

Notes: Error bars represent standard error of the mean of multiple sampling sites.

Dotted lines represent analytical detection limits.

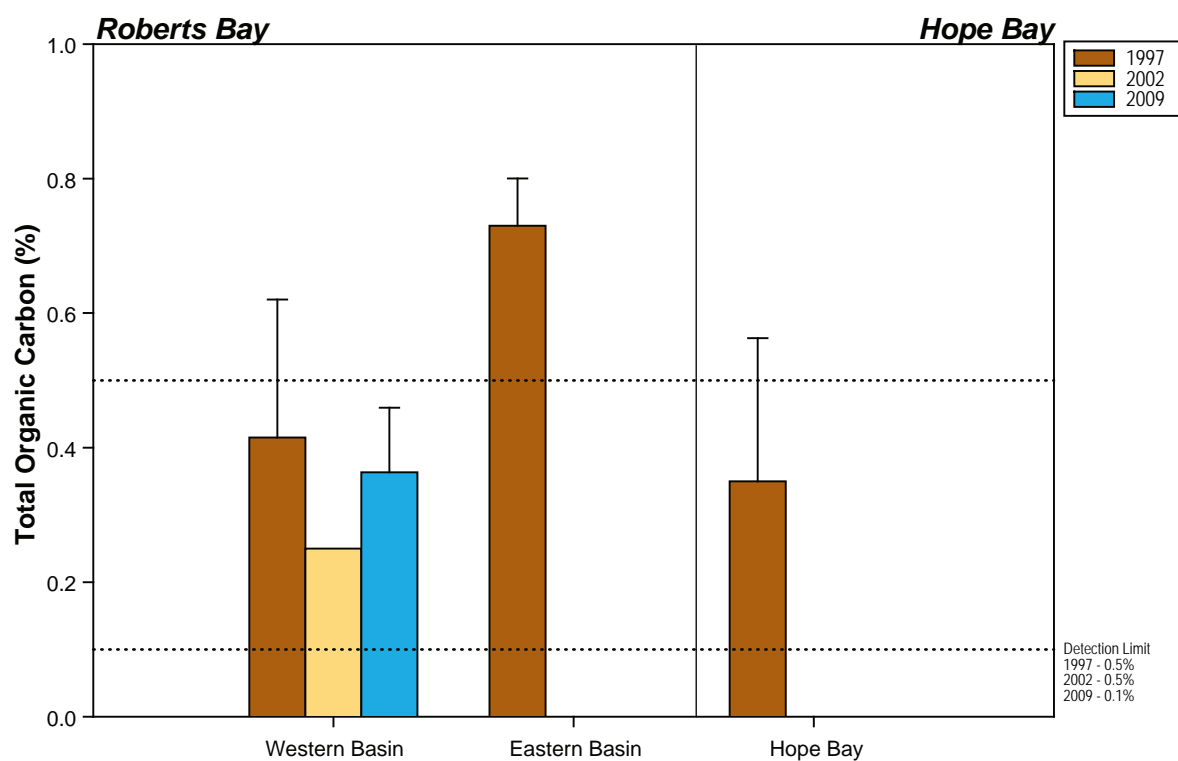
Mean sediment grain size represents an average of 4 sites in 2002 and 5 sites in 2009.

Only a subset of sites sampled in 2009 (ST7, ST8, ST2, ST9, and ST10) are plotted here;

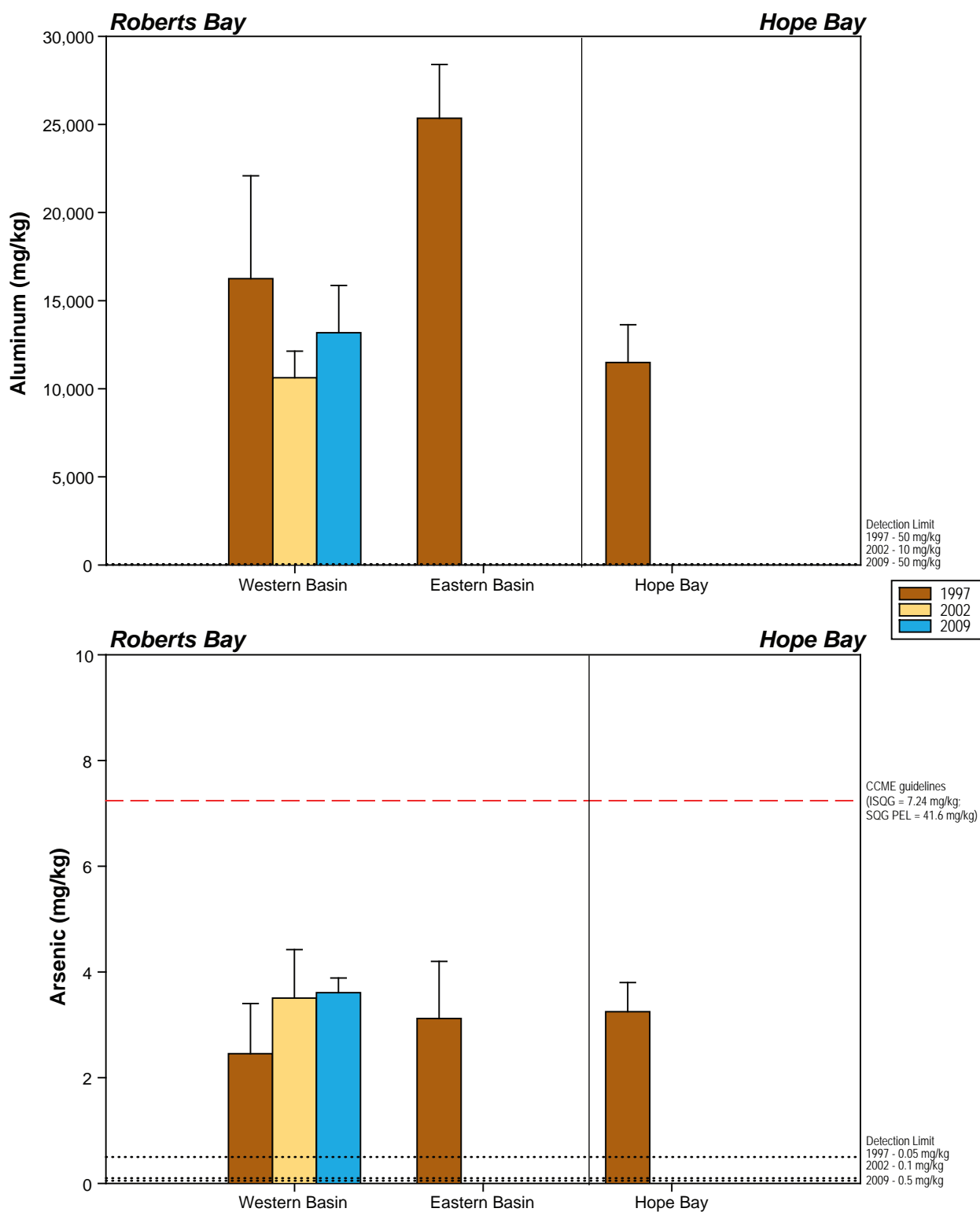
these sites were selected because they are comparable to historical sampling locations.

For 2002 data, sediment grain size categories were defined as: gravel = >2 mm, sand = 53  $\mu$ m to 2 mm, silt = 2  $\mu$ m to 53  $\mu$ m, clay = <2  $\mu$ m.

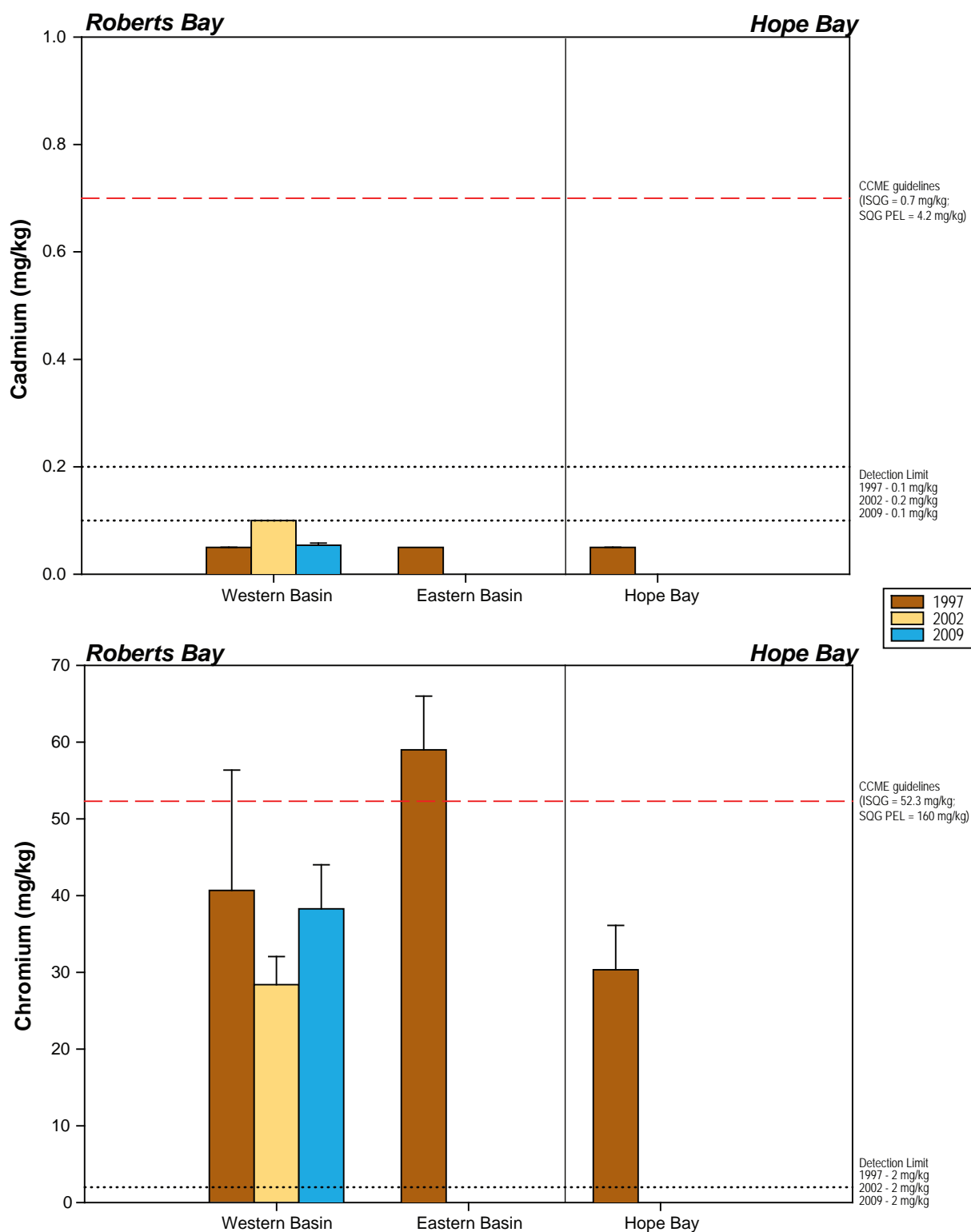
For 2009 data, sediment grain size categories were defined as: gravel = >2 mm, sand = 63  $\mu$ m to 2 mm, silt = 4  $\mu$ m to 63  $\mu$ m, clay = <4  $\mu$ m.



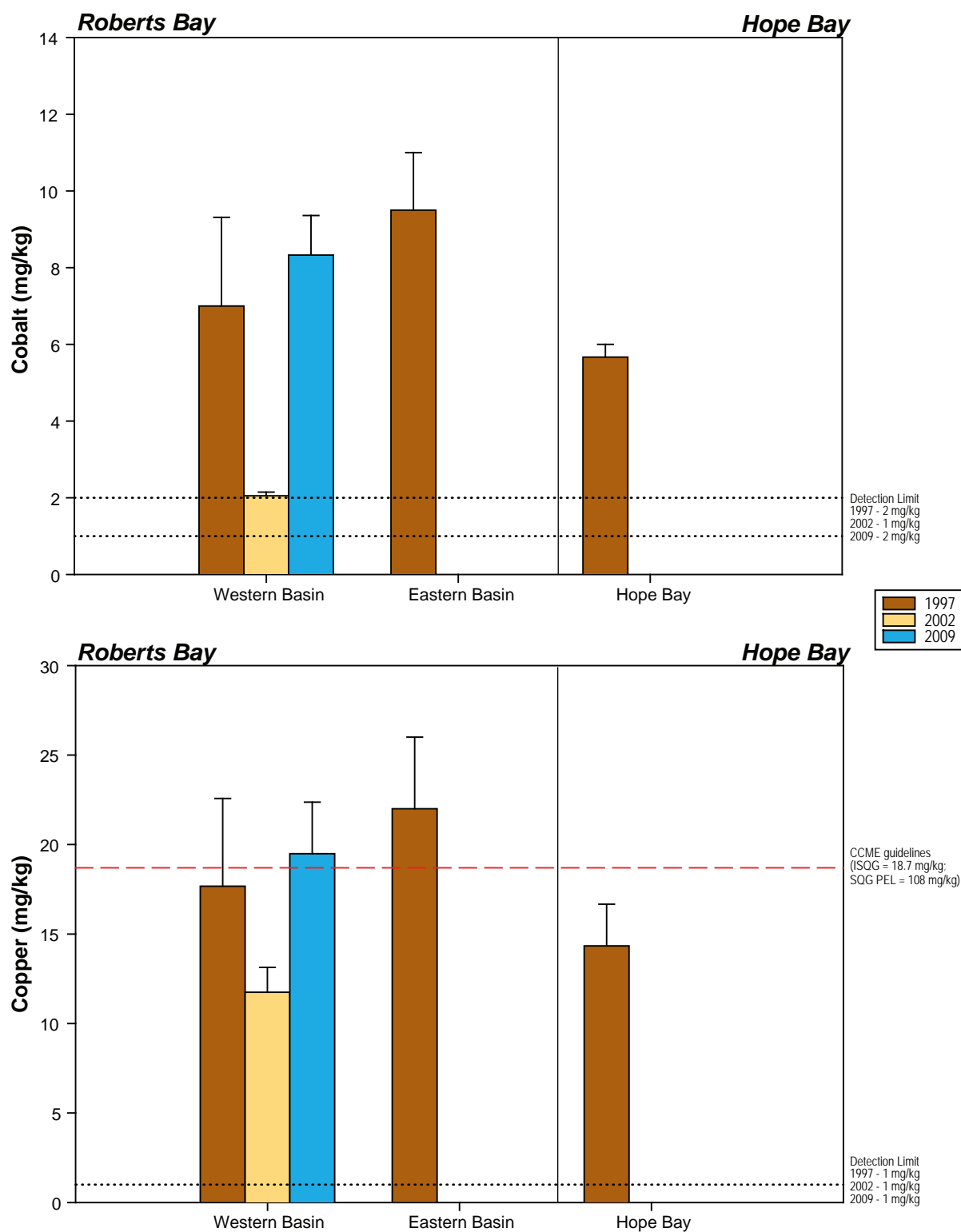
Notes: Error bars represent standard error of the mean of multiple sampling sites.  
Dotted lines represent analytical detection limits.  
Only a subset of sites sampled in 2009 (ST7, ST8, ST2, ST9, and ST10) are plotted here;  
these sites were selected because they are comparable to historical sampling locations.



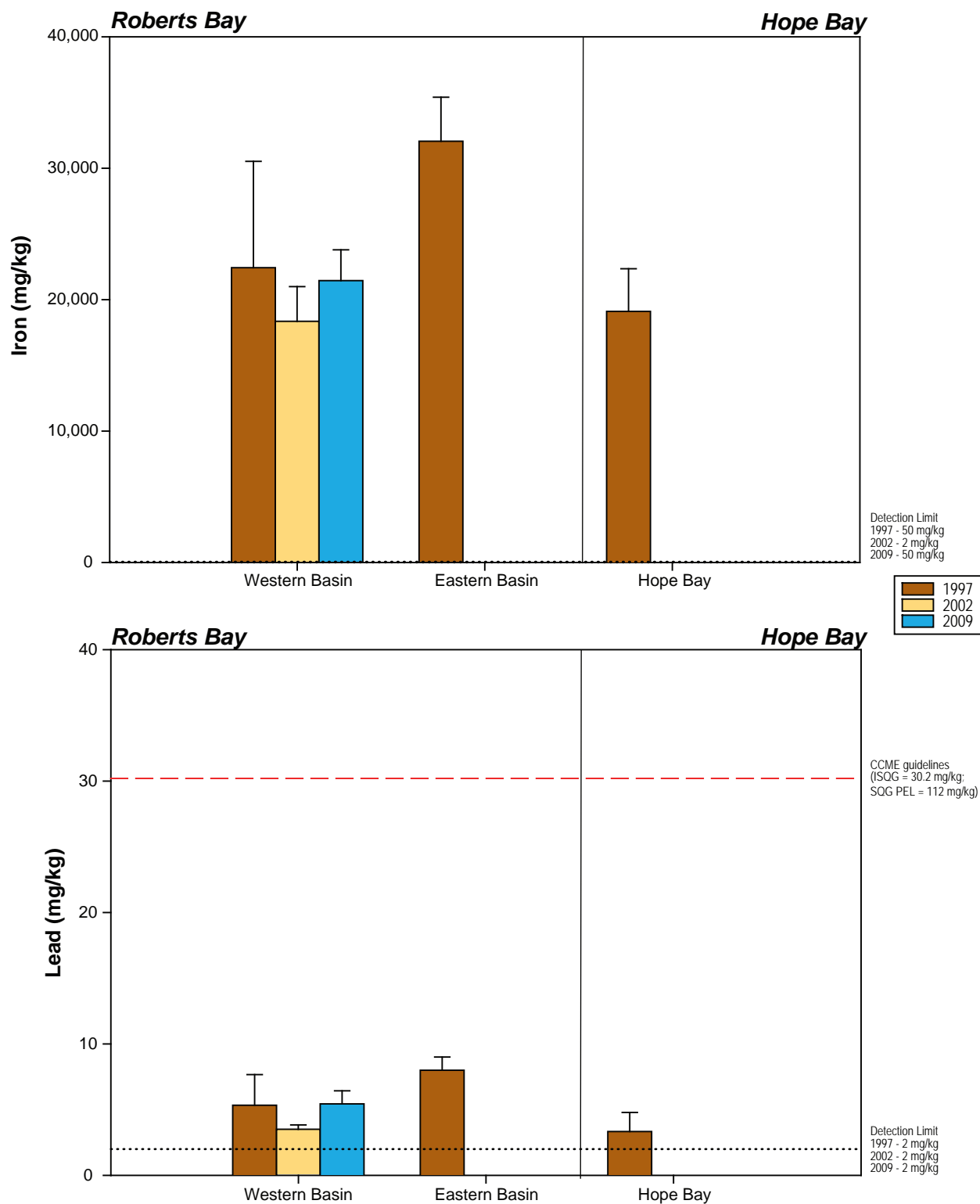
Notes: Error bars represent standard error of the mean of multiple sampling sites.  
 Dotted lines represent analytical detection limits.  
 Red dashed line represents CCME interim sediment quality guideline for the protection of marine aquatic life.  
 Only a subset of sites sampled in 2009 (ST7, ST8, ST2, ST9, and ST10) are plotted here;  
 these sites were selected because they are comparable to historical sampling locations.



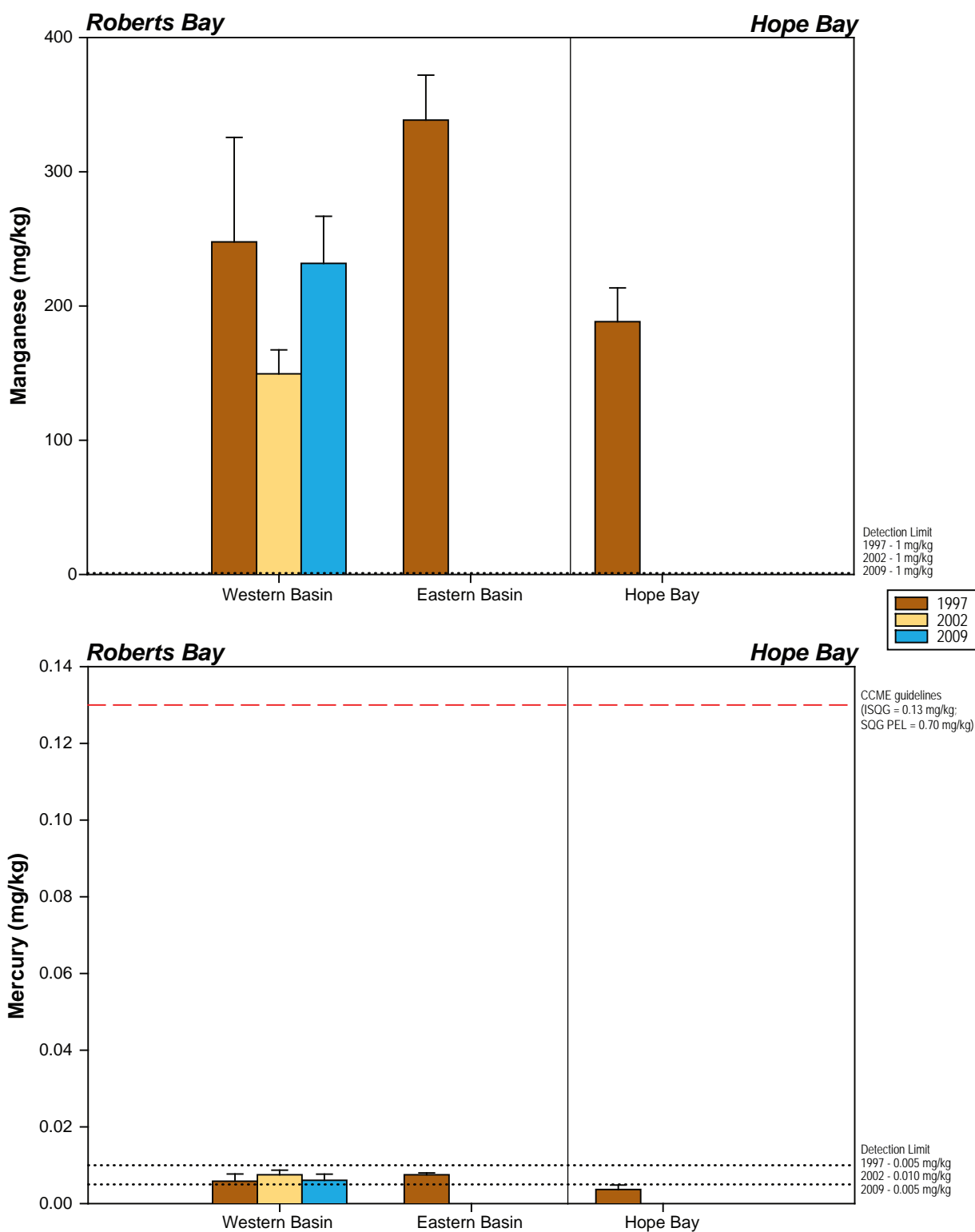
Notes: Error bars represent standard error of the mean of multiple sampling sites.  
 Dotted lines represent analytical detection limits.  
 Red dashed lines represent CCME interim sediment quality guidelines for the protection of marine aquatic life.  
 Only a subset of sites sampled in 2009 (ST7, ST8, ST2, ST9, and ST10) are plotted here;  
 these sites were selected because they are comparable to historical sampling locations.



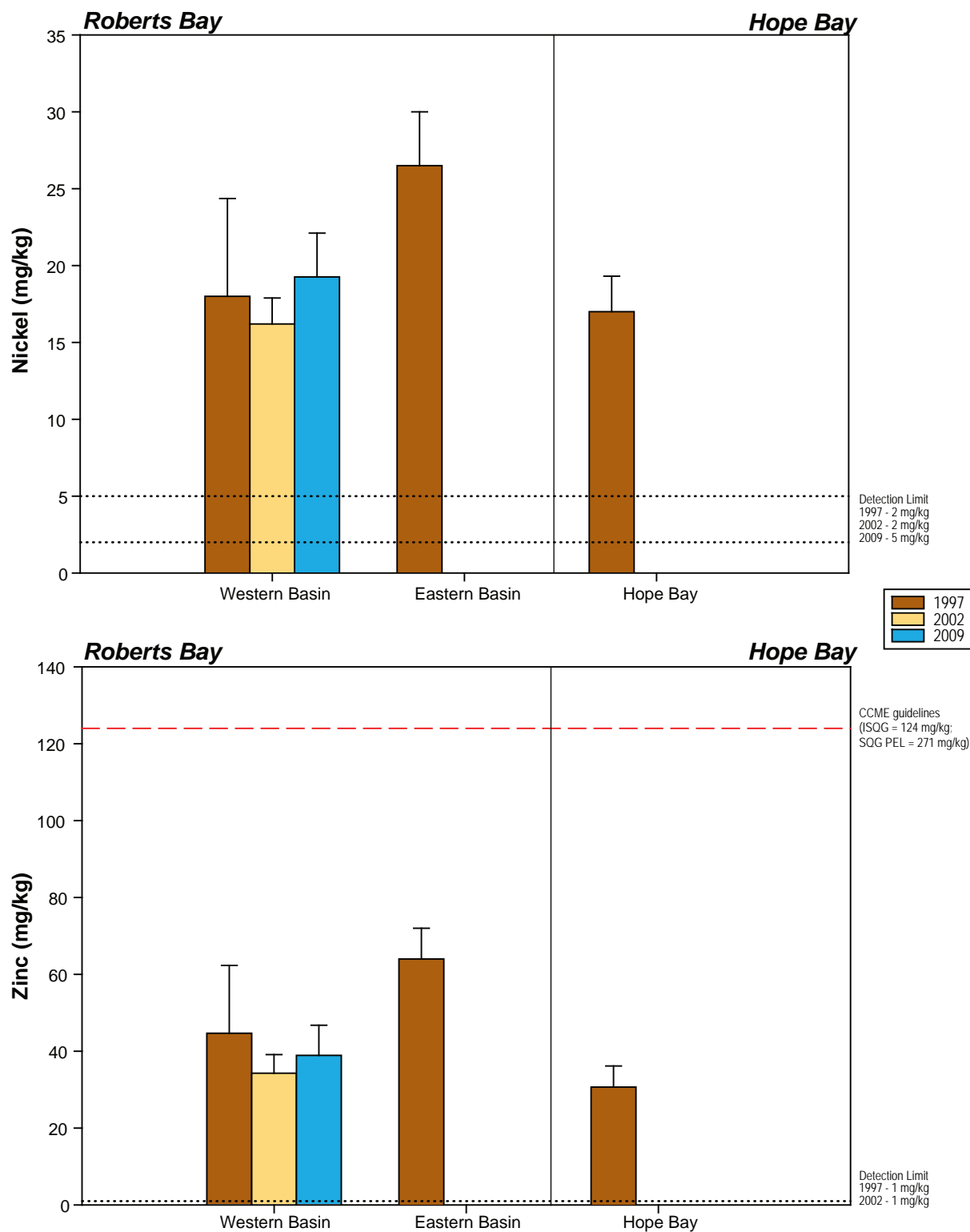
Notes: Error bars represent standard error of the mean of multiple sampling sites.  
 Dotted lines represent analytical detection limits.  
 Red dashed line represents CCME interim sediment quality guideline for the protection of marine aquatic life.  
 Only a subset of sites sampled in 2009 (ST7, ST8, ST2, ST9, and ST10) are plotted here;  
 these sites were selected because they are comparable to historical sampling locations.



Notes: Error bars represent standard error of the mean of multiple sampling sites.  
 Dotted lines represent analytical detection limits.  
 Red dashed line represents CCME interim sediment quality guideline for the protection of marine aquatic life.  
 Only a subset of sites sampled in 2009 (ST7, ST8, ST2, ST9, and ST10) are plotted here;  
 these sites were selected because they are comparable to historical sampling locations.



Notes: Error bars represent standard error of the mean of multiple sampling sites.  
 Dotted lines represent analytical detection limits.  
 Red dashed line represents CCME interim sediment quality guideline for the protection of marine aquatic life.  
 Only a subset of sites sampled in 2009 (ST7, ST8, ST2, ST9, and ST10) are plotted here;  
 these sites were selected because they are comparable to historical sampling locations.



Notes: Error bars represent standard error of the mean of multiple sampling sites.  
 Dotted lines represent analytical detection limits.  
 Red dashed line represents CCME interim sediment quality guideline for the protection of marine aquatic life.  
 Only a subset of sites sampled in 2009 (ST7, ST8, ST2, ST9, and ST10) are plotted here;  
 these sites were selected because they are comparable to historical sampling locations.



### 3.7 PHYTOPLANKTON

Phytoplankton are free-floating autotrophic algae that play an important role in many aquatic systems as primary producers and prey for higher trophic levels. Phytoplankton biomass (as chlorophyll *a*) and taxonomy samples were collected from seven sites in Roberts Bay and two sites in Reference Bay in August, 2009. Chlorophyll *a* results are provided in Appendix 3.7-1 and phytoplankton taxonomic results are provided in Appendices 3.7-2 and 3.7-3.

Phytoplankton biomass was low at all sites and depths sampled, ranging from below detection ( $<0.04 \mu\text{g chl } a/\text{L}$ ) in most samples to a maximum of  $0.18 \mu\text{g chl } a/\text{L}$  in deep water samples collected from REF4 (Figure 3.7-1). Nitrate-limitation was likely the cause of the low phytoplankton biomass, because nitrate concentrations were extremely low in surface waters of Roberts and Reference bays, and phytoplankton require nitrate for growth. It is likely the summer phytoplankton bloom typical of Arctic coastal regions occurred earlier than the August sampling period and was responsible for removing most of the nitrate from the surface waters.

Overall, phytoplankton abundance ranged from 120,030 cells/L at site ST3 to 298,020 cells/L at the more offshore site ST6. Abundance at ST6 was at least 100,000 cells/L higher than at any other site. Reference Bay phytoplankton abundances were within the range observed at Roberts Bay sites. Phytoplankton biomass (as carbon) ranged from  $5.2 \mu\text{g C/L}$  at the pelagic Reference Bay site REF4 to  $9.9 \mu\text{g C/L}$  at site ST0 in the eastern basin of Roberts Bay (Figure 3.7-2).

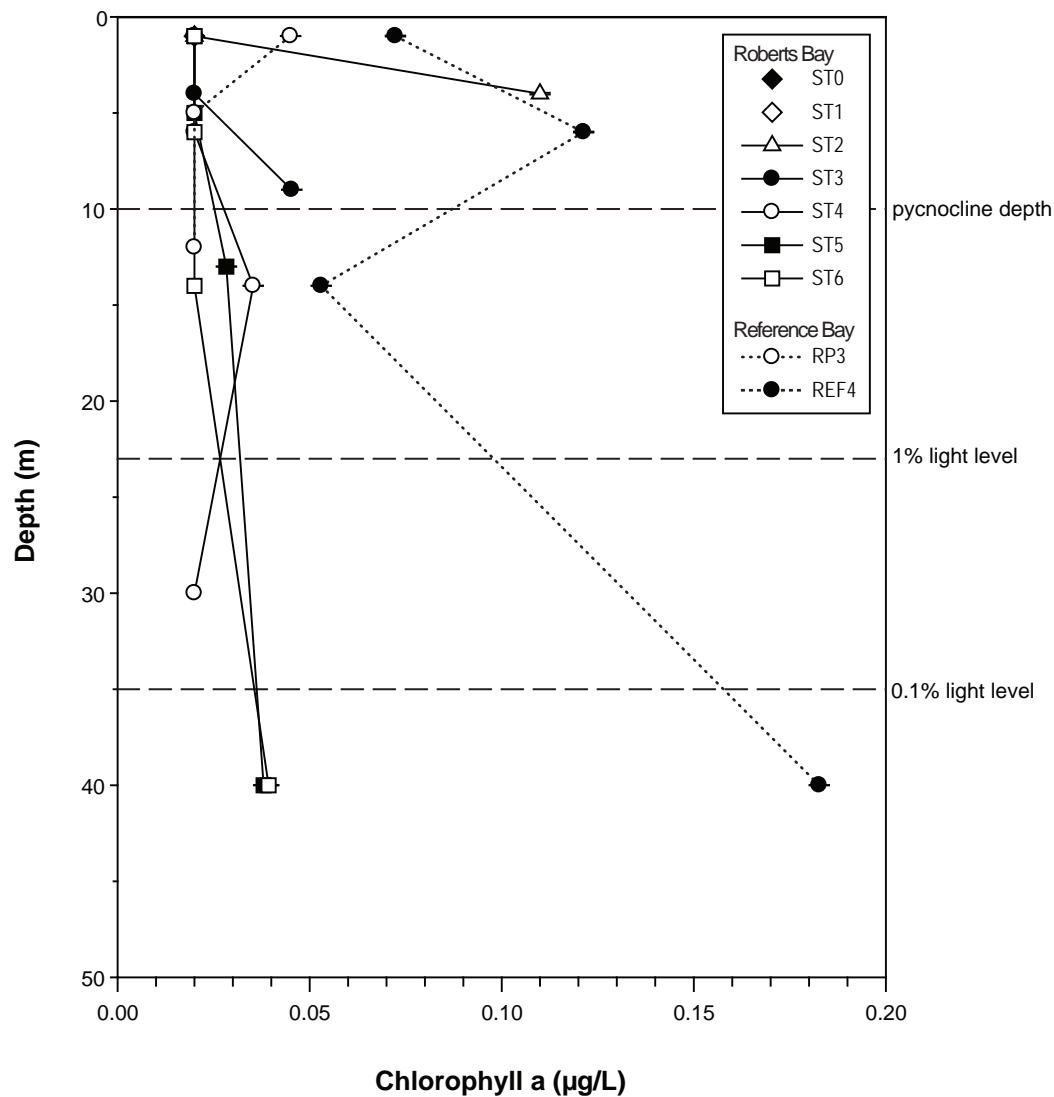
The phytoplankton assemblage in Roberts Bay was numerically dominated by the marine chrysophyte *Dinobryon balticum*. Cryptomonads were also abundant in Roberts Bay sites. These two groups accounted for  $\geq 85\%$  of the phytoplankton assemblage. However, dinoflagellates and other taxa (*Ebria tripartite*, *Myrionecta rubra*) generally dominated the algal assemblage in terms of carbon biomass as a result of their much larger cell size compared to chrysophytes and cryptomonads. The assemblage at site ST6 (i.e., the site located furthest offshore), was slightly different than other Roberts Bay sites, in that chrysophytes made up 82% of the phytoplankton assemblage, and also made the largest contribution to phytoplankton biomass levels (36%). This was followed closely by dinoflagellates (32%). Diatoms accounted for  $<6\%$  of the phytoplankton assemblage in Roberts Bay, but represented as much as 21% of the algal biomass. Cyanobacteria represented a minor fraction of algal abundance and biomass (Figure 3.7-3).

Very few chrysophytes were observed in Reference Bay, and the algal assemblage was numerically dominated by cryptomonads ( $>87\%$ ). Dinoflagellates accounted for the largest proportion of phytoplankton biomass in Reference Bay, though cryptomonads, diatoms, and other taxa also made significant contributions (Figure 3.7-3).

Phytoplankton taxa richness ranged from 11 at RP3 in Reference Bay to 17 at site ST5 in the pelagic region of Roberts Bay. Simpson's diversity index was variable among sites, ranging from 0.12 at RP3 in Reference Bay to 0.61 at both ST0 and ST3 in Roberts Bay (Figure 3.7-4). The low level of Simpson's diversity observed at RP3 was attributable to the dominance of cryptomonads at this site.

#### 3.7.1 Historical Trends in Phytoplankton

Prior to 2009, marine phytoplankton biomass samples (as chlorophyll *a*) were collected in 2006 and 2007, and taxonomy samples were collected in 2007. Figure 2.3-3 shows the historical phytoplankton sampling locations, and Table 2.3-3 presents the methodological details of historical phytoplankton sampling.



Notes: Dotted line represents analytical detection limit (0.04µg/L).

Error bars represent standard error of the mean.

Horizontal dashed lines represent the approximate depth of the pycnocline and the estimated euphotic zone depth (1% and 0.1% light level).

**Phytoplankton Biomass (as Chlorophyll a),  
Hope Bay Belt Project, August 2009**

Figure 3.7-1

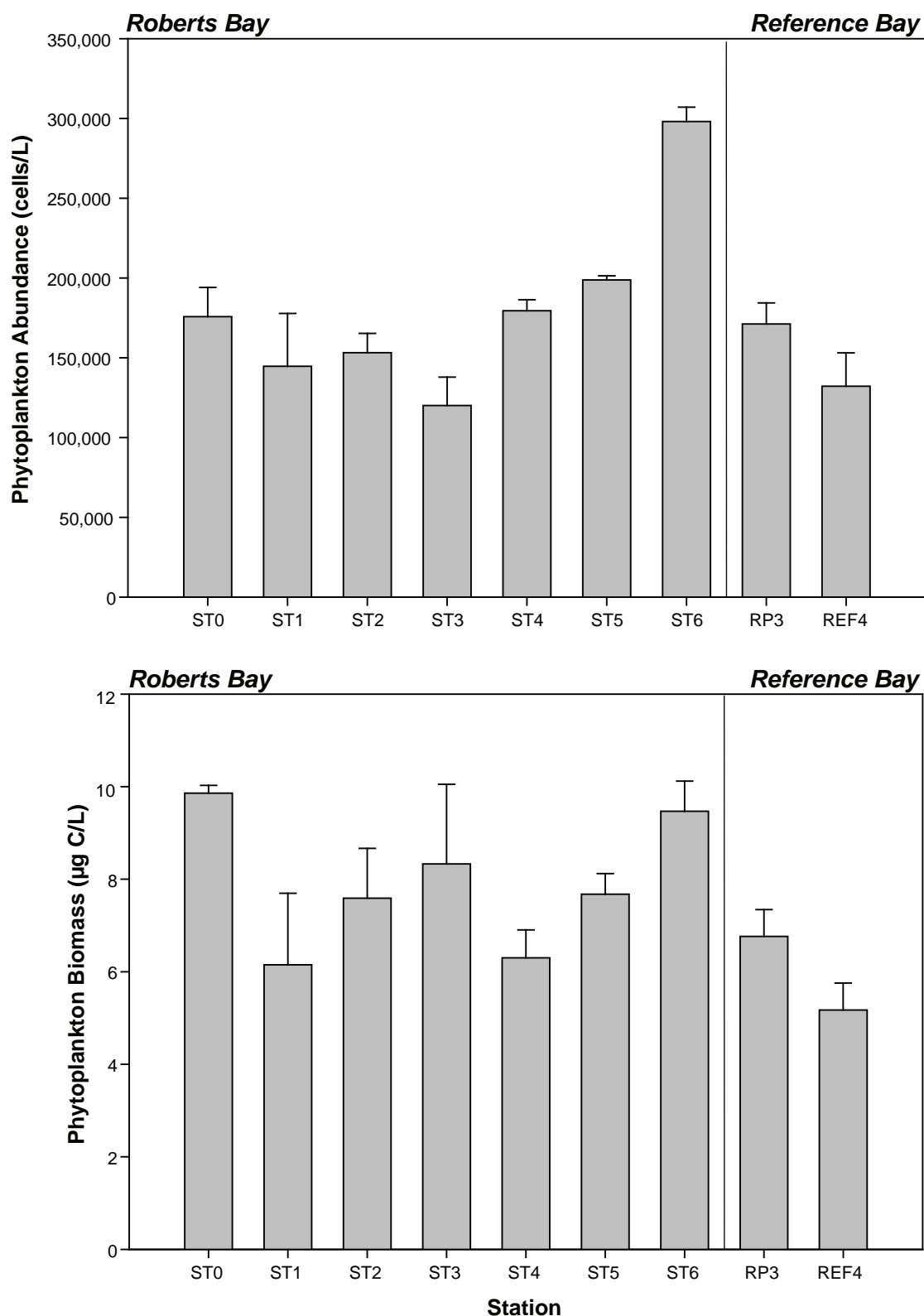


Figure 3.7-2

