Comparison of TreeBLOSSIM predictions with PhotoMARVL data:
FR8 (Tahorakuri), FR10 (Glengarry), FR54 (Mamaranui) and FR84 (Kawerau)

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Executive Summary

TreeBLOSSIM is an integrated tree and branch growth model for radiata pine. Given the limited database used to develop the branch model within TreeBLOSSIM, it is important to determine the performance of the model for a wide range of sites throughout New Zealand. To this end a non-destructive, ground-based photogrammetric method (PhotoMARVL / TreeD) is being used to provide branching data for comparison with TreeBLOSSIM predictions.

This report documents the performance of TreeBLOSSIM for four SGMC trials, FR8, FR10, FR54 and FR84:

- FR8 was planted in Tahorakuri Forest in 1987 to be representative of a medium site index in the Central North Island.
- FR10 was planted in Glengarry Forest in 1987 to be representative of a high basal area site in Hawkes Bay, North Island.
- FR54 was planted in Mamaranui Forest in 1988 to be representative of a high basal area site the Auckland Clays area of the North Island.
- FR84 was planted in Kawerau Forest in 1989 to be representative of a high basal area site in the Central North Island.

The results illustrate that the model performance is acceptable for many trees but that there is room for model improvements. In particular the model:

- Adequately captured the variability between trees within a plot for these trials
- Adequately captured the effect of silviculture for 3 of the 4 trials
- Performed equally well for all Growth and Form seedlots even though the functions were derived using GF14 data

The issues identified for future improvements include:

- Development of a separate model for Long Internode Seedlots as TreeBLOSSIM did not perform as well for this seedlot
- Revision of the functions accounting for the effects of stocking

Comparison of TreeBLOSSIM predictions with PhotoMARVL data: FR8(Tahorakuri), FR10(Glengarry), FR54(Mamaranui) and FR84(Kawerau)

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INTRODUCTION

TreeBLOSSIM is an integrated tree and branch growth model for radiata pine. The branching functions in Version 3 (see SGMC Report No. 125) are specifically for GF14 seedlots and were developed from destructively sampling a few radiata pine trees at a limited number of sites throughout New Zealand.

Given the limited database used to develop TreeBLOSSIM, it is important to determine the performance of the model for a wide range of sites throughout New Zealand. To this end a non-destructive, ground-based photogrammetric method (PhotoMARVL / TreeD (see Firth *et al.*, 2000; Brownlie *et al.*, 2007) is being used to provide data for comparison with TreeBLOSSIM predictions.

Two strategies are being used for data collection. One approach is to use SGMC trials. This allows TreeBLOSSIM to be tested across a range of silvicultural treatments and genetically improved seedlots at one site. The second approach is to use individual PSPs within a growth modelling region. This allows TreeBLOSSIM to be tested across a wider range of site conditions.

This report examines the performance of TreeBLOSSIM for four SGMC trials FR8, FR10, FR54 and FR84 using PhotoMARVL data collected in 2003-4:

- FR8 was planted in Tahorakuri Forest in 1987 to be representative of a medium site index in the Central North Island.
- FR10 was planted in Glengarry Forest in 1987 to be representative of a high basal area site in Hawkes Bay, North Island.
- FR54 was planted in Mamaranui Forest in 1988 to be representative of a high basal area site the Auckland Clays area of the North Island.
- FR84 was planted in Kawerau Forest in 1989 to be representative of a high basal area site in Central North Island.

Further details on the design and layout of these trial series are given in SGMC Reports Nos. 100 and 103.

METHODS

<u>Alternative Methods To Select Sample Trees</u>

Several alternative methods for selecting the sample trees were considered.

1. In previous PhotoMARVL studies, all the trees in the PSP have been ranked according to DBH and sample trees selected at given percentage ranks, i.e:
   - if there are n trees in the plot, then the ranks are 1….n
   - the percentage rank for j^{th} tree is $100 \times j/n$

   This gave values between $100 \times 1/n$ and 100.

2. A percentage rank was calculated based on the DBH of the sample tree relative to the maximum and minimum DBH in the plot, i.e. for the j^{th} tree, the percentage rank would be:
   - $100 \times (DBH_j - DBH_{min}) / (DBH_{max} - DBH_{min})$

   This gave values between 0 and 100.

3. A standardised DBH was calculated using the mean and standard deviation of the DBH distribution within the plot, i.e.
   - $(DBH_j - \mu) / \sigma$ where μ is the plot mean DBH and σ is the standard deviation

   The maximum and minimum values of this standardised DBH were dependent on the variation in DBH within the plot.

After consideration of these alternatives, method 1 was considered the most appropriate.

<u>Selection of Sample Trees</u>

These experiments generally have 2 or 3 replications of the same treatment. In some instances there was only one replication due to unscheduled silvicultural treatments. The first stage was to select which plot should be used for each treatment.

This was done by:
- Examining the stocking within the plots, to determine how well the plots matched the prescribed treatment.

The initial stocking was quite variable. There was also tree mortality in some plots.

Wood density increment cores have been proposed for 2 of these trials. It was considered best to keep these to one replicate of the trials. The same then applied to the PhotoMARVL images as we would like to be able link these two sources of data.

The trial data, from the last remeasurement, were examined to see if there were any significant differences in basal area and mean top height between replicates. Apart from FR84, Kawerau, there were no differences between replicates.
The following replicates were selected for the PHOTOMARVL studies:
- FR8, Tahorakuri, Replicate 1 as some treatments were missing from Replicate 2.
- FR10, Glengarry, Replicate 1.
- FR54, Mamaranui, Replicate 1 – this was the replicate visited during the February 2003 SGMC co-operative meeting.
- FR84, Kawerau, Replicate 2. This replicate was in the middle in terms of basal area.

The plots selected are shown in Tables 1a, b, c, d.

The trees within the selected plots were then ranked according to Method 1 above using the last DBH measurement. There was often several centimetres difference in DBH between the largest and the next largest tree. As we are attempting to cover the range in DBH, it was decided to select trees with no obvious damage (e.g. dead top) close to the following percentiles:
- 15, 35, 55, 75, and 95 %

This has advantages and disadvantages. These percentile positions are not evenly spaced around 50%, but they are likely to cover a greater range in DBH whilst avoiding the largest tree which might be anomalous. This is slightly different to previous studies. In the 1978 trials the 10, 30, 50, 70 and 90 percentiles were used. In the 1975 trials the 10, 40, 70 and 100 percentiles were used.

In previous studies, we selected to avoid trees that had been assigned a defect code at the last measurement. In this study we selected to avoid trees that had been assigned a defect code at any measurement.
There are two possible effects that might occur as a result of this selection:
- The sample trees may show fewer extremely large, apparently anomalous branches
- The effect of defects etc on other non-selected trees may have influenced the branching pattern of these trees.

Table 1a. Plot numbers for treatments assessed in Tahorakuri FR8

Plot	GF rating	Treatment
9/12	LI28/GF13	500→200
10/12	GF14	500→200
11/12	GF21	500→200
18/13	LI28/GF13	1000→400
19/13	GF21	1000→400
20/13	GF14	1000→400
25/14	GF14	1500→600
26/14	LI28/GF13	1500→600
28/14	GF21	1500→600
33/15	LI28/GF13	500→500
34/15	GF14	500→500
35/15	GF21	500→500

Table 1b. Plot numbers for treatments assessed in Glengarry FR10

Plot	GF rating	Treatment
9/12	LI28/GF13	500→200
10/12	GF21	500→200
11/12	GF7	500→200
12/12	GF14	500→200
17/13	GF14	1000→400
18/13	LI28/GF13	1000→400
19/13	GF21	1000→400
20/13	GF7	1000→400
25/14	GF7	1500→600
26/14	GF14	1500→600
27/14	LI28/GF13	1500→600
28/14	GF21	1500→600
33/15	GF21	500→500
34/15	GF14	500→500
35/15	LI28/GF13	500→500

Table 1c. Plot numbers for treatments assessed in Mamaranui FR54

Plot	GF rating	Treatment
7/12	GF22	500→200
8/12	LI23/GF9	500→200
9/12	GF17, cutting	500→200
10/12	GF14	500→200
15/13	GF14	1000→400
16/13	LI23/GF9	1000→400
17/13	GF22	1000→400
22/14	GF14	1500→600
23/14	LI23/GF9	1500→600
24/14	GF22	1500→600
29/15	GF14	500→500
30/15	GF22	500→500
31/15	LI23/GF9	500→500
41/17	GF17, cutting	200→200

Table 1d. Plot numbers for treatments assessed in Kawarau FR84

Plot	GF rating	Treatment
13/24	GF25	600→600
14/22	GF16	600→250 Late thin (20m)
16/24	GF25 Cutting	600→600
17/21	GF25	600→250 Early thin (6.2m)
18/22	GF25 Cutting	600→250 Late thin (20m)
19/21	GF16	600→250 Early thin (6.2m)
20/22	GF25	600→250 Late thin (20m)
21/24	GF16	600→600
23/21	GF25 Cutting	600→250 Early thin (6.2m)

Image analysis

The following measurements were extracted from the images using the PhotoMARVL system:

- stem diameter below the cluster,
- height to base and top of the cluster,
- diameter of the largest branch in the cluster that was visible on the image (*BDI)*.

Comparisons

For each tree, the TreeBLOSSIM branching pattern for the section of stem measured by PhotoMARVL was extracted. The position of each cluster and the diameter of the largest branch in that cluster were retained. A graph was plotted showing both the TreeBLOSSIM prediction for diameter of the largest branch in a cluster (*BDTB)* and the image measurement of the largest visible branch in a cluster (*BDI)* versus the height of the cluster (see Appendix 1 (FR8), Appendix 2 (FR10), Appendix 3 (FR54) and Appendix 4 (FR84). This approach gives a good visual impression of how the model performs for each tree. (Note: "Tree" is equivalent to "Tree-Key" in the PSP system).

The data for each tree was then summarised to give:

- BDI_{max} — The maximum branch diameter measured on the PhotoMARVL / TreeD image (i.e. maximum value of *BDI* for the tree)
- $BDTB_{max}$ — The maximum branch diameter predicted by TreeBLOSSIM for that stem section (i.e. the maximum value of *BDTB* for the stem section)
- BDI_{av} — The mean branch diameter measured by PhotoMARVL / TreeD (i.e. average value of *BDI* for the tree)
- $BDTB_{av}$ — The mean branch diameter predicted by TreeBLOSSIM for that stem section (i.e. average diameter *BDTB* for the stem section)
- *CLI* — Number of branch clusters on the stem section measured by PhotoMARVL / TreeD

- *CLTB* Number of branch clusters on the same stem sections in the TreeBLOSSIM prediction
- *zonelength* height to base of highest cluster – height to base of lowest cluster, both measured from the image

The following differences were then calculated for each tree:

$DIFF_{max} = BDI_{max} - BDTB_{max}$

$DIFF_{av} = BDI_{av} - BDTB_{av}$

$DIFF_{CL} = (CLI - CLTB) / zonelength$

These differences were then plotted against the relative position of the tree in the DBH distribution (equivalent to percentage rank) for each plot (Appendix 5 (FR8), Appendix 6 (FR10), Appendix 7 (FR54) and Appendix 8 (FR84).

RESULTS

In this study TreeBLOSSIM was considered to have performed well for predicting branch diameters on an individual tree if the absolute values of $DIFF_{max}$ and $DIFF_{av}$ are less than or equal to 20 mm. This was based on the fact that there is error in measuring branch diameters from PhotoMARVL (measured values are assumed to be within 10 mm of the true value); and that a model prediction within 10 mm of the true value would be reasonable. By definition these criteria are harsher for $DIFF_{max}$ compared to $DIFF_{av}$. The number of trees satisfying these criteria by experiment are shown in Tables 2 ($DIFF_{av}$) and Tables 3 ($DIFF_{max}$). A number of factors will be influencing these values – the suitability of the regional model for that site, the number of trees considered from different seedlots (TreeBLOSSIM is designed for GF14 seedlots) and the number of trees exhibiting abnormal branching characteristics due to stem damage. A more detailed examination of the results for each experiment follows.

Table 2. Summary of performance of TreeBLOSSIM with respect to $DIFF_{av}$.

Experiment	Number of trees	$DIFF_{av} \leq 20$ mm	$DIFF_{av} > 20$ mm	% acceptable
FR8	60	40	20	67
FR10	74	48	26	65
FR54	70	39	31	56
FR84	44	38	6	86

Table 3. Summary of performance of TreeBLOSSIM with respect to $DIFF_{max}$.

Experiment	Number of trees	$DIFF_{max} \leq 20$ mm	$DIFF_{max} > 20$ mm	% acceptable
FR8	60	25	35	42
FR10	74	35	39	47
FR54	70	23	47	33
FR84	44	18	26	41

FR8, Tahorakuri

Graphs showing the individual tree values of $DIFF_{max}$, $DIFF_{av}$, and $DIFF_{CL}$ versus relative position in the DBH distribution are shown in Appendix 5 and the actual and predicted branch diameters for individual trees in Appendix 1.

Individual tree values of $DIFF_{max}$, $DIFF_{av}$, and $DIFF_{CL}$ were analysed using the SAS procedure, PROC GLM with plot number as a "class" variable and relative position of the tree within the plot's DBH distribution as a continuous variable. The relative position in the DBH distribution not was significant for $DIFF_{av}$, and $DIFF_{CL}$ indicating that TreeBLOSSIM performance is varying with position of the tree in the DBH distribution. Relative position of the tree was significant for $DIFF_{max}$ but the trend was not consistent between plots and it is considered that the significant effect is due to the occasional tree with a large value of $DIFF_{max}$.

Branch diameter tended to be larger for the long internode seedlot compared to the GF14 and GF21 seedlots as shown by the larger values of $DIFF_{max}$ (Table 4) and $DIFF_{av}$ (Table 5). Not unexpectedly there were fewer branch clusters on the long internode trees as shown by the large negative values of $DIFF_{CL}$ (Table 6).

There were no consistent differences between the silvicultural treatments.

The images for trees where $DIFF_{max}$ was ≥ 60 mm were examined to determine reasons for the large differences (Table 7). The trees were mainly from the long-internode seedlot and did not show any obvious signs of stem damage.

Table 4. Least-square mean values for $DIFF_{max}$ in mm for FR8, Tahorakuri

Treatment	GF14	GF21	LI28 /GF13
500⇨200 stem/ha	12	29	34
1000⇨400 stem/ha	36	29	39
1500⇨600 stem/ha	14	19	30
500⇨500 stem/ha	11	44	58

Table 5. Least-square mean values for $DIFF_{av}$ in mm for FR8, Tahorakuri

Treatment	GF14	GF21	LI28 /GF13
500⇨200 stem/ha	10	12	16
1000⇨400 stem/ha	11	17	21
1500⇨600 stem/ha	13	17	22
500⇨500 stem/ha	4	16	33

Table 6. Least-square mean values for $DIFF_{CL}$ for FR8, Tahorakuri

Treatment	GF14	GF21	LI28 /GF13
500⇨200 stem/ha	-0.04	0.01	-0.50
1000⇨400 stem/ha	0.33	-0.06	-0.58
1500⇨600 stem/ha	-0.28	0.04	-0.50
500⇨500 stem/ha	-0.21	0.26	-0.55

Table 7. Comments on trees in FR8 (Tahorakuri) with large values of $DIFF_{max}$.

Plot	Tree	Relative Position (%)	$DIFF_{max}$ (mm)	Seedlot	Comments
9_12	16	15	67	LI28/GF13	No obvious damage
18_13	20	95	66	LI28/GF13	Large branches on one side of the stem
20_13	12	95	73	GF14	Difficult to determine whether any abnormalities
26_14	44	77	65	LI28/GF13	No obvious damage
33_15	16	95	69	LI28/GF13	No obvious damage
33_15	34	36	66	LI28/GF13	No obvious damage
33_15	46	74	88	LI28/GF13	No obvious damage
35_15	33	16	103	GF21	Large steeply angled branches in one cluster

FR10, Glengarry

Graphs showing the individual tree values of $DIFF_{max}$, $DIFF_{av}$, and $DIFF_{CL}$ versus relative position in the DBH distribution are shown in Appendix 6 and the actual and predicted branch diameters for individual trees in Appendix 2.

Individual tree values of $DIFF_{max}$, $DIFF_{av}$, and $DIFF_{CL}$ were analysed using the SAS procedure, PROC GLM with plot number as a “class” variable and relative position of the tree within the plot’s DBH distribution as a continuous variable. The relative position in the DBH distribution was not significant, indicating that TreeBLOSSIM is performing equally well for trees of different DBH within a plot.

TreeBLOSSIM performance was similar for the GF7, GF14 and GF21 seedlots, but noticeably poorer for the long internode seedlot as shown by the larger values positive values of $DIFF_{max}$ (Table 8) and $DIFF_{av}$ (Table 9) and the larger negative values of $DIFF_{CL}$ (Table 10).

The images for trees where $DIFF_{max}$ was ≥ 60 mm were examined to determine reasons for the large differences (Table 11). The trees were mainly from the long-internode seedlot some of which showed signs of stem damage.

Table 8. Least-square mean values for $DIFF_{max}$ in mm for FR10, Glengarry

Treatment	GF7	GF14	GF21	LI28/GF13
500⇨200 stem/ha	23	21	36	60
1000⇨400 stem/ha	22	9	2	30
1500⇨600 stem/ha	25	14	7	31
500⇨500 stem/ha		18	13	55

Table 9. Least-square mean values for $DIFF_{av}$ in mm for FR10, Glengarry

Treatment	GF7	GF14	GF21	LI28/GF13
500⇨200 stem/ha	21	15	20	41
1000⇨400 stem/ha	14	8	5	23
1500⇨600 stem/ha	14	8	5	29
500⇨500 stem/ha		13	7	35

Table 10. Least-square mean values for $DIFF_{CL}$ for FR10, Glengarry

Treatment	GF7	GF14	GF21	LI28/GF13
500⇨200 stem/ha	-0.31	-0.32	0.07	-0.79
1000⇨400 stem/ha	-0.09	-0.12	-0.17	-0.88
1500⇨600 stem/ha	-0.09	-0.03	0.08	-0.88
500⇨500 stem/ha		-0.11	0.30	-0.85

Table 11. Comments on trees in FR10 (Glengarry) with large values of $DIFF_{max}$.

Plot	Tree	Relative Position (%)	$DIFF_{max}$ (mm)	Seedlot	Comments
9_12	14	40	74	LI28/GF13	Branches large to one side, possible gap
9_12	30	90	70	LI28/GF13	Steep branch and possible stem sweep
9_12	50	60	89	LI28/GF13	Stem sweep and at least one steep/ spike branch
18_13	7	75	72	LI28/GF13	Steep / spike branch in lowest cluster
20_13	22	95	61	GF7	Difficult to determine whether any abnormalities
35_15	34	30	91	LI28/GF13	No obvious abnormalities
35_15	40	50	66	LI28/GF13	Large steep angled branch

FR54, Mamaranui

Graphs showing the individual tree values of $DIFF_{max}$, $DIFF_{av}$, and $DIFF_{CL}$ versus relative position in the DBH distribution are shown in Appendix 7 and the actual and predicted branch diameters for individual trees in Appendix 3.

Individual tree values of $DIFF_{max}$, $DIFF_{av}$, and $DIFF_{CL}$ were analysed using the SAS procedure, PROC GLM with plot number as a "class" variable and relative position of the tree within the plot's DBH distribution as a continuous variable. The relative position in the DBH distribution was not significant, indicating that TreeBLOSSIM is performing equally well for trees of different DBH within a plot.

At this site there is a tendency for TreeBLOSSIM prediction of branch diameter to be poorer for the treatments with a final crop stocking of 200 stems/ha (larger values of $DIFF_{max}$ (Table 12), and $DIFF_{av}$ (Table 13)). The prediction of the number of branch clusters is, as expected, poorer for the long internode seedlot as shown by the larger values of $DIFF_{CL}$ (Table 14).

The images for trees where $DIFF_{max}$ was ≥ 60 mm were examined to determine reasons for the large differences (Table 15). The trees were mainly from the long-internode seedlot and the GF14 seedlot. Many of the GF14 trees were from plot 10/12 (treatment: 500⇨200 stem/ha) and this contributes to the large values of $DIFF_{max}$ (Table 12), and $DIFF_{av}$ (Table13).

Table 12. Least-square mean values for $DIFF_{max}$ in mm for FR54, Mamaranui

Treatment	GF14	GF22	LI23/GF9	GF17, cutting
500⇨200 stem/ha	68	40	69	35
1000⇨400 stem/ha	23	16	26	
1500⇨600 stem/ha	17	8	23	
500⇨500 stem/ha	41	26	43	
200⇨200 stem/ha				52

Table 13. Least-square mean values for $DIFF_{av}$ in mm for FR54, Mamaranui

Treatment	GF14	GF22	LI23/GF9	GF17, cutting
500⇨200 stem/ha	35	23	41	24
1000⇨400 stem/ha	17	14	20	
1500⇨600 stem/ha	16	6	20	
500⇨500 stem/ha	11	11	14	
200⇨200 stem/ha				24

Table 14. Least-square mean values for $DIFF_{CL}$ for FR54, Mamaranui

Treatment	GF14	GF22	LI23/GF9	GF17, cutting
500⇨200 stem/ha	0.06	-0.16	-0.30	-0.05
1000⇨400 stem/ha	-0.26	-0.33	-0.64	
1500⇨600 stem/ha	-0.22	-0.23	-0.65	
500⇨500 stem/ha	-0.07	-0.06	-0.48	
200⇨200 stem/ha				-0.17

Table 15. Comments on trees in FR54 (Mamaranui) with large values of $DIFF_{max}$.

Plot	Tree	Relative Position (%)	$DIFF_{max}$ (mm)	Seedlot	Comments
7_12	37	89	61	GF22	Large steep-angled branch
8_12	22	79	102	LI23/GF9	No obvious damage
8_12	29	95	74	LI23/GF9	No obvious damage
8_12	50	37	96	LI23/GF9	Steep branches with bend in stem.
10_12	8	16	67	GF14	Possible bend in stem near top, but difficult to observe
10_12	23	37	85	GF14	No obvious damage
10_12	29	74	84	GF14	Obvious stem defect, very steep branches near base
10_12	34	89	62	GF14	Probable stem damage
29_15	12	91	83	GF14	Steep / spike branch
31_15	16	15	71	LI23/GF9	Large step-angled branch near base
41_17	13	32	63	GF17 cutting	Cluster of large steep branches

FR84, Kawerau

Graphs showing the individual tree values of $DIFF_{max}$, $DIFF_{av}$, and $DIFF_{CL}$ versus relative position in the DBH distribution are shown in Appendix 8 and the actual and predicted branch diameters for individual trees in Appendix 4.

Individual tree values of $DIFF_{max}$, $DIFF_{av}$, and $DIFF_{CL}$ were analysed using the SAS procedure, PROC GLM with plot number as a "class" variable and relative position of the tree within the plot's DBH distribution as a continuous variable. The relative position in the DBH distribution was not significant, indicating that TreeBLOSSIM is performing equally well for trees of different DBH within a plot.

Plot number was not significant for $DIFF_{max}$ (Table 16), $DIFF_{av}$ (Table 17), and $DIFF_{CL}$ (Table 18) at this site indicating that TreeBLOSSIM was performing equally for the three treatments and three seedlots.

The images for the 5 trees where $DIFF_{max}$ was ≥ 60 mm were examined to determine reasons for the large differences (Table 19). Two of these trees showed signs of stem damage.

Table 16. Least-square mean values for $DIFF_{max}$ in mm for FR84, Kawerau

Treatment	GF16	GF25	GF25 (cutting)
600 ⇨ 250 (6.2 m)	25	36	10
600 ⇨ 250 (20 m)	17	37	36
600 ⇨ 600	25	34	21

Table 17. Least-square mean values for $DIFF_{av}$ in mm for FR84, Kawerau

Treatment	GF16	GF25	GF25 (cutting)
600 ⇨ 250 (6.2 m)	16	15	11
600 ⇨ 250 (20 m)	11	16	15
600 ⇨ 600	16	6	12

Table 18. Least-square mean values for $DIFF_{CL}$ for FR84, Kawerau

Treatment	GF16	GF25	GF25 (cutting)
600 ⇨ 250 (6.2 m)	0.24	0.03	0.42
600 ⇨ 250 (20 m)	0.16	0.17	0.07
600 ⇨ 600	0.10	0.38	0.11

Table 19. Comments on trees in FR84 (Kawerau) with large values of $DIFF_{max}$.

Plot	Tree	Relative Position (%)	$DIFF_{max}$ (mm)	Seedlot	Comment
13_24	45	55	95	GF25	Leader change near base of tree; large steep-angled branches
17_21	1	13	73	GF25	Steep ramicorn
17_21	83	77	61	GF25	Tree in a fairly open situation with large branches
18_22	9	53	62	GF25 cutting	No obvious abnormalities
20_22	38	13	64	GF25	No obvious abnormalities

DISCUSSION

PhotoMARVL was used as a non-destructive tool to provide data to determine how well the branch model within TreeBLOSSIM performed for four SGMC trials, FR8, FR10, FR54 and FR84:

- FR8 was planted in Tahorakuri Forest in 1987 to be representative of a medium site index in the Central North Island.
- FR10 was planted in Glengarry Forest in 1987 to be representative of a high basal area site in Hawkes Bay, North Island.
- FR54 was planted in Mamaranui Forest in 1988 to be representative of a high basal area site the Auckland Clays area of the North Island.
- FR84 was planted in Kawerau Forest in 1989 to be representative of a high basal area site in the Central North Island.

In this study TreeBLOSSIM was considered to have performed well for predicting branch diameters on an individual tree if the absolute values of $DIFF_{max}$ and $DIFF_{av}$ are less than or equal to 20 mm. This was based on the fact that there is error in measuring branch diameters from PhotoMARVL (measured values are assumed to be within 10 mm of the true value); and that a model prediction within 10 mm of the true value would be reasonable.

For these sites $DIFF_{max}$ and $DIFF_{av}$ were always positive indicating that branch diameters at these sites tended to be larger than predicted by TreeBLOSSIM.

TreeBLOSSIM performed well in terms of $DIFF_{av}$ for over half the trees (see Table 2). TreeBLOSSIM performed less well in terms of $DIFF_{max}$ (Table 3) but this is a harsher criterion to satisfy. However there were only a few trees for which $DIFF_{max}$ was greater than 60 mm (Tables 7, 11, 15 and 19). These were mainly trees with stem damage or from the long internode seedlot.

TreeBLOSSIM performance was noticeably poorer for the long internode seedlots, particularly in FR8 (Tables 4-6) and FR10 (Tables 8-10). The long internode seedlot was less different from the GF14 seedlot in FR54 (Tables 12-14). Branch diameters were larger than predicted and the number of branch clusters less than predicted. These results indicate that a separate branch model should be developed for the long internode seedlot.

TreeBLOSSIM performance was similar for the growth and form seedlots considered (GF7, GF14, GF16, GF17, GF21, GF22, and GF25).

The effects of silviculture appear to have been captured reasonably well at FR8, FR10 and FR84, but the values of $DIFF_{av}$ were higher for the treatment with a final crop stocking of 200 stems/ha in FR54.

The high value of $DIFF_{max}$ for the GF17 cutting planted at 200 stems/ha and left is considered to be due to the fact that the spacing was rectangular (4 m × 11.3 m – see SGMC Report 46) and the wider spacing is equivalent to a square spacing of 78 stems/ha.

TreeBLOSSIM performed equally well for trees at different positions in the DBH distribution, suggesting that TreeBLOSSIM adequately models the between tree variability within a plot.

These results will be collated with the results from other PhotoMARVL / TreeD studies to determine further improvements required to the branch model.

ACKNOWLEDGMENTS

Thanks to Tony Evanson for assistance with the PhotoMARVL fieldwork.

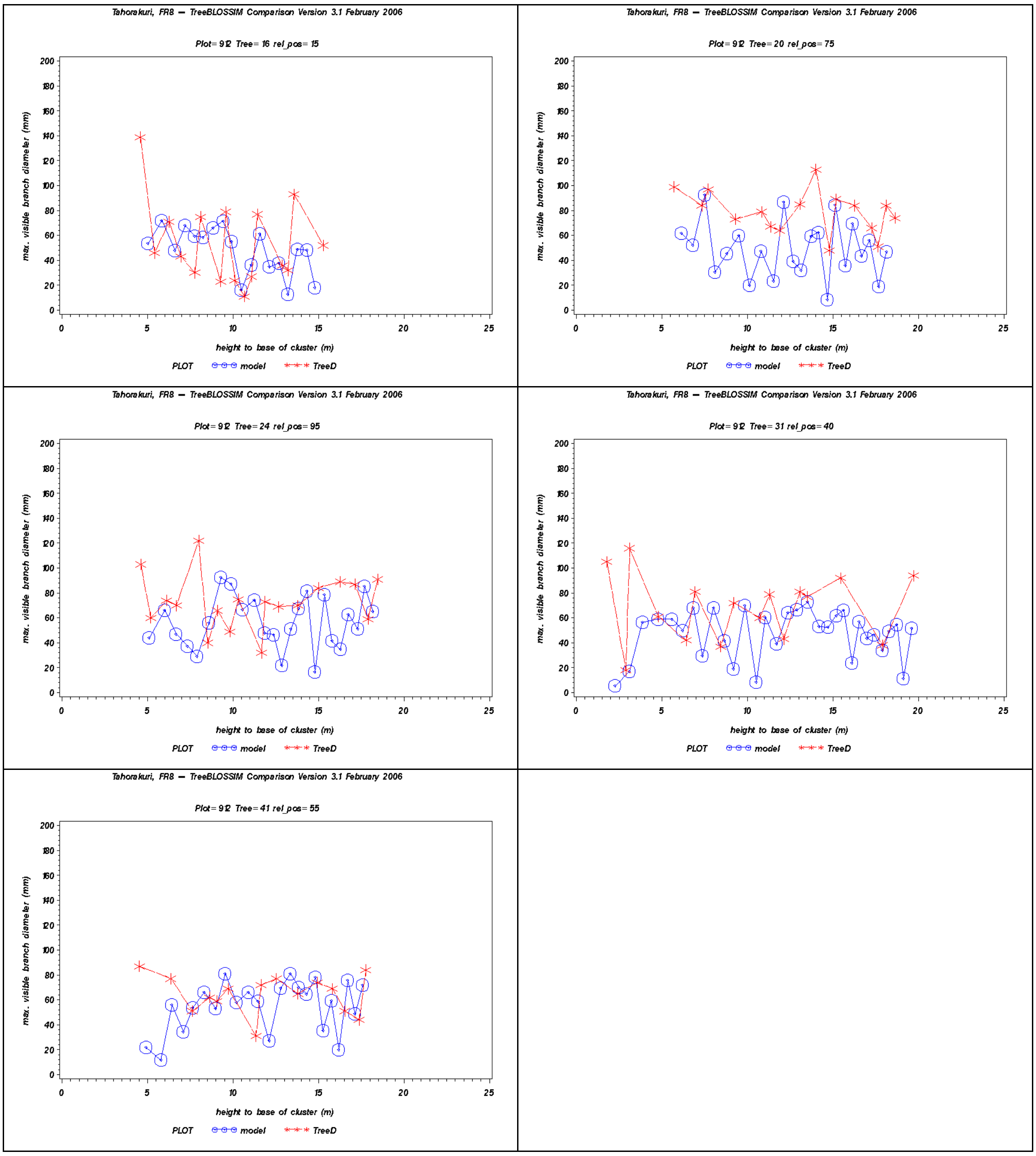
REFERENCES

Firth, J.G.; Brownlie, R.K.; Carson, W.W. 2000: Accurate stem measurements, key to new image-based system. New Zealand Journal of Forestry 45 (2): 25-29.

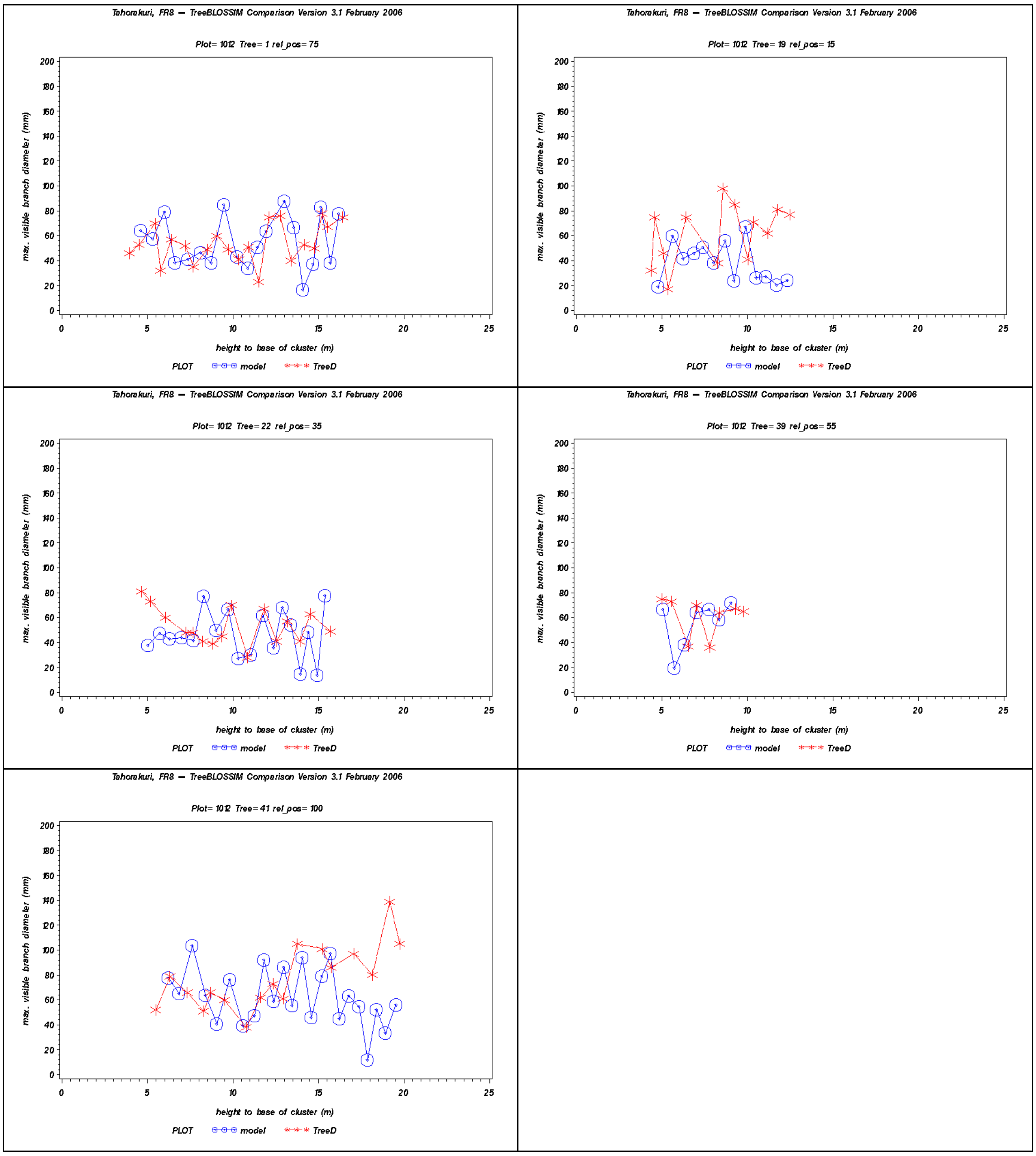
Brownlie, R.K.; Carson, W.W.; Firth, J.G.; Goulding, C.J. 2007: An image-based dendrometry tool for Standing Trees. New Zealand Journal of Forestry Science 37 (2): 153-168.

APPENDIX 1. Tahorakuri, FR8

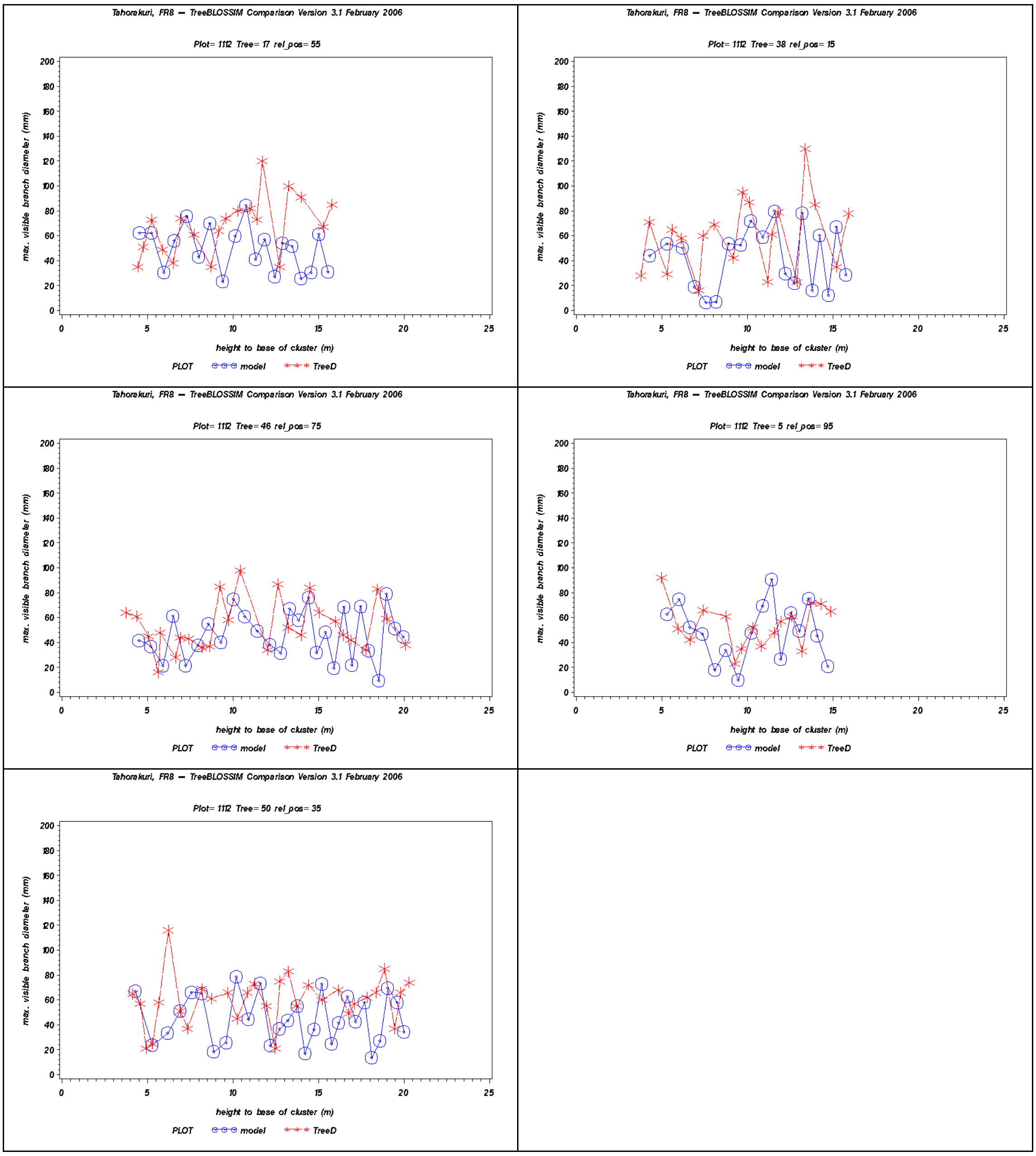
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR8, plot 09_12 (GF13 seedlot).



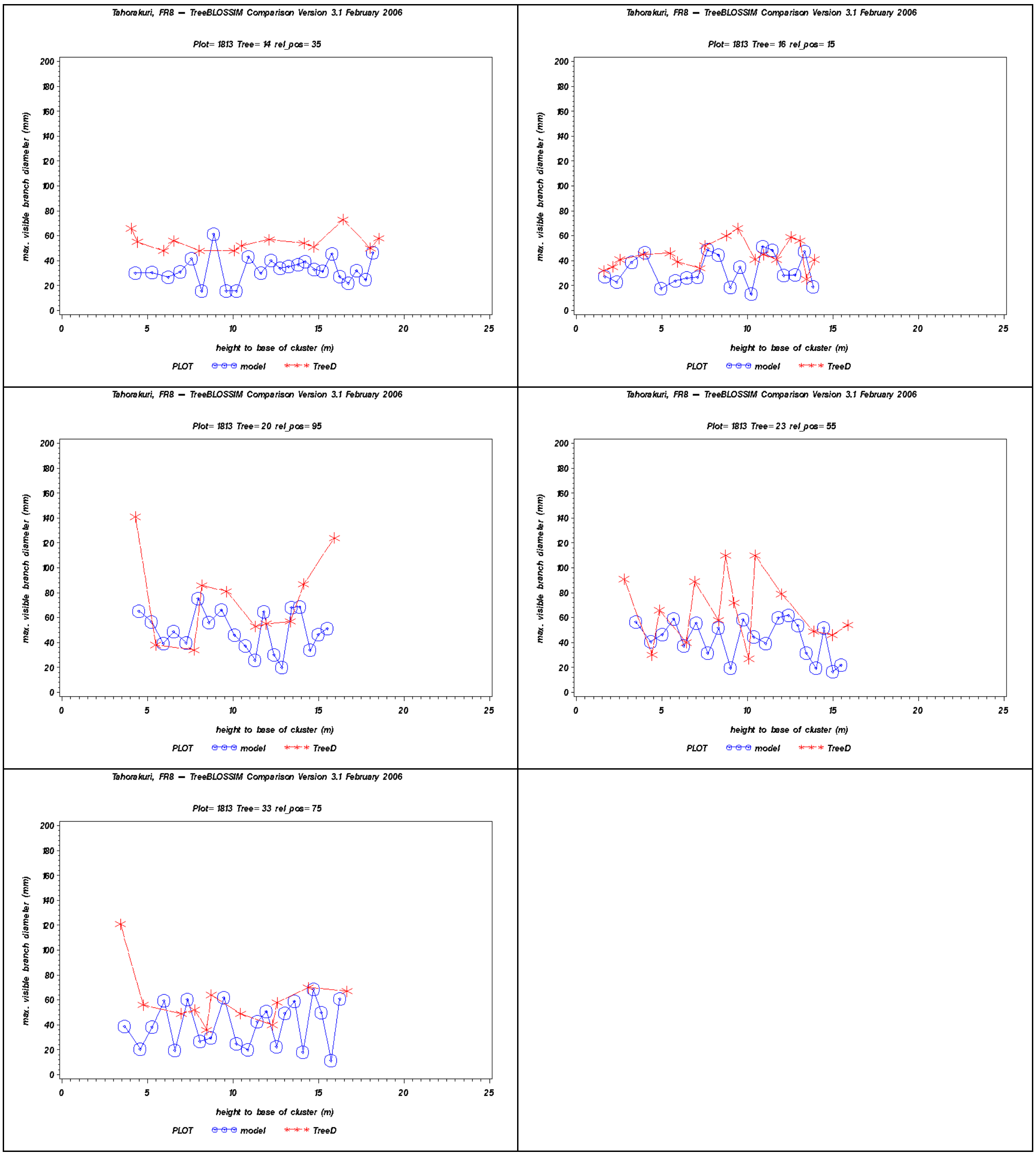
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR8, plot 10_12 (GF14 seedlot).



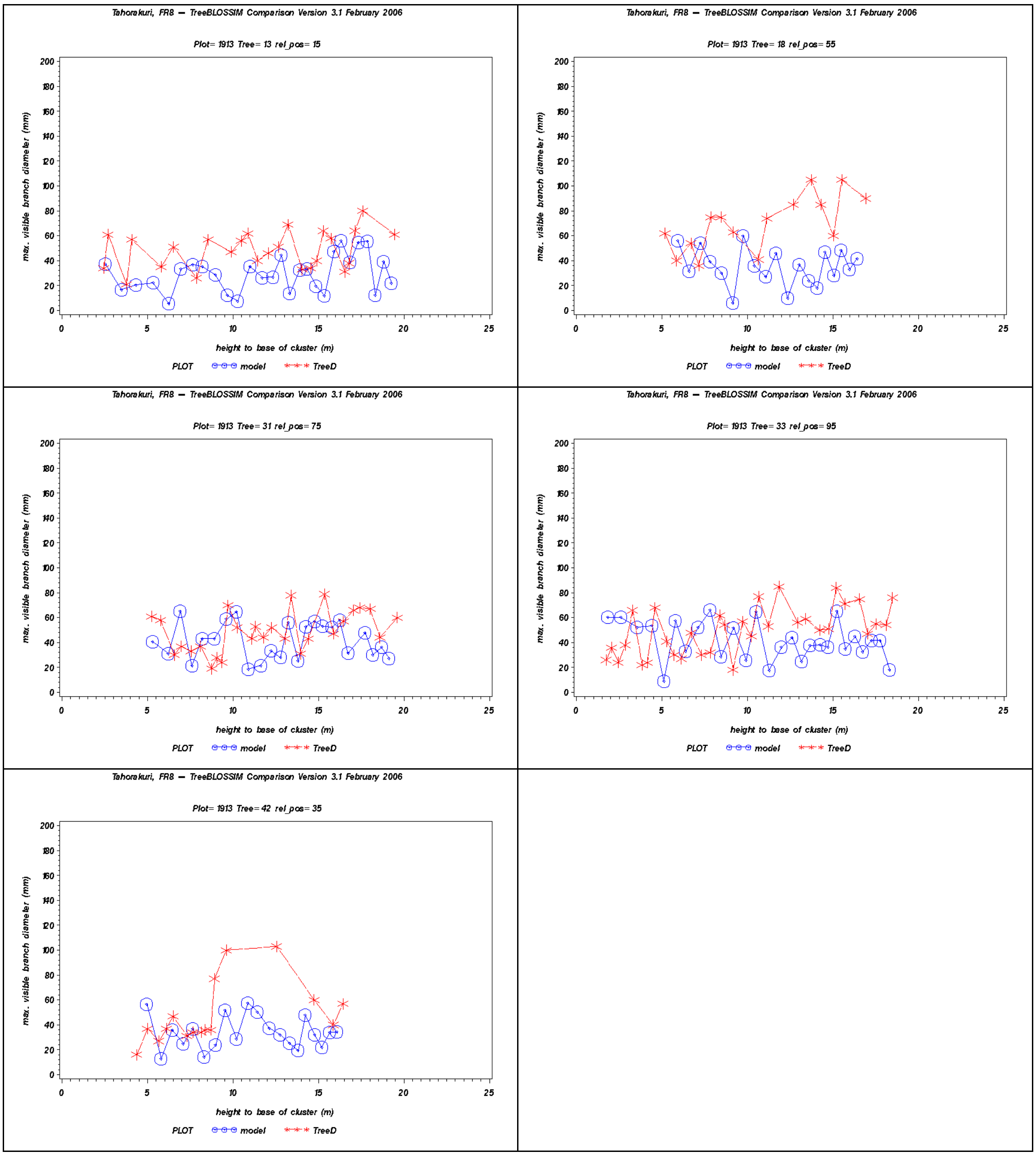
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR8, plot 11_12 (GF21 seedlot).



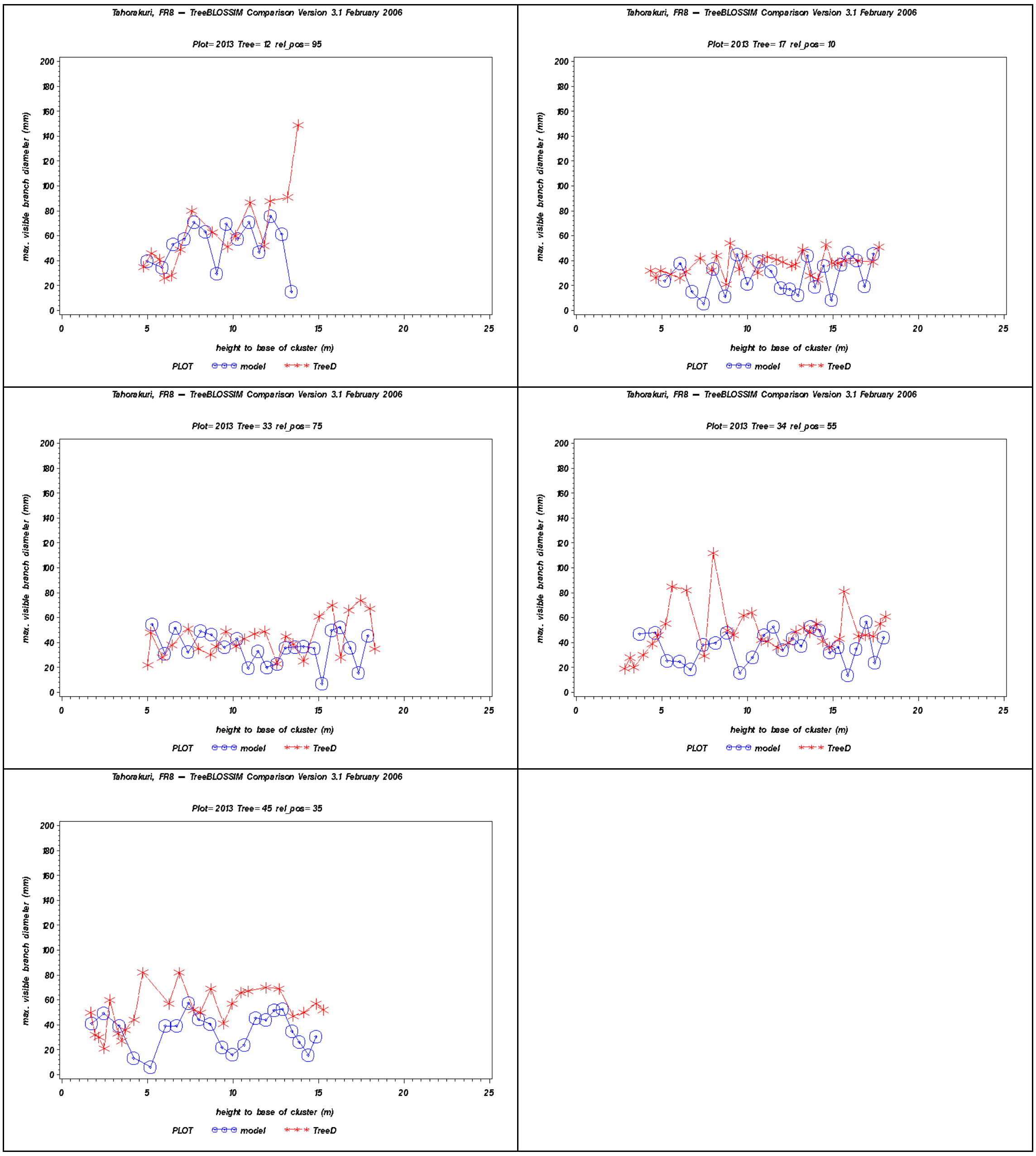
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR8, plot 18_13 (GF13 seedlot).



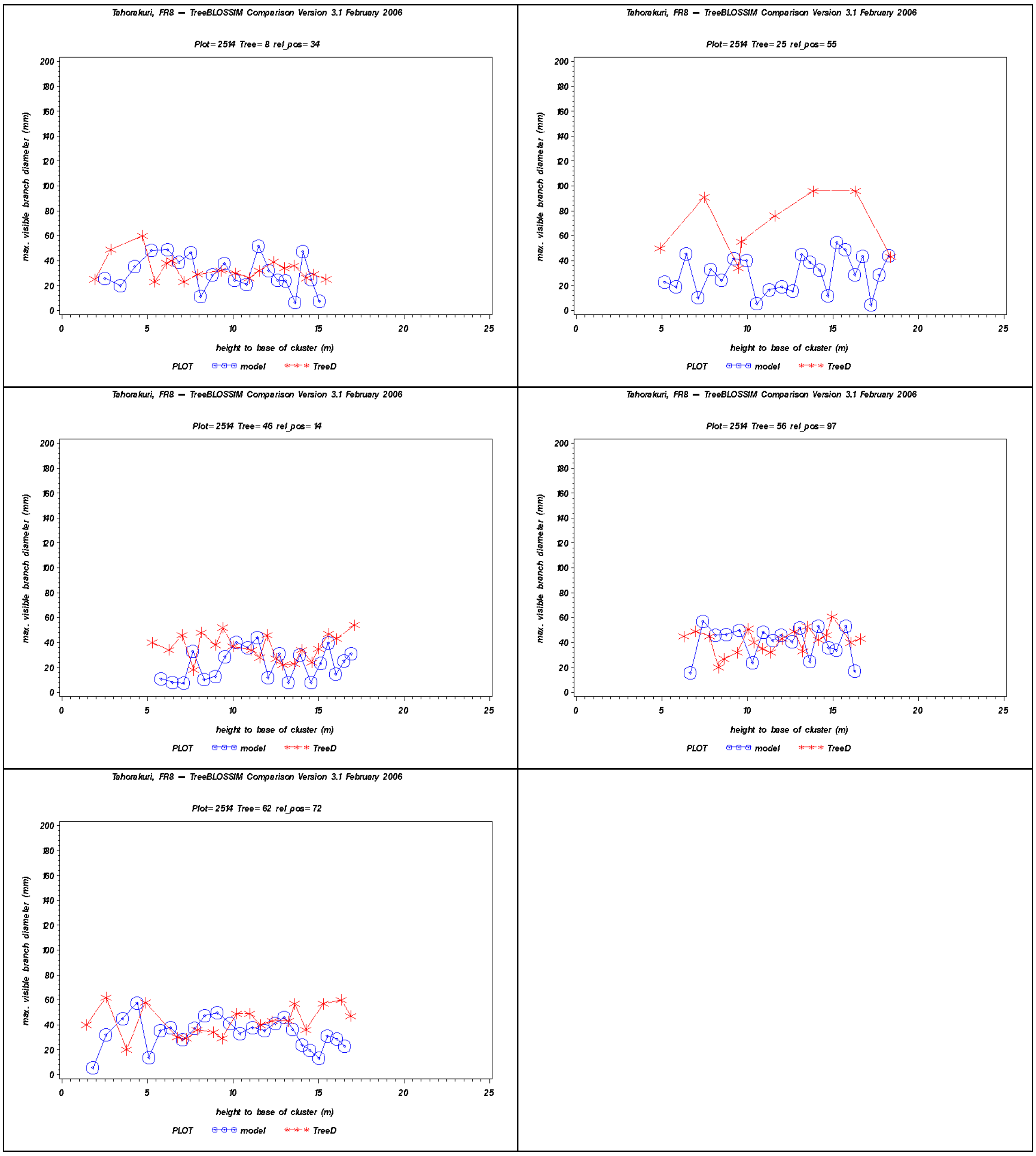
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR8, plot 19_13 (GF21 seedlot).



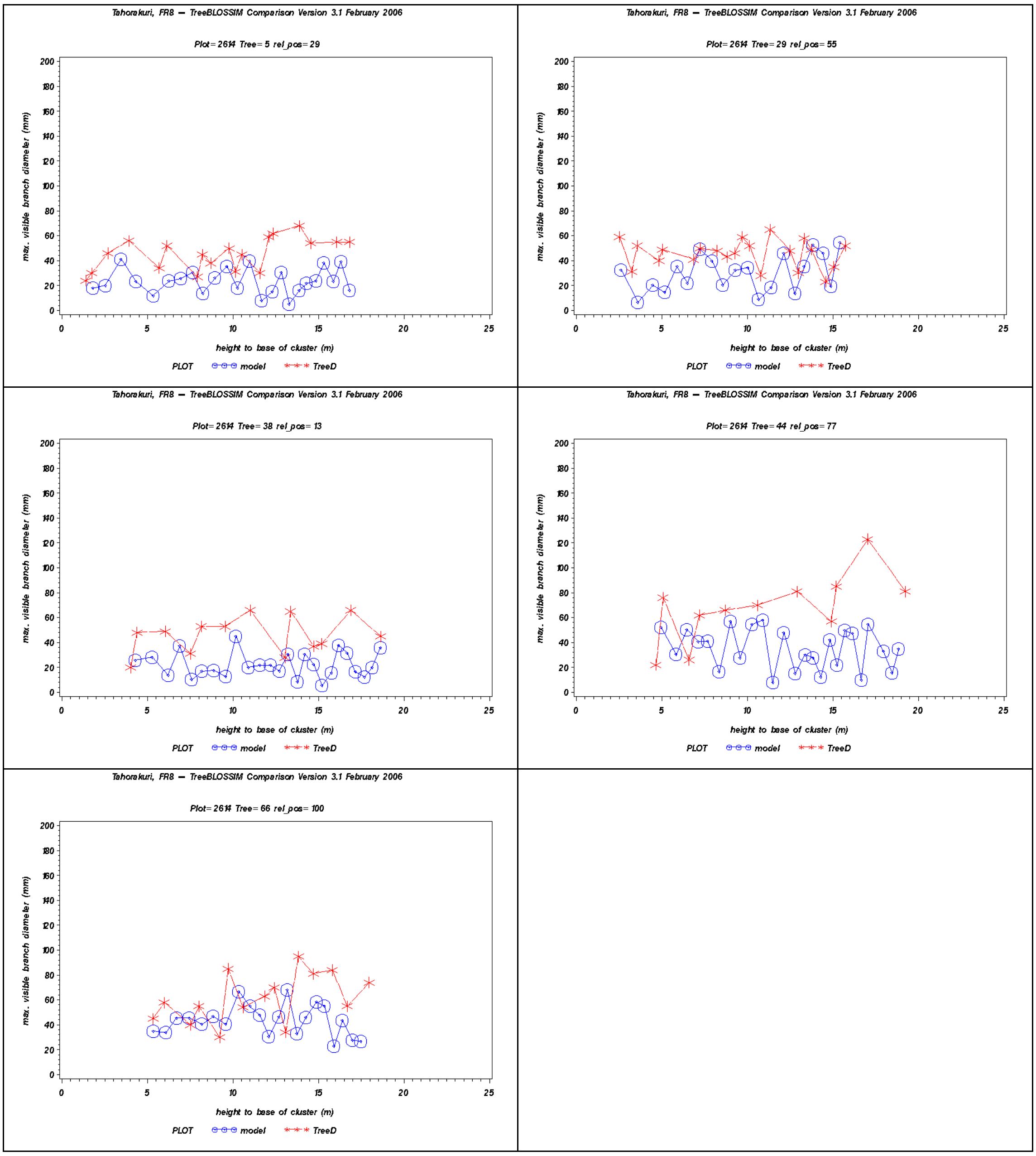
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR8, plot 20_13 (GF14 seedlot).



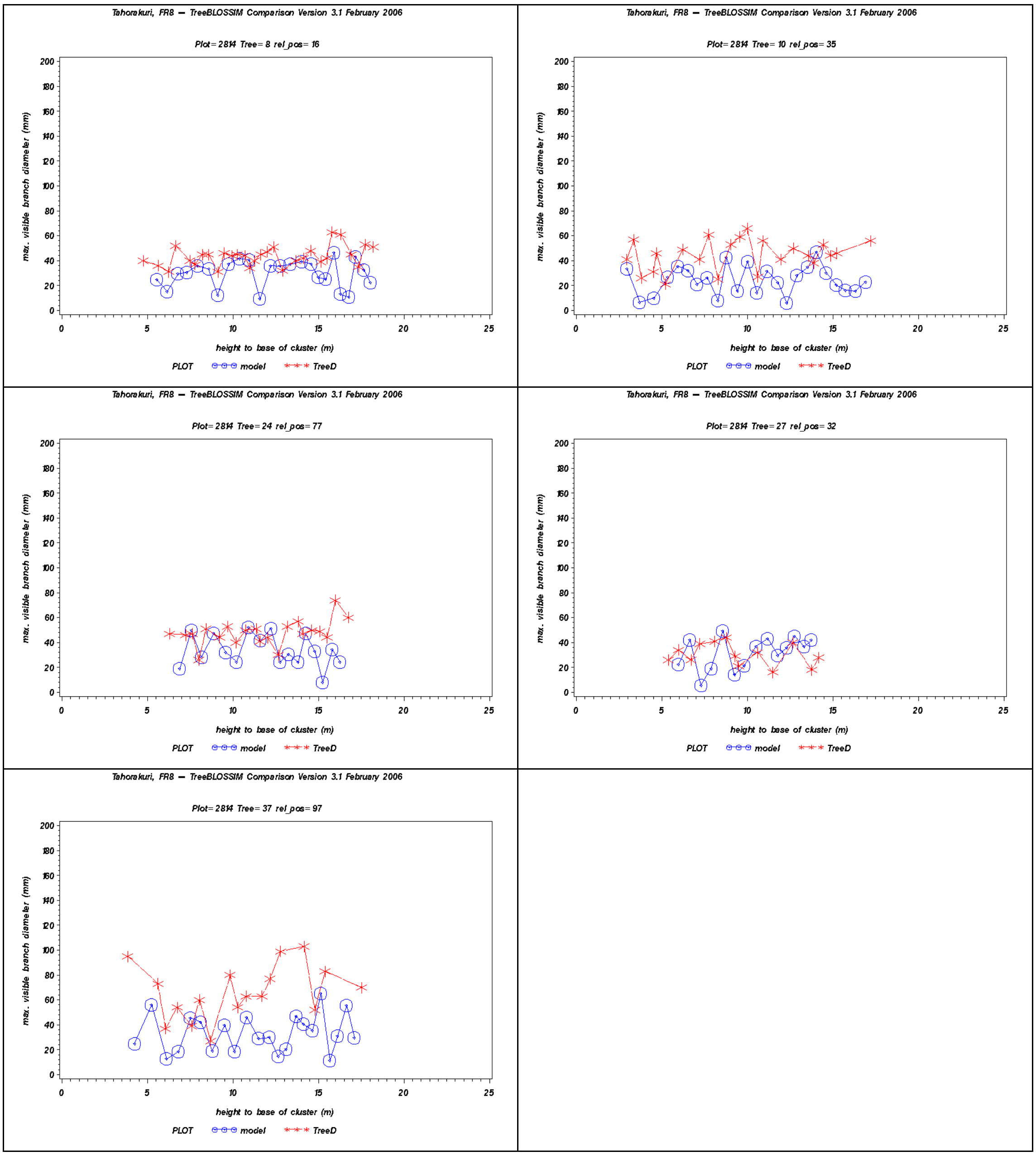
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR8, plot 25_14 (GF14 seedlot).



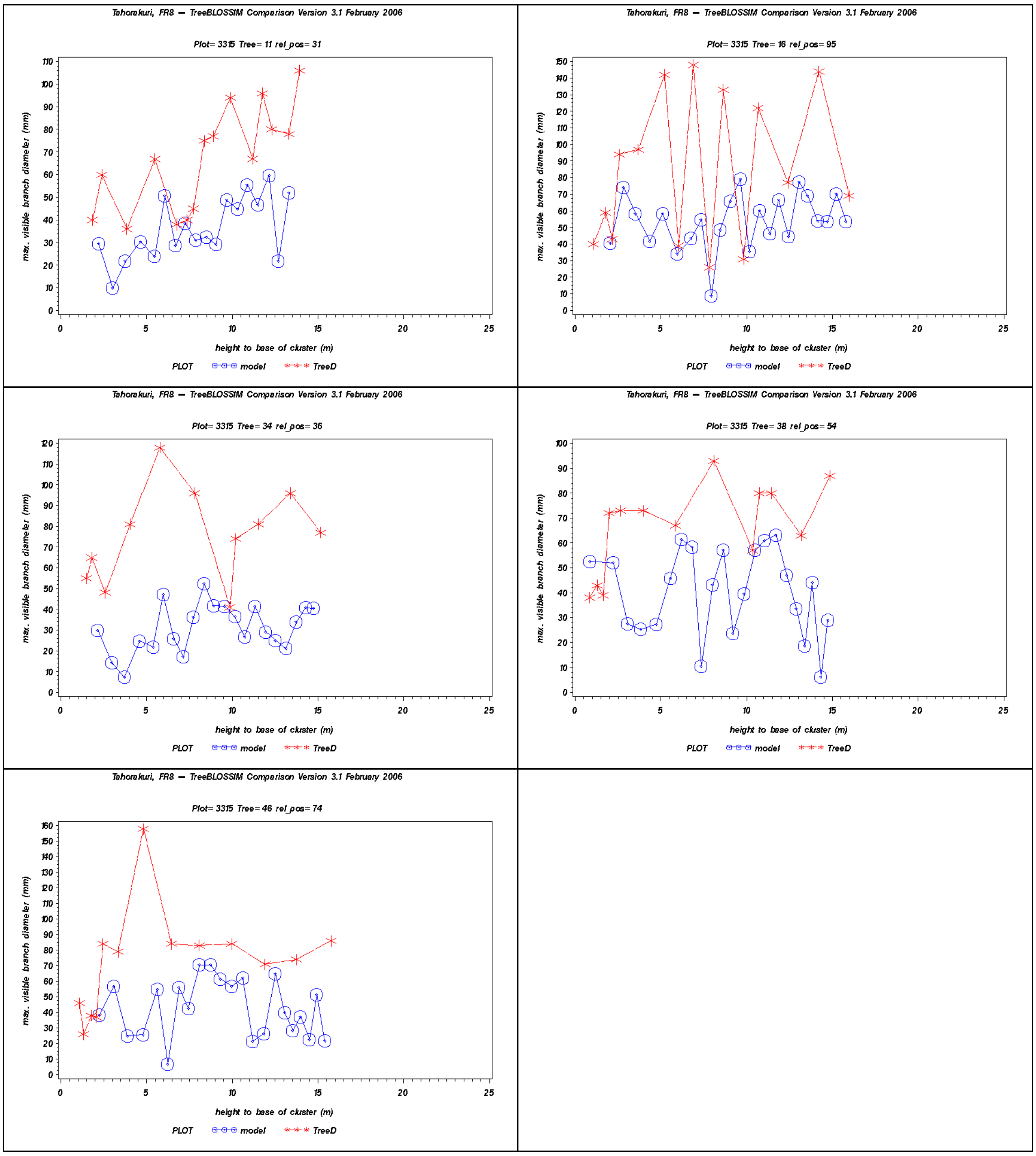
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR8, plot 26_14 (GF13 seedlot).



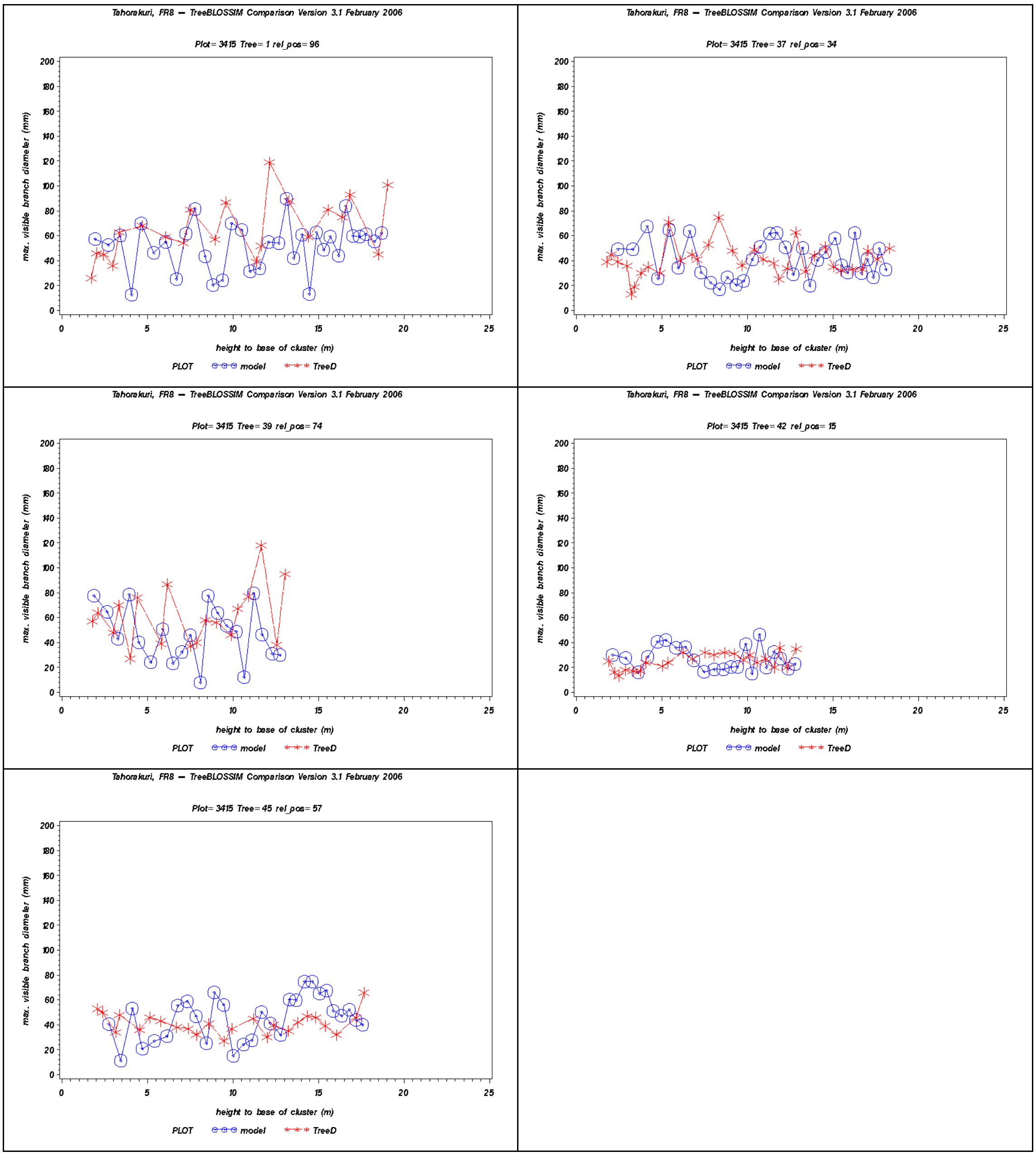
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR8, plot 28_14 (GF21 seedlot).



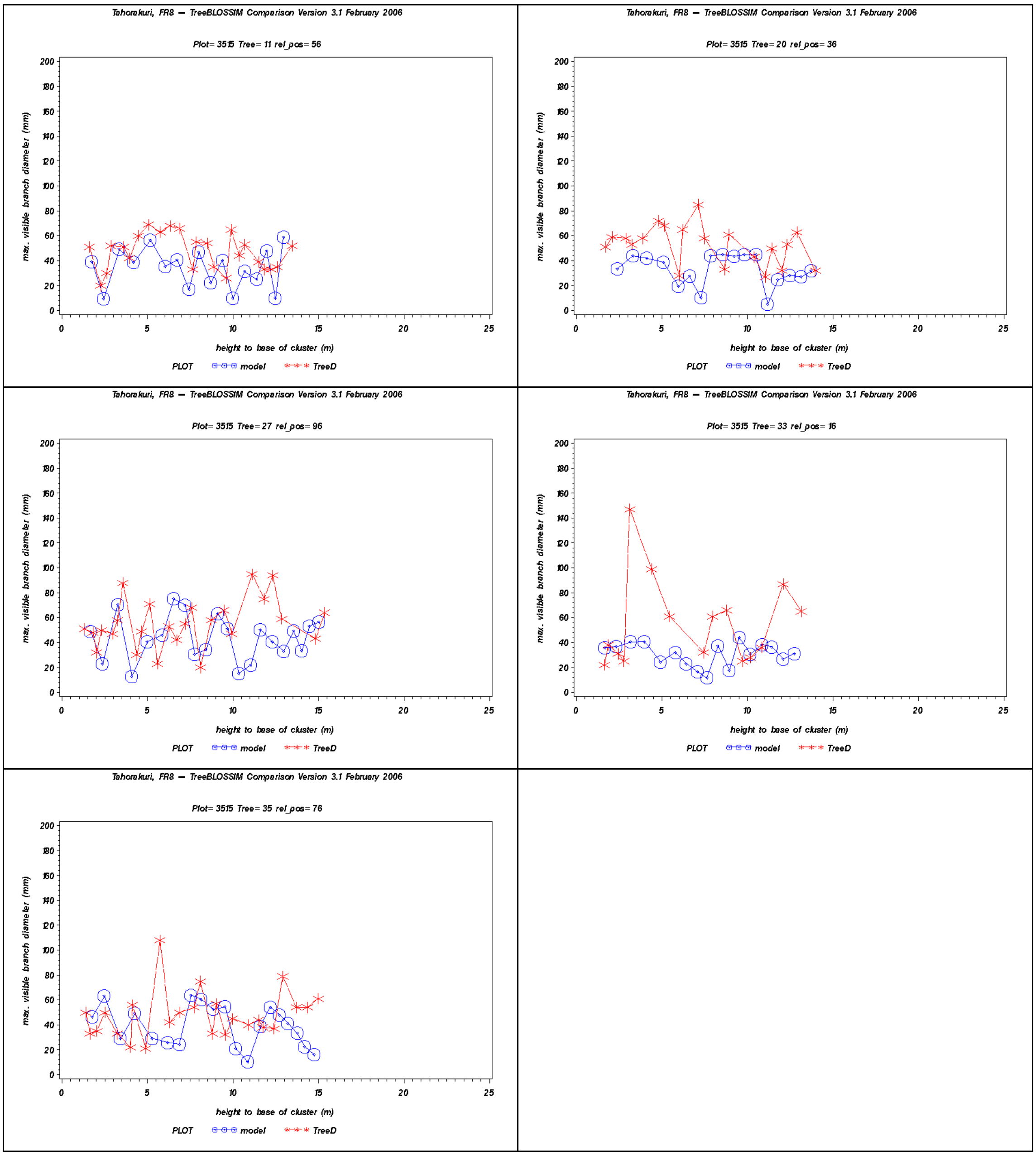
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR8, plot 33_15 (GF13 seedlot).



Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR8, plot 34_15 (GF14 seedlot).

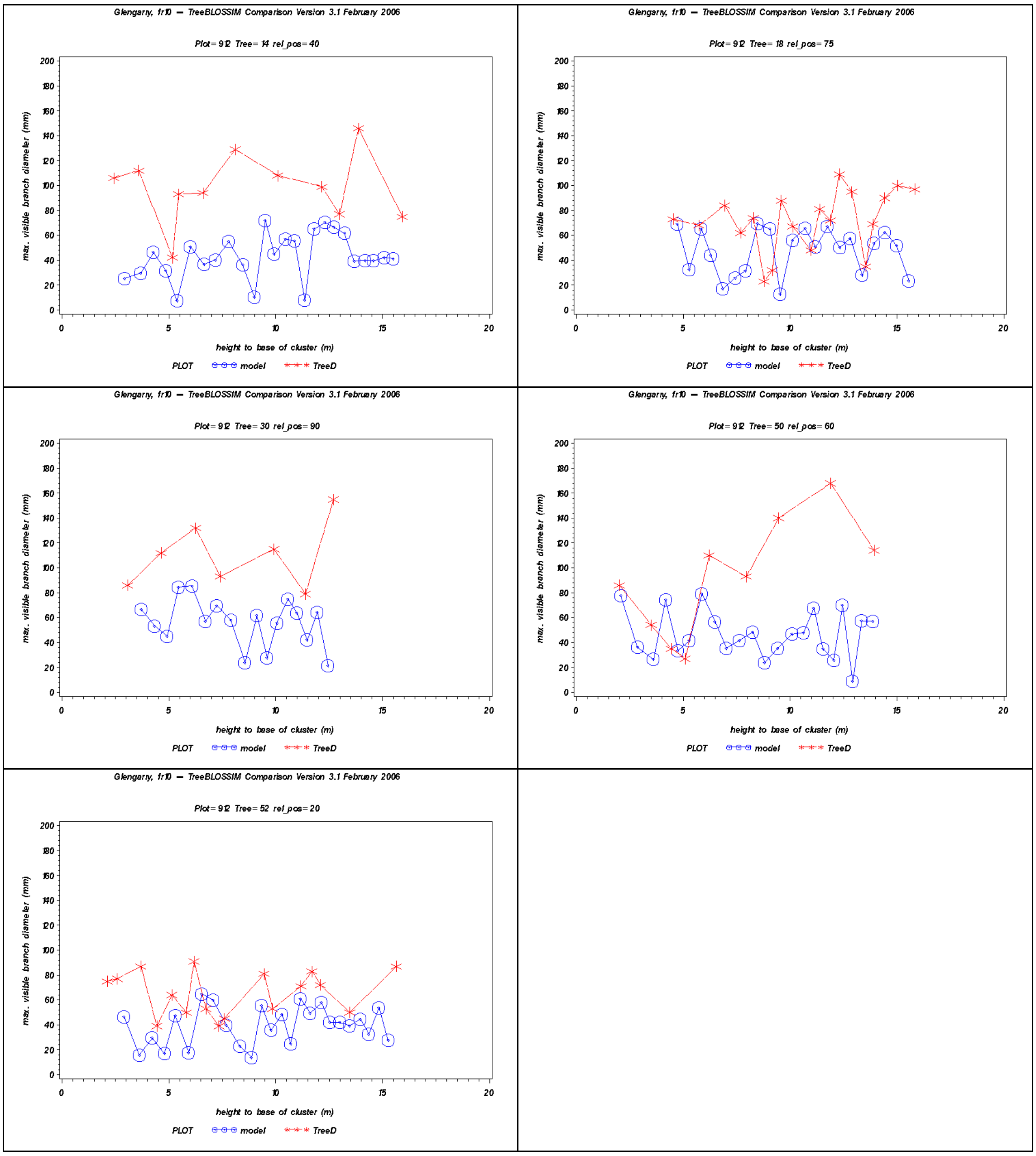


Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR8, plot 35_15 (GF21 seedlot).

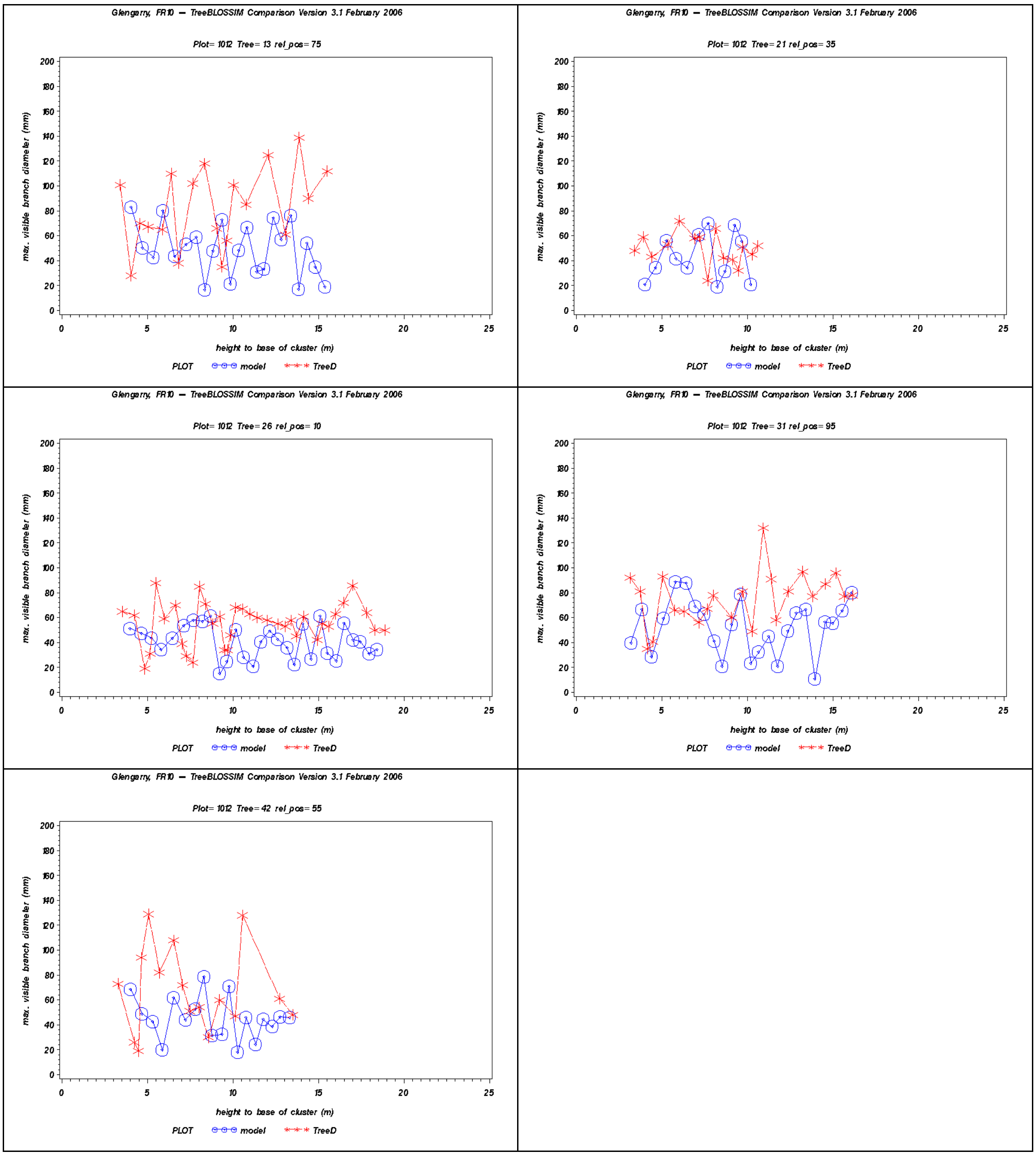


APPENDIX 2. Glengarry, FR10

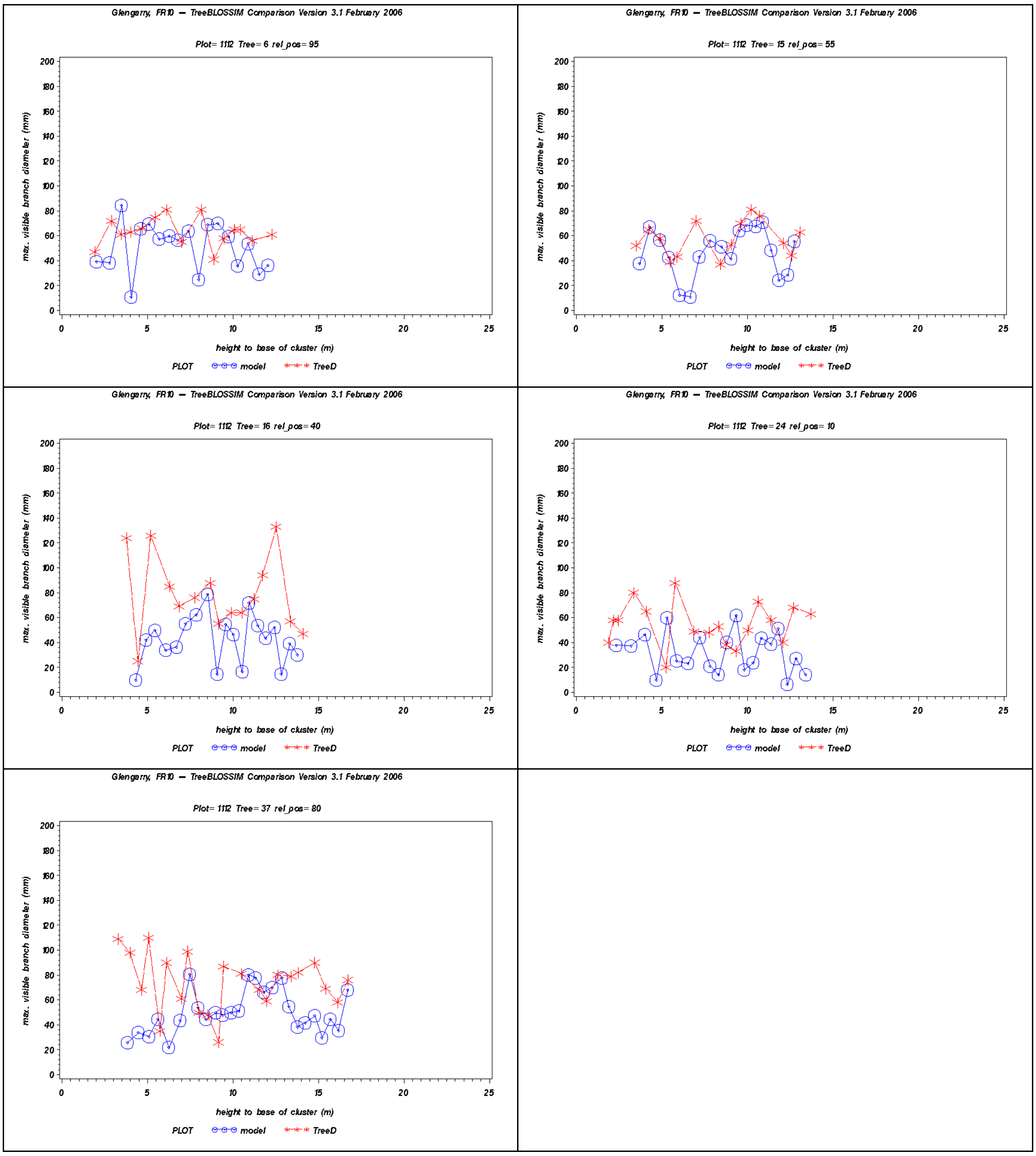
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR10, plot 09_12 (GF13 seedlot).



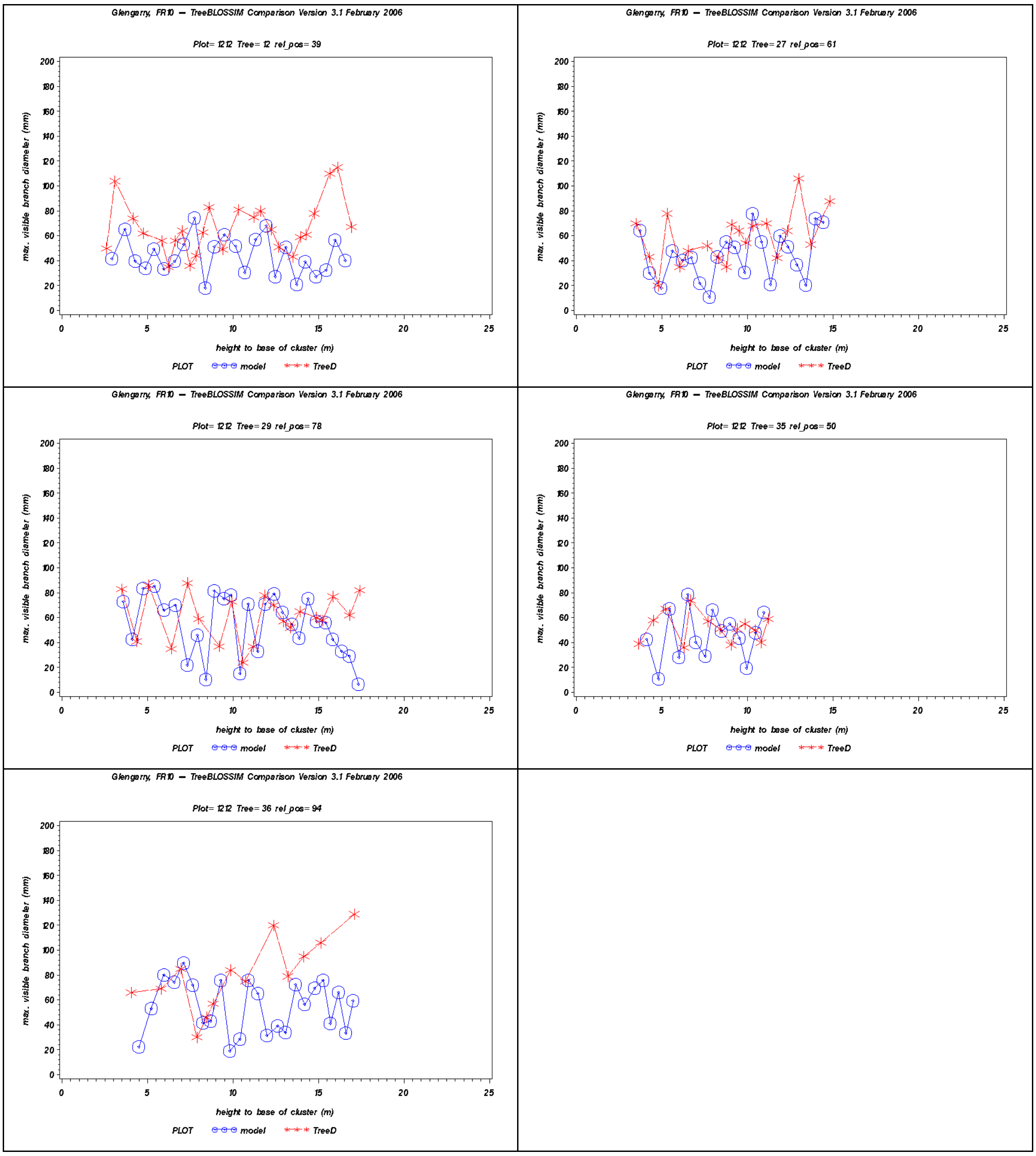
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR10, plot 10_12 (GF21 seedlot).



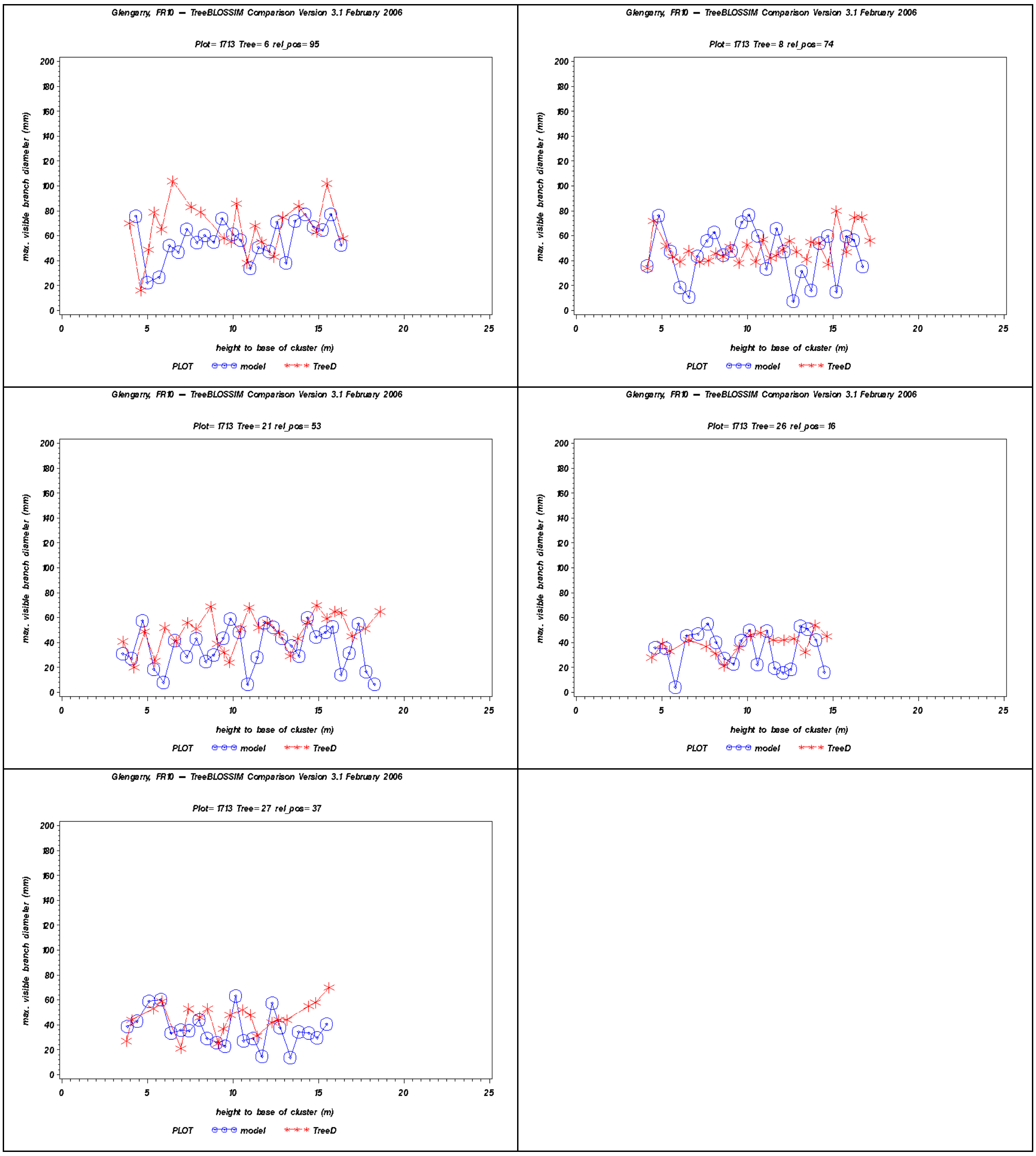
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR10, plot 11_12 (GF7 seedlot).



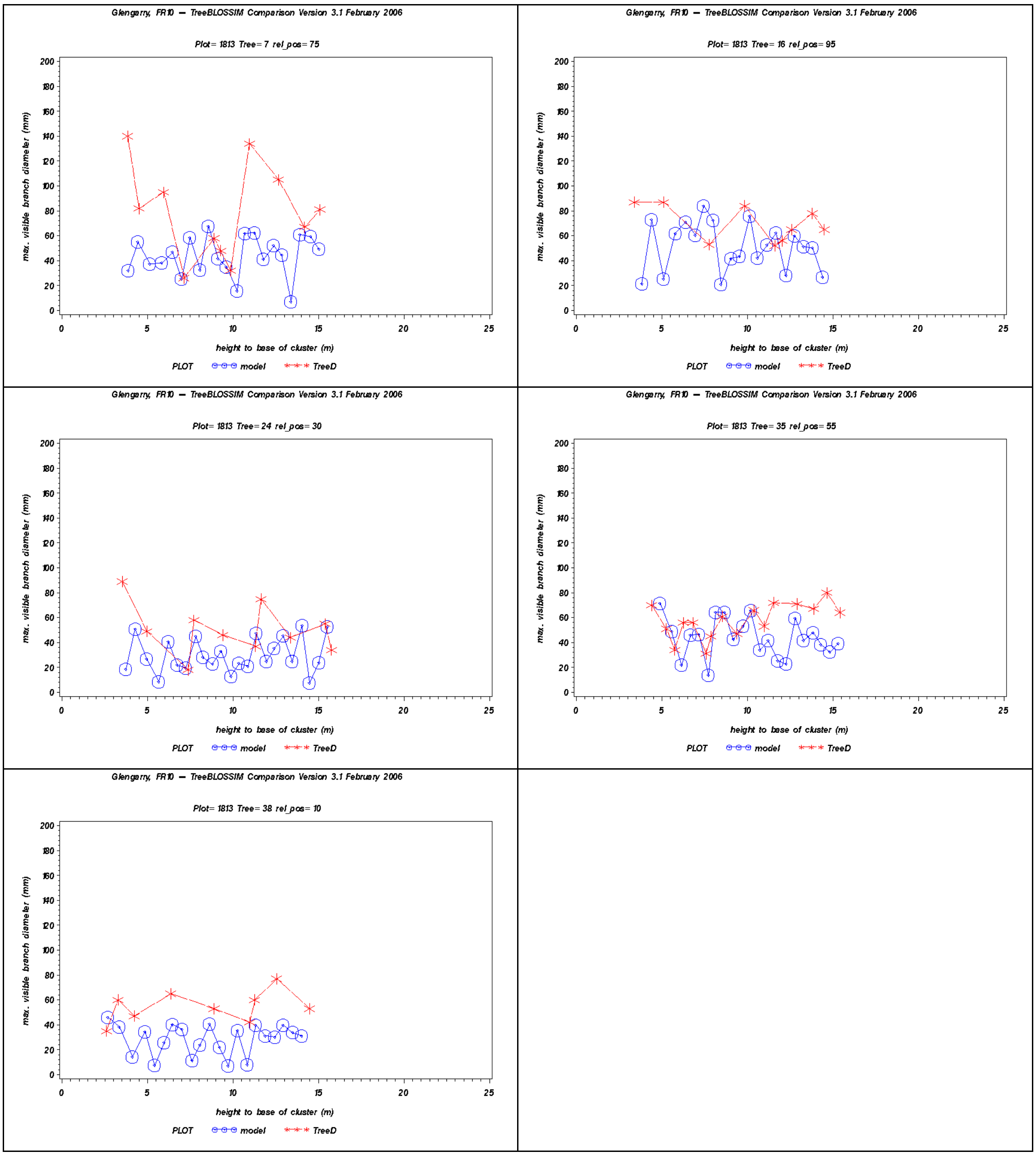
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR10, plot 12_12 (GF14 seedlot).



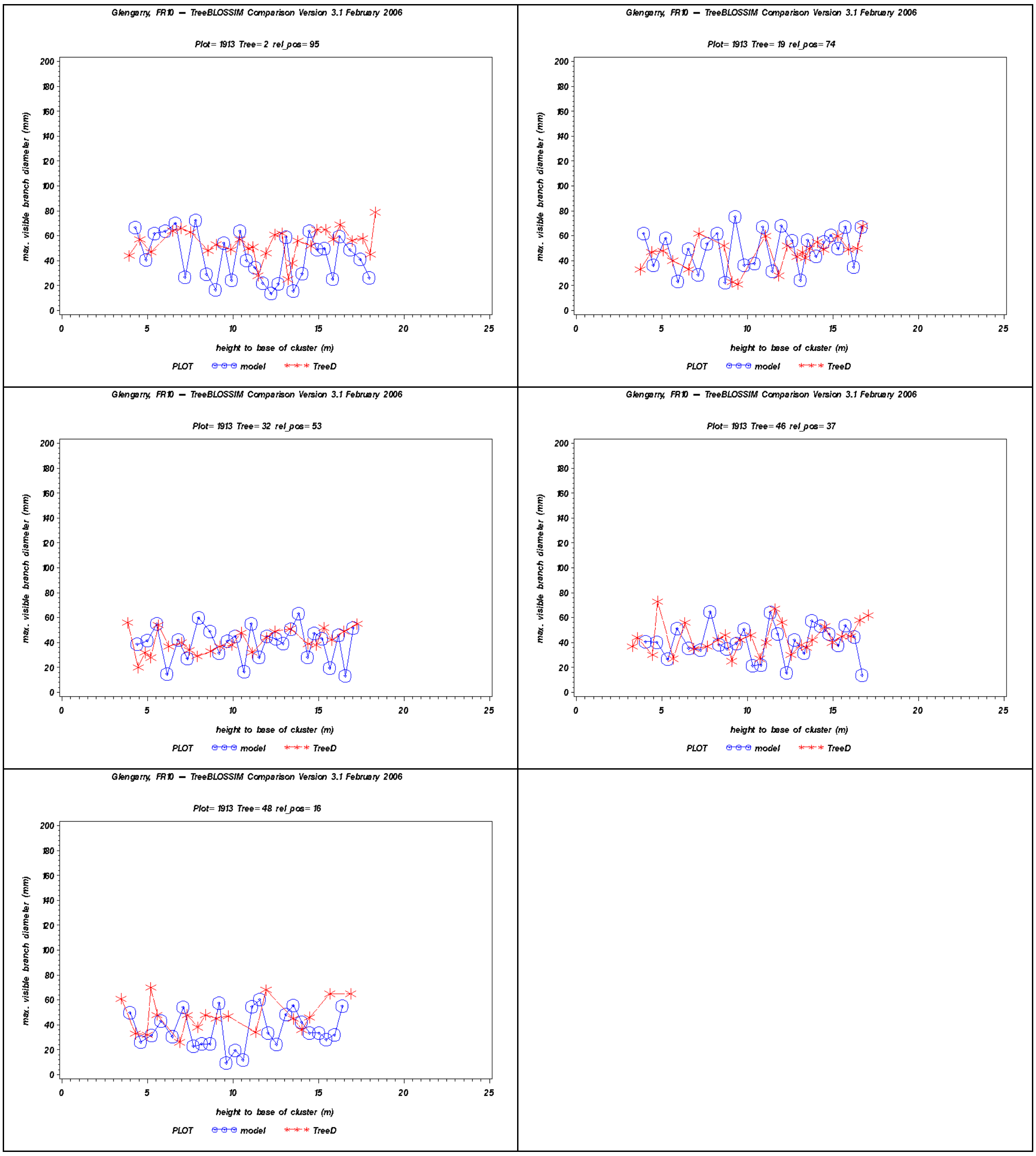
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR10, plot 17_13 (GF14 seedlot).



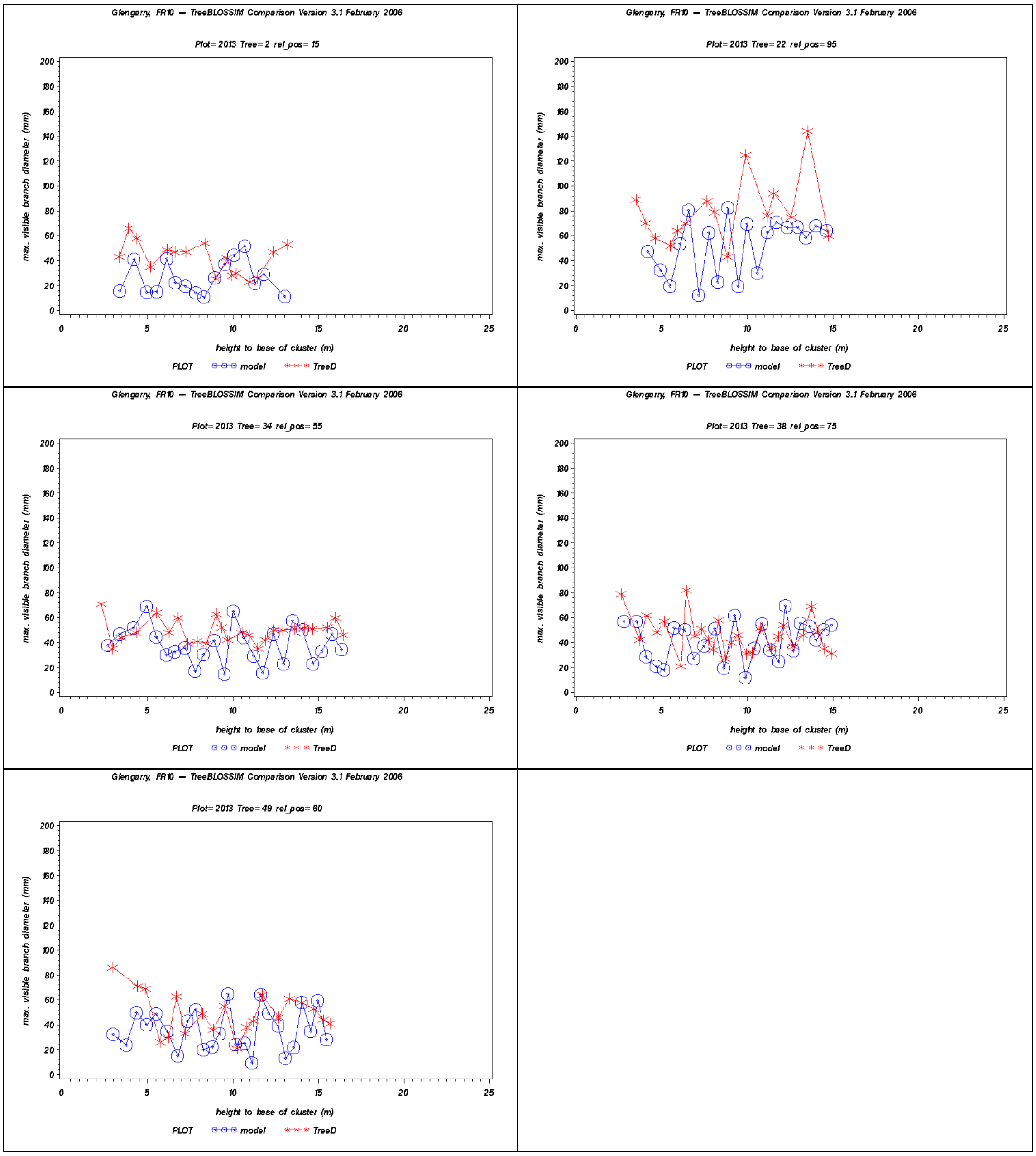
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR10, plot 18_13 (GF13 seedlot).



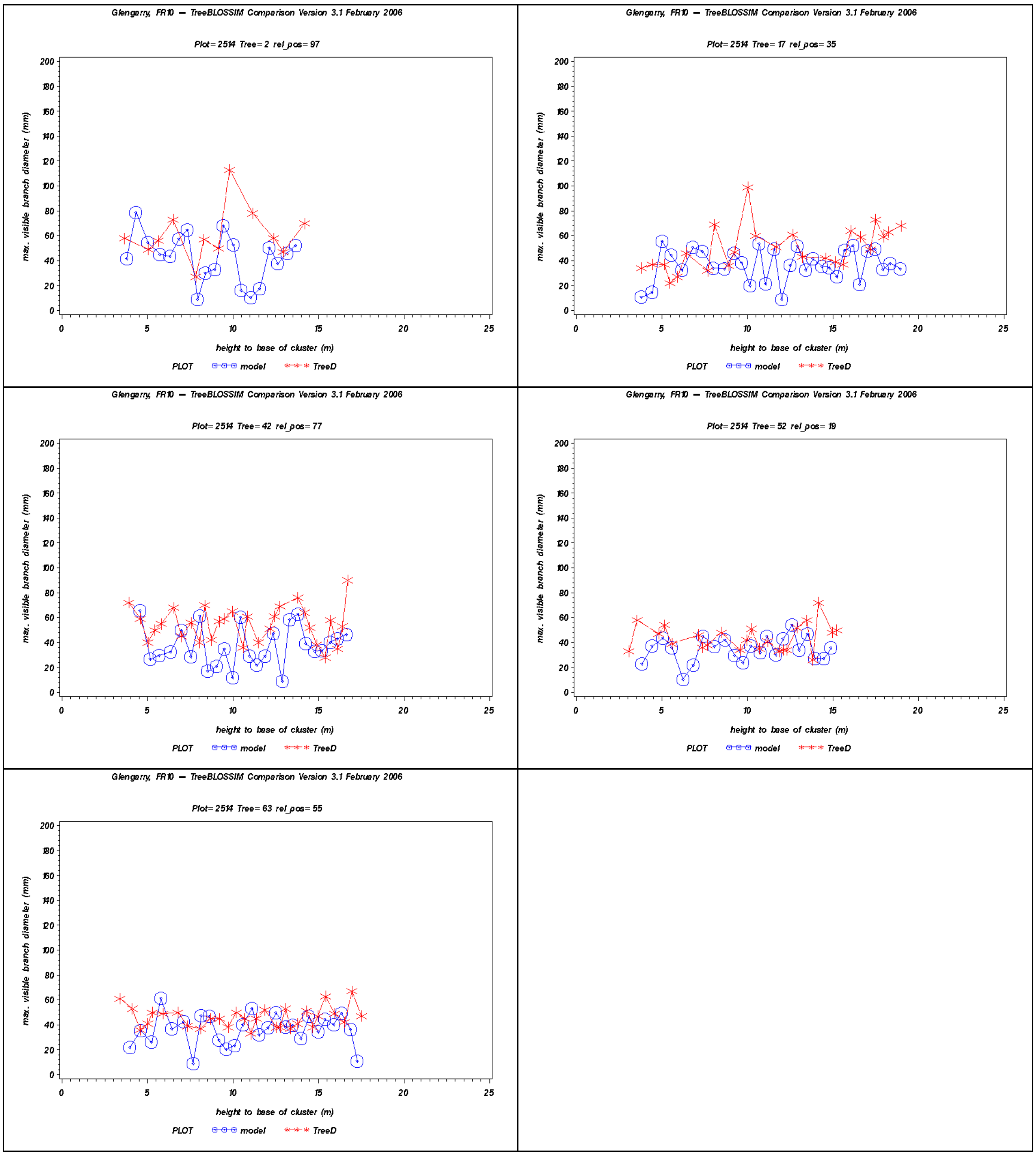
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR10, plot 19_13 (GF21 seedlot).



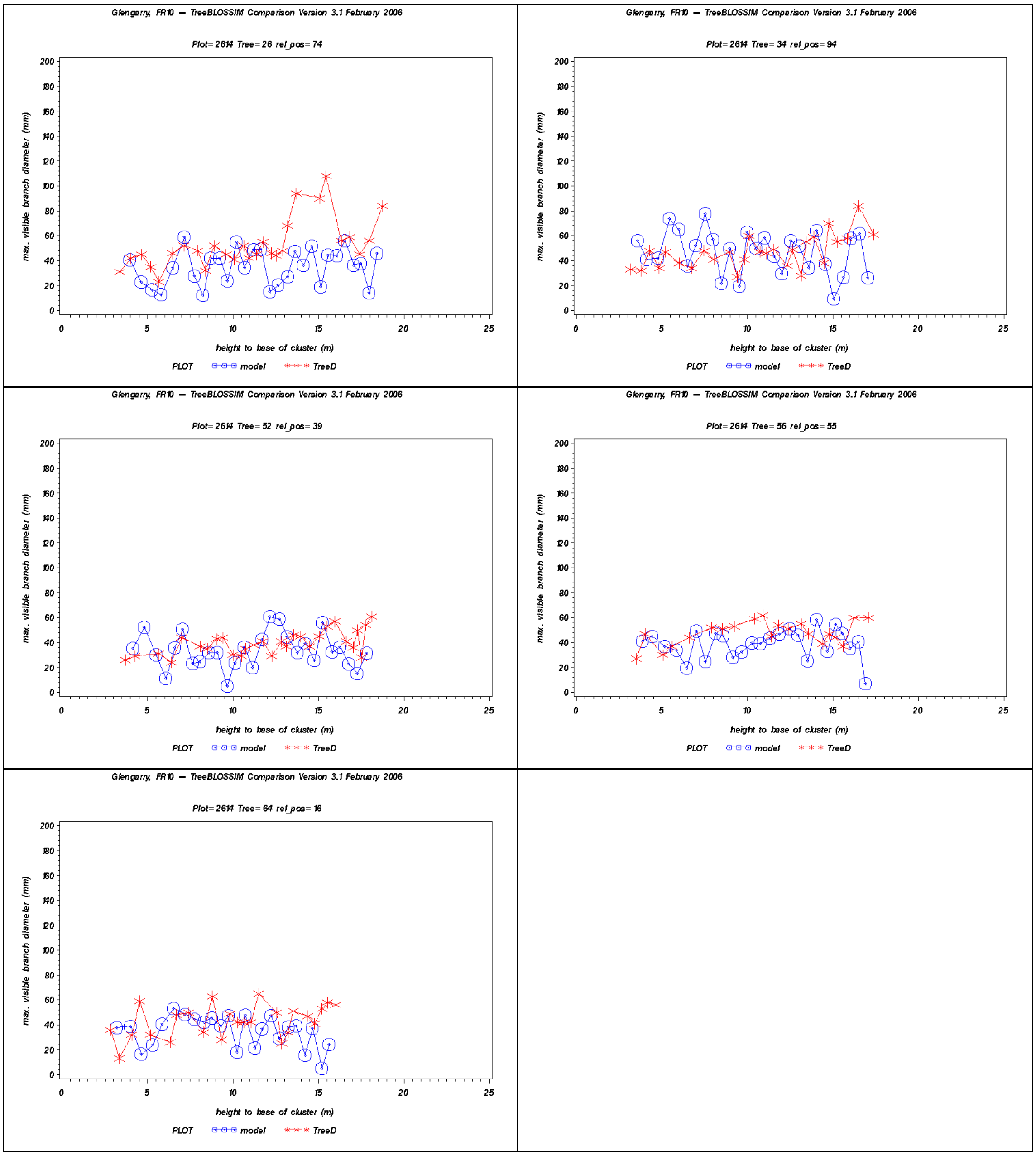
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR10, plot 20_13 (GF7 seedlot).



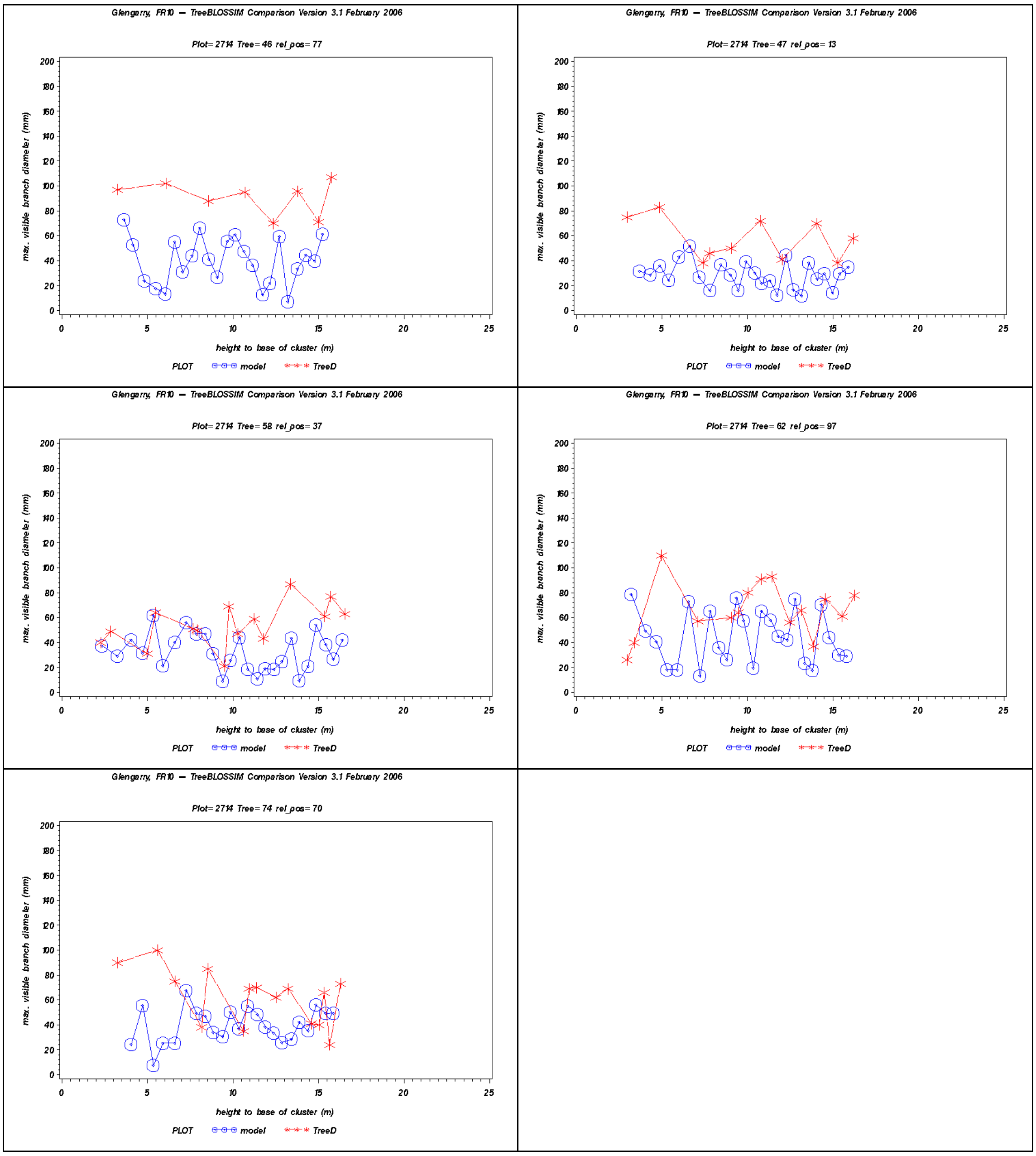
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR10, plot 25_14 (GF7 seedlot).



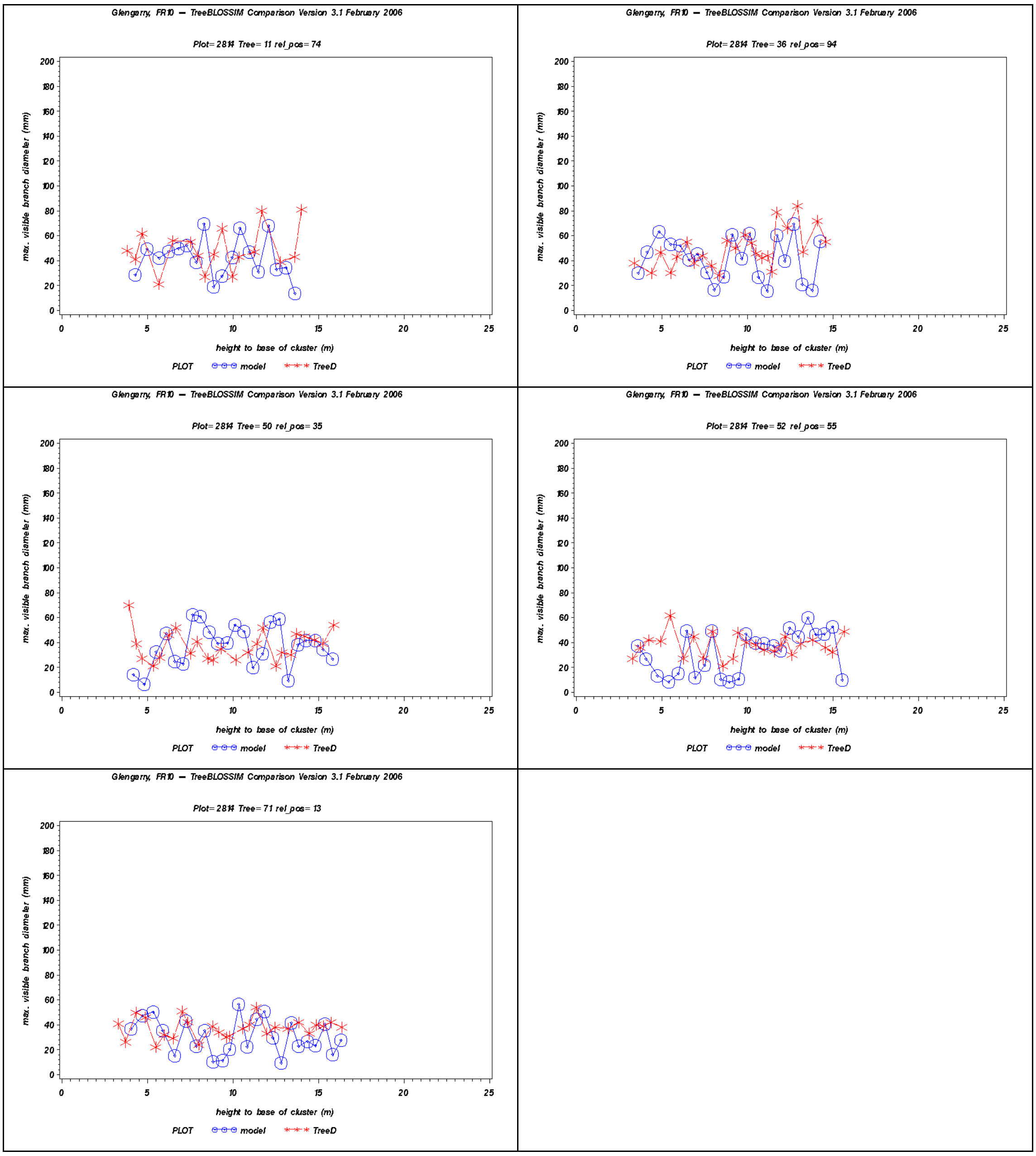
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR10, plot 26_14 (GF14 seedlot).



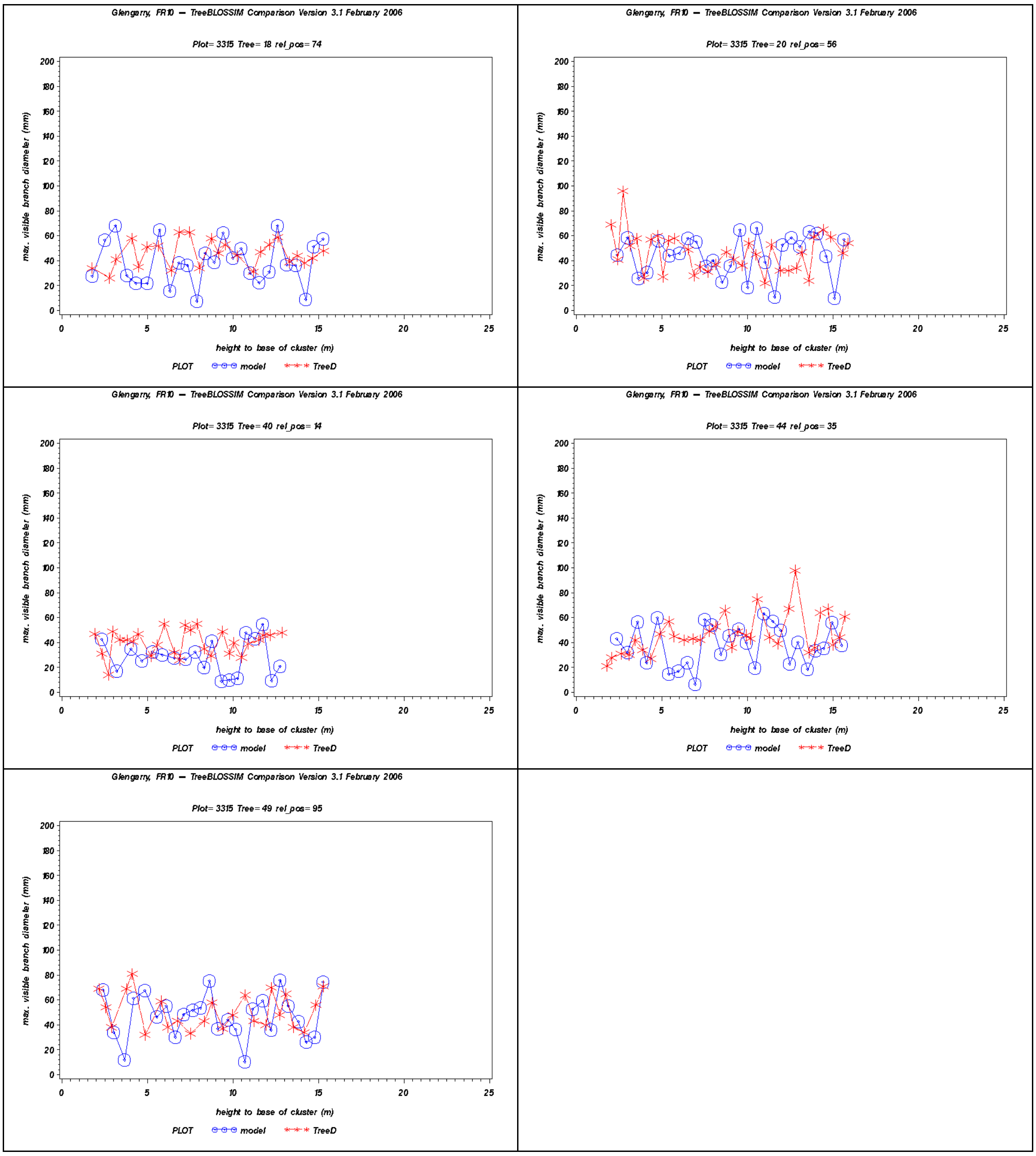
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR10, plot 27_14 (GF13 seedlot).



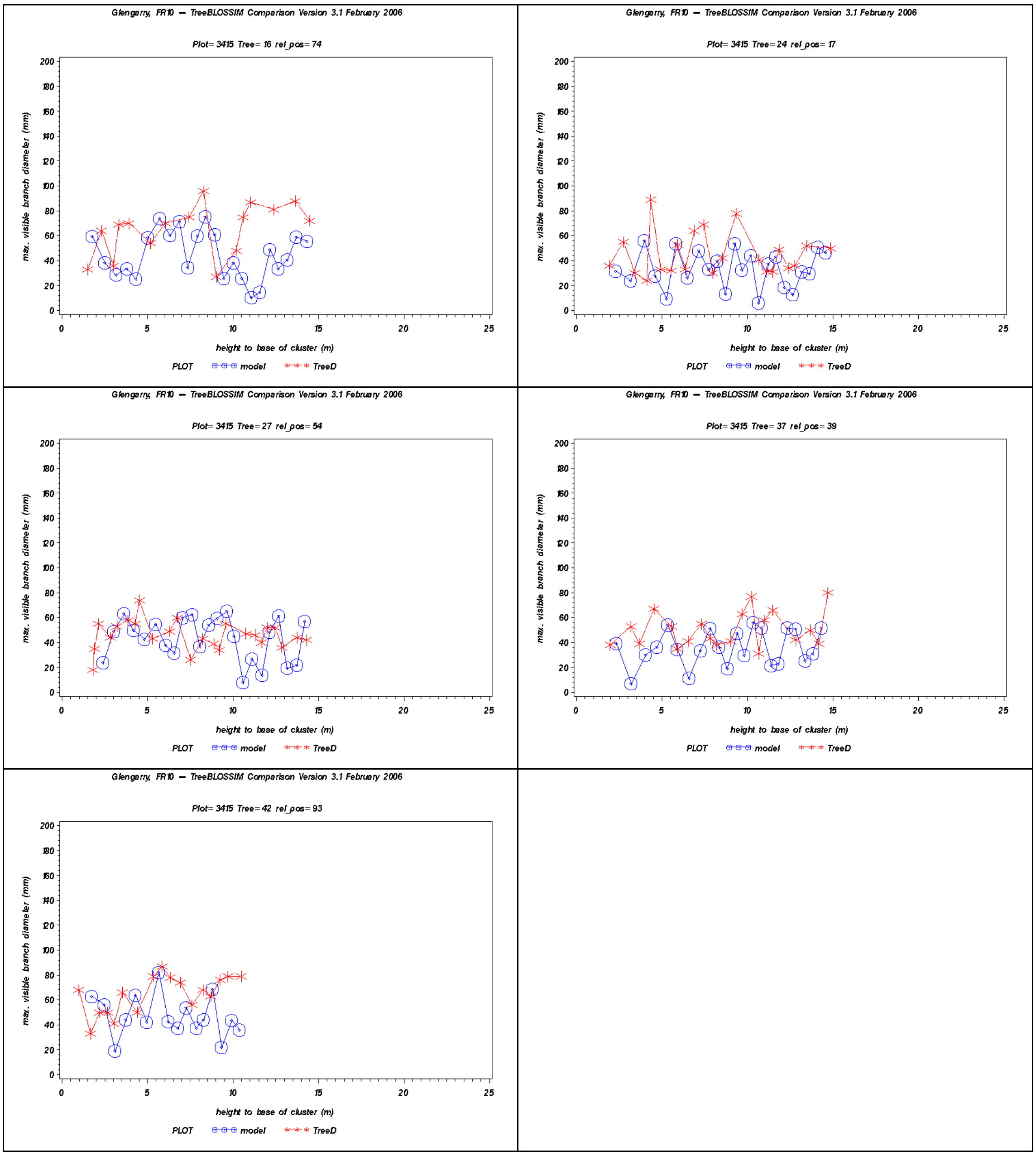
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR10, plot 28_14 (GF21 seedlot).



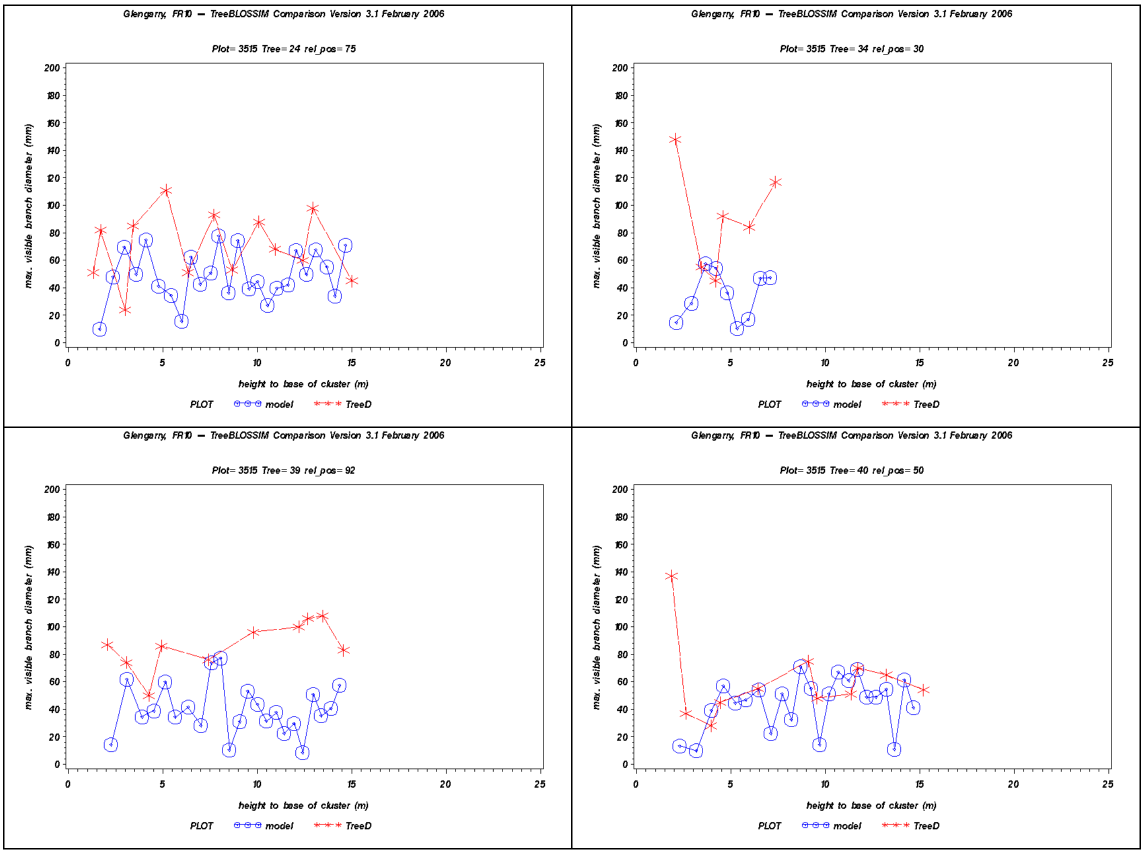
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR10, plot 33_15 (GF21 seedlot).



Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR10, plot 34_15 (GF14 seedlot).

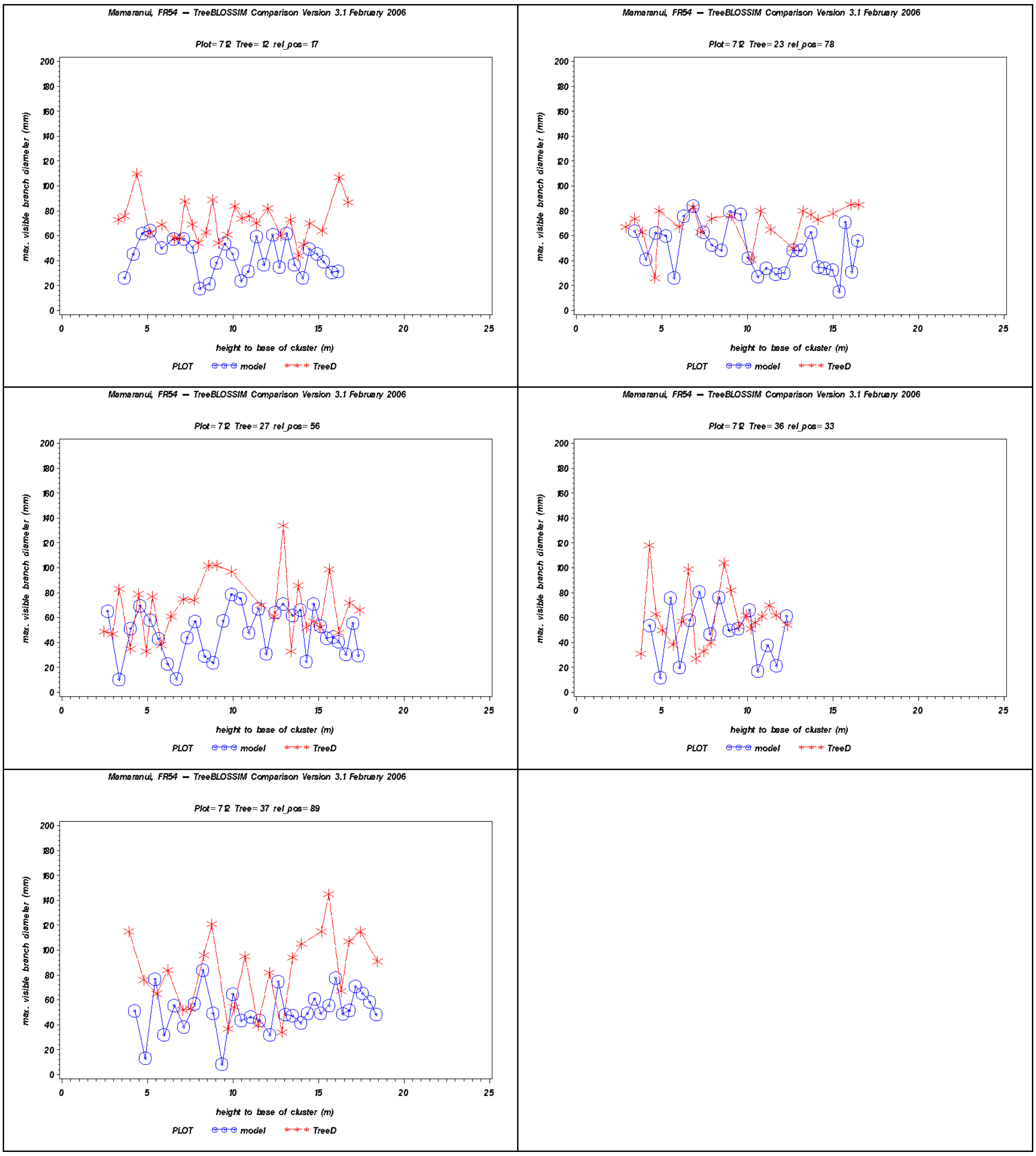


Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR10, plot 35_15 (GF13 seedlot).

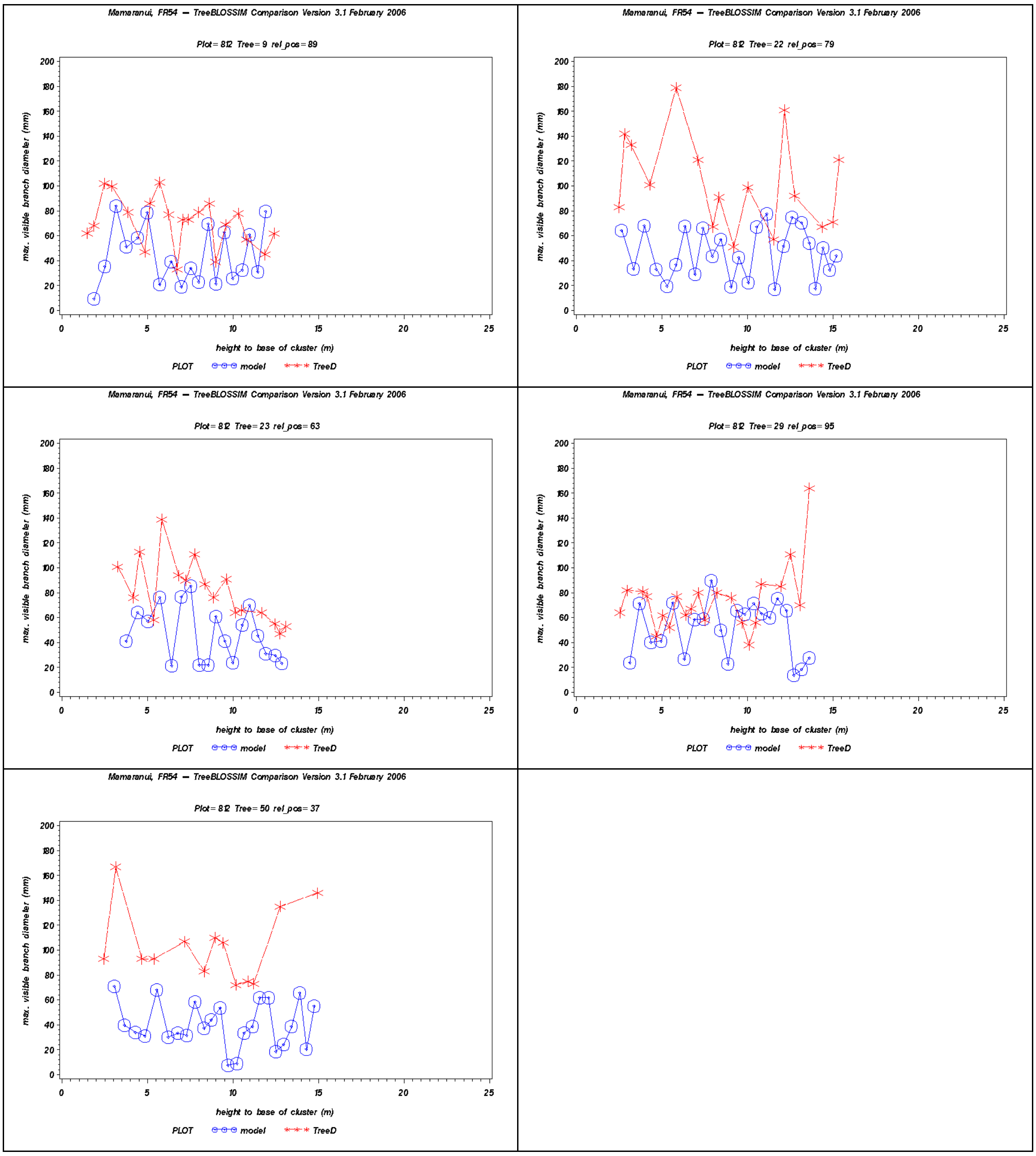


APPENDIX 3. Mamaranui, FR54

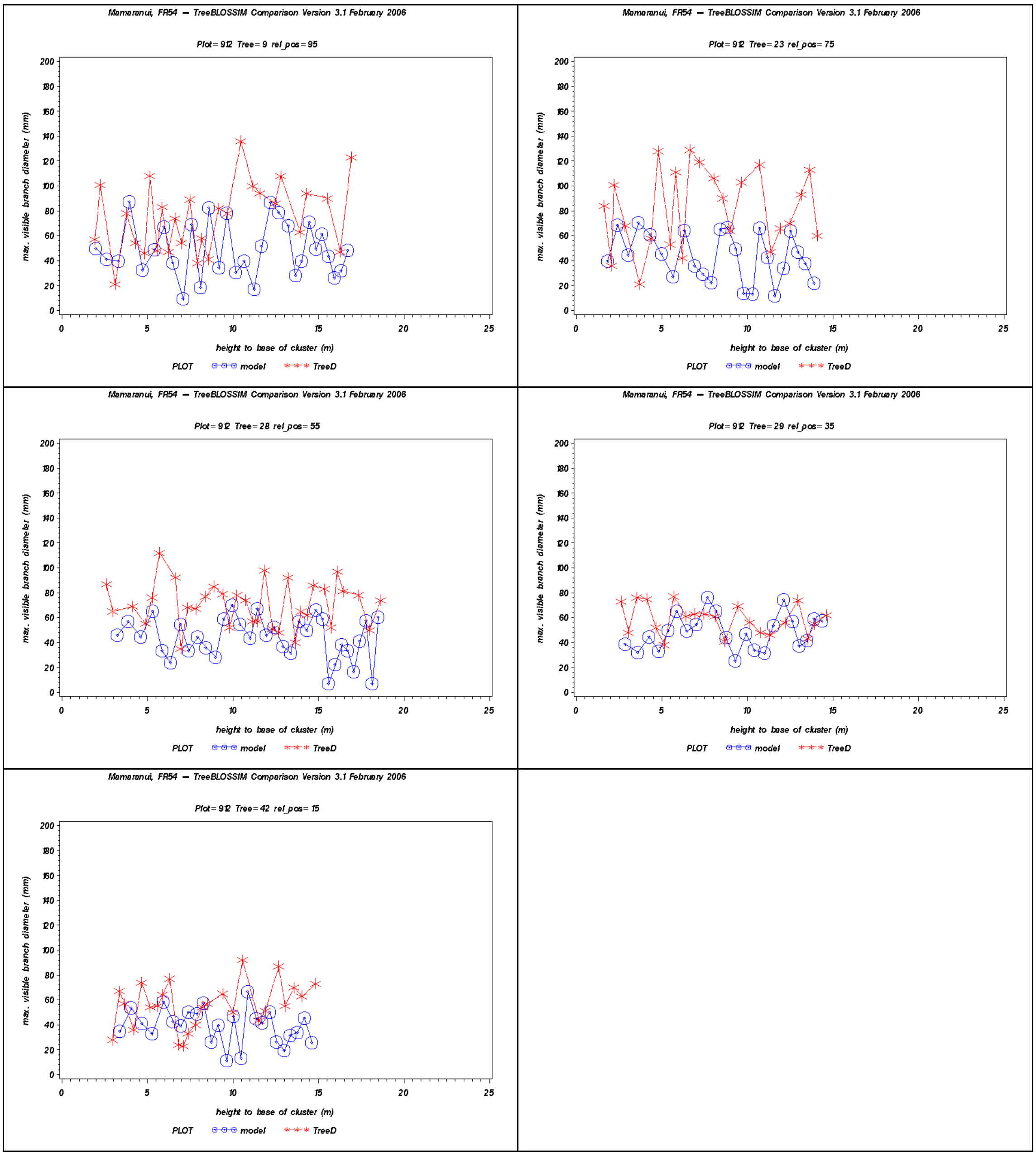
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR54, plot 07_12 (GF22 seedlot).



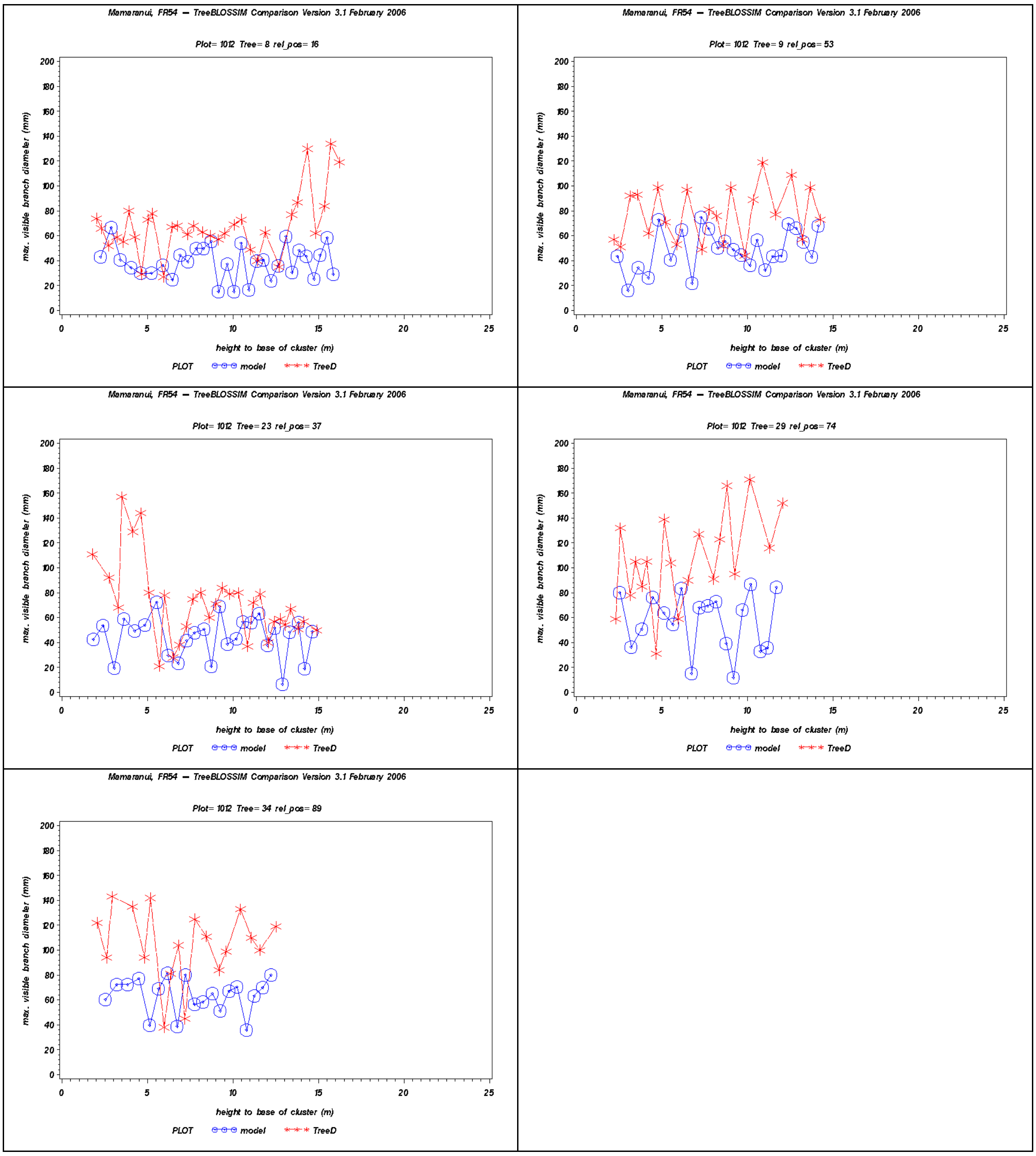
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR54, plot 08_12 (GF9 seedlot).



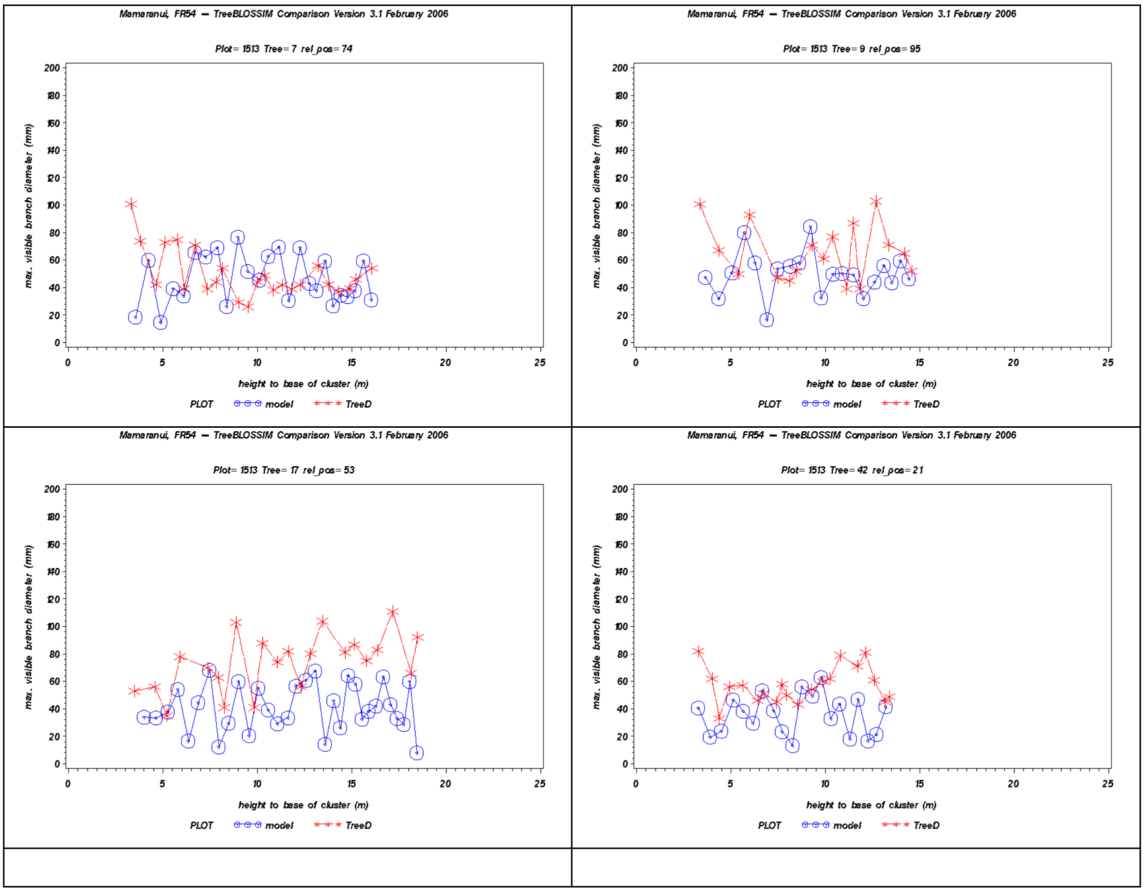
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR54, plot 09_12 (GF17 cuttings seedlot).



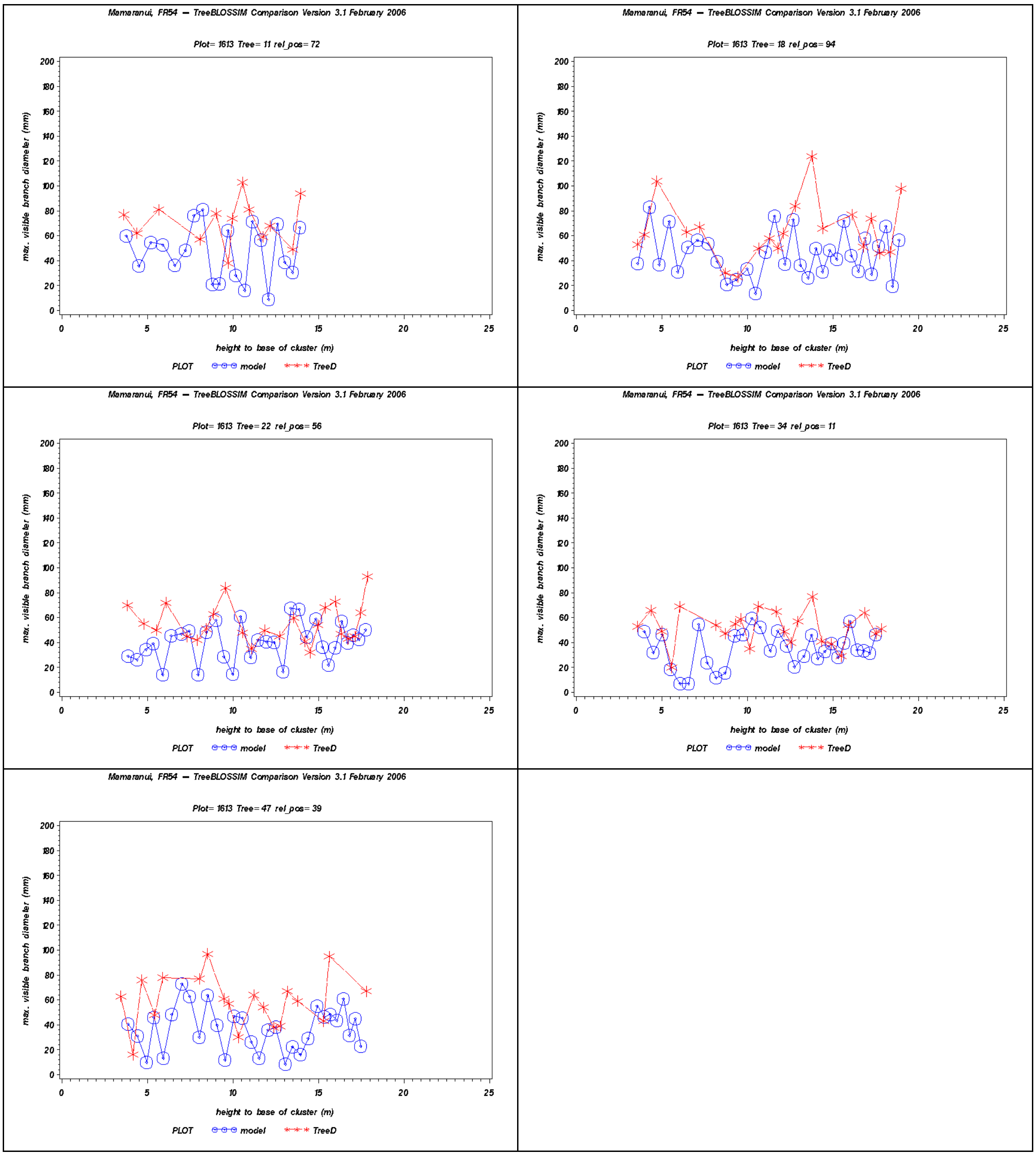
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR54, plot 10_12 (GF14 seedlot).



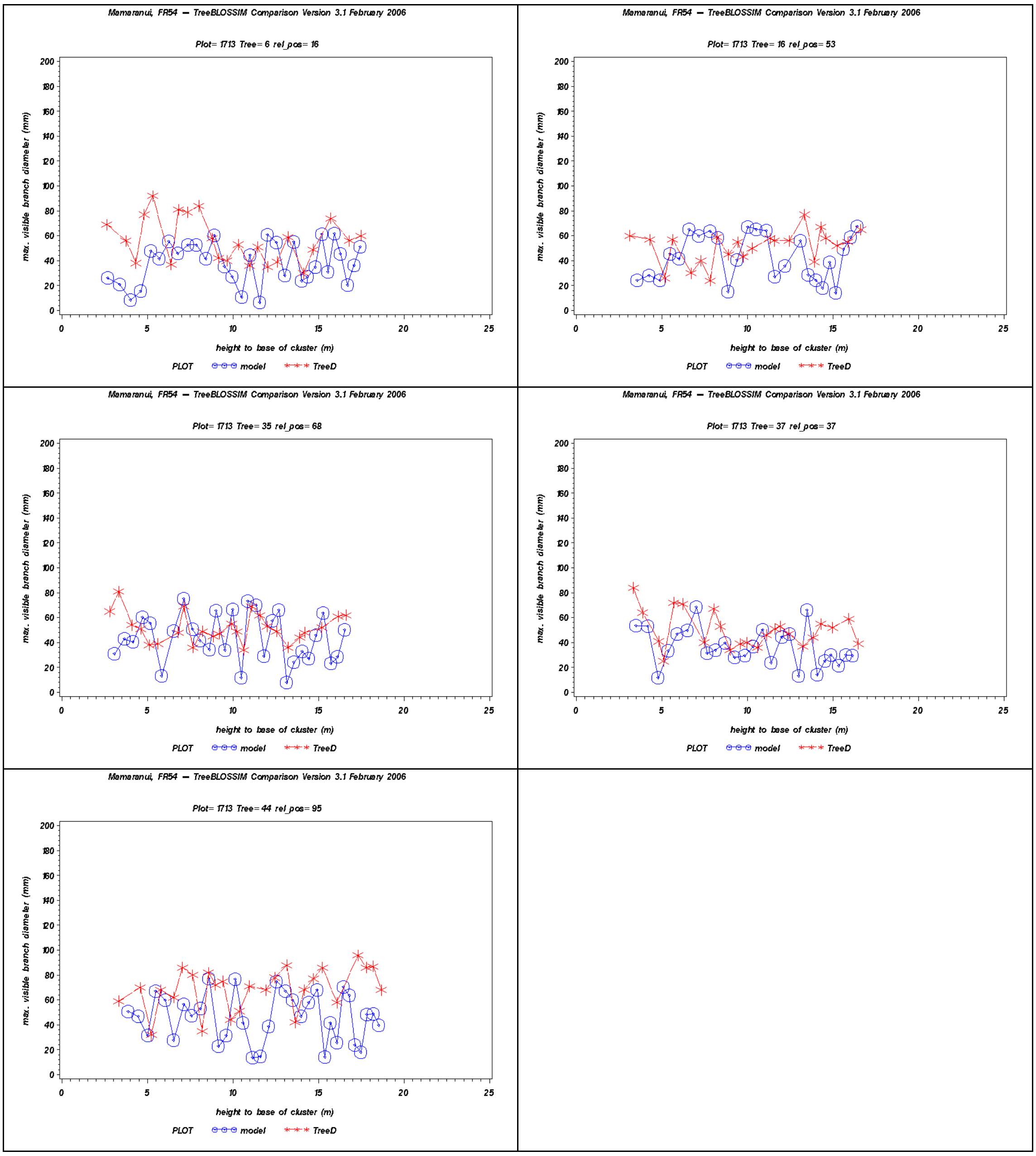
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR54, plot 15_13 (GF14 seedlot).



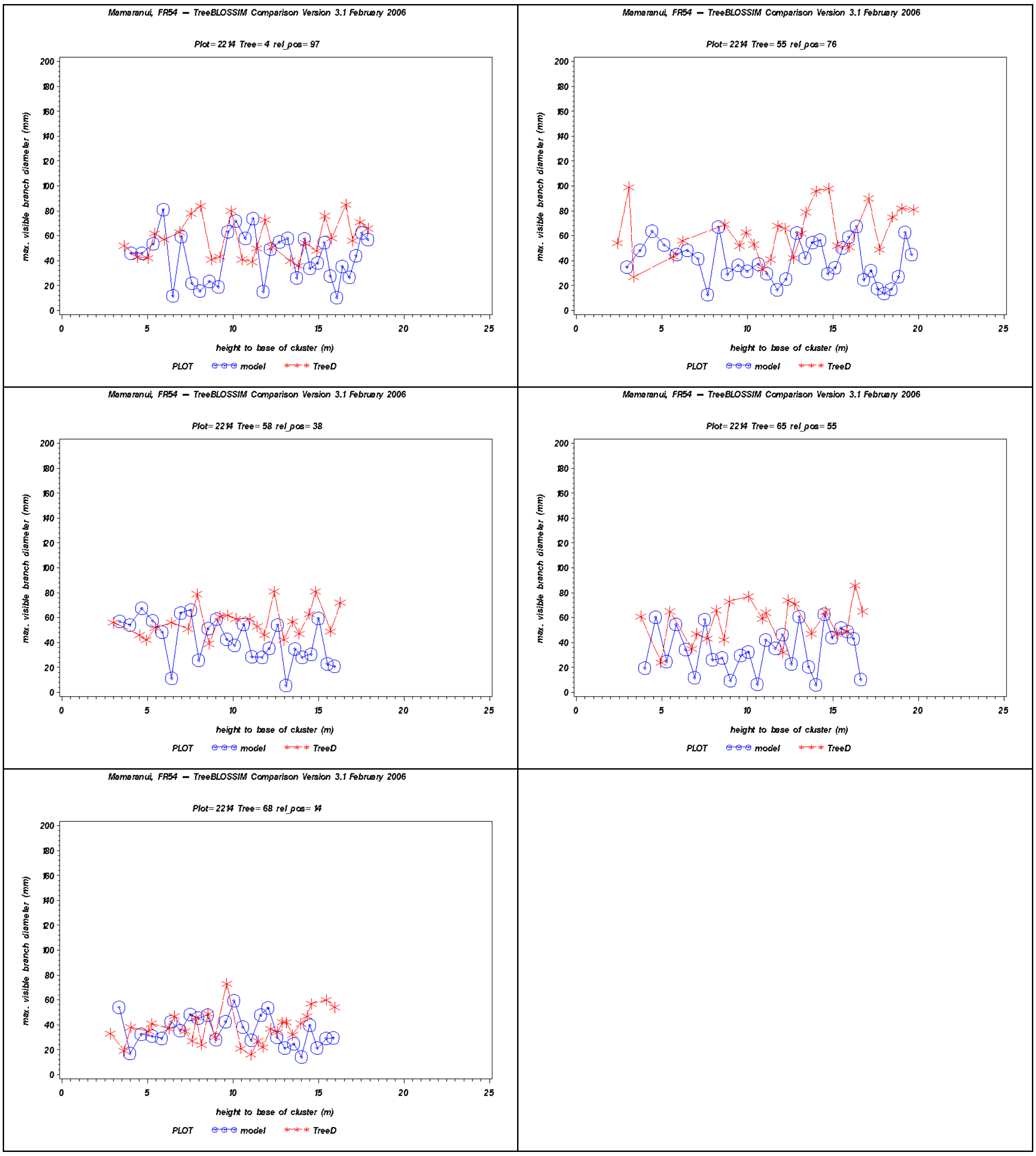
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR54, plot 16_13 (GF9 seedlot).



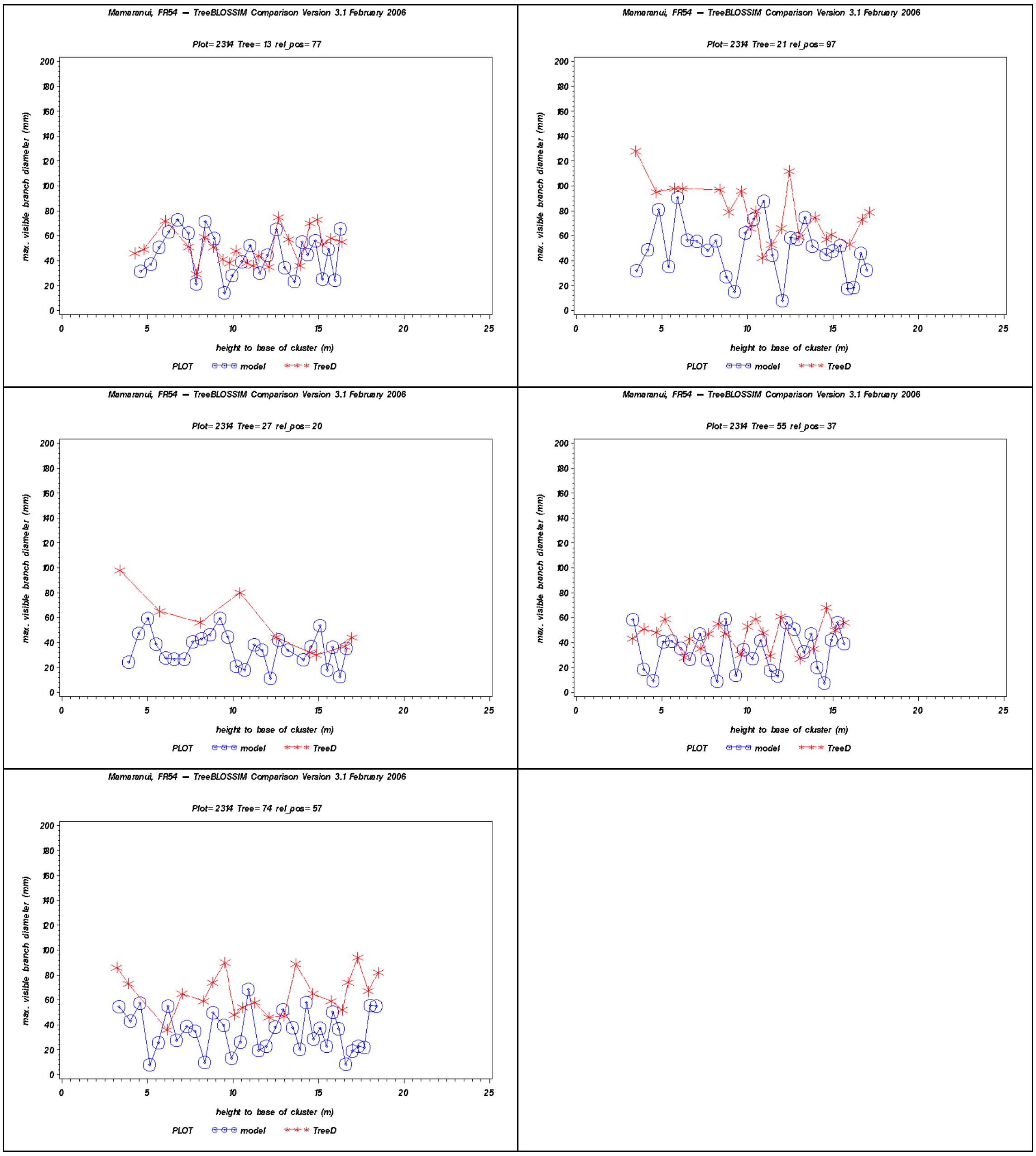
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR54, plot 17_13 (GF22 seedlot).



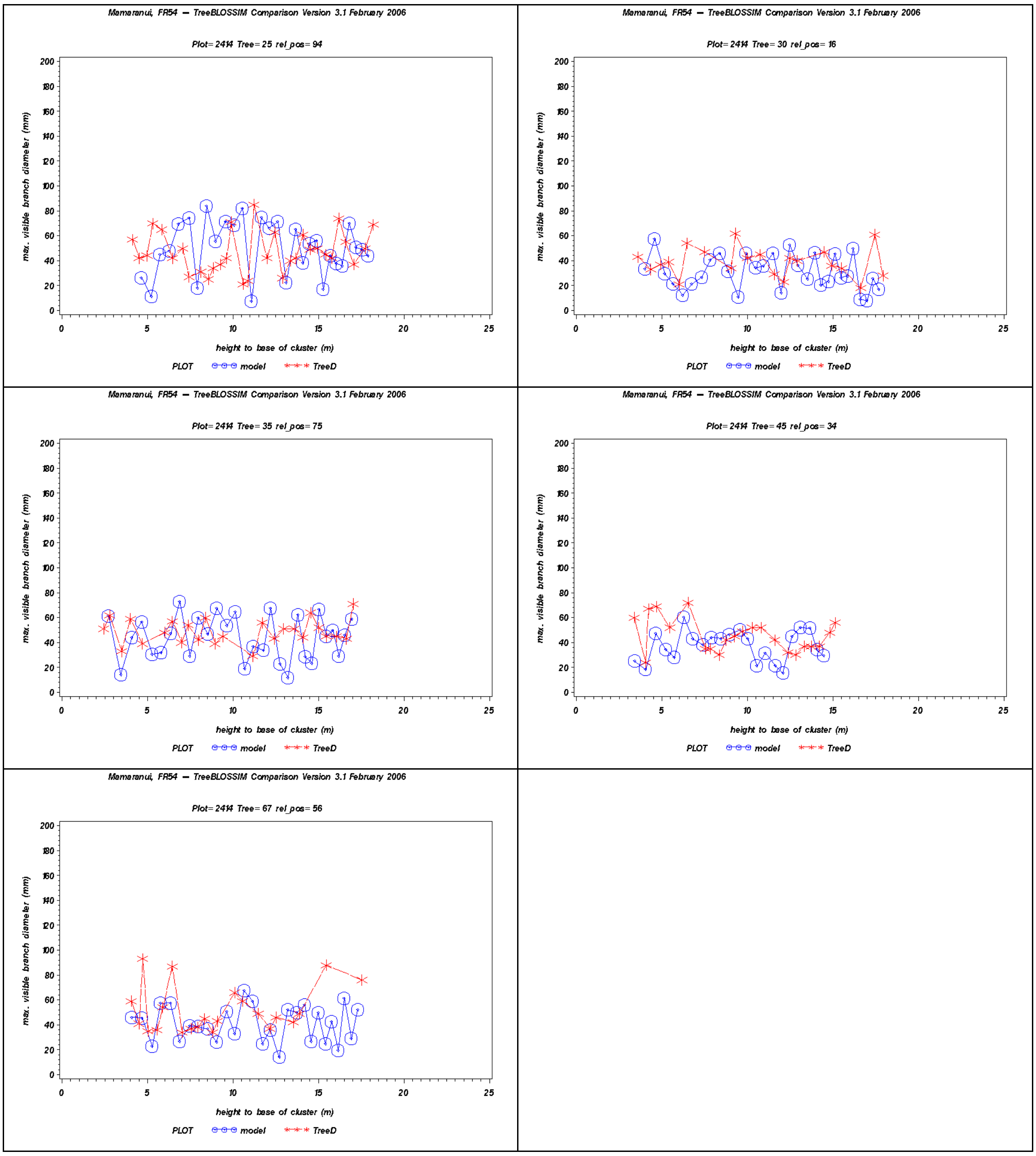
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR54, plot 22_14 (GF14 seedlot).



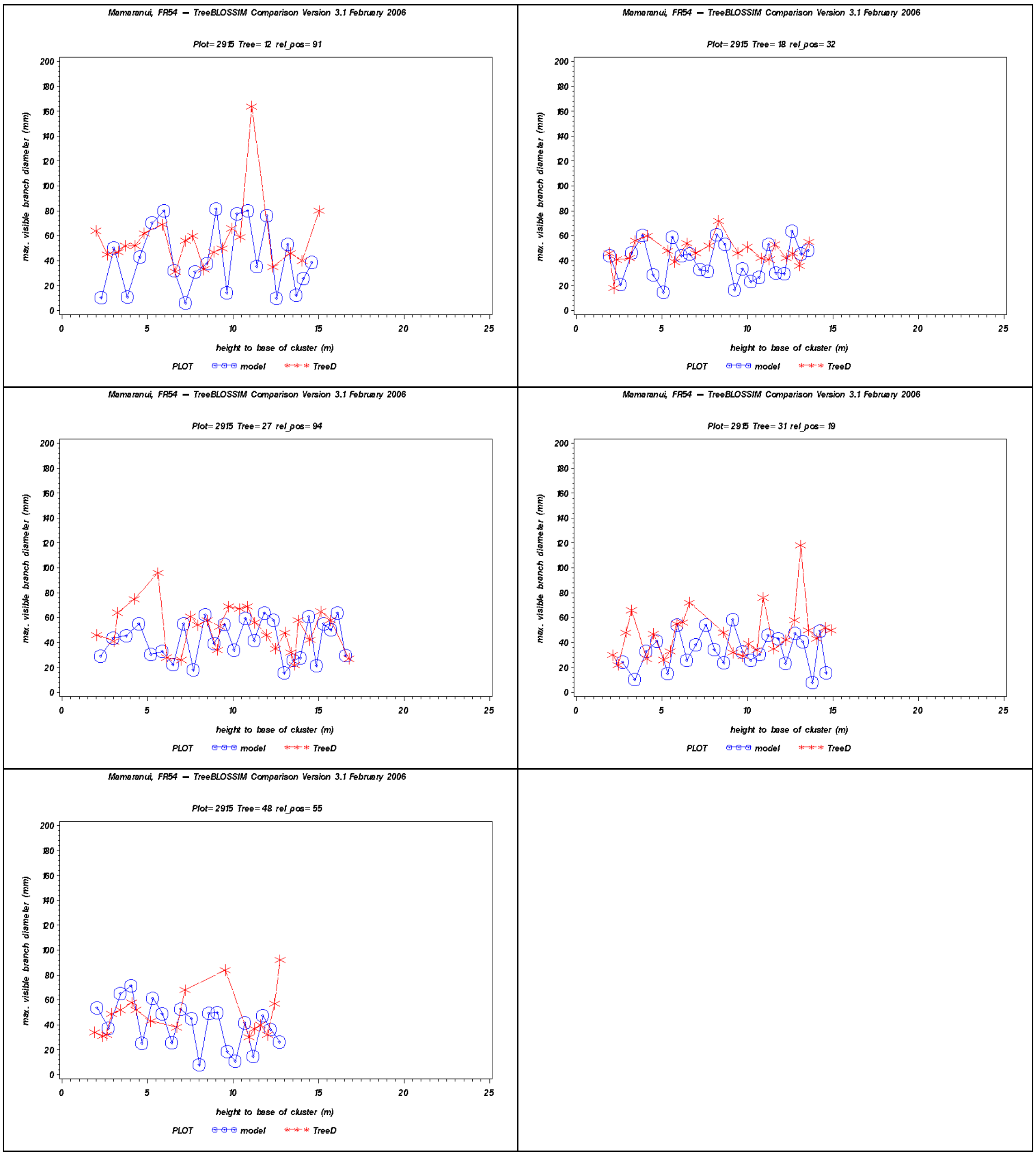
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR54, plot 23_14 (GF9 seedlot).



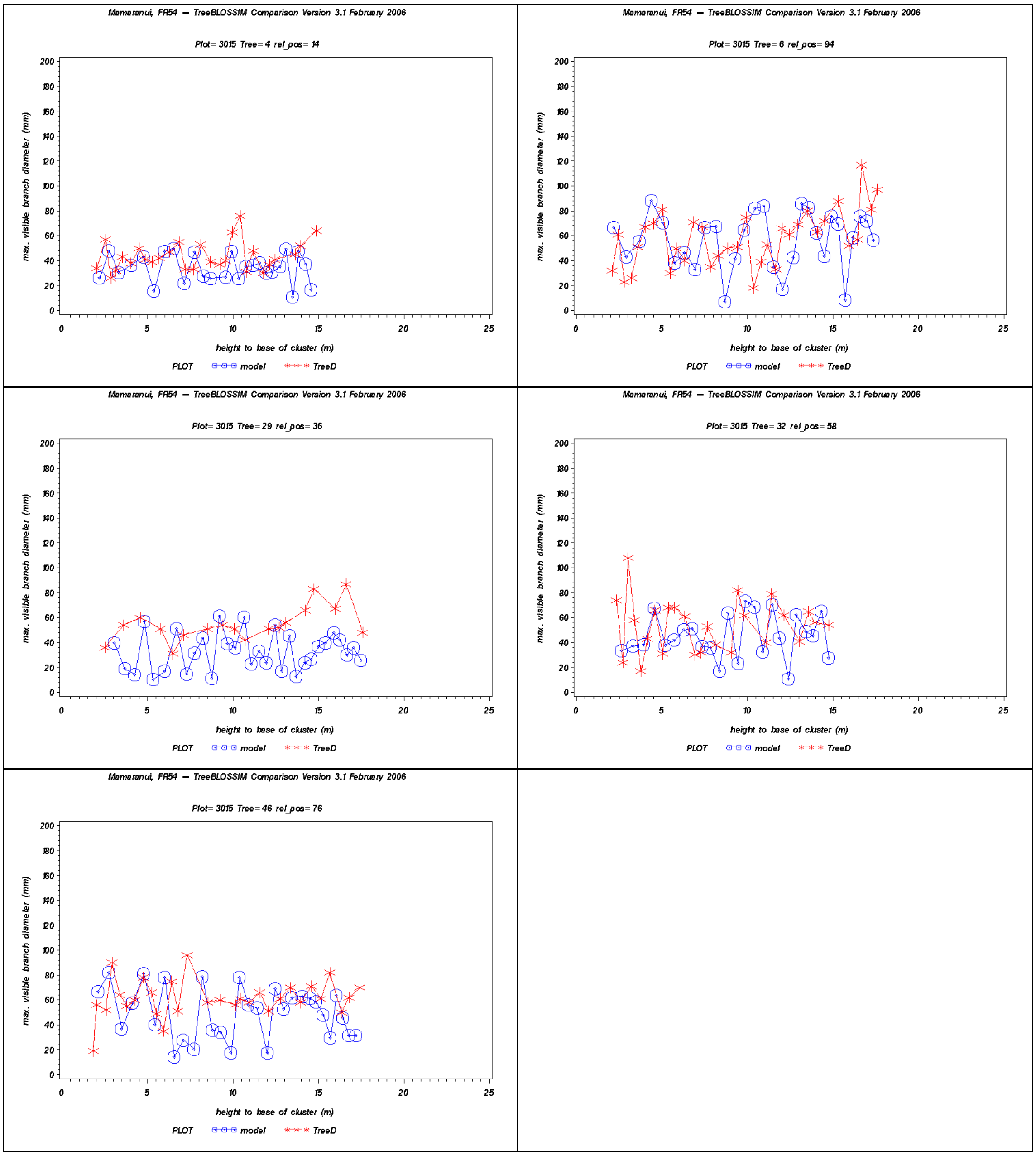
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR54, plot 24_14 (GF22 seedlot).



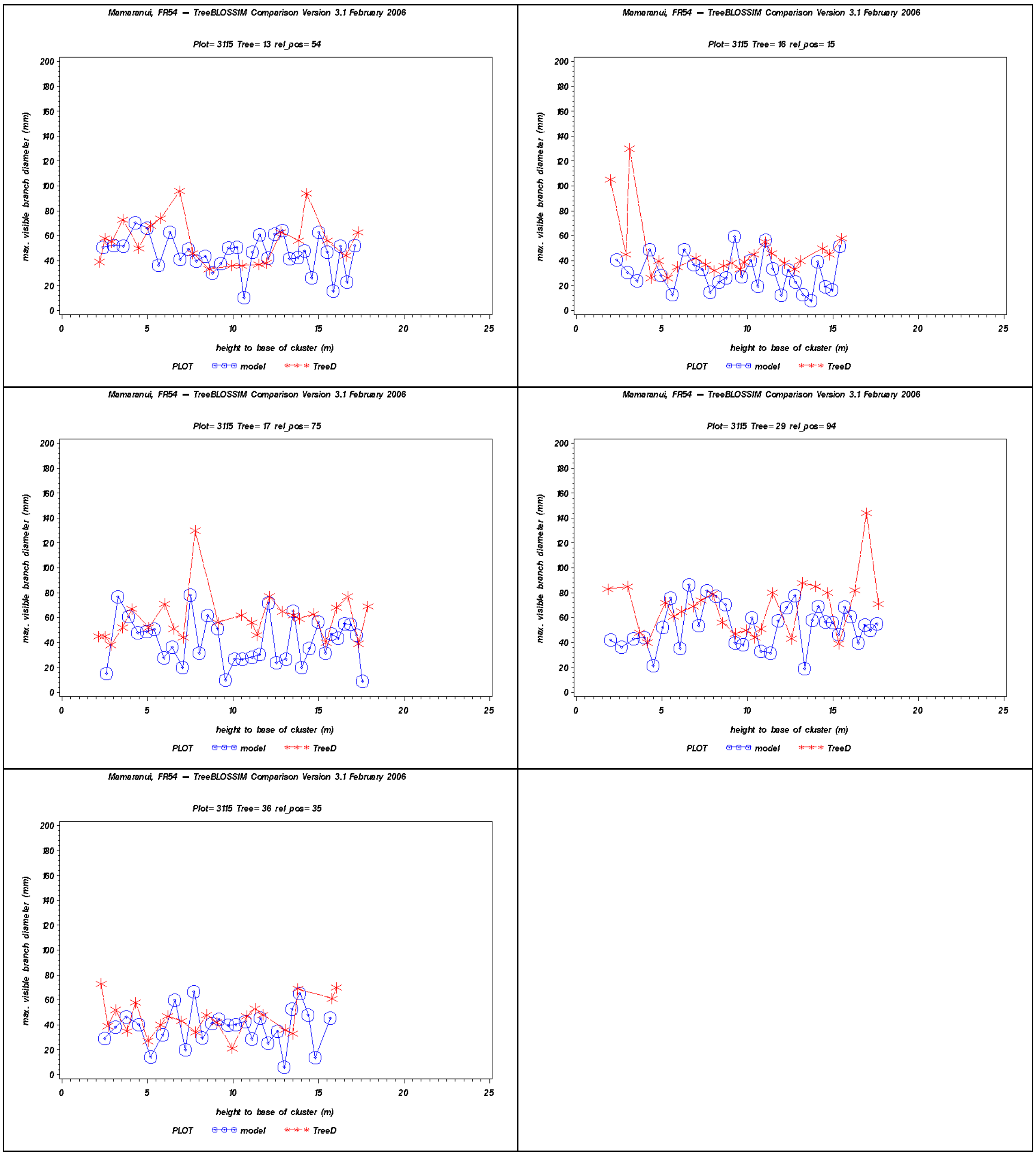
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR54, plot 29_15 (GF14 seedlot).



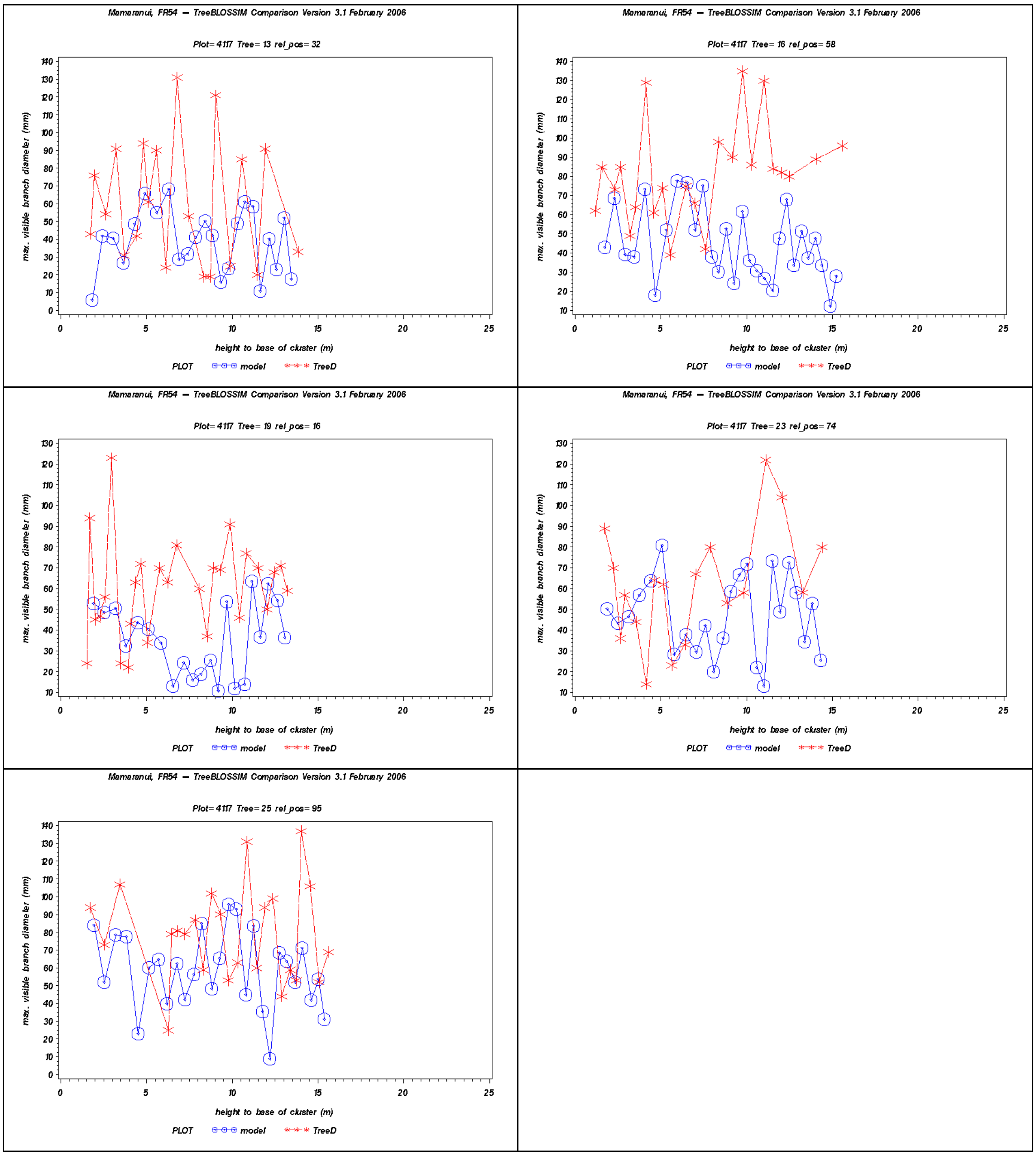
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR54, plot 30_15 (GF22 seedlot).



Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR54, plot 31_15 (GF9 seedlot).

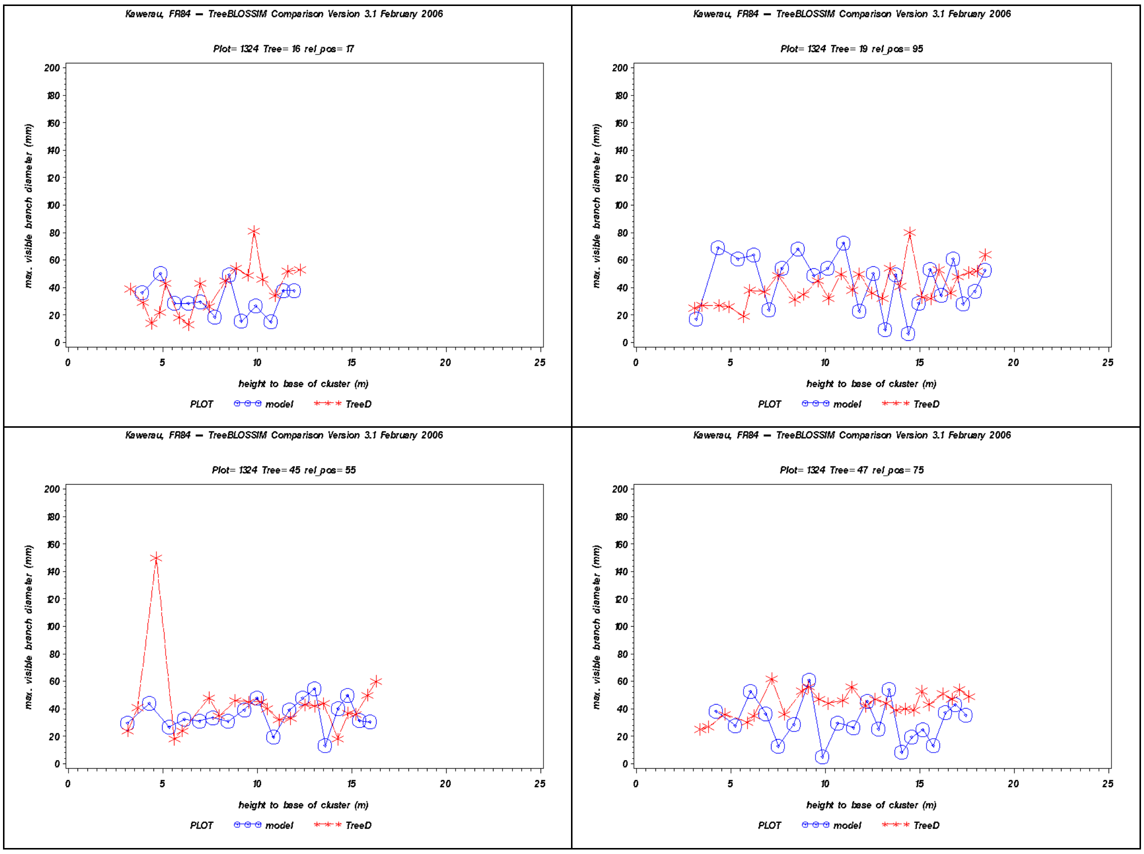


Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR54, plot 41_17 (GF17, cuttings seedlot).

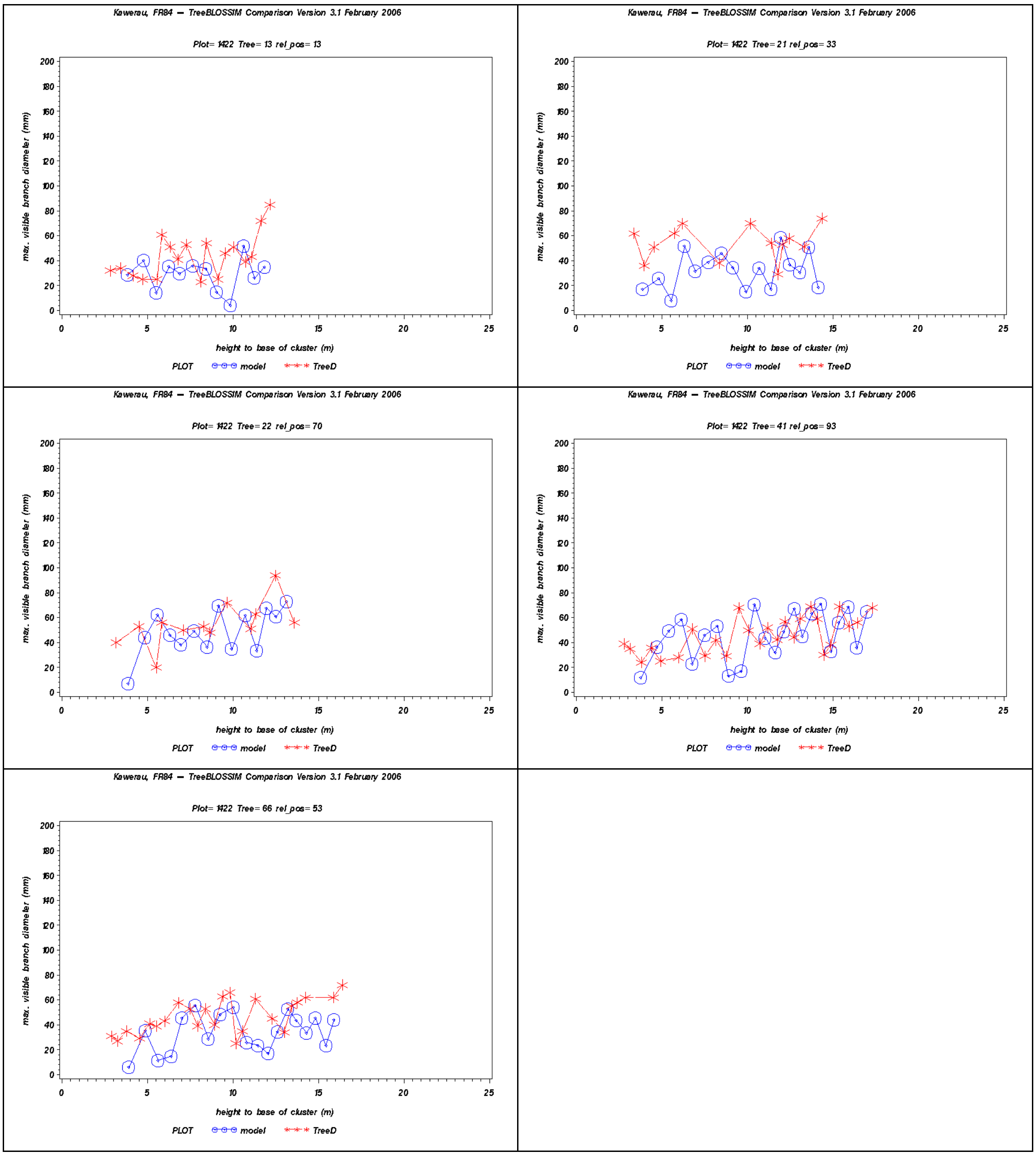


APPENDIX 4. Kawerau, FR84

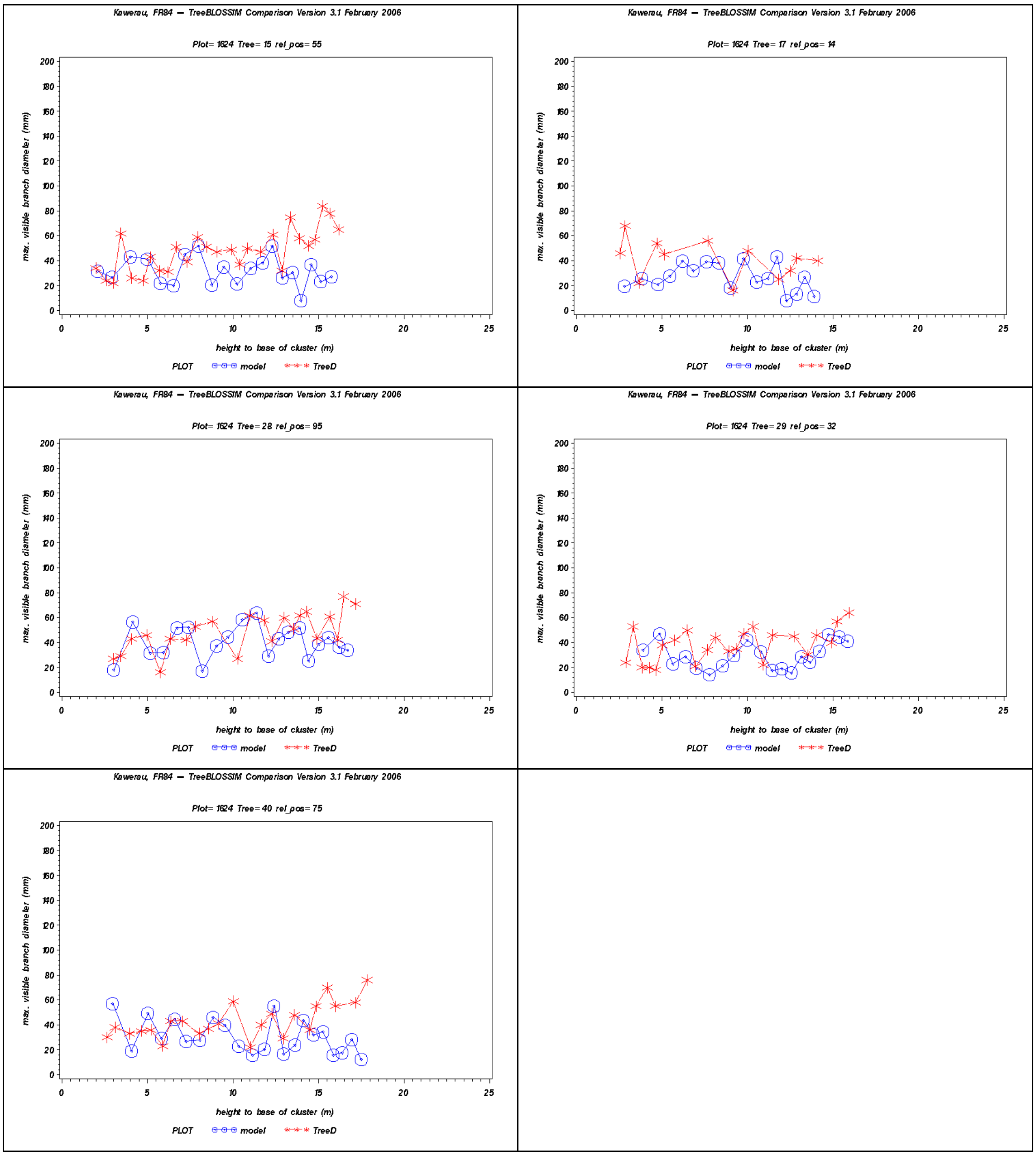
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR84, plot 13_24 (GF25 seedlot).



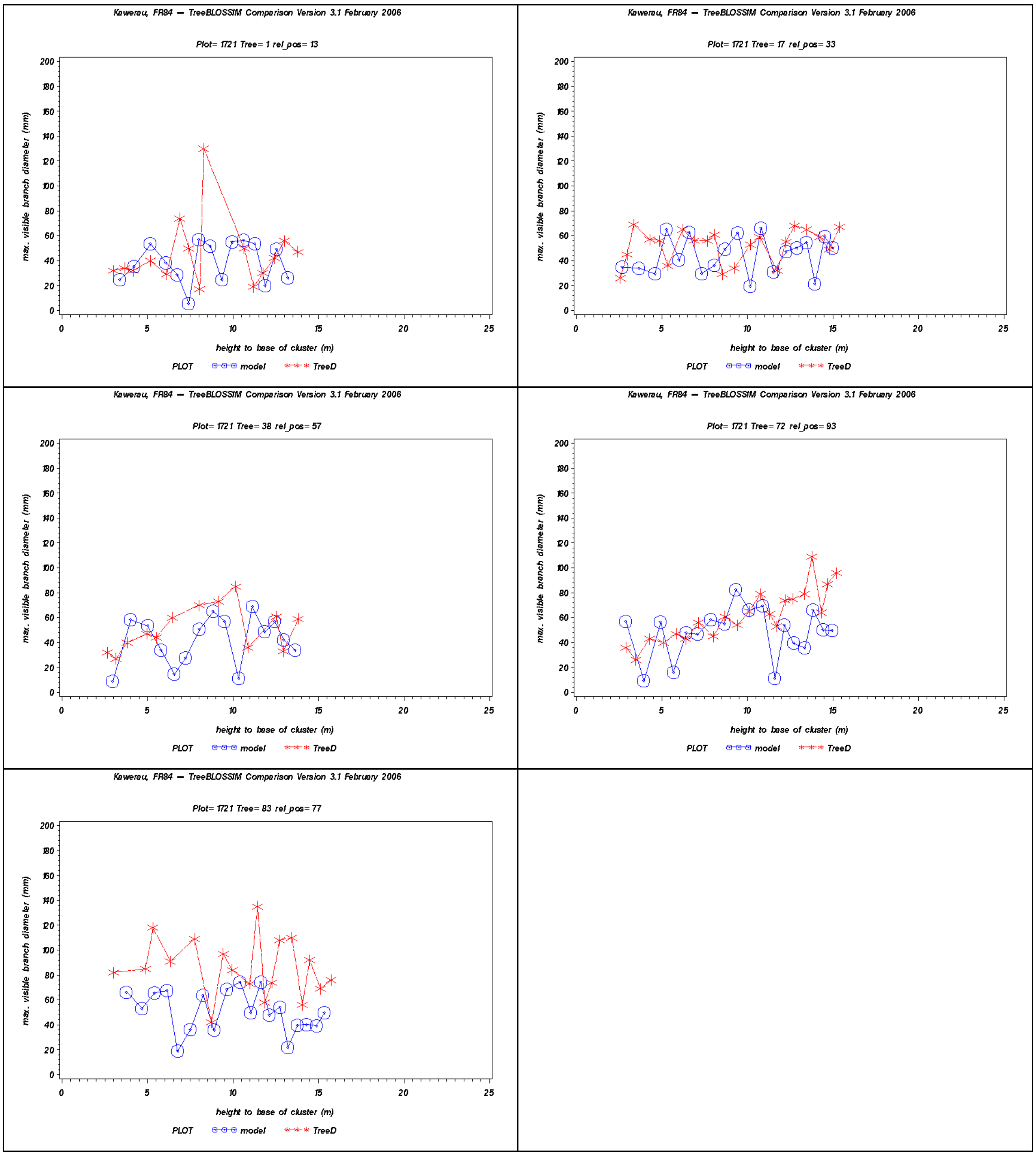
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR84, plot 14_22 (GF16 seedlot).



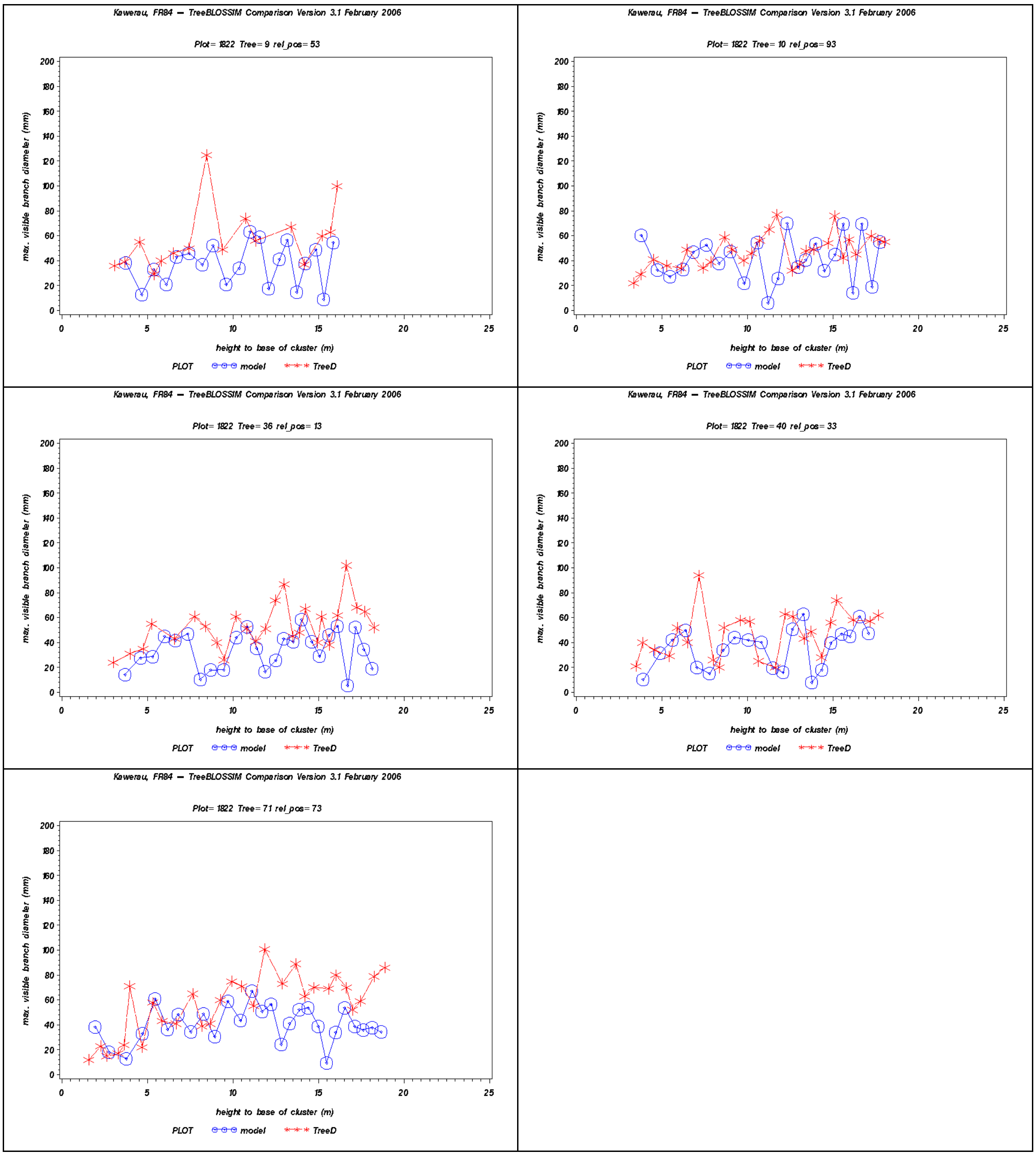
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR84, plot 16_24 (GF25 cutting).



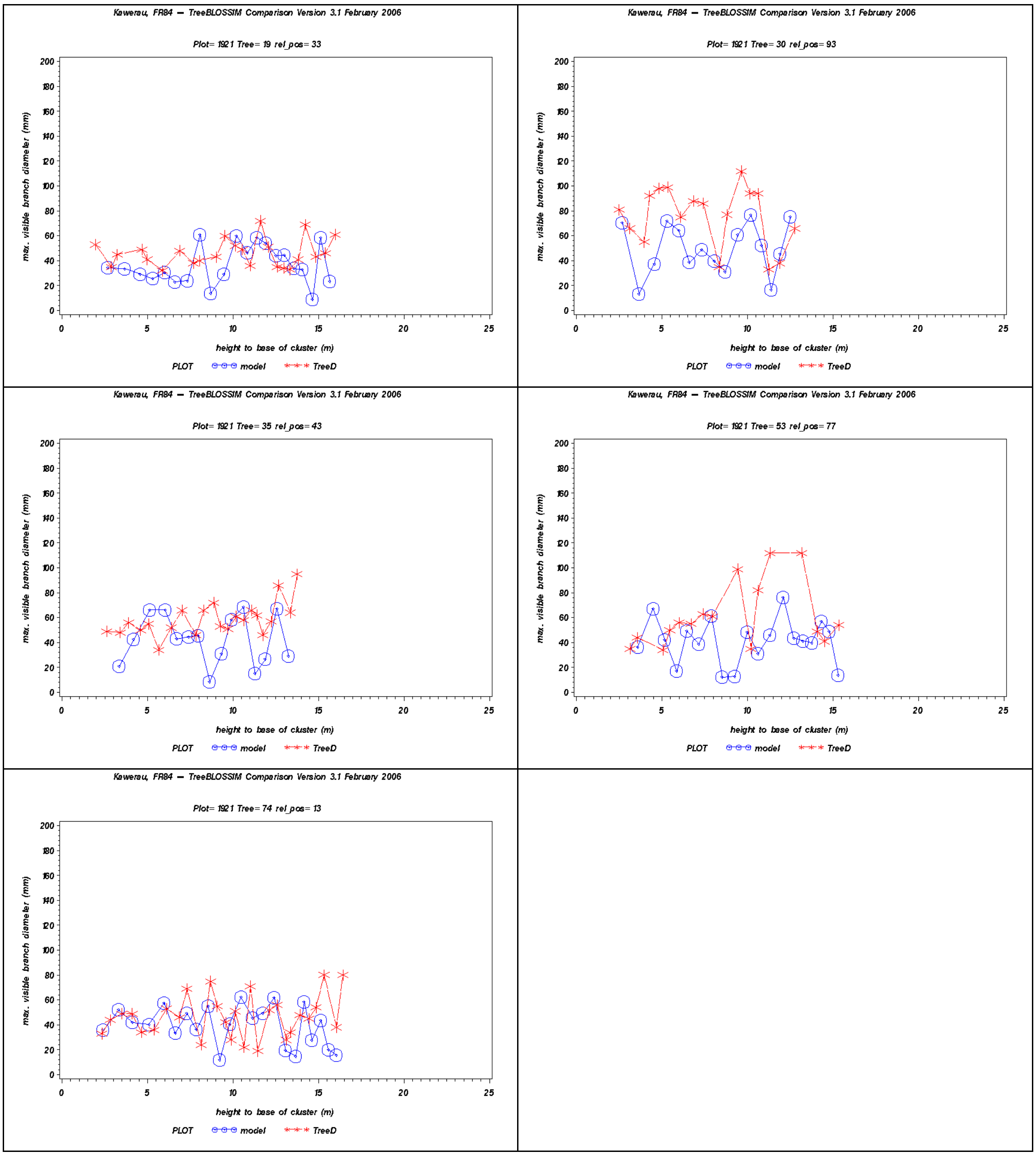
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR84, plot 17_21 (GF25 seedlot).



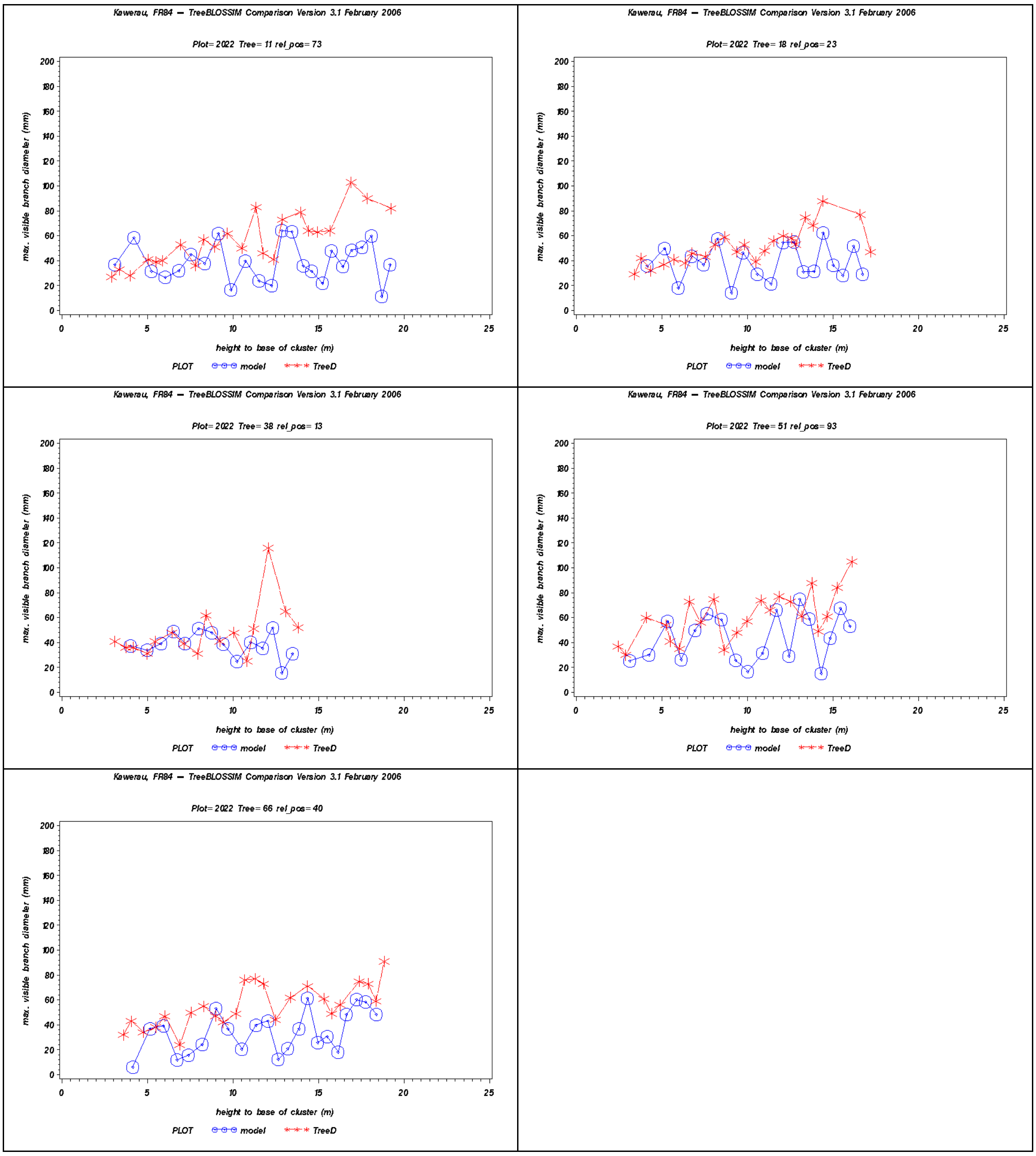
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR84, plot 18_22 (GF25 cutting).



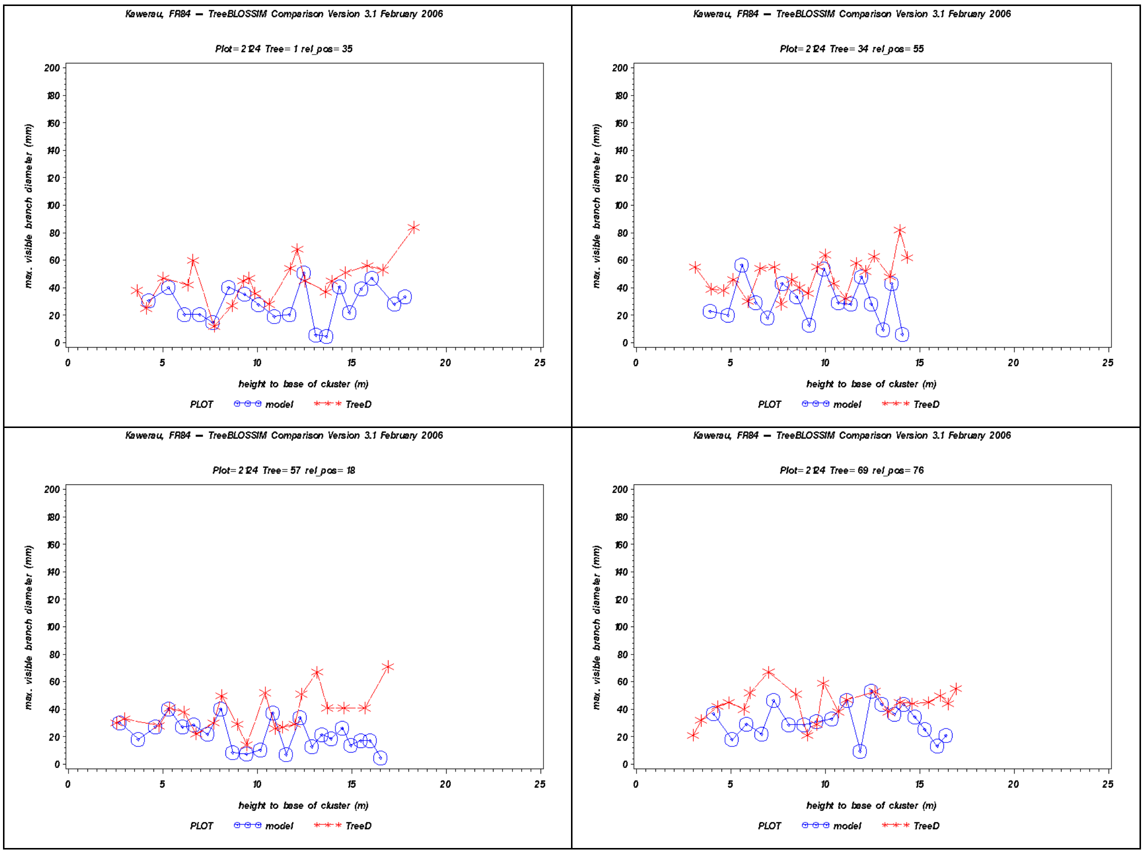
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR84, plot 19_21 (GF16 seedlot).



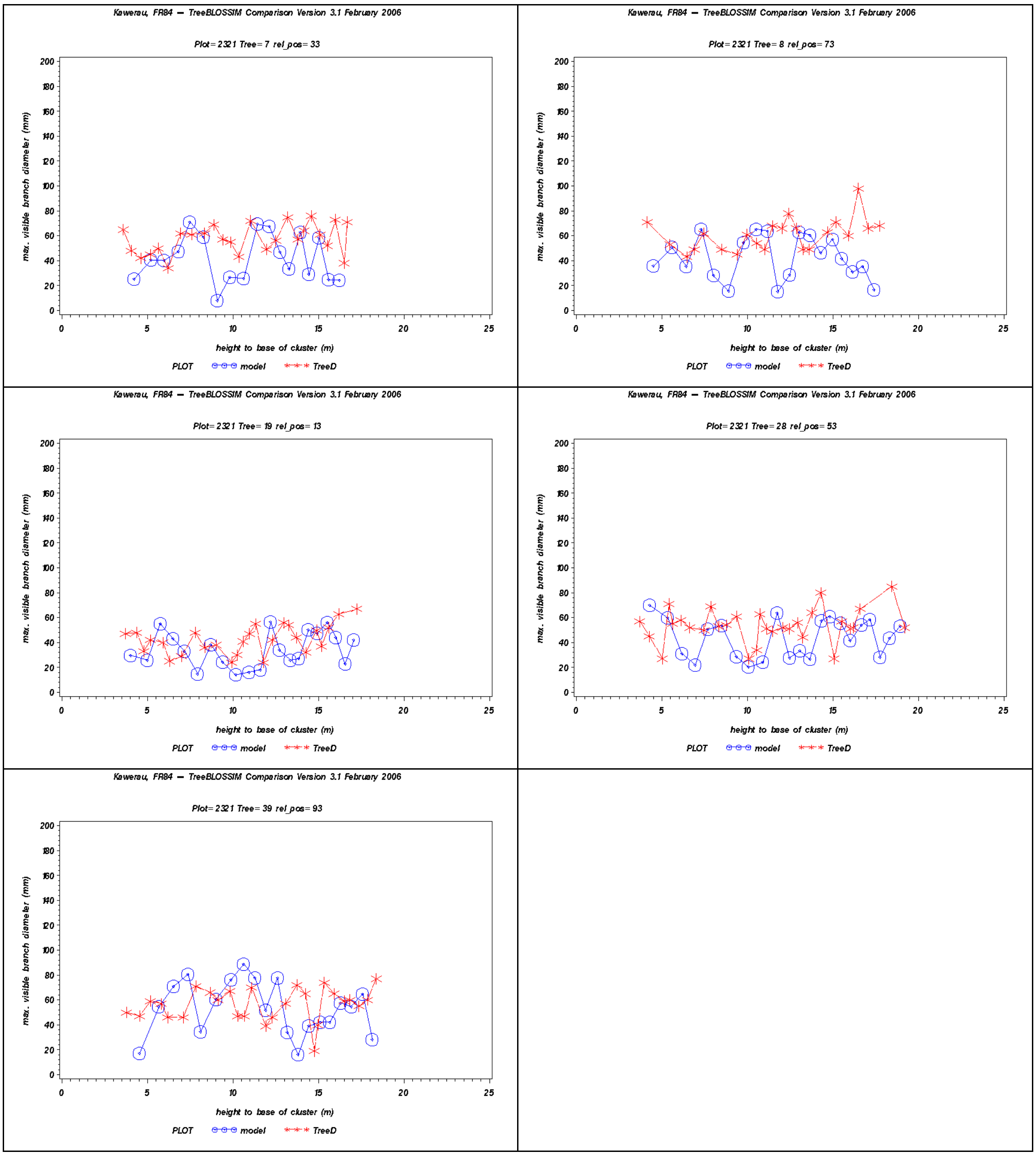
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR84, plot 20_22 (GF25 seedlot).



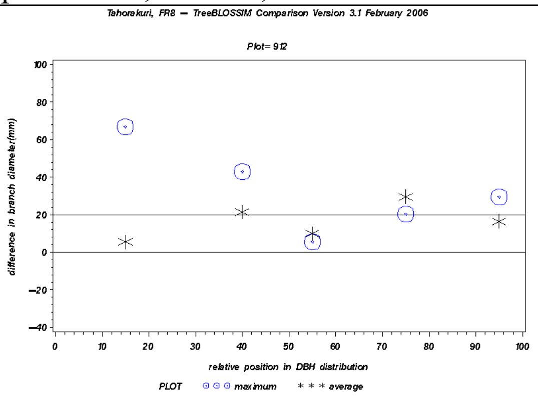
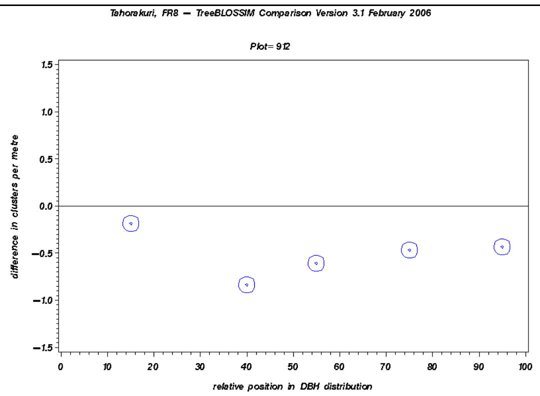
Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR84, plot 21_24 (GF16 seedlot).



Graph showing PhotoMARVL measurements and TreeBLOSSIM predictions of branch diameter versus height of cluster for individual trees in FR84, plot 23_21 (GF25 cutting).



APPENDIX 5. Tahorakuri, FR8

<table>
<tr><th>Stocking Treatment</th><th>Graphs showing the difference in branch diameter (maximum = $DIFF_{max}$ and average = $DIFF_{av}$) between image measurements and TreeBLOSSIM predictions, for FR8, GF13 seedlot</th><th>Graphs showing the difference between image and TreeBLOSSIM prediction of the number of branch clusters per metre ($DIFF_{CL}$) for FR8, GF13 seedlot</th></tr>
<tr><td>500 → 200</td><td>
</td><td>
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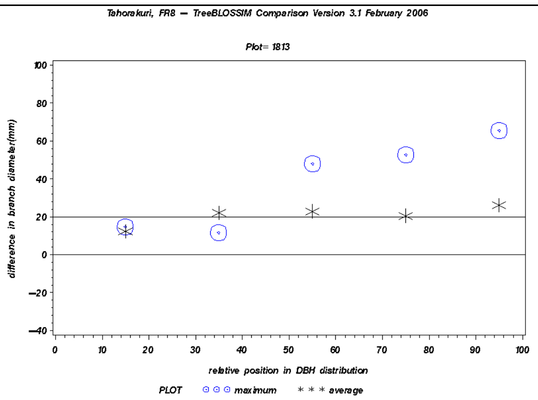
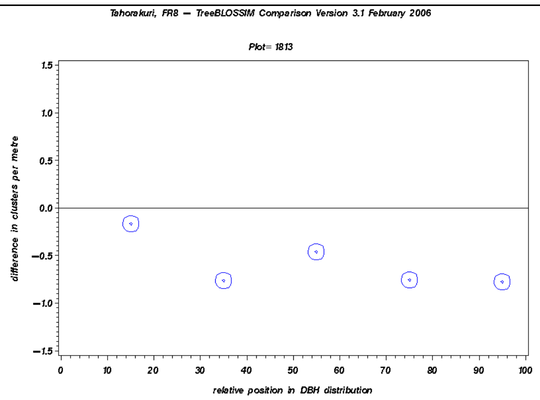
<tr><td>1000 → 400</td><td>
</td><td>
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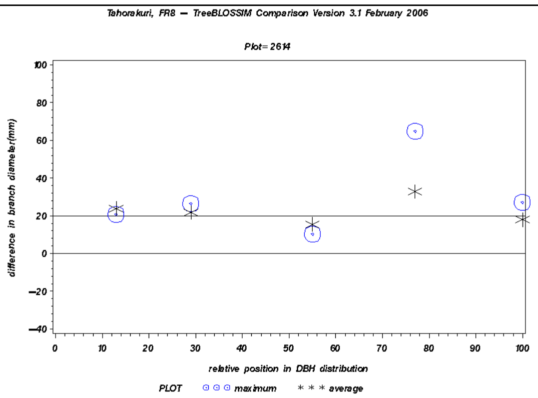
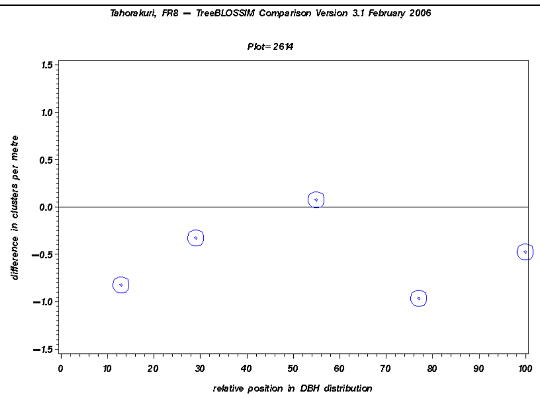
<tr><td>1500 → 600</td><td>
</td><td>
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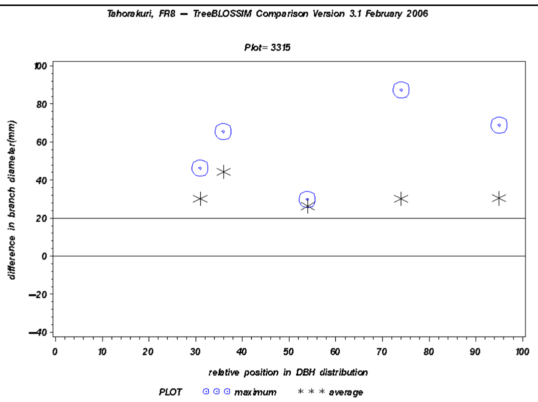
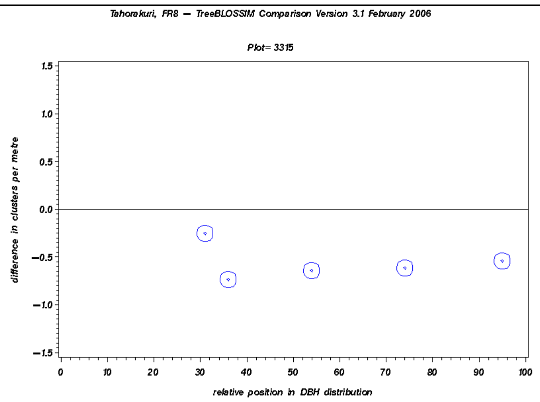
<tr><td>500 → 500</td><td>
</td><td>
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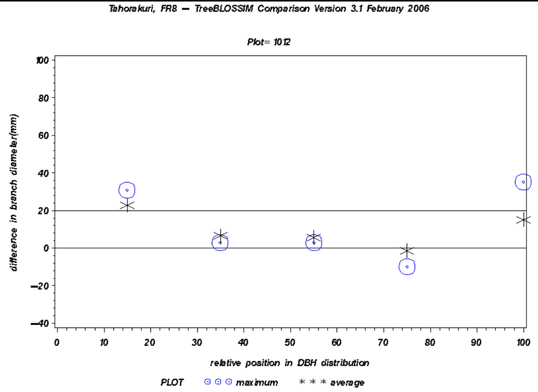
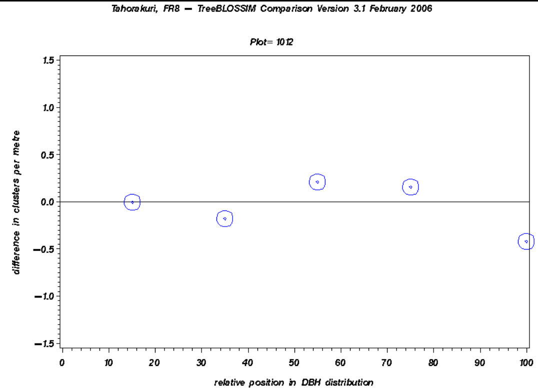
<tr><td>500 → 200</td><td>
</td><td>
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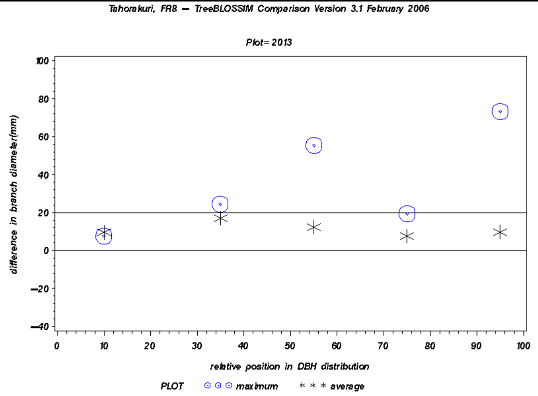
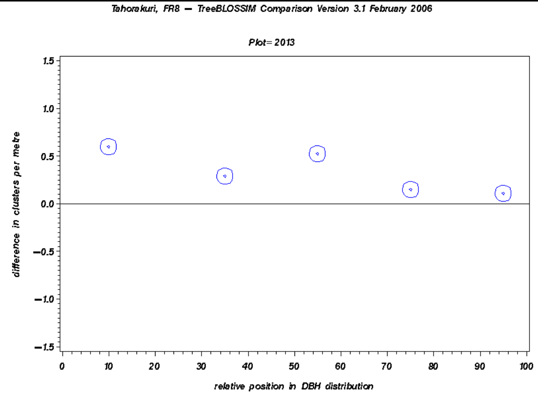
<tr><td>1000 → 400</td><td>
</td><td>
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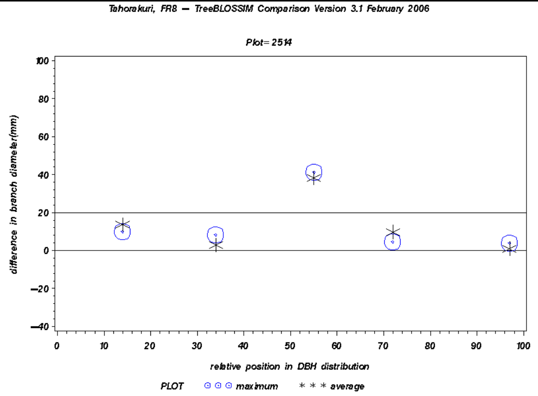
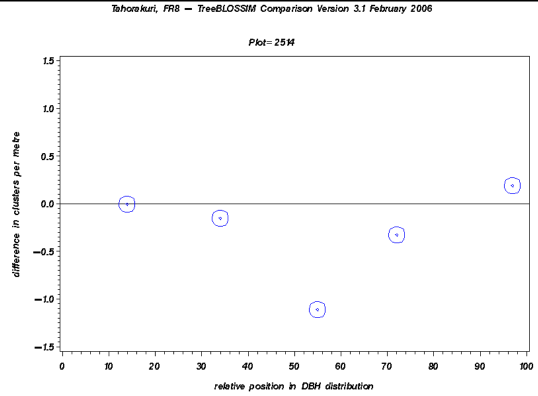
<tr><td>1500 → 600</td><td>
</td><td>
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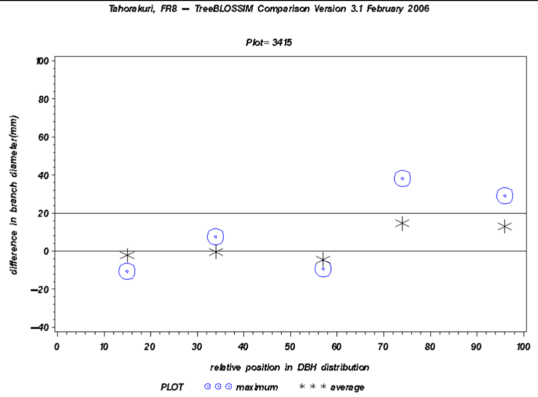
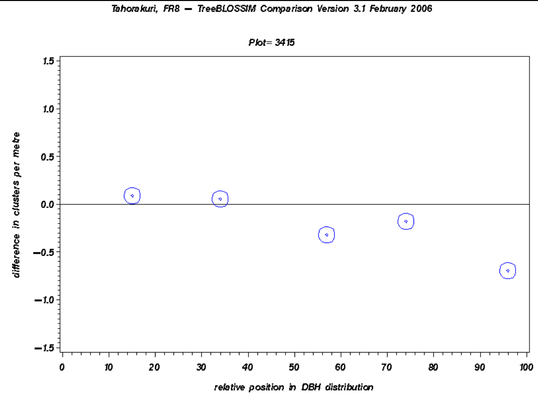
<tr><td>500 → 500</td><td>
</td><td>
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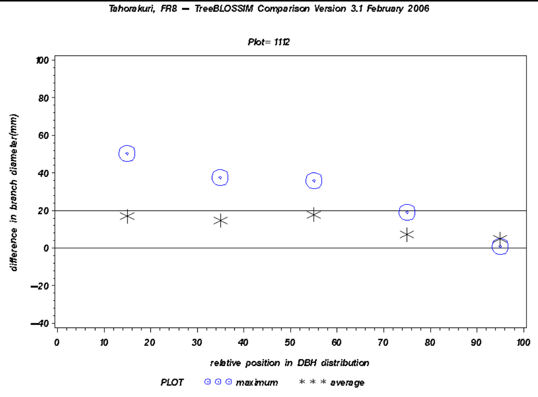
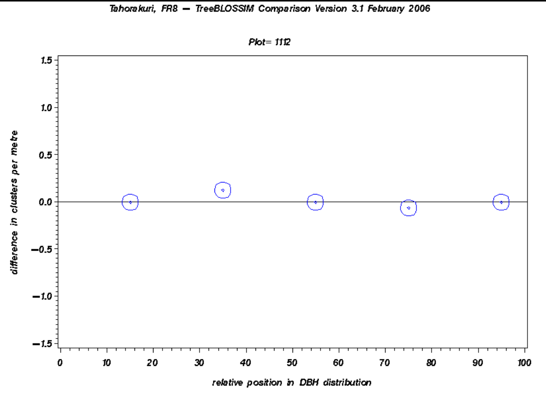
<tr><td>500 → 200</td><td>
</td><td>
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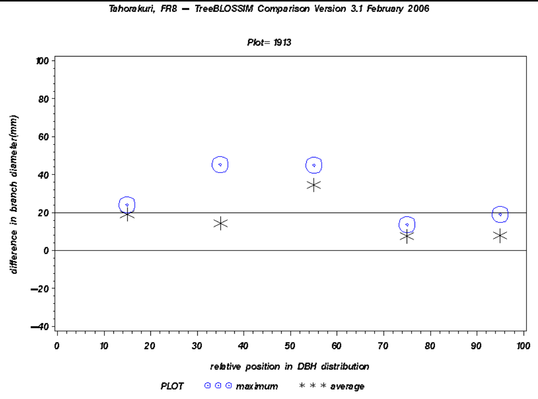
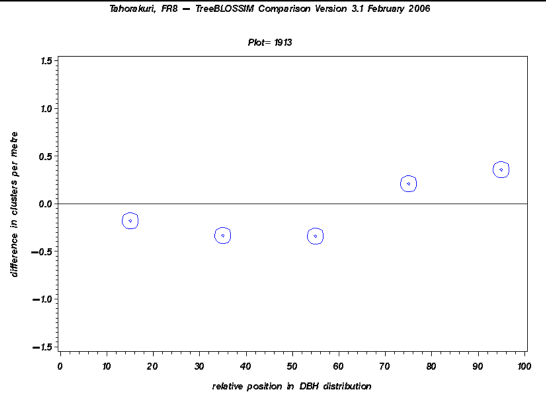
<tr><td>1000 → 400</td><td>
</td><td>
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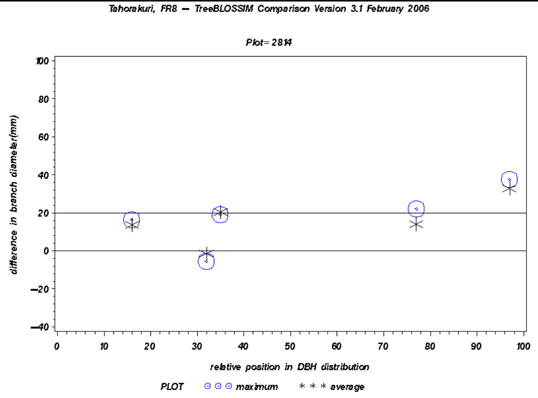
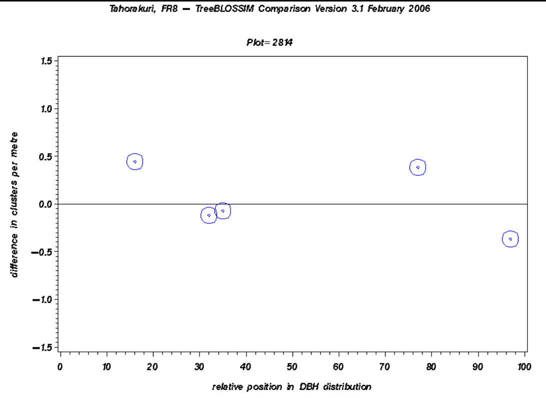
<tr><td>1500 → 600</td><td>
</td><td>
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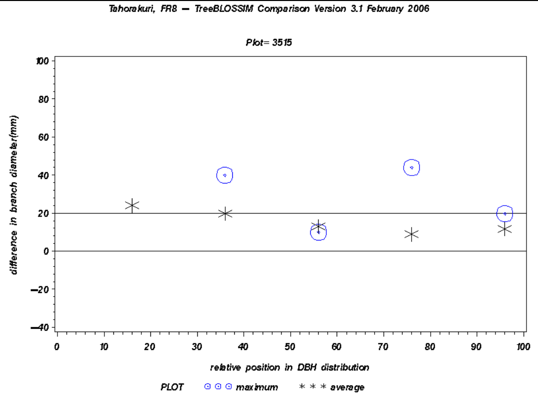
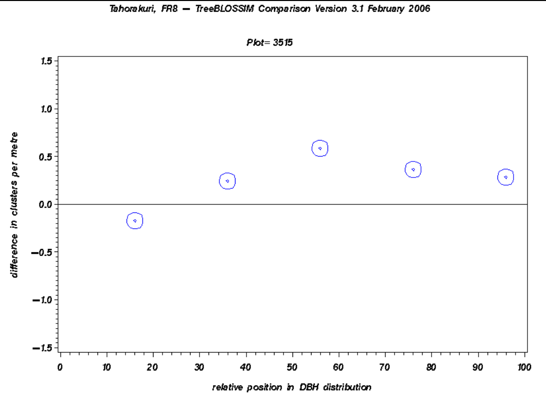
<tr><td>500 → 500</td><td>
</td><td>
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APPENDIX 6. Glengarry, FR10

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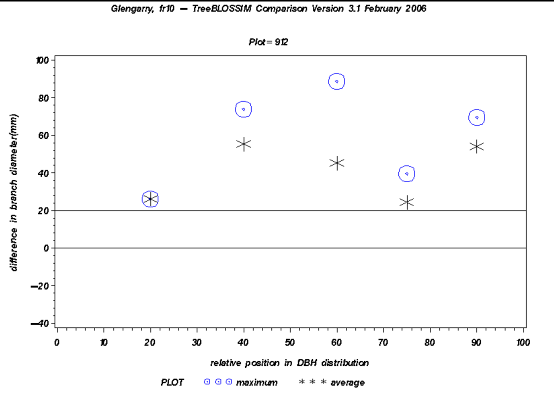
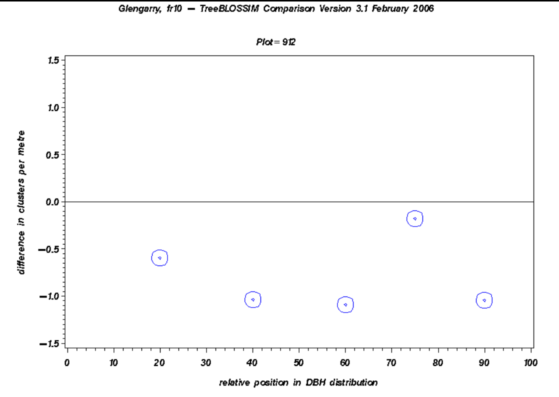
<tr><td>500 → 200</td><td>
</td><td>
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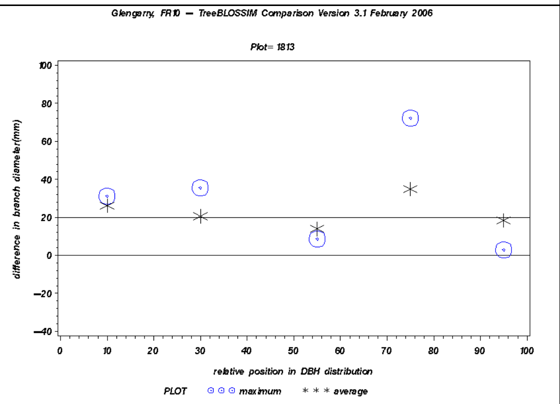
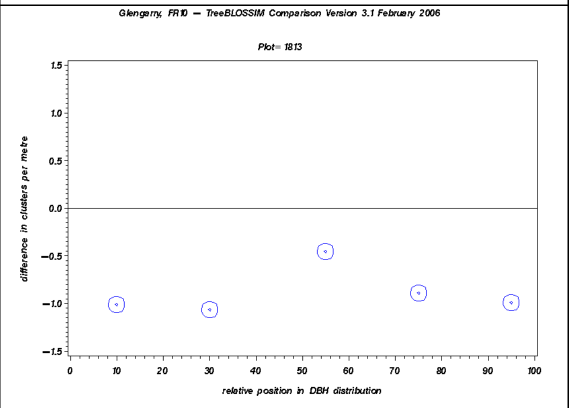
<tr><td>1000 → 400</td><td>
</td><td>
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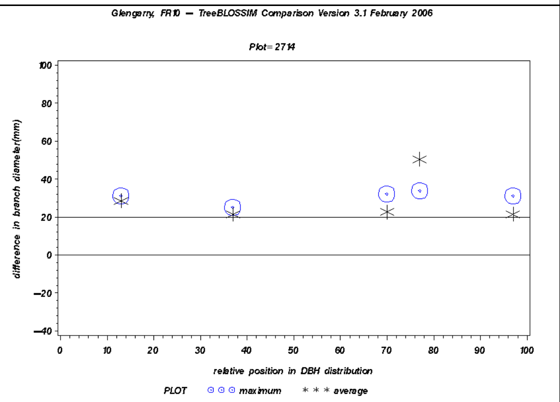
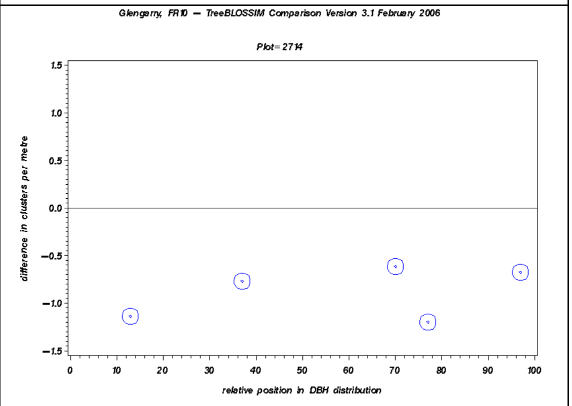
<tr><td>1500 → 600</td><td>
</td><td>
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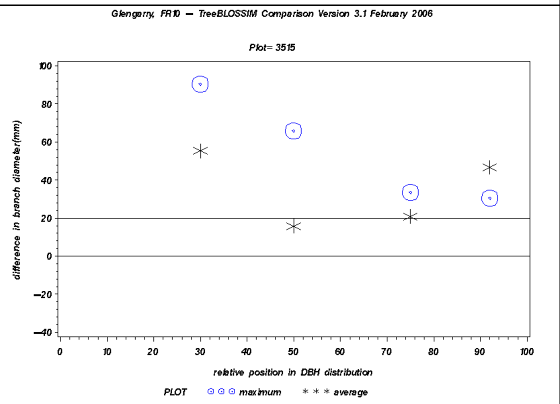
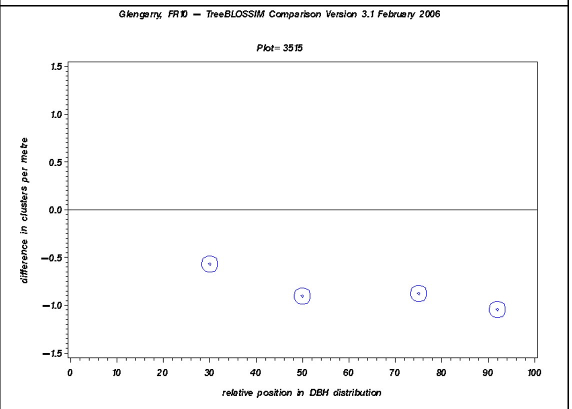
<tr><td>500 → 500</td><td>
</td><td>
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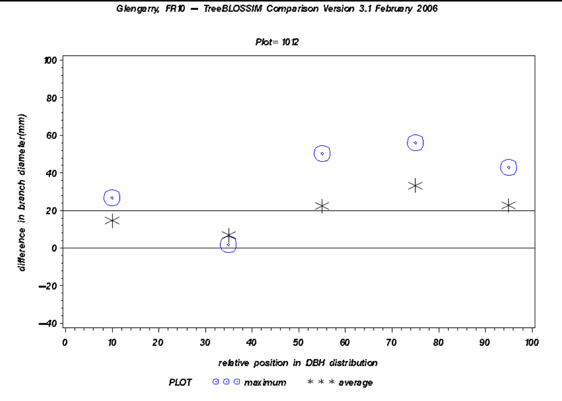
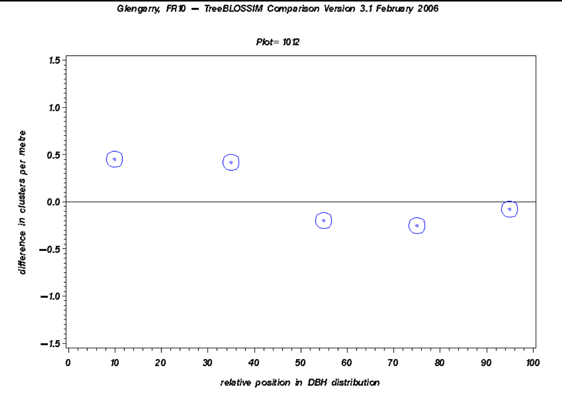
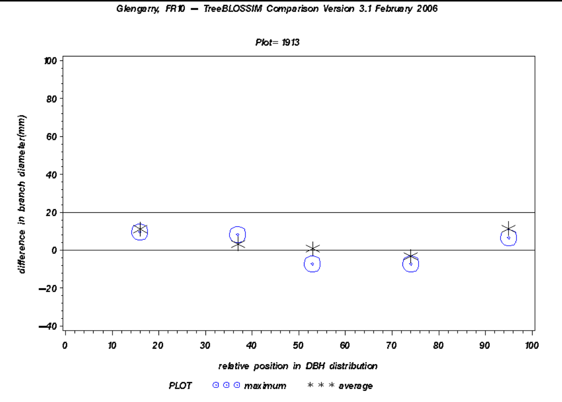
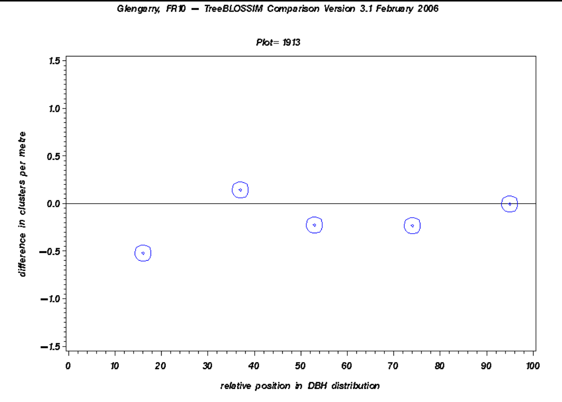
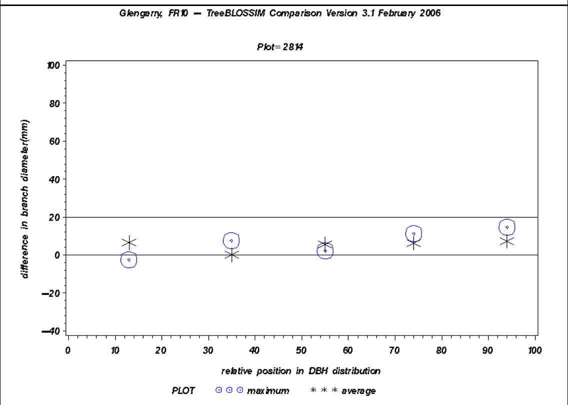
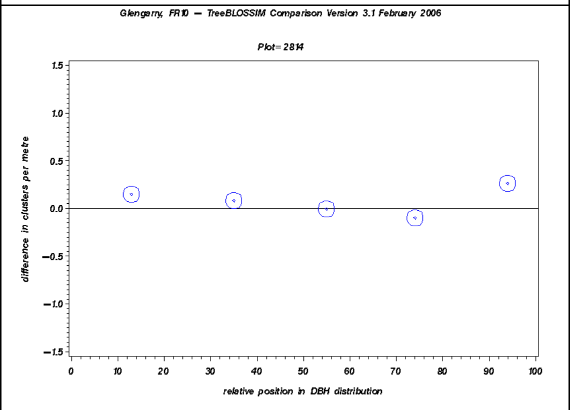
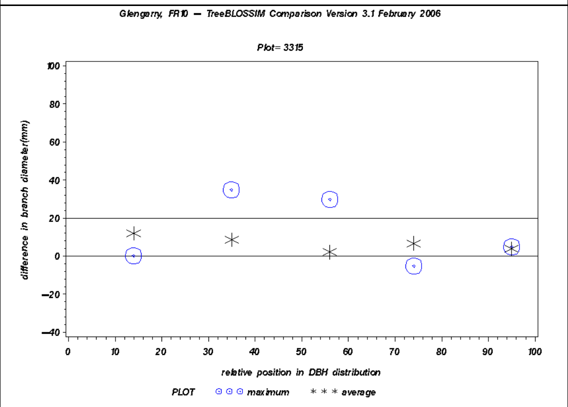
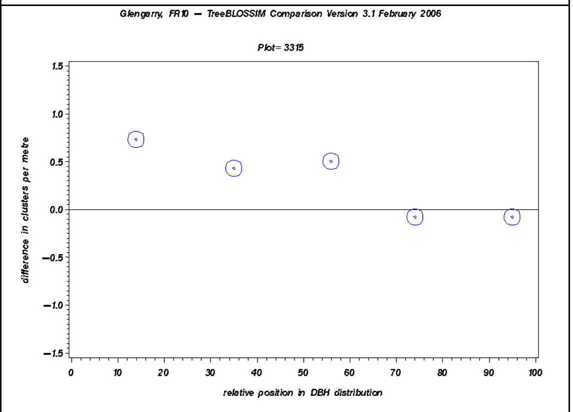
Stocking Treatment	Graphs showing the difference in branch diameter (maximum = $DIFF_{max}$ and average = $DIFF_{av}$) between image measurements and TreeBLOSSIM predictions, for FR10, GF21	Graphs showing the difference between image and TreeBLOSSIM prediction of the number of branch clusters per metre ($DIFF_{CL}$) for FR10, GF21
500 → 200		
1000 → 400		
1500 → 600		
500 → 500		

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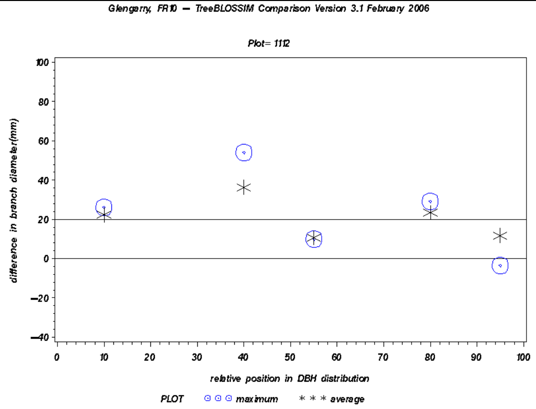
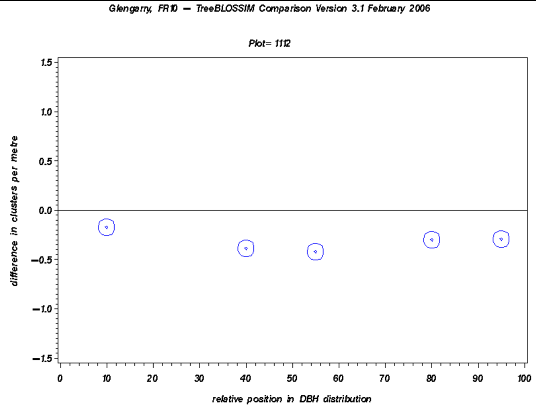
<tr><td>500 → 200</td><td>
</td><td>
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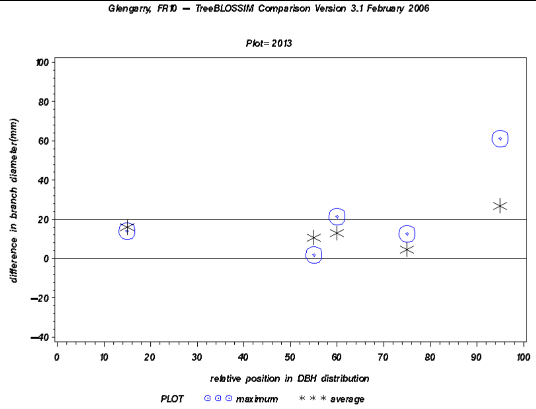
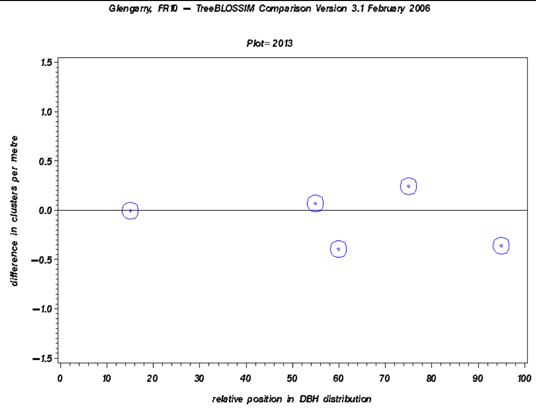
<tr><td>1000 → 400</td><td>
</td><td>
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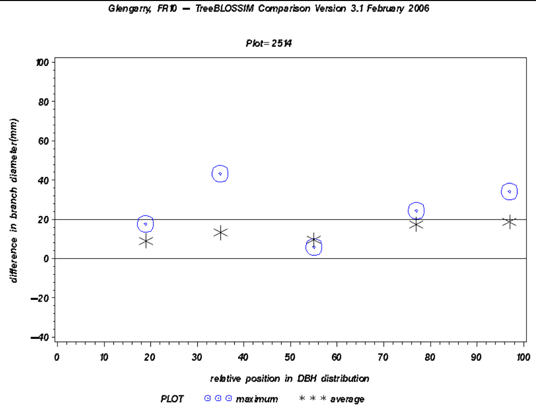
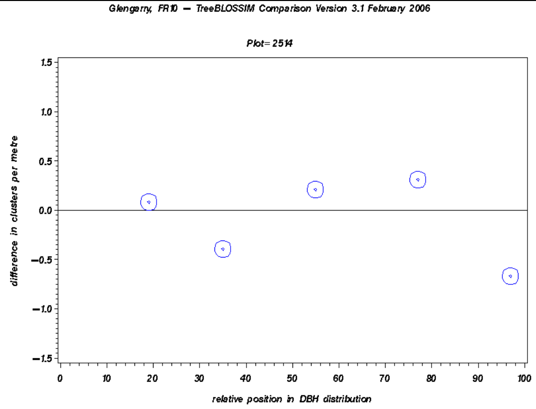
<tr><td>1500 → 600</td><td>
</td><td>
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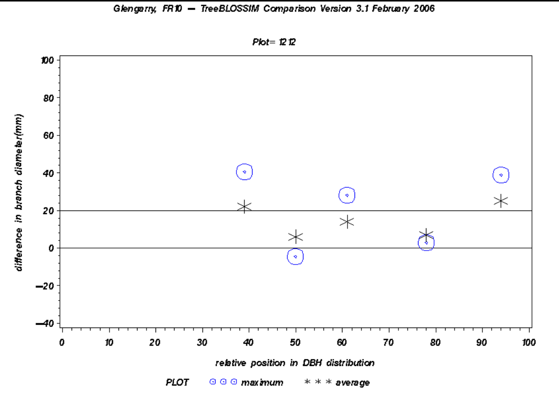
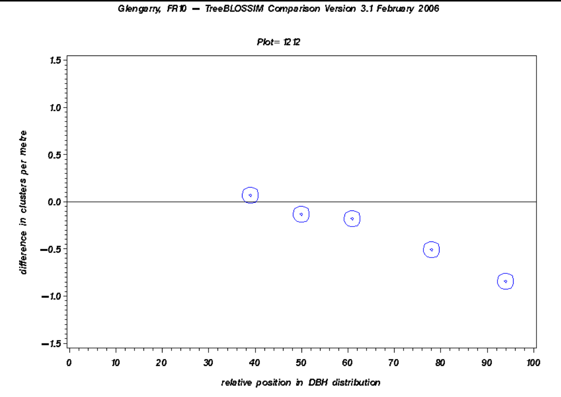
<tr><td>500 → 200</td><td>
</td><td>
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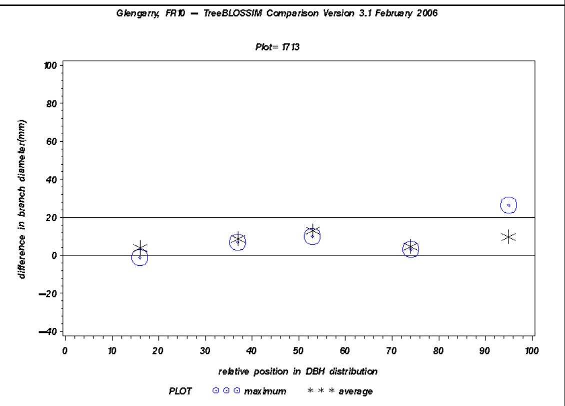
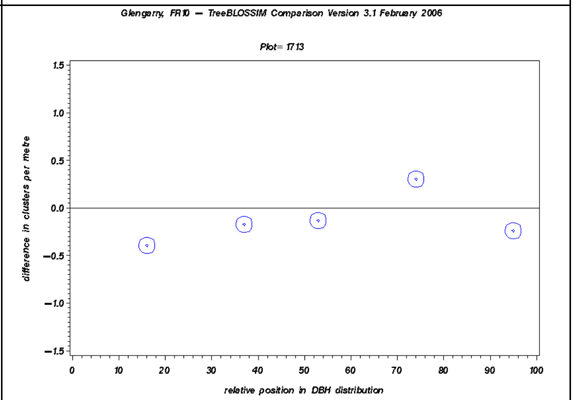
<tr><td>1000 → 400</td><td>
</td><td>
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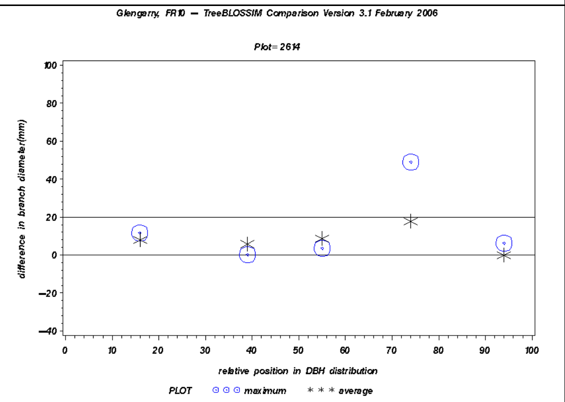
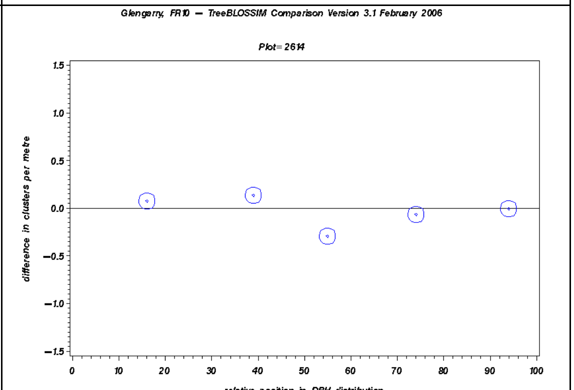
<tr><td>1500 → 600</td><td>
</td><td>
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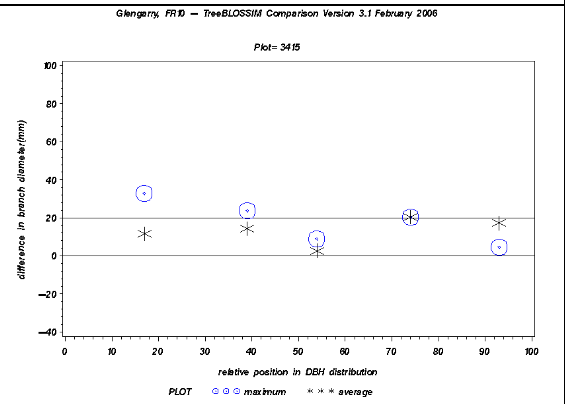
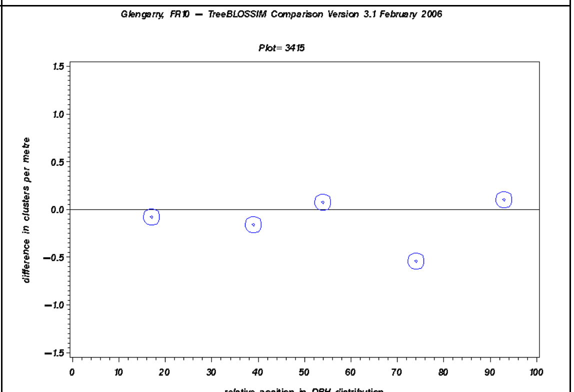
<tr><td>500 → 500</td><td>
</td><td>
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APPENDIX 7. Mamaranui, FR54

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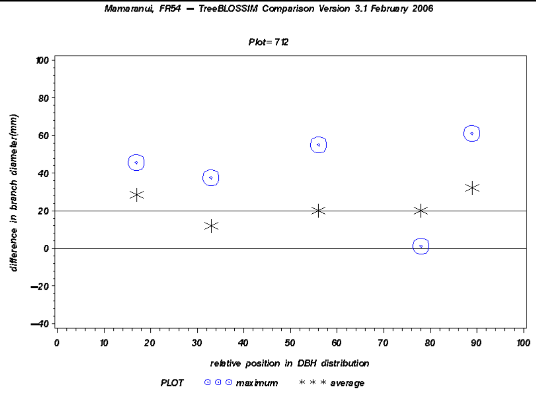
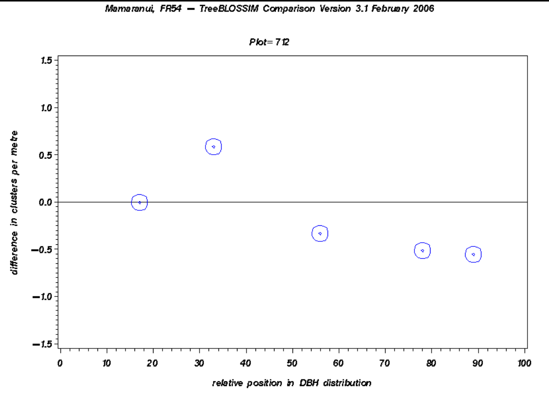
<tr><td>500 → 200</td><td>
</td><td>
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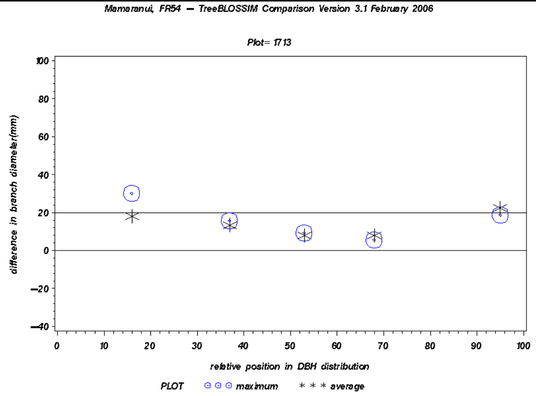
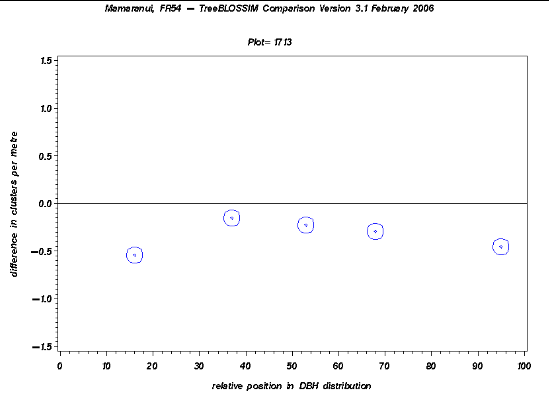
<tr><td>1000 → 400</td><td>
</td><td>
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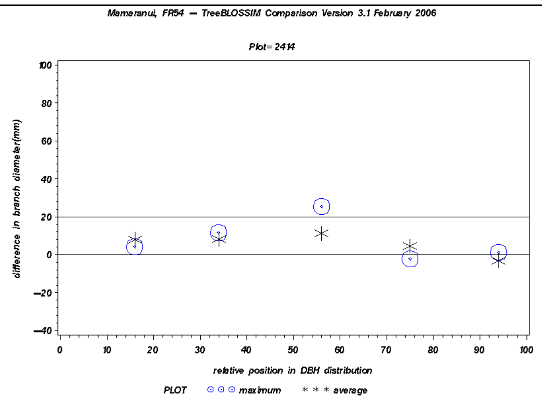
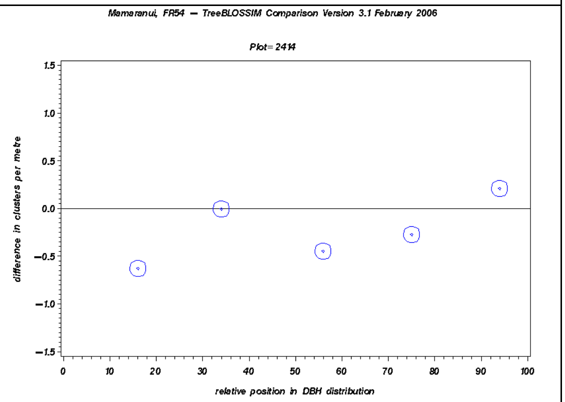
<tr><td>1500 → 600</td><td>
</td><td>
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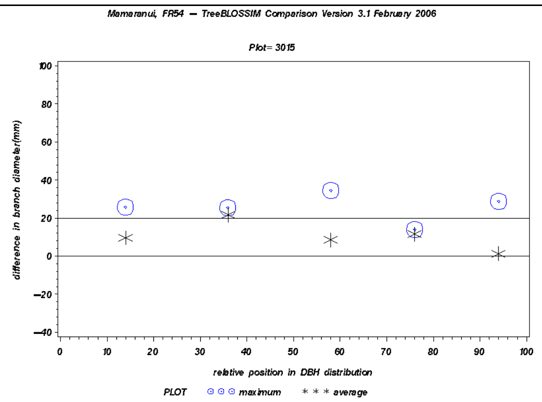
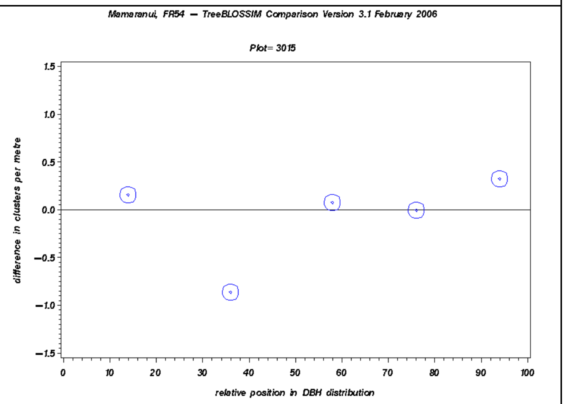
<tr><td>500 → 500</td><td>
</td><td>
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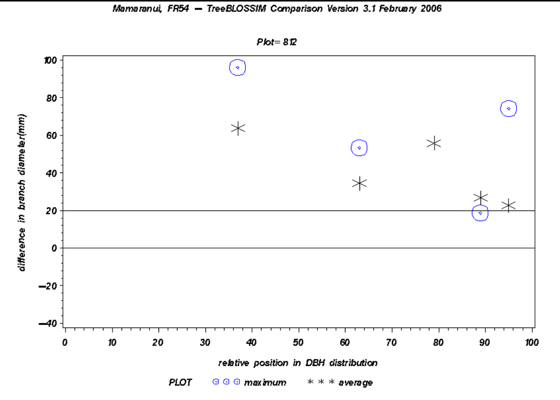
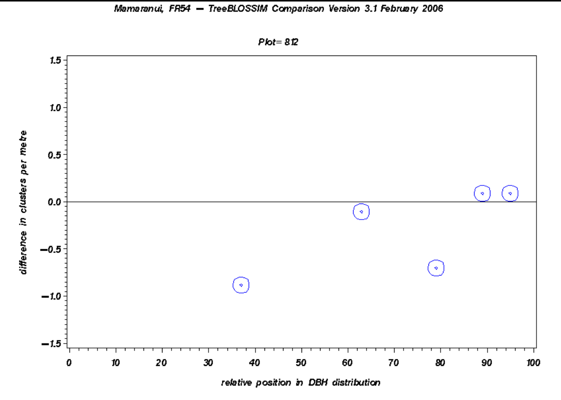
<tr><td>500 → 200</td><td>
</td><td>
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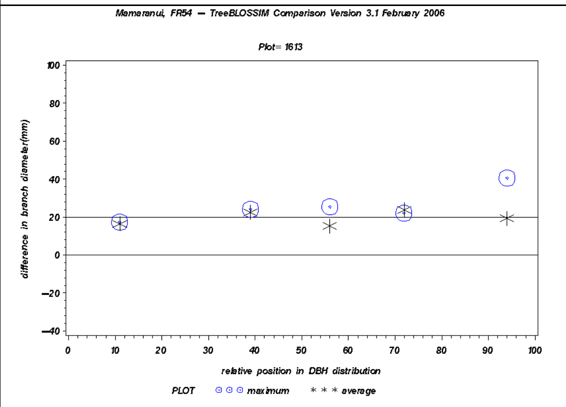
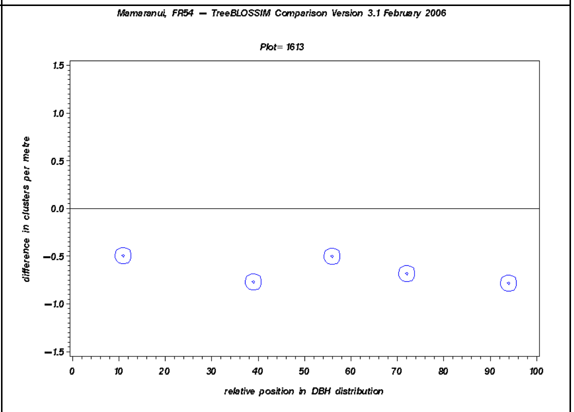
<tr><td>1000 → 400</td><td>
</td><td>
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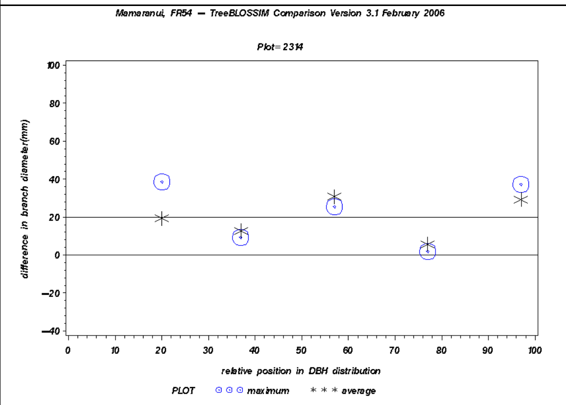
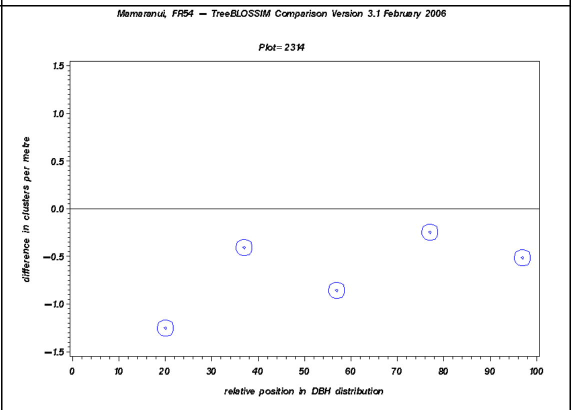
<tr><td>1500 → 600</td><td>
</td><td>
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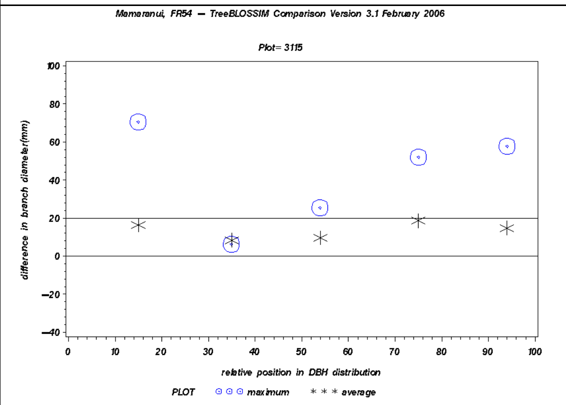
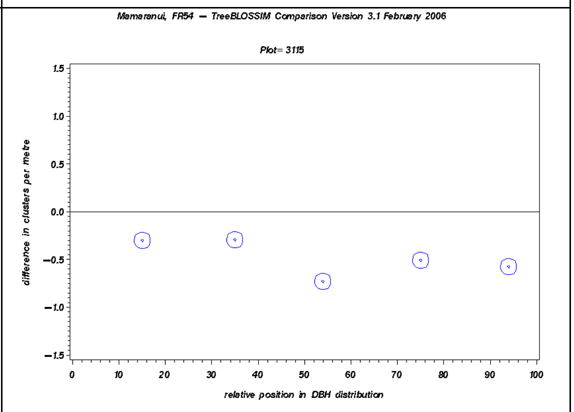
<tr><td>500 → 500</td><td>
</td><td>
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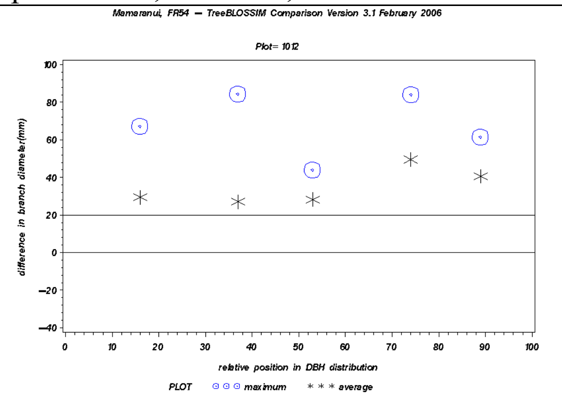
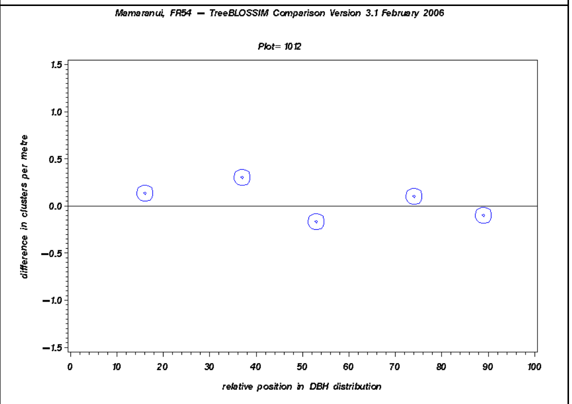
<tr><td>Stocking Treatment</td><td>Graphs showing the difference in branch diameter (maximum = $DIFF_{max}$ and average = $DIFF_{av}$) between image measurements and TreeBLOSSIM predictions, for FR54, GF14</td><td>Graphs showing the difference between image and TreeBLOSSIM prediction of the number of branch clusters per metre ($DIFF_{CL}$) for FR54, GF14</td></tr>
<tr><td>500 → 200</td><td>
</td><td>
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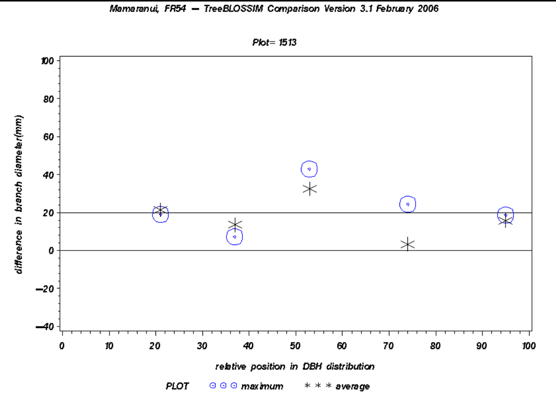
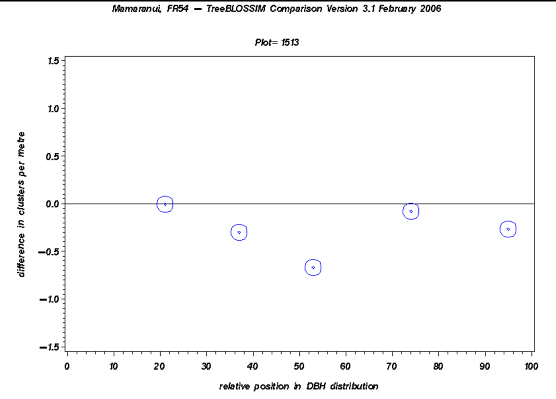
<tr><td>1000 → 400</td><td>
</td><td>
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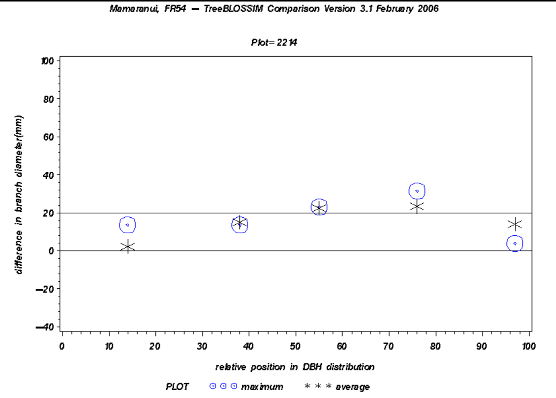
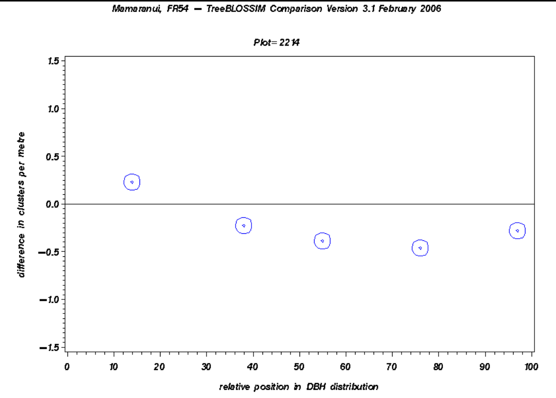
<tr><td>1500 → 600</td><td>
</td><td>
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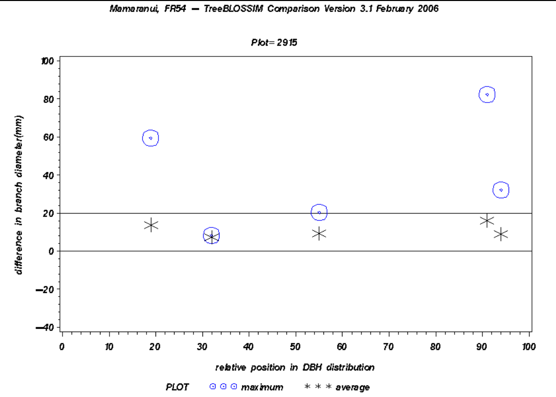
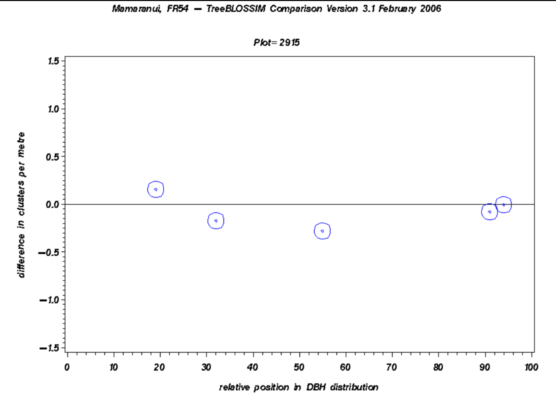
<tr><td>500 → 500</td><td>
</td><td>
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APPENDIX 8. Kawerau, FR84

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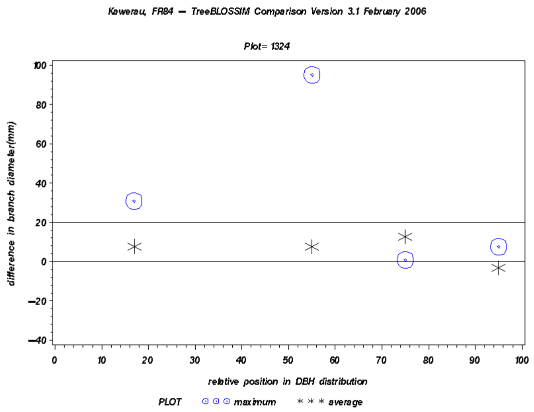
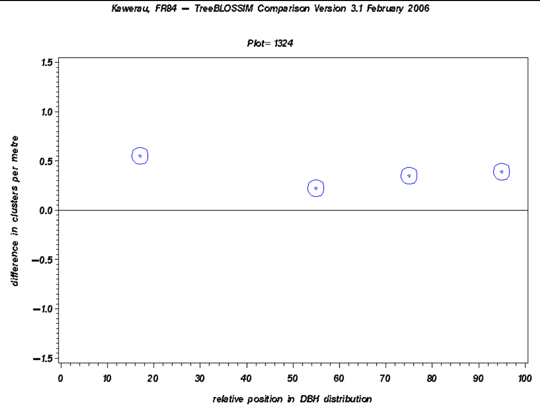
<tr><th>Stocking Treatment</th><th>Graphs showing the difference in branch diameter (maximum = $DIFF_{max}$ and average = $DIFF_{av}$) between image measurements and TreeBLOSSIM predictions, for FR84, GF25 seedlot</th><th>Graphs showing the difference between image and TreeBLOSSIM prediction of the number of branch clusters per metre ($DIFF_{CL}$) for FR84, GF25 seedlot</th></tr>
<tr><td>None</td><td>
</td><td>
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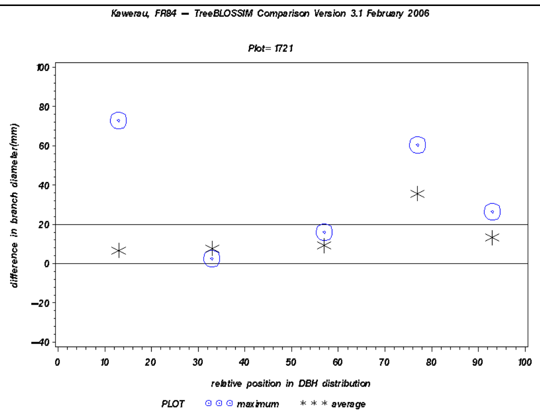
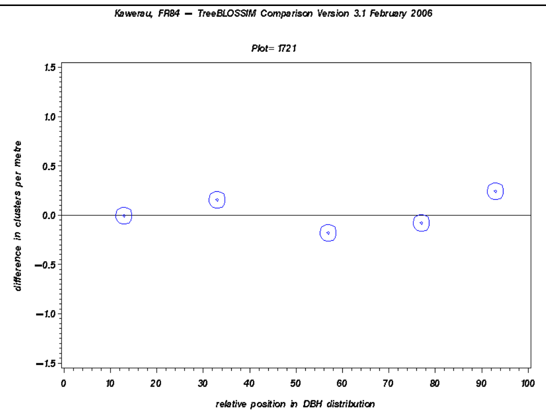
<tr><td>Early Thin</td><td>
</td><td>
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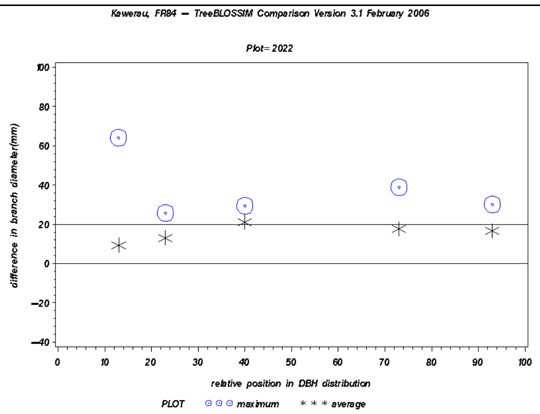
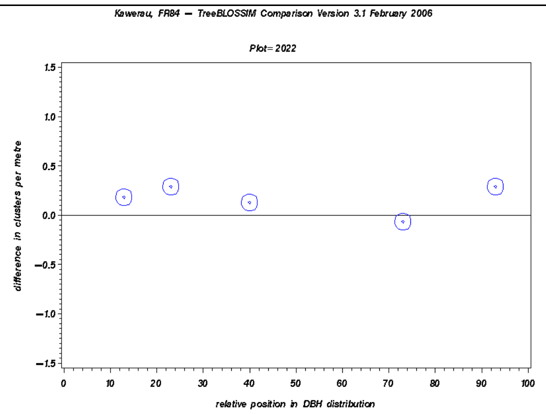
<tr><td>Late Thin</td><td>
</td><td>
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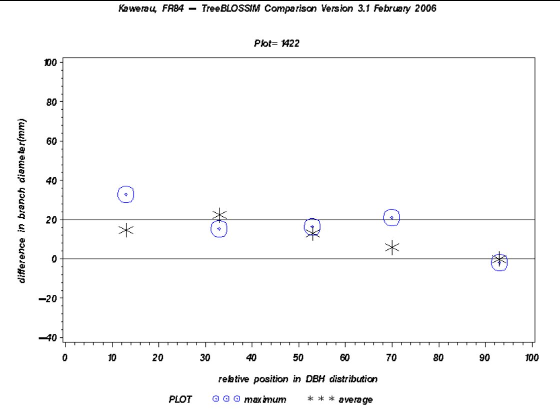
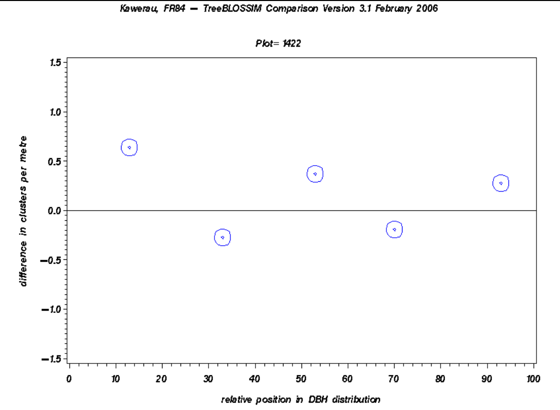
<tr><td>Late Thin</td><td>
</td><td>
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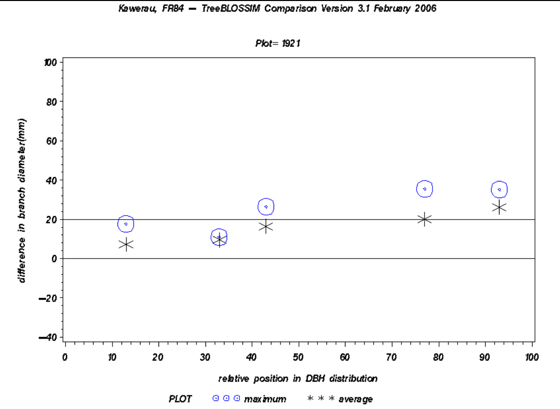
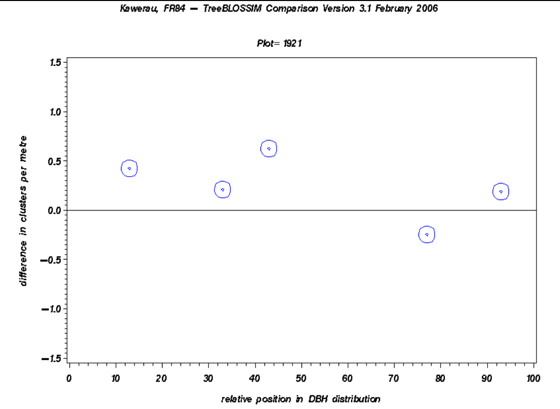
<tr><td>Early Thin</td><td>
</td><td>
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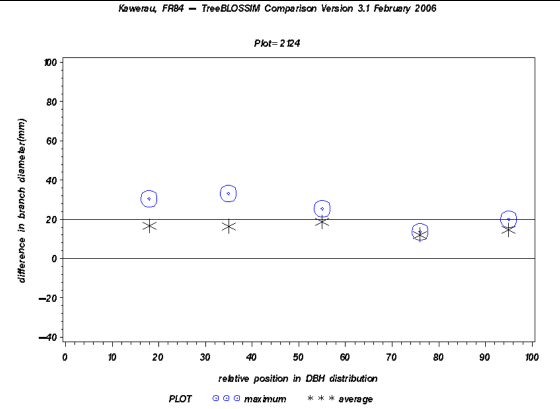
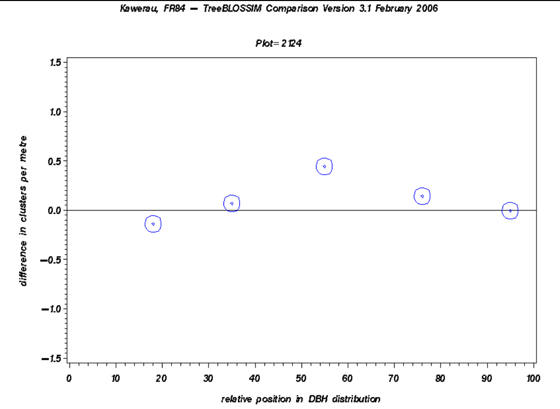
<tr><td>None</td><td>
</td><td>
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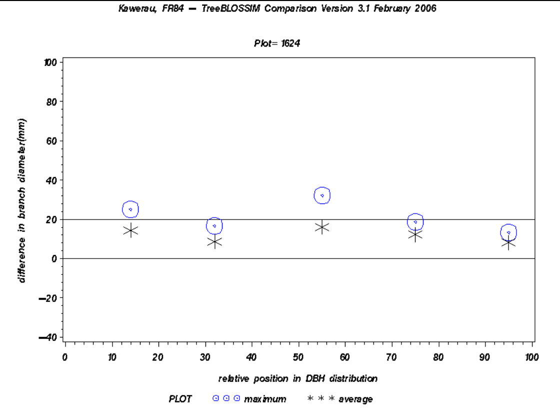
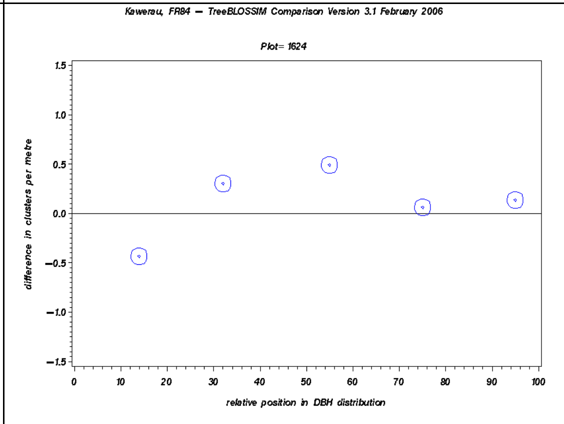
<tr><td>None</td><td>
</td><td>
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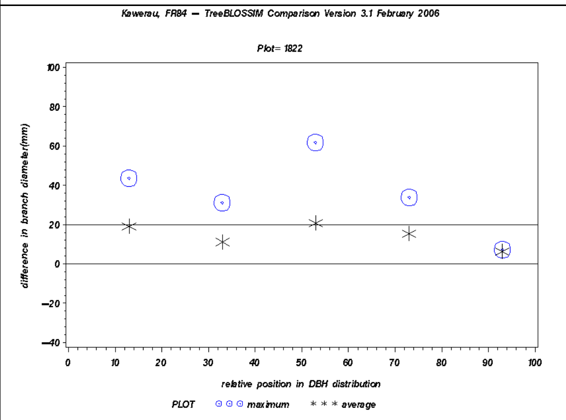
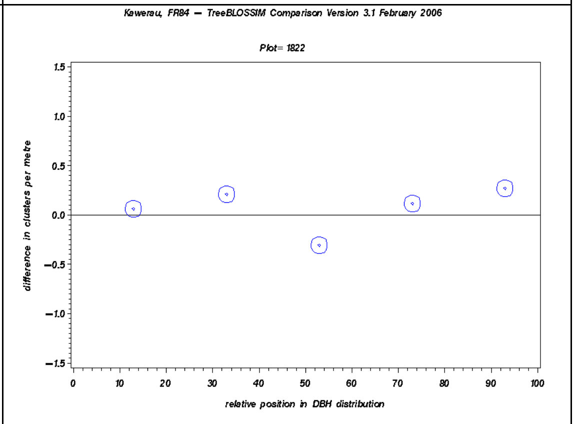
<tr><td>Late Thin</td><td>
</td><td>
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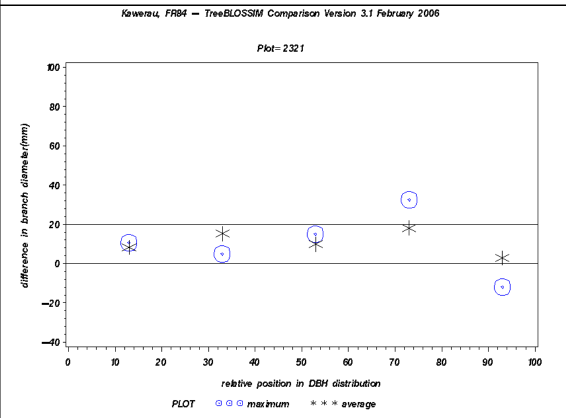
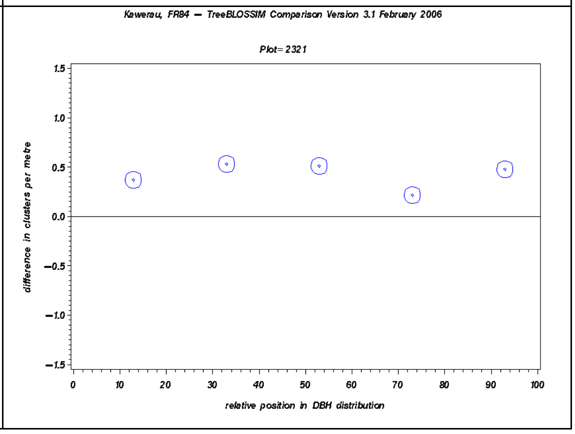
<tr><td>Early Thin</td><td>
</td><td>
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