



Figure S1. To determine the scute sampling strategy that would maximize the chance of correctly assigning individual spotted turtles *Clemmys guttata* to their population of origin, we tested four annotation areas (A1, A2, A3 and A4) (Fig. 1) on 29 spotted turtles from four sites (EO2, EO3, GH1 and HC; (Davy & Murphy 2009)). We used ^{13}S Spot to annotate all carapacial spots in each annotation area, then calculated pairwise similarity scores for each pair of turtles. Similarity scores for turtles matched to individuals from the same site (gray box) and to individuals from other sites (white box) are shown for each site and annotation area. Annotation Area 2 resulted in the largest difference between median (horizontal line) and mean (star) similarity scores, therefore, we used this sampling strategy to annotate spot patterns for all 126 turtle photos.

Table S1. Comparison of four annotation areas (Fig. 1) used to calculate similarity scores for carapacial spot patterns in 29 spotted turtles *Clemmys guttata* from four test sites (EO2, EO3, HC and GH1; (Davy & Murphy 2009). We compared median and mean I³S Spot similarity scores between turtles matched within and among capture sites to determine the scute sampling strategy that would maximize the chance of correctly assigning individuals to their population of origin. Largest among-site differences (in **bold**) were attained using Annotation Area 2.

Site	Annotation Area	Matched to Site	N	Median I ³ S Spot Similarity Score	Difference in Median I ³ S Scores	Mean I ³ S Spot Similarity Score	Difference in Mean I ³ S Scores
EO2	1	EO2	49	18.53		30.36	
		Other	154	30.80	12.27	46.63	16.27
	2	EO2	49	35.89		54.59	
		Other	154	56.49	20.60	100.43	45.83
	3	EO2	49	24.10		40.97	
		Other	154	37.51	13.41	57.87	16.89
	4	EO2	49	26.17		43.11	
		Other	154	39.27	13.10	50.34	7.24
EO3	1	EO3	56	15.79		24.90	
		Other	147	31.32	15.54	52.31	27.41
	2	EO3	64	26.06		43.51	
		Other	168	57.71	31.65	85.11	41.60
	3	EO3	64	17.95		31.92	
		Other	168	39.27	21.32	62.00	30.08
	4	EO3	64	18.33		32.62	
		Other	168	39.27	20.54	62.00	25.62

	Other	168	38.87		58.24		
HC	1	HC	64	23.16	15.53	28.44	30.74
		Other	168	38.69		59.18	
	2	HC	64	37.79	30.76	46.31	78.64
		Other	168	68.55		124.95	
	3	HC	64	31.66	12.67	34.20	50.21
		Other	168	44.32		84.41	
	4	HC	64	28.17	16.53	34.09	44.66
		Other	168	44.70		78.75	
GH1	1	GH1	36	22.07	18.33	31.05	37.97
		Other	138	40.40		69.02	
	2	GH1	36	56.73	29.71	65.23	43.63
		Other	138	86.44		108.87	
	3	GH1	36	47.79	10.18	54.64	24.07
		Other	138	57.97		78.70	
	4	GH1	36	50.36	9.10	107.24	-28.24
		Other	138	59.46		79.00	