

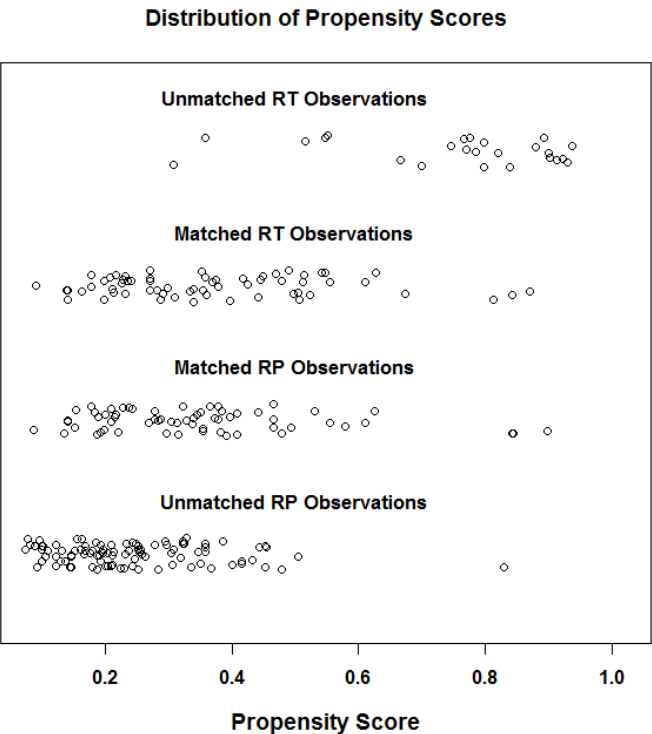
Supplementary Data

Supplemental Figure 1. A) Dot plot and B) histogram of distribution of propensity scores for matched and unmatched RT and RP cohorts.

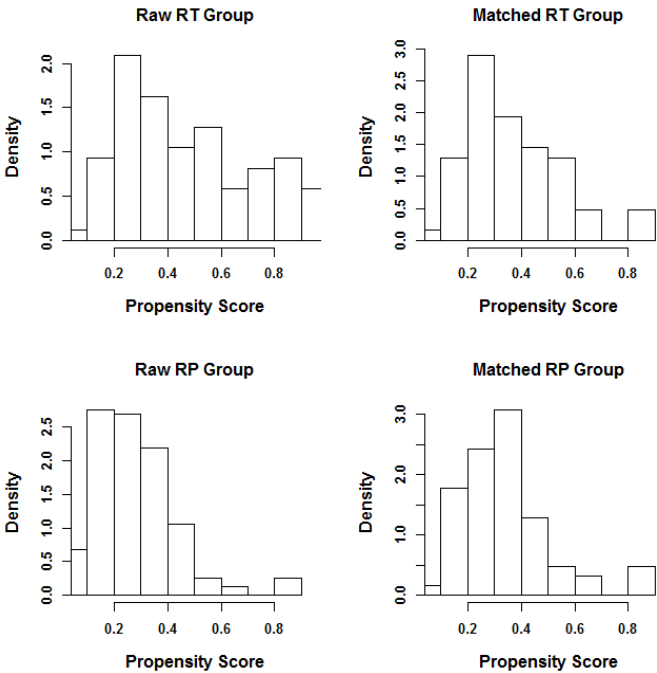
Supplemental Figure 2. Kaplan Meier plot of A) distant metastasis free survival and B) overall survival in matched patients undergoing RP or RT for primary treatment of HR-PCa specifically without ADT.

Supplemental Figure 1

A

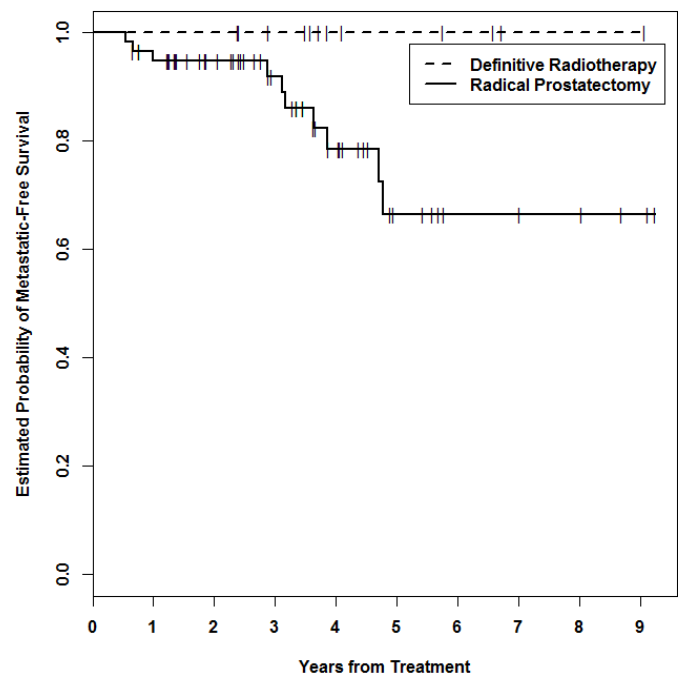


B

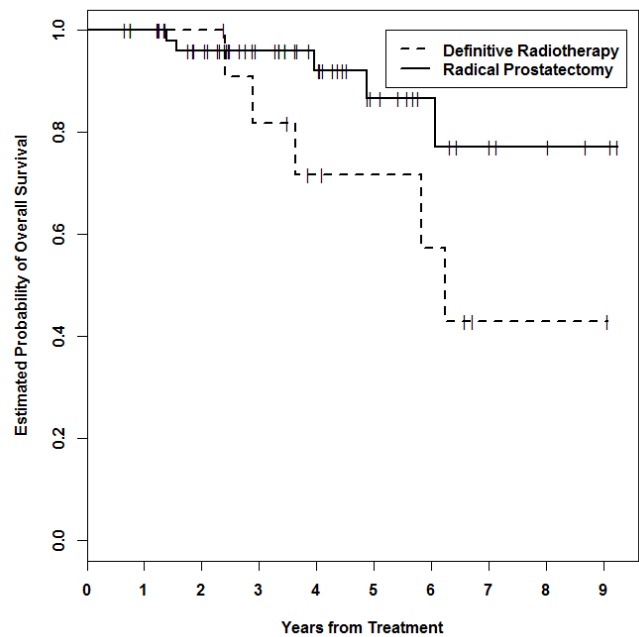


Supplemental Figure 2

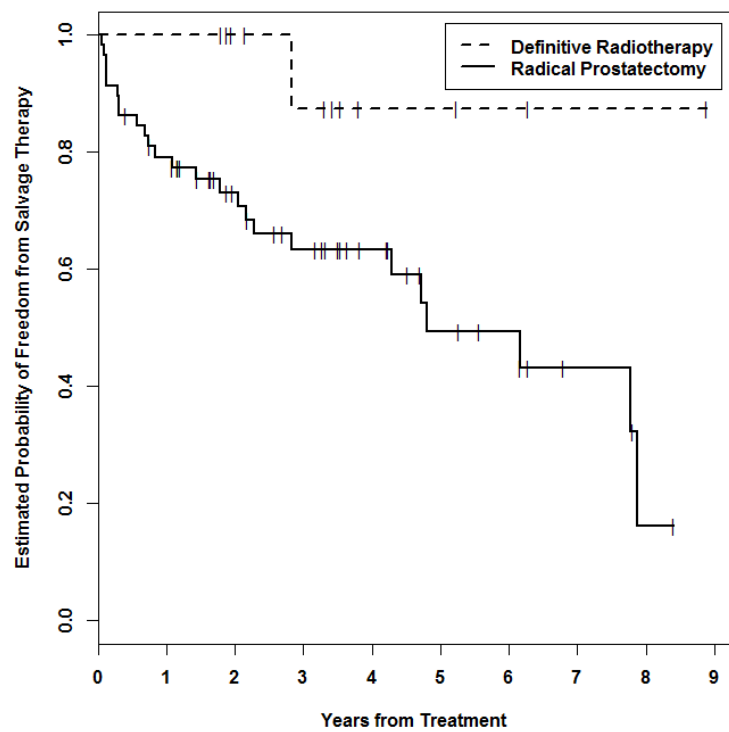
A



B



C



Supplemental Table 1. Patient Characteristics – Unmatched Cohort

	RP (N = 160)	RT (N = 86)	P-Value
Clinical T-Stage			<0.001
T1	114	36	
T2	42	29	
T3	4	21	
PSA			0.014
<10	96	35	
10-20	12	11	
>20	52	40	
Biopsy Gleason Score			0.09
6 or 7	33	28	
8	86	36	
9 or 10	41	22	
ACE 27			0.292
0	52	20	
1	75	44	
≥2	33	22	
Age			0.255
Mean	62.2	64	
Standard Deviation	7.2	9.2	
Follow-up (Months)*			<0.001
Median	42.7	51.4	
Standard Deviation	25.5	28.7	
Days to Treatment from Dx			<0.001
Median	57.5	135	
Standard Deviation	39	311	

* Calculated from the completion of RT or date of RP

Supplemental Table 2. Matching Diagnostics

Matching Method	Variable	% Improvement	Mean Difference: Unmatched Cohort	Mean Difference: Matched Cohort
Exact + Nearest Neighbor	Overall Distance	87.6	0.19	0.02
Nearest Neighbor	Age: Years (Numeric)	24.7	1.76	1.32
	ACE = 0	12.0	-9.2%	-8.1%
	ACE = 1	24.8	4.3%	3.2%
	ACE 2+	2.4	5.0%	4.8%
Exact	cT1	100.0	-29.4%	0.0%
	cT2	100.0	7.5%	0.0%
	cT3	100.0	21.9%	0.0%
	PSA: <10	100.0	-19.3%	0.0%
	PSA: 10 to 20	100.0	5.3%	0.0%
	PSA: >20	100.0	14.0%	0.0%
	Gleason: 6 or 7	100.0	11.9%	0.0%
	Gleason = 8	100.0	-11.9%	0.0%
	Gleason >8	100.0	0.0%	0.0%

Supplemental Table 3. Cox-Proportional Hazards Models – Unmatched Cohort**Distant Metastasis Free Survival (27 events)**

Cox PH Model	Hazard Ratio	95% Confidence Interval		P-value
		Lower	Upper	
RT vs. RP	0.27	0.10	0.73	0.010
Age	1.00	0.95	1.06	0.895
cT2 vs. cT1	0.81	0.26	2.56	0.725
cT3 vs. cT1	1.18	0.34	4.14	0.794
PSA 20+ vs. <20	8.07	3.15	20.67	<0.001
Gleason 8 vs. 6 to 7	5.81	1.76	19.25	0.004
Gleason 8+ vs. 6 to 7	8.77	2.45	31.35	0.001
ACE 1 vs. 0	0.97	0.40	2.37	0.943
ACE 2+ vs. 0	1.03	0.31	3.45	0.967

Overall Survival (33 events)

Cox PH Model	Hazard Ratio	95% Confidence Interval		P-value
		Lower	Upper	
RT vs. RP	1.90	0.83	4.32	0.128
Age	1.02	0.98	1.07	0.381
cT2 vs. cT1	0.51	0.19	1.40	0.192
cT3 vs. cT1	0.76	0.27	2.17	0.613
PSA 20+ vs. <20	2.38	1.04	5.46	0.040
Gleason 8 vs. 6 to 7	1.62	0.59	4.45	0.350
Gleason 8+ vs. 6 to 7	3.88	1.37	10.97	0.011
ACE 1 vs. 0	0.56	0.23	1.38	0.211
ACE 2+ vs. 0	1.40	0.54	3.59	0.489

Salvage Treatment (68 events)

Cox PH Model	Hazard Ratio	95% Confidence Interval		P-value
		Lower	Upper	

RT vs. RP	0.15	0.07	0.33	<0.001
Age	0.96	0.92	0.99	0.010
cT2 vs. cT1	1.22	0.69	2.16	0.493
cT3 vs. cT1	0.56	0.16	1.98	0.369
PSA 20+ vs. <20	3.22	1.64	6.33	0.001
Gleason 8 vs. 6 to 7	1.94	0.94	3.99	0.071
Gleason 8+ vs. 6 to 7	2.31	0.99	5.37	0.053
ACE 1 vs. 0	1.37	0.76	2.46	0.295
ACE 2+ vs. 0	2.16	1.06	4.43	0.034

Supplemental Table 4. Pathologic Findings - RP Group

	cT1c	cT2	cT3
Pathologic T-Stage			
pT2a	2	2	0
pT2c	9	6	0
pT3a	11	8	1
pT3b	14	7	1
pT4	0	0	1
RP Gleason Score			
3+3		3	
3+4		13	
4+3		17	
4+4		3	
5+3 or 3+5		2	
9 or 10		23	
Unknown		1	
Surgical Margins			
Positive		34	
Negative		28	
Pathologic N Stage			
pNx		5	
pN0		46	
pN1		11	