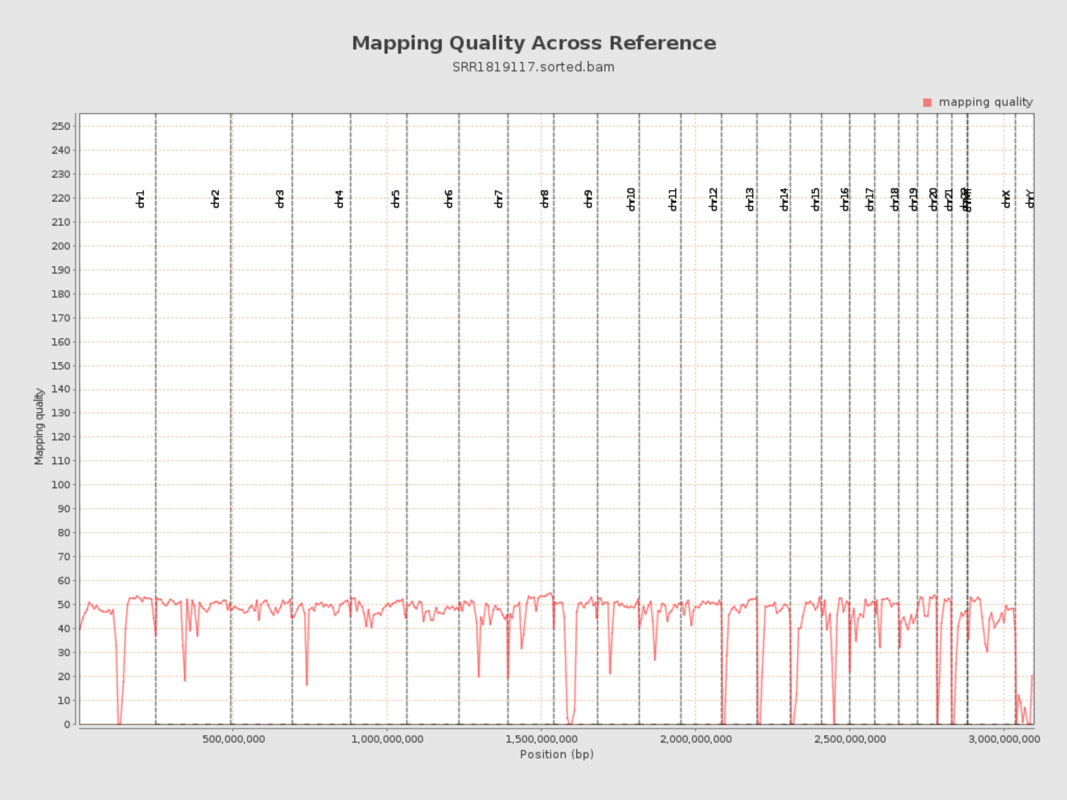
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram