Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 06:33:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818903.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_SRR1818903 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818903.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 06:33:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818903.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,019,650
Mapped reads	1,985,242 / 98.3%
Unmapped reads	34,408 / 1.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,802 / 1.38%
Read min/max/mean length	30 / 101 / 101.53
Duplicated reads (estimated)	405,153 / 20.06%
Duplication rate	17.01%
Clipped reads	1,990,756 / 98.57%

2.2. ACGT Content

Number/percentage of A's	51,135,964 / 27.79%
Number/percentage of C's	38,521,865 / 20.94%
Number/percentage of T's	52,891,285 / 28.75%
Number/percentage of G's	41,448,855 / 22.53%
Number/percentage of N's	2,549 / 0%
GC Percentage	43.46%

2.3. Coverage

Mean	0.0595

Standard Deviation	0.7431

2.4. Mapping Quality

Mean Mapping Quality	49.22

2.5. Mismatches and indels

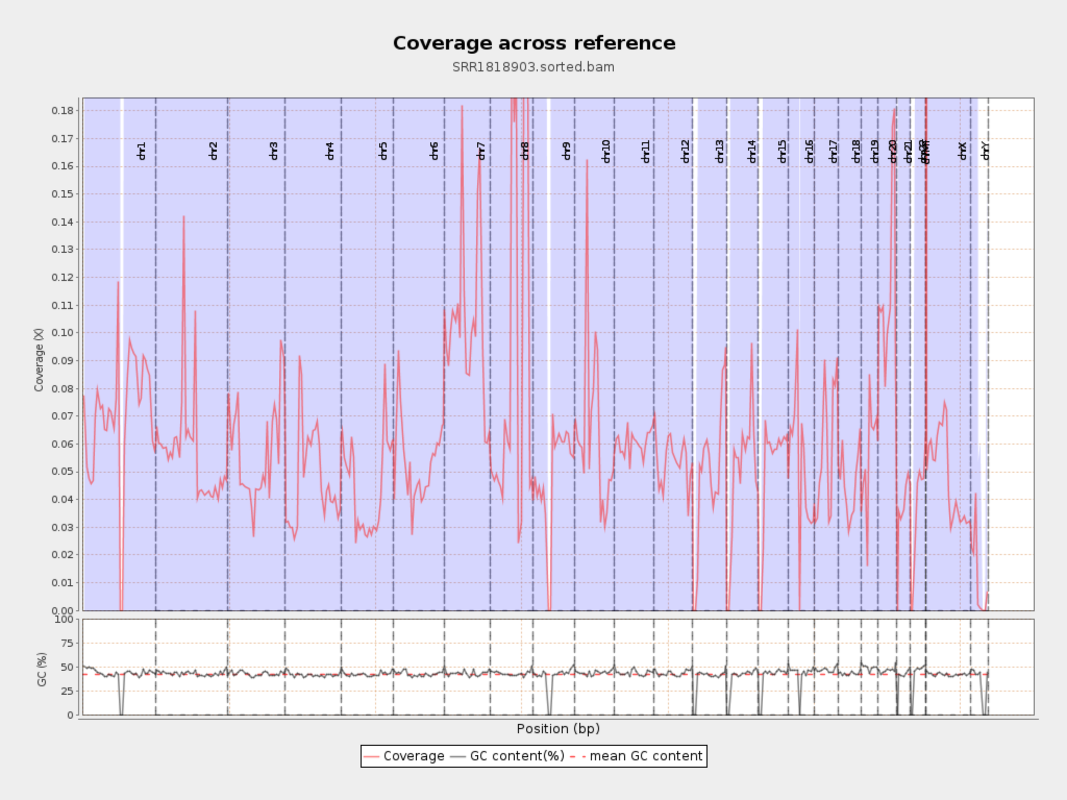
General error rate	0.65%
Mismatches	1,132,849
Insertions	25,628
Mapped reads with at least one insertion	1.25%
Deletions	58,679
Mapped reads with at least one deletion	2.89%
Homopolymer indels	41.85%

2.6. Chromosome stats

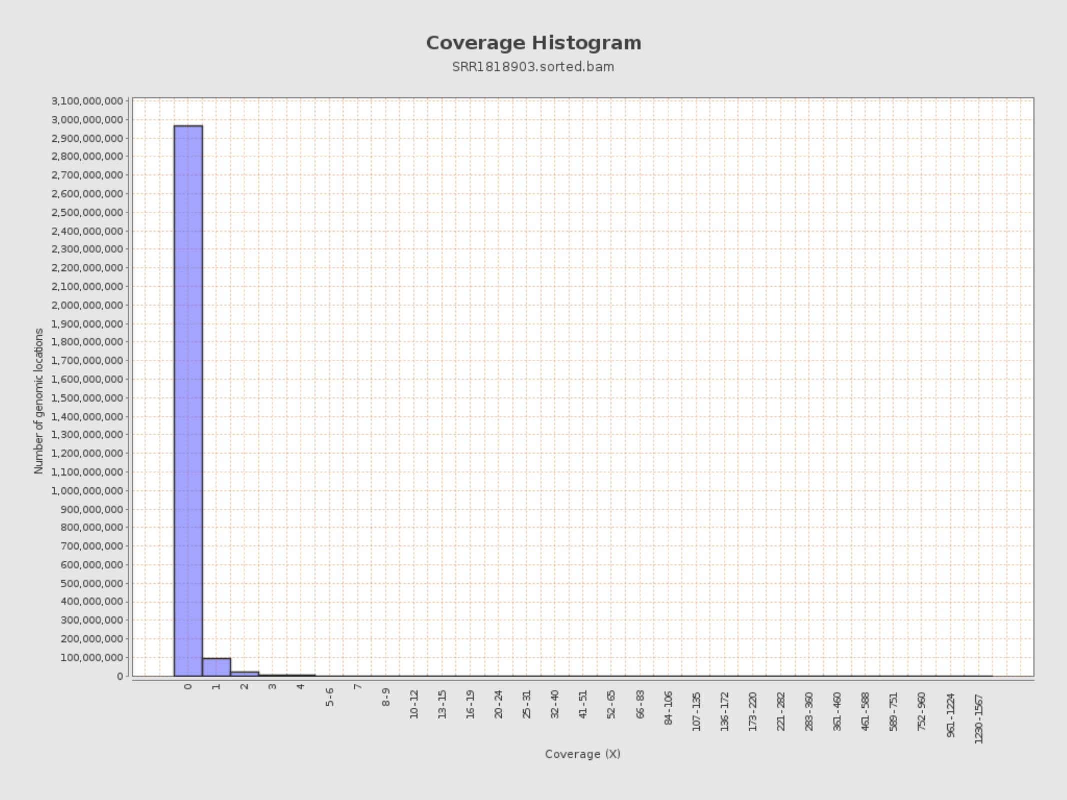
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17469511	0.0701	1.1675
chr2	243199373	13950428	0.0574	0.9973
chr3	198022430	11362737	0.0574	0.3169
chr4	191154276	9157659	0.0479	0.4189
chr5	180915260	8124553	0.0449	0.2954
chr6	171115067	9123109	0.0533	0.3465
chr7	159138663	16497276	0.1037	1.6802

chr8	146364022	15945125	0.1089	0.6014
chr9	141213431	6827120	0.0483	0.6385
chr10	135534747	8605073	0.0635	1.036
chr11	135006516	8135346	0.0603	0.4283
chr12	133851895	7208432	0.0539	0.3127
chr13	115169878	5610628	0.0487	0.2893
chr14	107349540	5401731	0.0503	0.3335
chr15	102531392	5062461	0.0494	0.2917
chr16	90354753	4588210	0.0508	0.6927
chr17	81195210	4655046	0.0573	0.4691
chr18	78077248	3567649	0.0457	0.7224
chr19	59128983	3321761	0.0562	1.0632
chr20	63025520	7570468	0.1201	0.5001
chr21	48129895	1770598	0.0368	0.3196
chr22	51304566	1735285	0.0338	0.2715
chrMT	16571	302300	18.2427	13.0477
chrX	155270560	7442886	0.0479	0.3736
chrY	59373566	680164	0.0115	0.8209

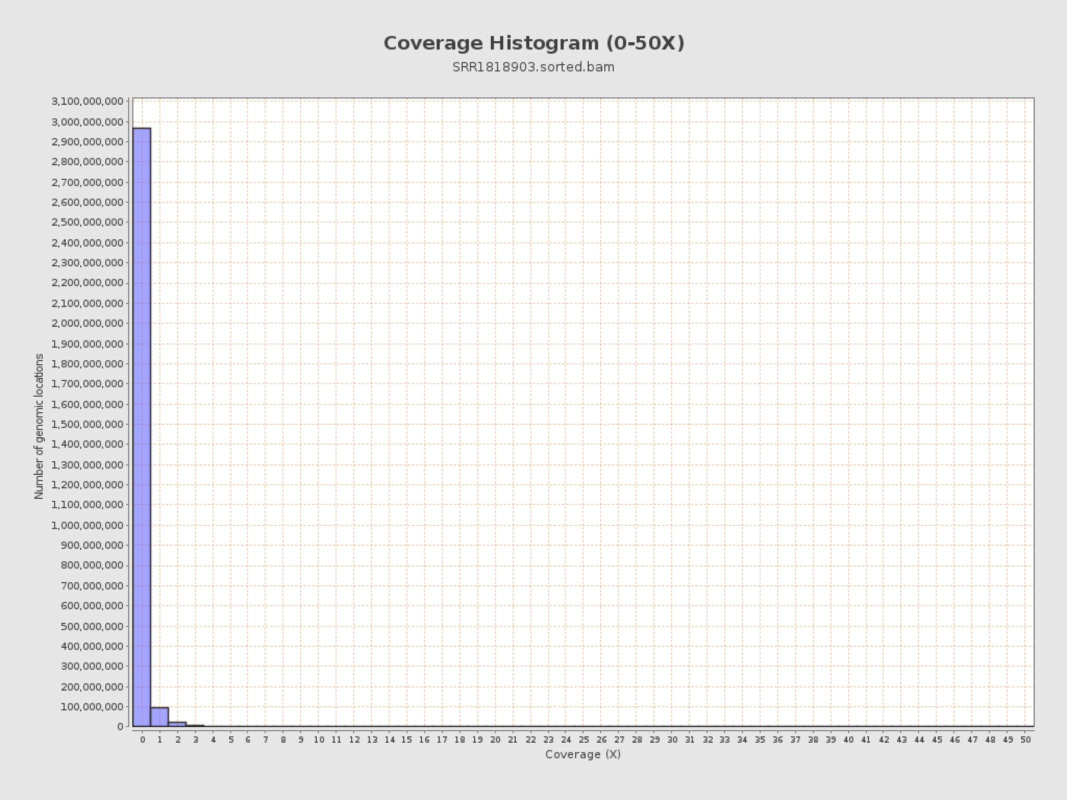
3. Results : Coverage across reference



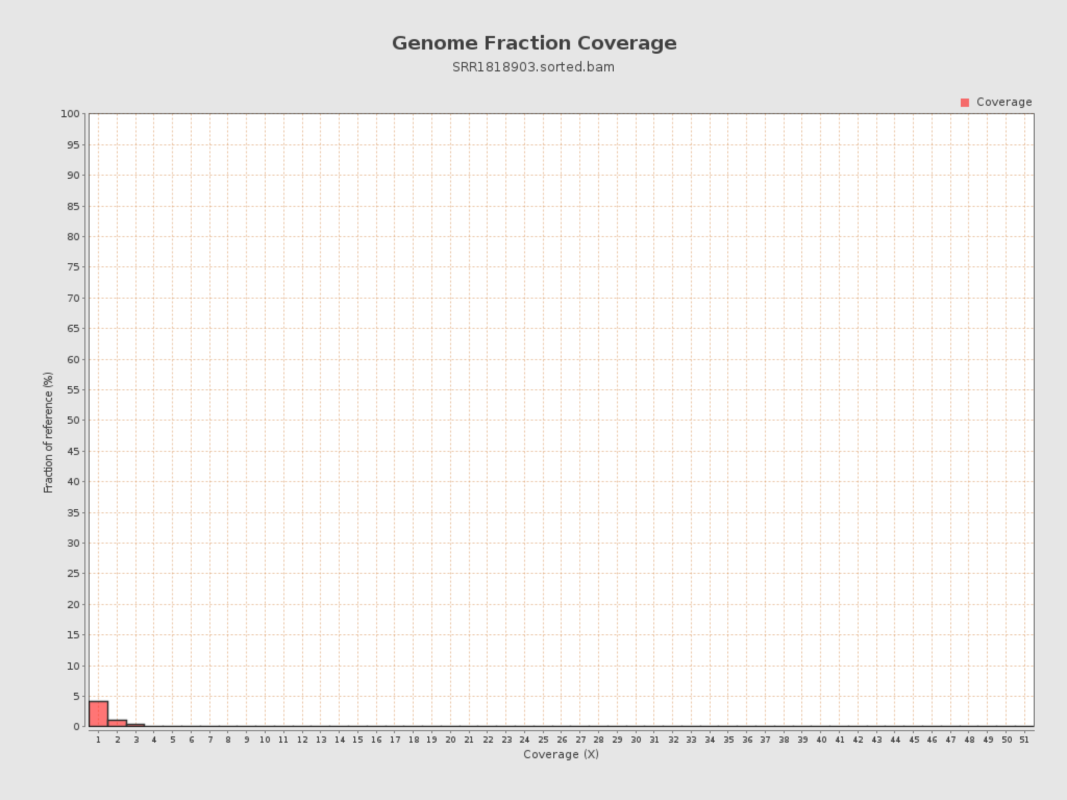
4. Results : Coverage Histogram



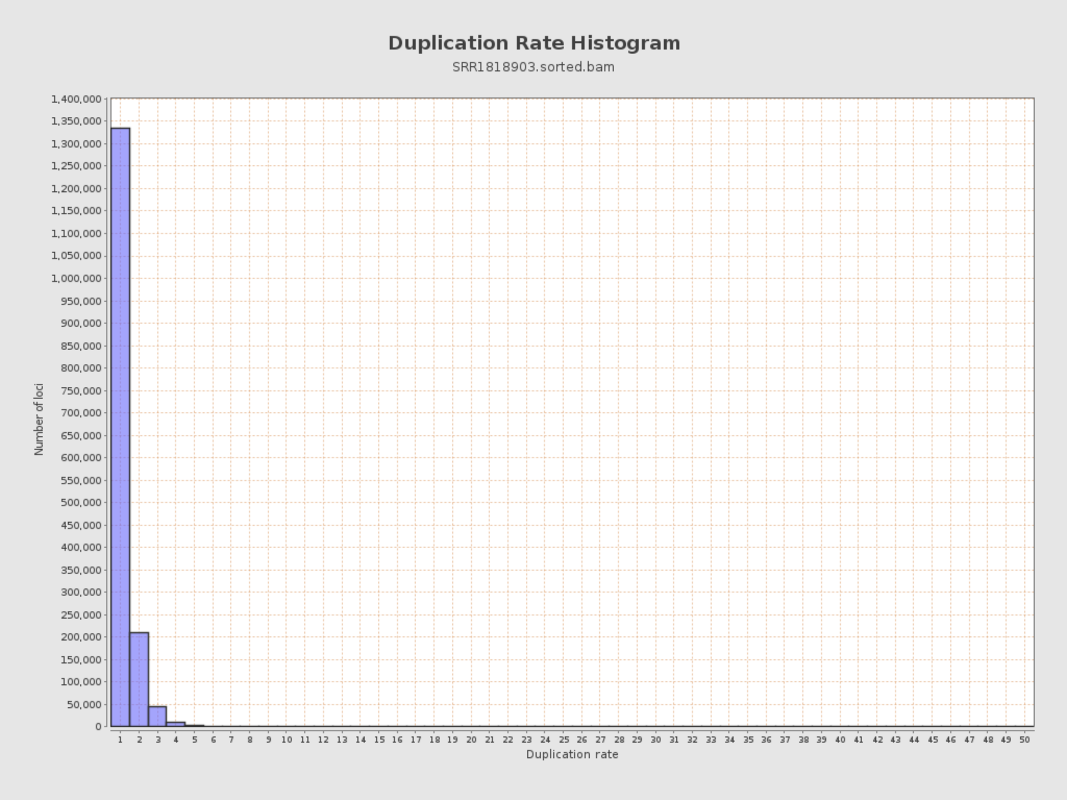
5. Results : Coverage Histogram (0-50X)



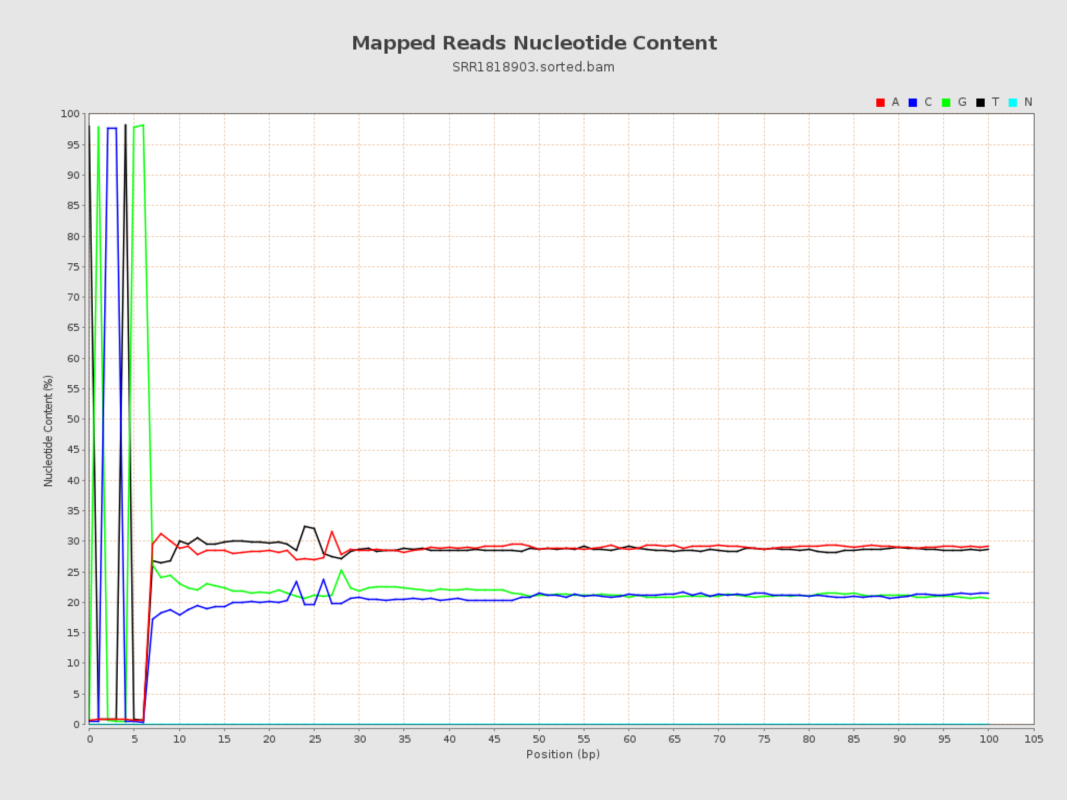
6. Results : Genome Fraction Coverage



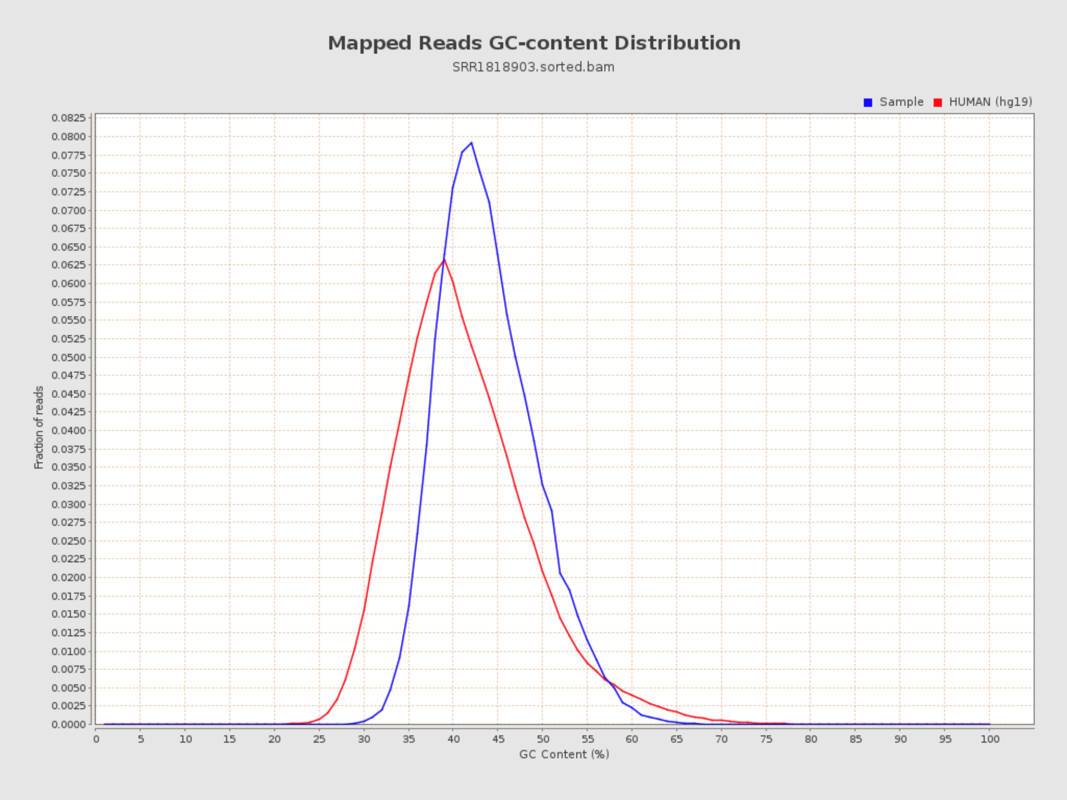
7. Results : Duplication Rate Histogram



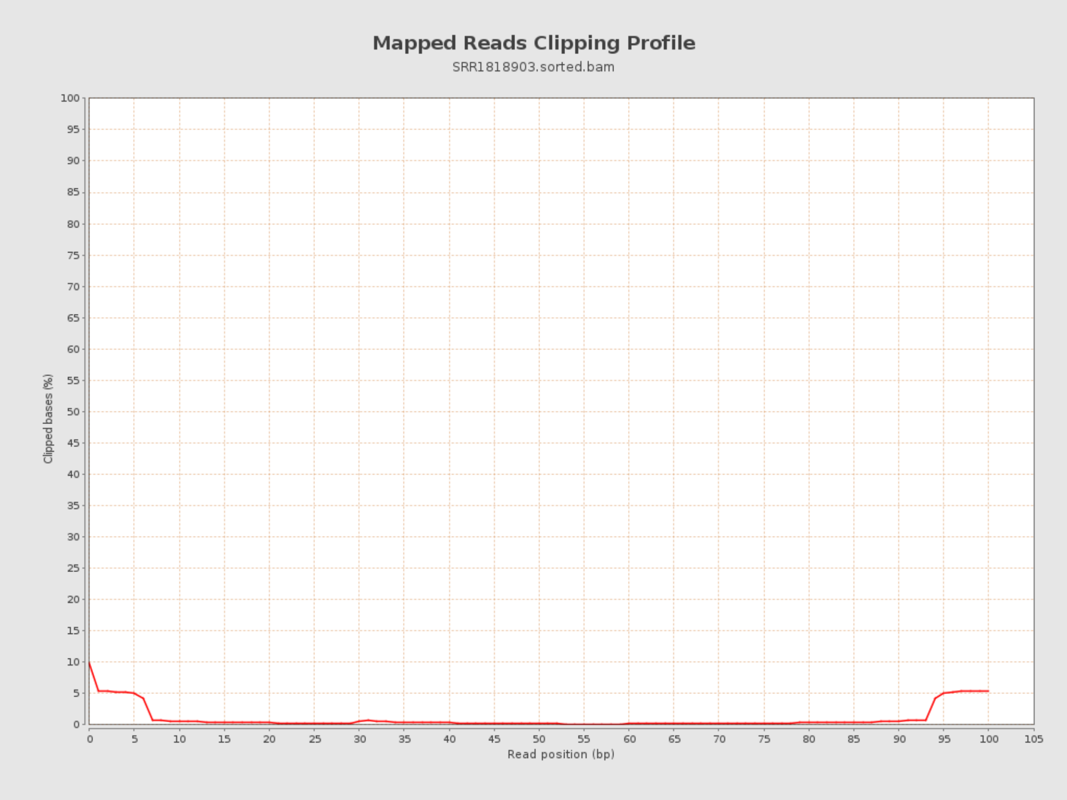
8. Results : Mapped Reads Nucleotide Content



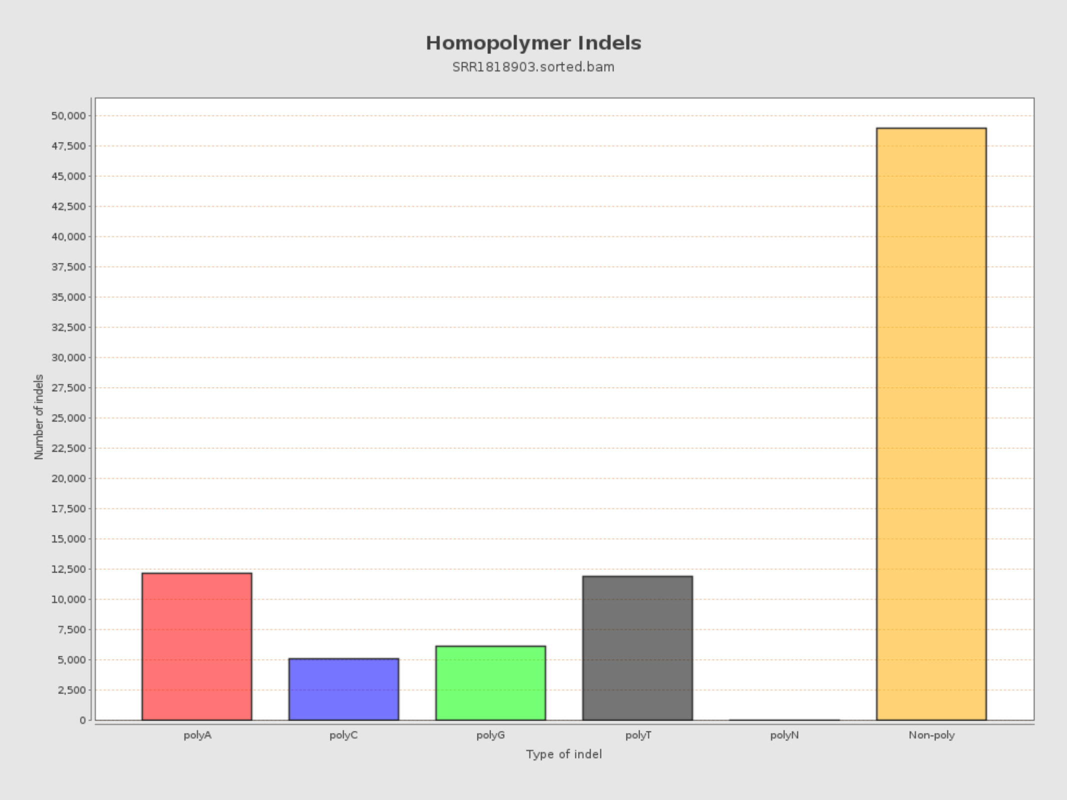
9. Results : Mapped Reads GC-content Distribution



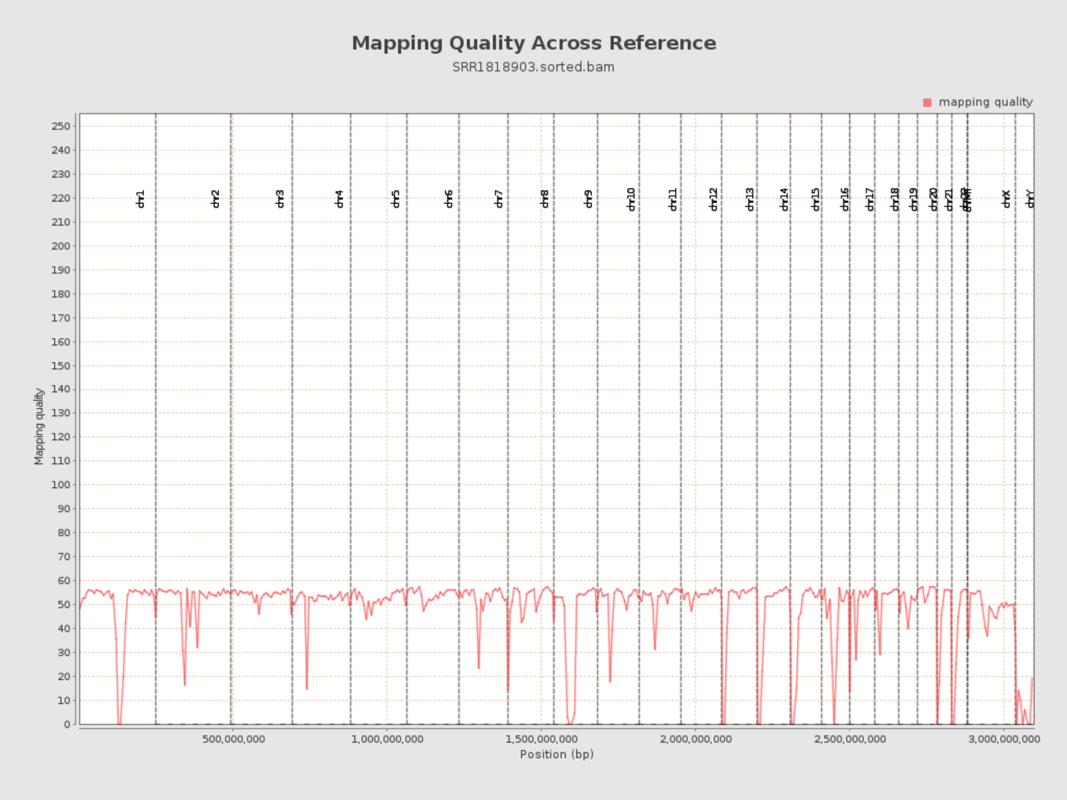
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram