Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 21:21:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089700.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_SRR089700 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089700.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 21:21:40 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089700.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,696,728
Mapped reads	17,253,119 / 76.02%
Unmapped reads	5,443,609 / 23.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	728 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,535,372 / 6.76%
Duplication rate	6.88%
Clipped reads	2,936,144 / 12.94%

2.2. ACGT Content

Number/percentage of A's	261,724,814 / 32.71%
Number/percentage of C's	159,019,956 / 19.87%
Number/percentage of T's	209,113,655 / 26.13%
Number/percentage of G's	169,954,417 / 21.24%
Number/percentage of N's	392,613 / 0.05%
GC Percentage	41.11%

2.3. Coverage

Mean	0.2585

Standard Deviation	1.4366

2.4. Mapping Quality

Mean Mapping Quality	42.6

2.5. Mismatches and indels

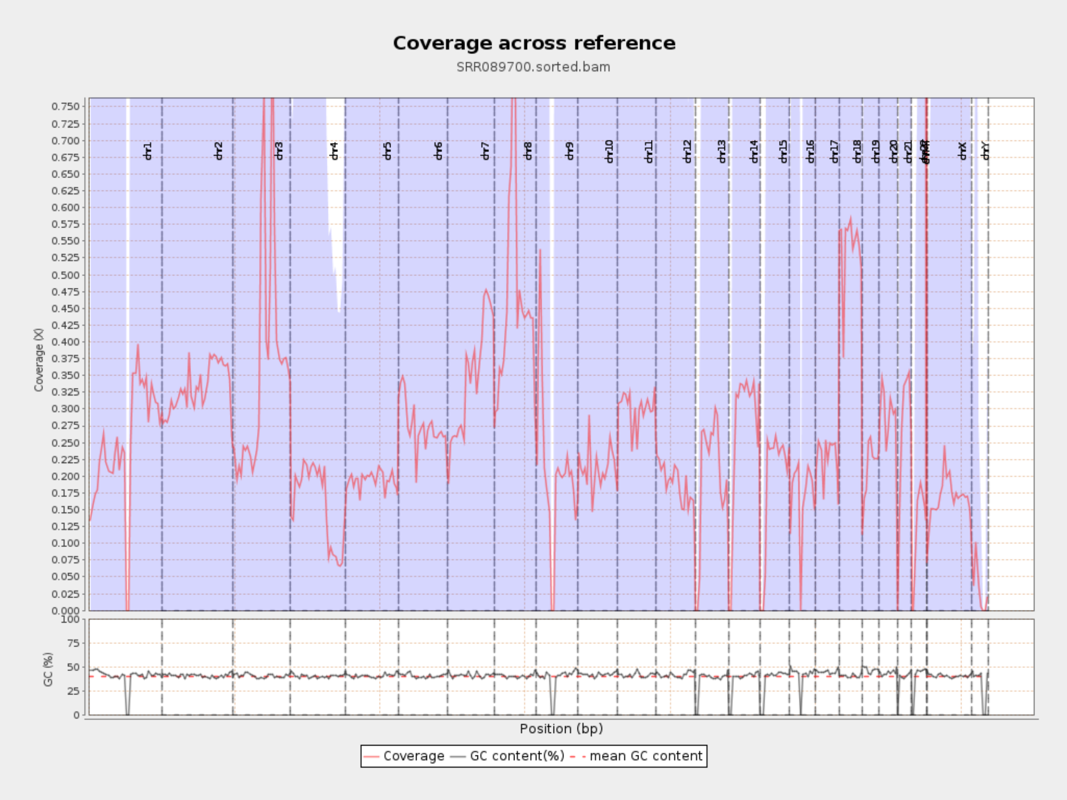
General error rate	0.6%
Mismatches	4,709,619
Insertions	39,390
Mapped reads with at least one insertion	0.23%
Deletions	115,099
Mapped reads with at least one deletion	0.67%
Homopolymer indels	42.87%

2.6. Chromosome stats

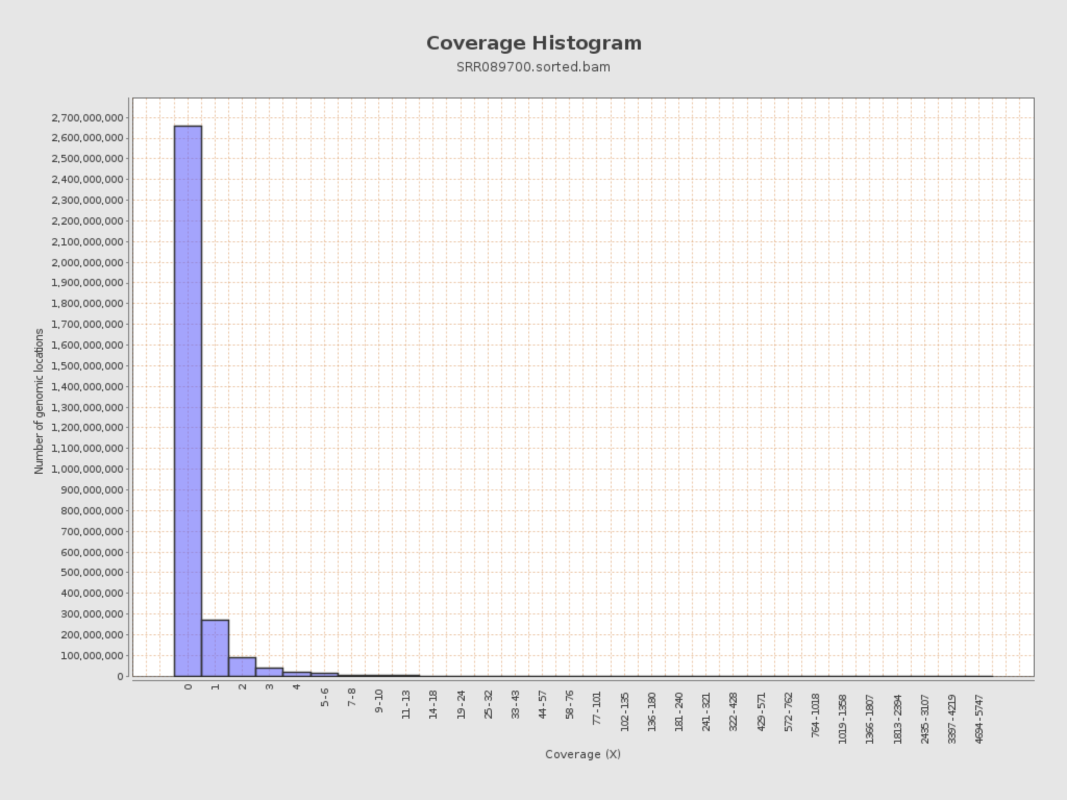
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	62026670	0.2489	1.6113
chr2	243199373	80845947	0.3324	1.9463
chr3	198022430	72205594	0.3646	1.0922
chr4	191154276	30282432	0.1584	0.6896
chr5	180915260	35151457	0.1943	0.7292
chr6	171115067	47079110	0.2751	1.0456
chr7	159138663	55604592	0.3494	2.0806

chr8	146364022	68615672	0.4688	3.4352
chr9	141213431	29522077	0.2091	1.1775
chr10	135534747	28882642	0.2131	1.2786
chr11	135006516	40327644	0.2987	1.2242
chr12	133851895	25227743	0.1885	0.7449
chr13	115169878	22517661	0.1955	0.7344
chr14	107349540	28595027	0.2664	0.9609
chr15	102531392	19666473	0.1918	0.7204
chr16	90354753	15552695	0.1721	0.7789
chr17	81195210	18363735	0.2262	0.9008
chr18	78077248	42142862	0.5398	2.0173
chr19	59128983	12740055	0.2155	1.5
chr20	63025520	18305843	0.2905	0.9572
chr21	48129895	12632808	0.2625	0.9871
chr22	51304566	6179029	0.1204	0.5618
chrMT	16571	196268	11.8441	10.3275
chrX	155270560	25857337	0.1665	0.9635
chrY	59373566	1856982	0.0313	0.5276

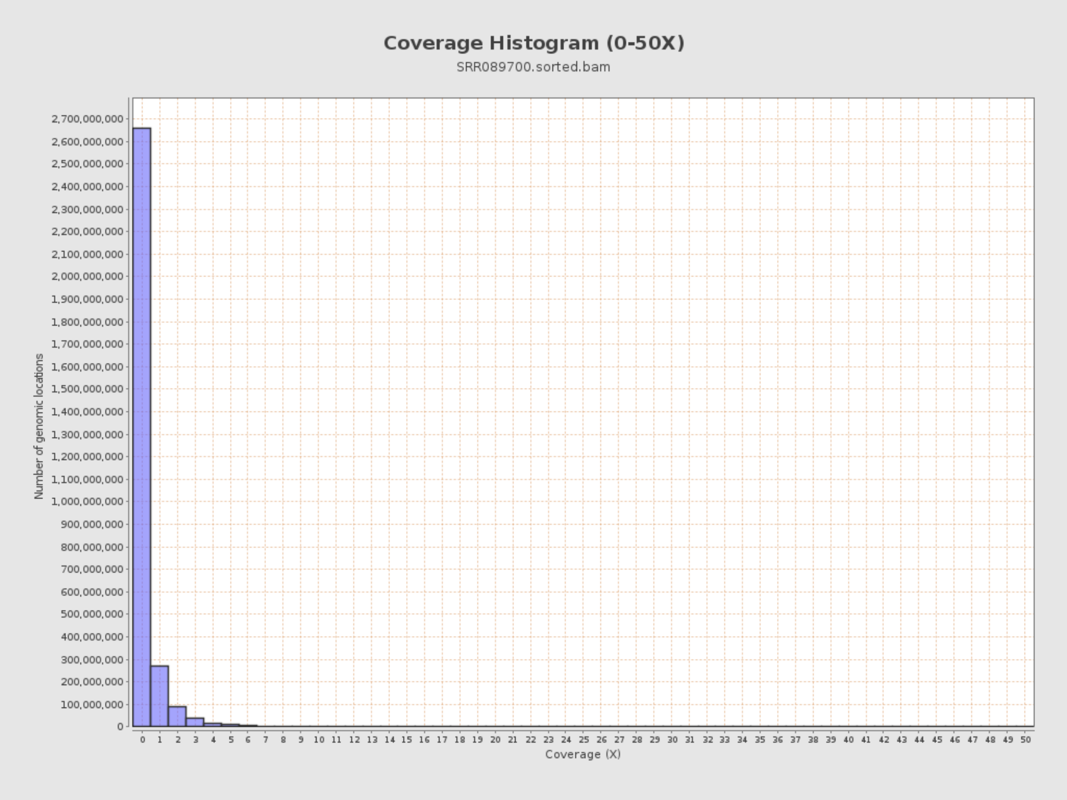
3. Results : Coverage across reference



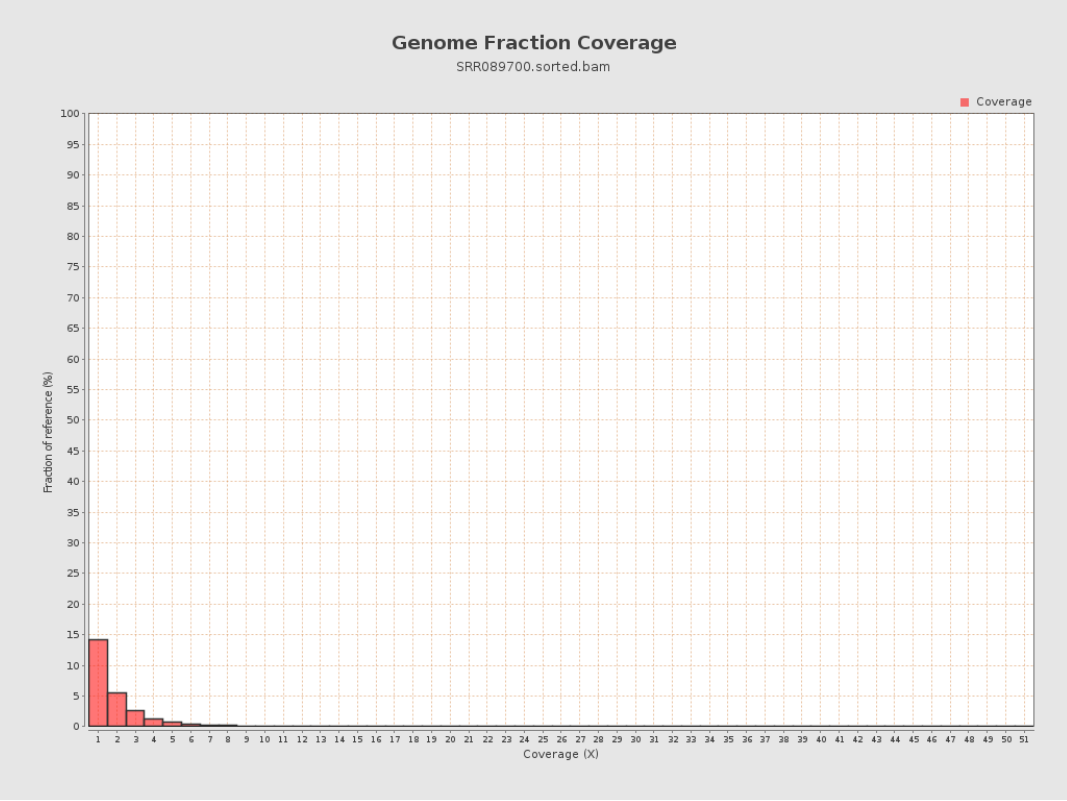
4. Results : Coverage Histogram



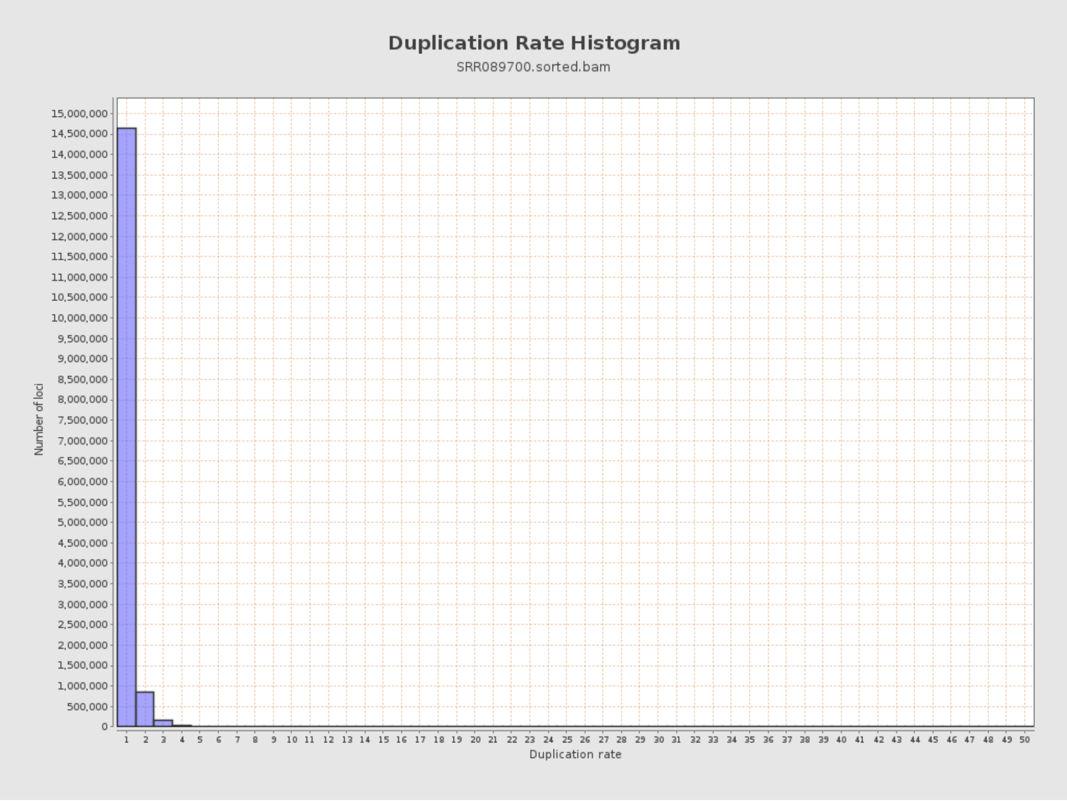
5. Results : Coverage Histogram (0-50X)



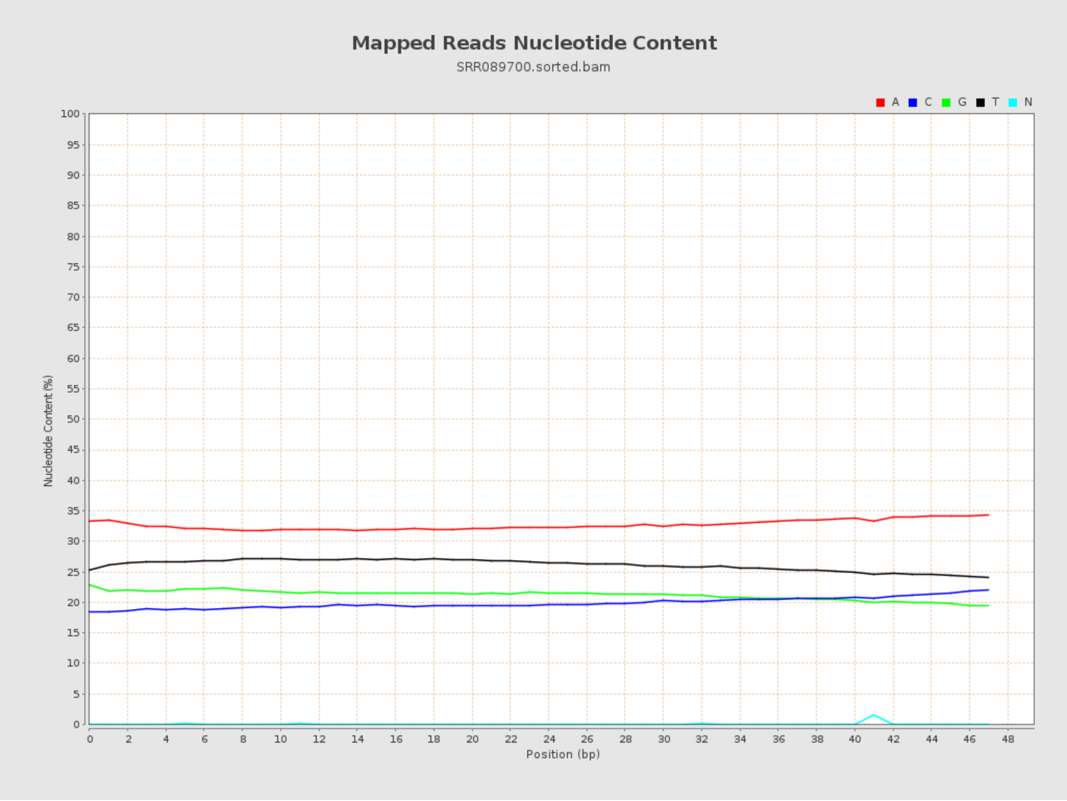
6. Results : Genome Fraction Coverage



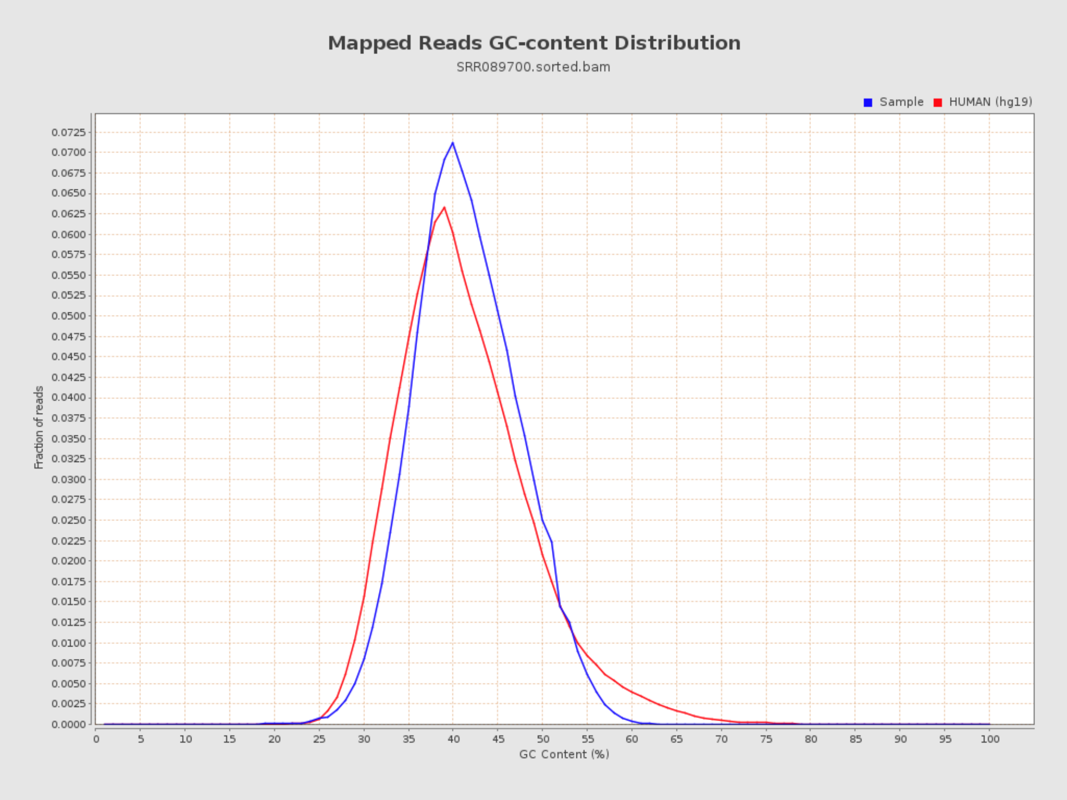
7. Results : Duplication Rate Histogram



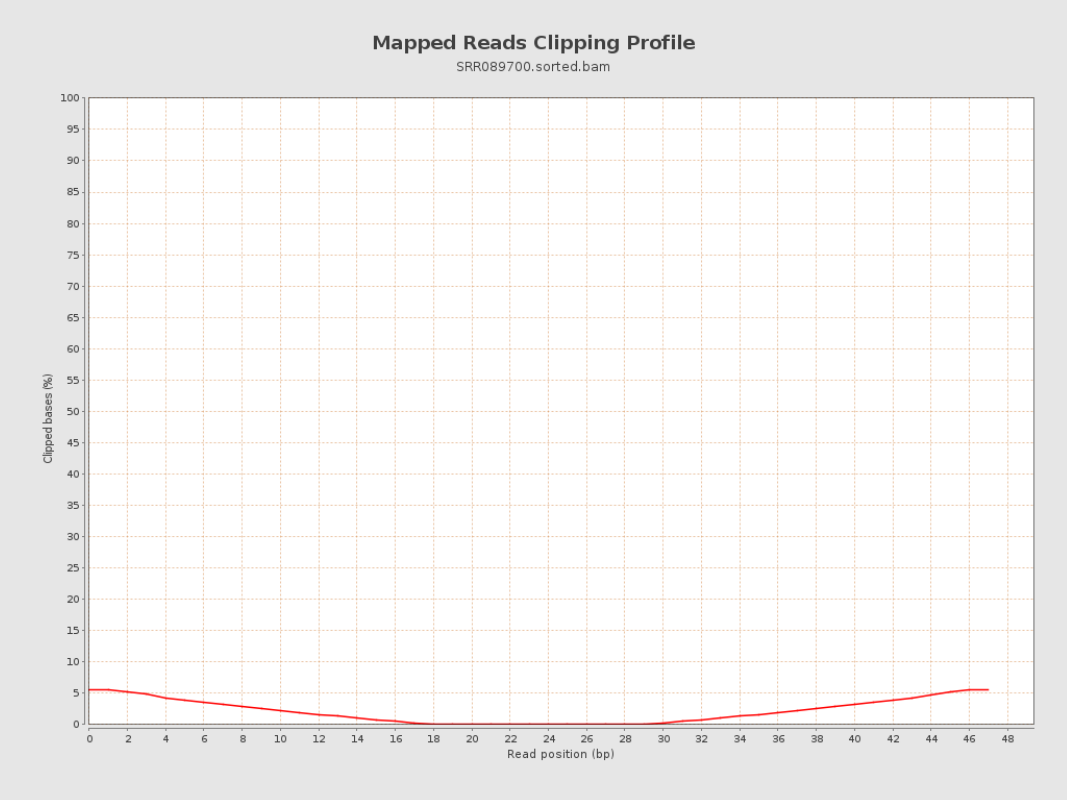
8. Results : Mapped Reads Nucleotide Content



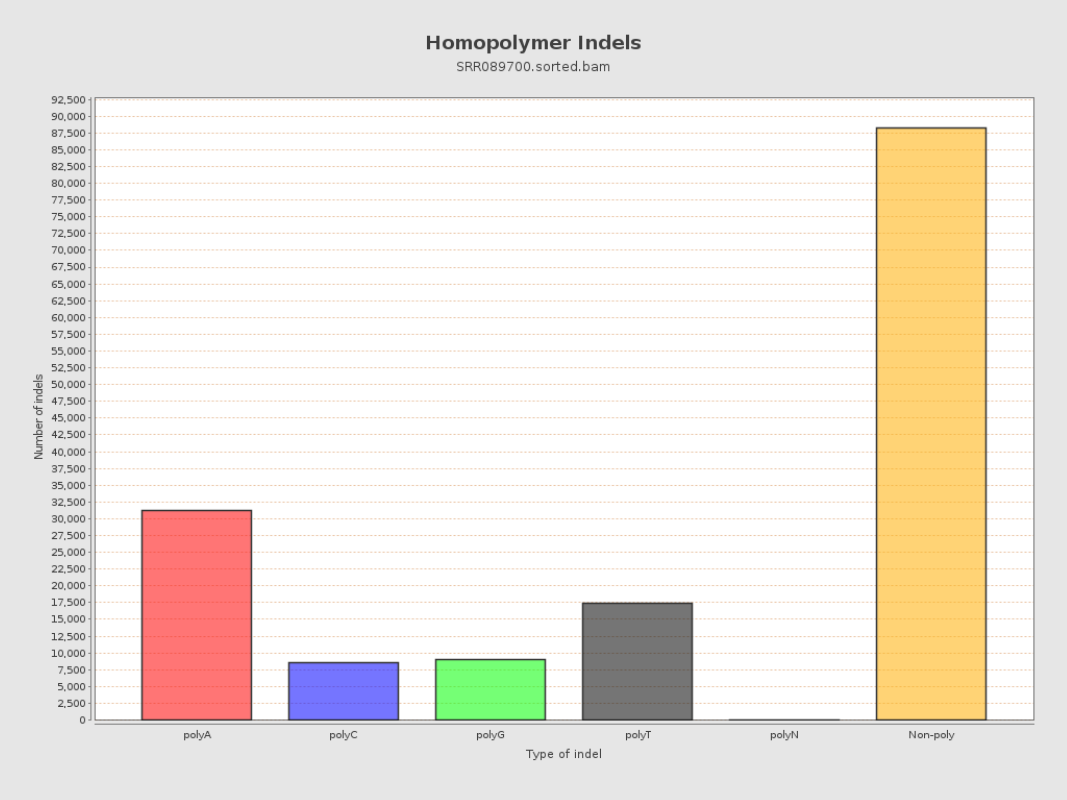
9. Results : Mapped Reads GC-content Distribution



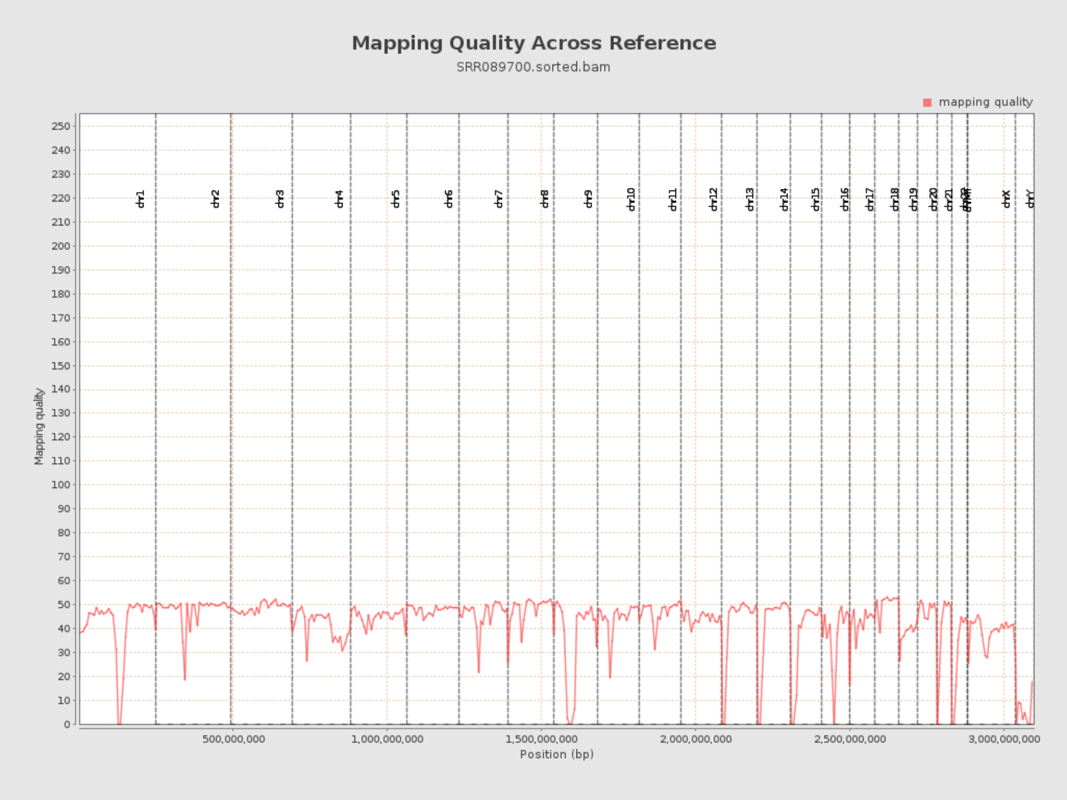
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram