

**Table S3.** Model selection results from Huggins closed population models of black bear abundance in the Bow Valley of Banff National Park, Alberta, Canada in 2006 and 2008; results from Program MARK, April 2011 build.

Model <sup>a</sup>	AIC <sub>c</sub> <sup>b</sup>	$\Delta$ AIC <sub>c</sub> <sup>c</sup>	w <sub>i</sub> <sup>d</sup>	Model Likelihood	No. parameters	Deviance
<b>2006</b>						
CS: p(CSE <sub>hair</sub> ) HT: p(t + sex + HTE <sub>full</sub> ) BR: p(DTE)	271.66	0.00	0.55	1.00	11	248.75
CS: p(DTE) HT: p(t + sex + HTE <sub>hair</sub> ) BR: p(.)	275.14	3.48	0.10	0.18	10	254.38
CS: p(.) HT: p(t + sex + HTE <sub>hair</sub> ) BR: p(.)	275.20	3.54	0.09	0.17	9	256.58
CS: p(.) HT: p(t + sex + HTE <sub>hair</sub> + DTE) BR: p(.)	276.21	4.55	0.06	0.10	10	255.45
CS: p(DTE) HT: p(t + sex + HTE <sub>full</sub> ) BR: p(.)	276.72	5.05	0.04	0.08	10	255.96
CS: p(DTE) HT: p(t + sex + HTE <sub>hair</sub> ) BR: p(DTE)	277.20	5.54	0.03	0.06	11	254.29
CS: p(DTE) HT: p(t + sex + HTE <sub>full</sub> + DTE) BR: p(DTE); M10km, F5km	278.37	6.71	0.02	0.03	11	255.46
CS: p(DTE) HT: p(t + sex + HTE <sub>full</sub> + DTE) BR: p(DTE); MF5km	278.37	6.71	0.02	0.03	11	255.46
CS: p(DTE) HT: p(t + sex + HTE <sub>full</sub> + DTE) BR: p(DTE)	278.37	6.71	0.02	0.03	11	255.46
CS: p(.) HT: p(t + sex + DTE) BR: p(.)	278.54	6.88	0.02	0.03	9	259.92
<b>2008</b>						
CS: p(DTE) HT: p(t + sex + HTE <sub>full</sub> ) BR: p(DTE); MF5km	437.77	0.00	0.16	1.00	11	415.16
CS: p(DTE) HT: p(t + sex + HTE <sub>full</sub> ) BR: p(DTE); M10km, F5km	437.77	0.00	0.16	1.00	11	415.16
CS: p(DTE) HT: p(t + sex + HTE <sub>full</sub> ) BR: p(DTE)	437.77	0.00	0.16	1.00	11	415.16
CS: p(DTE) HT: p(t + sex + HTE <sub>full</sub> ) BR: p(.)	438.13	0.36	0.14	0.84	10	417.62
CS: p(DTE) HT: p(t + sex + HTE <sub>hair</sub> ) BR: p(DTE)	438.15	0.38	0.14	0.83	11	415.53
CS: p(DTE) HT: p(t + sex + HTE <sub>hair</sub> ) BR: p(.)	438.33	0.56	0.12	0.76	10	417.82
CS: p(CSE <sub>full</sub> + DTE) HT: p(t + sex + HTE <sub>full</sub> ) BR: p(DTE)	439.51	1.74	0.07	0.42	12	414.78
CS: p(DTE) HT: p(t × sex + HTE <sub>full</sub> ) BR: p(DTE)	442.89	5.12	0.01	0.08	15	411.76
CS: p(DTE) HT: p(t × sex + DTE) BR: p(DTE)	443.20	5.43	0.01	0.07	15	412.07
CS: p(DTE) HT: p(t × sex + HTE <sub>hair</sub> ) BR: p(DTE)	443.32	5.55	0.01	0.06	15	412.19

<sup>a</sup> Models estimated capture probabilities,  $p$ , for three noninvasive genetic sampling methods (HT=hair traps, BR=bear rubs, CS=crossing structures) and contained method-specific sampling effort covariates calculated by summing the number of hair traps (HTE), bear rub days (BRE), and crossing structures (CSE) that were located within each bear's idealized detection range each session. Models also included distance to edge of grid (DTE) covariates; thresholds for DTE, if any, appear at the end of model names after a semicolon (M=males, F=females; km=kilometers).

<sup>b</sup> Akaike's Information Criterion for small sample sizes.

<sup>c</sup> The difference in AIC<sub>c</sub> value between the  $i$ th model and the model with the lowest AIC<sub>c</sub> value.

<sup>d</sup> Akaike wt used in model averaging.