

**Variant Call Report: HUMAN BAC sequencing**

**BAC Library Identifier:** \_\_\_\_\_

**Galaxy Workflow used (cut and paste screen shot or otherwise share):**

**Outcome, Variants identified (give dbSNP rs### identifier code):**

**Please identify # of variants and whether the variants identified do or do not have human disease associations. What are the clinical associations? Provide one or two peer reviewed references that describe any clinically relevant SNPs.**