Table 1: Troubleshooting

Step	Problem	Possible reason	Solution
B.3.	At the end of the cryomilling step, the sample is thawed.	The cryomilling racks were not cold enough.	Dip the rack into liquid nitrogen for a longer time prior to this step.
	At the end of the cryomilling step, the sample is not pulverized.	The cryomilling conditions are not adapted to the sample.	Repeat the cryomilling step or empirically optimize the number and size of stainless steel milling balls according to the consistency of the sample.
E.1.	The sample did not entirely pass through the column.	The column is clogged.	Repeat the centrifugation for 4 additional minutes. If the entire volume still does not pass through the column, transfer it to a second column. Both columns will need to be eluted later in the protocol. In case of recurrent clogging, the quantity and pre-treatment of starting material should be adapted.
F.1.	The isolated biomolecules are not representative of the sample composition.	Cell lysis was not indiscriminate.	Test and optimize the efficiency of cell lysis as previously described [1,2].
F.1.	The RNA is degraded.	Presence of RNases	Prevent RNase contamination of reagents and labware. Make sure that the entire sample was snap-frozen on site. Keep the sample in cold conditions from steps A to D, and reduce handling time to a minimum.
F.1.	The DNA is degraded (be sure that you are really seeing degradation and not shearing of genomic DNA during the bead milling steps).	Presence of DNases	Prevent DNase contamination of reagent and labware. Make sure that the entire sample was snap-frozen on site. Check that from steps A to D, the sample was in cold conditions