



## Table of contents

1. Summary de novo report .....	3
1.1 Nucleotide distribution .....	3
1.2 Contig measurements .....	3
1.3 Accumulated contig lengths .....	4
1.4 Summary statistics .....	5
1.5 Distribution of read length .....	5
1.6 Distribution of matched read length .....	6
1.7 Distribution of non-matched read length .....	7

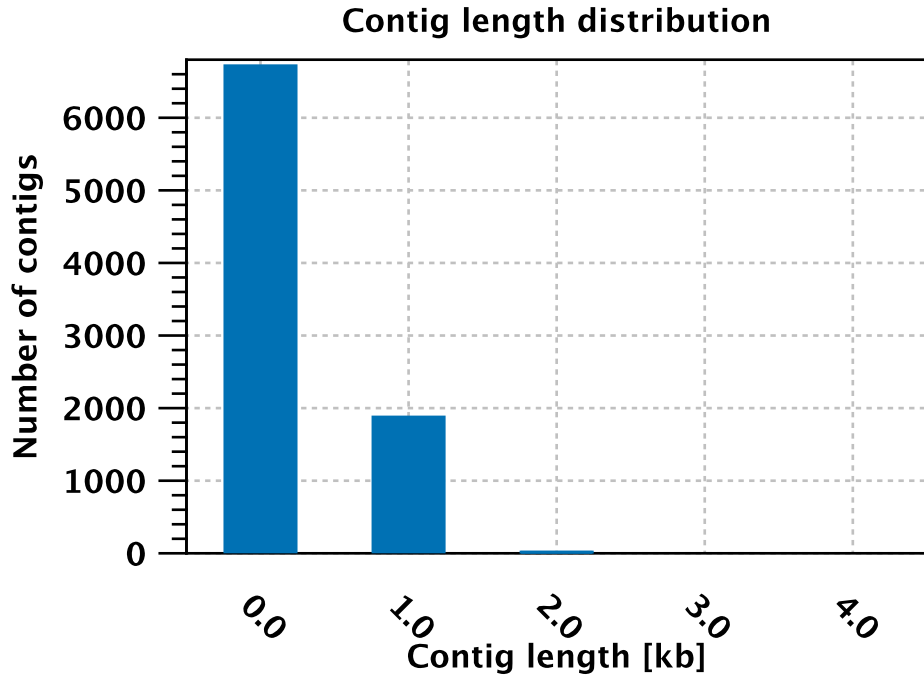
# 1. Summary de novo report

## 1.1 Nucleotide distribution

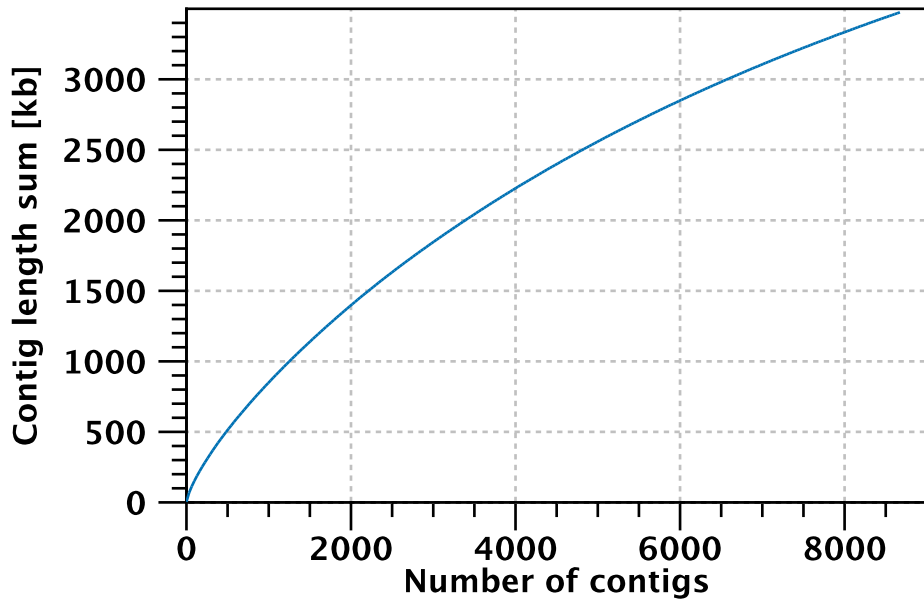
Nucleotide	Count	Frequency
Adenine (A)	1,067,587	30.7%
Cytosine (C)	671,212	19.3%
Guanine (G)	667,721	19.2%
Thymine (T)	1,068,106	30.7%

## 1.2 Contig measurements

N75	304
N50	427
N25	611
Minimum	199
Maximum	3,571
Average	401
Count	8,673



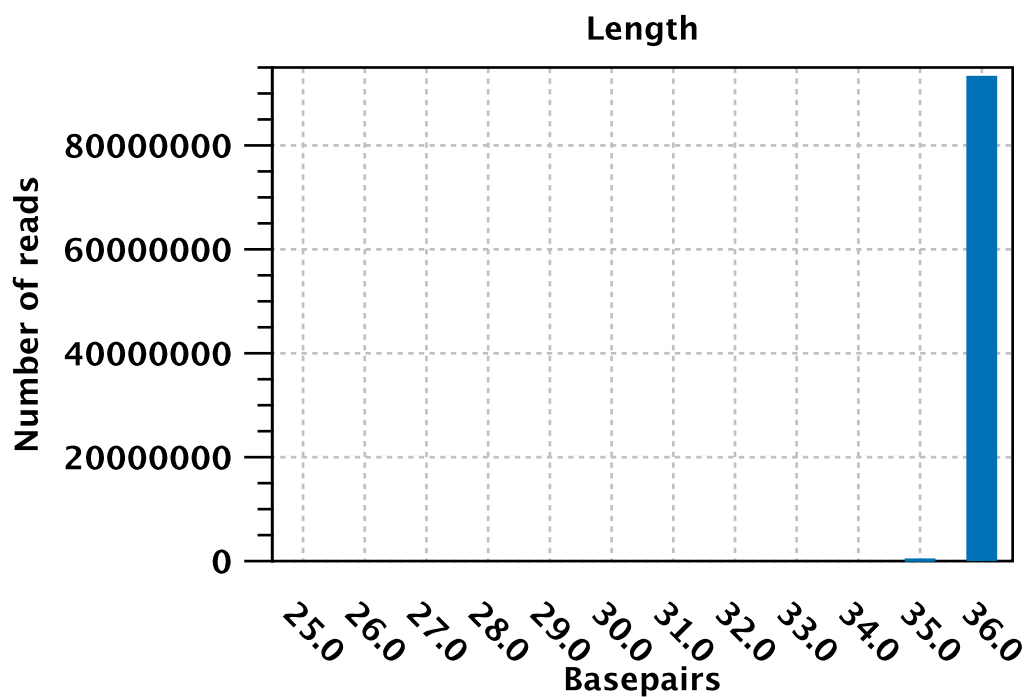
### 1.3 Accumulated contig lengths



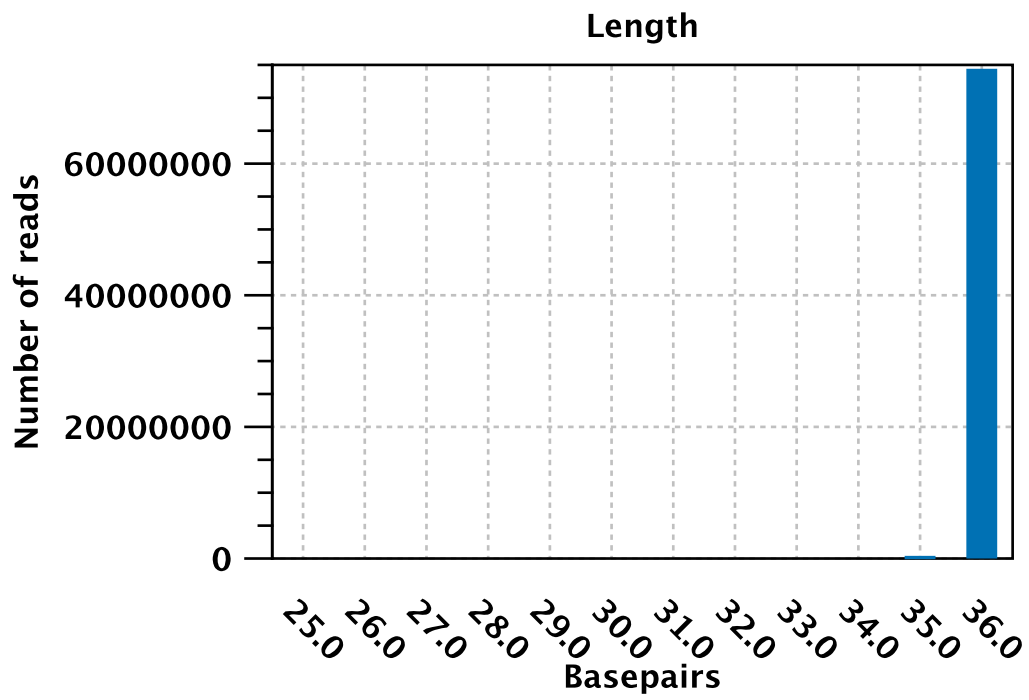
## 1.4 Summary statistics

	Count	Average length	Total bases
Reads	94,777,799	35.95	3,406,883,609
Matched	75,462,078	35.95	2,712,844,324
Not matched	19,315,721	35.93	694,039,285
Contigs	8,673	400	3,474,626

## 1.5 Distribution of read length



## 1.6 Distribution of matched read length



## 1.7 Distribution of non-matched read length

