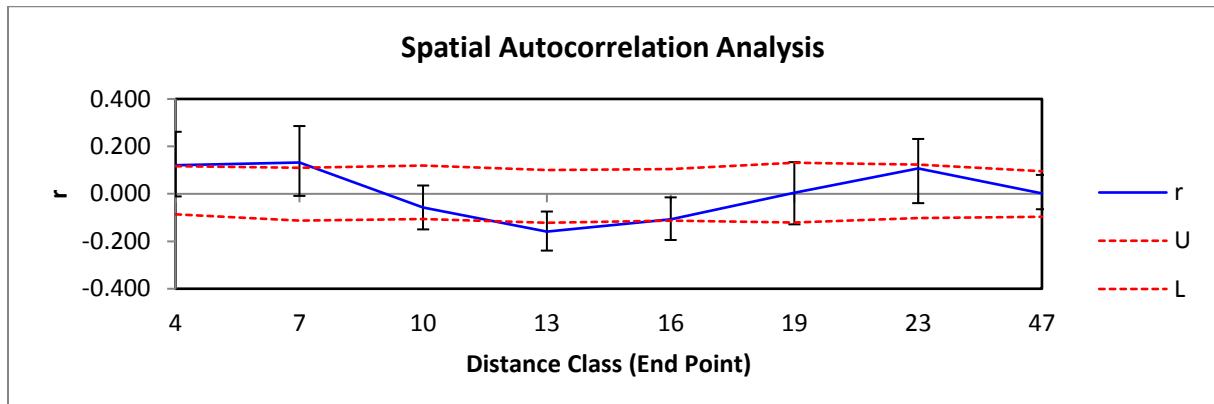


S1 Fig. Results of spatial autocorrelation analysis for all lynx individuals genotyped at 11 microsatellite loci. Bold indicates significant correlation (r) and probability (p).



Genetic Distance GD all
Geographic Distance GGD all
Data Title All genotypes

No. Samples 18
Even Sample Sizes
No. Dist. Classes 8
No. Permutations 999
No. Bootstraps 1000

n	22	19	19	19	23	15	15	16
Distance Class (End Point)	4	7	10	13	16	19	23	47
r	0.121	0.132	-0.057	-0.159	-0.108	0.004	0.107	0.002
U	0.116	0.109	0.119	0.100	0.105	0.131	0.123	0.095
L	-0.086	-0.113	-0.106	-0.122	-0.113	-0.121	-0.103	-0.096
P(r-rand >= r-data)	0.019	0.010	0.853	0.993	0.973	0.456	0.044	0.497
P(r-rand <= r-data)	0.982	0.991	0.148	0.008	0.028	0.545	0.957	0.504
Correction	0.059	0.059	0.059	0.059	0.059	0.059	0.059	0.059
r uc	0.062	0.073	-0.116	-0.218	-0.166	-0.055	0.048	-0.057
U uc	0.058	0.051	0.060	0.042	0.046	0.072	0.064	0.037
L uc	-0.145	-0.172	-0.165	-0.181	-0.172	-0.180	-0.161	-0.155
Mean Bootstrap r	0.120	0.131	-0.055	-0.159	-0.108	0.005	0.106	0.006
Ur error	0.141	0.154	0.092	0.085	0.093	0.129	0.124	0.078
Lr error	0.132	0.141	0.093	0.080	0.087	0.133	0.146	0.067
Ur	0.262	0.286	0.035	-0.075	-0.015	0.134	0.231	0.080
Lr	-0.011	-0.009	-0.150	-0.239	-0.194	-0.128	-0.039	-0.065
Intercept	9.095							