

Table.xxx BRMS model outputs: maternal width effects analysis across species. Model structure per species: (log(max height) ~ log(maternal height) + Site.

	Estimate	Est. Error	Lower 95% CI (log)	Upper 95% CI (log)	Rhat	Bulk Effective Sample Size	Tail Effective Sample Size	Effect	Sample Size	Species
Intercept	3.03	1.04	0.94	5.09	1.00	6219.59	6833.35	fixed	45	Salix richardsonii
log(Mother Canopy Width)	0.19	0.22	-0.25	0.64	1.00	6080.73	6779.84	fixed	45	Salix richardsonii
Site:Qikiqtaruk	-1.36	0.29	-1.92	-0.78	1.00	6290.31	6781.08	fixed	45	Salix richardsonii
Sigma	0.68	0.08	0.55	0.84	1.00	7811.80	7880.60	residual	45	Salix richardsonii
Intercept	4.48	1.01	2.52	6.43	1.00	4783.95	3610.84	fixed	58	Salix pulchra
log(Mother Canopy Width)	-0.16	0.20	-0.53	0.22	1.00	4718.68	3792.01	fixed	58	Salix pulchra
Site:Qikiqtaruk	-1.05	0.21	-1.46	-0.63	1.00	4926.07	3542.28	fixed	58	Salix pulchra
Sigma	0.74	0.07	0.61	0.90	1.00	4725.79	3765.90	residual	58	Salix pulchra
Intercept	2.38	0.87	0.62	4.08	1.00	5169.71	3634.35	fixed	20	Salix arctica
log(Mother Canopy Width)	0.18	0.21	-0.22	0.60	1.00	5231.34	3708.63	fixed	20	Salix arctica
Site:Qikiqtaruk	-0.18	0.30	-0.77	0.41	1.00	4257.33	3273.71	fixed	20	Salix arctica
Sigma	0.54	0.10	0.38	0.77	1.00	3929.29	3595.36	residual	20	Salix arctica