

Supplementary Materials

Nucleotide-resolution analysis of *TMPRSS2* and *ERG* rearrangements in prostate cancer

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Table of Contents

	<u>Page</u>
Supplementary Methods	2
Supplementary Figure 1	3
Supplementary Figure 2	4
Supplementary Figure 3	5
Supplementary Figure 4	6
Supplementary Figure 5	7
Supplementary Figure 6	8
Supplementary Figure 7	9
Supplementary Figure 8	10
Supplementary Figure 9	11
Supplementary Figure 10	12
Supplementary Table 1	13
Supplementary Table 2	14
Supplementary Table 3	15
Supplementary Table 4	16

Additional Supplementary Material not included in this PDF:

Supplementary File containing chromosomal coordinates of RNA Baits used in geBACS.

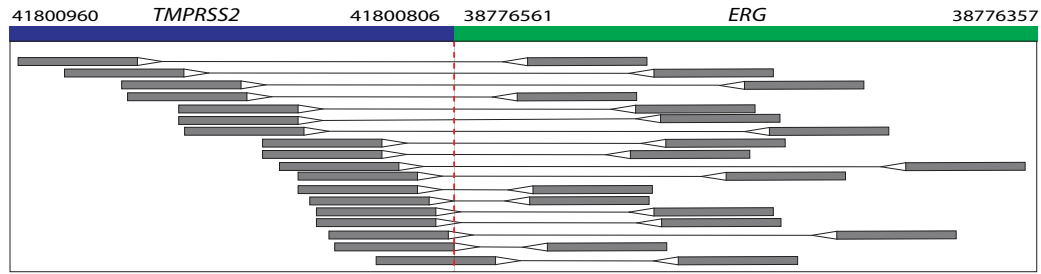
SUPPLEMENTARY METHODS

PCR reactions for validation and case-specific breakpoint assignment

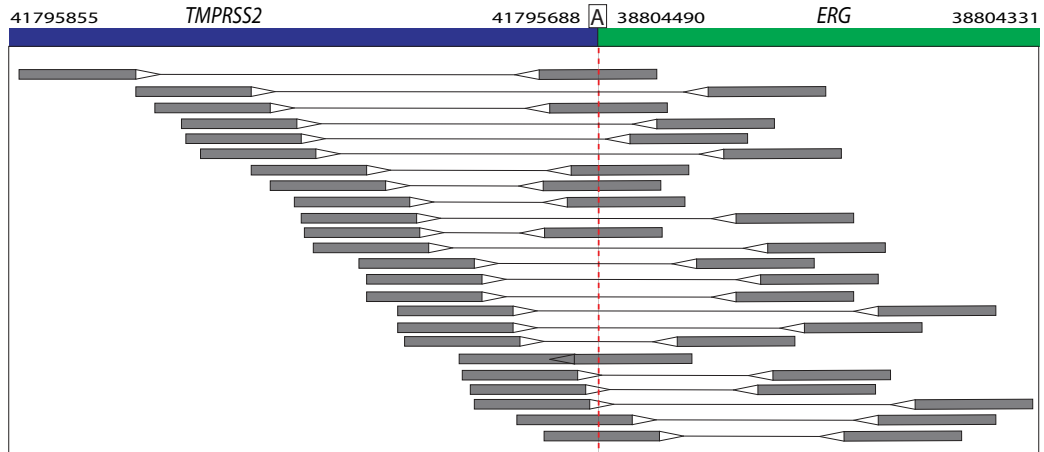
PCR reactions consisted of 40 µl reactions containing 50 ng of DNA, 1× Platinum Taq buffer (Invitrogen, Carlsbad, CA), 1.5 U Platinum Taq polymerase (Invitrogen), 250 µM each dNTPs, 1.5 mM MgCl₂, 0.25 µg/µl BSA, 2 µl dimethyl sulfoxide, 400 nM each forward and reverse primers. A touchdown PCR approach was utilized as follows: 95°C for 3 min, 4 cycles of denaturing at 94°C for 30 s, annealing at 70°C for 30 s and extension at 72°C for 45 s, repeating with successive annealing temperatures of 68°C, 65°C, and 60°C for 4 cycles each and finally 36 cycles at an annealing temperature of 55°C, followed by a 7 min extension step at 72°C.

A

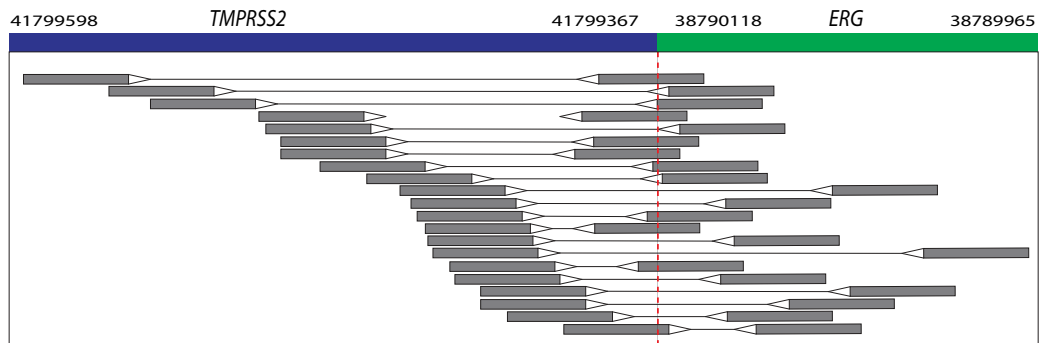
Case 45



Case 66



Case 77



B

Characteristics of rearrangement junctions identified in reference samples.*

Reference Case #	Junctions	Gene 1	Gene 2	Orientation	^A Microhomology	^B Reads	^C Junction Reads
Case 45	<i>TMPRSS2-ERG</i>	chr21:41800806	chr21:38776561	s/s	-	18	5
Case 66	<i>TMPRSS2-ERG</i>	chr21:41795687	chr21:38804491	s/s	A	24	11
Case 77	<i>TMPRSS2-ERG</i>	chr21:41799367	chr21:38790118	s/s	-	21	12

*, Conventions are same as for Supplementary Table 2.

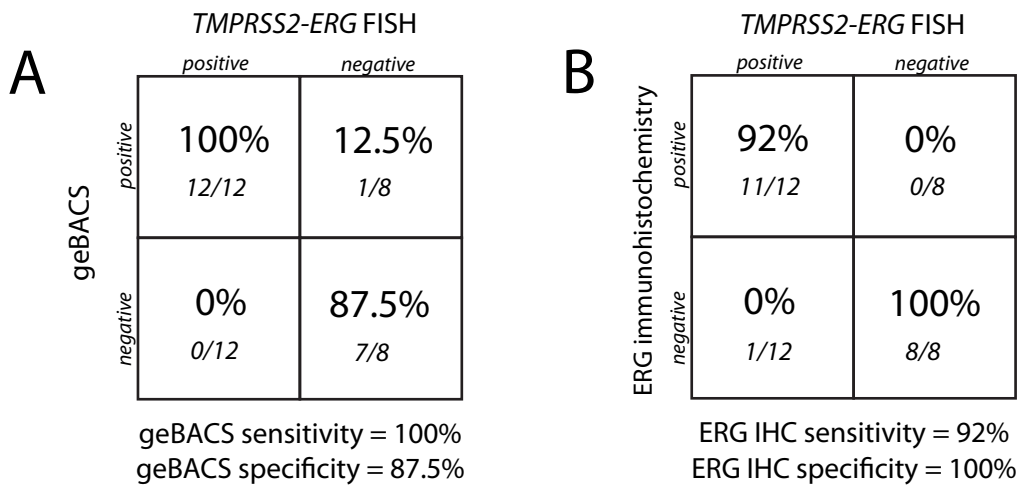
A. Bases at the junction that are shared by both genes in the rearrangement.

B. Number of paired-end reads flanking or directly overlapping the rearrangement junction.

C. Number of reads directly overlapping the rearrangement junction.

Supplementary Figure 1. Detection of rearrangement junctions in reference samples.

(A) Paired-end read distribution surrounding 3 known *TMPRSS2-ERG* rearrangements from 3 reference samples allowing assessment of effectiveness of the geBACS strategy. The position of the breakpoint is indicated by the red line and by the Chr21 positions of the *TMPRSS2* and *ERG* breakpoints at the top of each panel. (B) Characteristics of *TMPRSS2-ERG* breakpoints of reference samples.



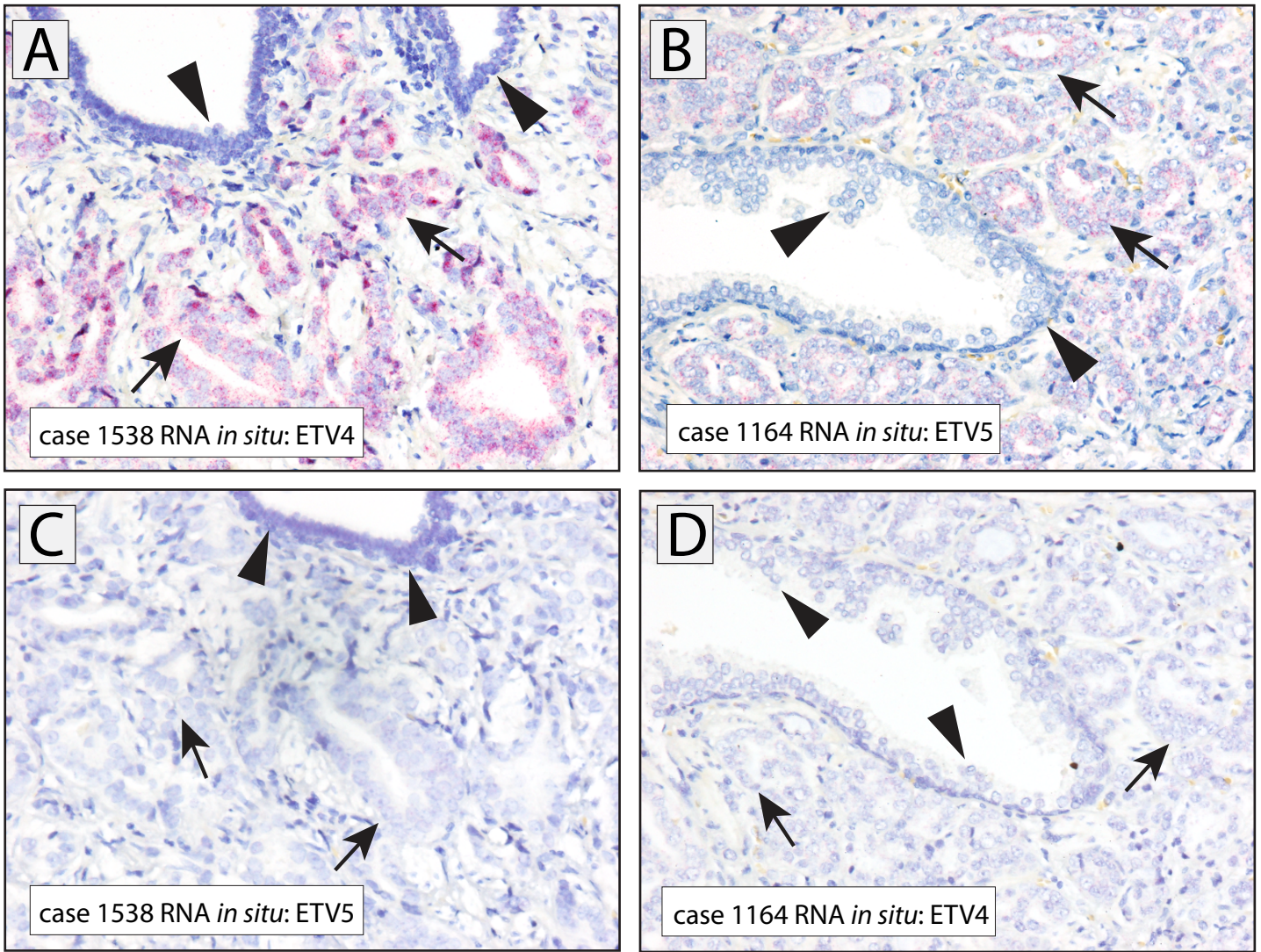
C

Patient Bank #	Junctions	ERG Stain	FISH
4	TMPRSS2-ERG	positive	D
372	TMPRSS2-ERG SLC45A3-ERG	negative	N
535	TMPRSS2-ERG	positive	D
652	TMPRSS2-ERG ERG-ERG	positive	T
675	TMPRSS2-ERG	positive	D
682	TMPRSS2-ERG	positive	D
808	TMPRSS2-ERG TMPRSS2-ERG	positive	T
814	TMPRSS2-ERG	positive	T
816	TMPRSS2-ERG TMPRSS2-TMPRSS2	positive	T
981	TMPRSS2-ERG	positive	T
989	FAM177A-ERG	positive	D
995	TMPRSS2-ERG ERG-ERG TMPRSS2-TMPRSS2 TMPRSS2-TMPRSS2 TMPRSS2-TMPRSS2	positive	T
1273	ELK4-ERG	negative	T, ERG*
170	-	negative	N
178	-	negative	N
700	-	negative	N
913	-	negative	N
994	-	negative	N
1048	-	negative	N
1508	-	negative	N

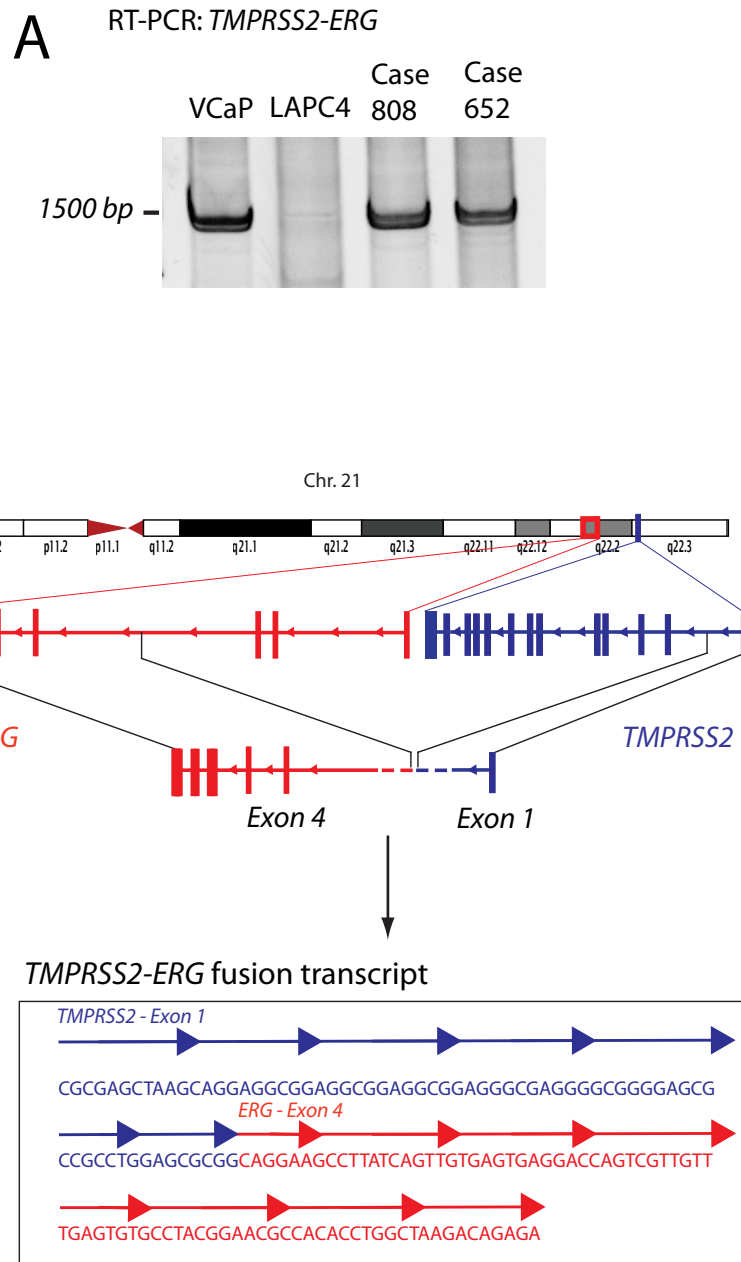
Rearrangement status by FISH; rearrangement with deletion (D), rearrangement with translocation (T), no rearrangement (N). *, Case 1273 showed translocation only of the 3' ERG probe.

Supplementary Figure 2. Sensitivity and specificity determination of geBACS by FISH.

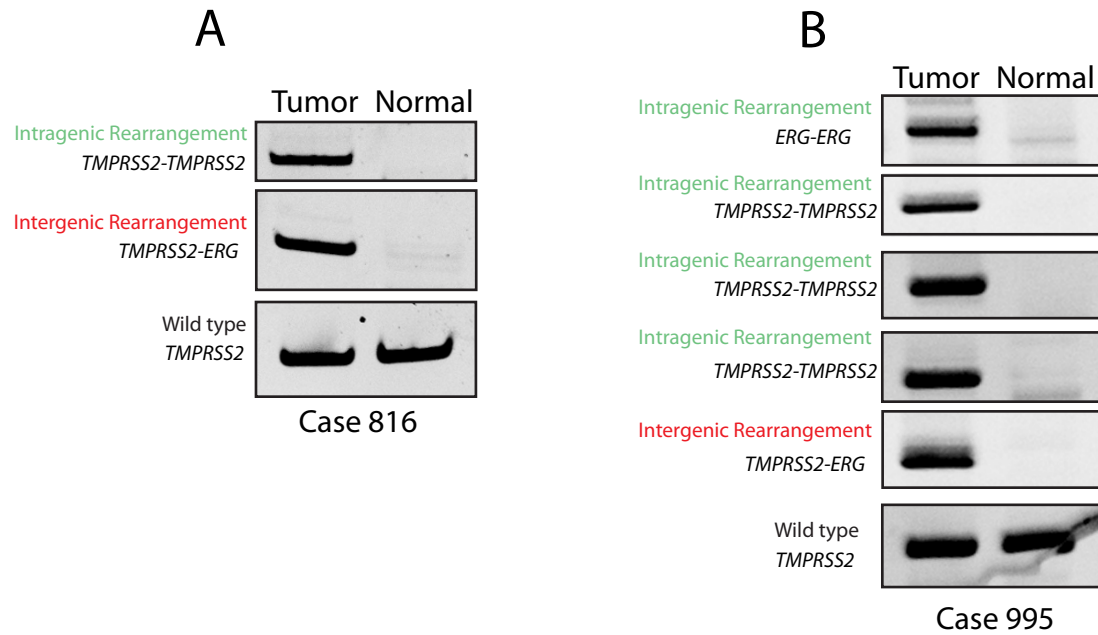
(A) Specificity and sensitivity of the geBACS pipeline in identifying TMPRSS2-ERG rearrangements, determined by using TMPRSS2-ERG FISH. (B) Correlation between ERG IHC and TMPRSS2-ERG FISH. (C) Table summarizing IHC and FISH data.



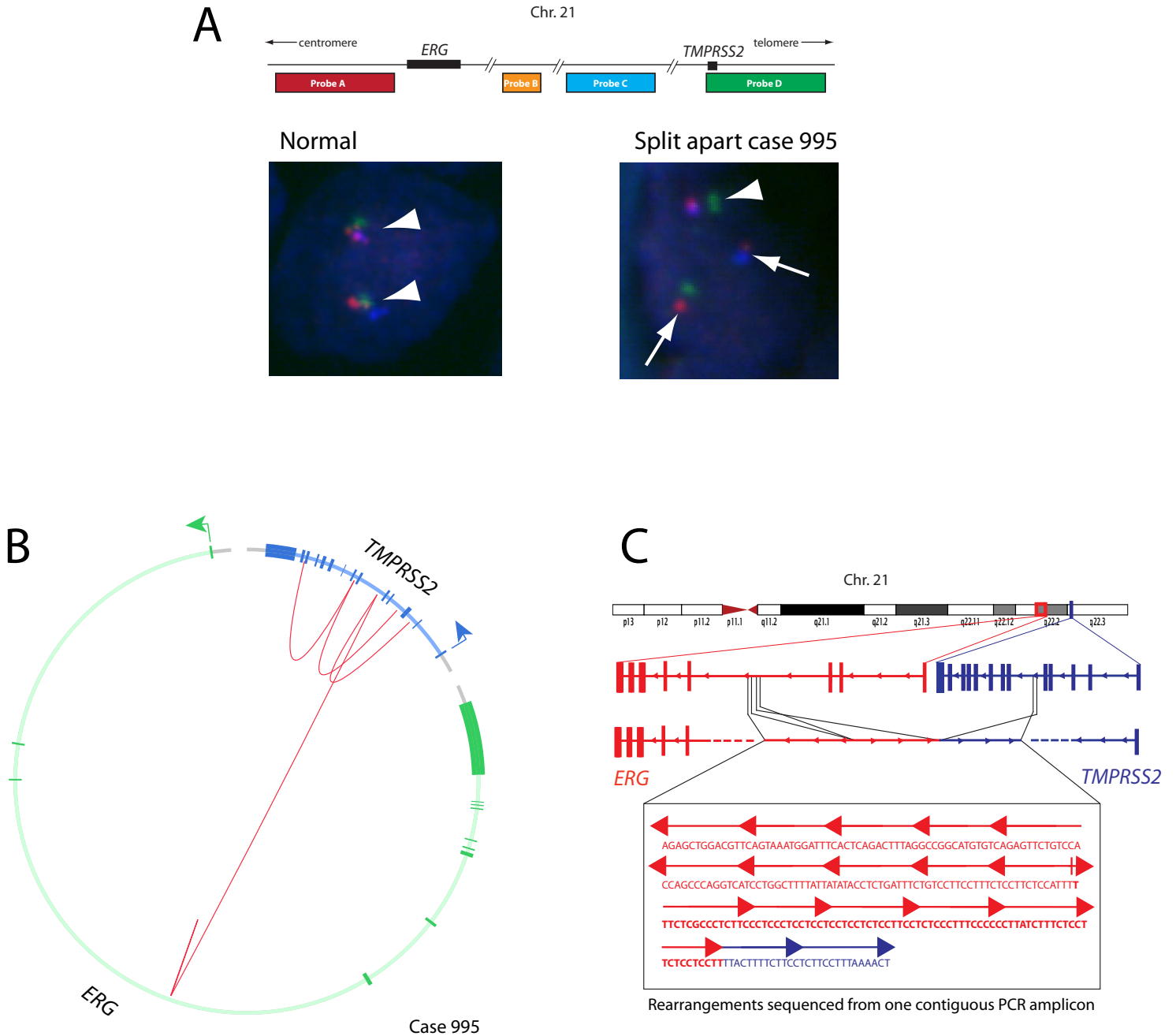
Supplementary Figure 3. In situ RNA detection of ETV4 and ETV5 in cases harboring TMPRSS2-ETV4 and TMPRSS2-ETV5 rearrangements. Case 1538 with geBACS-confirmed ETV4 rearrangement shows positive reactivity for ETV4 expression in neoplastic cells (arrows) (A), but no reactivity with ETV5 specific probes (C). Case 1164 with geBACS confirmed TMPRSS2-ETV5 rearrangement shows positive reactivity for ETV5 expression in tumor cells (arrows) (B), but no reactivity with ETV4 probes (D). Arrows indicate representative prostate cancer cells, and Arrowheads indicate representative normal prostate epithelial cells.



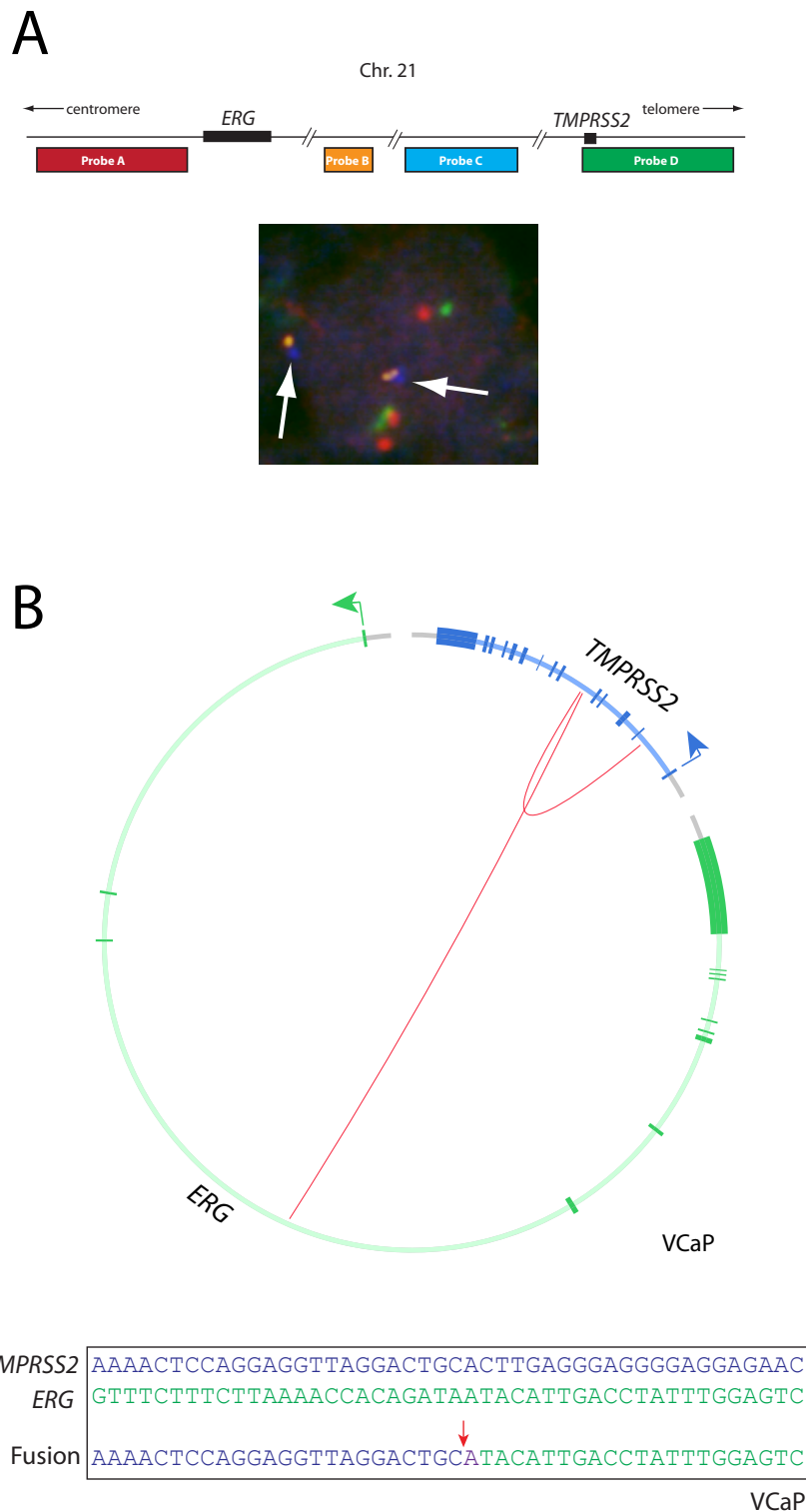
Supplementary Figure 4. The most common *TMPRSS2-ERG* rearrangement involves the first intron of *TMPRSS2* and the third intron of *ERG* resulting in an exon 1 – exon 4 *TMPRSS2-ERG* fusion transcript. (A) RT-PCR showing the expected exon 1 – exon 4 fusion previously noted in the VCaP cell line. Lane 2 shows no amplification of the transcript from the rearrangement negative LAPC4 cell line while lanes 3 and 4 show a similar exon 1 – exon 4 transcript in Cases 808 and 652 respectively, in which geBACS identified rearrangements occurring in intron 1 of *TMPRSS2* and intron 3 or *ERG*. Bands were excised and sequenced to verify the expected rearrangement transcript. (B) Detailed schematic showing the configuration of the most common *TMPRSS2-ERG* rearrangement sites identified by geBACS and the structure of the expected fusion transcript sequence.



Supplementary Figure 5. Inter- and Intra- genic rearrangements in TMPRSS2 and ERG are only detected in tumor, and not in normal adjacent tissue. All inter- and intra- genic rearrangements identified by geBACS for case 816 (A) and case 995 (B) were detected by PCR using primers flanking the rearrangement breakpoint only in tumor, but not adjacent normal tissues. (A,B) Primers targeting a TMPRSS2 sequence not involved in rearrangement (Wild type TMPRSS2) were used as an input control for the PCR reactions.

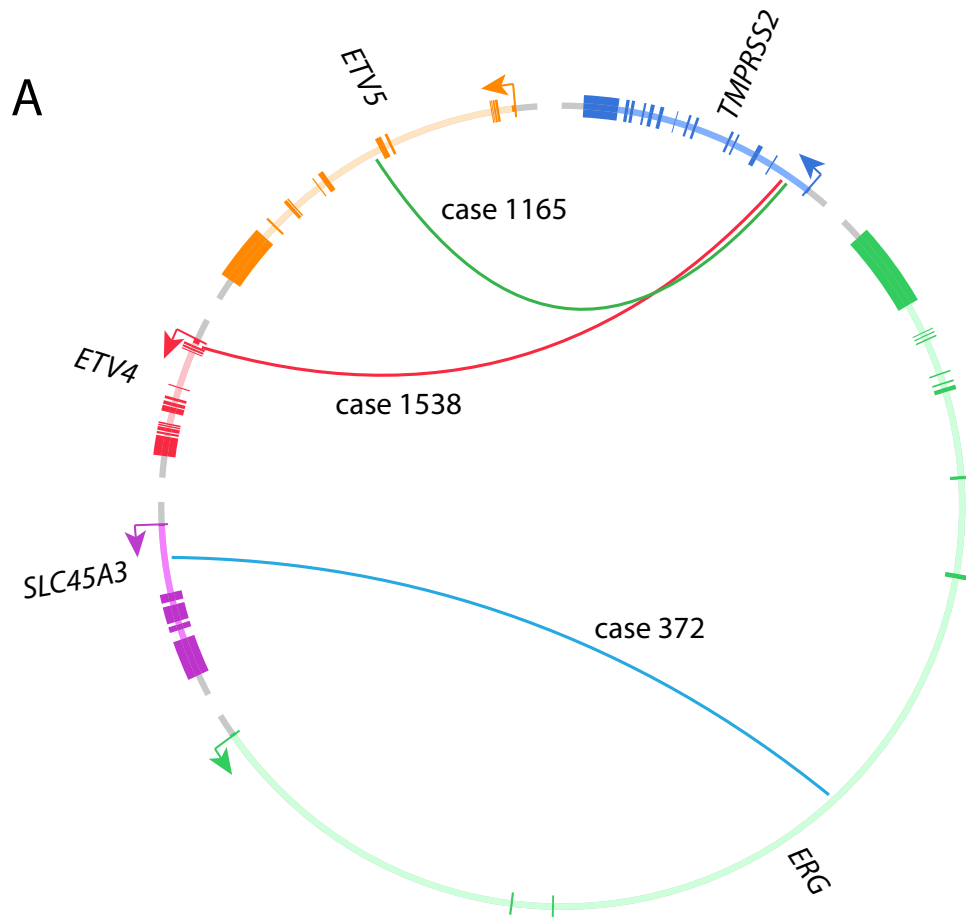


Supplementary Figure 6. Detailed characterization of rearrangements in Case 995. (A) Mono-allelic rearrangement associated with translocation by FISH. White arrowheads indicate normal alleles, white arrows indicate rearranged alleles. (B) Circos plot depicting complex interand intra-genic rearrangements involving *TMPRSS2* and *ERG*. (C) A schematic representing the location and orientation of a complex rearrangement in case 995 involving inversion of an *ERG* segment, inversion of a *TMPRSS2* segment, and the rearrangement of *TMPRSS2* with *ERG* is shown. A PCR amplicon spanning multiple contiguous complex rearrangement junctions was sequenced and used to generate this schematic (see Supplementary Table 3 for the PCR primers).



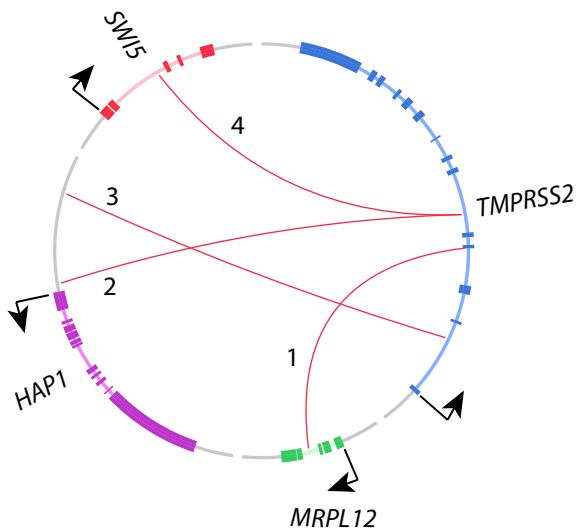
Supplementary Figure 7. Detailed characterization of rearrangements in VCaP cell line.

(A). *TMPRSS2-ERG* FISH of VCaP cells confirmed the presence of a rearrangement, and revealed a bi-allelic rearrangement for *TMPRSS2-ERG* associated with translocation of intervening sequences. (B) Circos plot depicting inter- and intra-genic rearrangements in VCaP. (C) Genomic sequence of the *TMPRSS2-ERG* fusion in VCaP, as identified by geBACS and confirmed by PCR and Sanger sequencing.



Supplementary Figure 8. Genomic rearrangements involving *TMPRSS2*, *SLC45A3*, *ERG*, *ETV4* and *ETV5*. (A) Circos plots showing architecture of genomic rearrangements in cases harboring *TMPRSS2-ETV4* (case 1538), *TMPRSS2-ETV5* (case 1165) and *SLC45A3-ERG* (case 372) fusions. (B) Nucleotide resolution of breakpoint sequence of the above cases. Sequences showing flanking microhomologies are highlighted in boxes. Note that case 1165 shows extensive microhomology overlapping and flanking the fusion breakpoint.

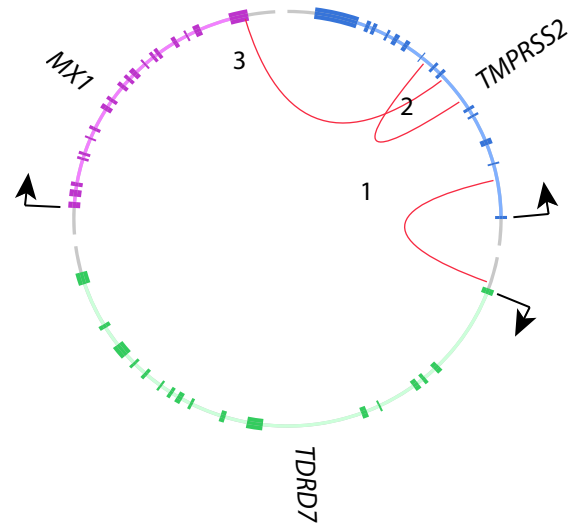
case 70



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1 CCTCCTCTCCAGAGACTAAGCAATCCAGTTTACACAACAGGCTCTACAGT
2 GCCAGTGCATTAGGGCAGCGCTGACTGGTTTCTGTAAAGCCCTCGC
3 GAAGCCGGCCCCACTCTACTTCAGGATACTTAACACAGGTGAGCCCCACC
4 CCCCTCTCTAAGGGCCATCCTTGTTG AGGACGCTGAGGCCaGAGAATTA
    
```

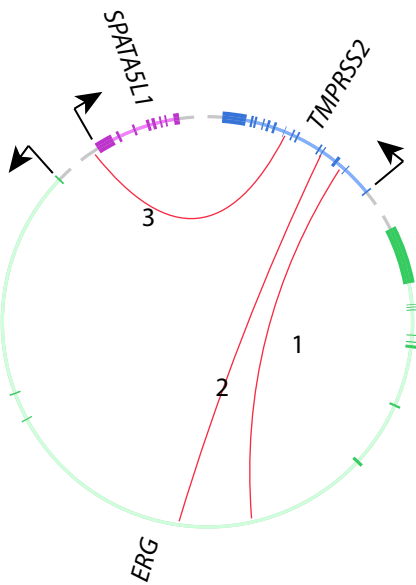
case 558



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1 GTAAAATACATATAGTGTCTAGATATGAGTATTGATTCTTCACTCCTTT
2 TACAATAATAGGTCCTTCTGACACCT/AATAAGTTTTAAAGGAAGAGGAA
3 CTAGAAACTGACACATGCTGAACATaaagGAGCATAAGGTCTTCAGCACT
    
```

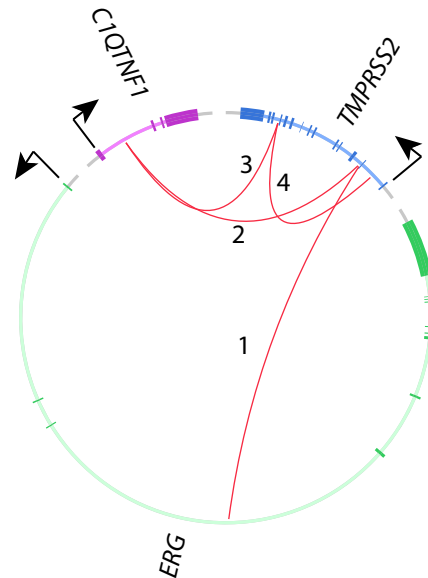
case 808



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1 AGAAGGGGAAGATGTGGGCTGGTGGGGCCCTGCAAAACATCACAAGAGCACT
2 GAGGAAGGTCCCCAGGGTCAAGGTGAGATGTTTAATACCTACAAATACAG
3 TATCTACGTTATTAAGACAACCTGCCTGACGCTCAGTGAAATAATTCAGGT
    
```

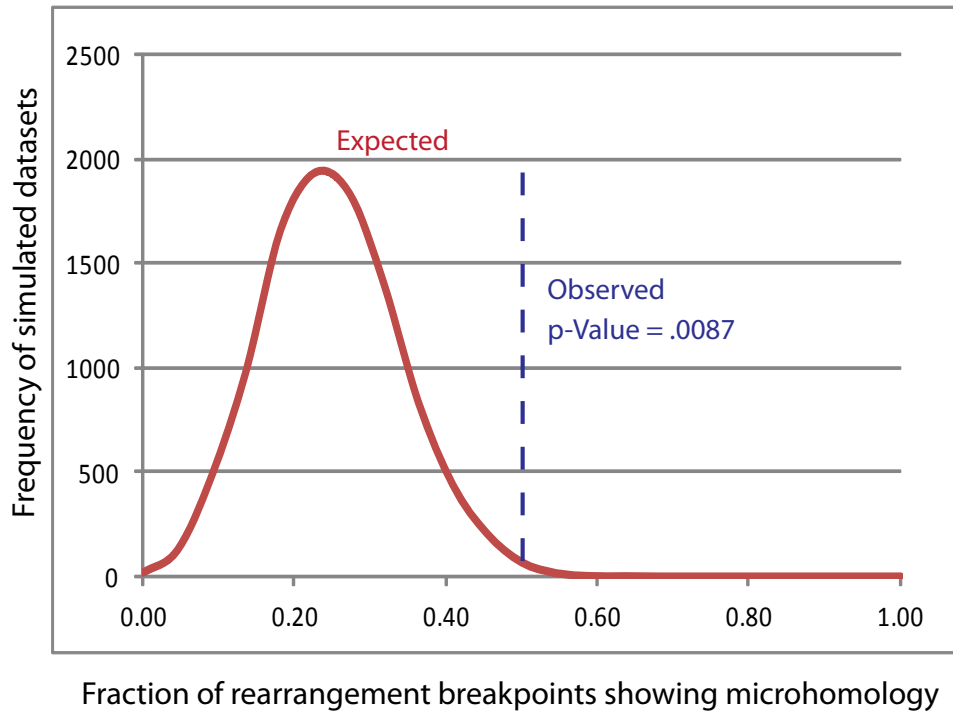
case 816



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1 ACACAGCTGCCAGGTGAGTCGCAAGAGCAGACTGAGATAGGCTTCCCGA
2 GTGGCTCGTAGCCACTGTACTGACTCAGGAATTTTCAGGGACAAACCTGC
3 AAATGTTTAAGTCAGTACAGTGGCcTGAGGACGGGCATCCTGGACCCATG
4 TGGACCCATGGTGGCCACATCTAAGC/AAATGAGTAAGATGAAATTTAGCA
    
```

Supplementary Figure 9. Cases showing complex genomic rearrangements involving TMPRSS2 and ERG. Representative circos plots of various cases exhibiting complex intra- and inter-chromosomal rearrangements involving TMPRSS2 or ERG. The sequences of the breakpoint for the junctions from each case are shown below.



Supplementary Figure 10. Strong enrichment of microhomologies at breakpoint junctions.

Groups of 22 randomly generated rearrangements between the introns of Tmprss2 and ERG were simulated 10,000 times. The red distribution shows the fraction of rearrangements in each simulated dataset displaying microhomologies (1+ nucleotides) at the junction. The dashed blue line indicates the fraction of rearrangement breakpoints with microhomologies in our observed dataset, and shows that our observed dataset is significantly enriched for microhomology compared to what would be expected by random chance ($p = 0.0087$).

Supplementary Table 1: Clinical and pathological characteristics of study samples

Median Age (range)	61 (34-72)
Ethnicity	N (%)
Caucasian	74 (89.2)
African American	6 (7.2)
Hispanic	1 (1.2)
Other	1 (1.2)
N/A	1 (1.2)
Gleason Sum*	N (%)
5	1 (1.3)
6	11 (14.1)
7	43 (55.1)
8	11 (14.1)
9	12 (15.4)
Surgical Margins*	N (%)
Positive	28 (36)
Negative	50 (64)
Median Gland Weight (range)*	55.05 (27-155)
TNM***	N (%)
T1	0 (0)
T2	6 (7.7)
T3	71 (91)
T4	0 (0)
TX	1 (1.3)
N0	62 (79.5)
N1	16 (20.5)

* Data based on 78 specimens; surgical data unavailable for 5 specimens

**Distant metastases were not assessed at time of prostatectomy

Supplementary Table 2: Detailed clinical and pathological characteristics of cohort

Patient Bank #	Age	Ethnicity	MarginsPositive	GleasonSum	Primary	Nodes	Tumor Cellularity %
4	59	W	Negative	7	T3	N0	80
10	62	W	Negative	7	T3	N1	NA
13	64	W	Negative	5	T3	N0	NA
70	67	W	Positive	6	T3	N0	NA
82	71	W	Negative	7	T3	N0	NA
96	48	W	Negative	9	T3	N1	NA
116	64	W	Negative	6	T3	N0	NA
134	60	W	Negative	6	T3	N0	NA
144	59	W	Negative	7	T3	N0	NA
146	63	W	Negative	7	T3	N0	NA
178	51	W	Negative	7	T3	N0	NA
179	63	W	Negative	9	T3	N1	NA
199	70	W	Negative	7	T3	N1	NA
202	58	W	Negative	6	T3	N1	NA
206	57	W	Negative	9	T3	N0	NA
214	69	W	Positive	7	T3	N0	65
219	66	W	Positive	8	T3	N0	NA
243	52	W	Negative	7	T3	N1	NA
270	61	W	Negative	7	T3	N0	80
327	62	W	Positive	7	T3	N0	75
341	66	W	Negative	7	T2	N0	80
353	65	W	Negative	6	T3	N0	85
357	57	W	Positive	7	T3	N0	70
358	57	W	Negative	7	T3	N1	65
362	55	W	Negative	9	T3	N0	70
372	68	W	Positive	7	T3	N0	80
388	72	W	Negative	7	T3	N0	70
460	68	W	Negative	9	T3	N0	75
535	54	W	Negative	8	T3	N0	70
541	67	W	Negative	8	T3	N0	65
558	62	W	Negative	6	T3	N0	NA
580	52	W	Negative	7	T3	N0	NA
594	54	W	Positive	6	T3	N0	NA
652	66	W	Positive	7	T3	N1	85
667	65	W	Positive	7	T3	N1	75
675	57	W	Negative	6	T3	N0	70
682	56	W	Positive	7	T3	N0	65
700	66	W	Negative	7	T3	N1	75
731	52	W	Negative	9	T3	N0	NA
733	67	W	Positive	9	T3	N0	65
735	62	B	Positive	9	T3	N0	90
738	55	W	Negative	7	T3	N0	70
741	66	W	Negative	9	T2	N0	NA
759	68	W	Positive	7	TX	N0	NA
774	71	W	Negative	7	T3	N0	NA
780	53	W	Negative	8	T3	N1	NA
782	58	W	Negative	7	T3	N0	NA
808	57	W	Negative	7	T3	N0	70
814	67	W	Positive	7	T3	N0	65
816	62	W	Negative	6	T2	N0	70
823	70	W	Positive	7	T3	N0	70
913	57	W	Positive	7	T2	N0	NA
926	66	B	Negative	7	T3	N0	70
938	53	W	Positive	7	T3	N0	80
981	48	H	Positive	7	T3	N0	75
982	61	W	Positive	7	T3	N1	70
986	66	B	Negative	7	T3	N0	65
989	58	W	Positive	7	T3	N0	70
994	53	B	Positive	7	T3	N0	NA
995	54	W	Negative	7	T3	N0	65
1009	51	W	Positive	7	T3	N0	80
1048	43	W	Negative	6	T3	N0	70
1070	66	W	Positive	8	T3	N0	75
1138	49	W	Negative	8	T3	N1	70
1164	57	W	Negative	8	T3	N0	65
1203	59	W	Negative	6	T2	N0	NA
1273	63	W	Positive	8	T3	N0	70
1355	59	W	Negative	8	T3	N0	65
1422	64	W	Positive	9	T3	N0	70
1437	48	W	Negative	8	T3	N0	80
1508	61	O	Negative	7	T3	N0	70
1518	51	W	Positive	9	T3	N1	75
1538	45	W	Negative	7	T3	N0	65
1665	61	B	Negative	7	T3	N1	70
1704	65	W	Positive	9	T3	N1	65
1756	51	W	Negative	8	T3	N0	90
1863	42	B	Positive	7	T3	N0	80
4441	55	W	Negative	7	T2	N0	NA

* Data for 78 specimens

Supplementary Table 3: Junction Specific Primer Sets

^A Patient Bank #	^B Junctions	^C Gene 1	^D Gene 2	^E Forward	^F Reverse
4	<i>TMPRSS2-ERG</i>	chr21:41794326	chr21:38753597	GCAGGCTGTGGGGTTTTAT	ACATCCATGACCCAAAACCA
10	<i>TMPRSS2-ERG</i>	chr21:41792775	chr21:38792757	GGTCAAATGTTGGCTCTG	AAGGAAACTTTGCAGGTGGA
70	<i>TMPRSS2-MPRL12</i>	chr21:41783383	chr17:77283404	CACCTCATGCCTGAGAAGTGG	CTTCTCCTGTTGGTCTCCA
	<i>HAP1*-TMPRSS2</i>	chr17:37144837	chr21:41779769	GAGAATGGTCTGCCCAAAG	AGACTGTGCTGAGGAAAGG
	<i>TMPRSS2-HAP1*</i>	chr21:41794230	chr17:37149531	CTGACCCCCACTCTGAAGTT	CCTGTTGGGTGAGGTTTCTC
	<i>TMPRSS2-SWI5</i>	chr21:41779767	chr9:130085490	CTCCCTCAAGTGCACTCTAA	AGTGGCATGATTTGGCTCA
82	<i>EIF3K-TMPRSS2</i>	chr19:43815389	chr21:41788584	GGAATCACCCTGGACACCT	AGGTCCAATAGCTGGTGGTG
	<i>NF1-TMPRSS2</i>	chr17:26590306	chr21:41774186	TCTGACCAGATGACCACAGC	TCTTCAAGTGGCCAGACT
134	<i>TMPRSS2-ERG</i>	chr21:41795069	chr21:38803391	TACTGCCAGCATCACTCTGG	CAGCCAAACAAACAACCTGC
	<i>ACPP-TMPRSS2</i>	chr3:133565489	chr21:41795096	CCAGGGGCCAGTTTTAGAG	CCAGAGGCAGTCACAGGATA
144	<i>TMPRSS2-ERG</i>	chr21:41779065	chr21:38796877	AAATGGGTTTCATCAATGTTGTC	CCGGCCAATAACCTTTTGTG
	<i>TMPRSS2-TMPRSS2</i>	chr21:41789960	chr21:41781176	TCATACCTGTGCCAGTCTCG	AAGGAAAGGAAATCCGTGTG
199	<i>TMPRSS2-ERG</i>	chr21:41786586	chr21:38748712	CATGTAGGTTTCATATTTCCCTTA	TGGATTTTCAAACCAAGTATCTACC
206	<i>TMPRSS2-ERG</i>	chr21:41793812	chr21:38763138	CATGGAGAGTGAGTGGCTGA	AGTCCAGCCTCATCTCAGA
214	<i>TMPRSS2-ERG</i>	chr21:41797467	chr21:38749676	TGGAGAAATGATCCTCCAGTC	CTGGCAAGCAAAGATAGGG
341	<i>TMPRSS2-ERG</i>	chr21:41785537	chr21:38798302	AGATGCCTGTCCAGCAAAGT	TTTCATAAGCATCCACACCG
353	<i>TMPRSS2-ERG</i>	chr21:41789358	chr21:38799621	AGAGCTTTGCTGCCCTTGAT	AATCCTGCCTCAAGGATTTT
357	<i>TMPRSS2-ERG</i>	chr21:41794131	chr21:38797829	CATGTTGGTAGCTGGGAAT	CCAGCACTCCATGGAACCTT
372	<i>TMPRSS2-ERG</i>	chr21:41797622	chr21:38784847	TAAGGCCATTGCTTCCAAG	GGATGCCACGAAGAAATACAG
	<i>SLC45A3-ERG</i>	chr1:203908669	chr21:38798718	TTGGTAGGAGCCATGAAAG	TCTGAGTCGGGGTAGAGTG
535	<i>TMPRSS2-ERG</i>	chr21:41790462	chr21:38748584	ATGGGGGCCCTTAGATACAG	GGACAGTTAAATGGGCCAAA
558	<i>TDRD7*-TMPRSS2</i>	chr9:99213679	chr21:41794880	CCTCAGGCTTGACAACACAA	TCGTGTGCTAGGCACACTCT
	<i>TMPRSS2-TMPRSS2</i>	chr21:41771407	chr21:41780399	CAACCTCACCAACTCTGTT	GAGCGACGGACGTTTCTTTA
	<i>MX1-TMPRSS2</i>	chr21:41752881	chr21:41775109	GCTGGGTGAGCAGAATAGGAT	GGGATTGAAGGATGCTGTCT
580	<i>MX1-TMPRSS2</i>	chr21:41752819	chr21:41775553	GCTGGGTGAGCAGAATAGGAT	GGGATTGAAGGATGCTGTCT
652	<i>TMPRSS2-ERG</i>	chr21:41792424	chr21:38775810	ACTCACACATCGACACTTCCAG	ATGCCAAATCTGGATAAATGCT
	<i>ERG-ERG</i>	chr21:38830023	chr21:38872708	ATGAGCAATTAGCCCCCTCT	ATTCAGTTGCTCCTGGGAAG
675	<i>TMPRSS2-ERG</i>	chr21:41798800	chr21:38789416	GAAAGTGGCCTTGCTAGTGG	TGGCTCTCCACATCTTCT
682	<i>TMPRSS2-ERG</i>	chr21:41796887	chr21:38791968	AGCTTGAGGCACCTGGACT	CAGGCACCGTTAGGGATAGT
733	<i>TMPRSS2-ERG</i>	chr21:41794661	chr21:38816717	CTTCTGAGCTGGGAGAGCTG	TCAAGCCAGTTCCAAGACA
738	<i>THSD7A-TMPRSS2</i>	chr7:11743984	chr21:41788390	GTTCTTGTAGTGCATGGCTTATATT	AGACGACGGGGTGGGAAG
780	<i>TMPRSS2-ERG</i>	chr21:41792243	chr21:38787029	GGTTAAGTCCAGCAGGATGC	CCCATGTGCTCAATAATTC
808	<i>TMPRSS2-ERG</i>	chr21:41790468	chr21:38780232	ATGGGGGCCCTTAGATACAG	TATTAGCCTGGTACATGCT
	<i>TMPRSS2-ERG</i>	chr21:41783369	chr21:38805184	TCCTACATATGTGCAGTCTAATTC	GCTCAGAGCACTGGGGACT
	<i>SPATA5L1*-TMPRSS2</i>	chr15:43481074	chr21:41771055	GATGGATTTGTAGCACACCAA	GGGAGTCAAACATCCCAGGT
814	<i>TMPRSS2-ERG</i>	chr21:41792783	chr21:38784111	TCCTTTTCATAGATCCCTGATT	AGGAACTGAGGAAGAGCAGGTG
	<i>MORC3-TMPRSS2</i>	chr21:36673099	chr21:41762272	ACTGAGGAGGCTCTGCTGAC	CACCCCAAACAACTACCCA
816	<i>TMPRSS2-ERG</i>	chr21:41791718	chr21:38797360	TTTGTCCCTTGTCCCTCTG	AGAAAACCCAGAAACGCTCA
	<i>C1qTNF1-TMPRSS2</i>	chr17:74540999	chr21:41791286	GCACACAGAGGGAAACACA	TATGGCAGCTGTAGTCAGG
	<i>C1qTNF1-TMPRSS2</i>	chr17:74540985	chr21:41764084	TCTTTCTGCCTGTCTGGTC	TGCAGATTGCAAAGGAAGTG
	<i>TMPRSS2-TMPRSS2</i>	chr21:41764044	chr21:41796946	GTTTAGAGCTGCCCTGGAGA	AGCTTGAGGCACCTGGACT
981	<i>TMPRSS2-ERG</i>	chr21:41795091	chr21:38796469	TACAGGCACCCACCATCATA	TGGCAGCAGAACAGTATTGG
989	<i>FAM177A1-ERG</i>	chr14:34584342	chr21:38756847	TCCTTTCTCTGTGCCAAA	CCAGGGCTCTCTAACACTGC
995	<i>TMPRSS2-ERG¹</i>	chr21:41780434	chr21:38793491	-	CCTTTAAAACCTTATTCTGGCC
	<i>TMPRSS2-TMPRSS2</i>	chr21:41762098	chr21:41773713	TCCCATGGAAAACAAAGTGG	CGGTTTTTCAGAGGGTGTGT
	<i>TMPRSS2-TMPRSS2</i>	chr21:41780464	chr21:41790293	TTTTTGAGGGTGATTTCAAGG	GATAGGCACCAAGTGAAGGA
	<i>TMPRSS2-TMPRSS2</i>	chr21:41786495	chr21:41773659	GATGCCAACAGTGTTCCTTAAA	CGTAGCTGAGGGGAAGGTG
	<i>ERG*-ERG</i>	chr21:38793472	chr21:38793604	AGAGCTGGACGTTCAAGTAAATG	-
1164	<i>TMPRSS2-ETV5</i>	chr21:41797113	chr3:187278460	CCCCCTTCACTCAATTACC	CCCTGCAACACCCCTATTTT
1273	<i>ELK4-ERG</i>	chr1:203858916	chr21:38746745	CTGTATGTCTGCCTTAGAAAATAAGA	GTAAGCCAAGATCGCACCAT
1355	<i>TMPRSS2-ERG</i>	chr21:41788584	chr21:38799738	TATAGGCGCCACCATCATA	TGCCAGCTAGGACAGACAGA
1422	<i>TMPRSS2-ERG</i>	chr21:41795553	chr21:38788443	TCAGCCAAGATTAGGCCACT	AAGACAACAGAAATGGTTGTTCA
1538	<i>TMPRSS2-ETV4</i>	chr21:41795742	chr17:38978855	GCTGTGTGCCATTGTGAGAT	CGGGCTCGGTTACATAAGAA
1665	<i>TMPRSS2-ERG</i>	chr21:41791298	chr21:38729732	GCCCGTTTGCCTTATACCTA	TGAAAACCTGGAGGAAATGC
1863	<i>TMPRSS2-TMPRSS2</i>	chr21:41761944	chr21:41777674	CACCTGACCAGGCCTAGAGGA	TCAGTCACTGGCTATTGCAG
VCAP	<i>TMPRSS2-ERG</i>	chr21:41779893	chr21:38798223	GAGGGCTTAAACAGGAAACAGT	ACAATTTATAAGCATCCACA
	<i>TMPRSS2-TMPRSS2</i>	chr21:41793823	chr21:41779387	GAGTGGCTGAGCCTGAGTTT	CACGTGGAATGGCTTTTCT
Case 45	<i>TMPRSS2-ERG</i>	chr21:41800806	chr21:38776561	CCCCATGTCAGAAAGTTTG	AGATGGAATCTCAGTCTGTTGC
Case 66	<i>TMPRSS2-ERG</i>	chr21:41795687	chr21:38804491	CCAGGAATGGAGCCTGAGT	CCTTGTGCTCTTTGTGAGTT
Case 77	<i>TMPRSS2-ERG</i>	chr21:41799367	chr21:38790118	TGCTCCCTAGCAGTATGACA	CCAAGGGAAATGATGGTAAGA

¹Complex rearrangement containing a *TMPRSS2-ERG* junction and an *ERG-ERG* junction were discovered with a single set of primers.

A. Patient Bank # indicates the subject identification number used for each patient specimen.

B. Genes involved in rearrangements with 5' rearrangement partner listed first.

C. Genomic position of the rearrangement breakpoint for the 5' partner.

D. Genomic position of the rearrangement breakpoint for the 3' partner.

E,F. Forward and Reverse primer sequences respectively, shown 5' to 3'.

* Indicates nearest gene when rearrangement occurs in intergenic space

