Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 03:00:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080750.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_SRR3080750 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080750.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 03:00:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080750.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,160,262
Mapped reads	4,260,522 / 82.56%
Unmapped reads	899,740 / 17.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,579 / 0.48%
Read min/max/mean length	30 / 66 / 66.16
Duplicated reads (estimated)	499,410 / 9.68%
Duplication rate	9.08%
Clipped reads	637,842 / 12.36%

2.2. ACGT Content

Number/percentage of A's	79,931,096 / 29.4%
Number/percentage of C's	56,055,902 / 20.62%
Number/percentage of T's	76,278,532 / 28.06%
Number/percentage of G's	58,981,891 / 21.7%
Number/percentage of N's	620,610 / 0.23%
GC Percentage	42.31%

2.3. Coverage

Mean	0.0879

Standard Deviation	0.5565

2.4. Mapping Quality

Mean Mapping Quality	45.32

2.5. Mismatches and indels

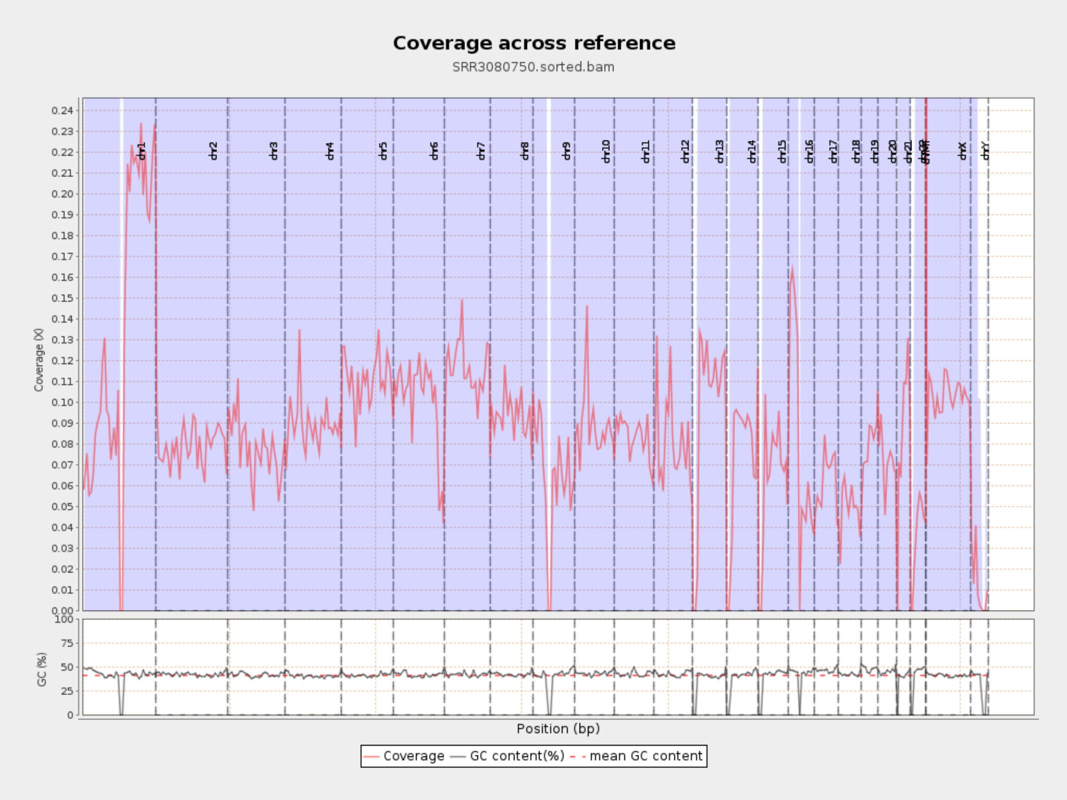
General error rate	1%
Mismatches	2,679,727
Insertions	18,346
Mapped reads with at least one insertion	0.43%
Deletions	48,021
Mapped reads with at least one deletion	1.12%
Homopolymer indels	44.37%

2.6. Chromosome stats

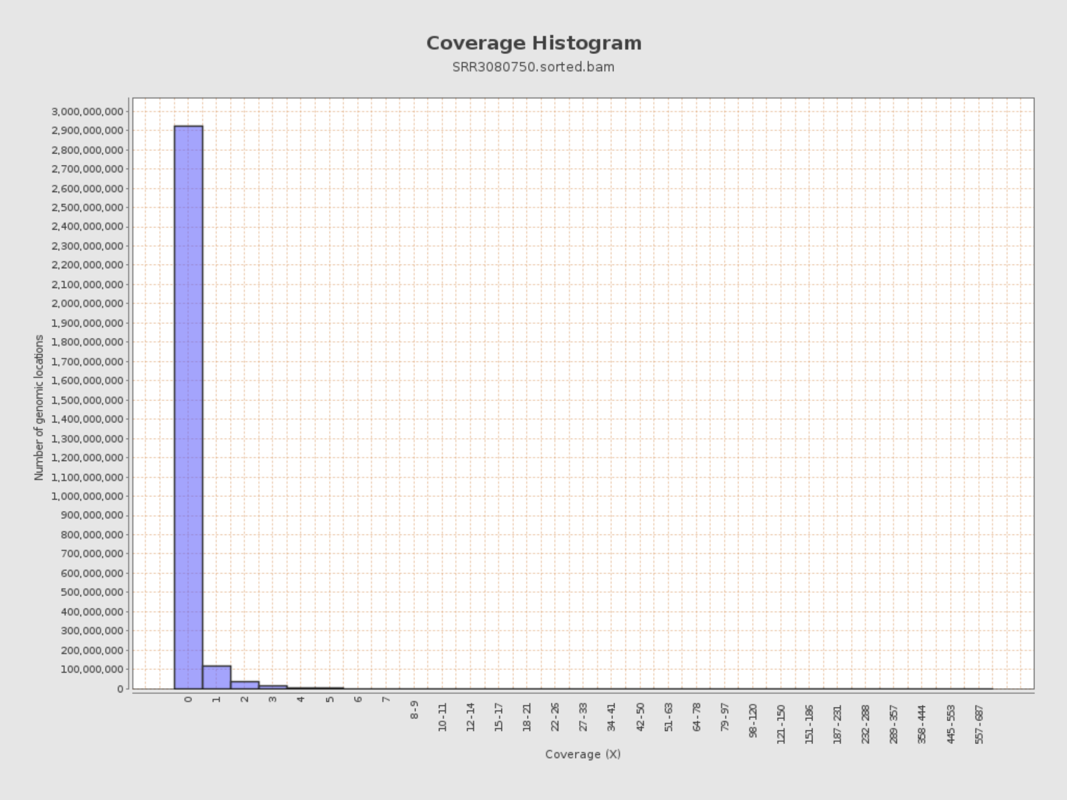
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33366635	0.1339	0.746
chr2	243199373	19324387	0.0795	0.5154
chr3	198022430	15401892	0.0778	0.4069
chr4	191154276	17134201	0.0896	0.4852
chr5	180915260	20025282	0.1107	0.4882
chr6	171115067	17469195	0.1021	0.6446
chr7	159138663	18519629	0.1164	0.8757

chr8	146364022	13710342	0.0937	0.6304
chr9	141213431	8963780	0.0635	0.4329
chr10	135534747	12081833	0.0891	0.7036
chr11	135006516	11255500	0.0834	0.5219
chr12	133851895	10919116	0.0816	0.4263
chr13	115169878	11273251	0.0979	0.4666
chr14	107349540	7766343	0.0723	0.4599
chr15	102531392	6442083	0.0628	0.367
chr16	90354753	7258423	0.0803	0.447
chr17	81195210	5162698	0.0636	0.3867
chr18	78077248	3858231	0.0494	0.6602
chr19	59128983	4707905	0.0796	0.6862
chr20	63025520	4532578	0.0719	0.4172
chr21	48129895	4199262	0.0872	0.5348
chr22	51304566	1808709	0.0353	0.2741
chrMT	16571	108754	6.5629	5.5238
chrX	155270560	15924398	0.1026	0.4945
chrY	59373566	742461	0.0125	0.3031

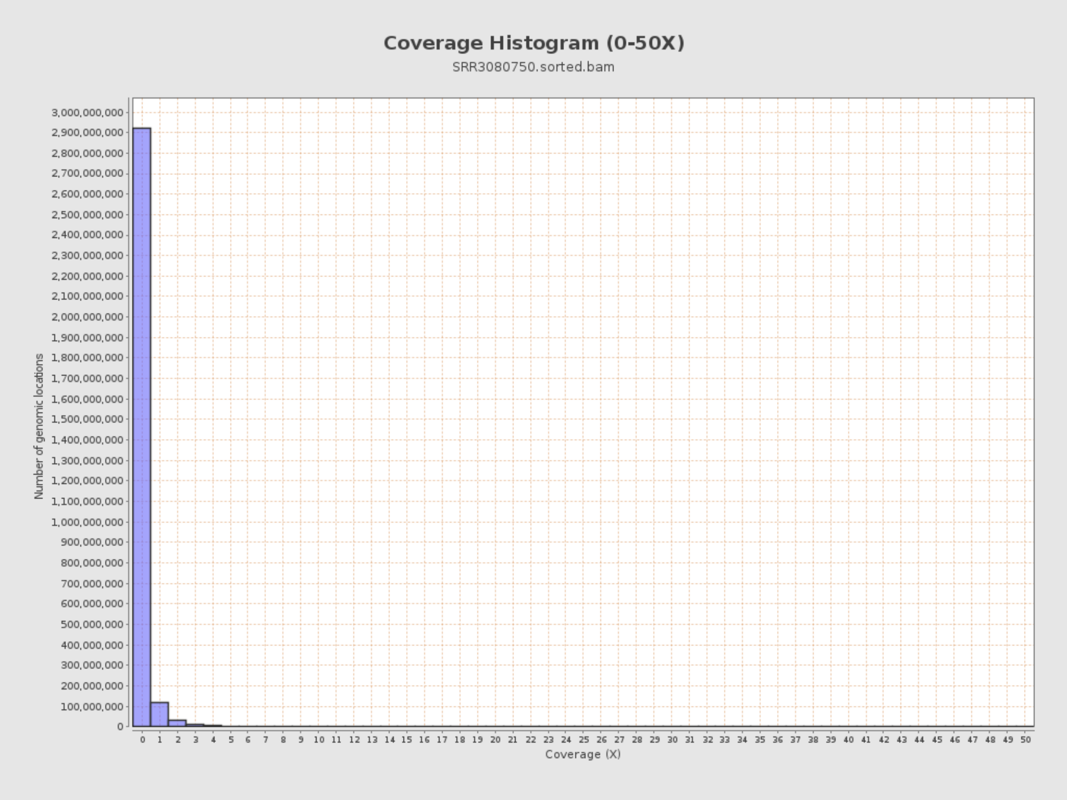
3. Results : Coverage across reference



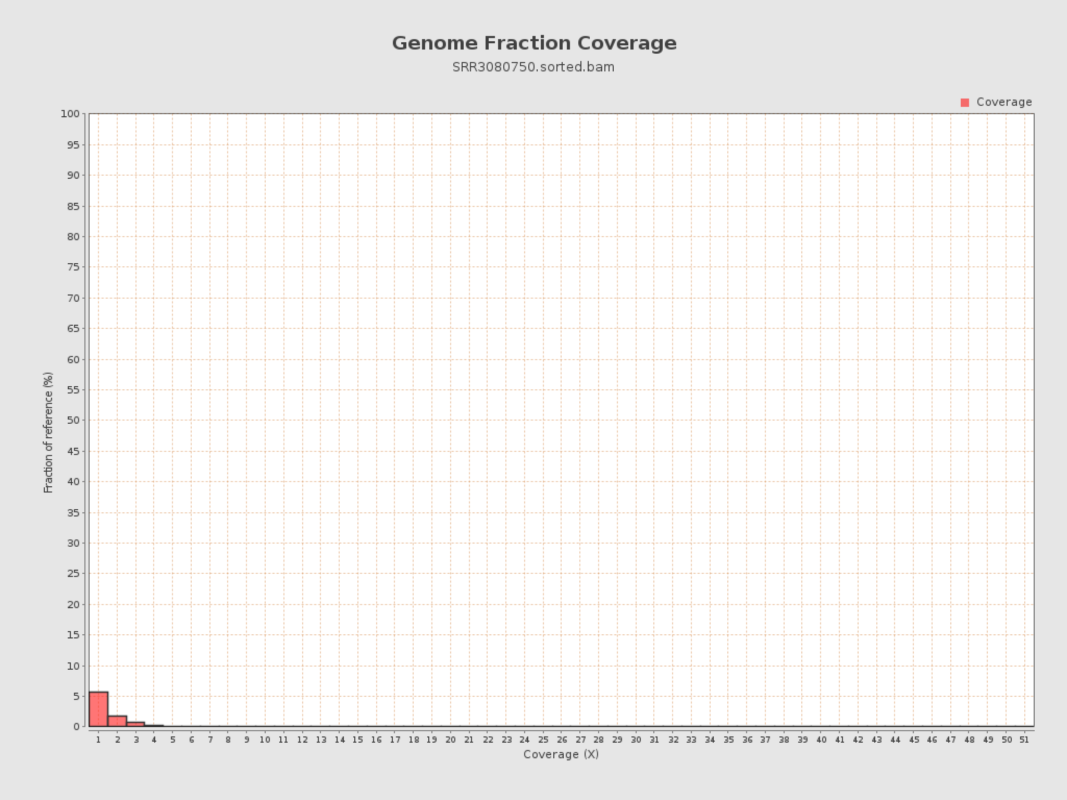
4. Results : Coverage Histogram



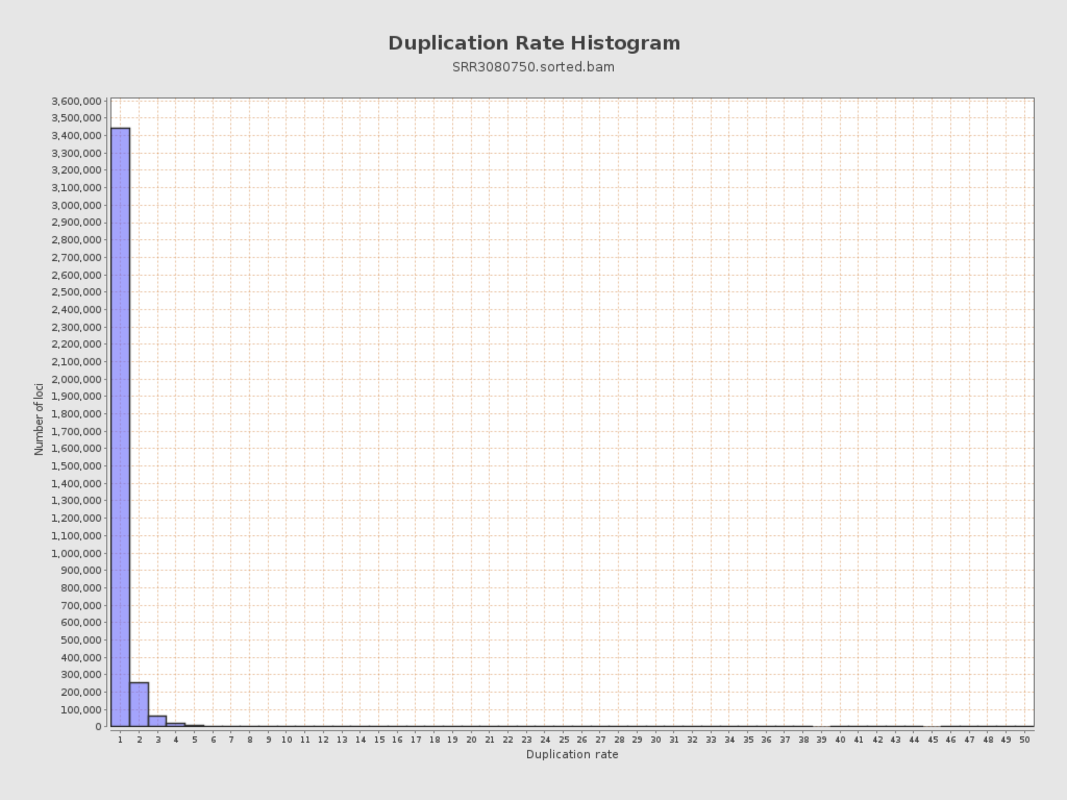
5. Results : Coverage Histogram (0-50X)



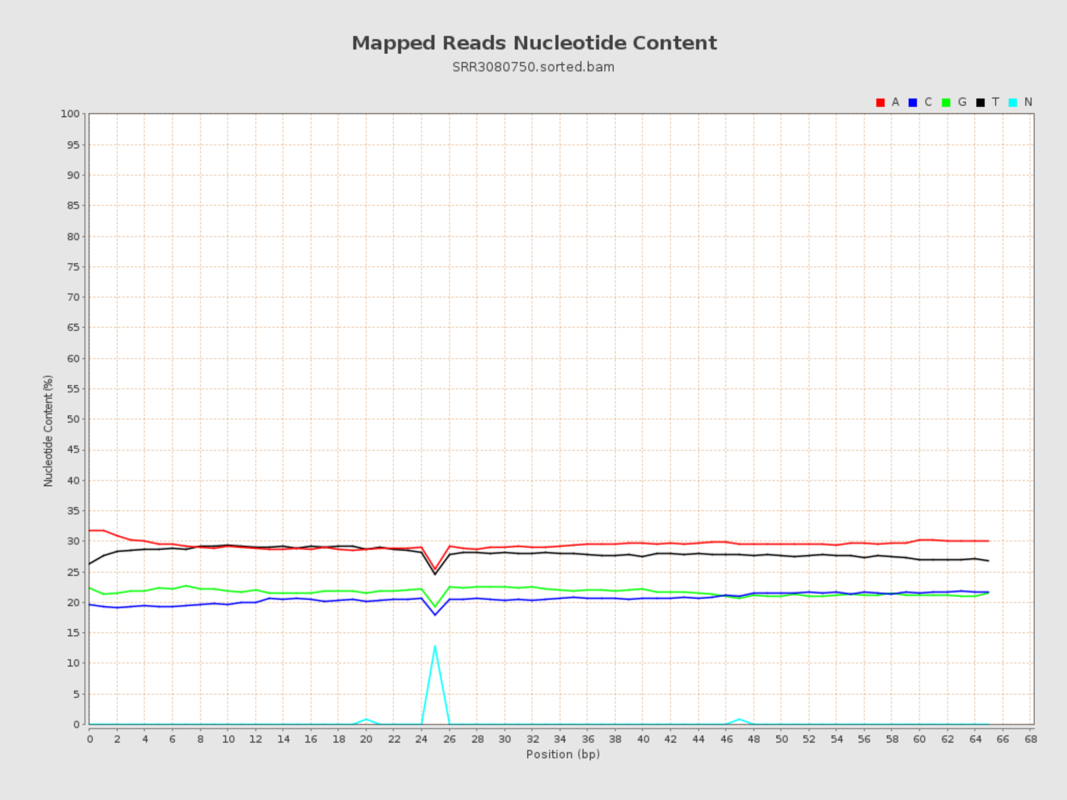
6. Results : Genome Fraction Coverage



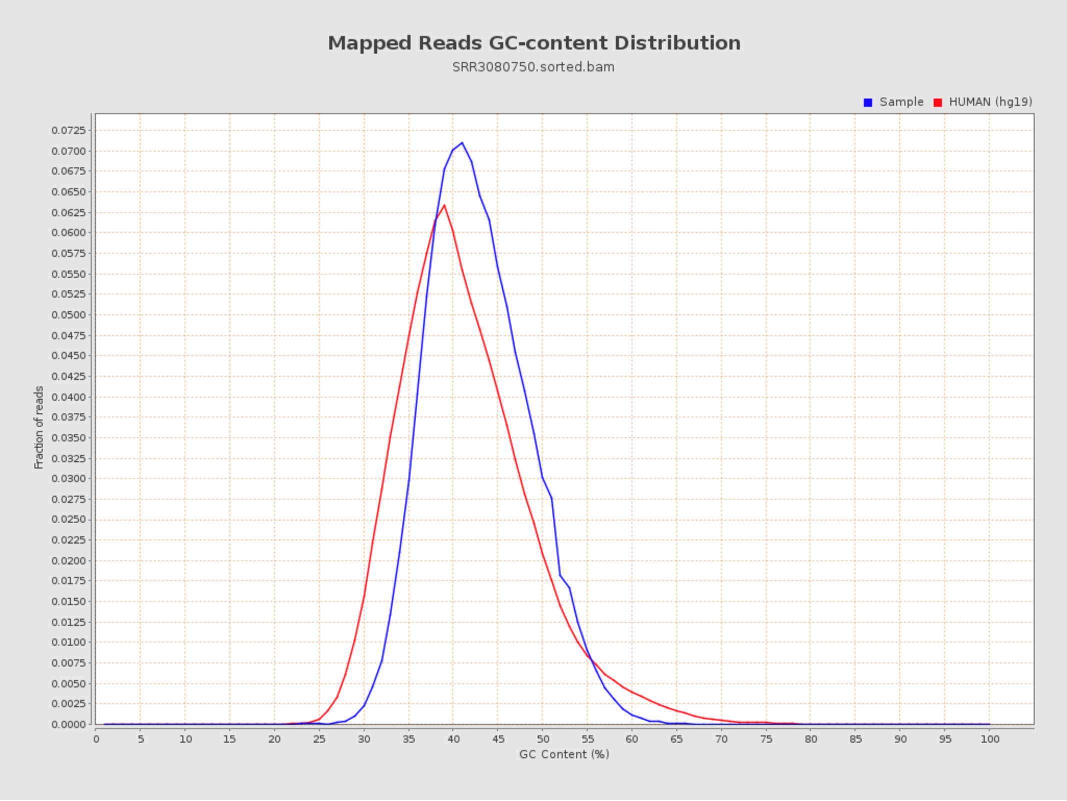
7. Results : Duplication Rate Histogram



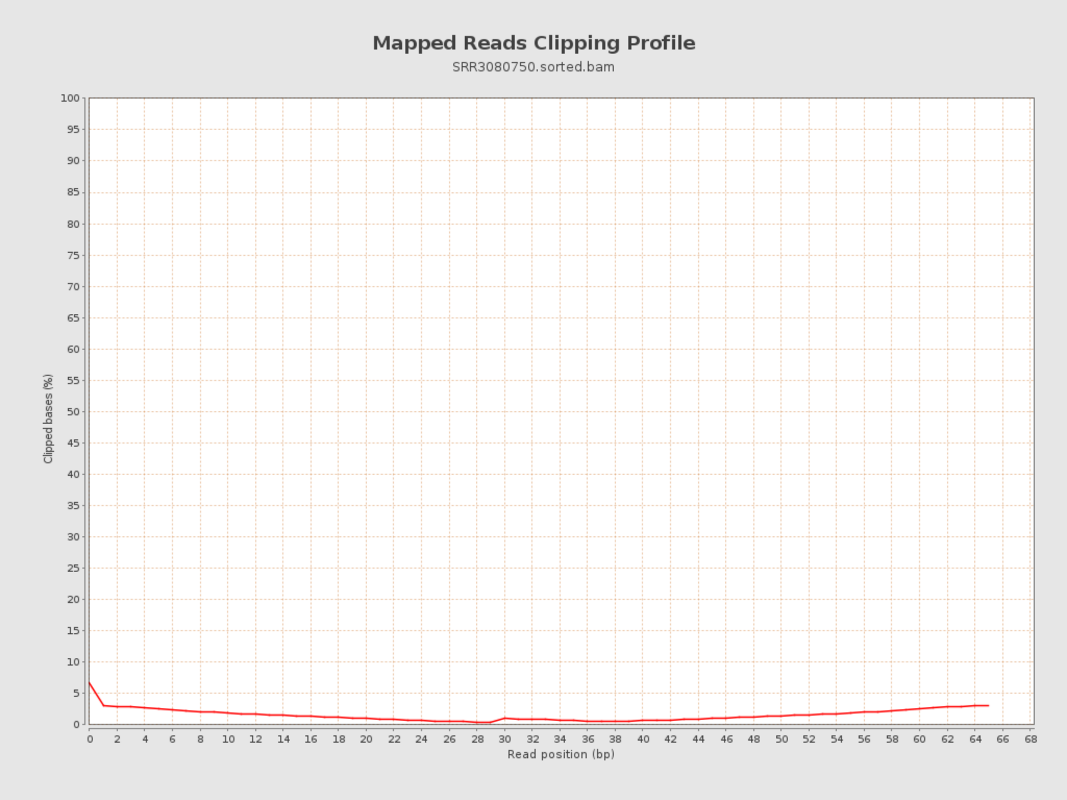
8. Results : Mapped Reads Nucleotide Content



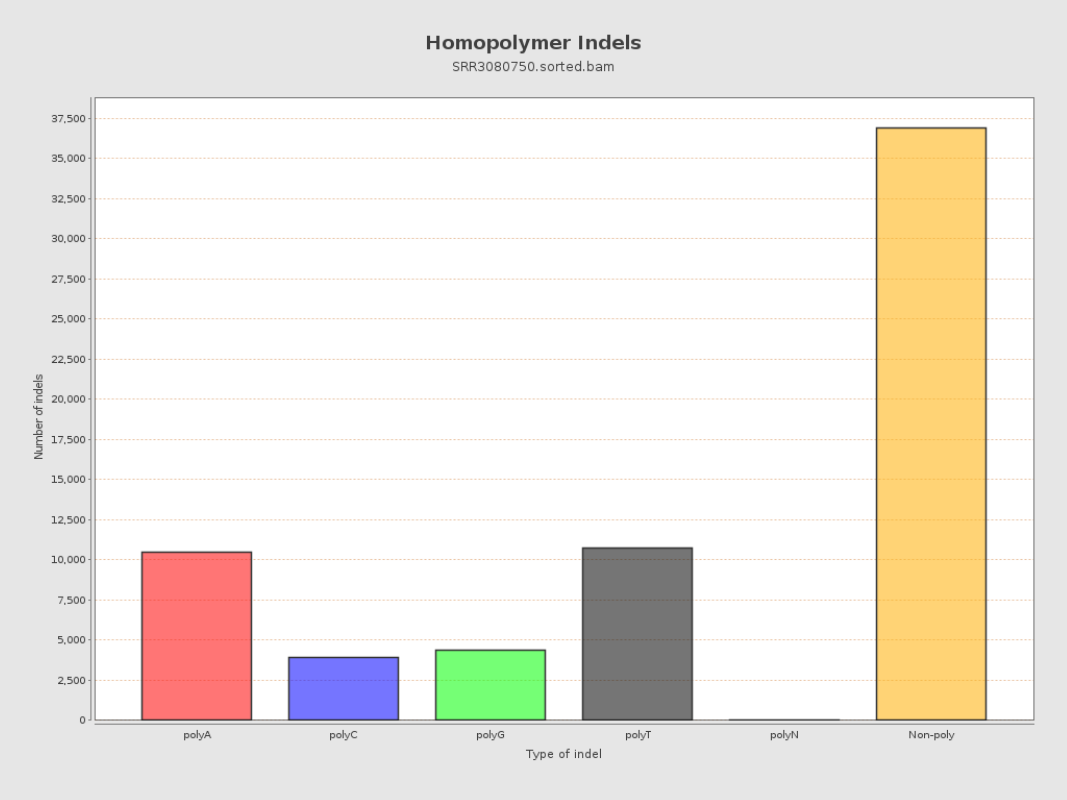
9. Results : Mapped Reads GC-content Distribution



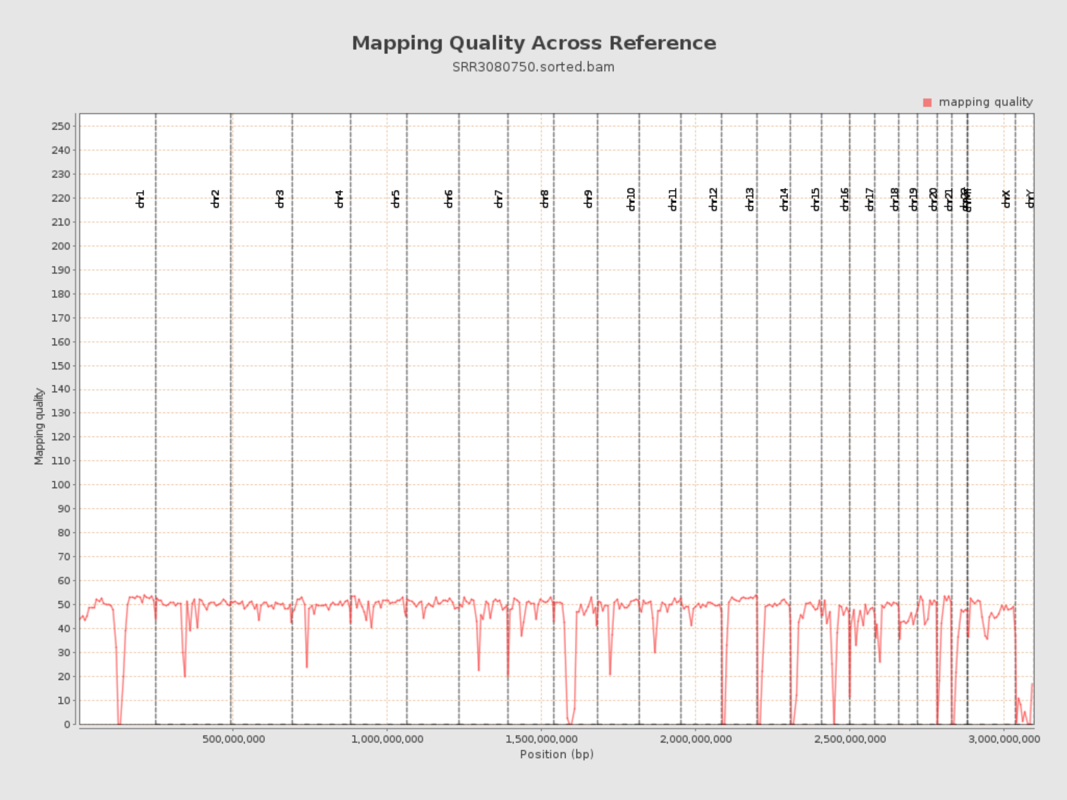
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram