









# Throughput NGS

Key specifications	 <a href="#">iSeq 100 System</a>	 <a href="#">MiniSeq System</a>	 <a href="#">MiSeq System</a>	 <a href="#">MiSeq i100 Series</a>	 <a href="#">NextSeq 550 System</a>	 <a href="#">NextSeq 1000 and 2000 Systems</a>	 <a href="#">NovaSeq 6000 System</a>	 <a href="#">NovaSeq X Series</a>
Max output per flow cell	1.2 Gb <sup>b</sup>	7.5 Gb <sup>c</sup>	15 Gb <sup>d</sup>	30 Gb <sup>a</sup>	120 Gb <sup>c</sup>	540 Gb <sup>e</sup>	3 Tb <sup>b</sup>	8 Tb <sup>c</sup>
Run time (range) <sup>e</sup>	~9.5–19 hr	~5–24 hr	~5.5–56 hr	~4–15.5 hr	~11–29 hr	~8–44 hr	~13–44 hr	~17–48 hr
Max reads per run (single reads)	4M <sup>ab</sup>	25M <sup>c</sup>	25M <sup>d</sup>	100M <sup>a</sup>	400M <sup>c</sup>	1.8B <sup>e</sup>	10B (single flow cell) <sup>b</sup> 20B (dual flow cells)	26B (single flow cell) <sup>c</sup> 52B (dual flow cells) <sup>c,e</sup>
Human genome depth	0.4x	2.5x	5x	10x	40x	180x	1000x	2600x

# Pra que tanto?

- Cada read é uma evidência de observação biológica:
  - Expressão de um gene
  - Existência de mutação
- Quanto mais evidências, maior o suporte para as inferências.

```
##gff-version 3
ctg123 . mRNA                1300   9000   .   +   .   ID=mrna0001;Name=sonichedgehog
ctg123 . exon                 1300   1500   .   +   .   ID=exon00001;Parent=mrna0001
ctg123 . exon                 1050   1500   .   +   .   ID=exon00002;Parent=mrna0001
ctg123 . exon                 3000   3902   .   +   .   ID=exon00003;Parent=mrna0001
ctg123 . exon                 5000   5500   .   +   .   ID=exon00004;Parent=mrna0001
ctg123 . exon                 7000   9000   .   +   .   ID=exon00005;Parent=mrna0001
```

