1   Fig. S1 Iteratively reweighted least square regressions of cumulative biomass of all species
2   combined (g) and read abundance of all species combined (number of mapped reads) for each of
3   the six primer sets. Iteratively reweighted least square regression analysis results in fitting the
4   linear model to reweighted data (closed points) exclusive of outliers (open points). Data pooled
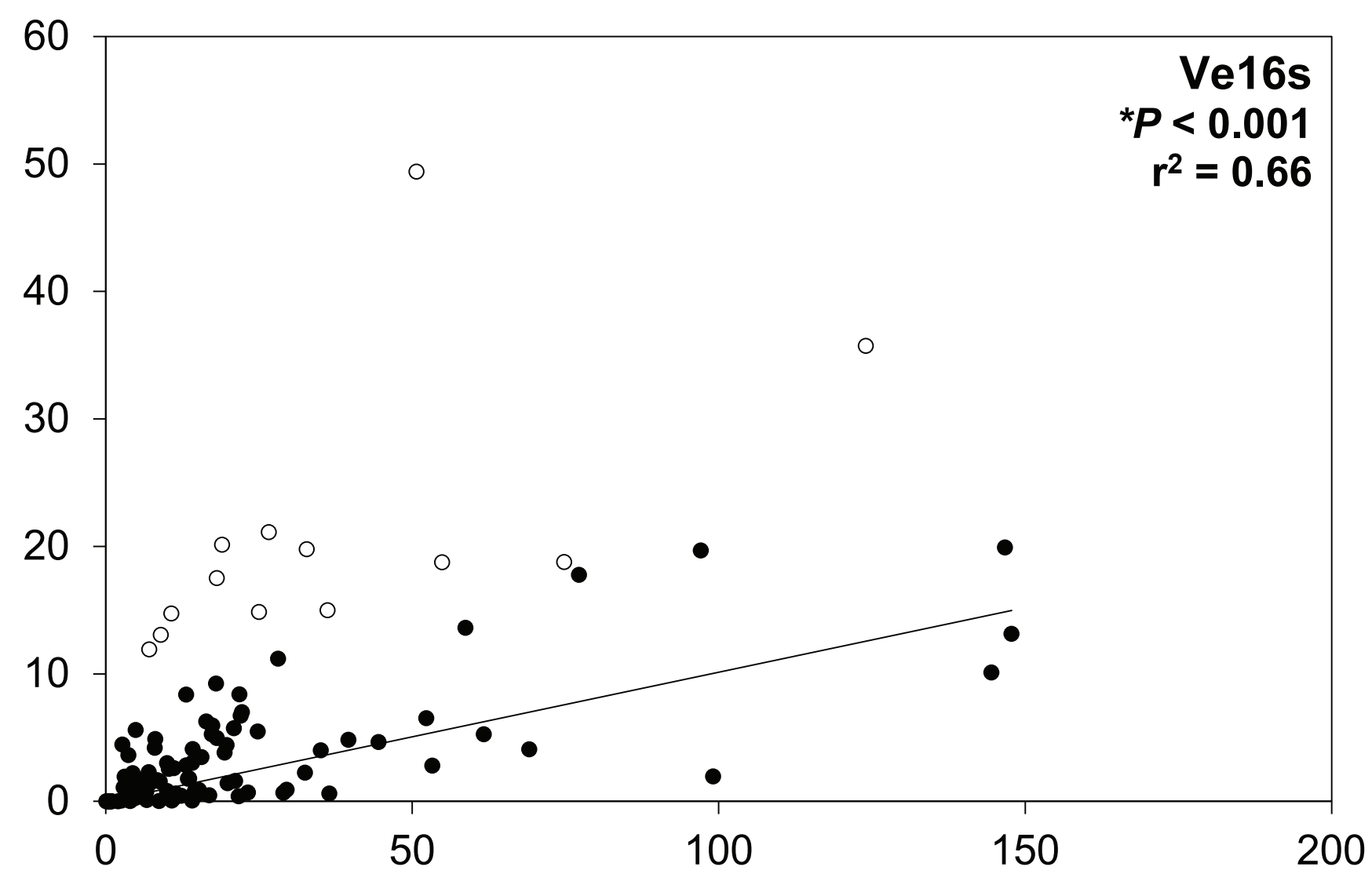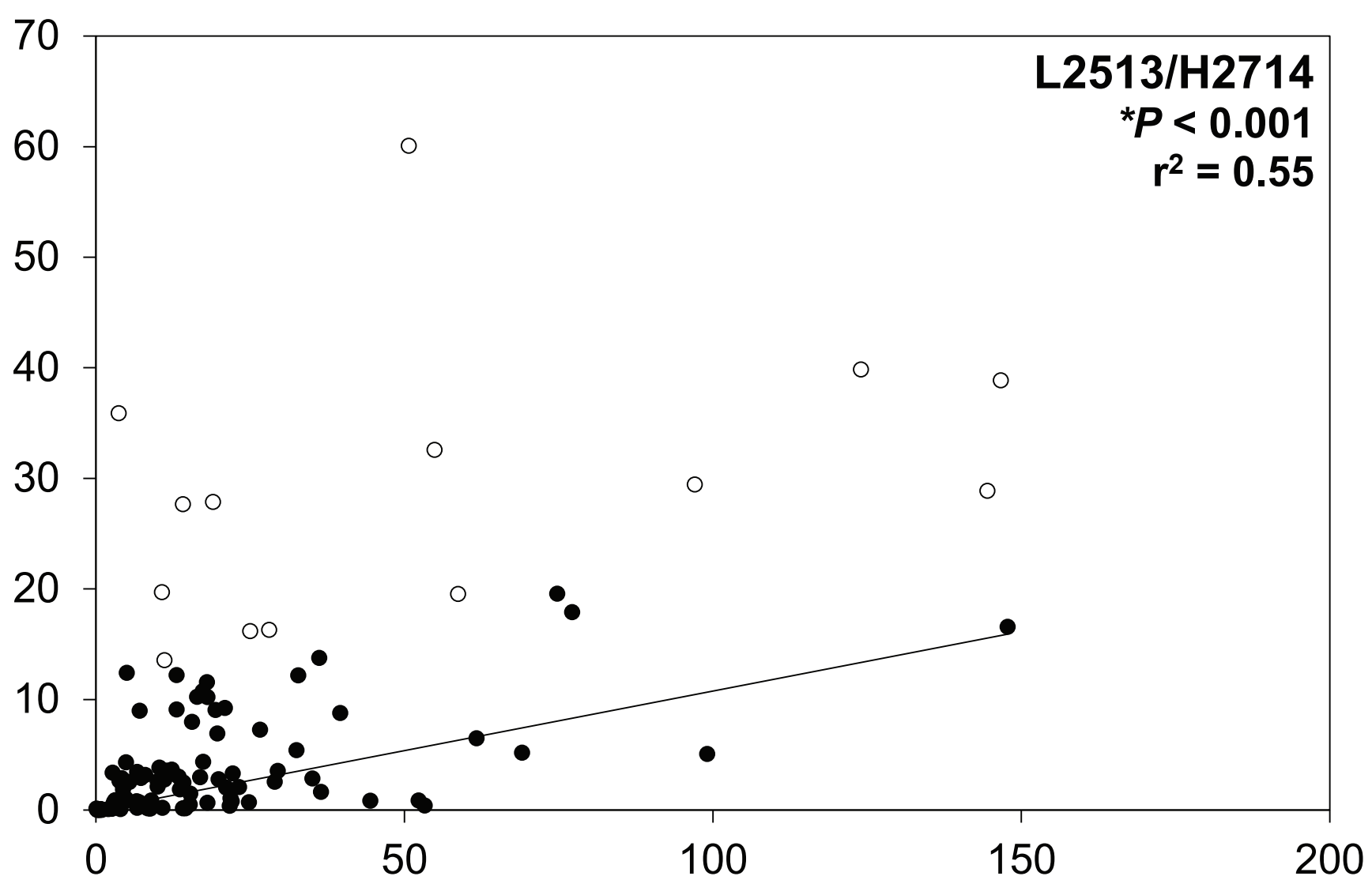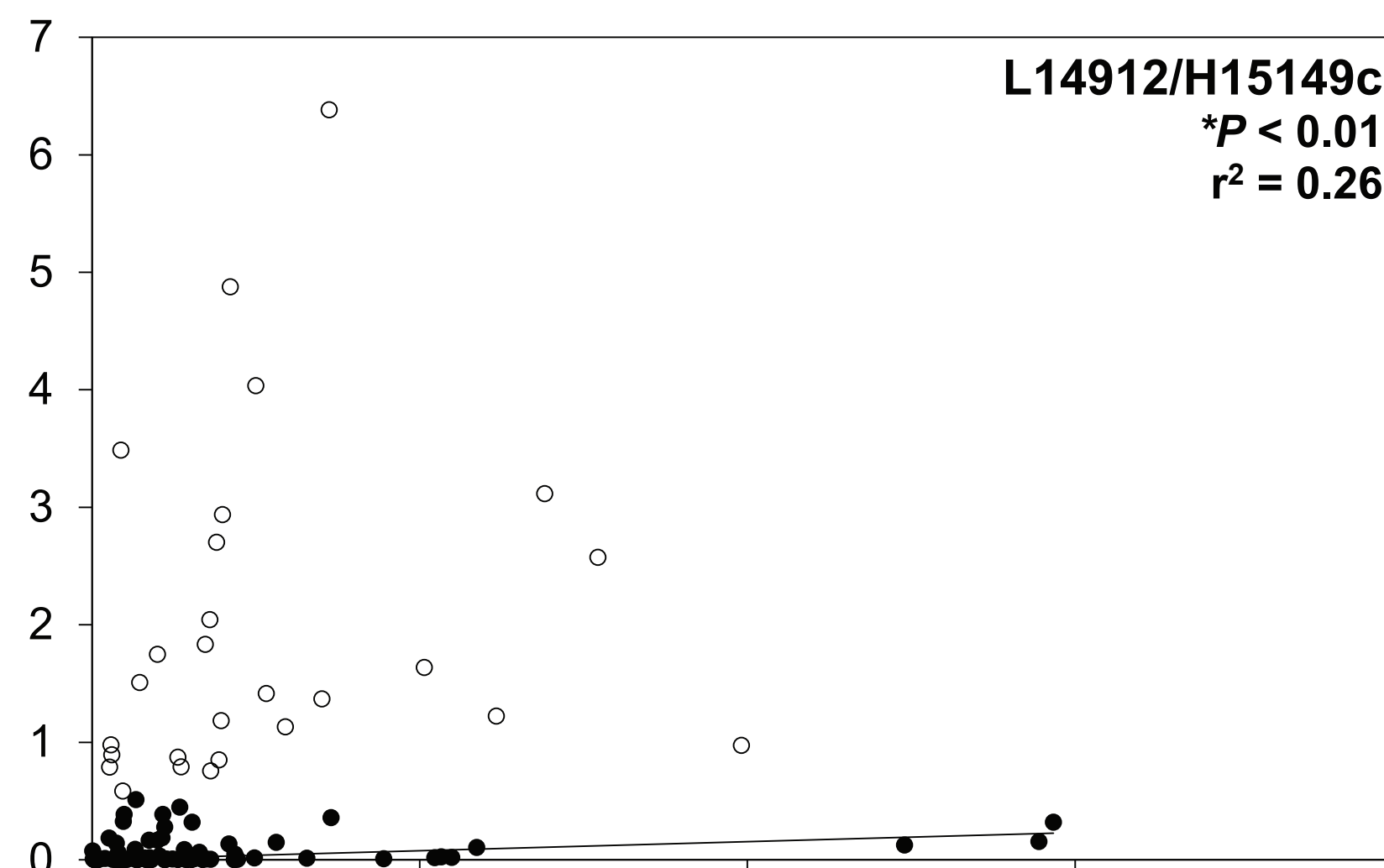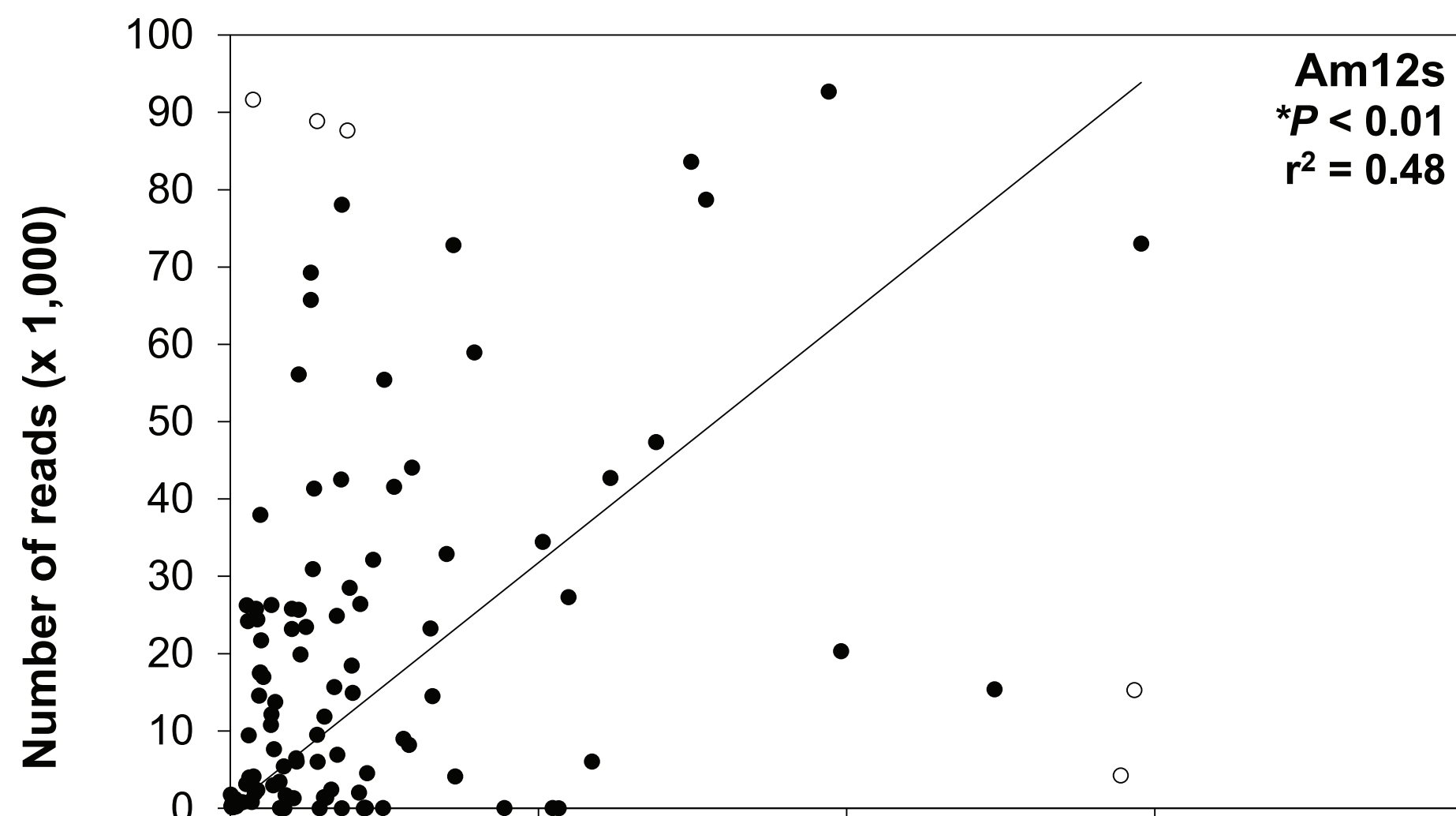5   from all mesocosms (n=108).

6   Fig. S2 Iteratively reweighted least square regressions of standing stock biomass (g) and read
7   abundance (number of mapped reads) for each species for the Ac12s primer. Iteratively
8   reweighted least square regression analysis results in fitting the linear model to reweighted data
9   (closed points) exclusive of outliers (open points). Data pooled by species from each of the
10   independent mesocosms (n=12).

11   Fig. S3 Iteratively reweighted least square regressions of standing stock biomass (g) and read
12   abundance (number of mapped reads) for each species for the Ac16s primer. Iteratively
13   reweighted least square regression analysis results in fitting the linear model to reweighted data
14   (closed points) exclusive of outliers (open points). Data pooled by species from each of the
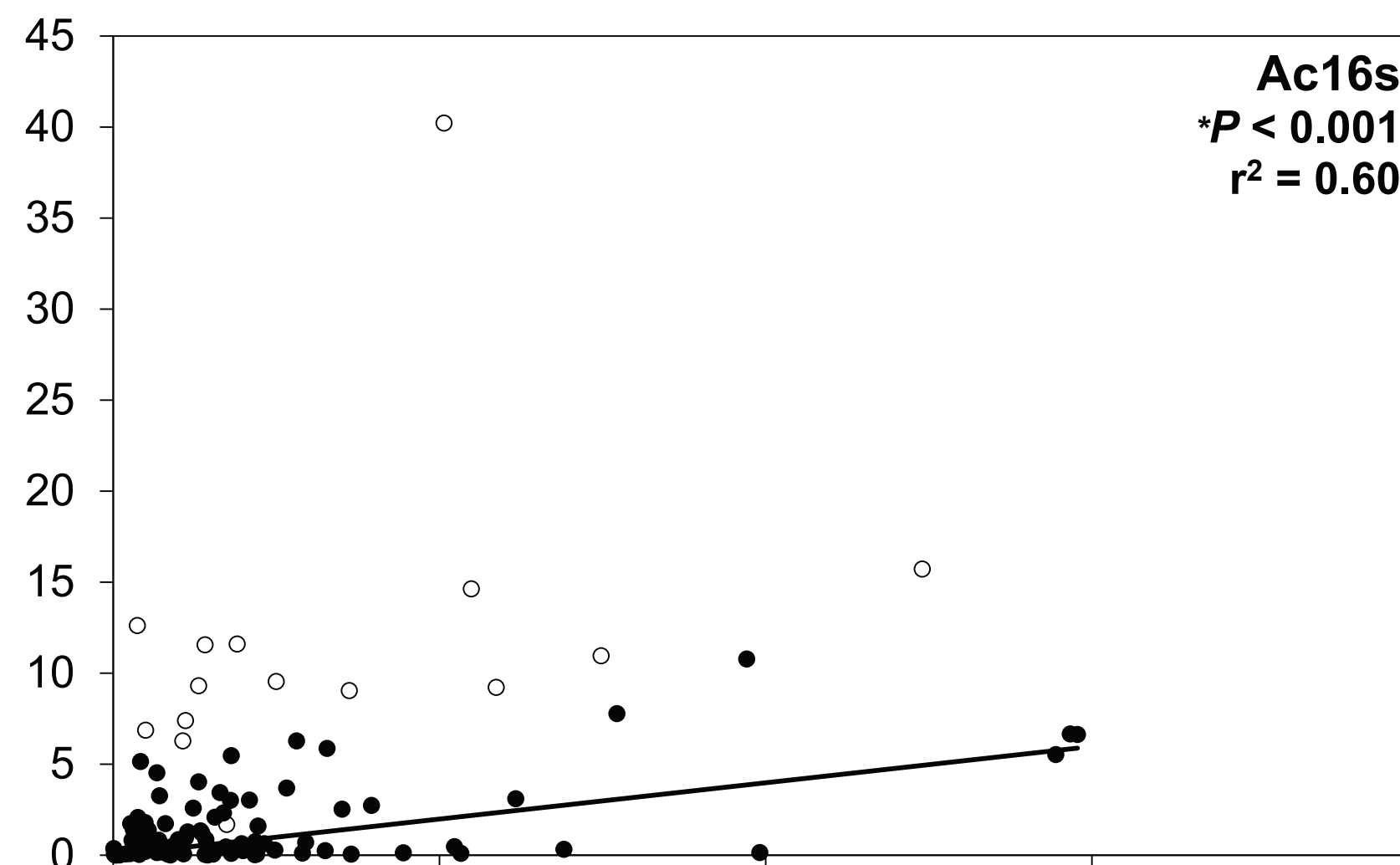15   independent mesocosms (n=12).

16   Fig. S4 Iteratively reweighted least square regressions of standing stock biomass (g) and read
17   abundance (number of mapped reads) for each species for the L14912/H15149c primer.
18   Iteratively reweighted least square regression analysis results in fitting the linear model to
19   reweighted data (closed points) exclusive of outliers (open points). Data pooled by species from
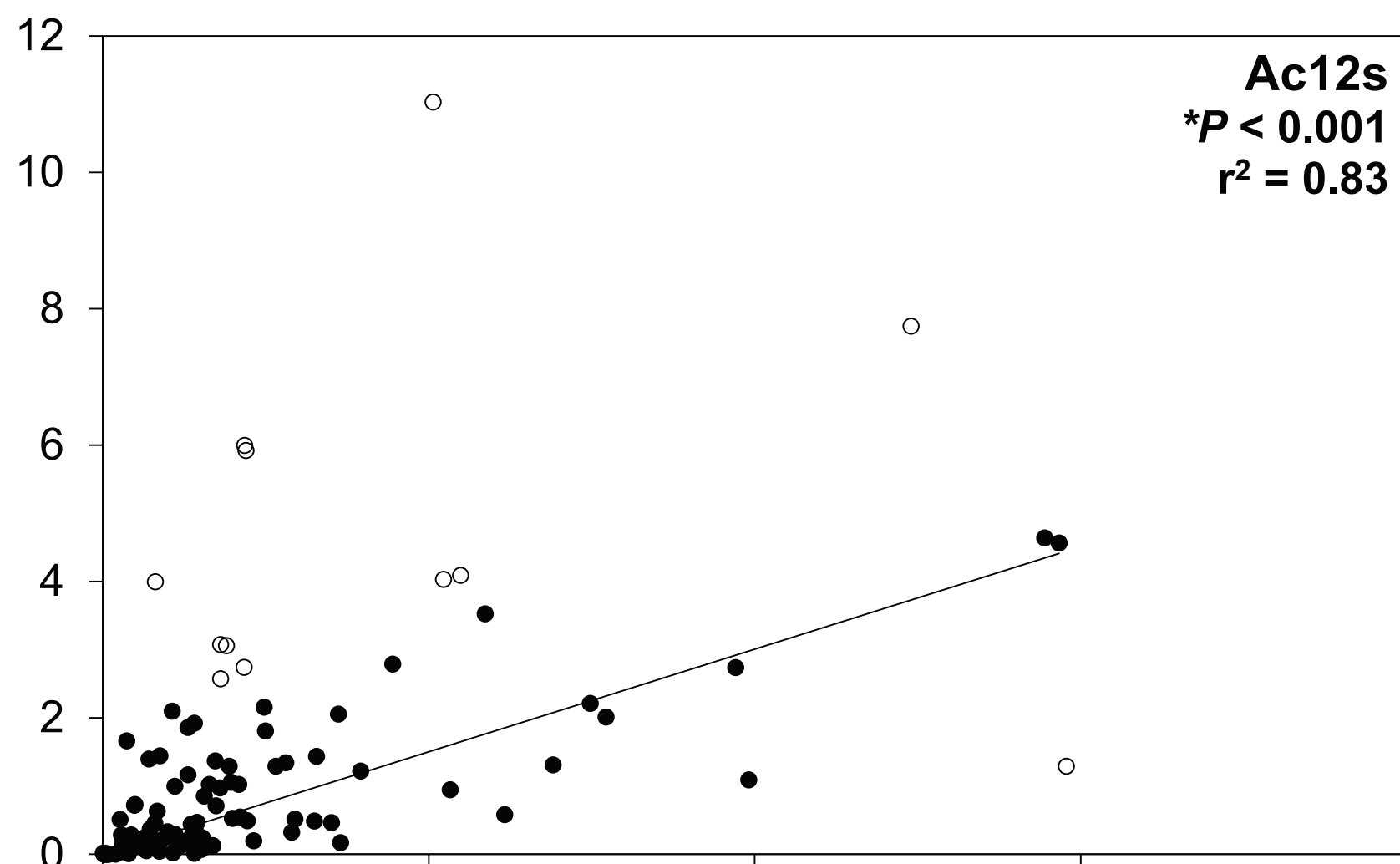20   each of the independent mesocosms (n=12).

21   Fig. S5 Iteratively reweighted least square regressions of standing stock biomass (g) and read
22   abundance (number of mapped reads) for each species for the L2513/H2714 primer. Iteratively
23   reweighted least square regression analysis results in fitting the linear model to reweighted data
24   (closed points) exclusive of outliers (open points). Data pooled by species from each of the
25   independent mesocosms (n=12).

26   Fig. S6 Iteratively reweighted least square regressions of standing stock biomass (g) and read
27   abundance (number of mapped reads) for each species for the Ve16s primer. Iteratively
28   reweighted least square regression analysis results in fitting the linear model to reweighted data
29   (closed points) exclusive of outliers (open points). Data pooled by species from each of the
30   independent mesocosms (n=12).

Figure legend (axis labels):

Number of reads (x 1,000)

Cumulative Biomass (g)

Panel annotations:

Ac12s
*P < 0.001
r² = 0.83

Ac16s
*P < 0.001
r² = 0.60

Am12s
*P < 0.01
r² = 0.48

L14912/H15149c
*P < 0.01
r² = 0.26

L2513/H2714
*P < 0.001
r² = 0.55

Ve16s
*P < 0.001
r² = 0.66

Figure showing nine scatter plots of Number of reads (x 1,000) versus Biomass (g) for different species.

central stoneroller
*P < 0.001
r² = 0.69

white sucker
P = 0.09
r² = 0.81

common carp
P = 0.06
r² = 0.65

blackstripe topminnow
P = 0.24
r² = 0.54

eastern mosquitofish
*P < 0.02
r² = 0.41

bluegill sunfish
P = 0.07
r² = 0.57

fathead minnow
*P < 0.01
r² = 0.84

bullfrog tadpole
*P < 0.01
r² = 0.50

creek chub
*P < 0.001
r² = 0.77

Number of reads (x 1,000)

Biomass (g)

central stoneroller
*P < 0.01
r² = 0.40

white sucker
*P < 0.001
r² = 0.73

common carp
P = 0.08
r² = 0.71

blackstripe topminnow
*P = 0.001
r² = 0.65

eastern mosquitofish
*P < 0.01
r² = 0.50

bluegill sunfish
*P < 0.01
r² = 0.71

fathead minnow
*P = 0.02
r² = 0.60

bullfrog tadpole
*P = 0.02
r² = 0.50

creek chub
*P = 0.02
r² = 0.64

Number of reads (x 1,000)

Biomass (g)

Central stoneroller: *P < 0.01, r² = 0.49. White sucker: P = 0.10, r² = 0.66. Common carp: *P < 0.01, r² = 0.53. Blackstripe topminnow: *P = 0.03, r² = 0.39. Eastern mosquitofish: *P = 0.001, r² = 0.64. Bluegill sunfish: *P < 0.01, r² = 0.60. Fathead minnow: *P < 0.001, r² = 0.67. Bullfrog tadpole: *P < 0.001, r² = 0.73. Creek chub: *P = 0.01, r² = 0.62.

Number of reads (x 1,000) versus Biomass (g).