Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 14:31:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089586.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_SRR089586 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089586.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 14:31:41 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089586.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,640,150
Mapped reads	17,805,029 / 78.64%
Unmapped reads	4,835,121 / 21.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	715 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,836,704 / 8.11%
Duplication rate	7.74%
Clipped reads	2,027,299 / 8.95%

2.2. ACGT Content

Number/percentage of A's	257,303,566 / 30.78%
Number/percentage of C's	169,305,258 / 20.26%
Number/percentage of T's	228,175,094 / 27.3%
Number/percentage of G's	180,818,675 / 21.63%
Number/percentage of N's	213,401 / 0.03%
GC Percentage	41.89%

2.3. Coverage

Mean	0.27

Standard Deviation	1.3891

2.4. Mapping Quality

Mean Mapping Quality	43.63

2.5. Mismatches and indels

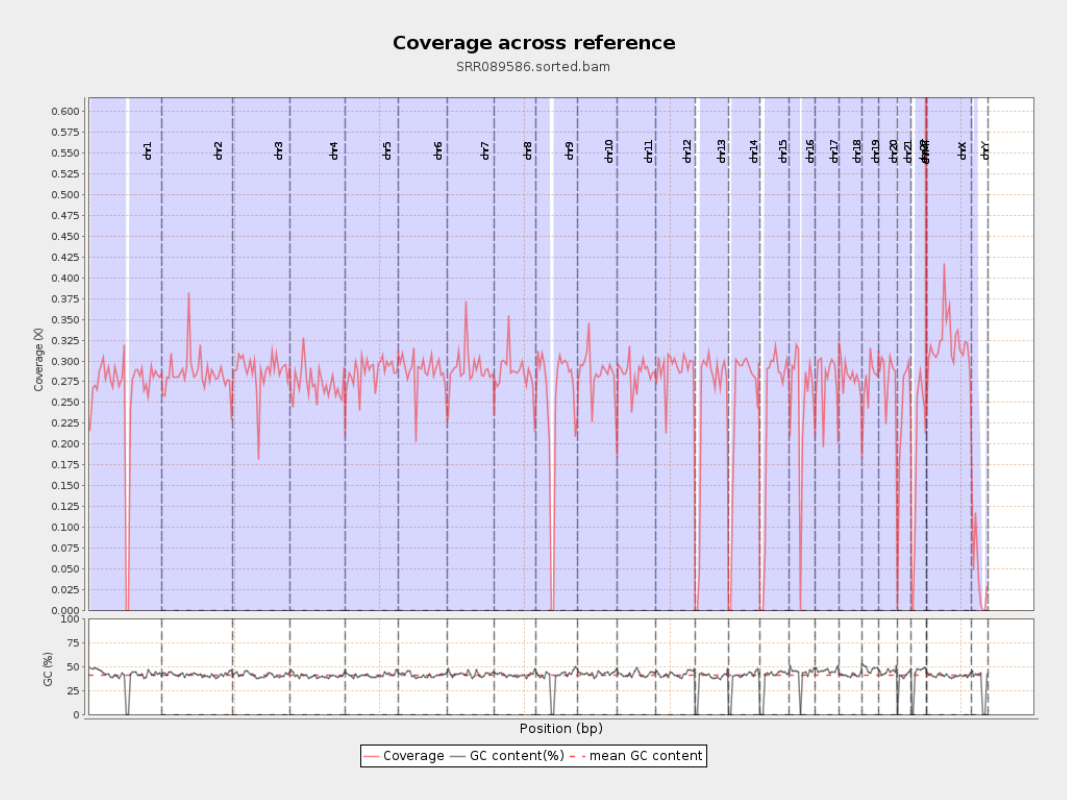
General error rate	0.62%
Mismatches	5,086,286
Insertions	38,008
Mapped reads with at least one insertion	0.21%
Deletions	115,723
Mapped reads with at least one deletion	0.65%
Homopolymer indels	44.01%

2.6. Chromosome stats

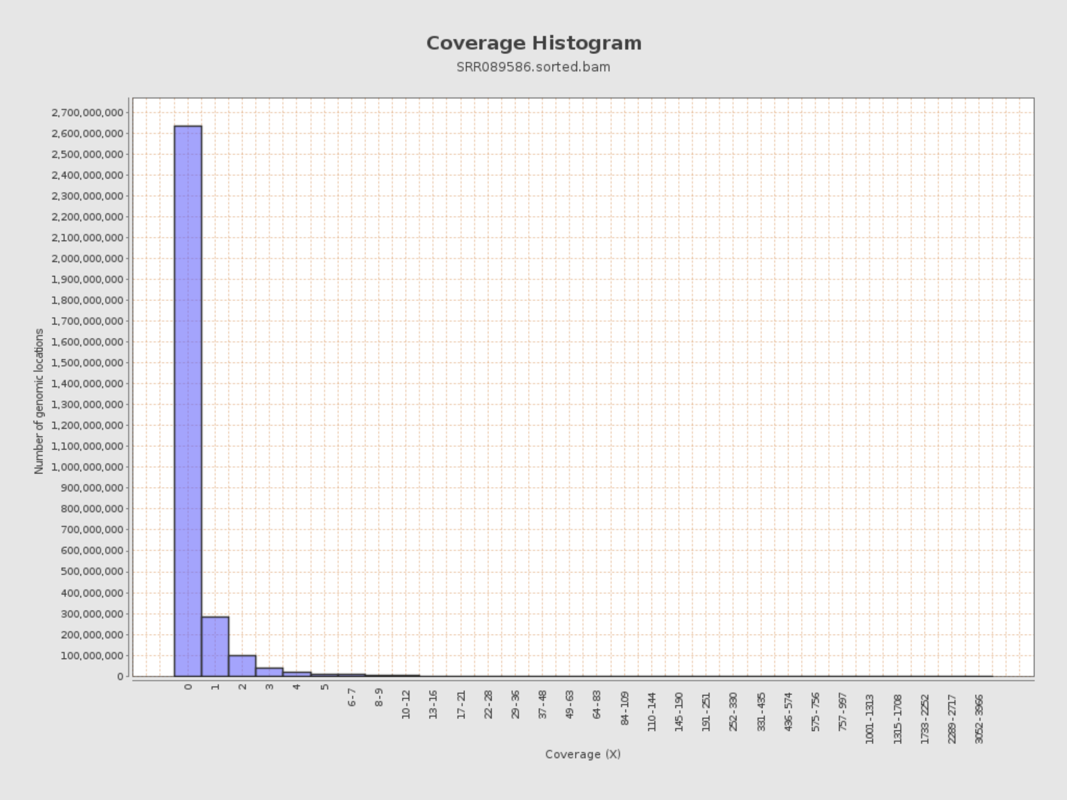
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	65162580	0.2614	1.9785
chr2	243199373	69413511	0.2854	1.6532
chr3	198022430	56900874	0.2873	0.9066
chr4	191154276	52077738	0.2724	0.9577
chr5	180915260	52040298	0.2877	0.9228
chr6	171115067	49286590	0.288	1.102
chr7	159138663	46547162	0.2925	1.9192

chr8	146364022	41814901	0.2857	2.384
chr9	141213431	35284924	0.2499	1.2904
chr10	135534747	38854583	0.2867	1.2871
chr11	135006516	38310928	0.2838	1.3249
chr12	133851895	38800374	0.2899	0.972
chr13	115169878	27683998	0.2404	0.8374
chr14	107349540	26002924	0.2422	1.0406
chr15	102531392	24053627	0.2346	0.8293
chr16	90354753	22713241	0.2514	0.9668
chr17	81195210	22257996	0.2741	1.0567
chr18	78077248	22111956	0.2832	2.0985
chr19	59128983	16362676	0.2767	1.8657
chr20	63025520	17554782	0.2785	0.9829
chr21	48129895	10990382	0.2283	0.9741
chr22	51304566	9347893	0.1822	0.7265
chrMT	16571	225767	13.6242	12.6242
chrX	155270560	49706341	0.3201	1.2324
chrY	59373566	2482946	0.0418	0.5822

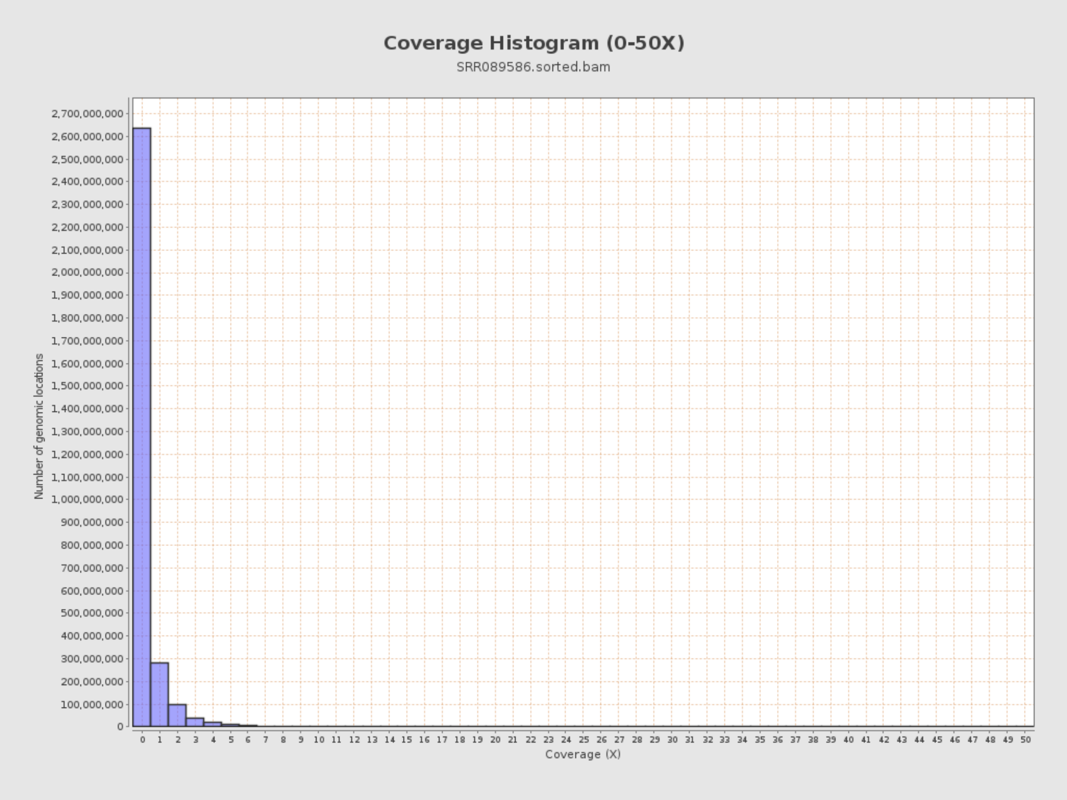
3. Results : Coverage across reference



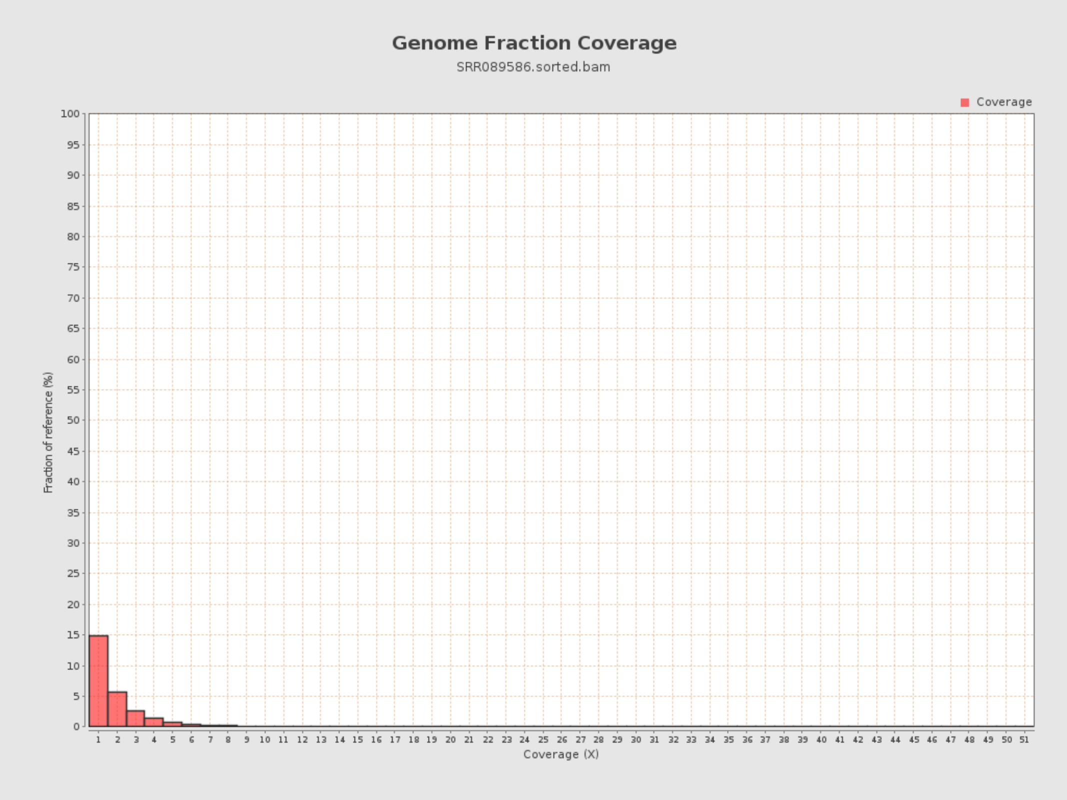
4. Results : Coverage Histogram



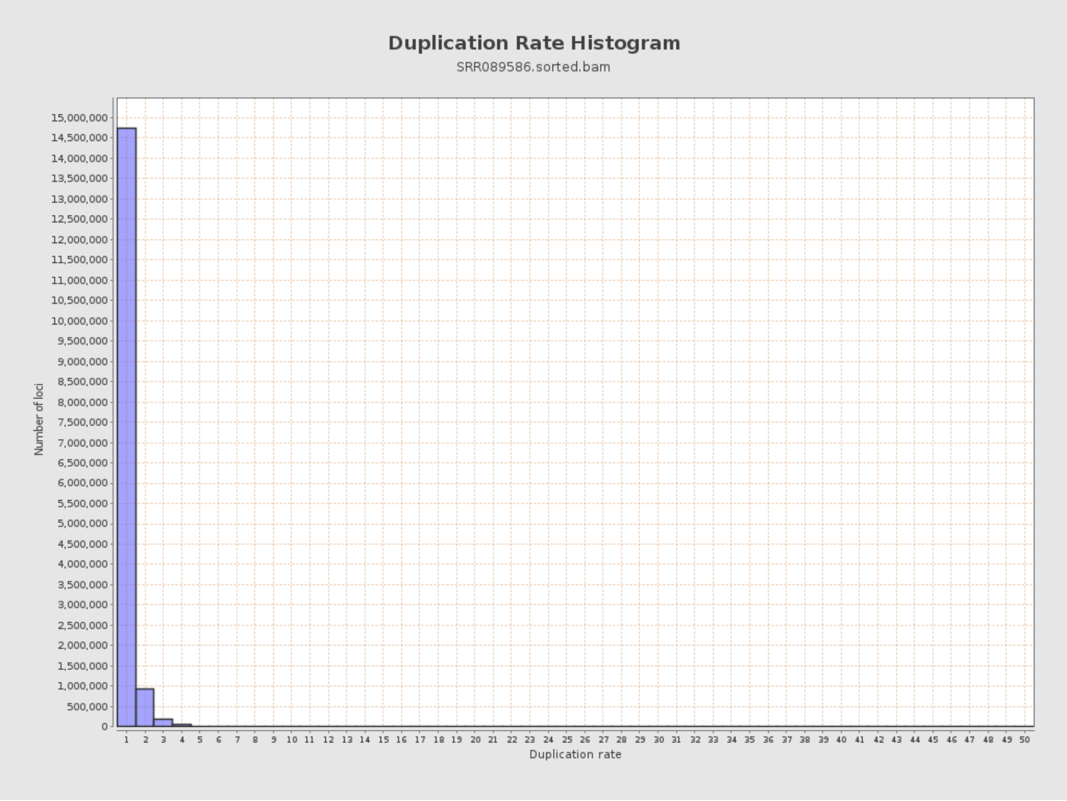
5. Results : Coverage Histogram (0-50X)



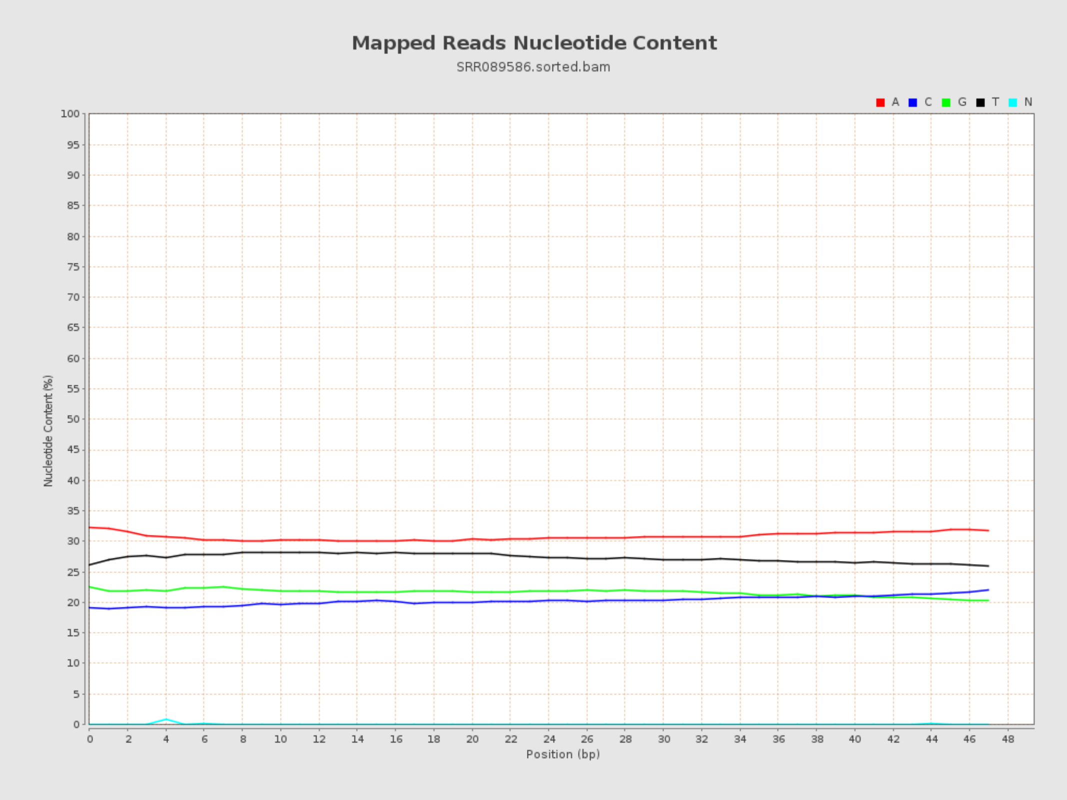
6. Results : Genome Fraction Coverage



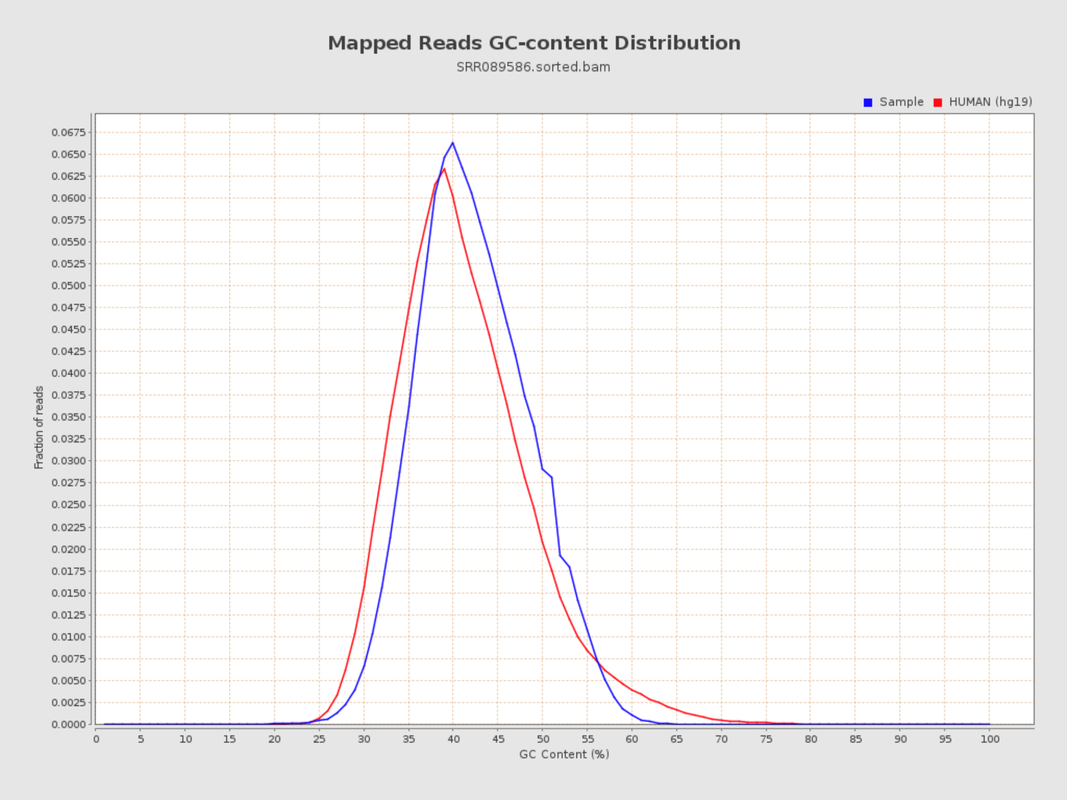
7. Results : Duplication Rate Histogram



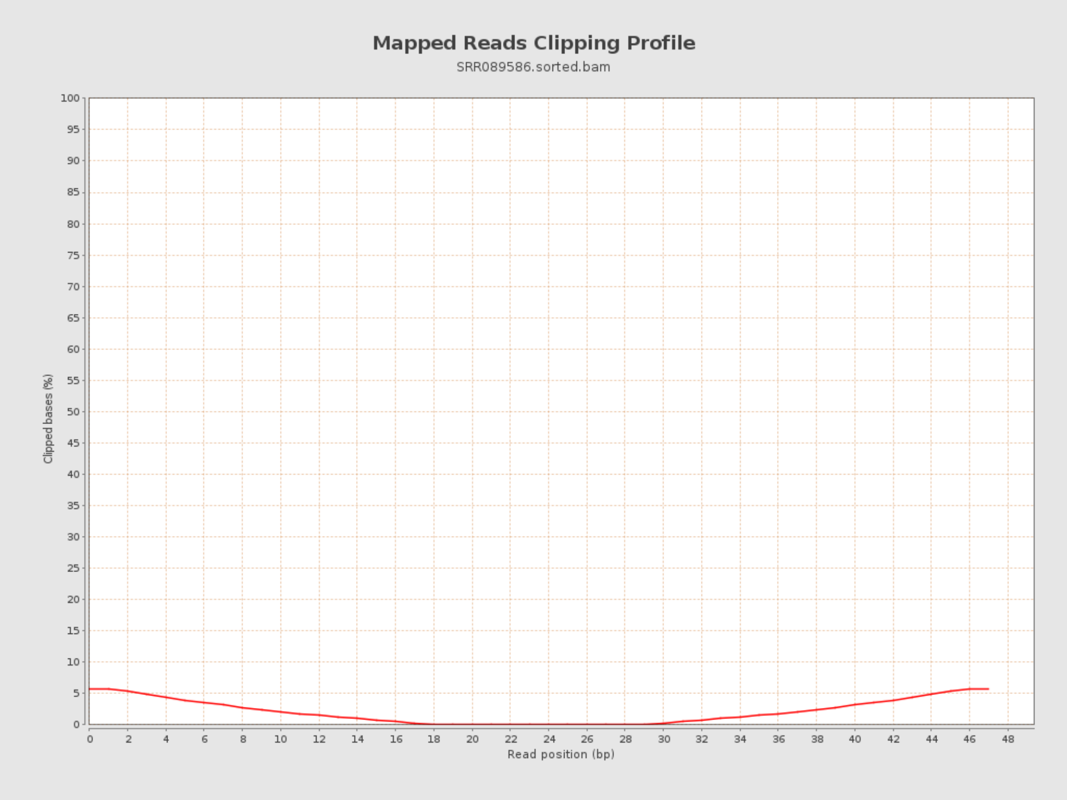
8. Results : Mapped Reads Nucleotide Content



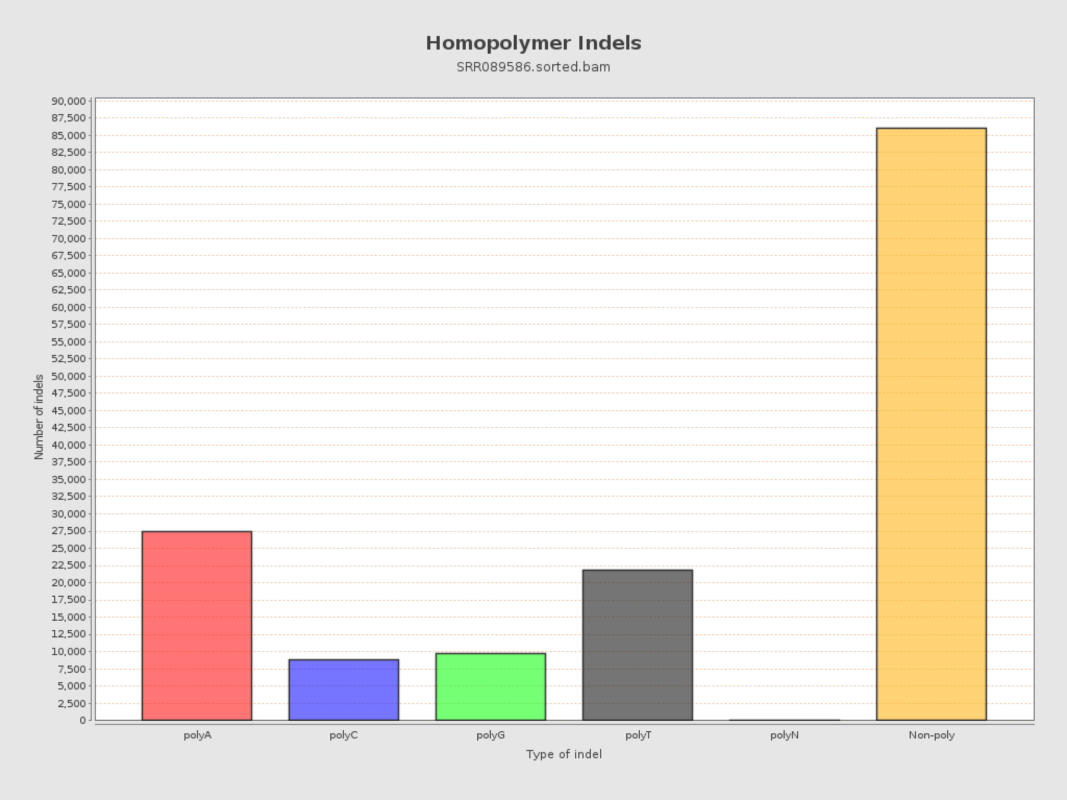
9. Results : Mapped Reads GC-content Distribution



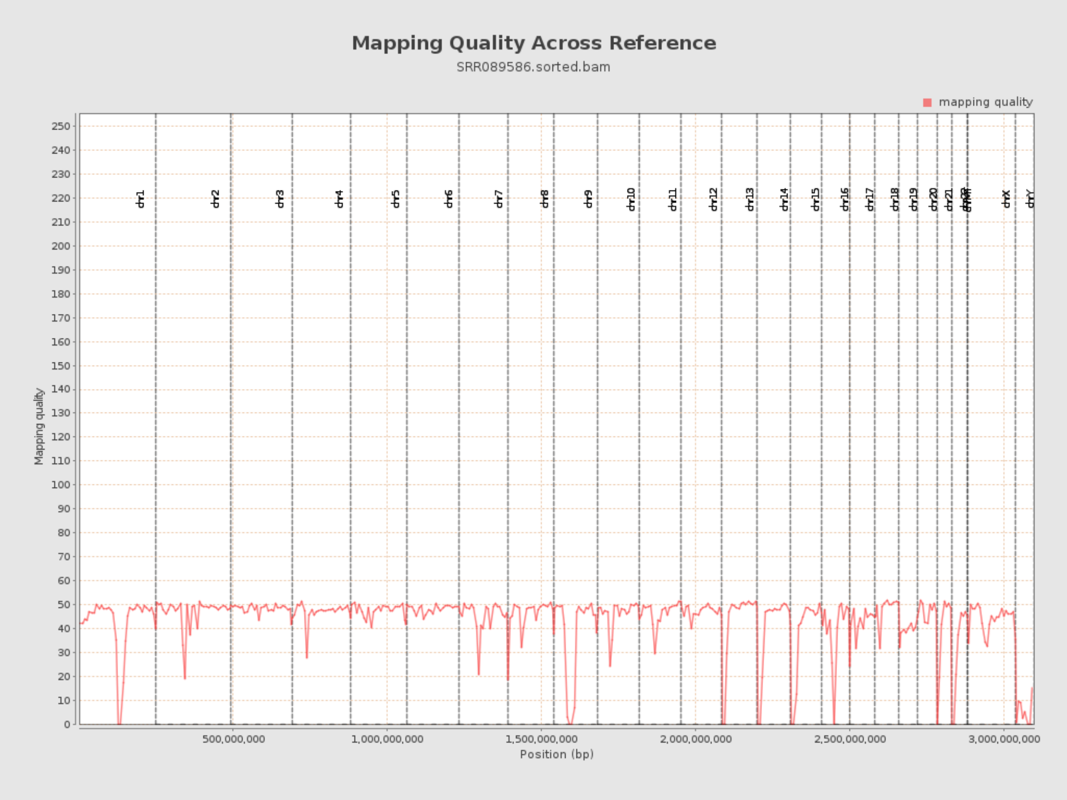
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram