Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:23:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818884.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_SRR1818884 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818884.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:22:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818884.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,487,441
Mapped reads	1,457,978 / 98.02%
Unmapped reads	29,463 / 1.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,259 / 1.43%
Read min/max/mean length	30 / 101 / 101.55
Duplicated reads (estimated)	238,591 / 16.04%
Duplication rate	13.47%
Clipped reads	1,455,651 / 97.86%

2.2. ACGT Content

Number/percentage of A's	38,319,481 / 28.38%
Number/percentage of C's	27,694,134 / 20.51%
Number/percentage of T's	39,296,240 / 29.1%
Number/percentage of G's	29,721,392 / 22.01%
Number/percentage of N's	1,954 / 0%
GC Percentage	42.52%

2.3. Coverage

Mean	0.0436

Standard Deviation	0.5341

2.4. Mapping Quality

Mean Mapping Quality	49.37

2.5. Mismatches and indels

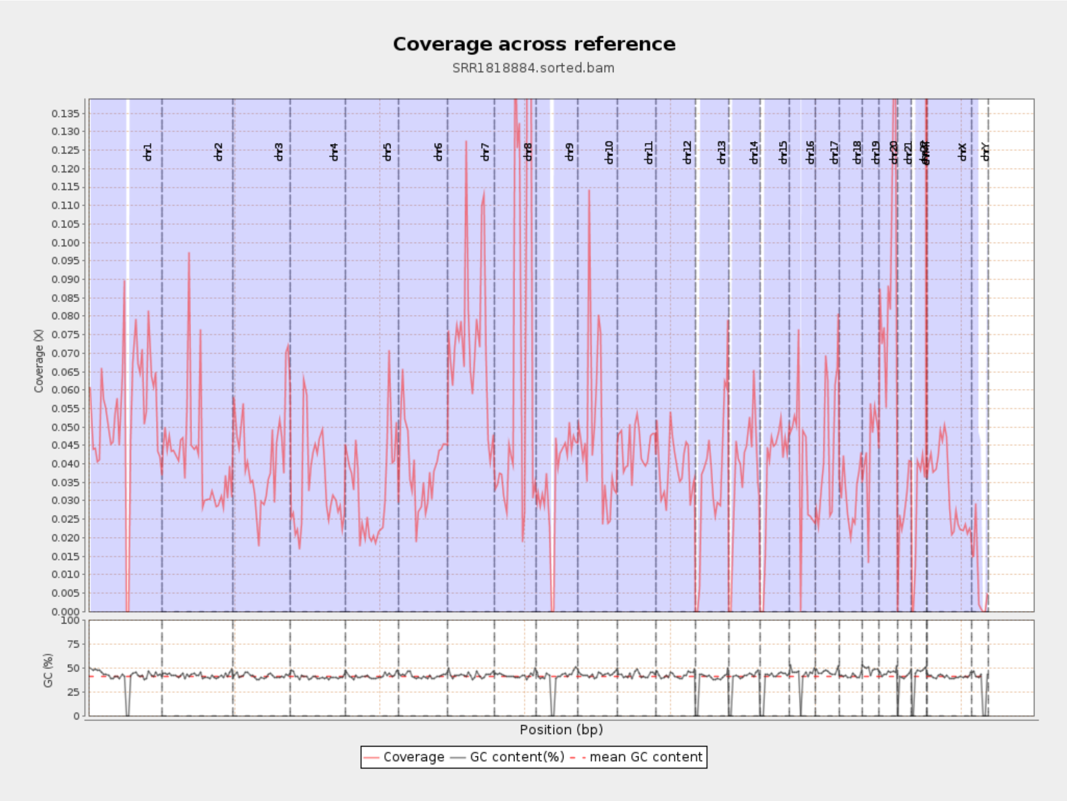
General error rate	0.66%
Mismatches	839,729
Insertions	21,357
Mapped reads with at least one insertion	1.42%
Deletions	43,354
Mapped reads with at least one deletion	2.91%
Homopolymer indels	40.06%

2.6. Chromosome stats

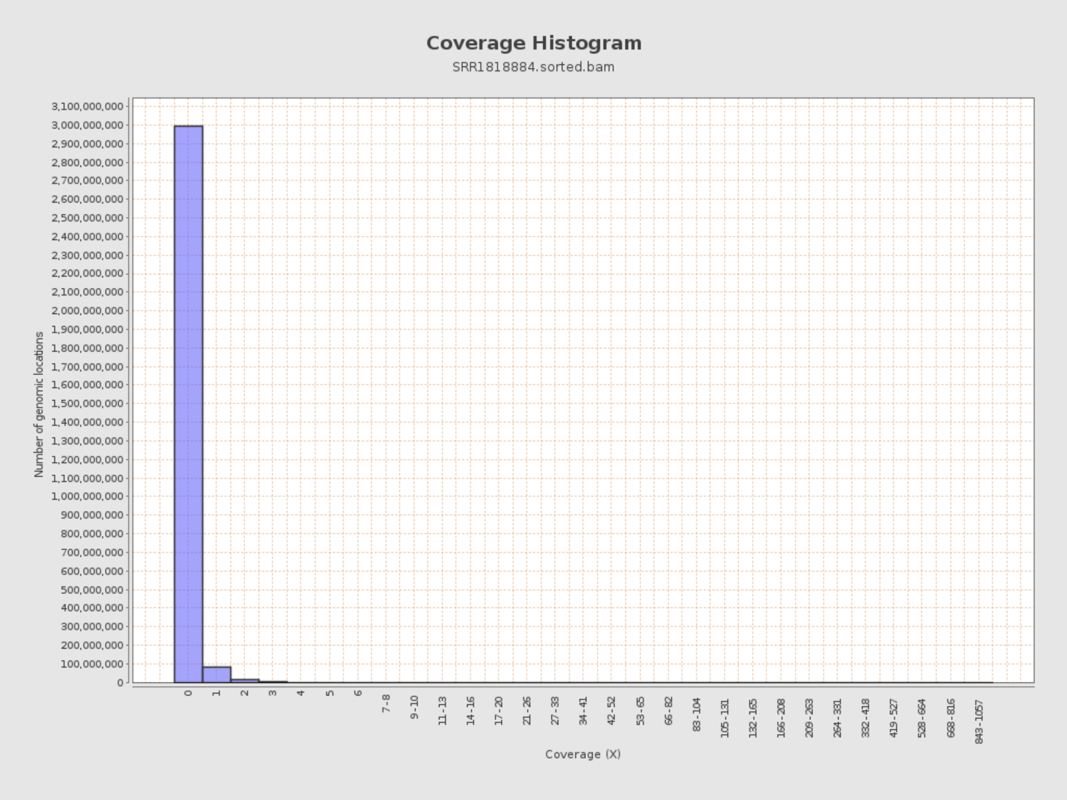
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13350053	0.0536	0.8073
chr2	243199373	10115369	0.0416	0.7383
chr3	198022430	8327648	0.0421	0.2572
chr4	191154276	6483615	0.0339	0.3114
chr5	180915260	5925948	0.0328	0.2392
chr6	171115067	6638308	0.0388	0.2736
chr7	159138663	11768744	0.074	1.1646

chr8	146364022	11284520	0.0771	0.4303
chr9	141213431	4958550	0.0351	0.4325
chr10	135534747	6449978	0.0476	0.7622
chr11	135006516	6014307	0.0445	0.3231
chr12	133851895	5276884	0.0394	0.2513
chr13	115169878	3967318	0.0344	0.228
chr14	107349540	4022193	0.0375	0.2603
chr15	102531392	3790925	0.037	0.2381
chr16	90354753	3552232	0.0393	0.5276
chr17	81195210	3710956	0.0457	0.3394
chr18	78077248	2464096	0.0316	0.486
chr19	59128983	2560565	0.0433	0.7197
chr20	63025520	5834426	0.0926	0.4073
chr21	48129895	1335892	0.0278	0.2551
chr22	51304566	1397482	0.0272	0.2245
chrMT	16571	292347	17.6421	10.8589
chrX	155270560	5117033	0.033	0.2748
chrY	59373566	479542	0.0081	0.6405

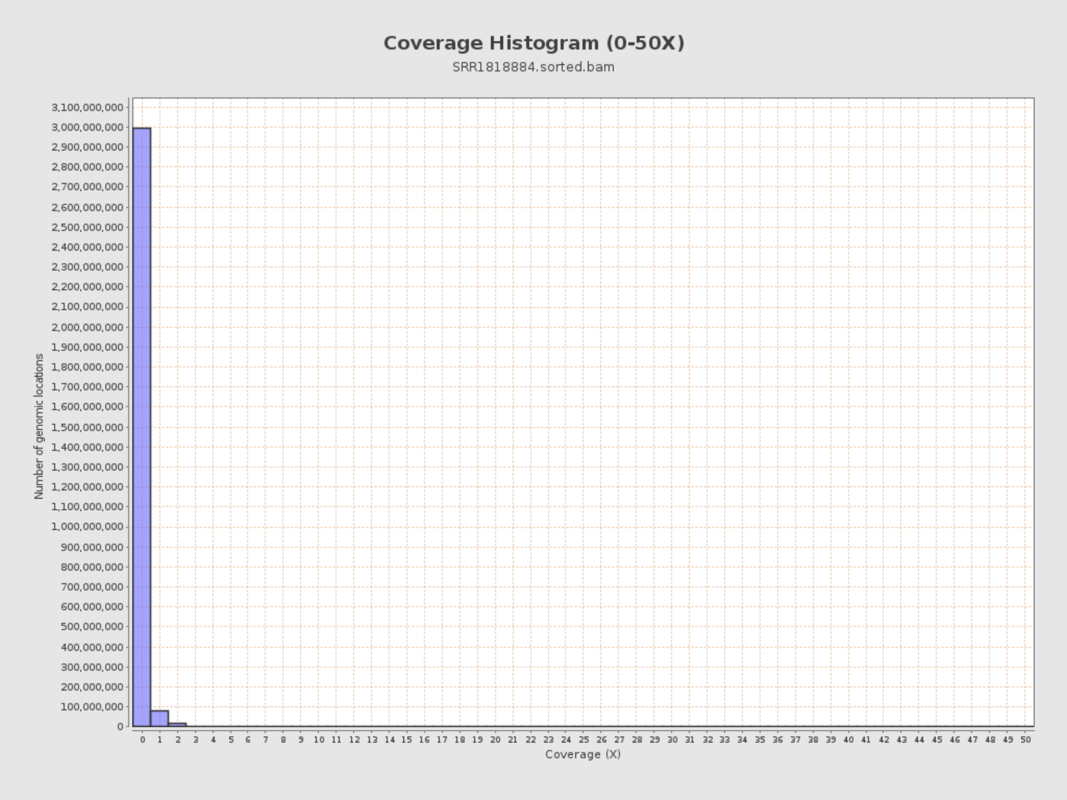
3. Results : Coverage across reference



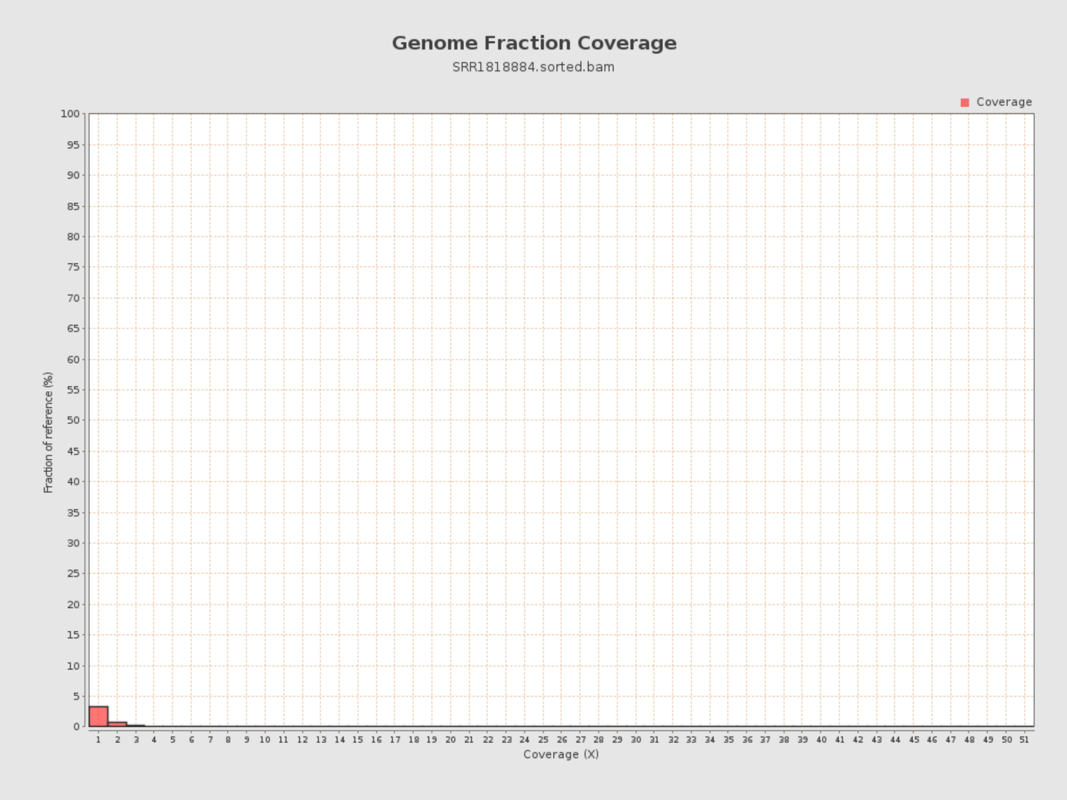
4. Results : Coverage Histogram



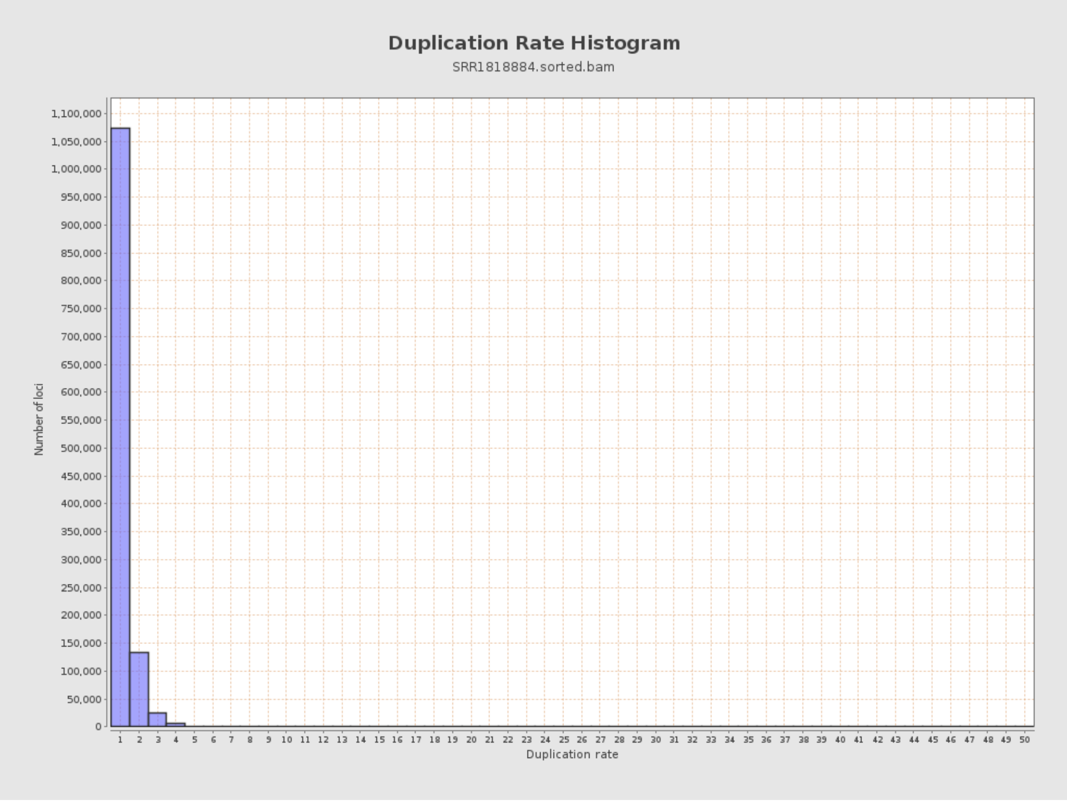
5. Results : Coverage Histogram (0-50X)



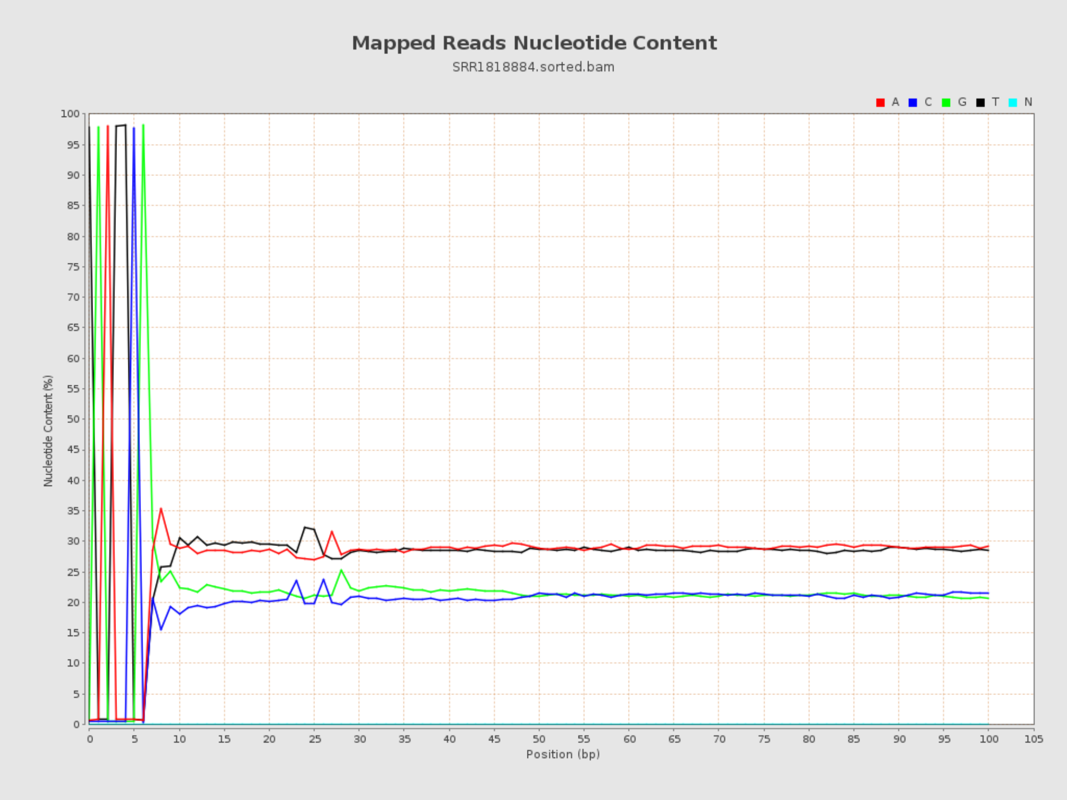
6. Results : Genome Fraction Coverage



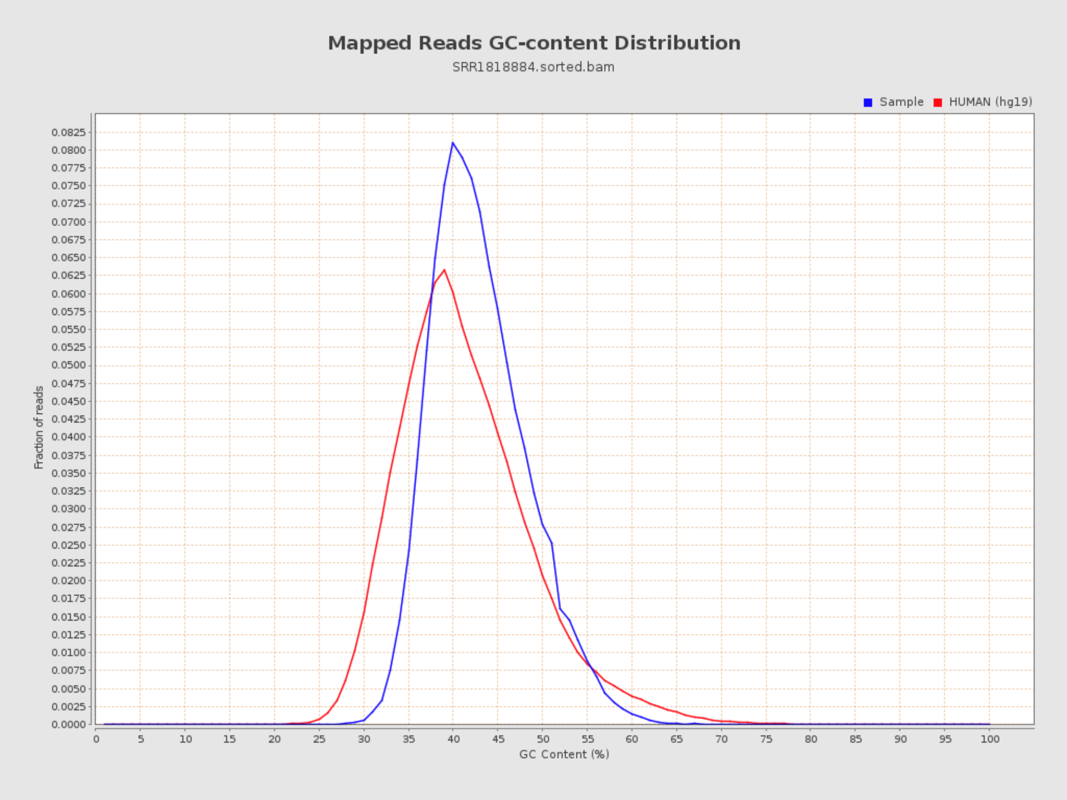
7. Results : Duplication Rate Histogram



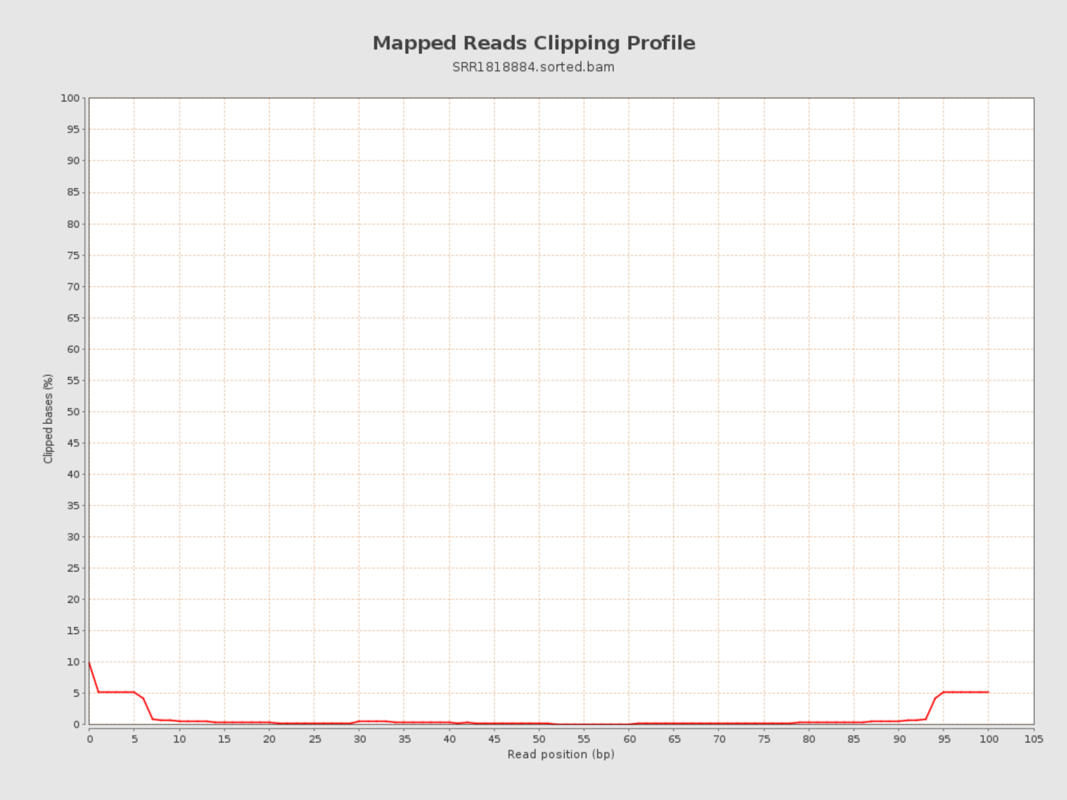
8. Results : Mapped Reads Nucleotide Content



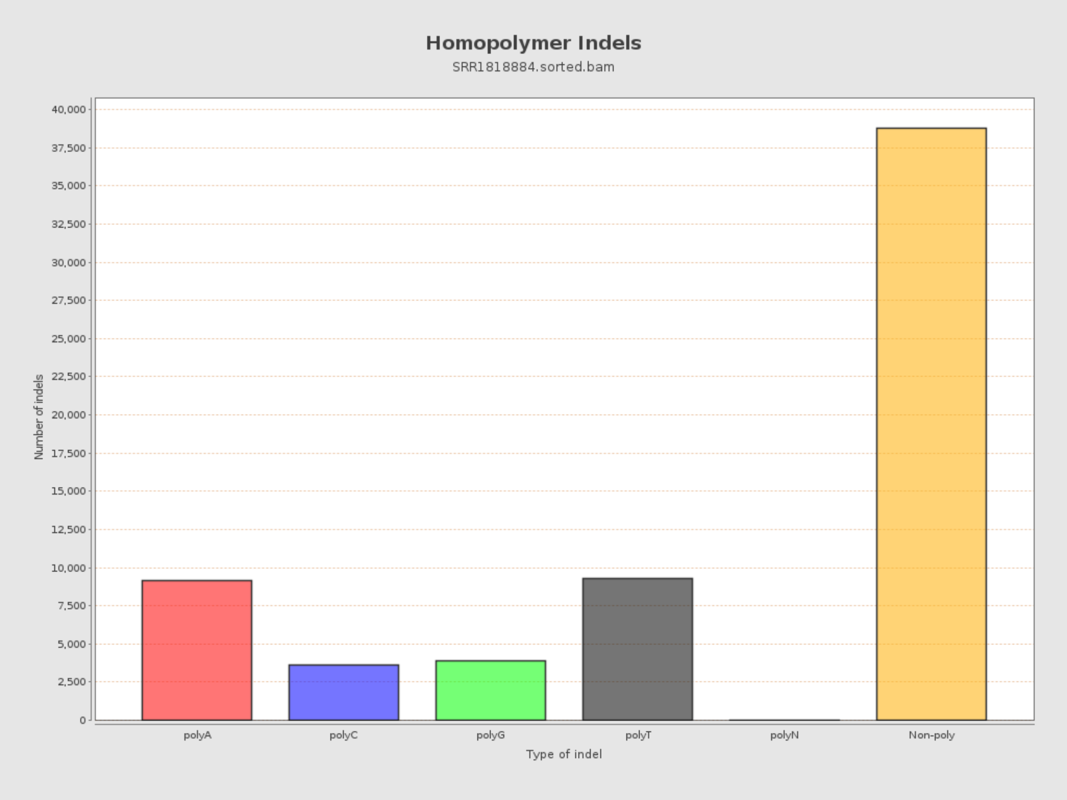
9. Results : Mapped Reads GC-content Distribution



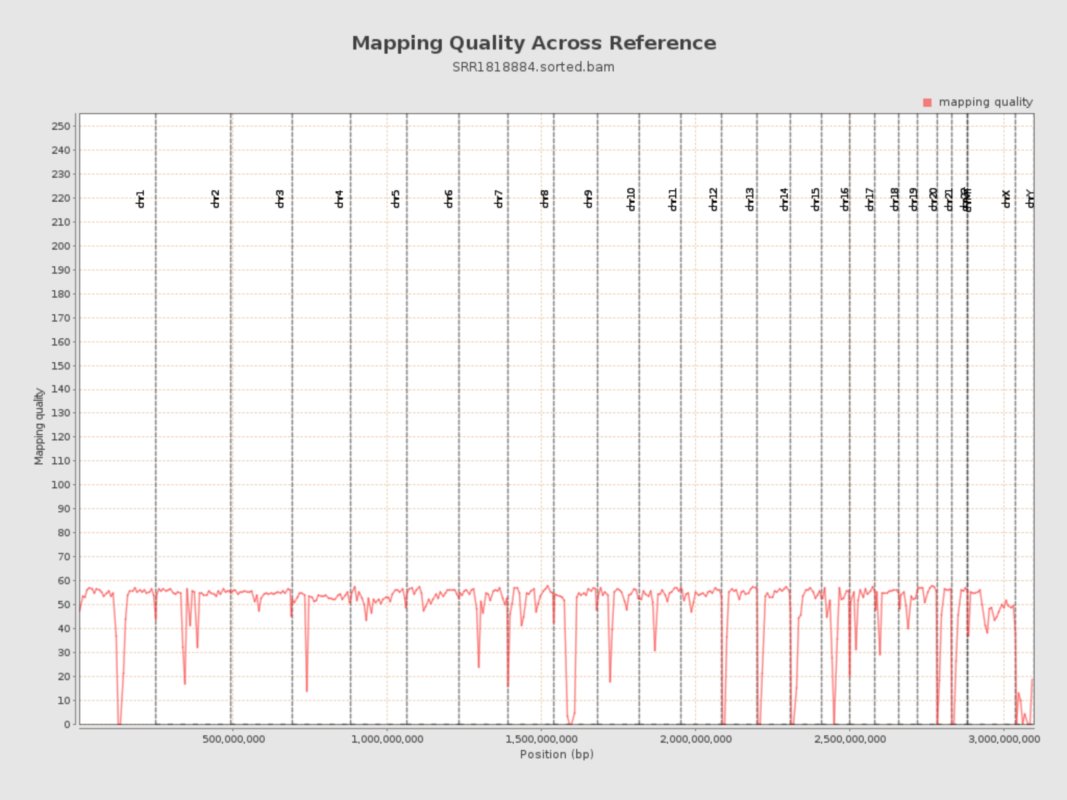
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram