CALIFORNIA REGIONAL WATER QUALITY CONTROL BOARD
LAHONTAN REGION

MEETING OF JUNE 10-11, 2015
BISHOP

ITEM: **10**

SUBJECT: **ASSESSMENT OF BACTERIAL WATER QUALITY**

DISCUSSION: Under contract with the State Water Board, Principal Investigator, Roland Knapp, Ph.D. with the University of California's Sierra Nevada Aquatic Research Laboratory, Center for Eastern Sierra Aquatic Microbial (CESAME) investigated the spatial and temporal patterns of fecal indicator bacteria (FIB) concentrations in streams in the eastern Sierra Nevada portions of the Lahontan Region. The work performed under the contract (1) utilized traditional and modern methods for measuring various bacterial indicators in surface water, and (2) applied statistical analysis to landscape-scale variables and site-specific data to determine the primary drivers of FIB concentrations.

Traditional measurements of FIB based on over 700 samples collected throughout the study area indicated that *Escherichia coli* (E. coli) concentrations were generally low, typically less than 20 colony forming units (CFU) per 100 milliliters (mL). Areas that exhibited bacterial levels greater than 100 CFU/ml included Bridgeport Valley, Owens River above Crowley Reservoir, Round Valley, and in and around the City of Bishop.

Modern measurements of FIB that rely on quantitative polymerase chain reaction (qPCR) methods were used to identify the primary sources of FIB in 165 samples collected from streams in the study area. Microbial Source Tracking (MST) assays were applied to analyze the DNA extracted from bacterial cells collected from filtered water samples. Bacterial cells were compared to assays that targeted general bacterial groups found in vertebrate species and specific subgroups associated with ruminants (which include cattle, goats, sheep, and deer) and humans.

MST results showed that fecal bacteria attributable to ruminants were widespread throughout the study area.

Additionally, ruminants were a more significant source of the measured fecal contamination than were humans.

The source of the fecal bacteria measured in the multiple samples collected in and around the City of Bishop were also dominated by ruminant sources even though human development and cattle grazing are intermixed.

Statistical analysis and modeling determined that the presence or absence of livestock had the strongest effect on E.coli concentrations. Other primary landscape-scale drivers (land use, elevation, precipitation amount, presence/absence of an upstream waterbody, day of year) had a significant effect on FIB concentrations, but none as strong of a predictor as the presence or absence of livestock upstream of the sampling location.

This research provides an important step toward evaluating the spatial and temporal variation in water-borne fecal bacteria throughout the region and identifying sources of contamination. Additional contract work being conducted by CESAME plans to (1) test a broader set of source-specific MST assays to determine the extent to which other sources contribute to the concentrations of fecal bacteria, and (2) test additional ruminant assays to evaluate their specificity on the Sierra Nevada landscape.

RECOMMENDATION: This is a discussion item only. No Water Board action is required for this item.

ENCLOSURE	ITEM	Bates Number
1	Final Report with Appendices: Assessment of Bacterial Water Quality in the Lahontan Region	**10-5**
2	PowerPoint presentation by Roland Knapp, PhD	**10-83**

ENCLOSURE 1

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Final Report

Project Title: Assessment of Bacterial Water Quality in the Lahontan Region

State Water Resource Control Board Contract Number: 12-067-160

Contract Period: 10/19/2012 – 03/31/2015

Contract Amount: $130,000

Date Submitted: March 10, 2015

Principal Investigators:

Roland Knapp, Ph.D., Center for Eastern Sierra Aquatic Microbial Ecology, Sierra Nevada Aquatic Research Laboratory, University of California, 1016 Mount Morrison Road, Mammoth Lakes, CA 93546 (roland.knapp@lifesci.ucsb.edu)

Craig Nelson, Ph.D., Center for Microbial Oceanography, University of Hawaiʻi at Mānoa, 1950 East-West Road, Honolulu, HI 96822 (craig.nelson@hawaii.edu)

Contract Managers:

Thomas Suk and Mary Fiore-Wagner, California Regional Water Quality Control Board - Lahontan Region, 2501 Lake Tahoe Blvd., South Lake Tahoe, CA 96150

Executive Summary

Project Scope

This study had three primary objectives: (1) describe the spatial and temporal patterns of fecal indicator bacteria (FIB) concentrations in streams in the eastern Sierra Nevada portion of the Lahontan Region, (2) identify the primary drivers of FIB concentrations using statistical analyses of landscape-scale and site-specific data, and (3) test modern microbial source tracking (MST) assays that are based on quantitative real-time polymerase chain reaction (qPCR) methods as a means to identify the primary sources of FIB to streams in the study area.

Findings and Interpretations

Based on 705 samples collected at 111 sites, *Escherichia coli* concentrations in the study area were generally low, typically less than 20 colony forming units (CFU) per 100 milliliters (mL). However, a few areas were characterized by high *E. coli* concentrations, in some cases exceeding 100 and/or 126 CFU per 100 mL. These areas included Bridgeport Valley, Owens River above Crowley Reservoir, Round Valley, and in and around the City of Bishop.

Results of statistical analyses suggested that the primary drivers of *E. coli* concentrations in the study area were the presence of livestock (primarily cattle), day of the year, and time of sample collection. The presence of upstream lakes, intensity of upstream human development, rainfall during the days preceding sampling, and site elevation all had much weaker, but still significant effects on *E. coli* concentrations. The number of upstream campsites and sampling year did not have significant effects. Predictive modeling suggested that if management measures are implemented to effectively address fecal inputs from livestock into streams, virtually all of the streams in the study area would meet the current 20 CFU per 100 mL standard used by the Lahontan Region.

The importance of livestock as a driver of fecal bacteria concentrations in the study streams was further indicated by the results from microbial source tracking (MST) assays. MST results showed that ruminants (including cattle) were a much more significant source of fecal bacteria than were humans. This was the case even in the vicinity of the City of Bishop, where human development and cattle grazing are closely intermixed. Analysis of a larger number of samples collected over additional seasons should be conducted to confirm this preliminary finding. In addition, analysis of at least a subset of samples using a broader set of source-specific MST assays will be necessary to determine the extent to which other sources contribute to the concentrations of fecal bacteria in the study area streams.

Introduction

The Clean Water Act (CWA) was passed in 1972 in response to severe and increasing water pollution in many fresh waters of the United States. The CWA regulates the discharge of pollutants into U.S. waters and although the original focus was on point sources of pollution, in 1987 the CWA was amended to specifically address nonpoint sources (Section 319 Nonpoint Source Management Program). The CWA and subsequent amendments have allowed considerable progress in controlling water pollution (Smith et al. 1987), but not surprisingly controlling point sources has proven much easier than nonpoint sources. By definition, nonpoint source pollution is diffuse and the sources can often be difficult to identify. As a result, nonpoint sources remain largely uncontrolled and continue to be a major cause of water quality impairment (Brown and Froemke 2012).

For both point and non-point sources, one of the primary causes of water quality impairment is the presence of pathogens associated with human and animal feces. Such feces can originate from a wide variety of sources, including sewage treatment facilities, septic tanks, farms, rangeland livestock, pets, and wildlife. In a 2004 assessment that ranked the ten most important causes of impairment of U.S. streams and rivers, pathogens affected the greatest number of stream/river miles (U.S. Environmental Protection Agency 2009). Fecal-associated pathogens in waters can cause illnesses in humans, including those caused by bacteria such as *Escherichia coli*, *Enterococcus*, and *Campylobacter*, protozoans such as *Giardia* and *Cryptosporidium*, and viruses (e.g., rotaviruses). Some of these microorganisms can be pathogenic even at very low concentrations, but such low concentrations can make their detection difficult. Therefore, water quality monitoring often relies on detecting the presence of bacteria that are common in vertebrate feces and that can provide useful indicators of the presence of fecal material and associated pathogens. The most commonly tested for fecal indicator bacteria (FIB) include fecal coliforms, *E. coli*, and *Enterococcus*. For recreational waters, fecal coliform bacteria were the primary FIB until relatively recently (U.S. Environmental Protection Agency 1976). However, some of the bacteria included within the "fecal coliforms" are in fact not fecal in origin, suggesting that they may not always provide an accurate indication of human health risks. Subsequent research indicated that *E. coli* and *Enterococcus* were better predictors than fecal coliforms of the presence of gastrointestinal illness-causing pathogens, and in 1986 fecal coliforms were replaced by *E. coli* and *Enterococcus* as the primary FIB recommended by the U.S. Environmental Protection Agency (U.S. Environmental Protection Agency 1986).

Under the CWA, the U.S. Environmental Protection Agency (USEPA) is charged with developing water quality criteria, but this authority and the implementation and enforcement of these criteria can be delegated to individual states. In California, this is the responsibility of the State Water Resources Control Board (State Water Board) and nine Regional Water Quality Control Boards (Regional Water Boards). The State Water Board and Regional Water Boards adopt and enforce standards and policies at the statewide and regional/local levels, respectively. Regional/local standards can differ from state standards because of region-specific or smaller-scale differences in climate, topography, geology, and hydrology, as well as in local and regional economies (see State Water Board 2013 Fact Sheet; included here as Supplement A). The Lahontan Regional Water Quality Control Board (Lahontan Water Board) manages the Lahontan Region that covers the area of eastern California in which the current study was conducted.

In the mid-1970s, the State Water Board adopted the then-current federal recreational water quality criterion of 200 fecal coliform colony forming units (CFU) per 100 mL. Soon thereafter, in recognition of the very high-quality waters of the Lahontan Region and the importance of associated

water-based recreation to the Region's economy, the Lahontan Water Board adopted a more protective fecal coliform standard ("objective") of 20 CFU per 100 mL for numerous water bodies within the Region (including Eagle Lake and Lake Tahoe, and the Susan, Truckee, Carson, Walker, and other rivers). In 1995, the Lahontan Water Board extended this more protective objective (i.e., 20 CFU per 100 mL) to all surface waters of the Lahontan Region. This objective remains in place today, although the USEPA has revised its bacterial water quality criteria twice since the mid-1970s (when the State Water Board and Lahontan Water Board adopted their current criteria/objectives). In 1986 the USEPA changed its bacterial water quality criterion for recreational waters from 200 fecal coliform CFU per 100 mL to 126 *E. coli* CFU per 100 mL (U.S. Environmental Protection Agency 1986). The USEPA updated this criterion again in 2012, and under this latest guidance the bacterial water quality criterion for recreational waters is either 100 or 126 *E. coli* CFU per 100 mL (U.S. Environmental Protection Agency 2012). The State Water Board recently began the process of updating its bacterial water quality objectives based on these latest criteria. It remains uncertain whether or how any *E. coli* standards ultimately adopted by the State Water Board will apply to the Lahontan Region, and/or whether the Lahontan Water Board will adopt the State Water Board's "statewide" objective or will instead adopt an objective that more closely matches the protection provided by its current fecal coliform objective.

The general aim of the current study was to provide a science-based framework to inform the modernization of FIB standards within the Lahontan Region. As such, the study had three primary objectives: (1) describe the spatial and temporal patterns of FIB concentrations in streams in the eastern Sierra Nevada portion of the Lahontan Region, (2) identify the primary drivers of FIB concentrations using statistical analyses of landscape-scale and site-specific data, and (3) test modern microbial source tracking (MST) assays that are based on quantitative real-time polymerase chain reaction (qPCR) methods as a means to identify the primary sources of FIB to streams in the study area.

Methods

Study area description

The study area is located at the base of the eastern escarpment of the southern Sierra Nevada and includes both Sierra Nevada and Great Basin ecoregions. Elevations in the vicinity range from 1098 m (lower Owens River upstream of Owens Dry Lake) to 4421 m (Mt. Whitney), and the area is characterized by cold winters and warm to hot summers. Precipitation amounts are highest near the crest of the Sierra Nevada, and decrease rapidly east of the crest. Most precipitation falls as winter snow, and precipitation events during summer are typically associated with convective thunderstorms. During the three year duration of the study (2012-2014) the area was in the midst of an extreme drought, with total annual precipitation generally <50% of the long-term average. The majority of lands in the study area are under the jurisdiction of either the U.S Forest Service (Humboldt-Toiyabe National Forest, Inyo National Forest), Bureau of Land Management (Bishop Resource Area), or Los Angeles Department of Water and Power (LADWP).

To characterize FIB concentrations in streams within the study area, we repeatedly sampled 111 sites located on 35 streams in Mono County and northern Inyo County, California (Figure 1). The 35 streams represent most perennial streams in the two counties. The majority of the streams (33) drained watersheds originating in the Sierra Nevada, and two additional streams were located in the adjacent White Mountains (Figure 1). Most streams were relatively small with base flow discharges of 0.05 to 4 $m^3 \cdot s^{-1}$. Sampling sites were selected to represent all major land uses in the study area, including natural landscapes subject to minimal alteration, dispersed recreation areas with designated campgrounds,

suburban and urban areas, and areas subject to grazing by domestic livestock. Sampling sites were typically located above and below areas of distinct land uses (e.g., above and below areas grazed by cattle), were generally separated by at least 1 km, and each stream contained 1-14 sampling sites (average = 3). Coordinates of each sampling site were determined using a geographic information system (ArcGIS 10.2). Attributes of all sampling sites are provided in Appendix A.

Collection of water samples

Samples were collected from March through October during 2012-2014, with start dates in each year dependent on snow and stream discharge conditions (see Appendix B and C for details on the State Water Board contracts under which samples were collected). All samples were collected during baseflow or near-baseflow conditions. Sampling in 2012 and 2013 focused primarily on sites located in Mono County (Figure 1) and for most sites was conducted approximately once per month. Sampling in 2014 was expanded to also include sites in the northern half of Inyo County (Figure 1). Also, to assess finer-scale temporal variability in FIB levels, in 2014 two sites in Mono County were sampled approximately weekly between May and August. Across all sites, the total number of samples collected per site during the study ranged from 1-26 (average = 6).

Water samples were collected by hand in mid-stream, approximately 3 cm below the water surface and upstream of the collector. For each sample, a new pair of disposable gloves was used by the collector. Prior to use, the 1000 mL polypropylene sample bottles were autoclaved to ensure they were sterile. Sample bottles were filled to within 1-2 cm of the rim, and immediately placed into a cooler with ice packs and transported to the Sierra Nevada Aquatic Research Laboratory (SNARL) for analysis. The time between sample collection and arrival at SNARL was always ≤ 6 hours (range 0.1-6.0, average = 2.7).

Culturing of fecal indicator bacteria

FIB were cultured from the samples using standard membrane filtration methods, specifically "Standard Methods" for fecal coliform bacteria (9222D) and *E. coli* (9222G; American Public Health Association et al. 1998). To process a sample, the 1000 mL sample bottle was first shaken vigorously to mix the contents, and then 1-3 subsamples were removed from the sample using a sterile serological pipette. Each subsample was placed into a separate filtration unit, and pulled through a 0.45 µm mixed cellulose ester membrane filter (Millipore HAWG) using vacuum filtration (< 250 mm Hg). Subsample filtration volumes ranged from 5 to 100 mL; the number and volume of subsamples were based on the bacteria culturing results from previous samples from a site and observations made during sample collection (e.g., presence or absence of cattle upstream), with the goal of obtaining 20-60 colony forming units (CFUs) per filter. Following filtration, each filter was transferred face-up to a petri dish containing a filter pad and 2.0 mL of m-FC Broth with Rosolic Acid (Millipore MHA000P2F). A lid was placed on the petri dish, and the dish was inverted, placed into a waterproof container, and submerged in a water bath where it was incubated for fecal coliform bacteria: 22-26 hours at 44.5 ± 0.2 °C. All samples were processed within two hours of arriving at the laboratory (range = 0.3-2.0, average = 1.1) and incubation of each filter began within 30 minutes after filtration. Filtration "blanks" were run regularly during sample processing to ensure that rinsing procedures were sufficient to remove all bacteria in previous samples from the filtration unit. Blanks were created by filtering 100 mL of autoclaved deionized (Milli-Q) water using the same methods as described above for field samples. For

each batch of samples, every tenth filter and the first and last filter was a blank. In addition, one of the subsamples in each batch was run in duplicate to evaluate within-subsample variation in FIB counts.

At the conclusion of the fecal coliform incubation period, filters were removed from the water bath and fecal coliform CFUs were counted under a low-power binocular microscope. Fecal coliform CFUs were distinguished from non-fecal coliforms by their characteristic blue color. For each sample, the filter with a CFU count that most closely matched the 20-60 CFU target was selected for subsequent *E. coli* culturing. To do this, the filter was removed from the m-FC media and transferred to a sterile petri dish containing nutrient agar with 4-methylumbelliferyl-β-D-glucuronide (NA-MUG; BD Difco 223100). The dish was then placed into a waterproof container and incubated in a water bath for 4 hours at 35 ± 0.5 °C as described above. Following incubation, *E. coli* CFUs were enumerated under a 6W 365nm long wave-length ultraviolet light source (UVP 95-0006-02). *E. coli* CFUs were distinguished from non-*E. coli* CFUs by their distinctive blue fluorescence.

Quality assurance and quality control practices

All samples were collected, processed, and analyzed, and all data were reviewed and managed, in accordance with all relevant provisions of the project's Quality Assurance Project Plan (Knapp and Nelson 2012).

Spatial and temporal patterns in FIB concentrations

To describe the general spatial patterns in FIB concentrations across the study area, for each site we calculated the geometric mean *E. coli* concentration for all samples collected during the May-September period. Filters that produced no FIB colonies were given a CFU value of zero. Site-specific results were projected onto digital maps of the study area. By focusing on the summer-fall period when FIB concentrations are likely to be the highest (see Results: *Landscape-scale drivers of FIB concentrations*), this analysis served to identify those areas for which FIB concentrations typically exceeded regional and federal bacterial water quality criteria/standards.

The landscape-scale analysis conducted as part of this study (see Methods: *Analysis of landscape-scale drivers of FIB concentrations*) provides a description of temporal patterns in FIB concentrations across the study area. However, this description is based on relatively low-frequency sampling (i.e., monthly or less frequently). To provide a more detailed description of FIB temporal patterns we analyzed data collected at two sites that were sampled more intensively in 2014: MAM.50, located on lower Mammoth Creek immediately below the Chance Ranch; and OWE.40, located on the Owens River at the Benton Crossing Road bridge. In 2013 both sites were sampled approximately once per month from March to November, and in 2014 they were sampled weekly during May to August and approximately monthly in September and October.

As summarized in the Introduction, for recreational waters the current FIB water quality standard in the Lahontan Region is 20 fecal coliform CFU per 100 mL and the USEPA recommended federal criteria for recreational fresh waters is 100 or 126 *E. coli* CFU per 100 mL. To allow comparison of our FIB results against these different standards/criteria, we opted to analyze and present all of our FIB results as counts of *E. coli* CFU per 100 mL. Counts based on *E. coli* provide a more accurate description of the concentration of fecal-derived bacteria than do results based on fecal coliforms because some bacteria categorized as fecal coliforms are actually not derived from feces (U.S. Environmental Protection Agency 1986). In addition, counts of fecal coliform and *E. coli* CFU per 100 mL from individual samples were highly correlated (r = 0.95) and the slope of their relationship was not significantly

different from 1. This indicates that the Lahontan Region fecal coliform standard of 20 CFU per 100 mL is approximately equal to 20 *E. coli* CFU per 100 mL (for additional details see Results: *Membrane filtration quality control measures*).

Analysis of landscape-scale drivers of FIB concentrations

Data set development. Project data were compiled into a SQL relational database (Microsoft Access v. 2013) and geographic information system (ArcGIS v. 10.2). As mentioned above, during the 2012-2014 study period sampling at nearly all sites was conducted monthly or less frequently. However, at two sites sampling in 2014 was conducted weekly. To ensure that sample collection intervals were relatively consistent across all sites included in the landscape analysis, for the sites subject to weekly sampling only the first sample collected per month in 2014 was included in the "landscape" data set. The final data set used for the landscape analysis included FIB results based on 681 samples from 110 sites, and 13 predictor variables (Table 1).

Several of the predictor variables describe the extent or presence/absence of a particular land use in the vicinity of each sampling location (i.e., campsite density, presence of lakes, road density, area of low or high-intensity land use, and presence of livestock). These variables were calculated for a "sector" that circumscribes the area in the immediate vicinity of a sampling location, regardless of watershed boundaries (see Methods: *Justification for using a "sector" to calculate land-use variables* below for additional details). Sectors were created using the ArcGIS Sectors tool. Each sector was centered on a sampling site, oriented upstream, and had a radius of 1.5 km and an angle of 90° (Figure 2). The 1.5 km radius was chosen based on the bacteria attenuation results of Willden (2006), and FIB results for the study area that suggested similar high attenuation rates. Importantly, preliminary analyses in which land use variables were calculated using sectors with a range of radius values (0.5-3.0 km) indicated that within this range values of land use variables were relatively insensitive to the actual sector radius used. Finally, the majority of sectors fell entirely or almost entirely within the watershed that contained the associated sampling site (e.g., Figure 2).

The following provides a detailed description of each of the predictor variables used in the landscape analysis (see also Table 1).

- SITEID: A unique five-digit alphanumeric code identifying each sampling location.
- HUC12M: The hydrologic unit in which each sampling site was located. This 12-digit hydrologic unit code was extracted from the U.S. Geological Survey (USGS) Watershed Boundary Dataset. In a few cases, a watershed was divided into more than one hydrologic unit, and in these cases a single HUC12 code was assigned to the entire watershed. In addition, because of its length the Owens River traversed multiple hydrologic units, and the areas circumscribed by those units were relatively arbitrary. Therefore, these hydrologic units were modified to better delineate discrete river reaches, including (1) Owens River headwaters downstream to Pleasant Valley Reservoir, (2) Pleasant Valley Reservoir downstream to Tinemaha Reservoir, and (3) Tinemaha Reservoir downstream to Owens Dry Lake.
- ELEV: Elevation of sampling sites, obtained from Google Earth. Although elevation is unlikely to influence FIB concentrations directly, indirect effects are possible because the extent of human use of the study landscapes generally decreases with increasing elevation.
- CAMP, LAKE, ROAD, LANDUSE21, LANDUSE23, COW: These six variables were calculated for the area within a 1.5 km radius sector (as described above; Figure 2). Because land uses within each

sector are upstream and in close proximity to the sampling site they have the potential to strongly influence FIB concentrations.

- CAMP: The number of designated campsites within each sector, based on information from the Humboldt-Toiyabe National Forest, Inyo National Forest, Bureau of Land Management, and Mono and Inyo Counties. If any part of a campground was within the sector perimeter, all campsites were considered as being inside the sector.
- LAKE: The presence or absence of lakes on the sampled stream within the associated sector. For example, as shown in Figure 2, upstream sectors for MAM.10 and MAM.20 both contain one or more lakes but that for MAM.30 does not. LAKE was included because preliminary analyses indicated that FIB concentrations were always very low immediately below lakes even when FIB concentrations were relatively high immediately above the water body. This might be due to dilution of the incoming FIB, settling and/or death of FIB in the water body, or some combination of these or other factors.
- ROAD: Total length of roads within each sector, calculated from 2014 U.S. Census Bureau TIGER/Line shapefiles. These files include both primary roads (paved) and secondary roads (paved and unpaved). Road length was included as an indicator of the intensity of human development and/or activity, which may affect FIB concentrations.
- LANDUSE21, LANDUSE23: The area of low and high-intensity land use within each sector, calculated from the 2011 National Land Cover Data Set (NLCDS). The “low intensity” land use category included NLCDS category 21 (“developed – open space”). The “high intensity” land use category included categories 22-24 (“developed – low/medium/high intensity”).
- COW: The presence or absence of livestock in a sector at the time of sample collection. This was estimated visually for all sites, except those on Bishop Creek and lower Owens River. Visibility in these two areas was often limited due to dense riparian vegetation (e.g., *Populus fremontii*, *Salix* spp.), and livestock presence was therefore determined from the LADWP Owens Valley Land Management Plan which identified the locations of grazing allotments and associated grazing periods. Along Bishop Creek, in addition to livestock grazing on LADWP lands grazing also occurs year-round on the Bishop Paiute Reservation. Most livestock grazing within the study area is by cattle, but some parcels are grazed by domestic horses or sheep. Domestic livestock are well-documented as a potential source of FIB to surface waters (e.g., Collins et al. 2007, Lewis et al. 2009, Roche et al. 2013), including in the study area (Nilson et al. 2012) where cattle are often found in close proximity to streams, including in natural stream-side meadows and in flood-irrigated pastures.
- RAIN: Rainfall intensity during the three days preceding sample collection. Precipitation data for the study area were downloaded from the MesoWest web portal. The MesoWest project provides access to current and archived weather observations from government agencies, private firms, and educational institutions. Daily total precipitation data for the 2012-2014 period were available from 11 stations scattered across the study area. Total precipitation during the three days preceding sample collection was calculated using data from the closest station. Precipitation from summer thunderstorms is often highly spatially variable in intensity, and even precipitation amounts recorded at a station in close proximity to a sampling site may not accurately reflect the actual precipitation at the site. Therefore, the numeric precipitation data (millimeters per day) was transformed into categorical data using a cut-off of 2 mm. When total precipitation during the previous three days was ≤2 mm, data were categorized as “no-to-

light precipitation", and when the precipitation amount was > 2 mm, data were categorized as "moderate-to-heavy precipitation". Precipitation during the three days preceding sampling was quantified because of its potential effect on FIB concentrations via influences on overland runoff and the associated transport of sediment and fecal material into streams (e.g., Reeves et al. 2004, Lewis et al. 2009).

- YEAR, DAY, TIME: Sampling year and sampling day (i.e., day of the year) were included to account for yearly and seasonal variation in FIB concentrations due to factors such as inter-year differences in precipitation amounts, seasonal variation in human use (in the study area, highest in mid-summer), and seasonal variation in livestock grazing intensity that is not captured by the livestock presence/absence variable (e.g., stocking densities are often lowest early and late in the grazing season). Sampling time was included because of possible diel variation in FIB concentrations due to inactivation of bacteria by sunlight (Whitman et al. 2004) or temperature (Howell et al. 1996).

Justification for using a "sector" to calculate land-use variables. The sector-based land-use variables described above could instead have been calculated for the entire watershed that lies upstream of a sampling point. However, there are several drawbacks of a watershed-based approach. First, in the eastern Sierra Nevada large portions of some watersheds lack any surface water and these areas will have little or no effect on fecal bacteria concentrations in streams. In this situation, watershed-based land use calculations could be broadly misleading. The Owens River is one of the best such examples. The eastern half of the Owens River watershed is made up of dry mountain ranges whose minimal surface water never reaches the Owens River (e.g., Glass Mountains, White Mountains, Inyo Mountains; Figure 1). As such, there is no reason to expect that land uses in these portions of the Owens River watershed will affect bacterial water quality in the Owens River. Second, calculating land-use variables across the entire watershed for the purpose of assessing land use effects on stream bacterial water quality is based on the assumption that land uses in even distant portions of a watershed can affect downstream bacterial water quality. However, in cold-water streams FIB concentrations may attenuate quickly downstream of a fecal source (e.g., Willden 2006; also R. A. Knapp, unpublished data). For example, the study by Willden (2006) included an attenuation experiment conducted in a Utah mountain stream using tracer bacteria, and showed that <20% of bacteria introduced at an upstream site were recovered from the water column only 1.2 km downstream. If FIB in our study streams show similar attenuation rates then land uses in the area immediately upstream of the sampling sites will have much stronger effects on FIB concentrations than those in more distant areas within the watershed, arguing for making calculations based on areas in the immediate vicinity of sampling locations. Third, making land use calculations strictly within the watershed of the stream being sampled ignores the fact that in many areas within the study area ditches have been constructed to move water between adjacent watersheds, thereby broadening the area in which land uses could affect water quality at a sampling location. This is particularly the case in areas subject to intensive livestock grazing, in which meadows are typically watered using flood irrigation (e.g., Bridgeport Valley, Long Valley, Round Valley, Bishop Creek).

Statistical analysis. We used multivariate generalized linear and generalized additive models to quantify the strength of associations between predictor variables and *E. coli* concentrations. In all analyses we were primarily interested in the effects of the landscape variables but included other

covariates to reduce the chances of confounding effects caused by not including important predictors. Our general regression analysis approach followed the protocol of Zuur et al. (2009, Section 4.2.3). All statistical analyses were conducted using R (R Development Core Team 2014) and the R packages *nlme* and *mgcv*. Our approach, which included a model with both fixed and random effects (see below), allowed us to account for between-sample dependencies and thereby include every sample as a separate record in the analysis. This allows for a much more informative and statistically powerful analysis than is possible using a simpler approach in which *E. coli* results are averaged for each sampling site and only the averaged values are included in the analysis.

Prior to analysis, we evaluated the continuous predictor variables for collinearity by calculating correlation coefficients and variance inflation factors (VIF). ROAD was the only variable with VIF > 3 and when it was dropped from the data set all other VIF values were less than 3. Therefore, ROAD was not included in regression models. In addition LANDUSE21 and LANDUSE23 were highly correlated (r = 0.6) so LANDUSE21 was also not included in regression models. The response variable in this analysis was counts of *E. coli* CFU per 100 mL (ECOLI100).

The regression analysis started with a generalized linear model that contained all categorical and non-collinear continuous predictor variables (Table 1). A $\log_{10}(Y + 1)$ transformation was applied to the ECOLI100 variable to meet assumptions of normality (transformed variable = LECOLI). The starting model was as follows:

(1) *LECOLI ~ ELEV + CAMP + LAKE + LANDUSE23 + COW + RAIN + YEAR + DAY + TIME*

A key assumption underlying regression analysis is that residuals are homogeneous. We assessed the validity of this assumption for Model 1 by plotting the standardized residuals versus fitted values and versus each individual predictor variable. Heterogeneity in residuals was detected, and was at least partly due to consistent differences between sampling sites and between watersheds in *E. coli* concentrations. Therefore, in the next iteration of the model we made several changes to allow us to find the optimal residual variance structure. We included both SITEID and HUC12M as random effects in the model to account for consistent differences in *E. coli* concentrations between sites/watersheds, and the lack of independence in intra-site results due to repeated sampling of the same location through time. Including SITE and HUC12M as random effects instead of as fixed effects has two important advantages: (1) it allows general conclusions to be made, not only conclusions restricted to the sampling sites and watersheds, and (2) it reduces the number of estimated parameters and thereby increases statistical power to detect effects.

To implement these changes we developed two new models, each of which included both fixed and random effects and are therefore referred to as mixed effects models. In one model the random effect term was simply SITEID and in the second model the random effect term was SITEID nested within watershed (HUC12M). These models were as follows:

(2) *LECOLI ~ ELEV + CAMP + LAKE + LANDUSE23 + COW + RAIN + YEAR + DAY + TIME | SITEID*
(3) *LECOLI ~ ELEV + CAMP + LAKE + LANDUSE23 + COW + RAIN + YEAR + DAY + TIME | HUC12M/SITEID*

Likelihood ratio tests indicated that Models 2 and 3 provided much better fits to the data than Model 1 and that Model 3 provided a significantly better fit than Model 2, although the difference between the two models was small.

The next step in the modeling process was to find the optimal fixed effect structure for Model 3. To do this, we sequentially dropped the least significant variable and refit the model until all remaining fixed effect variables were significant ($P \leq 0.05$). Using this reduced model, we again assessed the homogeneity of residuals as described above and detected some evidence of patterns in the residuals for two of the continuous predictor variables, DAY and TIME. To evaluate whether model fit could be further improved by using non-linear terms, we fit a generalized additive mixed effects (GAM) model in which the linear DAY and TIME terms were replaced by terms that used smoothing splines. Both terms had effective degrees of freedom >1, indicating that the terms were non-linear and that the smoothers improved model fit.

Microbial source tracking

Microbial source tracking (MST) methods are based on the fact that vertebrate species or related groups of species typically have characteristic bacterial communities in their digestive tracts and feces. By quantifying the abundance of source-specific bacteria in water samples containing fecal contamination it is therefore possible to attribute the contamination to particular vertebrate sources. MST methods have rarely been used to identify fecal sources in Sierra Nevada water bodies, and therefore it is important to evaluate MST assays (that usually were developed elsewhere) using local samples prior to their broader application. In this study, we applied six assays (3 general bacterial assays and 3 source-specific assays) to 165 samples to evaluate their general utility, and then used the results to describe the relative contribution of ruminant and human sources to fecal bacteria in streams in the study area.

Bacterial cells were collected from water samples by filtering 100-800 mL of water (average = 719 mL) from the 1000 mL sample using the methods described above for the membrane filtration assays. One filtration blank was collected on every date on which samples were processed. Following filtration, all filters were placed into sterile microcentrifuge tubes and stored at -40 °C until analysis. The 165 filters used in this study were selected to represent a diversity of land uses, and included 63 samples collected by SNARL personnel during the 2012 field season and filtered at SNARL (referred to as the "*2012*" set), 48 samples collected by personnel from the Surface Water Ambient Monitoring Program (SWAMP) from the Bishop Creek region in 2013 and filtered at SNARL ("*BSP*"), and 54 samples collected by SWAMP personnel from the northern Lahontan Region in 2013 at filtered at the Lahontan Water Board lab in South Lake Tahoe ("*SWA*"). Collection locations for all SWAMP MST samples are provided in Appendix D.

A description of MST standard operating procedures is provided in Appendix E, and these procedures are summarized here. DNA was extracted from filters using MoBio PowerSoil® DNA Isolation Kits (MoBio 12888). All samples were analyzed using a suite of six targeted 5' exonuclease quantitative polymerase chain reaction (qPCR)-based MST assays (Table 2). Three of these assays targeted general bacterial groups found in vertebrate feces (*Enterococcus*, Bacteroidales, and *Escherichia* including *E. coli*). The remaining three assays targeted two specific subgroups of Bacteroidales that are associated with particular animal sources of fecal contamination: ruminants (including cattle) and humans. Assays were conducted using widely established methods including those approved by the USEPA [summarized in Boehm et al. (2013) and references in Table 2]. A subset of preliminary MST data using assays for *Enterococcus* and *Escherichia* from 63 samples collected in 2012 was previously published in the final report for Contract 11-167-160.

The source-specific assays we used (Table 2) are those recommended following thorough testing for sensitivity and specificity (Boehm et al. 2013, Layton et al. 2013, Raith et al. 2013). Sensitivity is the ability of an assay to detect the target bacteria (and by extension, its vertebrate source) when it is present in a sample. Specificity is the ability of an assay to discriminate the target bacteria from bacteria of other potential sources. Therefore, assays with high sensitivity always detect the target bacteria when it is present, and those with high specificity identify as negative all samples lacking the target bacteria. Names of source-specific assays used in this report are those by which each assay was originally described in the peer-reviewed scientific literature. The ruminant assay (BacCow; Kildare 2007) was originally developed as a cow-specific assay but was subsequently discovered to cross-react with fecal bacteria from other ruminants (Boehm et al. 2013, Raith et al. 2013). Therefore, it is now classified as a ruminant-specific assay. The two human assays (BacHum: Kildare et al. 2007; HF183: Haugland et al. 2010, Green et al. 2014) differ somewhat in their sensitivity and specificity, with BacHum being highly sensitive but not 100% specific to human feces, and HF183 less sensitive but 100% human-specific (Layton et al. 2013). Because these differences are complimentary, it is generally recommended that samples be analyzed using both assays (Boehm et al. 2013, Layton et al. 2013).

Results

Spatial and temporal patterns of FIB concentrations

FIB results for all samples collected during the study period are provided in Appendix B. Across the study area, the average *E. coli* concentration was low for most sites, typically below 20 CFU per 100 mL (Figure 3a-e, Appendix B). However, several areas were characterized by average *E. coli* concentrations that were substantially higher, including some that exceeded 100 and/or 126 CFU per 100 mL. In the East Walker River headwaters, this included sites along the middle reaches of Swauger Creek (SWA.05, SWA.06), the lower reaches of Buckeye (BUC. 04, BUC.05, BUC.08) and Robinson Creeks (RBS.07, RBS.08, RBS.10), and the lower reaches of the East Walker River (EWK.06, EWK.08; Figure 3a). In the Mono Basin all sampling sites except one had low average *E. coli* concentrations; the exception (RUS.20) was located in the headwaters of Rush Creek downstream of suburban developments and the June Mountain Ski Area (Fig. 3b). In the headwaters of the Owens River above Crowley Reservoir most sampling sites also had low *E. coli* concentrations (Figure 3b), but sites along lower Mammoth Creek (MAM.40, MAM.50), on Convict Creek below SNARL (CON.20), and on the Owens River at the Benton Crossing Road bridge (OWE.40) were notable exceptions (Figure 3b). The *E. coli* concentrations at OWE.40 were particularly high. The central Owens River watershed contained several areas with elevated *E. coli* concentrations, in particular sampling sites along lower Pine Creek (PIN.50) and Horton Creek (HOR.70) in Round Valley (Figure 3c), and nearly all sites located in and around the City of Bishop (Figure 3c, d). *E. coli* concentrations at these sites typically exceeded 126 CFU per 100 mL, and for PIN.50 averaged > 400 CFU per 100 mL. Average *E. coli* concentrations were also somewhat elevated on the Owens River below Pleasant Valley Reservoir (OWE.66), Baker Creek (BAK.50), Big Pine Creek (BIG.40, BIG.70), and Birch Creek (BIR.50) (Figure 3c). In the lower Owens River watershed, *E. coli* concentrations were typically low (Figure 3e), exceeding 20 CFU per 100 mL only in lower Lone Pine Creek (LON.70) and on the Owens River just upstream of Owens Dry Lake (OWE.90).

For the two intensive sampling sties (MAM.50, OWE.40), during the 2013-2014 sampling period both sites were subject to grazing by cattle from approximately May to October. Mammoth Creek through most of the Chance Ranch is corridor-fenced to exclude cattle, but cattle have access to some portions of the creek and also to tributaries that enter Mammoth Creek within the Chance Ranch reach.

The Owens River above the OWE.40 sampling site is divided into a series of riparian pastures that based on our observations appear to be grazed on a rotational basis. Several tributaries enter the Owens River upstream of OWE.40 including Hot Creek, and cattle also have access to these tributaries both inside and outside of the Owens River riparian pastures. Temporal variation in *E. coli* concentrations at MAM.50 and OWE.40 was high, with concentrations generally low in the early spring and late fall when cattle were absent and relatively high during the summer when cattle were present (Figure 4a, b). In addition to variation between grazing and non-grazing periods, *E. coli* concentrations within the grazing period also showed considerable fluctuations. On Mammoth Creek, *E. coli* concentrations when cattle were present typically exceeded 20 CFU per 100 mL but were usually below the 100 or 126 CFU per 100 mL *E. coli* criteria (Figure 4a). On the Owens River, *E. coli* concentrations were close to 20 CFU per 100 mL early and late in the grazing season but were much higher during the main portion of the grazing season, usually exceeding both the 100 and 126 CFU per 100 mL *E. coli* criteria (Figure 4b).

Landscape-scale drivers of FIB concentrations

The final GAM regression model met the assumption of homogeneity of residuals, provided a good fit to the data, and explained 61% of the variation in *E. coli* concentrations (adjusted $R^2 = 0.61$). Significant predictors of *E. coli* concentrations were COW, DAY, TIME, LAKE, LANDUSE23, RAIN, and ELEV (Table 3a, b). CAMP and YEAR did not have significant effects and were dropped during the procedure used to find the optimal fixed structure. Of the four continuous predictor variables retained in the final model, response curves for two (DAY, TIME) were significantly non-linear (Table 3b). The results of the final GAM regression model are shown graphically in a series of plots (Figure 5). Each plot describes the relationship between one of the significant predictor variables and per-sample *E. coli* concentration, after accounting for the effects of all other significant predictor variables. The plotted terms are based on partial residuals, and the y-axis is standardized to have an average value of zero.

The predictor variable COW, which describes the presence or absence of livestock (primarily cattle) upstream of sampling sites, had the strongest effects on *E. coli* concentrations. After accounting for the effects of all other significant predictor variables, *E.coli* concentrations were markedly higher in the presence of livestock compared to when livestock were absent (Table 3a, Figure 5a). In Table 3a the "estimate" for COW(yes) is 0.85 and the fact that this coefficient is positive indicates that the presence of livestock has a positive effect on *E. coli* concentrations relative to the absence of livestock (see also Figure 5a).

Of the three temporal variables included in the model (YEAR, DAY, TIME), two had significant effects. The predictor variable DAY indicates the number of days since January 1 and in the model describes seasonal trends in *E. coli* concentrations. The effect of DAY was highly significant and non-linear (Table 3b), being lowest in spring and fall and highest in mid-summer (Figure 5b). (The reason no estimate for DAY is provided in Table 3b is because for continuous variables the estimate is the slope of the line describing the effect of a predictor variable on the response variable; given that the effect of DAY is non-linear, the slope of this effect cannot be described with a single number.) TIME describes the time of day at which a sample was collected, and had a significant, non-linear effect on *E. coli* concentrations (Table 3b). After accounting for the effects of all other significant predictor variables, *E. coli* concentrations were high and relatively constant for samples collected during the morning and early afternoon, but decreased in late-afternoon (Figure 5c).

The predictor variables LAKE, LANDUSE23, RAIN, and ELEV also had significant effects on *E. coli* concentrations, but their importance was substantially less than that of COW, DAY, and TIME (Table 3).

LAKE indicates the presence or absence of larger lakes (>1 ha) on the sampled stream within the upstream sector. The presence of upstream lakes reduced *E. coli* concentrations compared to when lakes were absent (Table 3a, Figure 5d). The area of high intensity land use within a sector (LANDUSE23) had a significant linear effect on *E. coli* concentrations, and this effect was positive (Table 3a, Figure 5e). However, relatively few sampling sites had a substantial area of high-intensity land use upstream. RAIN indicated whether or not sampling sites had received moderate-to-heavy rain during the three days prior to sample collection. Moderate-to-heavy rain increased *E. coli* concentrations (Table 3a), although only by a relatively small amount (Figure 5f). Finally, sampling site elevation (ELEV) had a significant linear effect on *E. coli* concentrations (Table 3a), and *E. coli* concentration decreased with increasing elevation (Figure 5g). However, this effect was relatively weak after accounting for the effects of other significant predictor variables.

Given both the success of the final GAM model in identifying the drivers of *E. coli* concentrations in study area streams and the strength of the COW variable in predicting these concentrations, an interesting additional application of the model is to predict expected site-specific *E. coli* concentrations in the absence of livestock fecal inputs to streams within the study area (i.e., "background" *E. coli* concentrations). Such an approach allows forecasting scenarios in which livestock access to streams is effectively mitigated by management practices such as corridor fencing, off-stream water sources, and/or other measures. To do this, we used the *predict.gam* function and the final GAM model to predict *E. coli* concentrations using (1) the original data set, and (2) using a modified data set in which the variables COW and RAIN were set to zero for all records. The modified data set allowed us to predict *E. coli* concentrations in the absence of moderate-to-heavy rain events during the three days prior to sampling and in the absence of livestock fecal inputs to the study streams. The prediction routine using the original data set and the final GAM model indicated that the percentage of samples predicted to exceed 20 *E. coli* CFU per 100 mL was similar to the actual percentage in the original data set, as expected (Figure 6a, b; 24% versus 33%, respectively). Importantly, the model also predicted that under "baseline" conditions (i.e., in the absence of moderate-to-heavy rain during the three days prior to sample collection and in the absence of livestock fecal inputs to streams), the percentage of samples exceeding 20 CFU per 100 mL would be reduced to only 2% (Figure 6c).

Membrane filtration quality control measures

Results from membrane filtration incubation blanks demonstrated the adequacy of our sterile techniques when culturing FIB. Of the 203 blanks, fecal coliform colonies were observed on only one filter and included only a single CFU. Therefore, the between-sample rinsing protocol was successful in removing bacteria from the filtration unit. Membrane filtration duplicates indicated the repeatability of FIB counts. Subsamples from 64 samples were run in duplicate, and the number of *E. coli* colonies on duplicate filters was very similar (Model II (reduced major axis) regression: $R^2 = 0.98$, $P << 0.0001$; slope = 1.04, 95% confidence interval = 0.96-1.13).

Based on results from the 681 field samples, the number of fecal coliform CFU counted per filter was closely associated with the number *E. coli* CFU counted on the same filter (Figure 7; Model II (reduced major axis) regression: LECOLI = 0.9720(LFECAL) – 0.0242, $R^2 = 0.98$, $P << 0.0001$; 95% confidence interval for slope = 0.96-0.98). Using this equation, the current Lahontan Water Board FIB objective of 20 fecal coliform CFU per 100 mL is equivalent to 17 *E. coli* CFU per 100 mL.

Microbial source tracking

MST results from all samples/assays are provided in Appendix F. Ribosomal subunit gene copies from *Enterococcus*, *Escherichia*, and Bacteroidales were found in concentrations ranging over five orders of magnitude, from 10^2 to 10^6 copies per 100 mL (Figure 8; as determined using the three general assays, Entero1a, EC23S857, and GenBac3, respectively). The source-specific ruminant Bacteroidales assay (BacCow) showed similar ranges (Figure 8). The human-specific Bacteroidales assays (BacHum and HF183) exhibited positive "hits" in only five samples, ranging from 626 to 4195 copies per 100 mL: Sites RBS.07 and RBS.08 on 8/14/12, and Sites BSP.002, BSP.003 and BSP.004 on 9/4/2013 (Figure 9). Four of the five samples were positive for both assays.

The relative contribution of ruminant Bacteroidales (BacCow) to total Bacteroidales (GenBac3) ranged widely ["%Cow": (BacCow/GenBac3)*100; Figure 10], with ruminant contribution for the vast majority of the samples (90%) falling between 1% and 100%. For the remaining 10% of samples (13 out of a total of 136 BacCow-positive samples), the relative ruminant contribution exceeded 100%, suggesting imprecision in the higher ranges of one or both of the assays. The proportion of total Bacteroidales attributable to ruminant sources ("%Cow") was strongly correlated with absolute concentrations of BacCow gene copies (Figure 10), indicating that quantities of ruminant-derived Bacteroidales varied across a relatively homogenous background of non-ruminant Bacteroidales. The black guidelines in Figure 10 highlight that above ~ 7000 BacCow gene copies per 100 mL ruminant sources exceed 10% of the Bacteroidales. It is notable that most of the *2012* samples (collected mostly from sites not subject to cattle grazing) fall below these thresholds while the *BSP* and *SWA* samples (collected primarily from sites grazed by cattle) fall above these thresholds. For the *2012* data set (the only MST data set for which data on site conditions was available), %Cow was nearly five times higher for sites at which cattle were observed upstream during sampling than for sites without cattle (lognormal means: 10% versus 2%; $P = 0.0003$, $r^2 = 0.29$). Ruminant source contribution was not significantly influenced by other predictor variables described above, including prior precipitation, time of day, day of year, elevation, or latitude/longitude ($P > 0.05$).

Membrane filtration-based *E. coli* concentrations strongly and significantly predicted qPCR-based *Escherichia* gene copy concentrations in each of the three sample sets (Figure 11; $r = 0.87$, 0.66, 0.83 for *2012*, *BSP*, and *SWA* respectively, $P < 0.0001$). This provides an important validation that the qPCR *Escherichia* assay is detecting the same organisms as those detected by the *E. coli* membrane filtration assay. Using this relationship, we estimate that 20 CFU (from the membrane filtration assay) is roughly equivalent to 2000 *Escherichia* genes and 126 CFU is roughly equivalent to 10,000 genes (Figure 11). The slopes of the relationship between membrane filtration and qPCR-based *E. coli* concentrations did not differ significantly among the three datasets (95% confidence intervals overlap the slope estimates) but the intercept of the *SWA* dataset is significantly (~4X) lower than those of the *2012* and *BSP* datasets. This suggests either higher *E. coli* CFU counts or lower qPCR efficiency in the *SWA* samples (Figure 11). Using the four qPCR assays that frequently exhibited positive "hits" (Entero1a, EC23S857, GenBac3, BacCow), results from all assays were significantly related to both membrane filtration-based fecal coliform and *E. coli* CFU. This was true within each of the three sample sets ($P < 0.01$) with the exception that *Enterococcus* values in set *SWA* were not correlated with FIB ($P = 0.55$). Coefficients of determination for the prediction of *Escherichia* gene concentrations from FIB were nearly twice those of the other assays (~0.6 versus 0.3), suggesting that the *Escherichia* assay is most closely representing the fecal coliform and *E. coli* bacteria detected by membrane filtration, as expected. The coefficients of determination for the three MST assays averaged across the *2012*, *BSP*, and *SWA* sample sets were 0.52,

0.29, and 0.28, respectively, suggesting some variation among sites in the degree of predictability of the results of all MST assays from FIB concentrations.

During preliminary assay testing, we evaluated two additional ruminant-specific Bacteroidales MST assays for specificity and consistency, BacR (Reischer et al. 2006) and BoBac (Layton et al. 2006). Results from BacR were virtually identical to those from the BacCow assay, with a lognormal regression (r^2 = 0.93 P < 0.0001) exhibiting a slope not significantly different from 1 (95% confidence interval spans 1 when intercept is set to zero; intercept not significantly different from 0). BoBac showed a similar relationship (slope not significantly different from 1), but had an intercept significantly different from 0 (consistently 100 copies higher than BacCow; 95% confidence interval = 30 – 260 copies) and was equivalent to the more general GenBac3 assay (slope not significantly different from 1, intercept nonsignificant). This suggests that for the included samples, the BoBac assay is not specific to ruminants. Based on these results, and considering the added expense of the minor groove binding probes required for the BacR assay, we used the BacCow assay and the corresponding BacHum assay (Kildare et al. 2007).

All MST standards were tested on every run against every assay and exhibited predictable specificity among assays and no detectable cross-reaction; as predicted, standards for human and ruminant Bacteroidales both were detected by the GenBac3 assay in addition to the respective source-specific assays. The empirically determined minimum stable limit of detection was estimated at 20 gene copies per qPCR reaction, effectively limiting the sensitivity of the assays to 250 copies per 100 mL of sample collected (depending on the volume filtered); this limit of detection is less than 1 *E. coli* CFU per 100 mL as obtained by membrane filtration (Figure 11). All filter blanks from 2012 and 2013 samples yielded zero resolvable gene copies. Similarly, no-template qPCR contamination controls yielded no contamination, with no resolvable gene copies and no detectable amplification threshold (C_T) values.

To test methodological replicability of MST assays we analyzed each *BSP* sample (n = 48) for both human (BacHum, HF183) and ruminant (BacCow) gene copies on three qPCR runs (Figure 12). For any given sample we observed an among-run variance averaging 0.5 log copies (equivalent to approximately 3-fold raw copy concentration variance) in the BacCow assay, with some runs consistently higher (e.g., 28 October) than others. However, all runs had statistically identical slopes such that relationships among samples were preserved across runs and there was no evidence that any given run is superior. Very few samples contained bacteria that were detected by the human Bacteroidales assays; those samples in which the human Bacteroidales marker was detected showed consistency in detection among runs. Our results emphasize that the accepted approach of “running samples in triplicate” by loading samples three times onto one plate run is pseudo-replication and will increase precision within a run but sacrifice accuracy by reinforcing run-to-run bias. Running in triplicate within a plate is a tradeoff with running large groups of samples together within the same plate. When samples run on separate plates are to be compared across runs the lack of accounting for run-to-run variance can create artificial differences. When entire sample “sets” can be run on a single plate in triplicate it is advantageous to reduce instrument “noise” through pseudo-replication within the plate run, but in most cases it is preferable to run all samples from a given sample set in singletons on a single plate. Running additional plates can increase precision and accuracy, but should be secondary to including more samples per plate.

To provide a preliminary assessment of the association between MST results and the variables used in the “landscape-scale drivers of FIB” regression analysis, we relied on the *2012* set of MST samples because these were the only sites for which MST results were available that were included in

the regression analysis (n = 63 filters). Because the two human assays rarely exhibited positive "hits" this assessment focused solely on the results from the Entero1a, EC23S857, GenBac3, and BacCow assays. The bacteria targeted by these four assays were all found at significantly higher concentration in sites with cattle present, and/or that experienced >2 mm of rain during the three days preceding sample collection. All four measurements were significantly reduced at higher versus lower elevations, and declined throughout the season ($P < 0.01$). There was no effect of longitude, time of day, or land use on gene concentrations on any of the qPCR assays ($P > 0.05$).

Except for Bishop Creek, MST results for our study area are so far available only from a single sample and therefore may not be representative of general patterns. As such, these MST results were not mapped. The MST results for Bishop Creek were mapped because these results are available for multiple samples per site collected across the Bishop region. These results are presented as the proportion of total Bacteroidales attributable to ruminant sources ("%Cow"), averaged (as geometric means) across all samples per site. The results indicate that during the summer-fall 2013 sampling period, average %Cow values in Bishop Creek were low upstream of developed areas (upstream of Mumy Lane), and increased markedly in downstream reaches (Figure 13). Absolute gene concentrations (BacCow) produced very similar patterns, indicating that both the magnitude of ruminant-derived feces and the proportional ruminant contribution to total vertebrate feces increased from upstream to downstream reaches.

Discussion

Patterns and drivers of fecal indicator bacteria

Based on more than 700 samples collected at 111 sites during 2012-2014, *E. coli* concentrations in streams from the headwaters of the East Walker River to the lower Owens River were generally low, typically less than 20 CFU per 100 mL. However, a few areas were characterized by high *E. coli* concentrations, in some cases exceeding 100 and/or 126 CFU per 100 mL. These areas included Bridgeport Valley, Owens River above Crowley Reservoir, Round Valley, and in and around the City of Bishop. The relatively low FIB concentrations obtained for the middle and lower reaches of the Owens River are encouraging, but may in part reflect the fact that this area is grazed by livestock primarily in winter and spring, and sampling of these reaches was conducted only in mid-summer. As such, additional sampling during the grazing season will be necessary to more fully describe seasonal patterns in FIB concentrations for this portion of the study area. *Note added to draft*: Sampling of the Owens River conducted at eight sites from Pleasant Valley to Owens Dry Lake on February 26, 2015 also showed low FIB concentrations, with *E. coli* counts ≤21 CFU per 100 mL at all sites.

The primary drivers of *E. coli* concentrations in the study area were the presence of livestock (primarily cattle) and day of the year. The association between livestock and elevated *E. coli* concentrations in streams is well-documented (e.g., Collins et al. 2007, Lewis et al. 2009, Nilson et al. 2012, Roche et al. 2013) and in the study area likely results from both direct deposition of cattle feces into waterways and transport of fecal material from land to streams via overland runoff caused by rainfall or flood irrigation of pastures. The return to streams of water that was used to irrigate pastures, including pastures being actively grazed by cattle, was commonly observed in Bridgeport Valley and Round Valley, and has the potential to transport high concentrations of FIB from terrestrial areas into aquatic habitats. Limiting these return flows via changes in irrigation practices could result in significant reductions in *E. coli* concentations in receiving waters. Fencing cattle away from streams, providing alternative water sources, and other livestock management measures also have been shown to reduce

FIB and pathogen concentrations in receiving waters (e.g., Collins et al. 2007, George et al. 2011, Osmond et al. 2007, Zeckoski et al. 2012). Recent fencing projects implemented by the LADWP as part of livestock operations management in Long Valley, including those along lower McGee, Convict, and Mammoth Creeks may have contributed to the low-to-moderate *E. coli* concentrations observed at associated sampling sites (e.g., CON.30, CON.40, MCG.30, MAM.50). However, the occasionally high *E. coli* concentations at the MAM.50 site and the regularly high concentrations observed at the OWE.40 site (Figure 4) suggest that *E. coli* concentrations can sometimes remain high even in the presence of riparian fencing installed to reduce direct contact of cattle with streams. In such cases, MST should be used to determine if the observed FIB are derived from ruminants or from other sources.

Day-of-the-year was also a strong predictor of *E. coli* concentrations. The hump-shaped relationship between DAY and *E. coli* concentration is likely a consequence of DAY serving as a surrogate for seasonal patterns of livestock and human use in the study area. For example, cattle stocking densities often appear to be lower early and late in the grazing season compared to during the main (i.e., summer) portion of the season. However, the effect of DAY remained significant even when all grazed sites were excluded from the analysis. This suggests that feces from other sources, including humans, pets, and wildlife, may also be partially responsible for the significant seasonal pattern in *E. coli* concentrations. The shape of the response curve describing the relationship between day of the year and *E. coli* concentration qualitatively matches patterns of human use of the study area (e.g., anglers, hikers), being relatively low in spring and fall and peaking in mid-summer.

The results from the analysis in which we predicted the *E. coli* concentrations of sampling sites across the study area has implications for water managers and regulators who are in the process of developing future *E. coli* objectives for implementation by the Lahontan and State Water Boards. The final statistical model provided a good fit to the data, and predictions of *E. coli* concentrations using the model were similar to measured concentrations (percentage exceeding 20 *E. coli* CFU per 100 mL = 24% and 33%, respectively). More importantly, predictions of baseline *E. coli* concentrations (i.e., in the absence of moderate-to-heavy rain and in the absence of livestock fecal inputs to streams) suggested that the percentage of samples exceeding 20 CFU per 100 mL would be reduced to only 2%. These results have at least three significant management/policy implications: (1) the majority of sites in the study area are predicted to have *E. coli* concentrations that already meet the current Lahontan Water Board standard of 20 CFU per 100 mL; (2) if management measures are implemented to effectively address fecal inputs from livestock into streams, nearly all of the streams in the study area are predicted to meet the current 20 CFU per 100 mL standard; and (3) because most streams already meet the Lahontan Water Board's current standard (i.e., 20 CFU per 100 mL), adoption by the Lahontan Water Board and/or State Water Board of the current federal FIB criteria (i.e., 100 or 126 *E. coli* CFU per 100 mL) would allow substantial degradation of the generally high water quality that currently characterizes streams in the study area.

Microbial source tracking

Results from the six qPCR-based bacteria assays indicate that the three general assays and three source-specific assays have significant utility for improving our ability to accurately quantify FIB concentrations in streams and identify FIB sources. All qPCR assays produced reliable results, characterized by a lack of filtration-blank or template contamination, high reproducibility among instrument runs, and strong predictability of qPCR-based *E. coli* gene concentrations from membrane filtration-based *E. coli* concentrations. Despite these promising results, the number of samples analyzed

to date using the qPCR assays is still relatively small, and limits our ability to make broad generalizations about the MST results. However, some important patterns are evident and deserve mention.

First, gene concentrations of *Enterococcus*, Bacteroidales (general and ruminant-specific) and *Escherichia* produced by qPCR assays were highly correlated with fecal coliform and *E. coli* concentrations quantified using the membrane filtration assay. This association was particularly strong for *Escherichia*, and confirms that the *E. coli* membrane filtration and *Escherichia* qPCR assays are targeting the same bacteria. Associations between membrane filtration-based FIB concentrations and gene concentrations of *Enterococcus* and Bacteroidales were less precise, as expected. Using the relationship between qPCR-based and membrane filtration-based estimation of *Escherichia* concentrations, we estimate that 2000 gene copies per 100 mL is equivalent to the Lahontan Water Board's current fecal coliform standard of 20 CFU per 100 mL, and that 10,000 gene copies per 100 mL is equivalent to the USEPA's recommended criterion of 126 CFU per 100 mL.

Second, gene concentrations from all assays were generally enriched in areas with cattle and after rain events. Bacteroidales attributable to ruminants were widespread across the study area, and were often detected in high concentrations. The proportion of Bacteroidales attributable to ruminant sources was nearly five times higher for sites at which cattle were observed upstream during sampling than for sites without cattle, and Bacteroidales attributable to ruminant sources contributed substantially more to total Bacteroidales at sites where cows were present versus absent. Collectively, these results suggest that cattle were often the primary contributor to the ruminant-specific fraction of Bacteroidales, and confirm that the ruminant-specific qPCR assay BacCow will provide a useful tool to detect feces in streams that originated from cattle. Detailed spatial analyses of MST results across the study area will be conducted pending results from additional MST samples.

Third, human Bacteroidales were detected only rarely (five samples), and even when detected concentrations were relatively low. This was particularly informative for the Bishop Creek watershed. This watershed is characterized by high FIB concentrations, but land uses that could contribute importantly to FIB concentrations (i.e., human development, livestock grazing) are closely intermixed (Figure 3d), making it difficult to identify the dominant sources of bacterial contamination solely by evaluating spatial associations between land uses and FIB concentrations. Of the 48 Bishop Creek samples analyzed using the BacCow and BacHum assays, all showed evidence of ruminant Bacteroidales and in 31 samples concentrations were high (>50,000 gene copies per 100 mL). Spatial patterns of ruminant Bacteroidales in Bishop Creek were very similar to those of *E. coli* from membrane filtration assays. In contrast, human Bacteroidales were detected in only three samples by BacHum and two samples by HF183 and always at low concentration (<5000 gene copies per 100 mL). Therefore, based on the current set of samples cattle appear to be a much more significant source of fecal bacteria in the Bishop Creek watershed than are humans. However, analysis of a larger number of samples collected over several seasons should be conducted to assess the generality of this preliminary finding. In addition, analysis of at least a subset of samples using a broader set of source-specific assays would be needed to determine whether other fecal sources (e.g., horses, pets, wildlife) also contribute significantly to FIB concentrations.

Conclusions

Results from the current study provide an important landscape-scale assessment of patterns of FIB concentrations across the study area, with particular relevance for the development of science-based bacterial water quality standards for the Lahontan Region. Application of the modeling techniques

used in the current study to sites across the Lahontan Region are needed to extend the generality of these results and to assess their broader applicability. In addition, application of the MST assays to a larger set of samples will serve to further test the human and ruminant assays used in the current study, and significantly advance our understanding of sources of fecal contamination to streams in the study area and across the Lahontan Region. An expanded water quality monitoring program that uses modern statistical and molecular approaches has the potential to significantly improve the water quality in this region, with important benefits to users of this limited water resource.

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Tables

Table 1. Predictor variables used to identify the drivers of fecal indicator bacteria concentrations in streams in the eastern Sierra Nevada, California.

Variable	Code	Description	Type	Model effect
Site identification number	SITEID	Unique five-digit alphanumeric code used to identify each sampling location	Categorical	Random
Hydrologic unit	HUC12M	U.S. Geological Survey 12-digit hydrologic unit, modified in some cases as described in Methods.	Categorical	Random
Elevation	ELEV	Height above sea level (in meters)	Continuous	Fixed
Campsites	CAMP	Number of designated campsites within a 1.5 km radius upstream-oriented sector	Continuous	Fixed
Upstream lakes	LAKE	Presence/absence of one or more water bodies (>1 ha in surface area, >3 m deep) within a 1.5 km radius upstream-oriented sector	Continuous	Fixed
Road length	ROAD	Total length of all road segments (paved and unpaved) within a 1.5 km radius upstream-oriented sector (in kilometers)	Continuous	Fixed
Low-intensity land use	LANDUSE21	Area of low-intensity land use within a 1.5 km radius upstream-oriented sector, including golf courses and low density of buildings (in km^2)	Continuous	Fixed
High-intensity land use	LANDUSE23	Area of moderate and high-intensity land use within a 1.5 km radius upstream-oriented sector, including high density of buildings (in km^2)	Continuous	Fixed
Livestock grazing	COW	Presence/absence of livestock (usually cows) within a 1.5 km radius upstream-oriented sector	Categorical	Fixed
Precipitation amount	RAIN	Presence/absence of total rainfall during previous 3 days of ≥2 mm.	Categorical	Fixed
Sampling year	YEAR	Year during which sample was collected	Categorical	Fixed
Sampling day	DAY	Day of the year (since January 1) on which sample was collected.	Continuous	Fixed
Sampling time	TIME	Time of day when sample was collected	Continuous	Fixed

Table 2. Description of six qPCR-based microbial source tracking assays used in the current study.

Assay Target	Assay Name	Gene Target	References	Nucleotide Sequences (Forward, Reverse, 5' Exonuclease Probe)
Enterococcus	Entero1a	23S rRNA	Ludwig and Schleifer (2000), Haugland et al. (2005), U.S. Environmental Protection Agency (2010a)	AGAAATTCCAAACGAACTTG CAGTGCTCTACCTCCATCATT 6-FAM™/TGGTTCTCT/ZEN™/CCGAAATAGCTTTAGGGCTA/IB®FQ/
Escherichia	EC23S857	23S rRNA	Chern et al. (2011)	GGTAGAGCACTGTTTTGGCA TGTCTCCCGTGATAACTTTCTC 6-FAM™/TCATCCCGA/ZEN™/CTTACCAACCCG/IB®FQ/
Bacteroidales	GenBac3	16S rRNA	Dick and Field (2004), Siefring et al. (2008), U.S. Environmental Protection Agency (2010b)	GGGGTTCTGAGAGGAAGGT CCGTCATCCTTCACGCTACT 6-FAM™/CAATATTCC/ZEN™/TCACTGCTGCCTCCCGTA/IB®FQ/
Human Bacteroidales	HF183	16S rRNA	Haugland et al. (2010), Green et al. (2014)	ATCATGAGTTCACATGTCCG CTTCCTCTCAGAACCCCTATCC 6-FAM™/CTAATGGAA/ZEN™/CGCATCCCCAT/IB®FQ/
Human Bacteroidales	BacHum	16S rRNA	Kildare et al. (2007)	TGAGTTCACATGTCCGCATGA CGTTACCCCGCCTACTATCTAATG 6-FAM™/TCCGGTAGA/ZEN™/CGATGGGGATGCGTT/IB®FQ/
Ruminant Bacteroidales	BacCow	16S rRNA	Kildare et al. (2007)	CCAACYTTCCCGWTACTC GGACCGTGTCTCAGTTCCAGTG 6-FAM™/TAGGGGTTC/ZEN™/TGAGAGGAAGGTCCCCC/IB®FQ/

Table 3. Estimated parameters for the final GAM model used to identify significant predictors of *E. coli* concentrations across the study area: (a) parametric coefficients, and (b) smooth terms.

a.

Variable name	Estimate	Std. error	*t*	*P*
Intercept	1.09	0.20	5.50	5.27×10^{-8}
COW(yes)	0.85	0.06	13.54	$< 1.00 \times 10^{-10}$
LAKE(yes)	-0.46	0.13	-3.59	3.60×10^{-4}
LANDUSE23	0.58	0.20	2.90	3.89×10^{-3}
RAIN(yes)	0.14	0.05	2.61	9.20×10^{-3}
ELEV	-0.23	0.10	-2.29	2.22×10^{-2}

b.

Variable name	EDF[1]	*F*	*P*
s(DAY)	5.35	34.06	$< 1.00 \times 10^{-10}$
s(TIME)	4.63	8.61	2.33×10^{-7}

1. Effective degrees of freedom: 1 indicates a straight line, and higher values indicate an increasingly non-linear smoothing spline.

Figures

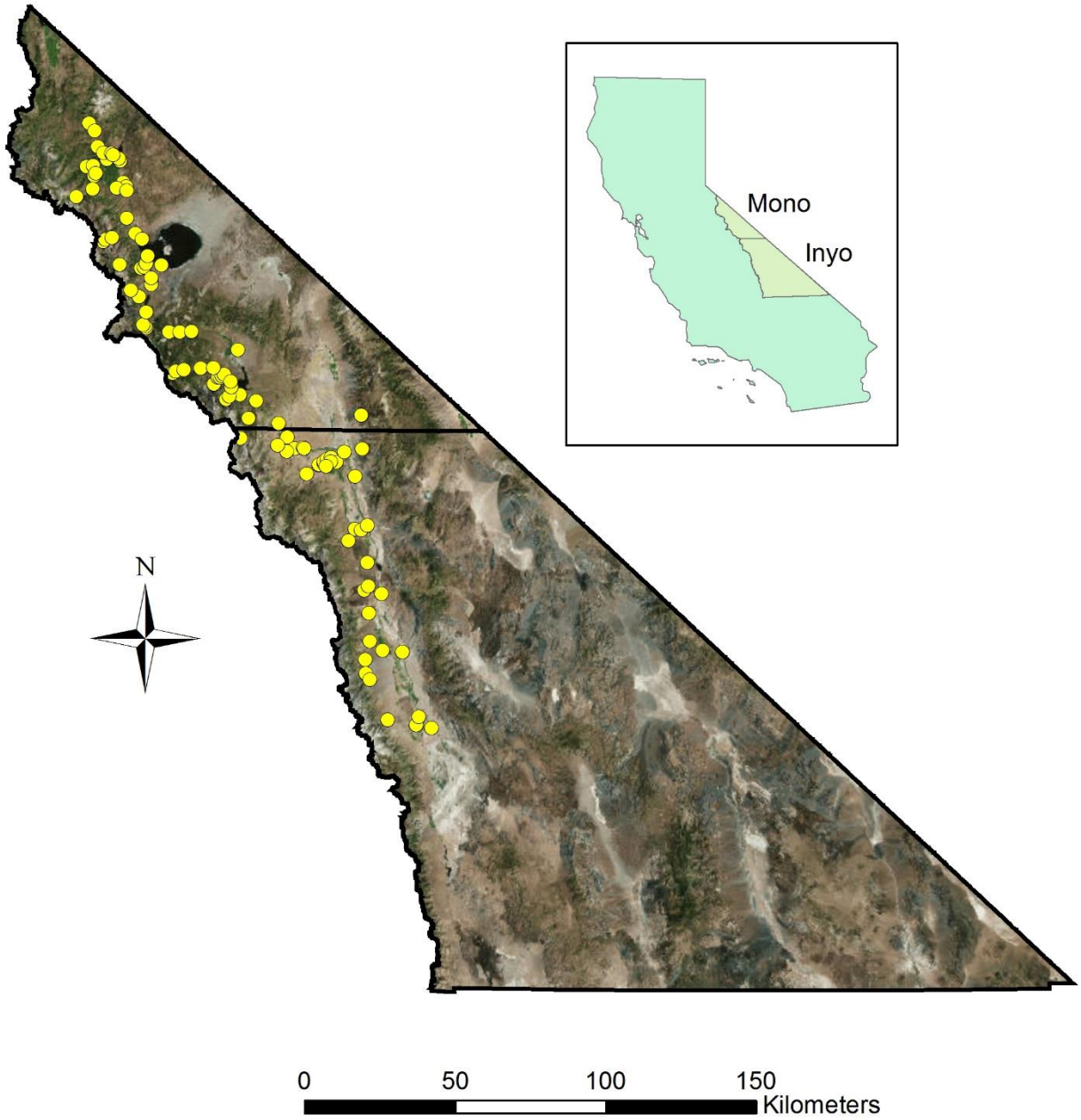


Figure 1. Map of the study area showing the sampling sites (yellow circles) within Mono and Inyo Counties, California. The inset map locates the two counties within California. The Sierra Nevada crest forms the western border of the study area. Most study sites were located along the eastern base of the Sierra Nevada, and few perennial streams exist in more easterly portions of the two counties.

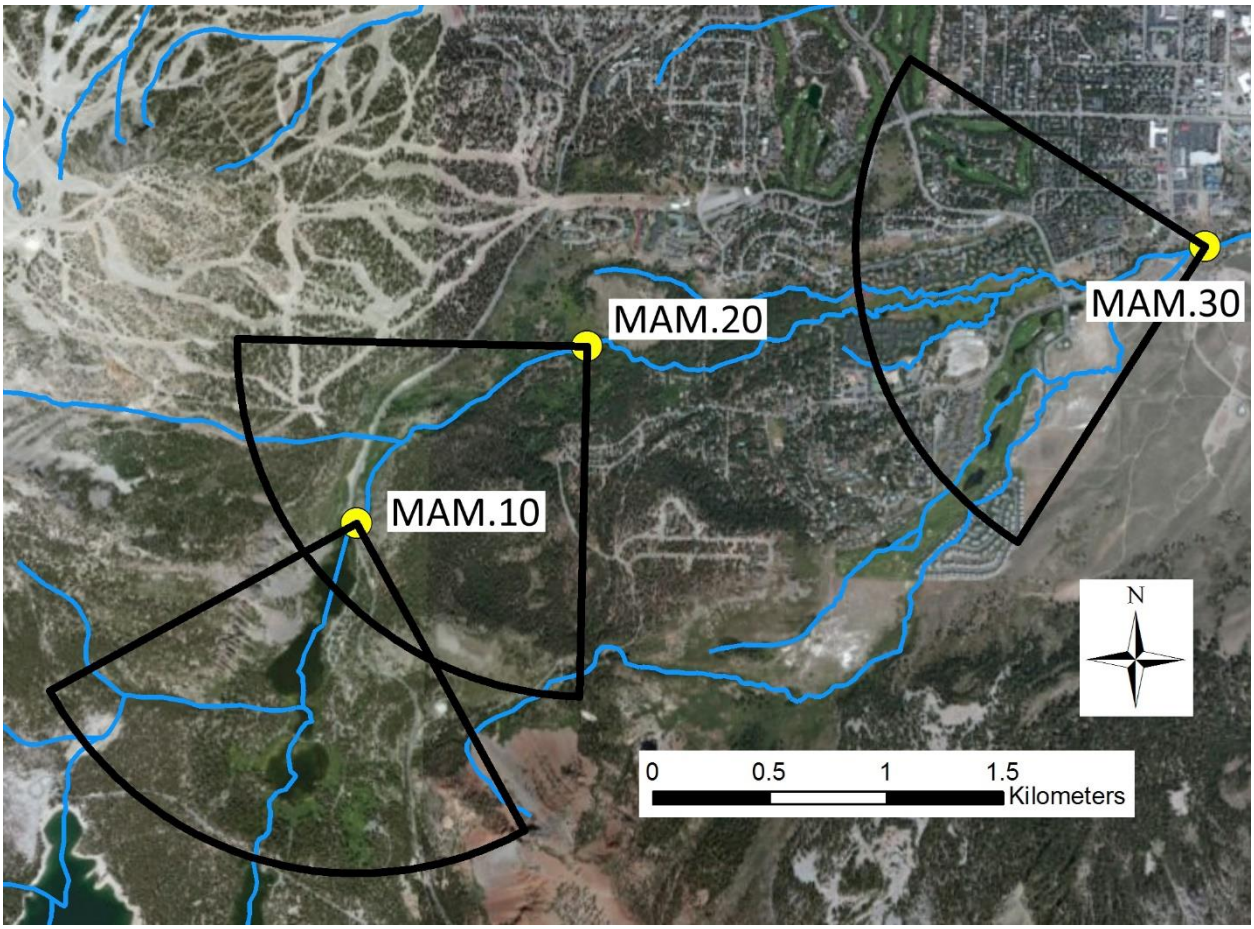


Figure 2. Image from the Geographic Information System used in this study, showing sectors associated with three sampling sites (yellow circles) on Mammoth Creek (MAM.10, MAM.20, MAM.30). Each sector has a 1.5 km radius, an angle of 90°, and is oriented upstream. The sectors for MAM.10 and MAM.20 include mostly undeveloped national forest lands, and the sector for MAM.30 includes the highly developed areas associated with the town of Mammoth Lakes. Streams are indicated with blue lines.

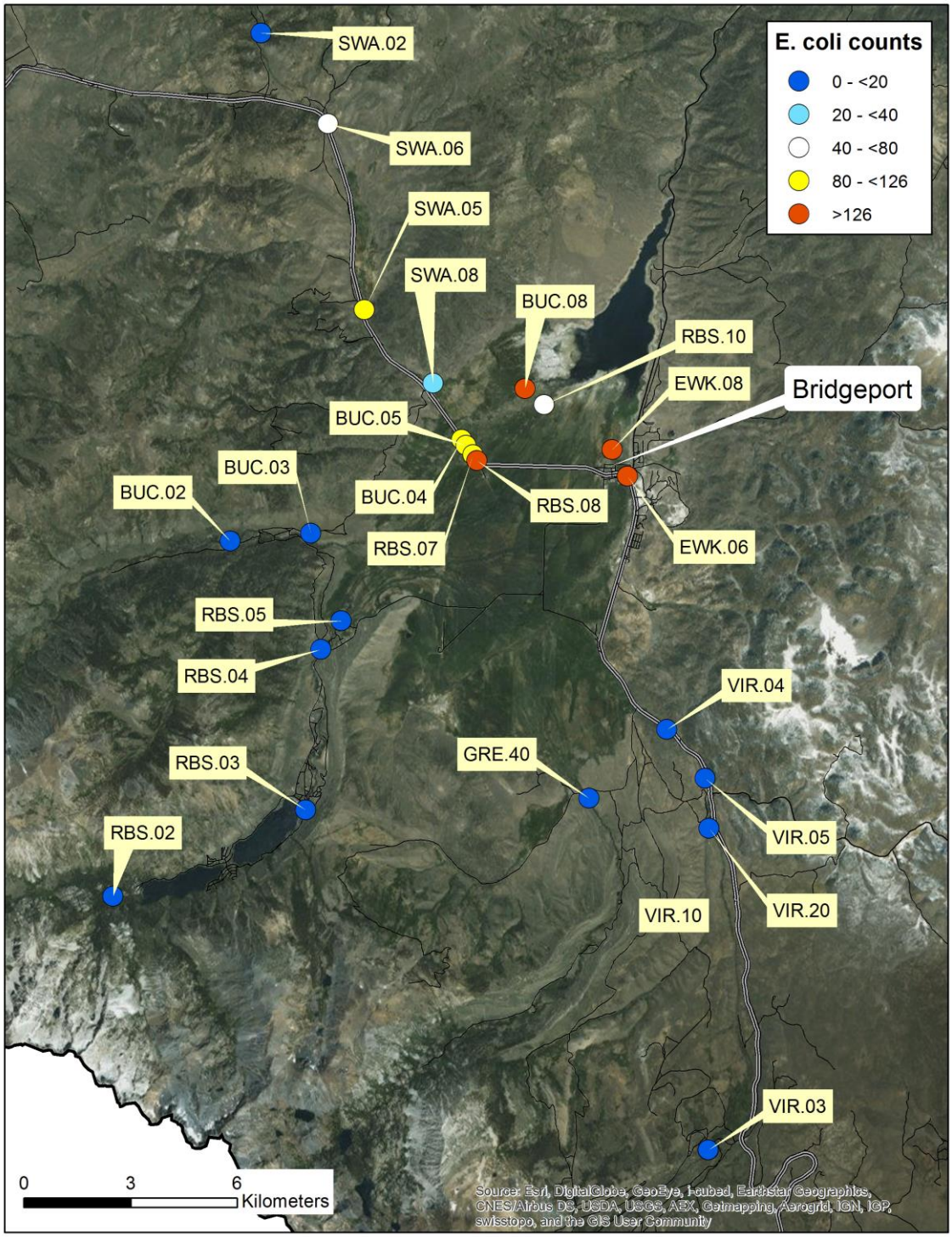


Figure 3a. Map of the East Walker River headwaters, from Swauger Creek in the north to Virginia Creek in the south, showing *E. coli* concentrations. The large water body in the upper-right is Bridgeport Reservoir. Circles show the locations of sampling sites and their colors indicate the geometric mean *E. coli* concentrations (CFU per 100 mL) during May to September of the study period. Highway 395 is shown as a wide gray and black line, and more minor roads are shown as thin black lines. Yellow labels identify sampling sites listed in Appendix A, and white labels identify towns.

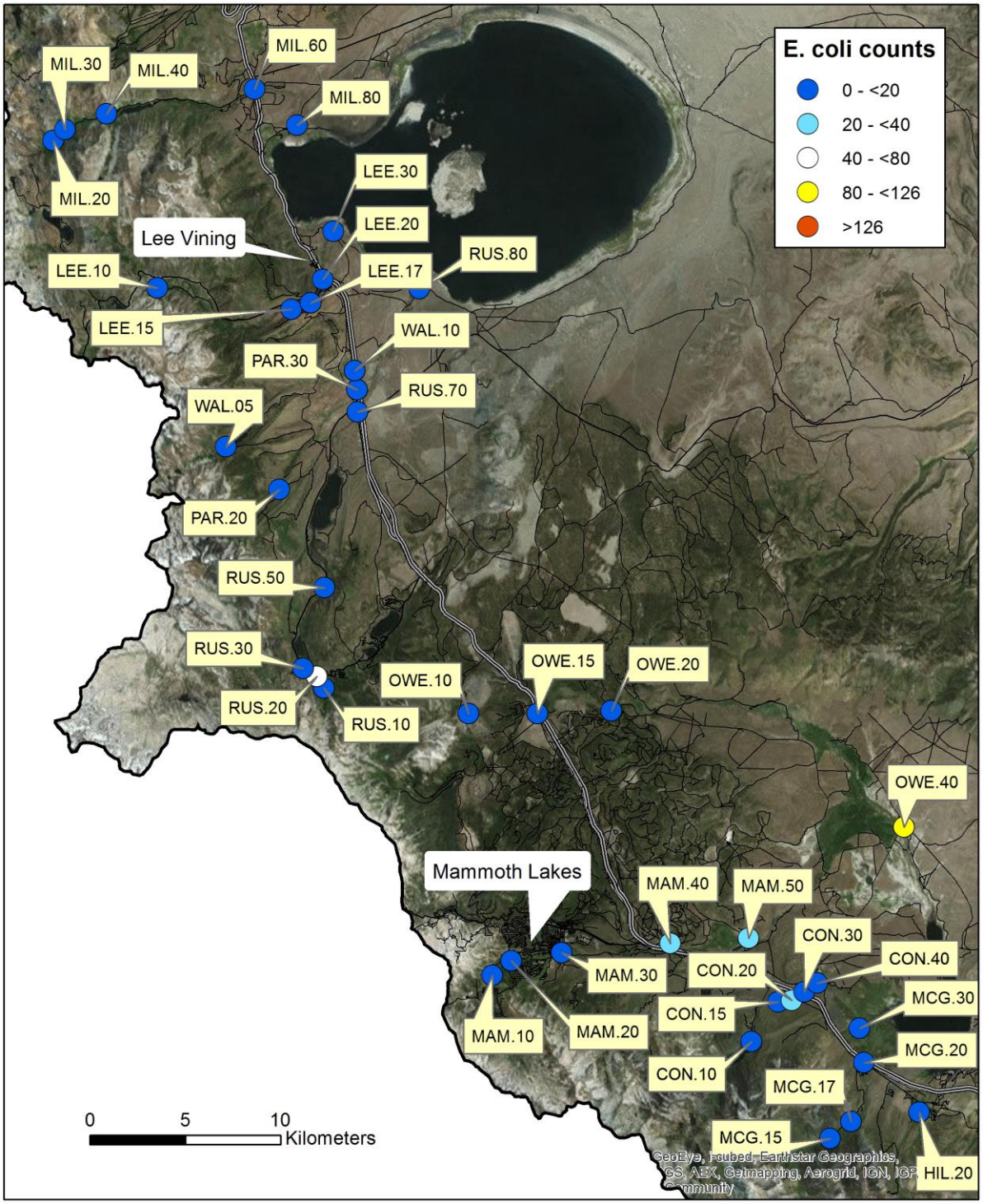


Figure 3b. Map of the Mono Basin and Owens River headwaters, from Lundy Canyon and Mono Lake in the north (just south of Virginia Creek) to Crowley Reservoir in the south, showing *E. coli* concentrations. Circles show the locations of sampling sites and their colors indicate the geometric mean *E. coli* concentrations (CFU per 100 mL) during May to September of the study period. Highway 395 is shown as a wide gray and black line, and more minor roads are shown as thin black lines. Labeling is as described in Figure 3a.

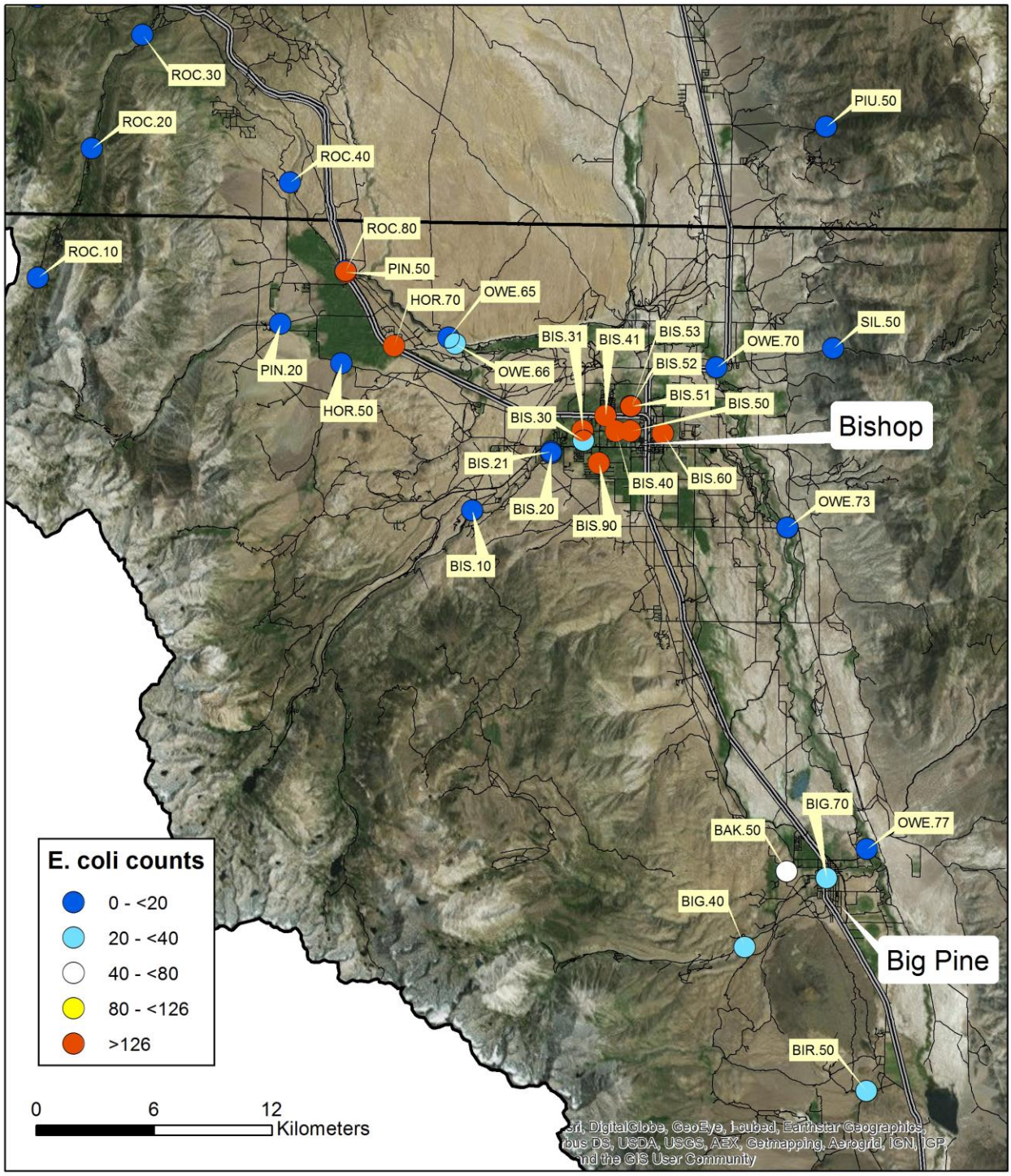


Figure 3c. Map of the central Owens River watershed, from Rock Creek in the north (just south of Crowley Reservoir) to Tinemaha Reservoir in the south, showing *E. coli* concentrations. Circles show the locations of sampling sites and their colors indicate the geometric mean *E. coli* concentrations (CFU per 100 mL) during May to September of the study period. Highways 395 and 6 are shown as wide gray and black lines, and more minor roads are shown as thin black lines. Labeling is as described in Figure 3a. A enlarged map of the Bishop area is shown in Figure 3d.

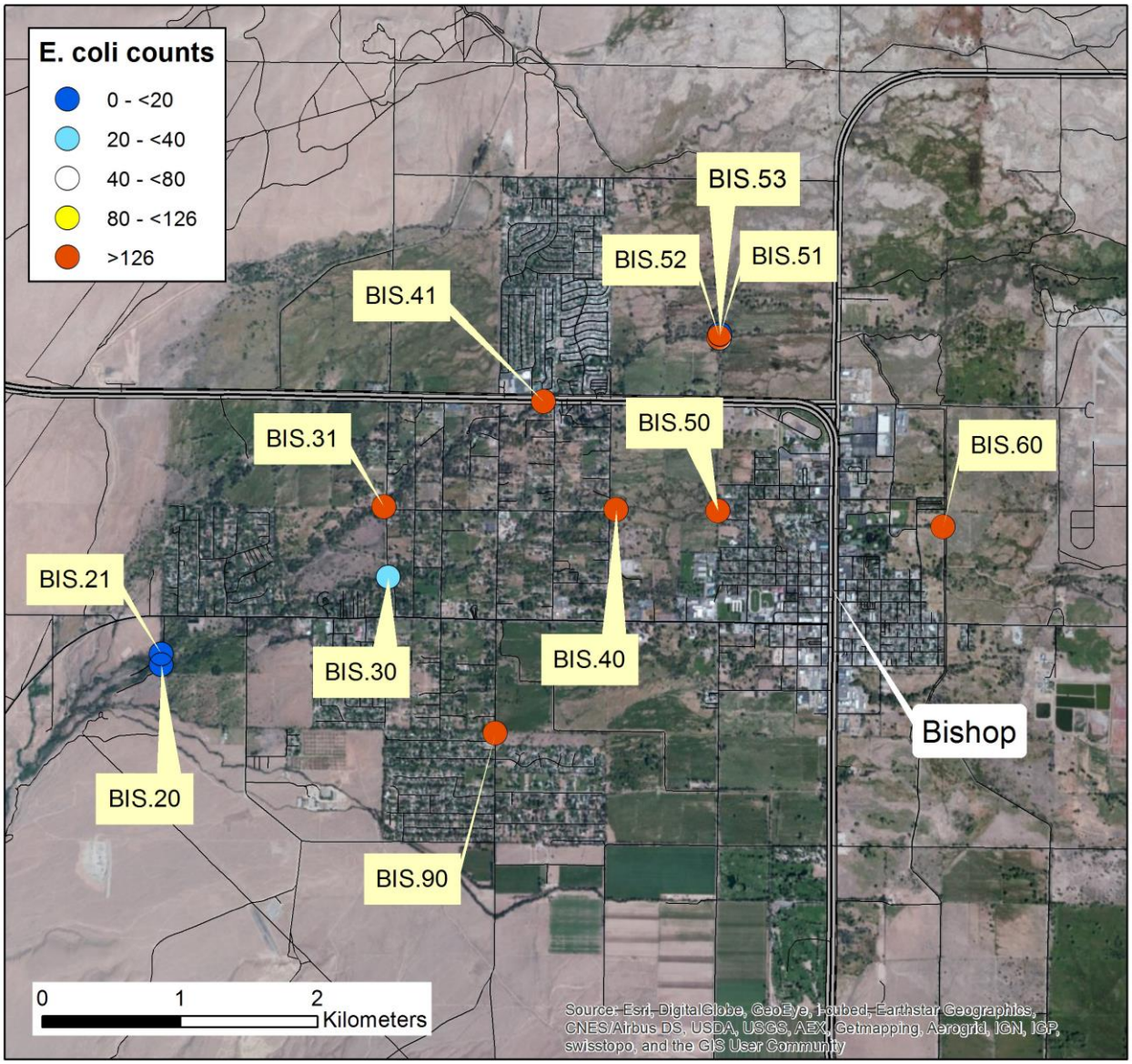


Figure 3d. Map of the City of Bishop and outlying areas, showing *E. coli* concentrations (same data as in Figure 3c). Circles show the locations of sampling sites and their colors indicate the geometric mean *E. coli* concentrations (CFU per 100 mL) during May to September of the study period. Highways 395 and 6 are shown as wide gray and black lines, and more minor roads are shown as thin black lines. Labeling is as described in Figure 3a.

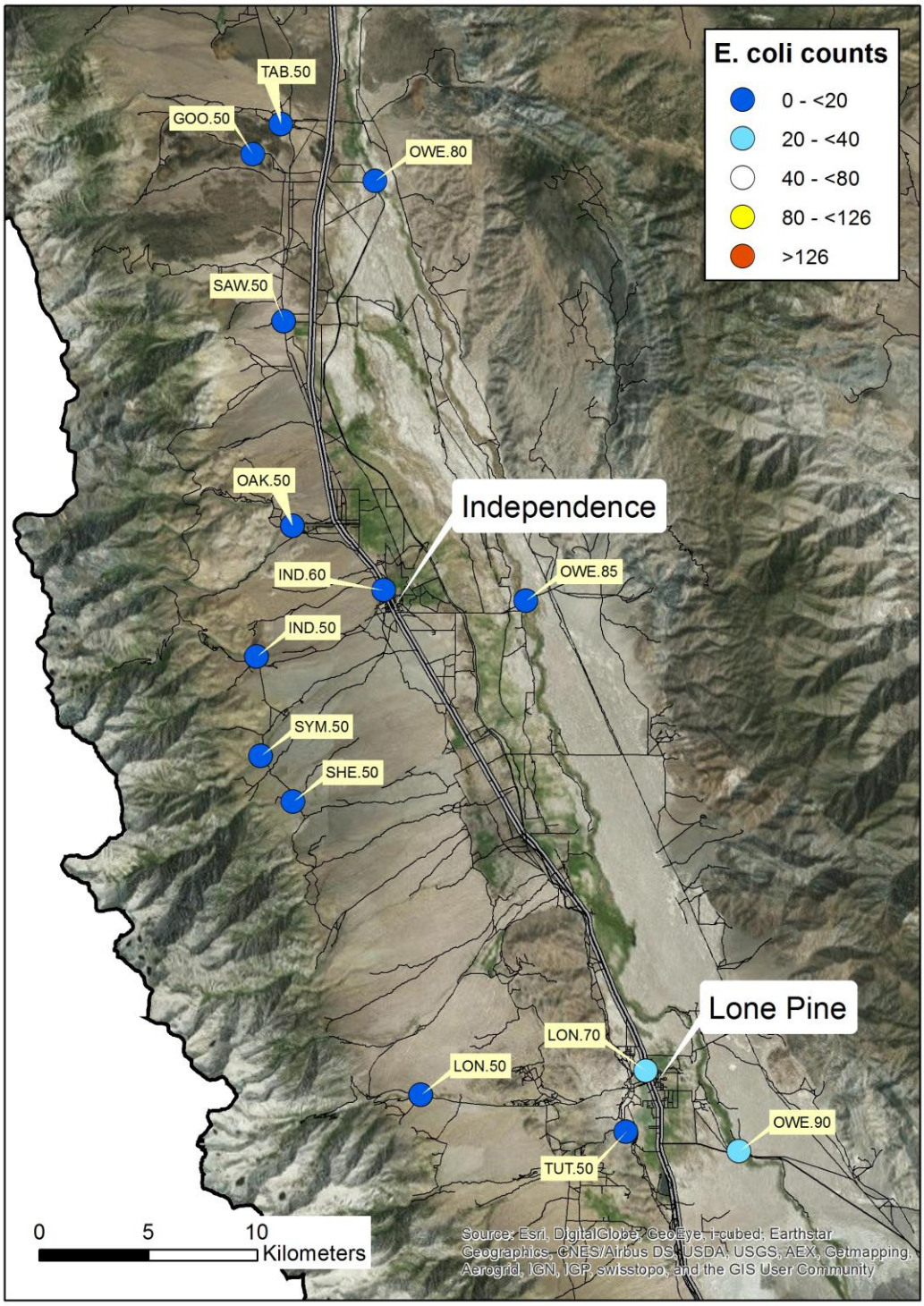


Figure 3e. Map of the lower Owens River watershed, from Taboose Creek in the north (just south of Tinemaha Reservoir) to Owens Dry Lake and the town of Lone Pine in the south, showing *E. coli* concentrations. Circles show the locations of sampling sites and their colors indicate the geometric mean *E. coli* concentrations (CFU per 100 mL) during May to September of the study period. Highway 395 is shown as a wide gray and black line, and more minor roads are shown as thin black lines. Labeling is as described in Figure 3a.

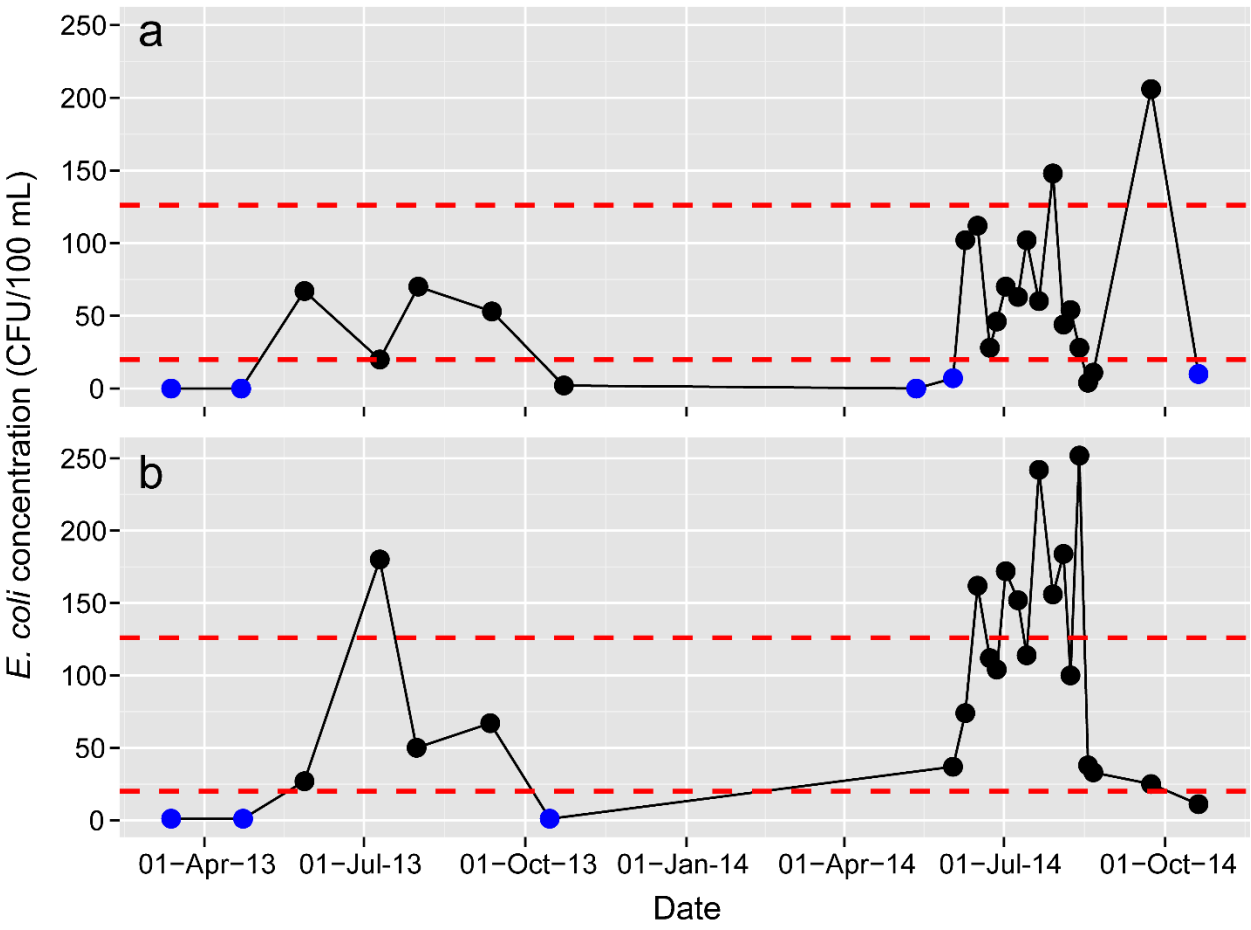


Figure 4. Temporal patterns of *E. coli* concentrations at two intensively sampled sites: (a) Lower Mammoth Creek (MAM.50), and (b) Owens River at the Benton Crossing bridge (OWE.40). Blue points indicate samples collected when cattle were not observed upstream and black points indicate samples collected when cattle were observed. Red lines indicate *E. coli* concentrations of 20 and 126 CFU per 100 mL.

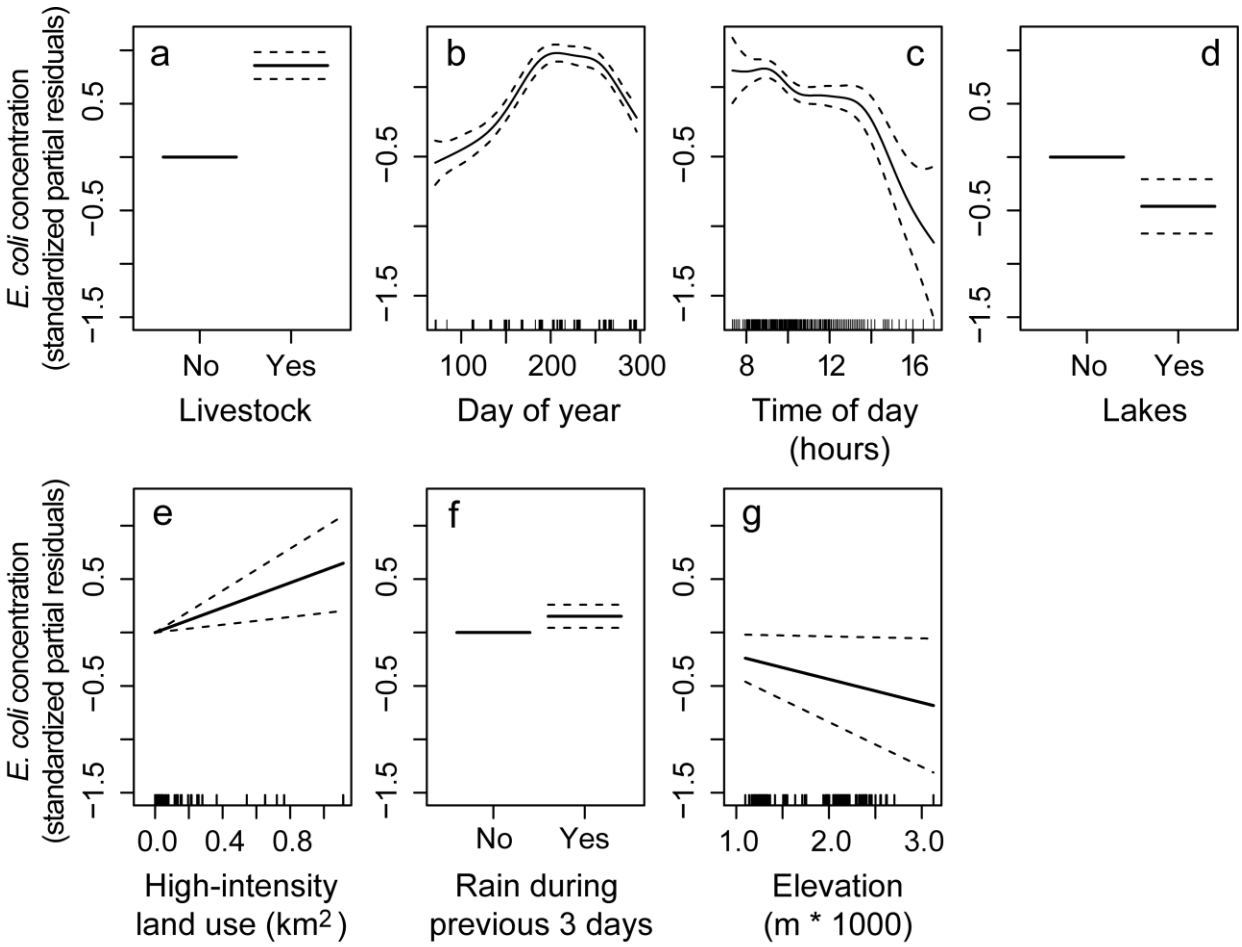


Figure 5. Plots showing the relationships (based on standardized partial residuals) between *E. coli* concentrations ($\log_{10}$(CFU 100 · mL^{-1} + 1) and all significant predictor variables ($P < 0.05$) in the final GAM model: (a) presence/absence of livestock, (b) day of year, (c) time of day, (d) presence/absence of lakes, (e) area of high-intensity land use, (f) presence/absence of rain during the previous 3 days, and (g) site elevation. Confidence intervals (95%) are shown as dashed lines. Plots are arranged in order of the strength of each predictor variable's effect, from strongest (a) to weakest (g). Hatch marks above the x-axis for the continuous variables indicate the observed values. In (b), x-axis values correspond to the following dates: 100 = 10 April, 200 = 19 July, 300 = 27 October.

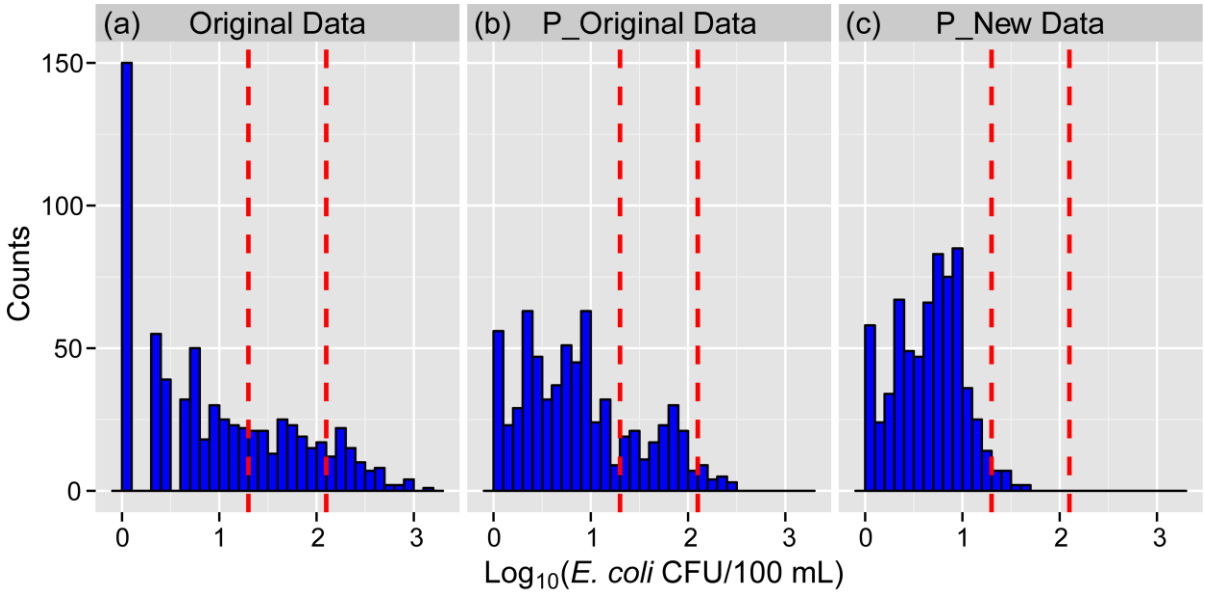


Figure 6. Frequency histograms of the number of *E. coli* CFU per 100 mL (a) calculated from the original data set, (b) predicted from the original data set using the final GAM model, and (c) predicted from a modified data set where COW = 0 and RAIN = 0 for all records using the final GAM model. Red lines indicate *E. coli* concentrations of 20 and 126 CFU per 100 mL.

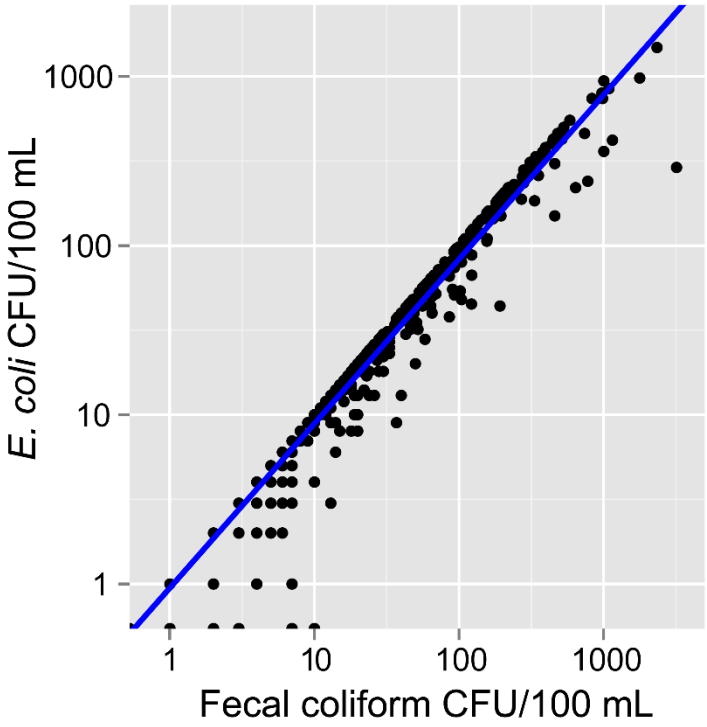
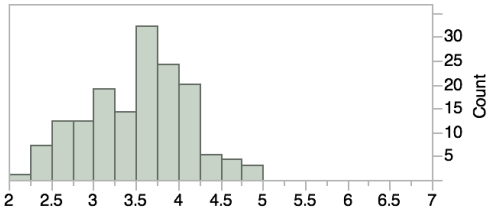


Figure 7. Plot showing the relationship between fecal coliform and *E. coli* bacteria counts (colony forming units per 100 mL). Each point represents the counts made from a single filter. The line describing the relationship was obtained using Model II (reduced major axis) regression methods, as is appropriate when regressing two variables both with quantifiable error.

Distributions

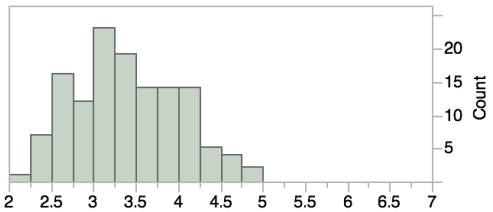
Log10[Copies/100mL Entero1a]



Quantiles		
100.0%	maximum	4.88994
99.5%		4.88994
97.5%		4.72332
90.0%		4.17704
75.0%	quartile	3.93343
50.0%	median	3.62476
25.0%	quartile	3.07975
10.0%		2.65636
2.5%		2.40147
0.5%		2.16235
0.0%	minimum	2.16235

Summary Statistics	
Mean	3.5162894
Std Dev	0.5836983
Std Err Mean	0.0471892
Upper 95% Mean	3.6095208
Lower 95% Mean	3.4230579
N	153
Median	3.6247636

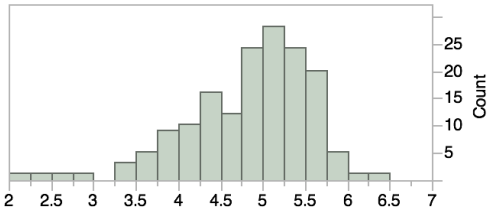
Log10[Copies/100mL Escherichia]



Quantiles		
100.0%	maximum	4.9268
99.5%		4.9268
97.5%		4.6495
90.0%		4.22738
75.0%	quartile	3.8582
50.0%	median	3.31566
25.0%	quartile	2.90454
10.0%		2.5547
2.5%		2.42389
0.5%		2.2304
0.0%	minimum	2.2304

Summary Statistics	
Mean	3.3892895
Std Dev	0.6161014
Std Err Mean	0.053829
Upper 95% Mean	3.4957838
Lower 95% Mean	3.2827952
N	131
Median	3.3156646

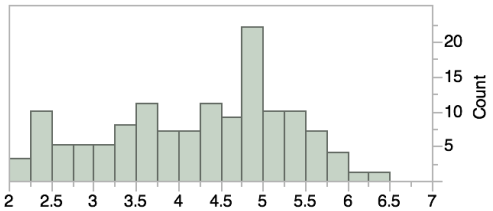
Log10[Copies/100mL GenBac3]



Quantiles		
100.0%	maximum	6.40105
99.5%		6.40105
97.5%		5.91147
90.0%		5.59934
75.0%	quartile	5.34071
50.0%	median	4.98882
25.0%	quartile	4.37938
10.0%		3.85292
2.5%		2.93561
0.5%		2.18331
0.0%	minimum	2.18331

Summary Statistics	
Mean	4.841689
Std Dev	0.7197211
Std Err Mean	0.0565466
Upper 95% Mean	4.9533577
Lower 95% Mean	4.7300202
N	162
Median	4.9888218

Log10[Copies/100mL BacCow]



Quantiles		
100.0%	maximum	6.48001
99.5%		6.48001
97.5%		5.95712
90.0%		5.50284
75.0%	quartile	4.99261
50.0%	median	4.4135
25.0%	quartile	3.46996
10.0%		2.51174
2.5%		2.23927
0.5%		2.15491
0.0%	minimum	2.15491

Summary Statistics	
Mean	4.2216675
Std Dev	1.0553387
Std Err Mean	0.0904945
Upper 95% Mean	4.4006379
Lower 95% Mean	4.0426971
N	136
Median	4.4135021

Figure 8. Histogram distributions, quantiles and summary statistics of $\log_{10}$concentrations of each of the four widespread qPCR assays. A total of 165 samples were analyzed by each assay. Samples that produced results that were below the limits of detection by qPCR were not included in the statistical summaries; sample size (N) is noted for each distribution.

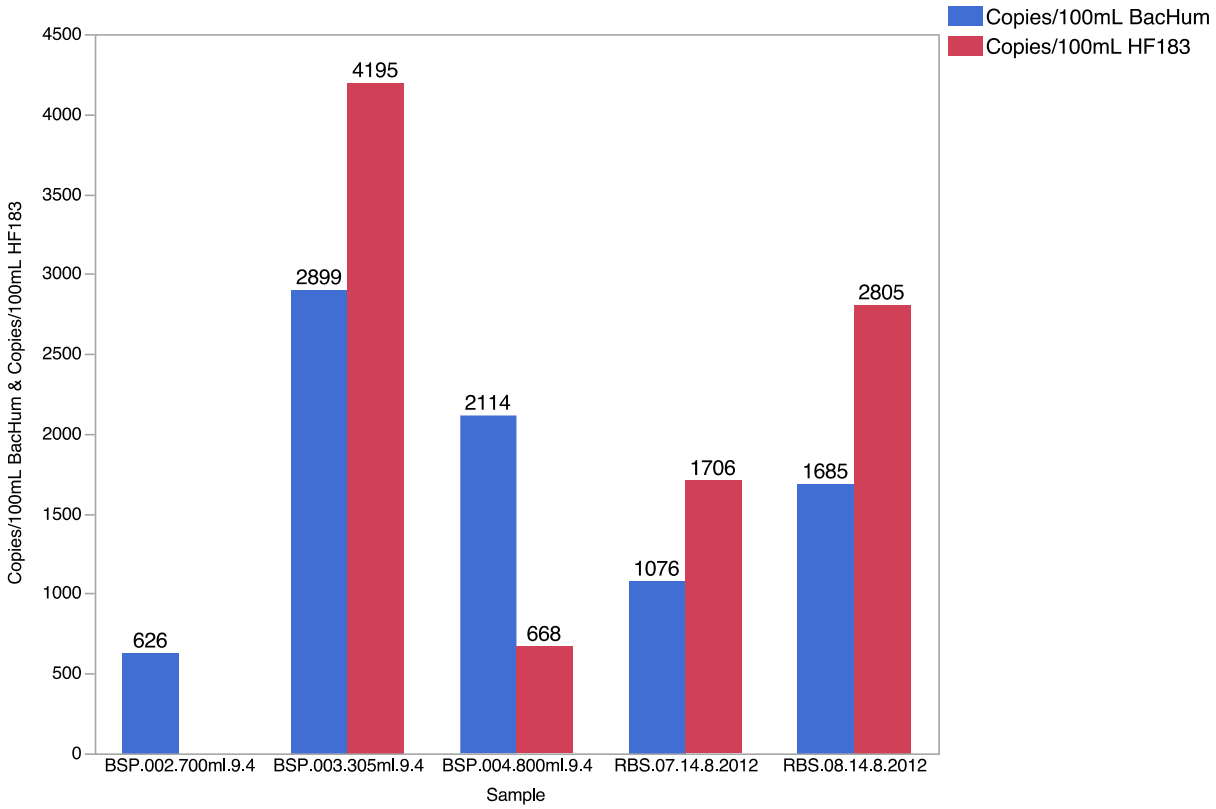


Figure 9. Gene copy concentrations of human Bacteroidales markers for the five sites where genes were detected using either of the human-specific assays BacHum and HF183. Three of the samples were collected from Bishop Creek (BSP.002, BSP.003, BSP.004) on 4 Sept 2013, and two remaining samples were collected from Robinson Creek (RBS.07, RBS.08) on 14 Aug 2012.

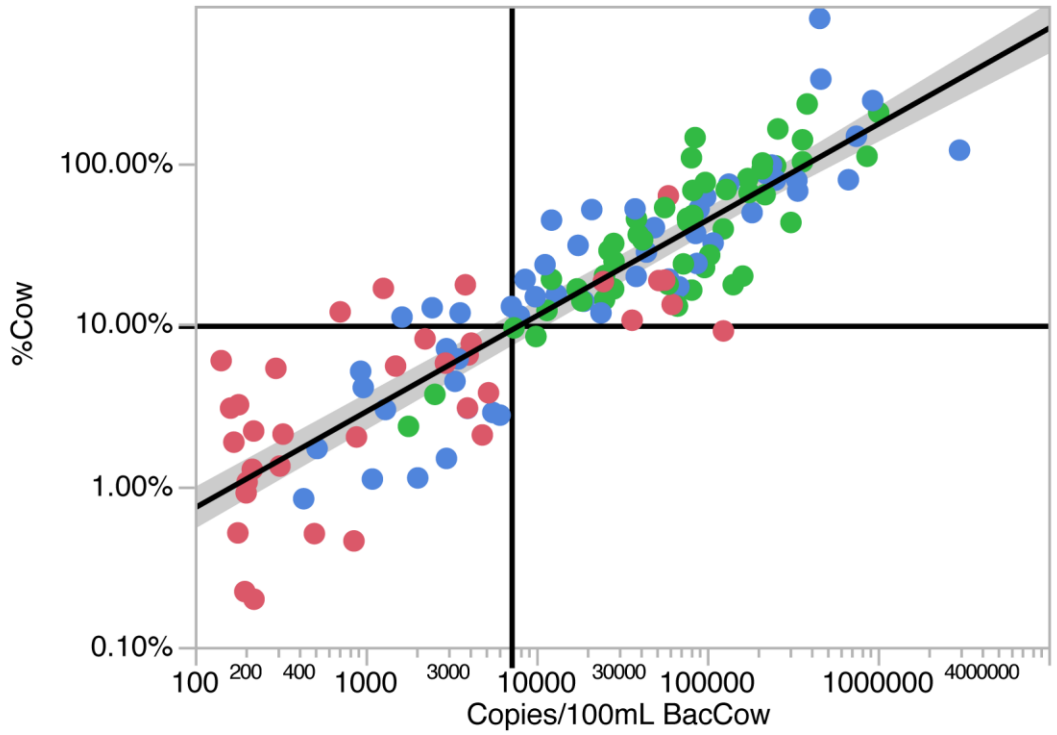


Figure 10. Correlation between gene copy concentrations of ruminant Bacteroidales genes (BacCow) and the proportion of total Bacteroidales genes (GenBac3) attributable to ruminant sources (BacCow) assuming perfect specificity (%Cow). Samples are color coded according to sample set as follows: Red – *2012*, Blue – *SWA*, Green – *BSP*. For details on the black horizontal and vertical lines, see Results.

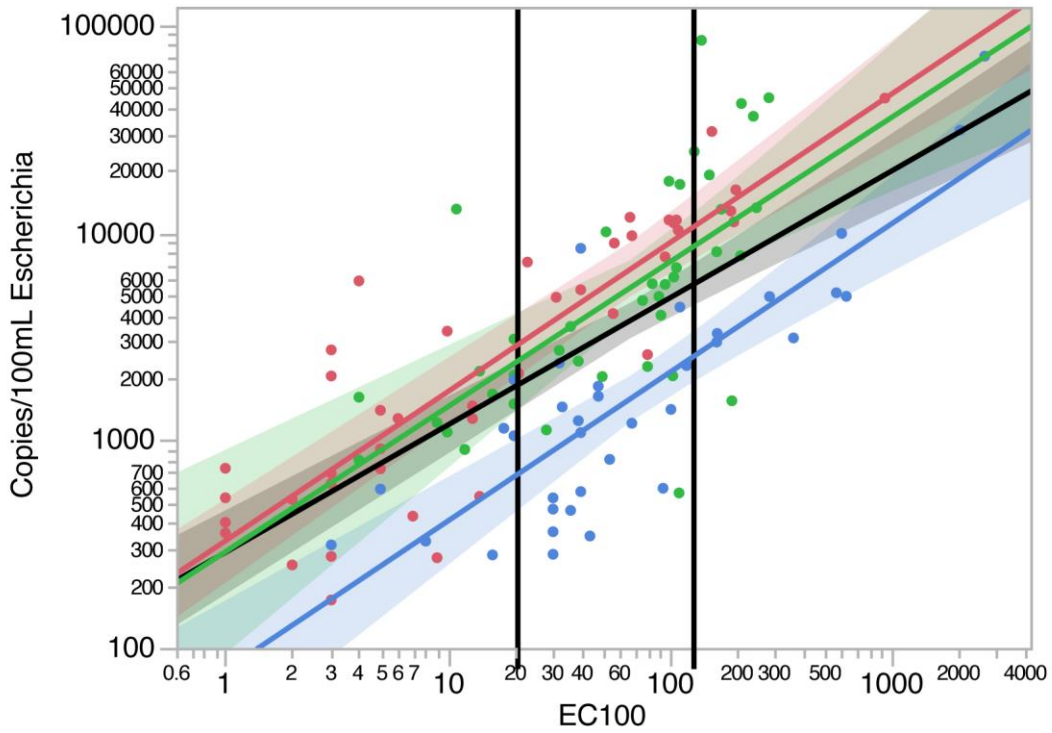


Figure 11. Correlation of *E. coli* CFU (EC100; x-axis) and *Escherichia* gene copy concentrations (y-axis) across the three datasets. Samples are color coded according to sample set as follows: Red – 2012, Blue – SWA, Green – BSP. The black line is the regression through all of the points and vertical black lines are provided for reference of *E. coli* concentrations of 20 and 126 CFU per 100 mL.

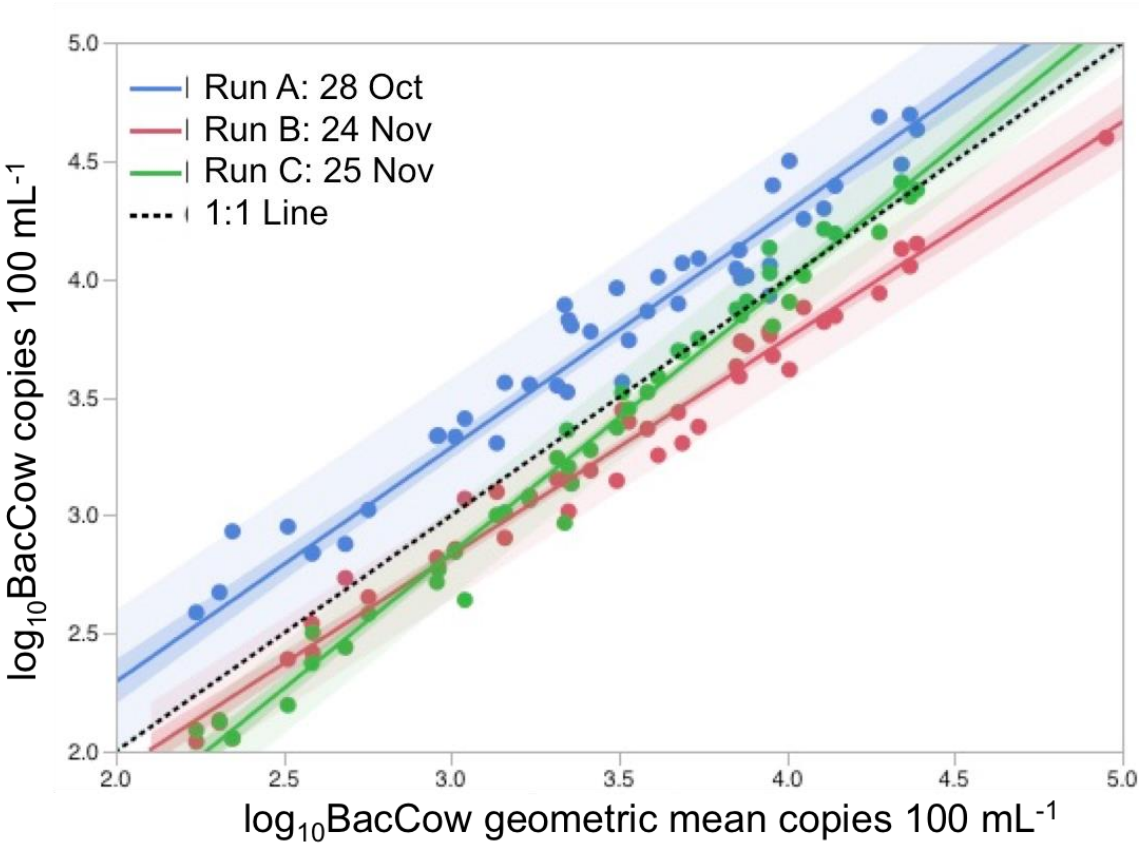


Figure 12. Replicability of qPCR assays among runs. The bivariate plot shows regressions of three individual runs (A, B, C; y-axis, prepped and run on separate dates as noted) against the geometric mean of all three runs (x-axis); each colored dot is a sample run on one of three days. The 1:1 line is dashed black for reference.

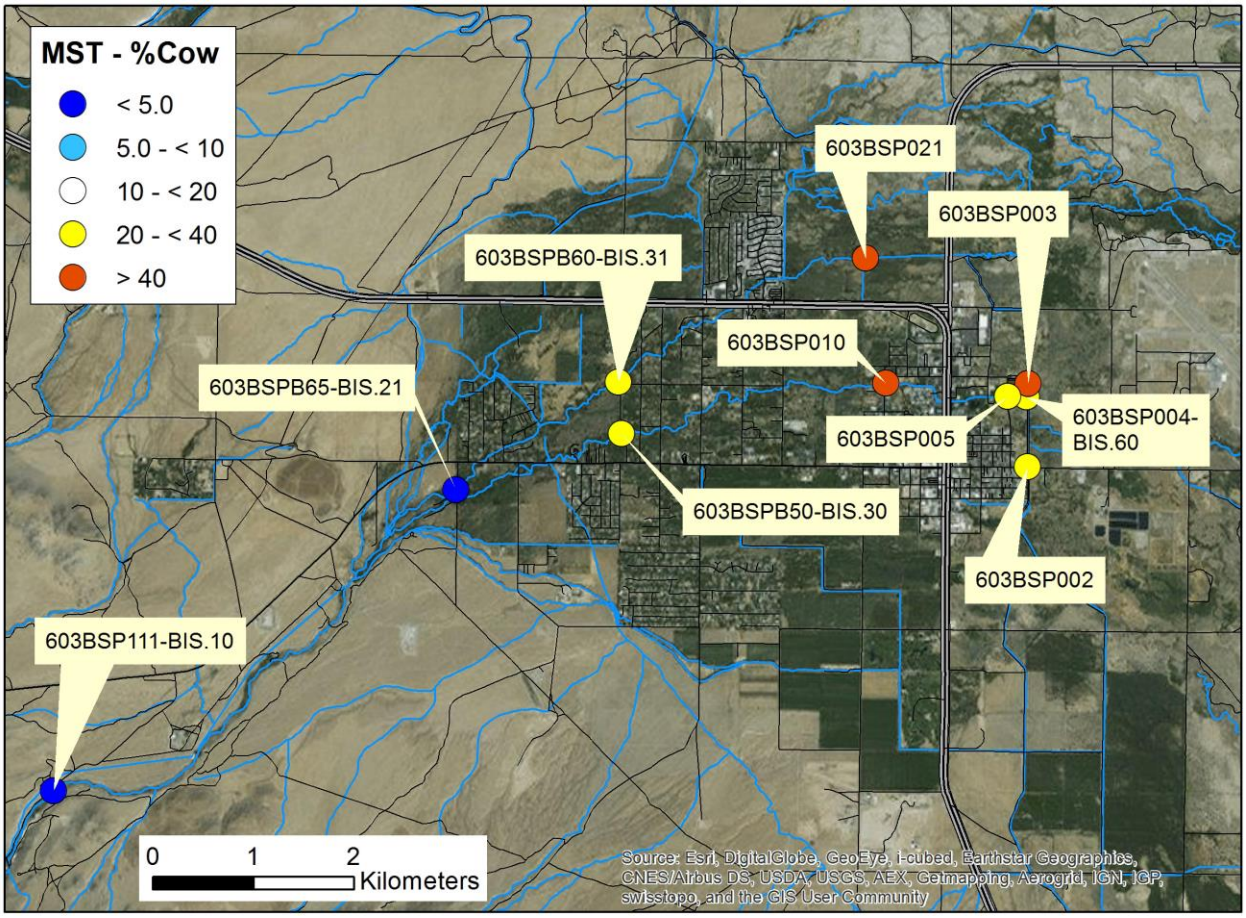


Figure 13. Map of the City of Bishop and outlying areas, showing the microbial source tracking results from the BacCow (ruminant) assay. Circles identify the locations of sampling sites and their colors indicate the geometric mean "%Cow" values [(BacCow/GenBac3)*100] during June to October 2013. The position of 603BSP003 was shifted slightly northward to reduce symbol overlap. Streams and ditches are shown as blue lines, Highways 395 and 6 are shown as wide gray and black lines, and more minor roads are shown as thin black lines. Labels show the site ids listed in Appendix D (SWAMP ID only, or SWAMP ID and SNARL ID).

Appendix A. Description of all sites sampled by personnel from the Sierra Nevada Aquatic Research Laboratory and included in the landscape analysis.

SNARL ID	SWAMP ID	Stream	Drainage	County	Elevation	Latitude	Longitude	Location Description
BAK.50		Baker_Ck	Owens	Inyo	1279	37.1678	-118.3116	Baker Creek at LADWP diversion structure above Baker Creek Campground
BIG.40		Big_Pine_Ck	Owens	Inyo	1550	37.1328	-118.3349	Big Pine Creek at base of Glacier Lodge Road switchbacks
BIG.70		Big_Pine_Ck	Owens	Inyo	1213	37.1649	-118.2885	Big Pine Creek below Hwy 395, at southern end of Pine Street
BIR.50		Tinemaha_Ck	Owens	Inyo	1252	37.0674	-118.2641	Tinemaha Creek immediately above Birch Creek Road culvert
BIS.10	603BSP111	Bishop_Ck	Owens	Inyo	1527	37.3311	-118.4952	At USFS boundary (Inyo NF sign), above Plant 5 on E. Bishop Creek Road
BIS.20	603BSPB55	Bishop_Ck_SF	Owens	Inyo	1342	37.3581	-118.4504	South Fork, immediately above Mumy Lane
BIS.21	603BSPB65	Bishop_Ck_NF	Owens	Inyo	1341	37.3587	-118.4504	North Fork, immediately above Mumy Lane
BIS.30	603BSPB50	Bishop_Ck_SF	Owens	Inyo	1305	37.3640	-118.4318	South Fork, immediately above Brockman Lane
BIS.31	603BSPB60	Bishop_Ck_NF	Owens	Inyo	1297	37.3686	-118.4323	North Fork, immediately above Brockman Lane
BIS.40		Bishop_Ck_SF	Owens	Inyo	1277	37.3687	-118.4132	South Fork, below See-Vee Lane
BIS.41	603BSPB20	Bishop_Ck_NF	Owens	Inyo	1282	37.3757	-118.4193	North Fork, immediately above Hwy 395
BIS.50	603BSP011	Bishop_Ck_SF	Owens	Inyo	1272	37.3687	-118.4048	South Fork, 190 m S of end of Sierra Street
BIS.51	603BSPB22	Bishop_Ck_NF	Owens	Inyo	1269	37.3801	-118.4050	North Fork, 35 m above confluence with Bishop Canal, just upstream of B-1 drain
BIS.52	603BSPB23	Bishop_Ck	Owens	Inyo	1269	37.3800	-118.4049	B-1 Drain, immediately before confluence with North Fork Bishop Creek
BIS.53		Bishop_Ck	Owens	Inyo	1269	37.3802	-118.4049	Bishop Canal, immediately upstream of confluence with North Fork Bishop Creek
BIS.60	603BSP004	Bishop_Ck_SF	Owens	Inyo	1259	37.3678	-118.3863	South Fork, immediately upstream of confluence with Bishop Canal, below Hanby Avenue
BIS.90		Bishop_Ck_SF	Owens	Inyo	1295	37.3539	-118.4229	South Fork Bishop Creek, North Indian Ditch, 53 m N of Highland Dr-Barlow Ln intersection
BUC.02		Buckeye_Ck	Walker	Mono	2181	38.2364	-119.3509	At bridge that crosses Buckeye Ck in Lower Buckeye Meadow, above campground
BUC.03		Buckeye_Ck	Walker	Mono	2105	38.2389	-119.3252	Immediately below Buckeye Hot Springs
BUC.04	630BUC004	Buckeye_Ck	Walker	Mono	1985	38.2637	-119.2773	North branch of Buckeye Creek @ Hwy 395, 860 m N of Centennial Ranch driveway
BUC.05	630BUC005	Buckeye_Ck	Walker	Mono	1985	38.2622	-119.2759	Middle branch of Buckeye Creek @ Hwy 395, 630 m N of Centennial Ranch drivewa
BUC.08		Buckeye_Ck	Walker	Mono	1972	38.2769	-119.2574	780 m W of Buckeye Creek-Robinson Creek confluence
CON.10		Convict_Ck	Owens	Mono	2324	37.5952	-118.8510	80 m downstream from Convict Lake
CON.15		Convict_Ck	Owens	Mono	2173	37.6141	-118.8359	At top-most diversion structure where overflow channel leaves main stream
CON.20		Convict_Ck	Owens	Mono	2154	37.6148	-118.8276	Within SNARL property, immediately downstream of confluence of Channels 3 and 4
CON.30		Convict_Ck	Owens	Mono	2141	37.6190	-118.8202	120 m below Highway 395 crossing
CON.40		Convict_Ck	Owens	Mono	2128	37.6234	-118.8127	Dirt road off of Benton Crossing Rd on E just before Whitmore ball fields, follow for 500 m
EWK.06	630EWK006	East_Walker_Rvr	Walker	Mono	1976	38.2553	-119.2237	30 m upstream of Hwy 395 bridge
EWK.08		East_Walker_Rvr	Walker	Mono	1966	38.2619	-119.2288	400 m N of Stock Drive, just downstream of mid-channel island
GOO.50		Goodale_Ck	Owens	Inyo	1237	36.9858	-118.2729	Goodale Creek at Goodale Creek Campground, immediately below Goodale Road culvert
GRE.40		Green_Ck	Walker	Mono	2096	38.1734	-119.2336	Immediately upstream of Upper Summers Meadow Road bridge over creek
HIL.20		Hilton_Ck	Owens	Mono	2186	37.5632	-118.7506	Just below culvert under Juniper Drive
HOR.50		Horton_Ck	Owens	Inyo	1418	37.3977	-118.5720	Immediately upstream of Round Valley Road, at turn-off for Horton Creek Campground
HOR.70		Horton_Ck	Owens	Inyo	1364	37.4061	-118.5417	Horton Creek, immediately below Hwy 395 off of Mill Creek Road
IND.50		Independence_Ck	Owens	Inyo	1635	36.7782	-118.2674	Independence Creek 390 m NW of Foothill Rd-Onion Valley Rd junction, just above weir
IND.60		Independence_Ck	Owens	Inyo	1194	36.8064	-118.2024	Independence Creek at Dehy Park
LEE.10		Lee_Vining_Ck	Mono	Mono	2379	37.9448	-119.2145	Last pullout on Poole Plant Road, on R before reaching Poole Plant (150 m upstream)

SNARL ID	SWAMP ID	Stream	Drainage	County	Elevation	Latitude	Longitude	Location Description
LEE.15		Lee_Vining_Ck	Mono	Mono	2197	37.9362	-119.1342	30 m below LADWP diversion dam
LEE.17		Lee_Vining_Ck	Mono	Mono	2179	37.9394	-119.1228	Immediately above culvert under Hwy 120
LEE.20		Lee_Vining_Ck	Mono	Mono	2074	37.9506	-119.1159	10 m above culvert under Hwy 395
LEE.30		Lee_Vining_Ck	Mono	Mono	1963	37.9735	-119.1102	Immediately above Test Station Road ford of creek
LON.50		Lone_Pine_Ck	Owens	Inyo	1755	36.5980	-118.1803	Lone Pine Creek below Lone Pine Campground, at Whitney Portal Road crossing of creek
LON.70		Lone_Pine_Ck	Owens	Inyo	1138	36.6090	-118.0651	Lone Pine Creek immediately above Hwy 395 in Spainhower Park
MAM.10		Mammoth_Ck	Owens	Mono	2615	37.6238	-119.0057	Outlet of lowermost Twin Lake, immediately downstream of Lake Mary Road bridge
MAM.20		Mammoth_Ck	Owens	Mono	2459	37.6308	-118.9947	Valentine Reserve, immediately upstream of easternmost trail bridge
MAM.30		Mammoth_Ck	Owens	Mono	2393	37.6352	-118.9648	S of Mammoth Creek Road, 185 m E of Old Mammoth Road, 75 m W of pedestrian bridge
MAM.40		Mammoth_Ck	Owens	Mono	2200	37.6407	-118.9004	Below bridge on Old Highway 395, immediately below USGS weir
MAM.50		Mammoth_Ck	Owens	Mono	2154	37.6438	-118.8540	160 m upstream of confluence with Hot Creek, 50 m below Chance Ranch fenceline
MCG.15		McGee_Ck	Owens	Mono	2406	37.5500	-118.8034	110 m up trail from trailhead parking lot
MCG.17		McGee_Ck	Owens	Mono	2344	37.5582	-118.7910	760 m (on road) below McGee Creek Pack Station, pullout on S side of road below meadow
MCG.20		McGee_Ck	Owens	Mono	2111	37.5861	-118.7840	Immediately upstream of Crowley Lake Drive bridge
MCG.30		McGee_Ck	Owens	Mono	2075	37.6024	-118.7872	500 m upstream (straight-line distance) from Convict Creek junction, at fence corner
MIL.20		Mill_Ck	Mono	Mono	2623	38.0132	-119.2788	1.8 km upstream (straight-line distance) of Lundy Canyon trailhead
MIL.30		Mill_Ck	Mono	Mono	2559	38.0185	-119.2719	Tributary from Burro Lakes, immediately above trail crossing tributary
MIL.40		Mill_Ck	Mono	Mono	2440	38.0263	-119.2473	Immediately below first beaver pond complex above Lundy Reservoir
MIL.60		Mill_Ck	Mono	Mono	2101	38.0397	-119.1591	Immediately upstream of Hwy 395 culvert
MIL.80		Mill_Ck	Mono	Mono	1975	38.0232	-119.1334	Immediately upstream of Cemetery Road culvert
OAK.50		Oak_Ck	Owens	Inyo	1327	36.8324	-118.2498	Oak Creek 470 m WNW of Mt. Whitney Fish Hatchery
OWE.10		Owens_Rvr	Owens	Mono	2501	37.7471	-119.0233	Glass Ck at trailhead S of Obsidian Dome
OWE.15		Owens_Rvr	Owens	Mono	2289	37.7479	-118.9822	Deadman Ck immediately above Hwy 395 culvert
OWE.20		Owens_Rvr	Owens	Mono	2212	37.7500	-118.9383	Owens R immediately upstream of Forest Road 2S04, below Big Springs Campground
OWE.40		Owens_Rvr	Owens	Mono	2079	37.6977	-118.7629	Immediately upstream of Benton Crossing Road bridge over Owens River
OWE.65		Owens_Rvr	Owens	Inyo	1316	37.4102	-118.5105	Owens River at Pleasant Valley Dam Rd-Chalk Bluff Rd intersection
OWE.66		Owens_Rvr	Owens	Inyo	1311	37.4061	-118.5020	Owens River at footbridge below Pleasant Valley Campground
OWE.70		Owens_Rvr	Owens	Inyo	1245	37.3985	-118.3560	Owens River immediately below Hwy 6 bridge
OWE.73		Owens_Rvr	Owens	Inyo	1222	37.3255	-118.3138	Owens River above Warms Springs Road bridge
OWE.77		Owens_Rvr	Owens	Inyo	1193	37.1786	-118.2658	Owens River above Hwy 168 bridge
OWE.80		Owens_Rvr	Owens	Inyo	1167	36.9754	-118.2097	Owens River immediately below LA Aqueduct intake structure, at end of Goodale Road
OWE.85		Owens_Rvr	Owens	Inyo	1140	36.8028	-118.1293	Owens River at Mazourka Canyon Road overcrossing
OWE.90		Owens_Rvr	Owens	Inyo	1098	36.5763	-118.0168	Upstream of Hwy 136 at LADWP weir, under high voltage power lines
PAR.20		Parker_Ck	Mono	Mono	2405	37.8510	-119.1389	430 m (straight-line distance) WSW of Parker Lake trailhead
PAR.30		Parker_Ck	Mono	Mono	2091	37.8989	-119.0939	Immediately above Hwy 395 culvert
PIN.20		Pine_Ck	Owens	Inyo	1531	37.4153	-118.6073	Pine Creek Road culvert immediately below Rovana
PIN.50		Pine_Ck	Owens	Inyo	1363	37.4396	-118.5702	Pine Creek, immediately below Hwy 395 in Round Valley, 100 m S of Rock Ck site (ROC.80)
PIU.50		Piute_Ck	Owens	Mono	1939	37.5095	-118.2947	Piute Creek at hydro intake structure
RBS.02		Robinson_Ck	Walker	Mono	2181	38.1455	-119.3857	At west end of meadow that is west of Mono Village

SNARL ID	SWAMP ID	Stream	Drainage	County	Elevation	Latitude	Longitude	Location Description
RBS.03		Robinson_Ck	Walker	Mono	2162	38.1686	-119.3245	120 m below outlet dam on Lower Twin Lake, access from S. Twin Road
RBS.04		Robinson_Ck	Walker	Mono	2088	38.2095	-119.3209	On Road 017 bridge over Robinson Creek, 100 m upstream of bridge
RBS.05		Robinson_Ck	Walker	Mono	2063	38.2169	-119.3146	At NE end of Hackamore Place, immediately above Hunewill fenceline
RBS.07	630RBS007	Robinson_Ck	Walker	Mono	1986	38.2598	-119.2736	North branch of Robinson Creek @ Hwy 395, 290 m N of Centennial Ranch driveway
RBS.08	630RBS008	Robinson_Ck	Walker	Mono	1987	38.2584	-119.2723	South branch of Robinson Creek @ Hwy 395, 120 m N of Centennial Ranch driveway
RBS.10		Robinson_Ck	Walker	Mono	1971	38.2730	-119.2512	600 m SW of Buckeye Creek-Robinson Creek confluence
ROC.10		Rock_Ck	Owens	Inyo	3125	37.4345	-118.7474	At Mosquito Flat trailhead, 30 m upstream of pedestrian bridge to walk-in campground
ROC.20		Rock_Ck	Owens	Mono	2704	37.4943	-118.7177	Immediately upstream of culvert NE of Palisade Campground
ROC.30		Rock_Ck	Owens	Mono	2298	37.5468	-118.6898	Immediately downstream of first creek crossing Rock Creek Road above Hwy 395
ROC.40		Rock_Ck	Owens	Mono	1509	37.4802	-118.6033	Lower Rock Creek Rd in Paradise, immediately below Rock Creek culvert
ROC.80		Rock_Ck	Owens	Inyo	1363	37.4400	-118.5704	Rock Creek, immediately below Hwy 395 in Round Valley
RUS.10		Rush_Ck	Mono	Mono	2363	37.7577	-119.1096	Yost Ck at end of Venice St, just above June Lake PUD diversion structure
RUS.20		Rush_Ck	Mono	Mono	2221	37.7631	-119.1140	Reverse Ck at first culvert upstream of Double Eagle Resort
RUS.30		Rush_Ck	Mono	Mono	2208	37.7667	-119.1224	Immediately above Hwy 158, below SCE hydro plant
RUS.50		Rush_Ck	Mono	Mono	2193	37.8051	-119.1107	Above gauging station, upstream of Grant Reservoir
RUS.70		Rush_Ck	Mono	Mono	2093	37.8885	-119.0934	20 m downstream of old Hwy 395 bridge
RUS.80		Rush_Ck	Mono	Mono	1962	37.9473	-119.0581	Immediately upstream of Test Station Rd culvert over Rush Creek
SAW.50		Sawmill_Ck	Owens	Inyo	1189	36.9168	-118.2558	Sawmill Creek at Blackrock Springs Rd-Old Hwy 395 Junction
SHE.50		Shepherd_Ck	Owens	Inyo	1711	36.7186	-118.2478	Shepherd Creek immediately upstream of Foothill Road culvert
SIL.50		Silver_Ck	Owens	Inyo	1506	37.4080	-118.2891	Silver Creek at 3rd creek crossing of Silver Canyon Road
SWA.02		Swauger_Ck	Walker	Mono	2368	38.3654	-119.3452	Immediately downstream of Swauger Creek Road at first creek crossing, 2 km N of Hwy 395
SWA.05	630SWA005	Swauger_Ck	Walker	Mono	2059	38.2959	-119.3097	Below Huntoon Valley, 2.9 km N of Buckeye Road/Forest Service compound on Hwy 395
SWA.06	630SWA006	Swauger_Ck	Walker	Mono	2208	38.3429	-119.3229	Above Huntoon Valley, 2 km S of Swauger Ck Rd on Hwy 395 @ dirt road that crosses creek
SWA.08		Swauger_Ck	Walker	Mono	2002	38.2777	-119.2870	At USFS compound, immediately upstream of bridge over creek and private land boundary
SYM.50		Symmes_Ck	Owens	Inyo	1738	36.7373	-118.2647	Symmes Creek upstream of Foothill Road culvert, at LADWP weir
TAB.50		Taboose_Ck	Owens	Inyo	1201	36.9983	-118.2586	Taboose Creek at footbridge at W end of Taboose Creek Campground
TUT.50		Tuttle_Ck	Owens	Inyo	1186	36.5837	-118.0749	Tuttle Creek at LADWP diversion structure, 450 m upstream of LA Aqueduct
VIR.03		Virginia_Ck	Walker	Mono	2553	38.0849	-119.1927	Immediately upstream of Virginia Lakes Road culvert over Virginia Creek
VIR.04	630VIR004	Virginia_Ck	Walker	Mono	2045	38.1914	-119.2092	450 m N of Willow Springs Resort on Hwy 395, at USGS stream gage
VIR.05	630VIR005	Virginia_Ck	Walker	Mono	2078	38.1792	-119.1965	430 m N of Bodie Road (Hwy 270) junction
VIR.10		Virginia_Ck	Walker	Mono	2112	38.1665	-119.1948	Immediately upstream of Dog Creek-Virginia Creek confluence, on Virginia Creek
VIR.20		Virginia_Ck	Walker	Mono	2112	38.1665	-119.1948	Immediately upstream of Dog Creek-Virginia Creek confluence, on Dog Creek
WAL.05		Walker_Ck	Mono	Mono	2436	37.8706	-119.1713	At trail crossing of creek, 145 m (straight-line distance) upstream of Walker Lake
WAL.10		Walker_Ck	Mono	Mono	2075	37.9079	-119.0955	Immediately upstream of Hwy 395 culvert

Appendix B. Concentrations of fecal indicator bacteria in all samples collected from sites in Appendix A, and included in landscape-scale analyses. Concentrations of fecal coliform (fcoli100) and *E. coli* (ecoli100) bacteria are described as the number of colony forming units per 100 mL. The contract under which the sample was collected is also listed.

SNARL ID	SWAMP ID	Sampling Date	Stream	Drainage	County	Contract ID	fcoli100	ecoli100
BAK.50		7/31/2014	Baker_Ck	Owens	Inyo	12-067-160	69	52
BAK.50		8/20/2014	Baker_Ck	Owens	Inyo	12-067-160	64	64
BIG.40		7/31/2014	Big_Pine_Ck	Owens	Inyo	12-067-160	29	29
BIG.40		8/20/2014	Big_Pine_Ck	Owens	Inyo	12-067-160	25	25
BIG.70		7/31/2014	Big_Pine_Ck	Owens	Inyo	12-067-160	26	26
BIG.70		8/20/2014	Big_Pine_Ck	Owens	Inyo	12-067-160	44	44
BIR.50		7/31/2014	Tinemaha_Ck	Owens	Inyo	12-067-160	26	24
BIR.50		8/19/2014	Tinemaha_Ck	Owens	Inyo	12-067-160	18	18
BIS.10	603BSP111	5/14/2014	Bishop_Ck	Owens	Inyo	13-054-160	0	0
BIS.10	603BSP111	6/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	1	1
BIS.10	603BSP111	7/23/2014	Bishop_Ck	Owens	Inyo	13-054-160	10	4
BIS.10	603BSP111	8/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	66	61
BIS.10	603BSP111	9/24/2014	Bishop_Ck	Owens	Inyo	13-054-160	5	3
BIS.10	603BSP111	10/22/2014	Bishop_Ck	Owens	Inyo	13-054-160	48	48
BIS.20	603BSP55	5/14/2014	Bishop_Ck	Owens	Inyo	13-054-160	4	3
BIS.20	603BSP55	6/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	7	3
BIS.20	603BSP55	7/23/2014	Bishop_Ck	Owens	Inyo	13-054-160	16	12
BIS.20	603BSP55	8/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	4	4
BIS.20	603BSP55	9/24/2014	Bishop_Ck	Owens	Inyo	13-054-160	4	1
BIS.20	603BSP55	10/22/2014	Bishop_Ck	Owens	Inyo	13-054-160	0	0
BIS.21	603BSPB65	5/14/2014	Bishop_Ck	Owens	Inyo	13-054-160	1	1
BIS.21	603BSPB65	6/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	7	4
BIS.21	603BSPB65	7/23/2014	Bishop_Ck	Owens	Inyo	13-054-160	86	38
BIS.21	603BSPB65	8/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	5	5
BIS.21	603BSPB65	9/24/2014	Bishop_Ck	Owens	Inyo	13-054-160	3	2
BIS.21	603BSPB65	10/22/2014	Bishop_Ck	Owens	Inyo	13-054-160	12	12
BIS.30	603BSPB50	5/14/2014	Bishop_Ck	Owens	Inyo	13-054-160	45	43
BIS.30	603BSPB50	6/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	50	20
BIS.30	603BSPB50	7/23/2014	Bishop_Ck	Owens	Inyo	13-054-160	43	40
BIS.30	603BSPB50	8/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	54	47
BIS.30	603BSPB50	9/24/2014	Bishop_Ck	Owens	Inyo	13-054-160	64	44
BIS.30	603BSPB50	10/22/2014	Bishop_Ck	Owens	Inyo	13-054-160	254	221
BIS.31	603BSPB60	5/14/2014	Bishop_Ck	Owens	Inyo	13-054-160	324	276
BIS.31	603BSPB60	6/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	80	74
BIS.31	603BSPB60	7/23/2014	Bishop_Ck	Owens	Inyo	13-054-160	24	18
BIS.31	603BSPB60	8/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	514	426
BIS.31	603BSPB60	9/24/2014	Bishop_Ck	Owens	Inyo	13-054-160	340	335
BIS.31	603BSPB60	10/22/2014	Bishop_Ck	Owens	Inyo	13-054-160	45	45
BIS.40		5/14/2014	Bishop_Ck	Owens	Inyo	13-054-160	104	90
BIS.40		6/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	1150	420
BIS.40		7/23/2014	Bishop_Ck	Owens	Inyo	13-054-160	90	82

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BIS.40		8/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	172	144
BIS.40		9/24/2014	Bishop_Ck	Owens	Inyo	13-054-160	78	72
BIS.40		10/22/2014	Bishop_Ck	Owens	Inyo	13-054-160	28	18
BIS.41	603BSPB20	5/14/2014	Bishop_Ck	Owens	Inyo	13-054-160	156	106
BIS.41	603BSPB20	6/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	102	54
BIS.41	603BSPB20	7/23/2014	Bishop_Ck	Owens	Inyo	13-054-160	195	150
BIS.41	603BSPB20	8/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	160	160
BIS.41	603BSPB20	9/24/2014	Bishop_Ck	Owens	Inyo	13-054-160	448	424
BIS.41	603BSPB20	10/22/2014	Bishop_Ck	Owens	Inyo	13-054-160	64	56
BIS.50	603BSP011	5/14/2014	Bishop_Ck	Owens	Inyo	13-054-160	40	40
BIS.50	603BSP011	6/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	240	230
BIS.50	603BSP011	7/23/2014	Bishop_Ck	Owens	Inyo	13-054-160	72	72
BIS.50	603BSP011	8/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	1000	360
BIS.50	603BSP011	9/24/2014	Bishop_Ck	Owens	Inyo	13-054-160	275	255
BIS.50	603BSP011	10/22/2014	Bishop_Ck	Owens	Inyo	13-054-160	40	40
BIS.51	603BSPB22	5/14/2014	Bishop_Ck	Owens	Inyo	13-054-160	104	80
BIS.51	603BSPB22	6/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	135	135
BIS.51	603BSPB22	7/23/2014	Bishop_Ck	Owens	Inyo	13-054-160	780	240
BIS.51	603BSPB22	8/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	400	350
BIS.51	603BSPB22	9/24/2014	Bishop_Ck	Owens	Inyo	13-054-160	45	35
BIS.51	603BSPB22	10/22/2014	Bishop_Ck	Owens	Inyo	13-054-160	124	112
BIS.52	603BSPB23	5/14/2014	Bishop_Ck	Owens	Inyo	13-054-160	3190	290
BIS.52	603BSPB23	6/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	740	460
BIS.52	603BSPB23	7/23/2014	Bishop_Ck	Owens	Inyo	13-054-160	110	100
BIS.52	603BSPB23	8/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	3	0
BIS.52	603BSPB23	9/24/2014	Bishop_Ck	Owens	Inyo	13-054-160	46	40
BIS.52	603BSPB23	10/22/2014	Bishop_Ck	Owens	Inyo	13-054-160	198	178
BIS.53		5/14/2014	Bishop_Ck	Owens	Inyo	13-054-160	2	0
BIS.53		6/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	20	20
BIS.53		7/23/2014	Bishop_Ck	Owens	Inyo	13-054-160	26	13
BIS.53		8/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	5	2
BIS.53		9/24/2014	Bishop_Ck	Owens	Inyo	13-054-160	6	4
BIS.53		10/22/2014	Bishop_Ck	Owens	Inyo	13-054-160	2	1
BIS.60	603BSP004	5/14/2014	Bishop_Ck	Owens	Inyo	13-054-160	460	305
BIS.60	603BSP004	6/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	125	125
BIS.60	603BSP004	7/23/2014	Bishop_Ck	Owens	Inyo	13-054-160	460	150
BIS.60	603BSP004	8/18/2014	Bishop_Ck	Owens	Inyo	13-054-160	280	280
BIS.60	603BSP004	9/24/2014	Bishop_Ck	Owens	Inyo	13-054-160	65	50
BIS.60	603BSP004	10/22/2014	Bishop_Ck	Owens	Inyo	13-054-160	270	188
BIS.90		7/31/2014	Bishop_Ck	Owens	Inyo	12-067-160	640	220
BUC.02		9/18/2012	Buckeye_Ck	Walker	Mono	11-167-160	5	3
BUC.02		3/25/2013	Buckeye_Ck	Walker	Mono	11-167-160	0	0
BUC.02		4/23/2013	Buckeye_Ck	Walker	Mono	12-067-160	1	1
BUC.02		5/29/2013	Buckeye_Ck	Walker	Mono	12-067-160	2	2
BUC.02		7/6/2013	Buckeye_Ck	Walker	Mono	12-067-160	44	44
BUC.02		7/29/2013	Buckeye_Ck	Walker	Mono	12-067-160	5	4
BUC.02		9/16/2013	Buckeye_Ck	Walker	Mono	12-067-160	4	4

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BUC.02		10/16/2013	Buckeye_Ck	Walker	Mono	12-067-160	5	4
BUC.03		9/18/2012	Buckeye_Ck	Walker	Mono	11-167-160	3	2
BUC.03		3/25/2013	Buckeye_Ck	Walker	Mono	11-167-160	1	1
BUC.03		4/23/2013	Buckeye_Ck	Walker	Mono	12-067-160	0	0
BUC.03		5/29/2013	Buckeye_Ck	Walker	Mono	12-067-160	6	6
BUC.03		7/6/2013	Buckeye_Ck	Walker	Mono	12-067-160	43	43
BUC.03		7/29/2013	Buckeye_Ck	Walker	Mono	12-067-160	5	5
BUC.03		9/16/2013	Buckeye_Ck	Walker	Mono	12-067-160	24	13
BUC.03		10/16/2013	Buckeye_Ck	Walker	Mono	12-067-160	5	5
BUC.03		5/13/2014	Buckeye_Ck	Walker	Mono	13-054-160	1	1
BUC.03		6/17/2014	Buckeye_Ck	Walker	Mono	13-054-160	4	4
BUC.03		7/22/2014	Buckeye_Ck	Walker	Mono	13-054-160	58	28
BUC.03		8/17/2014	Buckeye_Ck	Walker	Mono	13-054-160	0	0
BUC.03		9/22/2014	Buckeye_Ck	Walker	Mono	13-054-160	0	0
BUC.03		10/21/2014	Buckeye_Ck	Walker	Mono	13-054-160	0	0
BUC.04	630BUC004	8/14/2012	Buckeye_Ck	Walker	Mono	11-167-160	80	68
BUC.04	630BUC004	9/18/2012	Buckeye_Ck	Walker	Mono	11-167-160	23	23
BUC.04	630BUC004	3/25/2013	Buckeye_Ck	Walker	Mono	11-167-160	19	18
BUC.04	630BUC004	4/23/2013	Buckeye_Ck	Walker	Mono	12-067-160	5	5
BUC.04	630BUC004	5/29/2013	Buckeye_Ck	Walker	Mono	12-067-160	19	13
BUC.04	630BUC004	7/6/2013	Buckeye_Ck	Walker	Mono	12-067-160	440	400
BUC.04	630BUC004	7/29/2013	Buckeye_Ck	Walker	Mono	12-067-160	187	187
BUC.04	630BUC004	9/16/2013	Buckeye_Ck	Walker	Mono	12-067-160	123	113
BUC.04	630BUC004	10/16/2013	Buckeye_Ck	Walker	Mono	12-067-160	58	58
BUC.04	630BUC004	5/13/2014	Buckeye_Ck	Walker	Mono	13-054-160	2	2
BUC.04	630BUC004	6/17/2014	Buckeye_Ck	Walker	Mono	13-054-160	62	59
BUC.04	630BUC004	7/22/2014	Buckeye_Ck	Walker	Mono	13-054-160	980	740
BUC.04	630BUC004	8/17/2014	Buckeye_Ck	Walker	Mono	13-054-160	530	500
BUC.04	630BUC004	9/22/2014	Buckeye_Ck	Walker	Mono	13-054-160	190	170
BUC.04	630BUC004	10/21/2014	Buckeye_Ck	Walker	Mono	13-054-160	107	107
BUC.05	630BUC005	8/14/2012	Buckeye_Ck	Walker	Mono	11-167-160	196	196
BUC.05	630BUC005	3/25/2013	Buckeye_Ck	Walker	Mono	11-167-160	0	0
BUC.05	630BUC005	4/23/2013	Buckeye_Ck	Walker	Mono	12-067-160	20	13
BUC.05	630BUC005	5/29/2013	Buckeye_Ck	Walker	Mono	12-067-160	16	15
BUC.05	630BUC005	7/6/2013	Buckeye_Ck	Walker	Mono	12-067-160	156	156
BUC.05	630BUC005	7/29/2013	Buckeye_Ck	Walker	Mono	12-067-160	193	167
BUC.05	630BUC005	9/16/2013	Buckeye_Ck	Walker	Mono	12-067-160	300	260
BUC.05	630BUC005	10/16/2013	Buckeye_Ck	Walker	Mono	12-067-160	40	38
BUC.05	630BUC005	5/13/2014	Buckeye_Ck	Walker	Mono	13-054-160	2	2
BUC.05	630BUC005	6/17/2014	Buckeye_Ck	Walker	Mono	13-054-160	33	29
BUC.05	630BUC005	7/22/2014	Buckeye_Ck	Walker	Mono	13-054-160	1090	850
BUC.05	630BUC005	8/17/2014	Buckeye_Ck	Walker	Mono	13-054-160	120	120
BUC.05	630BUC005	9/22/2014	Buckeye_Ck	Walker	Mono	13-054-160	210	203
BUC.05	630BUC005	10/21/2014	Buckeye_Ck	Walker	Mono	13-054-160	107	107
BUC.08		6/3/2014	Buckeye_Ck	Walker	Mono	13-054-160	240	224
BUC.08		8/21/2014	Buckeye_Ck	Walker	Mono	13-054-160	330	310
CON.10		7/25/2012	Convict_Ck	Owens	Mono	11-167-160	0	0

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CON.10		4/22/2013	Convict_Ck	Owens	Mono	12-067-160	0	0
CON.10		5/28/2013	Convict_Ck	Owens	Mono	12-067-160	0	0
CON.10		7/8/2013	Convict_Ck	Owens	Mono	12-067-160	0	0
CON.10		7/29/2013	Convict_Ck	Owens	Mono	12-067-160	3	3
CON.10		9/11/2013	Convict_Ck	Owens	Mono	12-067-160	0	0
CON.10		10/15/2013	Convict_Ck	Owens	Mono	12-067-160	0	0
CON.15		7/7/2013	Convict_Ck	Owens	Mono	12-067-160	13	13
CON.15		7/29/2013	Convict_Ck	Owens	Mono	12-067-160	32	24
CON.15		9/11/2013	Convict_Ck	Owens	Mono	12-067-160	23	17
CON.15		10/17/2013	Convict_Ck	Owens	Mono	12-067-160	4	4
CON.20		7/25/2012	Convict_Ck	Owens	Mono	11-167-160	22	21
CON.20		3/13/2013	Convict_Ck	Owens	Mono	11-167-160	0	0
CON.20		4/22/2013	Convict_Ck	Owens	Mono	12-067-160	2	2
CON.20		5/30/2013	Convict_Ck	Owens	Mono	12-067-160	19	19
CON.20		7/7/2013	Convict_Ck	Owens	Mono	12-067-160	39	38
CON.20		7/29/2013	Convict_Ck	Owens	Mono	12-067-160	51	35
CON.20		9/11/2013	Convict_Ck	Owens	Mono	12-067-160	46	32
CON.20		10/17/2013	Convict_Ck	Owens	Mono	12-067-160	7	7
CON.30		7/25/2012	Convict_Ck	Owens	Mono	11-167-160	0	0
CON.30		3/13/2013	Convict_Ck	Owens	Mono	11-167-160	0	0
CON.30		4/23/2013	Convict_Ck	Owens	Mono	12-067-160	0	0
CON.30		5/28/2013	Convict_Ck	Owens	Mono	12-067-160	4	4
CON.30		7/10/2013	Convict_Ck	Owens	Mono	12-067-160	11	11
CON.30		7/31/2013	Convict_Ck	Owens	Mono	12-067-160	18	14
CON.30		9/11/2013	Convict_Ck	Owens	Mono	12-067-160	17	17
CON.30		10/15/2013	Convict_Ck	Owens	Mono	12-067-160	2	2
CON.40		7/25/2012	Convict_Ck	Owens	Mono	11-167-160	123	67
CON.40		3/13/2013	Convict_Ck	Owens	Mono	11-167-160	0	0
CON.40		4/23/2013	Convict_Ck	Owens	Mono	12-067-160	0	0
CON.40		5/28/2013	Convict_Ck	Owens	Mono	12-067-160	5	5
CON.40		7/10/2013	Convict_Ck	Owens	Mono	12-067-160	12	12
CON.40		7/31/2013	Convict_Ck	Owens	Mono	12-067-160	16	16
CON.40		9/11/2013	Convict_Ck	Owens	Mono	12-067-160	8	8
CON.40		10/15/2013	Convict_Ck	Owens	Mono	12-067-160	4	2
EWK.06	630EWK006	8/14/2012	East_Walker_Rvr	Walker	Mono	11-167-160	230	200
EWK.06	630EWK006	3/25/2013	East_Walker_Rvr	Walker	Mono	11-167-160	7	6
EWK.06	630EWK006	4/23/2013	East_Walker_Rvr	Walker	Mono	12-067-160	14	6
EWK.06	630EWK006	5/29/2013	East_Walker_Rvr	Walker	Mono	12-067-160	830	740
EWK.06	630EWK006	7/6/2013	East_Walker_Rvr	Walker	Mono	12-067-160	287	247
EWK.06	630EWK006	7/29/2013	East_Walker_Rvr	Walker	Mono	12-067-160	250	220
EWK.06	630EWK006	9/16/2013	East_Walker_Rvr	Walker	Mono	12-067-160	67	60
EWK.06	630EWK006	10/16/2013	East_Walker_Rvr	Walker	Mono	12-067-160	30	22
EWK.06	630EWK006	5/13/2014	East_Walker_Rvr	Walker	Mono	13-054-160	7	7
EWK.06	630EWK006	6/17/2014	East_Walker_Rvr	Walker	Mono	13-054-160	395	380
EWK.06	630EWK006	7/22/2014	East_Walker_Rvr	Walker	Mono	13-054-160	160	160
EWK.06	630EWK006	8/17/2014	East_Walker_Rvr	Walker	Mono	13-054-160	135	135
EWK.06	630EWK006	9/22/2014	East_Walker_Rvr	Walker	Mono	13-054-160	96	96

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EWK.06	630EWK006	10/21/2014	East_Walker_Rvr	Walker	Mono	13-054-160	16	14
EWK.08		6/3/2014	East_Walker_Rvr	Walker	Mono	13-054-160	360	330
EWK.08		8/21/2014	East_Walker_Rvr	Walker	Mono	13-054-160	280	250
GOO.50		7/29/2014	Goodale_Ck	Owens	Inyo	12-067-160	4	4
GOO.50		8/19/2014	Goodale_Ck	Owens	Inyo	12-067-160	2	2
GRE.40		6/3/2014	Green_Ck	Walker	Mono	13-054-160	1	1
GRE.40		8/21/2014	Green_Ck	Walker	Mono	13-054-160	73	66
HIL.20		9/17/2012	Hilton_Ck	Owens	Mono	11-167-160	3	3
HIL.20		3/13/2013	Hilton_Ck	Owens	Mono	11-167-160	0	0
HIL.20		4/22/2013	Hilton_Ck	Owens	Mono	12-067-160	1	1
HIL.20		5/28/2013	Hilton_Ck	Owens	Mono	12-067-160	0	0
HIL.20		7/8/2013	Hilton_Ck	Owens	Mono	12-067-160	11	11
HIL.20		7/31/2013	Hilton_Ck	Owens	Mono	12-067-160	13	13
HIL.20		9/12/2013	Hilton_Ck	Owens	Mono	12-067-160	10	10
HIL.20		10/15/2013	Hilton_Ck	Owens	Mono	12-067-160	14	14
HOR.50		7/31/2014	Horton_Ck	Owens	Inyo	12-067-160	3	3
HOR.50		8/20/2014	Horton_Ck	Owens	Inyo	12-067-160	6	6
HOR.70		5/14/2014	Horton_Ck	Owens	Inyo	13-054-160	512	460
HOR.70		6/18/2014	Horton_Ck	Owens	Inyo	13-054-160	148	144
HOR.70		7/23/2014	Horton_Ck	Owens	Inyo	13-054-160	92	78
HOR.70		8/18/2014	Horton_Ck	Owens	Inyo	13-054-160	124	124
HOR.70		8/20/2014	Horton_Ck	Owens	Inyo	12-067-160	112	108
HOR.70		9/24/2014	Horton_Ck	Owens	Inyo	13-054-160	378	358
HOR.70		10/22/2014	Horton_Ck	Owens	Inyo	13-054-160	80	80
IND.50		7/29/2014	Independence_Ck	Owens	Inyo	12-067-160	2	2
IND.50		8/19/2014	Independence_Ck	Owens	Inyo	12-067-160	5	5
IND.60		7/29/2014	Independence_Ck	Owens	Inyo	12-067-160	28	28
IND.60		8/19/2014	Independence_Ck	Owens	Inyo	12-067-160	8	8
LEE.10		7/26/2012	Lee_Vining_Ck	Mono	Mono	11-167-160	0	0
LEE.10		8/13/2012	Lee_Vining_Ck	Mono	Mono	11-167-160	0	0
LEE.10		3/12/2013	Lee_Vining_Ck	Mono	Mono	11-167-160	0	0
LEE.10		4/24/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	0	0
LEE.10		5/31/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	0	0
LEE.10		7/7/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	1	0
LEE.10		7/30/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	2	2
LEE.10		9/17/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	2	2
LEE.10		10/17/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	2	2
LEE.15		8/13/2012	Lee_Vining_Ck	Mono	Mono	11-167-160	1	1
LEE.15		3/12/2013	Lee_Vining_Ck	Mono	Mono	11-167-160	0	0
LEE.15		4/24/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	1	0
LEE.15		5/31/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	0	0
LEE.15		7/7/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	8	7
LEE.15		7/30/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	9	9
LEE.15		9/17/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	6	6
LEE.15		10/17/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	4	4
LEE.17		8/13/2012	Lee_Vining_Ck	Mono	Mono	11-167-160	5	5
LEE.17		3/12/2013	Lee_Vining_Ck	Mono	Mono	11-167-160	2	2

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LEE.17		4/24/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	0	0
LEE.17		5/31/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	0	0
LEE.17		7/7/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	6	6
LEE.17		7/30/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	11	10
LEE.17		9/17/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	2	2
LEE.17		10/17/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	1	1
LEE.20		7/26/2012	Lee_Vining_Ck	Mono	Mono	11-167-160	66	56
LEE.20		8/13/2012	Lee_Vining_Ck	Mono	Mono	11-167-160	14	14
LEE.20		3/12/2013	Lee_Vining_Ck	Mono	Mono	11-167-160	0	0
LEE.20		4/24/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	7	0
LEE.20		5/31/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	0	0
LEE.30		8/13/2012	Lee_Vining_Ck	Mono	Mono	11-167-160	0	0
LEE.30		3/12/2013	Lee_Vining_Ck	Mono	Mono	11-167-160	0	0
LEE.30		4/24/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	6	6
LEE.30		5/31/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	5	5
LEE.30		7/7/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	47	43
LEE.30		7/30/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	31	28
LEE.30		9/17/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	10	8
LEE.30		10/17/2013	Lee_Vining_Ck	Mono	Mono	12-067-160	4	3
LON.50		7/29/2014	Lone_Pine_Ck	Owens	Inyo	12-067-160	3	3
LON.50		8/19/2014	Lone_Pine_Ck	Owens	Inyo	12-067-160	2	2
LON.70		7/29/2014	Lone_Pine_Ck	Owens	Inyo	12-067-160	90	55
LON.70		8/19/2014	Lone_Pine_Ck	Owens	Inyo	12-067-160	22	14
MAM.10		7/25/2012	Mammoth_Ck	Owens	Mono	11-167-160	1	1
MAM.10		4/22/2013	Mammoth_Ck	Owens	Mono	12-067-160	0	0
MAM.10		5/30/2013	Mammoth_Ck	Owens	Mono	12-067-160	0	0
MAM.10		7/8/2013	Mammoth_Ck	Owens	Mono	12-067-160	0	0
MAM.10		8/1/2013	Mammoth_Ck	Owens	Mono	12-067-160	4	4
MAM.10		9/11/2013	Mammoth_Ck	Owens	Mono	12-067-160	2	2
MAM.10		10/15/2013	Mammoth_Ck	Owens	Mono	12-067-160	0	0
MAM.10		5/12/2014	Mammoth_Ck	Owens	Mono	13-054-160	0	0
MAM.20		7/25/2012	Mammoth_Ck	Owens	Mono	11-167-160	19	10
MAM.20		4/22/2013	Mammoth_Ck	Owens	Mono	12-067-160	0	0
MAM.20		5/30/2013	Mammoth_Ck	Owens	Mono	12-067-160	1	0
MAM.20		7/7/2013	Mammoth_Ck	Owens	Mono	12-067-160	1	1
MAM.20		7/29/2013	Mammoth_Ck	Owens	Mono	12-067-160	8	8
MAM.20		9/11/2013	Mammoth_Ck	Owens	Mono	12-067-160	18	18
MAM.20		10/15/2013	Mammoth_Ck	Owens	Mono	12-067-160	0	0
MAM.20		5/12/2014	Mammoth_Ck	Owens	Mono	13-054-160	1	1
MAM.30		7/25/2012	Mammoth_Ck	Owens	Mono	11-167-160	6	4
MAM.30		3/13/2013	Mammoth_Ck	Owens	Mono	11-167-160	0	0
MAM.30		4/22/2013	Mammoth_Ck	Owens	Mono	12-067-160	3	3
MAM.30		5/12/2013	Mammoth_Ck	Owens	Mono	12-067-160	6	6
MAM.30		5/30/2013	Mammoth_Ck	Owens	Mono	12-067-160	1	1
MAM.30		7/7/2013	Mammoth_Ck	Owens	Mono	12-067-160	53	52
MAM.30		7/29/2013	Mammoth_Ck	Owens	Mono	12-067-160	78	69
MAM.30		9/12/2013	Mammoth_Ck	Owens	Mono	12-067-160	49	40

SNARL ID	SWAMP ID	Sampling Date	Stream	Drainage	County	Contract ID	fcoli100	ecoli100
MAM.30		10/17/2013	Mammoth_Ck	Owens	Mono	13-054-160	1	1
MAM.30		6/16/2014	Mammoth_Ck	Owens	Mono	13-054-160	3	3
MAM.30		7/9/2014	Mammoth_Ck	Owens	Mono	13-054-160	93	51
MAM.30		7/21/2014	Mammoth_Ck	Owens	Mono	13-054-160	59	57
MAM.30		8/21/2014	Mammoth_Ck	Owens	Mono	13-054-160	32	31
MAM.30		9/23/2014	Mammoth_Ck	Owens	Mono	13-054-160	6	6
MAM.30		10/20/2014	Mammoth_Ck	Owens	Mono	13-054-160	13	13
MAM.40		7/25/2012	Mammoth_Ck	Owens	Mono	11-167-160	0	0
MAM.40		3/13/2013	Mammoth_Ck	Owens	Mono	11-167-160	0	0
MAM.40		4/22/2013	Mammoth_Ck	Owens	Mono	12-067-160	1	0
MAM.40		5/30/2013	Mammoth_Ck	Owens	Mono	12-067-160	7	7
MAM.40		7/8/2013	Mammoth_Ck	Owens	Mono	12-067-160	99	88
MAM.40		7/29/2013	Mammoth_Ck	Owens	Mono	12-067-160	56	51
MAM.40		9/11/2013	Mammoth_Ck	Owens	Mono	12-067-160	123	88
MAM.40		10/15/2013	Mammoth_Ck	Owens	Mono	12-067-160	11	11
MAM.40		5/12/2014	Mammoth_Ck	Owens	Mono	13-054-160	8	8
MAM.40		6/16/2014	Mammoth_Ck	Owens	Mono	13-054-160	11	11
MAM.40		7/9/2014	Mammoth_Ck	Owens	Mono	13-054-160	192	192
MAM.40		7/21/2014	Mammoth_Ck	Owens	Mono	13-054-160	142	142
MAM.40		8/21/2014	Mammoth_Ck	Owens	Mono	13-054-160	125	125
MAM.40		9/23/2014	Mammoth_Ck	Owens	Mono	13-054-160	15	15
MAM.40		10/20/2014	Mammoth_Ck	Owens	Mono	13-054-160	2	2
MAM.50		7/25/2012	Mammoth_Ck	Owens	Mono	11-167-160	0	0
MAM.50		3/13/2013	Mammoth_Ck	Owens	Mono	11-167-160	0	0
MAM.50		4/22/2013	Mammoth_Ck	Owens	Mono	12-067-160	0	0
MAM.50		5/28/2013	Mammoth_Ck	Owens	Mono	12-067-160	67	67
MAM.50		7/10/2013	Mammoth_Ck	Owens	Mono	12-067-160	20	20
MAM.50		8/1/2013	Mammoth_Ck	Owens	Mono	12-067-160	80	70
MAM.50		9/12/2013	Mammoth_Ck	Owens	Mono	12-067-160	53	53
MAM.50		10/23/2013	Mammoth_Ck	Owens	Mono	12-067-160	2	2
MAM.50		5/12/2014	Mammoth_Ck	Owens	Mono	13-054-160	0	0
MAM.50		6/2/2014	Mammoth_Ck	Owens	Mono	13-054-160	7	7
MAM.50		6/9/2014	Mammoth_Ck	Owens	Mono	13-054-160	117	102
MAM.50		6/16/2014	Mammoth_Ck	Owens	Mono	13-054-160	120	112
MAM.50		6/23/2014	Mammoth_Ck	Owens	Mono	13-054-160	30	28
MAM.50		6/27/2014	Mammoth_Ck	Owens	Mono	13-054-160	46	46
MAM.50		7/2/2014	Mammoth_Ck	Owens	Mono	13-054-160	84	70
MAM.50		7/9/2014	Mammoth_Ck	Owens	Mono	13-054-160	63	63
MAM.50		7/14/2014	Mammoth_Ck	Owens	Mono	13-054-160	106	102
MAM.50		7/21/2014	Mammoth_Ck	Owens	Mono	13-054-160	60	60
MAM.50		7/29/2014	Mammoth_Ck	Owens	Mono	13-054-160	164	148
MAM.50		8/4/2014	Mammoth_Ck	Owens	Mono	13-054-160	56	44
MAM.50		8/8/2014	Mammoth_Ck	Owens	Mono	13-054-160	54	54
MAM.50		8/13/2014	Mammoth_Ck	Owens	Mono	13-054-160	30	28
MAM.50		8/18/2014	Mammoth_Ck	Owens	Mono	13-054-160	4	4
MAM.50		8/21/2014	Mammoth_Ck	Owens	Mono	13-054-160	11	11
MAM.50		9/23/2014	Mammoth_Ck	Owens	Mono	13-054-160	206	206

SNARL ID	SWAMP ID	Sampling Date	Stream	Drainage	County	Contract ID	fcoli100	ecoli100
MAM.50		10/20/2014	Mammoth_Ck	Owens	Mono	13-054-160	10	10
MCG.15		9/17/2012	McGee_Ck	Owens	Mono	11-167-160	0	0
MCG.15		4/22/2013	McGee_Ck	Owens	Mono	12-067-160	0	0
MCG.15		5/28/2013	McGee_Ck	Owens	Mono	12-067-160	0	0
MCG.15		7/8/2013	McGee_Ck	Owens	Mono	12-067-160	1	1
MCG.15		7/31/2013	McGee_Ck	Owens	Mono	12-067-160	1	1
MCG.15		9/12/2013	McGee_Ck	Owens	Mono	12-067-160	5	5
MCG.15		10/15/2013	McGee_Ck	Owens	Mono	12-067-160	0	0
MCG.17		9/17/2012	McGee_Ck	Owens	Mono	11-167-160	0	0
MCG.17		4/22/2013	McGee_Ck	Owens	Mono	12-067-160	1	1
MCG.17		5/28/2013	McGee_Ck	Owens	Mono	12-067-160	0	0
MCG.17		7/8/2013	McGee_Ck	Owens	Mono	12-067-160	1	1
MCG.17		7/31/2013	McGee_Ck	Owens	Mono	12-067-160	6	6
MCG.17		9/12/2013	McGee_Ck	Owens	Mono	12-067-160	18	17
MCG.17		10/15/2013	McGee_Ck	Owens	Mono	12-067-160	4	4
MCG.20		7/26/2012	McGee_Ck	Owens	Mono	11-167-160	13	3
MCG.20		9/17/2012	McGee_Ck	Owens	Mono	11-167-160	6	6
MCG.20		3/13/2013	McGee_Ck	Owens	Mono	11-167-160	1	1
MCG.20		4/22/2013	McGee_Ck	Owens	Mono	12-067-160	4	1
MCG.20		5/28/2013	McGee_Ck	Owens	Mono	12-067-160	4	4
MCG.20		7/8/2013	McGee_Ck	Owens	Mono	12-067-160	7	7
MCG.20		7/31/2013	McGee_Ck	Owens	Mono	12-067-160	6	3
MCG.20		9/12/2013	McGee_Ck	Owens	Mono	12-067-160	4	3
MCG.20		10/15/2013	McGee_Ck	Owens	Mono	12-067-160	3	3
MCG.30		9/17/2012	McGee_Ck	Owens	Mono	11-167-160	1	1
MCG.30		4/22/2013	McGee_Ck	Owens	Mono	12-067-160	0	0
MCG.30		5/28/2013	McGee_Ck	Owens	Mono	12-067-160	5	4
MCG.30		7/10/2013	McGee_Ck	Owens	Mono	12-067-160	60	60
MCG.30		8/1/2013	McGee_Ck	Owens	Mono	12-067-160	55	49
MCG.30		9/12/2013	McGee_Ck	Owens	Mono	12-067-160	9	7
MCG.30		10/23/2013	McGee_Ck	Owens	Mono	12-067-160	1	1
MIL.20		9/24/2012	Mill_Ck	Mono	Mono	11-167-160	0	0
MIL.20		5/31/2013	Mill_Ck	Mono	Mono	12-067-160	0	0
MIL.30		9/24/2012	Mill_Ck	Mono	Mono	11-167-160	0	0
MIL.30		5/31/2013	Mill_Ck	Mono	Mono	12-067-160	0	0
MIL.40		9/24/2012	Mill_Ck	Mono	Mono	11-167-160	3	2
MIL.40		5/31/2013	Mill_Ck	Mono	Mono	12-067-160	1	1
MIL.40		7/7/2013	Mill_Ck	Mono	Mono	12-067-160	0	0
MIL.40		7/30/2013	Mill_Ck	Mono	Mono	12-067-160	17	16
MIL.40		9/17/2013	Mill_Ck	Mono	Mono	12-067-160	0	0
MIL.40		10/17/2013	Mill_Ck	Mono	Mono	12-067-160	0	0
MIL.60		9/24/2012	Mill_Ck	Mono	Mono	11-167-160	5	5
MIL.60		3/12/2013	Mill_Ck	Mono	Mono	11-167-160	0	0
MIL.60		4/24/2013	Mill_Ck	Mono	Mono	12-067-160	6	6
MIL.60		5/31/2013	Mill_Ck	Mono	Mono	12-067-160	1	1
MIL.60		7/7/2013	Mill_Ck	Mono	Mono	12-067-160	21	18
MIL.60		7/30/2013	Mill_Ck	Mono	Mono	12-067-160	4	4

SNARL ID	SWAMP ID	Sampling Date	Stream	Drainage	County	Contract ID	fcoli100	ecoli100
MIL.60		9/17/2013	Mill_Ck	Mono	Mono	12-067-160	1	1
MIL.60		10/17/2013	Mill_Ck	Mono	Mono	12-067-160	2	2
MIL.80		9/24/2012	Mill_Ck	Mono	Mono	11-167-160	13	13
MIL.80		3/12/2013	Mill_Ck	Mono	Mono	11-167-160	0	0
MIL.80		4/24/2013	Mill_Ck	Mono	Mono	12-067-160	1	1
MIL.80		5/31/2013	Mill_Ck	Mono	Mono	12-067-160	2	2
MIL.80		7/7/2013	Mill_Ck	Mono	Mono	12-067-160	31	27
MIL.80		7/30/2013	Mill_Ck	Mono	Mono	12-067-160	32	23
MIL.80		9/17/2013	Mill_Ck	Mono	Mono	12-067-160	20	18
MIL.80		10/17/2013	Mill_Ck	Mono	Mono	12-067-160	3	3
OAK.50		7/29/2014	Oak_Ck	Owens	Inyo	12-067-160	5	3
OAK.50		8/19/2014	Oak_Ck	Owens	Inyo	12-067-160	0	0
OWE.10		9/26/2012	Owens_Rvr	Owens	Mono	11-167-160	0	0
OWE.10		5/30/2013	Owens_Rvr	Owens	Mono	12-067-160	0	0
OWE.10		7/6/2013	Owens_Rvr	Owens	Mono	12-067-160	1	1
OWE.10		7/30/2013	Owens_Rvr	Owens	Mono	12-067-160	4	3
OWE.10		9/11/2013	Owens_Rvr	Owens	Mono	12-067-160	4	4
OWE.10		10/23/2013	Owens_Rvr	Owens	Mono	12-067-160	1	1
OWE.15		9/26/2012	Owens_Rvr	Owens	Mono	11-167-160	5	5
OWE.15		4/23/2013	Owens_Rvr	Owens	Mono	12-067-160	0	0
OWE.15		5/30/2013	Owens_Rvr	Owens	Mono	12-067-160	0	0
OWE.15		7/6/2013	Owens_Rvr	Owens	Mono	12-067-160	15	8
OWE.15		8/1/2013	Owens_Rvr	Owens	Mono	12-067-160	33	25
OWE.15		9/11/2013	Owens_Rvr	Owens	Mono	12-067-160	4	4
OWE.15		10/23/2013	Owens_Rvr	Owens	Mono	12-067-160	0	0
OWE.20		9/26/2012	Owens_Rvr	Owens	Mono	11-167-160	0	0
OWE.20		4/24/2013	Owens_Rvr	Owens	Mono	12-067-160	0	0
OWE.20		5/29/2013	Owens_Rvr	Owens	Mono	12-067-160	1	1
OWE.20		7/8/2013	Owens_Rvr	Owens	Mono	12-067-160	60	56
OWE.20		8/1/2013	Owens_Rvr	Owens	Mono	12-067-160	13	11
OWE.20		9/11/2013	Owens_Rvr	Owens	Mono	12-067-160	0	0
OWE.20		10/23/2013	Owens_Rvr	Owens	Mono	12-067-160	0	0
OWE.40		3/13/2013	Owens_Rvr	Owens	Mono	11-167-160	1	1
OWE.40		4/23/2013	Owens_Rvr	Owens	Mono	12-067-160	1	1
OWE.40		5/28/2013	Owens_Rvr	Owens	Mono	12-067-160	33	27
OWE.40		7/10/2013	Owens_Rvr	Owens	Mono	12-067-160	180	180
OWE.40		7/31/2013	Owens_Rvr	Owens	Mono	12-067-160	63	50
OWE.40		9/11/2013	Owens_Rvr	Owens	Mono	12-067-160	70	67
OWE.40		10/15/2013	Owens_Rvr	Owens	Mono	12-067-160	1	1
OWE.40		6/2/2014	Owens_Rvr	Owens	Mono	13-054-160	37	37
OWE.40		6/9/2014	Owens_Rvr	Owens	Mono	13-054-160	106	74
OWE.40		6/16/2014	Owens_Rvr	Owens	Mono	13-054-160	204	162
OWE.40		6/23/2014	Owens_Rvr	Owens	Mono	13-054-160	132	112
OWE.40		6/27/2014	Owens_Rvr	Owens	Mono	13-054-160	144	104
OWE.40		7/2/2014	Owens_Rvr	Owens	Mono	13-054-160	180	172
OWE.40		7/9/2014	Owens_Rvr	Owens	Mono	13-054-160	160	152
OWE.40		7/14/2014	Owens_Rvr	Owens	Mono	13-054-160	114	114

SNARL ID	SWAMP ID	Sampling Date	Stream	Drainage	County	Contract ID	fcoli100	ecoli100
OWE.40		7/21/2014	Owens_Rvr	Owens	Mono	13-054-160	266	242
OWE.40		7/29/2014	Owens_Rvr	Owens	Mono	13-054-160	164	156
OWE.40		8/4/2014	Owens_Rvr	Owens	Mono	13-054-160	192	184
OWE.40		8/8/2014	Owens_Rvr	Owens	Mono	13-054-160	108	100
OWE.40		8/13/2014	Owens_Rvr	Owens	Mono	13-054-160	292	252
OWE.40		8/18/2014	Owens_Rvr	Owens	Mono	13-054-160	38	38
OWE.40		8/21/2014	Owens_Rvr	Owens	Mono	13-054-160	43	33
OWE.40		9/23/2014	Owens_Rvr	Owens	Mono	13-054-160	26	25
OWE.40		10/20/2014	Owens_Rvr	Owens	Mono	13-054-160	11	11
OWE.65		7/31/2014	Owens_Rvr	Owens	Inyo	12-067-160	5	5
OWE.65		8/20/2014	Owens_Rvr	Owens	Inyo	12-067-160	0	0
OWE.66		8/20/2014	Owens_Rvr	Owens	Inyo	12-067-160	21	21
OWE.70		7/31/2014	Owens_Rvr	Owens	Inyo	12-067-160	0	0
OWE.70		8/20/2014	Owens_Rvr	Owens	Inyo	12-067-160	0	0
OWE.73		7/31/2014	Owens_Rvr	Owens	Inyo	12-067-160	20	10
OWE.73		8/20/2014	Owens_Rvr	Owens	Inyo	12-067-160	0	0
OWE.77		7/31/2014	Owens_Rvr	Owens	Inyo	12-067-160	33	23
OWE.77		8/20/2014	Owens_Rvr	Owens	Inyo	12-067-160	10	0
OWE.80		7/29/2014	Owens_Rvr	Owens	Inyo	12-067-160	4	2
OWE.80		8/19/2014	Owens_Rvr	Owens	Inyo	12-067-160	2	0
OWE.85		7/29/2014	Owens_Rvr	Owens	Inyo	12-067-160	8	8
OWE.85		8/19/2014	Owens_Rvr	Owens	Inyo	12-067-160	5	5
OWE.90		7/29/2014	Owens_Rvr	Owens	Inyo	12-067-160	22	22
OWE.90		8/19/2014	Owens_Rvr	Owens	Inyo	12-067-160	18	18
PAR.20		9/24/2012	Parker_Ck	Mono	Mono	11-167-160	0	0
PAR.20		4/24/2013	Parker_Ck	Mono	Mono	12-067-160	5	5
PAR.20		5/31/2013	Parker_Ck	Mono	Mono	12-067-160	0	0
PAR.20		7/7/2013	Parker_Ck	Mono	Mono	12-067-160	0	0
PAR.20		7/30/2013	Parker_Ck	Mono	Mono	12-067-160	3	3
PAR.20		9/17/2013	Parker_Ck	Mono	Mono	12-067-160	2	2
PAR.20		10/17/2013	Parker_Ck	Mono	Mono	12-067-160	0	0
PAR.30		9/24/2012	Parker_Ck	Mono	Mono	11-167-160	5	4
PAR.30		3/12/2013	Parker_Ck	Mono	Mono	11-167-160	0	0
PAR.30		4/24/2013	Parker_Ck	Mono	Mono	12-067-160	0	0
PAR.30		5/29/2013	Parker_Ck	Mono	Mono	12-067-160	0	0
PAR.30		7/7/2013	Parker_Ck	Mono	Mono	12-067-160	0	0
PAR.30		7/29/2013	Parker_Ck	Mono	Mono	12-067-160	1	1
PAR.30		9/17/2013	Parker_Ck	Mono	Mono	12-067-160	6	3
PAR.30		10/17/2013	Parker_Ck	Mono	Mono	12-067-160	0	0
PIN.20		7/31/2014	Pine_Ck	Owens	Inyo	12-067-160	0	0
PIN.20		8/20/2014	Pine_Ck	Owens	Inyo	12-067-160	5	5
PIN.50		5/14/2014	Pine_Ck	Owens	Inyo	13-054-160	976	796
PIN.50		6/18/2014	Pine_Ck	Owens	Inyo	13-054-160	2340	1480
PIN.50		7/23/2014	Pine_Ck	Owens	Inyo	13-054-160	310	310
PIN.50		8/18/2014	Pine_Ck	Owens	Inyo	13-054-160	56	56
PIN.50		8/20/2014	Pine_Ck	Owens	Inyo	12-067-160	1780	980
PIN.50		9/24/2014	Pine_Ck	Owens	Inyo	13-054-160	354	260

SNARL ID	SWAMP ID	Sampling Date	Stream	Drainage	County	Contract ID	fcoli100	ecoli100
PIN.50		10/22/2014	Pine_Ck	Owens	Inyo	13-054-160	100	98
PIU.50		7/31/2014	Piute_Ck	Owens	Mono	12-067-160	0	0
RBS.02		9/18/2012	Robinson_Ck	Walker	Mono	11-167-160	3	3
RBS.02		4/23/2013	Robinson_Ck	Walker	Mono	12-067-160	0	0
RBS.02		5/29/2013	Robinson_Ck	Walker	Mono	12-067-160	1	1
RBS.02		7/6/2013	Robinson_Ck	Walker	Mono	12-067-160	15	15
RBS.02		7/29/2013	Robinson_Ck	Walker	Mono	12-067-160	20	20
RBS.02		9/16/2013	Robinson_Ck	Walker	Mono	12-067-160	13	9
RBS.02		10/16/2013	Robinson_Ck	Walker	Mono	12-067-160	1	1
RBS.03		5/13/2014	Robinson_Ck	Walker	Mono	13-054-160	0	0
RBS.03		6/17/2014	Robinson_Ck	Walker	Mono	13-054-160	0	0
RBS.03		7/22/2014	Robinson_Ck	Walker	Mono	13-054-160	2	2
RBS.03		8/17/2014	Robinson_Ck	Walker	Mono	13-054-160	0	0
RBS.03		9/22/2014	Robinson_Ck	Walker	Mono	13-054-160	1	1
RBS.03		10/21/2014	Robinson_Ck	Walker	Mono	13-054-160	4	4
RBS.04		9/18/2012	Robinson_Ck	Walker	Mono	11-167-160	15	13
RBS.04		3/25/2013	Robinson_Ck	Walker	Mono	11-167-160	0	0
RBS.04		4/23/2013	Robinson_Ck	Walker	Mono	12-067-160	1	1
RBS.04		5/29/2013	Robinson_Ck	Walker	Mono	12-067-160	2	2
RBS.04		7/6/2013	Robinson_Ck	Walker	Mono	12-067-160	4	3
RBS.04		7/29/2013	Robinson_Ck	Walker	Mono	12-067-160	15	13
RBS.04		9/16/2013	Robinson_Ck	Walker	Mono	12-067-160	7	6
RBS.04		10/16/2013	Robinson_Ck	Walker	Mono	12-067-160	1	1
RBS.05		9/16/2013	Robinson_Ck	Walker	Mono	12-067-160	9	9
RBS.05		10/16/2013	Robinson_Ck	Walker	Mono	12-067-160	7	1
RBS.05		5/13/2014	Robinson_Ck	Walker	Mono	13-054-160	0	0
RBS.05		6/17/2014	Robinson_Ck	Walker	Mono	13-054-160	7	7
RBS.05		7/22/2014	Robinson_Ck	Walker	Mono	13-054-160	24	18
RBS.05		8/17/2014	Robinson_Ck	Walker	Mono	13-054-160	41	40
RBS.05		9/22/2014	Robinson_Ck	Walker	Mono	13-054-160	27	26
RBS.05		10/21/2014	Robinson_Ck	Walker	Mono	13-054-160	3	3
RBS.07	630RBS007	8/14/2012	Robinson_Ck	Walker	Mono	11-167-160	164	156
RBS.07	630RBS007	9/18/2012	Robinson_Ck	Walker	Mono	11-167-160	57	57
RBS.07	630RBS007	3/25/2013	Robinson_Ck	Walker	Mono	11-167-160	2	2
RBS.07	630RBS007	4/23/2013	Robinson_Ck	Walker	Mono	12-067-160	15	13
RBS.07	630RBS007	5/29/2013	Robinson_Ck	Walker	Mono	12-067-160	58	52
RBS.07	630RBS007	7/6/2013	Robinson_Ck	Walker	Mono	12-067-160	220	196
RBS.07	630RBS007	7/29/2013	Robinson_Ck	Walker	Mono	12-067-160	163	143
RBS.07	630RBS007	9/16/2013	Robinson_Ck	Walker	Mono	12-067-160	220	220
RBS.07	630RBS007	10/16/2013	Robinson_Ck	Walker	Mono	12-067-160	66	64
RBS.07	630RBS007	5/13/2014	Robinson_Ck	Walker	Mono	13-054-160	8	8
RBS.07	630RBS007	6/17/2014	Robinson_Ck	Walker	Mono	13-054-160	84	74
RBS.07	630RBS007	7/22/2014	Robinson_Ck	Walker	Mono	13-054-160	480	460
RBS.07	630RBS007	8/17/2014	Robinson_Ck	Walker	Mono	13-054-160	110	110
RBS.07	630RBS007	9/22/2014	Robinson_Ck	Walker	Mono	13-054-160	76	68
RBS.07	630RBS007	10/21/2014	Robinson_Ck	Walker	Mono	13-054-160	120	120
RBS.08	630RBS008	8/14/2012	Robinson_Ck	Walker	Mono	11-167-160	1000	940

SNARL ID	SWAMP ID	Sampling Date	Stream	Drainage	County	Contract ID	fcoli100	ecoli100
RBS.08	630RBS008	3/25/2013	Robinson_Ck	Walker	Mono	11-167-160	8	8
RBS.08	630RBS008	4/23/2013	Robinson_Ck	Walker	Mono	12-067-160	10	8
RBS.08	630RBS008	5/29/2013	Robinson_Ck	Walker	Mono	12-067-160	332	184
RBS.08	630RBS008	7/6/2013	Robinson_Ck	Walker	Mono	12-067-160	167	160
RBS.08	630RBS008	7/29/2013	Robinson_Ck	Walker	Mono	12-067-160	240	227
RBS.08	630RBS008	9/16/2013	Robinson_Ck	Walker	Mono	12-067-160	200	200
RBS.08	630RBS008	10/16/2013	Robinson_Ck	Walker	Mono	12-067-160	92	92
RBS.08	630RBS008	5/13/2014	Robinson_Ck	Walker	Mono	13-054-160	11	11
RBS.08	630RBS008	6/17/2014	Robinson_Ck	Walker	Mono	13-054-160	114	105
RBS.08	630RBS008	7/22/2014	Robinson_Ck	Walker	Mono	13-054-160	280	235
RBS.08	630RBS008	8/17/2014	Robinson_Ck	Walker	Mono	13-054-160	64	64
RBS.08	630RBS008	9/22/2014	Robinson_Ck	Walker	Mono	13-054-160	132	128
RBS.08	630RBS008	10/21/2014	Robinson_Ck	Walker	Mono	13-054-160	332	316
RBS.10		6/3/2014	Robinson_Ck	Walker	Mono	13-054-160	28	28
RBS.10		8/21/2014	Robinson_Ck	Walker	Mono	13-054-160	200	200
ROC.10		7/26/2012	Rock_Ck	Owens	Inyo	11-167-160	2	2
ROC.10		5/28/2013	Rock_Ck	Owens	Inyo	12-067-160	0	0
ROC.10		7/8/2013	Rock_Ck	Owens	Inyo	12-067-160	0	0
ROC.10		7/31/2013	Rock_Ck	Owens	Inyo	12-067-160	0	0
ROC.10		9/12/2013	Rock_Ck	Owens	Inyo	12-067-160	9	9
ROC.10		10/15/2013	Rock_Ck	Owens	Inyo	12-067-160	0	0
ROC.20		7/26/2012	Rock_Ck	Owens	Mono	11-167-160	1	1
ROC.20		4/22/2013	Rock_Ck	Owens	Mono	12-067-160	0	0
ROC.20		5/28/2013	Rock_Ck	Owens	Mono	12-067-160	0	0
ROC.20		7/8/2013	Rock_Ck	Owens	Mono	12-067-160	1	1
ROC.20		7/31/2013	Rock_Ck	Owens	Mono	12-067-160	5	5
ROC.20		9/12/2013	Rock_Ck	Owens	Mono	12-067-160	4	4
ROC.20		10/15/2013	Rock_Ck	Owens	Mono	12-067-160	0	0
ROC.30		7/26/2012	Rock_Ck	Owens	Mono	11-167-160	3	3
ROC.30		4/22/2013	Rock_Ck	Owens	Mono	12-067-160	0	0
ROC.30		5/28/2013	Rock_Ck	Owens	Mono	12-067-160	0	0
ROC.30		7/8/2013	Rock_Ck	Owens	Mono	12-067-160	6	6
ROC.30		7/31/2013	Rock_Ck	Owens	Mono	12-067-160	6	6
ROC.30		9/12/2013	Rock_Ck	Owens	Mono	12-067-160	22	22
ROC.30		10/15/2013	Rock_Ck	Owens	Mono	12-067-160	1	1
ROC.40		7/31/2014	Rock_Ck	Owens	Mono	12-067-160	7	7
ROC.40		8/20/2014	Rock_Ck	Owens	Mono	12-067-160	1	1
ROC.80		5/14/2014	Rock_Ck	Owens	Inyo	13-054-160	6	2
ROC.80		6/18/2014	Rock_Ck	Owens	Inyo	13-054-160	128	120
ROC.80		7/23/2014	Rock_Ck	Owens	Inyo	13-054-160	24	24
ROC.80		8/18/2014	Rock_Ck	Owens	Inyo	13-054-160	7	7
ROC.80		8/20/2014	Rock_Ck	Owens	Inyo	12-067-160	7	7
ROC.80		9/24/2014	Rock_Ck	Owens	Inyo	13-054-160	25	25
ROC.80		10/22/2014	Rock_Ck	Owens	Inyo	13-054-160	5	5
RUS.10		9/26/2012	Rush_Ck	Mono	Mono	11-167-160	0	0
RUS.10		4/24/2013	Rush_Ck	Mono	Mono	12-067-160	0	0
RUS.10		5/30/2013	Rush_Ck	Mono	Mono	12-067-160	0	0

SNARL ID	SWAMP ID	Sampling Date	Stream	Drainage	County	Contract ID	fcoli100	ecoli100
RUS.10		7/7/2013	Rush_Ck	Mono	Mono	12-067-160	4	4
RUS.10		7/30/2013	Rush_Ck	Mono	Mono	12-067-160	5	5
RUS.10		9/17/2013	Rush_Ck	Mono	Mono	12-067-160	1	1
RUS.10		10/17/2013	Rush_Ck	Mono	Mono	12-067-160	0	0
RUS.20		9/26/2012	Rush_Ck	Mono	Mono	11-167-160	90	80
RUS.20		3/13/2013	Rush_Ck	Mono	Mono	11-167-160	5	5
RUS.20		4/24/2013	Rush_Ck	Mono	Mono	12-067-160	2	2
RUS.20		5/30/2013	Rush_Ck	Mono	Mono	12-067-160	18	8
RUS.20		7/7/2013	Rush_Ck	Mono	Mono	12-067-160	43	43
RUS.20		7/30/2013	Rush_Ck	Mono	Mono	12-067-160	168	160
RUS.20		9/17/2013	Rush_Ck	Mono	Mono	12-067-160	93	74
RUS.20		10/17/2013	Rush_Ck	Mono	Mono	12-067-160	19	19
RUS.30		9/26/2012	Rush_Ck	Mono	Mono	11-167-160	0	0
RUS.30		3/13/2013	Rush_Ck	Mono	Mono	11-167-160	0	0
RUS.30		4/24/2013	Rush_Ck	Mono	Mono	12-067-160	0	0
RUS.30		5/30/2013	Rush_Ck	Mono	Mono	12-067-160	0	0
RUS.30		7/7/2013	Rush_Ck	Mono	Mono	12-067-160	0	0
RUS.30		7/30/2013	Rush_Ck	Mono	Mono	12-067-160	0	0
RUS.30		9/17/2013	Rush_Ck	Mono	Mono	12-067-160	0	0
RUS.30		10/17/2013	Rush_Ck	Mono	Mono	12-067-160	0	0
RUS.50		9/26/2012	Rush_Ck	Mono	Mono	11-167-160	0	0
RUS.50		4/24/2013	Rush_Ck	Mono	Mono	12-067-160	1	1
RUS.50		5/30/2013	Rush_Ck	Mono	Mono	12-067-160	3	3
RUS.50		7/7/2013	Rush_Ck	Mono	Mono	12-067-160	4	3
RUS.50		7/30/2013	Rush_Ck	Mono	Mono	12-067-160	10	9
RUS.50		9/17/2013	Rush_Ck	Mono	Mono	12-067-160	6	6
RUS.50		10/17/2013	Rush_Ck	Mono	Mono	12-067-160	2	2
RUS.70		9/26/2012	Rush_Ck	Mono	Mono	11-167-160	37	9
RUS.70		3/12/2013	Rush_Ck	Mono	Mono	11-167-160	0	0
RUS.70		4/24/2013	Rush_Ck	Mono	Mono	12-067-160	0	0
RUS.70		5/30/2013	Rush_Ck	Mono	Mono	12-067-160	0	0
RUS.70		7/7/2013	Rush_Ck	Mono	Mono	12-067-160	11	10
RUS.70		7/30/2013	Rush_Ck	Mono	Mono	12-067-160	6	4
RUS.70		9/17/2013	Rush_Ck	Mono	Mono	12-067-160	6	5
RUS.70		10/17/2013	Rush_Ck	Mono	Mono	12-067-160	1	1
RUS.80		9/26/2012	Rush_Ck	Mono	Mono	11-167-160	7	7
RUS.80		3/12/2013	Rush_Ck	Mono	Mono	11-167-160	0	0
RUS.80		4/24/2013	Rush_Ck	Mono	Mono	12-067-160	2	2
RUS.80		5/30/2013	Rush_Ck	Mono	Mono	12-067-160	4	4
RUS.80		7/7/2013	Rush_Ck	Mono	Mono	12-067-160	10	8
RUS.80		7/30/2013	Rush_Ck	Mono	Mono	12-067-160	43	30
RUS.80		9/17/2013	Rush_Ck	Mono	Mono	12-067-160	6	6
RUS.80		10/17/2013	Rush_Ck	Mono	Mono	12-067-160	0	0
SAW.50		7/29/2014	Sawmill_Ck	Owens	Inyo	12-067-160	18	14
SAW.50		8/19/2014	Sawmill_Ck	Owens	Inyo	12-067-160	23	22
SHE.50		7/29/2014	Shepherd_Ck	Owens	Inyo	12-067-160	1	1
SHE.50		8/19/2014	Shepherd_Ck	Owens	Inyo	12-067-160	0	0

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SIL.50		7/31/2014	Silver_Ck	Owens	Inyo	12-067-160	2	0
SIL.50		8/20/2014	Silver_Ck	Owens	Inyo	12-067-160	0	0
SWA.02		9/18/2012	Swauger_Ck	Walker	Mono	11-167-160	5	5
SWA.02		3/25/2013	Swauger_Ck	Walker	Mono	11-167-160	6	6
SWA.02		4/23/2013	Swauger_Ck	Walker	Mono	12-067-160	3	3
SWA.02		5/29/2013	Swauger_Ck	Walker	Mono	12-067-160	3	3
SWA.02		7/6/2013	Swauger_Ck	Walker	Mono	12-067-160	30	18
SWA.02		7/29/2013	Swauger_Ck	Walker	Mono	12-067-160	46	46
SWA.02		9/16/2013	Swauger_Ck	Walker	Mono	12-067-160	43	42
SWA.02		10/16/2013	Swauger_Ck	Walker	Mono	12-067-160	3	3
SWA.02		5/13/2014	Swauger_Ck	Walker	Mono	13-054-160	0	0
SWA.02		6/17/2014	Swauger_Ck	Walker	Mono	13-054-160	3	3
SWA.02		7/22/2014	Swauger_Ck	Walker	Mono	13-054-160	16	16
SWA.02		8/17/2014	Swauger_Ck	Walker	Mono	13-054-160	7	7
SWA.02		9/22/2014	Swauger_Ck	Walker	Mono	13-054-160	5	2
SWA.02		10/21/2014	Swauger_Ck	Walker	Mono	13-054-160	4	2
SWA.05	630SWA005	8/14/2012	Swauger_Ck	Walker	Mono	11-167-160	95	95
SWA.05	630SWA005	9/18/2012	Swauger_Ck	Walker	Mono	11-167-160	157	110
SWA.05	630SWA005	3/25/2013	Swauger_Ck	Walker	Mono	11-167-160	15	14
SWA.05	630SWA005	4/23/2013	Swauger_Ck	Walker	Mono	12-067-160	2	2
SWA.05	630SWA005	5/29/2013	Swauger_Ck	Walker	Mono	12-067-160	30	29
SWA.05	630SWA005	7/6/2013	Swauger_Ck	Walker	Mono	12-067-160	460	400
SWA.05	630SWA005	7/29/2013	Swauger_Ck	Walker	Mono	12-067-160	93	93
SWA.05	630SWA005	9/16/2013	Swauger_Ck	Walker	Mono	12-067-160	107	90
SWA.05	630SWA005	10/16/2013	Swauger_Ck	Walker	Mono	12-067-160	64	60
SWA.05	630SWA005	5/13/2014	Swauger_Ck	Walker	Mono	13-054-160	8	8
SWA.05	630SWA005	6/17/2014	Swauger_Ck	Walker	Mono	13-054-160	583	550
SWA.05	630SWA005	7/22/2014	Swauger_Ck	Walker	Mono	13-054-160	185	185
SWA.05	630SWA005	8/17/2014	Swauger_Ck	Walker	Mono	13-054-160	184	184
SWA.05	630SWA005	9/22/2014	Swauger_Ck	Walker	Mono	13-054-160	18	18
SWA.05	630SWA005	10/21/2014	Swauger_Ck	Walker	Mono	13-054-160	10	9
SWA.06	630SWA006	8/14/2012	Swauger_Ck	Walker	Mono	11-167-160	120	108
SWA.06	630SWA006	9/18/2012	Swauger_Ck	Walker	Mono	11-167-160	197	190
SWA.06	630SWA006	3/25/2013	Swauger_Ck	Walker	Mono	11-167-160	4	4
SWA.06	630SWA006	4/23/2013	Swauger_Ck	Walker	Mono	12-067-160	2	0
SWA.06	630SWA006	5/29/2013	Swauger_Ck	Walker	Mono	12-067-160	7	7
SWA.06	630SWA006	7/6/2013	Swauger_Ck	Walker	Mono	12-067-160	130	114
SWA.06	630SWA006	7/29/2013	Swauger_Ck	Walker	Mono	12-067-160	77	67
SWA.06	630SWA006	9/16/2013	Swauger_Ck	Walker	Mono	12-067-160	80	80
SWA.06	630SWA006	10/16/2013	Swauger_Ck	Walker	Mono	12-067-160	14	9
SWA.06	630SWA006	5/13/2014	Swauger_Ck	Walker	Mono	13-054-160	1	1
SWA.06	630SWA006	6/17/2014	Swauger_Ck	Walker	Mono	13-054-160	18	17
SWA.06	630SWA006	7/22/2014	Swauger_Ck	Walker	Mono	13-054-160	222	192
SWA.06	630SWA006	8/17/2014	Swauger_Ck	Walker	Mono	13-054-160	104	48
SWA.06	630SWA006	9/22/2014	Swauger_Ck	Walker	Mono	13-054-160	36	34
SWA.06	630SWA006	10/21/2014	Swauger_Ck	Walker	Mono	13-054-160	12	10
SWA.08		5/13/2014	Swauger_Ck	Walker	Mono	13-054-160	11	11

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SWA.08		6/17/2014	Swauger_Ck	Walker	Mono	13-054-160	18	15
SWA.08		7/22/2014	Swauger_Ck	Walker	Mono	13-054-160	54	46
SWA.08		8/17/2014	Swauger_Ck	Walker	Mono	13-054-160	192	44
SWA.08		9/22/2014	Swauger_Ck	Walker	Mono	13-054-160	86	66
SWA.08		10/21/2014	Swauger_Ck	Walker	Mono	13-054-160	30	30
SYM.50		7/29/2014	Symmes_Ck	Owens	Inyo	12-067-160	26	26
SYM.50		8/19/2014	Symmes_Ck	Owens	Inyo	12-067-160	7	5
TAB.50		7/29/2014	Taboose_Ck	Owens	Inyo	12-067-160	0	0
TAB.50		8/19/2014	Taboose_Ck	Owens	Inyo	12-067-160	1	1
TUT.50		7/29/2014	Tuttle_Ck	Owens	Inyo	12-067-160	21	21
TUT.50		8/19/2014	Tuttle_Ck	Owens	Inyo	12-067-160	13	11
VIR.03		3/25/2013	Virginia_Ck	Walker	Mono	11-167-160	0	0
VIR.03		4/23/2013	Virginia_Ck	Walker	Mono	12-067-160	0	0
VIR.03		5/29/2013	Virginia_Ck	Walker	Mono	12-067-160	1	1
VIR.03		7/6/2013	Virginia_Ck	Walker	Mono	12-067-160	20	8
VIR.03		7/29/2013	Virginia_Ck	Walker	Mono	12-067-160	50	45
VIR.03		9/16/2013	Virginia_Ck	Walker	Mono	12-067-160	37	37
VIR.03		10/16/2013	Virginia_Ck	Walker	Mono	12-067-160	1	1
VIR.04	630VIR004	8/14/2012	Virginia_Ck	Walker	Mono	11-167-160	34	31
VIR.04	630VIR004	3/25/2013	Virginia_Ck	Walker	Mono	11-167-160	0	0
VIR.04	630VIR004	4/23/2013	Virginia_Ck	Walker	Mono	12-067-160	0	0
VIR.04	630VIR004	5/29/2013	Virginia_Ck	Walker	Mono	12-067-160	2	2
VIR.04	630VIR004	7/6/2013	Virginia_Ck	Walker	Mono	12-067-160	142	118
VIR.04	630VIR004	7/29/2013	Virginia_Ck	Walker	Mono	12-067-160	14	14
VIR.04	630VIR004	9/16/2013	Virginia_Ck	Walker	Mono	12-067-160	40	13
VIR.04	630VIR004	10/16/2013	Virginia_Ck	Walker	Mono	12-067-160	3	3
VIR.04	630VIR004	5/13/2014	Virginia_Ck	Walker	Mono	13-054-160	1	1
VIR.04	630VIR004	6/17/2014	Virginia_Ck	Walker	Mono	13-054-160	27	21
VIR.04	630VIR004	7/22/2014	Virginia_Ck	Walker	Mono	13-054-160	20	20
VIR.04	630VIR004	8/17/2014	Virginia_Ck	Walker	Mono	13-054-160	7	7
VIR.04	630VIR004	9/22/2014	Virginia_Ck	Walker	Mono	13-054-160	19	19
VIR.04	630VIR004	10/21/2014	Virginia_Ck	Walker	Mono	13-054-160	22	22
VIR.05	630VIR005	8/14/2012	Virginia_Ck	Walker	Mono	11-167-160	96	96
VIR.05	630VIR005	3/25/2013	Virginia_Ck	Walker	Mono	11-167-160	0	0
VIR.05	630VIR005	4/23/2013	Virginia_Ck	Walker	Mono	12-067-160	0	0
VIR.05	630VIR005	5/29/2013	Virginia_Ck	Walker	Mono	12-067-160	1	1
VIR.05	630VIR005	7/6/2013	Virginia_Ck	Walker	Mono	12-067-160	122	45
VIR.05	630VIR005	7/29/2013	Virginia_Ck	Walker	Mono	12-067-160	38	38
VIR.05	630VIR005	9/16/2013	Virginia_Ck	Walker	Mono	12-067-160	7	7
VIR.05	630VIR005	10/16/2013	Virginia_Ck	Walker	Mono	12-067-160	2	2
VIR.10		6/3/2014	Virginia_Ck	Walker	Mono	13-054-160	0	0
VIR.20		6/3/2014	Virginia_Ck	Walker	Mono	13-054-160	2	2
VIR.20		8/21/2014	Virginia_Ck	Walker	Mono	13-054-160	22	19
WAL.05		9/24/2012	Walker_Ck	Mono	Mono	11-167-160	0	0
WAL.10		7/26/2012	Walker_Ck	Mono	Mono	11-167-160	6	3
WAL.10		9/24/2012	Walker_Ck	Mono	Mono	11-167-160	65	40
WAL.10		3/12/2013	Walker_Ck	Mono	Mono	11-167-160	0	0

SNARL ID	SWAMP ID	Sampling Date	Stream	Drainage	County	Contract ID	fcoli100	ecoli100
WAL.10		4/24/2013	Walker_Ck	Mono	Mono	12-067-160	0	0
WAL.10		5/31/2013	Walker_Ck	Mono	Mono	12-067-160	0	0
WAL.10		7/7/2013	Walker_Ck	Mono	Mono	12-067-160	4	4
WAL.10		7/29/2013	Walker_Ck	Mono	Mono	12-067-160	9	9
WAL.10		9/17/2013	Walker_Ck	Mono	Mono	12-067-160	52	32
WAL.10		10/17/2013	Walker_Ck	Mono	Mono	12-067-160	0	0

Appendix C. Description of the State Water Resources Control Board contracts under which samples included in the landscape-scale analyses were collected.

To maximize the generality of our landscape-scale analyses, we did not limit the samples that were included in the analysis to those collected under Contract 12-067-160 (the contract for which the current report was prepared). Instead, all samples collected under Contracts 11-167-160, 12-067-160, and 13-054-160 during the 2012-2014 period were included. The following table provides a description of the samples that were collected under each contract.

Contract number	Number of samples	Samples per county	Collection dates (range)
11-167-160	98	Mono: 97 Inyo: 1	25-Jul-2012 to 25-Mar-2013
12-067-160	377	Mono: 317 Inyo: 60	22-Apr-2013 to 20-Aug-2014
13-054-160	230	Mono: 140 Inyo: 90	12-May-2014 to 22-Oct-2014

Appendix D. Description of all sites sampled for microbial source tracking (MST) analyses by personnel from the Surface Water Ambient Monitoring Program. MST results are provided in Appendix F.

SWAMP ID	SNARL ID	Location Description	Latitude	Longitude
603BSP002		Bishop Ck Canal at East Line St.	37.3616	-118.3861
603BSP003		Bishop Ck Canal above South Fork Bishop Ck	37.3679	-118.3862
603BSP004	BIS.60	South Fork Bishop Ck above Bishop Ck Canal	37.3679	-118.3863
603BSP005		South Fork Bishop Ck at Hanby St.	37.3678	-118.3885
603BSP010		South Fork Bishop Ck at Home St.	37.3689	-118.4022
603BSP021		North Fork Bishop Ck above Bishop Ck Canal	37.3801	-118.4047
603BSP111	BIS.10	Bishop Ck at National Forest Boundary	37.3303	-118.4958
603BSPB50	BIS.30	South Fork Bishop Ck @ Brockman Lane	37.3640	-118.4318
603BSPB60	BIS.31	North Fork Bishop Ck @ Brockman Lane	37.3686	-118.4322
603BSPB65	BIS.21	North Fork Bishop Ck @ Mumy Lane	37.3588	-118.4503
630BUC004		North Branch Buckeye Ck, upstream of bridge	38.2637	-119.2773
630BUC005		Middle Branch Buckeye Ck, upstream of bridge	38.2622	-119.2758
630RBS007		North Branch Robinson Ck, upstream of bridge	38.2597	-119.2735
630RBS008		South Branch Robinson Ck, upstream of bridge	38.2585	-119.2723
630SWA005		Swauger Ck below Huntoon Valley	38.2959	-119.3097
630SWA006		Swauger Ck above Huntoon Valley	38.3428	-119.3231
630VIRB01		Virginia Ck below Green Ck Road	38.1983	-119.2206
632ECR005		East Fork Carson River, at USGS gage below Markleeville	38.7154	-119.7644
632ECRB10		East Fork Carson River, above Hangmans bridge	38.6896	-119.7639
632MLBB01		Confluence Millberry Ck with Markleeville Ck	38.6950	-119.7785
632MLBB03		Millberry Ck at 30 mph Sign	38.6969	-119.7818
632MRKB02		Markeeville Ck at USFS Campground	38.6965	-119.7740
632MRKB03		Markleeville Ck at Swim Hole	38.6938	-119.7795
632MRKB04		Markleeville Ck at Library Bridge	38.6933	-119.7818
632WLFB01		Wolf Ck, above East Fork Carson River	38.6137	-119.6924
632WLFB10		Wolf Ck, below Ranch	38.6007	-119.6889
633WFCB02		West Fork Carson River at Paynesville Bridge	38.8089	-119.7771
634TRTB02		Trout Ck, at confluence with South Upper Truckee	38.9416	-119.9960
637SUS001		Susan River @ Litchfield	40.3777	-120.3951

Appendix E. *Enterococcus*, Bacteroidales, and *Escherichia* qPCR assay Standard Operating Procedures.

Dr. Craig E. Nelson, January 2015
Standardized to USEPA document EPA-821-R-10-004: "Method A: Enterococci in Water by TaqMan® Quantitative Polymerase Chain Reaction (qPCR) Assay" (April 2010)

Laboratory Details and Sample Handling:
Sample collection and handling are described in the CESAME QA/QC Section E: Appendix. All equipment guidelines in EPA-821-R-10-004 are met. Reagent preparation is done in a bleach- and UV-sterilized laminar flow hood. Sample preparation (membrane filtration and subsequent DNA extraction) is done in separate laboratories, with DNA extraction done in benchtop area separated from reagent preparation that is bleach- and ethanol- cleaned after each use. Handling of amplified DNA is isolated to a separate room to avoid contamination of samples and reagents. All materials are disposed of according to institutional guidelines for biohazardous waste. Quantitative PCR is done on an Applied Biosystems StepOnePlus or ABI7300 or Eppendorf Mastercycler® ep realplex. All recommended safety guidelines are followed in accordance with EPA-821-R-10-004 and institutional recommendations.

Reagents and Standards:

1) DNA Extraction Kits: MoBio PowerSoil® DNA Isolation Kit (12888)
2) qPCR Master Mix: 5Prime RealMasterMix Probe (2200710)
3) Primer and Probes – Table 2 above: Integrated DNA Technologies PrimeTime® Assays
4) Standards: Genomic DNA from the American Type Culture Collection or IDT gBlocks synthetics:
    a. Entero1a: *Enterococcus faecalis* strain V583 (ATCC® 700802D-5™)
    b. EC23S857: *Escherichia coli* strain Crooks (ATCC® 8739D-5™)
    c. GenBac3: *Bacteroides thetaiotamicron* Strain VPI 5482 [ATCC® 29148™]
    d. BacHum and HF183: IDT gBlocks dsDNA sequence AB242142.1 (Green et al. 2014). 16S rRNA gene sequence for the type strain of *Bacteroides dorei* Strain DSM 17855.
    e. BacCow: IDT gBlocks dsDNA sequence AF233400.1 (Bernhardt et al. 2000, Layton et al. 2009) – 16S rRNA gene sequence for uncultured clone CF123.

Quality Control Summary:

1) Method Blanks: A volume of 800 mL autoclaved deionized (Milli-Q) sterile water is filtered on every sampling date (4-8 samples) & filter and DNA extraction proceeds as for samples.
2) Positive and Negative Controls: Every day that samples are analyzed, or when reagents are changed,both control cultures are run for each assay (20,000 copies) to check for both positive and negative results for the target and non-target assay respectively.
3) No Template Controls (NTCs): Every day that samples are analyzed, on every plate, three wells are devoted to NTCs consisting of DNA elution buffer (Tris-EDTA).
4) DNA Standards and Standard Curves: Extracted genomic DNA or gBlocks synthetic DNA (see above) is quantitated (see below) and. Calculations are used to estimate copy number (see below). A composite standard dilution series is run in triplicate on each assay plate (see below) and analyzed using least squares log-linear regressions predicting Ct from Standard Quantity (Copies per Well).

These regressions are standard curve equations to calculate Quantity from Ct for Samples and Controls.

Sample Analysis

1) DNA Extractions – Follow the MoBio Kit Directions with filter in bead tube: Elute 100 uL
2) Standard Dilution Series – See Below
3) qPCR Assays:
    a. Dilute working stocks of Standards and Control Samples to target correct copies per well in 5 uL volumes.
    b. Dilute Samples 1:5 to reduce inhibition; thus 5uL of Diluted = 1 uL sample per well
    c. Prepare qPCR Master Mix as follows for each sample (plus 10% extra for pipet error)
        i. 10uL of 5Prime RealMasterMix Probe (2.5X, without ROX), 0.25uL BSA 100X stock for 0.1 mg/mL final, 0.05uL Probe and 0.10 uL Primer (both 100 uM stock) for 200/400 nM final, 10uL Water. Multiply everything 100X for a full 96-well plate.
    d. Prepare assay plate 20 uL Master Mix per well for the following 96 well layout:
        i. Single wells for each of 64 samples or Triplicate wells for each of 21 samples (including method blanks) – 64 or 63 wells, respectively
        ii. Triplicate wells for each 8-position standard dilution series – 24 wells
        iii. Triplicate wells for NTCs, Positive Controls, Negative Controls – 8 wells
    e. Aliquot Samples, Standards, and Controls 5 uL each to wells
    f. Cap and centrifuge plate 1000 RPM for 1 min, check for bubbles
    g. Set up Run Details with FAM Detection, ROX Background (depending on machine used), Auto Baseline, Ct Threshold = 0.03 or 300, depending on machine
    h. Run Reactions 2 min 95°C followed by 45 cycles of 15s 95°C and 30s 60°C
4) Data analysis and calculation of sample copy numbers from standards.
    a. Standard curves yield gene copies per 1 uL of sample analyzed
    b. 1 uL sample analyzed is 1% of total sample collected if using a 100 uL elution.
    c. sample volume filtered (e.g. 800 mL) = 8 mL sample per 1 uL DNA analyzed
    d. Data are reported and calculated as Copies/100 mL = Quantity/8 mL

Standard Dilution and Preparation

1) Standards are purchased at a nominal amount of 5000 ng (typically more)
2) Genomic Standards are converted to gene copies using the following conversion factors:
   6.02E23 bp mol^{-1} / 660 g mol^{-1} = 9.12E11 bp ng^{-1} * ng purchased = total bp
   bp / bp $genome^{-1}$ = genomes * rRNA genes $genome^{-1}$ = total rRNA genes purchased
   Enterococcus faecalis V583: 3,359,974 bp genome with 4 copies of 23S gene
   Escherichia coli 8739: 4,746,218 bp genome with 7 copies of 23S gene
3) Standards are diluted with Tris-EDTA (TE) 750 uL – Primary Stock
4) Primary Stock is quantitated with PicoGreen on Invitrogen Qubit system
    a. Final concentrations typically 5-20 ng/uL, 10-20 million copies/uL
5) Standard Stock Solutions are aliquotted from the Primary Stock as follows:
    a. Master Stock is prepped at 1 million copies/uL (~5-10%) (1m storage)

b. Working Stock is prepped at 10,000 copies/uL (1:100) (destroy after thaw)
c. Dilution series are prepped by serial dilution planning for 15 uL per well. This is then aliquotted across three wells of the plate for a final of 5 uL per well in triplicate.
    i. 50,000 copies (15uL Working Stock - WS)
    ii. 10,000 copies (3uL WS + 12uL water)
    iii. 5,000 copies (1:10 of row A)
    iv. 1,000 copies (1:10 of row B)
    v. 500 copies (1:10 of row C)
    vi. 100 copies (1:10 of row D)
    vii. 50 copies (1:10 of row E)
    viii. 10 copies (1:10 of row F)
    ix. This series is best accomplished as follows according to Rows
        A. 17 uL of WS, remove 1.7uL for Row C
        B. 3.4 uL of WS, add 13.6 water, remove 1.7ul for Row D
        C. 15.3uL of water, add 1.7uL Row A, remove 1.7uL for Row E
        D. 15.3uL of water, add 1.7uL Row B, remove 1.7uL for Row F
        E. 15.3uL of water, add 1.7uL Row C, remove 1.7uL for Row G
        F. 15.3uL of water, add 1.7uL Row D, remove 1.7uL for Row H
        G. 15.3uL of water, add 1.7uL Row E
        H. 15.3uL of water, add 1.7uL Row F

Appendix F. MST gene concentrations obtained from the six qPCR assays applied to each of the 165 samples. ND = Not detected. Sampling locations for samples collected by the Sierra Nevada Aquatic Research Laboratory (Project = SNARL) are provided in Appendix A, and those collected under the Surface Water Ambient Monitoring Program (Project = SWAMP) are provided in Appendix D.

Site ID	Date	Project	Laboratory for Filter Collection	mL Filtered	BacCow Copies/ 100mL	BacHum Copies/ 100mL	HF183 Copies/ 100mL	GenBac3 Copies/ 100mL	Entero1a Copies/ 100mL	*E. coli* Copies/ 100mL
BUC.02	9/18/2012	SNARL	SNARL	800	ND	ND	ND	ND	ND	170
BUC.03	9/18/2012	SNARL	SNARL	800	712	ND	ND	5967	1248	251
BUC.04	8/14/2012	SNARL	SNARL	800	5261	ND	ND	140029	7575	9667
BUC.04	9/18/2012	SNARL	SNARL	800	2941	ND	ND	51271	4618	7214
BUC.05	8/14/2012	SNARL	SNARL	800	3960	ND	ND	131011	5621	11267
CON.10	7/25/2012	SNARL	SNARL	800	ND	ND	ND	5463	1644	ND
CON.20	7/25/2012	SNARL	SNARL	800	1274	ND	ND	7639	4497	2098
CON.30	7/25/2012	SNARL	SNARL	800	52342	ND	ND	280636	11048	19858
CON.40	7/25/2012	SNARL	SNARL	800	59464	ND	ND	95127	3432	11861
EWK.06	8/14/2012	SNARL	SNARL	800	56655	ND	ND	301950	8524	16082
HIL.20	9/17/2012	SNARL	SNARL	800	329	ND	ND	15797	1618	619
LEE.10	7/26/2012	SNARL	SNARL	800	ND	ND	ND	2804	2075	540
LEE.10	8/13/2012	SNARL	SNARL	800	ND	ND	ND	2642	2008	325
LEE.15	8/13/2012	SNARL	SNARL	800	ND	ND	ND	3398	1044	528
LEE.17	8/13/2012	SNARL	SNARL	800	ND	ND	ND	21724	2844	1394
LEE.20	7/26/2012	SNARL	SNARL	800	ND	ND	ND	13180	3298	4075
LEE.20	8/13/2012	SNARL	SNARL	800	315	ND	ND	23895	5046	536
LEE.30	8/13/2012	SNARL	SNARL	800	217	ND	ND	17243	5844	1426
MAM.10	7/25/2012	SNARL	SNARL	800	ND	ND	ND	23429	6498	358
MAM.20	7/25/2012	SNARL	SNARL	800	ND	ND	ND	13272	10157	3354
MAM.30	7/25/2012	SNARL	SNARL	800	886	ND	ND	44352	10015	5856
MAM.40	7/25/2012	SNARL	SNARL	800	4168	ND	ND	54619	10014	7043
MAM.50	7/25/2012	SNARL	SNARL	800	2234	ND	ND	27570	4439	1354
MCG.15	9/17/2012	SNARL	SNARL	800	143	ND	ND	2403	1139	ND
MCG.17	9/17/2012	SNARL	SNARL	800	ND	ND	ND	15080	2086	322
MCG.20	7/26/2012	SNARL	SNARL	800	ND	ND	ND	3479	1021	2724
MCG.20	9/17/2012	SNARL	SNARL	800	162	ND	ND	5373	2148	1274
MCG.30	9/17/2012	SNARL	SNARL	800	203	ND	ND	19285	1716	733
MIL.20	9/24/2012	SNARL	SNARL	800	ND	ND	ND	348	605	ND
MIL.30	9/24/2012	SNARL	SNARL	800	ND	ND	ND	793	145	ND
MIL.40	9/24/2012	SNARL	SNARL	800	197	ND	ND	89363	1667	519
MIL.60	9/24/2012	SNARL	SNARL	800	ND	ND	ND	9240	5335	ND
MIL.80	9/24/2012	SNARL	SNARL	800	3849	ND	ND	21936	11832	1465
OWE.10	9/26/2012	SNARL	SNARL	800	ND	ND	ND	6918	6817	ND
OWE.15	9/26/2012	SNARL	SNARL	800	ND	ND	ND	5845	1097	729
OWE.20	9/26/2012	SNARL	SNARL	800	ND	ND	ND	153	242	ND
PAR.20	9/24/2012	SNARL	SNARL	800	181	ND	ND	5705	3614	ND
PAR.30	9/24/2012	SNARL	SNARL	800	ND	ND	ND	8230	3259	ND
RBS.02	9/18/2012	SNARL	SNARL	800	200	ND	ND	22225	4501	276
RBS.04	9/18/2012	SNARL	SNARL	800	1502	ND	ND	27303	8039	1271
RBS.07	8/14/2012	SNARL	SNARL	800	62618	1076	1706	472452	14066	30722
RBS.07	9/18/2012	SNARL	SNARL	800	36493	ND	ND	344801	6716	8906
RBS.08	8/14/2012	SNARL	SNARL	800	125008	1685	2805	1376360	15854	44492

Site ID	Date	Project	Laboratory for Filter Collection	mL Filtered	BacCow Copies/ 100mL	BacHum Copies/ 100mL	HF183 Copies/ 100mL	GenBac3 Copies/ 100mL	Entero1a Copies/ 100mL	*E. coli* Copies/ 100mL
ROC.10	7/26/2012	SNARL	SNARL	800	ND	ND	ND	12968	2442	ND
ROC.20	7/26/2012	SNARL	SNARL	800	ND	ND	ND	12040	3085	402
ROC.30	7/26/2012	SNARL	SNARL	800	ND	ND	ND	19945	6360	2039
RUS.10	9/26/2012	SNARL	SNARL	800	ND	ND	ND	ND	287	ND
RUS.20	9/26/2012	SNARL	SNARL	800	221	ND	ND	10174	5812	2585
RUS.30	9/26/2012	SNARL	SNARL	800	ND	ND	ND	293	236	263
RUS.50	9/26/2012	SNARL	SNARL	800	299	ND	ND	5612	2963	ND
RUS.70	9/26/2012	SNARL	SNARL	800	170	ND	ND	9134	9246	272
RUS.80	9/26/2012	SNARL	SNARL	800	179	ND	ND	35215	4580	431
SWA.02	9/18/2012	SNARL	SNARL	800	ND	ND	ND	41703	4215	910
SWA.05	8/14/2012	SNARL	SNARL	800	4838	ND	ND	235232	15714	11148
SWA.05	9/18/2012	SNARL	SNARL	800	24759	ND	ND	134778	9063	10277
SWA.06	8/14/2012	SNARL	SNARL	800	502	ND	ND	99848	12855	11513
SWA.06	8/14/2012	SNARL	SNARL	800	502	ND	ND	99848	12855	11513
SWA.06	9/18/2012	SNARL	SNARL	800	3997	ND	ND	61970	5419	12713
VIR.04	8/14/2012	SNARL	SNARL	800	222	ND	ND	112712	10973	4884
VIR.05	8/14/2012	SNARL	SNARL	800	856	ND	ND	188924	12524	7651
WAL.05	9/24/2012	SNARL	SNARL	800	ND	ND	ND	ND	ND	ND
WAL.10	7/26/2012	SNARL	SNARL	800	ND	ND	ND	9923	8634	693
WAL.10	9/24/2012	SNARL	SNARL	800	ND	ND	ND	10060	3608	5308
603BSP002	6/11/2013	SWAMP	SNARL	400	18521	ND	ND	132847	2084	ND
603BSP002	9/4/2013	SWAMP	SNARL	700	28447	626	ND	171761	4552	1497
603BSP002	9/23/2013	SWAMP	SNARL	800	82748	ND	ND	122541	6914	1612
603BSP002	10/22/2013	SWAMP	SNARL	400	26702	ND	ND	93289	1885	ND
603BSP002	10/24/2013	SWAMP	SNARL	600	38684	ND	ND	85958	5344	1215
603BSP003	6/11/2013	SWAMP	SNARL	150	59304	ND	ND	335379	10663	ND
603BSP003	9/4/2013	SWAMP	SNARL	305	17356	2899	4195	104848	4107	2711
603BSP003	10/22/2013	SWAMP	SNARL	600	85320	ND	ND	59467	1698	ND
603BSP003	10/24/2013	SWAMP	SNARL	600	81205	ND	ND	75521	2141	803
603BSP004	6/11/2013	SWAMP	SNARL	350	867053	ND	ND	788955	17690	44671
603BSP004	7/25/2013	SWAMP	SNARL	400	176480	ND	ND	269397	8117	17699
603BSP004	8/21/2013	SWAMP	SNARL	700	82752	ND	ND	175216	11580	5676
603BSP004	9/4/2013	SWAMP	SNARL	800	96930	2114	668	431849	8663	18973
603BSP004	9/23/2013	SWAMP	SNARL	800	67233	ND	ND	519201	21628	41901
603BSP004	10/22/2013	SWAMP	SNARL	800	103876	ND	ND	387046	23611	6111
603BSP004	10/24/2013	SWAMP	SNARL	600	162240	ND	ND	815885	77615	36362
603BSP005	9/4/2013	SWAMP	SNARL	700	124732	ND	ND	320042	12252	24592
603BSP005	9/23/2013	SWAMP	SNARL	750	81552	ND	ND	501325	18878	84490
603BSP005	10/22/2013	SWAMP	SNARL	400	72843	ND	ND	308158	5751	ND
603BSP005	10/24/2013	SWAMP	SNARL	600	142671	ND	ND	811833	52299	17086
603BSP010	6/11/2013	SWAMP	SNARL	350	363227	ND	ND	261234	5549	1549
603BSP010	7/25/2013	SWAMP	SNARL	700	129764	ND	ND	189745	5160	2058
603BSP010	8/21/2013	SWAMP	SNARL	800	260528	ND	ND	160340	7739	2404
603BSP010	9/4/2013	SWAMP	SNARL	800	1014546	ND	ND	493984	4459	7745
603BSP010	9/23/2013	SWAMP	SNARL	750	42047	ND	ND	126233	2574	1094
603BSP010	10/22/2013	SWAMP	SNARL	800	39615	ND	ND	110375	1537	ND
603BSP010	10/24/2013	SWAMP	SNARL	750	25145	ND	ND	177095	1778	903
603BSP021	6/11/2013	SWAMP	SNARL	350	219375	ND	ND	345236	14029	12972
603BSP021	7/25/2013	SWAMP	SNARL	400	76914	ND	ND	169552	9735	557

Site ID	Date	Project	Laboratory for Filter Collection	mL Filtered	BacCow Copies/ 100mL	BacHum Copies/ 100mL	HF183 Copies/ 100mL	GenBac3 Copies/ 100mL	Entero1a Copies/ 100mL	*E. coli* Copies/ 100mL
603BSP021	8/21/2013	SWAMP	SNARL	800	386912	ND	ND	166855	7986	6779
603BSP021	9/4/2013	SWAMP	SNARL	800	211680	ND	ND	211899	4960	8097
603BSP021	9/23/2013	SWAMP	SNARL	750	362927	ND	ND	357343	19236	10090
603BSP021	10/22/2013	SWAMP	SNARL	800	173701	ND	ND	217240	5215	2266
603BSP021	10/24/2013	SWAMP	SNARL	800	97893	ND	ND	129439	4376	4930
603BSP111	6/11/2013	SWAMP	SNARL	400	1787	ND	ND	76825	4126	ND
603BSPB50	7/25/2013	SWAMP	SNARL	600	12287	ND	ND	64720	13940	4003
603BSPB50	8/21/2013	SWAMP	SNARL	800	11568	ND	ND	95061	9052	1121
603BSPB50	9/4/2013	SWAMP	SNARL	800	25138	ND	ND	125629	5622	2151
603BSPB50	9/23/2013	SWAMP	SNARL	700	28588	ND	ND	116484	7562	3070
603BSPB50	10/22/2013	SWAMP	SNARL	600	28472	ND	ND	89897	2265	1671
603BSPB50	10/24/2013	SWAMP	SNARL	100	310712	ND	ND	727167	46119	12990
603BSPB60	7/25/2013	SWAMP	SNARL	600	7421	ND	ND	78199	10714	13185
603BSPB60	8/21/2013	SWAMP	SNARL	800	56551	ND	ND	107127	5986	3533
603BSPB60	9/4/2013	SWAMP	SNARL	800	9974	ND	ND	118934	7224	5633
603BSPB60	9/23/2013	SWAMP	SNARL	800	252913	ND	ND	263796	11131	4716
603BSPB60	10/22/2013	SWAMP	SNARL	800	210637	ND	ND	229469	4991	2043
603BSPB60	10/24/2013	SWAMP	SNARL	800	77214	ND	ND	178012	1731	2028
603BSPB65	9/4/2013	SWAMP	SNARL	350	2551	ND	ND	69481	5549	ND
630BUC004	7/10/2013	SWAMP	Lahontan	800	11271	ND	ND	48200	423	2290
630BUC005	7/10/2013	SWAMP	Lahontan	600	937	ND	ND	18354	ND	ND
630RBS007	7/10/2013	SWAMP	Lahontan	600	184093	ND	ND	374399	1100	2970
630RBS008	7/10/2013	SWAMP	Lahontan	700	90038	ND	ND	173753	656	4380
630SWA005	7/10/2013	SWAMP	Lahontan	600	340459	ND	ND	508818	765	4935
630SWA005	10/24/2013	SWAMP	Lahontan	800	6141	ND	ND	224915	3462	ND
630SWA006	7/10/2013	SWAMP	Lahontan	600	435	ND	ND	52494	ND	ND
630VIRB01	10/24/2013	SWAMP	Lahontan	500	23965	ND	ND	203951	704	1115
632ECR005	8/19/2013	SWAMP	Lahontan	700	751056	ND	ND	513431	1356	3270
632ECR005	8/21/2013	SWAMP	Lahontan	800	457933	ND	ND	58244	770	3600
632ECR005	9/25/2013	SWAMP	Lahontan	350	134468	ND	ND	182110	ND	ND
632ECR005	9/27/2013	SWAMP	Lahontan	800	44269	ND	ND	158106	471	313
632ECR005	10/7/2013	SWAMP	Lahontan	800	7975	ND	ND	70842	18204	ND
632ECRB10	9/5/2013	SWAMP	Lahontan	800	7162	ND	ND	55643	6555	ND
632MLBB01	8/6/2013	SWAMP	Lahontan	700	3488	ND	ND	57286	293	346
632MLBB01	8/13/2013	SWAMP	Lahontan	800	ND	ND	ND	26097	ND	282
632MLBB03	6/18/2013	SWAMP	Lahontan	800	1637	ND	ND	14790	525	ND
632MLBB03	7/1/2013	SWAMP	Lahontan	600	239069	ND	ND	246558	359	809
632MLBB03	7/22/2013	SWAMP	Lahontan	800	9890	ND	ND	66800	ND	1407
632MLBB03	7/24/2013	SWAMP	Lahontan	750	12303	ND	ND	27837	ND	587
632MLBB03	9/10/2013	SWAMP	Lahontan	800	ND	ND	ND	79673	ND	ND
632MRKB02	6/18/2013	SWAMP	Lahontan	800	17602	ND	ND	57114	254	3111
632MRKB02	7/1/2013	SWAMP	Lahontan	800	2461	ND	ND	19455	453	280
632MRKB02	7/22/2013	SWAMP	Lahontan	800	2982	ND	ND	42301	627	466
632MRKB02	7/31/2013	SWAMP	Lahontan	400	222673	ND	ND	259980	3803	9915
632MRKB02	8/6/2013	SWAMP	Lahontan	600	3020039	ND	ND	2517952	3830	70868
632MRKB02	8/13/2013	SWAMP	Lahontan	800	21167	ND	ND	41211	919	1051
632MRKB02	9/10/2013	SWAMP	Lahontan	800	3346	ND	ND	75620	297	1242
632MRKB03	6/18/2013	SWAMP	Lahontan	425	85931	ND	ND	235290	1157	8407
632MRKB03	8/6/2013	SWAMP	Lahontan	600	674734	ND	ND	857696	700	31185

Site ID	Date	Project	Laboratory for Filter Collection	mL Filtered	BacCow Copies/ 100mL	BacHum Copies/ 100mL	HF183 Copies/ 100mL	GenBac3 Copies/ 100mL	Entero1a Copies/ 100mL	*E. coli* Copies/ 100mL
632MRKB03	8/13/2013	SWAMP	Lahontan	800	37961	ND	ND	73192	391	1208
632MRKB03	9/10/2013	SWAMP	Lahontan	800	1310	ND	ND	44279	453	ND
632MRKB04	7/1/2013	SWAMP	Lahontan	800	971	ND	ND	23974	755	566
632MRKB04	7/22/2013	SWAMP	Lahontan	800	3586	ND	ND	30523	ND	459
632WLFB01	8/19/2013	SWAMP	Lahontan	800	38549	ND	ND	194831	691	1208
632WLFB01	8/21/2013	SWAMP	Lahontan	600	252283	ND	ND	322210	ND	2069
632WLFB01	9/5/2013	SWAMP	Lahontan	800	465026	ND	ND	140581	35850	ND
632WLFB01	9/25/2013	SWAMP	Lahontan	800	935883	ND	ND	384113	334	2355
632WLFB01	9/27/2013	SWAMP	Lahontan	800	49298	ND	ND	124184	884	582
632WLFB10	10/7/2013	SWAMP	Lahontan	800	336735	ND	ND	431998	65908	1088
633WFCB02	6/18/2013	SWAMP	Lahontan	800	521	ND	ND	30722	387	ND
633WFCB02	7/1/2013	SWAMP	Lahontan	800	59741	ND	ND	313751	44061	4923
633WFCB02	7/22/2013	SWAMP	Lahontan	800	1098	ND	ND	100121	1609	528
633WFCB02	7/24/2013	SWAMP	Lahontan	800	2982	ND	ND	202612	938	362
633WFCB02	7/31/2013	SWAMP	Lahontan	800	13144	ND	ND	86164	3745	5133
633WFCB02	8/6/2013	SWAMP	Lahontan	800	3963	ND	ND	131698	462	327
633WFCB02	8/13/2013	SWAMP	Lahontan	800	98454	ND	ND	160184	1322	1821
633WFCB02	8/19/2013	SWAMP	Lahontan	800	108799	ND	ND	341535	259	1629
633WFCB02	9/5/2013	SWAMP	Lahontan	800	19008	ND	ND	136958	395	1142
633WFCB02	9/10/2013	SWAMP	Lahontan	800	68605	ND	ND	402069	56324	1447
633WFCB02	9/26/2013	SWAMP	Lahontan	800	8613	ND	ND	45450	462	ND
634TRTB02	7/1/2013	SWAMP	Lahontan	300	2025	ND	ND	181656	2179	ND
637SUS001	9/18/2013	SWAMP	Lahontan	200	5573	ND	ND	196612	1504	1956
637SUS001	11/14/2013	SWAMP	Lahontan	300	87476	ND	ND	367612	ND	692

Appendix G. Description of deliverables that were required under Contract 12-067-160.

Task 2.1: Quality Assurance Plan

Required: Prepare a quality assurance plan that specifies the quality assurance and quality control methods and processes to be used for the field and laboratory elements of the project.
Delivered: A final quality assurance plan was submitted to and accepted by the State's Contract Manager, Thomas Suk.

Task 3.1: Longitudinal stream surveys

Required: At not fewer than eight watersheds, conduct longitudinal stream surveys for bacterial indicators. At each selected watershed, collect not fewer than ten water samples and transport the samples to the laboratory for analysis.
Delivered: A total of 378 samples were collected from 33 watersheds. Therefore, actual deliverables far exceeded what was required.

Task 3.2: Laboratory analysis:

Required: At the laboratory, analyze all water samples collected under Task 3.1 for fecal coliform bacteria and *Escherichia coli* using USEPA-approved methods. Conduct a preliminary source tracking assessment on not fewer than 50 samples using qPCR assays to differentiate human and bovine sources of Bacteroidales, and develop ratio-based metrics of relative source levels (humans vs. bovine).
Delivered: All 378 samples were analyzed for fecal coliform and *E. coli* using membrane filtration methods. A total of 164 DNA samples were analyzed, of which 62 were collected by SNARL in 2012 and 102 were collected by SWAMP in 2013. All 165 samples were subjected to six qPCR assays, three general assays (EC23S857: *Escherichia*; Entero1a: *Enterococcus*; GenBac3: Bacteroidales), and three source-specific assays (BacCow: ruminants; BacHum: humans; HF183: humans). For the 2012 samples, results from the EC23S857 and Entero1a assays were presented in the final report for Contract 11-167-160. Results from all other assays are new. Estimates of contributions from each source are provided in the final report. In summary, actual deliverables far exceeded what was required.

Task 4: Submit electronic data

Required: Submit the results of Task 3 in electronic data formats to the California Environmental Data Exchange Network (CEDEN).
Delivered: Data collected in 2013 and 2014 was submitted to CEDEN on 1/25/2014 and 2/27/2015, respectively. Digital files of study data were provided to Lahontan staff on 3/10/2015.

Task 5: Draft and final project reports.

Required: Submit to the Contract Manager a draft Project Report that details the findings of Task 3. This draft report was originally due on 01/16/2015 but given the interest of the investigators to brief Lahontan staff on the contents of the report and the availability of Lahontan staff only on 01/23/2015, by agreement with the Contract Manager the draft Project Report is due on 01/23/2015. Submit a final Project Report by 3/20/2015.
Delivered: The draft Project Report was submitted on 1/23/2015, and a project briefing was provided at the Lahontan Water Board office in South Lake Tahoe on the same date. The final Project Report is hereby submitted on 03/10/2015.

Supplement A. State Water Resources Control Board fact sheet published in 2013.

Water Board Strategic Goals:

Goal 1: Implement strategies to fully support the beneficial uses for all 2006-listed water bodies by 2030.

Goal 2: Improve and protect groundwater quality in high-use basins by 2030.

Goal 3: Increase sustainable local water supplies available for meeting existing and future beneficial uses by 1,725,000 acre-feet per year, in excess of 2002 levels, by 2015, and ensure adequate flows for fish and wildlife habitat.

Goal 4: Comprehensively address water quality protection and restoration, and the relationship between water supply and water quality, and describe the connections between water quality, water quantity, and climate change, throughout California's water planning processes.

Goal 5: Improve transparency and accountability by ensuring that Water Board goals and actions are clear and accessible, by demonstrating and explaining results achieved with respect to the goals and resources available, by enhancing and improving accessibility of data and information, and by encouraging the creation of organizations or cooperative agreements that advance this goal, such as establishment of a statewide water data institute.

Goal 6: Enhance consistency across the Water Boards, on an ongoing basis, to ensure our processes are effective, efficient, and predictable, and to promote fair and equitable application of laws, regulations, policies, and procedures.

Goal 7: Ensure that the Water Boards have access to information and expertise, including employees with appropriate knowledge and skills, needed to effectively and efficiently carry out the Water Boards' mission.

Information Links

The State Water Board has easy to use information on surface water, groundwater, water rights and other programs at its website. Key sites include:

About the Water Board: The "About Us" tab on the State Water Board website is a one stop location to find information such as Board membership, meetings, budget information, important policy documents, fact sheets and important contact information. http://www.waterboards.ca.gov/about_us/

My Water Quality: This site provides information to the public from multiple perspectives and presents California water quality monitoring data and assessment information that may be viewed across space and time in order to better address the public's questions. http://www.waterboards.ca.gov/mywaterquality/

Electronic Water Rights Information Management System (eWRIMS): This water rights tracking system contains information on water right permits and licenses issued by the Water Board that is available to the public and staff. http://www.waterboards.ca.gov/water_issues/programs/ewrims

GeoTracker Groundwater Ambient Monitoring and Assessment Program (GAMA): GeoTracker GAMA is an online groundwater information system that provides access to water quality data and connects users to groundwater basics and protection information. http://www.waterboards.ca.gov/gama/geotracker_gama.shtml

State Water Board Performance Reports: This annual report provides information on the Water Boards' efforts to protect and allocate the state's waters for beneficial uses. http://www.waterboards.ca.gov/about_us/performance_report/

Additional information can be found at www.waterboards.ca.gov.

CALIFORNIA
Water Boards
STATE WATER RESOURCES CONTROL BOARD
REGIONAL WATER QUALITY CONTROL BOARDS

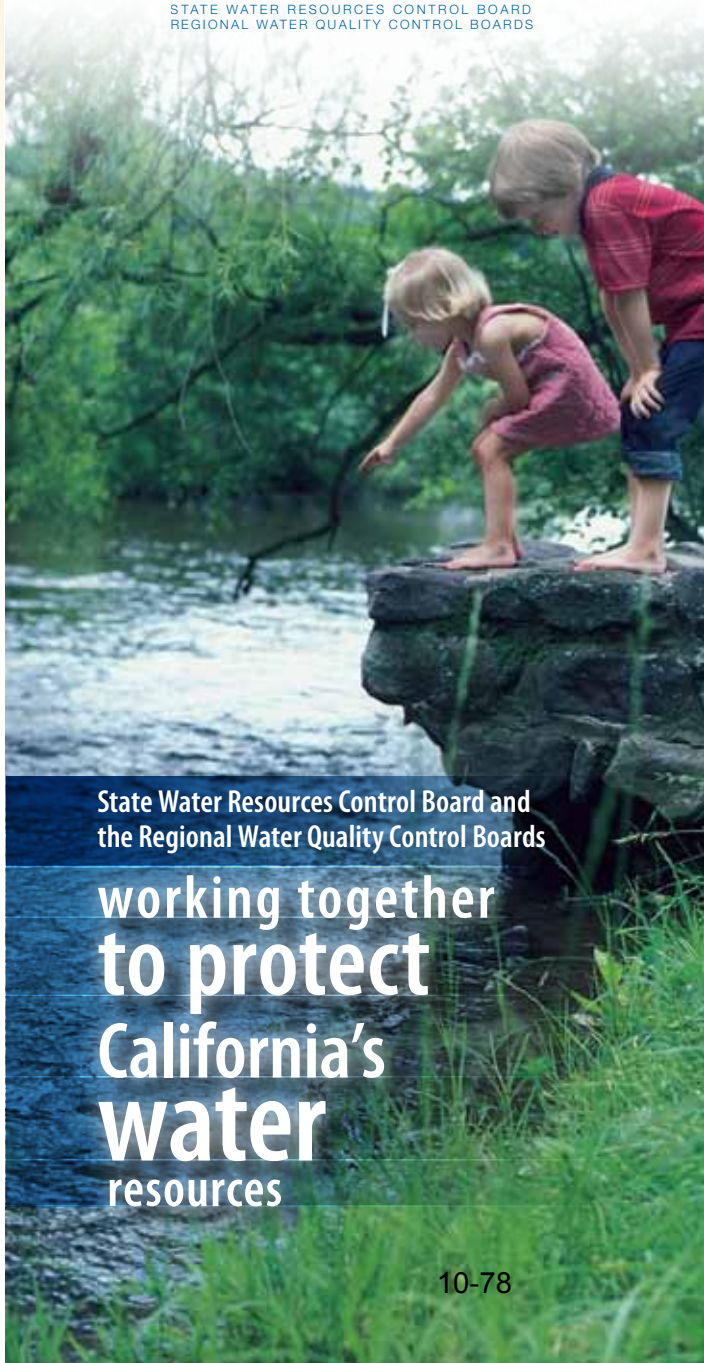
For more information, or if you have any questions, contact:

OFFICE OF PUBLIC AFFAIRS
http://www.waterboards.ca.gov/press_room/
(916) 341-5254

CALIFORNIA ENVIRONMENTAL PROTECTION AGENCY

REVISED: MAY 2013

CALIFORNIA
Water Boards
STATE WATER RESOURCES CONTROL BOARD
REGIONAL WATER QUALITY CONTROL BOARDS



State Water Resources Control Board and the Regional Water Quality Control Boards

working together to protect California's water resources

OUR MISSION: To preserve, enhance, and restore the quality of California's water resources, and ensure their proper allocation and efficient use for the benefit of present and future generations.

What the State Water Resources Control Board does

Created by the State Legislature in 1967, the five-member Board protects water quality by setting statewide policy, coordinating and supporting the Regional Water Board efforts, and reviewing petitions that contest Regional Board actions. Together with the Regional Boards, the State Board is authorized to implement the federal Clean Water Act in California. The State Board also is solely responsible for allocating surface water rights.

Each of the five full-time salaried board members fills a different specialized position (representing the public, engineering expertise, water quality expertise and water supply). The members are appointed to four-year terms by the Governor and confirmed by the Senate.

FELICIA MARCUS, Board Chair:
Qualified in the field of water quality

FRANCES SPIVY-WEBER, Vice-Chair:
Represents the public

TAM M. DODUC, Board Member:
Civil engineer qualified in the fields of water supply, water rights and irrigated agriculture

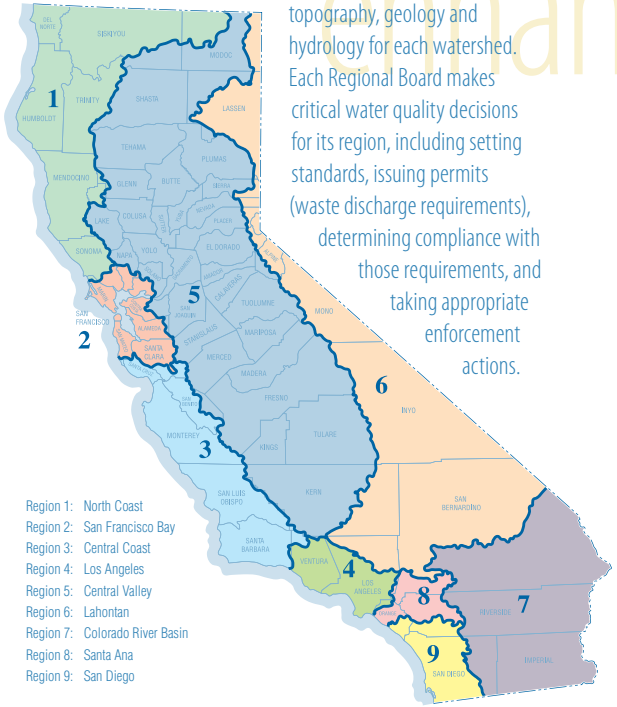
DORENE D'ADAMO, Board Member:
Attorney qualified in the fields of water supply and water rights

STEVEN MOORE, Board Member:
Professional engineer qualified in the field of water quality

THOMAS HOWARD, Executive Director

What the Regional Water Quality Control Boards do

There are nine regional water quality control boards statewide. The nine Regional Boards are semi-autonomous and are comprised of seven part-time Board members appointed by the Governor and confirmed by the Senate. Regional boundaries are based on watersheds and water quality requirements are based on the unique differences in climate, topography, geology and hydrology for each watershed. Each Regional Board makes critical water quality decisions for its region, including setting standards, issuing permits (waste discharge requirements), determining compliance with those requirements, and taking appropriate enforcement actions.



Region 1: North Coast
Region 2: San Francisco Bay
Region 3: Central Coast
Region 4: Los Angeles
Region 5: Central Valley
Region 6: Lahontan
Region 7: Colorado River Basin
Region 8: Santa Ana
Region 9: San Diego

State Water Board programs

The State Water Board has three major programs:

WATER QUALITY: The State Water Board works in coordination with the Regional Water Boards to preserve, protect, enhance and restore water quality. Major areas of focus include:

- Stormwater
- Wastewater treatment
- Water quality monitoring
- Wetlands protection
- Ocean protection
- Environmental education
- Environmental justice
- Clean up contaminated sites, including brownfields
- Low-impact development
- Underground Storage Tank Cleanups
- Groundwater Protection

The State Water Board and the nine Regional Water Boards are responsible for swift and fair enforcement when the laws and regulations protecting our waterways are violated. The Water Boards also work with federal, state and local law enforcement, as well as other environmental agencies to ensure a coordinated approach to protecting human health and the environment.

FINANCIAL ASSISTANCE: The State Water Board provides loans and grants for constructing municipal sewage and water recycling facilities, remediation for underground storage tank releases, watershed protection projects, and for nonpoint source pollution control projects. The State Water Board has several financial programs to help local agencies and individuals prevent or clean up pollution of the state's water.

WATER RIGHTS: Anyone wanting to divert water from a stream or river not adjacent to their property must first apply for a water right permit from the State Water Board. The State Water Board issues permits for water rights specifying amounts, conditions and construction timetables for diversion and storage. Decision-making stems from water availability, prior water rights and flows needed to preserve instream uses, such as recreation and fish habitat.

The State Water Board's Bay-Delta Program facilitates the development and review of plans and policies to protect beneficial uses of the San Francisco Bay / Sacramento - San Joaquin Delta Estuary. This Program also implements a nine-point Strategic Workplan to protect this important natural resource.

The State Water Board is also home to the Delta Watermaster. The Office of Delta Watermaster oversees the monitoring and enforcement of water right activities regarding water diversions in the Sacramento-San Joaquin Delta. The Watermaster's authority extends to all diversions within the Sacramento - San Joaquin Delta and includes water appropriations within the Delta watershed.

SWAMP ID	SNARL ID	Location	Latitude	Longitude
603BSP002		Bishop Ck Canal at East Line St.	37.3616	-118.3861
603BSP003		Bishop Ck Canal above South Fork Bishop Ck	37.3679	-118.3862
603BSP004	BIS.60	South Fork Bishop Ck above Bishop Ck Canal	37.3679	-118.3863
603BSP005		South Fork Bishop Ck at Hanby St.	37.3678	-118.3885
603BSP010		South Fork Bishop Ck at Home St.	37.3689	-118.4022
603BSP021		North Fork Bishop Ck above Bishop Ck Canal	37.3801	-118.4047
603BSP111	BIS.10	Bishop Ck at National Forest Boundary	37.3303	-118.4958
603BSPB50	BIS.30	South Fork Bishop Ck @ Brockman Lane	37.3640	-118.4318
603BSPB60	BIS.31	North Fork Bishop Ck @ Brockman Lane	37.3686	-118.4322
603BSPB65	BIS.21	North Fork Bishop Ck @ Mumy Lane	37.3588	-118.4503
630BUC004		North Branch Buckeye Ck, upstream of bridge	38.2637	-119.2773
630BUC005		Middle Branch Buckeye Ck, upstream of bridge	38.2622	-119.2758
630RBS007		North Branch Robinson Ck, upstream of bridge	38.2597	-119.2735
630RBS008		South Branch Robinson Ck, upstream of bridge	38.2585	-119.2723
630SWA005		Swauger Ck below Huntoon Valley	38.2959	-119.3097
630SWA006		Swauger Ck above Huntoon Valley	38.3428	-119.3231
630VIRB01		Virginia Ck below Green Ck Road	38.1983	-119.2206
632ECR005		East Fork Carson River, at USGS gage below Markleeville	38.7154	-119.7644
632ECRB10		East Fork Carson River, above Hangmans bridge	38.6896	-119.7639
632MLBB01		Confluence Millberry Ck with Markleeville Ck	38.6950	-119.7785
632MLBB03		Millberry Ck at 30 mph Sign	38.6969	-119.7818
632MRKB02		Markeeville Ck at USFS Campground	38.6965	-119.7740
632MRKB03		Markleeville Ck at Swim Hole	38.6938	-119.7795
632MRKB04		Markleeville Ck at Library Bridge	38.6933	-119.7818
632WLFB01		Wolf Ck, above East Fork Carson River	38.6137	-119.6924
632WLFB10		Wolf Ck, below Ranch	38.6007	-119.6889
633WFCB02		West Fork Carson River at Paynesville Bridge	38.8089	-119.7771
634TRTB02		Trout Ck, at confluence with South Upper Truckee	38.9416	-119.9960
637SUS001		Susan River @ Litchfield	40.3777	-120.3951

ENCLOSURE 2

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LANDSCAPE-SCALE PATTERNS OF FECAL INDICATOR BACTERIA IN STREAMS OF THE EASTERN SIERRA:

Insights gained from modern statistical and molecular approaches

Roland Knapp, Sierra Nevada Aquatic Research Laboratory

Craig Nelson, University of Hawai'i at Mānoa

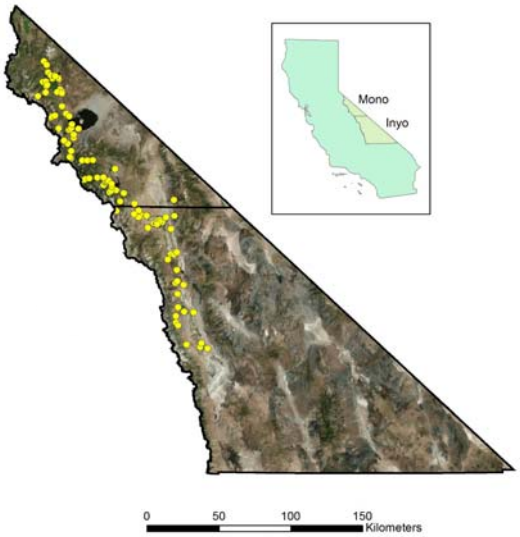
STUDY OBJECTIVES

1. Identify the primary drivers of fecal indicator bacteria (FIB) concentrations in streams in the eastern Sierra Nevada portion of the Lahontan region.

2. Use modern microbial source tracking (MST) assays to identify the primary sources of FIB.

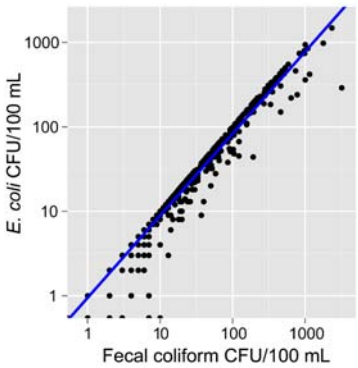
STUDY DESIGN

- 111 sites along 35 streams/rivers.
- Sites arranged longitudinally, 1-14 sites per stream.
- Encompassed all major land-use classes: undeveloped, dispersed recreation, livestock grazing, suburban and urban development.
- Monthly sampling during spring-summer-fall, 2012-2014.
- Standard membrane filtration methods to estimate fecal coliform and *E. coli* concentrations (CFU per 100 mL).



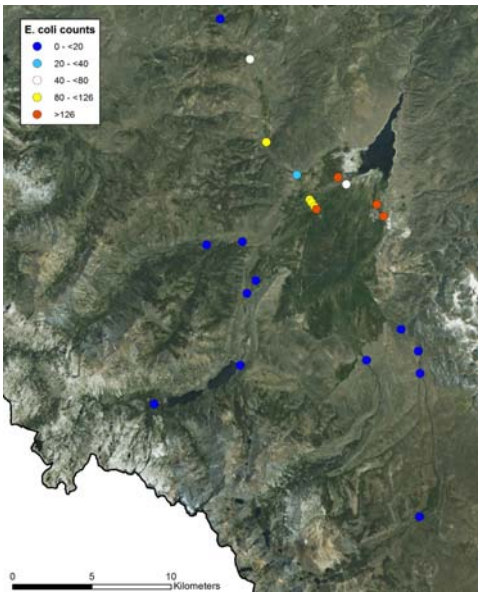
FIB STANDARDS FOR THE LAHONTAN REGION

- Current standard: 20 fecal coliform colony forming units (CFU) per 100 mL.
- Proposed statewide standard (for recreational waters): 100 or 126 *E. coli* CFU per 100 mL.
- Concentration of fecal coliform and *E. coli* bacteria highly correlated, *E. coli* concentrations provide a more accurate description of the concentration of fecal bacteria.



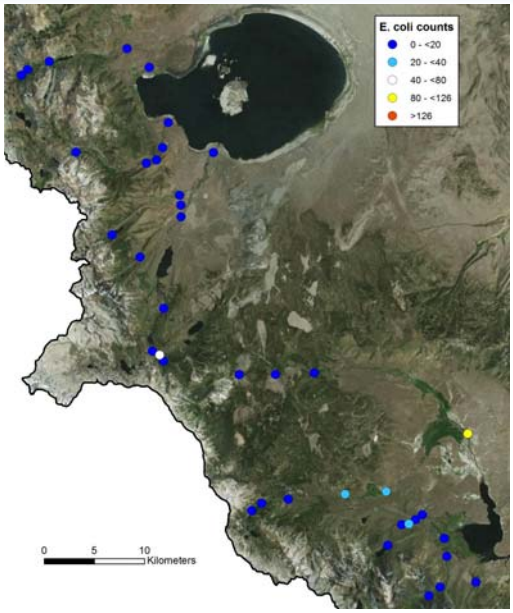
SPATIAL PATTERNS

- *E. coli* concentrations: CFU per 100 mL.
- Categorized to reflect current/proposed FIB objectives.
- Average of May-September sample results.
- Headwaters of East Walker River
  - Swauger Creek
  - Buckeye Creek
  - Robinson Creek
  - East Walker River
  - Virginia Creek
  - Green Creek



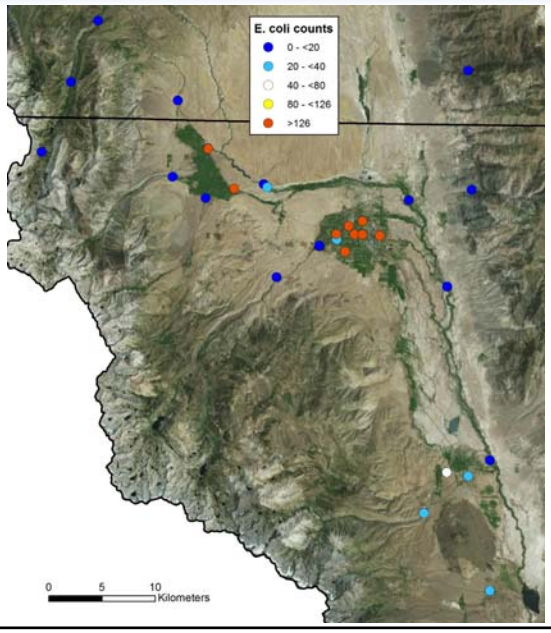
SPATIAL PATTERNS

- Mono Basin
  - Mill Creek
  - Lee Vining Creek
  - Walker Creek
  - Parker Creek
  - Rush Creek
- Upper Owens River
  - Upper Owens River
  - Mammoth Creek
  - Convict Creek
  - McGee Creek
  - Hilton Creek



SPATIAL PATTERNS

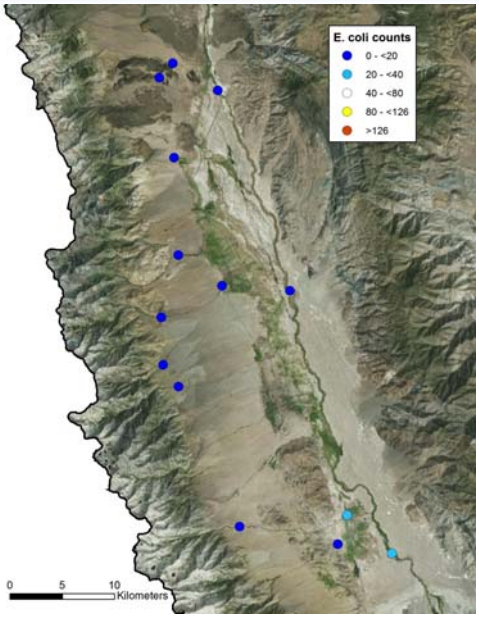
- Middle Owens River
  - Rock Creek
  - Pine Creek
  - Horton Creek
  - Owens River
  - Bishop Creek – NF & SF
  - Baker Creek
  - Big Pine Creek
  - Birch Creek
- White Mountains
  - Piute Creek
  - Silver Canyon Creek



SPATIAL PATTERNS

- Lower Owens River
  - Owens River
  - Taboose Creek
  - Goodale Creek
  - Sawmill Creek
  - Oak Creek
  - Independence Creek
  - Symmes Creek
  - Shepherd Creek
  - Lone Pine Creek
  - Tuttle Creek

Summary:
- Majority of sites have *E. coli* concentrations of <20 CFU per 100 mL.
- Some localized areas of high *E. coli* concentrations.

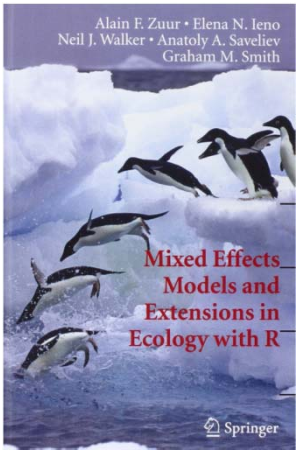


LANDSCAPE-SCALE DRIVERS OF FIB

Variable	Code	Description
Site identification number	SITEID	Unique five-digit alphanumeric code used to identify each sampling location
Hydrologic unit	HUC12M	U.S. Geological Survey 12-digit hydrologic unit, modified in some cases as described in Methods.
Elevation	ELEV	Height above sea level (in meters)
Campsites	CAMP	Number of designated campsites within a 1.5 km radius upstream-oriented sector
Upstream lakes	LAKE	Presence/absence of one or more water bodies (>1 ha in surface area, >3 m deep) within a 1.5 km radius upstream-oriented sector
Road length	ROAD	Total length of all road segments (paved and unpaved) within a 1.5 km radius upstream-oriented sector (in kilometers)
Low-intensity land use	LANDUSE21	Area of low-intensity land use within a 1.5 km radius upstream-oriented sector, including golf courses and low density of buildings (in km^2)
High-intensity land use	LANDUSE23	Area of moderate and high-intensity land use within a 1.5 km radius upstream-oriented sector, including high density of buildings (in km^2)
Livestock grazing	COW	Presence/absence of livestock (usually cows) within a 1.5 km radius upstream-oriented sector
Precipitation amount	RAIN	Presence/absence of total rainfall during previous 3 days of ≥2 mm.
Sampling year	YEAR	Year during which sample was collected
Sampling day	DAY	Day of the year (since January 1) on which sample was collected.
Sampling time	TIME	Time of day when sample was collected

MODELING APPROACH

- Generalized additive mixed models (GAMM), allow each sample to be included in analysis as an independent observation.
- Followed protocol of Zuur et al. (2009).



RESULTS

a.

Variable name	Estimate	Std. error	*t*	*P*
Intercept	1.09	0.20	5.50	5.27×10^{-8}
COW(yes)	0.85	0.06	13.54	$< 1.00 \times 10^{-10}$
LAKE(yes)	-0.46	0.13	-3.59	3.60×10^{-4}
LANDUSE23	0.58	0.20	2.90	3.89×10^{-3}
RAIN(yes)	0.14	0.05	2.61	9.20×10^{-3}
ELEV	-0.23	0.10	-2.29	2.22×10^{-2}

b.

Variable name	EDF[1]	*F*	*P*
s(DAY)	5.35	34.06	$< 1.00 \times 10^{-10}$
s(TIME)	4.63	8.61	2.33×10^{-7}

1. Effective degrees of freedom: 1 indicates a straight line, and higher values indicate an increasingly non-linear smoothing spline.

CONCLUSIONS: LANDSCAPE-SCALE ANALYSIS

1. Majority of sites in the study area (76%) have *E. coli* concentrations that meet the current LRWQCB standard of 20 CFU per 100 mL
2. If effective measures are adopted to control fecal inputs from livestock into streams, virtually all of the streams in the study area are predicted to meet the current LRWQCB standard.
3. MST study is necessary to directly link observed fecal contamination to potential sources.

MICROBIAL SOURCE TRACKING (MST)

- Based on the fact that vertebrate species (or groups of closely-related species) have characteristic bacteria in their intestinal tracts.
- Molecular assays (qPCR) allow identification of sources of fecal contamination.
- Most assays target Bacteroidales bacteria, several types are common in feces of mammals.
- Ideal assay has both high sensitivity and high specificity.
  - Sensitivity: ability to detect the target bacteria when it is present in a sample.
  - Specificity: ability to discriminate the target bacteria from bacteria contributed by other sources.

MICROBIAL SOURCE TRACKING ASSAYS

Assay Target	Assay Name	Assay Type
Bacteroidales	GenBac3	Broad
Human Bacteroidales	HF183	Source-specific
Human Bacteroidales	BacHum	Source-specific
Ruminant Bacteroidales	BacCow	Source-specific
Cattle Bacteroidales	CowM2	Source-specific

MICROBIAL SOURCE TRACKING RESULTS

Human Bacteroidales assays (BacHum, HF183):

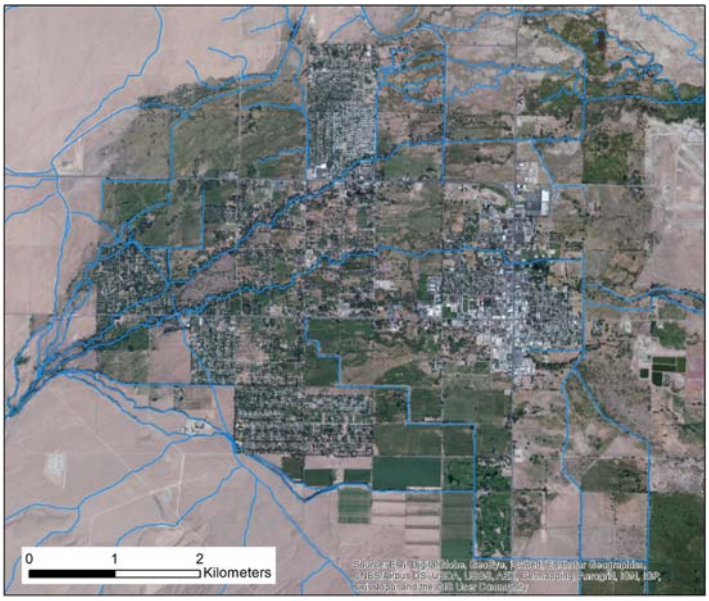
- 2 assays gave very similar results: Human Bacteroidales rarely detected, found in only 5 of samples.
- When detected, concentrations of human Bacteroidales always low.

Ruminant Bacteroidales assay (BacCow):

- Ruminant Bacteroidales widespread across study area, and were often detected in high concentrations.
- Concentrations of ruminant Bacteroidales ~5X higher for sites with cattle compared to those without cattle.
- Effective method of identifying cattle-derived fecal sources.

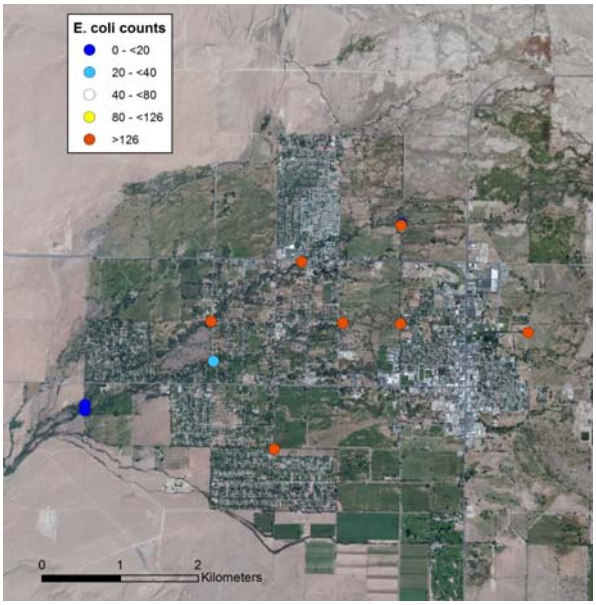
Use of MST to identify sources of fecal contamination in areas with multiple potential sources: Bishop Creek.

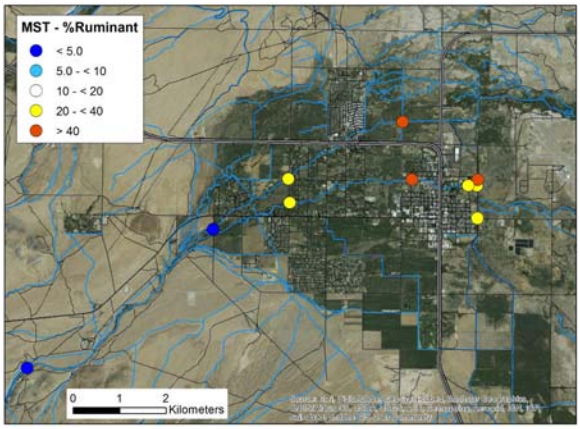
BISHOP CREEK



BISHOP CREEK: FIB RESULTS

- Average *E. coli* concentrations from monthly samples collected May-Sept.
- Potential fecal sources: humans, cattle, dogs, waterfowl, beavers.



BISHOP CREEK: RESULTS FROM MST

- Of 48 samples, human markers detected in 3, ruminant markers detected in all.
- Ruminant Bacteroidales concentrations much higher than human Bacteroidales.
- → At the time of sample collection (summer 2013), cattle were a more significant source of fecal contamination than were humans.
- Analysis of more samples underway, using wider array of source-specific assays.
- Results will provide a sound basis for future management efforts.