Second Five-Year Review Report
Hudson River PCBs Superfund Site

APPENDIX 3

ASSESSMENT OF PCB LEVELS IN FISH TISSUE

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1 INTRODUCTION

This Appendix examines PCB concentrations in fish collected from approximately 1993 to 2016, representing a period of natural attenuation (1993-2008), dredging (2008-2015) and one year post-dredging (2016). The analyses presented include both Upper Hudson and Lower Hudson River data, focusing on those species that were modeled and forecast as part of the 2002 Record of Decision (ROD) (EPA, 2002). Fish tissue data are examined on both wet weight and lipid normalized bases to assess the rates of change in fish concentrations throughout the Hudson. The fish data are also compared with forecasts of fish tissue concentrations under monitored natural attenuation (MNA) developed for the ROD using the FISHRAND bioaccumulation model. These results are then integrated to assess the rates of decline, also referred to as decay or recovery rates, in fish tissue concentrations throughout the Hudson.

Prior to the commencement of the second Five Year Review, EPA prepared a *White Paper: Responses to NOAA Manuscript Entitled: "Re-Visiting Projections of PCBs in Lower Hudson River Fish Using Model Emulation" (Field, Kern, Rosman, 2015) ("White Paper"; EPA, 2016)* evaluating trends in water column, fish, and sediment data. The White Paper explained that a comprehensive approach that considers multiple lines of evidence from all three media together is necessary to understand the recovery of PCB concentrations (as represented by Tri+ PCB[1]) in the Hudson River system. The evaluations presented in this Appendix, along with Appendix 1 (Evaluation of Water Column PCB Concentrations and Loadings) and Appendix 4 (Surface Sediment Concentrations), incorporate additional data now available to build upon and update the analysis of trends presented in EPA (2016). These evaluations demonstrate that, although sediment sampling designs and collection methods were not always consistent through time, the rates of recovery displayed by Upper Hudson water column and fish PCB data prior to dredging

[1] Tri + PCBs represents the sum of all measured PCB congeners with three or more chlorine atoms per molecule. PCBs are a group of chemicals consisting of 209 individual compounds known as congeners. The congeners can have from one to ten chlorine atoms per molecule, each with its own set of chemical properties.

are internally consistent, are consistent with sediment data for the same period, and are consistent with expectations described in the ROD.

This Appendix begins with a summary of relevant background on Remedial Action Objectives (RAOs) for fish tissue PCB levels in the ROD to provide the context for the analysis presented in this five-year review and to highlight why PCBs in fish tissue represent an important long-term monitoring measurement for evaluating remedy effectiveness. Subsequent sections examine the trends in fish body burdens though time and compare these trends with ROD expectations for periods before dredging. Operational considerations that resulted in short-term and localized impacts on fish tissue and water column PCB concentrations are discussed in Appendix 8. Because there is only one year of post-dredging data available, we do not yet have sufficient data to evaluate post-dredging trends. Furthermore, as noted in the ROD (*e.g.*, pp 68-69), EPA's expectation was that following dredging, the system would require at least a year or more to equilibrate to post-dredging conditions and exposures. The expectation as presented in the ROD was that the Upper Hudson River would proceed along a path of MNA until dredging occurred, at which time the system would be "reset" through a temporary disruption with the potential for transient impacts at localized spatial and temporal scales due to active dredging, followed by a new period of MNA.

The accuracy and comparability of monitoring programs relies on consistent sampling methods, sample preparation, and accounting for naturally varying processes that may influence data interpretation. In long-term monitoring programs such as that implemented at the Hudson River, technologies improve over time and sampling and analysis methods may change. In this program, uncertainty in temporal trend analyses due to unforeseen events in the river itself, changes in sample preparation in 2007 through 2013, and naturally varying lipid content in the fish themselves require reconciliation to provide a consistent basis for comparison. Therefore, EPA estimated temporal trends in fish using several complementary statistical approaches to control for the influence of these factors.

To address varying analytical methods, the Aroclor data have been corrected to a common homologue-based metric to permit consistent comparisons of data over time. EPA minimized the effects of differing fillet preparation and processing methods in largemouth bass, brown bullhead, yellow perch and white perch by focusing the wet weight based analysis on fillet data from 1995 through 2006. All samples during this time period included the ribcage and were processed in a consistent manner. Finally, EPA adjusted for variation in lipid content using lipid normalization as well as a data subsetting technique (*i.e.,* restricting the analysis to include only lipid within a narrow range to control for collinearity between time and lipid).

Measurements of organic contaminants such as PCBs are typically accompanied by lipid content measurements, and interpretations of spatial and temporal trends in concentration are conducted on both a wet weight as well as lipid normalized basis. Lipid normalization minimizes variability associated with changes in lipid content and facilitates comparisons across sampling times, locations, and species, although the approach is only useful when a direct and proportional relationship can be observed between lipid content and contaminant concentrations (Randall et al. 1991; Hebert and Keenleyside 1995; van der Heijden and Jonker 2011). Generally, tissue contaminant burdens in two equally exposed organisms will vary proportionally to their lipid content, assuming a correlation between lipid content and contaminant concentration. However, these correlations are not always observed and fail to account for the role of protein (independent of lipid) in absorbing PCBs. At low lipid levels, the role of protein, referred to as non-lipid organic matter (NLOM), increases in importance with respect to absorption capacity relative to primary lipid, particularly in specimens with observed lipids less than 1 percent (de Bruyn and Gobas 2007; Mäenpää et al. 2015; Jahnke et al. 2015), with observed proportionality constants (to lipid) of approximately 0.035 to 0.05 in species with observed lipids less than 1 percent. This can lead to non-linearities in the observed relationship between lipid content and contaminant concentrations.

For example, Panel A in Figure A3-1 shows a plot of median Total PCB ($TPCB^2$)$_{HE}$ (red) and median percent lipid (blue) over time for white perch at RM152. This plot shows that both wet weight $TPCB_{HE}$ and percent lipid have declined similarly over the period of study, indicating an apparent correlation between tissue $TPCB_{HE}$ and lipid. If percent lipid and wet weight PCB were perfectly correlated, then each year in which lipid increased, wet weight PCB would also increase, but this is not always the case. For example, looking at the period 2000 through 2008, in some years lipid decreases, but wet weight PCB increases, and conversely, in some years lipid increases, and yet wet weight PCB decreases. As described above, this may be indicative of sorption of PCBs by NLOM, but is also characteristic of the combined effects of documented measurement error in lipid more generally (e.g., Schlectriem et al. 2012).

Panel B in Figure A3-1 shows this same relationship between wet weight PCBs and lipid content for RM152 for individual white perch samples for two periods, 1997-2002 and 2003-2008. A best fitting line is fit to the data for each subperiod. Absent measurement error in lipid levels, the downward shift of this line between 1997-2002 and 2003-2008 would be an unbiased estimator of the substantial reduction in the average wet weight concentration for white perch with a given lipid content over this 12-year period. Measurement error in the lipid content tends to flatten these best fit lines, amplifying the apparent difference in PCBs for a given lipid level. Because of this flattening effect, the observed shift represents a combination of the effects of changes over time and differences in lipid content between the two time periods.

Each line can be interpreted with reference to the following equation:

$$\text{Wet weight PCB} = \alpha * \text{NLOM} + \beta * \text{Lipid}$$

[2] Total PCBs represents the sum of all measured PCB congeners. PCBs are a group of chemicals consisting of 209 individual compounds known as congeners. The congeners can have from one to ten chlorine atoms per molecule, each with its own set of chemical properties.

where α and β are partition coefficients for NLOM and lipids, respectively. Both best-fitting lines have positive intercepts, representing a combination of the sorption of PCBs by NLOM and the effect of measurement error in lipid content which tends to inflate estimates of the intercepts. Other deviations from a strictly proportional relationship between PCBs and lipid content may also contribute to these intercepts.

Consequently, this appendix evaluates fish tissue trends over time based on several approaches, including a wet weight basis, lipid-normalized basis (*i.e.*, PCBs in fish tissue divided by the fraction lipid) and a lipid-restricted basis (focusing on a narrow and consistent range of lipid levels over time to control for collinearity between lipid content and PCB levels). The third approach, lipid-restricted analysis, looks at trends over time in fish that have similar lipid content to remove the effect of changes in lipid. EPA uses these different approaches because PCB levels in fish can decline in response to declines in both lipid content and environmental exposures. In addition, several factors in the Hudson River system can influence fish PCB-tissue levels in populations, including species, natural variability in fish ages and locations within a reach (exposure), different fish species life cycles, and environmental factors such as flooding, storms, flow conditions, and the possibility of other PCB sources (in the Lower Hudson River). These complementary data evaluation approaches presented here serve as multiple lines of evidence that help address these sources of uncertainty, along with the underlying uncertainties in sampling and measurement techniques, lipid measurements, and spatial and temporal differences in lipid content. Concordance in results across approaches provides a more robust basis for interpreting trends in tissue concentrations over time.

2 RELEVANT BACKGROUND

To provide context for this evaluation, relevant elements of the 2002 ROD are reviewed below.

2.1 Elements of the Remedy

Two of the RAOs identified in the 2002 ROD addressed reductions in concentrations of PCBs in fish tissue that would lead to a reduction in potential risks associated with PCB exposure to humans and the environment:

- Reduce the cancer risks and non-cancer health hazards for people eating fish from the Hudson River by reducing the concentration of PCBs in fish. The risk-based [preliminary remediation goal (PRG)] for the protection of human health is 0.05 mg/kg PCBs in fish fillet based on non-cancer hazard indices for the [reasonable maximum exposure (RME)] adult fish consumption rate of one halfpound meal per week (this level is protective of cancer risks as well). Other target concentrations are 0.2 mg/kg PCBs in fish fillet, which is protective at a fish consumption rate of one half-pound meal per month and 0.4 mg/kg PCBs in fish fillet, which is protective of the [central tendency (CT)] or average angler, who consumes one half-pound meal every two months.
- Reduce the risks to ecological receptors by reducing the concentration of PCBs in fish. The risk-based PRG for the ecological exposure pathway is a range from 0.3 to 0.03 mg/kg PCBs in fish (largemouth bass, whole body), based on the [lowest observed adverse effect level (LOAEL)] and the [no-observed adverse effect level (NOAEL)] for consumption of fish by the river otter… In addition, a range from 0.7 to 0.07 mg/kg PCBs in spottail shiner (whole fish) was developed based on the NOAEL and LOAEL for the mink, which is a species known to be sensitive to PCBs (2002 ROD, p. 50). In the ROD, EPA adopted the PRGs as the remedial goals for the Site.

In addition to the removal of approximately 2.6 million cubic yards of PCB-contaminated contaminated sediment, the remedy also includes MNA of PCB contamination remaining

in the river after dredging until remedial goals are met, and a long-term monitoring program, including fish tissue monitoring.

3 COMPILATION OF DATA FOR ANALYSIS

3.1 Data Used in the Analysis

The New York State Department of Environmental Conservation (NYSDEC) has been collecting fish and monitoring PCB levels in fish tissue in the Hudson River since approximately 1975 (NYSDEC 2005). NYSDEC monitoring has focused on Upper Hudson River (UHR) fish at the Glens Falls Feeder Dam Pool (river mile (RM) 201), Thompson Island Pool (RM189), and the Stillwater Pool from either Coveville (RM176) or Stillwater (RM168) from 1975 to 2007. NYSDEC data from other UHR locations (*e.g.*, Remnant Deposit sites) exist through 2011. In the Lower Hudson River, NYSDEC has been monitoring fish tissue from 1976 through 2016 at various locations and focused on Albany/Troy (RM152-142), Catskill (RM112/113), Poughkeepsie (RM76), Newburgh (RM59), Haverstraw/Croton/Piermont/Tappan Zee (approximately RM36-27), and the George Washington Bridge (RM12). General Electric Company (GE) has been monitoring PCB levels in Hudson River fish from 2004-2016 at many of these same monitoring locations.

Details regarding local fish monitoring stations and species for this project and the rationale behind their selection are presented in the Baseline Monitoring Report [BMR] (and revisions, EPA 2000a); the Baseline Ecological Risk Assessment [BERA] (and revisions), EPA 2000c); the Feasibility Study ([FS] EPA, 2000b); the ROD (EPA 2002); the Quality Assurance Project Plan Baseline Monitoring Program [BMP] (General Electric 2004);) and Phase 2 (General Electric 2012). Remedial Action Monitoring Program Quality Assurance Program Plans (RAMP QAPPs) and are not repeated here. All data presented in this appendix have undergone quality control and validation. The data span much of the length of the Site, from the Thompson Island Pool (RM194 to 188.5) to RM50 in the Lower Hudson River. Several fish collection areas have been reoccupied from year to year, resulting in a limited number of river areas with long-term records. For consistent presentation, the data have been grouped into seven primary locations to represent those areas, three of which are in the Upper Hudson. The locations are listed in Table A3-1, along with the river miles included in each location and the number of species at each station

with long-term collection records. Data were restricted to the period 1993 to 2016, representing the period following the largest releases associated with the Allen Mill event, which began in September 1991. The analyses conducted for this appendix focus on the period 1995 and later because by 1995 the releases from the Allen Mill were largely controlled. The fish monitoring by NYSDEC yielded long-term records of PCB levels in a total of eleven species, of which seven were modeled and forecast as part of the ROD. GE collected additional fish tissue samples as part of the baseline monitoring period prior to dredging (2004-2008). Table A3-2 summarizes the available data collected by NYSDEC and GE, listing the species with long-term records, identifying the associated monitoring locations for each species, the length of the record, and data sources (NYSDEC or NYSDEC+GE).

3.2 Determination of the TPCB Concentration and its Relationship to Tri+ PCB

For both the NYSDEC and GE data, fish tissue analyses were primarily conducted using an Aroclor-based analysis, with a subset of the samples analyzed using a more quantitative procedure based on PCB congeners. Because of the subjective nature of Aroclor identification and quantitation by the analyst, it is important to reference the Aroclor-based results to a more objective method based on PCB homologues or PCB congeners to facilitate comparisons and analyses across the long-term database. In this manner, changes or trends in reported PCB concentrations in fish tissue can be attributed to actual changes in the environment, and not due to changes in analytical procedures, analytical laboratories or personnel. Therefore, all Aroclor-based results were converted to estimates of total PCB homologue equivalent ($TPCB_{HE}$) concentrations following the procedures described in Appendix 5, and for the remainder of this appendix, total PCB concentrations will be referred to as $TPCB_{HE}$. These procedures are specific to laboratory and analytical method. That is, each unique combination of laboratory and time was assigned a specific factor to convert Aroclor-based results to total PCB homologue or congener-based values. In Section 4.2 of this appendix, there is a comparison between fish tissue trends developed based on $TPCB_{HE}$ results and trends similarly developed based on the sum of Aroclors.

Note that for most of the time, $TPCB_{HE}$ is equivalent to the sum of trichloro and higher congeners of PCBs in fish tissue, and the FISHRAND and HUDTOX modeling was conducted based on the sum of trichloro and higher congeners. This is because lighter PCB molecules (*i.e.*, mono- and di-substituted PCB congeners) are generally not stored in fish tissues, as originally presented in the EPA RI for the Hudson (EPA1999; EPA 2000b). Thus, $TPCB_{HE}$ is functionally similar to Tri+ PCBs (the sum of congeners with at least three chlorine substitutions), which was the PCB measure used in the models.

However, as Appendices 1, 5, and 8 discuss, mono- and dichloro congeners comprised a substantial portion of the observed fish tissue burdens of PCBs during the dredging period itself (*i.e.*, 2009 to 2015). During the BMP, mono- and dichloro congeners comprised 1 percent or less of the total fish tissue PCB burden (expressed as the fraction of Aroclor 1221). In 2009-2010, this increased to 3-4 percent, likely due to the non-aqueous phase liquid (NAPL) released in dissolved form during dredging operations as reflected in the water column (see Appendix 1). However, mono and dichloro forms comprised approximately 11-18 percent of the total fish tissue burden between 2011 and 2015 consistent with the short-term transient impact during the dredging. More recent data indicate that mono- and dichloro congeners accounted for only 3 percent of the fish tissue burden in 2016, and it is expected that the proportion of these congeners will further decline to 1 percent or less in a few years.

In summary, nearly all PCB concentrations in fish were analyzed as the sum of Aroclors. However, this sum is not always the most accurate representation of total PCB concentration in fish. To address this, EPA developed relationships between the total PCB concentration based on PCB congener or homologue values ($TPCB_{HE}$) and the sum of Aroclors (see Appendix 5) for each unique lab-time period pair. For all years up to the actual dredging period itself, $TPCB_{HE}$ in fish is essentially equal to the sum of trichloro through decachloro PCB homologues (Tri+ PCB) because fish do not generally retain the lighter congeners.

3.3 Variations in Fish Sample Preparation

The various fish tissue samples collected by NYSDEC and GE include individual whole body samples, whole body composites (typically multiple individual specimens combined to make a single blended sample), NYS standard fillet samples (the fillet including the rib portion of the fillet), various internal organs, whole body minus head and viscera, and fillets prepared by GE which excluded the rib portion of the animal. NYSDEC has historically collected the most extensive record of fish tissue samples, and thus, those data form the primary basis for examination of long-term trends occurring prior to dredging. NYSDEC processed most samples as one of the following: whole body, whole body composite, NYS standard fillet, or whole body minus head and viscera. The first two sample types are considered equivalent because both include all components of the fish in their natural proportions. The latter two sample types are considered essentially equivalent because whole body minus head and viscera is approximately equivalent to two fillet samples.

Between 2007 and 2013, for some species at some locations, GE laboratory contractors used a non-NYSDEC-standard fillet approach by not including the rib cage material in the fillet harvested for analyses. Because this method of preparing samples differs from the NYSDEC method, EPA evaluated the difference between rib-in (NYSDEC-standard fillet) and rib-out (non-NYSDEC-standard fillet) samples during a special study in 2014. EPA found that on a wet weight basis, the difference between fillets prepared as rib-in *vs*. rib-out is variable and can be greater than a factor of two, while for lipid normalized data, the difference averages less than 20 percent. EPA's evaluation establishes that the lipid-normalized rib-out data are useable for trend analyses. Thus, for the pre-dredging trend calculations presented here, the rib-out GE fillet samples are excluded from the wet weight analyses but included for the lipid normalized analyses. In the interest of clarity and transparency, non-NYSDEC standard fillet data points are shown using a unique symbol when presented in the charts prepared for this report to provide a complete record of the results. The lipid-restricted analysis focuses on a narrow range of lipid values to completely remove any collinearity between lipid and time (that is, the analyses evaluate decay rates independent of trends in lipid). This approach also controls for changes in sample processing by excluding non-NYSDEC standard fillet samples. This exclusion of non-

NYSDEC-standard fillet samples from the lipid-restricted analysis is necessary to control for lipid covariation caused by sample preparation, and other dissimilarities in sample media, by using only identically processed samples.

4 PRE-DREDGING TRENDS IN FISH TISSUE: MNA PERIOD

In this section, long-term fish tissue trends are empirically examined using several data-based statistical approaches, including on a wet weight basis ($TPCB_{HE}$ in fish tissue), lipid-normalized basis ($TPCB_{HE}$ in fish tissue divided by the lipid content expressed as a fraction) and a lipid-restricted basis using only those samples with roughly equivalent lipid content. Specific details and the basis of the lattermost analysis are explained in subsection 4.3. This section examines the estimated rates of observed decline in $TPCB_{HE}$ over time for the period beginning in 1995 and ending just prior to the start of dredging (April 2009). This period begins when the releases from the Allen Mill were brought under control and the Site was undergoing natural attenuation (see EPA, 2016). This period of natural attenuation ends with initiation of dredging and its associated disturbances of the river bottom. Because the HUDTOX and FISHRAND models were used to predict an MNA scenario, the data-based trend analyses can be compared to trends as predicted by the model, providing another line of evidence for model performance. Detailed comparisons are presented in Appendix 1 for water column concentrations and in this appendix for fish tissue concentrations.

Data from the dredging period, 2009-2015, are also presented in this section to document the changes in fish tissue levels in response to dredging (General Electric 2004, 2009, 2012). Appendix 8 provides a more detailed evaluation of transient impacts of dredging with respect to fish tissue concentrations on a station-by-station basis. In this appendix, predicted fish tissue concentrations from the FISHRAND model, adjusted to account for resuspension observed during the dredging period, are presented for comparison purposes, although as noted, the models were designed to predict long-term rather than short-term impacts of exposure to PCBs, and on a river reach basis rather than a station-by-station basis. Lastly, this section presents the first post-dredging data for 2016 obtained by GE. Depending on the specific location, the 2016 data still reflect residual dredging impacts, given that sampling occurred during the spring of 2016 and dredging was only completed in the fall of 2015. Further, as discussed in the ROD (EPA 2002), there is at least a one-year equilibration period following dredging.

The three complementary bases for estimating the rates of decline in fish tissue $TPCB_{HE}$ levels (*i.e.,* wet weight, lipid-normalized, and lipid-restricted) are examined here to provide several perspectives on observed decay rates. The straightforward observation of the decline in $TPCB_{HE}$ levels over time on a wet-weight basis provides one means of estimating how fish tissue concentrations will decline under MNA, and is the basis for estimating risks to human health and the environment. In general, declines in fish tissue $TPCB_{HE}$ levels are attributable to declines in sediment and water exposure concentrations. However, to the extent wet weight concentrations are correlated with lipid content, declines in lipid content can confound wet-weight-based trend analyses. That is, declines in wet weight concentrations may be associated with declines in lipid in addition to declines in exposure concentrations. Thus, an alternative basis to determine the rate of decline in $TPCB_{HE}$ levels is to express the $TPCB_{HE}$ concentrations on a lipid-normalized basis. Lipid normalized values are derived by dividing $TPCB_{HE}$ concentrations by the fraction of lipid in the fish sample as given by the following formula:

$$TPCB_{HE}(mg\ PCB/kg\ lipid) = \frac{TPCB_{HE}(mg\ PCB/kg\ tissue)}{Fract_{lipid}\ (kg\ lipid/kg\ tissue)}$$

The change in lipid-normalized $TPCB_{HE}$ concentrations through time provides an estimate of the decay rate of PCB levels in fish focusing on the effect of the exposure of fish to PCBs, rather than changes in lipid.

Finally, while $TPCB_{HE}$ and lipid levels in fish are often correlated, the relationship may not always be linear, because PCBs adsorb to other fish tissue such as protein, and sorption to other tissue is relatively more important for fish with low lipids (Randall et al. 1991; Hebert and Keenleyside 1995; van der Heijden and Jonker 2011). To address this non-linearity, $TPCB_{HE}$ levels in fish are examined through time for a limited range of lipid levels (*i.e.,* a lipid-restricted basis). Using data over a narrow range in lipid level reduces the variation in $TPCB_{HE}$ attributable to lipid variation, identifying change in $TPCB_{HE}$ that is independent of trends in lipid content.

In preparing these time trends, analyses are focused on those fish species for which model results are available and that were used in the human health and ecological risk assessments supporting the 2002 ROD. These species include largemouth bass, brown bullhead, yellow perch, pumpkinseed, spottail shiner and white perch. The largemouth bass, brown bullhead, and yellow perch were used in the human health risk assessment to develop a species-weighted average concentration consistent with typical angler's creel exposure. Striped bass were also included, as they are an important sport fish for the Lower Hudson, although this species was not modeled to support the ROD. In addition to these, smallmouth bass were also examined because they are often caught in lieu of largemouth bass, although smallmouth bass is also not a modeled species. Finally, these species offer the longest and most complete data sets.

Trends of $TPCB_{HE}$ were examined for the eight species listed above collected at the NYSDEC monitoring stations. Data from these stations through 1997 were also used in the modeling analysis conducted for the ROD, which included forecasts of fish tissue concentrations at these locations under various scenarios starting in 1998 and going forward. As mentioned above, the period 1995 to 2008 represents a fourteen-year MNA period, much of which transpired after the issuance of the modeling reports in 2000. Thus, the monitoring data from 1995 to 2008 can be used to empirically estimate the rate of recovery, or decay rates, in fish tissue concentrations under MNA.

Prior to comparing trends based on empirical observations to those originally forecast by EPA models in Section 5, Subsections 4.1 through 4.3 first present the empirical observations of the rates of decline in $TPCB_{HE}$ levels in fish tissue. In this discussion, Upper Hudson data are represented on a river section basis, corresponding to the three river sections defined in the ROD and shown in Table A3-1. The data presented for these sections represent all available data obtained in these river sections. Thus, RS1 (RM189) comprises the monitoring stations TD1 through TD5 and RS2 consists of data from ND1 to ND5. RS3 is represented as one location, with corresponding fish data collected in the vicinity of RM168. In the Lower Hudson, the river sections are referenced by a nominal river mile, as given in Table A3-1. Similar to the Upper Hudson River sections, each Lower

Hudson River section graph for each species presents all the available data for that section. For each species at each station, data were examined for the MNA period to estimate the observed rate of decline. In evaluating the data, EPA established a minimum data requirement of at least 25 samples spanning at least 5 years during the MNA period to support decay rate calculations. These criteria were established to avoid using smaller data sets that might reflect short-term fluctuations that are not representative of longer term trends. Additionally, the MNA calculation was restricted to samples prepared on a consistent basis over time. Thus, for forage fish such as pumpkinseed and spottail shiner, only whole body and whole body composite samples, respectively, were used in the calculation of the rate of decline. For larger fish, the rates were calculated based only on standard fillet samples and whole body samples minus head and viscera. As described in Section 3.3, rib-out fillet samples (*e.g.*, excluding rib cage material) are identified by triangles in the figures discussed below. To avoid introducing uncertainties into the wet-weight decay estimates during the MNA period, wet weight and lipid-restricted decay rates excluded rib-out samples. However, as based on EPA's analysis discussed above in Section 3.3, to avoid introducing unnecessary uncertainty into trend analysis, these data were included in the lipid normalized estimates. In all figures, samples collected from 1993 through the MNA period are shown in blue, dredging period samples (2009 to 2015) are shown in orange, and 2016 sample results are shown in green.

4.1 Trends in Wet Weight-Based Results

Figures A3-2 through A3-8 present the wet weight $TPCB_{HE}$ levels in fish across the river sections listed in Table A3-1. All available data for each species are shown in the figures, even if the amount of data was not sufficient to support a rate of decline estimate. Also shown on each figure are regression curves providing the best fit to the trend in fish tissue data for the 1995 – 2008 MNA period. As discussed previously, these regression curves are based on NYSDEC and GE data where available, and do not include any rib-out samples. The regression results are used to calculate an average rate of decline, also referred to as a decay or recovery rate. When the slope of the regression line is significantly less than zero in a statistical sense, a half-life estimate is also calculated. The rates of

decline for these results, along with the estimates of uncertainty on those rates, are summarized in Table A3-3.

Evident in Figures A3-2 to A3-4 is the relatively rapid decline of wet weight concentrations of PCBs across nearly all species and stations in the Upper Hudson. While rates of decline vary across individual species, average rates of decline are approximately 16 percent per year, corresponding to a 4-year half-life. In the Lower Hudson at RM152, wet weight rates of decline in fish tissue PCB concentrations (average of 16 percent per year) are consistent with those observed in the Upper Hudson, as shown in Figure A3-5, suggesting a link between exposure conditions in the Upper Hudson and this region of the Lower Hudson. However, downstream of this river section, fish tissue concentrations do not decline as rapidly as observed in upstream river sections. Figures A3-6 through A3-8 present the results for RM113, RM90, and RM50, respectively. Rates of decline at RM113 are somewhat less rapid than those observed upstream, on average approximately 11 percent per year. In RM90, the rate of decline averages 8 percent per year. At RM50, the data sets are limited, but using the three species with records containing at least 25 samples, the average rate of decline is low (about 1 percent per year).

To summarize, the results for wet weight fish tissue PCB concentrations indicate a substantial lessening in the rate of decline moving downstream in the Lower Hudson. During the MNA years, fish tissue wet-weight PCB concentrations in the Upper Hudson declined at a rapid rate, typically 12 to 20 percent per year, coincident with substantive declines in lipid levels in many species at several stations. Therefore, the rates of decline were also examined by adjusting for lipid variations. These analyses are discussed in the next two subsections.

4.2 Trends in Lipid-Normalized Results

The fish results described in the previous section were also examined on a lipid-normalized basis, calculated as described in Section 4.0. Figures A3-9 through A3-15 parallel the presentation of fish tissue data shown in Figures A3-2 through A3-8. In normalizing to lipid concentration, this analysis implicitly assumes that PCB concentrations correlate

linearly with lipid content, such that a doubling of the lipid content in fish at the identical level of exposure will double the wet weight concentration by maintaining a constant lipid-normalized concentration. While lipids and PCBs are often strongly correlated, this relationship is stronger for some species and locations than for others. In addition, there is recent evidence to suggest that the relationship can exhibit non-linearities (Garvey et al. 2016; Randall et al. 1991; Seston et al. 2015). The observed relationships in the literature suggest that a strict lipid-normalized calculation is likely to provide a lower bound on the rate of decline of $TPCB_{HE}$ exposures for fish, when lipid content also has a declining trend. Less rapid rates of decline were obtained for essentially all fish and stations based on lipid-normalized concentrations relative to wet weight decay rates.

Figures A3-9 through A3-11 and Table A3-3 present the lipid normalized trends for the Upper Hudson River sections. The average rate of decline across adult sport fish species (*i.e.,* not including pumpkinseed or spottail shiner) for the entire Upper Hudson River is approximately 8 percent per year, corresponding to an 8-year half-life. This rate is substantially less rapid than the average 16 percent per year rate of decline for wet weight concentrations, suggesting that changes in lipid account for a portion of the observed decreases on a wet weight basis. As discussed below, these average decay rates calculated on a lipid-normalized basis are consistent with the lipid-normalized decay rates estimated as part of the ROD, indicating satisfactory model performance with respect to capturing trends over time. Similarly, across all fish species at RM152, the estimated lipid-normalized rate of decline averages about 10 percent per year, compared to the average of 16 percent on a wet weight basis (Figure A3-12).

Downstream of RM152, the rates of decline based on lipid-normalized concentrations were again slower relative to estimated wet-weight based rates and were also slower than the lipid-normalized rates observed upstream. Figures A3-13 through A3-15 present the results for RM113, RM90, and RM50, respectively. At RM113, the estimated average decay rate is approximately 3 percent per year, while most rates estimated at RM90 and RM50 were not significantly different from zero. Thus, overall the results for the latter two stations are

not distinguishable from a zero rate of change (*i.e.*, no trend with time), based on the available data.

There are significant differences in lipid-normalized decay rates across species and locations. For example, as shown in Figure A3-10 and summarized in Table A3-3, in RS2 (RM184), the estimated decay rate for yellow perch is 18 percent and for smallmouth bass is 15 percent per year, while for brown bullhead, the estimated decay rate is 2 percent. Largemouth bass fall in-between at 7 percent per year. Brown bullhead, a species closely associated with sediments due to their foraging strategy and life history, consistently demonstrates among the lowest decay rate across all species.

The rates of decline based on lipid-normalized results spatially parallel those obtained on a wet weight basis, although the rate values calculated when accounting for lipid content are generally less than half those obtained from the wet weight results (see Table A3-3). The spatial pattern exhibited by the rates of decline on both a wet weight and a lipid-normalized basis indicate that the Lower Hudson recovers more slowly than the Upper Hudson under MNA. This is illustrated in the left side diagrams of Figure A3-16A, where the average rates of decline for each river section *vs.* distance downstream are plotted. Both wet weight and lipid-normalized decay rates exhibit the lowest values for RM50. While the apparent lack of decline in RM50 may be due to the difficulty in estimating statistically significant changes in low absolute fish tissue concentrations, it is unclear how the exposure concentrations in surface sediments have changed over time in this reach of the river. Limited surface water concentrations collected at Poughkeepsie (RM 75) in the Lower Hudson River showed declining trends in water column concentrations (see Appendix 1 for details).

The calculations described above were repeated using the sum of Aroclor data as reported, and compared to the PCB homologue equivalent ($TPCB_{HE}$)-based results. This was done as a check and to evaluate possible artifacts arising when converting the fish tissue data to the $TPCB_{HE}$ basis. The results of this analysis are shown in Figure A3-16A. The rates of decline, as well as trends with river mile, are nearly identical when comparing results

obtained using sum of Aroclors values versus on a $TPCB_{HE}$ basis. Because of the importance of these observations regarding the rates of decline within the Hudson River, the findings in Figure A3-16A were further analyzed by focusing on only the most robust and temporally extensive of the data sets. To this end, only those species-station pairs with at least 8 years of data and at least 100 samples were plotted. This filtering step removed almost half of the available data sets in refining the presentation to those data sets best suited to support long-term trend estimates. The results (shown in Figure A3-16B) further confirm the conclusions drawn above, specifically, that MNA rates of decline in the Upper Hudson and RM152 for wet weight tissue concentrations declined at approximately 15 to 20 percent, with lower rates observed at locations further downstream in the Lower Hudson River. Similarly, lipid-normalized tissue concentrations declined at approximately 8 percent per year in the Upper Hudson and in RM152, with slower rates observed downstream at RM113 and below.

The lipid-normalized results presented in Figures A3-16A and A3-16B, included the non-NYSDEC-standard fillet data. A sensitivity analysis excluding the non-NYSDEC-standard fillet data was performed and the results are presented in Figure A3-16C. The results of this sensitivity analysis indicate a similar distribution of the estimated rates of decline, with or without the non-NYSDEC standard fillet data. Therefore, EPA's conclusion on the rates of decline and their distributions across the Hudson River, on a lipid-normalized basis, is consistent regardless of whether the non-NYSDEC-standard fillet data are used or not.

4.3 Trends in Lipid-Restricted Results

Sections 4.1 and 4.2 report trends in wet weight and lipid normalized fish tissue concentrations, with the objective of bounding the trend in PCB exposures to fish: wet weight trends may overstate the decline by confounding it with declines in lipids, whereas lipid normalization may overcompensate where tissue concentrations are not strictly proportional to lipid content, especially at low lipid levels.

This section employs a third method, controlling for lipid covariation through experimental design, rather than statistical adjustments, avoiding the assumption of strict proportionality

assumed in the lipid normalization approach. This approach estimates trends in $TPCB_{HE}$ PCBs for fish within bins of similar lipid content, to control for lipid content without assuming proportionality between PCBs and lipid content. This approach is similar to how the effects of size are controlled by limiting the range of fish lengths collected in the field. Generally, the effects of lipid-PCB covariation would be similarly controlled if it were known at the time of collection.

Since the late 1990s, the data show that lipid content in fish tissue has declined across many species and locations in both the Upper and Lower Hudson River. TPCBs in some species have also followed this declining pattern, and as a result, a proportion of apparent temporal changes in exposure, as indicated by changes in body burdens, may be conflated with temporal changes in lipid content as discussed previously. Furthermore, because of the effect of NLOM, the associations between lipid and PCB may not be simple, suggesting that the assumptions of the lipid-normalized trend analysis are not fully satisfied, motivating this third method of analysis.

To apply the regression approach to lipid restricted groups of fish, tissue concentrations are fit to the following temporal trend model:

$$C_f = C_0 \times f_L^B e^{kt}$$

which is linearized prior to fitting as

$$\mathrm{Ln}\left(C_f\right) = \mathrm{Ln}(C_0) + B \times Ln(f_L) + k \times t$$

where C_f is the PCB concentration in fish, f_L is the fraction lipid in fish, and k is the exponential decay rate, and the parameter B determines the response of PCB concentrations to the lipid content.

This approach provides a compromise between maximizing sample size and minimizing lipid variability. When fish tissue concentration varies linearly with lipids, B equals 1,

while B would be 0 in the extreme case that tissue concentrations are independent of lipids. By allowing B to vary freely, the method avoids the strict proportionality required for lipid normalization, and by focusing on a narrow range of lipids it attempts to avoid mixing high-lipid concentrations, where the PCBs tend to be proportional to lipids, with low-lipid concentrations, where other tissue becomes more important and proportionality to lipids is less reliable.

The first step in the lipid-restricted analysis was to determine the representative lipid levels for each fish species and river mile. For each species and river mile, a systematic search approach was used to identify a range of lipid content, maximizing the number of years in which 5 or more samples were present. The width and center of this range was varied systematically and the number of years with at least 5 samples was identified. The results of the systematic search were inspected visually to ensure that obvious visually recognizable intervals were not missed by the automated algorithm.

For example, the top panel of Figure A3-17 shows the full set of lipid values for brown bullhead from 1995 through 2006. Two red lines, determined from the systematic search algorithm, illustrate that a consistent range of lipid values is approximately 1.5 to 2.5 percent. The second panel shows just the selected samples that demonstrate a relatively even lipid distribution within the selected range across these years. However, the number of samples per year is also relatively small, which may negatively influence precision of estimates (*i.e.*, a wide confidence interval). The third panel shows the sample $TPCB_{HE}$ concentrations for these selected samples with the fitted exponential decay curve overlaid, including the estimated decay rate and associated confidence interval. This figure illustrates the competing effects of restricting the lipid range - accuracy is improved by restricting the analysis to a consistent lipid level, but precision of decay estimates decreases due to lower sample sizes per year. The rate of decay obtained for brown bullhead (1 percent per year, with a confidence interval of a decline of 7 to a rise of 4 percent per year) is in general agreement with the results based on lipid normalization.

Figure A3-18 provides the same analysis for largemouth bass and shows that temporal changes in lipid content preclude identification of a consistent representative range of lipid content. In this case, the estimated exponential decay rate may be somewhat conflated with lipid covariation. However, the rate of decline (12 percent per year with a confidence interval of 18 to 6 percent per year), as shown in the third panel, falls within the range of estimates obtained based on the wet weight and lipid-normalized calculations described previously (22 and 8 percent per year respectively).

The right panel of Table A-3 presents results obtained with this method. In general, the standard errors of estimates are higher than are shown for the wet weight and lipid-normalized trends, reflecting the smaller sample sizes inherent in limiting lipid variation. The expectation is that these estimated rates of decline would be bounded below by the lipid-normalized rates and above by wet weight rates of decline, and in many cases this is true, as shown in the right panel of Table A-3. In most cases, lipid-normalization, which takes advantage of the full data set, represents a more conservative decay rate estimate (*e.g.*, a slower rate of decline than estimated from using the lipid-restricted approach, which controls for both lipid trend and changes in sample processing over time).

4.4 Summary of Pre-Dredging Fish Tissue Trend Analyses

Calculated decay rates demonstrate that:

- In general, fish monitoring results in the Upper Hudson River show that decay rate estimates are variable across species and locations, with the brown bullhead demonstrating the slowest recovery, followed by more rapid recovery in largemouth bass, yellow perch, and smallmouth bass, in that order;
- Decay rate estimates are consistently more rapid when calculated on a wet weight basis as compared to a lipid-normalized or lipid-restricted basis. This indicates that a portion of the decline in fish tissue concentrations is due to declining lipids, with the remainder due to declining exposures;
- Decay rates that use the lipid-restricted approach to control for lipid variability and differences in sample processing over time show faster observed recovery across several species and locations than the estimates obtained using lipid-normalized

data, suggesting that lipid-normalization provides a conservative estimate of pre-dredging MNA decay rates;

- PCBs in fish tissue in the Upper Hudson River and downstream to RM152 in the Lower Hudson River are declining more rapidly than in the remainder of the Hudson River below RM113; and,
- Estimated decay rates are consistently less rapid moving downstream in the Lower Hudson River, with estimated rates not statistically different from zero for several species at RM113, RM90 and RM50, indicating different trends in exposure and suggesting a disconnect in exposure sources between the Upper and Lower Hudson.

5 COMPARISON OF ROD MODEL FORECASTS WITH MNA OBSERVATIONS

In this section, data trends observed over the MNA period 1995 to 2008 are compared to MNA forecasts developed as part of the ROD for this period. Model forecasts presented here were taken directly from the ROD (for example, Table 11-3 for largemouth bass and the Species-Weighted Fish Fillet Average PCB Concentration forecast presented in Table 11-2). The ROD did not present model results for all species and locations, but these were obtained from archived output from the original model runs. Data from the MNA period are also contrasted with forecast curves generated as part of EPA's 2010 Phase 1 Evaluation Report reflecting actual rather than estimated flows and external solids loads (EPA 2010). As part of EPA's Phase 1 evaluation, the model forecasts were revised to reflect actual river flows between 1998 and 2009 (the ROD forecasts incorporated a synthetic series of future flows based on historical daily flows from selected prior years). All other aspects of the model remained unchanged. Model output can be used to forecast rates of recovery under MNA for comparison to the empirical estimates presented in Section 4.

The model calibration period ended in 1997, and thus data now available for this period provide a unique opportunity to examine the reliability of model forecasts for MNA relative to actual observations. Note that the calibration period (1976 – 1997) included the 1993-1997 timeframe, and data obtained subsequent to this period were not used in model calibration. The original ROD model forecast curves (indicated on ROD Tables 11-2 and 11-3) were prepared between 1998 and 2000. The data in figures A3-2 to A3-15 cover the period 1993 to 2016, and include the regression curves discussed previously. Figures A3-2 to A3-8 present the wet weight data and forecast curves, while Figures A3-9 to A3-15 provide lipid-normalized data and forecast curves.

These figures include smallmouth bass and striped bass data, although these species were not modeled using FISHRAND as part of the RI/FS. As mentioned previously, these species are likely to be sought after and consumed by local fishermen and are, therefore, routinely monitored. For smallmouth bass, the diagrams include the model curves for

largemouth bass as a basis for comparison to the observed data trends, based on the physical similarity of the two species and their similar trophic levels.

There is generally good agreement between model forecasts and actual observations of wet weight tissue concentrations for Upper Hudson River sections and the uppermost Lower River section at RM152. In general, observed tissue concentrations have declined comparably to, or in several instances more rapidly than, model predictions, particularly in the Upper Hudson River and the first two locations in the Lower River, indicating the model has adequately captured trends in fish concentrations. On an absolute basis (*e.g.*, comparison of predicted means to observed means), Table A3-4 shows the percentage of comparisons for each species and location that fall within factors of two, three and five. At RM90 and RM50, the model tends to underpredict fish tissue concentrations and shows a faster rate of decline than indicated by data (for example, pumpkinseed at RM90 in Figure A3-7A, brown bullhead at RM50 in Figure A3-8A, and white perch at RM50 in Figure A3-8B). Overall, the Upper Hudson model forecasts and fish tissue observations agree more closely than the Lower Hudson comparisons, but it is important to note that the FISHRAND model was not calibrated for the lower river, and relied on a different model for sediment and water input exposure concentrations (Farley et al. 1999) as opposed to the HUDTOX model. Appendix 1 shows that the Farley model underpredicted water column Tri+ PCB concentrations at Poughkeepsie during the 2004-2008 baseline monitoring period, which has implications for performance of the FISHRAND model (which was not explicitly calibrated for Lower Hudson River fish data, relying on calibration to Upper Hudson River fish data using HUDTOX-predicted exposures as inputs). It also should be noted that while the Farley model was calibrated to sediment and fish data, very little water column data for the Lower Hudson River was available to constrain the model calibration.

Also evident in Figures A3-2 to A3-15 is the close agreement between the original model forecasts and the Phase 1 Report forecasts using actual flows and external solids loads. Based on the good agreement between data and the model, the remainder of this appendix focuses on the original ROD model forecasts.

The comparison of lipid-normalized data and model results also shows good agreement across the Upper Hudson and RM152, as shown in Figures A3-12A and A3-12B and summarized in Table A3-4. Again, the model curves both agree well in absolute magnitude with the actual observations in most instances, and the model curves typically show comparable or slower decay rates than those observed in the data.

Note that the FISHRAND model was calibrated to data on a wet weight basis over many years, species, and locations, and it assumed that lipid content was a calibrated parameter as described in the modeling report and associated documentation (EPA 2000c). FISHRAND is a probabilistic model, which does not predict lipid content, fish weight, or feeding preferences. These are all imperfectly known and dynamic inputs to the model that vary not only from year to year but also within a year. Through the calibration process, these inputs, represented by distributions, were fixed for the forecast period and do not change over time. In any given year, the actual lipid content, weight, and feeding preferences of sample fish may or may not exactly match the optimized distributions used as inputs to the model. As demonstrated here, the model successfully predicted observed wet weight and lipid-normalized concentrations without any further adjustment to inputs, as is expected of a predictive model for which future inputs cannot be known.

6 POST-DREGING $TPCB_{HE}$ CONCENTRATIONS

This section provides a brief discussion of the one year of post-dredging data (2016) that exists for the Hudson River. Dredging ended in the fall of 2015, thus, it has been less than a year between the completion of dredging and sampling of fish tissue. Model results as presented in the ROD suggest that the system continues to reflect the transient impacts of dredging for some time following the end of remedial activities, depending on the size and ages of the fish population. Nonetheless, this first year of data relative to model results provides perspective on current observations and expectations as presented in the ROD.

During-dredging fish tissue concentrations are discussed in greater detail in Appendix 8 in the context of operational modifications to remedy implementation. During-dredging tissue concentrations are also shown in this appendix by the orange markers on Figures A3-2 through A3-8 for wet weight concentrations, and Figures A3-9 through A3-15 on a lipid-normalized basis. Fish tissue concentrations during the dredging period, for which the ROD expected transient increases in response to remedial activities, generally fall within the variability observed in the years just prior to dredging. The models were designed to predict long-term impacts, and the expected trajectory of sediment, water, and tissue concentrations following the transient disturbance of remedial activities.

The risk-based human health remediation goal presented in the ROD is 0.05 ppm (or mg/kg) PCBs (wet weight) in fillet, based on the reasonable maximum exposure adult fish consumption rate of one half-pound meal per week. In addition, EPA considered a target level of 0.2 ppm PCBs (wet weight) in fillet based on one half-pound meal per month, and a target concentration of 0.4 ppm based on the average (central tendency) consumption rate of one half-pound meal every 2 months. The target levels correspond to points at which the fish consumption advisories might be relaxed from the current "eat none" recommendation. However, it is the New York State Department of Health that determines fish consumption advisories.

Modeling presented as species-weighted averages in Table 11-2 of the ROD did not project that neither MNA or the selected remedy would achieve the human health remediation goal

of 0.05 ppm PCBs for RS1, RS2, and for the Upper Hudson River as a whole, within the modeling time frame (to 2067), unless the upstream source was virtually eliminated, but did forecast that the remedial goal would be achieved within 40 years in RS3 (RM168-154). The model results averaged over three species in the entire Upper Hudson River, as presented in Table 11-2 of the ROD, showed that a target level of 0.4 mg/kg wet weight could be achieved several years after completing dredging and after 15 years for the 0.2 mg/kg wet weight target level.

There is one year of post-dredging fish tissue data available for some species and locations, and these are shown in green in Figures A3-2 through A3-15. The median is presented as a large green circle. Overall, these data show rapid declines in observed PCB tissue concentrations relative to those observed during the dredging period for the Upper Hudson. The ROD anticipated at least a year of equilibration in the system in response to remedial activities; therefore, since these data reflect only the first year since the completion of dredging, it is likely these species still reflect some impact from dredging. The expectation is that concentrations would be comparable to what the FISHRAND model predicted for the first year following dredging (2010). Figure A3-19 provides a summary of species-specific means predicted by the model for the first year following dredging, as compared to monitoring data for 2016. However, it is important to note that FISHRAND's predictions for RS3 assume a population of fish foraging at the downstream end of the reach (*i.e.*, closer to RM154) whereas the sample fish were collected at RM168, so that model and data are not directly comparable. Nonetheless, these results show that the model anticipated concentrations in the first year post-dredging that are similar to what has been observed.

Panel A of this figure shows the species-weighted average concentrations from Table 11-2 of the ROD for 2010 as compared to monitoring data. Panel B of this figure shows that on an individual species basis, the model somewhat underpredicted brown bullhead concentrations but performed well for largemouth bass.

Ongoing monitoring over several more years beyond completion of dredging will be required to draw conclusions and calculate new post-dredging trends with any confidence

on a statistically robust basis. Nonetheless, these early data are encouraging, and when compared to model predictions, indicate that the model has performed as expected.

In terms of target levels, Figure A3-2 shows that in RS1 (RM189), the 2016 post-dredging data are lower than the concentrations observed during the dredging period. The median largemouth bass concentration of PCBs is close to the 0.4 mg/kg target level, and the yellow perch median is below this target level. Similarly, Figures A3-3 and A3-4 show that in RS2 (RM184) and RS3 (RM154-168), largemouth bass median tissue concentrations are close to 0.4 mg/kg and median yellow perch levels have achieved the 0.4 mg/kg target concentration.

Striped bass and the forage fish species median PCB concentrations in 2016 have also reached the 0.4 mg/kg target level in the uppermost river section RM152 in the Lower Hudson, and yellow perch have achieved the 0.05 mg/kg remedial goal, as shown in Figure A3-5.

At RM113, Figure A3-6, the brown bullhead median concentration in 2016 was at the 0.4 mg/kg target level and striped bass are close to this concentration. Note that striped bass concentrations observed in RM113 were somewhat higher than observed in the upstream RM152, which is not unexpected given the large home range and migratory habits of this species that integrates exposures over larger spatial and temporal scales than other species.

Although fewer data are available for RM90 and RM50, the concentrations observed during the dredging period indicated that several species were at or near the 0.4 and 0.2 mg/kg target levels and are approaching the 0.05 mg/kg remedial goal.

It is important to note there are many factors contributing to model prediction uncertainty and environmental variability as reflected in monitoring data, and these will impact specific timelines with respect to achieving target levels. Model predictions as presented in the ROD represent annualized average fish tissue concentrations. Both predicted and observed concentrations increase and decrease throughout the year, as well as across years, and

should be viewed in terms of statistical ranges and distributions rather than strict point estimates. In addition, particularly in RS2, there are notable differences between anticipated surface sediment concentration reductions as presented in the ROD and the actual reductions due to dredging. Appendices 4 and 8 of this document and Appendix A of the 2012 FYR provide additional information on these topics.

In general, these initial, post-dredging data are encouraging and suggest that predictions made in the ROD for the post-dredging period are consistent with current observations. Although further monitoring will be required to verify that RAOs are being achieved, the lines of evidence to this point indicate that the system is responding as anticipated.

7 OVERALL CONCLUSIONS

- Wet weight tissue concentrations declined at approximately 12 to 20 percent per year in the Upper Hudson and at RM152 during the MNA period, with slower recovery observed at further downstream locations in the Lower Hudson River.
- Lipid normalized tissue concentrations declined at approximately 8 percent per year in the Upper Hudson and at RM152, with slower rates of recovery observed at RM113.
- Decay rates at RM90 and RM50 for the MNA period are not significantly different from zero.
- All three decay rate estimation methods show similar patterns of decline across species and locations and show that a portion of the decline in fish tissue concentration is due to declining lipids, with the remainder due to declining exposures.
- Lack of correspondence between the rates of decline in fish tissue PCBs between Upper and Lower Hudson River monitoring locations indicates that Lower Hudson exposures are not directly related to Upper Hudson conditions. Differences in exposure could relate to other sources in the Lower Hudson watershed and/or fate and transport of PCBs within the Lower Hudson River. The difference in Upper Hudson and Lower Hudson exposures is further demonstrated by the lack of response in Lower Hudson fish to dredging-related releases during 2009-2015 as discussed in Appendix 8.
- Model forecasts of fish tissue under MNA agree well with observations of fish tissue $TPCB_{HE}$ levels for the Upper Hudson and RM152 and RM113 river sections on both a wet weight and lipid normalized basis, with most comparisons within a factor of 2. The model performs comparatively less well in downstream Lower Hudson River sections where it was not calibrated to data and was driven by inputs from the Farley model, which tended to underpredict water column concentrations.
- ROD forecasts for the Lower Hudson did not predict significant impacts from dredging implementation. Some improvements because of remedy implementation were predicted for the Lower Hudson as compared to MNA. Both predictions are consistent with observations. Overall, observations support a lack of significant

response between Upper Hudson processes, *e.g.*, dredging releases, and Lower Hudson impacts.

- Overall, EPA's evaluation of the available data, including post-dredging data from 2016, indicates declines in tissue concentrations consistent with ROD predictions. Although further monitoring will be required to verify that RAOs are being achieved, the lines of evidence to this point indicate that the system is responding as anticipated and that target levels will be achieved within the timeframes predicted in the ROD.

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APPENDIX 3

Assessment of PCB Levels in Fish Tissue

Tables and Figures

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Table A3-1. Fish Monitoring Locations by River Section (RS) and Baseline Monitoring Program (BMP) and Remedial Action Monitoring Program (RAMP) Station in the Upper and Lower Hudson.

Domain	River Section	River Mile (RM) Range	Monitoring Stations	RS or RM for Appendix 3 Figures	Number of Species Examined
Upper Hudson River (UHR)	RS1	194.5 to 188.5	TD1 – TD5 (RM 189)	RS1	7
	RS2	188.5 to 183.4	ND1- ND5 (RM 183.5)	RS2	6
	RS3*	183.4 to 154	SW1 – SW5 (RM 168 and RM154)	RS3	6
Lower Hudson River (LHR)	RS4	153.9 to 123.5	Albany/Troy (AT, RM142-153.9)	RM 152	11
	RS5	123.5 to 93.5	Catskill (CS, RM113)	RM113	8
	RS6	93.5 to 63.5	Poughkeepsie (RM76)	RM90	8
	RS7	63.5 to 33.5	Newburgh (RM60)	RM50	8

* As described in the BMP QAPP (GE 2004) and RAMP QAPP (GE 2009, GE 2012) RS3 is represented by Reach 5 (Stillwater Pool, RM 183.4 through RM168). For the FS and 2002 ROD data analyses, RS3 was characterized at RM154.

Table A3-2
Hudson River Species with Long-Term Records

Species	River Section	Period of Data		Sources
Brown Bullhead	RS1	1993	2016	NYSDEC & GE
	RS2	1997	2016	NYSDEC & GE
	RS3	1993	2016	NYSDEC & GE
	RS4	1993	2007	NYSDEC & GE
	RS5	1998	2016	NYSDEC & GE
	RS6	1998	2011	NYSDEC
	RS7	1999	2002	NYSDEC
Channel Catfish*	RS4	1999	2016	NYSDEC & GE
	RS5	2000	2011	NYSDEC
	RS6	1999	2011	NYSDEC
Largemouth Bass	RS1	1993	2016	NYSDEC & GE
	RS2	1997	2016	NYSDEC & GE
	RS3	1993	2016	NYSDEC & GE
	RS4	1993	2012	NYSDEC & GE
	RS5	1993	2015	NYSDEC & GE
	RS6	1998	2011	NYSDEC
	RS7	1999	1999	NYSDEC
Pumpkinseed	RS1	1993	2016	NYSDEC & GE
	RS2	1997	2016	NYSDEC & GE
	RS3	1993	2016	NYSDEC & GE
	RS4	1993	2016	NYSDEC & GE
	RS5	1993	2011	NYSDEC
	RS6	1993	2011	NYSDEC
	RS7	1993	2003	NYSDEC
Smallmouth Bass	RS1	1998	2016	NYSDEC & GE
	RS2	1999	2016	NYSDEC & GE
	RS3	1997	2016	NYSDEC & GE
	RS4	1993	2016	NYSDEC & GE
	RS5	1996	2015	NYSDEC & GE
	RS6	1998	2011	NYSDEC
	RS7	1999	2001	NYSDEC
Spottail Shiner	RS1	1993	2016	NYSDEC & GE
	RS2	2004	2016	GE
	RS3	1993	2016	NYSDEC & GE
	RS4	1993	2016	NYSDEC & GE
	RS5	1993	1993	NYSDEC
	RS6	1993	1993	NYSDEC
	RS7	1993	1993	NYSDEC

Species	River Section	Period of Data		Sources
Striped Bass	RS4	1993	2016	NYSDEC & GE
	RS5	1993	2016	NYSDEC & GE
	RS6	1993	2015	NYSDEC
	RS7	1993	2015	NYSDEC
White Catfish*	RS4	1993	2012	NYSDEC & GE
	RS5	1997	2007	NYSDEC
White Perch	RS4	1993	2016	NYSDEC & GE
	RS5	1993	2011	NYSDEC
	RS6	1998	2011	NYSDEC
	RS7	1999	2003	NYSDEC
Yellow Bullhead*	RS1	1993	2014	NYSDEC & GE
Yellow Perch	RS1	1993	2016	NYSDEC & GE
	RS2	1999	2016	NYSDEC & GE
	RS3	1993	2016	NYSDEC & GE
	RS4	1993	2016	NYSDEC & GE
	RS5	1993	2011	NYSDEC
	RS6	1999	2011	NYSDEC
	RS7	1999	2002	NYSDEC

Note:

* Fish Species not plotted in Appendix 3 Figures

Table A3-3 Estimated Exponential Rates of Decline for Fish Species - Rates of Decline are Shown by Negative Values and Rates of Increase are Shown by Positive Values

River Mile	Species	Wet Weight Rate of Decline	Standard Error	*p* Value	Lipid-Normalized Rate of Decline	Standard Error	*p* Value	Lipid-Restricted Rate of Decline	Standard Error	*p* Value
RS1 - 189	Largemouth Bass	**-20%**	**2%**	**<0.01**	**-9%**	**1%**	**<0.01**	**-12%**	**3%**	**<0.01**
	Brown Bullhead	**-17%**	**1%**	**<0.01**	**-7%**	**1%**	**<0.01**	-1.2%	3%	0.67
	Yellow Perch	**-24%**	**1%**	**<0.01**	**-14%**	**1%**	**<0.01**	**-12%**	**2%**	**<0.01**
	Spottail Shiner	na			na			na		
	Smallmouth Bass	**-33%**	**5%**	**<0.01**	**-14%**	**3%**	**<0.01**	na		
	Striped Bass	nd			nd			na		
	White Perch	nd			nd			na		
	Pumpkinseed	**-6%**	**1%**	**<0.01**	**-5%**	**1%**	**<0.01**	-1.6%	1%	0.29
RS2 - 184	Largemouth Bass	**-18%**	**3%**	**0.00**	**-7%**	**2%**	**<0.01**	na		
	Brown Bullhead	-3%	3%	0.25	-2%	2%	0.21	na		
	Yellow Perch	**-26%**	**4%**	**<0.01**	**-18%**	**2%**	**<0.01**	na		
	Spottail Shiner	na			na			na		
	Smallmouth Bass	**-29%**	**4%**	**<0.01**	**-15%**	**2%**	**<0.01**	na		
	Striped Bass	nd			nd			na		
	White Perch	nd			nd			na		
	Pumpkinseed	-2%	2%	0.37	**-5%**	**2%**	**0.01**	na		
RS3 - 168 & 154	Largemouth Bass	**-15%**	**2%**	**<0.01**	**-10%**	**1%**	**<0.01**	**-39%**	**7%**	**0.03**
	Brown Bullhead	**-10%**	**2%**	**<0.01**	**-2%**	**1%**	**0.02**	-7%	5%	0.20
	Yellow Perch	**-20%**	**2%**	**<0.01**	**-12%**	**1%**	**<0.01**	-19%	11%	0.10
	Spottail Shiner	na			na			na		
	Smallmouth Bass	**-10%**	**4%**	**0.01**	**-8%**	**3%**	**<0.01**	na		
	Striped Bass	nd			nd			na		
	White Perch	nd			nd			na		
	Pumpkinseed	**-10%**	**1%**	**<0.01**	**-10%**	**1%**	**<0.01**	**-13%**	**1%**	**<0.01**
RS4 - 152	Smallmouth Bass	**-14%**	**2%**	**<0.01**	**-9%**	**1%**	**<0.01**	**-8%**	**3%**	**<0.01**
	Largemouth Bass	-12%	6%	0.07	**-14%**	**3%**	**<0.01**	na		
	Brown Bullhead	**-16%**	**5%**	**<0.01**	**-9%**	**3%**	**<0.01**	-12%	15%	0.43
	Yellow Perch	**-13%**	**3%**	**<0.01**	**-10%**	**3%**	**<0.01**	**-12%**	**4%**	**<0.01**
	Pumpkinseed	**-15%**	**1%**	**<0.01**	**-13%**	**1%**	**<0.01**	**-13%**	**1%**	**<0.01**
	Spottail Shiner	**-33%**	**5%**	**<0.01**	**-12%**	**3%**	**<0.01**	na		
	Striped Bass	**-9%**	**1%**	**<0.01**	**-10%**	**1%**	**<0.01**	na		
	White Perch	**-16%**	**1%**	**<0.01**	**-4%**	**1%**	**<0.01**	**-9%**	**2%**	**<0.01**
RS5 - 113	Smallmouth Bass	**-16%**	**2%**	**<0.01**	**-7%**	**1%**	**<0.01**	**-17%**	**2%**	**<0.01**
	Largemouth Bass	**-18%**	**2%**	**<0.01**	**-5%**	**1%**	**<0.01**	na		
	Brown Bullhead	**-17%**	**1%**	**<0.01**	-1%	1%	0.42	**-7%**	**2%**	**<0.01**
	Yellow Perch	**-16%**	**2%**	**<0.01**	**-4%**	**2%**	**0.04**	**-14%**	**2%**	**<0.01**
	Pumpkinseed	**7%**	**3%**	**0.04**	-3%	2%	0.24	-1.8%	4%	0.63
	Spottail Shiner	nd			nd			nd		
	Striped Bass	**-7%**	**1%**	**<0.01**	**-4%**	**1%**	**0.01**	na		
	White Perch	**-12%**	**2%**	**<0.01**	2%	1%	0.05	0.3%	2%	0.86
RS6 - 90	Smallmouth Bass	**-11%**	**3%**	**<0.01**	-1%	2%	0.81	**-9%**	**3%**	**0.01**
	Largemouth Bass	**-15%**	**5%**	**<0.01**	1%	3%	0.84	na		
	Brown Bullhead	**-8%**	**3%**	**0.01**	**4%**	**2%**	**0.04**	5%	8%	0.55
	Yellow Perch	**-5%**	**2%**	**0.02**	3%	2%	0.14	-2%	2%	0.40
	Pumpkinseed	-1%	1%	0.25	**-9%**	**1%**	**<0.01**	**-8%**	**1%**	**<0.01**
	Spottail Shiner	nd			nd			nd		
	Striped Bass	**-4%**	**1%**	**<0.01**	1%	1%	0.33	na		
	White Perch	**-10%**	**2%**	**<0.01**	1%	1%	0.30	**-4%**	**1%**	**0.02**
RS7 - 50	Smallmouth Bass	na			na			na		
	Largemouth Bass	na			na			na		
	Brown Bullhead	na			na			na		
	Yellow Perch	na			na			na		
	Pumpkinseed	-4%	2%	0.06	4%	2%	0.06	na		
	Spottail Shiner	nd			nd			nd		
	Striped Bass	**-3%**	**1%**	**<0.01**	-1%	1%	0.12	na		
	White Perch	5%	4%	0.14	4%	3%	0.23	na		

Values shown in bold $p < 0.05$

nd = no data

na = not enough data to meet the inclusion criteria

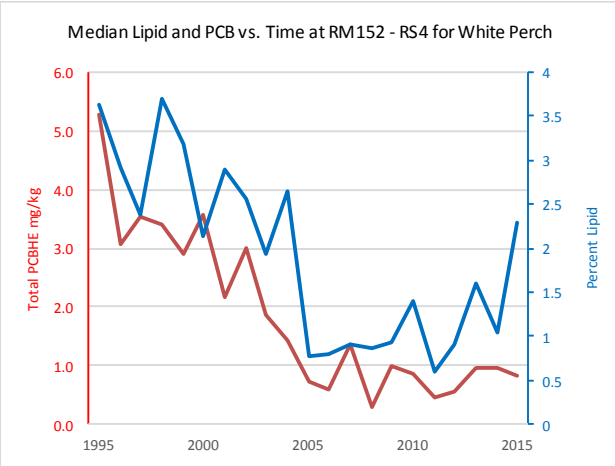
Table A3-4: Percentage of Comparisons Within Specified Factors for Model Results versus Data for the MNA Period (1998-2008)

WET WEIGHT BASIS														
	Within a factor of 2							Within a factor of 3						
Species	RS1 (RM189)	RS2 (RM184)	RS3 (RM168)	RM152	RM113	RM90	RM50	RS1 (RM189)	RS2 (RM184)	RS3 (RM168)	RM152	RM113	RM90	RM50
LMB	73%	75%	91%	75%	82%	88%	100%	100%	100%	100%	75%	100%	factor of 5	<2
BB	73%	38%	100%	83%	100%	83%	0%	100%	75%	<2	100%	<2	100%	0%[a]
YP	73%	57%	82%	86%	100%	89%	67%	100%	86%	100%	100%	<2	100%	100%
WP	x	x	x	100%	82%	45%	0%	x	x	x	<2	100%	100%	60%
PKSD	91%	71%	91%	100%	88%	100%	100%	100%	86%	100%	<2	88%	<2	<2
SPSH	25%	25%	20%	60%	x	x	x	100%	25%	100%	100%	x	x	x
LIPID-NORMALIZED BASIS														
	Within a factor of 2							Within a factor of 3						
Species	RS1 (RM189)	RS2 (RM184)	RS3 (RM168)	RM152	RM113	RM90	RM50	RS1 (RM189)	RS2 (RM184)	RS3 (RM168)	RM152	RM113	RM90	RM50
LMB	91%	63%	100%	75%	91%	63%	100%	100%	100%	<2	factor of 5	factor of 5	88%	100%
BB	100%	63%	82%	67%	factor of 5	factor of 5	0%	<2	88%	100%	67%	factor of 5	20%	factor of 5
YP	82%	14%	91%	86%	91%	33%	67%	100%	86%	100%	86%	100%	67%	factor of 5
WP	x	x	x	91%	factor of 5	9%	0%	x	x	x	100%	factor of 5	18%	factor of 6
PKSD	91%	57%	100%	91%	100%	100%	100%	100%	86%	<2	100%	100%	100%	100%
SPSH	50%	50%	60%	factor of 5	x	x	x	100%	75%	100%	factor of 5	x	x	x

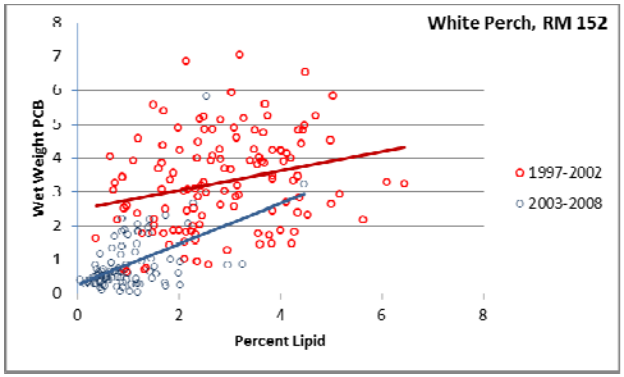
x - no data are available for this location

factor of 5 - 100% of comparisons within a factor of five rather than three

a - two of four available comparisons at this location within a factor of 5; four out of four within a factor of 6



Panel A: Lipid content (blue line) and wet weight PCB concentration (red line) over time showing similar trends, but differences in increases and decreases (e.g., some years lipid content increases but wet weight PCB increases and vice versa).

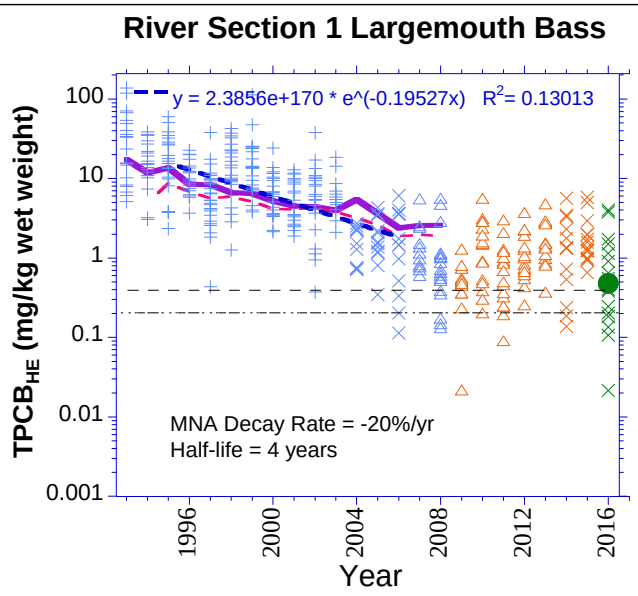


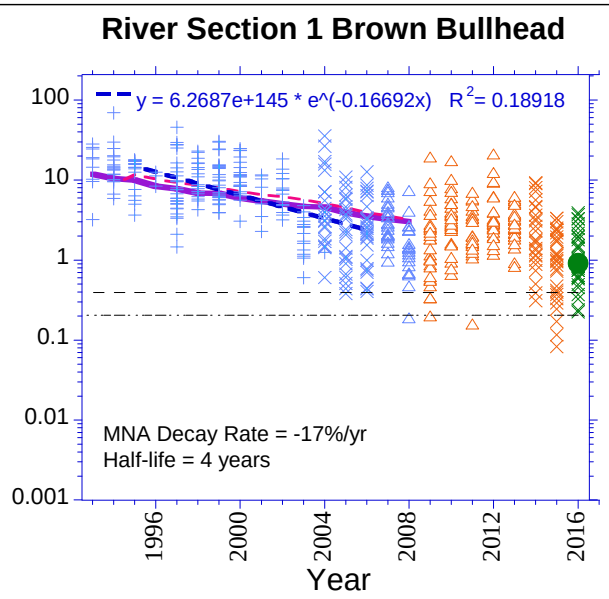
Panel B: The downward shift of the best-fit line between lipid and wet weight PCB for two time periods 1997-2002, representing a combination of measurement error, the effects of lipid changes over time, the role of NLOM, and differences in lipid content between the two time periods.

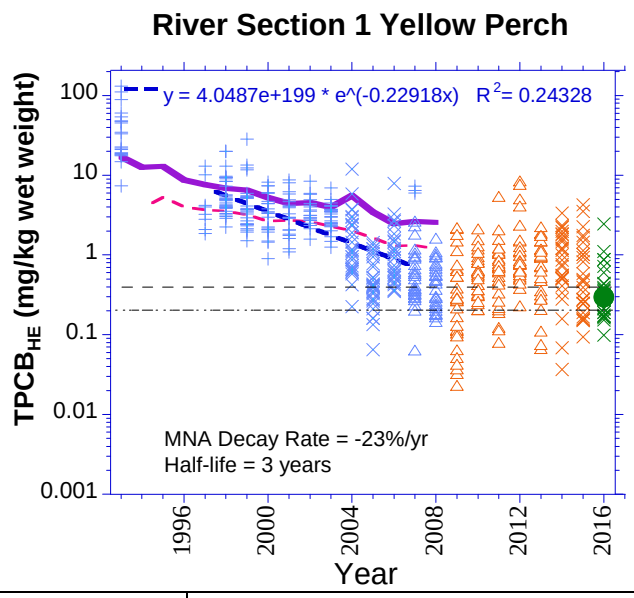
Lipid Content versus Wet Weight $TPCB_{HE}$ in White Perch at RM152

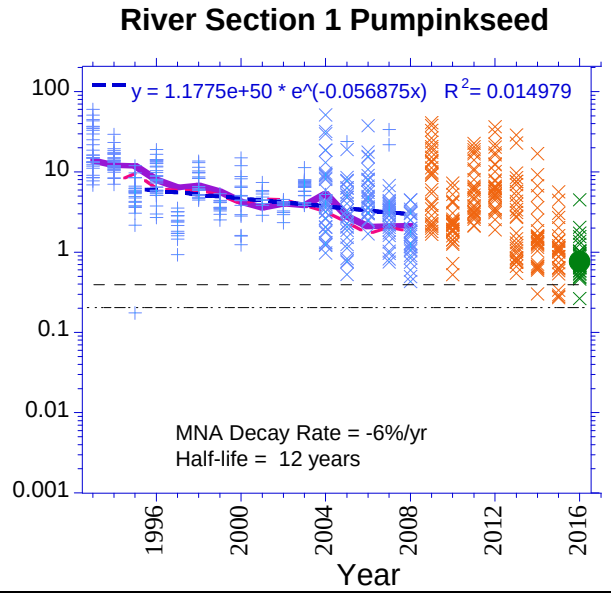
Figure A3-1

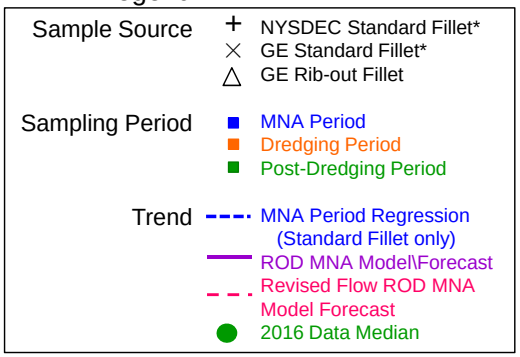
May 2017









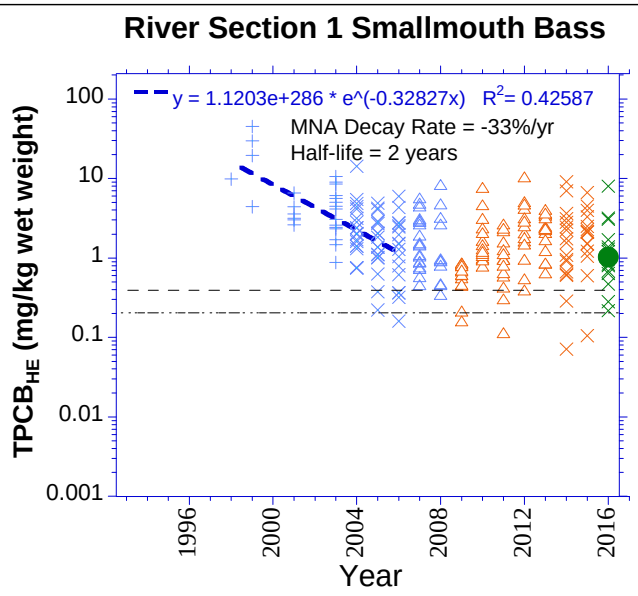


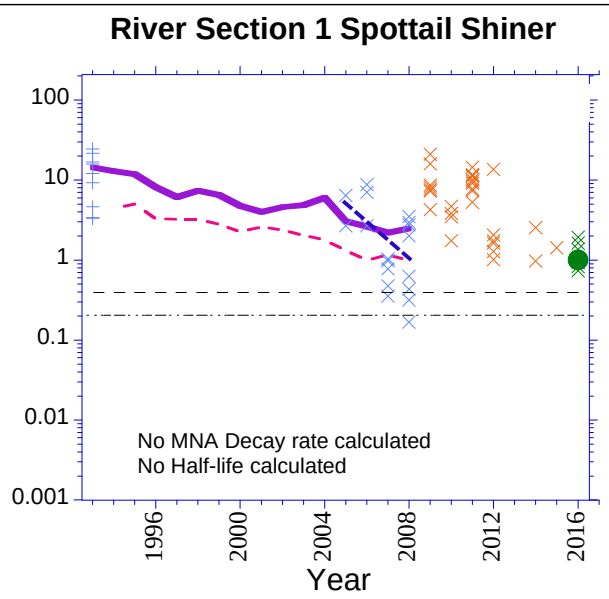
Notes:

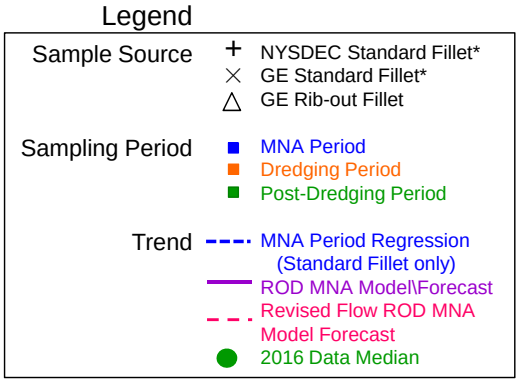
*For Pumpkinseed and spot tail shiner, samples are whole body composites.
1.PCB concentrations are expressed as Total PCB homologue equivalent values ($TPCB_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.
2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

$TPCB_{HE}$ in Fish Tissue Samples at River Section 1 - Wet Weight Basis

Figure A3-2A
May 2017





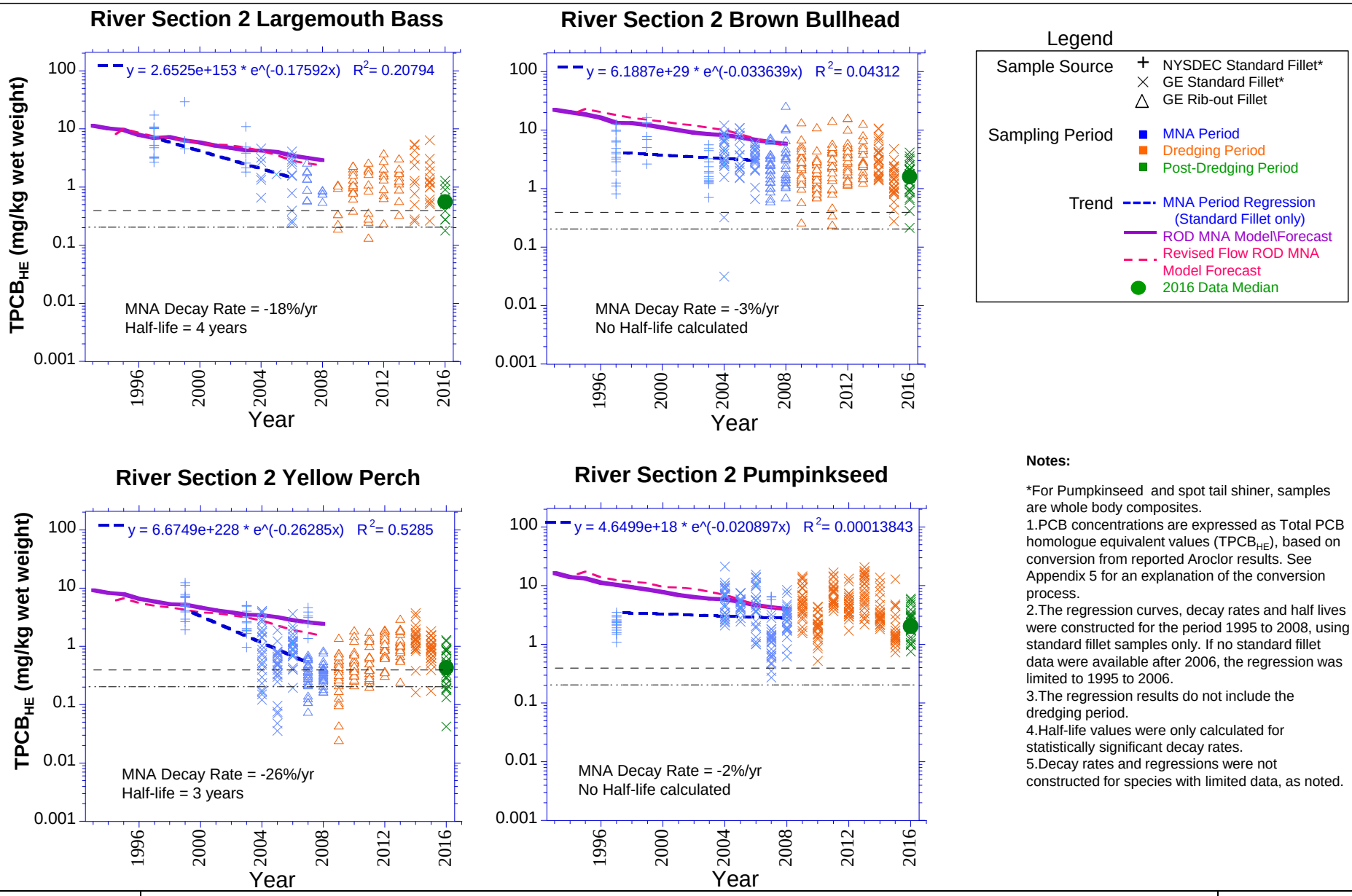


Notes:

*For Pumpkinseed and spot tail shiner, samples are whole body composites.
1.PCB concentrations are expressed as Total PCB homologue equivalent values ($TPCB_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.
2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

$TPCB_{HE}$ in Fish Tissue Samples at River Section 1 - Wet Weight Basis

Figure A3-2B
May 2017

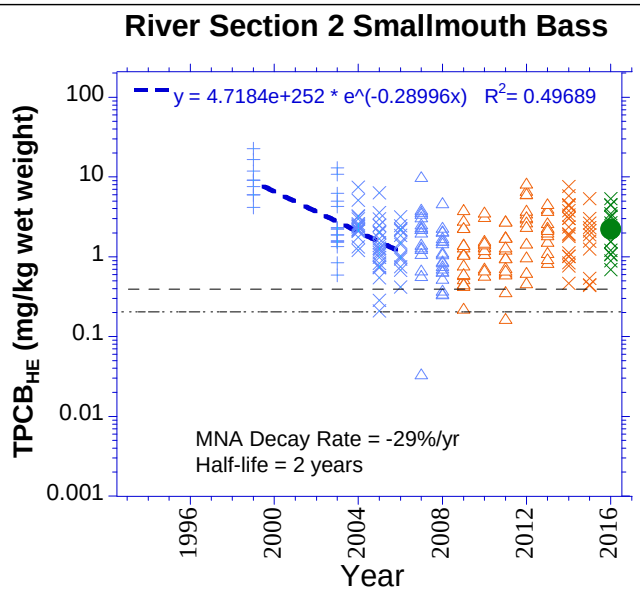


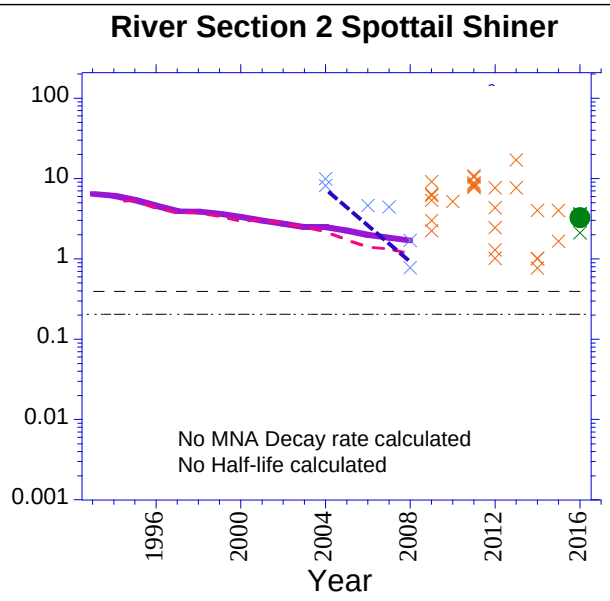
Notes:

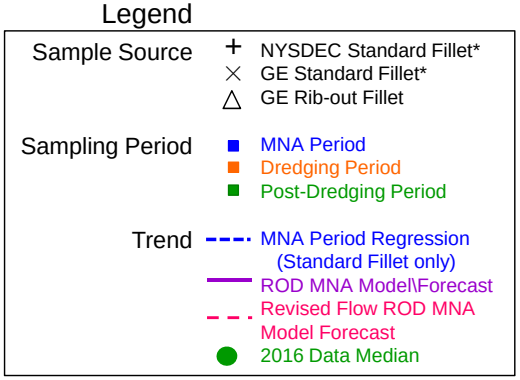
*For Pumpkinseed and spot tail shiner, samples are whole body composites.
1.PCB concentrations are expressed as Total PCB homologue equivalent values ($TPCB_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.
2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

$TPCB_{HE}$ in Fish Tissue Samples at River Section 2 - Wet Weight Basis

Figure A3-3A
May 2017





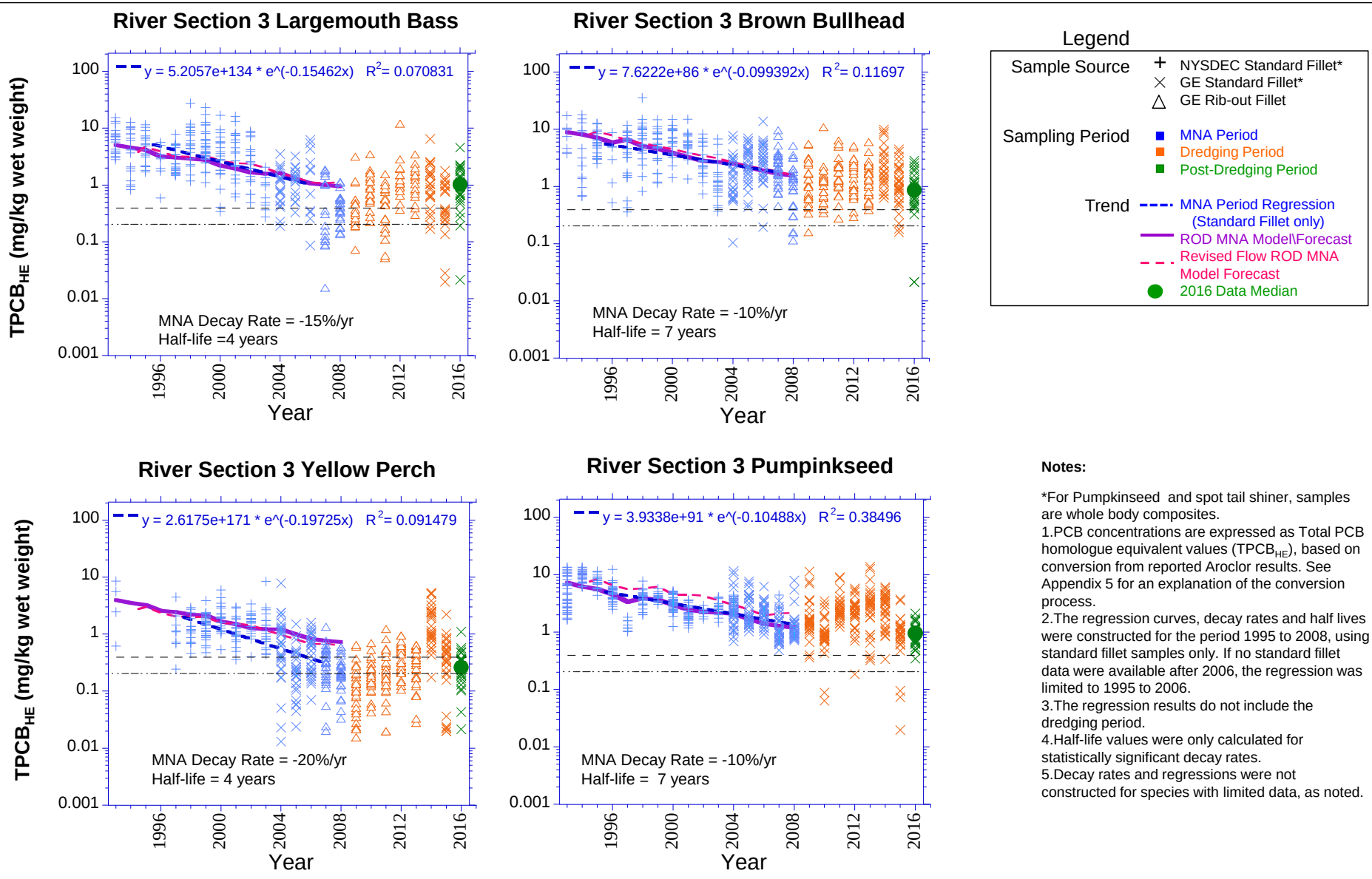


Notes:

*For Pumpkinseed and spot tail shiner, samples are whole body composites.
1.PCB concentrations are expressed as Total PCB homologue equivalent values ($TPCB_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.
2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

$TPCB_{HE}$ in Fish Tissue Samples at River Section 2 - Wet Weight Basis

Figure A3-3B
May 2017



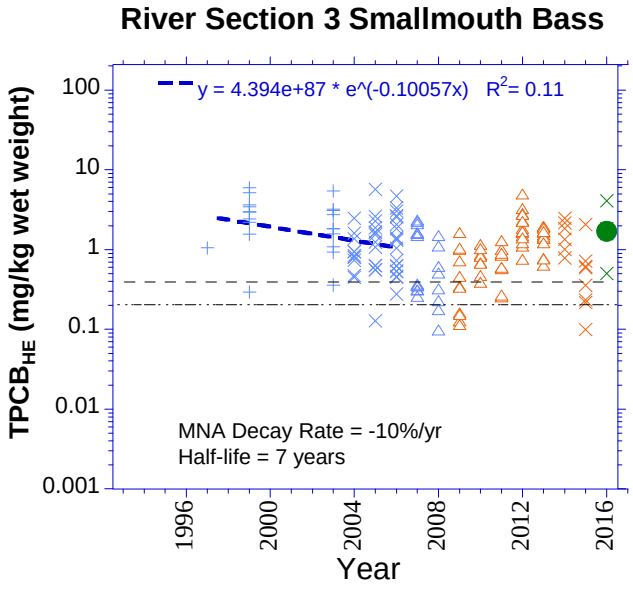
Notes:

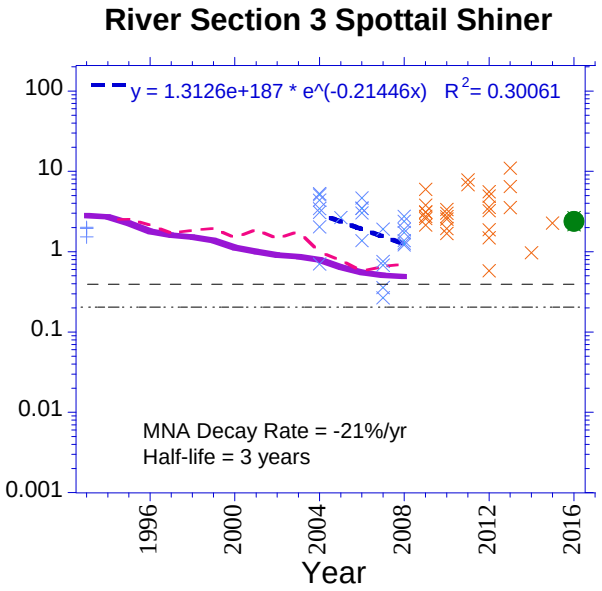
*For Pumpkinseed and spot tail shiner, samples are whole body composites.
1.PCB concentrations are expressed as Total PCB homologue equivalent values ($TPCB_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.
2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

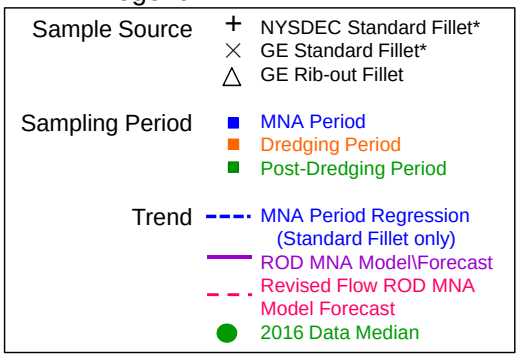
$TPCB_{HE}$ in Fish Tissue Samples at River Section 3 - Wet Weight Basis

Figure A3-4A

May 2017







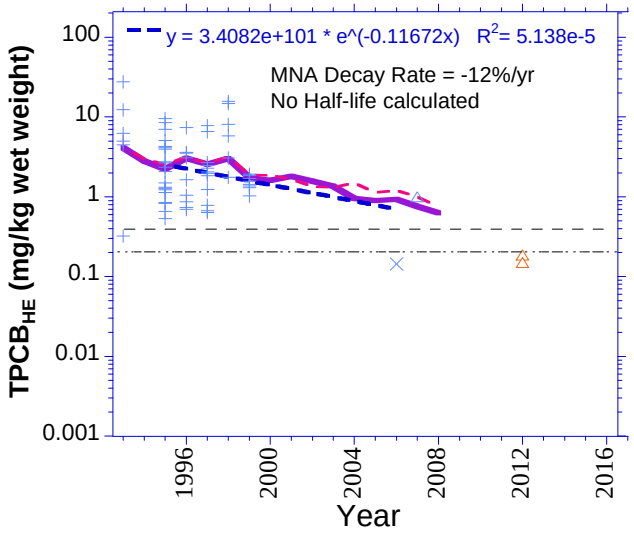
Notes:

*For Pumpkinseed and spot tail shiner, samples are whole body composites.
1.PCB concentrations are expressed as Total PCB homologue equivalent values ($TPCB_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.
2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

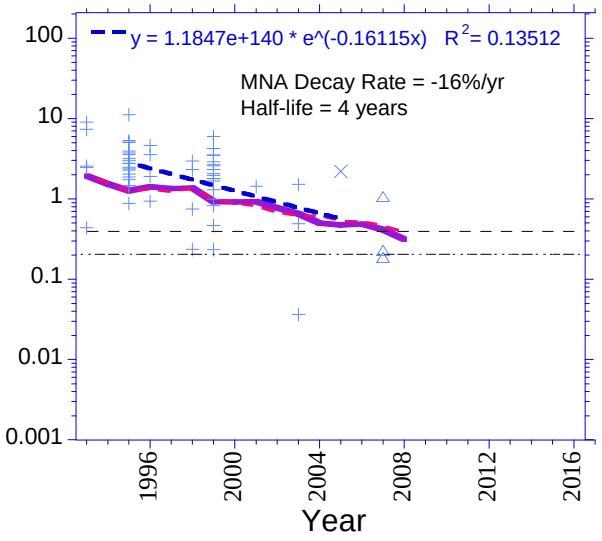
$TPCB_{HE}$ in Fish Tissue Samples at River Section 3 - Wet Weight Basis

Figure A3-4B
May 2017

RM 152 Largemouth Bass



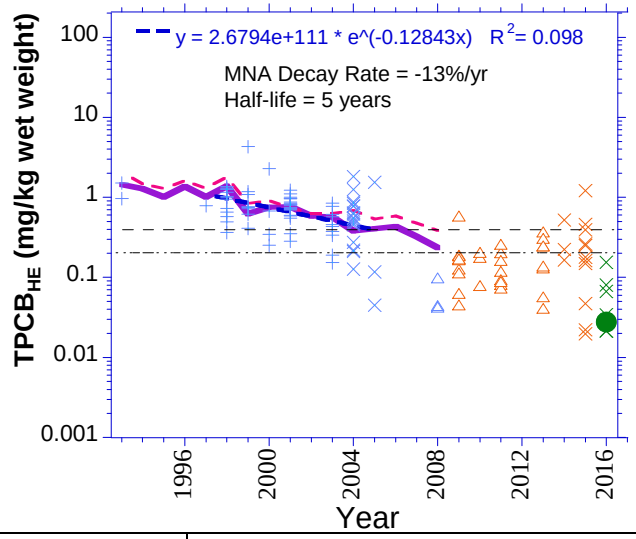
RM 152 Brown Bullhead



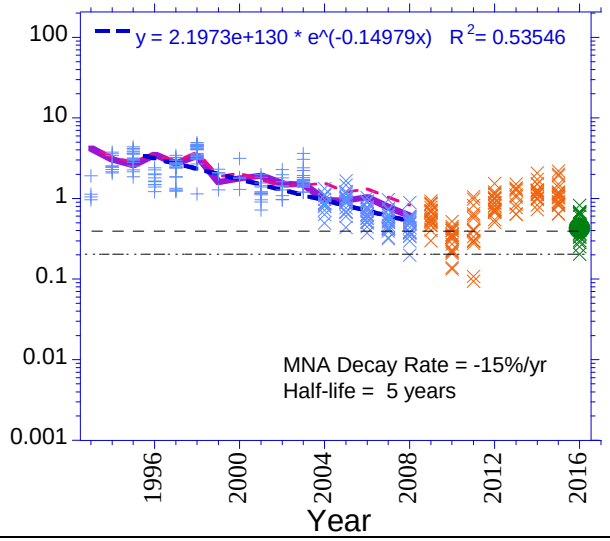
Legend

Sample Source	+ NYSDEC Standard Fillet*
	× GE Standard Fillet*
	△ GE Rib-out Fillet
Sampling Period	■ MNA Period
	■ Dredging Period
	■ Post-Dredging Period
Trend	MNA Period Regression (Standard Fillet only)
	ROD MNA Model\Forecast
	Revised Flow ROD MNA Model Forecast
	2016 Data Median

RM 152 Yellow Perch



RM 152 Pumpinkseed



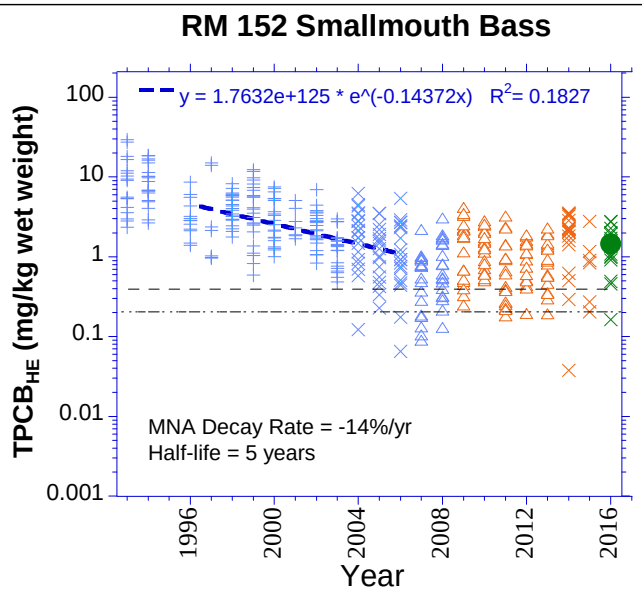
Notes:

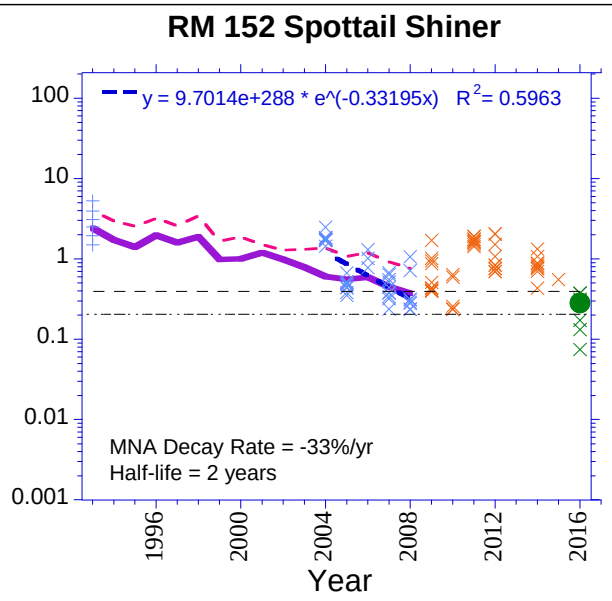
*For Pumpkinseed and spot tail shiner, samples are whole body composites.
1.PCB concentrations are expressed as Total PCB homologue equivalent values ($TPCB_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.
2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

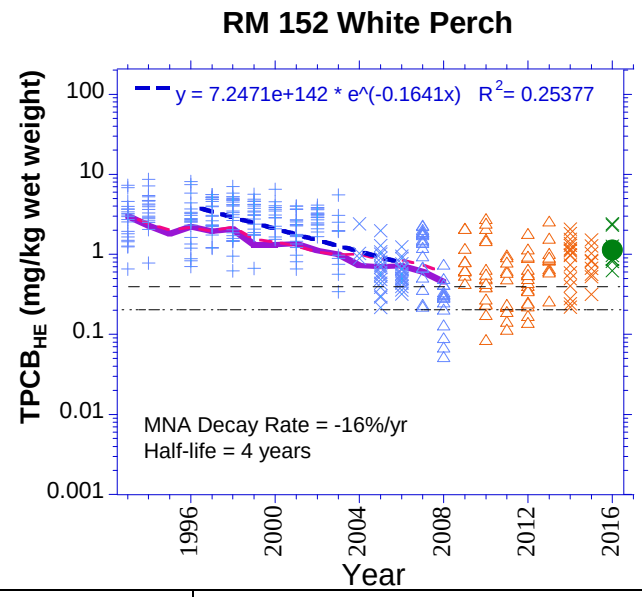
$TPCB_{HE}$ in Fish Tissue Samples at RM 152 - Wet Weight Basis

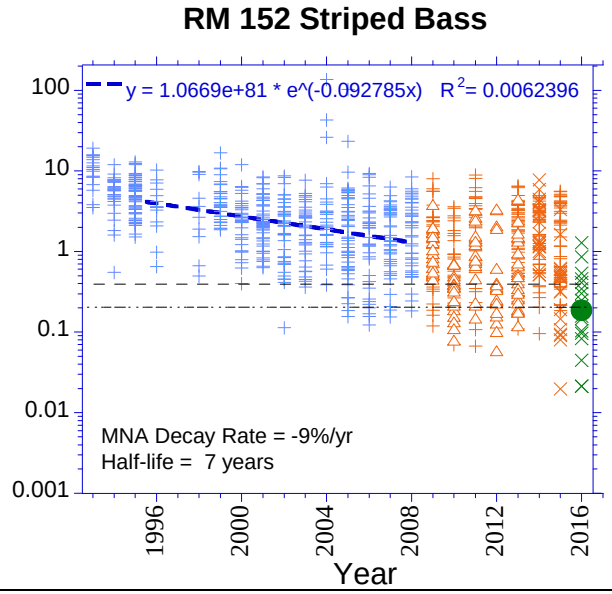
Figure A3-5A

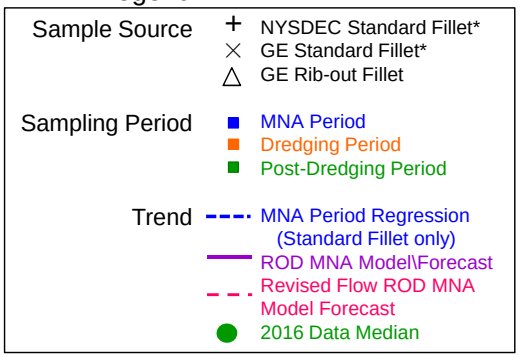
May 2017











Notes:

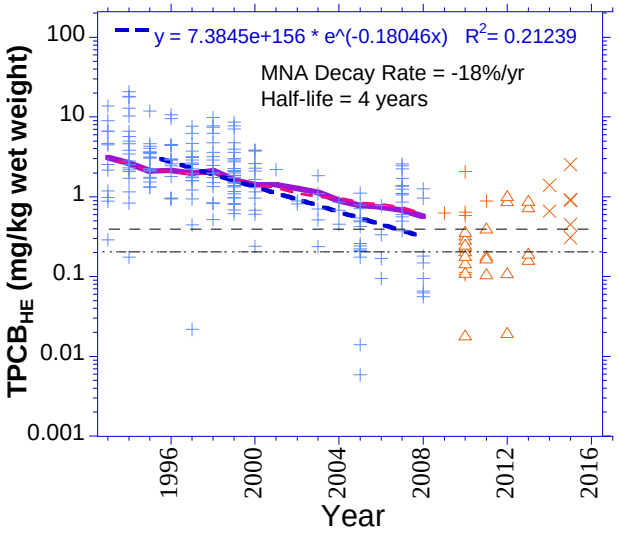
*For Pumpkinseed and spot tail shiner, samples are whole body composites.
1.PCB concentrations are expressed as Total PCB homologue equivalent values ($TPCB_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.
2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

$TPCB_{HE}$ in Fish Tissue Samples at RM 152 - Wet Weight Basis

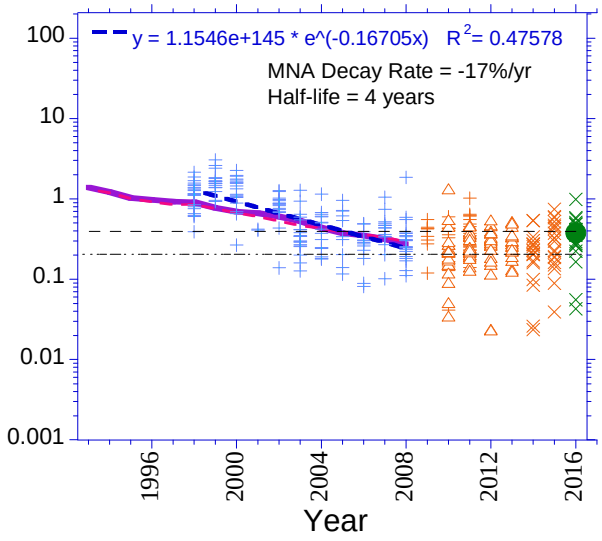
Figure A3-5B

May 2017

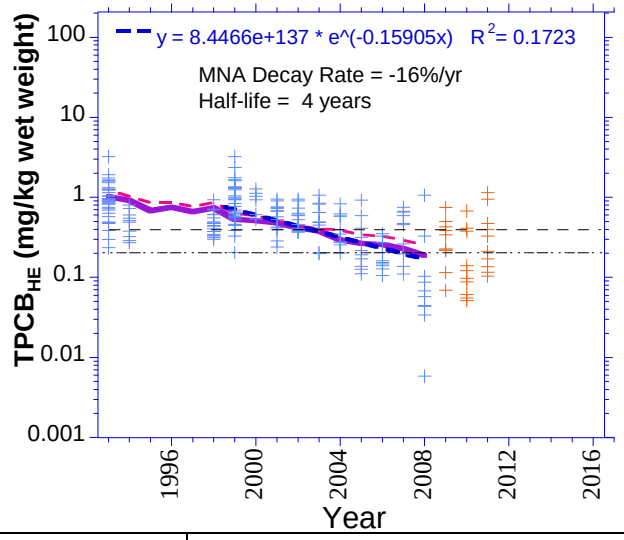
RM 113 Largemouth Bass



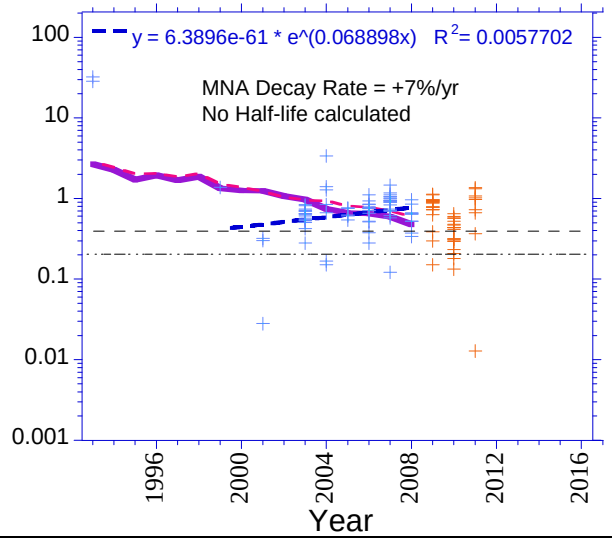
RM 113 Brown Bullhead



RM 113 Yellow Perch



RM 113 Pumpinkseed



Legend

- Sample Source
  - NYSDEC Standard Fillet*
  - GE Standard Fillet*
  - GE Rib-out Fillet
- Sampling Period
  - MNA Period
  - Dredging Period
  - Post-Dredging Period
- Trend
  - MNA Period Regression (Standard Fillet only)
  - ROD MNA Model\Forecast
  - Revised Flow ROD MNA Model Forecast
  - 2016 Data Median

Notes:

*For Pumpkinseed and spot tail shiner, samples are whole body composites.

1.PCB concentrations are expressed as Total PCB homologue equivalent values ($TPCB_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.

2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.

3.The regression results do not include the dredging period.

4.Half-life values were only calculated for statistically significant decay rates.

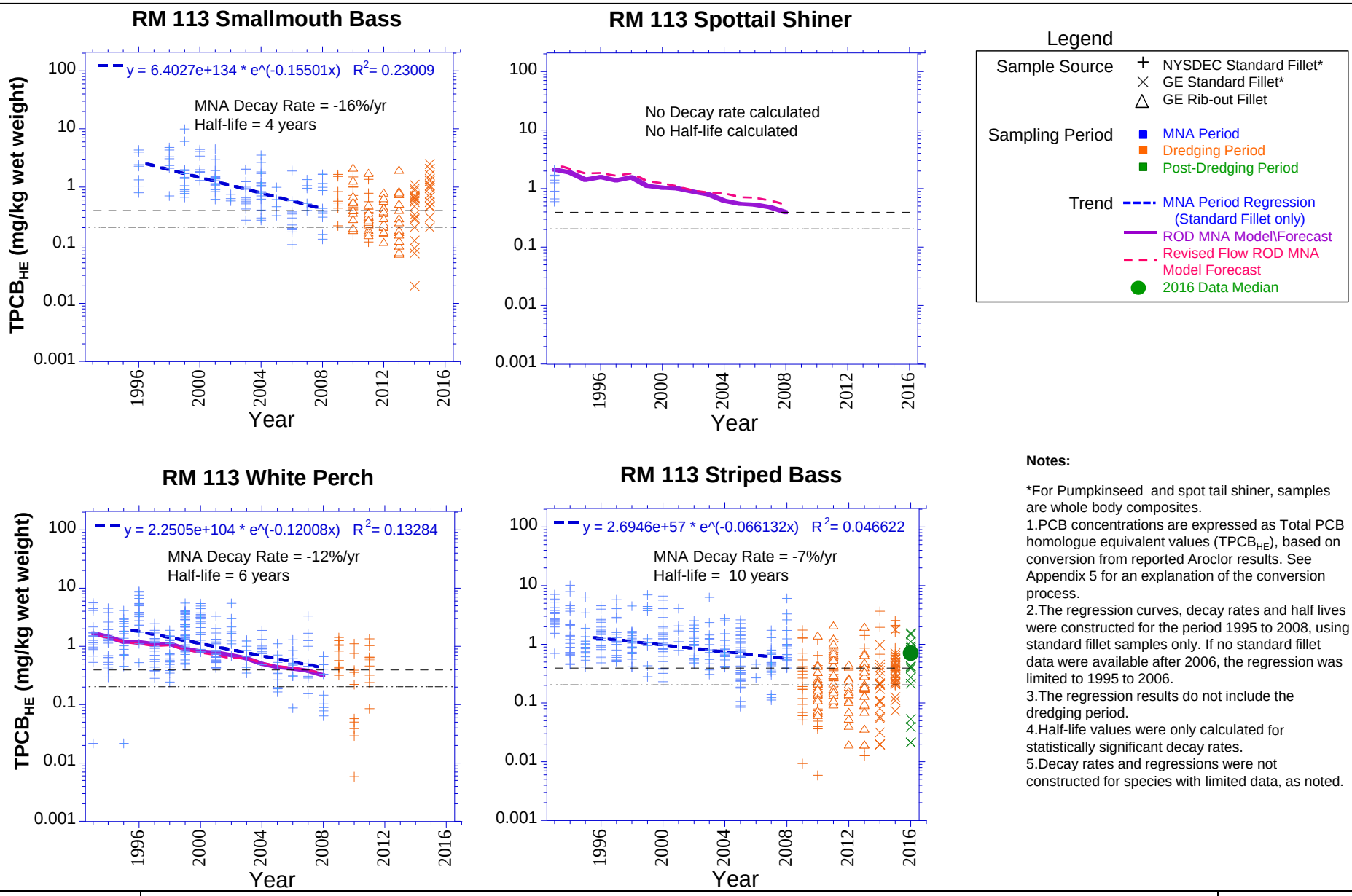
5.Decay rates and regressions were not constructed for species with limited data, as noted.

Hudson River PCBs Superfund Site

$TPCB_{HE}$ in Fish Tissue Samples at RM 113 - Wet Weight Basis

Figure A3-6A

May 2017

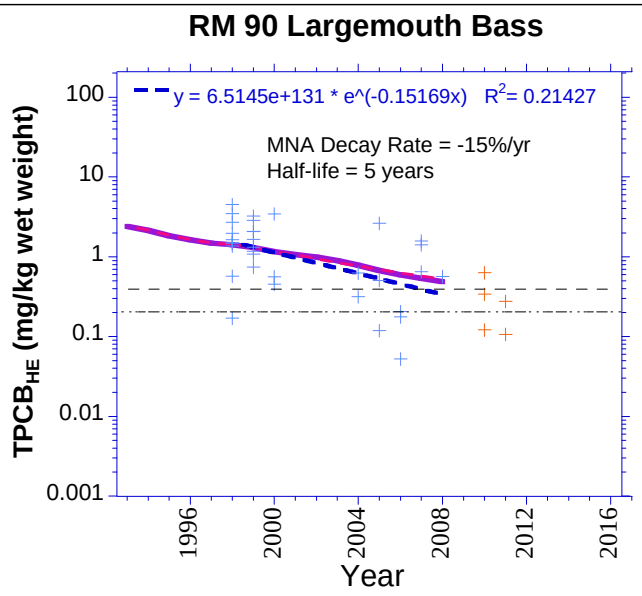


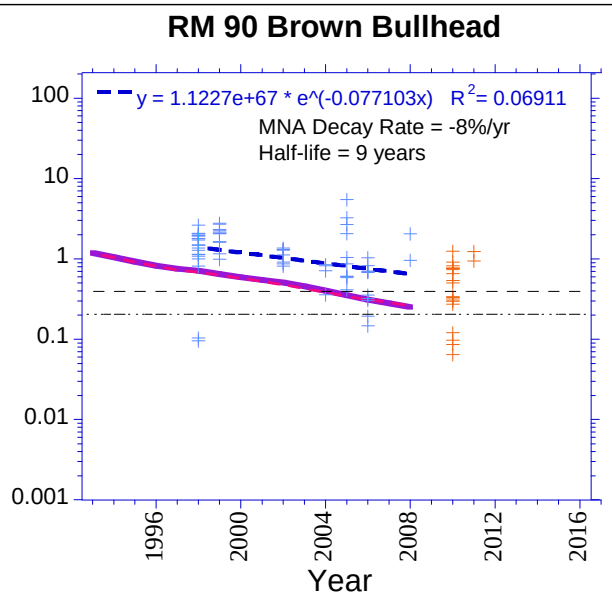
Notes:

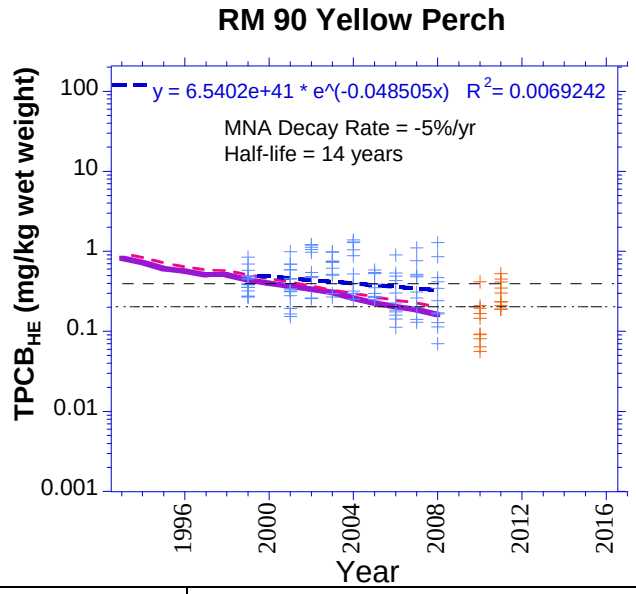
*For Pumpkinseed and spot tail shiner, samples are whole body composites.
1.PCB concentrations are expressed as Total PCB homologue equivalent values ($TPCB_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.
2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

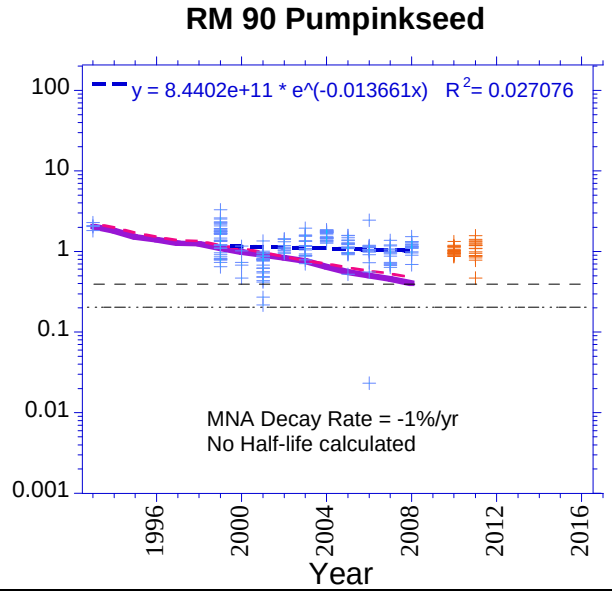
$TPCB_{HE}$ in Fish Tissue Samples at RM 113 - Wet Weight Basis

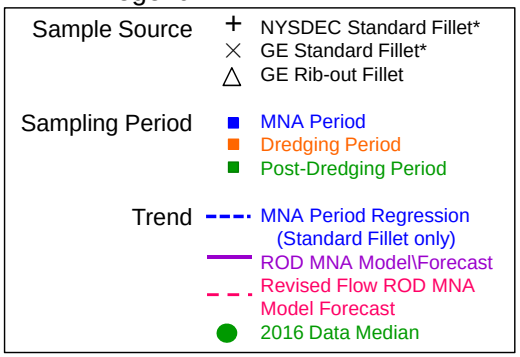
Figure A3-6B
May 2017











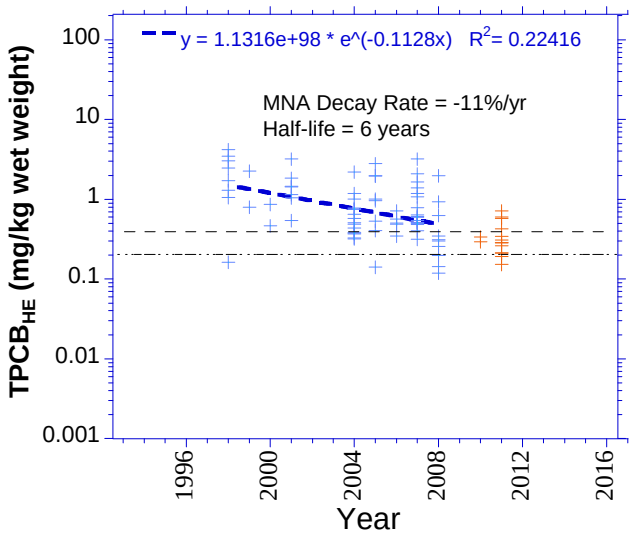
Notes:

*For Pumpkinseed and spot tail shiner, samples are whole body composites.
1.PCB concentrations are expressed as Total PCB homologue equivalent values ($TPCB_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.
2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

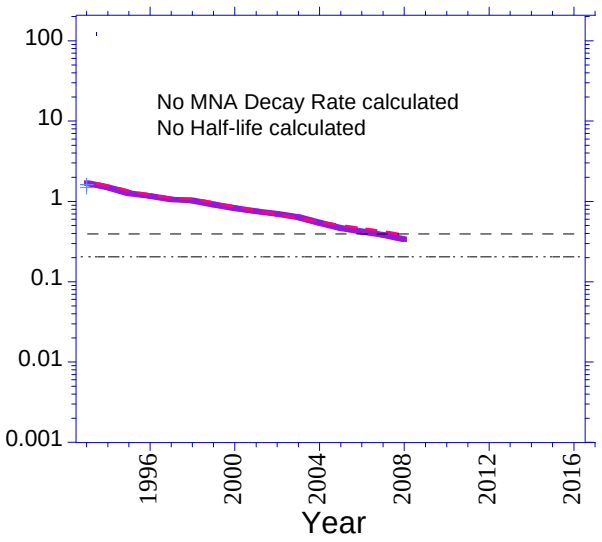
$TPCB_{HE}$ in Fish Tissue Samples at RM 90 - Wet Weight Basis

Figure A3-7A
May 2017

RM 90 Smallmouth Bass



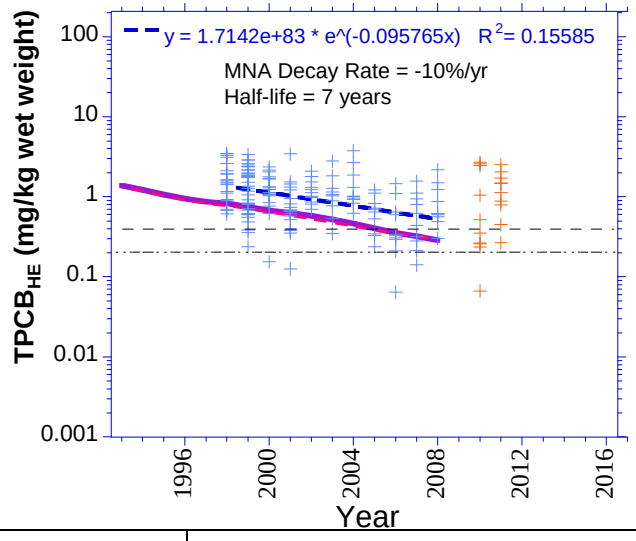
RM 90 Spottail Shiner



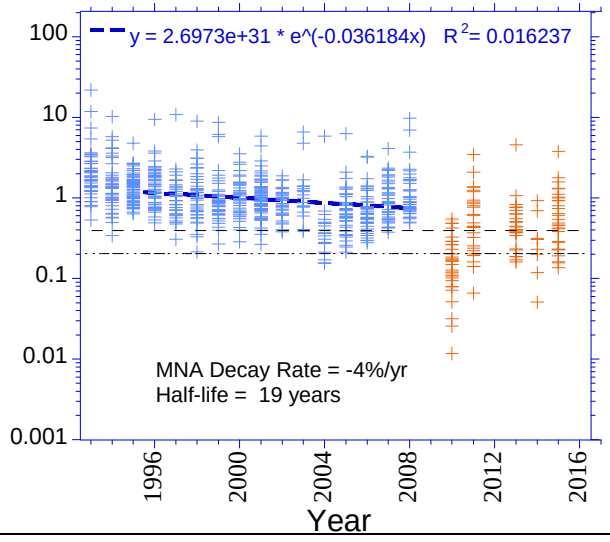
Legend

Sample Source	+ NYSDEC Standard Fillet*
	× GE Standard Fillet*
	△ GE Rib-out Fillet
Sampling Period	■ MNA Period
	■ Dredging Period
	■ Post-Dredging Period
Trend	MNA Period Regression (Standard Fillet only)
	ROD MNA Model\Forecast
	Revised Flow ROD MNA Model Forecast
	● 2016 Data Median

RM 90 White Perch



RM 90 Striped Bass



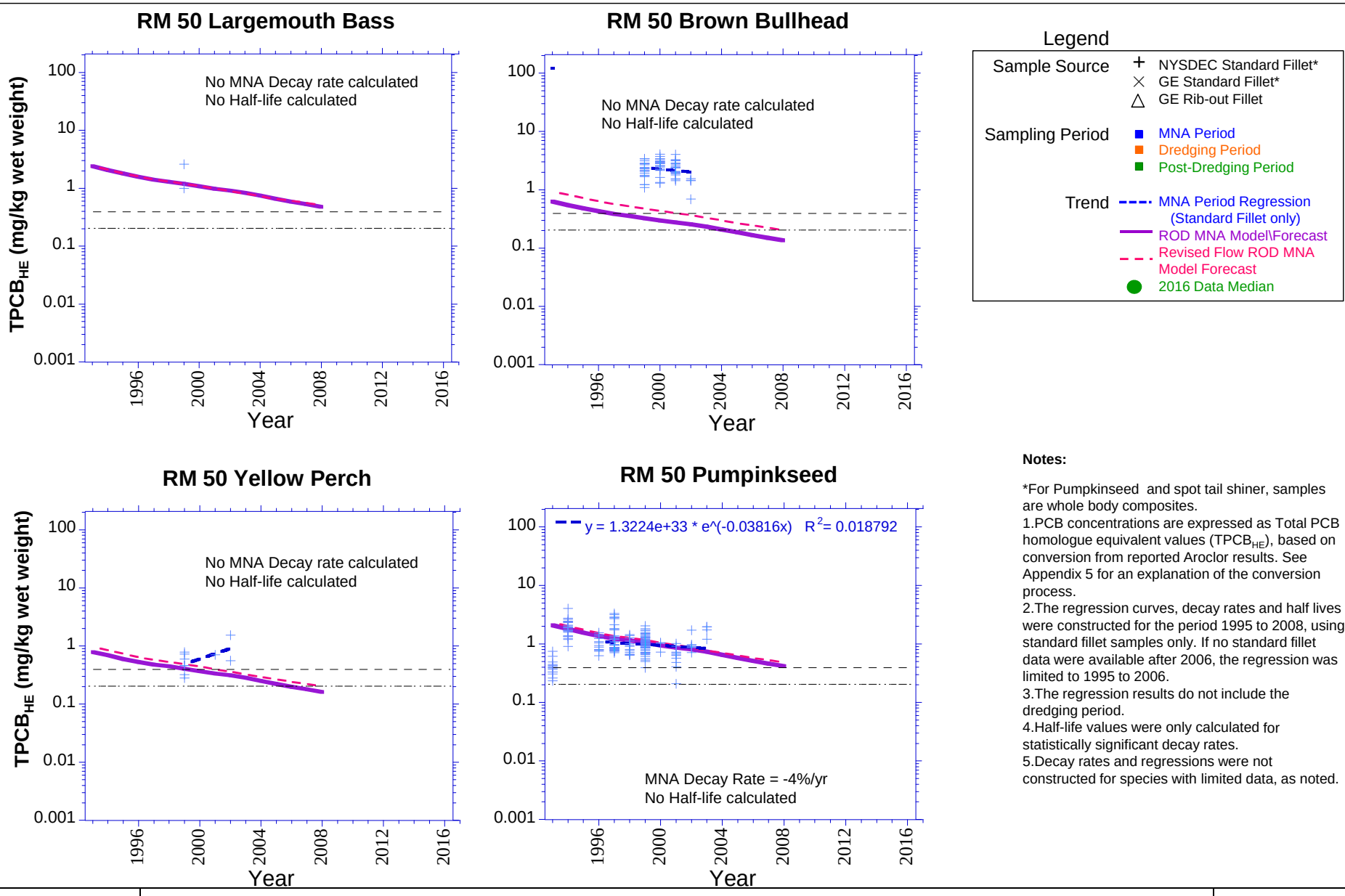
Notes:

*For Pumpkinseed and spot tail shiner, samples are whole body composites.
1.PCB concentrations are expressed as Total PCB homologue equivalent values ($TPCB_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.
2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

$TPCB_{HE}$ in Fish Tissue Samples at RM 90 - Wet Weight Basis

Figure A3-7B

May 2017

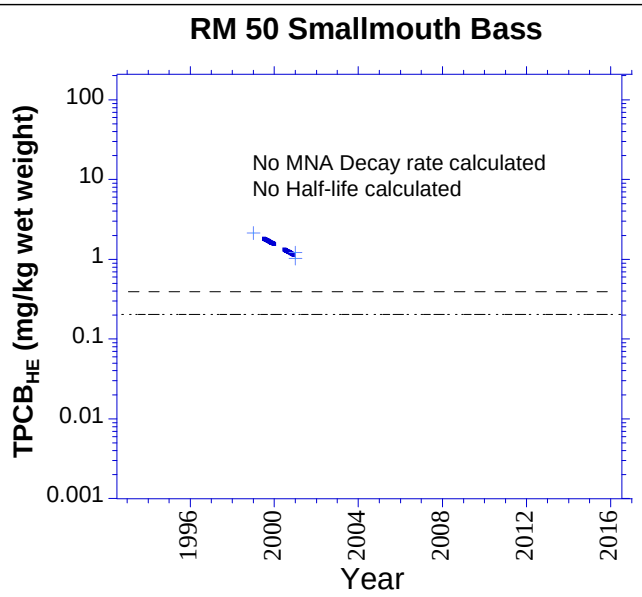


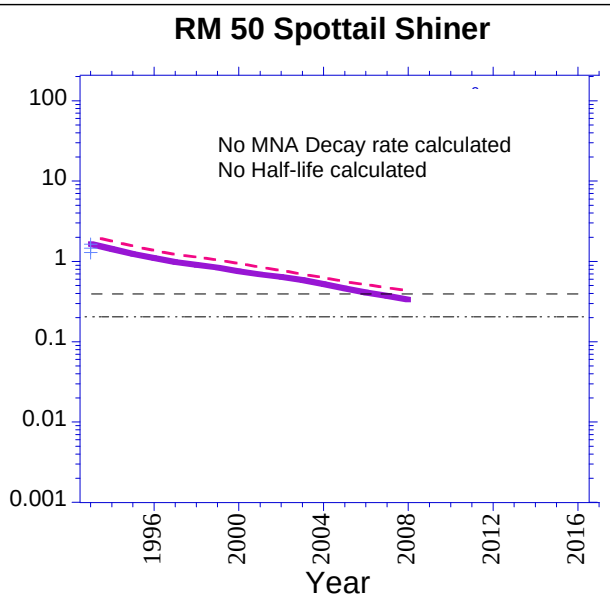
Notes:

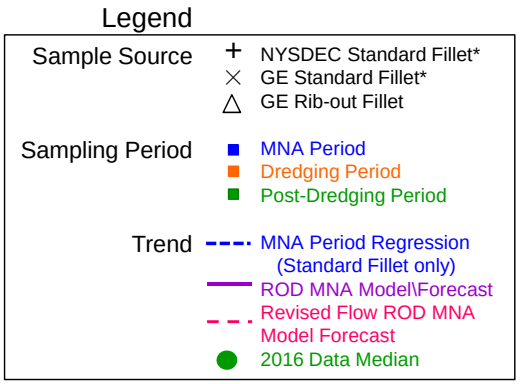
*For Pumpkinseed and spot tail shiner, samples are whole body composites.
1.PCB concentrations are expressed as Total PCB homologue equivalent values ($TPCB_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.
2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

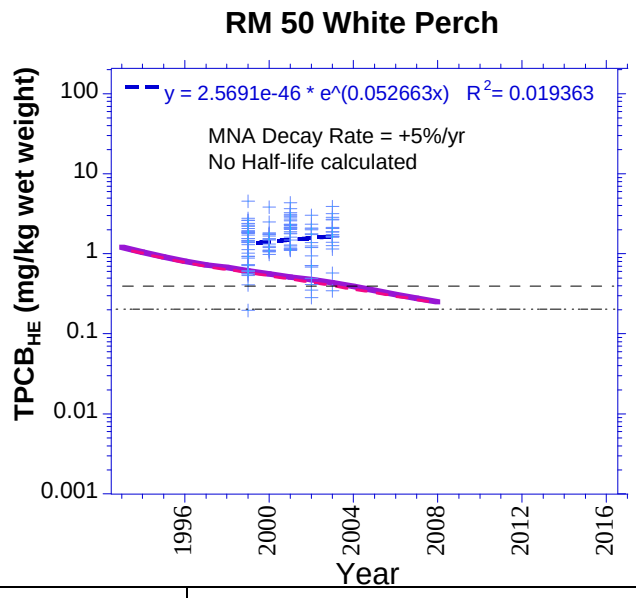
$TPCB_{HE}$ in Fish Tissue Samples at RM 50 - Wet Weight Basis

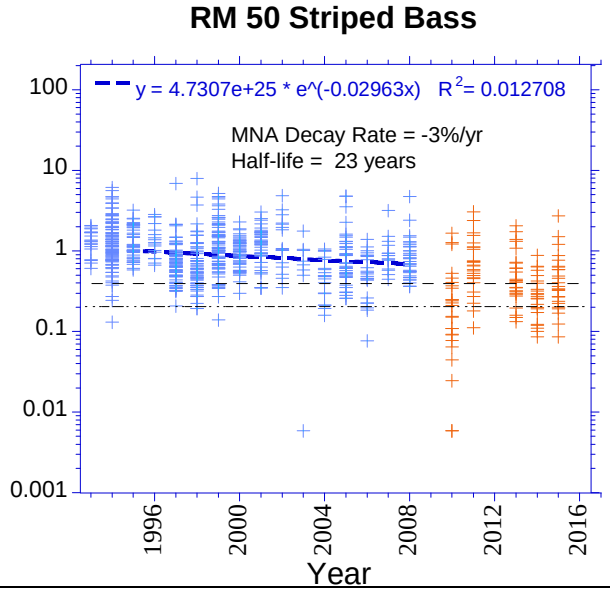
Figure A3-8A
May 2017











Notes:

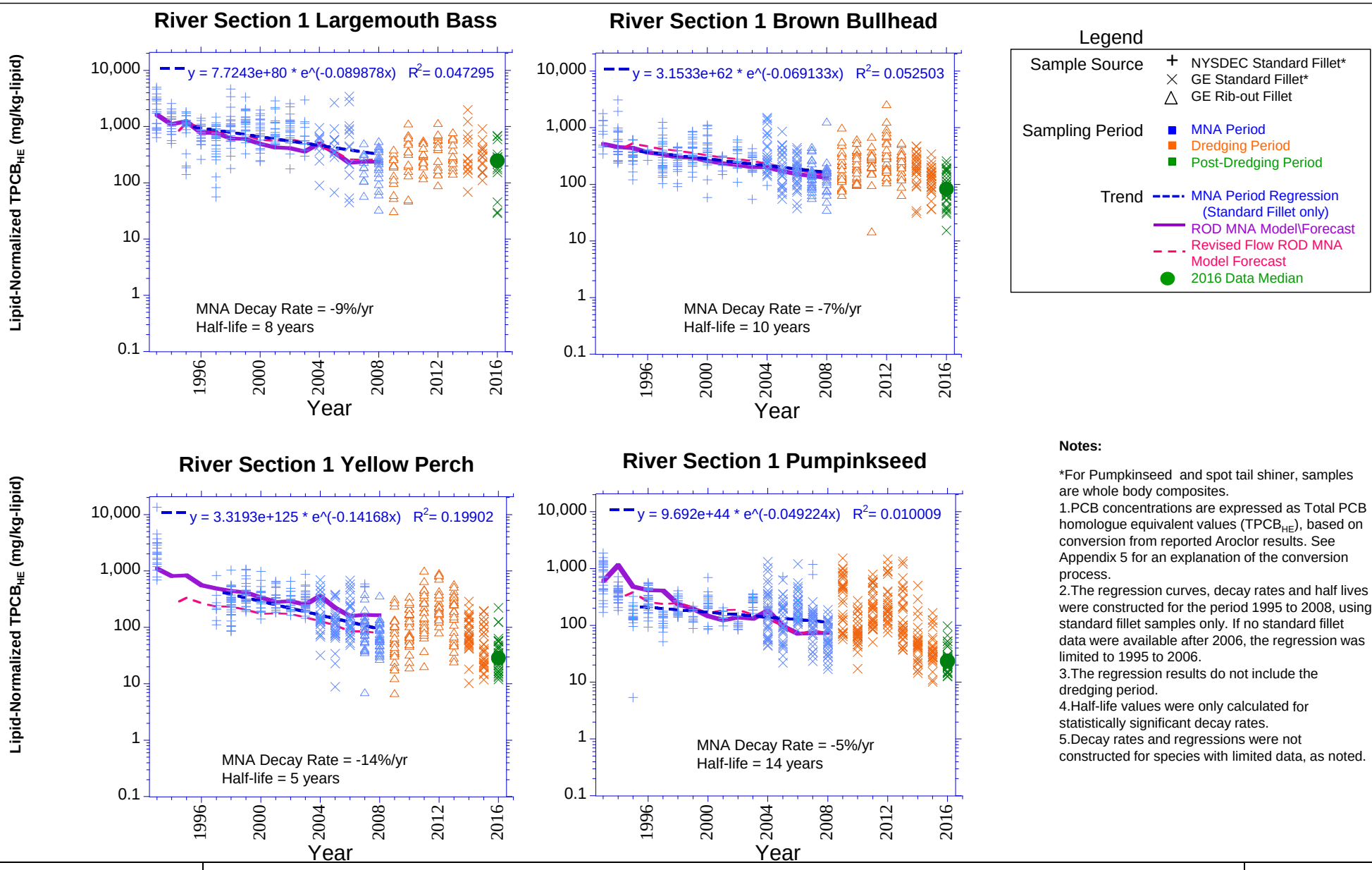
*For Pumpkinseed and spot tail shiner, samples are whole body composites.
1.PCB concentrations are expressed as Total PCB homologue equivalent values (TPCB$_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.
2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

Hudson River PCBs Superfund Site

TPCB$_{HE}$ in Fish Tissue Samples at RM 50 - Wet Weight Basis

Figure A3-8B

May 2017



Notes:

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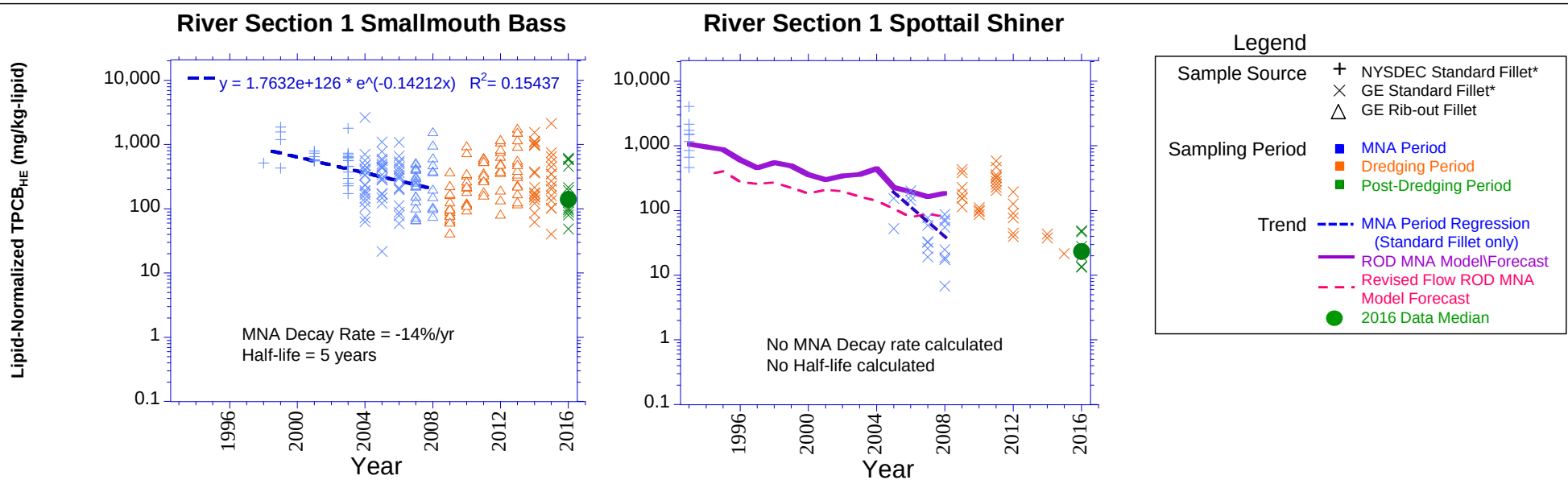
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

$TPCB_{HE}$ in Fish Tissue Samples at River Section 1 - Lipid Normalized Basis

Figure A3-9A

May 2017



Notes:

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3.The regression results do not include the dredging period.
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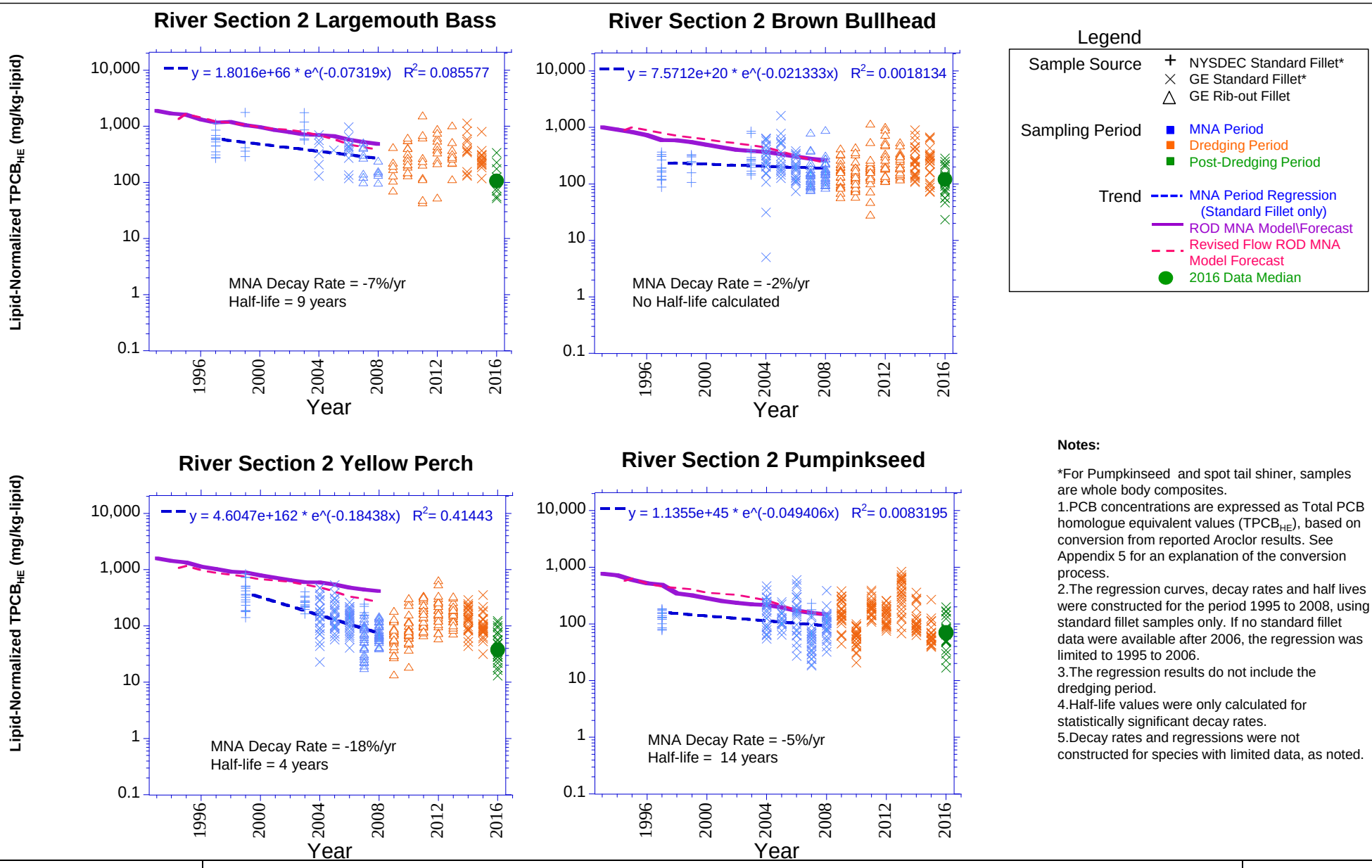
TPCB$_{HE}$ in Fish Tissue Samples at River Section 1 - Lipid Normalized Basis

Figure A3-9B

May 2017



Notes:

*For Pumpkinseed and spot tail shiner, samples are whole body composites.
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2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.
3.The regression results do not include the dredging period.
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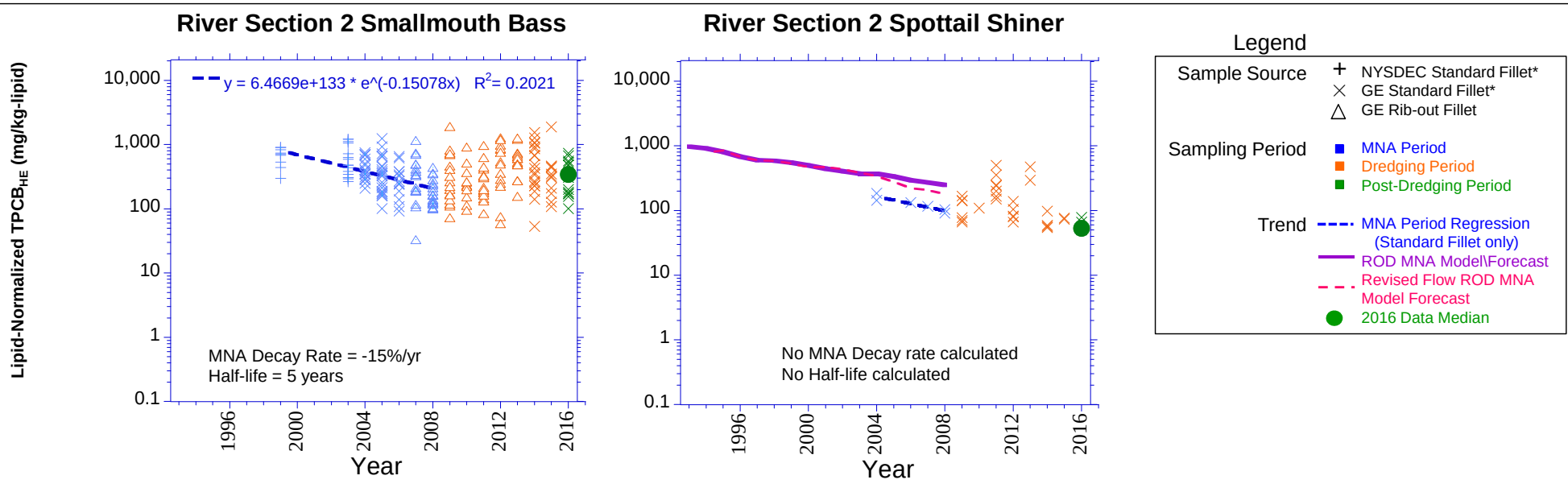
$TPCB_{HE}$ in Fish Tissue Samples at River Section 2 - Lipid Normalized Basis

Figure A3-10A

May 2017



Notes:

*For Pumpkinseed and spot tail shiner, samples are whole body composites.
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3.The regression results do not include the dredging period.
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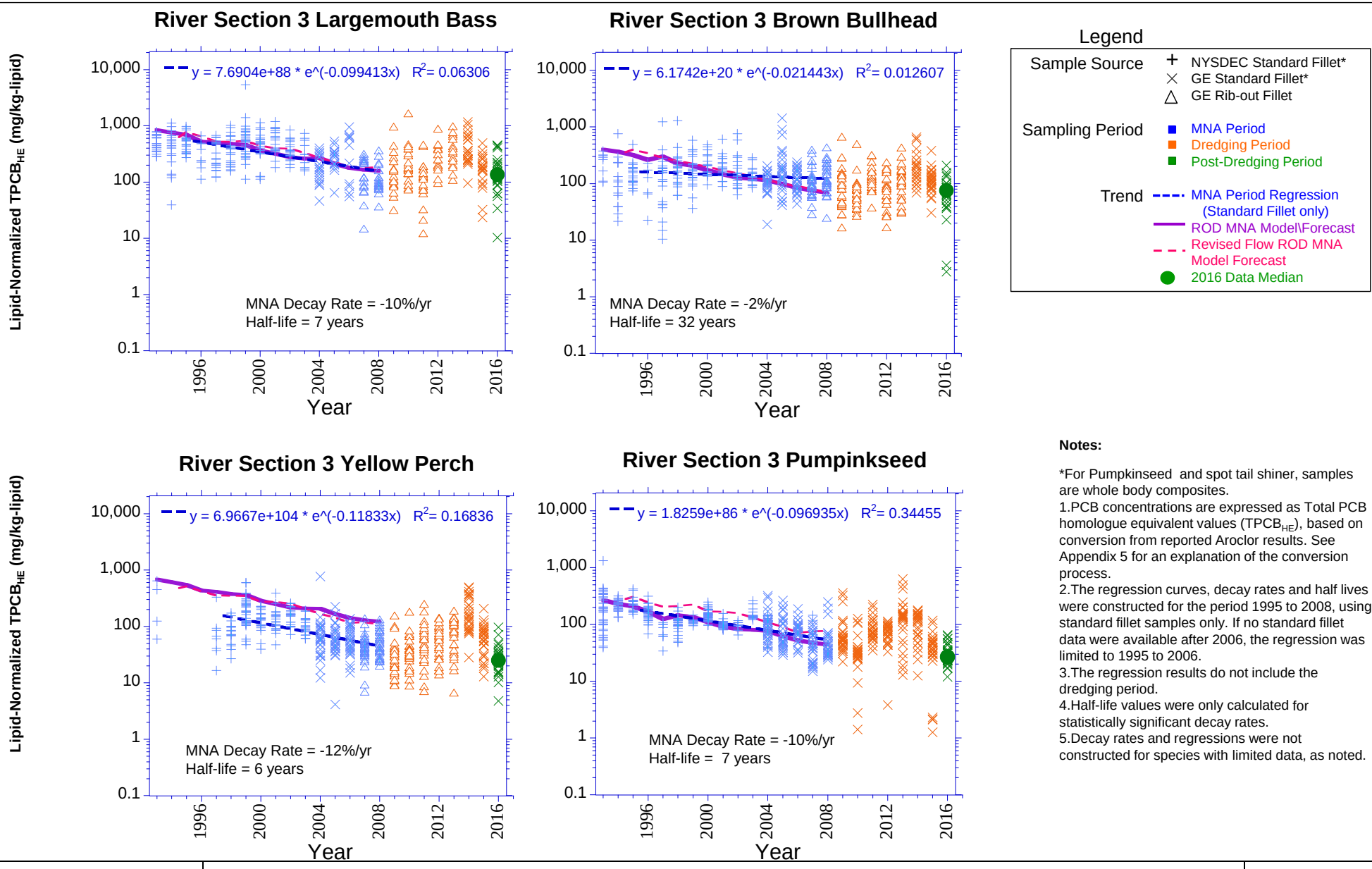
5.Decay rates and regressions were not constructed for species with limited data, as noted.

Hudson River PCBs Superfund Site

TPCB$_{HE}$ in Fish Tissue Samples at River Section 2 - Lipid Normalized Basis

Figure A3-10B

May 2017



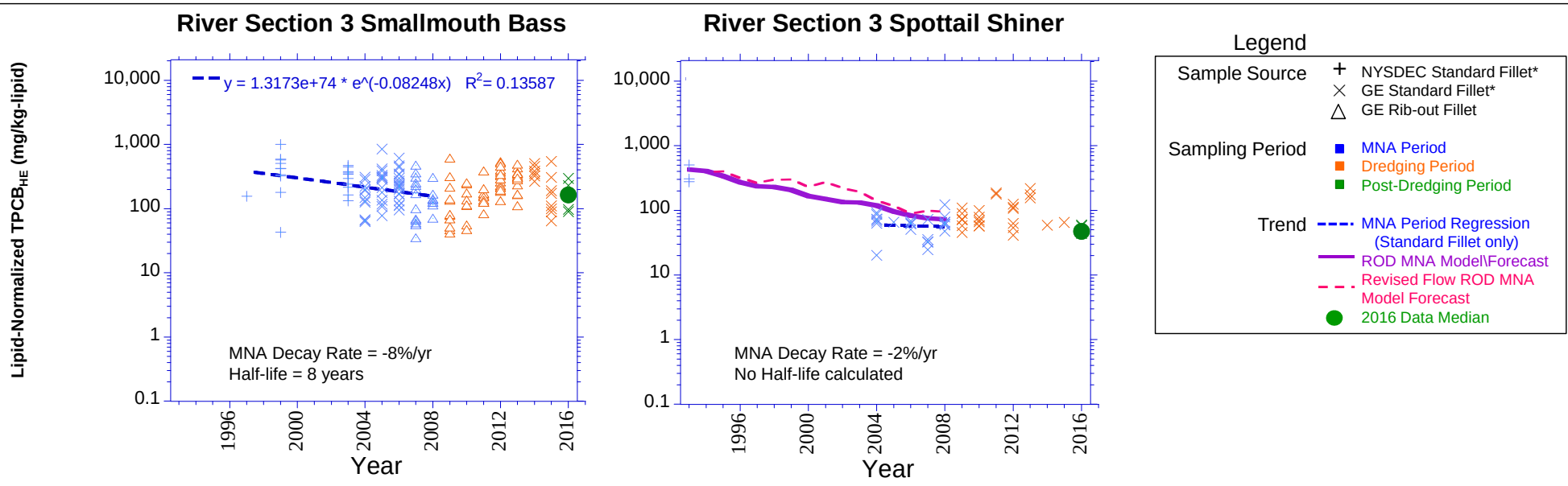
Notes:

*For Pumpkinseed and spot tail shiner, samples are whole body composites.
1.PCB concentrations are expressed as Total PCB homologue equivalent values ($TPCB_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.
2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

$TPCB_{HE}$ in Fish Tissue Samples at River Section 3 - Lipid Normalized Basis

Figure A3-11A

May 2017



Notes:

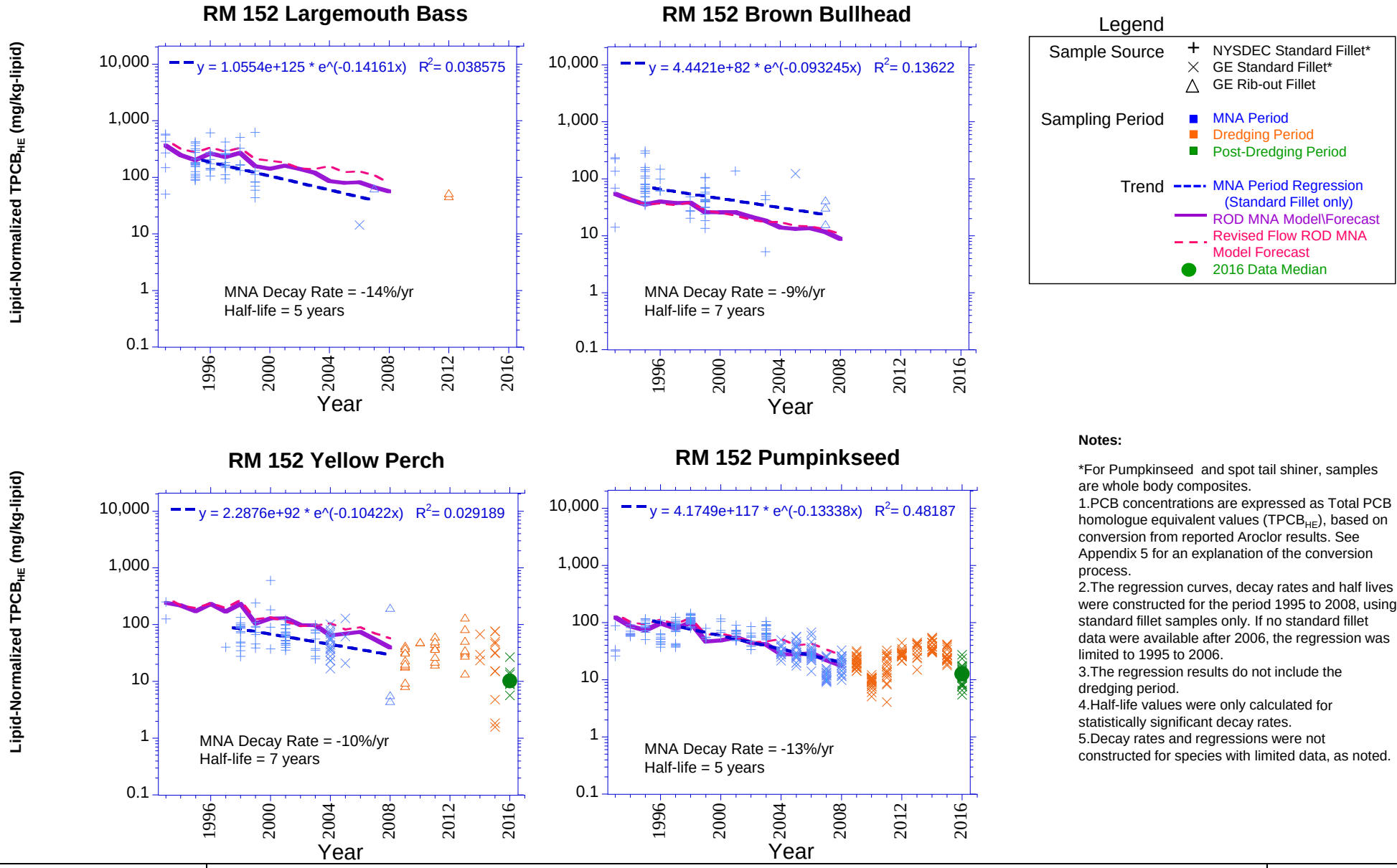
*For Pumpkinseed and spot tail shiner, samples are whole body composites.
1.PCB concentrations are expressed as Total PCB homologue equivalent values (TPCB$_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.
2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

Hudson River PCBs Superfund Site

TPCB$_{HE}$ in Fish Tissue Samples at River Section 3 - Lipid Normalized Basis

Figure A3-11B

May 2017



Notes:

*For Pumpkinseed and spot tail shiner, samples are whole body composites.
1.PCB concentrations are expressed as Total PCB homologue equivalent values ($TPCB_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.
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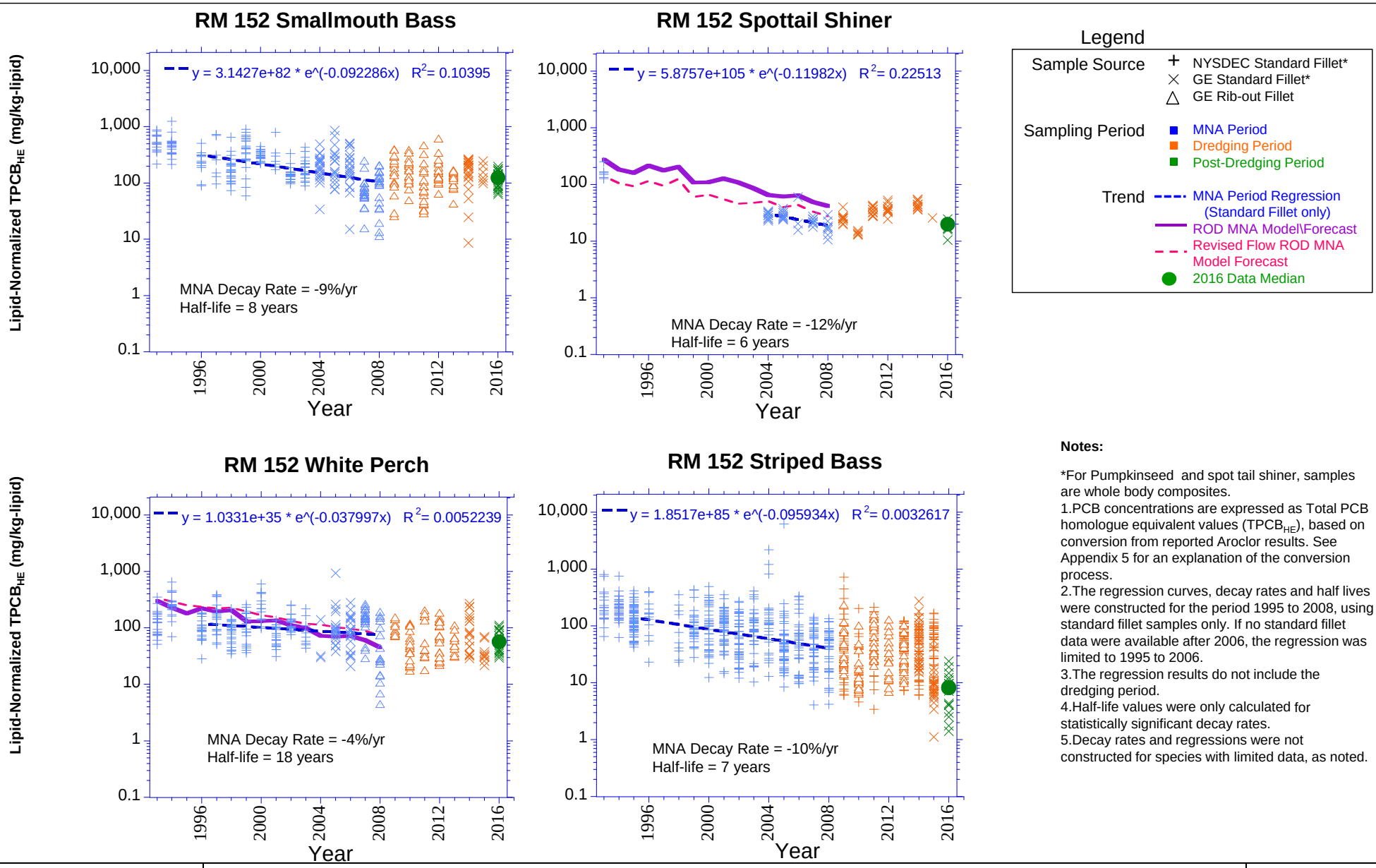
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

$TPCB_{HE}$ in Fish Tissue Samples at RM 152 - Lipid Normalized Basis

Figure A3-12A

May 2017



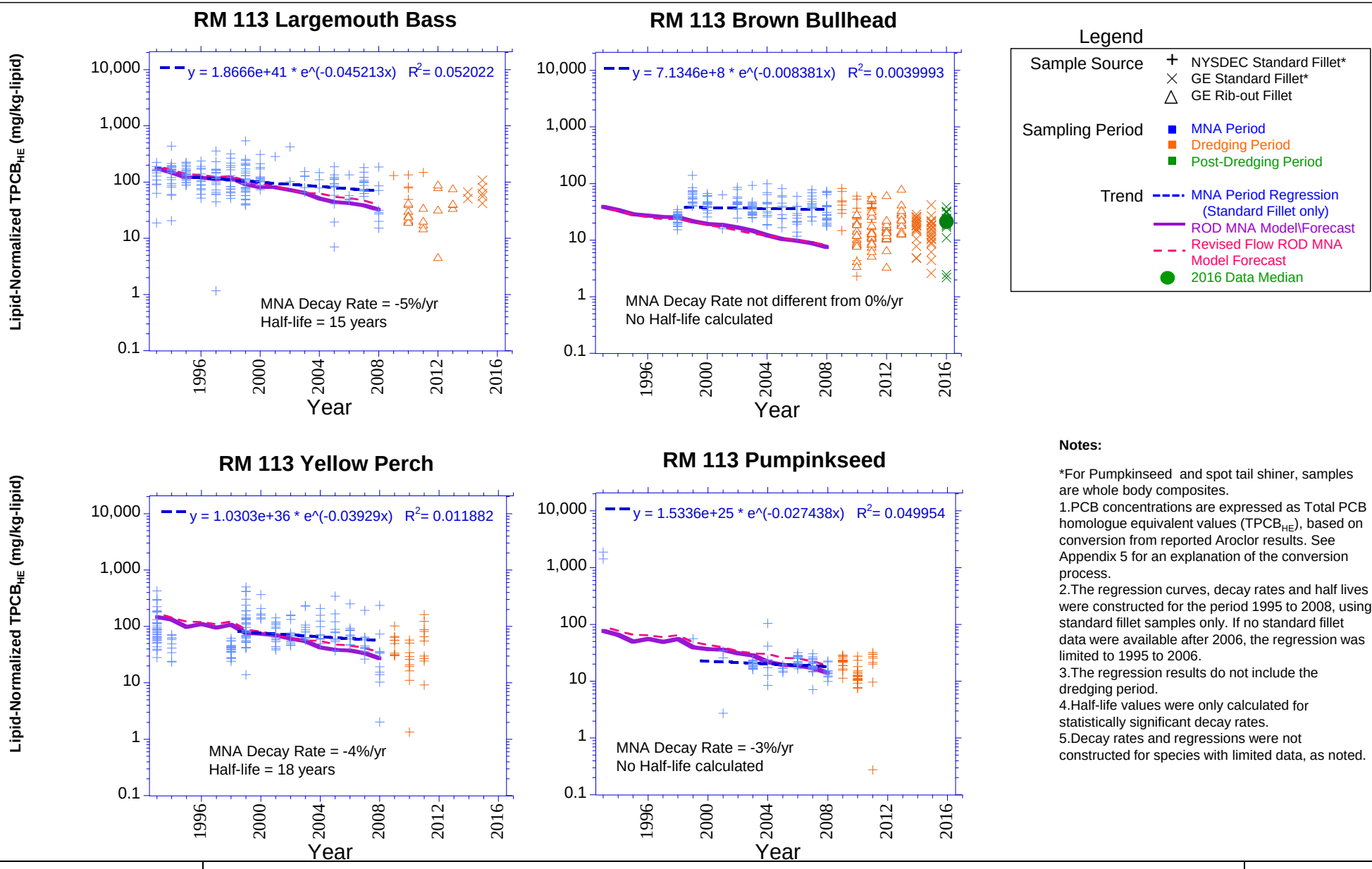
Notes:

*For Pumpkinseed and spot tail shiner, samples are whole body composites.
1.PCB concentrations are expressed as Total PCB homologue equivalent values ($TPCB_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.
2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

$TPCB_{HE}$ in Fish Tissue Samples at RM 152 - Lipid Normalized Basis

Figure A3-12B

May 2017



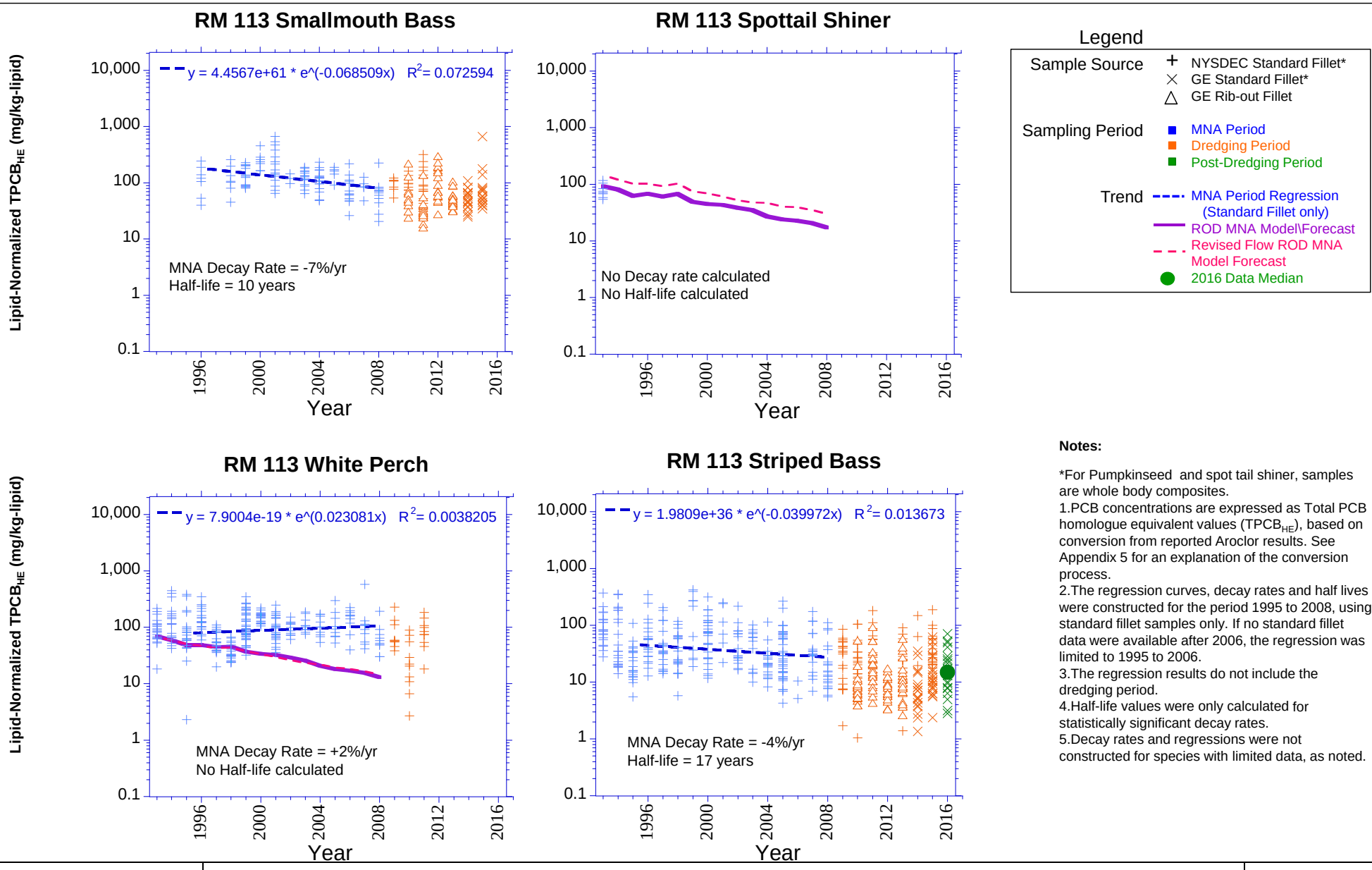
Notes:

*For Pumpkinseed and spot tail shiner, samples are whole body composites.
1.PCB concentrations are expressed as Total PCB homologue equivalent values ($TPCB_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.
2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

$TPCB_{HE}$ in Fish Tissue Samples at RM 113 - Lipid Normalized Basis

Figure A3-13A

May 2017



Notes:

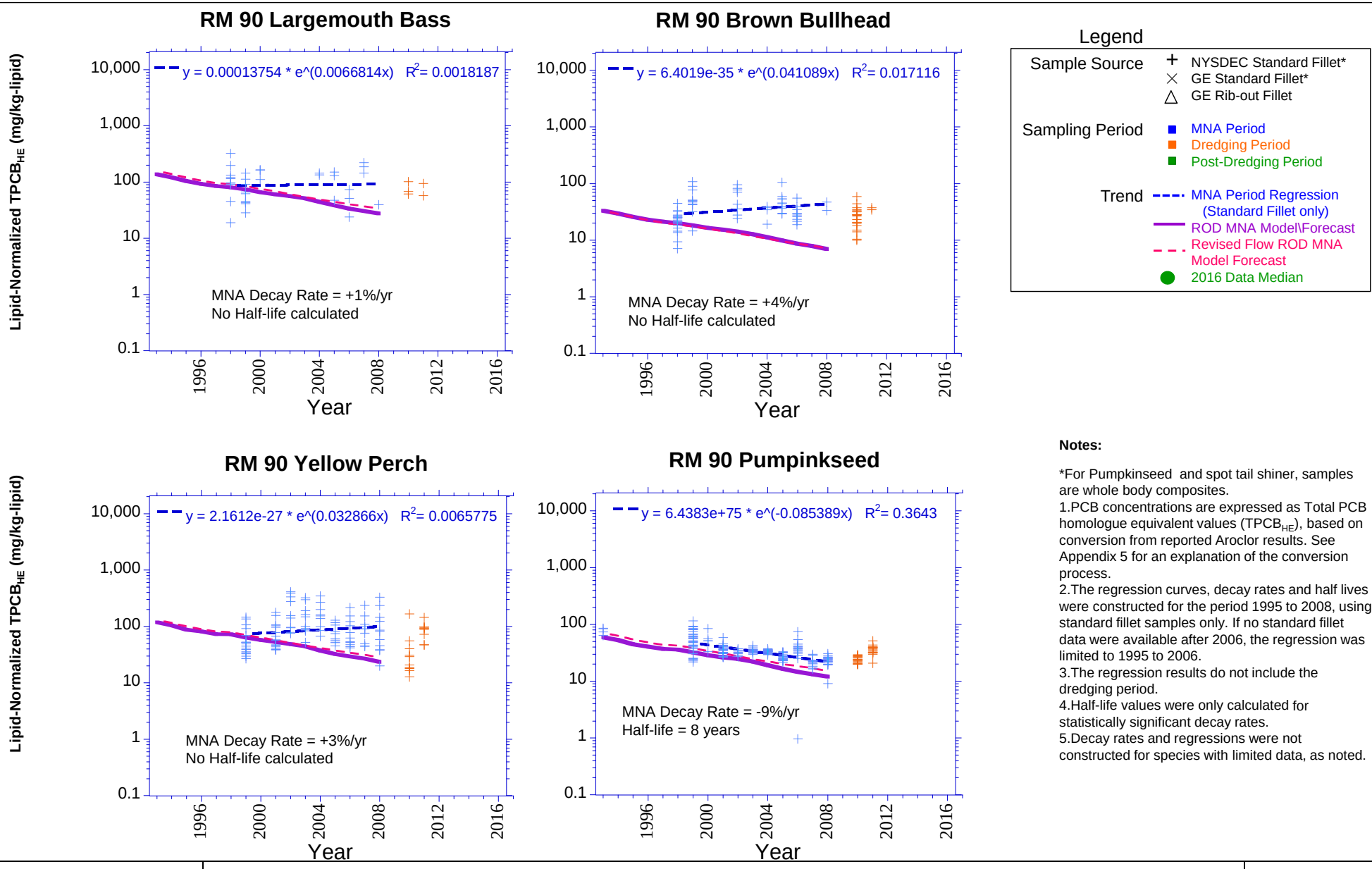
*For Pumpkinseed and spot tail shiner, samples are whole body composites.
1.PCB concentrations are expressed as Total PCB homologue equivalent values ($TPCB_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.
2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

Hudson River PCBs Superfund Site

$TPCB_{HE}$ in Fish Tissue Samples at RM 113 - Lipid Normalized Basis

Figure A3-13B

May 2017



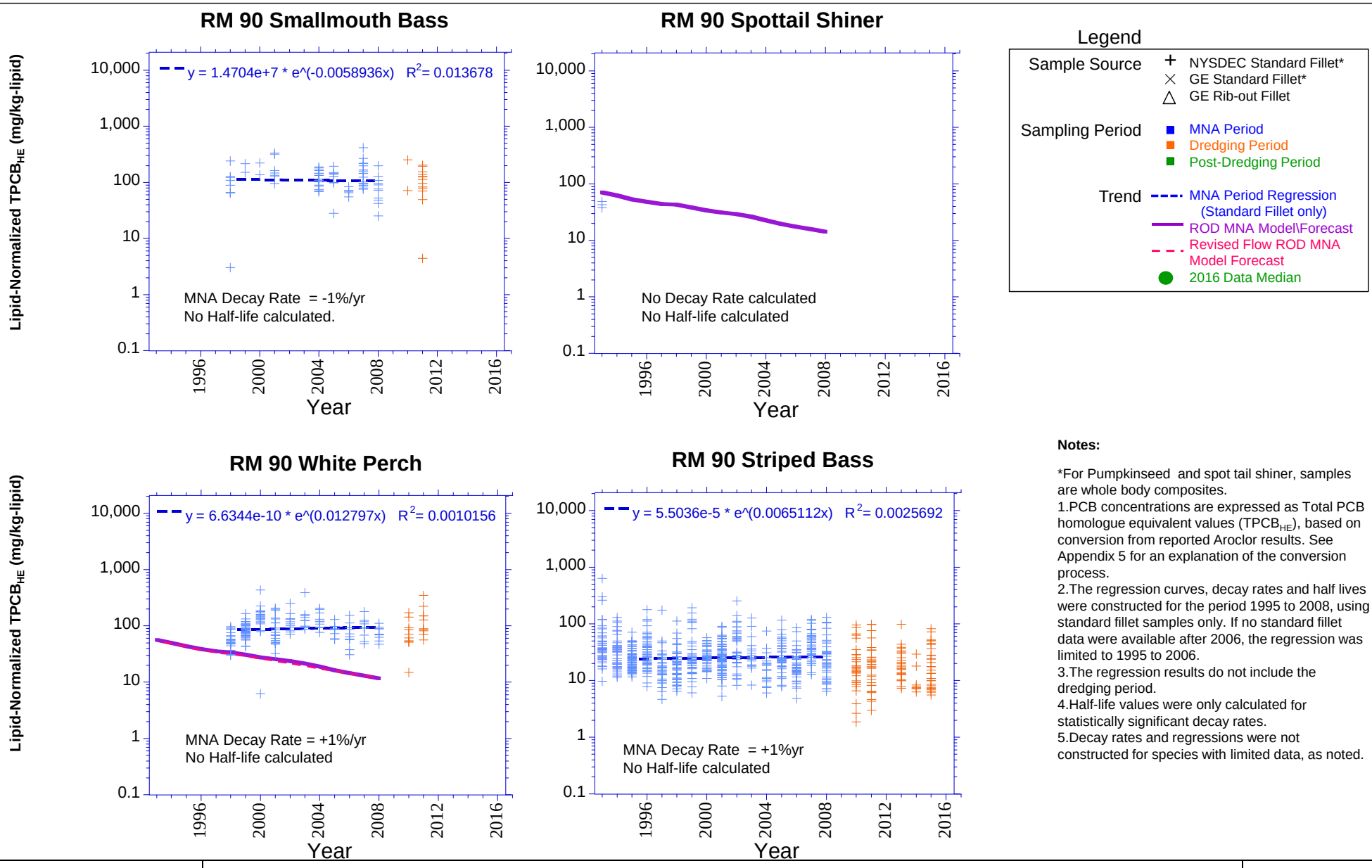
Notes:

*For Pumpkinseed and spot tail shiner, samples are whole body composites.
1.PCB concentrations are expressed as Total PCB homologue equivalent values ($TPCB_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.
2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

$TPCB_{HE}$ in Fish Tissue Samples at RM 90 - Lipid Normalized Basis

Figure A3-14A

May 2017



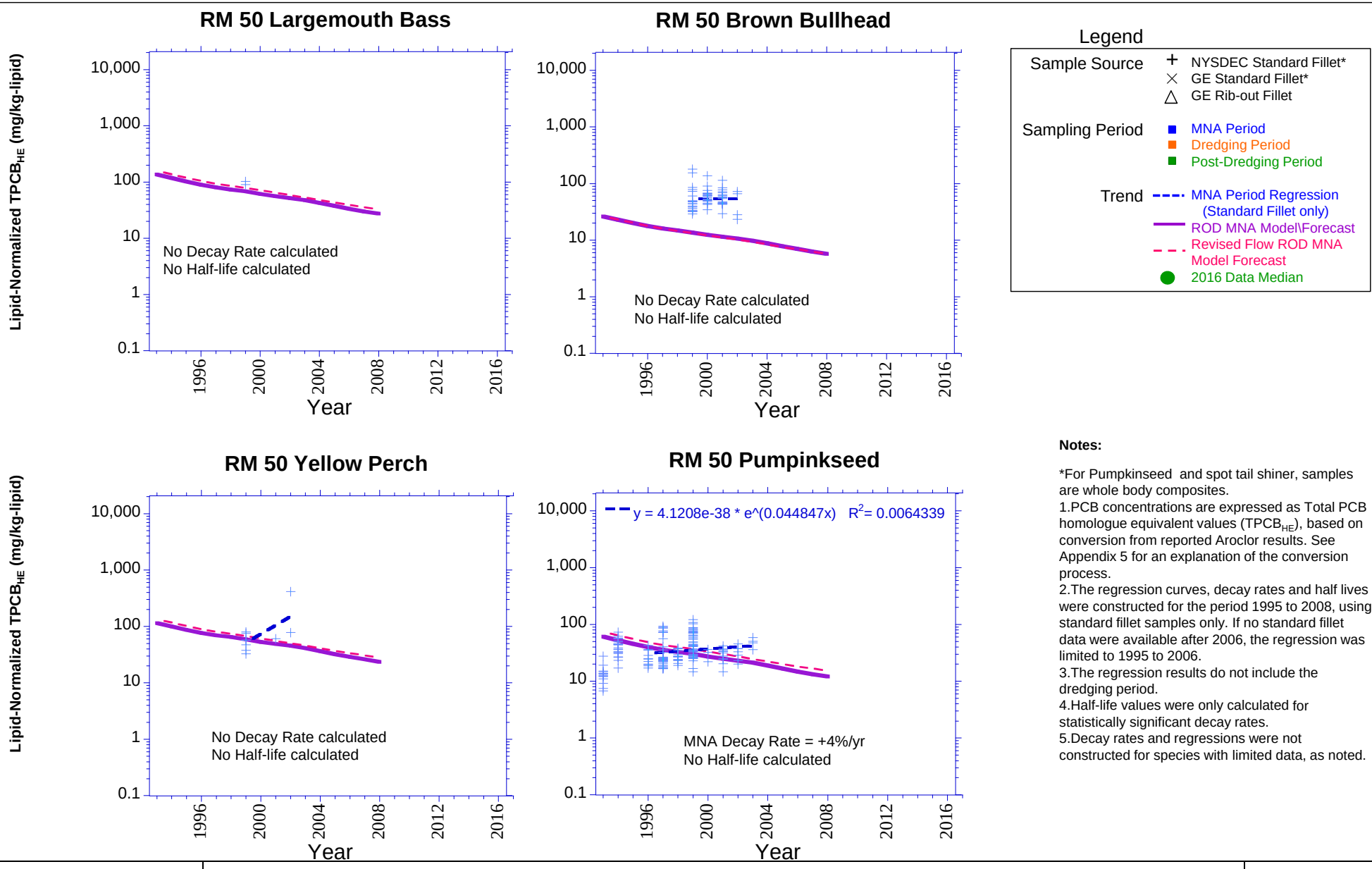
Notes:

*For Pumpkinseed and spot tail shiner, samples are whole body composites.
1.PCB concentrations are expressed as Total PCB homologue equivalent values ($TPCB_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.
2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

$TPCB_{HE}$ in Fish Tissue Samples at RM 90 - Lipid Normalized Basis

Figure A3-14B

May 2017



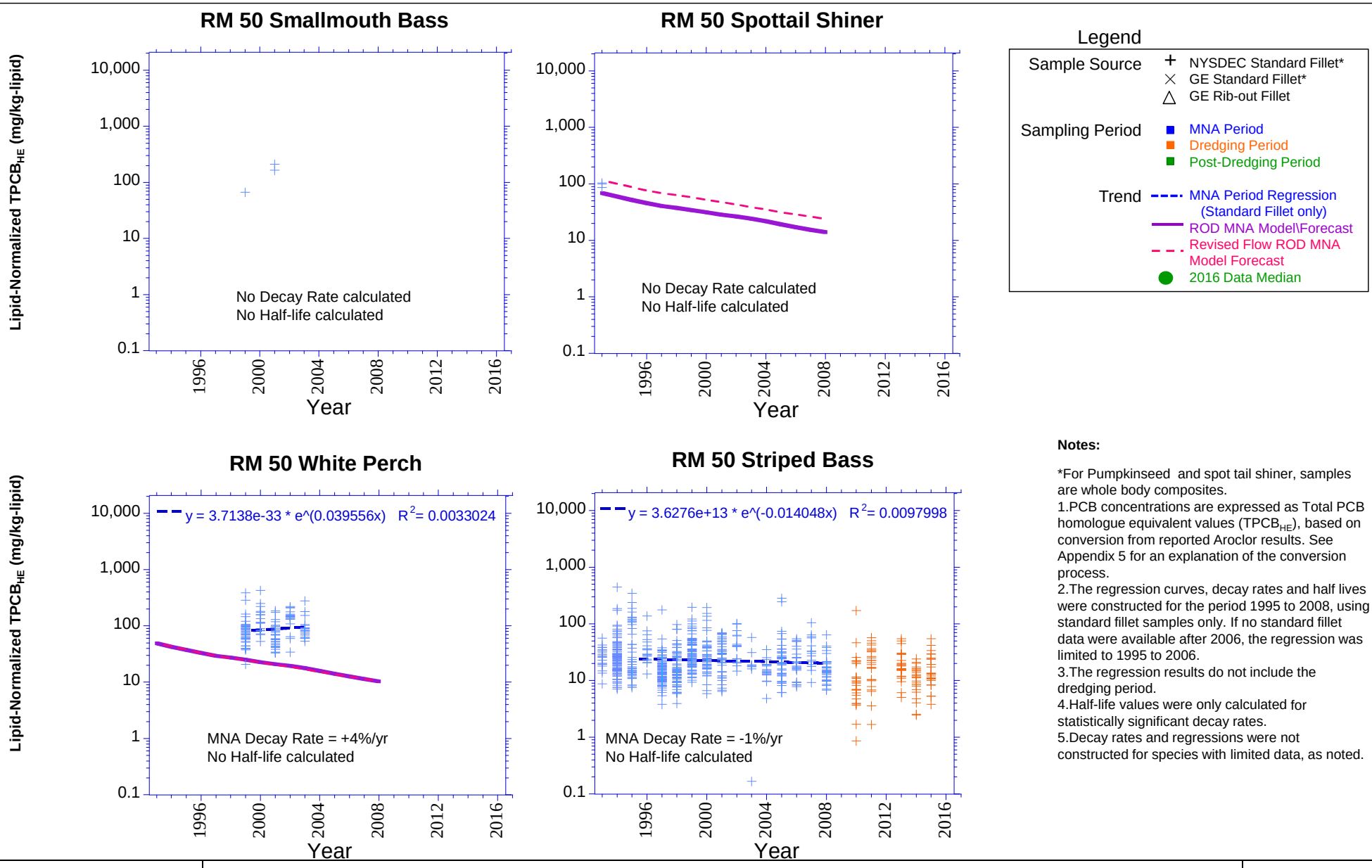
Notes:

*For Pumpkinseed and spot tail shiner, samples are whole body composites.
1.PCB concentrations are expressed as Total PCB homologue equivalent values (TPCB$_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.
2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

TPCB$_{HE}$ in Fish Tissue Samples at RM 50 - Lipid Normalized Basis

Figure A3-15A

May 2017



Notes:

*For Pumpkinseed and spot tail shiner, samples are whole body composites.
1.PCB concentrations are expressed as Total PCB homologue equivalent values ($TPCB_{HE}$), based on conversion from reported Aroclor results. See Appendix 5 for an explanation of the conversion process.
2.The regression curves, decay rates and half lives were constructed for the period 1995 to 2008, using standard fillet samples only. If no standard fillet data were available after 2006, the regression was limited to 1995 to 2006.
3.The regression results do not include the dredging period.
4.Half-life values were only calculated for statistically significant decay rates.
5.Decay rates and regressions were not constructed for species with limited data, as noted.

$TPCB_{HE}$ in Fish Tissue Samples at RM 50 - Lipid Normalized Basis

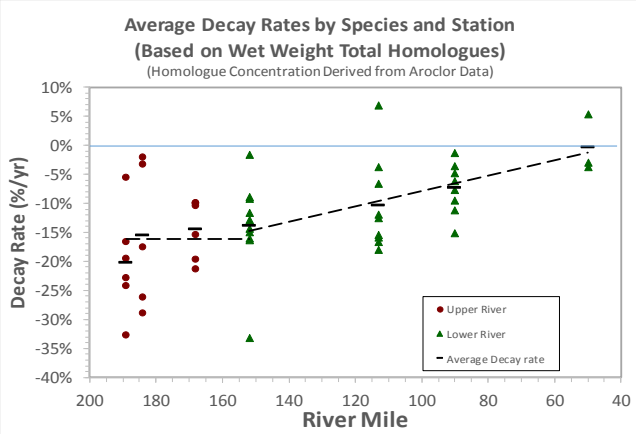
Figure A3-15B

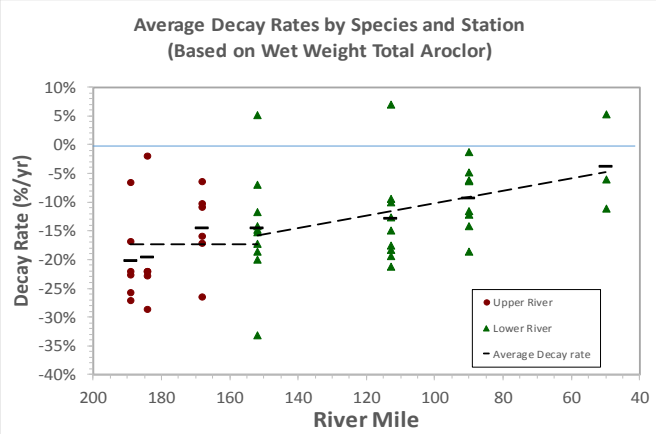
May 2017

Total PCB $_{HE}$

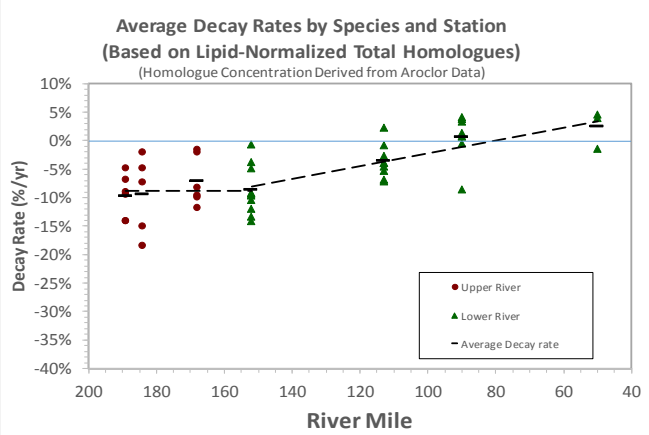
Total PCB $_{Aroclor}$

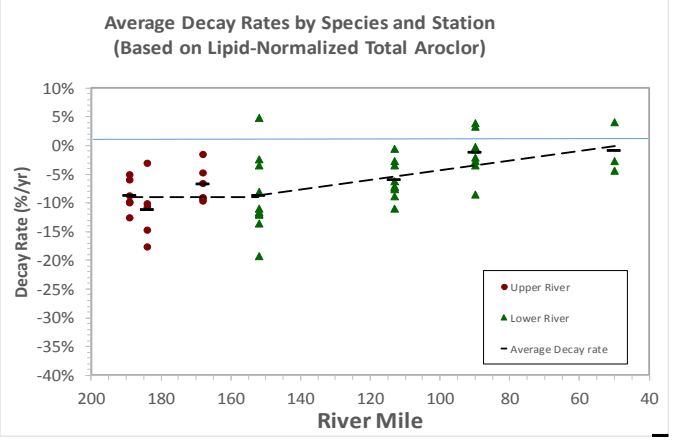
Wet Weight Basis





Lipid-Normalized Basis





Notes:
1. Wet Weight Basis average data do not include rib-out samples
2. Lipid Normalized Basis average data include rib-out samples

Fish Tissue Decay Rates as a Function of River Mile Stations with 5+ years of Data and at Least 25 Samples

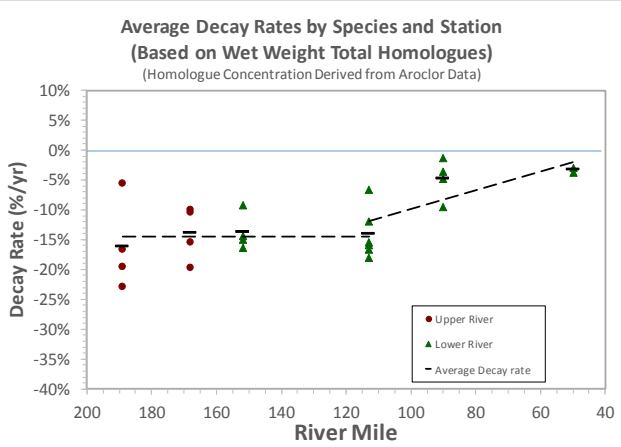
Figure A3-16A

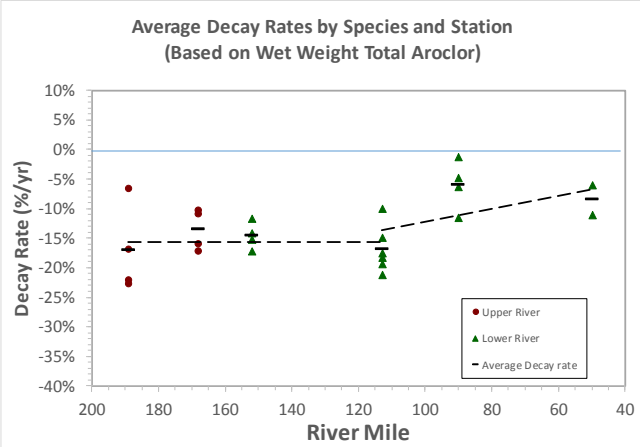
May 2017

Total PCB $_{HE}$

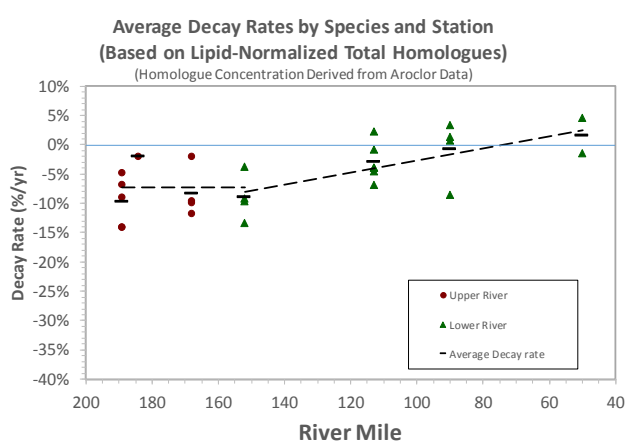
Total PCB $_{Aroclor}$

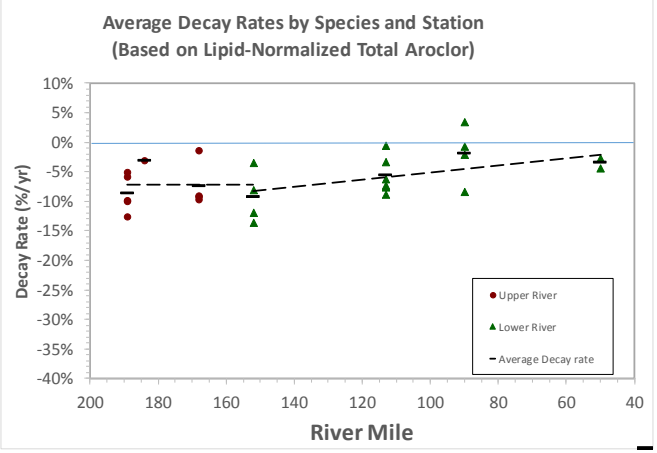
Wet Weight Basis





Lipid-Normalized Basis





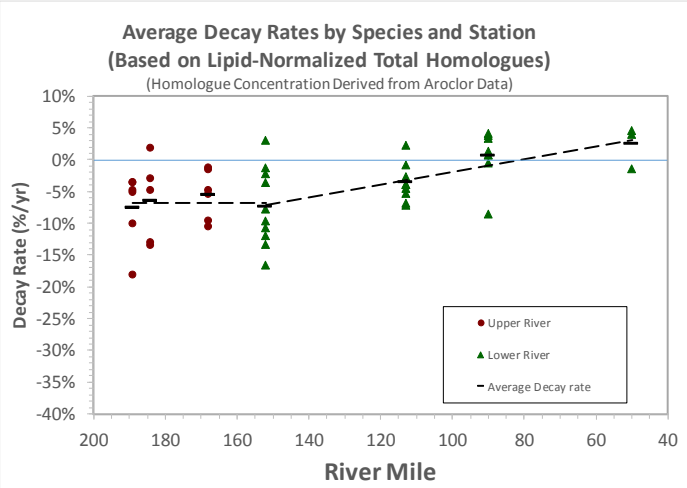
Notes:
1. Wet Weight Basis average data do not include rib-out samples
2. Lipid Normalized Basis average data include rib-out samples

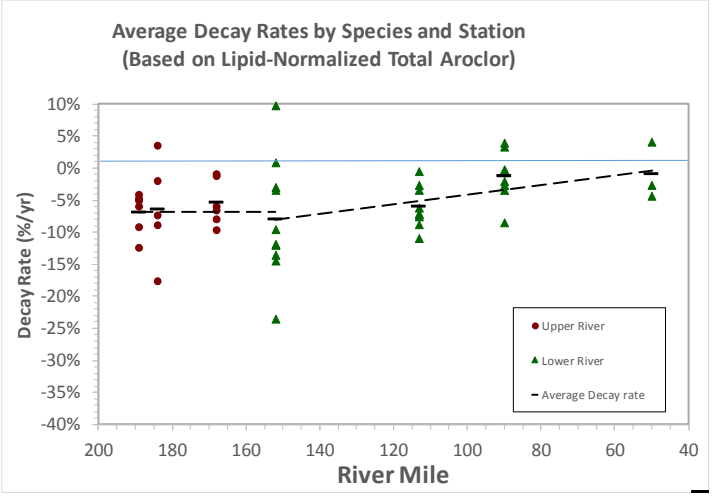
Fish Tissue Decay Rates as a Function of River Mile Stations with 8+ years of Data and at Least 100 Samples

Figure A3-16B

May 2017

Lipid-Normalized Basis



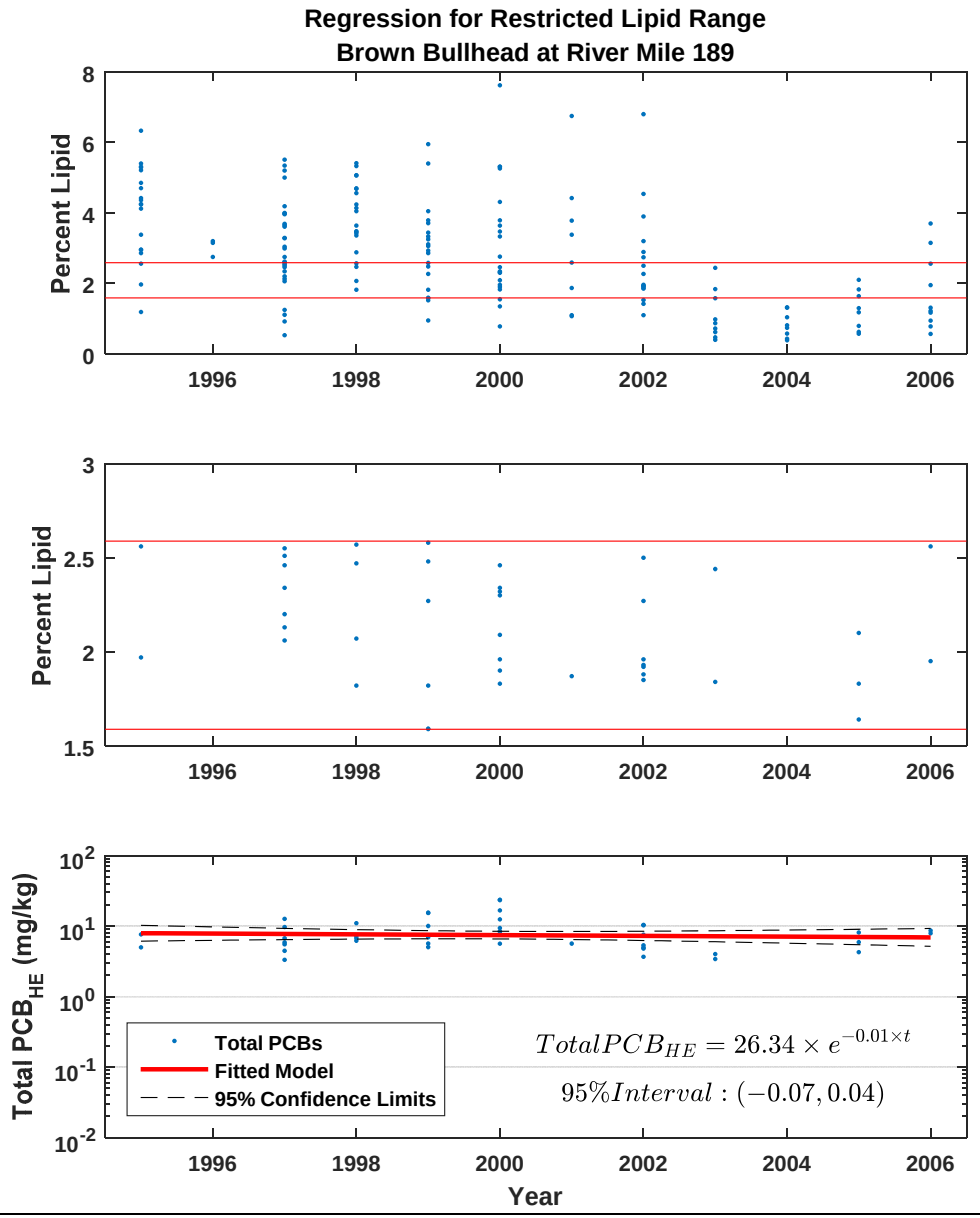


Notes:
1. Lipid Normalized Basis average data do not include rib-out samples

Sensitivity Analysis of non-NYSDEC standard Fillet Data on Fish Tissue Decay Rates as a Function of River Mile Stations with 5+ years of Data and at Least 25 Samples

Figure A3-16C

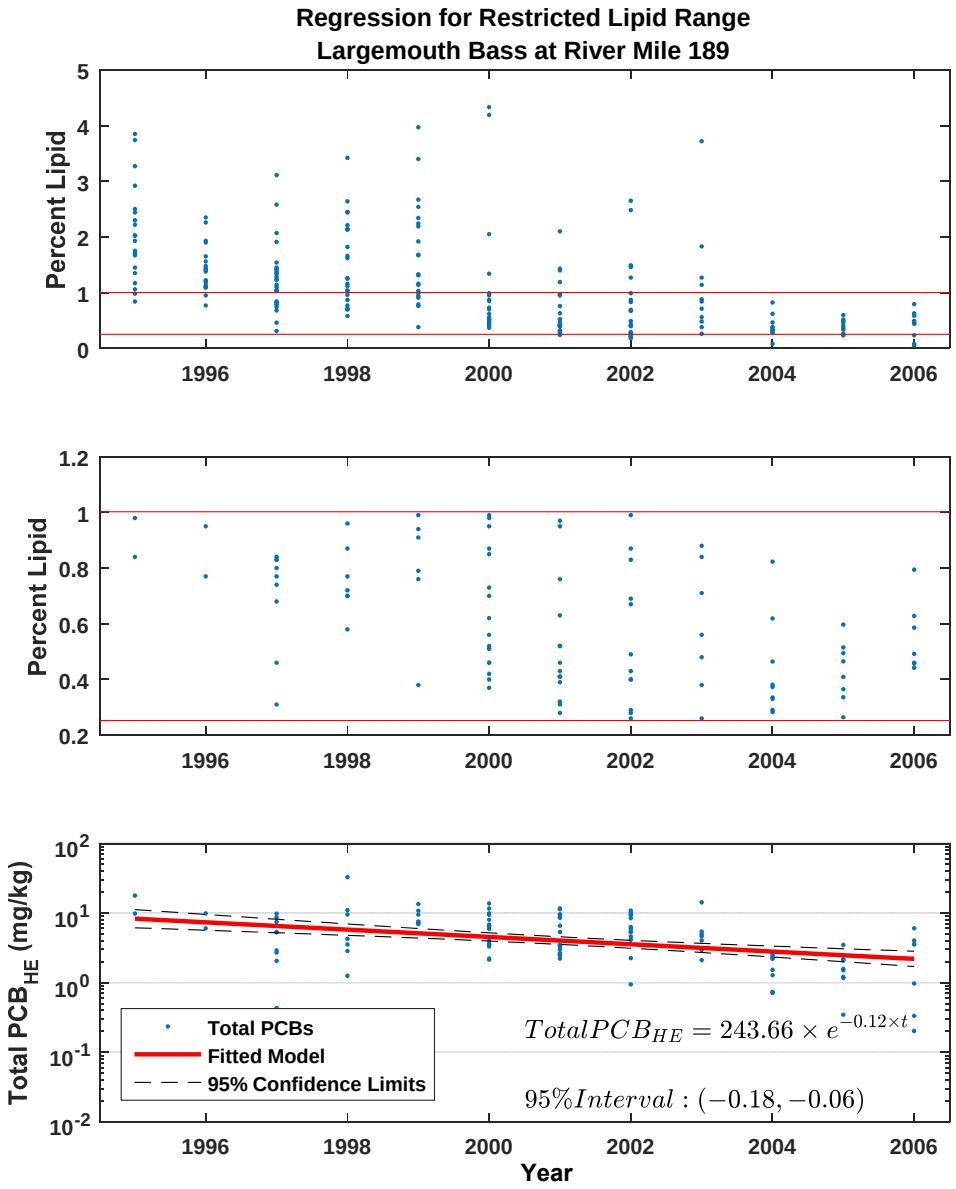
May 2017



Temporal distribution of percent lipid and range selected for analysis (top 2 panels) and temporal distribution of total PCBs (Homologue basis) for Brown Bullhead with fitted exponential decay function at River Mile 189 (Thompson Island Pool).

Figure A3-17

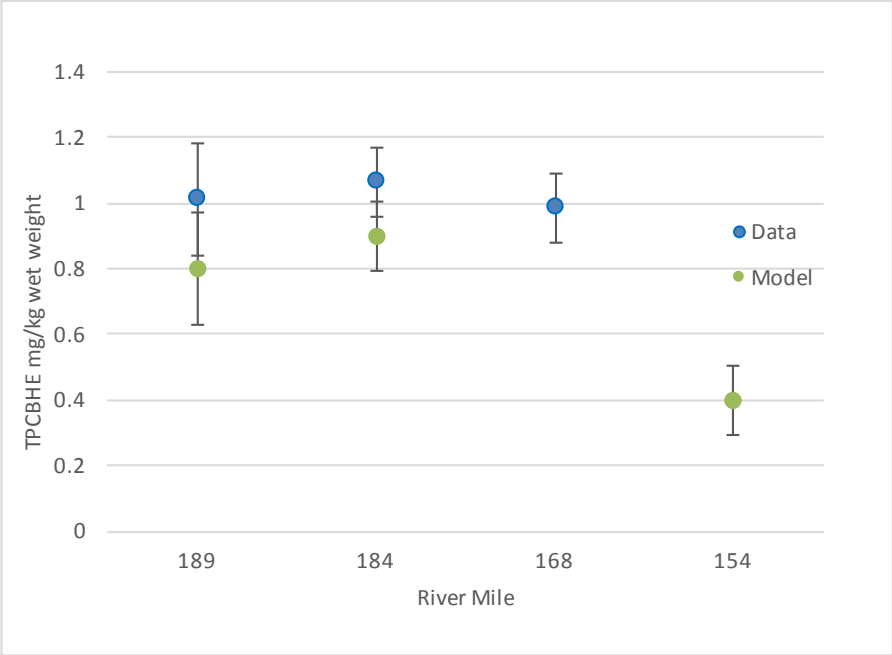
May 2017



Temporal distribution of percent lipid and range selected for analysis (top 2 panels) and temporal distribution of total PCBs (Homologue basis) for Largemouth Bass with fitted exponential decay function at River Mile 189 (Thompson Island Pool)

Figure A3-18

May 2017



Panel A: Species-Weighted average concentrations in the Upper Hudson River. Model (green) results taken from the first post-dredging year (2010) of Table 11-2 in the 2002 ROD and observed first post-dredging year data (blue) from the 2016 monitoring program.

Comparison of Model Results to 2016 Monitoring Data (mg/kg wet weight)

Species	RS1-RM189		RS2-RM184		RS3-RM154-168	
	Data Mean (Standard Error)	Model Mean (Standard Error)	Data Mean (Standard Error)	Model Mean (Standard Error)	RM168 Data Mean (Standard Error)	RM154 Model Mean (Standard Error)
BB	1.3 (0.2)	0.7 (0.2)	1.7 (0.2)	1.3 (0.2)	1.0 (0.1)	0.6 (0.1)
LMB	0.9 (0.3)	1.0 (0.3)	0.6 (0.1)	0.7 (0.1)	1.0 (0.2)	0.4 (0.2)
YP	0.4 (0.08)	0.7 (0.08)	0.5 (0.07)	0.5 (0.07)	0.3 (0.04)	0.4 (0.04)
Species-Weighted Mean	1.0 (0.2)	0.8 (0.2)	1.1 (0.1)	0.9 (0.1)	1.0 (0.1)	0.4 (0.1)
Note:						
Data are obtained from RM168 while model results are for RM154 -- both within RS3						
Species-Weighted Mean taken from Year 10 of Table 11-2 of the ROD						
Species-specific model results for year 2010 for the preferred alternative						

Panel B: Species-specific model results (Model Mean) for the selected remedy for the year 2010 (first post-dredging year) and observed monitoring data for first-post dredging year 2016 (Data Mean)

Comparison of Expected PCB Concentrations in Fish Tissue for the Preferred Alternative as Presented in the ROD (2002) to Monitoring Data for 2016

Figure A3-19

May 2017