Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 04:35:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089753.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_SRR089753 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089753.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 04:35:43 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089753.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	30,131,967
Mapped reads	25,449,443 / 84.46%
Unmapped reads	4,682,524 / 15.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,341 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	5,647,778 / 18.74%
Duplication rate	13.21%
Clipped reads	1,880,297 / 6.24%

2.2. ACGT Content

Number/percentage of A's	360,985,974 / 30%
Number/percentage of C's	242,155,896 / 20.12%
Number/percentage of T's	341,563,447 / 28.38%
Number/percentage of G's	258,550,948 / 21.48%
Number/percentage of N's	173,315 / 0.01%
GC Percentage	41.61%

2.3. Coverage

Mean	0.3888

Standard Deviation	2.5245

2.4. Mapping Quality

Mean Mapping Quality	45.16

2.5. Mismatches and indels

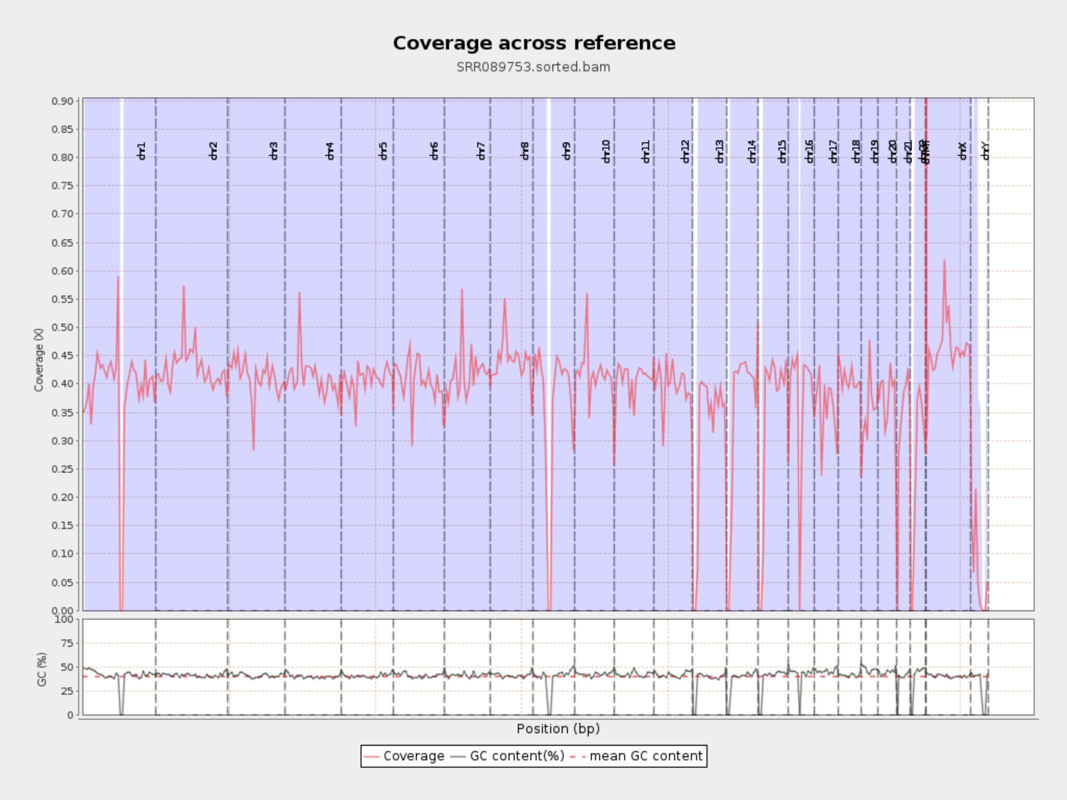
General error rate	0.4%
Mismatches	4,788,010
Insertions	44,574
Mapped reads with at least one insertion	0.17%
Deletions	142,795
Mapped reads with at least one deletion	0.56%
Homopolymer indels	47.11%

2.6. Chromosome stats

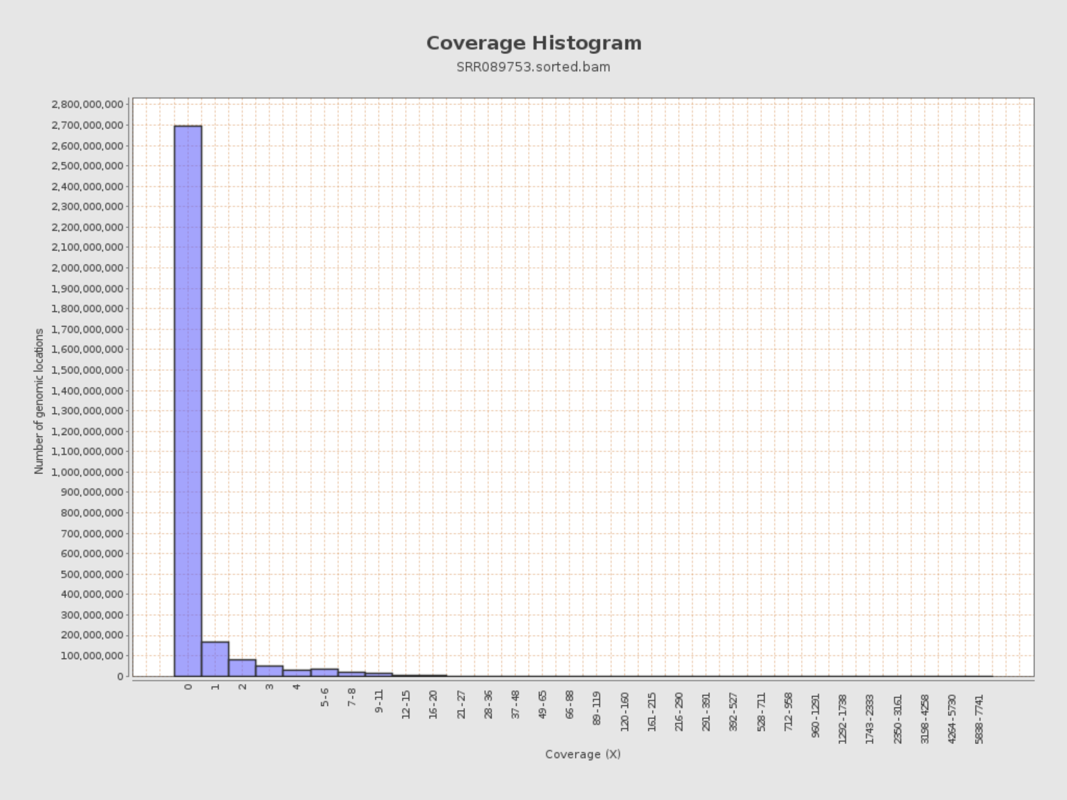
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	96114197	0.3856	4.639
chr2	243199373	104516658	0.4298	2.3331
chr3	198022430	81465454	0.4114	1.5338
chr4	191154276	79077626	0.4137	1.7208
chr5	180915260	73762760	0.4077	1.5319
chr6	171115067	69619822	0.4069	1.7104
chr7	159138663	66385113	0.4172	3.0844

chr8	146364022	64677500	0.4419	4.4144
chr9	141213431	50995900	0.3611	2.1791
chr10	135534747	56971068	0.4203	2.2824
chr11	135006516	54946055	0.407	2.2921
chr12	133851895	53228721	0.3977	1.6088
chr13	115169878	35858132	0.3113	1.3317
chr14	107349540	37582819	0.3501	1.5048
chr15	102531392	34267943	0.3342	1.3812
chr16	90354753	33063459	0.3659	1.5766
chr17	81195210	29132509	0.3588	1.7652
chr18	78077248	31952170	0.4092	4.3205
chr19	59128983	21012242	0.3554	3.1526
chr20	63025520	23885927	0.379	1.5984
chr21	48129895	15812339	0.3285	1.7165
chr22	51304566	12915559	0.2517	1.188
chrMT	16571	606472	36.5984	25.8119
chrX	155270560	71866431	0.4628	1.8891
chrY	59373566	3928593	0.0662	1.5753

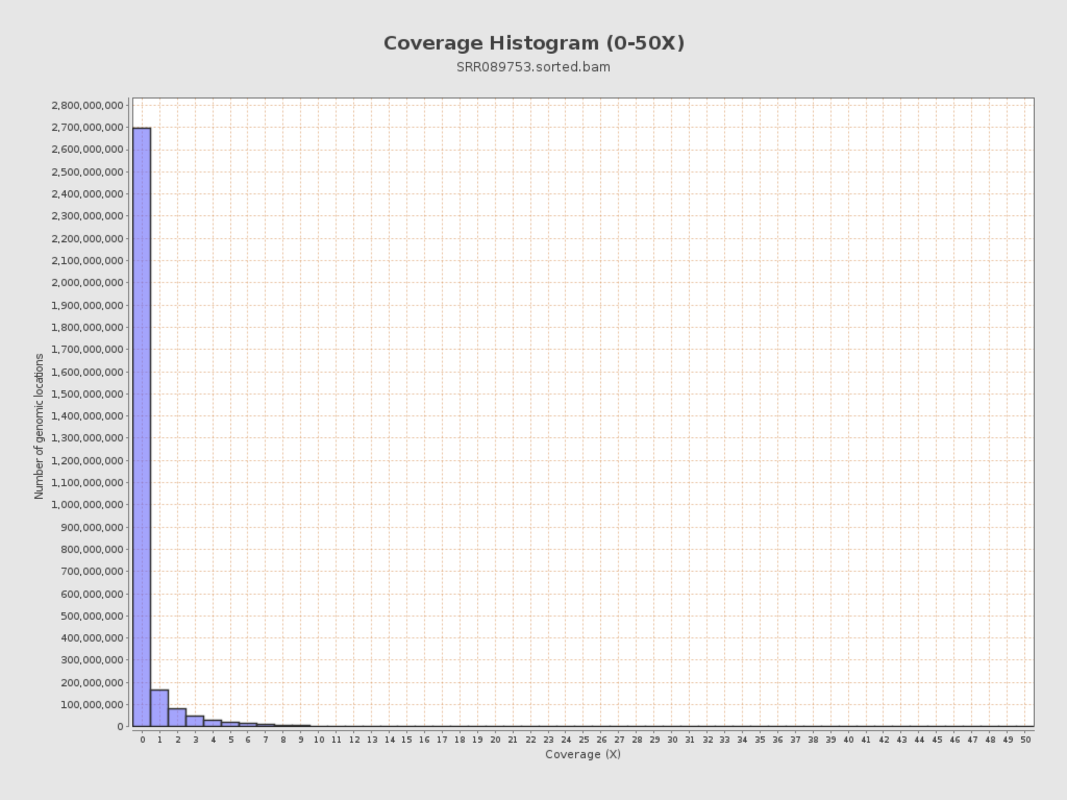
3. Results : Coverage across reference



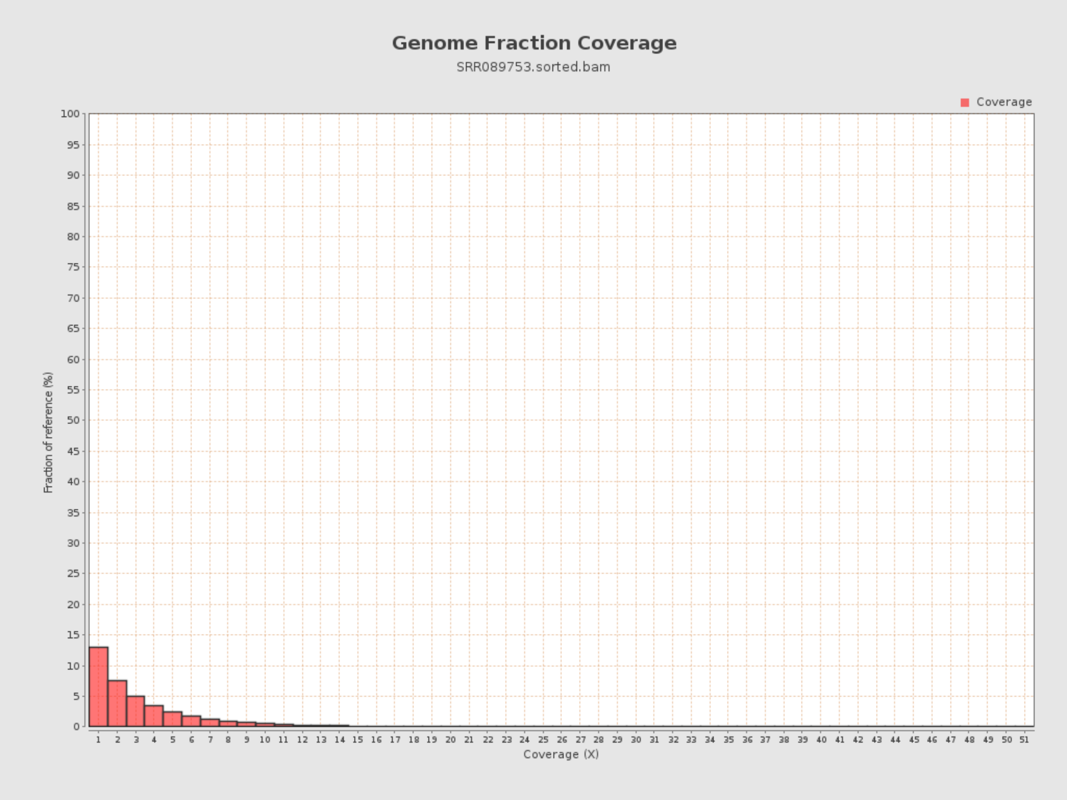
4. Results : Coverage Histogram



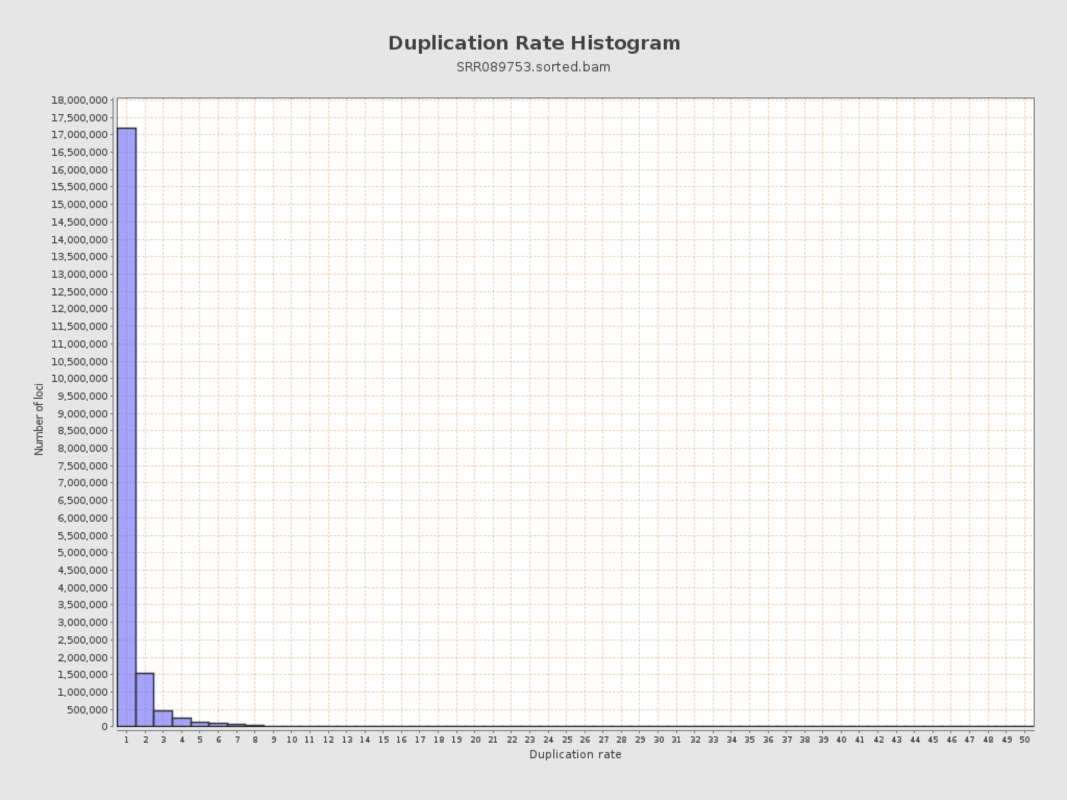
5. Results : Coverage Histogram (0-50X)



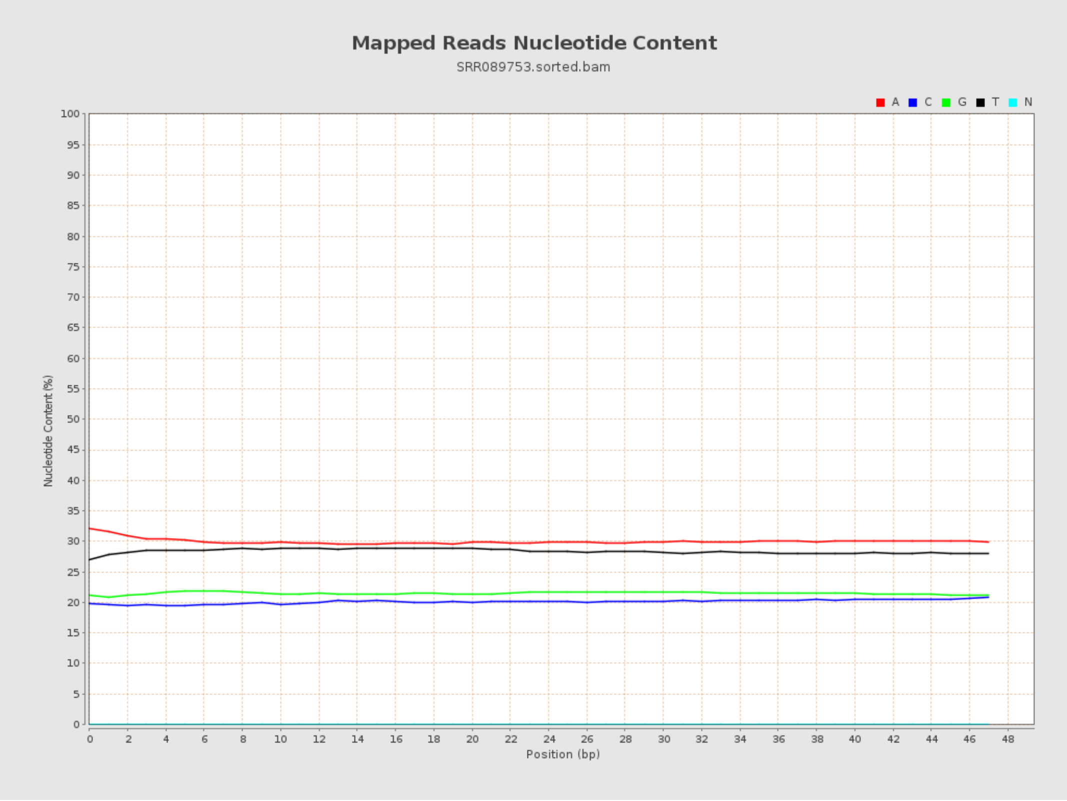
6. Results : Genome Fraction Coverage



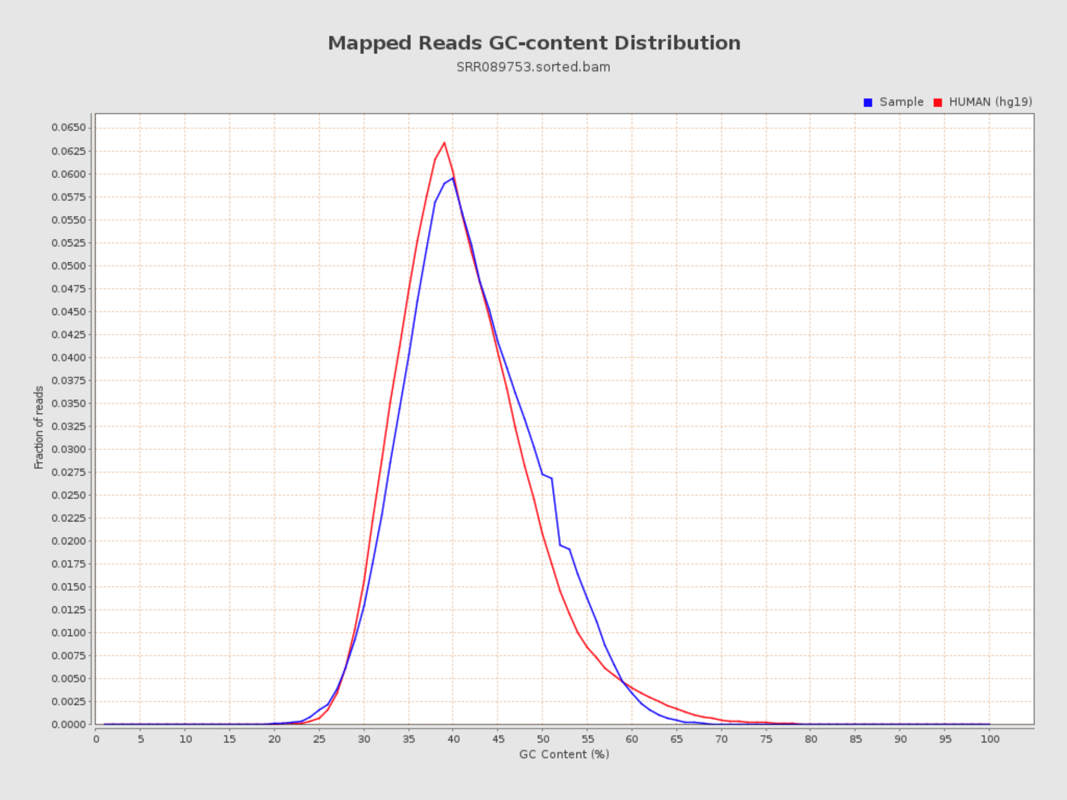
7. Results : Duplication Rate Histogram



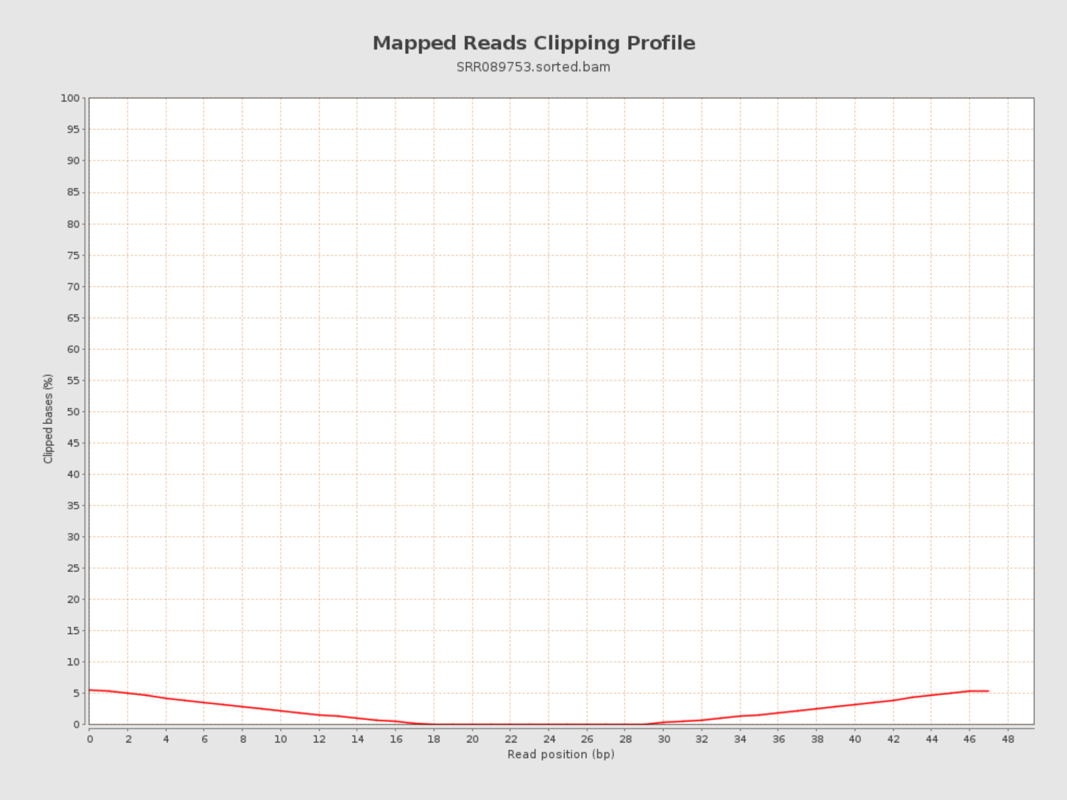
8. Results : Mapped Reads Nucleotide Content



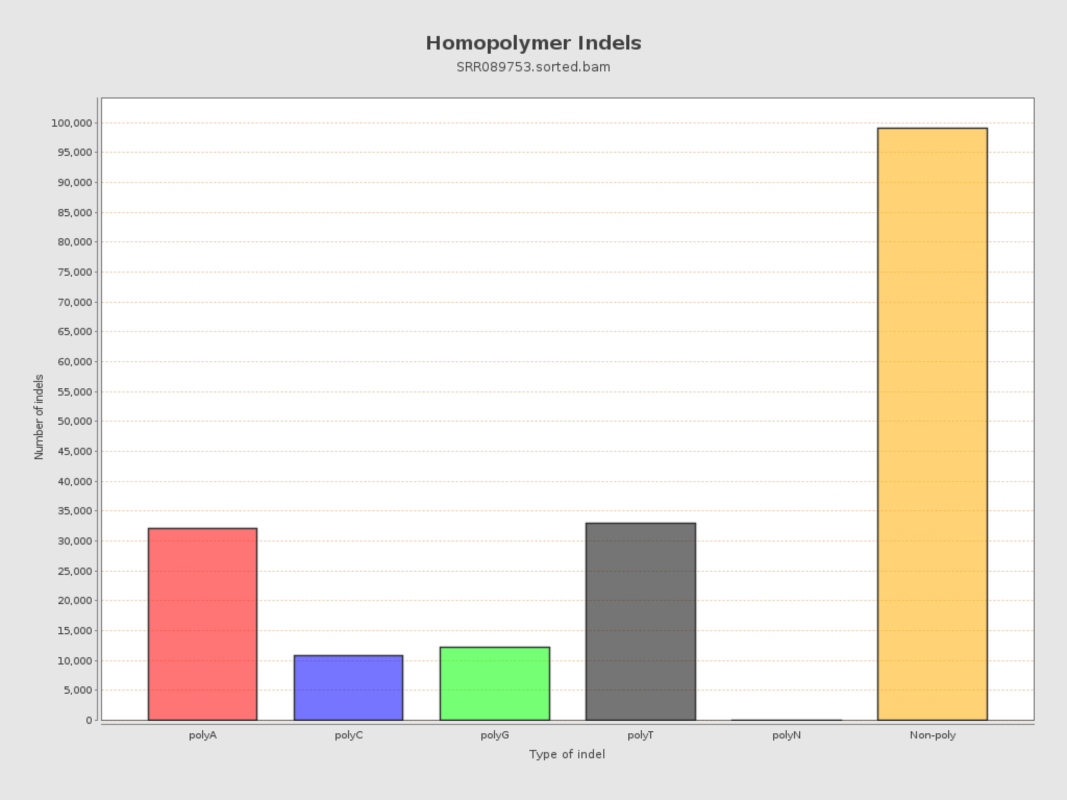
9. Results : Mapped Reads GC-content Distribution



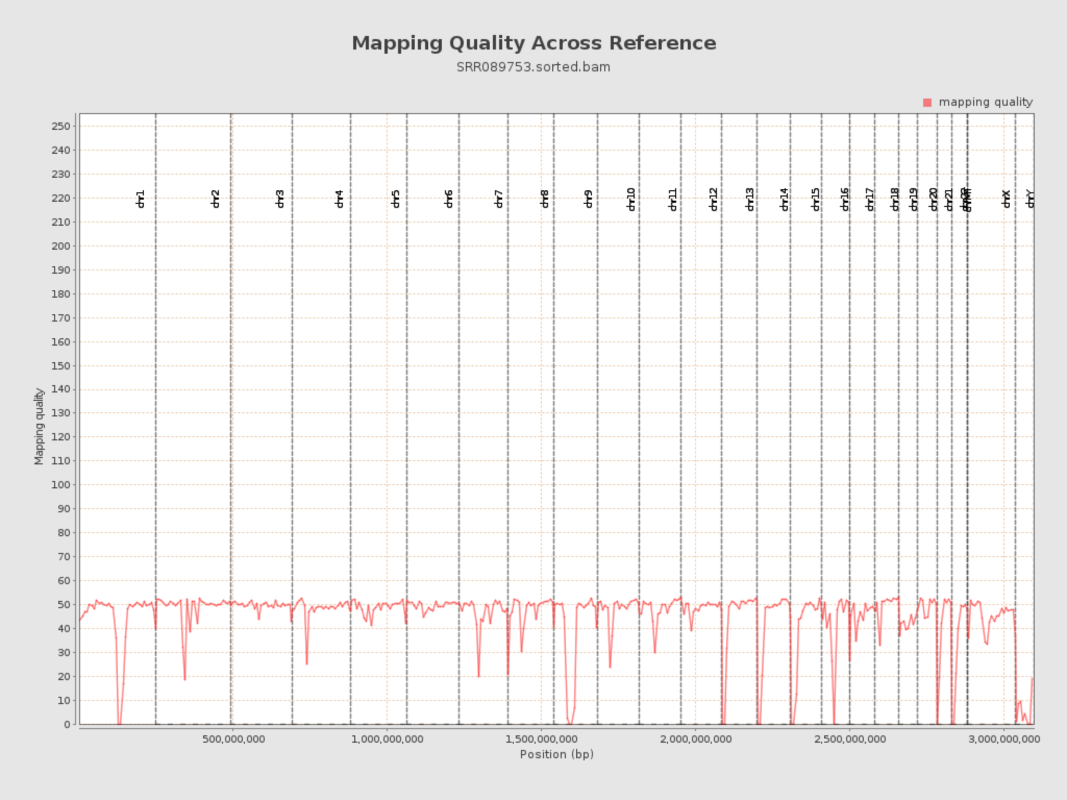
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram