1. Run the program with no beans and a reflector so that it can calibrate
2. When the program finishes calibration, add the beans to the MedBeanis. Pay attention to the “**SettingsUsed**” picture in the folder, it says the amount used.
3. Continue the program
4. When the bean scan group is complete, mix the beans and continue the program.
5. Repeat step 4 until all 10 scans have been completed.
6. Empty the beans out and restart at step 1.

**NOTES:**

For this particular test, I am replacing the beans with a new set of beans from that same bean type. This ensures that we see a larger number of varieties of sizes of beans and are not just testing off of one small sample group.