SUPPORTING INFORMATION

Low Resource Nucleic Acid Extraction Method Enabled by High-Gradient Magnetic Separation

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SUPPLEMENTARY VIDEO CAPTIONS

Video S1. Paramagnetic bead separation from a flowing fluid stream using high-gradient magnetic separation. An external magnet is applied next to the ferromagnetic matrix to magnetize it. When the magnetic force is sufficiently great, the magnetic force draws beads to the surface of the wire, capturing them in the matrix. After all of the bead suspension has passed, all of the particles are retained in the ferromagnetic matrix, and no beads remain in the flow through.

Video S2. Paramagnetic bead separation from a flowing fluid stream using a stationary magnet. An external magnet is applied alongside the flowing fluid stream to separate particles from suspension. After all of the bead suspension has passed, only some of the beads are retained in the flow channel, and many still remain in the flow through. This is because the viscous drag forces applied by the liquid medium overcome the magnetic forces applied to the beads.

SUPPLEMENTARY FIGURES

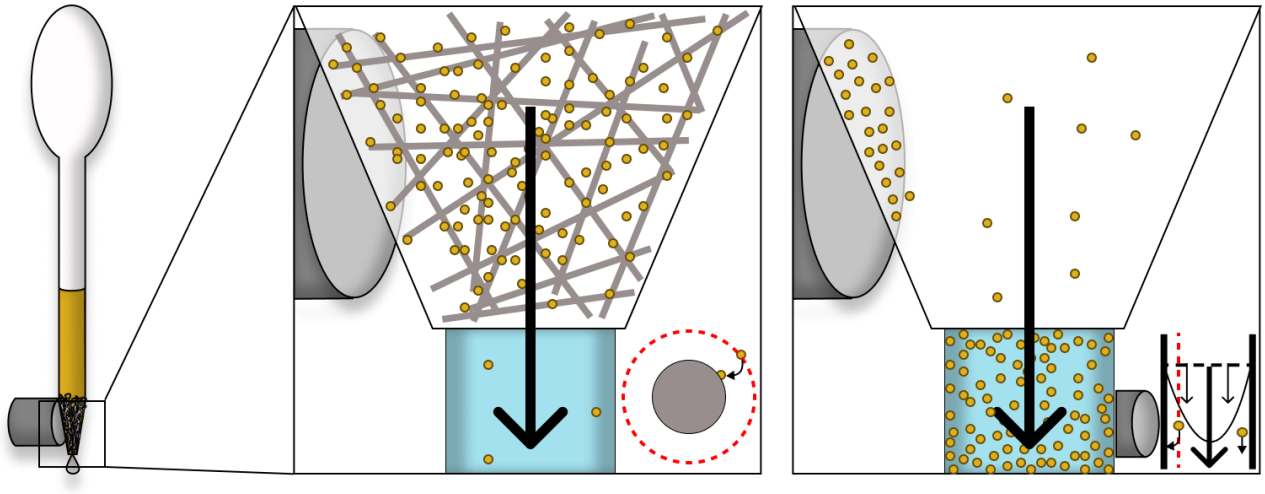

Figure S1. Overview of paramagnetic bead separation from a flowing fluid stream. **Left panel:** An external magnet is used to capture and contain magnetic beads in the ferromagnetic matrix (**see Video S1**). When the magnetic force is sufficiently great around a wire (red dashed line), the magnetic force draws beads to the surface, capturing them. **Right Panel:** Applying the magnetic field without the presence of the steel wool matrix results in significant loss of magnetic beads, because the viscous drag forces applied by the liquid medium overcome the magnetic forces on the bead when the bead is sufficiently far away from the magnet (red dashed line) (**see Video S2**).

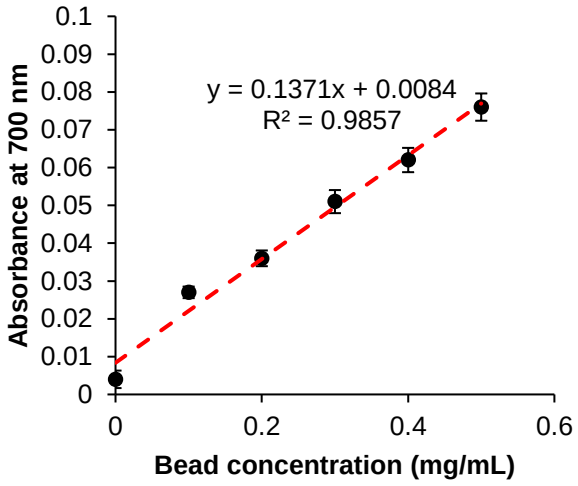

Figure S2. Nanodrop Spectrophotometer standard curve correlating absorbance at 700nm with known solution concentrations of MyOne Silane Dynabeads.

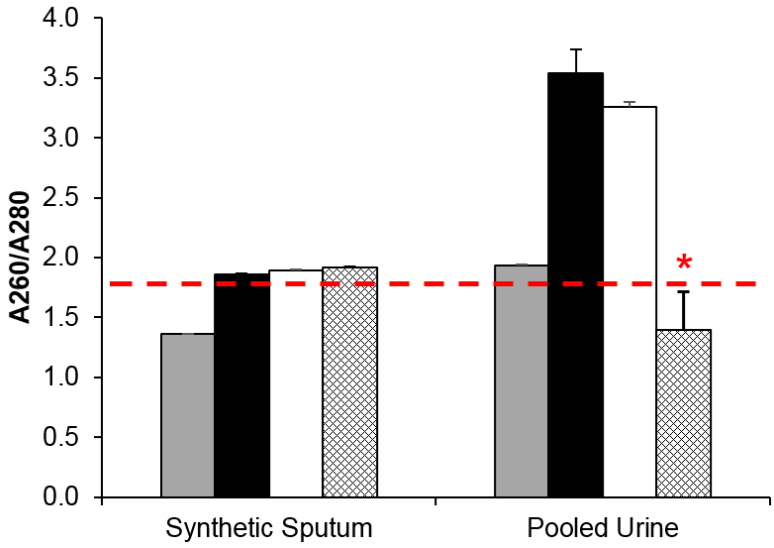

Figure S3. A260/A280 measurement for sample purity of DNA extracted sample. Samples with a value of 1.8 ± 0.1 (red dashed line) are considered to be pure and free from contaminating protein and salt that absorbs light at 280 nm. Values greater than 3.0 may indicate RNA contamination.[1] Gray bars = Raw sample; Black bars = HGMS-enabled extraction; White bars = Qiagen commercial extraction kits. Cross-hatched bars = Chargeswitch™ gDNA Mini Tissue Kit (mean ± s.d.), n ≥ 3. (*) indicates statistical significance at $p < 0.05$.

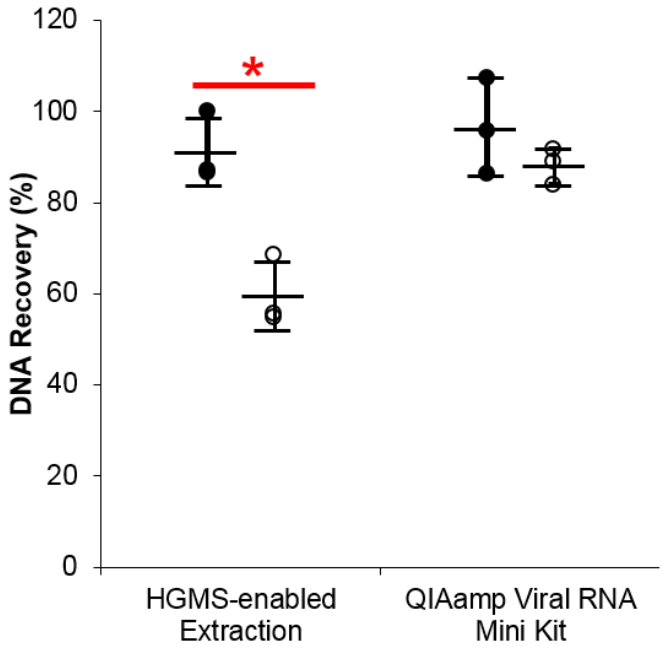

Figure S4: Extraction of IS6110 DNA from urine is statistically improved using the HGMS-enabled extraction method, with the addition of 5.6 µg of carrier RNA to the binding mixture.[2] (•) – with carrier RNA; (○) – without carrier RNA. (mean ± s.d., n ≥ 3). (*) indicates statistical significance at $p < 0.05$.

SUPPLEMENTARY REFERENCES

1. Farrell Jr., R. E., *RNA Methodologies: Laboratory Guide for Isolation and Characterization*. Fifth Edition ed.; Academic Press: 2017.
2. Kishore, R.; Reef Hardy, W.; Anderson, V. J.; Sanchez, N. A.; Buoncristiani, M. R., Optimization of DNA extraction from low-yield and degraded samples using the BioRobot EZ1 and BioRobot M48. *J Forensic Sci* **2006,** *51* (5), 1055-61.