## data homogenization processing summary and QC check results: ChronicN $\_$ Metabolite notes included with key file:

| source   | Var_long  | var                  | var_notes  |
|----------|---|----------------------|--|
| location | Google Directory  |                      | ChronicN_Metabolite  |
| location | Network (e.g. LTER, CZO, DIRT, NutNet, etc)                       | network              | LTER   |
| location | Site code (e.g. LUQ) or name                                      | $site\_code$         | HRF  |
| location | Location name   | location_name        | Harvard Forest   |
| location | control samples identifier  | $control\_id$        | Treatment = Control  |
| location | number of treatments  | $number\_treatments$ | high & low N   |
| location | merging datafiles required? please add details to alignment notes | merge_align          | align by plot with soil CN data?   |
| profile  | Effective Cation Exchange<br>Capacity                             | ecec                 | effective cation exchange<br>capacity (ECEC) calculated by<br>summation of milliequivalent<br>levels of Ca, K, Mg, Na, and<br>acidity, 100gm |

## files processed:

| type             | filename                            |
|------------------|-------------------------------------|
| provided data    | hf297-04-soil-chem-metabolite       |
| homogenized data | hf297-04-soil-chem-metabolite_HMGZD |

QC results: location data

location data checks passed

QC results: profile data, data range

profile data range checks passed

QC results: profile data, data type

profile data type checks passed