

1 **Vulnerability and life-history traits correlate with the load of** 2 **deleterious mutations in fish**

3 4 *Authors*

5 Jonathan Rolland^{1,2*} & Jonathan Romiguier^{3*}

6 7 *Authors' affiliations*

8 ¹*Department of Zoology, University of British Columbia, #4200-6270 University Blvd.,*
9 *Vancouver, B.C., Canada*

10 ²*Department of Computational Biology, University of Lausanne, Quartier Sorge, 1015*
11 *Lausanne, Switzerland*

12 ³*CNRS, UMR 5554 Institut des Sciences de l'Evolution (Université de Montpellier), Place*
13 *Eugène Bataillon, 34095 Montpellier, France*

14 15 *Authors for correspondence (*):*

16 Jonathan Rolland: jonathan.rolland@yahoo.fr

17 Jonathan Romiguier: jonathan.romiguier@umontpellier.fr

18
19 **Keywords:** mutational meltdown, dN/dS ratio, extinction, effective population size.

20 21 **Abstract**

22 Understanding why some species accumulate more deleterious substitutions than others is an
23 important question relevant in evolutionary biology and conservation sciences. Previous
24 studies conducted in terrestrial taxa suggest that life history traits correlate with the efficiency
25 of purifying selection and accumulation of deleterious mutations. Using a large genome
26 dataset of 76 species of fishes, we show that the rate of deleterious mutation accumulation
27 (measured via dN/dS, *i.e.* non-synonymous over synonymous substitution rate) is associated
28 to the vulnerability, the life-history strategies, and the latitude of species. Our results,
29 focusing on a large clade of aquatic species, generalizes previous patterns found so far in few
30 clades of terrestrial vertebrates. These results also suggest that vulnerable species accumulate
31 more deleterious substitutions than non-threatened ones, which give insights in how life-
32 history traits, populations sizes and genetic risk of extinction can be tightly interconnected.

33

34 **Main text**

35 **Introduction**

36 Determining the factors explaining why some species are more vulnerable than others is
37 urgent given the acceleration of species extinction rates in the last decades (Barnosky et al.
38 2011). While it is accepted that a combination of demographic, ecological (Jennings 1998;
39 Reynolds 2001) and genetic factors (Spielman et al. 2004) contribute to species extinction,
40 their relative importance is still unclear.

41 Based on metrics such as geographical range or population size, the widely used red
42 list IUCN index relies nearly exclusively on demographic and population dynamics criteria
43 (Strona et al. 2014). Such an approach reliably measures the conservation status of a species
44 under ongoing threats, but is not designed to assess the intrinsic vulnerability of a species to
45 potential future threats (Miranda et al. 2017). To fill this gap and better manage the increasing
46 problem of overfishing, an alternative vulnerability index has been developed for fish species:
47 the *Fishbase* vulnerability index (Cheung et al. 2005). Instead of relying on demographic
48 criteria, this index exploits the well-known fact that population size and population growth
49 depends on life history and ecological species features, such as body length, longevity,
50 fecundity or sexual maturity; as populations of large and long-lived species being smaller and
51 less resilient than small and short-lived ones (Cheung et al. 2005).

52 Because the effective population size and genome evolution are related, the genomic
53 sequence of a given species keeps track of the past variations in population size
54 (Nadachowska-Brzyska et al. 2015). Therefore, long-term population size can be tracked
55 down by measuring species genetic diversity (Romiguier et al. 2014) or the ratio of non-
56 synonymous mutations over synonymous mutations (dN/dS ; Popadin et al. 2007; Nikolaev et
57 al. 2007; Romiguier et al. 2013; Figuet et al. 2016; Botero-Castro et al. 2017). In this study,
58 we propose to test whether vulnerable species accumulate more deleterious alleles than non-
59 threatened ones. We choose to focus our study on teleostean fishes, a large taxa with various
60 life-history traits, for which i) several genomes have been recently sequenced (Malmstrøm et
61 al. 2017) and ii) unmatched resources in terms of vulnerability index are available due to their
62 economic importance for fishing activities. Furthermore, studies trying to link effective
63 population size, life history traits and genome evolution focused so far exclusively on
64 terrestrial species (mammals: Nikolaev et al. 2007; Popadin 2007; Romiguier et al. 2012,
65 2013; birds: Botero-Castro et al. 2017; reptiles: Figuet et al. 2016). These studies concluded
66 that species with a “K-strategy” (i.e. large body size, long-lived and low fecundity) are more

67 likely to exhibit small effective population sizes on the long-term (MacArthur & Wilson
68 1967). By comparing the life history traits and species vulnerability to the genome-wide
69 efficiency of purifying selection in 76 teleostean species, we test here whether commonly
70 assumed patterns in terrestrial habitats can be generalized to aquatic environments.

71

72 **Results and Discussion**

73 For several decades, studies in conservation sciences have aimed to identify the causes
74 of species vulnerability to extinction. Large body size, low fecundity and low rate of niche
75 evolution have already been identified in previous studies as correlates of high extinction risk
76 in mammals or birds (Fritz et al. 2009; Lavergne et al. 2013). Based on a dataset of 76 species
77 of fish, our genomic analyses showed that the rate of non-synonymous over synonymous
78 substitutions (dN/dS) was strongly associated to vulnerability ($P = 1.68 \times 10^{-5}$, $R^2_{\text{adjust}} = 0.24$,
79 Figure 1, Table 1). This association was found when dN/dS was estimated with *mapnh* and
80 *PAML* and when we controlled for phylogenetic correlation (Figure 1, Table 1,
81 Supplementary Material S2). We also found a strong relationship between dN/dS and life
82 history traits (dN/dS and body length: $P = 1.65 \times 10^{-5}$, $R^2_{\text{adjust}} = 0.25$; dN/dS and longevity: $P =$
83 3.69×10^{-2} , $R^2_{\text{adjust}} = 0.11$; Table 1), which is consistent with previous studies on terrestrial clades
84 in mammals, birds and metazoa (Nikolaev et al. 2007; Popadin 2007; Romiguier et al. 2012,
85 2013, 2014; Botero-Castro et al. 2017; Figuet et al. 2016). Our analyses indicate that these
86 results are not due to substitution saturation that could bias dN/dS estimations (Supplementary
87 Material S3). Additional test showed that the relationship between dN/dS and vulnerability
88 remained significant even when we removed the 15% of the longest branches that are
89 potentially more affected by saturation ($P < 0.05$, Supplementary Material S4).

90 One potential interpretation of the strong relationship found between vulnerability and dN/dS
91 is that the accumulation of deleterious mutation is playing a role in the extinction of species.
92 Indeed, the decrease of the efficiency of purifying selection in populations with small
93 effective sizes (Ohta et al. 1992) has been linked to a snow-ball mechanism for species
94 extinction known as mutational meltdown (Lynch et al. 1995). The accumulation of
95 deleterious mutations can lead, in the long term, to a decrease of fitness resulting in a decrease
96 of population size which ultimately will also increase the accumulation of deleterious alleles,
97 leading to a further decrease of population size. Such negative demographic/genetic feedbacks
98 loops toward extinction have already been proposed as a potential explanation for the local
99 extirpation of large vertebrates (e.g. woolly mammoth, Rogers et al. 2017). In the present

100 study, it is however difficult to disentangle causation from correlation. Indeed, the *Fishbase*
101 vulnerability index is directly built from life-history traits, which is reflected in our data by
102 the strong correlation between vulnerability and body size ($R^2_{\text{ajust}} = 0.60$, $P = 3.29 \times 10^{-14}$). Given
103 the fact that dN/dS correlates equally with vulnerability and other life-history traits, it is
104 difficult to conclude that genetic factors (dN/dS) are directly causing species extinction. A
105 more parsimonious explanation is that life-history traits (e.g. body size), vulnerability and
106 dN/dS are all correlated simply because they are all different proxies of effective population
107 size (Jennings and Blanchard 2004). Because they all correlate with each other, it is
108 consequently difficult to disentangle demographic, ecological and genetic components of
109 extinction risks, even if low population sizes, large body sizes and high rates of deleterious
110 mutations seems to be all directly or indirectly associated to high species vulnerability. Future
111 studies using a different metric of species vulnerability calculated independently from life
112 history traits might help to better measure the relative contribution of ecological and genetic
113 factor on fish extinction risk (Polishchuk et al. 2015).

114 Our estimate of dN/dS was also significantly higher in species distributed at higher
115 latitude ($P = 2.17 \times 10^{-3}$, $R^2_{\text{ajust}} = 0.13$, Table 1), although this relationship was not significant for
116 the *PAML* analysis (Supplementary material S2). This result suggests that species distributed
117 at high latitude may have generally lower or less stable population sizes. We found a
118 significant relationship between latitude and vulnerability (PGLS, $P = 5.32 \times 10^{-3}$, $R^2_{\text{ajust}} = 0.10$,
119 Supplementary material S1) but, surprisingly, latitude was not associated with either body
120 size (PGLS, $P > 0.05$, $R^2_{\text{ajust}} = 0.03$) or longevity ($P > 0.05$, $R^2_{\text{ajust}} = -0.01$). We thus hypothesize
121 that latitude may be associated to population size by other mechanisms than an increase of
122 body size and longevity. For example, population dynamics at high latitude might be related
123 to other ecological factors, such as strong seasonal and long-term climatic oscillations which
124 reduce periodically the carrying capacity of high latitude ecosystems (Dynesius and Jansson
125 2000). This result also implies that particular attention should be paid to vulnerable species at
126 high latitude, given that they might have lower long-term effective population sizes, which
127 would lead to accumulate more deleterious mutations, compared to tropical species.

128 The strong correlations found between vulnerability and dN/dS and between body size
129 and dN/dS suggest that vulnerability and body size might be generally better proxies of
130 effective population size than latitude or longevity. In theory, longevity should be also related
131 to population size and dN/dS (Romiguier et al. 2013), but in practice the difficulty to measure
132 longevity in the wild may lead to spurious life span measures that may blur the relationship
133 with dN/dS. Similarly, latitude might be related to population size but species distribution is

134 also depending on other factors such as dispersal contingencies and species interactions
135 (Sexton et al. 2009), which are not expected to be directly related to the effective population
136 size.

137

138 **Conclusion**

139 Based on genomes of 76 species of fishes, our study shows that large, long-lived and
140 vulnerable species accumulate more deleterious mutations than small, short-lived and not
141 vulnerable species. Our results extend to aquatic environments the association between the
142 efficiency of natural selection and species life-history strategies previously found in few
143 clades of terrestrial vertebrates. Finally, this work also highlights for the first time a positive
144 relationship between dN/dS and latitude, suggesting that species distributed at higher latitude
145 might have small long-term effective population sizes, and consequently accumulates more
146 deleterious mutations than tropical species.

147

148 **Material & Methods**

149

150 *Molecular data and phylogeny*

151 We used the alignments and the phylogenetic tree provided by the authors of Malmstrøm et
152 al. (2017). The authors aligned 1938 exons, from 120 to 1764 bp (Supplementary Material
153 S7), in 76 fish species using a multi-step blast procedure with 33,737 annotated zebrafish
154 genes (from the Ensembl release 78; Cunningham et al. 2014). All alignments provided by
155 Malmstrøm et al. are available in the zenodo dataset repository
156 (<https://zenodo.org/record/3516455#.XbjIMad7R3m>) and correspond to the less strictly
157 filtered dataset before removal of 3rd codon position. The phylogenetic tree was constructed
158 with RAxML v. 8.1.17 (Stamatakis 2014) and BEAST v.2.2 (Bouckaert 2014) using 567
159 exons from 111 genes, with a total alignment length of 71,418 bp and 17 fossil calibrations
160 (see Malmstrøm et al. 2017 for more details).

161

162 *Data*

163 Body length, latitude and vulnerability data were obtained for all 76 species in *Fishbase*
164 (<http://www.fishbase.org/>, Froese & Pauly 2014). Longevity was obtained for 33 species. The
165 *Fishbase* vulnerability index is calculated from a method averaging several traits related to
166 the rate of reproduction, such as body size and generation time (Cheung et al. 2005).

167

168 *Molecular evolution and dN/dS*

169 We estimated the number of synonymous and non-synonymous substitutions in the terminal
170 branches of the 76 teleost species from the alignment of 1938 concatenated genes (378,663 bp
171 for the concatenated alignment) using the probabilistic substitution mapping implemented in
172 the software *mapnh* (Romiguier et al. 2012; <https://github.com/BioPP/testnh>). The *mapnh*
173 analysis estimates a probabilistic count of synonymous and non-synonymous substitutions.
174 We used the ratio of the sum of non-synonymous substitutions and the sum of synonymous
175 substitutions as our dN/dS measure. For the *PAML* analysis, we first estimated dN and dS on
176 each individual genes (see Supplementary Material S7 for the details), and then computed the
177 average dN and average dS by weighting with gene length.

178 Estimates of dN/dS can be poorly estimated when the total number of substitutions is
179 small (short branches). We controlled for this bias by running all analyses after the removal of
180 the terminal branches with less than 10,000 synonymous substitutions (~15% smallest
181 branches). We chose this threshold because it allowed to eliminate atypical short branches,
182 which were difficult to compare with the others branches for accurate dN/dS estimations.
183 These small branches belonged mostly to closely related species inside taxa that were over-
184 sampled compared to the other clades, such as the *Gadinae* subfamily. We replicated the
185 analysis with the dN/dS estimations produced by *codeml* from the *PAML* package (Yang
186 2007).

187

188 *Relationship between dN/dS, life history traits and vulnerability.*

189 We tested whether dN/dS was associated with life history traits and vulnerability with
190 phylogenetic generalized least squares regressions (*pgls* function of the *R* package *caper*). The
191 *pgls* function allows to model a linear relationship while taking into account the phylogenetic
192 structure of correlation between variables. For plotting the phylogenetic generalized least
193 squares regressions, we transformed the x and y-axis in order to take into account the
194 phylogenetic correlation in variables (code provided in Supplementary Material S6, Figure1).
195 We then tested the robustness of the association between dN/dS and life history
196 traits/vulnerability with two other set of analyses: one set of analyses with all species
197 (including branches with less than 10,000 synonymous substitutions, Supplementary Material
198 S5), and one set of analyses removing the ~15% longest branches (branches with more than
199 35,000 synonymous substitution) to test whether substitution saturation was affecting our

200 results (Supplementary Material S4). We also tested whether substitution saturation affected
201 our results with the entropy index of substitution of Xia et al. 2003 in the software *DAMBE 7*
202 following the procedure described in Xia & Lemey (2009; see Supplementary Material S3 for
203 more details).

204

205

206 **Acknowledgments**

207 We thank Xuhua Xia, Matthew Hahn for advices on the analyses. We also thank Dolph
208 Schluter for providing the code to plot the phylogenetic generalized least squares regressions.
209 JR received funding from the European Union's Horizon 2020 research and innovation
210 programme under the Marie Skłodowska-Curie grant agreement No. 785910 and the Banting
211 postdoctoral fellowship (151042)

212

213 **Authors contributions**

214 J.R. and J.R. designed the study, ran the analyses and wrote the manuscript.

215

216 **References**

217

218 Barnosky AD, Matzke N, Tomiya S, Wogan, GO, Swartz, B, Quental, TB *et al.* 2011. Has the
219 Earth's sixth mass extinction already arrived? *Nature* 471:51.

220

221 Botero-Castro F, Figuet E, Tilak MK, Nabholz B, Galtier N. 2017. Avian genomes revisited:
222 hidden genes uncovered and the rates versus traits paradox in birds. *Mol Biol Evol* 34:3123-
223 3131.

224

225 Bouckaert R, Heled J, Kühnert D, Vaughan T, Wu CH, Xie D, Suchard MA, Rambaut A,
226 Drummond AJ. 2014. BEAST 2: a software platform for Bayesian evolutionary analysis.
227 *PLoS comput biol*, 10:p.e1003537.

228

229 Cheung WW, Pitcher TJ, Pauly D. 2005. A fuzzy logic expert system to estimate intrinsic
230 extinction vulnerabilities of marine fishes to fishing. *Biol Cons.* 124:97-111.

231

232 Cunningham F, Amode MR, Barrell D, Beal K, Billis K, Brent S, Carvalho-Silva D, Clapham
233 P, Coates G, Fitzgerald S, Gil L. 2014. Ensembl 2015. *Nucleic Acids Res*, 43:D662-D669.

234
235 Dynesius M, Jansson R. 2000. Evolutionary consequences of changes in species' geographical
236 distributions driven by Milankovitch climate oscillations. *Proc Natl Acad Sc USA*. 97:9115-
237 9120.

238
239 Figuet E, Nabholz B, Bonneau M, Mas Carrio E, Nadachowska-Brzyska K, Ellegren H,
240 Galtier N. 2016. Life history traits, protein evolution, and the nearly neutral theory in
241 amniotes. *Mol Biol Evol*. 33:1517-1527.

242
243 Froese R, Pauly D. 2018. *FishBase*. <https://www.fishbase.org/>. World Wide Web Electron.
244 Publ. version. (04/2018).

245
246 Fritz SA, Bininda-Emonds OR, Purvis A. 2009. Geographical variation in predictors of
247 mammalian extinction risk: big is bad, but only in the tropics. *Ecol. Lett*. 12:538-549.

248
249 Jennings S, Reynolds JD, Mills SC. 1998. Life history correlates of responses to fisheries
250 exploitation. *Proc R Soc Lond*. 265:333-339.

251
252 Jennings S, Blanchard JL. 2004. Fish abundance with no fishing: predictions based on
253 macroecological theory. *J Anim Ecol*. 73:632-642.

254
255 Lavergne S, Evans ME, Burfield IJ, Jiguet F, Thuiller W. 2013. Are species' responses to
256 global change predicted by past niche evolution? *Phil Trans Roy Soc B-Biol Sci*.
257 368:20120091.

258
259 Lynch M, Conery J, Burger R. 1995. Mutation accumulation and the extinction of small
260 populations. *Am Nat*. 146:489-518.

261
262 MacArthur, R. and Wilson, E. O. 1967. *The Theory of Island Biogeography*. Princeton
263 University Press.

264

- 265 Malmstrøm M, Matschiner M, Tørresen OK, Jakobsen KS, Jentoft S. 2017. Whole genome
266 sequencing data and *de novo* draft assemblies for 66 teleost species. *Sci Data*. 4, 160132.
267
- 268 Mace GM, Redford KH, Robinson JG. 2001. *Conservation of Exploited Species*. Cambridge
269 University Press, Cambridge, pp. 147–169.
270
- 271 Michael L, Conery J, & Burger R. 1995. Mutation accumulation and the extinction of small
272 populations. *Am Nat*. 146, 489–518.
273
- 274 Miranda R. 2017. The misguided comparison of vulnerability and conservation status. *Aquat*
275 *Conserv: Mar Freshw Ecosyst*. 27:898-899.
276
- 277 Nadachowska-Brzyska K, Li C, Smeds L, Zhang G, Ellegren H. 2015. Temporal dynamics of
278 avian populations during Pleistocene revealed by whole-genome sequences. *Curr*
279 *Biol*. 25:1375-1380.
280
- 281 Nikolaev SI, Montoya-Burgos JI, Popadin K, Parand L, Margulies EH. 2007. Life-history
282 traits drive the evolutionary rates of mammalian coding and noncoding genomic elements.
283 *Proc Natl Acad Sc USA*. 104:20443-20448.
284
- 285 Ohta T. 1992. The nearly neutral theory of molecular evolution. *Annu Rev Ecol Evol Syst*.
286 23:263-286.
287
- 288 Pinsky ML, Jensen OP, Ricard D, Palumbi SR. 2011. Unexpected patterns of fisheries
289 collapse in the world's oceans. *Proc Natl Acad Sc USA*. 108:8317-8322.
290
- 291 Popadin K, Polishchuk LV, Mamirova L, Knorre D, Gunbin K. 2007. Accumulation of
292 slightly deleterious mutations in mitochondrial protein-coding genes of large versus small
293 mammals. *Proc Natl Acad Sc USA*. 104:13390-13395.
294
- 295 Reynolds JD, Jennings S, Dulvy NK. 2001. *Life histories of fishes and population responses*
296 *to exploitation*. Conservation biology series - Cambridge.
297

- 298 Rogers RL, Slatkin M. 2017. Excess of genomic defects in a woolly mammoth on wrangel
299 Island. *PLOS Genet.* 13:e1006601.
300
- 301 Romiguier J, Figuet E, Galtier N, Douzery EJP, Boussau B, Dutheil JY, Ranwez V. 2012.
302 Fast and robust characterization of time-heterogeneous sequence evolutionary processes using
303 substitution mapping. *PLoS One* 7:e33852.
304
- 305 Romiguier J, Ranwez V, Douzery EJP, Galtier N. 2013. Genomic evidence for large, long-
306 lived ancestors to placental mammals. *Mol Biol Evol.* 30:5-13.
307
- 308 Romiguier J, Gayral P, Ballenghien M, Bernard A, Cahais V, Chenuil A, Chiari Y, Dernat R,
309 Duret L, Faivre N, Loire E. 2014. Comparative population genomics in animals uncovers the
310 determinants of genetic diversity. *Nature.* 515:261.
311
- 312 Sexton JP, McIntyre PJ, Angert AL, Rice KJ. 2009. Evolution and ecology of species range
313 limits. *Annu. Rev. Ecol. Evol. Syst.* 40, 415-436.
314
- 315 Spielman D, Brook BW, Frankham R. 2004. Most species are not driven to extinction before
316 genetic factors impact them. *Proc Natl Acad Sc USA.* 101:15261-15264.
317
- 318 Stamatakis, A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of
319 large phylogenies. *Bioinformatics* 30.9: 1312-1313.
320
- 321 Strona G. 2014. Assessing fish vulnerability: IUCN vs FishBase. *Aquat Conserv: Mar Freshw*
322 *Ecosyst.* 24:153-154.
323
- 324 Xia X, Xie Z, Salemi M, Chen L, & Wang Y. 2003. An index of substitution saturation and its
325 application. *Mol Phyl Evol*, 26: 1-7.
326
- 327 Xia X., Lemey P. 2009. Assessing substitution saturation with DAMBE. *The phylogenetic*
328 *handbook: a practical approach to DNA and protein phylogeny*, 2, 615-630.
329

330 Yang Z. 2007. PAML 4: phylogenetic analysis by maximum likelihood. *Mol Biol Evol.*
331 24:1586-1591.

332

333

334

335

336

337 **Tables et Figures**

338

339 **Table 1. Phylogenetic generalized least squares regressions between dN/dS,**
340 **vulnerability, latitude, body length and longevity.** Our analyses were ran with the *pgls*
341 function which allows us to model the relationship between variables accounting for
342 phylogenetical non-independence. dN/dS was computed using *mapnh*.

343

Variable	Intercept (Std. Error)	Estimate (Std. Error)	t value	P-value	R^2_{ajust}
Vulnerability	5.74×10^{-2} (9.27×10^{-3})	3.72×10^{-4} (7.99×10^{-5})	4.66	1.68×10^{-5}	0.24
Latitude	5.27×10^{-2} (1.04×10^{-2})	4.21×10^{-4} (1.32×10^{-4})	3.2	2.17×10^{-3}	0.13
log(Body length)	4.51×10^{-2} (1.04×10^{-2})	7.56×10^{-3} (1.62×10^{-3})	4.67	1.65×10^{-5}	0.25
log(Longevity)	6.01×10^{-2} (1.20×10^{-2})	6.02×10^{-3} (2.75×10^{-3})	2.19	3.69×10^{-2}	0.11

344

345

346

347

348

349

350

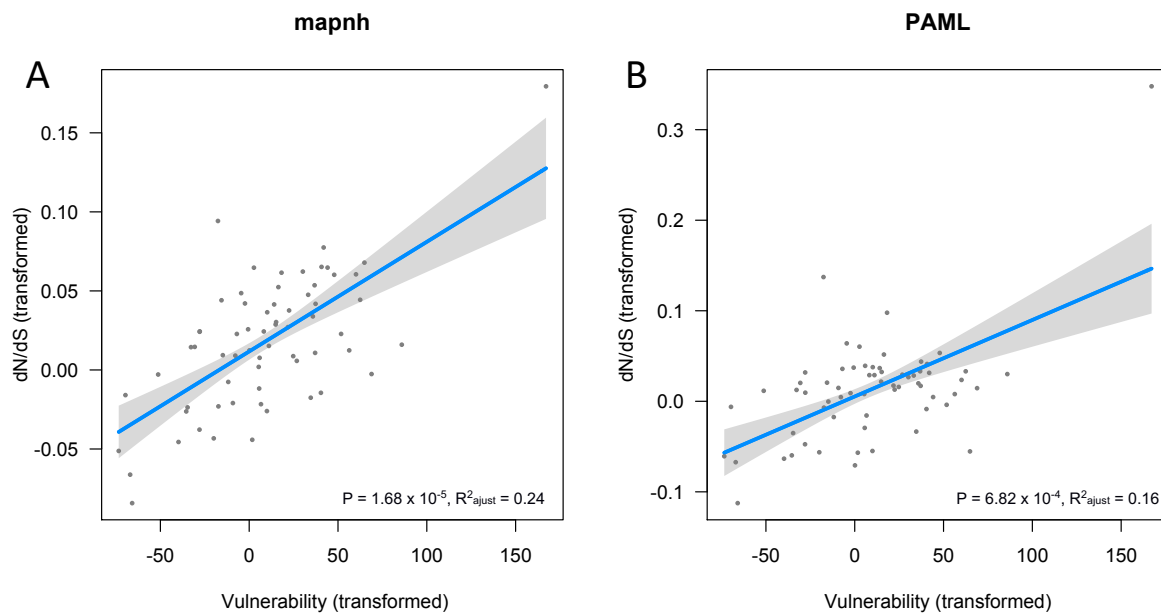
351

352

353

354

355 **Figure 1. dN/dS is associated with vulnerability.** dN/dS was computed using either (A)
356 *mapnh* or (B) *PAML*. Regression line, P-values and R^2_{adjust} of the phylogenetically generalized
357 least squares regressions were shown on each panel respectively for all terminal branches of
358 more than 10,000 synonymous substitutions. The shaded grey represents the 95% confidence
359 intervals. x and y axes have been transformed in order to account for the phylogenetic
360 relatedness between variables (script available in Supplementary material S6).
361



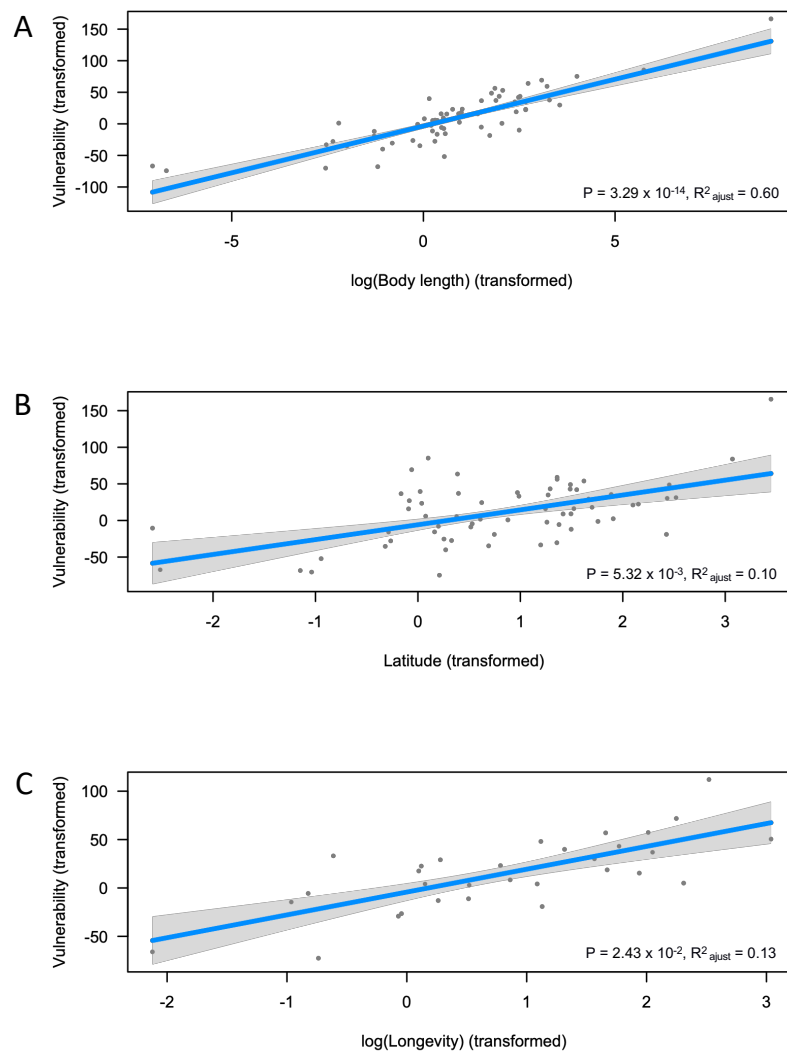
362

363

1 Vulnerability and life-history traits correlate with the load of 2 deleterious mutations in fish - Supplementary Material

3

4 **Supplementary Material S1. Relationship between vulnerability and (A) body length,**
5 **(B) latitude and (C) longevity.** Regression line, P -value and R^2_{ajust} of the phylogenetic least
6 squared regressions are shown for each variable. The shaded grey represents the 95%
7 confidence intervals. Body length and longevity have been log-transformed, and latitude is
8 shown in absolute values. These results were expected given that *Fishbase* vulnerability index
9 is a metric directly computed from multiple life history traits (Cheung et al. 2005). x and y
10 axes have been transformed in order to account for the phylogenetic relatedness between
11 variables (script available in Supplementary material S6).



12

13

14

15

16Supplementary Material S2. Phylogenetic generalized least squares regressions between
17dN/dS, vulnerability, latitude, body length and longevity. Our analyses were ran with the
18*pgls* function which allows us to model the relationship between variables accounting for
19phylogenetical non-independence. dN/dS was computed using *PAML*. We show here that our
20results are consistent with the results obtained with *mapnh* for vulnerability and body length.

21

Variable	Intercept (Std. Error)	Estimate (Std. Error)	t value	P-value	R^2_{adjust}
Vulnerability	2.15×10^{-2} (1.53×10^{-2})	4.73×10^{-4} (1.32×10^{-4})	3.57	6.82×10^{-4}	0.16
Latitude	3.39×10^{-2} (1.75×10^{-2})	1.52×10^{-4} (2.22×10^{-4})	0.69	4.95×10^{-1}	-8.35×10^{-3}
log(Body length)	1.00×10^{-2} (1.77×10^{-2})	8.40×10^{-3} (2.76×10^{-3})	3.05	3.31×10^{-3}	0.12
log(Longevity)	3.78×10^{-2} (2.25×10^{-2})	3.22×10^{-4} (5.17×10^{-3})	0.06	9.50×10^{-1}	-3.43×10^{-2}

22

23

24

25

26

27

28

29

30

31

32 **Supplementary Material S3. Substitution saturation analyses using the entropy index of**
33 **substitution of Xia *et al.* 2003 in the software DAMBE 7.** Estimates of the index of
34 substitution saturation (Iss) were obtained for a proportion of invariant of $P = 0.166$.
35 Substitution saturation is considered negligible only in the cases noted in bold in the table,
36 that is to say when the Iss is significantly smaller ($P < 0.05$) than the critical Iss value (Iss.c) at
37 which the sequences will begin to fail to recover the true tree. Iss.cSym corresponds to the
38 critical Iss value for symmetrical tree while the Iss.cAsym corresponds to critical Iss value for
39 unrealistic asymmetrical tree. Because the Iss.c is based on simulations limited to 32 species
40 in DAMBE, we have randomly sampled 200 times subsets of 4, 8, 16 and 32 species and
41 performed the test for each subset (see NumOTU in the table). Our results suggest that
42 substitution saturation remains very limited when the tree is symmetrical, but might be
43 potentially problematic for recovering the true topology when the tree is extremely
44 asymmetrical. Although our data is very unlikely falling into this category of extreme
45 asymmetrical topology as it is considered unrealistic (Xia & Lemey 2009), we also tested
46 whether removing long branches - with potentially more saturation - affect our results in
47 Supplementary Material S4.

NumOTU	Iss	Iss.cSym	T	DF	P	Iss.cAsym	T	DF	P
4	0.575	0.862	269.33	378662	$P < 10^{-4}$	0.857	265.01	378662	$P < 10^{-4}$
8	0.612	0.859	202.812	378662	$P < 10^{-4}$	0.785	142.26	378662	$P < 10^{-4}$
16	0.674	0.848	129.067	378662	$P < 10^{-4}$	0.707	24.68	378662	2.236
32	0.76	0.821	41.686	378662	$P < 10^{-4}$	0.607	102.78	378662	$P < 10^{-4}$

48

49

50

51

52

53

54

55

56

57

58

59

60

61

62 **Supplementary Material S4. Phylogenetic generalized least squares regressions between**
63 **dN/dS, vulnerability, latitude, body length and longevity obtained when long branches**
64 **were removed (potentially more affected by substitution saturation). dN/dS were**
65 **obtained with *mapnh*. We show here that the results presented in the main manuscript still**
66 **hold when we removed the branches with more than 35,000 synonymous substitutions (~15%**
67 **longest branches; as in all other analyses, this analysis also excludes branches with less than**
68 **10,000 synonymous substitutions).**

69

Variable	Intercept (Std. Error)	Estimate (Std. Error)	t value	P-value	R^2_{ajust}
Vulnerability	6.99×10^{-2} (8.68×10^{-3})	3.13×10^{-4} (8.26×10^{-5})	3.79	3.96×10^{-4}	0.20
Latitude	6.72×10^{-2} (8.87×10^{-3})	-4.80×10^{-4} (1.22×10^{-4})	3.92	2.66×10^{-4}	0.22
log(Body length)	6.00×10^{-2} (1.08×10^{-2})	5.98×10^{-3} (1.85×10^{-3})	3.24	2.13×10^{-3}	0.15
log(Longevity)	7.41×10^{-2} (1.29×10^{-2})	5.56×10^{-3} (2.79×10^{-3})	1.99	5.77×10^{-2}	0.1

70

71

72

73 **Supplementary Material S5. Phylogenetic generalized least squares regressions between**
74 **dN/dS, vulnerability, latitude, body length and longevity obtained with all species (also**
75 **include branches with less than 10,000 synonymous substitutions). dN/dS were obtained**
76 **with *mapnh*. We show here that the results presented in the main manuscript still hold for**
77 **vulnerability, body length and longevity.**

78

Variable	Intercept (Std. Error)	Estimate (Std. Error)	t value	P-value	R^2_{ajust}
Vulnerability	6.31×10^{-2} (1.47×10^{-2})	2.69×10^{-4} (9.24×10^{-5})	2.92	4.71×10^{-3}	0.09
Latitude	7.51×10^{-2} (1.57×10^{-2})	-6.81×10^{-5} (1.32×10^{-4})	-0.52	6.01×10^{-1}	-0.01
log(Body length)	5.69×10^{-2} (1.68×10^{-2})	4.68×10^{-3} (2.37×10^{-3})	1.96	5.27×10^{-2}	0.04
log(Longevity)	6.08×10^{-2} (1.22×10^{-2})	5.84×10^{-3} (2.78×10^{-3})	2.1	4.36×10^{-2}	0.10

79

80

**81Supplementary Material S6. Script permitting to transform x and y axis for accounting
82for phylogenetic correlation when plotting a phylogenetic generalized least squares
83regression.**

```
84
85 library(visreg)
86
87 inv<-function(x){solve(x)}
88
89 generaleastsquares <- function(x, y, v, save = TRUE){
90 # Function to implement general least squares. X, Y and V must be matrices (use "as.matrix" to make them conform). V is
91 the weight matrix. X must have a column of 1's to include an intercept. The most intuitive way to solve the regression
92 equations is to imagine that there is a transformation of the X and Y variables that would fulfill the assumptions of
93 uncorrelated residuals having equal variances (see Draper, N. R., & Smith, H. (1998). Applied regression analysis (Vol.
94 326). John Wiley & Sons. p 108 in the case of weighted least squares for uncorrelated data; p156 for the case with serially
95 correlated data). The transformation (P) is obtained by solving P'P=V as follows:
96     ve <- eigen(v)
97     pv <- ve$eigenvectors %*% sqrt(diag(ve$values)) %*% t(ve$eigenvectors)
98     xnew <- inv(pv) %*% x
99     ynew <- inv(pv) %*% y
100    beta <- inv(t(xnew) %*% xnew) %*% (t(xnew) %*% ynew)
101    mse <- sum( (ynew-xnew%*%beta)^2 ) / ( nrow(xnew)-ncol(xnew) )
102    sbeta <- sqrt( diag(inv(t(xnew) %*% xnew)) * mse )
103    result <- list(beta = as.vector(beta), sbeta = as.vector(sbeta))
104    if(save){
105        result$xnew <- xnew
106        result$ynew <- ynew
107    }
108    result
109 }
110
111 # Load data here
112 y <- dNdS
113 x <- Vulnerability
114
115 x <- cbind(rep(1, length(x)), x)
116 colnames(x) <- c("x1", "x2")
117
118 # Compute the vcv matrix according to the phylogenetic tree and a Brownian motion model
119 v <- vcv(tree, model = "Brownian", corr = TRUE)
120
121 # Run the phylogenetic generalized least squares regressions
122 result <- generaleastsquares(x=x, y=as.matrix(y), v=v, save=TRUE)
123
124 #Organize the new x and y axes
125 X <- as.data.frame(cbind(ynew=result$ynew[,1], result$xnew))
126
127 #Plot the PGLS
128 z <- lm(ynew ~ x1 + x2 - 1, data = X)
129 visreg(z, "x2", main= "mapnh", ylab= "dN/dS transformed to account for the phylogeny", xlab="Vulnerability")
```

130Supplementary Material S7. Information on the fish genomes. This table contains the
131detailed gene length in bp for each gene, the number of synonymous sites and the number of
132non-synonymous sites (number of synonymous sites + number of non-synonymous sites = gene
133length).

Gene Name	Gene length	Number of synonymous sites	Number of non-synonymous sites
ENSDARE00000004235	180	43.6	136.4
ENSDARE00000004308	177	45.3	131.7
ENSDARE00000004382	240	66.7	173.3
ENSDARE00000004480	303	62.4	240.6
ENSDARE00000011348	147	35.1	111.9
ENSDARE00000013761	186	45.7	140.3
ENSDARE00000013815	195	47.4	147.6
ENSDARE00000014930	162	41	121
ENSDARE00000016462	249	49.1	199.9
ENSDARE00000016629	159	32.4	126.6
ENSDARE00000017677	141	30.5	110.5
ENSDARE00000022514	186	42.8	143.2
ENSDARE00000022574	174	38.1	135.9
ENSDARE00000025213	390	85.8	304.2
ENSDARE00000025928	240	37.8	202.2
ENSDARE00000027640	183	35.8	147.2
ENSDARE00000027777	213	38.9	174.1
ENSDARE00000028455	156	32.5	123.5
ENSDARE00000028706	186	22.3	163.7
ENSDARE00000030359	228	35.9	192.1
ENSDARE00000030430	198	58.5	139.5
ENSDARE00000032670	219	43.5	175.5
ENSDARE00000033326	159	31.8	127.2
ENSDARE00000033633	153	31	122
ENSDARE00000034079	153	43.1	109.9
ENSDARE00000035008	168	48.5	119.5
ENSDARE00000035506	192	30	162
ENSDARE00000035819	201	42.4	158.6
ENSDARE00000036153	168	48.7	119.3
ENSDARE00000037408	210	30	180
ENSDARE00000038723	165	27.5	137.5
ENSDARE00000040663	171	40.2	130.8
ENSDARE00000041603	186	45.5	140.5

ENSDARE00000043490	192	37.2	154.8
ENSDARE00000044276	168	37.5	130.5
ENSDARE00000044609	156	23.3	132.7
ENSDARE00000048510	207	56.9	150.1
ENSDARE00000048616	147	37.1	109.9
ENSDARE00000048671	150	24.1	125.9
ENSDARE00000048937	189	27.1	161.9
ENSDARE00000049143	138	31.4	106.6
ENSDARE00000049680	159	34.8	124.2
ENSDARE00000049796	306	54.3	251.7
ENSDARE00000051029	255	58.8	196.2
ENSDARE00000052383	246	30.2	215.8
ENSDARE00000053703	153	27.9	125.1
ENSDARE00000058489	186	31.5	154.5
ENSDARE00000058500	147	43.3	103.7
ENSDARE00000058618	186	24.9	161.1
ENSDARE00000061321	360	71.4	288.6
ENSDARE00000061506	165	40.4	124.6
ENSDARE00000062898	261	72.8	188.2
ENSDARE00000063368	195	40.9	154.1
ENSDARE00000064283	168	30.4	137.6
ENSDARE00000065727	174	50.1	123.9
ENSDARE00000067613	162	41.4	120.6
ENSDARE00000067812	147	26.7	120.3
ENSDARE00000068333	126	37.9	88.1
ENSDARE00000069031	201	51.9	149.1
ENSDARE00000070430	249	49.3	199.7
ENSDARE00000070683	180	41.7	138.3
ENSDARE00000070983	150	29.2	120.8
ENSDARE00000072636	198	45.5	152.5
ENSDARE00000072940	171	44.9	126.1
ENSDARE00000073696	153	29.5	123.5
ENSDARE00000074578	165	41.9	123.1
ENSDARE00000076062	141	38.6	102.4
ENSDARE00000077727	171	29.1	141.9
ENSDARE00000077898	180	43.9	136.1
ENSDARE00000078420	165	29.5	135.5
ENSDARE00000078747	204	33.7	170.3
ENSDARE00000080957	174	41.9	132.1
ENSDARE00000081038	195	50.6	144.4
ENSDARE00000081137	165	37	128
ENSDARE00000081243	225	32.9	192.1

ENSDARE0000084947	291	48	243
ENSDARE0000084965	159	32.9	126.1
ENSDARE0000086184	147	31.9	115.1
ENSDARE0000087130	123	27.3	95.7
ENSDARE0000088400	276	48.2	227.8
ENSDARE0000090314	225	36.5	188.5
ENSDARE0000090814	195	32.2	162.8
ENSDARE0000091411	195	38.4	156.6
ENSDARE0000091637	243	60.2	182.8
ENSDARE0000094396	288	45.6	242.4
ENSDARE0000094570	165	35.5	129.5
ENSDARE0000096996	213	30.3	182.7
ENSDARE0000099680	153	37.6	115.4
ENSDARE00000100150	192	36.4	155.6
ENSDARE00000100785	189	45	144
ENSDARE00000101931	156	24.9	131.1
ENSDARE00000102661	159	24.8	134.2
ENSDARE00000103201	165	36.7	128.3
ENSDARE00000103910	207	29.1	177.9
ENSDARE00000104927	150	30.9	119.1
ENSDARE00000105971	168	25.8	142.2
ENSDARE00000107373	183	48.5	134.5
ENSDARE00000107691	153	45.3	107.7
ENSDARE00000107763	177	35.1	141.9
ENSDARE00000108129	147	32.1	114.9
ENSDARE00000109772	150	32.4	117.6
ENSDARE00000112506	150	17.4	132.6
ENSDARE00000113382	162	43.4	118.6
ENSDARE00000115339	228	48.3	179.7
ENSDARE00000116607	165	24.9	140.1
ENSDARE00000118053	171	27.2	143.8
ENSDARE00000118916	195	49.8	145.2
ENSDARE00000121440	207	67.8	139.2
ENSDARE00000121918	195	44.2	150.8
ENSDARE00000122333	180	33.8	146.2
ENSDARE00000122354	186	32.1	153.9
ENSDARE00000123434	159	28.6	130.4
ENSDARE00000123835	153	40.3	112.7
ENSDARE00000124868	159	31.8	127.2
ENSDARE00000125320	261	56.3	204.7
ENSDARE00000125484	174	42.1	131.9
ENSDARE00000125780	210	28.7	181.3

ENSDARE00000125787	192	39	153
ENSDARE00000126058	195	40.4	154.6
ENSDARE00000126479	150	29.2	120.8
ENSDARE00000126733	210	48.3	161.7
ENSDARE00000126765	204	47.4	156.6
ENSDARE00000127465	150	21.6	128.4
ENSDARE00000127604	165	40.5	124.5
ENSDARE00000128359	144	30	114
ENSDARE00000129628	222	42	180
ENSDARE00000130310	153	28.6	124.4
ENSDARE00000131361	207	64.3	142.7
ENSDARE00000132754	213	32.6	180.4
ENSDARE00000132910	162	32.6	129.4
ENSDARE00000134141	168	53.1	114.9
ENSDARE00000134724	165	41	124
ENSDARE00000137614	165	29.3	135.7
ENSDARE00000137754	207	38	169
ENSDARE00000137775	210	45.8	164.2
ENSDARE00000139292	171	33.9	137.1
ENSDARE00000140320	195	55.7	139.3
ENSDARE00000148296	183	41.7	141.3
ENSDARE00000150261	174	38.5	135.5
ENSDARE00000151375	180	30.9	149.1
ENSDARE00000152347	174	34.8	139.2
ENSDARE00000153026	162	55.6	106.4
ENSDARE00000154183	171	40.3	130.7
ENSDARE00000154487	186	44.4	141.6
ENSDARE00000155277	204	35.4	168.6
ENSDARE00000160687	195	54.1	140.9
ENSDARE00000164776	186	37	149
ENSDARE00000165484	237	63.9	173.1
ENSDARE00000166085	132	29.7	102.3
ENSDARE00000166758	237	34.7	202.3
ENSDARE00000166793	177	35.5	141.5
ENSDARE00000172393	162	36.2	125.8
ENSDARE00000172958	159	38	121
ENSDARE00000173051	177	42.1	134.9
ENSDARE00000173073	177	50.3	126.7
ENSDARE00000177117	204	46.3	157.7
ENSDARE00000178146	177	44.3	132.7
ENSDARE00000178165	219	42.3	176.7
ENSDARE00000178193	153	28.8	124.2

ENSDARE00000178648	165	38.2	126.8
ENSDARE00000180981	237	59.1	177.9
ENSDARE00000182322	162	43.5	118.5
ENSDARE00000189560	189	38.1	150.9
ENSDARE00000198896	177	42.1	134.9
ENSDARE00000198987	183	40.4	142.6
ENSDARE00000209100	177	40.4	136.6
ENSDARE00000209111	168	36.1	131.9
ENSDARE00000209689	303	47.8	255.2
ENSDARE00000212642	150	46	104
ENSDARE00000212705	204	48.2	155.8
ENSDARE00000212718	186	57.7	128.3
ENSDARE00000215713	144	28.1	115.9
ENSDARE00000223494	147	28.8	118.2
ENSDARE00000223534	135	25.4	109.6
ENSDARE00000223547	153	33.5	119.5
ENSDARE00000223962	177	27.8	149.2
ENSDARE00000224100	165	34.3	130.7
ENSDARE00000226236	156	30.2	125.8
ENSDARE00000227454	183	25.7	157.3
ENSDARE00000228023	282	55.4	226.6
ENSDARE00000228062	153	30.6	122.4
ENSDARE00000230619	192	35.4	156.6
ENSDARE00000233631	144	28.2	115.8
ENSDARE00000235757	171	24.6	146.4
ENSDARE00000237574	174	23.5	150.5
ENSDARE00000239780	213	35.9	177.1
ENSDARE00000239812	210	35.7	174.3
ENSDARE00000239836	195	32.2	162.8
ENSDARE00000241860	132	16.6	115.4
ENSDARE00000251375	168	48.6	119.4
ENSDARE00000251577	267	61.9	205.1
ENSDARE00000251731	168	45	123
ENSDARE00000251750	123	34.2	88.8
ENSDARE00000252160	168	32.5	135.5
ENSDARE00000252184	162	35.2	126.8
ENSDARE00000252236	150	41.7	108.3
ENSDARE00000254666	588	153.2	434.8
ENSDARE00000264561	129	24.4	104.6
ENSDARE00000267335	192	38.7	153.3
ENSDARE00000267689	171	42.3	128.7
ENSDARE00000267765	159	30.4	128.6

ENSDARE00000275889	213	31.2	181.8
ENSDARE00000277608	168	30.3	137.7
ENSDARE00000279026	165	18.8	146.2
ENSDARE00000279036	189	31.3	157.7
ENSDARE00000281507	186	38.7	147.3
ENSDARE00000281658	165	20.5	144.5
ENSDARE00000288910	171	45.2	125.8
ENSDARE00000289101	159	50.8	108.2
ENSDARE00000290587	162	33.6	128.4
ENSDARE00000294244	219	61.9	157.1
ENSDARE00000294926	162	39.7	122.3
ENSDARE00000295849	189	44.3	144.7
ENSDARE00000297146	156	31.8	124.2
ENSDARE00000303600	159	35.4	123.6
ENSDARE00000303888	156	32.2	123.8
ENSDARE00000306147	264	71.2	192.8
ENSDARE00000308377	180	32.3	147.7
ENSDARE00000309685	153	31.7	121.3
ENSDARE00000311092	150	25.2	124.8
ENSDARE00000311899	765	179.8	585.2
ENSDARE00000317534	156	42.1	113.9
ENSDARE00000318811	150	36.3	113.7
ENSDARE00000319833	153	29.1	123.9
ENSDARE00000320695	150	37.1	112.9
ENSDARE00000322331	162	41.6	120.4
ENSDARE00000323268	219	23.6	195.4
ENSDARE00000323720	150	47.8	102.2
ENSDARE00000324373	153	46.5	106.5
ENSDARE00000325218	216	50	166
ENSDARE00000326118	240	48.6	191.4
ENSDARE00000326400	156	40.9	115.1
ENSDARE00000326477	153	31	122
ENSDARE00000328606	165	37.8	127.2
ENSDARE00000331276	147	33.2	113.8
ENSDARE00000334266	192	38.9	153.1
ENSDARE00000339344	132	30.3	101.7
ENSDARE00000340546	195	41.3	153.7
ENSDARE00000341330	162	23.6	138.4
ENSDARE00000341443	144	32.8	111.2
ENSDARE00000343901	213	42.7	170.3
ENSDARE00000344236	201	46.8	154.2
ENSDARE00000345547	174	28.3	145.7

ENSDARE00000346449	162	33.1	128.9
ENSDARE00000346686	165	25.8	139.2
ENSDARE00000347824	150	42	108
ENSDARE00000348439	192	35.7	156.3
ENSDARE00000348874	177	35.1	141.9
ENSDARE00000348937	171	22.2	148.8
ENSDARE00000349395	216	51.1	164.9
ENSDARE00000349696	147	18.6	128.4
ENSDARE00000351117	147	30.6	116.4
ENSDARE00000351453	204	27.6	176.4
ENSDARE00000355082	141	32.7	108.3
ENSDARE00000355222	186	34.9	151.1
ENSDARE00000355248	168	44.5	123.5
ENSDARE00000357236	255	46.2	208.8
ENSDARE00000359261	165	33.7	131.3
ENSDARE00000362140	243	41.9	201.1
ENSDARE00000362911	174	47.1	126.9
ENSDARE00000366347	159	32.6	126.4
ENSDARE00000366349	168	33.3	134.7
ENSDARE00000366350	174	39.7	134.3
ENSDARE00000366351	195	51	144
ENSDARE00000366352	228	64.4	163.6
ENSDARE00000366382	174	30.4	143.6
ENSDARE00000366385	210	35.5	174.5
ENSDARE00000366387	183	27.4	155.6
ENSDARE00000366389	174	34.2	139.8
ENSDARE00000366391	150	37.6	112.4
ENSDARE00000366395	201	45.4	155.6
ENSDARE00000366397	174	33.8	140.2
ENSDARE00000366398	174	41.9	132.1
ENSDARE00000371704	183	32.7	150.3
ENSDARE00000371715	216	41.9	174.1
ENSDARE00000371716	219	43.2	175.8
ENSDARE00000371717	207	39.6	167.4
ENSDARE00000371718	225	37.8	187.2
ENSDARE00000371723	159	25.1	133.9
ENSDARE00000372898	150	37.1	112.9
ENSDARE00000372900	171	42.1	128.9
ENSDARE00000374445	138	25.7	112.3
ENSDARE00000375731	123	27.7	95.3
ENSDARE00000375760	153	26.9	126.1
ENSDARE00000375763	207	53.9	153.1

ENSDARE00000375766	177	35.9	141.1
ENSDARE00000376018	189	37.9	151.1
ENSDARE00000376022	246	42	204
ENSDARE00000376030	213	34.5	178.5
ENSDARE00000376032	144	25.9	118.1
ENSDARE00000376036	186	32.6	153.4
ENSDARE00000376039	213	60.7	152.3
ENSDARE00000376041	138	35.1	102.9
ENSDARE00000376042	156	44.1	111.9
ENSDARE00000382771	159	40.8	118.2
ENSDARE00000382773	138	30.6	107.4
ENSDARE00000385802	153	42.9	110.1
ENSDARE00000385804	546	123.2	422.8
ENSDARE00000385810	183	41.4	141.6
ENSDARE00000385813	165	40.6	124.4
ENSDARE00000385815	234	55.9	178.1
ENSDARE00000386166	135	27.7	107.3
ENSDARE00000386167	198	43.4	154.6
ENSDARE00000386169	207	38.9	168.1
ENSDARE00000386171	177	34.8	142.2
ENSDARE00000386175	195	45.1	149.9
ENSDARE00000386176	201	39.4	161.6
ENSDARE00000389406	222	53.1	168.9
ENSDARE00000389857	165	44.8	120.2
ENSDARE00000389876	852	269.5	582.5
ENSDARE00000389893	237	65.6	171.4
ENSDARE00000389928	255	67.6	187.4
ENSDARE00000393774	183	36.9	146.1
ENSDARE00000397253	165	29.6	135.4
ENSDARE00000397315	150	29.8	120.2
ENSDARE00000399344	180	35.9	144.1
ENSDARE00000399353	177	44.7	132.3
ENSDARE00000401798	147	27.4	119.6
ENSDARE00000401799	273	59.3	213.7
ENSDARE00000402489	171	40	131
ENSDARE00000402490	159	37.9	121.1
ENSDARE00000402497	162	23.4	138.6
ENSDARE00000402561	153	40.2	112.8
ENSDARE00000402563	156	33.1	122.9
ENSDARE00000402564	180	32.8	147.2
ENSDARE00000402972	174	52.6	121.4
ENSDARE00000402979	177	46.2	130.8

ENSDARE00000402982	156	47.4	108.6
ENSDARE00000407906	150	30.9	119.1
ENSDARE00000408780	153	28.2	124.8
ENSDARE00000408809	192	37.9	154.1
ENSDARE00000408813	213	51	162
ENSDARE00000408815	153	39.4	113.6
ENSDARE00000408817	189	39.7	149.3
ENSDARE00000413898	189	29.1	159.9
ENSDARE00000413900	162	27.5	134.5
ENSDARE00000413903	219	35.5	183.5
ENSDARE00000413909	216	30.2	185.8
ENSDARE00000416314	183	37.9	145.1
ENSDARE00000416315	231	37.2	193.8
ENSDARE00000416316	171	43.7	127.3
ENSDARE00000416323	147	24.1	122.9
ENSDARE00000416326	222	40.4	181.6
ENSDARE00000416327	159	39.5	119.5
ENSDARE00000416328	174	31.6	142.4
ENSDARE00000416329	204	40.9	163.1
ENSDARE00000416341	159	31.3	127.7
ENSDARE00000416343	177	37.7	139.3
ENSDARE00000416345	192	44.8	147.2
ENSDARE00000416347	180	50.9	129.1
ENSDARE00000420020	138	35.4	102.6
ENSDARE00000422536	180	23.8	156.2
ENSDARE00000422540	201	44.1	156.9
ENSDARE00000424684	183	29.8	153.2
ENSDARE00000424686	156	38.1	117.9
ENSDARE00000425118	228	24.3	203.7
ENSDARE00000428437	165	34.7	130.3
ENSDARE00000428440	195	38.5	156.5
ENSDARE00000428445	168	35.2	132.8
ENSDARE00000439469	156	46.7	109.3
ENSDARE00000439473	177	37.5	139.5
ENSDARE00000439477	174	38.7	135.3
ENSDARE00000439484	189	57.2	131.8
ENSDARE00000439488	294	79.8	214.2
ENSDARE00000439491	333	69.5	263.5
ENSDARE00000439497	189	44.8	144.2
ENSDARE00000439499	165	47.6	117.4
ENSDARE00000439502	156	42	114
ENSDARE00000439505	153	36.2	116.8

ENSDARE00000443878	177	39.1	137.9
ENSDARE00000443884	243	26.8	216.2
ENSDARE00000444017	174	58.3	115.7
ENSDARE00000444026	174	50.6	123.4
ENSDARE00000446813	168	32.8	135.2
ENSDARE00000446836	270	51.1	218.9
ENSDARE00000446858	192	37.2	154.8
ENSDARE00000446862	174	31	143
ENSDARE00000446867	243	42.5	200.5
ENSDARE00000446871	162	44.2	117.8
ENSDARE00000446881	213	51.5	161.5
ENSDARE00000447487	153	44.9	108.1
ENSDARE00000450451	186	46.4	139.6
ENSDARE00000450459	162	43.8	118.2
ENSDARE00000450810	147	33.5	113.5
ENSDARE00000451744	216	47	169
ENSDARE00000451753	156	28.6	127.4
ENSDARE00000453028	198	38.7	159.3
ENSDARE00000456412	147	29.3	117.7
ENSDARE00000456480	177	41.7	135.3
ENSDARE00000456502	144	34.2	109.8
ENSDARE00000456512	228	42	186
ENSDARE00000456519	138	39.5	98.5
ENSDARE00000456534	153	22.4	130.6
ENSDARE00000456569	210	42.9	167.1
ENSDARE00000456717	213	44.3	168.7
ENSDARE00000456729	132	31.9	100.1
ENSDARE00000457758	204	36	168
ENSDARE00000458979	159	37.8	121.2
ENSDARE00000458983	186	43.2	142.8
ENSDARE00000458985	210	36	174
ENSDARE00000458993	144	26	118
ENSDARE00000459428	156	41.5	114.5
ENSDARE00000459433	234	55.9	178.1
ENSDARE00000459435	288	62.1	225.9
ENSDARE00000459456	183	35.8	147.2
ENSDARE00000459464	168	41.5	126.5
ENSDARE00000459473	159	41	118
ENSDARE00000459479	198	50.9	147.1
ENSDARE00000459492	249	68.5	180.5
ENSDARE00000459505	192	46.8	145.2
ENSDARE00000459514	150	39.2	110.8

ENSDARE00000459519	168	44	124
ENSDARE00000459521	183	43.3	139.7
ENSDARE00000459530	273	77.9	195.1
ENSDARE00000459532	144	31.3	112.7
ENSDARE00000465123	231	31.7	199.3
ENSDARE00000465146	126	33.2	92.8
ENSDARE00000465151	168	39.9	128.1
ENSDARE00000465152	162	19	143
ENSDARE00000468545	189	36.3	152.7
ENSDARE00000468552	168	46.1	121.9
ENSDARE00000468560	153	41.5	111.5
ENSDARE00000468629	156	31.5	124.5
ENSDARE00000468684	252	39.1	212.9
ENSDARE00000468775	189	47	142
ENSDARE00000472748	201	37.2	163.8
ENSDARE00000472764	162	34.4	127.6
ENSDARE00000472768	180	39.5	140.5
ENSDARE00000472821	195	50.7	144.3
ENSDARE00000472827	198	40.7	157.3
ENSDARE00000472831	183	46.6	136.4
ENSDARE00000472833	228	38.8	189.2
ENSDARE00000472841	150	20.1	129.9
ENSDARE00000473568	153	33.2	119.8
ENSDARE00000478911	198	38.7	159.3
ENSDARE00000479753	171	37.3	133.7
ENSDARE00000483307	180	38.7	141.3
ENSDARE00000483315	159	33.9	125.1
ENSDARE00000485532	189	46.8	142.2
ENSDARE00000485565	186	33.3	152.7
ENSDARE00000485576	264	57.6	206.4
ENSDARE00000485597	171	23.2	147.8
ENSDARE00000486982	195	38	157
ENSDARE00000486984	186	43.8	142.2
ENSDARE00000489631	153	27.9	125.1
ENSDARE00000490003	129	27.7	101.3
ENSDARE00000490006	174	32.7	141.3
ENSDARE00000490008	186	29	157
ENSDARE00000490009	192	43.2	148.8
ENSDARE00000490010	255	37	218
ENSDARE00000490014	198	48.4	149.6
ENSDARE00000490015	234	49.3	184.7
ENSDARE00000496668	189	36.3	152.7

ENSDARE00000497324	159	38.7	120.3
ENSDARE00000497332	261	77.2	183.8
ENSDARE00000501488	177	48.8	128.2
ENSDARE00000503458	198	32.2	165.8
ENSDARE00000504303	189	39.4	149.6
ENSDARE00000504759	195	31.2	163.8
ENSDARE00000504760	174	44.1	129.9
ENSDARE00000504763	177	27.6	149.4
ENSDARE00000505244	165	23.1	141.9
ENSDARE00000506166	177	43.2	133.8
ENSDARE00000506558	135	42.3	92.7
ENSDARE00000508566	126	26.5	99.5
ENSDARE00000508573	159	37.5	121.5
ENSDARE00000508577	168	37	131
ENSDARE00000508579	159	18.9	140.1
ENSDARE00000508581	168	49	119
ENSDARE00000508584	177	40.6	136.4
ENSDARE00000508588	153	34.1	118.9
ENSDARE00000508589	174	40.7	133.3
ENSDARE00000508592	198	45.8	152.2
ENSDARE00000508594	201	33.2	167.8
ENSDARE00000508597	192	26.6	165.4
ENSDARE00000508599	168	37	131
ENSDARE00000508612	150	24.6	125.4
ENSDARE00000508772	153	23.6	129.4
ENSDARE00000508848	159	25.8	133.2
ENSDARE00000509941	156	37	119
ENSDARE00000509943	207	52.3	154.7
ENSDARE00000509946	231	45.6	185.4
ENSDARE00000509950	204	45.6	158.4
ENSDARE00000513313	159	29.8	129.2
ENSDARE00000513321	162	29.3	132.7
ENSDARE00000513323	450	116.7	333.3
ENSDARE00000513331	129	17.5	111.5
ENSDARE00000523058	171	36.7	134.3
ENSDARE00000523062	153	32.1	120.9
ENSDARE00000523073	123	31.7	91.3
ENSDARE00000523079	177	31.6	145.4
ENSDARE00000523834	156	46.3	109.7
ENSDARE00000523835	129	33.5	95.5
ENSDARE00000523837	177	42.6	134.4
ENSDARE00000523839	189	52.2	136.8

ENSDARE00000523840	198	53.3	144.7
ENSDARE00000526274	210	40.2	169.8
ENSDARE00000526277	144	27.9	116.1
ENSDARE00000526279	168	42.6	125.4
ENSDARE00000526284	162	30.2	131.8
ENSDARE00000526781	159	32	127
ENSDARE00000526790	168	30.9	137.1
ENSDARE00000526816	192	45.1	146.9
ENSDARE00000526820	210	55	155
ENSDARE00000529148	180	36.6	143.4
ENSDARE00000529160	177	29.6	147.4
ENSDARE00000530930	153	23.1	129.9
ENSDARE00000530935	168	37.9	130.1
ENSDARE00000530942	159	32.9	126.1
ENSDARE00000530947	150	32.2	117.8
ENSDARE00000530950	138	22.6	115.4
ENSDARE00000533901	159	34.9	124.1
ENSDARE00000533907	162	37.9	124.1
ENSDARE00000533915	216	46.7	169.3
ENSDARE00000533920	189	44.2	144.8
ENSDARE00000533921	153	33.6	119.4
ENSDARE00000533933	153	34.4	118.6
ENSDARE00000533952	171	48.8	122.2
ENSDARE00000533965	168	35.4	132.6
ENSDARE00000533998	177	42	135
ENSDARE00000534001	177	34.5	142.5
ENSDARE00000534004	198	34.1	163.9
ENSDARE00000534009	231	63.5	167.5
ENSDARE00000534031	162	39.5	122.5
ENSDARE00000534038	222	42.3	179.7
ENSDARE00000534061	198	53.6	144.4
ENSDARE00000534100	156	37.9	118.1
ENSDARE00000534136	195	48.8	146.2
ENSDARE00000534139	177	54.5	122.5
ENSDARE00000535855	159	34.9	124.1
ENSDARE00000535865	159	32.6	126.4
ENSDARE00000535873	159	45.3	113.7
ENSDARE00000536226	237	43	194
ENSDARE00000536231	135	30	105
ENSDARE00000537215	156	34.4	121.6
ENSDARE00000537228	147	29.4	117.6
ENSDARE00000537268	225	47.3	177.7

ENSDARE00000537287	162	33.5	128.5
ENSDARE00000537310	162	29.1	132.9
ENSDARE00000537366	165	37.8	127.2
ENSDARE00000537409	150	37.5	112.5
ENSDARE00000537564	207	52.9	154.1
ENSDARE00000538436	255	63.5	191.5
ENSDARE00000544279	231	55	176
ENSDARE00000544282	168	49.3	118.7
ENSDARE00000544296	120	30.7	89.3
ENSDARE00000544992	177	41.7	135.3
ENSDARE00000546183	183	50.2	132.8
ENSDARE00000546198	183	39.9	143.1
ENSDARE00000546213	189	55.1	133.9
ENSDARE00000548381	150	25.2	124.8
ENSDARE00000548487	150	27.5	122.5
ENSDARE00000548535	156	33.6	122.4
ENSDARE00000548618	171	29.2	141.8
ENSDARE00000551653	150	41.5	108.5
ENSDARE00000553760	177	37.8	139.2
ENSDARE00000553769	150	40.7	109.3
ENSDARE00000553777	168	48.2	119.8
ENSDARE00000553792	147	30.4	116.6
ENSDARE00000556339	141	31.4	109.6
ENSDARE00000556709	213	37.4	175.6
ENSDARE00000556737	240	34.9	205.1
ENSDARE00000556780	243	50.6	192.4
ENSDARE00000556793	180	33.3	146.7
ENSDARE00000556816	192	46.6	145.4
ENSDARE00000556832	192	36.6	155.4
ENSDARE00000558520	168	35.6	132.4
ENSDARE00000562216	174	33.6	140.4
ENSDARE00000562231	192	43.5	148.5
ENSDARE00000562278	234	51.6	182.4
ENSDARE00000562365	198	37.8	160.2
ENSDARE00000562369	207	47.1	159.9
ENSDARE00000562431	165	43	122
ENSDARE00000562462	213	44	169
ENSDARE00000562476	249	71.1	177.9
ENSDARE00000562503	450	127.5	322.5
ENSDARE00000564106	150	28	122
ENSDARE00000564170	192	59.4	132.6
ENSDARE00000565432	186	40.7	145.3

ENSDARE00000565442	174	36	138
ENSDARE00000565444	180	33.6	146.4
ENSDARE00000565452	171	41.3	129.7
ENSDARE00000565466	237	50.2	186.8
ENSDARE00000565486	150	37.4	112.6
ENSDARE00000565499	165	38.5	126.5
ENSDARE00000565539	327	57.9	269.1
ENSDARE00000567260	246	57.5	188.5
ENSDARE00000567274	159	35	124
ENSDARE00000568871	144	25	119
ENSDARE00000569324	156	37	119
ENSDARE00000569362	231	52.8	178.2
ENSDARE00000569389	180	36.9	143.1
ENSDARE00000569406	228	47.2	180.8
ENSDARE00000569434	159	37.5	121.5
ENSDARE00000569498	189	41	148
ENSDARE00000569569	168	37.6	130.4
ENSDARE00000569582	228	54.1	173.9
ENSDARE00000571584	225	46.9	178.1
ENSDARE00000573221	183	34	149
ENSDARE00000574770	165	43.5	121.5
ENSDARE00000574783	273	58.6	214.4
ENSDARE00000574792	240	63.4	176.6
ENSDARE00000580006	201	36.8	164.2
ENSDARE00000580140	267	62.9	204.1
ENSDARE00000580160	198	42	156
ENSDARE00000581236	153	30.3	122.7
ENSDARE00000581255	195	37.8	157.2
ENSDARE00000581287	195	33.6	161.4
ENSDARE00000583666	165	36.1	128.9
ENSDARE00000583775	150	32.8	117.2
ENSDARE00000583807	183	42.5	140.5
ENSDARE00000583815	156	36.4	119.6
ENSDARE00000583835	156	34.7	121.3
ENSDARE00000583845	150	19.9	130.1
ENSDARE00000583885	162	35.4	126.6
ENSDARE00000583896	138	28.5	109.5
ENSDARE00000583908	975	266.3	708.7
ENSDARE00000585921	177	34.8	142.2
ENSDARE00000585929	168	34.2	133.8
ENSDARE00000585960	198	44.8	153.2
ENSDARE00000585974	174	44.5	129.5

ENSDARE00000586007	183	40.8	142.2
ENSDARE00000587231	216	37.9	178.1
ENSDARE00000587257	159	33.3	125.7
ENSDARE00000587275	189	48.3	140.7
ENSDARE00000587329	177	43	134
ENSDARE00000587342	213	61.5	151.5
ENSDARE00000587360	144	41.1	102.9
ENSDARE00000589576	195	36.9	158.1
ENSDARE00000589581	192	37.4	154.6
ENSDARE00000589604	171	27.3	143.7
ENSDARE00000589610	198	38.9	159.1
ENSDARE00000590769	153	44.6	108.4
ENSDARE00000590855	144	28.1	115.9
ENSDARE00000590979	198	54.4	143.6
ENSDARE00000590988	192	40.4	151.6
ENSDARE00000591013	156	33.4	122.6
ENSDARE00000591106	186	43.2	142.8
ENSDARE00000591114	237	47.2	189.8
ENSDARE00000591122	210	49	161
ENSDARE00000591140	183	51.4	131.6
ENSDARE00000591148	186	44.3	141.7
ENSDARE00000591155	150	39.5	110.5
ENSDARE00000591182	174	51.4	122.6
ENSDARE00000591202	228	64.8	163.2
ENSDARE00000591211	156	35.5	120.5
ENSDARE00000591230	135	35.4	99.6
ENSDARE00000592670	153	33.9	119.1
ENSDARE00000594244	201	45.1	155.9
ENSDARE00000594268	165	24.7	140.3
ENSDARE00000594317	159	16.5	142.5
ENSDARE00000594319	150	29	121
ENSDARE00000594328	246	35.6	210.4
ENSDARE00000595847	225	59	166
ENSDARE00000595869	135	35.8	99.2
ENSDARE00000595888	189	45.7	143.3
ENSDARE00000595896	174	46.9	127.1
ENSDARE00000595900	162	31	131
ENSDARE00000602242	174	35	139
ENSDARE00000602243	186	30.3	155.7
ENSDARE00000602248	159	35.1	123.9
ENSDARE00000602253	225	39.5	185.5
ENSDARE00000602255	129	29	100

ENSDARE00000602261	150	41	109
ENSDARE00000602266	234	44.6	189.4
ENSDARE00000602268	162	32.9	129.1
ENSDARE00000602270	246	49.6	196.4
ENSDARE00000602988	159	35.1	123.9
ENSDARE00000602989	150	29.6	120.4
ENSDARE00000603094	186	29.6	156.4
ENSDARE00000603632	192	50	142
ENSDARE00000603645	237	40.2	196.8
ENSDARE00000603661	159	36.4	122.6
ENSDARE00000603668	159	36.4	122.6
ENSDARE00000603671	246	64.9	181.1
ENSDARE00000603682	168	23.9	144.1
ENSDARE00000603685	180	42.1	137.9
ENSDARE00000603689	177	40.6	136.4
ENSDARE00000603693	195	34.6	160.4
ENSDARE00000603701	156	45.3	110.7
ENSDARE00000603709	174	27.3	146.7
ENSDARE00000603720	159	36.5	122.5
ENSDARE00000603725	192	49.9	142.1
ENSDARE00000603731	282	97.1	184.9
ENSDARE00000605727	165	44.9	120.1
ENSDARE00000605752	144	40.1	103.9
ENSDARE00000605759	159	35.3	123.7
ENSDARE00000605767	147	25.9	121.1
ENSDARE00000605816	171	47.1	123.9
ENSDARE00000606680	168	36.4	131.6
ENSDARE00000608517	195	55.1	139.9
ENSDARE00000608522	162	48.4	113.6
ENSDARE00000608534	195	49.7	145.3
ENSDARE00000608544	249	69.4	179.6
ENSDARE00000608549	150	41.8	108.2
ENSDARE00000608553	141	30.7	110.3
ENSDARE00000608554	132	31.5	100.5
ENSDARE00000608557	135	33.9	101.1
ENSDARE00000608731	144	35.9	108.1
ENSDARE00000611768	210	31.4	178.6
ENSDARE00000611777	144	36.5	107.5
ENSDARE00000611790	162	35	127
ENSDARE00000613322	183	34.4	148.6
ENSDARE00000613356	192	28.9	163.1
ENSDARE00000613365	174	23	151

ENSDARE00000613377	207	28.8	178.2
ENSDARE00000613408	171	23.5	147.5
ENSDARE00000613416	159	37.4	121.6
ENSDARE00000613420	198	36.2	161.8
ENSDARE00000613426	159	32.6	126.4
ENSDARE00000613434	195	45.8	149.2
ENSDARE00000613438	150	34.8	115.2
ENSDARE00000613483	159	35.1	123.9
ENSDARE00000613495	153	33.8	119.2
ENSDARE00000613501	171	34.3	136.7
ENSDARE00000613509	144	36.2	107.8
ENSDARE00000613512	162	37.6	124.4
ENSDARE00000613521	198	43.4	154.6
ENSDARE00000613523	174	43.9	130.1
ENSDARE00000613531	147	31.4	115.6
ENSDARE00000613548	177	45.8	131.2
ENSDARE00000613565	180	40.2	139.8
ENSDARE00000622317	168	42.2	125.8
ENSDARE00000622382	249	42.8	206.2
ENSDARE00000622479	171	31.8	139.2
ENSDARE00000622496	156	32.8	123.2
ENSDARE00000622516	363	79.8	283.2
ENSDARE00000626482	156	35.8	120.2
ENSDARE00000626490	141	38.1	102.9
ENSDARE00000626537	126	24.5	101.5
ENSDARE00000631104	177	37.8	139.2
ENSDARE00000631111	201	44.1	156.9
ENSDARE00000631113	156	42.3	113.7
ENSDARE00000631126	168	44.3	123.7
ENSDARE00000631133	150	31.9	118.1
ENSDARE00000631142	195	47	148
ENSDARE00000631157	186	41.2	144.8
ENSDARE00000631169	198	39.6	158.4
ENSDARE00000631180	150	31	119
ENSDARE00000631194	198	36.4	161.6
ENSDARE00000631349	213	36.7	176.3
ENSDARE00000631352	183	31.4	151.6
ENSDARE00000631359	177	32.6	144.4
ENSDARE00000631365	222	37.5	184.5
ENSDARE00000631390	207	30.3	176.7
ENSDARE00000638012	162	43.2	118.8
ENSDARE00000638027	204	47.1	156.9

ENSDARE00000638037	147	42.7	104.3
ENSDARE00000638051	156	45.7	110.3
ENSDARE00000638113	261	48.5	212.5
ENSDARE00000638598	1212	238.7	973.3
ENSDARE00000638639	180	45.6	134.4
ENSDARE00000638675	186	34.8	151.2
ENSDARE00000638723	204	52.1	151.9
ENSDARE00000638727	225	52.6	172.4
ENSDARE00000638734	156	34.3	121.7
ENSDARE00000638745	165	41.5	123.5
ENSDARE00000638764	162	39.4	122.6
ENSDARE00000639000	165	24.6	140.4
ENSDARE00000639007	159	28.5	130.5
ENSDARE00000639013	150	34.5	115.5
ENSDARE00000639034	156	36.3	119.7
ENSDARE00000639040	150	34.9	115.1
ENSDARE00000639401	192	31.5	160.5
ENSDARE00000639474	177	36.6	140.4
ENSDARE00000639484	195	40.7	154.3
ENSDARE00000639510	186	31	155
ENSDARE00000639922	189	51.8	137.2
ENSDARE00000639973	144	21.8	122.2
ENSDARE00000640009	183	42.3	140.7
ENSDARE00000640043	240	48.8	191.2
ENSDARE00000640053	219	43.3	175.7
ENSDARE00000642104	156	38.7	117.3
ENSDARE00000642113	150	32	118
ENSDARE00000642143	159	26	133
ENSDARE00000642191	180	40.5	139.5
ENSDARE00000642207	168	32.5	135.5
ENSDARE00000642237	237	42.5	194.5
ENSDARE00000643776	177	34.4	142.6
ENSDARE00000643815	759	144.5	614.5
ENSDARE00000643830	195	31.7	163.3
ENSDARE00000643853	162	30.4	131.6
ENSDARE00000643865	135	25.9	109.1
ENSDARE00000643873	159	37.3	121.7
ENSDARE00000645582	168	37.5	130.5
ENSDARE00000645589	150	38.9	111.1
ENSDARE00000645600	153	38.4	114.6
ENSDARE00000645622	162	37	125
ENSDARE00000646383	168	39.8	128.2

ENSDARE00000646475	189	43.5	145.5
ENSDARE00000646520	147	34.8	112.2
ENSDARE00000646559	141	37.7	103.3
ENSDARE00000649754	144	33.1	110.9
ENSDARE00000649836	156	32.2	123.8
ENSDARE00000655720	258	66.9	191.1
ENSDARE00000655752	171	36.2	134.8
ENSDARE00000656788	162	41.1	120.9
ENSDARE00000656808	219	41.5	177.5
ENSDARE00000656857	165	41.1	123.9
ENSDARE00000657082	174	38.5	135.5
ENSDARE00000657180	180	41.2	138.8
ENSDARE00000657193	213	51.3	161.7
ENSDARE00000657199	207	40	167
ENSDARE00000659145	141	29.3	111.7
ENSDARE00000659318	183	38.9	144.1
ENSDARE00000660583	138	23.5	114.5
ENSDARE00000663129	189	39	150
ENSDARE00000663151	153	40.2	112.8
ENSDARE00000663161	150	40.9	109.1
ENSDARE00000663942	147	29.5	117.5
ENSDARE00000664040	225	47.1	177.9
ENSDARE00000664051	153	37.8	115.2
ENSDARE00000664100	228	41.5	186.5
ENSDARE00000664110	147	32.5	114.5
ENSDARE00000664146	219	56.6	162.4
ENSDARE00000664175	186	44.6	141.4
ENSDARE00000664222	165	49.2	115.8
ENSDARE00000664236	147	37.9	109.1
ENSDARE00000668704	234	36.3	197.7
ENSDARE00000668740	291	64.8	226.2
ENSDARE00000668775	138	31.7	106.3
ENSDARE00000668799	195	36.8	158.2
ENSDARE00000668808	198	32.7	165.3
ENSDARE00000668820	150	32.4	117.6
ENSDARE00000668824	312	57.4	254.6
ENSDARE00000671990	180	33.9	146.1
ENSDARE00000672014	156	28.9	127.1
ENSDARE00000672050	180	30.3	149.7
ENSDARE00000672077	207	38.7	168.3
ENSDARE00000672096	156	30.7	125.3
ENSDARE00000672104	282	59.3	222.7

ENSDARE00000672124	198	30	168
ENSDARE00000672158	189	36.3	152.7
ENSDARE00000672176	210	43.1	166.9
ENSDARE00000672238	198	48.2	149.8
ENSDARE00000672265	180	44.9	135.1
ENSDARE00000672358	156	40.3	115.7
ENSDARE00000673691	177	43.4	133.6
ENSDARE00000673739	159	38.3	120.7
ENSDARE00000673792	186	31.4	154.6
ENSDARE00000677593	132	24.9	107.1
ENSDARE00000677597	312	69.6	242.4
ENSDARE00000678787	210	35.7	174.3
ENSDARE00000681411	195	52.6	142.4
ENSDARE00000681420	174	35.3	138.7
ENSDARE00000681437	243	49.8	193.2
ENSDARE00000681450	207	36.2	170.8
ENSDARE00000681468	177	30.7	146.3
ENSDARE00000681475	177	37.6	139.4
ENSDARE00000682848	198	45	153
ENSDARE00000682853	141	27.5	113.5
ENSDARE00000684137	204	38.5	165.5
ENSDARE00000684157	189	45.2	143.8
ENSDARE00000684190	195	39.3	155.7
ENSDARE00000684194	294	58	236
ENSDARE00000684201	162	34.5	127.5
ENSDARE00000684203	123	28.1	94.9
ENSDARE00000684230	135	29.1	105.9
ENSDARE00000684271	195	36.8	158.2
ENSDARE00000691606	147	36.6	110.4
ENSDARE00000693112	189	32.3	156.7
ENSDARE00000693114	159	36.2	122.8
ENSDARE00000693116	159	39.8	119.2
ENSDARE00000693117	162	46	116
ENSDARE00000693118	216	53.7	162.3
ENSDARE00000693126	174	34.3	139.7
ENSDARE00000693189	165	47.5	117.5
ENSDARE00000693190	183	39.4	143.6
ENSDARE00000693191	192	37.3	154.7
ENSDARE00000693487	186	38.9	147.1
ENSDARE00000693534	216	62.1	153.9
ENSDARE00000693537	273	47.5	225.5
ENSDARE00000693539	240	49	191

ENSDARE00000693579	195	47.2	147.8
ENSDARE00000694221	150	42.7	107.3
ENSDARE00000694225	162	30.6	131.4
ENSDARE00000694226	153	36.6	116.4
ENSDARE00000695869	240	48.8	191.2
ENSDARE00000699851	183	35.8	147.2
ENSDARE00000699853	171	29	142
ENSDARE00000699855	243	55.9	187.1
ENSDARE00000699857	186	37.4	148.6
ENSDARE00000702602	198	42.5	155.5
ENSDARE00000702612	156	39.7	116.3
ENSDARE00000702616	150	37.9	112.1
ENSDARE00000702631	135	35.4	99.6
ENSDARE00000704083	294	58.7	235.3
ENSDARE00000705628	207	52.8	154.2
ENSDARE00000705635	189	44.7	144.3
ENSDARE00000706012	165	39.9	125.1
ENSDARE00000706014	144	26.2	117.8
ENSDARE00000706606	174	48.5	125.5
ENSDARE00000706620	156	30.5	125.5
ENSDARE00000711507	174	25.8	148.2
ENSDARE00000711512	159	26.2	132.8
ENSDARE00000711514	162	34.6	127.4
ENSDARE00000712064	216	48.4	167.6
ENSDARE00000712066	219	47.9	171.1
ENSDARE00000712069	168	36.1	131.9
ENSDARE00000712090	213	45	168
ENSDARE00000712092	192	50.2	141.8
ENSDARE00000712106	210	44.1	165.9
ENSDARE00000712110	195	43.4	151.6
ENSDARE00000712115	153	22.8	130.2
ENSDARE00000712140	213	42	171
ENSDARE00000715295	180	32.6	147.4
ENSDARE00000715309	159	24.5	134.5
ENSDARE00000715313	183	29.7	153.3
ENSDARE00000715325	141	37.2	103.8
ENSDARE00000715607	153	37.4	115.6
ENSDARE00000715611	231	55.3	175.7
ENSDARE00000715621	171	40.7	130.3
ENSDARE00000715666	303	76.9	226.1
ENSDARE00000715680	159	31.2	127.8
ENSDARE00000715695	240	46.8	193.2

ENSDARE00000715950	228	54.5	173.5
ENSDARE00000715999	198	46.7	151.3
ENSDARE00000716007	162	32.1	129.9
ENSDARE00000716028	177	33	144
ENSDARE00000716057	213	44.8	168.2
ENSDARE00000716065	171	43	128
ENSDARE00000716795	201	34.3	166.7
ENSDARE00000716814	237	43.1	193.9
ENSDARE00000716819	192	38	154
ENSDARE00000716823	174	34.4	139.6
ENSDARE00000716830	237	38.5	198.5
ENSDARE00000716832	189	26.2	162.8
ENSDARE00000716836	159	33.5	125.5
ENSDARE00000716845	168	29.4	138.6
ENSDARE00000716855	177	31.9	145.1
ENSDARE00000716860	246	52.6	193.4
ENSDARE00000716869	210	33.2	176.8
ENSDARE00000716881	237	37.7	199.3
ENSDARE00000716885	186	30.8	155.2
ENSDARE00000716889	192	38.9	153.1
ENSDARE00000716898	162	31.8	130.2
ENSDARE00000716903	207	34.4	172.6
ENSDARE00000716906	195	30.9	164.1
ENSDARE00000717004	126	25	101
ENSDARE00000717015	207	54.2	152.8
ENSDARE00000717029	156	28.8	127.2
ENSDARE00000717035	189	46.1	142.9
ENSDARE00000717064	162	33.2	128.8
ENSDARE00000717073	150	26.7	123.3
ENSDARE00000717083	162	30.4	131.6
ENSDARE00000717094	225	43.8	181.2
ENSDARE00000717100	264	57.3	206.7
ENSDARE00000719716	525	122.9	402.1
ENSDARE00000719726	177	41.5	135.5
ENSDARE00000719729	168	42.8	125.2
ENSDARE00000719733	201	51.8	149.2
ENSDARE00000719735	153	45.3	107.7
ENSDARE00000719739	165	44.4	120.6
ENSDARE00000720776	183	52.7	130.3
ENSDARE00000730549	156	41.5	114.5
ENSDARE00000730555	150	36.3	113.7
ENSDARE00000730558	141	42.7	98.3

ENSDARE00000731457	213	24.5	188.5
ENSDARE00000732826	147	41.9	105.1
ENSDARE00000732832	153	36.4	116.6
ENSDARE00000732856	153	37.9	115.1
ENSDARE00000732860	138	34.5	103.5
ENSDARE00000735714	228	37.8	190.2
ENSDARE00000735719	162	28.5	133.5
ENSDARE00000737068	135	24	111
ENSDARE00000737103	141	36.7	104.3
ENSDARE00000737111	180	33.8	146.2
ENSDARE00000738962	150	33.2	116.8
ENSDARE00000738964	174	33.1	140.9
ENSDARE00000739397	186	44.4	141.6
ENSDARE00000740292	144	30.8	113.2
ENSDARE00000740294	180	48.5	131.5
ENSDARE00000740298	165	46.3	118.7
ENSDARE00000740565	162	35.1	126.9
ENSDARE00000743432	153	30.2	122.8
ENSDARE00000743763	132	28.6	103.4
ENSDARE00000743890	168	34.4	133.6
ENSDARE00000746292	168	35.6	132.4
ENSDARE00000746911	198	61.8	136.2
ENSDARE00000748012	243	49.3	193.7
ENSDARE00000749025	171	39.5	131.5
ENSDARE00000749316	150	26	124
ENSDARE00000749374	255	48.8	206.2
ENSDARE00000752332	141	32.4	108.6
ENSDARE00000754356	174	29.8	144.2
ENSDARE00000754365	174	34	140
ENSDARE00000754384	192	42.8	149.2
ENSDARE00000754398	165	35.8	129.2
ENSDARE00000754411	156	36.3	119.7
ENSDARE00000755277	192	32.1	159.9
ENSDARE00000757353	153	41.5	111.5
ENSDARE00000757369	180	34.3	145.7
ENSDARE00000757376	162	35	127
ENSDARE00000757379	174	35.4	138.6
ENSDARE00000757381	198	38.2	159.8
ENSDARE00000759869	189	46	143
ENSDARE00000759895	345	91.2	253.8
ENSDARE00000759901	150	41.8	108.2
ENSDARE00000759904	126	21.5	104.5

ENSDARE00000759916	153	32.9	120.1
ENSDARE00000766250	183	15.4	167.6
ENSDARE00000766253	144	15.3	128.7
ENSDARE00000766261	150	21.7	128.3
ENSDARE00000766670	165	30.3	134.7
ENSDARE00000766673	192	25.1	166.9
ENSDARE00000766676	252	48.6	203.4
ENSDARE00000770662	141	28.5	112.5
ENSDARE00000770664	213	47.1	165.9
ENSDARE00000771170	171	29.6	141.4
ENSDARE00000774381	129	30	99
ENSDARE00000774389	159	29.9	129.1
ENSDARE00000774395	192	27.9	164.1
ENSDARE00000775044	183	47.9	135.1
ENSDARE00000775302	324	54.6	269.4
ENSDARE00000775343	171	38.7	132.3
ENSDARE00000776025	195	52.1	142.9
ENSDARE00000776079	150	32.5	117.5
ENSDARE00000776742	189	49.9	139.1
ENSDARE00000776757	270	57.1	212.9
ENSDARE00000776784	150	41	109
ENSDARE00000777124	195	26.6	168.4
ENSDARE00000777574	198	34.3	163.7
ENSDARE00000777995	168	38.8	129.2
ENSDARE00000778247	225	51.8	173.2
ENSDARE00000778745	171	26.8	144.2
ENSDARE00000779188	153	23.2	129.8
ENSDARE00000779190	192	48.1	143.9
ENSDARE00000779264	156	47.4	108.6
ENSDARE00000779325	195	30.4	164.6
ENSDARE00000780128	156	41.9	114.1
ENSDARE00000780253	159	25.6	133.4
ENSDARE00000780432	252	51.2	200.8
ENSDARE00000781234	153	32.6	120.4
ENSDARE00000781662	171	48.4	122.6
ENSDARE00000782197	156	48.2	107.8
ENSDARE00000782271	216	35.6	180.4
ENSDARE00000782334	234	40.6	193.4
ENSDARE00000783156	261	57.3	203.7
ENSDARE00000783245	171	40.5	130.5
ENSDARE00000783283	174	35	139
ENSDARE00000783339	168	49.6	118.4

ENSDARE00000783733	156	38	118
ENSDARE00000783887	189	43.8	145.2
ENSDARE00000783991	168	45.2	122.8
ENSDARE00000784313	174	38.5	135.5
ENSDARE00000784351	150	35.3	114.7
ENSDARE00000785293	237	47.3	189.7
ENSDARE00000785412	171	36.8	134.2
ENSDARE00000786247	129	31.3	97.7
ENSDARE00000786297	270	52.2	217.8
ENSDARE00000786354	150	42.8	107.2
ENSDARE00000786445	159	50.2	108.8
ENSDARE00000786818	219	43.6	175.4
ENSDARE00000787103	198	51.7	146.3
ENSDARE00000787936	174	40.5	133.5
ENSDARE00000788204	153	44.5	108.5
ENSDARE00000788234	162	41.5	120.5
ENSDARE00000788394	258	41.8	216.2
ENSDARE00000788729	150	31.8	118.2
ENSDARE00000788991	180	54.9	125.1
ENSDARE00000789125	177	31.5	145.5
ENSDARE00000789215	138	41.5	96.5
ENSDARE00000789433	150	37.2	112.8
ENSDARE00000789684	153	25.5	127.5
ENSDARE00000789813	339	64.5	274.5
ENSDARE00000790100	285	63.2	221.8
ENSDARE00000790288	156	36.6	119.4
ENSDARE00000790691	234	53.2	180.8
ENSDARE00000790753	150	29.6	120.4
ENSDARE00000790887	216	49.5	166.5
ENSDARE00000790894	180	46.2	133.8
ENSDARE00000790909	228	45.2	182.8
ENSDARE00000790941	198	55.2	142.8
ENSDARE00000791415	198	36.1	161.9
ENSDARE00000791494	156	32.4	123.6
ENSDARE00000792274	204	41.2	162.8
ENSDARE00000792391	192	29.4	162.6
ENSDARE00000793059	564	148.3	415.7
ENSDARE00000793791	132	39.5	92.5
ENSDARE00000793870	213	49.9	163.1
ENSDARE00000794204	162	43.7	118.3
ENSDARE00000794426	246	46	200
ENSDARE00000794764	234	35.2	198.8

ENSDARE00000794970	159	34.6	124.4
ENSDARE00000795003	177	32.1	144.9
ENSDARE00000795290	168	36.2	131.8
ENSDARE00000795518	324	63.4	260.6
ENSDARE00000795619	180	40.7	139.3
ENSDARE00000795670	357	56.8	300.2
ENSDARE00000795729	216	48.5	167.5
ENSDARE00000795894	168	29.3	138.7
ENSDARE00000796087	270	64.3	205.7
ENSDARE00000796579	147	40.9	106.1
ENSDARE00000796678	204	50.3	153.7
ENSDARE00000796727	159	33.1	125.9
ENSDARE00000796817	537	162.5	374.5
ENSDARE00000796879	168	47.8	120.2
ENSDARE00000797212	150	26.5	123.5
ENSDARE00000797397	150	28.4	121.6
ENSDARE00000797539	201	37.7	163.3
ENSDARE00000797540	195	46.5	148.5
ENSDARE00000797568	183	51.4	131.6
ENSDARE00000797652	147	38.1	108.9
ENSDARE00000797905	147	36.2	110.8
ENSDARE00000797998	159	39.2	119.8
ENSDARE00000798810	150	31.7	118.3
ENSDARE00000798877	330	68.7	261.3
ENSDARE00000798886	138	27.8	110.2
ENSDARE00000799022	201	51.1	149.9
ENSDARE00000799093	168	30.6	137.4
ENSDARE00000799161	360	56.3	303.7
ENSDARE00000799450	183	38.1	144.9
ENSDARE00000799533	207	31.6	175.4
ENSDARE00000799619	147	42	105
ENSDARE00000800033	192	53.9	138.1
ENSDARE00000800164	228	56.7	171.3
ENSDARE00000800803	150	30.5	119.5
ENSDARE00000801111	144	35.6	108.4
ENSDARE00000801351	183	20	163
ENSDARE00000801486	309	76.8	232.2
ENSDARE00000801740	477	118	359
ENSDARE00000801914	180	42.1	137.9
ENSDARE00000802196	174	35.7	138.3
ENSDARE00000802337	135	32.8	102.2
ENSDARE00000802354	204	57.9	146.1

ENSDARE00000802418	183	48.5	134.5
ENSDARE00000802698	162	31.3	130.7
ENSDARE00000802781	198	43	155
ENSDARE00000803684	129	21.7	107.3
ENSDARE00000804051	288	71.9	216.1
ENSDARE00000804578	150	35.7	114.3
ENSDARE00000804672	156	24.3	131.7
ENSDARE00000804979	180	29.3	150.7
ENSDARE00000805045	171	31.6	139.4
ENSDARE00000805489	180	41.4	138.6
ENSDARE00000805632	243	48.6	194.4
ENSDARE00000805901	153	42.3	110.7
ENSDARE00000806090	144	35.1	108.9
ENSDARE00000806132	336	77.5	258.5
ENSDARE00000806191	144	38.9	105.1
ENSDARE00000806262	156	38.7	117.3
ENSDARE00000806445	171	48.9	122.1
ENSDARE00000806639	171	52.9	118.1
ENSDARE00000806729	180	37	143
ENSDARE00000806786	246	60.3	185.7
ENSDARE00000806900	177	51.1	125.9
ENSDARE00000807355	174	28	146
ENSDARE00000808052	159	38	121
ENSDARE00000808083	189	35.6	153.4
ENSDARE00000808131	198	58.4	139.6
ENSDARE00000808293	204	50.1	153.9
ENSDARE00000808308	195	36.6	158.4
ENSDARE00000808437	159	27.8	131.2
ENSDARE00000808746	144	48.1	95.9
ENSDARE00000808785	171	46.8	124.2
ENSDARE00000809134	198	54.6	143.4
ENSDARE00000809206	177	34.1	142.9
ENSDARE00000809352	144	39.6	104.4
ENSDARE00000809627	147	39.7	107.3
ENSDARE00000809914	144	34.5	109.5
ENSDARE00000810378	258	62.7	195.3
ENSDARE00000810518	147	28.4	118.6
ENSDARE00000810811	123	23.5	99.5
ENSDARE00000811634	150	33.5	116.5
ENSDARE00000811811	153	41.4	111.6
ENSDARE00000812117	174	30.3	143.7
ENSDARE00000812281	180	34.7	145.3

ENSDARE00000812370	156	17.5	138.5
ENSDARE00000812534	246	58.3	187.7
ENSDARE00000812760	222	54.7	167.3
ENSDARE00000812780	141	36.7	104.3
ENSDARE00000812856	174	36	138
ENSDARE00000813076	147	29.3	117.7
ENSDARE00000813166	150	30.2	119.8
ENSDARE00000813375	171	31.4	139.6
ENSDARE00000813397	153	24	129
ENSDARE00000813405	150	31.1	118.9
ENSDARE00000813435	156	35.5	120.5
ENSDARE00000813751	159	37.6	121.4
ENSDARE00000813952	186	52.3	133.7
ENSDARE00000814296	510	109.4	400.6
ENSDARE00000814841	228	44.6	183.4
ENSDARE00000814924	231	62.9	168.1
ENSDARE00000815243	195	44.3	150.7
ENSDARE00000815542	198	46.3	151.7
ENSDARE00000815924	177	45.5	131.5
ENSDARE00000816220	165	36.6	128.4
ENSDARE00000816539	228	43.9	184.1
ENSDARE00000816576	174	52.6	121.4
ENSDARE00000816831	171	43	128
ENSDARE00000817156	228	55	173
ENSDARE00000817380	228	47.6	180.4
ENSDARE00000817560	132	34.2	97.8
ENSDARE00000817618	144	27.2	116.8
ENSDARE00000817775	150	37	113
ENSDARE00000817963	213	27.4	185.6
ENSDARE00000818012	198	30.9	167.1
ENSDARE00000818079	183	54.7	128.3
ENSDARE00000818317	162	37.3	124.7
ENSDARE00000818682	156	38.5	117.5
ENSDARE00000818811	216	38.6	177.4
ENSDARE00000818964	189	47.9	141.1
ENSDARE00000819039	150	35	115
ENSDARE00000819046	261	67.3	193.7
ENSDARE00000819503	198	41.9	156.1
ENSDARE00000820232	147	34.7	112.3
ENSDARE00000820409	159	31.3	127.7
ENSDARE00000820615	156	25.7	130.3
ENSDARE00000820768	144	21.2	122.8

ENSDARE00000821274	609	145.7	463.3
ENSDARE00000821277	171	40	131
ENSDARE00000821346	150	34.5	115.5
ENSDARE00000821408	168	42.8	125.2
ENSDARE00000821541	237	68.2	168.8
ENSDARE00000821542	174	51.1	122.9
ENSDARE00000821850	159	23.4	135.6
ENSDARE00000821992	201	39.2	161.8
ENSDARE00000822056	192	39.2	152.8
ENSDARE00000822343	135	31.8	103.2
ENSDARE00000822533	156	36.4	119.6
ENSDARE00000822563	345	92.5	252.5
ENSDARE00000822637	216	56	160
ENSDARE00000822690	162	37.6	124.4
ENSDARE00000822883	168	42.2	125.8
ENSDARE00000822927	153	44.2	108.8
ENSDARE00000823099	252	63.5	188.5
ENSDARE00000823750	162	44.4	117.6
ENSDARE00000824062	150	33.7	116.3
ENSDARE00000824363	165	29	136
ENSDARE00000824642	168	36.4	131.6
ENSDARE00000824763	135	35.6	99.4
ENSDARE00000825015	210	47.2	162.8
ENSDARE00000825408	156	46.1	109.9
ENSDARE00000825507	231	48.3	182.7
ENSDARE00000825658	192	42.8	149.2
ENSDARE00000825799	159	40	119
ENSDARE00000826290	225	37.9	187.1
ENSDARE00000826493	174	45.1	128.9
ENSDARE00000826580	141	30.9	110.1
ENSDARE00000826893	138	31.2	106.8
ENSDARE00000826960	195	34	161
ENSDARE00000827161	288	74	214
ENSDARE00000827566	177	37.6	139.4
ENSDARE00000827579	213	57	156
ENSDARE00000827655	510	128.8	381.2
ENSDARE00000827926	186	41.2	144.8
ENSDARE00000828340	183	32.3	150.7
ENSDARE00000828481	183	53.8	129.2
ENSDARE00000828610	168	43	125
ENSDARE00000828878	141	23.7	117.3
ENSDARE00000829041	165	43.3	121.7

ENSDARE00000829341	138	38.7	99.3
ENSDARE00000830024	165	41.7	123.3
ENSDARE00000830343	180	43.2	136.8
ENSDARE00000830633	135	26.6	108.4
ENSDARE00000830916	198	49.8	148.2
ENSDARE00000831109	174	29.2	144.8
ENSDARE00000831113	177	32.1	144.9
ENSDARE00000831393	171	37.5	133.5
ENSDARE00000831838	201	49.1	151.9
ENSDARE00000832329	150	40.8	109.2
ENSDARE00000832789	1764	443.5	1320.5
ENSDARE00000833160	159	33.5	125.5
ENSDARE00000833305	264	62.9	201.1
ENSDARE00000833482	285	75.5	209.5
ENSDARE00000833793	294	80.8	213.2
ENSDARE00000833856	171	36.6	134.4
ENSDARE00000834049	156	46.9	109.1
ENSDARE00000834980	159	34.5	124.5
ENSDARE00000835905	159	35.2	123.8
ENSDARE00000836502	159	36.6	122.4
ENSDARE00000836834	252	68.8	183.2
ENSDARE00000836989	126	25.5	100.5
ENSDARE00000837186	174	42.4	131.6
ENSDARE00000837294	153	34.7	118.3
ENSDARE00000837639	171	46.5	124.5
ENSDARE00000838127	156	33.3	122.7
ENSDARE00000838329	189	42.2	146.8
ENSDARE00000838514	183	44.4	138.6
ENSDARE00000838794	204	54.2	149.8
ENSDARE00000838840	150	27.7	122.3
ENSDARE00000839011	162	26.6	135.4
ENSDARE00000839037	192	50.5	141.5
ENSDARE00000839081	177	27.5	149.5
ENSDARE00000839200	174	42.6	131.4
ENSDARE00000839263	147	38.1	108.9
ENSDARE00000839417	186	58.1	127.9
ENSDARE00000839475	228	56.3	171.7
ENSDARE00000839612	165	35	130
ENSDARE00000840333	159	55.9	103.1
ENSDARE00000840463	192	43.4	148.6
ENSDARE00000840477	159	40.8	118.2
ENSDARE00000841054	174	26.4	147.6

ENSDARE00000841136	195	48.4	146.6
ENSDARE00000841382	162	33	129
ENSDARE00000842080	159	41.7	117.3
ENSDARE00000842341	201	42	159
ENSDARE00000842702	162	55.6	106.4
ENSDARE00000842720	171	42.1	128.9
ENSDARE00000842722	153	46.1	106.9
ENSDARE00000842730	303	73.8	229.2
ENSDARE00000842970	213	62.6	150.4
ENSDARE00000843086	168	49.5	118.5
ENSDARE00000843309	135	30	105
ENSDARE00000843334	186	43.7	142.3
ENSDARE00000843492	666	166.1	499.9
ENSDARE00000843570	231	53.5	177.5
ENSDARE00000843714	174	35.4	138.6
ENSDARE00000843730	159	42	117
ENSDARE00000843812	228	46.8	181.2
ENSDARE00000843862	153	33.3	119.7
ENSDARE00000844002	189	32.9	156.1
ENSDARE00000844853	168	41.9	126.1
ENSDARE00000844876	363	109.7	253.3
ENSDARE00000845490	171	50.9	120.1
ENSDARE00000845596	147	33.5	113.5
ENSDARE00000845643	654	149.2	504.8
ENSDARE00000845764	147	31.9	115.1
ENSDARE00000845869	153	34.2	118.8
ENSDARE00000846016	660	176	484
ENSDARE00000846736	171	45.3	125.7
ENSDARE00000846776	168	28.2	139.8
ENSDARE00000847055	243	61.8	181.2
ENSDARE00000847084	168	42.3	125.7
ENSDARE00000847133	195	47.6	147.4
ENSDARE00000847255	222	40.9	181.1
ENSDARE00000848369	159	23.1	135.9
ENSDARE00000848654	207	42.7	164.3
ENSDARE00000848672	222	58.2	163.8
ENSDARE00000848699	192	24.9	167.1
ENSDARE00000848979	156	27.1	128.9
ENSDARE00000848998	177	41.8	135.2
ENSDARE00000849074	177	35.5	141.5
ENSDARE00000849207	183	37.3	145.7
ENSDARE00000849427	207	44.8	162.2

ENSDARE00000849593	150	36.9	113.1
ENSDARE00000849955	141	41	100
ENSDARE00000849972	156	38.1	117.9
ENSDARE00000849977	189	48.6	140.4
ENSDARE00000850269	189	47.9	141.1
ENSDARE00000850929	180	35	145
ENSDARE00000851126	123	37.9	85.1
ENSDARE00000851128	162	28.6	133.4
ENSDARE00000851512	183	45.7	137.3
ENSDARE00000851539	165	42.1	122.9
ENSDARE00000851682	153	34.6	118.4
ENSDARE00000851696	165	33.3	131.7
ENSDARE00000852106	162	21.2	140.8
ENSDARE00000852266	219	49.2	169.8
ENSDARE00000852603	144	33.4	110.6
ENSDARE00000852878	234	53	181
ENSDARE00000853503	129	21.1	107.9
ENSDARE00000854059	186	34	152
ENSDARE00000854326	165	47.3	117.7
ENSDARE00000854555	177	34.9	142.1
ENSDARE00000854915	162	38.2	123.8
ENSDARE00000854990	177	42.1	134.9
ENSDARE00000855476	186	30.5	155.5
ENSDARE00000856130	120	26.7	93.3
ENSDARE00000856390	165	29.1	135.9
ENSDARE00000856633	501	141.3	359.7
ENSDARE00000856857	189	36.3	152.7
ENSDARE00000857372	405	100.2	304.8
ENSDARE00000858832	153	32.8	120.2
ENSDARE00000858910	195	42.8	152.2
ENSDARE00000858953	195	37.2	157.8
ENSDARE00000858970	174	32.1	141.9
ENSDARE00000858979	126	29	97
ENSDARE00000859173	153	33.6	119.4
ENSDARE00000859291	177	42.4	134.6
ENSDARE00000859410	792	223.1	568.9
ENSDARE00000859927	174	29.2	144.8
ENSDARE00000860095	204	38.8	165.2
ENSDARE00000860252	159	34.3	124.7
ENSDARE00000860338	183	38.5	144.5
ENSDARE00000860702	213	49.5	163.5
ENSDARE00000861333	213	44.7	168.3

ENSDARE00000861379	165	36.3	128.7
ENSDARE00000861852	198	35.1	162.9
ENSDARE00000861925	141	32.8	108.2
ENSDARE00000862002	144	30.3	113.7
ENSDARE00000862055	153	37.1	115.9
ENSDARE00000862125	198	32.5	165.5
ENSDARE00000862658	330	66.9	263.1
ENSDARE00000862663	195	40.8	154.2
ENSDARE00000862912	207	50	157
ENSDARE00000863109	207	56.5	150.5
ENSDARE00000863323	171	36.4	134.6
ENSDARE00000863745	390	93.6	296.4
ENSDARE00000863766	726	189.1	536.9
ENSDARE00000864205	174	40.6	133.4
ENSDARE00000864404	153	38.3	114.7
ENSDARE00000864473	201	42.6	158.4
ENSDARE00000864664	156	40.2	115.8
ENSDARE00000865013	141	32.7	108.3
ENSDARE00000865311	129	33.9	95.1
ENSDARE00000865484	177	37.8	139.2
ENSDARE00000865566	192	39	153
ENSDARE00000865998	159	33.3	125.7
ENSDARE00000866016	126	27.8	98.2
ENSDARE00000866086	156	28.8	127.2
ENSDARE00000866149	159	40.4	118.6
ENSDARE00000866614	183	47.3	135.7
ENSDARE00000866755	165	36.1	128.9
ENSDARE00000867133	210	35.1	174.9
ENSDARE00000867912	264	47	217
ENSDARE00000867971	168	23.1	144.9
ENSDARE00000868720	156	40.8	115.2
ENSDARE00000869047	216	51.5	164.5
ENSDARE00000869051	138	22.6	115.4
ENSDARE00000869892	141	32	109
ENSDARE00000869900	162	43.5	118.5
ENSDARE00000869993	195	50.5	144.5
ENSDARE00000870665	180	40.2	139.8
ENSDARE00000870739	459	95.6	363.4
ENSDARE00000870882	171	37	134
ENSDARE00000871080	123	27.6	95.4
ENSDARE00000871192	186	44.7	141.3
ENSDARE00000871250	144	38.2	105.8

ENSDARE00000871433	264	43.4	220.6
ENSDARE00000871625	165	42.3	122.7
ENSDARE00000871626	168	43.9	124.1
ENSDARE00000871714	210	32.7	177.3
ENSDARE00000871986	576	154.3	421.7
ENSDARE00000872037	162	32.9	129.1
ENSDARE00000872202	147	24	123
ENSDARE00000873765	162	40	122
ENSDARE00000874287	171	34.6	136.4
ENSDARE00000874328	369	97.3	271.7
ENSDARE00000874675	186	44	142
ENSDARE00000874784	231	40.7	190.3
ENSDARE00000874860	168	36.5	131.5
ENSDARE00000875220	354	98.5	255.5
ENSDARE00000875533	177	45	132
ENSDARE00000875766	129	31.4	97.6
ENSDARE00000875799	159	27.3	131.7
ENSDARE00000876532	156	29.8	126.2
ENSDARE00000876657	123	35.2	87.8
ENSDARE00000877276	162	31.3	130.7
ENSDARE00000877773	213	55.1	157.9
ENSDARE00000878355	189	30.8	158.2
ENSDARE00000878713	150	30.8	119.2
ENSDARE00000879243	228	56.7	171.3
ENSDARE00000879257	156	32	124
ENSDARE00000879293	210	33.5	176.5
ENSDARE00000885922	174	38.3	135.7
ENSDARE00000886296	231	47.8	183.2
ENSDARE00000887651	222	56.9	165.1
ENSDARE00000887840	156	29.8	126.2
ENSDARE00000888203	195	40.5	154.5
ENSDARE00000888482	192	40.1	151.9
ENSDARE00000889689	153	40.3	112.7
ENSDARE00000890097	180	43.2	136.8
ENSDARE00000890536	204	38.8	165.2
ENSDARE00000890580	159	35.9	123.1
ENSDARE00000890630	216	41.5	174.5
ENSDARE00000891418	225	28.9	196.1
ENSDARE00000892955	168	34.4	133.6
ENSDARE00000893810	150	29.7	120.3
ENSDARE00000894372	213	39.1	173.9
ENSDARE00000894490	168	27.9	140.1

ENSDARE00000894712	171	34.7	136.3
ENSDARE00000895209	132	37.7	94.3
ENSDARE00000895680	237	66.3	170.7
ENSDARE00000896137	147	32	115
ENSDARE00000896354	183	22.6	160.4
ENSDARE00000896750	159	35.7	123.3
ENSDARE00000896933	204	37.6	166.4
ENSDARE00000898895	225	51.8	173.2
ENSDARE00000898918	213	54.9	158.1
ENSDARE00000898995	243	52.6	190.4
ENSDARE00000899093	156	36.4	119.6
ENSDARE00000899588	165	42	123
ENSDARE00000899783	141	36.5	104.5
ENSDARE00000900195	174	33.1	140.9
ENSDARE00000900330	249	55.3	193.7
ENSDARE00000900663	168	35.7	132.3
ENSDARE00000900948	183	38.3	144.7
ENSDARE00000901587	225	58.3	166.7
ENSDARE00000902062	132	23.1	108.9
ENSDARE00000902288	162	39.8	122.2
ENSDARE00000902729	222	46.6	175.4
ENSDARE00000902756	153	28.7	124.3
ENSDARE00000903114	120	19.3	100.7
ENSDARE00000903637	123	29	94
ENSDARE00000903870	228	42.6	185.4
ENSDARE00000903889	162	36.3	125.7
ENSDARE00000904318	204	50.4	153.6
ENSDARE00000904391	192	55.7	136.3
ENSDARE00000904535	144	29.9	114.1
ENSDARE00000905326	147	40.8	106.2
ENSDARE00000905670	291	68.5	222.5
ENSDARE00000906772	174	43	131
ENSDARE00000907316	180	26.6	153.4
ENSDARE00000907744	210	28.9	181.1
ENSDARE00000908151	174	37.4	136.6
ENSDARE00000908333	153	37	116
ENSDARE00000908534	168	26.9	141.1
ENSDARE00000908671	165	34.8	130.2
ENSDARE00000908822	291	64.6	226.4
ENSDARE00000909228	141	26.6	114.4
ENSDARE00000909467	234	60.8	173.2
ENSDARE00000909888	147	31.7	115.3

ENSDARE00000910087	228	46.2	181.8
ENSDARE00000910106	144	23.4	120.6
ENSDARE00000910233	177	36.6	140.4
ENSDARE00000910345	186	35.5	150.5
ENSDARE00000911821	180	40.9	139.1
ENSDARE00000911822	153	33.5	119.5
ENSDARE00000911979	150	29.5	120.5
ENSDARE00000913135	207	54.4	152.6
ENSDARE00000913273	141	29	112
ENSDARE00000913431	201	56.3	144.7
ENSDARE00000913727	171	49.1	121.9
ENSDARE00000913931	171	36.8	134.2
ENSDARE00000914404	237	57.2	179.8
ENSDARE00000914570	141	31.4	109.6
ENSDARE00000914613	150	21.7	128.3
ENSDARE00000914842	159	41.6	117.4
ENSDARE00000915604	192	35.7	156.3
ENSDARE00000915859	231	52.5	178.5
ENSDARE00000916402	153	33.2	119.8
ENSDARE00000916655	183	47.4	135.6
ENSDARE00000916846	156	29.9	126.1
ENSDARE00000917553	183	49.2	133.8
ENSDARE00000917741	123	23.2	99.8
ENSDARE00000917797	153	30.1	122.9
ENSDARE00000917924	267	59.4	207.6
ENSDARE00000918077	210	45.9	164.1
ENSDARE00000918202	165	44.5	120.5
ENSDARE00000918456	192	49.6	142.4
ENSDARE00000918805	153	40.3	112.7
ENSDARE00000918891	126	32	94
ENSDARE00000920084	198	40.1	157.9
ENSDARE00000920511	156	25.7	130.3
ENSDARE00000921298	156	36.1	119.9
ENSDARE00000921455	177	46.8	130.2
ENSDARE00000921553	198	37	161
ENSDARE00000922069	192	44.5	147.5
ENSDARE00000922088	186	32	154
ENSDARE00000922870	678	153.3	524.7
ENSDARE00000922979	162	23.6	138.4
ENSDARE00000923089	213	52.1	160.9
ENSDARE00000923574	186	47.8	138.2
ENSDARE00000923673	183	53.6	129.4

ENSDARE00000924161	180	31.9	148.1
ENSDARE00000924510	237	47.1	189.9
ENSDARE00000924926	171	29.6	141.4
ENSDARE00000925418	174	36.9	137.1
ENSDARE00000925844	207	33.5	173.5
ENSDARE00000925931	150	41.4	108.6
ENSDARE00000926275	138	29.6	108.4
ENSDARE00000926491	408	94.9	313.1
ENSDARE00000926701	153	46.5	106.5
ENSDARE00000927706	246	58	188
ENSDARE00000927805	189	38	151
ENSDARE00000927911	189	31.5	157.5
ENSDARE00000928006	162	26.5	135.5
ENSDARE00000928698	156	32.4	123.6
ENSDARE00000928900	192	41	151
ENSDARE00000929152	183	40.8	142.2
ENSDARE00000929498	162	38.5	123.5
ENSDARE00000929960	174	42.3	131.7
ENSDARE00000930022	180	39.2	140.8
ENSDARE00000930089	210	46.1	163.9
ENSDARE00000930718	177	43.6	133.4
ENSDARE00000930829	162	44.8	117.2
ENSDARE00000931208	165	38.8	126.2
ENSDARE00000931608	129	30.3	98.7
ENSDARE00000931765	213	51.9	161.1
ENSDARE00000932691	192	32.2	159.8
ENSDARE00000932793	210	43.4	166.6
ENSDARE00000933176	195	43.1	151.9
ENSDARE00000933274	180	26.2	153.8
ENSDARE00000933693	150	42.5	107.5
ENSDARE00000933706	225	55	170
ENSDARE00000936053	165	34	131
ENSDARE00000936148	228	49.9	178.1
ENSDARE00000936574	225	48.3	176.7
ENSDARE00000936724	147	33.1	113.9
ENSDARE00000936760	264	48.5	215.5
ENSDARE00000936881	159	45.6	113.4
ENSDARE00000937011	186	42.8	143.2
ENSDARE00000937190	180	39.8	140.2
ENSDARE00000937296	498	87.2	410.8
ENSDARE00000937479	150	31.9	118.1
ENSDARE00000937643	189	48.4	140.6

ENSDARE00000937708	192	49	143
ENSDARE00000938070	162	35.9	126.1
ENSDARE00000938436	162	39.7	122.3
ENSDARE00000938836	207	43.9	163.1
ENSDARE00000938892	231	45.7	185.3
ENSDARE00000938907	195	61	134
ENSDARE00000940014	156	33.7	122.3
ENSDARE00000940396	174	37.6	136.4
ENSDARE00000940413	177	25.1	151.9
ENSDARE00000941272	204	55.4	148.6
ENSDARE00000941898	159	32.9	126.1
ENSDARE00000942042	147	32.4	114.6
ENSDARE00000942567	183	33.5	149.5
ENSDARE00000942646	162	29.2	132.8
ENSDARE00000943340	144	32.6	111.4
ENSDARE00000943582	132	23.8	108.2
ENSDARE00000943995	213	47.3	165.7
ENSDARE00000944141	177	38.5	138.5
ENSDARE00000944152	174	38.4	135.6
ENSDARE00000944381	234	54.2	179.8
ENSDARE00000944430	147	34.5	112.5
ENSDARE00000944476	456	93.7	362.3
ENSDARE00000944614	156	28.3	127.7
ENSDARE00000945102	147	33.2	113.8
ENSDARE00000946025	162	38.7	123.3
ENSDARE00000946861	162	42.9	119.1
ENSDARE00000947692	171	38.1	132.9
ENSDARE00000947852	219	56.1	162.9
ENSDARE00000948339	153	34.7	118.3
ENSDARE00000948752	177	39.3	137.7
ENSDARE00000949063	132	33.4	98.6
ENSDARE00000949089	168	33.9	134.1
ENSDARE00000950013	120	31.7	88.3
ENSDARE00000950073	159	32.1	126.9
ENSDARE00000950368	171	31.9	139.1
ENSDARE00000950883	162	33.3	128.7
ENSDARE00000951279	165	24.5	140.5
ENSDARE00000952007	219	61.8	157.2
ENSDARE00000952025	183	46.7	136.3
ENSDARE00000952037	150	36.8	113.2
ENSDARE00000952051	147	29.4	117.6
ENSDARE00000952054	171	46	125

ENSDARE00000952085	342	76.3	265.7
ENSDARE00000952289	120	26	94
ENSDARE00000952304	246	51.9	194.1
ENSDARE00000952441	177	28.5	148.5
ENSDARE00000952657	159	34.9	124.1
ENSDARE00000953313	150	27	123
ENSDARE00000953981	225	41.4	183.6
ENSDARE00000954210	240	38.8	201.2
ENSDARE00000954305	156	40.3	115.7
ENSDARE00000954362	366	57	309
ENSDARE00000955520	168	34.8	133.2
ENSDARE00000955823	186	27.6	158.4
ENSDARE00000955876	150	41.7	108.3
ENSDARE00000956594	192	42.9	149.1
ENSDARE00000956801	363	97	266
ENSDARE00000956846	174	34.7	139.3
ENSDARE00000957211	282	38.2	243.8
ENSDARE00000957300	168	34.8	133.2
ENSDARE00000957385	165	42.4	122.6
ENSDARE00000958591	141	34.6	106.4
ENSDARE00000959487	150	37.1	112.9
ENSDARE00000960098	150	38.6	111.4
ENSDARE00000961039	444	85.6	358.4
ENSDARE00000961180	159	37.8	121.2
ENSDARE00000961987	222	44.3	177.7
ENSDARE00000962853	183	50.2	132.8
ENSDARE00000963124	186	27.6	158.4
ENSDARE00000963225	177	47.2	129.8
ENSDARE00000963369	384	78.8	305.2
ENSDARE00000964380	261	64	197
ENSDARE00000964891	150	32.6	117.4
ENSDARE00000965053	156	28.6	127.4
ENSDARE00000965088	183	44.9	138.1
ENSDARE00000965346	201	35.8	165.2
ENSDARE00000965578	129	34.3	94.7
ENSDARE00000966090	222	30	192
ENSDARE00000967506	159	33.9	125.1
ENSDARE00000967963	156	45.2	110.8
ENSDARE00000968081	162	39.4	122.6
ENSDARE00000968248	162	36.5	125.5
ENSDARE00000968490	186	49.2	136.8
ENSDARE00000968805	246	55.3	190.7

ENSDARE00000969266	237	58.1	178.9
ENSDARE00000969878	183	56.9	126.1
ENSDARE00000970000	174	37.3	136.7
ENSDARE00000970259	174	35	139
ENSDARE00000971065	129	29.2	99.8
ENSDARE00000971196	171	44.3	126.7
ENSDARE00000971525	144	32.5	111.5
ENSDARE00000971964	189	42.6	146.4
ENSDARE00000972047	498	129	369
ENSDARE00000972592	228	62.1	165.9
ENSDARE00000973010	177	30.7	146.3
ENSDARE00000973123	180	41.7	138.3
ENSDARE00000974248	150	32.2	117.8
ENSDARE00000974677	198	30.9	167.1
ENSDARE00000974859	153	32.6	120.4
ENSDARE00000974895	180	36.1	143.9
ENSDARE00000975067	231	40.1	190.9
ENSDARE00000975137	177	33.3	143.7
ENSDARE00000975486	147	29	118
ENSDARE00000977029	150	42.7	107.3
ENSDARE00000978211	165	33.9	131.1
ENSDARE00000978344	213	49.5	163.5
ENSDARE00000978552	237	33.2	203.8
ENSDARE00000978746	180	36.1	143.9
ENSDARE00000979167	189	40.1	148.9
ENSDARE00000980789	201	30.9	170.1
ENSDARE00000980893	150	29	121
ENSDARE00000981088	186	36.8	149.2
ENSDARE00000981217	159	34.3	124.7
ENSDARE00000981762	195	48.1	146.9
ENSDARE00000981851	258	40.8	217.2
ENSDARE00000982107	378	91.8	286.2
ENSDARE00000983648	183	37.3	145.7
ENSDARE00000983901	147	47.4	99.6
ENSDARE00000983921	243	51.3	191.7
ENSDARE00000985885	270	47.1	222.9
ENSDARE00000986356	180	32.9	147.1
ENSDARE00000986742	201	44.9	156.1
ENSDARE00000987684	192	38.8	153.2
ENSDARE00000988771	153	21.1	131.9
ENSDARE00000988844	156	32	124
ENSDARE00000990724	159	35.2	123.8

ENSDARE00000991833	147	49.8	97.2
ENSDARE00000991951	240	50.3	189.7
ENSDARE00000992140	273	42.1	230.9
ENSDARE00000992597	234	39.4	194.6
ENSDARE00000992963	186	38.1	147.9
ENSDARE00000995416	261	60.7	200.3
ENSDARE00000997219	222	44	178
ENSDARE00000997405	174	38.2	135.8
ENSDARE00000997751	207	41.5	165.5
ENSDARE00000997883	177	40	137
ENSDARE00000997999	198	39.9	158.1
ENSDARE00000998041	210	49.8	160.2
ENSDARE00000998218	180	43.4	136.6
ENSDARE00000998815	195	43.5	151.5
ENSDARE00000998915	459	98.4	360.6
ENSDARE00000999465	183	35.5	147.5
ENSDARE00001000184	300	88.2	211.8
ENSDARE00001004934	150	42.1	107.9
ENSDARE00001009096	171	36.2	134.8
ENSDARE00001011215	150	34.4	115.6
ENSDARE00001013968	132	28.1	103.9
ENSDARE00001015043	159	46	113
ENSDARE00001015287	237	41.2	195.8
ENSDARE00001015417	204	41.3	162.7
ENSDARE00001015641	201	45	156
ENSDARE00001017465	168	30	138
ENSDARE00001017982	234	46.8	187.2
ENSDARE00001018537	198	54.4	143.6
ENSDARE00001019419	531	148.5	382.5
ENSDARE00001020850	243	41.7	201.3
ENSDARE00001022236	144	38	106
ENSDARE00001023679	162	44.1	117.9
ENSDARE00001023925	195	45.5	149.5
ENSDARE00001024423	225	67.6	157.4
ENSDARE00001025754	159	36.4	122.6
ENSDARE00001027176	177	39.9	137.1
ENSDARE00001028933	183	36.7	146.3
ENSDARE00001030842	195	49.8	145.2
ENSDARE00001031756	213	43	170
ENSDARE00001032919	216	56.5	159.5
ENSDARE00001033342	132	20.2	111.8
ENSDARE00001034027	165	29.7	135.3

ENSDARE00001034157	207	38.1	168.9
ENSDARE00001035096	207	47.3	159.7
ENSDARE00001036844	147	39.3	107.7
ENSDARE00001037880	168	37.6	130.4
ENSDARE00001039509	147	25.1	121.9
ENSDARE00001041332	147	36.3	110.7
ENSDARE00001045381	138	32.8	105.2
ENSDARE00001048933	300	69.9	230.1
ENSDARE00001050052	168	40.4	127.6
ENSDARE00001051767	162	38.6	123.4
ENSDARE00001052212	168	34.6	133.4
ENSDARE00001055477	150	30.3	119.7
ENSDARE00001055696	255	65.4	189.6
ENSDARE00001058263	162	32.9	129.1
ENSDARE00001059227	192	42.8	149.2
ENSDARE00001059482	132	26.6	105.4
ENSDARE00001096846	189	44.3	144.7
ENSDARE00001103899	162	47.4	114.6
ENSDARE00001103965	153	28.1	124.9
ENSDARE00001105279	165	37.1	127.9
ENSDARE00001106157	162	32.1	129.9
ENSDARE00001106579	165	26.6	138.4
ENSDARE00001106867	159	38.2	120.8
ENSDARE00001107617	150	46.9	103.1
ENSDARE00001108087	120	32.9	87.1
ENSDARE00001109237	216	49.5	166.5
ENSDARE00001109606	183	33.1	149.9
ENSDARE00001109668	207	29.5	177.5
ENSDARE00001109720	162	28.3	133.7
ENSDARE00001110191	294	57.4	236.6
ENSDARE00001112120	162	48.1	113.9
ENSDARE00001112216	183	35.2	147.8
ENSDARE00001112373	555	121.8	433.2
ENSDARE00001113159	180	27.2	152.8
ENSDARE00001113164	153	30.2	122.8
ENSDARE00001113432	177	39.2	137.8
ENSDARE00001114068	150	34.1	115.9
ENSDARE00001114072	135	33.4	101.6
ENSDARE00001114321	246	35.1	210.9
ENSDARE00001114558	180	36.2	143.8
ENSDARE00001114709	165	45.3	119.7
ENSDARE00001114771	162	41	121

ENSDARE00001115145	159	41.7	117.3
ENSDARE00001115461	126	32	94
ENSDARE00001115467	243	52.5	190.5
ENSDARE00001115898	195	39.6	155.4
ENSDARE00001115950	150	38.3	111.7
ENSDARE00001116342	135	32.1	102.9
ENSDARE00001116400	162	41.9	120.1
ENSDARE00001116563	138	32.8	105.2
ENSDARE00001117046	183	32.6	150.4
ENSDARE00001117049	168	35.9	132.1
ENSDARE00001117370	165	44.5	120.5
ENSDARE00001117823	219	33.8	185.2
ENSDARE00001117971	144	33.3	110.7
ENSDARE00001118009	162	32	130
ENSDARE00001118059	189	43.9	145.1
ENSDARE00001118698	171	40.4	130.6
ENSDARE00001119059	162	46	116
ENSDARE00001119113	222	40.4	181.6
ENSDARE00001120012	153	44.6	108.4
ENSDARE00001120089	186	45.7	140.3
ENSDARE00001120437	171	36.2	134.8
ENSDARE00001121821	252	72.9	179.1
ENSDARE00001121868	459	125.7	333.3
ENSDARE00001121992	174	36.5	137.5
ENSDARE00001122021	186	37.1	148.9
ENSDARE00001122505	132	25.5	106.5
ENSDARE00001123458	153	28.4	124.6
ENSDARE00001123630	168	30.4	137.6
ENSDARE00001124287	138	38.8	99.2
ENSDARE00001124494	192	45.7	146.3
ENSDARE00001124527	171	28	143
ENSDARE00001124623	183	34	149
ENSDARE00001125825	210	39.1	170.9
ENSDARE00001128075	147	37.7	109.3
ENSDARE00001128145	219	35.9	183.1
ENSDARE00001128832	168	43.2	124.8
ENSDARE00001129008	147	42.1	104.9
ENSDARE00001129743	273	53.7	219.3
ENSDARE00001129760	186	47.9	138.1
ENSDARE00001129947	141	33.3	107.7
ENSDARE00001130422	210	35.9	174.1
ENSDARE00001131183	168	35.1	132.9

ENSDARE00001131185	171	19.8	151.2
ENSDARE00001131272	162	38.1	123.9
ENSDARE00001131346	291	71.3	219.7
ENSDARE00001132971	153	40.5	112.5
ENSDARE00001135126	198	47.9	150.1
ENSDARE00001136989	216	61.1	154.9
ENSDARE00001139078	165	26.6	138.4
ENSDARE00001140362	186	37.6	148.4
ENSDARE00001142165	180	39.6	140.4
ENSDARE00001142628	261	33.9	227.1
ENSDARE00001144758	144	44.9	99.1
ENSDARE00001146931	198	39	159
ENSDARE00001148110	225	48.9	176.1

134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150