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# 1. Summary mapping report

## 1.1 Summary statistics

	Count	Average length	Total bases
Reads	12,185,418	527.52	6,428,059,816
Matched	10,972,986	522.57	5,734,191,975
Not matched	1,212,432	572.29	693,867,841
Contigs	235,330	1,290	303,613,645

## 1.2 General algorithm parameters

Parameter	Value
Conflict resolution	Unknown nucleotide (N)
Non specific matches	random

## 1.3 Reads parameters

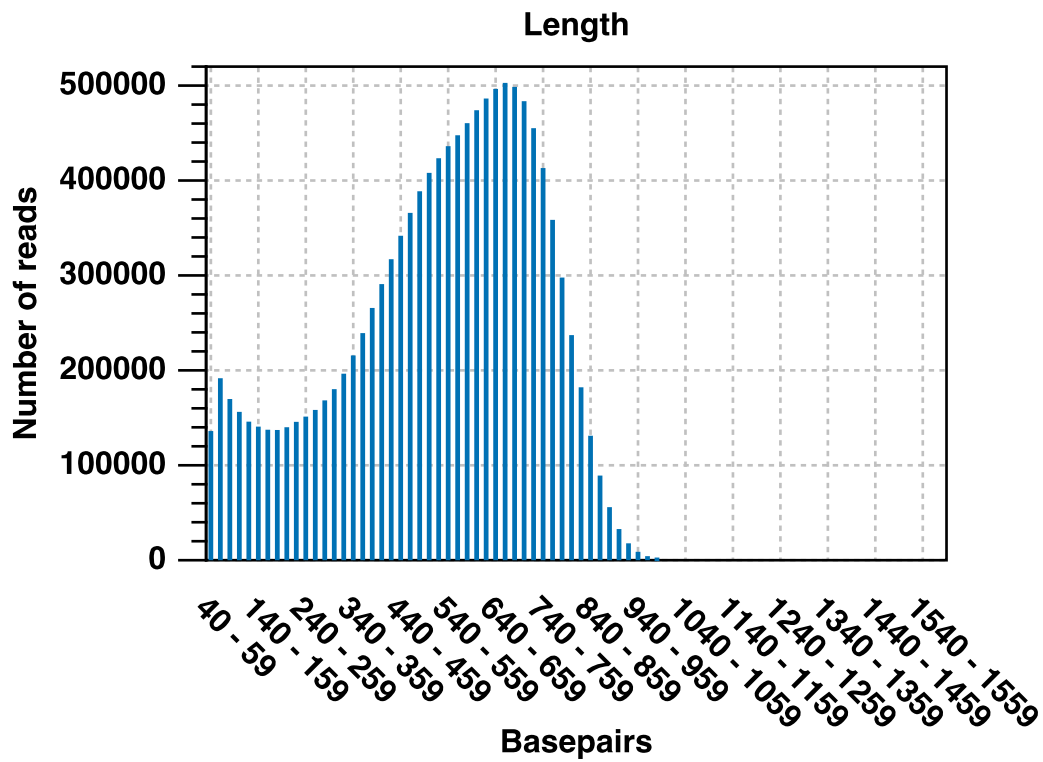
Reads	Length	Type	Parameters
G5UGEGY01 (single)	Long	Single	Default
G5UGEGY02 (single)	Long	Single	Default
G6IEU6N01 (single)	Long	Single	Default
G6IEU6N02 (single)	Long	Single	Default
G6P4JCY01 (single)	Long	Single	Default
G6P4JCY02 (single)	Long	Single	Default
G6IQQIE02 (single)	Long	Single	Default
G6IQQIE01 (single)	Long	Single	Default
G6MC6LA01 (single)	Long	Single	Default
G6MC6LA02 (single)	Long	Single	Default
G6NY9WP01 (single)	Long	Single	Default
G6NY9WP02 (single)	Long	Single	Default
G5T4LHD01 (single)	Long	Single	Default
G5T4LHD02 (single)	Long	Single	Default
G5YGYAB01 (single)	Long	Single	Default
G5YGYAB02 (single)	Long	Single	Default

Reads	Length	Type	Parameters
G5YGYJV01 (single)	Long	Single	Default
G5YGYJV02 (single)	Long	Single	Default
G5Z66BW01 (single)	Long	Single	Default
G5Z66BW02 (single)	Long	Single	Default

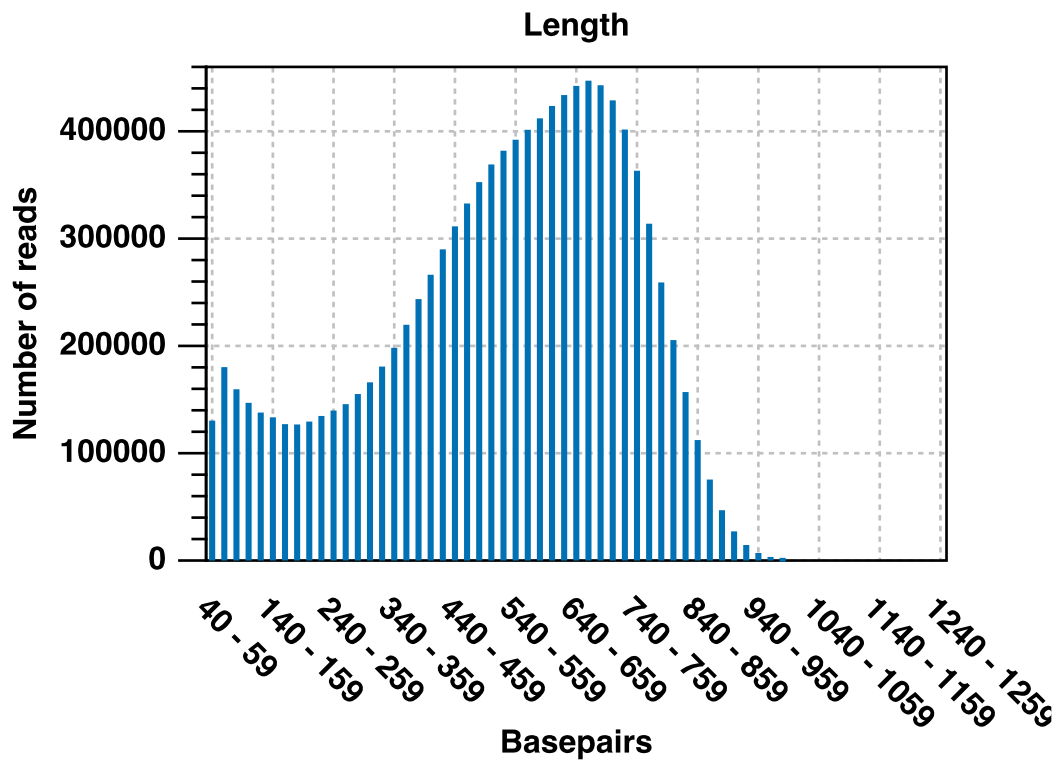
## 1.4 Quality measurement

N75	863
N50	1,592
N25	3,196

## 1.5 Distribution of read length



## 1.6 Distribution of matched read length



## 1.7 Distribution of non-matched read length

