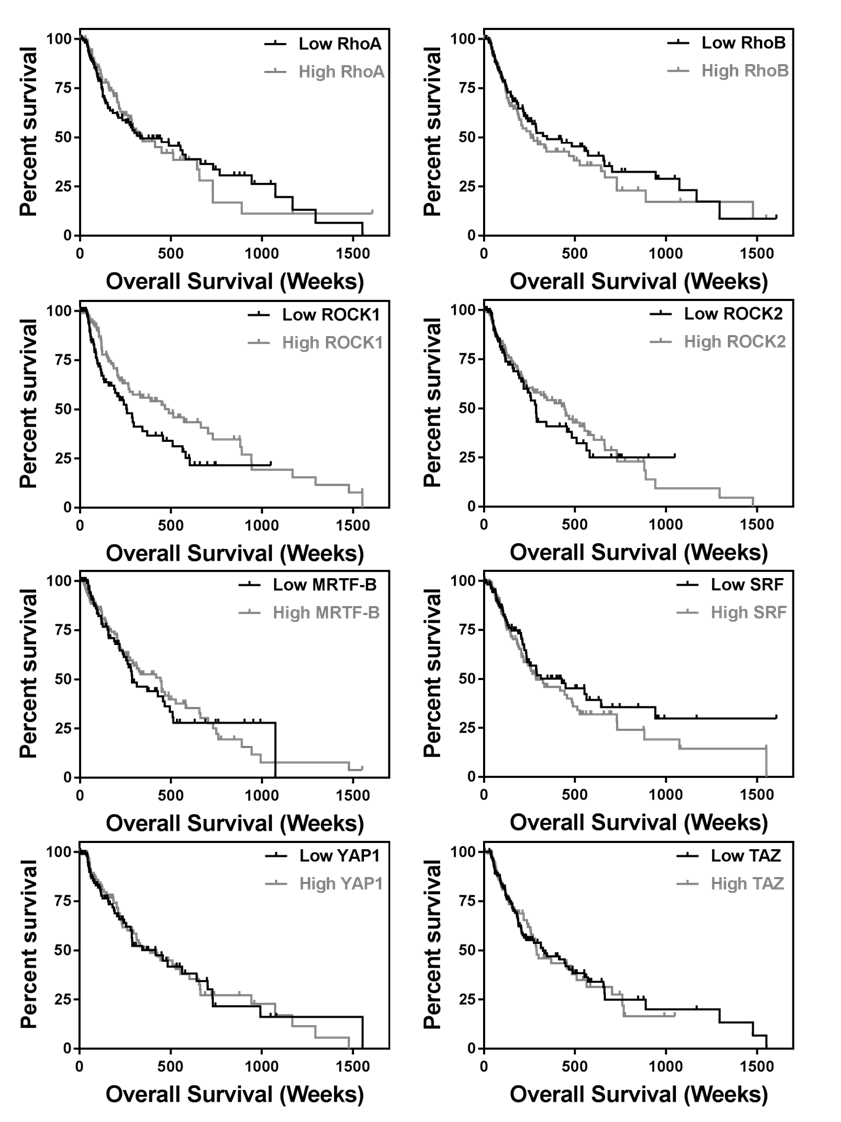
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**Figure S1.** The Cancer Genome Atlas (TCGA) cutaneous melanoma dataset was stratified into quartiles based upon expression ofindicated genes. Kaplan-Meier plots were generated from the highest (grey) and lowest (black) expressing quartiles. Survival curves were analyzed with the log-rank test with a cutoff of P < 0.05 as statistically significant.