Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 07:27:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867840.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_SRR9867840 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867840.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 07:27:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867840.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,404,735
Mapped reads	16,046,313 / 92.2%
Unmapped reads	1,358,422 / 7.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,988 / 0.21%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	906,684 / 5.21%
Duplication rate	1.38%
Clipped reads	16,014,820 / 92.01%

2.2. ACGT Content

Number/percentage of A's	397,528,675 / 27.79%
Number/percentage of C's	312,735,226 / 21.86%
Number/percentage of T's	402,496,897 / 28.14%
Number/percentage of G's	316,951,259 / 22.16%
Number/percentage of N's	691,099 / 0.05%
GC Percentage	44.02%

2.3. Coverage

Mean	0.4622

Standard Deviation	6.491

2.4. Mapping Quality

Mean Mapping Quality	50.35

2.5. Mismatches and indels

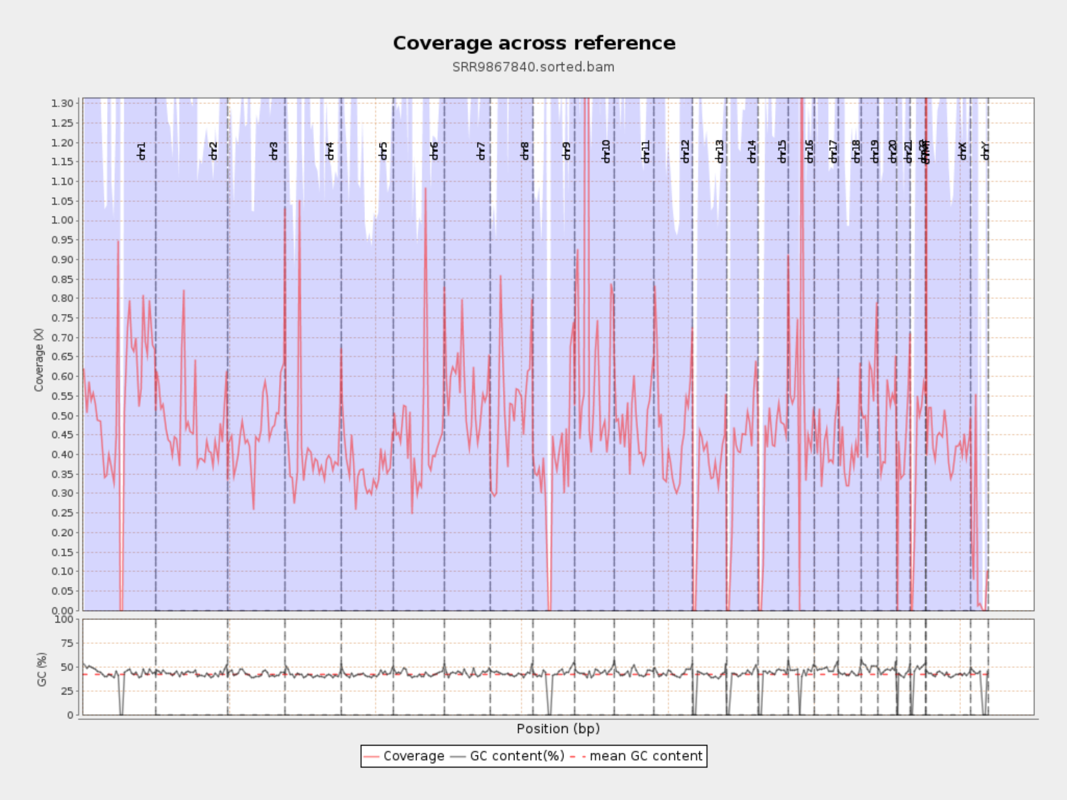
General error rate	0.48%
Mismatches	6,471,914
Insertions	146,267
Mapped reads with at least one insertion	0.89%
Deletions	150,401
Mapped reads with at least one deletion	0.91%
Homopolymer indels	35.38%

2.6. Chromosome stats

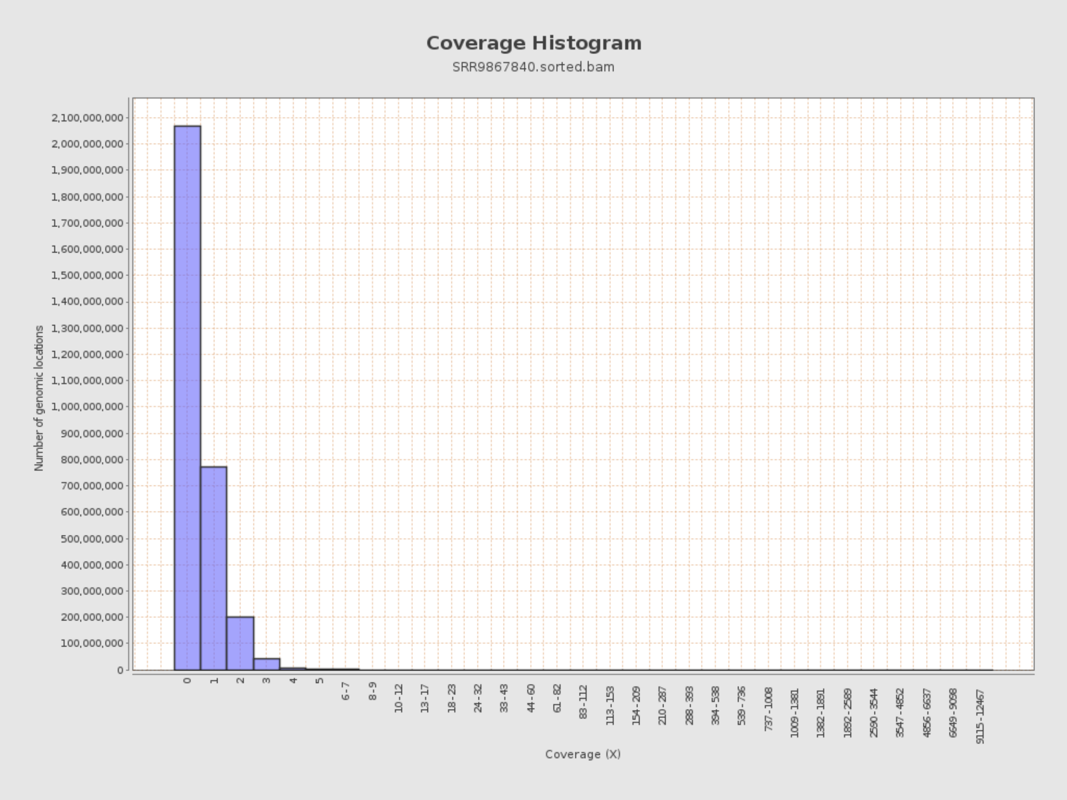
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	135256219	0.5427	10.3797
chr2	243199373	115410059	0.4745	3.2899
chr3	198022430	91576980	0.4625	4.5105
chr4	191154276	78195543	0.4091	3.7455
chr5	180915260	66756627	0.369	0.7268
chr6	171115067	76576334	0.4475	1.5521
chr7	159138663	90689952	0.5699	5.4377

chr8	146364022	77195187	0.5274	2.1053
chr9	141213431	52072153	0.3687	2.3854
chr10	135534747	99559893	0.7346	23.4933
chr11	135006516	65007652	0.4815	1.7267
chr12	133851895	61817355	0.4618	0.9804
chr13	115169878	39536580	0.3433	0.6639
chr14	107349540	42471338	0.3956	0.8882
chr15	102531392	38662694	0.3771	0.684
chr16	90354753	53272642	0.5896	6.8551
chr17	81195210	34947720	0.4304	1.6549
chr18	78077248	31908082	0.4087	4.9943
chr19	59128983	33275487	0.5628	6.3723
chr20	63025520	30497236	0.4839	1.32
chr21	48129895	19962330	0.4148	2.8766
chr22	51304566	19020055	0.3707	0.7458
chrMT	16571	3075917	185.6205	60.6102
chrX	155270560	67139354	0.4324	1.3174
chrY	59373566	6900618	0.1162	5.4531

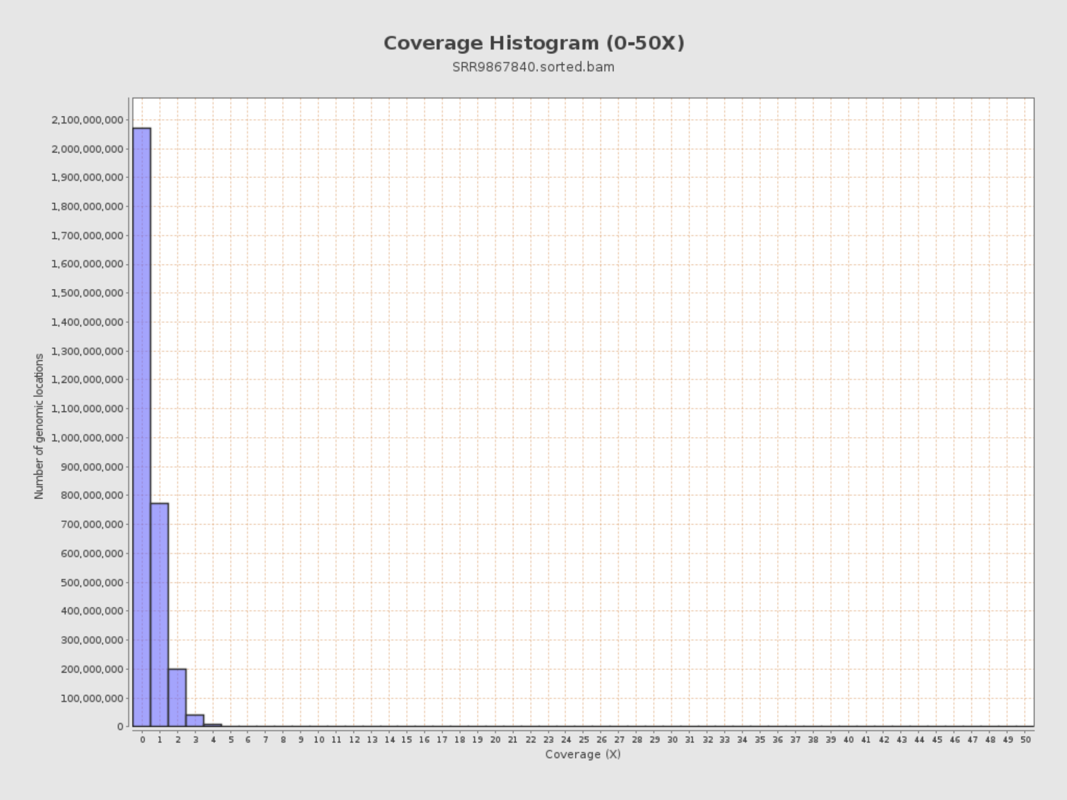
3. Results : Coverage across reference



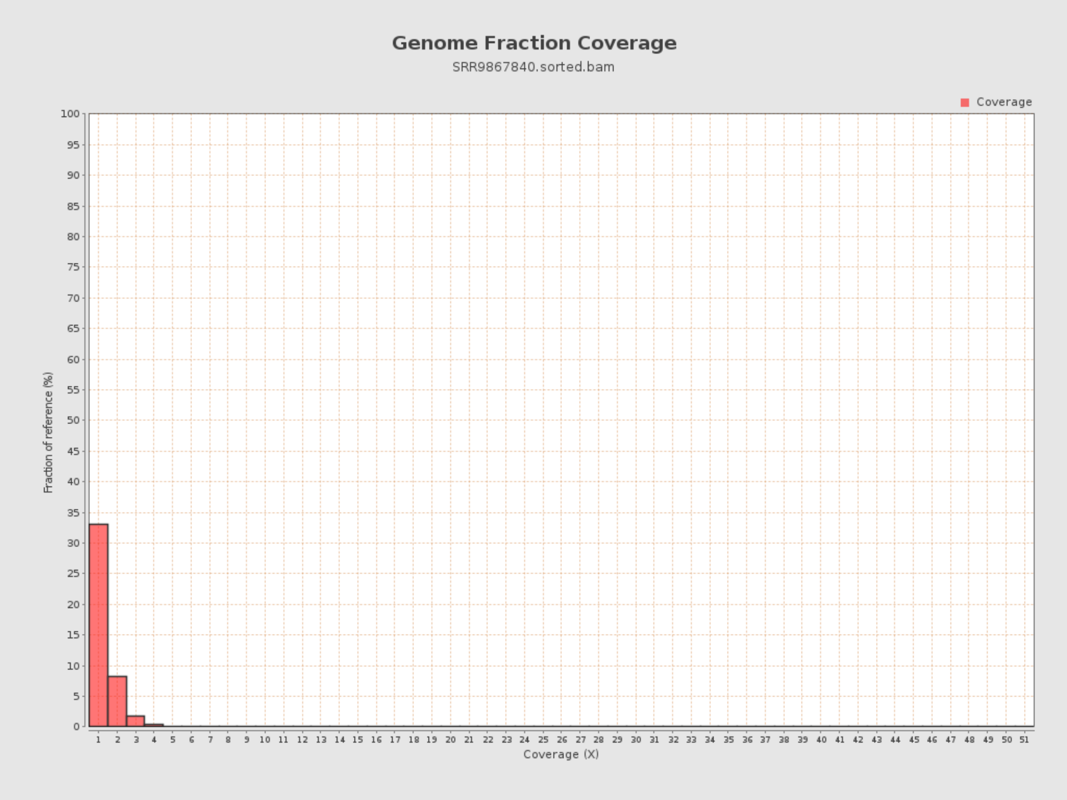
4. Results : Coverage Histogram



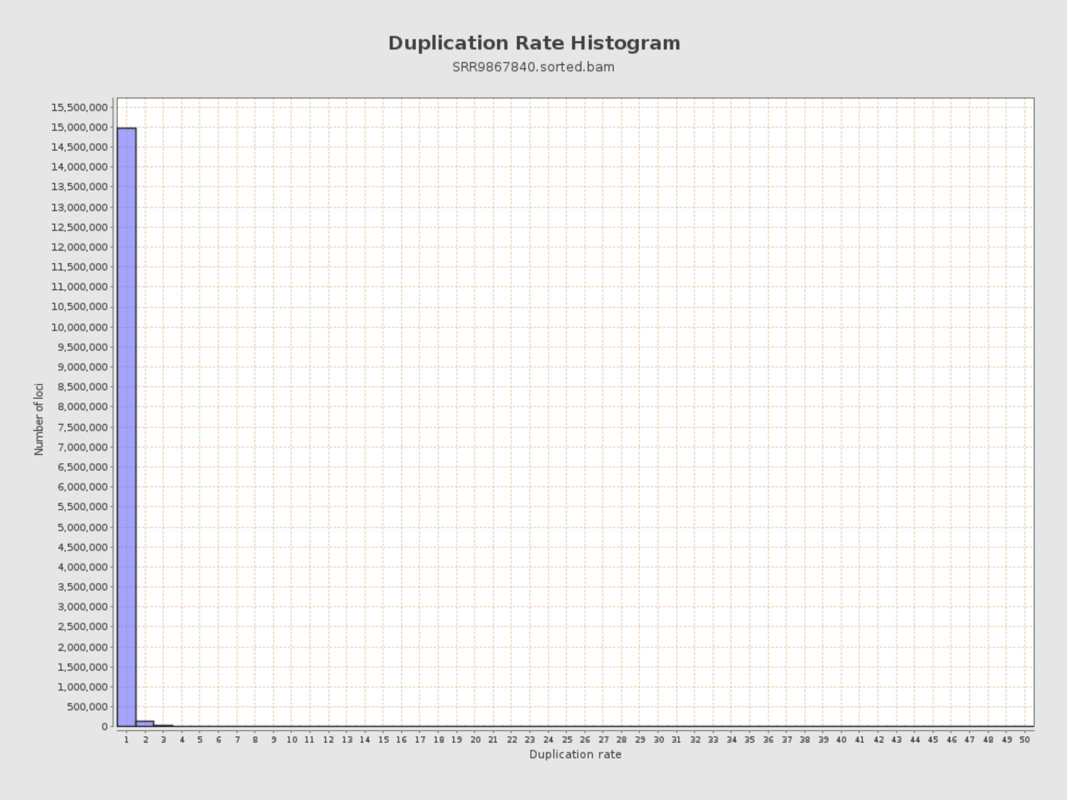
5. Results : Coverage Histogram (0-50X)



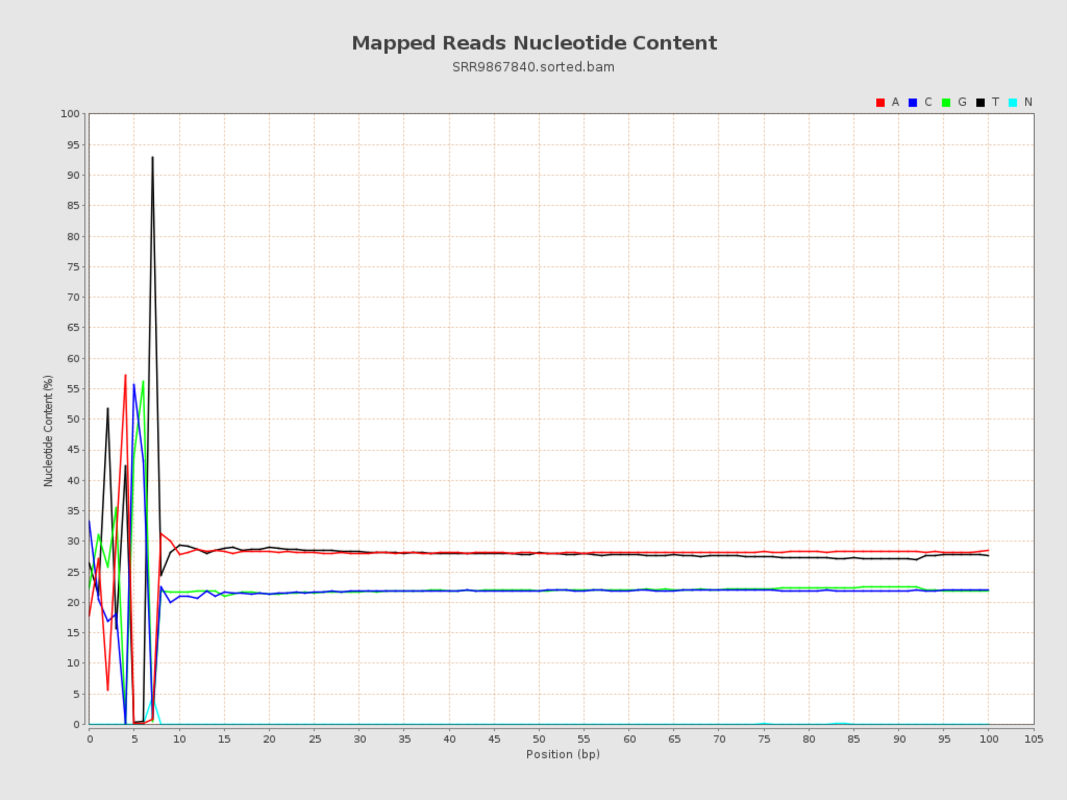
6. Results : Genome Fraction Coverage



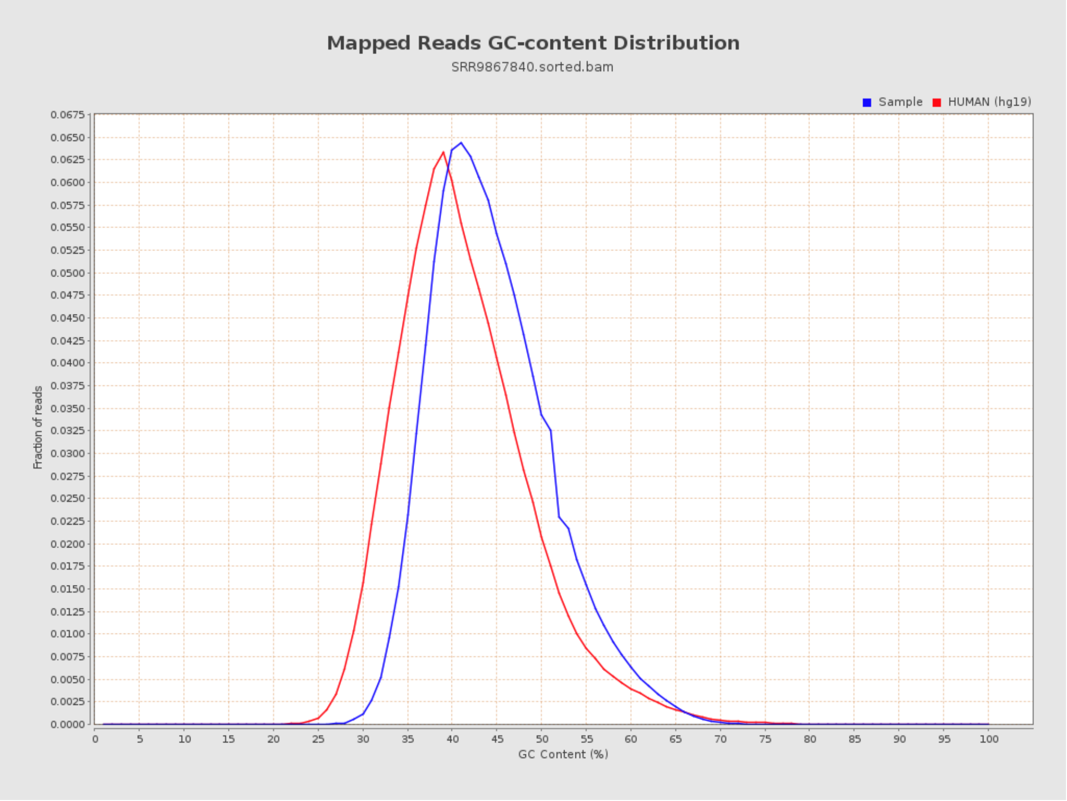
7. Results : Duplication Rate Histogram



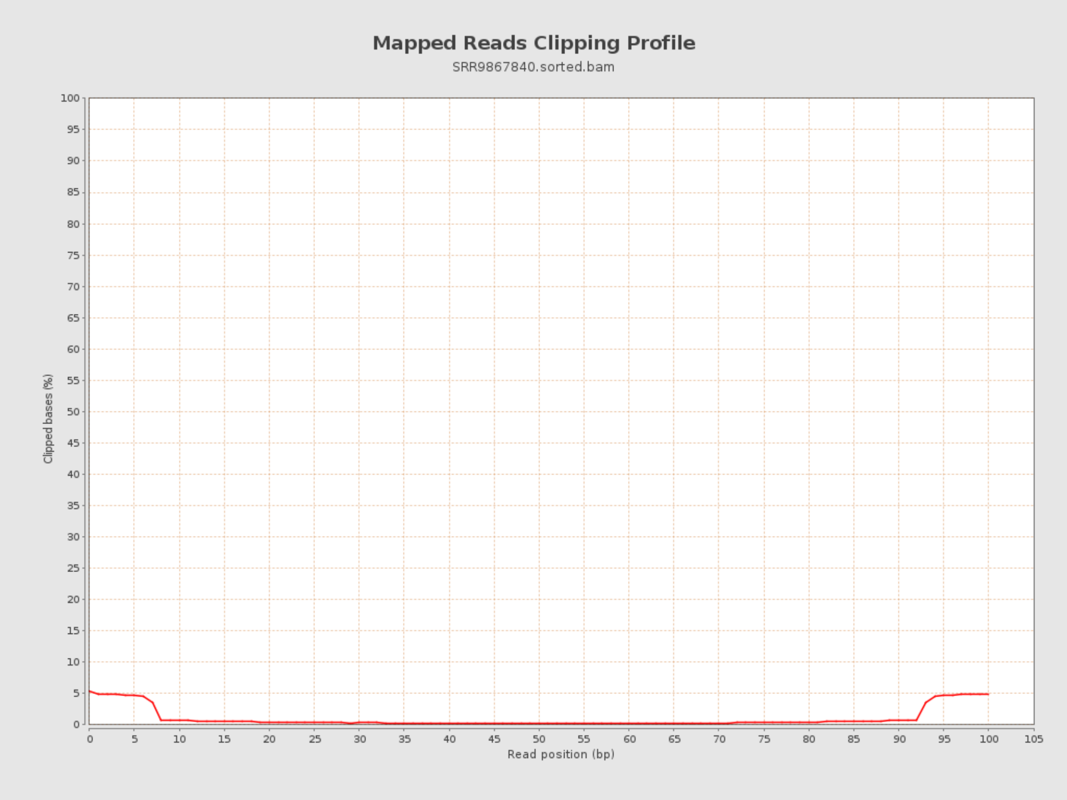
8. Results : Mapped Reads Nucleotide Content



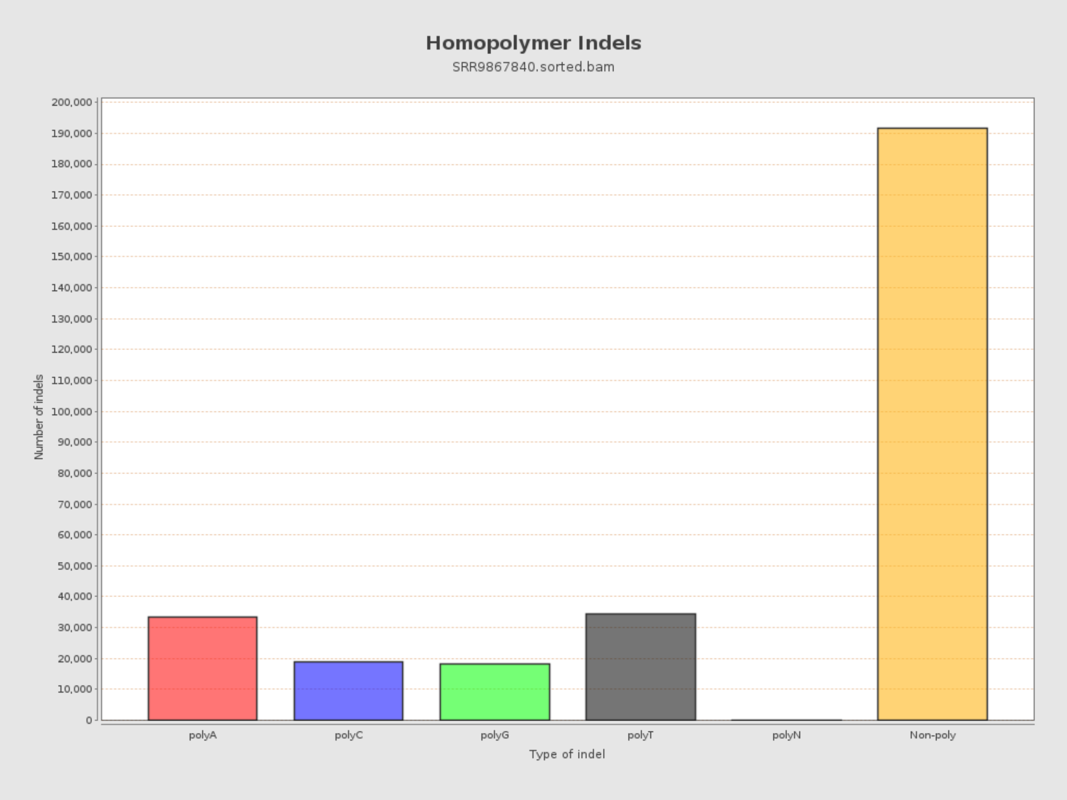
9. Results : Mapped Reads GC-content Distribution



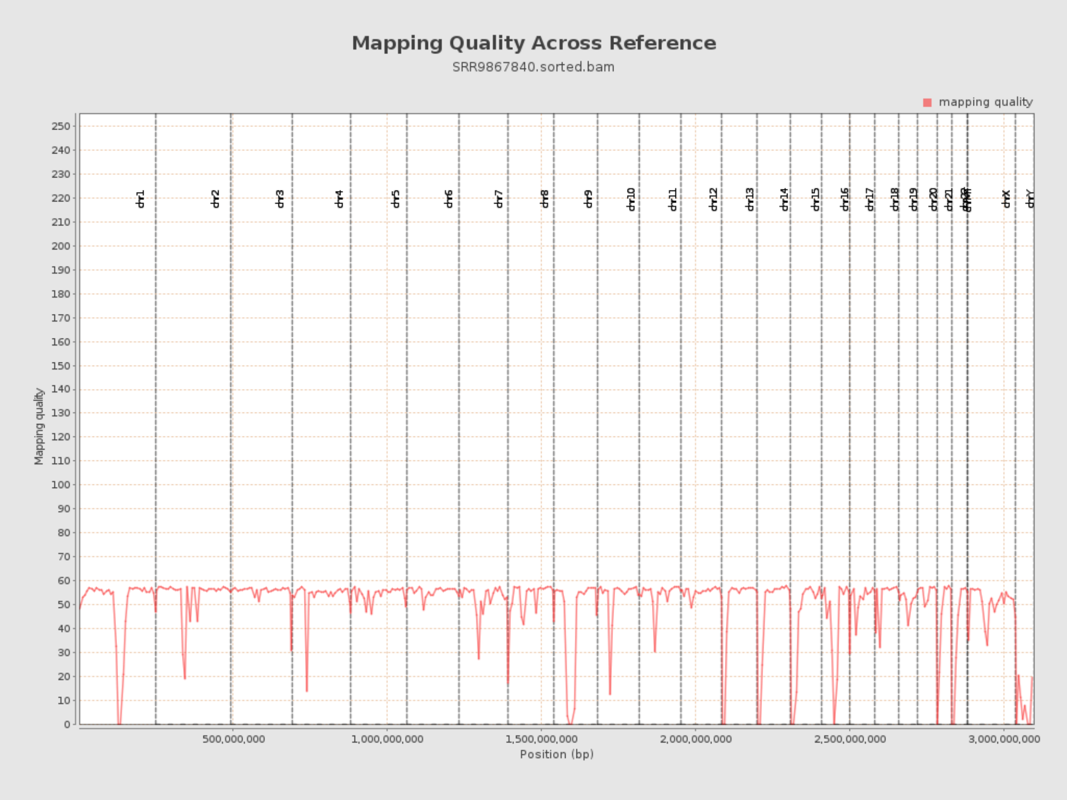
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram