APC 0.021 1.511(1.063-2.149) TP53 <0.001 1.788(1.273-2.513) TTN 0.065 1.378(0.981-1.937) KRAS <0.001 2.183(1.533-3.108) SYNE1 0.544 1.124(0.771-1.641) PIK3CA 0.388 1.184(0.807-1.738) MUC16 0.941 0.986(0.675-1.440) FAT4 0.790 0.946(0.631-1.420) CSMD3 0.262 1.276(0.833-1.954) DNAH5 0.268 1.277(0.828-1.968) RYR2 0.959 0.989(0.648-1.508) ZFHX4 0.446 1.185(0.765-1.836) OBSCN 0.736 0.928(0.600-1.434) RYR3 0.648 1.115(0.700-1.775) LRP1B 0.745 0.927(0.587-1.463) NEB 0.657 1.113(0.695-1.780) ABCA13 0.926 1.022(0.640-1.633) PCLO 0.715 0.917(0.576-1.460) CSMD1 0.783 0.936(0.584-1.500) FAT3 0.465 0.839(0.525-1.342) DST 0.753 0.925(0.572-1.498)	Genes	P-value	Hazard ratio
1	TP53 TTN KRAS SYNE1 PIK3CA MUC16 FAT4 CSMD3 DNAH5 RYR2 ZFHX4 OBSCN RYR3 LRP1B NEB ABCA13 PCLO CSMD1 FAT3	<0.001 0.065 <0.001 0.544 0.388 0.941 0.790 0.262 0.268 0.959 0.446 0.736 0.648 0.745 0.657 0.926 0.715 0.783 0.465	1.788(1.273-2.513) 1.378(0.981-1.937) 2.183(1.533-3.108) 1.124(0.771-1.641) 1.184(0.807-1.738) 0.986(0.675-1.440) 0.946(0.631-1.420) 1.276(0.833-1.954) 1.277(0.828-1.968) 0.989(0.648-1.508) 1.185(0.765-1.836) 0.928(0.600-1.434) 1.115(0.700-1.775) 0.927(0.587-1.463) 1.113(0.695-1.780) 1.022(0.640-1.633) 0.917(0.576-1.460) 0.936(0.584-1.500) 0.839(0.525-1.342)

## High Risk vs Low Risk

