Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 03:12:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080752.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_SRR3080752 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080752.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 03:12:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080752.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,344,035
Mapped reads	4,708,278 / 74.22%
Unmapped reads	1,635,757 / 25.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,551 / 0.47%
Read min/max/mean length	30 / 66 / 66.15
Duplicated reads (estimated)	479,715 / 7.56%
Duplication rate	8.16%
Clipped reads	1,021,773 / 16.11%

2.2. ACGT Content

Number/percentage of A's	88,823,276 / 30.16%
Number/percentage of C's	60,456,030 / 20.53%
Number/percentage of T's	78,804,169 / 26.76%
Number/percentage of G's	65,746,771 / 22.33%
Number/percentage of N's	649,224 / 0.22%
GC Percentage	42.86%

2.3. Coverage

Mean	0.0952

Standard Deviation	0.6624

2.4. Mapping Quality

Mean Mapping Quality	43.78

2.5. Mismatches and indels

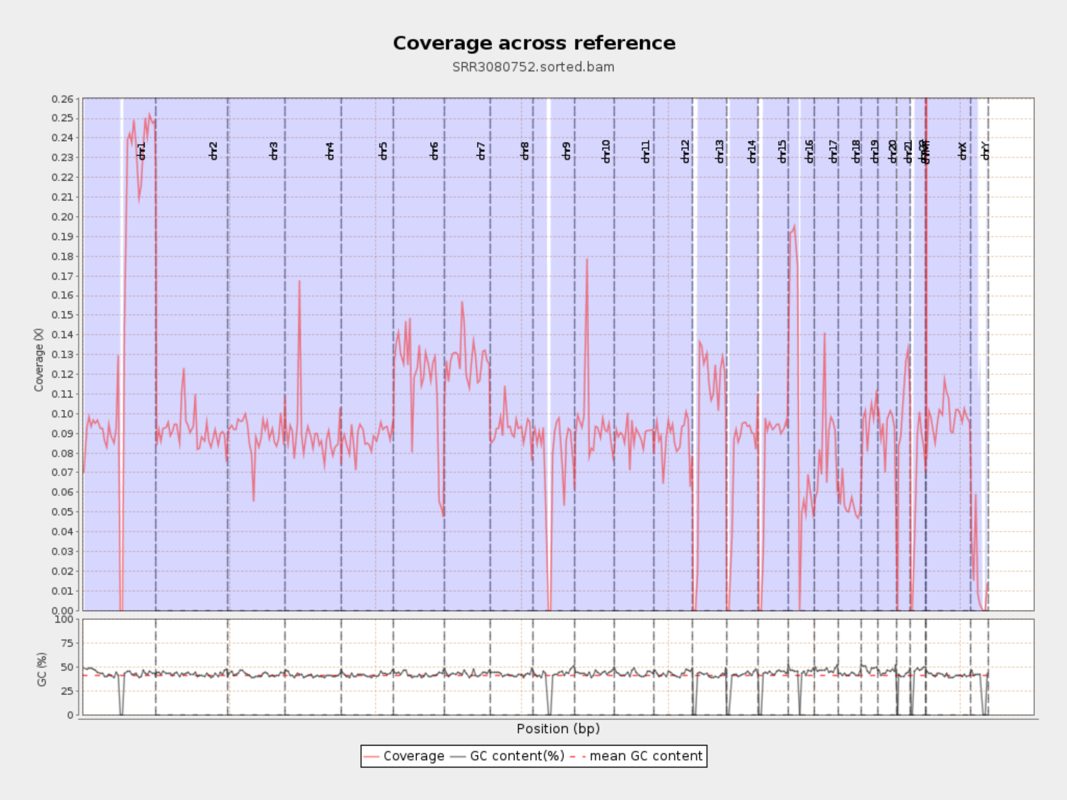
General error rate	1.08%
Mismatches	3,138,748
Insertions	22,497
Mapped reads with at least one insertion	0.47%
Deletions	52,556
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.28%

2.6. Chromosome stats

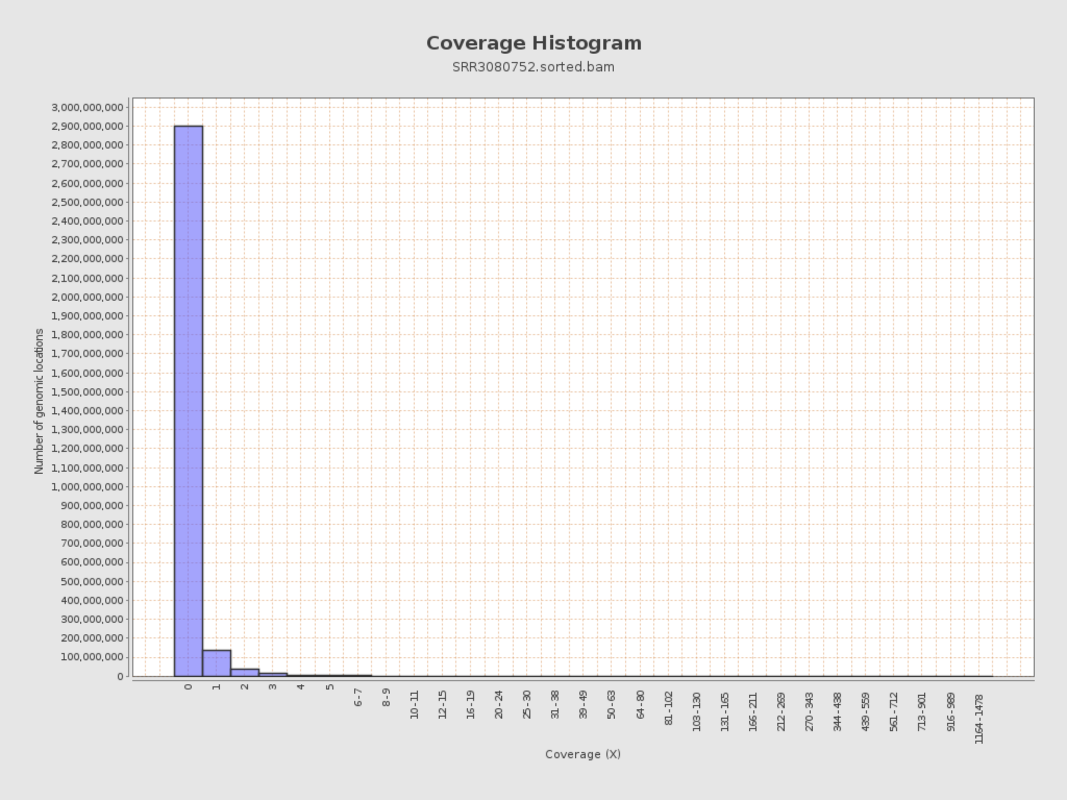
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	37037581	0.1486	0.9575
chr2	243199373	22309334	0.0917	0.6208
chr3	198022430	17743705	0.0896	0.4261
chr4	191154276	17278212	0.0904	0.5541
chr5	180915260	15900370	0.0879	0.4184
chr6	171115067	20078387	0.1173	0.9447
chr7	159138663	20291257	0.1275	1.0272

chr8	146364022	13507172	0.0923	0.6936
chr9	141213431	10520593	0.0745	0.5089
chr10	135534747	12928143	0.0954	0.8526
chr11	135006516	11995262	0.0888	0.6045
chr12	133851895	11722198	0.0876	0.4353
chr13	115169878	11632869	0.101	0.456
chr14	107349540	8091352	0.0754	0.4594
chr15	102531392	7752652	0.0756	0.3922
chr16	90354753	9035181	0.1	0.5183
chr17	81195210	6842038	0.0843	0.4465
chr18	78077248	4234452	0.0542	0.9366
chr19	59128983	5737522	0.097	0.8969
chr20	63025520	5747637	0.0912	0.4699
chr21	48129895	4738853	0.0985	0.5903
chr22	51304566	3208695	0.0625	0.364
chrMT	16571	43604	2.6313	2.6616
chrX	155270560	15244091	0.0982	0.4902
chrY	59373566	956113	0.0161	0.4721

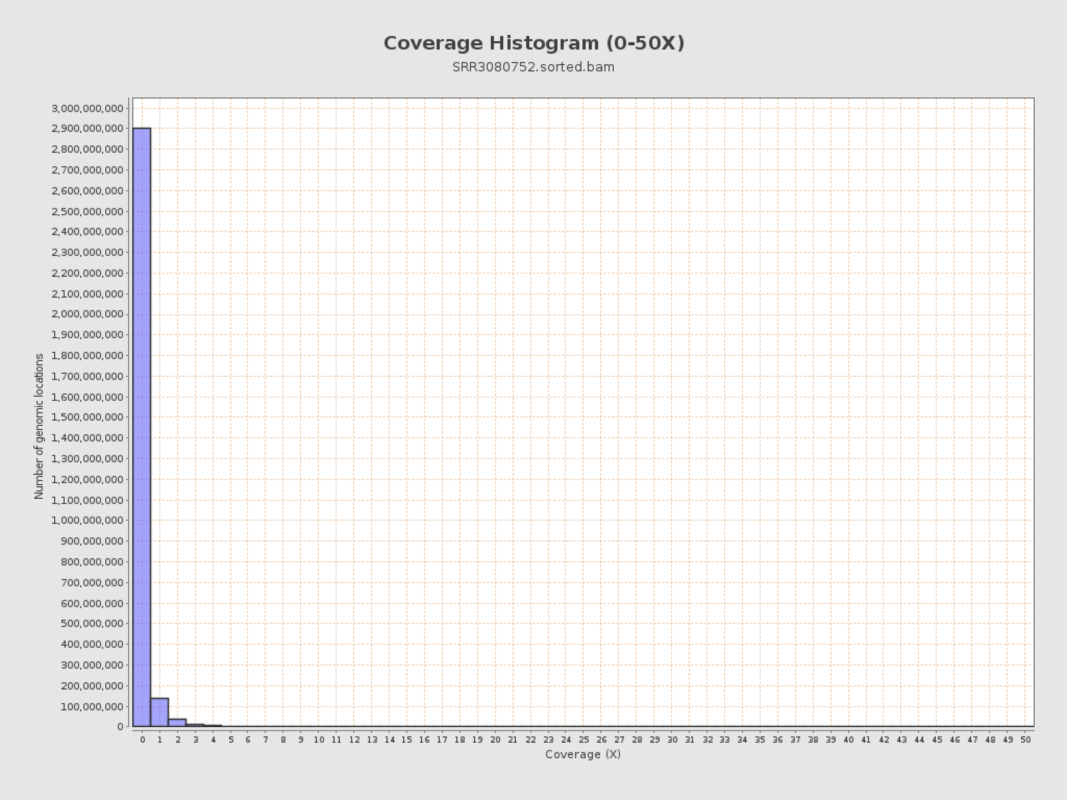
3. Results : Coverage across reference



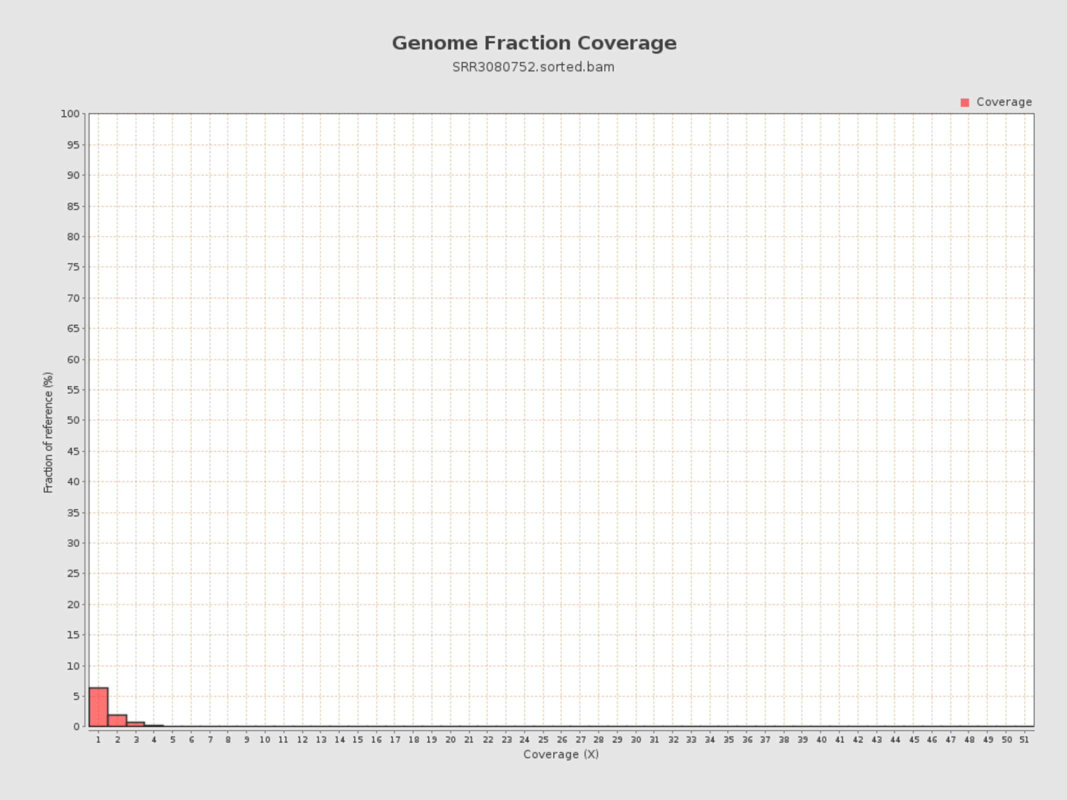
4. Results : Coverage Histogram



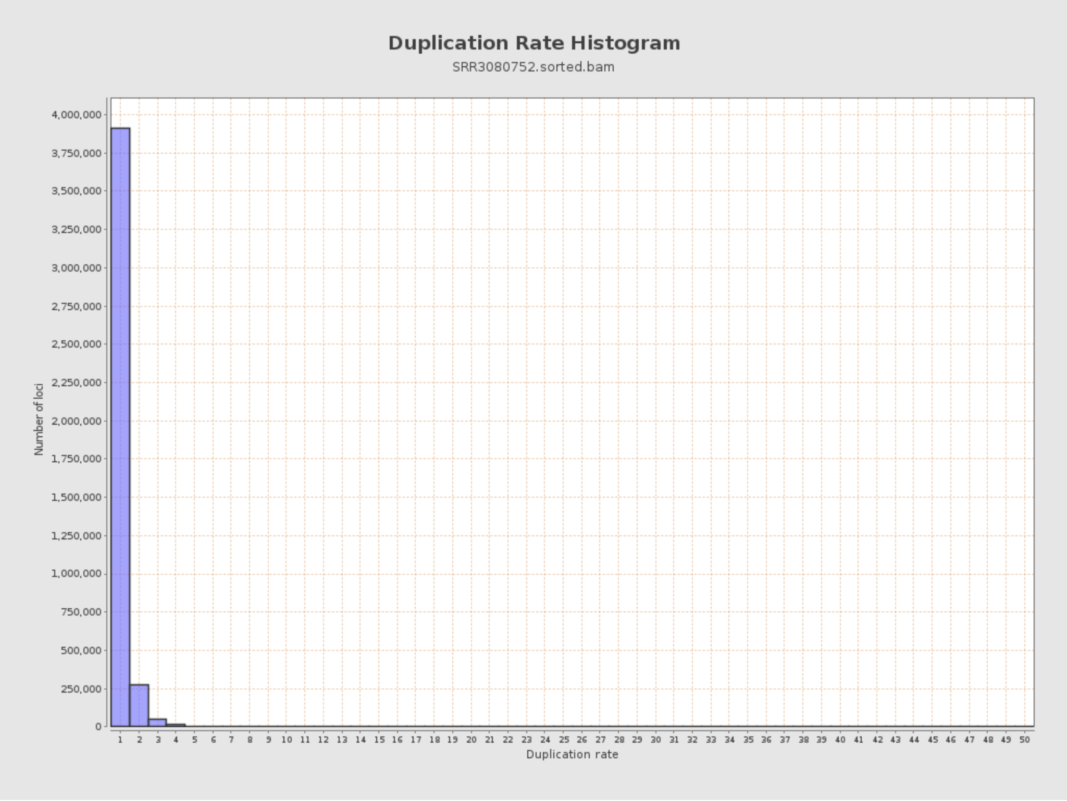
5. Results : Coverage Histogram (0-50X)



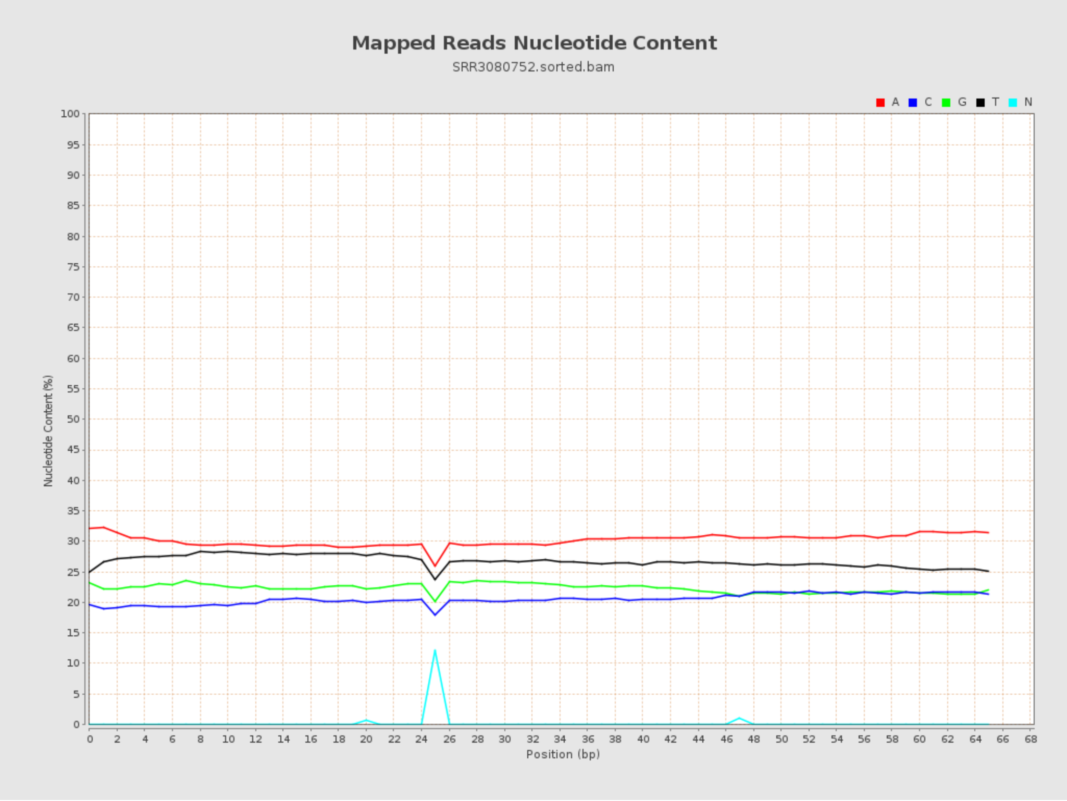
6. Results : Genome Fraction Coverage



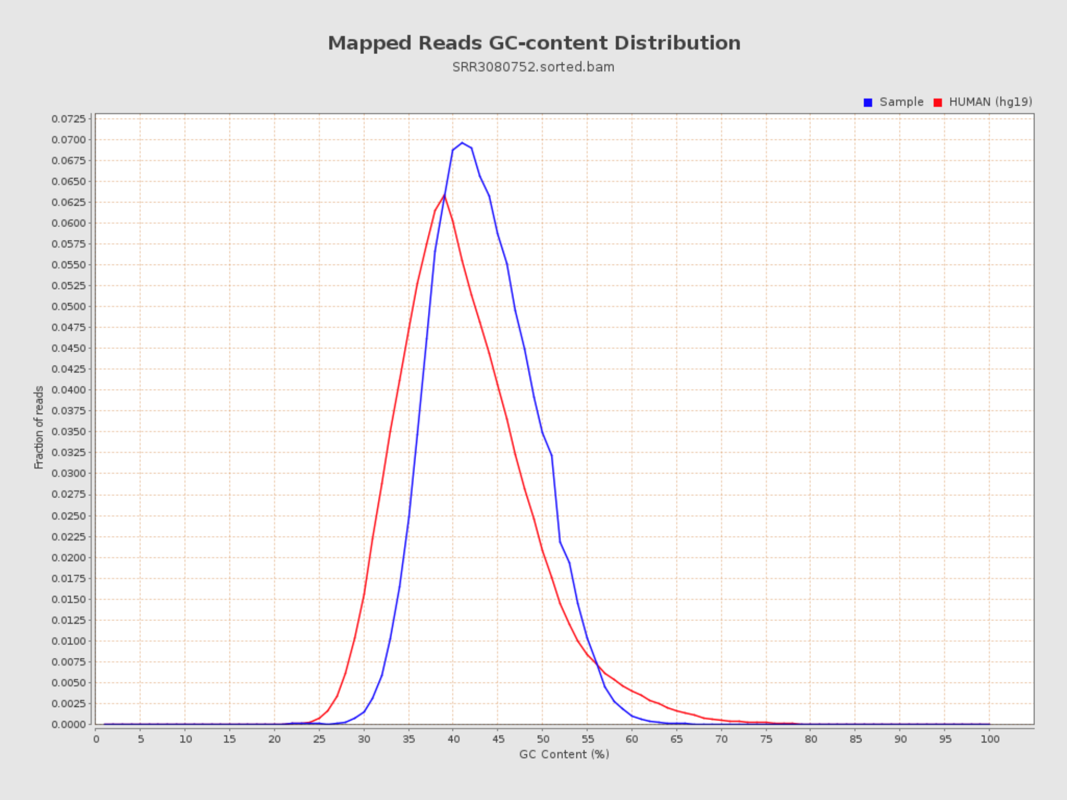
7. Results : Duplication Rate Histogram



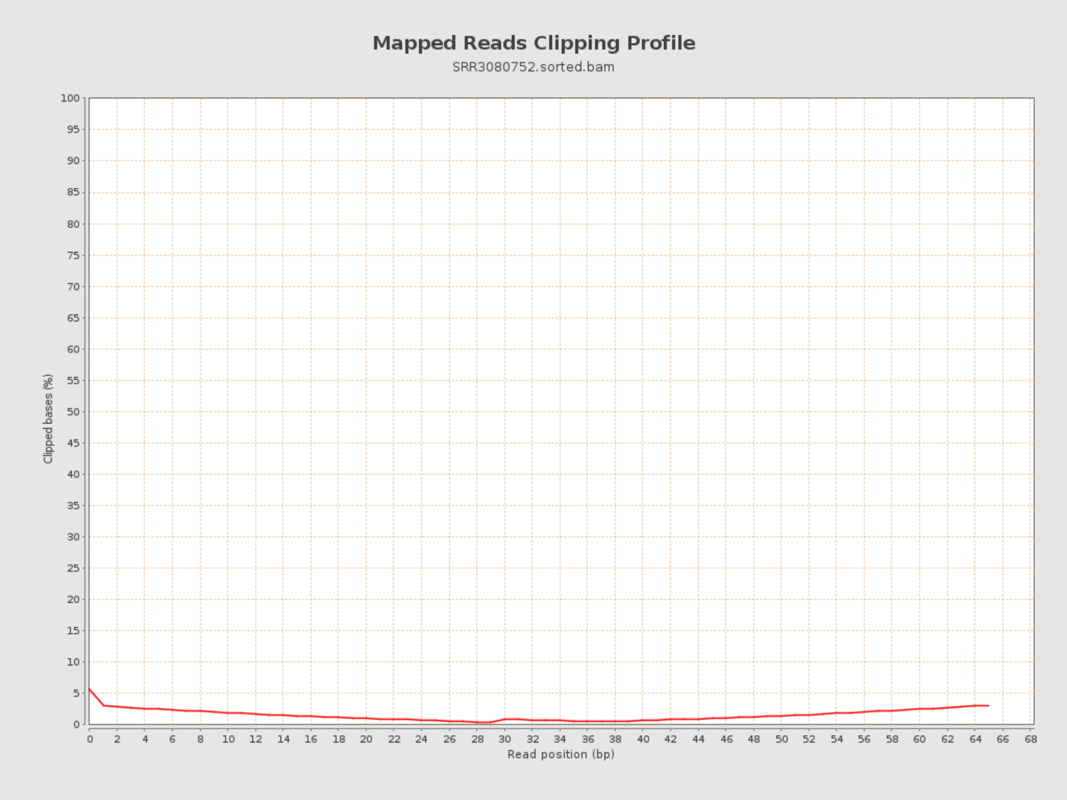
8. Results : Mapped Reads Nucleotide Content



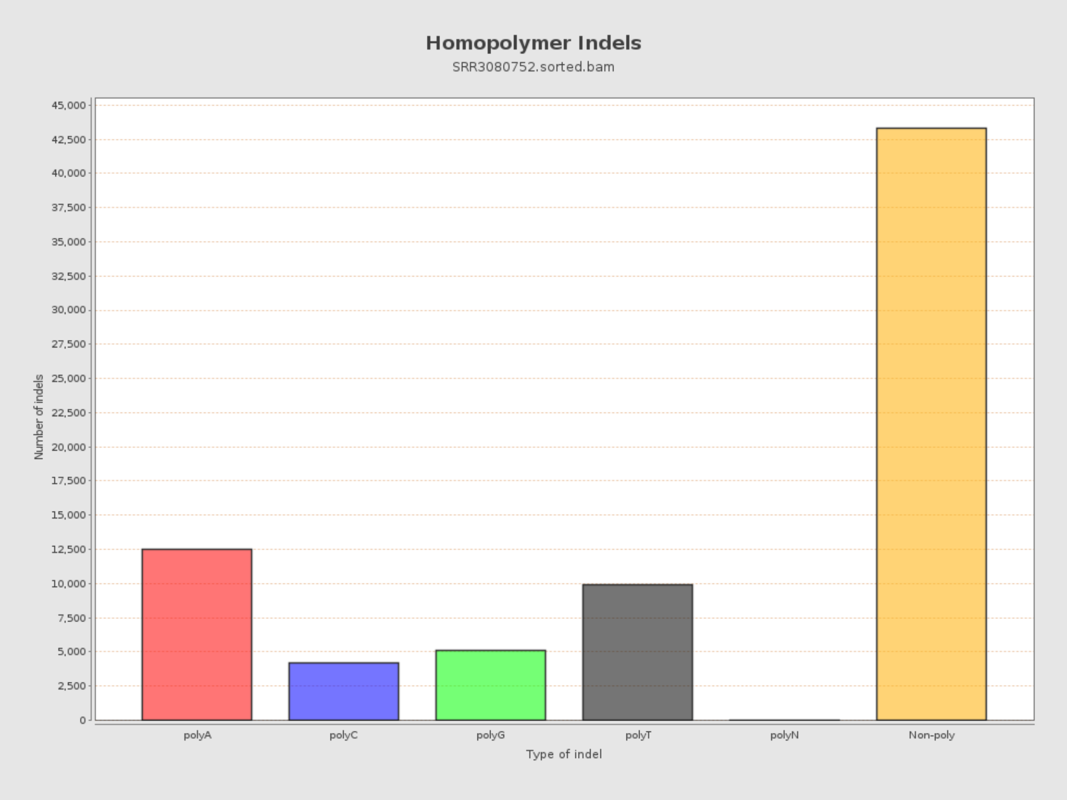
9. Results : Mapped Reads GC-content Distribution



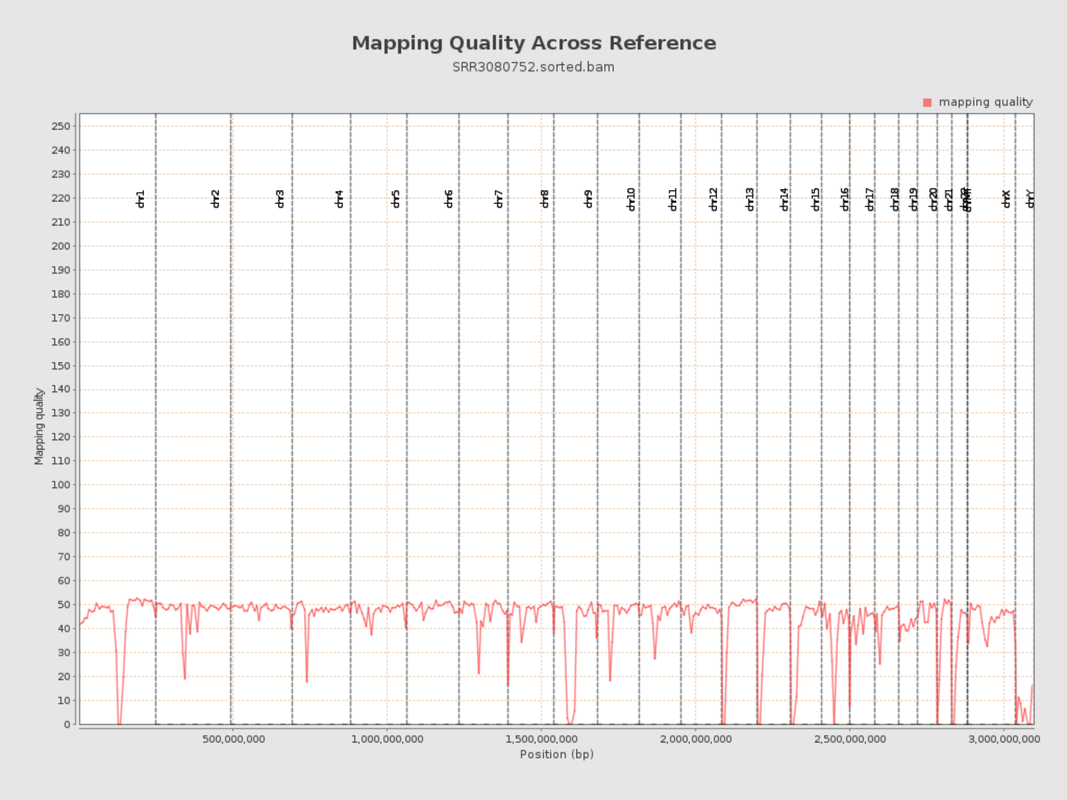
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram