Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 17:33:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089606.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_SRR089606 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089606.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 17:33:25 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089606.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,183,843
Mapped reads	9,302,190 / 83.18%
Unmapped reads	1,881,653 / 16.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	386 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,552,188 / 22.82%
Duplication rate	20.18%
Clipped reads	1,038,748 / 9.29%

2.2. ACGT Content

Number/percentage of A's	139,180,152 / 31.85%
Number/percentage of C's	82,569,431 / 18.89%
Number/percentage of T's	120,403,200 / 27.55%
Number/percentage of G's	94,689,169 / 21.67%
Number/percentage of N's	201,365 / 0.05%
GC Percentage	40.56%

2.3. Coverage

Mean	0.1412

Standard Deviation	1.0665

2.4. Mapping Quality

Mean Mapping Quality	45.02

2.5. Mismatches and indels

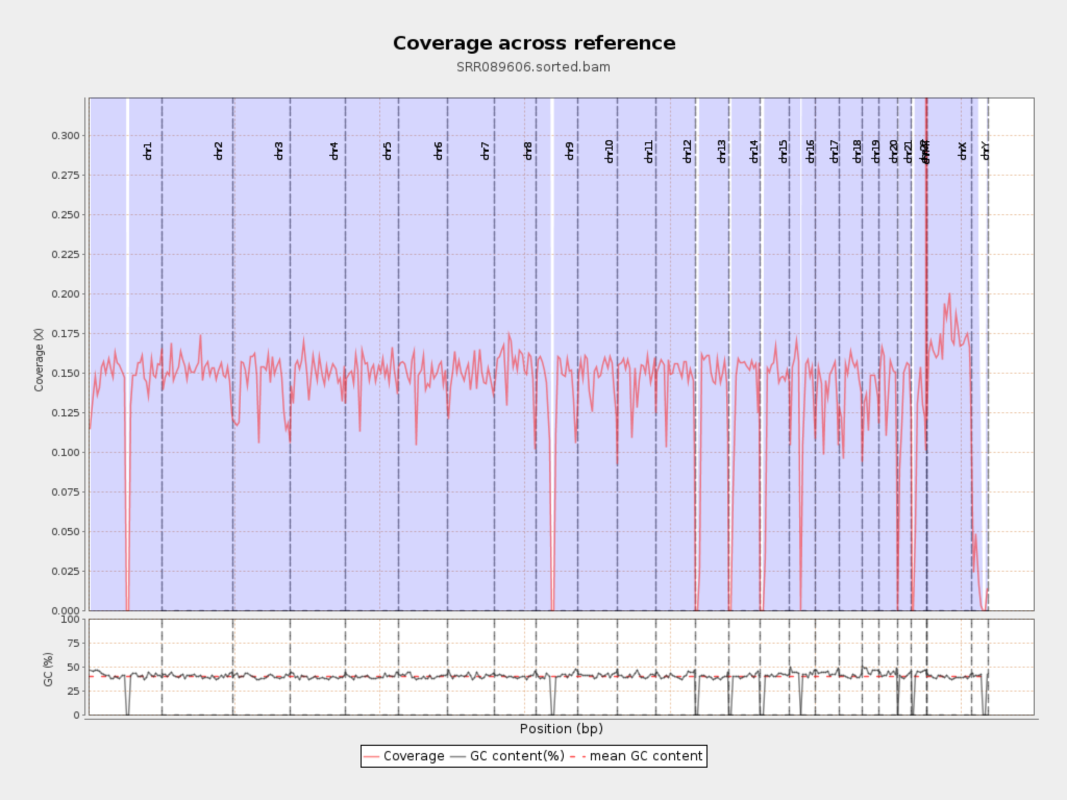
General error rate	0.58%
Mismatches	2,500,655
Insertions	18,850
Mapped reads with at least one insertion	0.2%
Deletions	59,468
Mapped reads with at least one deletion	0.64%
Homopolymer indels	46.55%

2.6. Chromosome stats

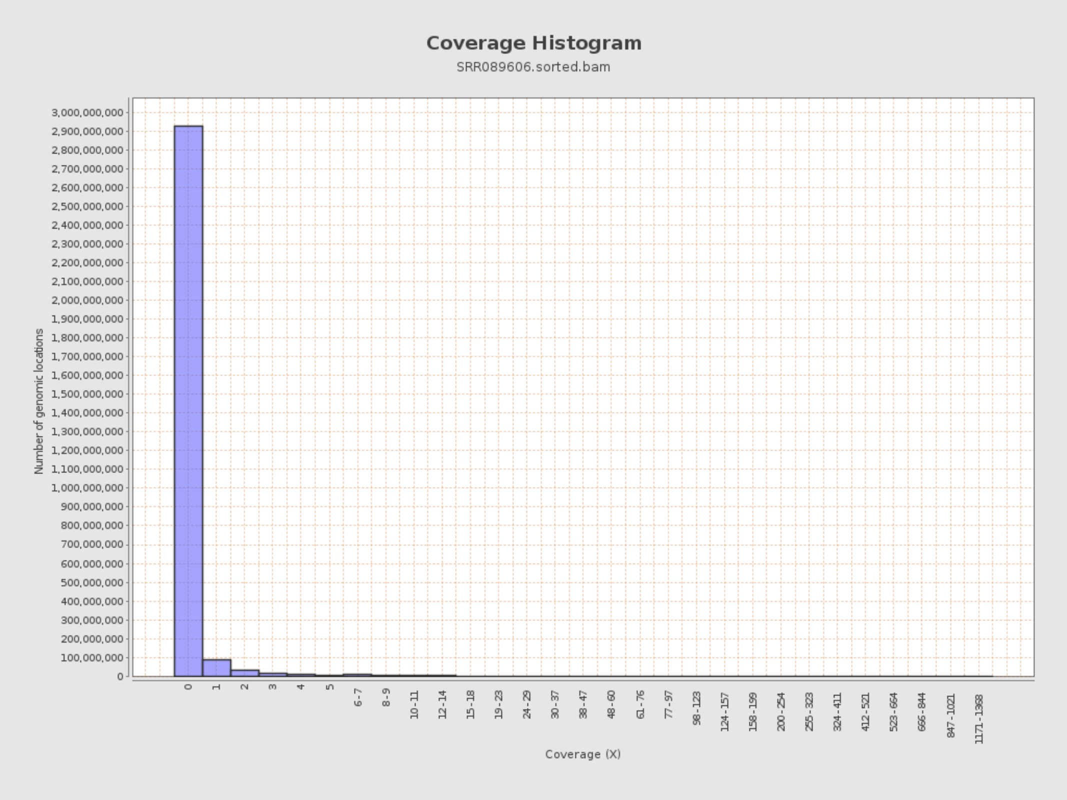
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	34834505	0.1398	1.1107
chr2	243199373	36988072	0.1521	1.2797
chr3	198022430	28367870	0.1433	0.9923
chr4	191154276	28674327	0.15	1.0643
chr5	180915260	27223744	0.1505	1.0048
chr6	171115067	25511341	0.1491	1.0677
chr7	159138663	23778763	0.1494	1.213

chr8	146364022	22677989	0.1549	1.2934
chr9	141213431	18171073	0.1287	0.9707
chr10	135534747	20314475	0.1499	1.0575
chr11	135006516	20048184	0.1485	1.0958
chr12	133851895	19926057	0.1489	0.9934
chr13	115169878	14627720	0.127	0.9401
chr14	107349540	13689652	0.1275	1.0263
chr15	102531392	12446040	0.1214	0.8859
chr16	90354753	12047665	0.1333	0.9555
chr17	81195210	11198814	0.1379	0.9591
chr18	78077248	11209532	0.1436	1.0871
chr19	59128983	7966002	0.1347	1.0531
chr20	63025520	9164758	0.1454	1.0153
chr21	48129895	5782490	0.1201	0.9618
chr22	51304566	4750875	0.0926	0.7347
chrMT	16571	110267	6.6542	11.9999
chrX	155270560	26502744	0.1707	1.1531
chrY	59373566	1119299	0.0189	0.4065

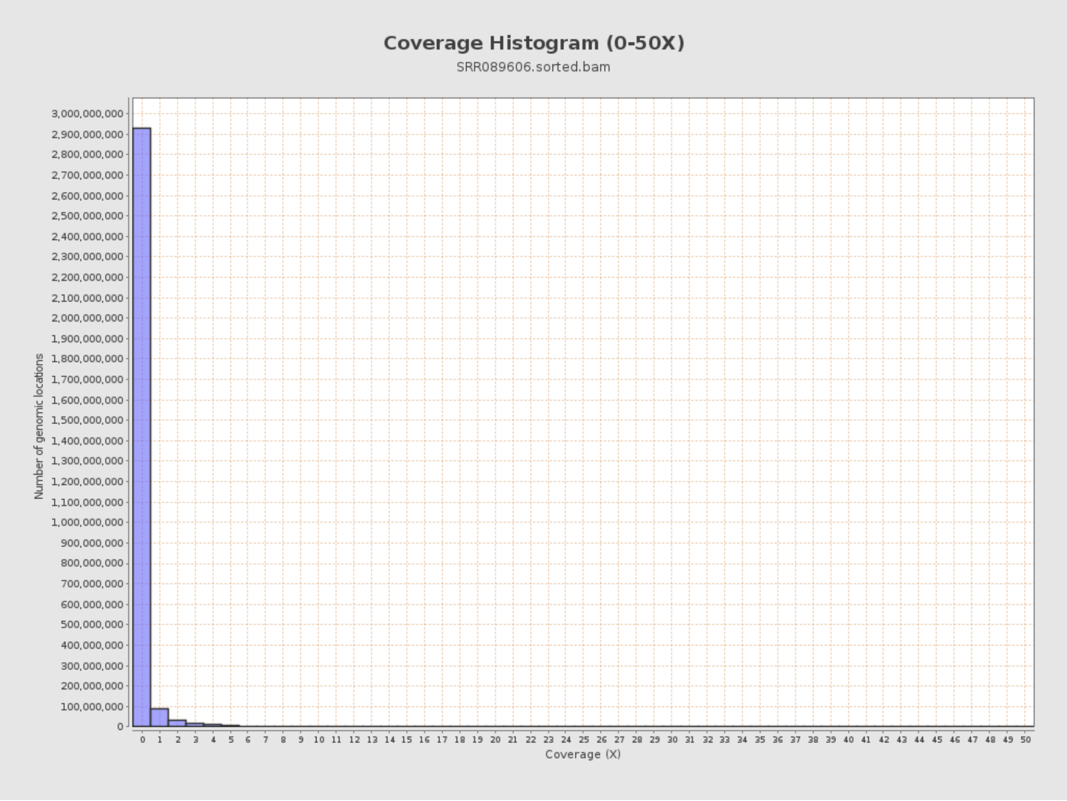
3. Results : Coverage across reference



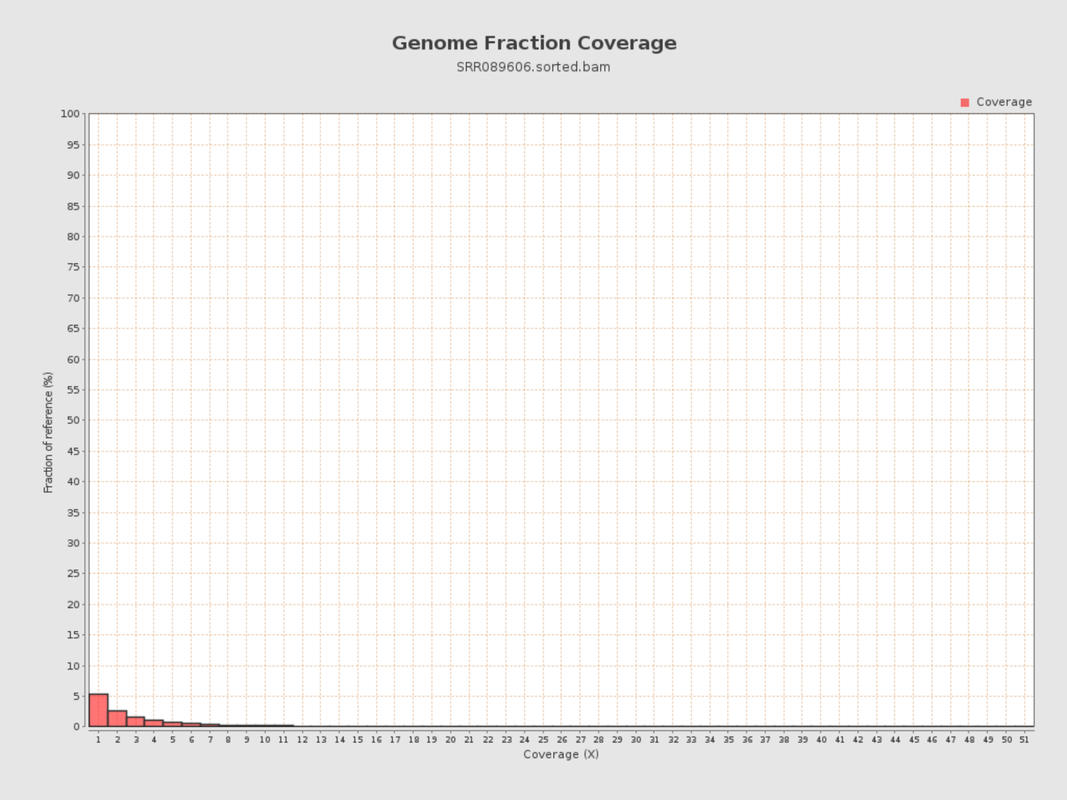
4. Results : Coverage Histogram



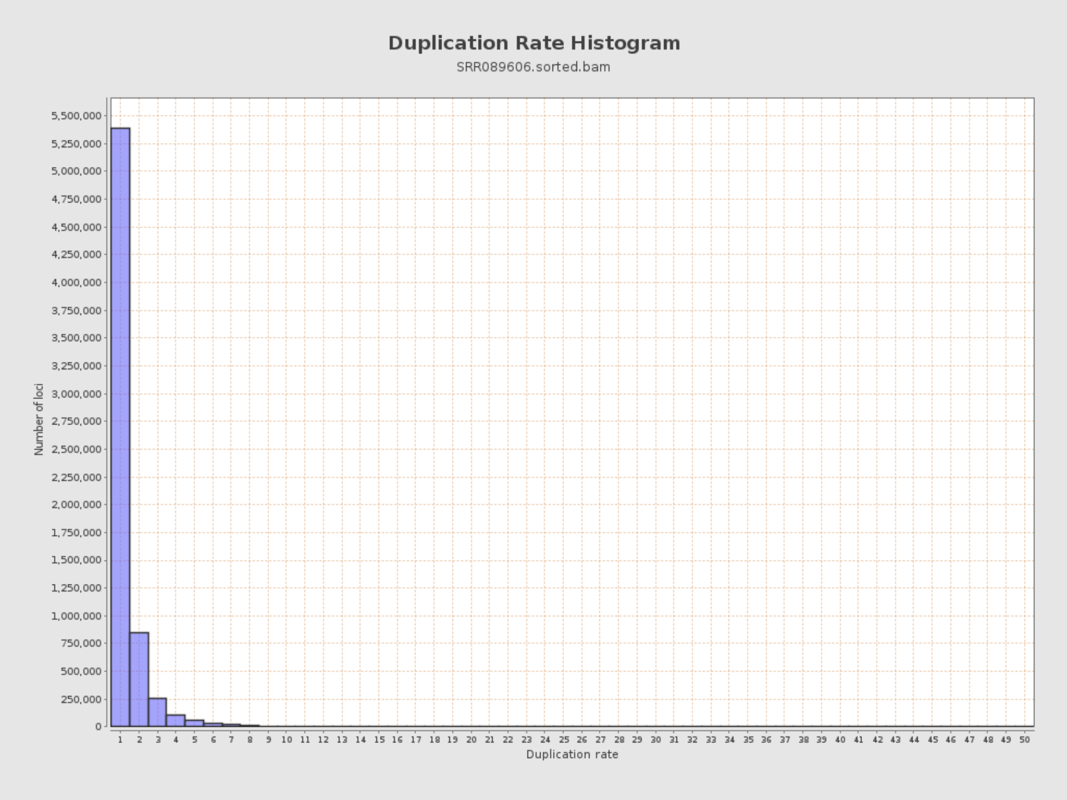
5. Results : Coverage Histogram (0-50X)



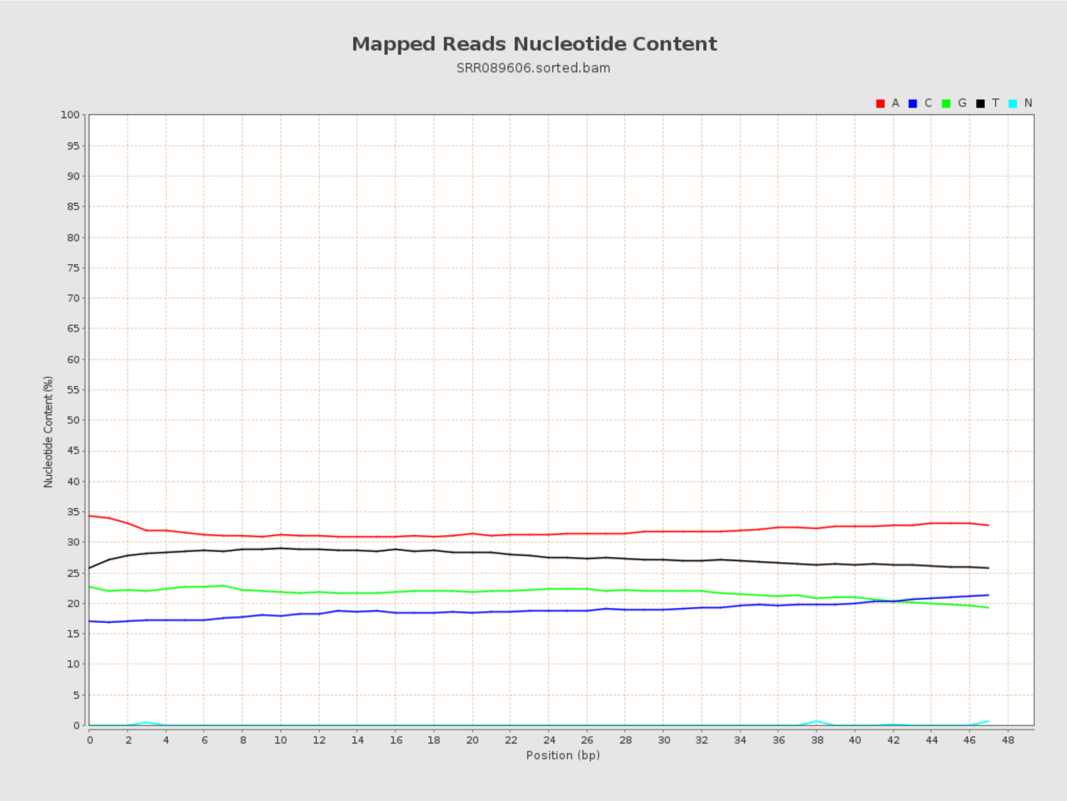
6. Results : Genome Fraction Coverage



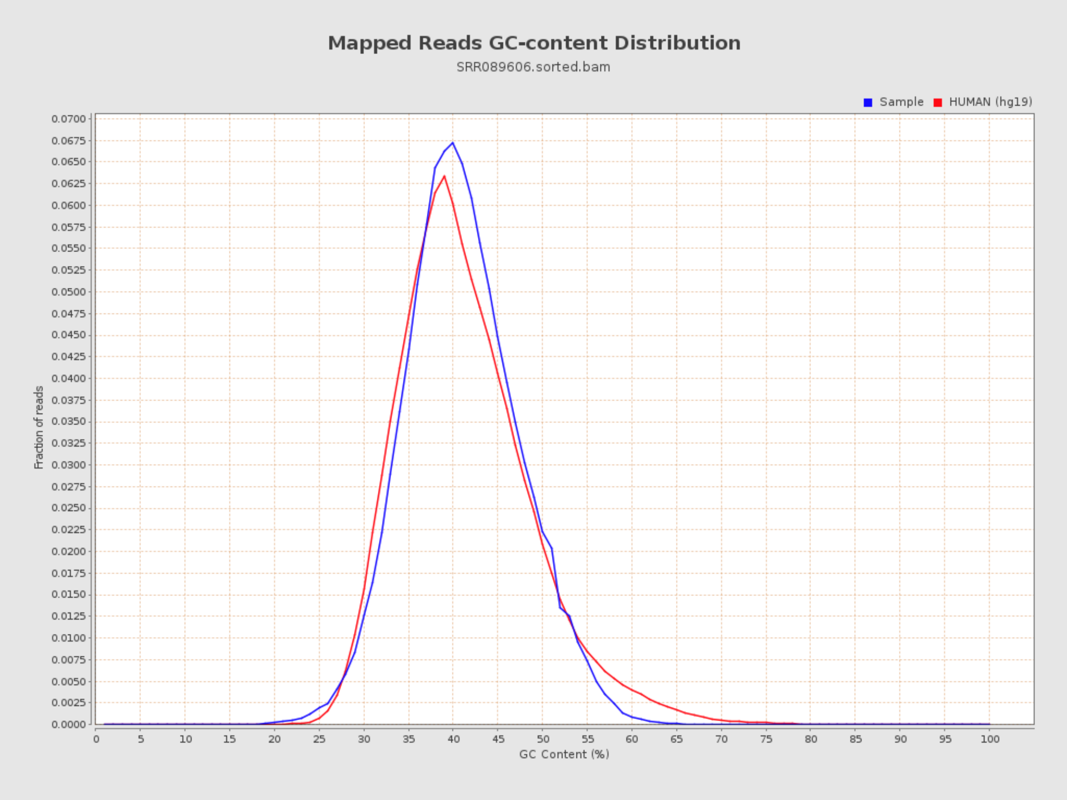
7. Results : Duplication Rate Histogram



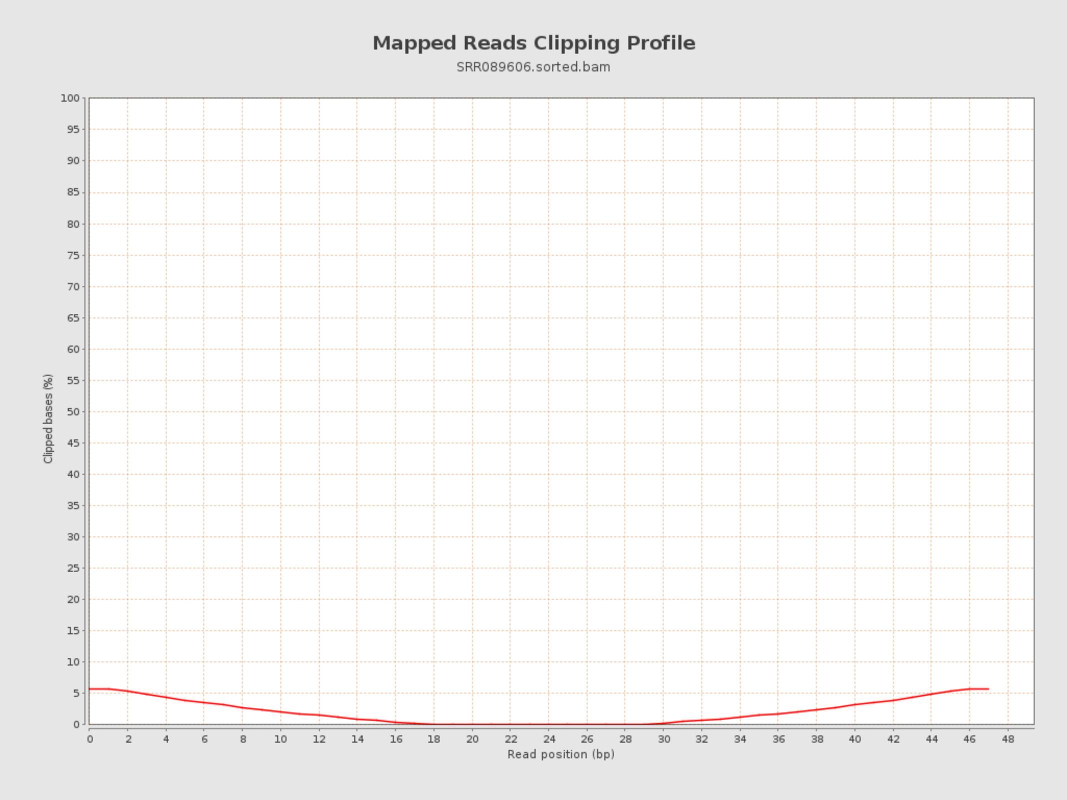
8. Results : Mapped Reads Nucleotide Content



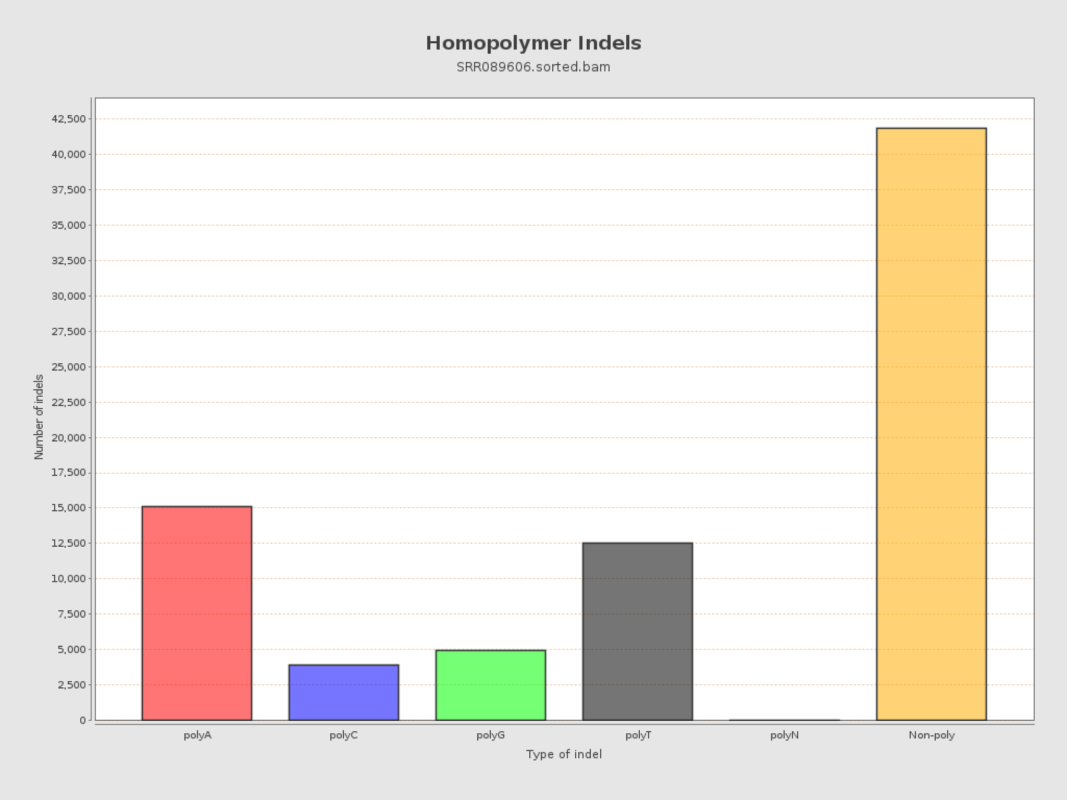
9. Results : Mapped Reads GC-content Distribution



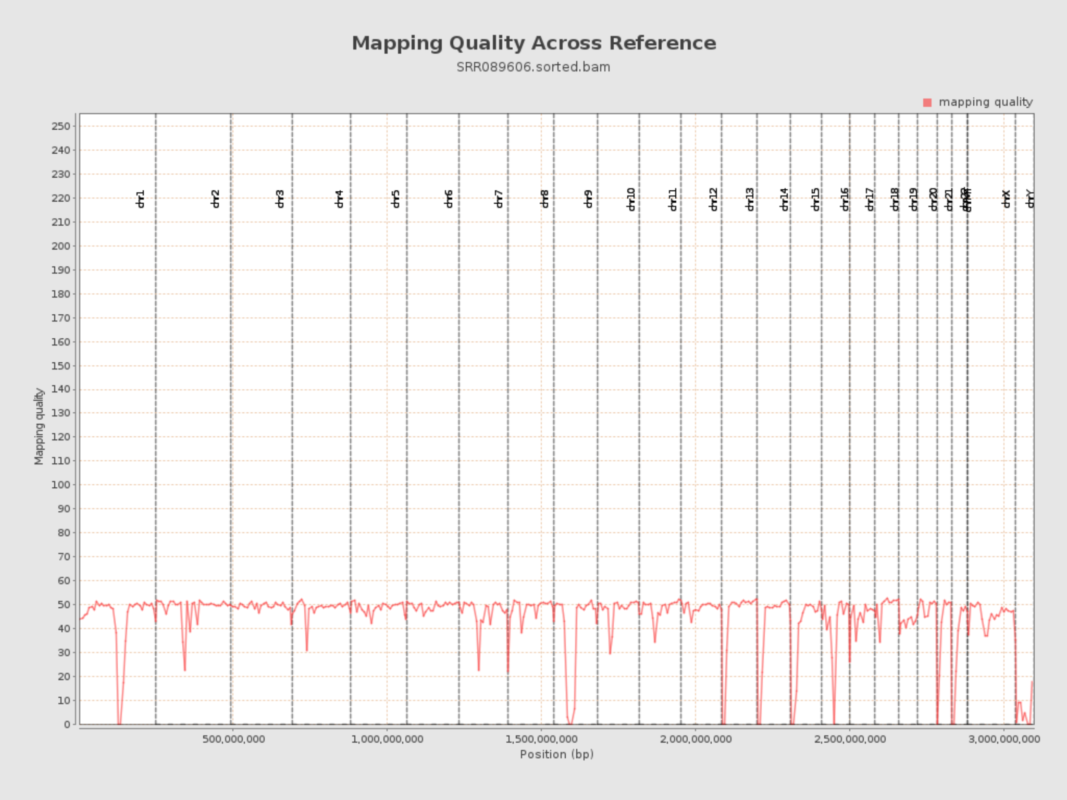
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram