Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 13:10:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089568.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_SRR089568 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089568.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 13:10:42 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089568.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,024,312
Mapped reads	16,644,375 / 79.17%
Unmapped reads	4,379,937 / 20.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	664 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,725,045 / 8.21%
Duplication rate	7.98%
Clipped reads	3,132,970 / 14.9%

2.2. ACGT Content

Number/percentage of A's	246,741,858 / 32.08%
Number/percentage of C's	155,759,082 / 20.25%
Number/percentage of T's	203,371,197 / 26.44%
Number/percentage of G's	163,171,465 / 21.22%
Number/percentage of N's	42,443 / 0.01%
GC Percentage	41.47%

2.3. Coverage

Mean	0.2485

Standard Deviation	1.3158

2.4. Mapping Quality

Mean Mapping Quality	43.6

2.5. Mismatches and indels

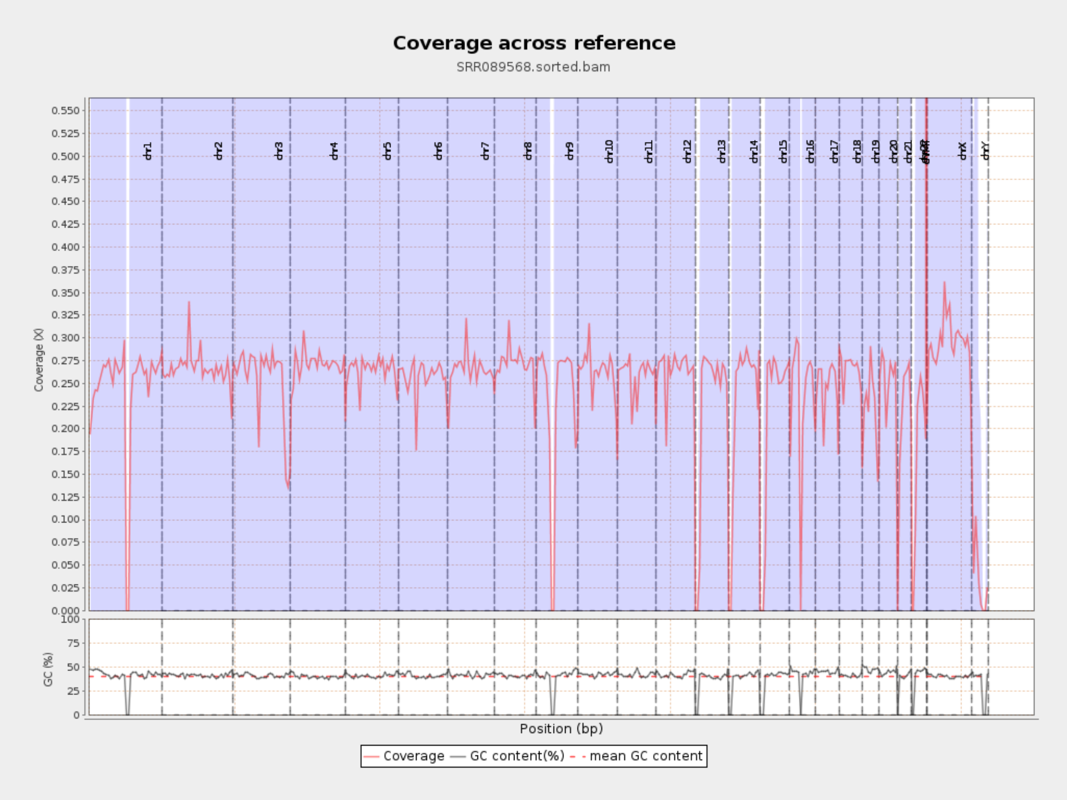
General error rate	0.47%
Mismatches	3,541,690
Insertions	36,256
Mapped reads with at least one insertion	0.22%
Deletions	109,608
Mapped reads with at least one deletion	0.66%
Homopolymer indels	43.09%

2.6. Chromosome stats

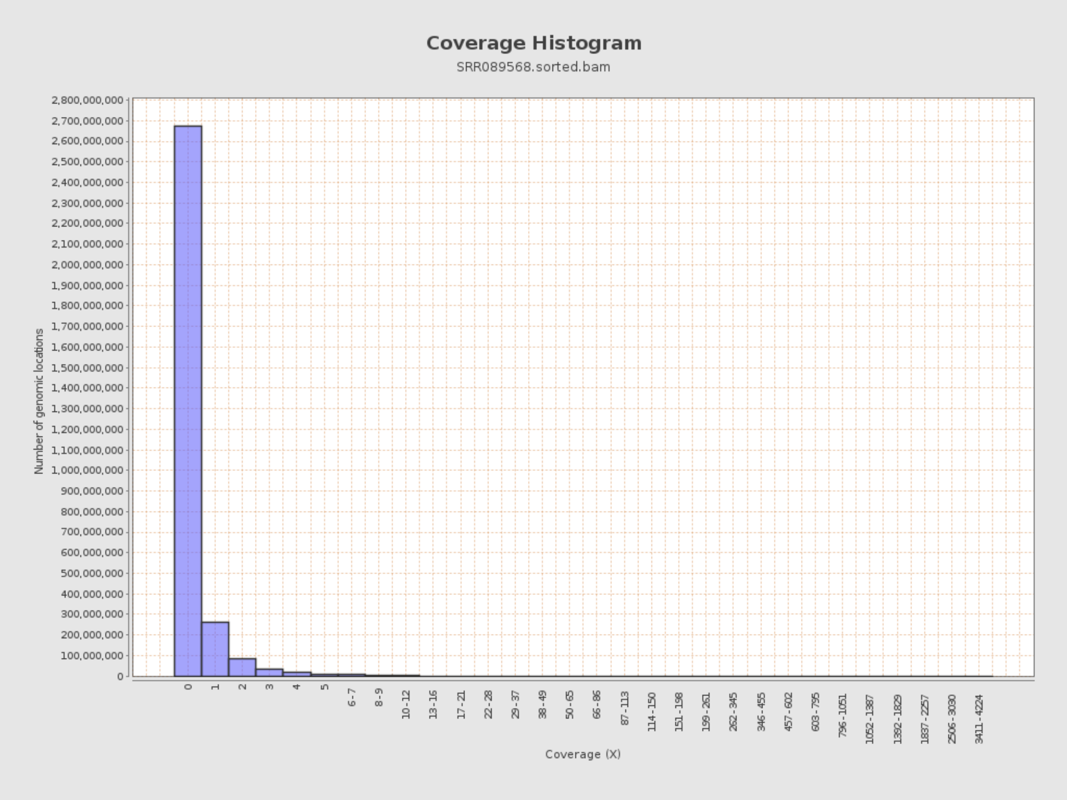
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	60773532	0.2438	1.7904
chr2	243199373	65023584	0.2674	1.5476
chr3	198022430	50432826	0.2547	0.8604
chr4	191154276	51768191	0.2708	0.9602
chr5	180915260	47917476	0.2649	0.8915
chr6	171115067	43998252	0.2571	0.9969
chr7	159138663	42395797	0.2664	1.7439

chr8	146364022	39765728	0.2717	2.4689
chr9	141213431	32330488	0.2289	1.1892
chr10	135534747	35969043	0.2654	1.2759
chr11	135006516	34908839	0.2586	1.2456
chr12	133851895	35297050	0.2637	0.9319
chr13	115169878	25375651	0.2203	0.8171
chr14	107349540	24060574	0.2241	0.9779
chr15	102531392	21677141	0.2114	0.7922
chr16	90354753	21241764	0.2351	0.9409
chr17	81195210	19746847	0.2432	0.9914
chr18	78077248	20810918	0.2665	1.8916
chr19	59128983	13196564	0.2232	1.6737
chr20	63025520	15970094	0.2534	0.9316
chr21	48129895	10060230	0.209	0.9512
chr22	51304566	8349821	0.1628	0.7126
chrMT	16571	162993	9.836	9.4317
chrX	155270560	45863844	0.2954	1.1936
chrY	59373566	2152424	0.0363	0.5442

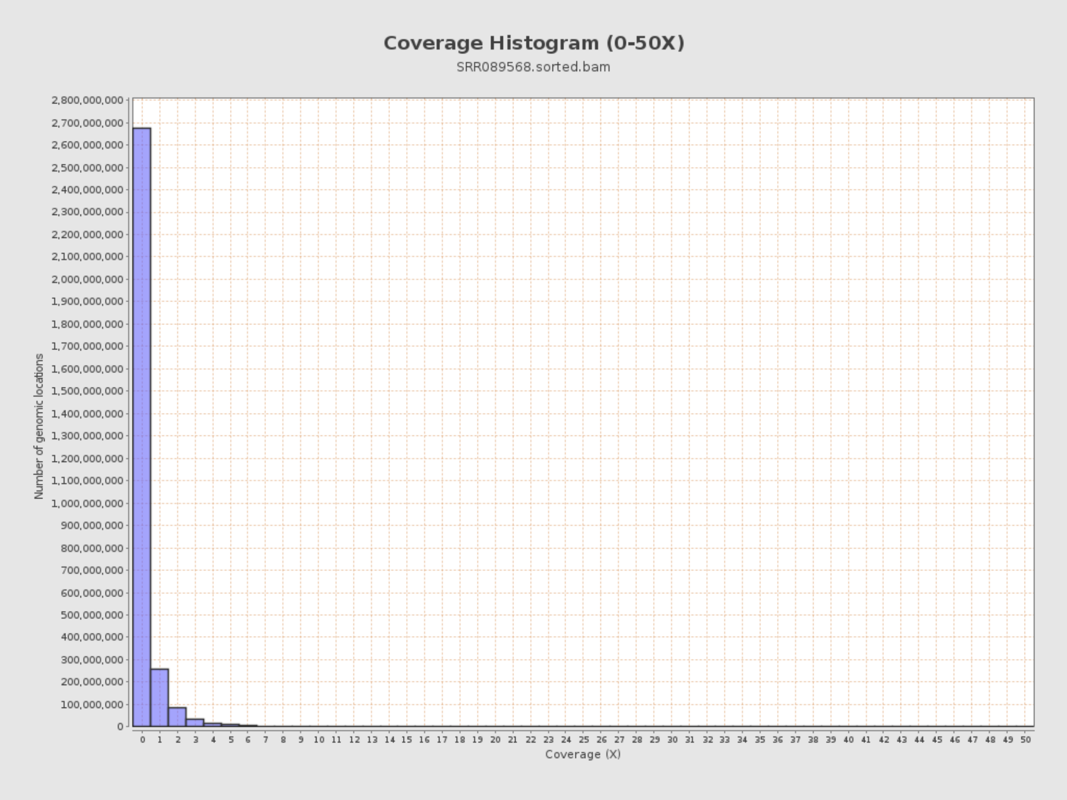
3. Results : Coverage across reference



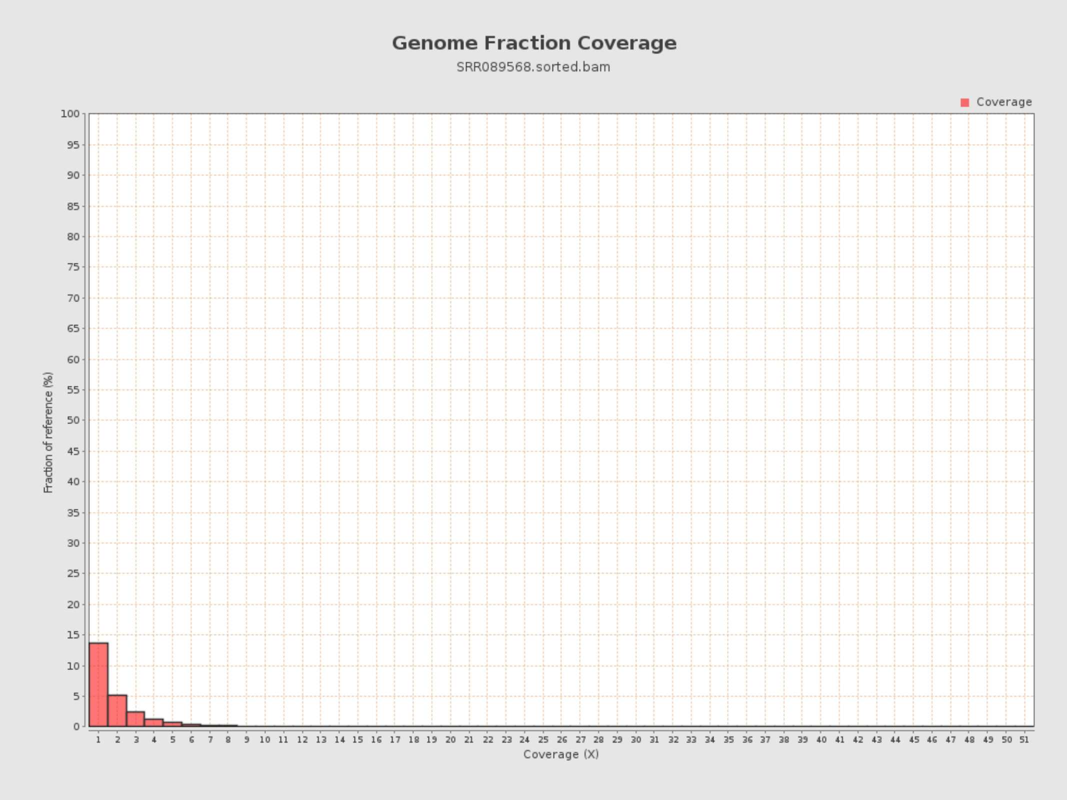
4. Results : Coverage Histogram



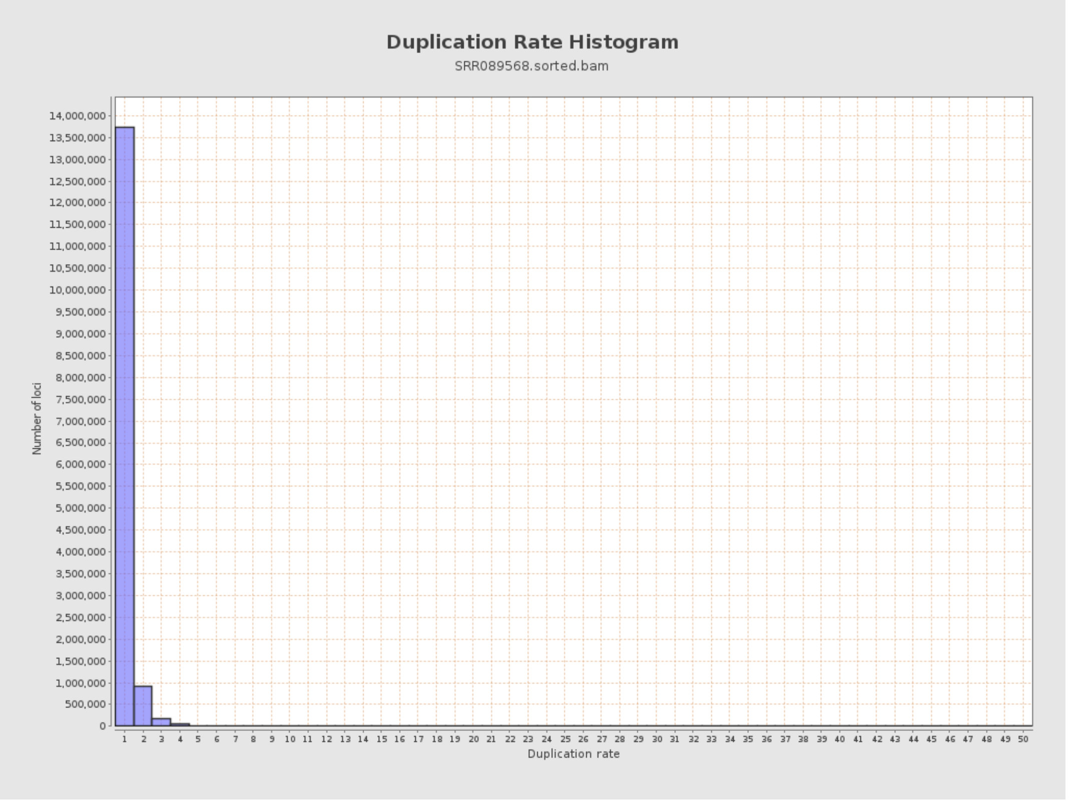
5. Results : Coverage Histogram (0-50X)



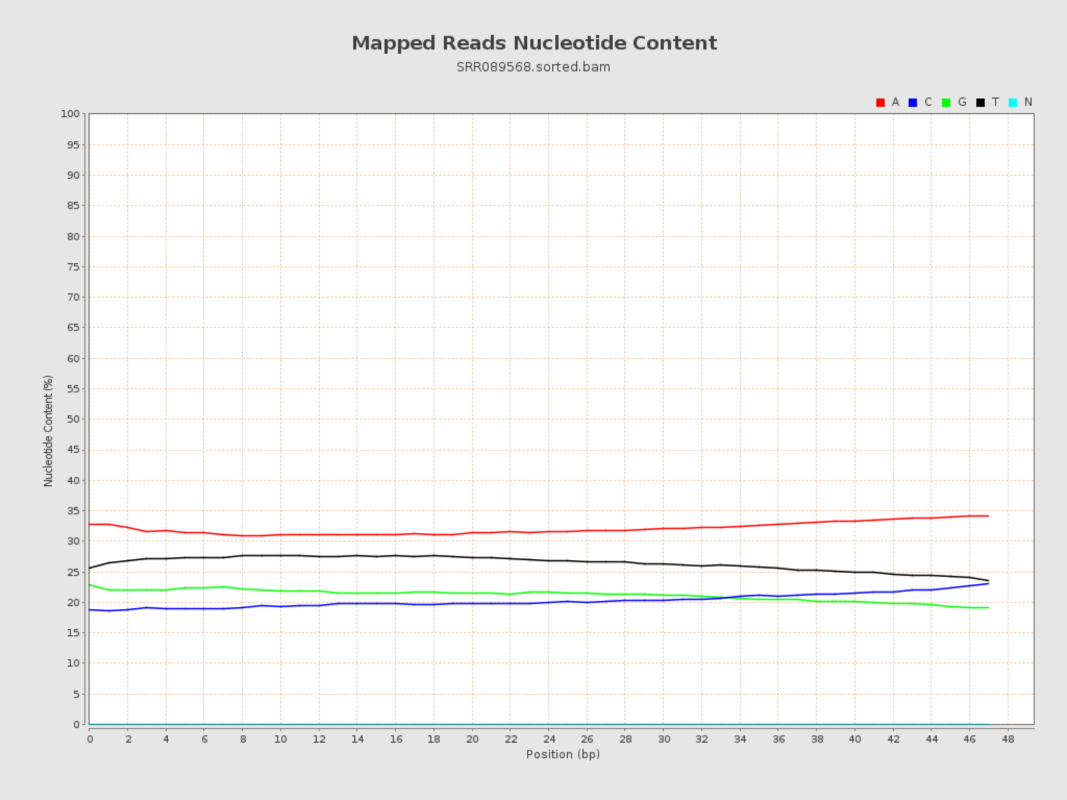
6. Results : Genome Fraction Coverage



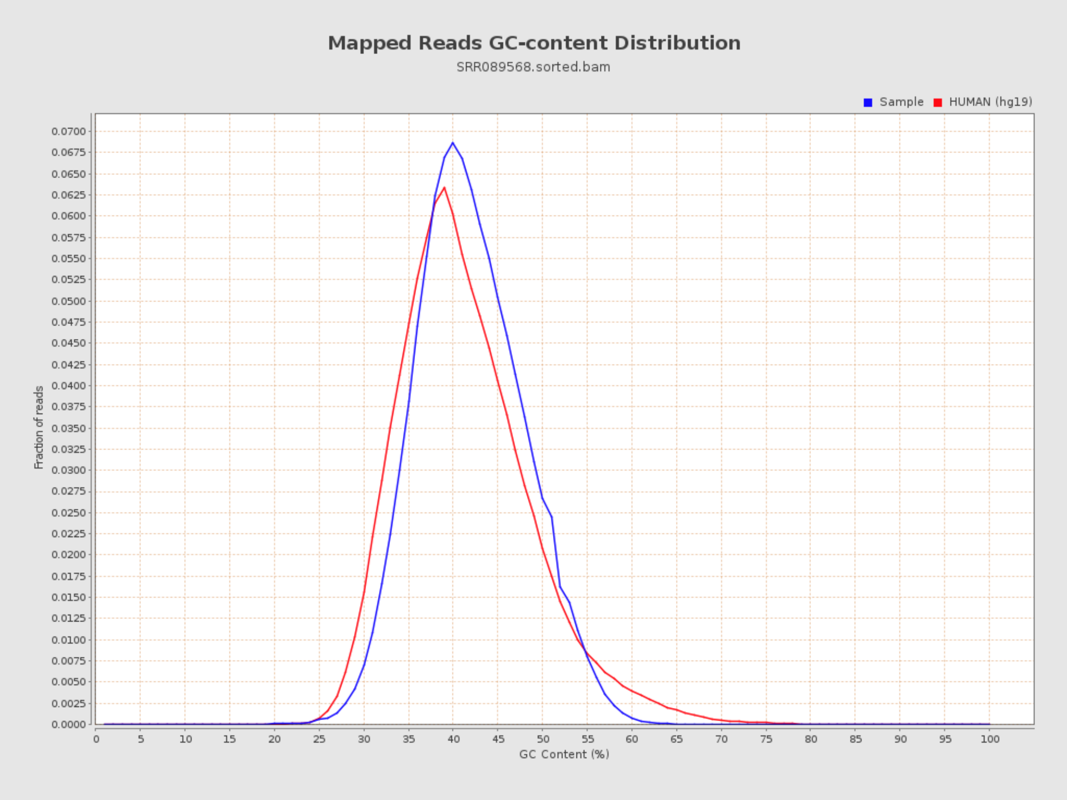
7. Results : Duplication Rate Histogram



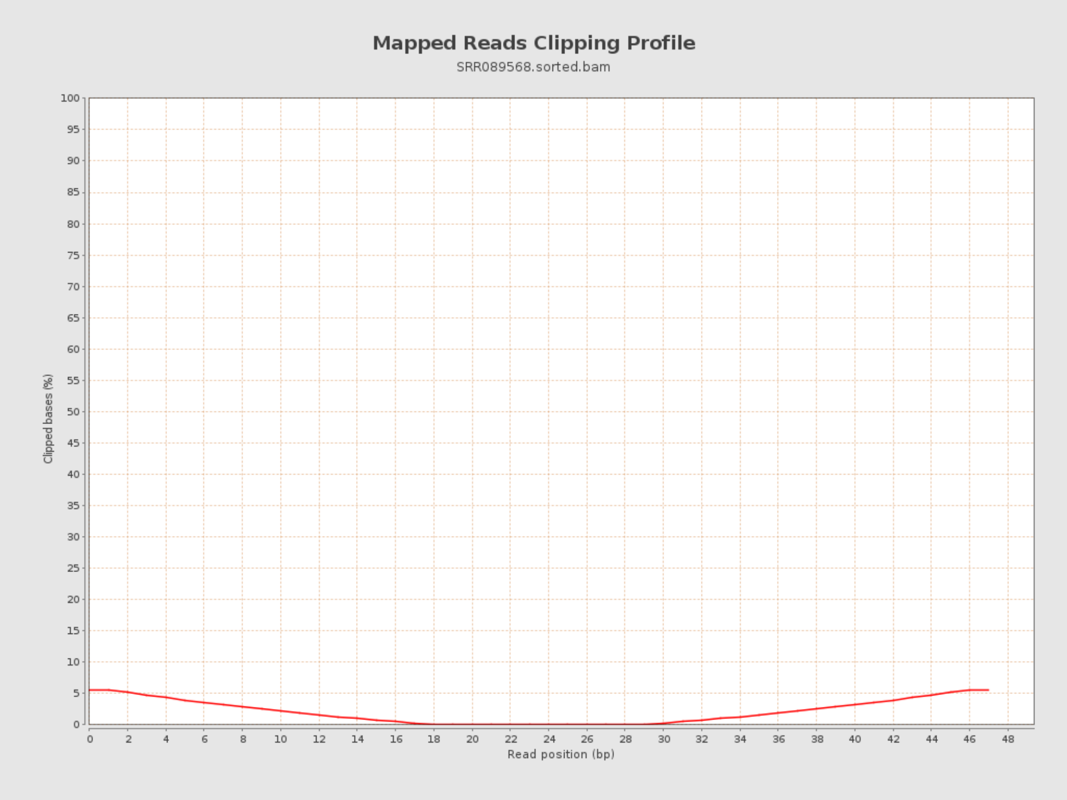
8. Results : Mapped Reads Nucleotide Content



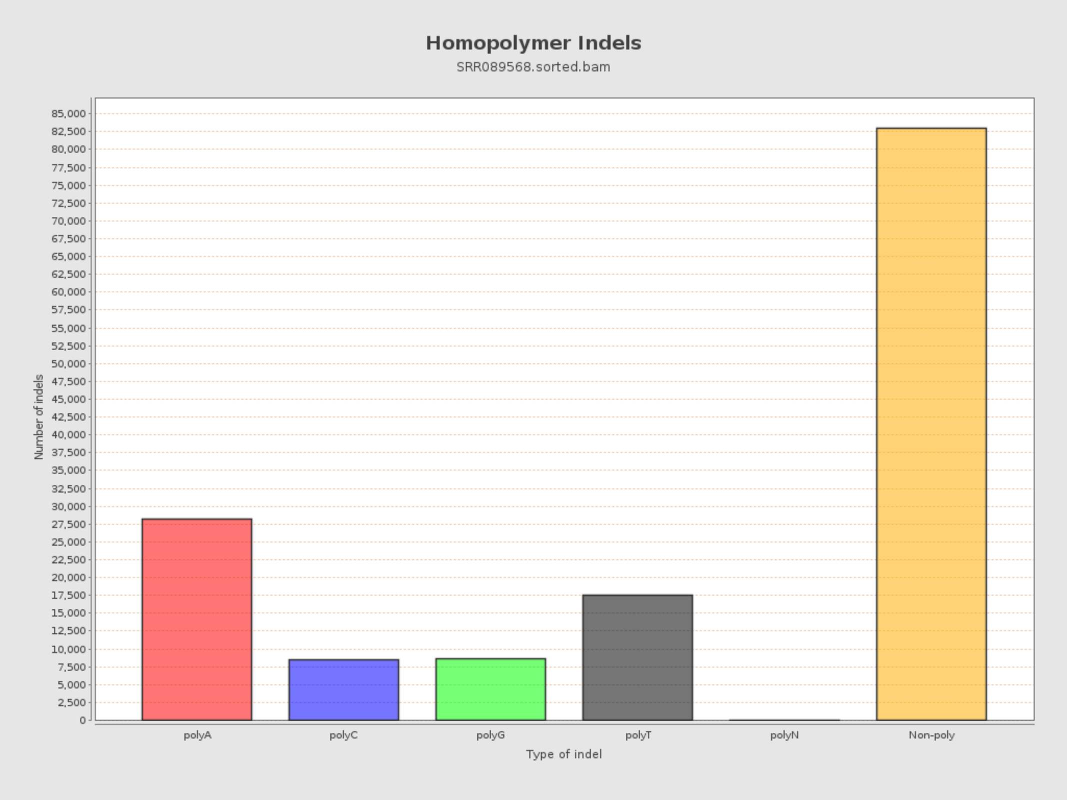
9. Results : Mapped Reads GC-content Distribution



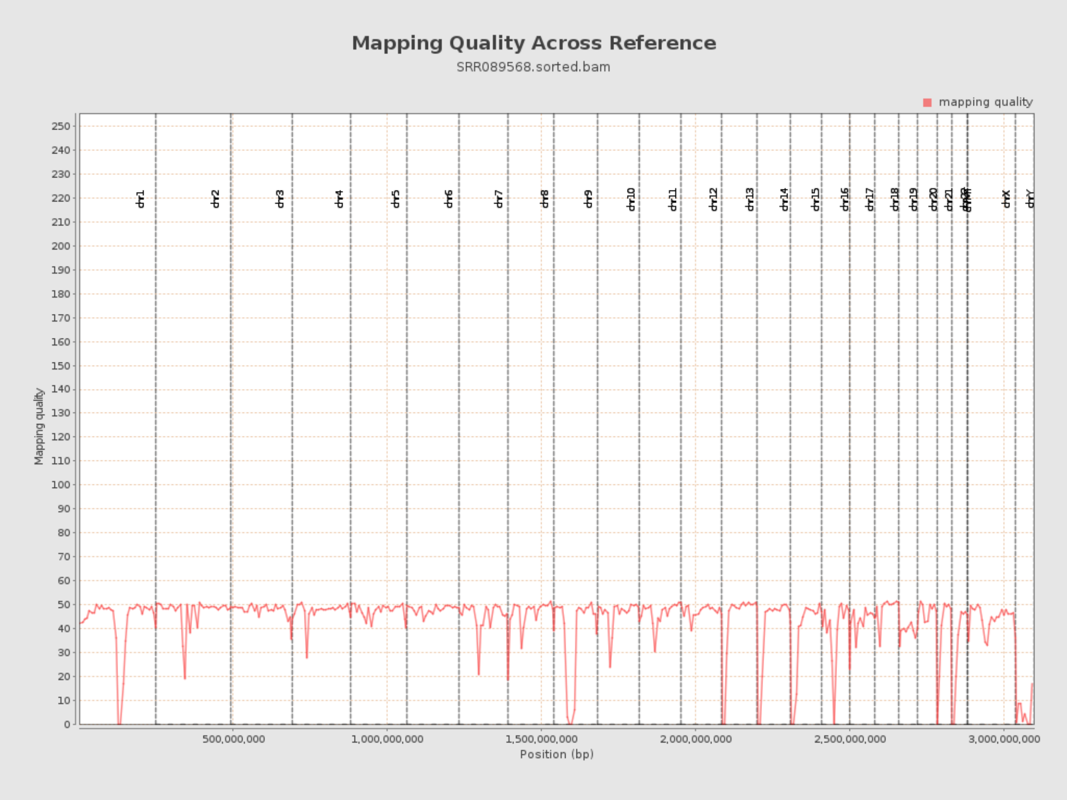
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram