AMPure XP- Gold Standard for bead based, Next-Generation Sequencing (NGS) clean-up

AMPure XP is suggested by over 200 library prep kits, including kits from trusted sequencing companies:

- Illumina®
- Oxford Nanopore Technologies
- Pacific Biosciences
- ThermoFisher Scientific

Over 15,000 publications used AMPure XP

- Referenced in articles in Science, Nature, and PNAS

AMPure XP maximizes recovery, consistency and speed

Nucleic acid purification and clean-up are mandatory for genomic applications, such as sequencing, qPCR/ddPCR/PCR, and microarrays. Maximizing recovery, consistency, and speed, AMPure XP meets the stringent needs of today’s genomic applications and minimizes the risk of losing important genetic information.

- High recovery of amplicons greater than 100bp
- Efficient removal of unincorporated dNTPs, primers, primer dimers, salts and other contaminants
- Predictable and consistent size selection


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SPRIselect vs AMPure XP Feature comparison

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**SPRIselect and AMPure XP**

- Can be substituted for each other in clean-up applications
- Use the same sample to bead ratios
- Are suggested for use by the most well-known library construction kit manufactures:
  - Illumnia®, Integrated DNA Technologies, Inc (IDT), Swift Biosciences, etc
- Have identical work flows

**SPRIselect benefits**

- Stability at room temperature allows:
  - Start clean-up steps without calibrating to room temperature
  - Frees up 4°C storage space
- Quality control for size selection allows:
  - Trust that lot to your size selection steps are accurate
  - Accurate and consistent size selection from lot to lot

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Sample to bead ratio for size selection matters

Not all bead based clean-up kits use the 1.8x ratio; the figure below shows that of 10 bead based clean-up kits only 3 suggest a 1.8x ratio for clean-up.

What switching to a kit with a different ratio could impact

- Clean-ups will require a different bead ratio that could lead to loss of fragments of interest
- Sample to bead ratios will need to be recalculated
- Lab protocols that use the standard sample to bead ratios that of AMpureXP or SPRIselect will have to be re-written