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# fastGEN QC Recommendation

**1.** Threshold default filter setting table:
- Minimal read depth: 500x
- Minimal variant allele frequency (VAF): 1%
- Synonymous variants: No

**2.** Provide a sheet with recommendations like min. raw reads per sample, min. coverage (1000), etc.
- Cluster density: 800–1 200K clusters/$mm^2$ (MiSeq)
- Total reads per sample in Genovesa:
  - Solid/Solid II Cancer kit: 100 000 reads per sample
  - Lung Cancer kit: 50 000 reads per sample
  - Brain Cancer kit: 25 000 reads per sample
  - POLE Cancer kit: 50 000 reads per sample
  - POLE/CTNNB1 Cancer kit: 70 000 reads per sample
  - PIK3CA Cancer kit: 125 000 reads per sample
  - TP53 Cancer kit: 200 000 reads per sample
- Minimal variant read depth: 500x
- Minimal Coverage/Depth
  Wild type samples > 1 000 for each exon/region
  Mutated samples
  - Minimal Total Depth > 500 for mutated variant VAF > 5 % (thus minimal variant count = 25)
  - Minimal Total Depth > 1000 for mutated variant VAF 2–5 % (thus minimal variant count = 20–50)
  - Minimal Total Depth > 2000 for mutated variant VAF 1–2 % (thus minimal variant count = 20–40)

**3.** Support e-mail address: support@biovendor-mdx.com