

Supplementary tables and figures (Whitman et al)

Table S1. Association of 8q24 SNPs with post-operative Gleason sum

Locus	Post-operative GS			P
	GS 2-6	GS 7	GS 8-10	
Region1				0.3
rs1447295 A				
CC	32(64%)	11(22%)	7(14%)	
CA	17(45%)	16(42%)	5(13%)	
AA	6(60%)	3(30%)	1(10%)	
Region2				0.4
rs6983561 C				
AA	11(50%)	7(32%)	4(18%)	
CA	29(58%)	17(34%)	4(8%)	
CC	16(57%)	7(25%)	5(18%)	
Region2				0.8
rs13254738 C				
AA	6(46%)	4(31%)	3(23%)	
CA	26(59%)	13(30%)	5(11%)	
CC	22(56%)	12(31%)	5(13%)	
Region2				0.2
Broad11934905				
A				
GG	49(58%)	26(31%)	9(11%)	
AG	6(40%)	5(33%)	4(27%)	
Region3				0.7
rs6983267 G				
TT+GT	14(58%)	6(25%)	4(17%)	
GG	41(55%)	24(32%)	9(12%)	
Region3				0.6
rs7000448 T				
CC	6(40%)	6(40%)	3(20%)	
TC	29(58%)	14(28%)	7(14%)	
TT	20(59%)	11(32%)	3(9%)	
Risk alleles¹				0.5
0 to 5	20(57%)	9(26%)	6(17%)	
6 to 10	36(55%)	22(34%)	7(11%)	
Risk alleles²				0.3
0 to 4	14(56%)	7(28%)	4(16%)	
5 to 7	31(65%)	13(27%)	4(8%)	
8 to 10	11(41%)	11(41%)	5(18%)	

Table S2. Distribution of total number of at-risk genotypes by region

Total number of risk alleles	N (%)
Region 1	
0	58 (50.0%)
1	45 (38.8%)
2	13 (11.2%)
Region 2	
0	9 (8.0%)
1	17 (15.0%)
2	31 (27.4%)
3	30 (26.6%)
4	21 (18.6%)
5	5 (4.4%)
Region 3	
0	9 (8.0%)
1	24 (21.2%)
2	40 (35.4%)
3	40 (35.4%)

Table S3. Association of total number of at-risk genotypes with age at diagnosis by region

Risk Locus	Total number of risk alleles	N	Age at diagnosis		
			Mean	SD	P
1	0	58	58.7	8.5	0.2954
	1	42	56.0	8.8	
	2	12	56.1	10.8	
2	0-1	25	58.9	9.7	0.1068
	2-3	60	58.4	8.5	
	4-5	25	54.3	8.3	
3	0	9	58.0	10.2	0.2791
	1	24	55.0	7.3	
	2	39	59.5	7.6	
	3	37	57.5	10.3	

Table S4. Association of total number of at-risk genotypes with pathological T stage by region

Risk locus	Total number of risk alleles	pT2	pT3-4	P value
1	<i>0</i>	34(68%)	16(32%)	0.0634
	<i>1</i>	19(49%)	20(51%)	
	<i>2</i>	9(82%)	2(18%)	
2	<i>0-1</i>	17(77%)	5(23%)	0.2141
	<i>2-3</i>	29(57%)	22(43%)	
	<i>4-5</i>	14(56%)	11(44%)	
3	<i>0</i>	5(83%)	1(17%)	0.6854
	<i>1</i>	14(61%)	9(39%)	
	<i>2</i>	20(57%)	15(43%)	
	<i>3</i>	21(62%)	13(38%)	

Table S5. Association between total number of at-risk genotypes and clinico-pathological features

Variable	Total number of risk alleles			P value
	N	Mean±SD	Median (range)	
CaP family history				0.3852
<i>No</i>	54	5.9±2.3	6 (0-10)	
<i>Yes</i>	44	5.5±2.1	6 (0-9)	
Pathologic T stage				0.1696
<i>pT2</i>	63	5.6+2.3	6 (0-10)	
<i>pT3-4</i>	39	6.2+2.1	6 (0-10)	
Postoperative Gleason sum				0.7567
<i>2 - 6</i>	57	5.9+2.1	6 (0-10)	
<i>7</i>	31	5.9+2.5	6 (0-9)	
<i>8 - 10</i>	14	5.6+2.6	5.5 (1-10)	

Figure S1. KM PSA recurrence-free survival curves across total number of at-risk genotypes at region 1

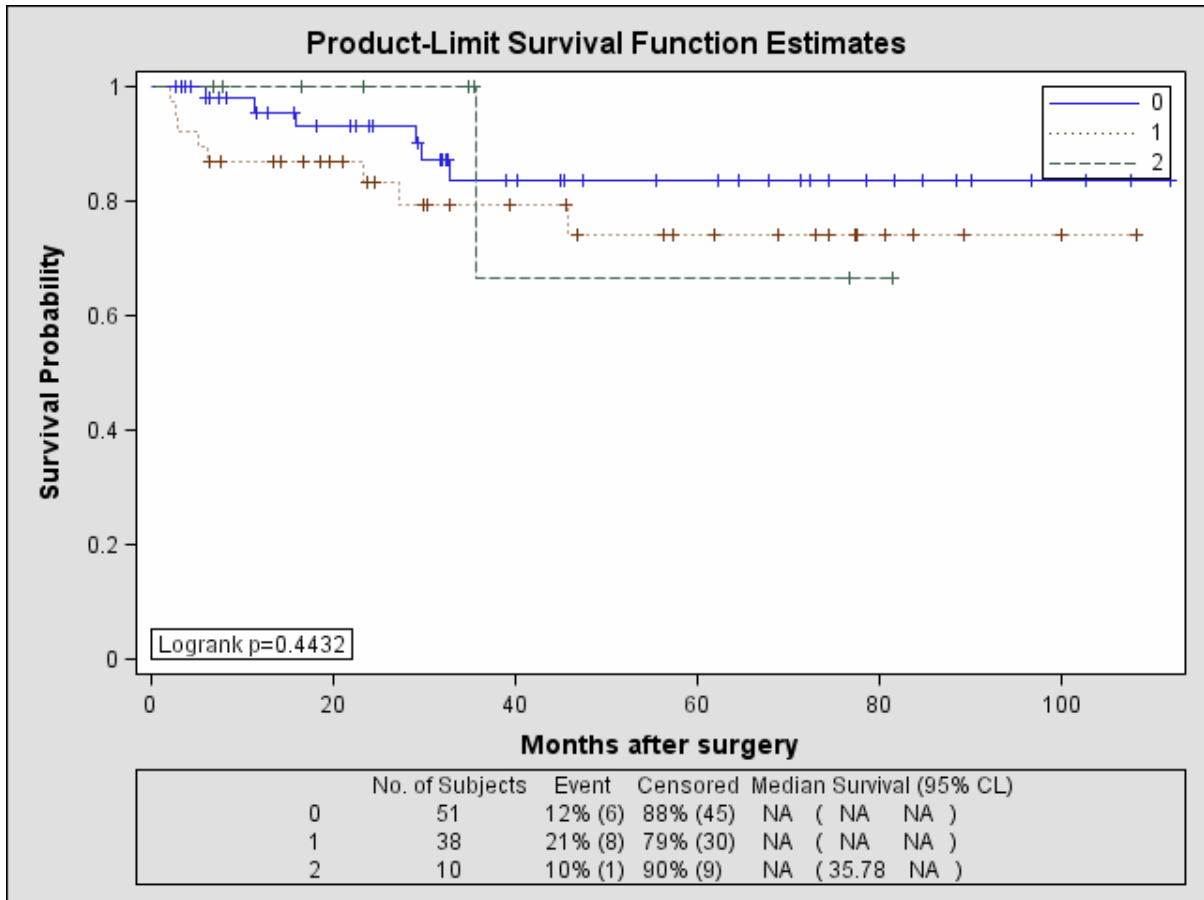


Figure S2. KM PSA recurrence-free survival curves across total number of at-risk genotypes at region 2

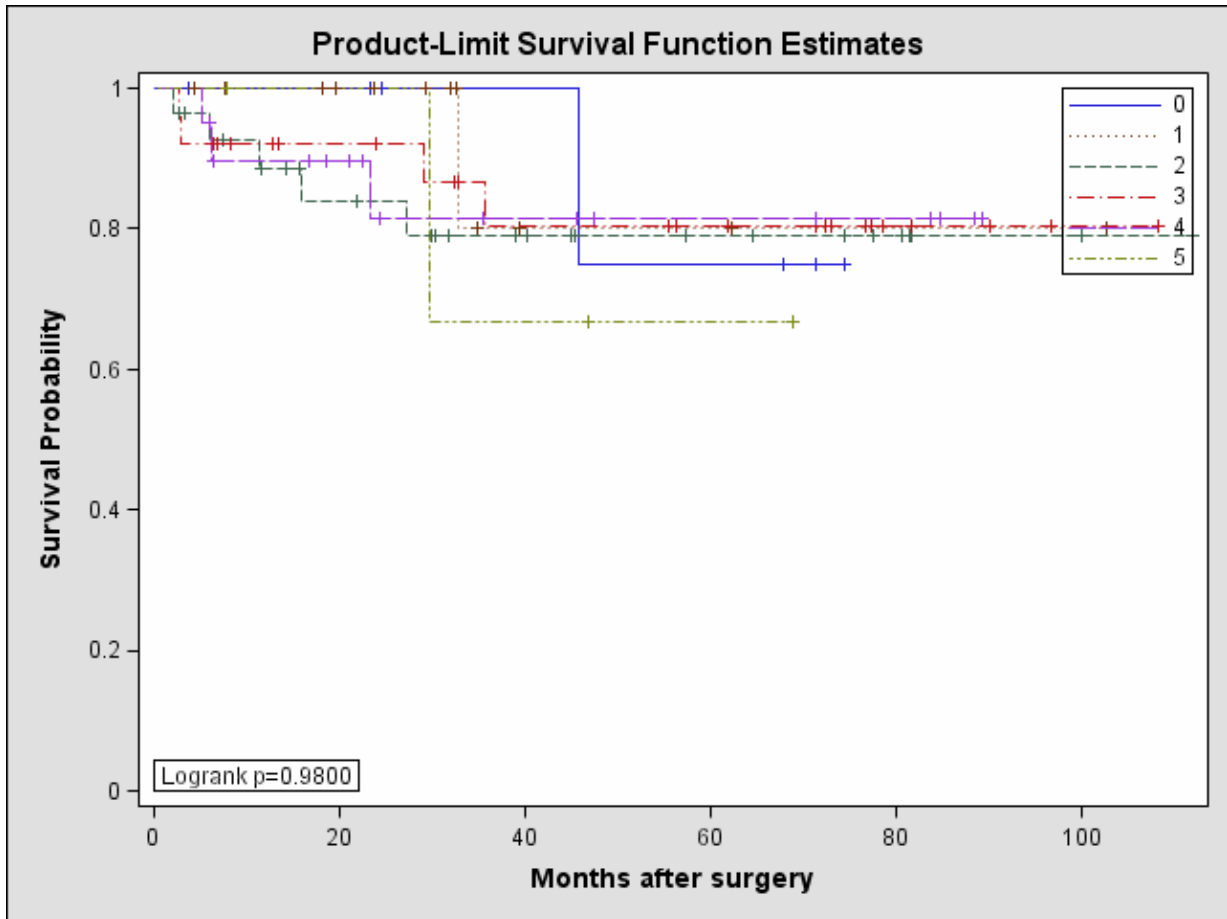


Figure S3. KM PSA recurrence-free survival curves across total number of at-risk genotypes at region 3

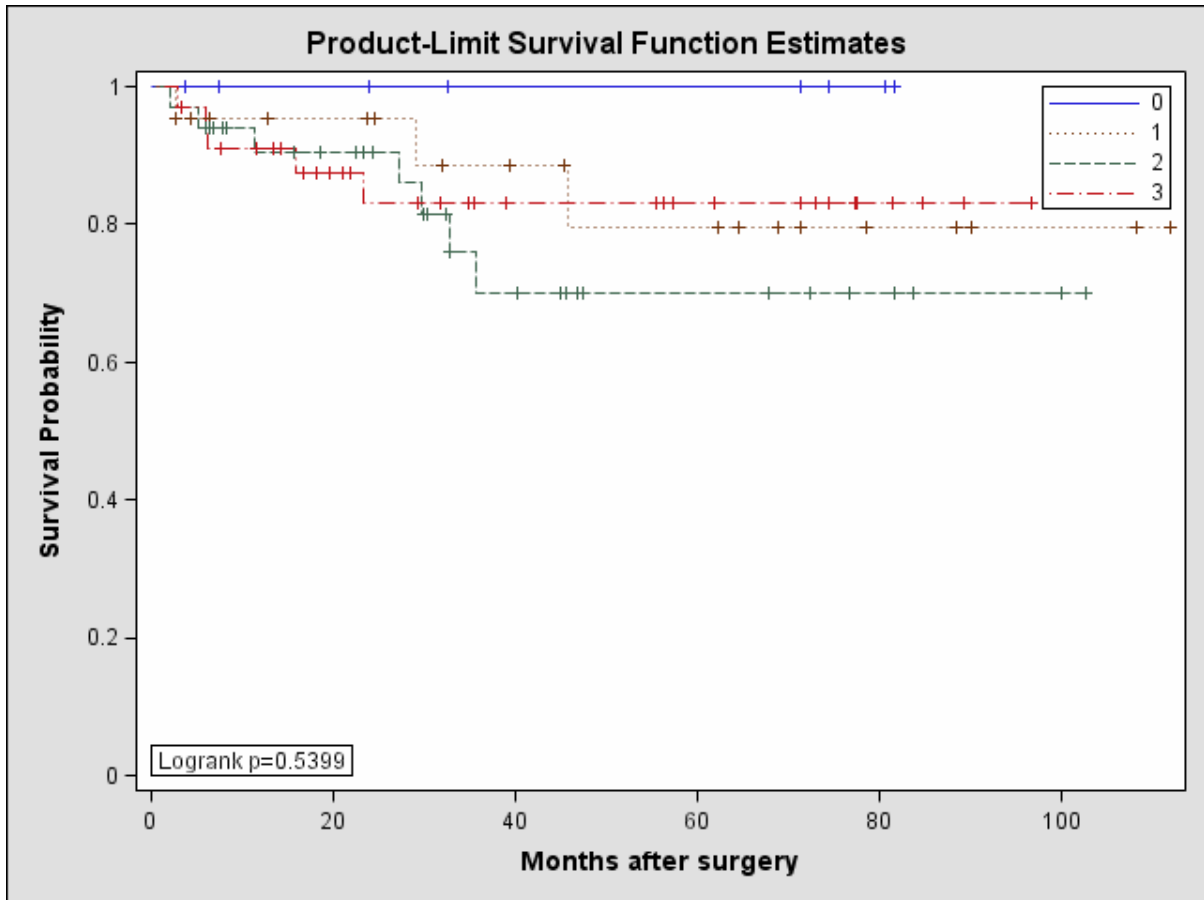


Figure S4. Association between total number of at-risk genotypes and age at diagnosis

