Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:28:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819004.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_SRR1819004 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819004.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:28:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819004.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,326,717
Mapped reads	1,302,581 / 98.18%
Unmapped reads	24,136 / 1.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,241 / 1.68%
Read min/max/mean length	30 / 101 / 101.64
Duplicated reads (estimated)	515,057 / 38.82%
Duplication rate	33.26%
Clipped reads	1,320,789 / 99.55%

2.2. ACGT Content

Number/percentage of A's	35,259,598 / 29.33%
Number/percentage of C's	26,604,337 / 22.13%
Number/percentage of T's	33,362,915 / 27.76%
Number/percentage of G's	24,969,703 / 20.77%
Number/percentage of N's	5,741 / 0%
GC Percentage	42.91%

2.3. Coverage

Mean	0.0389

Standard Deviation	0.5367

2.4. Mapping Quality

Mean Mapping Quality	49.09

2.5. Mismatches and indels

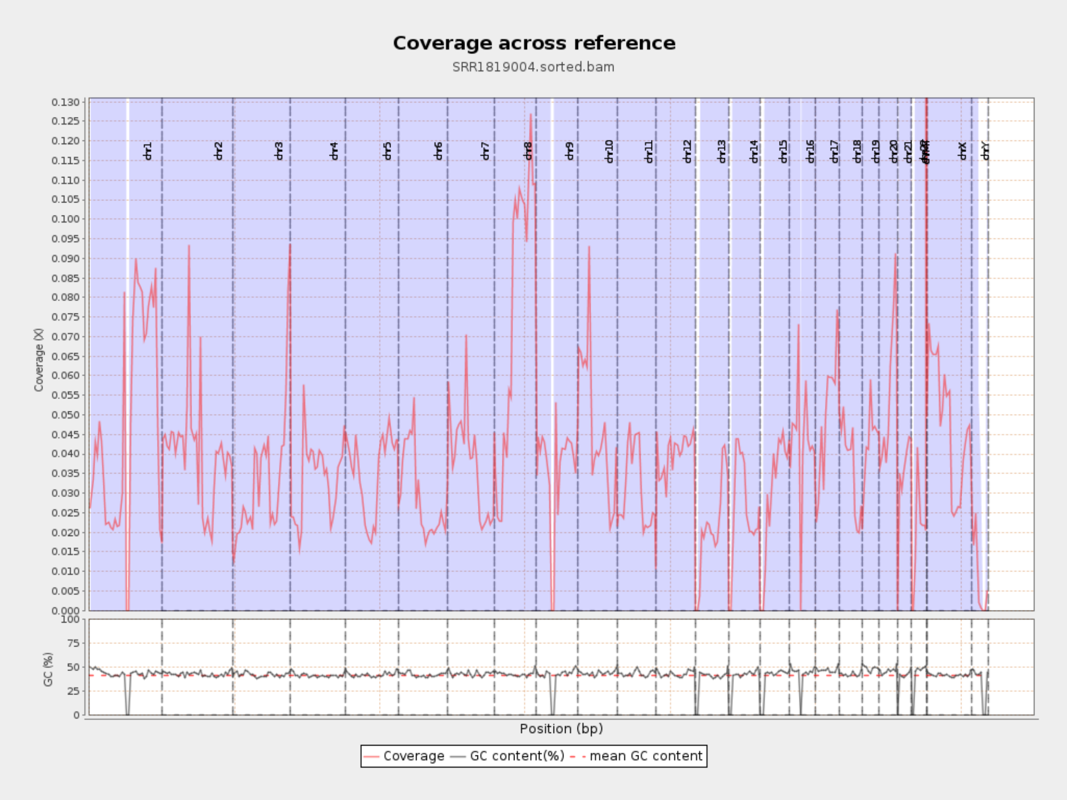
General error rate	0.7%
Mismatches	796,626
Insertions	17,820
Mapped reads with at least one insertion	1.32%
Deletions	39,132
Mapped reads with at least one deletion	2.94%
Homopolymer indels	42.33%

2.6. Chromosome stats

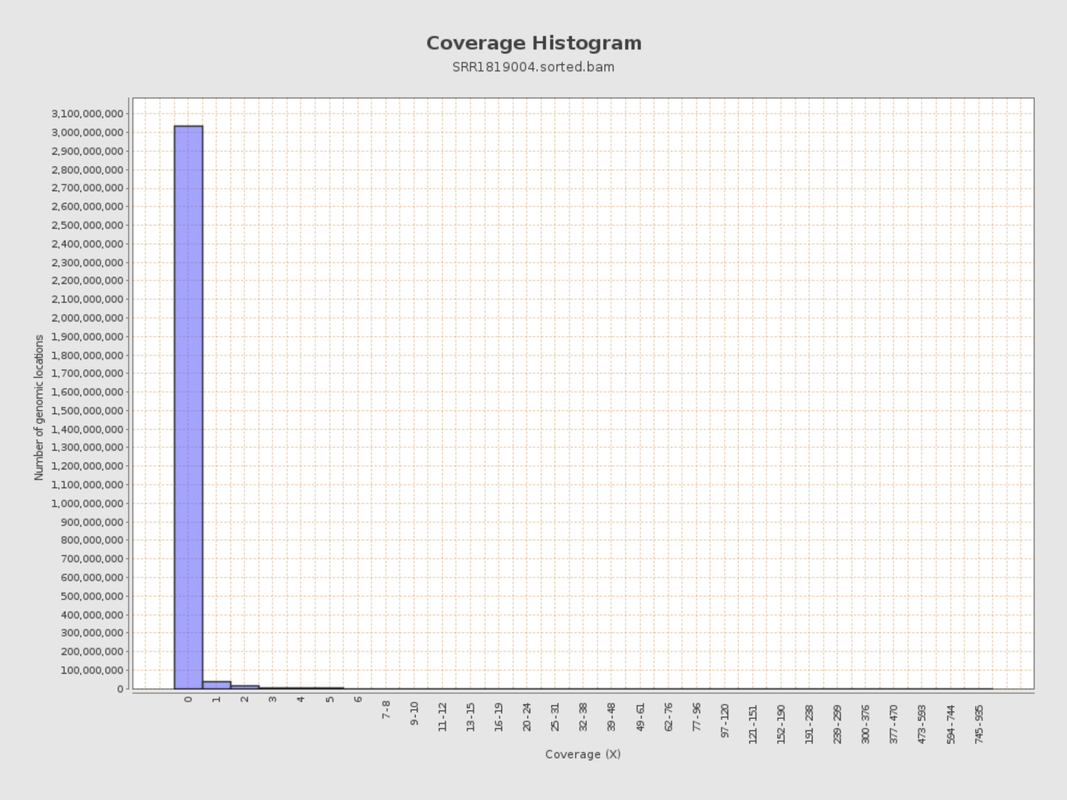
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11833150	0.0475	0.932
chr2	243199373	9893278	0.0407	0.8338
chr3	198022430	6507735	0.0329	0.3041
chr4	191154276	6394592	0.0335	0.3588
chr5	180915260	6398178	0.0354	0.3275
chr6	171115067	4980422	0.0291	0.3258
chr7	159138663	6015415	0.0378	0.6157

chr8	146364022	11297056	0.0772	0.5159
chr9	141213431	5085212	0.036	0.463
chr10	135534747	6352435	0.0469	0.6714
chr11	135006516	4192294	0.0311	0.3575
chr12	133851895	5405978	0.0404	0.3436
chr13	115169878	2460694	0.0214	0.2426
chr14	107349540	2730191	0.0254	0.2863
chr15	102531392	3054458	0.0298	0.2934
chr16	90354753	3906947	0.0432	0.6456
chr17	81195210	4101725	0.0505	0.4193
chr18	78077248	2891163	0.037	0.5601
chr19	59128983	2578398	0.0436	0.7228
chr20	63025520	3513555	0.0557	0.4219
chr21	48129895	1664630	0.0346	0.3336
chr22	51304566	972567	0.019	0.2545
chrMT	16571	129867	7.837	6.2364
chrX	155270560	7431613	0.0479	0.4128
chrY	59373566	484391	0.0082	0.6068

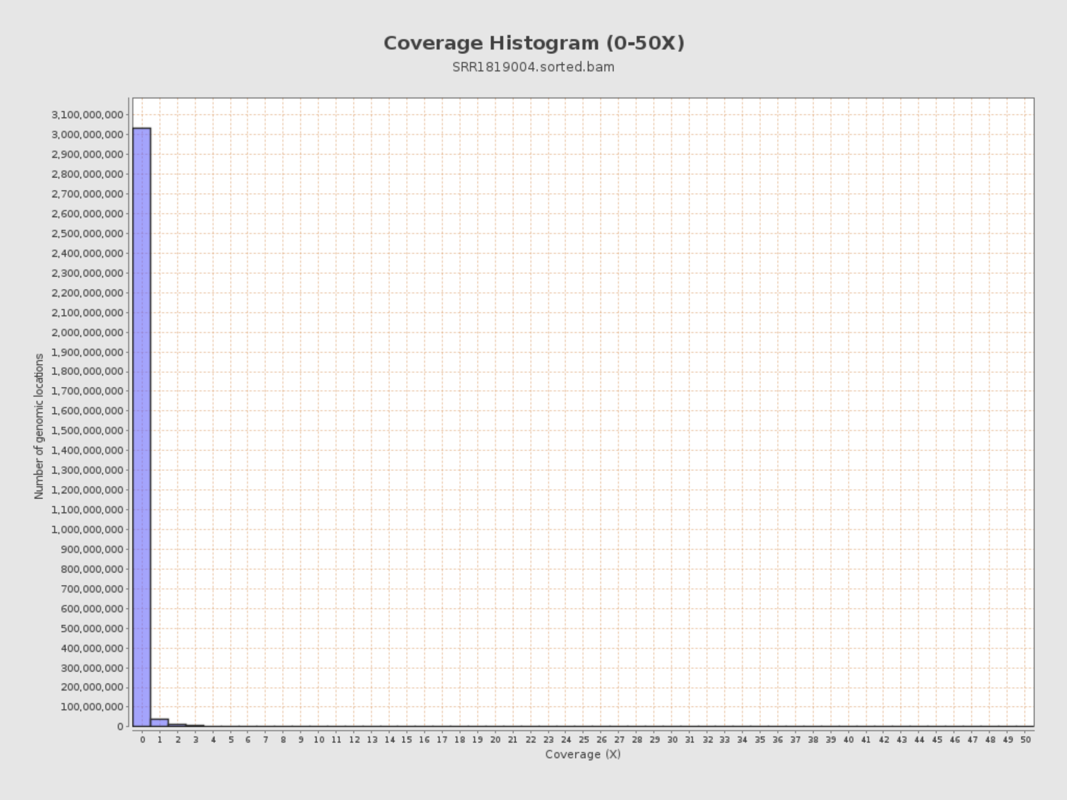
3. Results : Coverage across reference



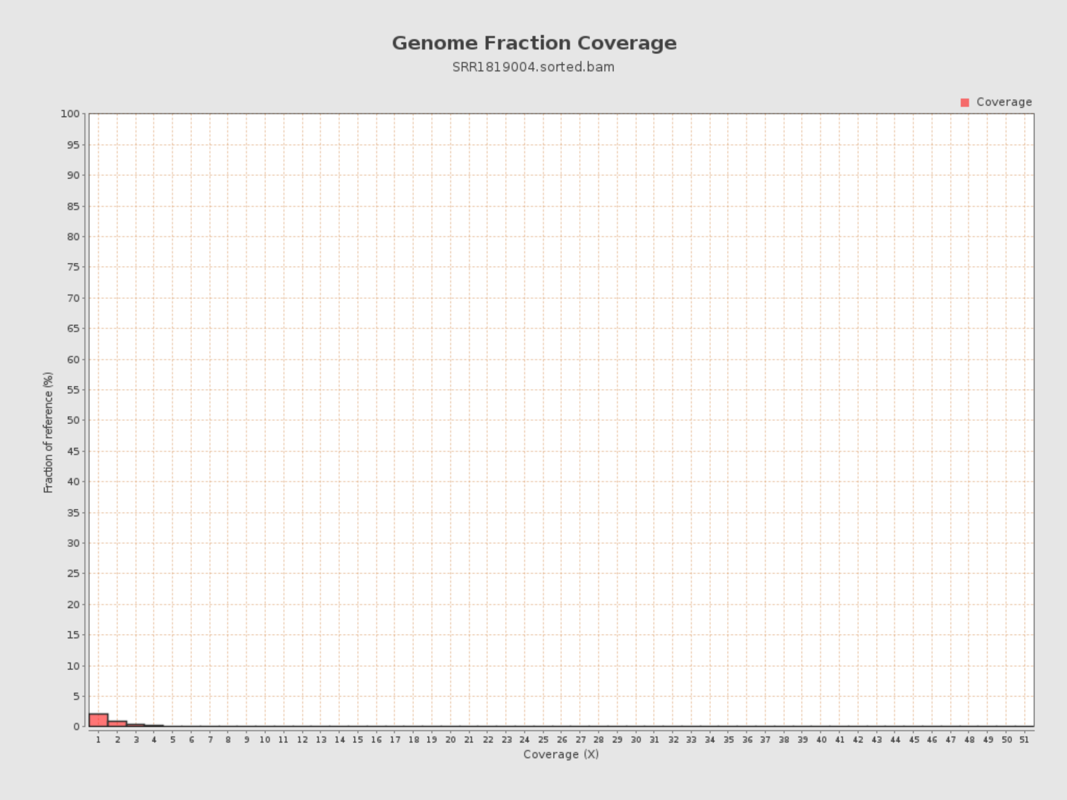
4. Results : Coverage Histogram



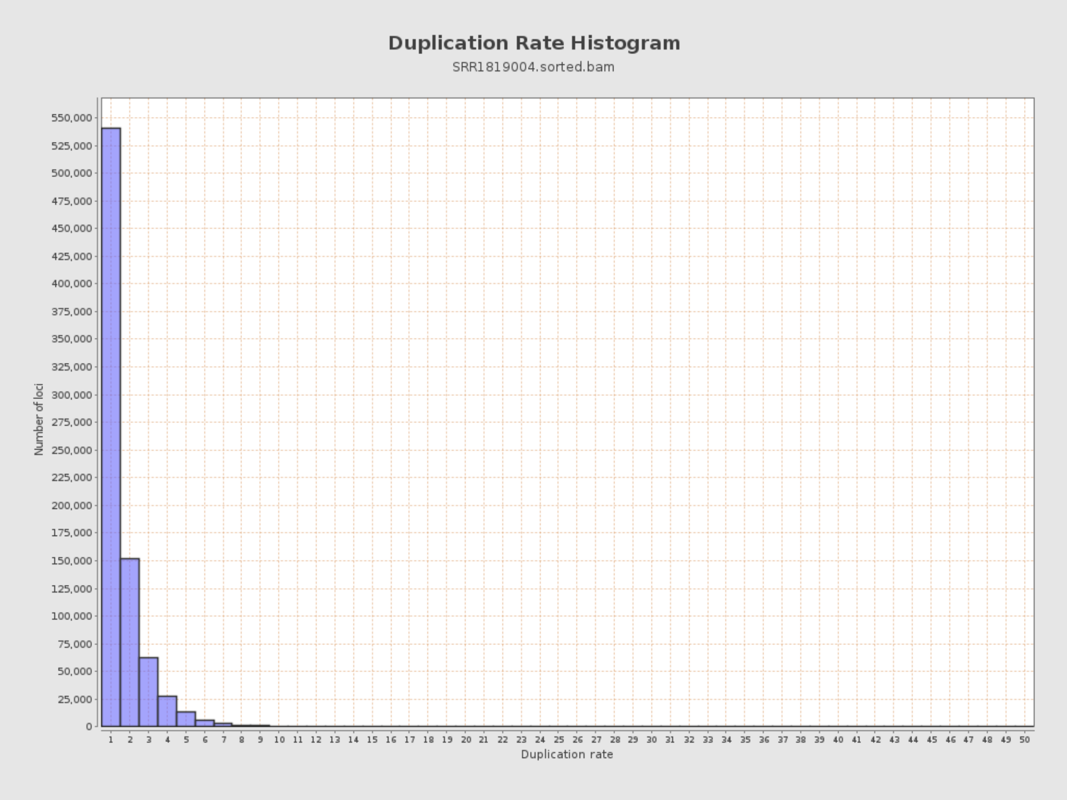
5. Results : Coverage Histogram (0-50X)



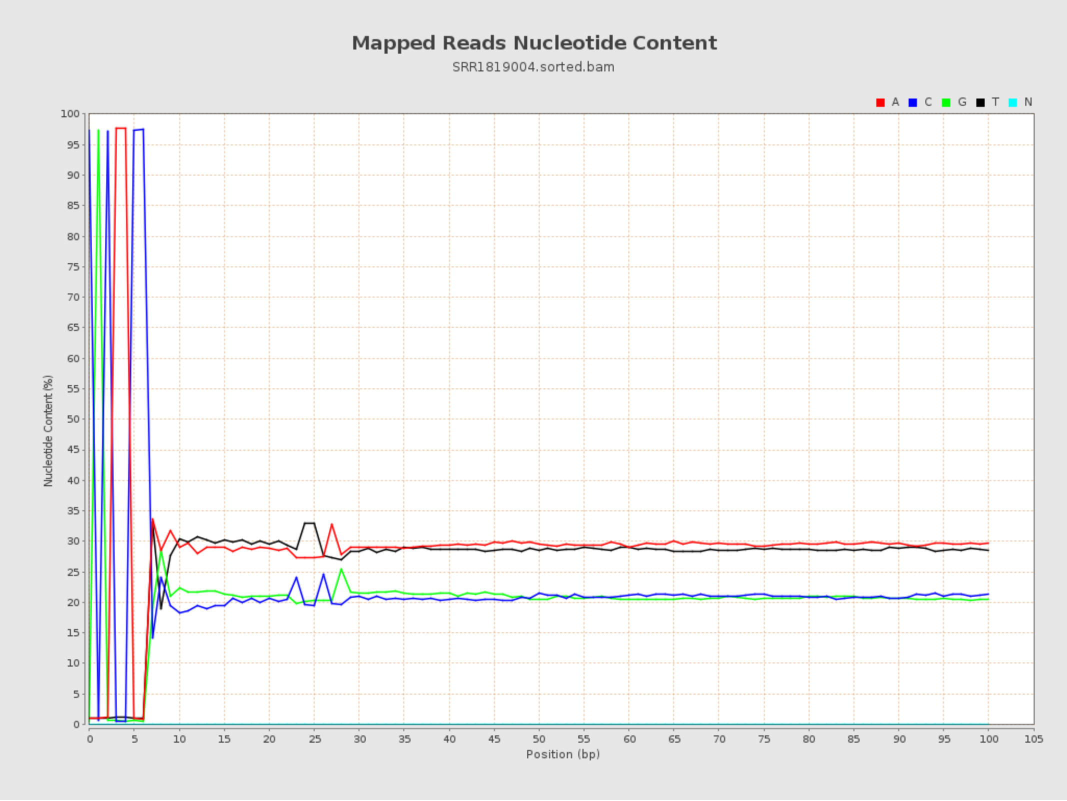
6. Results : Genome Fraction Coverage



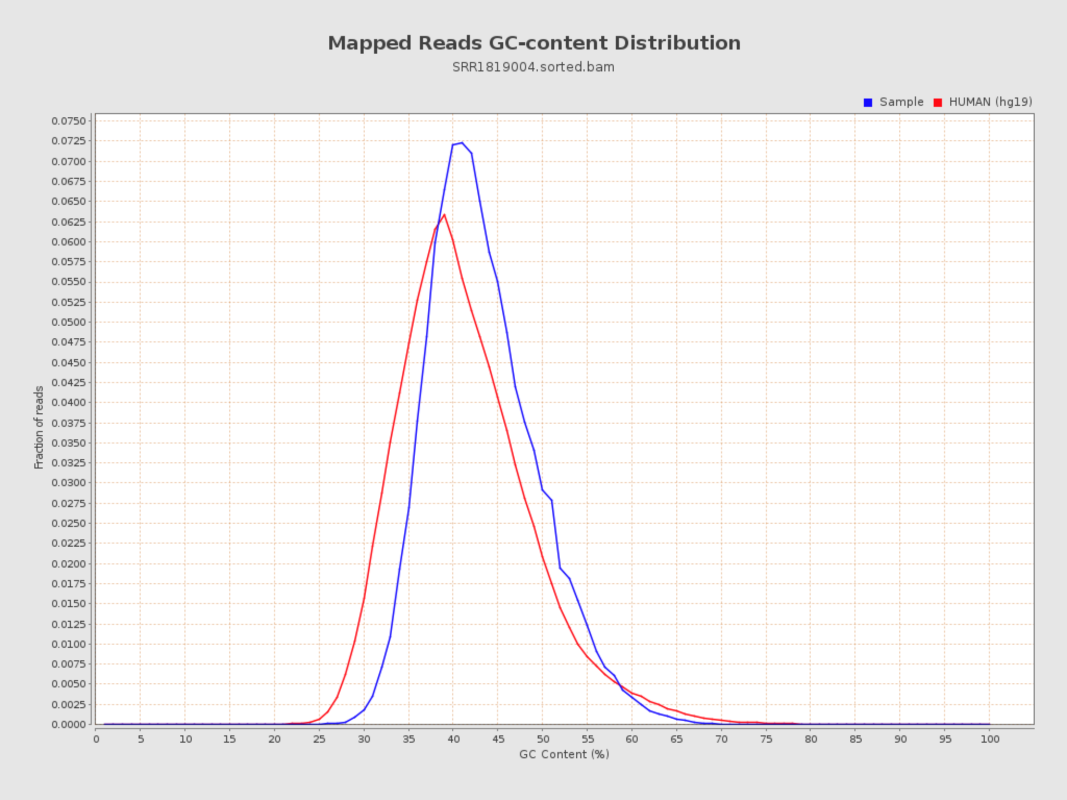
7. Results : Duplication Rate Histogram



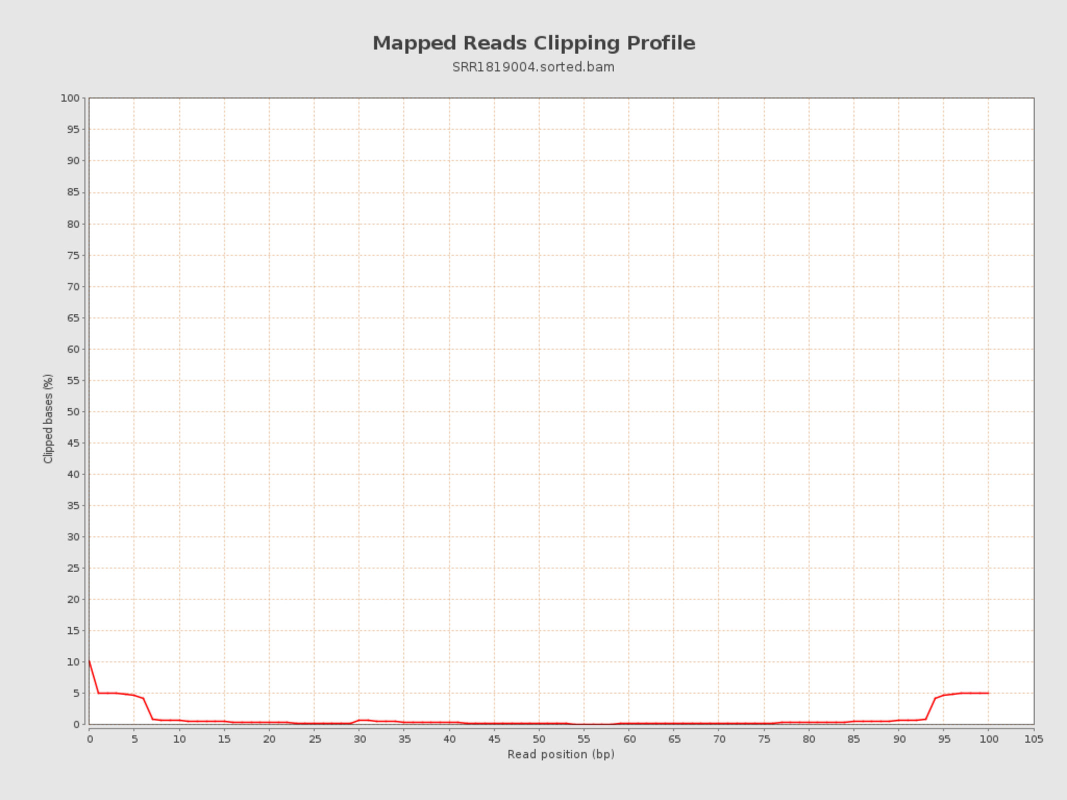
8. Results : Mapped Reads Nucleotide Content



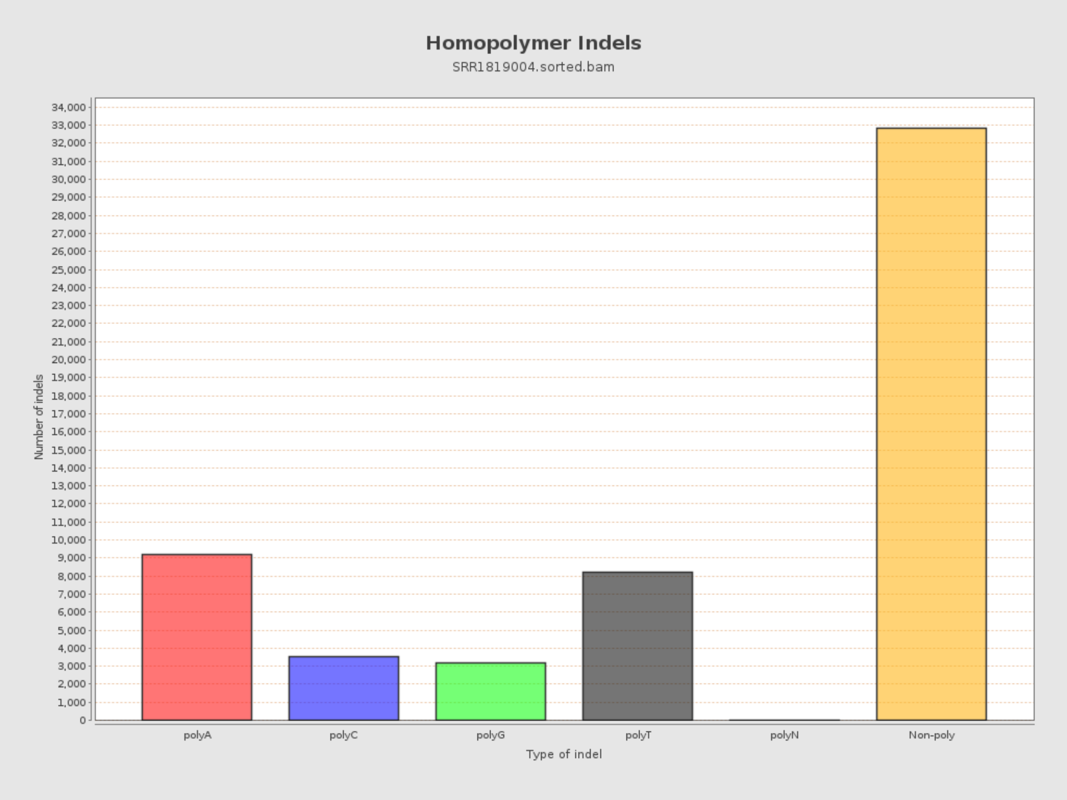
9. Results : Mapped Reads GC-content Distribution



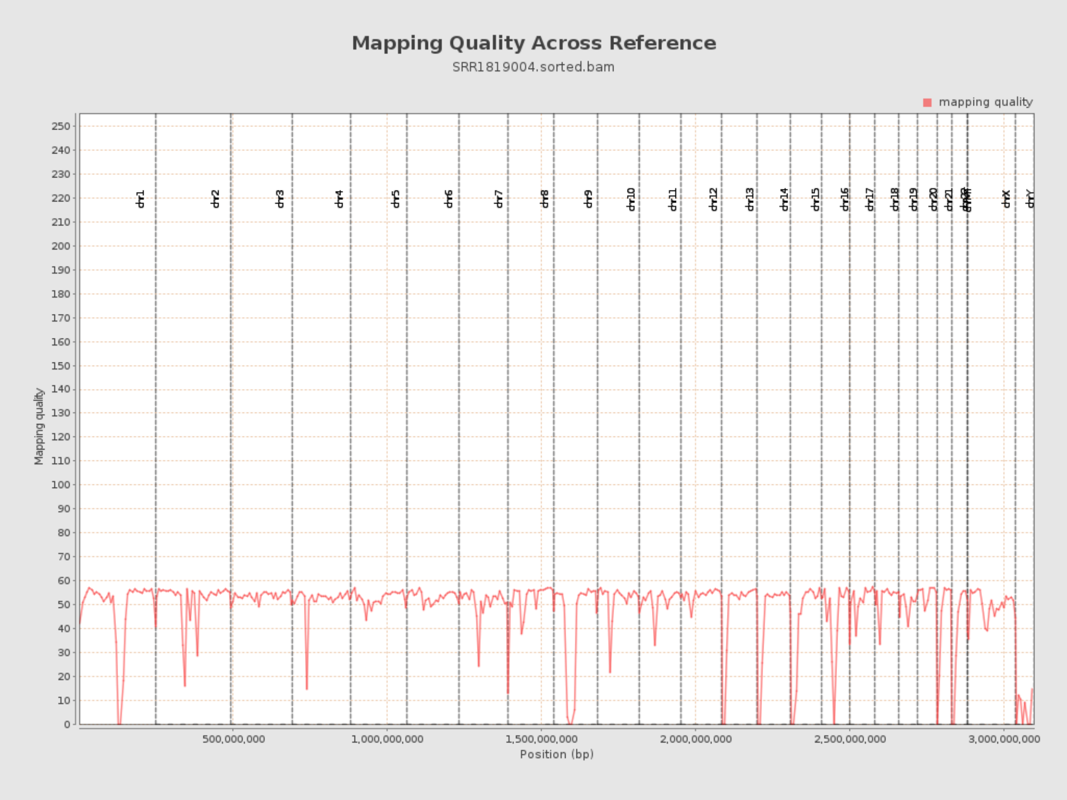
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram