Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 20:49:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089698.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_SRR089698 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089698.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 20:49:40 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089698.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,464,638
Mapped reads	17,254,213 / 73.53%
Unmapped reads	6,210,425 / 26.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	683 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,480,928 / 6.31%
Duplication rate	6.57%
Clipped reads	4,168,440 / 17.76%

2.2. ACGT Content

Number/percentage of A's	255,207,458 / 32.41%
Number/percentage of C's	161,170,990 / 20.46%
Number/percentage of T's	202,976,961 / 25.77%
Number/percentage of G's	167,684,001 / 21.29%
Number/percentage of N's	507,108 / 0.06%
GC Percentage	41.76%

2.3. Coverage

Mean	0.2545

Standard Deviation	1.3752

2.4. Mapping Quality

Mean Mapping Quality	41.86

2.5. Mismatches and indels

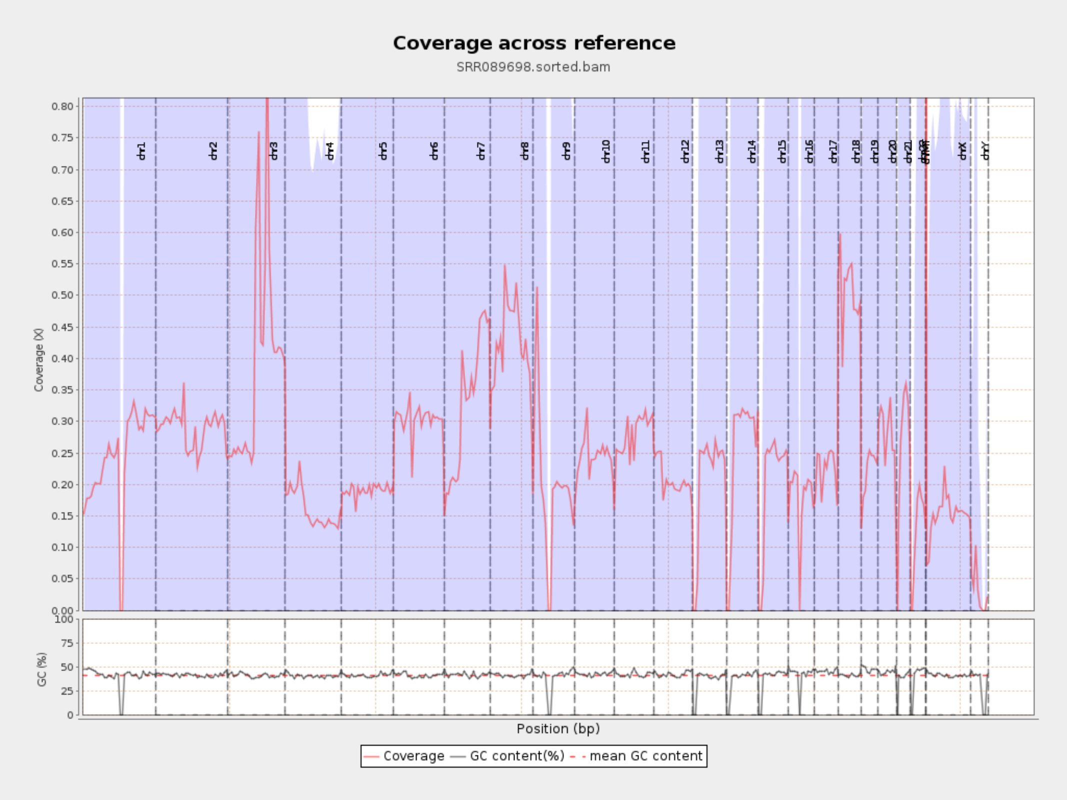
General error rate	0.57%
Mismatches	4,419,170
Insertions	39,426
Mapped reads with at least one insertion	0.23%
Deletions	111,036
Mapped reads with at least one deletion	0.64%
Homopolymer indels	41.28%

2.6. Chromosome stats

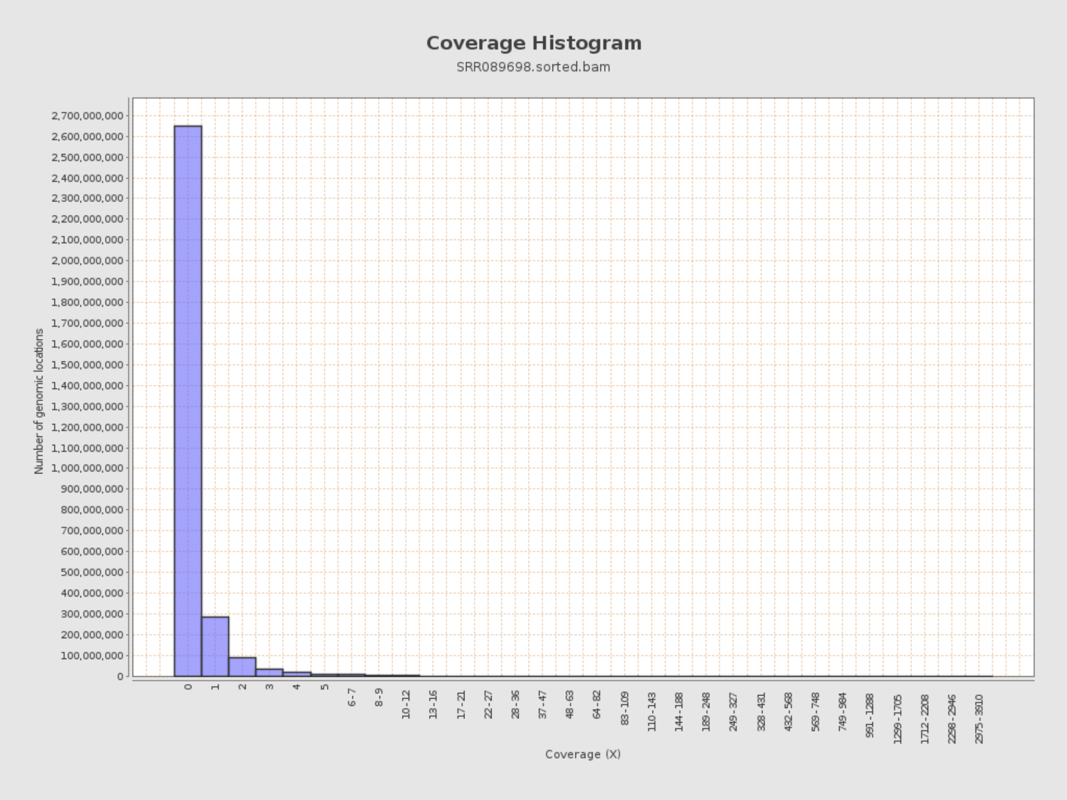
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	60055830	0.2409	1.5203
chr2	243199373	70529503	0.29	2.1077
chr3	198022430	76979889	0.3887	1.131
chr4	191154276	30762741	0.1609	0.7008
chr5	180915260	34462916	0.1905	0.7116
chr6	171115067	51966445	0.3037	1.1741
chr7	159138663	52545334	0.3302	2.2431

chr8	146364022	62440557	0.4266	2.529
chr9	141213431	28434071	0.2014	1.2059
chr10	135534747	33139732	0.2445	1.2731
chr11	135006516	37606264	0.2786	1.2487
chr12	133851895	27849807	0.2081	0.7785
chr13	115169878	23871874	0.2073	0.7543
chr14	107349540	27402651	0.2553	0.9508
chr15	102531392	20545239	0.2004	0.735
chr16	90354753	15908378	0.1761	0.7887
chr17	81195210	18355620	0.2261	0.9115
chr18	78077248	39517180	0.5061	1.8723
chr19	59128983	13187003	0.223	1.4617
chr20	63025520	17653999	0.2801	0.9439
chr21	48129895	12449798	0.2587	0.9929
chr22	51304566	6472638	0.1262	0.5736
chrMT	16571	165172	9.9675	9.7943
chrX	155270560	23570848	0.1518	1.0265
chrY	59373566	1837783	0.031	0.5305

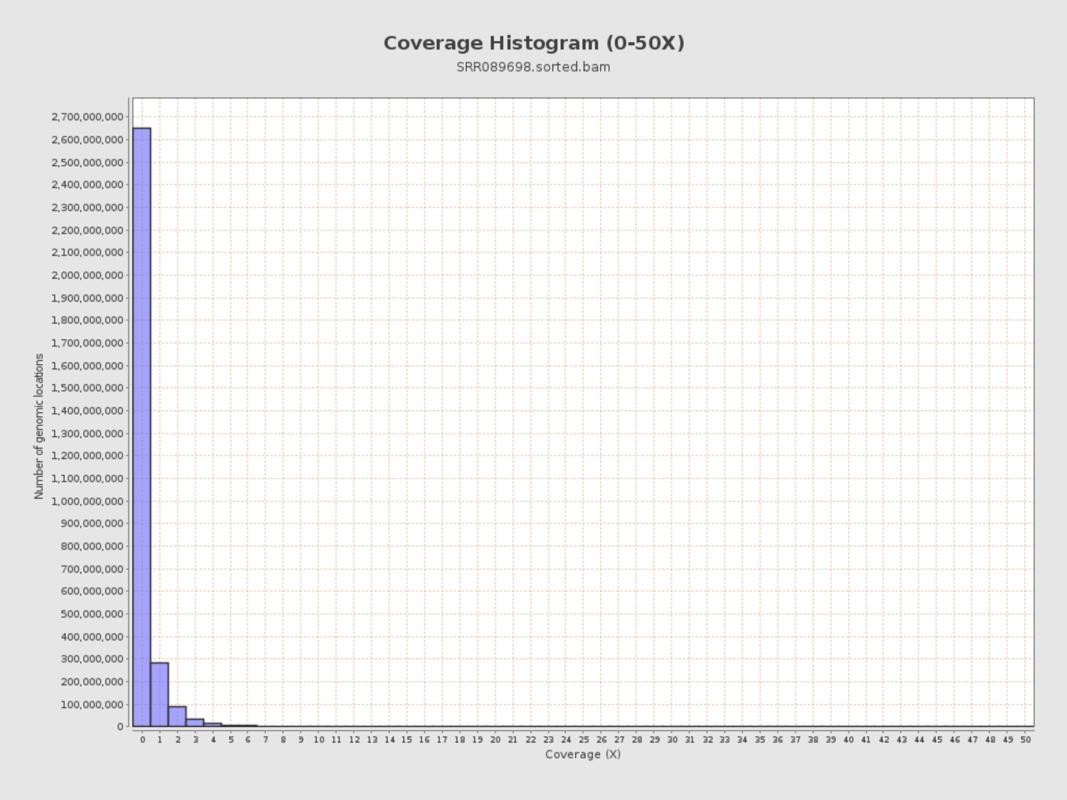
3. Results : Coverage across reference



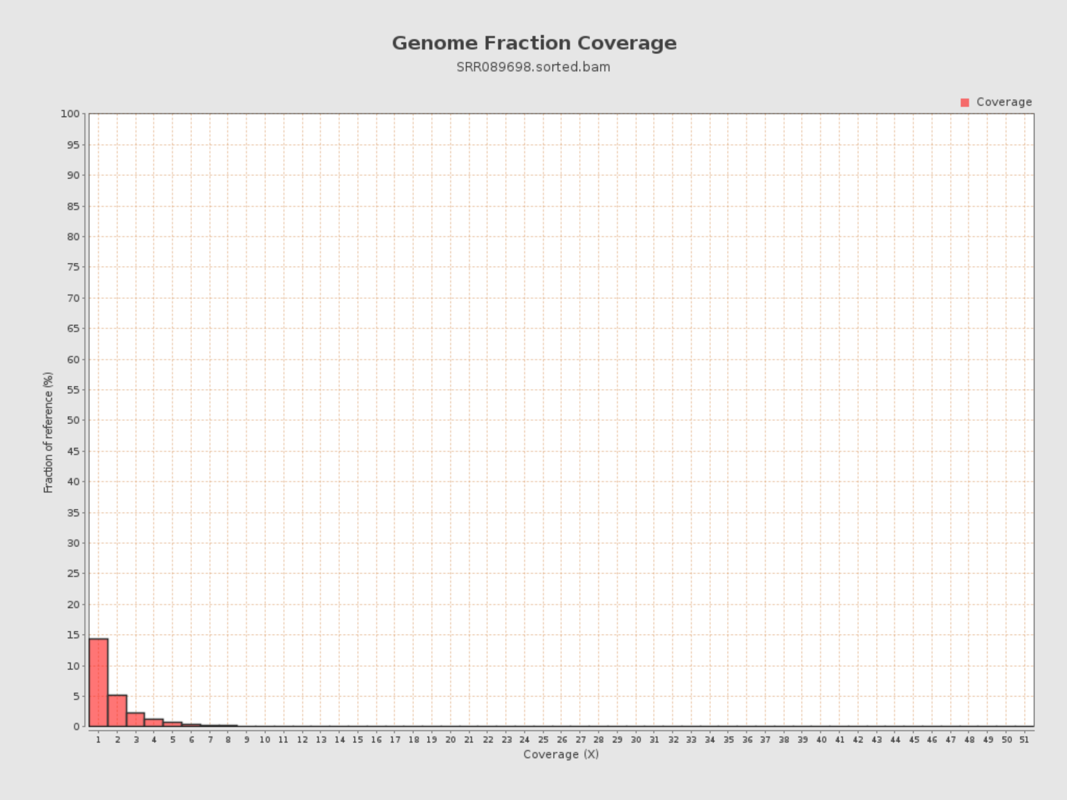
4. Results : Coverage Histogram



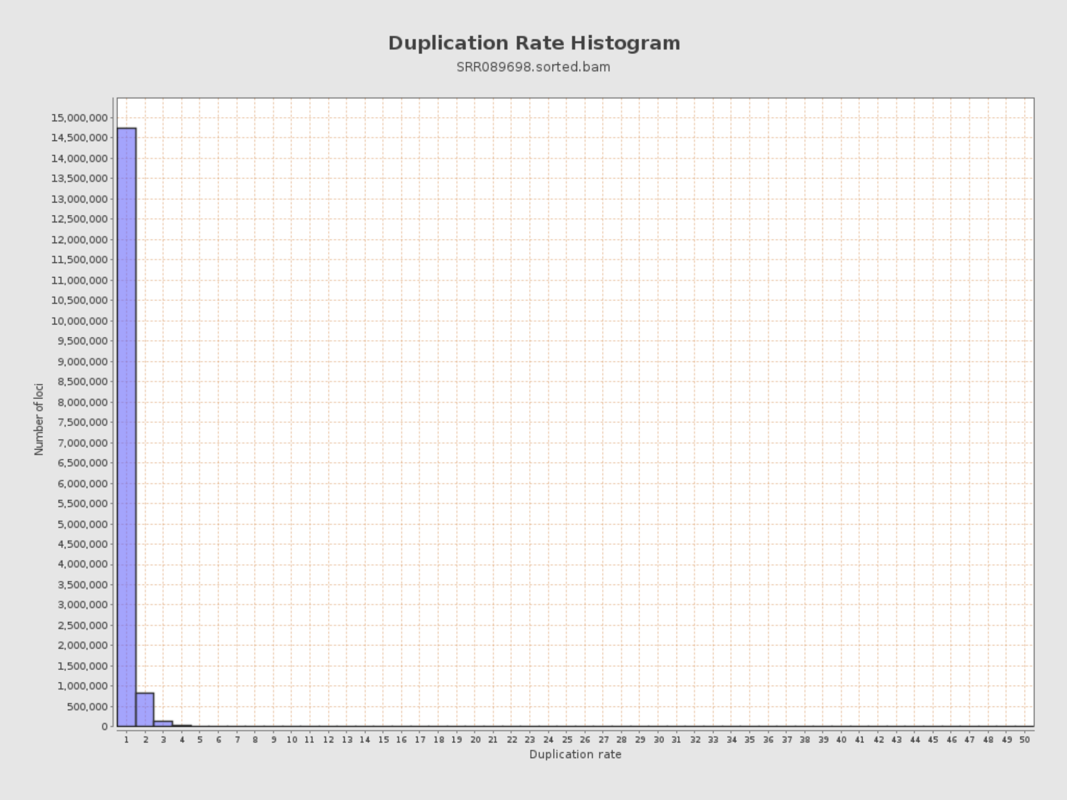
5. Results : Coverage Histogram (0-50X)



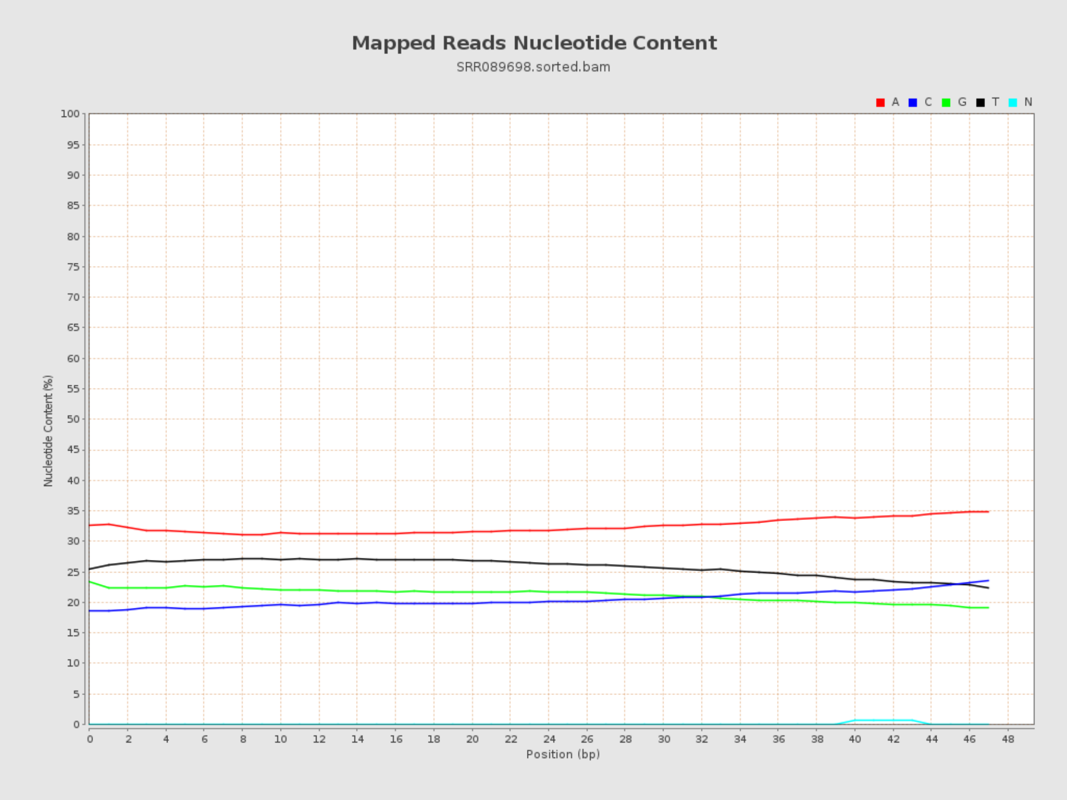
6. Results : Genome Fraction Coverage



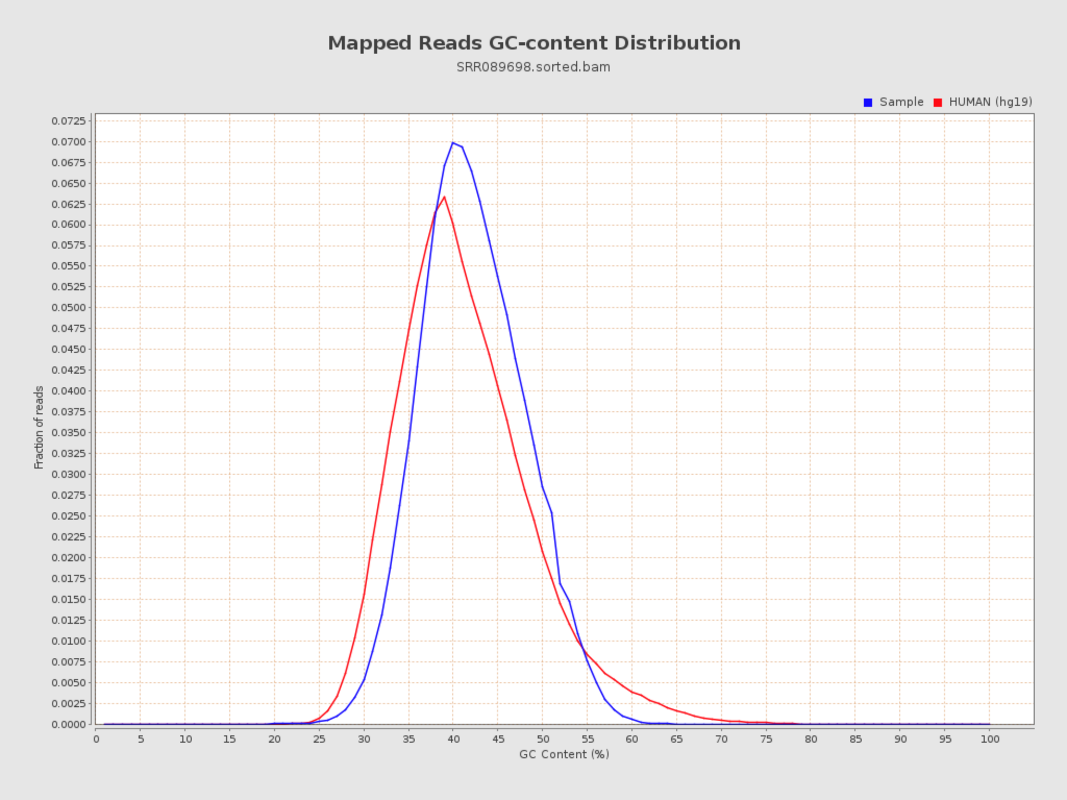
7. Results : Duplication Rate Histogram



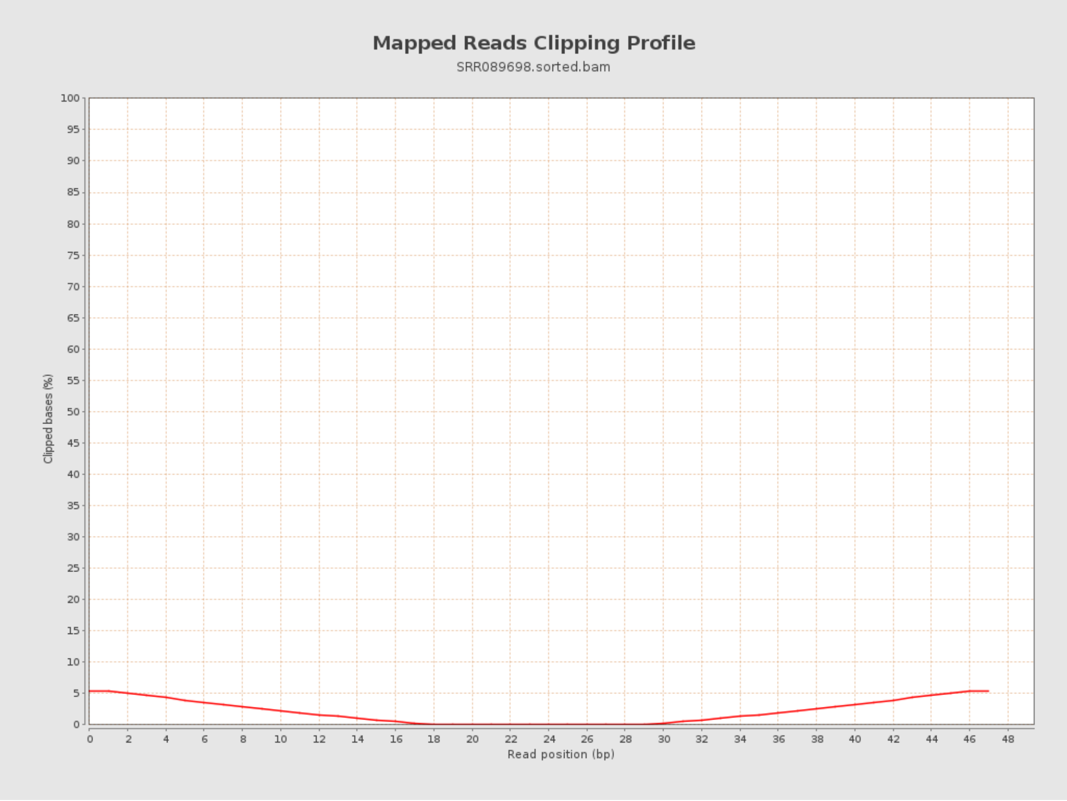
8. Results : Mapped Reads Nucleotide Content



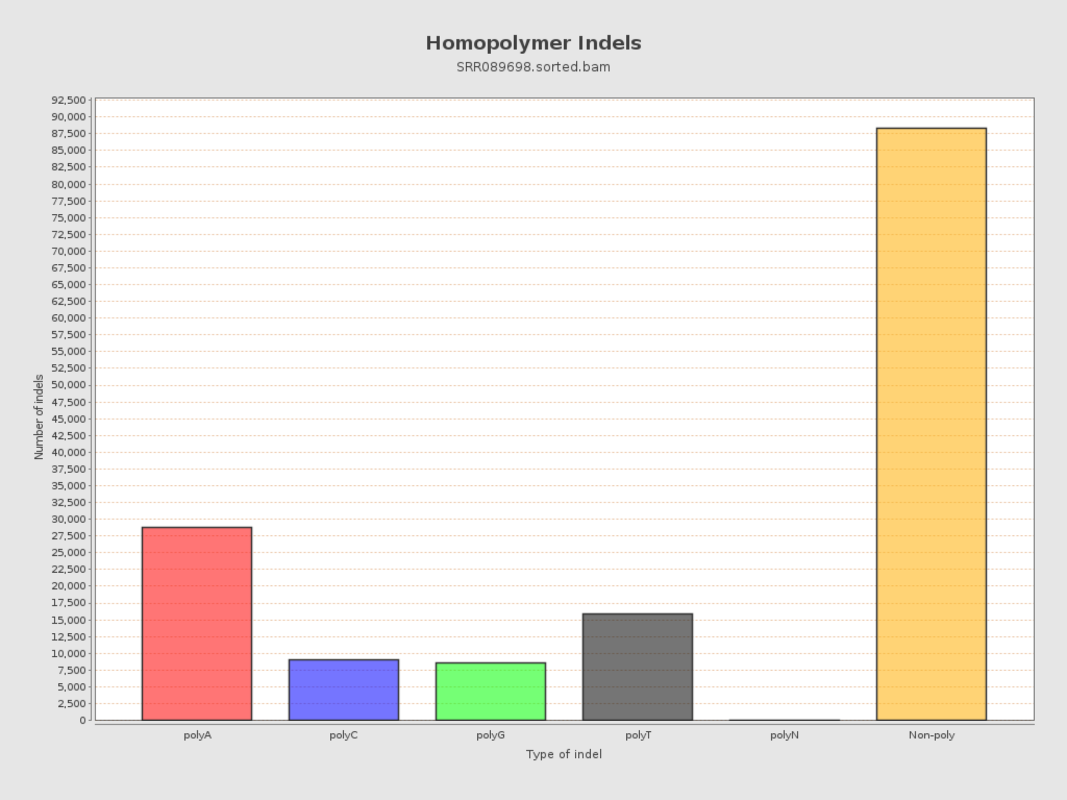
9. Results : Mapped Reads GC-content Distribution



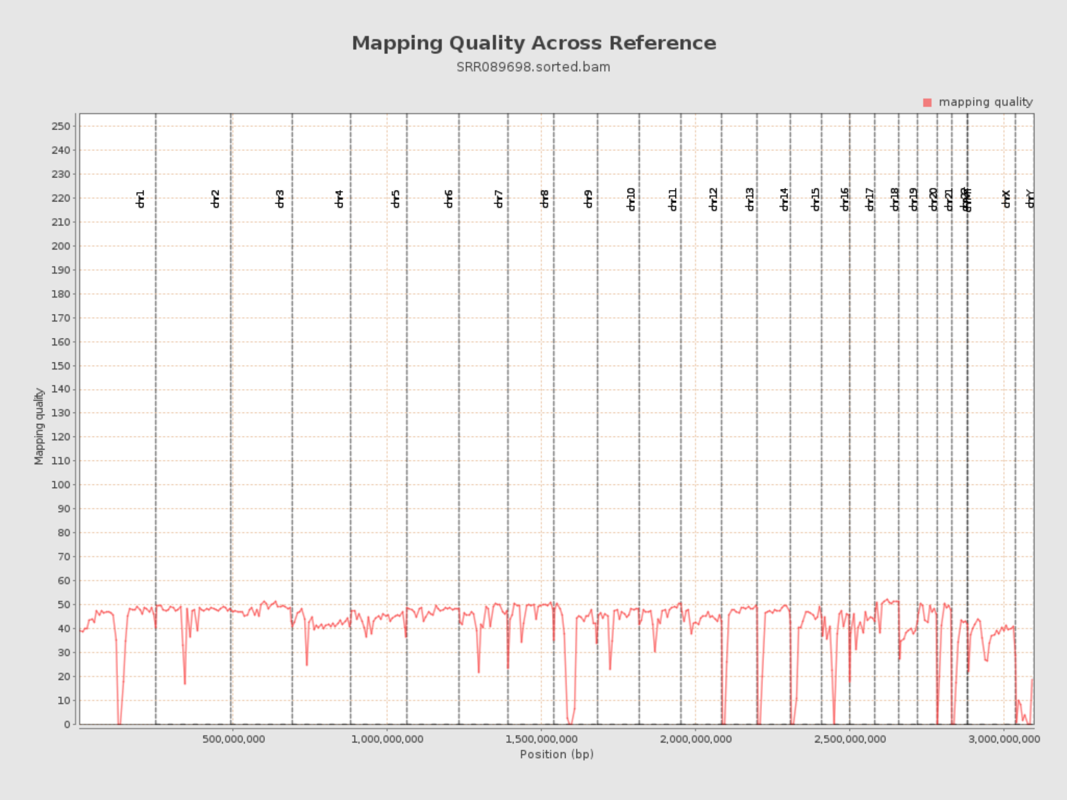
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram