AB mtDNA

		Matched		Mismatched	
	AB	ABxSD	ABxSCN	ABxSD	ABxSCN
AB	---	0.3984	1.0000	<0.0001	<0.0001
ABxSD	0.1670	---	0.1004	<0.0001	0.0068
ABxSCN	1.0000	0.2332	---	<0.0001	<0.0001
SDxAB	0.0002	<0.0001	<0.0001	---	1.0000
SCNxAB	0.0004	<0.0001	<0.0001	1.0000	---

SCN mtDNA

		Matched		Mismatched	
	SCN	SCNxSD	SCNxAB	SCNxSD	SCNxAB
SCN	---	1.0000	1.0000	<0.0001	0.0012
SCNxSD	1.0000	---	1.0000	<0.0001	0.0005
SCNxAB	0.6734	1.0000	---	<0.0001	<0.0001
SDxSCN	0.0489	0.0024	0.0001	---	0.0071
ABxSCN	1.0000	0.4030	0.0439	0.7301	---

SD mtDNA

		Matched		Mismatched	
	SD	SDxAB	SDxSCN	SDxAB	SDxSCN
SD	---	<0.0001	<0.0001	0.0009	0.0227
SDxAB	0.7900	---	1.0000	<0.0001	<0.0001
SDxSCN	1.0000	1.0000	---	<0.0001	<0.0001
ABxSD	0.3383	0.0046	0.0390	---	1.0000
SCNxSD	0.1051	0.0010	0.0151	1.0000	---

Table S2. ANOVA of primary discriminant functions No significant differences were found among control treatment genotype classes and all control treatment genotype classes were significantly different than all stress treatment genotype classes (data not shown). More complex results resulted from comparisons between genotypes within hypoosmotic stress treatment. Results for discriminant function 1 are shown above the diagonal; results for discriminant function 2 are shown below the diagonal. Data are grouped by mtDNA genotype. ANOVA with Bonferroni post-hoc comparisons (α=0.05).