

Gene	Tier 1 & 2		Tier 1 only	
	Aggressive	Non- aggressive	Aggressive	Non-aggressive
<i>ACVRL1</i>	0	3	0	0
<i>AXL</i>	10	1	0	0
<i>CHRNA3</i>	3	6	1	0
<i>CP</i>	0	5	0	0
<i>DHRS2</i>	3	12	0	0
<i>LUM</i>	5	0	0	0
<i>MTOR</i>	1	8	0	0
<i>PARK2</i>	0	6	0	0
<i>RYR1</i>	10	14	3	3
<i>WISP2</i>	0	1	0	0

Supplementary Table 5 – Burden of mutations between metastatic and non-aggressive cohorts for genes with BF ≥ 100 in the Bayesian Risk Index analysis of Hallmark Gene Sets. Counts of Tier 1 variants, or Tier 1 and 2 variants combined, stratified by aggressiveness status. The majority of rare disruptive variants within the genes identified through this analysis were non-protein truncating, and were enriched in the non-aggressive cohort, implying a protective effect against the likelihood of developing metastatic PrCa.