

# Evolution of Genome Sequencing

## Effect of Evolving Sequencing Technologies

### Phaseolus vulgaris (Bean) Genotype

	G19833 v1 (2012)	G19833 v2 (2015)	UI 111 v1 (2019)	Labor Ovalle v1 (2020)
Primary Technology	Roche 454	PacBio RSII	PacBio Sequel II	PacBio Sequel II
Average read length	-	-	8.5 kb	19.6 kb
Coverage	19.2X	83.2X	141.5X	51.2X
Main genome scaffold total	708	478	58	15
Main genome contig total	41,391	1,044	167	36
Main genome scaffold sequence total	521.1 Mb	537.2 Mb	554.9 Mb	571.9 Mb
Main genome contig sequence total	472.5 Mb (9.3% gap)	531.6 Mb (1.1% gap)	553.8 Mb (0.2% gap)	571.7 Mb (0.0% gap)
Main genome scaffold N50/L50	5/50.4 Mb	5/49.7 Mb	5/51.0 Mb	5/55.4 Mb
Main genome contig N50/L50	3,273/39.5 kb	73/1.9 Mb	23/8.5 Mb	9/20.5 Mb
Number of scaffolds > 50 Kb	28	87	36	13
% main genome in scaffolds >50 Kb	99.30%	99.10%	99.80%	100%

Best statistics to compare!!!