Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 18:31:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089646.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_SRR089646 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089646.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 18:31:21 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089646.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,755,171
Mapped reads	9,641,076 / 75.59%
Unmapped reads	3,114,095 / 24.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	388 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	576,508 / 4.52%
Duplication rate	4.6%
Clipped reads	1,088,881 / 8.54%

2.2. ACGT Content

Number/percentage of A's	133,685,443 / 29.53%
Number/percentage of C's	93,930,781 / 20.75%
Number/percentage of T's	129,279,805 / 28.56%
Number/percentage of G's	95,702,435 / 21.14%
Number/percentage of N's	114,923 / 0.03%
GC Percentage	41.89%

2.3. Coverage

Mean	0.1463

Standard Deviation	0.8459

2.4. Mapping Quality

Mean Mapping Quality	42.74

2.5. Mismatches and indels

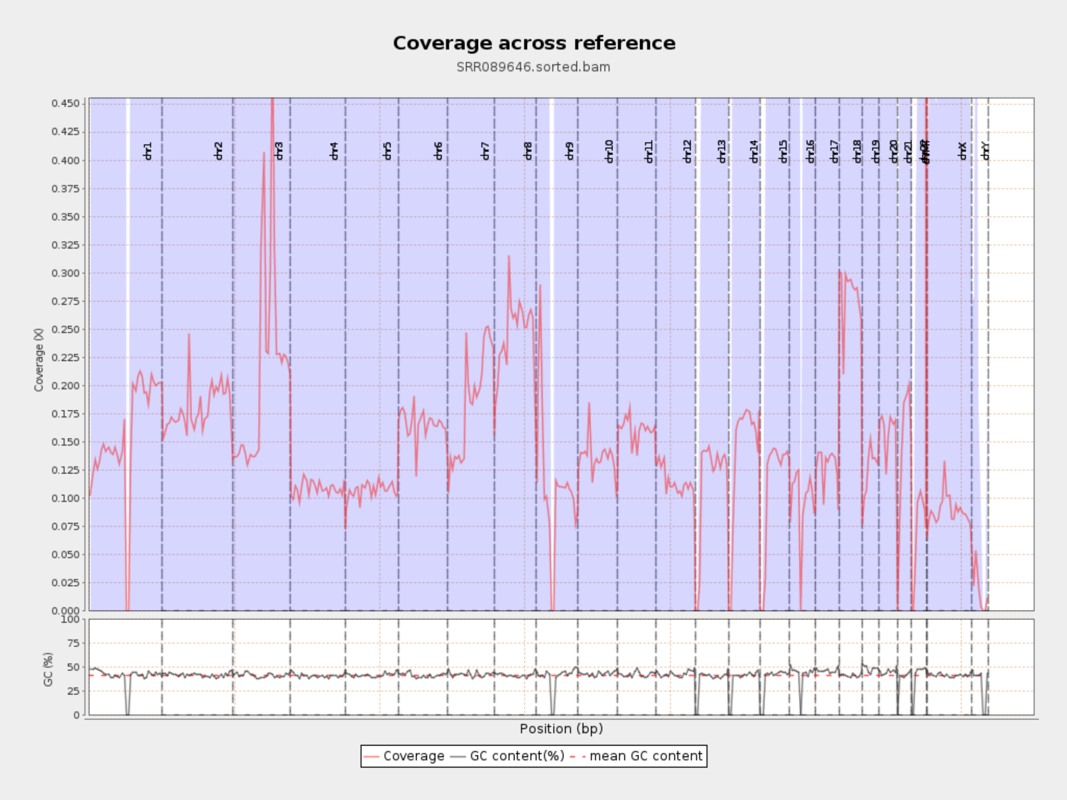
General error rate	0.68%
Mismatches	3,030,959
Insertions	20,052
Mapped reads with at least one insertion	0.21%
Deletions	63,066
Mapped reads with at least one deletion	0.65%
Homopolymer indels	44.44%

2.6. Chromosome stats

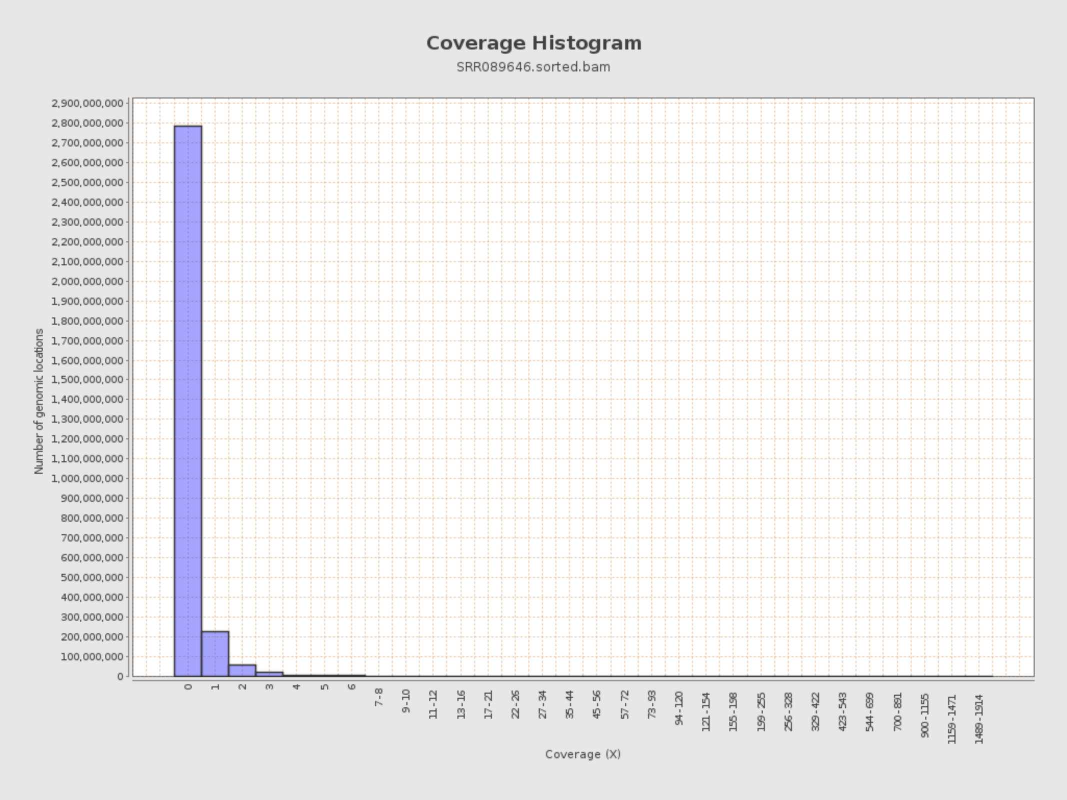
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	38597531	0.1549	1.0386
chr2	243199373	43785249	0.18	1.3032
chr3	198022430	42126971	0.2127	0.6797
chr4	191154276	20725116	0.1084	0.4707
chr5	180915260	19325806	0.1068	0.4523
chr6	171115067	28375006	0.1658	0.6976
chr7	159138663	29602483	0.186	1.3569

chr8	146364022	36013908	0.2461	1.3404
chr9	141213431	15769123	0.1117	0.7962
chr10	135534747	18530263	0.1367	0.7912
chr11	135006516	21629835	0.1602	0.8079
chr12	133851895	15243081	0.1139	0.49
chr13	115169878	12958795	0.1125	0.4591
chr14	107349540	14917166	0.139	0.585
chr15	102531392	11258111	0.1098	0.4569
chr16	90354753	8776598	0.0971	0.4942
chr17	81195210	10417824	0.1283	0.5654
chr18	78077248	21867719	0.2801	1.2079
chr19	59128983	7468993	0.1263	1.0455
chr20	63025520	9933579	0.1576	0.5812
chr21	48129895	6952133	0.1444	0.5905
chr22	51304566	3487206	0.068	0.3486
chrMT	16571	229588	13.8548	11.2624
chrX	155270560	13777167	0.0887	0.6097
chrY	59373566	1037181	0.0175	0.2777

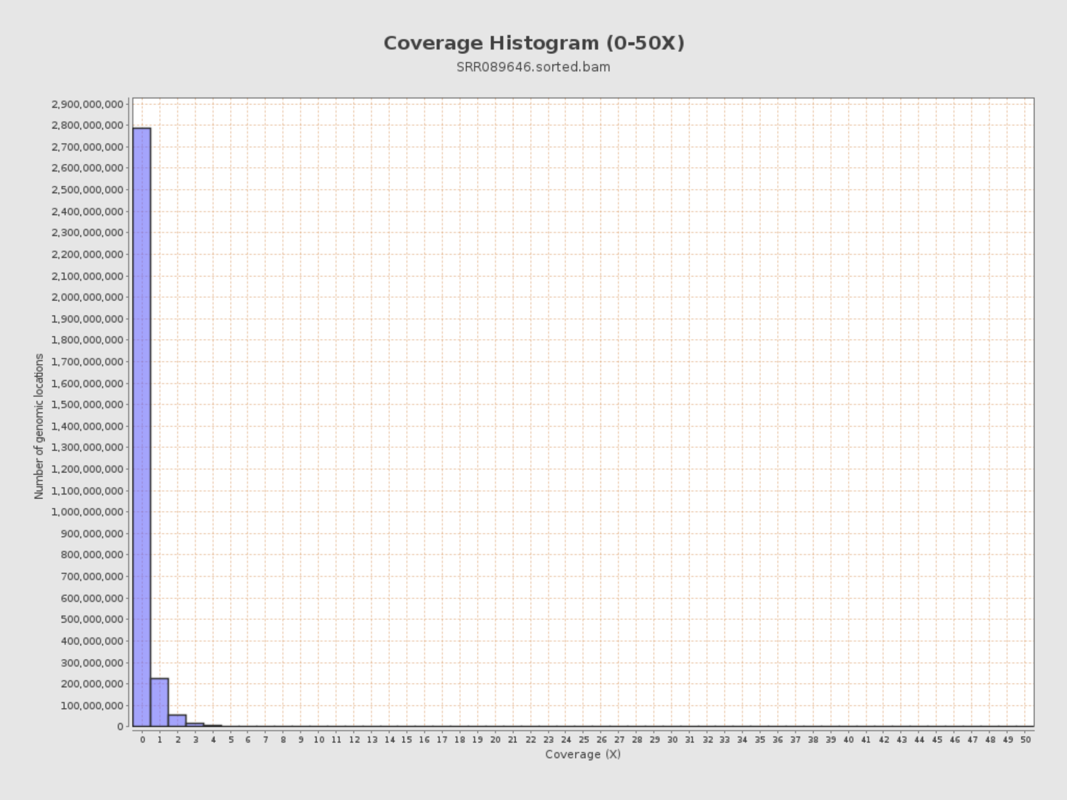
3. Results : Coverage across reference



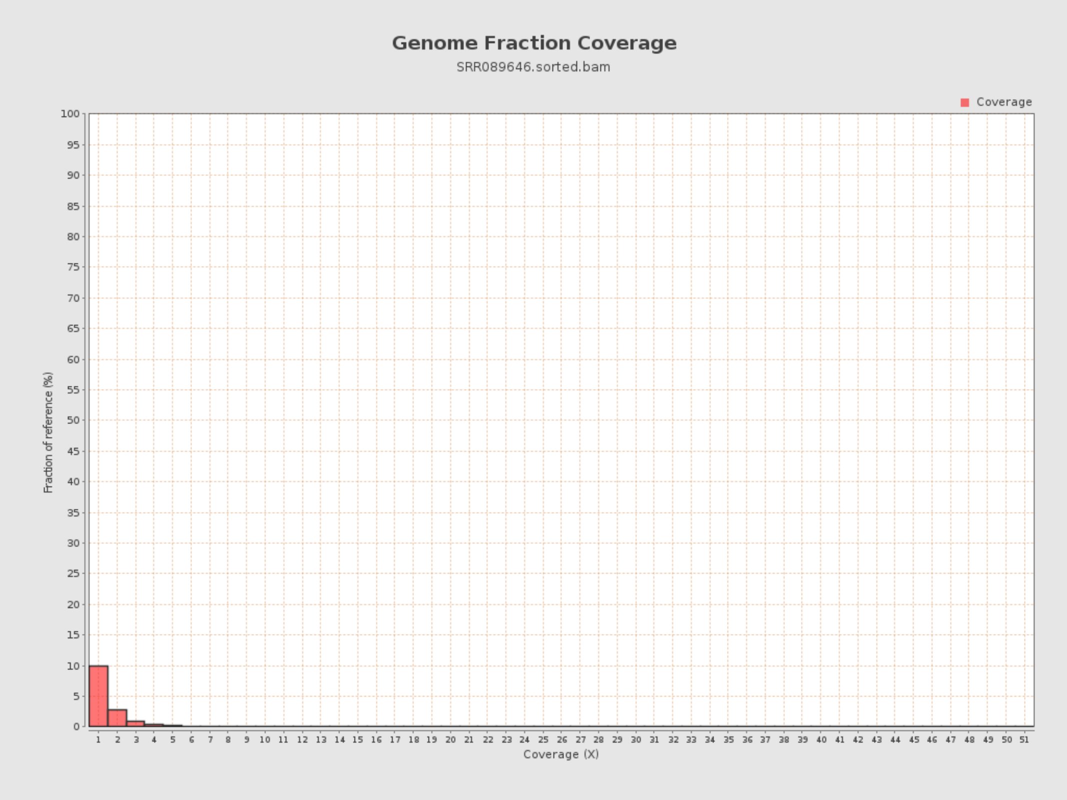
4. Results : Coverage Histogram



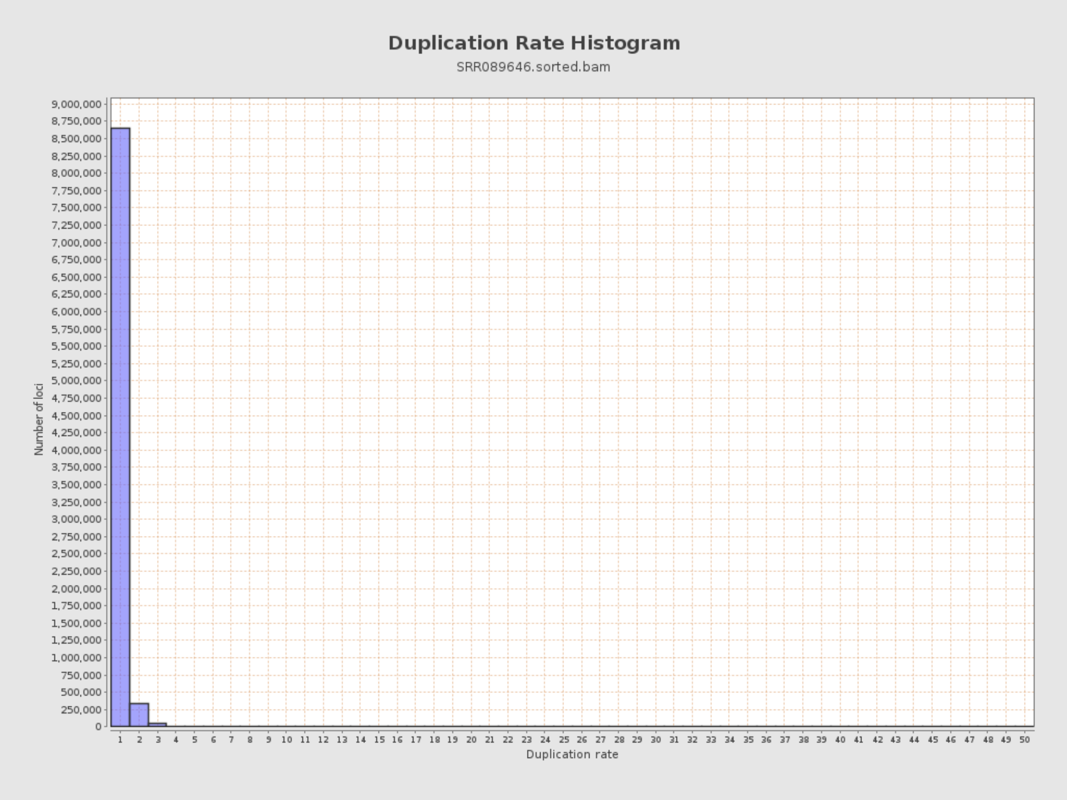
5. Results : Coverage Histogram (0-50X)



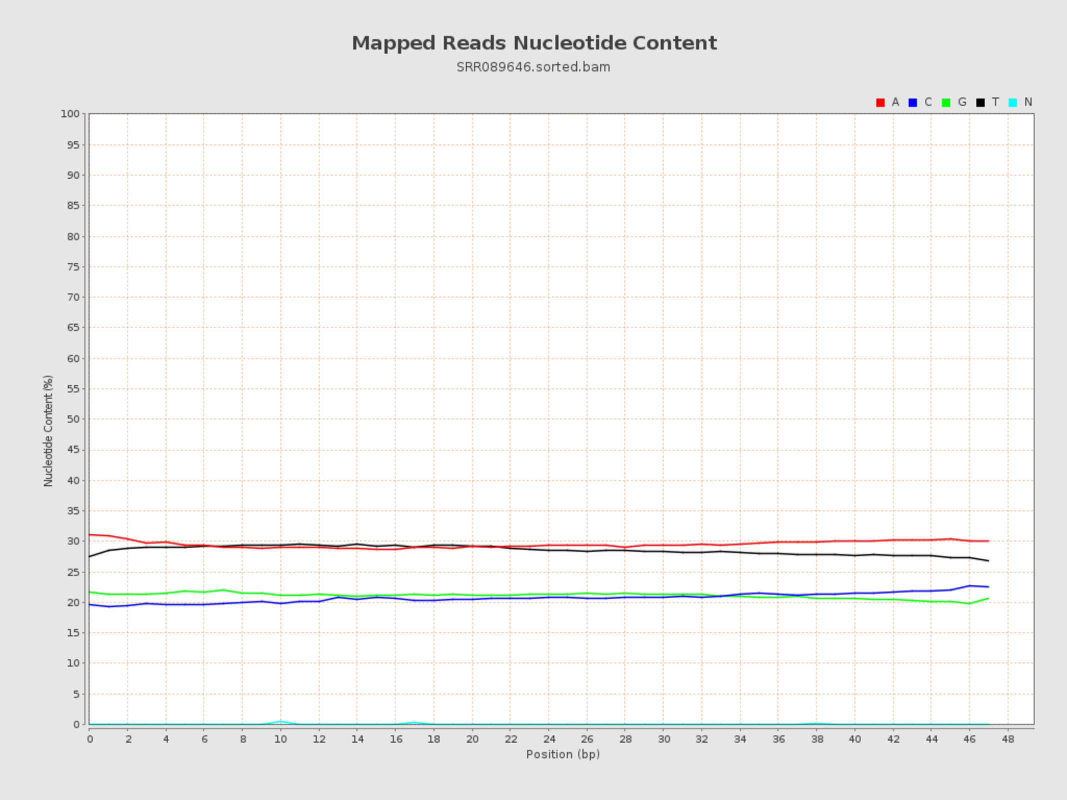
6. Results : Genome Fraction Coverage



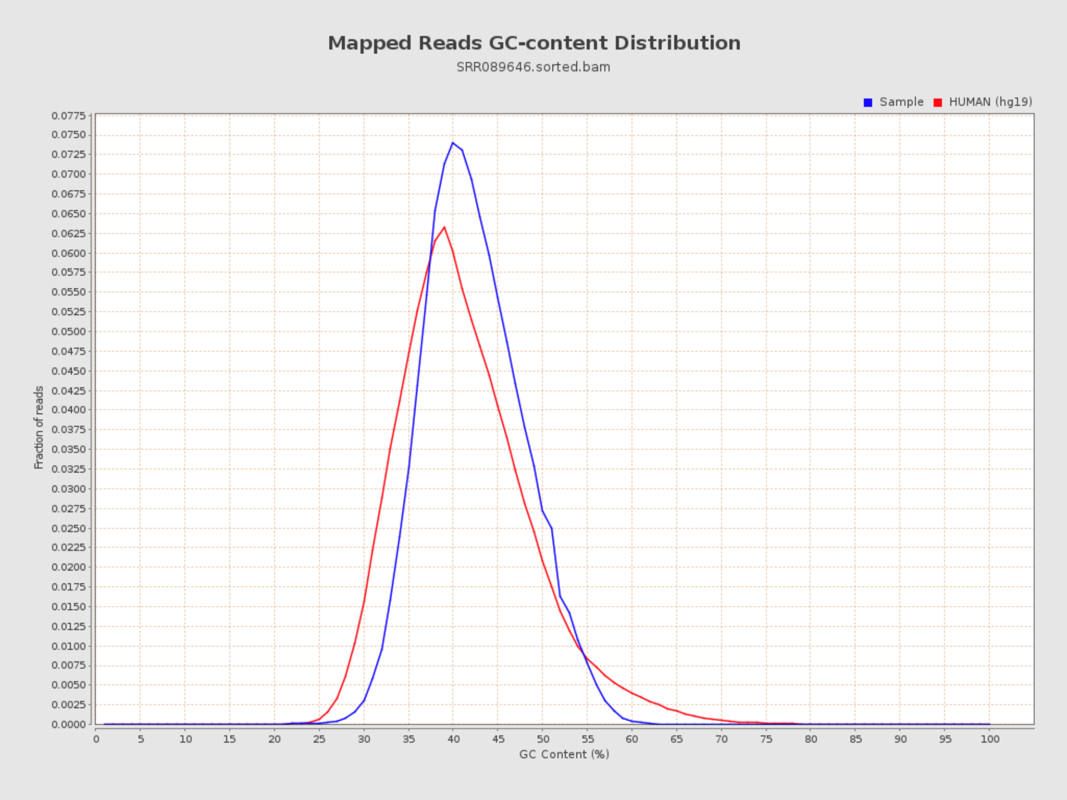
7. Results : Duplication Rate Histogram



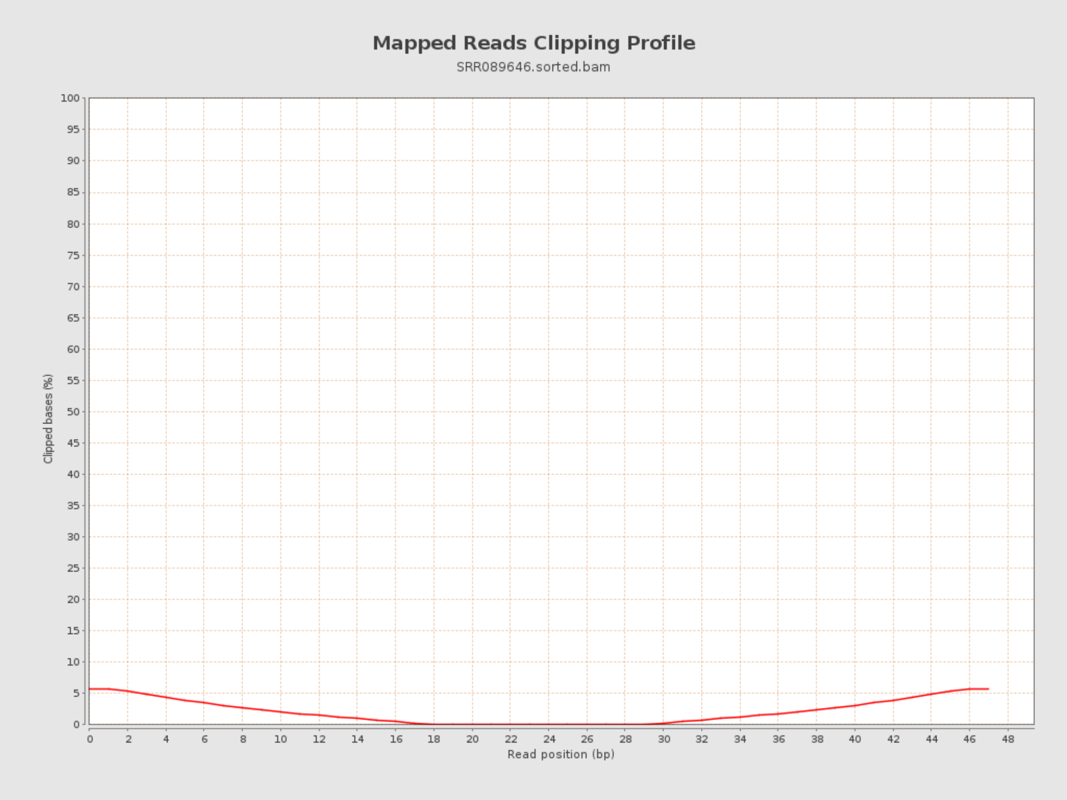
8. Results : Mapped Reads Nucleotide Content



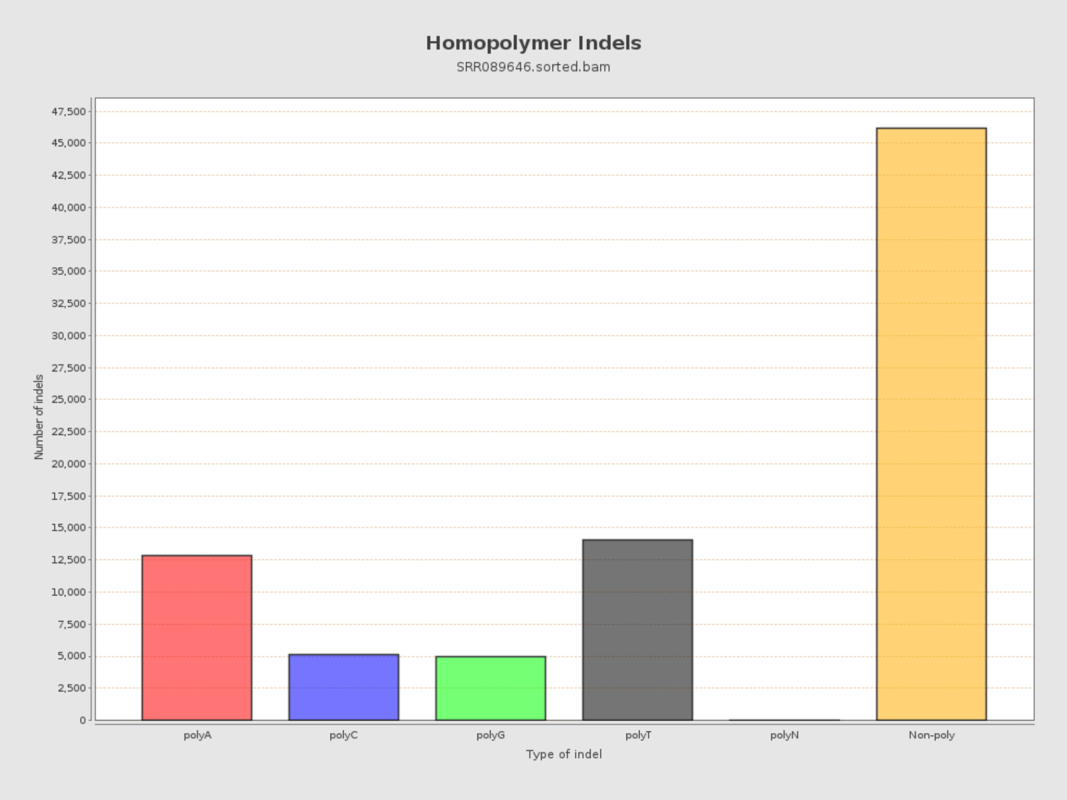
9. Results : Mapped Reads GC-content Distribution



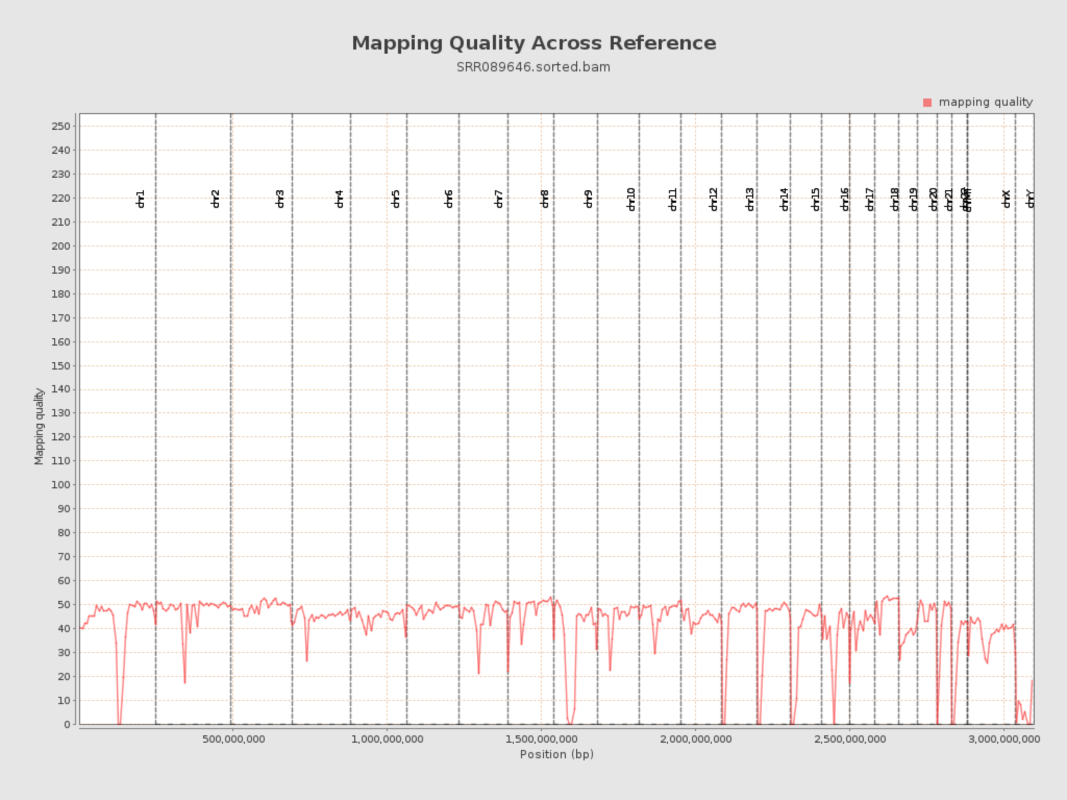
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram