

Online Supplementary Material

SUPPLEMENTARY METHODS

Estimating the Beavis effect.

We estimated the influence of the Beavis effect on the distribution of effect sizes with a parametric bootstrap procedure. Each bootstrap replicate involved the following steps.

First, we chose an effect size by randomly sampling an observation from the gamma distribution that best fit the empirical distribution of positive effect sizes in the data (Figure 4). Second, we chose a location for the QTL on the stickleback linkage map (Supplementary Figure S1) by randomly sampling a linkage group with probability proportional to group length (distance in cM between tip markers) and then choosing a location on this group using a uniform random number generator.

Third, we simulated a distribution of genotypes and phenotypes (single trait) in an F₂ cross for the single QTL using the `sim.cross` function in `Rqtl` 1.05-2 (Broman et al. 2003). The number of individuals in the cross was the same as that in the original data. We assumed that there were four unique genotypes at the QTL. AC and BD refer to the "pure" genotype combinations of the grandparents (two marine alleles A and C and two benthic alleles B and D). The mean for AC was set to zero and the mean for BD was fixed at the effect size obtained from the gamma distribution. The two other genotypes, AD and BC, refer to the mixed genotype combinations (having one marine allele and one benthic allele). The phenotype mean of both these genotypes was set to the average of the means of genotypes AC and BD.

1
2 The phenotype of each individual in the cross was modeled as the mean for its genotype
3 at the QTL locus plus a random residual. The residual was sampled from a normal
4 distribution having mean zero and a variance that depended on the effect size. The
5 variance of the residual was calculated using the observed relationship between the
6 effect sizes of QTL detected in the data for all traits and the unexplained variance from
7 the QTL mapping model. The unexplained variance is the total phenotypic variance of
8 the given trait multiplied by $(1 - \text{percent variance explained})$. We observed that
9 unexplained variance increased with QTL effect size in the data as a power function (Y
10 $= aX^b$), where $a = 0.50 \pm 0.07$ SE, and $b = 1.32 \pm 0.12$ SE. The residual variance for a
11 given individual was calculated from this power function. We explored the consequence
12 of adding an additional random term to the variance calculated using the above power
13 formula, to account for the greater heterogeneity of values for the unexplained variance
14 in the data when effect sizes were greater. However, this did not change the results and
15 we do not present them.

16
17 Fourth, we carried out QTL mapping on the simulated cross and "re-estimated" the
18 effect size of the largest QTL detected on the same linkage group as that chosen by the
19 random sampling process. We used the same LOD threshold as was used when
20 analyzing the original data (4.5).

21
22 Each of the four steps described above was procedure was repeated 500 times. In each
23 bootstrap replicate we recorded whether the simulated QTL was detected or not. If it

1 was detected, then we also recorded its re-estimated effect size. Simulation results were
2 analyzed using R (R Development Core Team 2007).

3

4 In Figure S2 we plot the re-estimated effect size against the "true" effect size of
5 simulated QTL. As the figure shows, the effect sizes of QTL of small effect that were
6 subsequently detected are slightly overestimated, on average, a reflection of the Beavis
7 effect. Note that the lower slope of the solid line in Figure S2, compared to the line of
8 equality $Y = X$, isn't an artifact of "regression toward the mean" (Kelly and Price 2005)
9 because the true effects are fixed in the simulation process.

10

11 *Estimating the probability of QTL detection.*

12 The results from the above simulation can also be used to estimate the probability of
13 QTL detection. A simulated QTL was given a score of 1 if it was subsequently detected
14 and a score of 0 otherwise. Detection score is plotted against the "true" effect size in
15 Figure S3. A logistic regression was fitted to these data to predict probability of
16 detection as a function of true effect size ($\ln(Y/1-Y) = a + b X$, where $a = -1.42 \pm 0.35$
17 SE and $b = 17.50 \pm 2.28$).

18

19

SUPPLEMENTARY REFERENCES

- 1
- 2 Broman, K. W., H. Wu, S. Sen, and G. A. Churchill. 2003. R/qtl: QTL mapping in
3 experimental crosses. *Bioinformatics* 19:889-880.
- 4 Kelly, C. and T. D. Price. 2005. Correcting for regression to the mean in behavior and
5 ecology. *American Naturalist* 166: 700–707.
- 6 R Development Core Team. 2007. R: A language and environment for statistical
7 computing. R Foundation for Statistical Computing, Vienna, Austria.
8 <http://www.R-project.org>.

SUPPLEMENTARY FIGURES

- 1
- 2 Figure S1. Linkage map used in QTL mapping. The number of linkage groups (LG)
- 3 corresponds to the known haploid number of chromosomes in stickleback (21).
- 4
- 5 Figure S2. Evaluation of the Beavis effect using the bootstrap. Each point indicates the
- 6 "true" and re-estimated effect size of a single QTL randomly placed on the linkage map.
- 7 The dashed line is $Y = X$. The solid line is the regression of re-estimated effects on true
- 8 effects ($Y = 0.026 + 0.92X$, with SE for intercept and slope 0.004 and 0.019,
- 9 respectively). The slight overestimation of effect sizes of detected QTL of small effect
- 10 represents a Beavis effect.
- 11
- 12 Figure S3. Estimated probability of detection of QTL with effect size. Symbols indicate
- 13 whether a QTL of specified effect size was subsequently detected (1) or not (0).
- 14 Detection score is jittered to reduce overlap of points. The curve is the best-fit logistic
- 15 regression. $n = 500$.

Figure S1

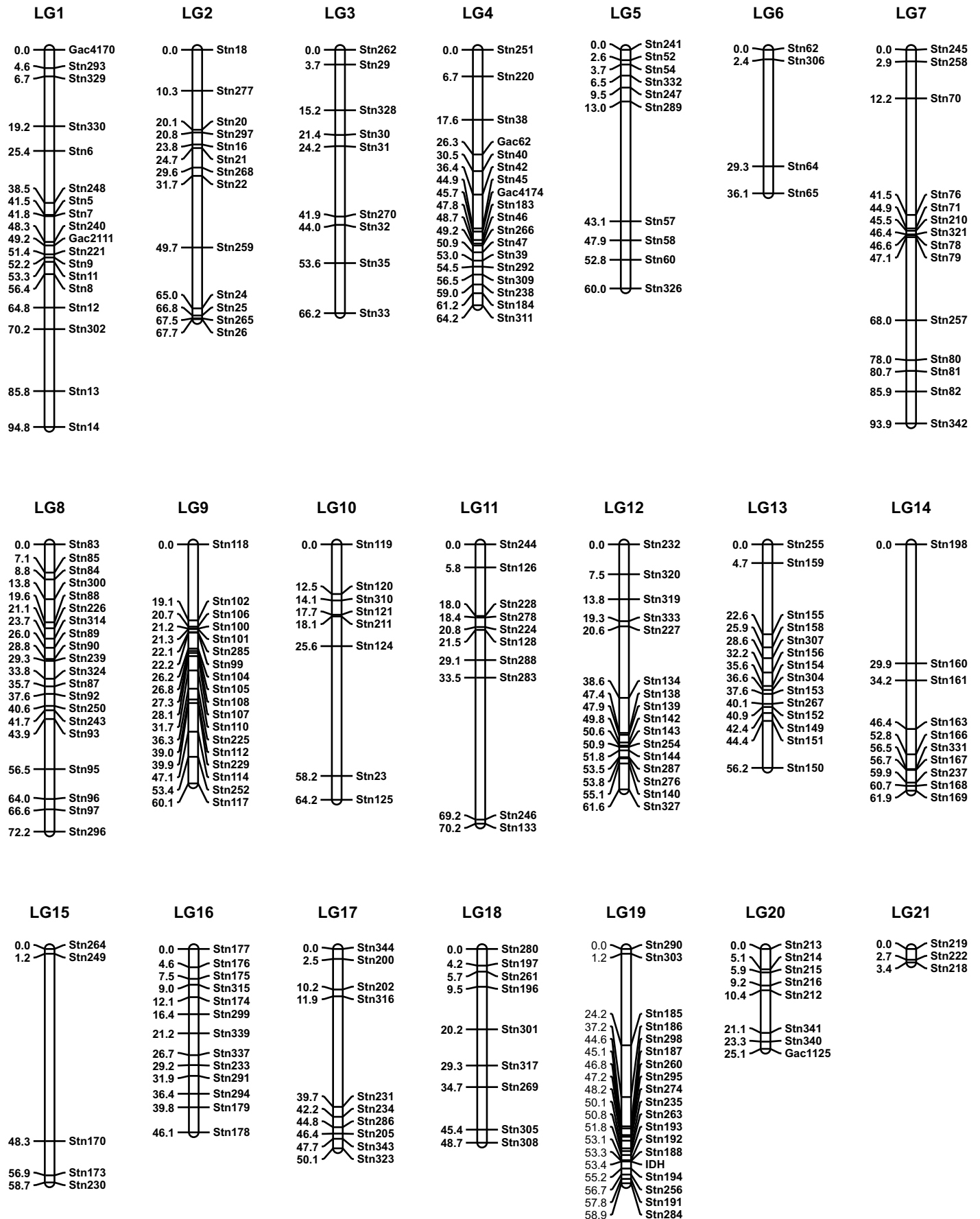


Figure S2

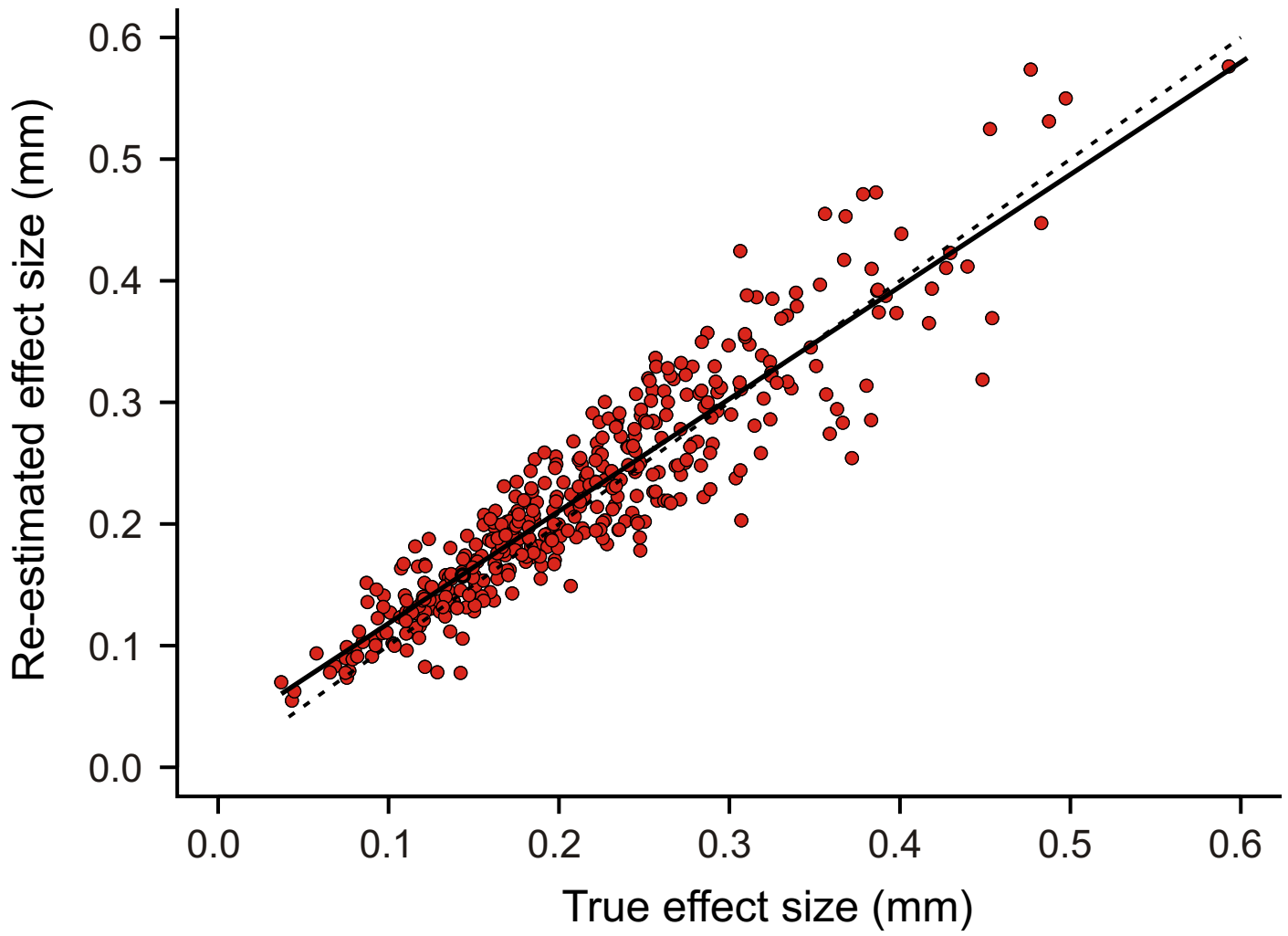
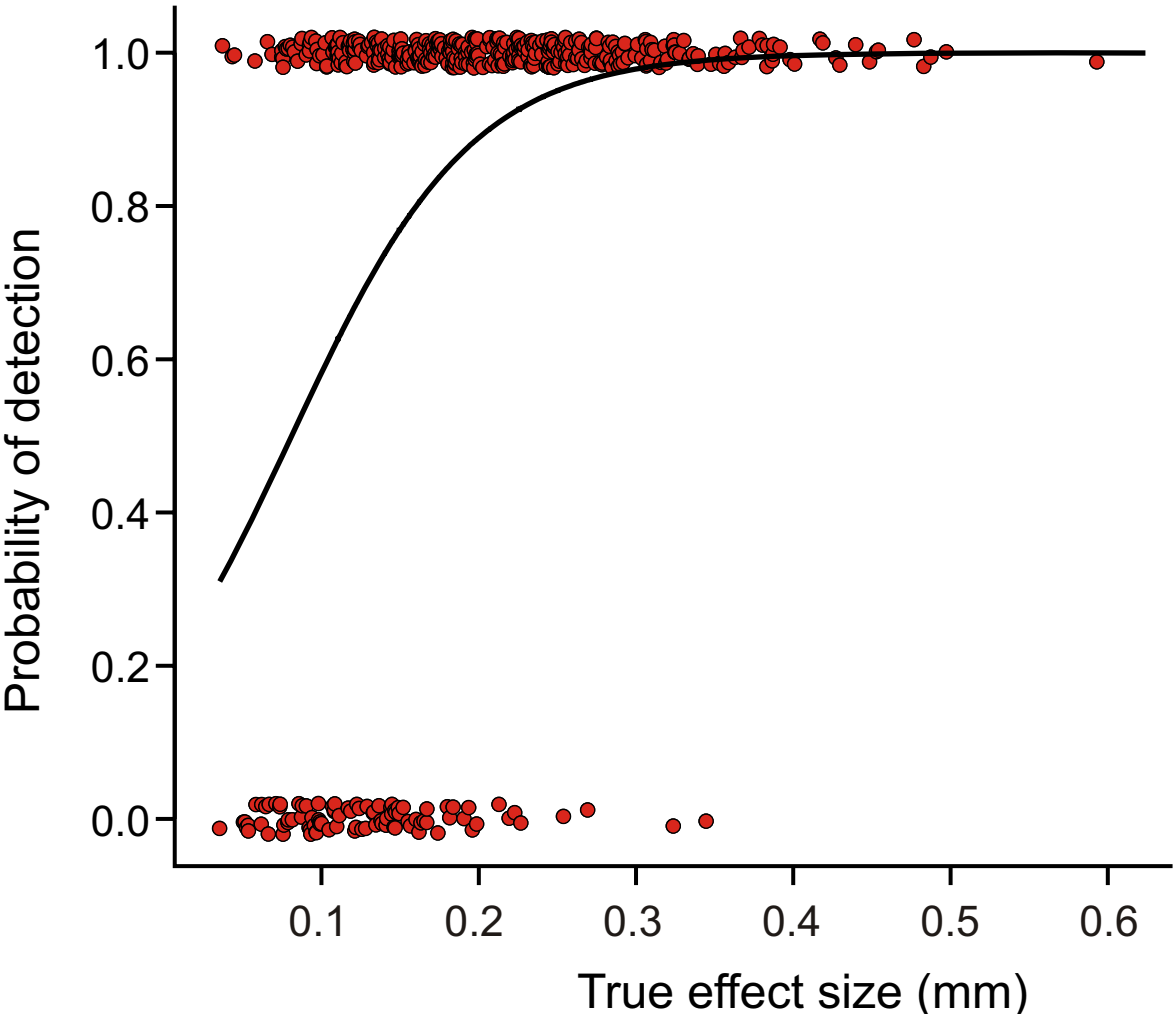


Figure S3



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SUPPLEMENTARY TABLE

2 Table S1. QTL from MQM mapping of all 54 landmark coordinates. Effects marked
 3 with a (-) are for coordinates associated with the pelvic girdle, which is absent in the
 4 Paxton benthics.

Linkage Group	QTL	Marker (locus nearest QTL)	Landmark coordinates affected	LOD score	Percent Variance Explained (PVE)	Individual effect and direction (mm)	Total effect size (Euclidean distance in mm)
1	1a	Stn5	x8	6.83	7.9	0.34	0.36
			y5	8.36	4.4	-	
			y16	7.18	8.0	-0.11	
1	1b	Stn221	x1	8.82	9.4	0.46	0.63
			x3	9.11	7.7	0.31	
			x5	8.21	6.5	-	
			x14	4.75	5.8	0.15	
			x22	5.1	5.9	-0.10	
			x26	4.5	4.5	0.19	
			y25	6.58	5.9	0.10	
2	2a	Stn259	x25	6.47	7.6	-0.22	0.22
3	3a	Stn270	x26	8.52	8.6	0.28	0.34
			y27	6.7	6.9	-0.19	
4	4a	Stn220	y5	5.23	3.2	-	-

4	4b	Gac4174	x4	5.54	5.1	-	0.53
			x10	8.53	6.1	0.19	
			x23	6.07	6.9	0.23	
			x24	16.75	13.4	0.36	
			y6	5.38	5.1	-0.13	
			y12	6.01	7.4	-0.14	
			y15	6.4	6.6	0.10	
			y16	8.51	8.5	0.12	
4	4c	Stn292	x5	5.43	4.2	-	0.25
			y11	5.11	6.1	-0.17	
			y5	4.88	2.5	-	
			y7	4.54	4.9	0.13	
			y23	5.32	4.9	0.14	
4	4d	Stn184	y14	17.76	18.1	0.27	0.27
5	5a	Stn60	x8	4.65	5.4	-0.27	0.27
7	7a	Stn321	x3	4.72	3.8	0.22	0.67
			x6	12.44	9.7	-0.30	
			x7	8.7	8.9	-0.23	
			x9	9.02	7.2	0.18	
			x10	4.76	3.2	0.16	
			x16	5.59	5.3	0.14	
			x17	5.22	3.6	0.14	
			x24	12.98	10.1	0.31	

			y8	7.69	7.5	0.21	
			y16	5.82	5.6	-0.10	
			y19	5.91	6.8	0.10	
7	7b	Stn342	x4	14.51	14.6	-	-
			x5	10.17	8.5	-	
			y4	6.63	6.6	-	
			y5	36.55	24.8	-	
8	8a	Stn85	x6	6.34	4.9	0.21	0.21
9	9a	Stn102	y5	4.94	2.8	-	-
12	12a	Stn143	x4	5.67	5.2	-	0.60
			x5	12.53	10.3	-	
			x9	6.05	4.8	0.14	
			x13	11.41	11.6	0.20	
			x26	6.72	7.7	0.23	
			y4	7.65	7.7	-	
			y5	6.48	4.1	-	
			y6	10.15	10.0	0.20	
			y7	10.17	12.2	0.21	
			y24	9.13	10.0	0.22	
			y25	13.57	12.4	0.24	
			y26	12.22	13.5	0.25	
13	13a	Stn149	x20	6.8	7.8	-0.09	0.09
15	15a	Stn170	x25	5.35	6.5	-0.21	0.21

16	16a	Stn174	x16	4.81	4.9	0.08	0.20
			y10	4.87	5.8	0.15	
			y17	4.67	5.6	0.10	
16	16b	Stn233	y11	4.73	5.4	0.11	0.11
16	16c	Stn178	x6	4.9	4.1	-0.15	0.20
			x15	5.52	6.9	0.13	
17	17a	Stn323	y5	6.26	3.6	-	-
18	18a	Stn280	y4	9.64	9.6	-	0.15
			y26	6.45	6.7	0.15	
18	18b	Stn261	y6	5.33	5.1	0.15	0.20
			y25	8.53	7.7	0.14	
18	18c	Stn317	x5	5.69	4.5	-	0.36
			x6	6.35	5.7	-0.22	
			x7	5.26	5.5	-0.17	
			x15	4.49	6.3	0.16	
			y8	5.56	5.7	0.17	
19	19	IDH	x2	5.14	6.4	0.38	1.23
			x3	25.23	23.4	0.47	
			x5	9.07	7.3	-	
			x6	11.8	9.3	-0.19	
			x7	9.07	9.4	-0.19	
			x9	21.71	19.0	0.21	
			x10	36.09	30.2	0.36	

x11	20.14	22.7	0.22
x12	16.21	18.8	0.20
x13	18.82	18.1	0.23
x16	7.12	7.6	0.10
x17	41.52	36.0	0.41
x18	25.74	28.0	0.27
x19	22.61	25.2	0.15
x20	4.99	5.7	0.05
x22	6.69	7.9	0.08
x23	8.79	10.0	0.05
x27	5.49	6.2	0.30
y3	7.77	9.5	0.21
y4	5.42	5.3	-
y6	8.29	8.1	0.16
y8	15.22	15.8	0.27
y14	14.02	13.1	0.17
y15	4.91	5.1	0.08
y18	7.33	9.0	0.15
y19	5.82	6.8	0.10
y20	13.53	15.9	0.10
y23	22.92	23.7	0.25
y24	9.8	11.0	0.23
y27	8.14	8.5	0.17

21	21a	Stn216	x1	7.79	8.2	0.43	0.79
			x6	9.85	7.8	0.22	
			x9	6.63	5.3	0.14	
			x24	6.32	4.8	0.21	
			x27	7.76	8.9	0.54	
			y5	7.82	4.3	-	
			y27	6.97	7.3	0.20	
22	22a	Stn219	x17	5.79	4.5	0.18	0.42
			x24	12.81	11.6	0.32	
			y15	5.16	6.5	0.09	
			y25	7.81	7.8	0.19	
