Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 22:40:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089707.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_SRR089707 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089707.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 22:40:26 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089707.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,714,027
Mapped reads	19,357,478 / 93.45%
Unmapped reads	1,356,549 / 6.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	152,149 / 0.73%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	5,897,992 / 28.47%
Duplication rate	17.91%
Clipped reads	9,716,413 / 46.91%

2.2. ACGT Content

Number/percentage of A's	326,733,818 / 25.98%
Number/percentage of C's	229,318,586 / 18.24%
Number/percentage of T's	399,507,493 / 31.77%
Number/percentage of G's	301,839,820 / 24%
Number/percentage of N's	59,313 / 0%
GC Percentage	42.24%

2.3. Coverage

Mean	0.4063

Standard Deviation	2.6465

2.4. Mapping Quality

Mean Mapping Quality	46.99

2.5. Mismatches and indels

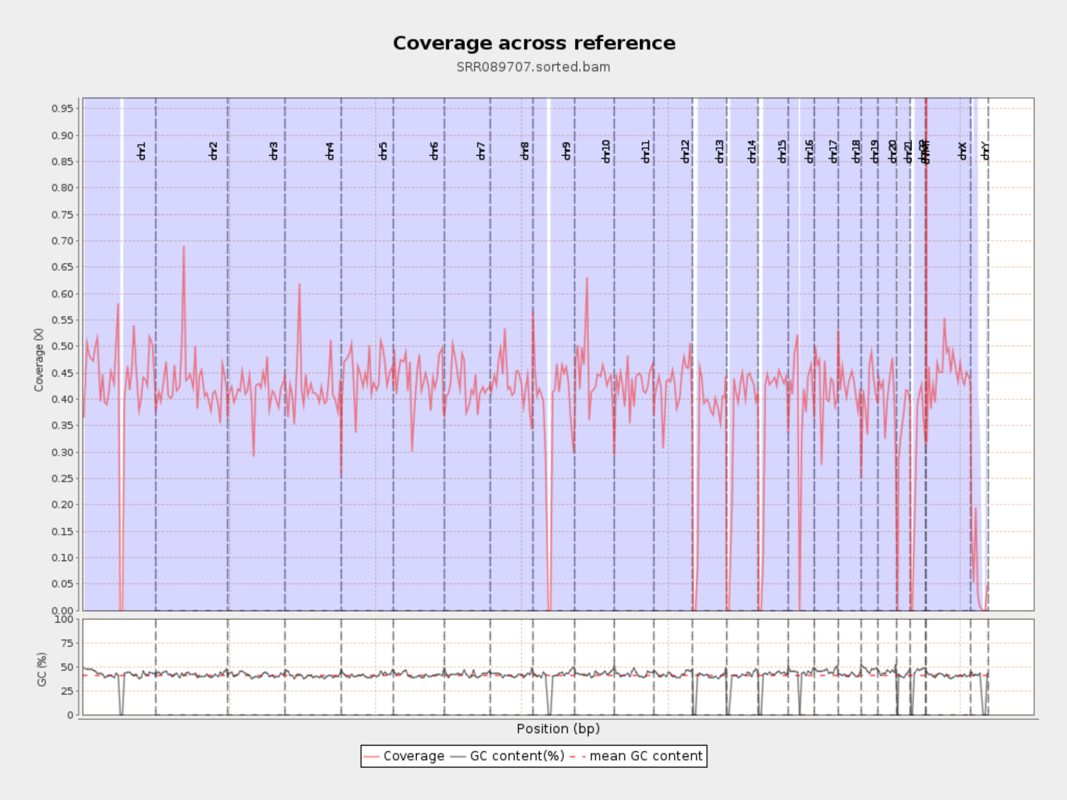
General error rate	0.61%
Mismatches	7,520,952
Insertions	82,563
Mapped reads with at least one insertion	0.42%
Deletions	260,704
Mapped reads with at least one deletion	1.33%
Homopolymer indels	48.23%

2.6. Chromosome stats

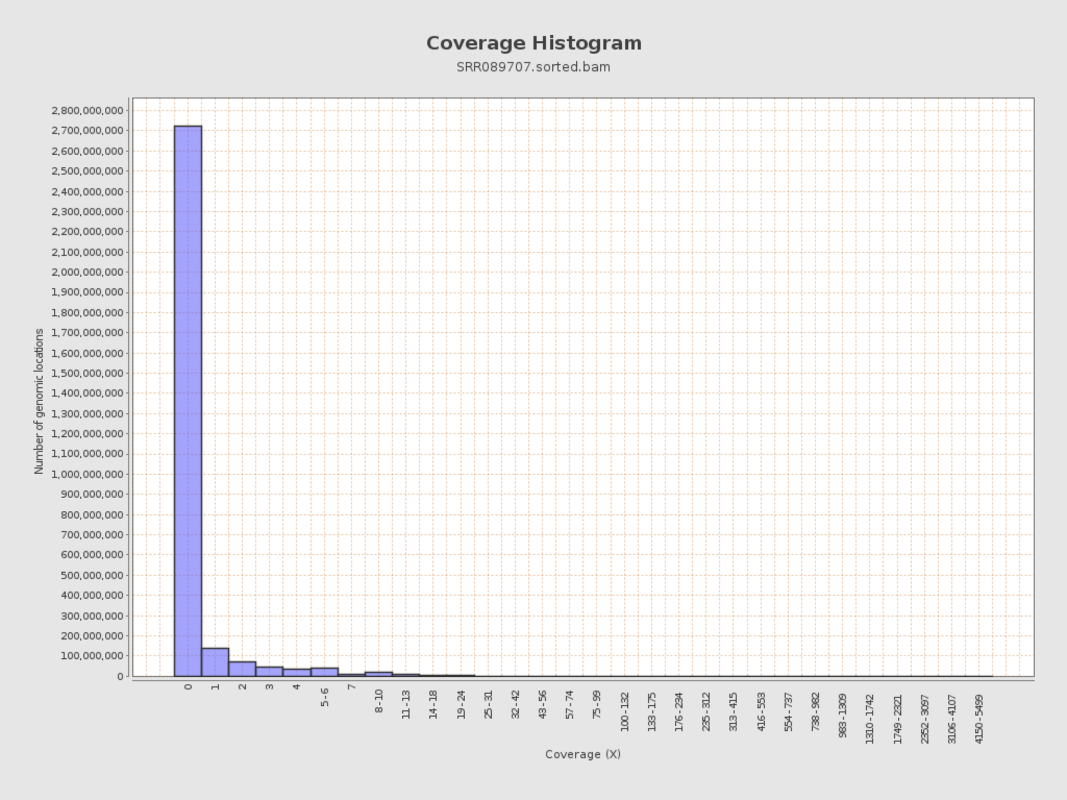
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	105984497	0.4252	4.4675
chr2	243199373	105224337	0.4327	3.2194
chr3	198022430	81966929	0.4139	1.6589
chr4	191154276	80928559	0.4234	1.9577
chr5	180915260	81163128	0.4486	1.7233
chr6	171115067	74860942	0.4375	2.4118
chr7	159138663	67740540	0.4257	2.6403

chr8	146364022	63308999	0.4325	3.6937
chr9	141213431	51781906	0.3667	2.4811
chr10	135534747	61127133	0.451	2.843
chr11	135006516	57493252	0.4259	2.4171
chr12	133851895	57592221	0.4303	2.0199
chr13	115169878	38498872	0.3343	1.4745
chr14	107349540	38184491	0.3557	1.6037
chr15	102531392	35828749	0.3494	1.9554
chr16	90354753	35014715	0.3875	1.8912
chr17	81195210	34337285	0.4229	2.023
chr18	78077248	33436894	0.4283	4.714
chr19	59128983	24197394	0.4092	2.826
chr20	63025520	25851276	0.4102	1.8569
chr21	48129895	16082219	0.3341	1.884
chr22	51304566	14003118	0.2729	1.3558
chrMT	16571	239741	14.4675	11.1977
chrX	155270560	69708783	0.449	1.9259
chrY	59373566	3360838	0.0566	1.3833

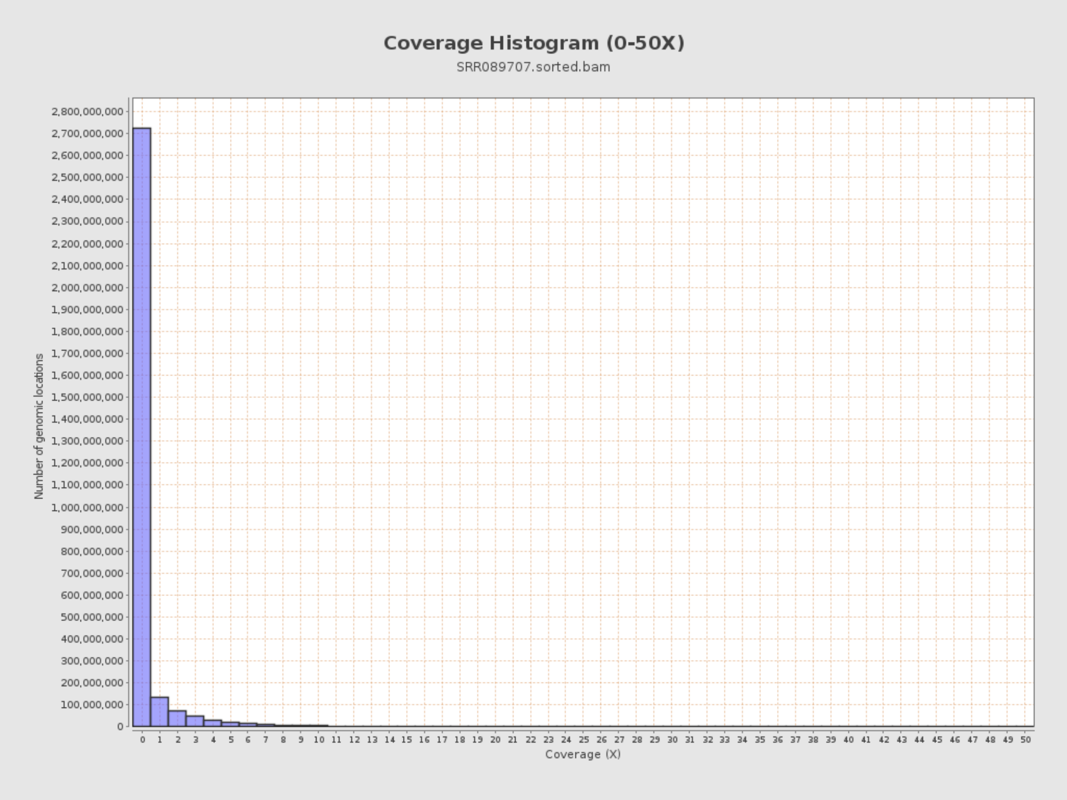
3. Results : Coverage across reference



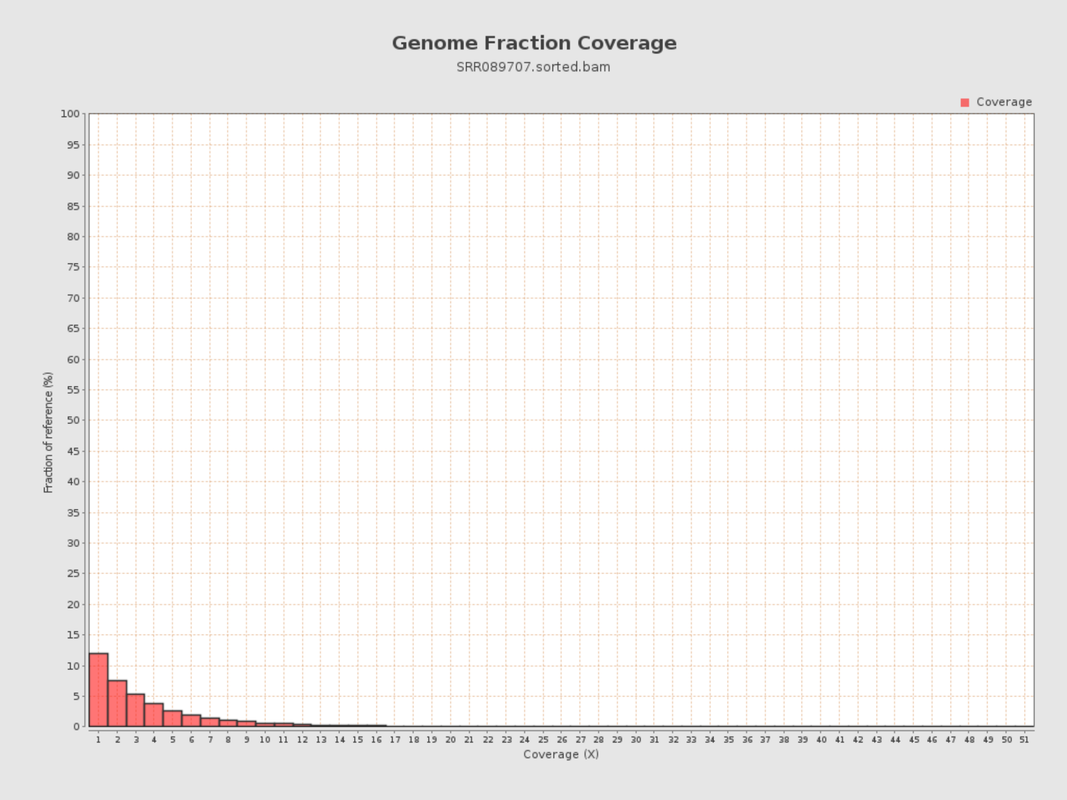
4. Results : Coverage Histogram



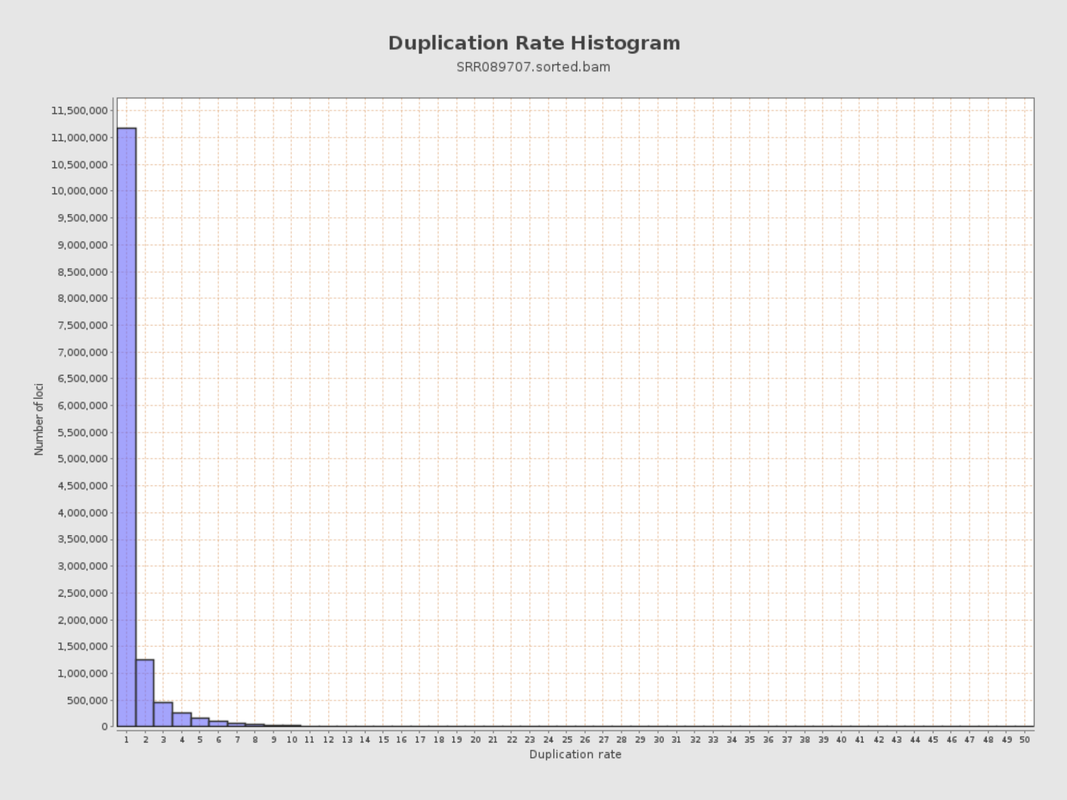
5. Results : Coverage Histogram (0-50X)



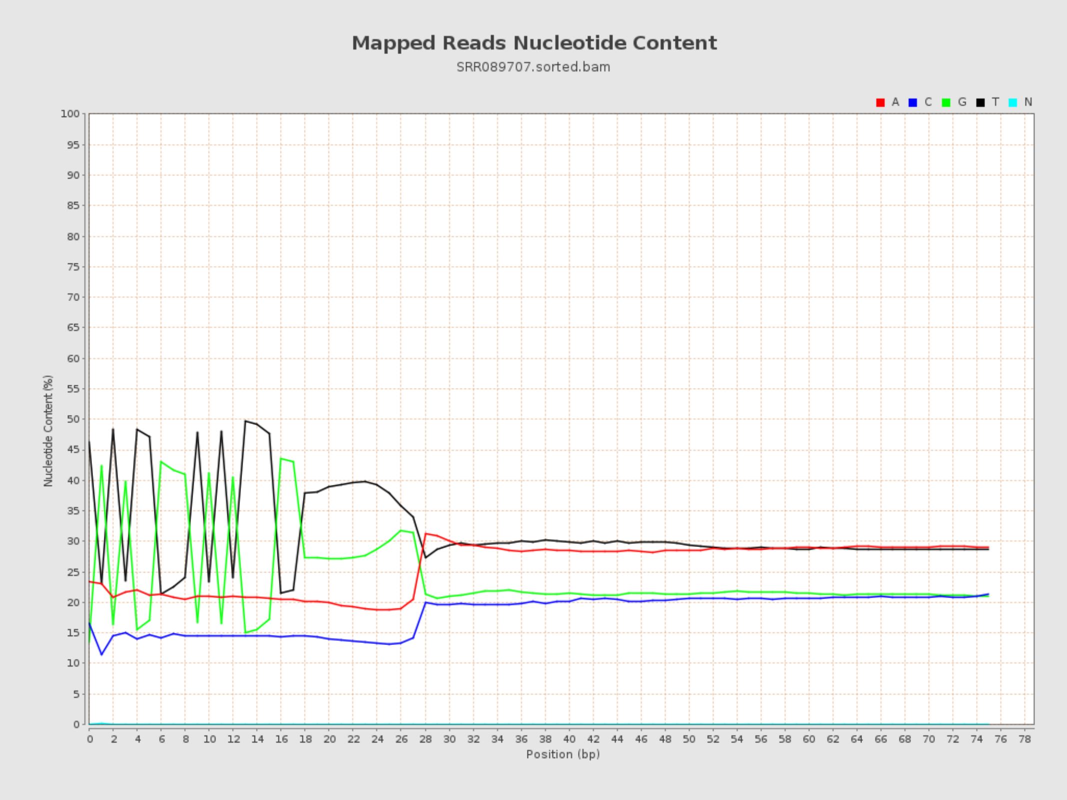
6. Results : Genome Fraction Coverage



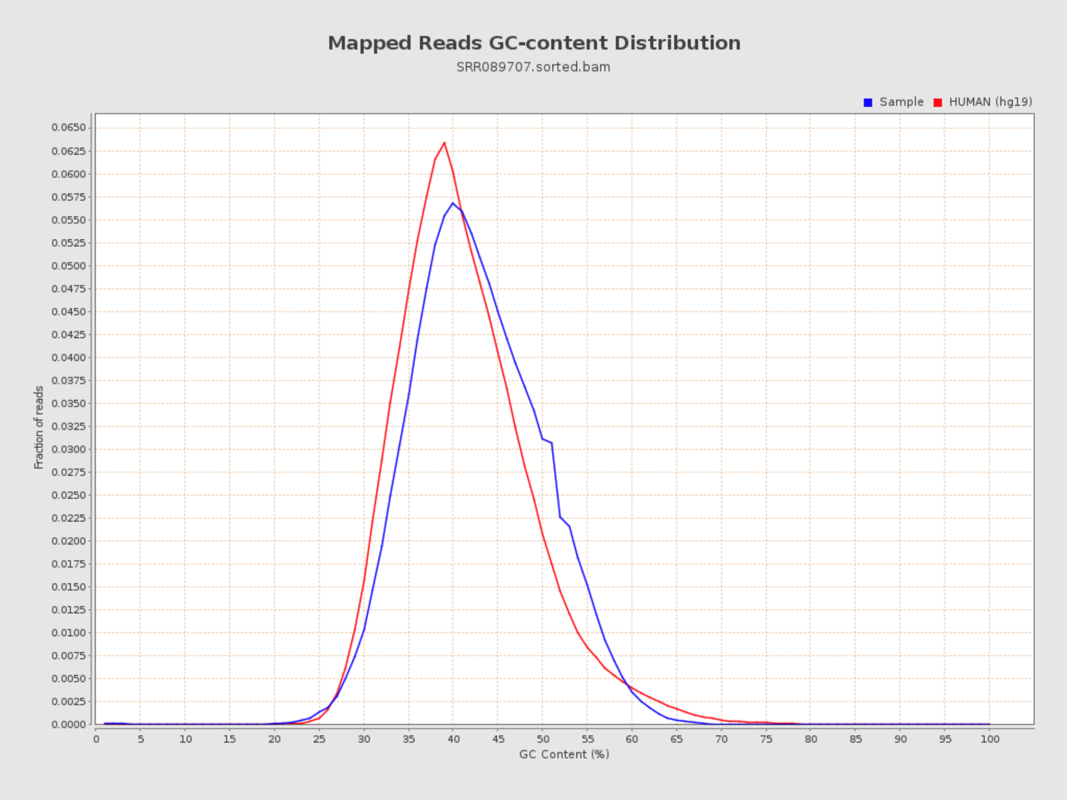
7. Results : Duplication Rate Histogram



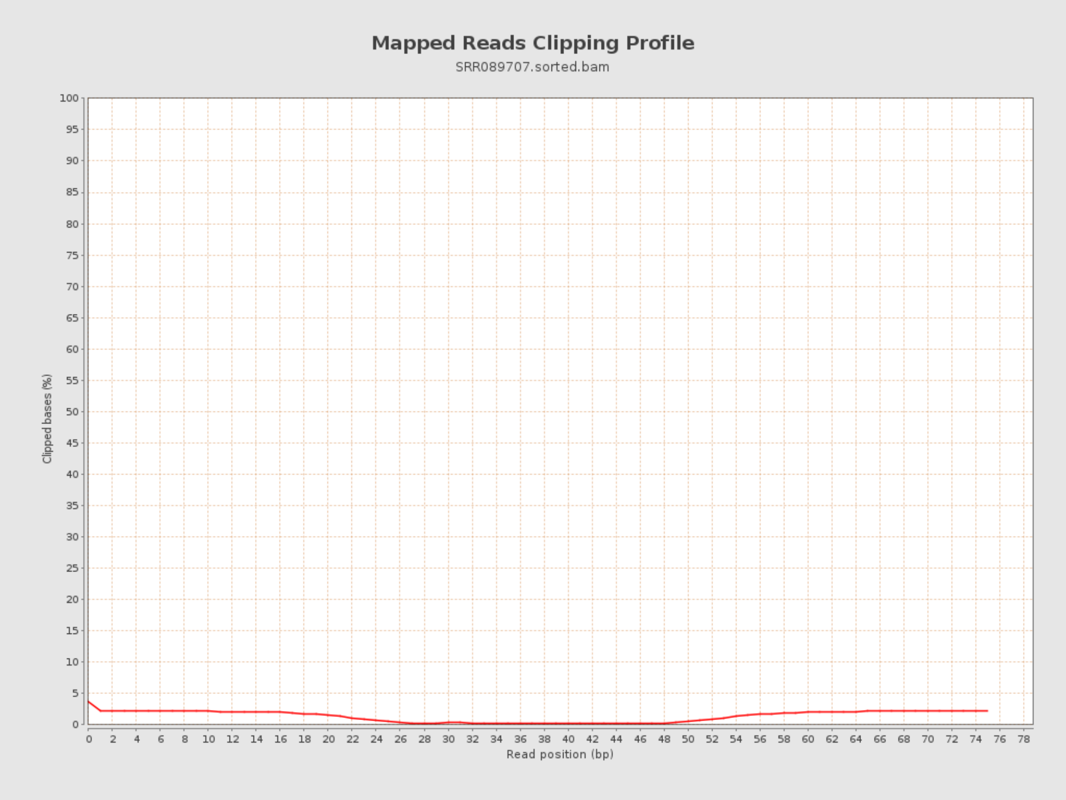
8. Results : Mapped Reads Nucleotide Content



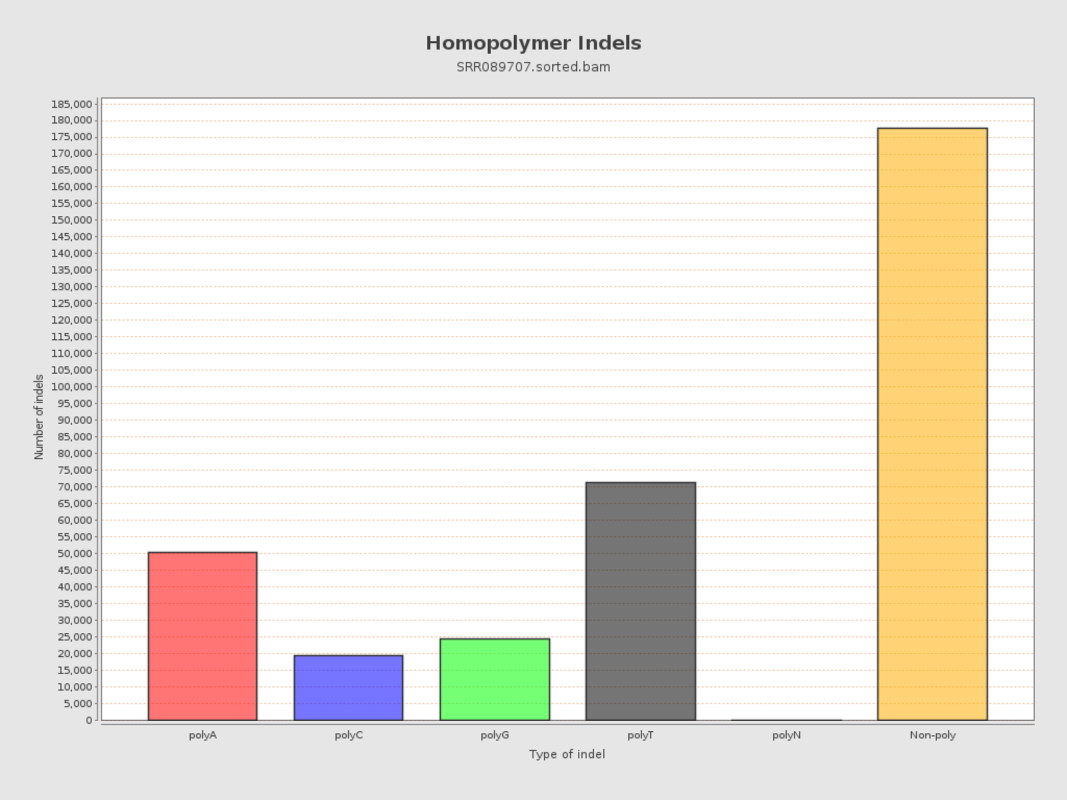
9. Results : Mapped Reads GC-content Distribution



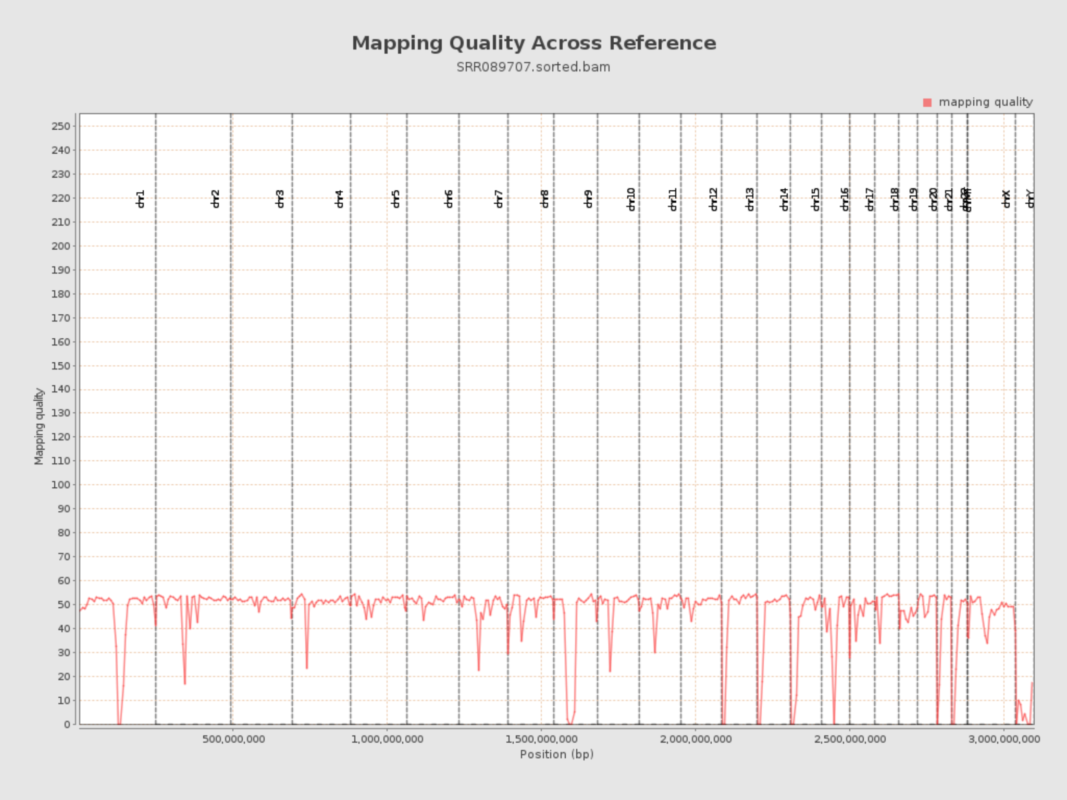
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram