Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 23:15:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089709.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_SRR089709 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089709.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 23:15:53 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089709.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,981,645
Mapped reads	19,752,491 / 85.95%
Unmapped reads	3,229,154 / 14.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	123,179 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	6,077,692 / 26.45%
Duplication rate	15.57%
Clipped reads	8,927,556 / 38.85%

2.2. ACGT Content

Number/percentage of A's	346,826,477 / 26.56%
Number/percentage of C's	244,363,741 / 18.71%
Number/percentage of T's	408,264,520 / 31.26%
Number/percentage of G's	305,993,043 / 23.43%
Number/percentage of N's	509,858 / 0.04%
GC Percentage	42.14%

2.3. Coverage

Mean	0.422

Standard Deviation	2.9162

2.4. Mapping Quality

Mean Mapping Quality	47.34

2.5. Mismatches and indels

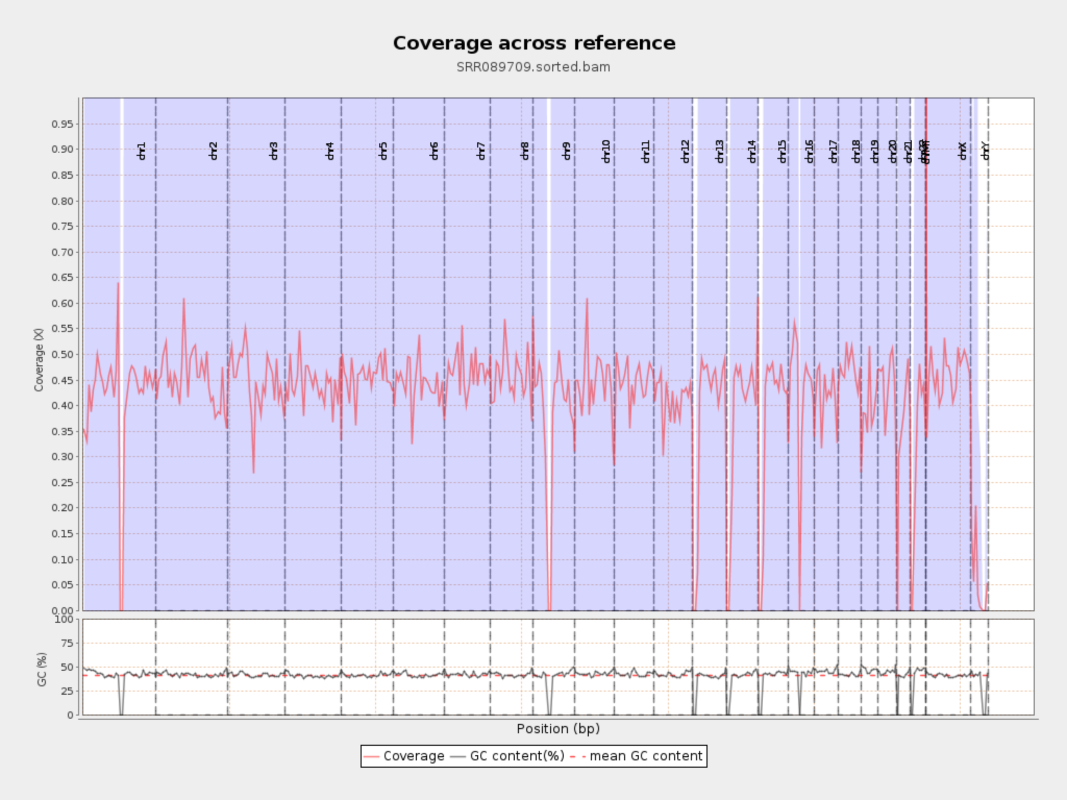
General error rate	0.66%
Mismatches	8,396,523
Insertions	84,770
Mapped reads with at least one insertion	0.42%
Deletions	256,420
Mapped reads with at least one deletion	1.28%
Homopolymer indels	46.95%

2.6. Chromosome stats

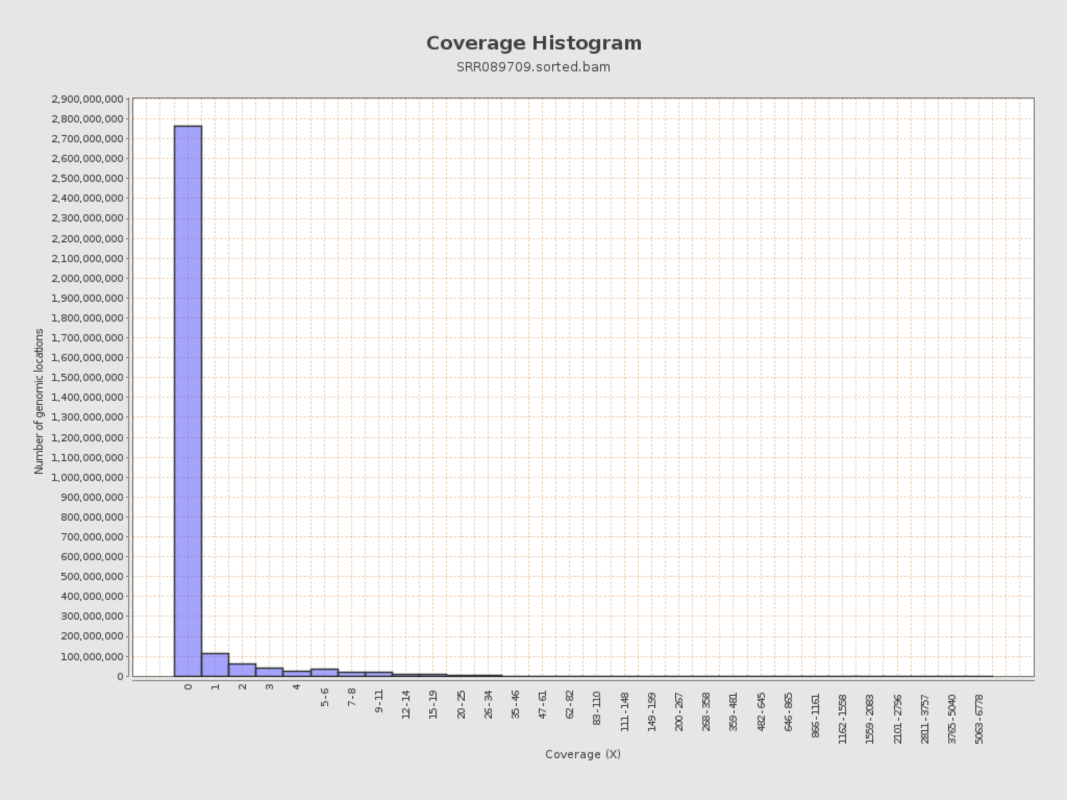
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	104095408	0.4176	5.3754
chr2	243199373	110450487	0.4542	3.6007
chr3	198022430	88574788	0.4473	1.9197
chr4	191154276	84954781	0.4444	2.1091
chr5	180915260	82885078	0.4581	1.9631
chr6	171115067	75806023	0.443	2.1628
chr7	159138663	73981640	0.4649	3.4024

chr8	146364022	66706231	0.4558	4.4041
chr9	141213431	53297019	0.3774	2.4904
chr10	135534747	60621313	0.4473	2.5744
chr11	135006516	60220960	0.4461	2.3103
chr12	133851895	55176920	0.4122	1.9628
chr13	115169878	43684158	0.3793	1.7716
chr14	107349540	40225491	0.3747	1.8562
chr15	102531392	37096798	0.3618	1.8274
chr16	90354753	37778987	0.4181	1.9761
chr17	81195210	34340138	0.4229	2.1953
chr18	78077248	36901985	0.4726	3.8994
chr19	59128983	23496331	0.3974	3.6227
chr20	63025520	28219440	0.4477	2.088
chr21	48129895	17067171	0.3546	1.9077
chr22	51304566	15420740	0.3006	1.6715
chrMT	16571	55934	3.3754	5.3446
chrX	155270560	71833977	0.4626	2.0968
chrY	59373566	3514901	0.0592	1.4896

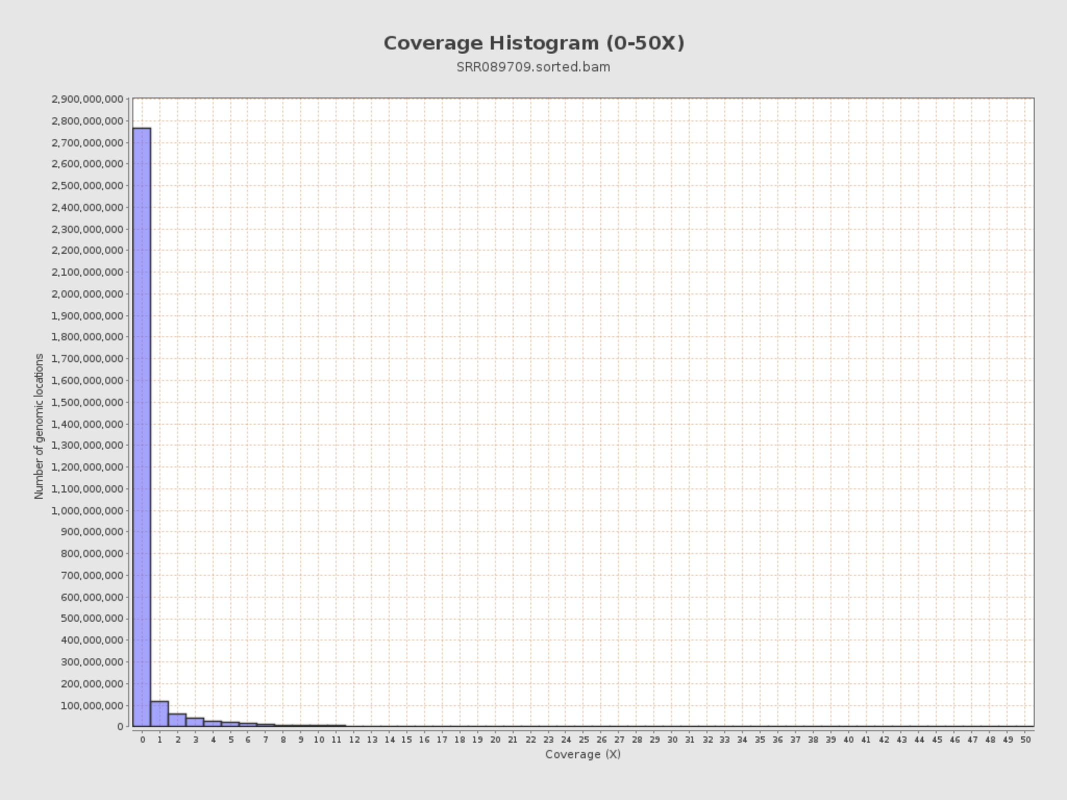
3. Results : Coverage across reference



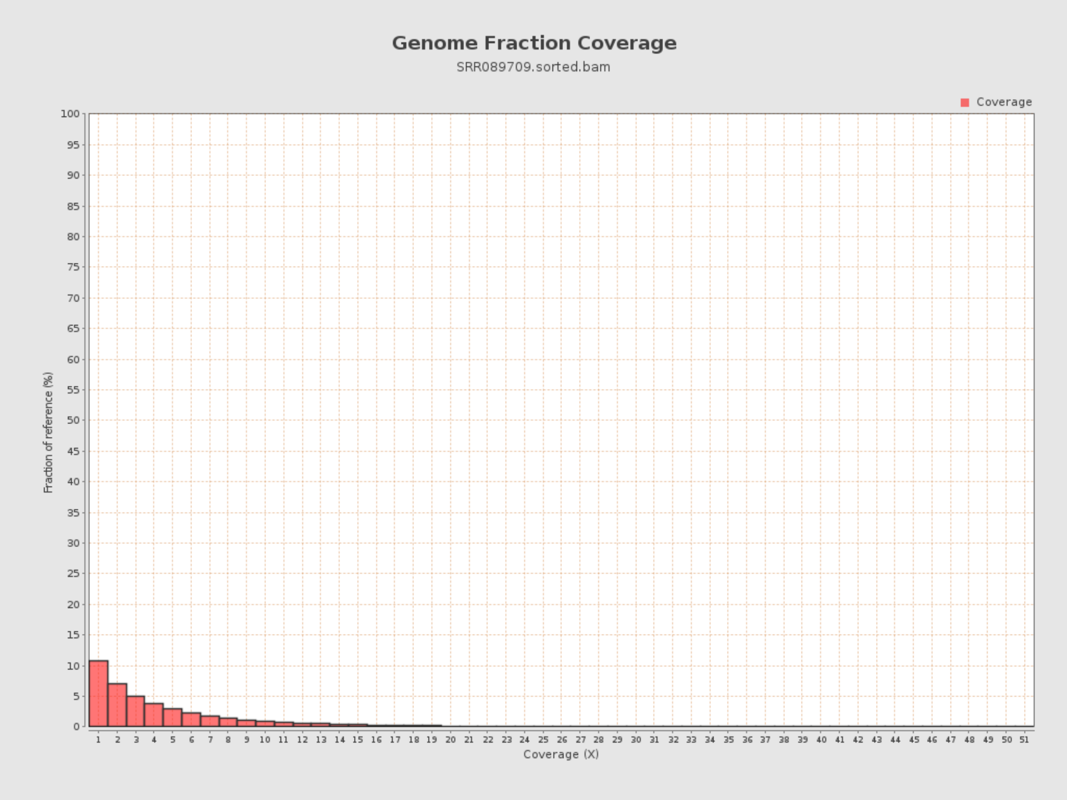
4. Results : Coverage Histogram



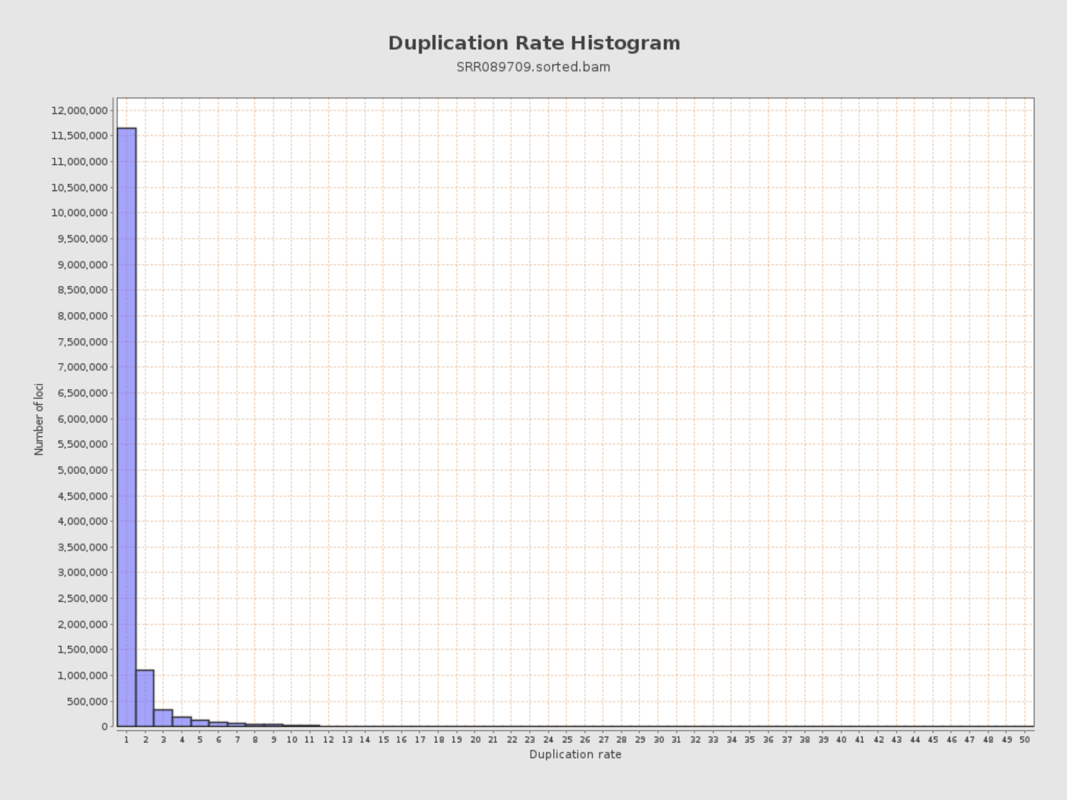
5. Results : Coverage Histogram (0-50X)



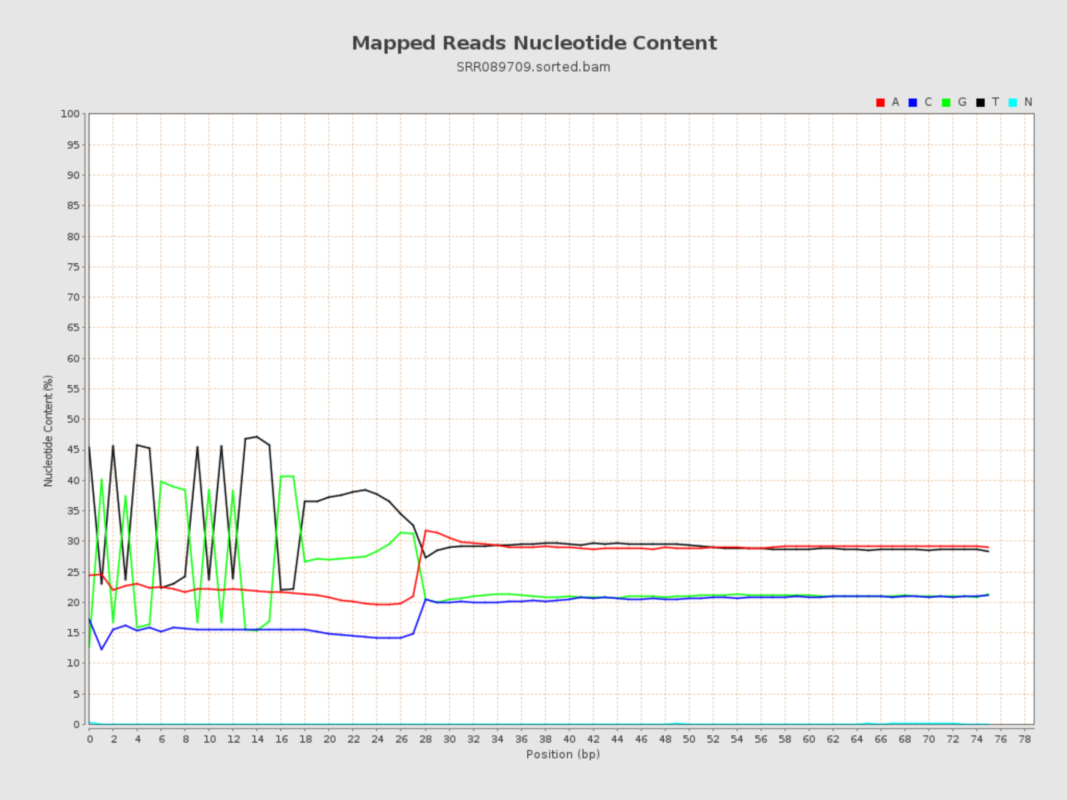
6. Results : Genome Fraction Coverage



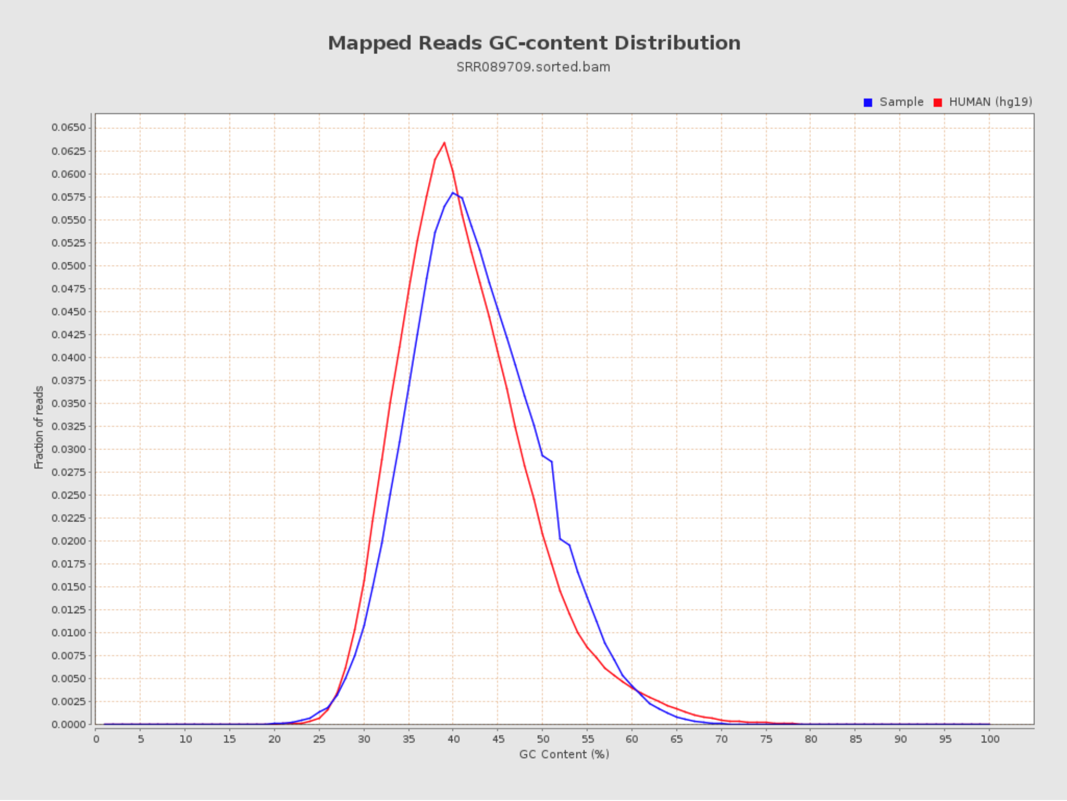
7. Results : Duplication Rate Histogram



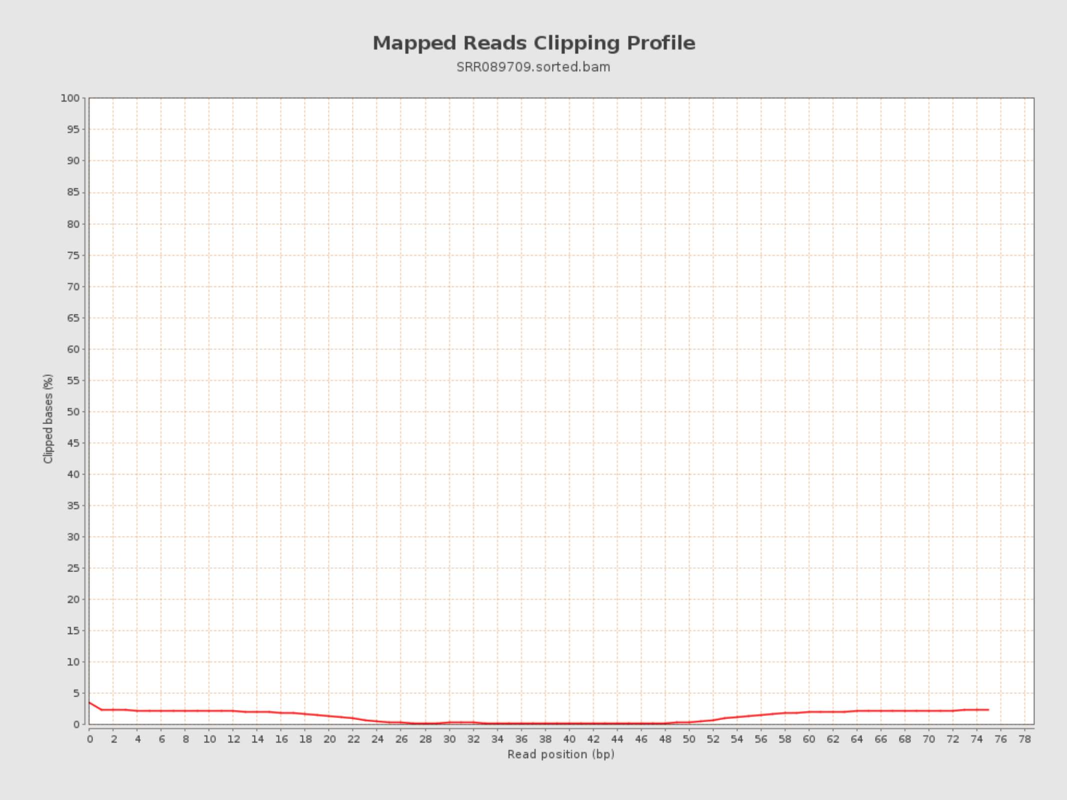
8. Results : Mapped Reads Nucleotide Content



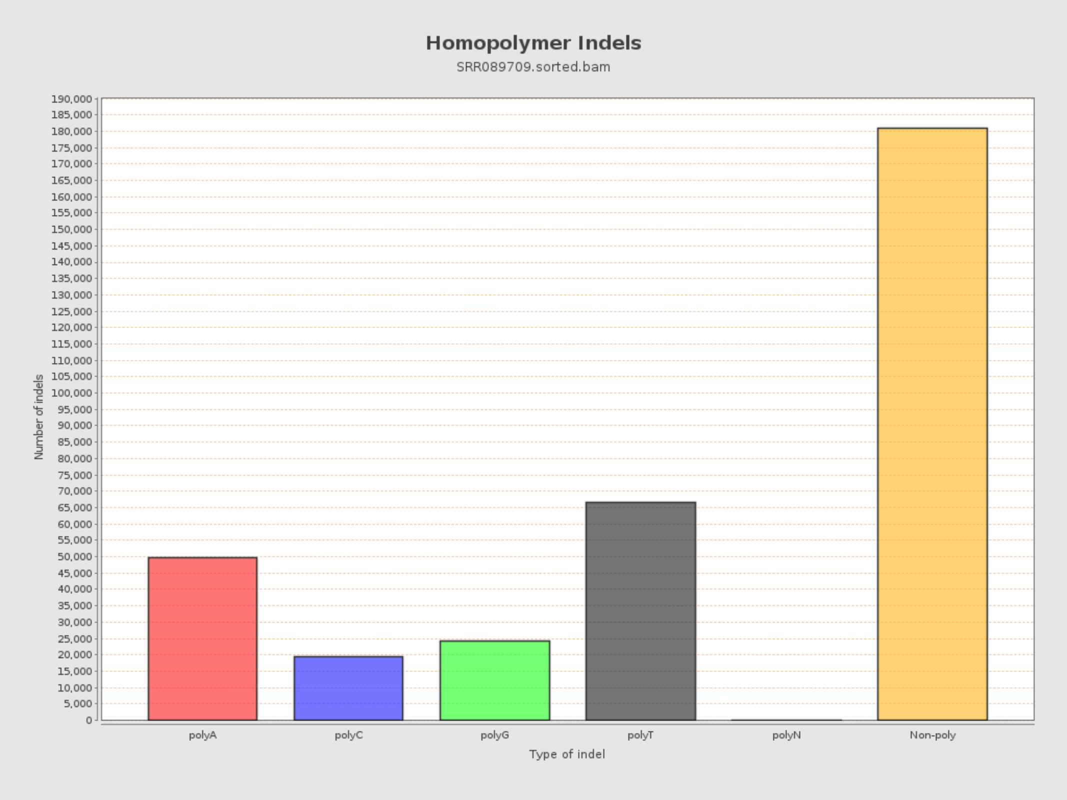
9. Results : Mapped Reads GC-content Distribution



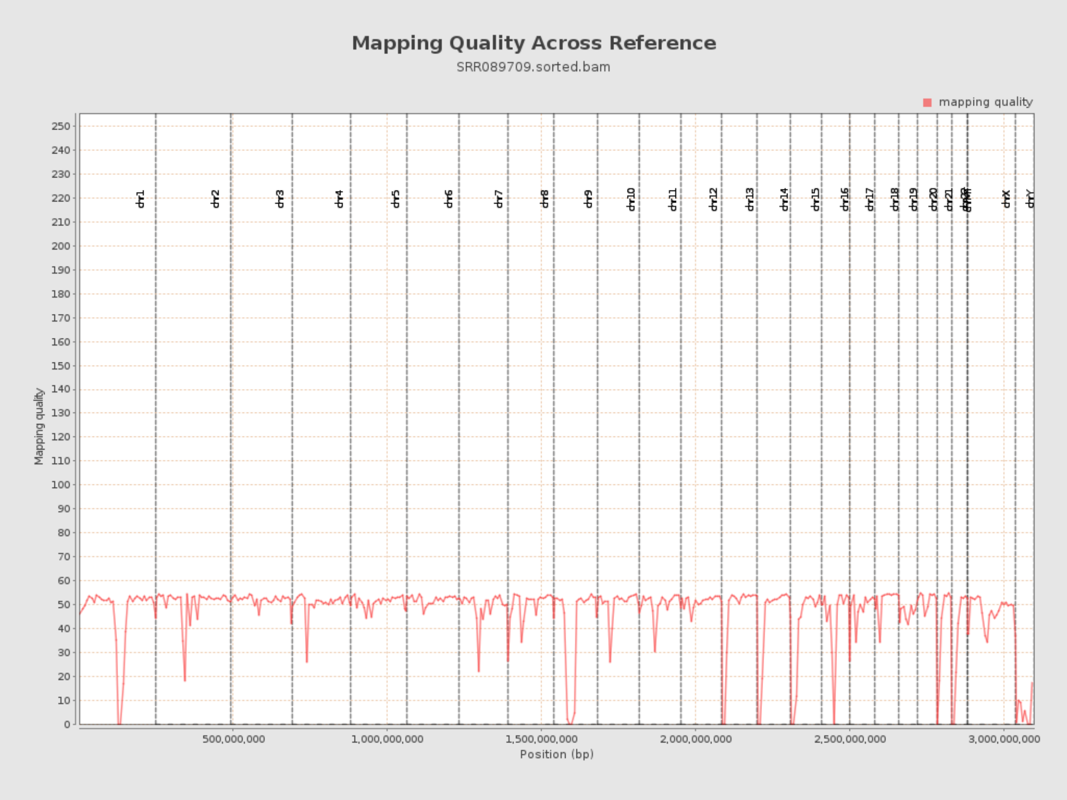
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram