

Supplementary Materials

Table S1. Details of patients used for NGS. BPH, benign prostate hyperplasia; LS, low stage (stage I and II); HS, high stage (stage III and IV).

Sample ID	Age	Gleason	PSA	pT	pN	pM	Stage	PCA3	RNA	Pool
2163	79	<5	6.50	-	-	pM0	-	35	69	BPH
1045	74	<5	0.27	-	-	pM0	-	30	35	BPH
1103	68	<5	4.10	-	-	pM0	-	34	48	BPH
1237	59	<5	4.45	-	-	pM0	-	14	38	BPH
2124	64	<5	6.94	-	-	pM0	-	32	41	BPH
1082	77	6	8.74	cT1a	pN0	pM0	IIA	44	24	LS
2039	71	6	4.17	pT2c	pN0	pM0	IIB	47	36	LS
2074	65	8	7.23	pT2c	pNx	pM0	IIB	24	34	LS
1272	63	7	3.17	pT2c	pNx	pM0	IIB	67	33	LS
2066	74	6	9.93	cT2c	pN0	pM0	IIA	60	33	LS
1145	61	9	12.37	pT3b	pN1	pM0	IV	51	63	HS
1200	70	8	1.86	pT3a	pN1	pM0	IV	nd	87	HS
1256	68	8	5.22	pT3a	pN0	pM0	III	73	35	HS
2002	67	7	26.46	pT3a	pN0	pM0	III	23	37	HS
2047	74	7	34.18	pT3a	pNx	pM0	III	26	47	HS

Table S2. Clinical details of individual patients and healthy controls of the centrifuged urine (CU) validation cohort.

Sample ID	Age	Gleason	PSA	Tumor (pT)	Lymph nodes (pN)	Metastasis (pM)	Stage
AC436	68	-	-	BPH	-	pM0	BPH
AC392	69	-	-	BPH	-	pM0	BPH
AC382	83	-	-	BPH	-	pM0	BPH
AC400	70	-	-	BPH	-	pM0	BPH
AC406	57	-	-	BPH	-	pM0	BPH
AC489	76	-	-	BPH	-	pM0	BPH
AC415	82	-	-	BPH	-	pM0	BPH
AC421	72	-	-	BPH	-	pM0	BPH
AC425	64	-	-	BPH	-	pM0	BPH
AC430	62	-	-	BPH	-	pM0	BPH
AC433	70	-	-	BPH	-	pM0	BPH
AC444	76	-	-	BPH	-	pM0	BPH
AC435	77	-	-	BPH	-	pM0	BPH
AC440	75	-	-	BPH	-	pM0	BPH
AC443	86	-	-	BPH	-	pM0	BPH
AC462	69	-	-	BPH	-	pM0	BPH
AC449	70	-	-	BPH	-	pM0	BPH
AC451	76	-	-	BPH	-	pM0	BPH
AC457	68	-	-	BPH	-	pM0	BPH
AC486	61	-	-	BPH	-	pM0	BPH
AC416	80	-	-	BPH	-	pM0	BPH
AC434	60	6		pT2a	pNx	pM0	Stage IIA
AC453	68	7		pT2c	pNx	pM0	Stage IIB
AC459	53	7		pT2c	pNx	pM0	Stage IIB
AC465	62	7		pT2c	pNx	pM0	Stage IIB
AC483	63	7		pT2c	pNx	pM0	Stage IIB
AC480	62	9		pT2a	pNx	pM0	Stage IIB
AC490	50	7		pT2c	pNx	pM0	Stage IIB
AC495	69	7		pT2c	pNx	pM0	Stage IIB
AC500	66	7		pT2c	pNx	pM0	Stage IIB
AC391	69	7		pT2c	-	pM0	Stage IIB
AC432	68	8		pT2c	pNx	pM0	Stage IIB
AC438	57	6		pT2c	pNx	pM0	Stage IIB

AC390V2	67	8		pT2c	pN0	pM0	Stage IIB
AC442	66	7		pT2c	pNx	pM0	Stage IIB
AC447	53	7		pT2c	pN0	pM0	Stage IIB
AC454	71	7		pT2c	pNx	pM0	Stage IIB
AC502	69	6		pT2c	pNx	pM0	Stage IIB
AC393	55	6		pT2c	pNx	pM0	Stage IIB
AC405	71	7		pT2c	pNx	pM0	Stage IIB
AC446	74	8		pT2c	pNx	pM0	Stage IIB
AC496	64	6		pT2c	pNx	pM0	Stage IIB
AC419	72	7		pT2c	pNx	pM0	Stage IIB
AC455	59	7		pT2c	pNx	pM0	Stage IIB
AC498	60	7		pT2c	pNx	pM0	Stage IIB
GARONK-003	77	9	11	T2a	pN0	pM0	Stage IIB
AC460	72	7		pT3a	pNx	pM0	Stage III
AC479	55	8		pT3a	pN0	pM0	Stage III
AC485	56	7		pT3a	pN0	pM0	Stage III
AC441	66	7		pT3a	pNx	pM0	Stage III
AC456	72	7		pT3a	pNx	pM0	Stage III
AC461	64	7		pT3a	pNx	pM0	Stage III
AC481	72	9		pT3b	pN0	pM0	Stage III
AC452	68	7		pT3a	pNx	pM0	Stage III
AC492	61	8		pT3a	pNx	pM0	Stage III
AC450	73	7		pT3a	pNx	pM0	Stage III
GARONK-001	70	6	5.69	T3a	pN0	pM0	Stage III
GARONK-002	70	9	6.94	T3b	pN0	pM0	Stage III
GARONK-006	73	7	3.44	T3a	pN0	pM0	Stage III
GARONK-008	77	9	15	T3a	pN0	pM0	Stage III
GARONK-009	66	8	6.85	T3a	pN0	pM0	Stage III
GARONK-012	74	6	7	T3a	pN0	pM0	Stage III
GARONK-013	78	7	4.9	T3a	pN0	pM0	Stage III
GARONK-017	63	9	7.7	T3b	pN0	pM0	Stage III
GARONK-018	72	9	6	T3b	pN0	pM0	Stage III
GARONK-019	75	7	4.8	T3a	pN0	pM0	Stage III
GARONK-011	81	9	16.5	T2c	pN0	pM0	Stage III
GARONK-014	71	7	13.9	T3b	pN0	pM0	Stage III
GARONK-015	64	6	3	T3a	pN0	pM0	Stage III
GARONK-016	79	7	6	T3a	pN0	pM0	Stage III
AC493	61	9		pT3b	pN1	pM0	Stage IV
AC505	61	8		pT3b	pN1	pM0	Stage IV
AC494	65	8		pT3a	pN1	pM0	Stage IV
30619	75	-	-	-	-	-	Control
30640	81	-	-	-	-	-	Control
30576	70	-	-	-	-	-	Control
30656	71	-	-	-	-	-	Control
30706	75	-	-	-	-	-	Control
30682	72	-	-	-	-	-	Control
30689	72	-	-	-	-	-	Control
30667	71	-	-	-	-	-	Control
30692	84	-	-	-	-	-	Control
30708	73	-	-	-	-	-	Control
30810	73	-	-	-	-	-	Control
HER_001	65	-	-	-	-	-	Control
HER_002	41	-	-	-	-	-	Control
HER_003	64	-	-	-	-	-	Control
HER_004	76	-	-	-	-	-	Control
HER_005	59	-	-	-	-	-	Control
HER_006	66	-	-	-	-	-	Control
HER_007	55	-	-	-	-	-	Control

HER_008	61	-	-	-	-	-	Control
HER_009	76	-	-	-	-	-	Control
HER_010	63	-	-	-	-	-	Control

Table S3. Clinical details of individual patients and healthy controls of the non-centrifuged (NCU) urine validation cohort.

Sample ID	Age	Gleason	PSA	Tumour (pT)	Lymph nodes (pN)	Metastasis (pM)	Stage
ONK-003	74	6	8.6	cT2a	pN0	pM0	Stage I
ONK-022	68	6	8.8	cT1c	pN0	pM0	Stage I
ONK-029	59	6	3.7	cT2a	pN0	pM0	Stage I
ONK-040	60	6	5.4	cT1c	pN0	pM0	Stage I
ONK-052	77	6	9.97	cT2a	pN0	pM0	Stage I
ONK-054	71	6	6.7	cT1c	pN0	pM0	Stage I
ONK-059	65	6	2.72	cT1c	pN0	pM0	Stage I
ONK-062	63	6	8.4	cT1c	pN0	pM0	Stage I
ONK-063	74	6	6	cT2a	pN0	pM0	Stage I
ONK-069	51	6	9.4	cT2a	pN0	pM0	Stage I
ONK-071	70	6	6.57	cT2a	pN0	pM0	Stage I
ONK-074	68	6	4.6	cT2a	pN0	pM0	Stage I
ONK-075	75	6	10	cT1c	pN0	pM0	Stage I
ONK-044	74	6	8.8	cT2a	pN0	pM0	Stage I
ONK-067	71	6	7.7	cT2a	pN0	pM0	Stage I
ONK-083	79	6	7	cT1c	pN0	pM0	Stage I
ONK-025	68	6	6.56	cT2a	pN0	pM0	Stage I
ONK-010	78	6	9.3	cT2a	pN0	pM0	Stage I
ONK-002	73	6	8.45	cT2a	pN0	pM0	Stage I
ONK-039	74	6	5.4	T2a	pN0	pM0	Stage I
ONK-041	72	6	7.6	T1a	pN0	pM0	Stage I
ONK-011	80	7	9.3	cT1c	pN0	pM0	Stage IIA
ONK-013	78	7	5	cT2a	pN0	pM0	Stage IIA
ONK-016	73	7	19.43	cT2a	pN0	pM0	Stage IIA
ONK-017	75	6	6	T2b	pN0	pM0	Stage IIA
ONK-024	63	6	7.14	cT2b	pN0	pM0	Stage IIA
ONK-028	63	7	5.5	cT2b	pN0	pM0	Stage IIA
ONK-037	71	6	19	cT2a	pN0	pM0	Stage IIA
ONK-065	72	6	15	cT2a	pN0	pM0	Stage IIA
ONK-076	67	7	10	cT2a	pN0	pM0	Stage IIA
ONK-082	63	7	8	cT2a	pN0	pM0	Stage IIA
ONK-068	69	6	5.7	T2b	pN0	pM0	Stage IIA
ONK-19-05	77	6	6.3	T2b	pN0	pM0	Stage IIA
ONK-009	68	6	6	cT2c	pN0	pM0	Stage IIB
ONK-027	64	6	22	cT2b	pN0	pM0	Stage IIB
ONK-046	51	6	8.14	cT2c	pN0	pM0	Stage IIB
ONK-061	62	7	X	cT2c	pN0	pM0	Stage IIB
ONK-084	72	7	6.35	cT2c	pN0	pM0	Stage IIB
ONK-004	63	4	2.8	cT2c	pN0	pM0	Stage IIB
ONK-057	79	8	20.87	T2b	pN0	pM0	Stage IIB
ONK-19-04	78	8	3.9	T2c	pN0	pM0	Stage IIB
ONK-006	68	7	16.48	cT3b	pN0	pM0	Stage III
ONK-015	62	7	34	cT3b	pN0	pM0	Stage III
ONK-019	62	8	87	cT3b	pN0	pM0	Stage III
ONK-023	74	6	12.8	cT3a	pN0	pM0	Stage III
ONK-026	68	8	6.8	cT3a	pN0	pM0	Stage III
ONK-034	73	8	8.45	cT3b	pN0	pM0	Stage III
ONK-035	72	8	16.29	cT3a	pN0	pM0	Stage III
ONK-042	70	6	12.88	cT3a	pN0	pM0	Stage III

ONK-072	60	6	5.24	cT3a	pN0	pM0	Stage III
ONK-078	75	6	8	cT3a	pN0	pM0	Stage III
ONK-19-01	74	7	7.3	T3b	pN0	pM0	Stage III
ONK-19-02	73	7	6.7	T3a	pN0	pM0	Stage III
ONK-19-03	71	6	10	T3a	pN0	pM0	Stage III
ONK-005	69	6	12.18	cT3a	pN0	pM0	Stage III
ONK-007	68	8	61.8	cT3b	pN0	pM0	Stage III
ONK-038	76	7	7.41	T3b	pN0	pM0	Stage III
ONK-001	64	6	5.66	cT3a	pN0	pM0	Stage III
ONK-19-06	80	8	79.3	T3b	pN0	pM0	Stage III
ONK-19-07	73	7	6.6	T3a	pN0	pM0	Stage III
HER_001	65	-	-	-	-	-	Control
HER_002	41	-	-	-	-	-	Control
HER_003	64	-	-	-	-	-	Control
HER_004	76	-	-	-	-	-	Control
HER_005	59	-	-	-	-	-	Control
HER_006	66	-	-	-	-	-	Control
HER_007	55	-	-	-	-	-	Control
CV001	63	-	-	-	-	-	Control
CV002	69	-	-	-	-	-	Control
CV003	70	-	-	-	-	-	Control
CV004	77	-	-	-	-	-	Control
CV005	66	-	-	-	-	-	Control
CV006	72	-	-	-	-	-	Control
CV008	72	-	-	-	-	-	Control
CV009	63	-	-	-	-	-	Control
CV013	68	-	-	-	-	-	Control
CV014	74	-	-	-	-	-	Control
CV015	70	-	-	-	-	-	Control
CV016	70	-	-	-	-	-	Control
CV017	73	-	-	-	-	-	Control
30656 NC	71	-	-	-	-	-	Control
CV010	66	-	-	-	-	-	Control
CV011	75	-	-	-	-	-	Control
CV012	72	-	-	-	-	-	Control

Table S4. Summary of NGS results from pooled RNA samples. *Average % of reads with Phred score >20.

<i>Pool</i>	<i>Reads (10⁶)</i>	<i>QC*</i>	<i>Mapped (10⁶) (%)</i>
BPH	11.6	81.7	7.07 (60.7)
LS PCa	11.3	89.8	8.49 (75.3)
HS PCa	12.7	81.8	6.48 (51.1)

Table S5. Top 50 most abundant transcripts by average read count normalized by transcript length. BPH, benign prostate hyperplasia; LS, low stage (stage I and II); HS, high stage (stage III and IV).

	BPH	LS	HS
<i>AL161626.1 (rRNA_pseudogene 17)</i>	1291565	277046	492569
<i>CTD-2328D6.1 (RNA28S5)</i>	585838	8833	815881
<i>AC079949.1 (lncRNA)</i>	447029	17369	476421
<i>AC010970.2 (lncRNA)</i>	75625	4125	81389
<i>MT-ND5</i>	52206	229273	28468
<i>MT-ND6</i>	49973	179344	26499
<i>MT-ND2</i>	22924	110066	13266
<i>MT-ND4</i>	16137	134277	10725
<i>MT-CYB</i>	13321	108790	4884
<i>ROCK1P1</i>	12991	4433	9493
<i>RN7SL1</i>	12078	1188	8756

<i>RN7SL2</i>	10758	1342	5709
<i>MT-CO1</i>	9185	51931	2750
<i>MT-ATP6</i>	9042	83226	4774
<i>MT-ND1</i>	8558	62964	3454
<i>MT-RNR2</i>	7359	78694	8921
<i>RNA5-8SP6</i>	6039	1518	16720
<i>Y-RNA3</i>	5863	14201	5720
<i>MT-CO2</i>	4301	30976	1287
<i>TTN</i>	3993	7975	3586
<i>MUC12</i>	3982	6952	4147
<i>MT-RNR1</i>	3861	12958	1265
<i>MIR663A</i>	3729	924	3927
(BRPF1*)	3674	1560	605
<i>RP11-91I20.3</i>	3630	3817	1485
<i>MT-CO3</i>	3344	14927	858
<i>RN7SL4P</i>	3300	286	3058
<i>KCNQ1OT1</i>	3212	8921	2816
<i>RN7SL5P</i>	3212	198	3740
<i>MUC16</i>	3201	3641	2981
<i>MUC3A</i>	2827	9031	6501
<i>MTND2P28</i>	2354	12815	770
<i>REXO1L1P</i>	2310	3036	1650
<i>HYDIN</i>	2288	1925	2398
<i>CDC27P1</i>	2068	3773	2585
<i>NBPF1</i>	1991	3806	2607
<i>MUC4</i>	1969	4565	3322
<i>MT-ND3</i>	1947	18403	1199
<i>snoU13</i>	1936	4400	2266
(PHC3*)	1903	3663	2200
<i>OBSCN</i>	1870	891	1870
<i>CDC27</i>	1837	1804	1221
<i>MICAL3</i>	1837	891	2068
<i>MUC6</i>	1837	3982	2112
<i>MTATP6P1</i>	1815	3036	660
<i>SSPO</i>	1782	550	704
<i>SYNE1</i>	1760	2706	1221
<i>RP11-413E6.7</i>	1749	440	1540
<i>COL6A3</i>	1727	2409	1155

Table 6. Differentially expressed ($P < 0.05$) transcripts in BPH and LS samples. Genes depicted in bold type are also present in the LS vs. HS list (Supplementary Table S6). Genes depicted in bold type and underlined are also present in the BPH vs. HS list (Supplementary Table S5).

<i>Genes</i>	BPH	LS	Fold Change	adj. <i>P</i>-value
<i>MTND1P23</i>	350	11858	33.89	4.69E-04
<u><i>EEF1A1P6</i></u>	1575	76	-20.66	1.24E-03
<i>PRRC1</i>	97	1722	17.72	1.53E-03
(<i>FTH1</i>*)	1844	117	-15.81	1.61E-03
<i>EFR3A</i>	136	1692	12.43	4.04E-03
<i>EIF3F</i>	136	1692	12.43	4.15E-03
<i>MLIP</i>	175	1844	10.54	4.34E-03
<i>RP11-96K19.4</i>	233	2241	9.61	4.56E-03
<i>CENPE</i>	117	1463	12.55	4.77E-03
<i>CBWD6</i>	253	2362	9.35	4.80E-03
<i>ANKRD36</i>	253	2271	8.99	4.95E-03
<i>CDK18</i>	1147	76	-15.05	4.97E-03
<u><i>SECISBP2L</i></u>	97	1128	11.60	5.73E-03
<i>STXBP5</i>	97	1341	13.80	6.05E-03
<i>FOXP2</i>	253	2103	8.32	6.78E-03

<u>DICER1</u>	117	1311	11.24	6.80E-03
MTND5P7	117	1448	12.41	6.87E-03
EEF1A1	1575	168	-9.39	8.08E-03
LDLR	1108	107	-10.39	8.14E-03
DHRS2	1069	91	-11.69	8.20E-03
XRNI	214	1844	8.62	8.64E-03
PPFIA2	97	1204	12.39	8.70E-03
CNTLN	253	1997	7.90	8.81E-03
TMEM45A	136	1357	9.97	8.84E-03
HAP1	953	76	-12.50	8.86E-03
FAM126B	136	1433	10.53	8.98E-03
CD55	97	1128	11.60	9.19E-03
GOLGA4	311	2271	7.30	9.61E-03
EIF4G3	272	2012	7.39	9.78E-03
MT-ATP8	991	10319	10.41	9.78E-03
DYNC2H1	330	2378	7.20	9.81E-03
TCAIM	136	1402	10.31	9.97E-03
KTN1	428	2926	6.84	1.06E-02
SEMA3A	214	1783	8.34	1.08E-02
GABRA2	233	1814	7.78	1.10E-02
<u>CTDSP2</u>	991	91	-10.84	1.11E-02
FIP1L1	97	1082	11.13	1.11E-02
CCDC144NL	156	1402	9.02	1.13E-02
ARHGEF38	97	1097	11.29	1.15E-02
(OSBP)*	5539	585	-9.47	1.20E-02
C8orf34	156	1402	9.02	1.22E-02
(PHC3)*	1903	122	-15.59	1.24E-02
ATAD5	214	1738	8.13	1.31E-02
ADAMTS14	836	76	-10.97	1.31E-02
<u>ZMAT1</u>	97	975	10.04	1.34E-02
TPH1	117	1174	10.06	1.35E-02
ATAD1	97	1036	10.66	1.36E-02
TRIP11	175	1402	8.02	1.37E-02
LUC7L3	156	1311	8.43	1.38E-02
PSMG3-AS1	816	76	-10.71	1.40E-02
MYO5BP2	97	1021	10.51	1.41E-02
SMC5	97	1006	10.35	1.43E-02
TAOK1	253	1799	7.12	1.45E-02
TMEM86A*	719	76	-9.44	1.46E-02
PABPC1	97	1006	10.35	1.48E-02
MYT1	1069	122	-8.77	1.48E-02
PLCH2	797	76	-10.46	1.51E-02
LHCGR	97	975	10.04	1.54E-02
MIER1	136	1235	9.07	1.56E-02
PLEKHA8	175	1402	8.02	1.56E-02
STX7	272	1783	6.55	1.56E-02
TMC05A	136	1265	9.30	1.57E-02
BTAF1	175	1387	7.93	1.57E-02
ANKRD18B	97	975	10.04	1.62E-02
SCFD1	97	975	10.04	1.62E-02
ANKS1A	1186	137	-8.64	1.63E-02
MTND5P27	156	1296	8.33	1.63E-02
PSMD6	175	1417	8.10	1.64E-02
RP11-848G14.5	875	91	-9.57	1.67E-02
GATAD2A	739	76	-9.69	1.67E-02
<u>RPL37</u>	136	1052	7.73	1.70E-02
COL9A3	758	76	-9.95	1.72E-02
SPATA6L	175	1296	7.41	1.73E-02
F7	680	76	-8.93	1.73E-02
HNRNPD	175	1402	8.02	1.74E-02
MITD1	97	930	9.57	1.75E-02
PTCHD2	816	91	-8.93	1.77E-02

PRPF4B	156	1311	8.43	1.82E-02
<i>PTAR1</i>	156	1296	8.33	1.84E-02
EDC4	739	76	-20.66	1.88E-02
NAALAD2	97	899	9.25	1.90E-02
<i>SQSTM1</i>	1575	244	-6.46	1.94E-02
PAPD4	156	1280	8.23	1.96E-02
<i>FAM47E</i>	175	1326	7.58	1.98E-02
<i>RALGAP1</i>	233	1494	6.40	1.99E-02
<i>EEF2</i>	1497	229	0.15	2.02E-02
<i>MSRB3</i>	97	899	9.25	2.03E-02
<i>GOLGA8T</i>	700	76	-9.18	2.09E-02
<i>ZNF638</i>	467	2637	5.65	2.10E-02
SLC37A2	953	122	-7.81	2.11E-02
STXBP5L	136	1143	8.40	2.11E-02
<i>GALC</i>	175	1250	7.14	2.13E-02
<i>C14orf164</i>	136	1113	8.18	2.14E-02
<i>DNAJB11</i>	117	1006	8.62	2.15E-02
<i>CCDC144CP</i>	136	1128	8.29	2.17E-02
<i>DNAH14</i>	428	2378	5.56	2.18E-02
<i>SLC25A29</i>	894	107	-8.38	2.20E-02
<i>ZCCHC11</i>	544	3018	5.54	2.24E-02
<i>MTND5P6</i>	97	869	8.94	2.24E-02
<i>HSPBAP1</i>	97	869	8.94	2.24E-02
KIRREL3	1225	198	-6.18	2.29E-02
<i>AB11</i>	97	854	8.78	2.30E-02
COL18A1	991	137	-7.23	2.34E-02
<i>ARFGAP1</i>	622	76	-8.16	2.34E-02
NLE1	680	76	-8.93	2.35E-02
<i>PATE4</i>	97	823	8.47	2.36E-02
<i>CTC-228N24.3</i>	117	975	8.36	2.37E-02
RAB21	136	1097	8.06	2.38E-02
PFKL	641	76	-8.42	2.44E-02
METTL14	136	1082	7.95	2.45E-02
<i>C1orf222</i>	1244	183	-6.80	2.45E-02
TONSL	758	91	-8.29	2.45E-02
FASN	797	107	-7.47	2.46E-02
<i>FBXW7</i>	117	960	8.23	2.47E-02
PKD1	1886	351	-5.38	2.47E-02
ANKRD27	1613	259	-6.23	2.50E-02
<i>AZIN1</i>	156	1128	7.25	2.51E-02
TNS3	1438	259	-5.55	2.53E-02
PARVG	1225	198	-6.18	2.54E-02
<i>U2SURP</i>	311	1814	5.83	2.55E-02
<i>ANAPC15</i>	622	76	-8.16	2.56E-02
<i>CAMK2D</i>	117	945	8.10	2.58E-02
<i>TMEM116</i>	97	823	8.47	2.60E-02
<i>CHFR</i>	1400	229	-6.12	2.60E-02
<i>SMAD1</i>	117	930	7.97	2.60E-02
<i>RCOR3</i>	233	1417	6.08	2.60E-02
<i>KCNQ2</i>	836	107	-7.83	2.63E-02
<i>TCP11L2</i>	136	1006	7.39	2.65E-02
<i>PRKCI</i>	136	1052	7.73	2.67E-02
<i>PLEKHA3</i>	408	2149	5.26	2.68E-02
MMAA	97	808	8.31	2.71E-02
<i>FRS2</i>	136	1036	7.62	2.72E-02
<i>ANKRD12</i>	311	1768	5.68	2.72E-02
<i>MAP3K19</i>	97	808	8.31	2.73E-02
<i>LY6E</i>	603	76	-7.91	2.75E-02
<i>APLNR</i>	564	76	-7.40	2.78E-02
<i>AGAP3</i>	1516	274	-5.53	2.78E-02
<i>SMARCD3</i>	816	107	-7.65	2.80E-02
<i>DHX29</i>	97	777	8.00	2.80E-02

<i>RP11-1281K21.6</i>	97	777	8.00	2.83E-02
TEX9	292	1738	5.96	2.83E-02
<i>ANKRD36</i>	641	3231	5.04	2.83E-02
<i>ENGASE</i>	816	107	-7.65	2.85E-02
<i>SCARA5</i>	505	76	-6.63	2.85E-02
<i>PTEN</i>	97	777	8.00	2.86E-02
<i>FER1L5</i>	1769	320	-5.53	2.87E-02
FLT4	1069	183	-5.85	2.87E-02
CAPS2	136	1021	7.50	2.88E-02
SMARCA4	797	122	-6.54	2.89E-02
<i>BAAT</i>	97	747	7.68	2.89E-02
<i>ICAM1</i>	525	76	-6.89	2.89E-02
<i>YAP1</i>	175	1189	6.80	2.90E-02
KIRREL	816	122	-6.70	2.91E-02
<i>HSPA4L</i>	175	1174	6.71	2.94E-02
<i>NT5DC2</i>	700	91	-7.65	2.94E-02
ERBB2IP	233	1494	6.40	2.94E-02
<i>ZC3H7B</i>	1283	213	-6.01	2.94E-02
NEK8	622	76	-8.16	2.95E-02
<i>POU3F3</i>	117	899	7.71	2.95E-02
<i>USP19</i>	894	122	-7.33	2.96E-02
<i>CRHR1</i>	680	91	-7.44	2.98E-02
<i>DNAJC2</i>	233	1433	6.14	3.00E-02
<i>RSPH3</i>	97	732	7.53	3.02E-02
<i>MKLN1</i>	136	1006	7.39	3.03E-02
<i>SLC12A2</i>	136	1006	7.39	3.03E-02
DSCAML1	1108	183	-6.06	3.03E-02
ESRP1	97	716	7.37	3.04E-02
<i>RP11-958N24.1</i>	525	76	-6.89	3.04E-02
<i>SNAPC4</i>	525	76	-6.89	3.04E-02
<i>RP11-112N13.1</i>	117	884	7.58	3.04E-02
<i>RP11-461G12.2</i>	117	884	7.58	3.05E-02
<i>DPCR1</i>	544	2713	4.98	3.05E-02
<i>C1orf216</i>	641	91	-7.01	3.07E-02
<i>VRK2</i>	97	747	7.68	3.07E-02
<i>SNN</i>	505	76	-6.63	3.07E-02
<i>RP11-597A11.1</i>	97	732	7.53	3.08E-02
<i>BDP1</i>	350	1814	5.18	3.09E-02
<i>IRX4</i>	272	76	-3.57	3.14E-02
<i>JOSD1</i>	564	76	-7.40	3.14E-02
<i>PAPOLA</i>	311	1692	5.44	3.14E-02
SPTLC3	311	1753	5.64	3.15E-02
<i>POT1-ASI</i>	117	869	7.45	3.16E-02
C9orf153	97	701	7.21	3.17E-02
HNRNPK	175	1204	6.88	3.17E-02
<i>OR11J2P</i>	292	76	-3.83	3.19E-02
<i>RP11-973H7.1</i>	292	76	-3.83	3.19E-02
<i>VWA2</i>	428	76	-5.61	3.19E-02
<i>KCNIP3</i>	1225	213	-5.74	3.21E-02
PRSS8	603	76	-7.91	3.22E-02
<i>CHRND</i>	311	76	-4.08	3.24E-02
<i>ZNF765</i>	953	137	-6.94	3.24E-02
<i>ITPKB</i>	855	122	-7.01	3.24E-02
<i>RHPN1</i>	661	91	-7.23	3.24E-02
<i>HGS</i>	661	91	-7.23	3.29E-02
<i>MIR3916</i>	350	76	-4.59	3.30E-02
<i>MISP</i>	350	76	-4.59	3.30E-02
<i>RP11-344P13.3</i>	350	76	-4.59	3.30E-02
<i>SRP68</i>	855	122	-7.01	3.32E-02
CYB5R4	233	1448	6.21	3.33E-02
<i>ELFN2</i>	1089	168	-6.49	3.35E-02
<i>MTND4P27</i>	97	747	7.68	3.35E-02

<i>RP11-383H13.1</i>	97	747	7.68	3.35E-02
<i>WDR43</i>	136	930	6.83	3.37E-02
<i>ART3</i>	97	701	7.21	3.38E-02
<i>ANKRD29</i>	117	854	7.32	3.40E-02
<i>UGP2</i>	97	747	7.68	3.40E-02
<i>ANXA9</i>	641	91	-7.01	3.41E-02
<i>NTRK1</i>	661	91	-7.23	3.42E-02
<i>SPATA17</i>	97	732	7.53	3.42E-02
<i>TDO2</i>	117	808	6.93	3.45E-02
<i>RP6-42F4.1</i>	136	945	6.94	3.46E-02
<i>ZBTB46</i>	758	107	-7.11	3.50E-02
<i>RP11-347C12.2</i>	117	838	7.19	3.51E-02
<i>GHDC</i>	447	76	-5.87	3.52E-02
<i>UFL1</i>	117	838	7.19	3.53E-02
<i>ZNF844</i>	739	107	-6.92	3.54E-02
<i>RP11-15B24.5</i>	117	838	7.19	3.55E-02
<i>TBCB</i>	505	76	-6.63	3.55E-02
<i>CYP4F12</i>	544	76	-7.14	3.55E-02
<i>TAF5L</i>	97	671	6.90	3.56E-02
<i>GRK1</i>	914	137	-6.66	3.58E-02
<i>RB1</i>	253	1417	5.61	3.61E-02
<i>ATG3</i>	97	655	6.74	3.64E-02
<i>PCYT2</i>	428	76	-5.61	3.65E-02
<i>CDIP1</i>	914	137	-6.66	3.65E-02
<i>ULK1</i>	1089	183	-5.95	3.67E-02
<i>ZBED3-AS1</i>	117	777	6.66	3.70E-02
<i>WDR7</i>	253	1311	5.19	3.72E-02
<i>RAB3D</i>	894	137	-6.52	3.72E-02
<i>L1CAM</i>	661	91	-7.23	3.72E-02
<i>PYGO1</i>	117	823	7.06	3.73E-02
<i>PAPD5</i>	136	930	6.83	3.74E-02
<i>MT-ND4L</i>	661	3018	4.57	3.76E-02
<i>TP53TG3D</i>	97	701	7.21	3.76E-02
<i>RPL3P4</i>	505	76	-6.63	3.76E-02
<i>SLC15A3</i>	739	107	-6.92	3.77E-02
<i>CUEDC1</i>	739	107	-6.92	3.78E-02
<i>RNF38</i>	156	975	6.27	3.80E-02
<i>ACAP3</i>	816	122	-6.70	3.82E-02
<i>NEDD4</i>	350	1768	5.05	3.83E-02
<i>LACCI</i>	175	1128	6.45	3.84E-02
<i>FAM78A</i>	603	91	-6.59	3.85E-02
<i>ZBTB21</i>	97	701	7.21	3.88E-02
<i>C19orf25</i>	700	107	-6.56	3.88E-02
<i>SVIP</i>	97	655	6.74	3.90E-02
<i>EMID1</i>	719	107	-6.74	3.92E-02
<i>PRPF38A</i>	156	960	6.17	3.92E-02
<i>ZNF213</i>	641	91	-7.01	3.96E-02
<i>USP15</i>	175	1021	5.84	3.98E-02
<i>NCOA3</i>	350	1738	4.97	4.01E-02
<i>SMCHD1</i>	525	2393	4.56	4.02E-02
<i>MTND6P9</i>	97	625	6.43	4.03E-02
<i>RERGL</i>	97	625	6.43	4.03E-02
<i>RFX6</i>	97	625	6.43	4.03E-02
<i>RRN3P1</i>	97	625	6.43	4.03E-02
<i>RIOK3</i>	97	686	7.06	4.09E-02
<i>DUX4L3</i>	797	122	-6.54	4.10E-02
<i>NPTX1</i>	700	107	-6.56	4.10E-02
<i>LSM5</i>	97	625	6.43	4.12E-02
<i>PTPLAD2</i>	272	1448	5.32	4.13E-02
<i>BLK</i>	758	122	-6.22	4.14E-02
<i>KDR</i>	233	1235	5.29	4.14E-02
<i>ATF3</i>	564	91	-6.16	4.18E-02

ASB14	214	1280	5.99	4.21E-02
KCNG2	330	76	-4.34	4.21E-02
TTLL9	525	76	-6.89	4.22E-02
CTD-2281E23.1	486	76	-6.38	4.23E-02
CYP2D8P	700	107	-6.56	4.23E-02
ADCY7	1089	183	-5.95	4.23E-02
CCDC14	272	1433	5.26	4.25E-02
DECRI	97	686	7.06	4.26E-02
FAFI	97	686	7.06	4.26E-02
SH3GLB2	544	91	-5.95	4.31E-02
MBOAT2	214	1250	5.84	4.33E-02
WDR5	855	137	-6.24	4.34E-02
KIF15	156	975	6.27	4.38E-02
SH3RF3	700	107	-6.56	4.38E-02
RNPEPL1	700	107	-6.56	4.38E-02
(BRPF1*)	3674	944	-3.95	4.40E-02
PTCD1	292	76	-3.83	4.43E-02
CYHR1	758	122	-6.22	4.45E-02
ATP13A1	505	76	-6.63	4.46E-02
AKR1A1	447	76	-5.87	4.51E-02
PRKCD	467	76	-6.12	4.51E-02
ABCC13	447	2012	4.50	4.52E-02
GPR98	875	3887	4.44	4.53E-02
FBRSL1	1147	229	-5.10	4.53E-02
RMDN3	680	107	-6.38	4.53E-02
CORO2B	505	91	-5.53	4.55E-02
EHD1	836	137	-6.09	4.57E-02
A1BG	272	76	-3.57	4.57E-02
ACSL5	136	854	6.27	4.58E-02
GUF1	97	640	6.59	4.59E-02
TANC2	525	2317	4.41	4.60E-02
HAX1	505	76	-6.63	4.61E-02
TBC1D31	136	838	6.16	4.61E-02
FLNC	1264	259	-4.88	4.63E-02
RP11-846F4.5	233	1250	5.36	4.64E-02
DNM1P47	1302	274	-4.75	4.67E-02
ST6GALNAC6	622	107	-5.83	4.67E-02
(UACA)*	991	183	-5.42	4.70E-02
SESN3	156	945	6.08	4.72E-02
TCF25	680	107	-6.38	4.72E-02
PGBD5	544	91	-5.95	4.72E-02
COPB1	156	945	6.08	4.74E-02
TXNDC16	156	945	6.08	4.74E-02
DCPS	505	76	-6.63	4.74E-02
TDRD7	156	945	6.08	4.76E-02
ABCB4	330	1494	4.52	4.76E-02
CNPY4	253	76	-3.32	4.79E-02
NBEA	253	1311	5.19	4.79E-02
SEZ6	486	76	-6.38	4.80E-02
YME1L1	156	930	5.98	4.81E-02
ZC3HC1	117	701	6.01	4.82E-02
EARS2	564	91	-6.16	4.82E-02
RP11-115N12.1	97	625	6.43	4.85E-02
RCOR1	117	686	5.88	4.85E-02
LRP1B	408	1783	4.37	4.87E-02
RSPH9	350	76	-4.59	4.90E-02
DYRK1B	233	76	-3.06	4.91E-02
PHF5A	233	76	-3.06	4.91E-02
CD3G	136	808	5.94	4.91E-02
LDLRAP1	739	122	-6.06	4.94E-02
FBXO44	447	76	-5.87	4.94E-02
TBX1	739	122	-6.06	4.96E-02

<i>ADCY9</i>	1380	290	-4.77	4.99E-02
<i>TMEM184A</i>	739	122	-6.06	5.00E-02

Table S7. Differentially expressed ($P < 0.05$) transcripts in BPH vs. HS samples. Genes depicted in bold type and underlined are also present in the BPH vs. LS list (Supp. Table S4). Genes depicted in red are also present in the LS vs. HS list (Supp. Table S6).

Genes	BPH	HS	Fold Change	adj. <i>P</i> -value
<u>SECISBP2L</u>	97	1325	13.63	3.17E-03
<u>RPL37</u>	136	1287	9.46	8.58E-03
<u>RANBP1</u>	97	1037	10.67	1.29E-02
<i>AKAP8</i>	97	999	10.27	1.45E-02
<u>ZBED3-AS1</u>	117	1056	9.06	1.48E-02
<i>RP13-279N23.2</i>	117	1095	9.38	1.62E-02
<u>SETSI</u>	175	1402	8.01	1.83E-02
<i>HNRNPA3P12</i>	136	1056	7.76	2.09E-02
<u>ZMAT1</u>	97	807	8.30	2.34E-02
<i>PDZD7</i>	816	96	-8.50	2.34E-02
<i>CLIC5</i>	156	1133	7.29	2.50E-02
<i>SV2C</i>	816	96	-8.50	2.53E-02
<i>COPS5</i>	97	826	8.50	2.54E-02
<i>FAM84A</i>	97	807	8.30	2.73E-02
<i>ADAMTS16</i>	97	787	8.10	2.75E-02
<u>(UACA)*</u>	991	101	-7.49	2.76E-02
<i>PRCD</i>	1127	154	-7.34	2.81E-02
<u>ANKRD27</u>	1613	269	-6.00	2.87E-02
<u>CTDSP2</u>	991	134	-7.38	2.90E-02
<i>METAP1</i>	97	787	8.10	2.91E-02
<u>NNT</u>	758	96	-7.90	2.97E-02
<i>SLC6A2</i>	136	999	7.34	3.03E-02
<i>PKLR</i>	1089	154	-7.09	3.11E-02
<i>PRDM11</i>	855	115	-7.42	3.14E-02
<i>RASGRP4</i>	719	96	-7.49	3.18E-02
<i>DENND2D</i>	156	1075	6.92	3.31E-02
<i>FAM118A</i>	214	1210	5.66	3.38E-02
<i>MTND5P11</i>	603	2996	4.97	3.39E-02
<u>TCEA3</u>	816	115	-7.09	3.53E-02
<i>F11</i>	97	730	7.51	3.58E-02
<i>ZDHHC17</i>	117	826	7.08	3.59E-02
<i>SAFB</i>	719	96	-7.49	3.62E-02
<i>PFKFB4</i>	700	96	-7.29	3.70E-02
<u>DECRI</u>	97	711	7.31	3.85E-02
<u>FAM177A1</u>	700	96	-7.29	3.90E-02
<i>CHIA</i>	797	115	-6.92	3.91E-02
<i>ZNF45</i>	117	807	6.92	3.92E-02
<i>POLD4</i>	622	96	0.15	4.04E-02
<u>EEF1A1P6</u>	1575	288	-5.47	4.05E-02
<i>RP11-576I22.2</i>	97	672	6.92	4.15E-02
<i>AP2A2</i>	1069	173	-6.19	4.15E-02
<i>DNTTIP2</i>	641	96	-6.68	4.16E-02
<u>POLR1C</u>	136	864	6.35	4.20E-02
<u>WDR7</u>	253	1248	4.94	4.26E-02
<i>SLAMF1</i>	117	749	6.42	4.27E-02
<i>LDLRAD3</i>	758	115	-6.58	4.34E-02
<i>PCDHAC1</i>	739	115	-6.41	4.35E-02
<u>(BRPF1)*</u>	3674	616	-5.96	4.41E-02
<i>WDFY2</i>	117	730	6.26	4.42E-02
<i>NEFH</i>	953	154	-6.20	4.44E-02
<u>PLCH1</u>	661	96	-6.88	4.46E-02
<u>(BPH3)*</u>	1903	96	-6.28	4.48E-02
<i>CNTNAP3</i>	641	96	-6.68	4.66E-02

<i>B3GNTL1</i>	156	941	6.05	4.68E-02
<i>STX4</i>	700	115	-6.07	4.68E-02
<i>DICER1</i>	117	691	5.93	4.77E-02
<i>MMAA</i>	97	653	6.72	4.77E-02
<i>NAMA</i>	894	154	-5.82	4.88E-02
<i>C22orf26</i>	117	691	5.93	4.89E-02
<i>VIL1</i>	719	115	-6.24	4.89E-02
<i>NFRKB</i>	622	96	-6.48	4.91E-02
<i>DTL</i>	97	615	6.32	4.97E-02
<i>TSPYL5</i>	97	634	6.52	5.00E-02

Table S8. Differentially expressed ($P < 0.05$) transcripts in HS vs. LS samples. Genes depicted in bold type are also present in the BPH vs. LS list (Supp. Table S4). Genes depicted in red are also present in the BPH vs. HS list (Supp. Table S5).

Genes	LS	HS	Fold Change	adj. <i>P</i> -value
<i>MTND1P23</i>	11858	422	-28.07	7.74E-04
<i>HSD17B4</i>	1875	96	-19.53	9.17E-04
<i>MPP5</i>	1859	96	-19.37	1.02E-03
<i>MT-ATP8</i>	10319	461	-22.39	1.18E-03
<i>LCOR</i>	1783	115	-15.48	1.90E-03
<i>MT-ND4L</i>	3018	269	-11.23	2.04E-03
<i>ITGAV</i>	1463	96	-15.24	3.16E-03
<i>BAZ1A</i>	1463	96	-15.24	3.57E-03
<i>ATAD5</i>	1738	134	-12.93	3.81E-03
<i>SMARCA4</i>	122	1440	11.81	4.04E-03
<i>RBPJ</i>	1357	96	-14.13	4.11E-03
<i>PFKL</i>	76	1133	14.87	4.12E-03
<i>XKR4</i>	1707	154	-11.11	4.19E-03
<i>WDR35</i>	1341	96	-13.97	4.39E-03
<i>INTU</i>	2561	288	-8.89	4.80E-03
<i>MTND5P7</i>	1448	115	-12.57	6.59E-03
<i>ASB14</i>	1280	96	-13.33	6.71E-03
<i>EPB41L2</i>	2210	269	-8.22	6.81E-03
<i>TEX9</i>	1738	173	-10.05	6.85E-03
<i>MYCBP2</i>	2225	288	-7.73	8.31E-03
<i>KIRREL</i>	122	1210	9.92	8.34E-03
<i>ASH1L</i>	1509	154	-9.82	8.58E-03
<i>CYBSR4</i>	1448	134	-10.77	8.60E-03
<i>FASN</i>	107	1095	10.26	9.12E-03
<i>CLUHP3</i>	76	941	12.35	9.14E-03
<i>PHLDB3</i>	76	941	12.35	9.16E-03
<i>SMCHD1</i>	2393	326	-7.33	9.35E-03
<i>FAM154A</i>	76	903	11.84	9.84E-03
<i>IPO8</i>	1463	154	-9.52	9.90E-03
<i>KCTD15</i>	122	1191	9.76	1.00E-02
<i>KTN1</i>	2926	422	-6.93	1.01E-02
<i>PHIP</i>	2210	307	-7.19	1.02E-02
<i>ERBB2IP</i>	1494	154	-9.72	1.03E-02
<i>APLP1</i>	76	903	11.84	1.04E-02
<i>NOTCH1</i>	76	903	11.84	1.04E-02
<i>CBWD6</i>	2362	326	-7.24	1.05E-02
<i>FLT4</i>	183	1440	7.87	1.06E-02
<i>TMC05A</i>	1265	115	-10.98	1.07E-02
<i>DNAJB2</i>	91	999	10.92	1.13E-02
<i>TRAPPC2L</i>	91	999	10.92	1.13E-02
<i>DNM3</i>	1265	134	-9.41	1.13E-02
<i>PTCHD2</i>	91	941	10.29	1.14E-02
<i>CNTN5</i>	1174	115	-10.19	1.15E-02
<i>PLEKHG7</i>	1204	115	-10.45	1.19E-02

<i>ADAM32</i>	1936	269	-7.20	1.21E-02
<i>PPFIA2</i>	1204	115	-10.45	1.25E-02
<i>CNOT4</i>	1143	115	-9.92	1.27E-02
<i>ANKRD36</i>	3231	499	-6.47	1.28E-02
<i>NCDN</i>	91	941	10.29	1.33E-02
<i>MLIP-AS1</i>	1143	115	-9.92	1.34E-02
<i>SPTLC3</i>	1753	230	-7.61	1.38E-02
<i>AP3B1</i>	1143	115	-9.92	1.41E-02
<i>DNAJB14</i>	1006	96	-10.48	1.42E-02
<i>ZNF142</i>	122	1095	8.98	1.43E-02
<i>PBXIP1</i>	107	1037	9.72	1.44E-02
<i>SLC8A1</i>	2317	365	-6.35	1.46E-02
<i>ORC4</i>	1357	154	-8.83	1.48E-02
<i>PRDM1</i>	1174	134	-8.73	1.50E-02
<i>SLC38A3</i>	91	903	9.87	1.51E-02
<i>ATP6AP1L</i>	975	96	-10.16	1.55E-02
<i>AKAP6</i>	1722	250	-6.90	1.56E-02
<i>LDLR</i>	107	903	8.46	1.57E-02
<i>CDC14A</i>	945	96	-9.84	1.63E-02
<i>SMAD4</i>	1082	115	-9.39	1.65E-02
<i>TTC3</i>	2561	422	-6.06	1.65E-02
<i>FEM1B</i>	1311	154	-8.53	1.65E-02
<i>METTL14</i>	1082	115	-9.39	1.69E-02
<i>ITGA4</i>	945	96	-9.84	1.70E-02
<i>STXBP5</i>	1341	154	-8.73	1.70E-02
<i>SSX2IP</i>	930	96	-9.68	1.78E-02
<i>TNS3</i>	259	1594	6.15	1.78E-02
<i>RGS3</i>	244	1555	6.38	1.80E-02
<i>MRPL45P2</i>	899	96	-9.37	1.83E-02
<i>ABCD3</i>	899	96	-9.37	1.84E-02
<i>CAPN14</i>	91	845	9.24	1.86E-02
<i>SLC41A3</i>	122	1018	8.35	1.87E-02
<i>KBTD4</i>	76	711	9.32	1.89E-02
<i>SYNJ1</i>	1143	134	-8.50	1.89E-02
<i>RANBP1</i>	122	1037	8.50	1.90E-02
<i>RMST</i>	884	96	-9.21	1.90E-02
<i>COL9A3</i>	76	730	9.58	1.91E-02
<i>EXOC2</i>	1036	115	-9.00	1.91E-02
<i>PPP6R2</i>	107	922	8.64	1.92E-02
<i>FGF12</i>	1036	115	-9.00	1.92E-02
<i>MTND6P8</i>	1036	115	-9.00	1.93E-02
<i>(OSBP)*</i>	585	96	6.10	1.94E-02
<i>KIRREL3</i>	198	1287	6.49	1.94E-02
<i>UBE2W</i>	1097	134	-8.16	1.95E-02
<i>ZNF469</i>	183	1287	7.03	1.95E-02
<i>ALPPL2</i>	76	691	9.07	1.96E-02
<i>CCSER2</i>	899	96	-9.37	1.96E-02
<i>PTBP3</i>	884	96	-9.21	1.97E-02
<i>SLC43A1</i>	91	826	9.03	1.99E-02
<i>RP11-435B5.5</i>	1890	307	-6.15	2.01E-02
<i>LITD1</i>	1143	134	-8.50	2.03E-02
<i>ZNF385D</i>	884	96	-9.21	2.04E-02
<i>TSNAXIP1</i>	76	711	9.32	2.05E-02
<i>NYNRIN</i>	213	1421	6.66	2.05E-02
<i>LACCI</i>	1128	134	-8.39	2.12E-02
<i>ATRNL1</i>	1113	134	-8.28	2.13E-02
<i>ZNF219</i>	137	1075	7.84	2.15E-02
<i>WDR55</i>	869	96	-9.05	2.15E-02
<i>MKKS</i>	854	96	-8.89	2.16E-02
<i>DDX55</i>	869	96	-9.05	2.17E-02
<i>(FTH1*)</i>	1844	11211	6.08	2.18E-02
<i>TONSL</i>	91	787	8.61	2.19E-02

<i>ZDHHC13</i>	1448	211	-6.85	2.20E-02
<i>PIDD</i>	107	883	8.28	2.20E-02
<i>SPEG</i>	427	2362	5.53	2.21E-02
<i>LSG1</i>	823	96	-8.57	2.25E-02
<i>NNT</i>	838	96	-8.73	2.25E-02
<i>PLEKHH2</i>	854	96	-8.89	2.26E-02
<i>TDO2</i>	808	96	-8.41	2.27E-02
<i>ZNF529</i>	854	96	-8.89	2.27E-02
<i>SUSD2</i>	107	883	8.28	2.28E-02
<i>SETSIP</i>	198	1402	7.07	2.32E-02
<i>PLCH1</i>	838	96	-8.73	2.34E-02
<i>MED12L</i>	1036	134	-7.71	2.39E-02
<i>SEMA3A</i>	1783	288	-6.19	2.42E-02
<i>SHQ1</i>	823	96	-8.57	2.43E-02
<i>PKN1</i>	107	864	8.10	2.44E-02
<i>WDR6</i>	107	864	8.10	2.44E-02
<i>PXN</i>	137	999	7.28	2.44E-02
<i>ADRBK1</i>	76	653	8.57	2.47E-02
<i>MANBA</i>	1250	173	-7.23	2.49E-02
<i>PGAP3</i>	76	634	8.32	2.49E-02
<i>TGM2</i>	107	845	7.92	2.54E-02
<i>USP33</i>	1143	154	-7.44	2.56E-02
<i>PTPRN2</i>	122	922	7.56	2.59E-02
<i>DCTN4</i>	930	115	-8.07	2.60E-02
<i>KPNA1</i>	930	115	-8.07	2.60E-02
<i>B9D1</i>	76	615	8.06	2.63E-02
<i>ZNF862</i>	274	1575	5.74	2.64E-02
<i>HMCN1</i>	2408	461	-5.23	2.65E-02
<i>EMID1</i>	107	826	7.74	2.65E-02
<i>EDC4</i>	76	653	8.57	2.66E-02
<i>SAMD3</i>	1036	134	-7.71	2.68E-02
<i>GCSAML</i>	793	96	-8.25	2.76E-02
<i>WRN</i>	1128	154	-7.34	2.77E-02
<i>NCKAP1</i>	2362	461	-5.13	2.77E-02
<i>VIL1</i>	884	115	-7.67	2.79E-02
<i>CAMK1G</i>	122	903	7.40	2.81E-02
<i>C12orf4</i>	777	96	-8.10	2.85E-02
<i>EDNRA</i>	777	96	-8.10	2.85E-02
<i>XPO4</i>	899	115	-7.80	2.85E-02
<i>MAN2B2</i>	213	1248	5.85	2.85E-02
<i>RP5-1112D6.8</i>	76	538	7.06	2.89E-02
<i>CPNE9</i>	107	787	7.38	2.90E-02
<i>PRSS1</i>	107	787	7.38	2.90E-02
<i>EXOC5</i>	1113	154	-7.24	2.90E-02
<i>MAP1S</i>	107	787	7.38	2.96E-02
<i>POLE3</i>	91	672	7.35	3.01E-02
<i>POLR1C</i>	122	864	7.09	3.02E-02
<i>SLC25A22</i>	76	595	7.81	3.03E-02
<i>LICAM</i>	91	711	7.77	3.04E-02
<i>LHCGR</i>	975	134	-7.26	3.05E-02
<i>HNRNPK</i>	1204	173	-6.97	3.06E-02
<i>IL7</i>	747	96	-7.78	3.07E-02
<i>PPHLN1</i>	1341	211	-6.35	3.08E-02
<i>FBXW12</i>	76	538	7.06	3.09E-02
<i>CACNA1H</i>	122	864	7.09	3.09E-02
<i>CHRNA9</i>	76	250	3.28	3.12E-02
<i>TRIM16L</i>	76	250	3.28	3.12E-02
<i>RDH13</i>	198	1229	6.20	3.12E-02
<i>KRT36</i>	76	499	6.55	3.13E-02
<i>SLC29A2</i>	76	595	7.81	3.15E-02
<i>BMP6</i>	76	269	3.53	3.17E-02
<i>RCOR1</i>	686	96	-7.14	3.20E-02

<i>AL592494.5</i>	76	288	3.78	3.21E-02
<i>CTD-2587H19.1</i>	76	288	3.78	3.21E-02
<i>SLC38A11</i>	716	96	-7.46	3.21E-02
<i>STARD13-AS</i>	76	307	4.03	3.26E-02
<i>RAN</i>	716	96	-7.46	3.26E-02
<i>MPDZ</i>	2515	518	-4.85	3.26E-02
<i>PIGO</i>	137	941	6.86	3.27E-02
<i>RP11-693J15.5</i>	960	134	-7.14	3.28E-02
<i>DAZAP1</i>	137	922	6.72	3.31E-02
<i>RP6-42F4.1</i>	945	134	-7.03	3.34E-02
<i>PSME4</i>	1326	230	-5.75	3.36E-02
<i>RP11-324H6.5</i>	91	653	7.14	3.38E-02
<i>SYCP1</i>	1158	173	-6.70	3.38E-02
<i>KCNB2</i>	198	1191	6.01	3.39E-02
<i>DEAF1</i>	122	845	6.93	3.40E-02
<i>SLC37A2</i>	122	807	6.61	3.41E-02
<i>AP3M1</i>	716	96	-7.46	3.42E-02
<i>PSMG3-AS1</i>	76	595	7.81	3.42E-02
<i>CD3G</i>	808	115	-7.01	3.43E-02
<i>ATG9B</i>	198	1171	5.91	3.48E-02
<i>YME1L1</i>	930	134	-6.92	3.49E-02
<i>GHc-362H12.3</i>	91	595	6.51	3.52E-02
<i>TCF12</i>	823	115	-7.14	3.53E-02
<i>CYP2A13</i>	76	518	6.80	3.54E-02
<i>FGF17</i>	137	922	6.72	3.54E-02
<i>LCE5A</i>	76	480	6.30	3.55E-02
<i>RP11-96K19.4</i>	2241	461	-4.86	3.55E-02
<i>PICK1</i>	91	653	7.14	3.55E-02
<i>USP5</i>	183	1133	6.19	3.55E-02
<i>MVP</i>	107	749	7.02	3.55E-02
<i>ADD3</i>	1128	173	-6.53	3.56E-02
<i>CTD-3195I5.5</i>	76	442	5.80	3.57E-02
<i>ZNF394</i>	107	711	6.66	3.57E-02
<i>RP11-143M1.3</i>	671	96	-6.98	3.58E-02
<i>MYSM1</i>	1341	230	-5.82	3.59E-02
<i>NCAM2</i>	716	96	-7.46	3.60E-02
<i>RP11-286B14.1</i>	655	96	-6.83	3.60E-02
<i>DUSP22</i>	229	1287	5.63	3.64E-02
<i>MTCYBP3</i>	793	115	-6.88	3.67E-02
<i>PDCD1</i>	91	615	6.72	3.68E-02
<i>PRPF4B</i>	1311	211	-6.21	3.69E-02
<i>NOBOX</i>	76	422	5.54	3.69E-02
<i>ZNF565</i>	107	730	6.84	3.69E-02
<i>TRPC2</i>	122	826	6.77	3.70E-02
<i>PRKRIR</i>	808	115	-7.01	3.72E-02
<i>COL18A1</i>	137	845	6.16	3.73E-02
<i>RSRC1</i>	686	96	-7.14	3.75E-02
<i>VWA7</i>	91	653	7.14	3.76E-02
<i>CHRA1</i>	76	480	6.30	3.76E-02
<i>HSD11B1L</i>	76	480	6.30	3.76E-02
<i>ASS1</i>	76	557	7.31	3.79E-02
<i>NR1D2</i>	808	115	-7.01	3.80E-02
<i>SMC5</i>	1006	154	-6.55	3.81E-02
<i>FAR1</i>	793	115	-6.88	3.82E-02
<i>ALOX12B</i>	76	518	6.80	3.88E-02
<i>ZNF682</i>	701	96	-7.30	3.89E-02
<i>NKTR</i>	2149	461	-4.66	3.90E-02
<i>SYCP2</i>	1097	173	-6.35	3.90E-02
<i>PTPN18</i>	899	134	-6.69	3.91E-02
<i>ABCA5</i>	1799	365	-4.93	3.92E-02
<i>CEP97</i>	899	134	-6.69	3.92E-02
<i>IFT81</i>	991	154	-6.45	3.93E-02

<i>IREB2</i>	899	134	-6.69	3.93E-02
<i>KCNQ1</i>	76	480	6.30	3.94E-02
<i>ARID2</i>	1296	230	-5.62	3.95E-02
<i>PPP1R16A</i>	122	807	6.61	3.95E-02
<i>HOXC-AS3</i>	76	499	6.55	3.96E-02
<i>ANKRD18DP</i>	625	96	-6.51	3.97E-02
<i>RAB21</i>	1097	173	-6.35	3.99E-02
<i>SUCO</i>	777	115	-6.75	4.03E-02
<i>CDCP1</i>	76	518	6.80	4.05E-02
<i>NLE1</i>	76	557	7.31	4.07E-02
<i>SRBD1</i>	1082	173	-6.26	4.10E-02
<i>GOLGA7B</i>	91	615	6.72	4.11E-02
<i>PLCH2</i>	76	557	7.31	4.11E-02
<i>SLC25A36</i>	777	115	-6.75	4.11E-02
<i>Clorf131</i>	107	653	6.12	4.11E-02
<i>FAM177A1</i>	686	96	-7.14	4.12E-02
<i>R3HDM2</i>	1082	173	-6.26	4.13E-02
<i>PAN2</i>	229	1191	5.21	4.15E-02
<i>UBB</i>	76	346	4.54	4.15E-02
<i>DCBLD2</i>	2088	461	-4.53	4.17E-02
<i>EIF3F</i>	1692	326	-5.18	4.17E-02
<i>FAM225A</i>	107	711	6.66	4.19E-02
<i>THNSL2</i>	107	711	6.66	4.19E-02
<i>MAT1A</i>	122	787	6.46	4.20E-02
<i>MOB1B</i>	975	154	-6.35	4.22E-02
<i>COPB2</i>	1311	250	-5.25	4.22E-02
<i>VLDLR</i>	777	115	-6.75	4.23E-02
<i>SPCS3</i>	777	115	-6.75	4.24E-02
<i>AGFG1</i>	960	154	-6.25	4.26E-02
<i>ESRP1</i>	716	115	-6.22	4.28E-02
<i>CNTRL</i>	2149	480	-4.48	4.29E-02
<i>SLC26A6</i>	290	1459	5.04	4.29E-02
<i>LRRK1</i>	274	1325	4.83	4.30E-02
<i>CCDC88B</i>	198	1114	5.62	4.30E-02
<i>CLCN2</i>	137	845	6.16	4.31E-02
<i>RP11-7M8.2</i>	76	442	5.80	4.31E-02
<i>THBS2</i>	945	154	-6.15	4.31E-02
<i>RP11-174G6.5</i>	640	96	-6.67	4.32E-02
<i>NF1</i>	2454	557	-4.41	4.33E-02
<i>GPR98</i>	3887	864	-4.50	4.35E-02
<i>PRSS8</i>	76	538	7.06	4.37E-02
<i>IVL</i>	76	307	4.03	4.37E-02
<i>CCDC18</i>	732	115	-6.35	4.39E-02
<i>ZFYVE16</i>	1158	211	-5.48	4.40E-02
<i>TOX4</i>	960	154	-6.25	4.41E-02
<i>DPP9</i>	274	1325	4.83	4.42E-02
<i>SYNJ2</i>	335	1613	4.81	4.43E-02
<i>MAPK12</i>	107	691	6.48	4.44E-02
<i>C5orf64</i>	655	96	-6.83	4.45E-02
<i>C9orf153</i>	701	115	-6.09	4.48E-02
<i>TCTE3</i>	76	288	3.78	4.50E-02
<i>TCEA3</i>	747	115	-6.48	4.50E-02
<i>PGLS</i>	76	499	6.55	4.50E-02
<i>USP37</i>	1280	250	-5.13	4.51E-02
<i>DHRS2</i>	91	595	6.51	4.55E-02
<i>GTF3C1</i>	320	1479	4.62	4.56E-02
<i>ZNF835</i>	91	518	5.67	4.58E-02
<i>RP11-115D19.1</i>	579	96	-6.03	4.58E-02
<i>MITD1</i>	930	154	-6.05	4.59E-02
<i>UGGT2</i>	945	154	-6.15	4.60E-02
<i>FAM27A</i>	91	595	6.51	4.61E-02
<i>SRSF5</i>	1036	173	-6.00	4.63E-02

<i>RP11-99J16_A.2</i>	76	269	3.53	4.66E-02
<i>RP1-18D14.7</i>	107	653	6.12	4.66E-02
<i>COL11A1</i>	1280	250	-5.13	4.66E-02
<i>UVRAG</i>	640	96	-6.67	4.67E-02
<i>MFSD2B</i>	244	1267	5.20	4.68E-02
PARVG	198	999	5.04	4.71E-02
<i>ADAM11</i>	107	672	6.30	4.71E-02
<i>NUCB2</i>	1021	173	-5.91	4.73E-02
<i>CSK</i>	91	595	6.51	4.74E-02
<i>RP11-17M15.2</i>	76	365	4.79	4.76E-02
<i>RP11-214L19.1</i>	76	365	4.79	4.76E-02
<i>C4orf29</i>	732	115	-6.35	4.76E-02
<i>DGKH</i>	1997	461	-4.33	4.77E-02
<i>TEKT5</i>	107	653	6.12	4.78E-02
<i>ABI3BP</i>	1951	442	-4.42	4.78E-02
CAPS2	1021	173	-5.91	4.80E-02
<i>SSBP2</i>	1021	173	-5.91	4.80E-02
<i>HMGCLL1</i>	930	154	-6.05	4.80E-02
<i>ZNF66</i>	625	96	-6.51	4.80E-02
NEK8	76	518	6.80	4.81E-02
<i>MMP11</i>	107	672	6.30	4.83E-02
<i>GBAPI</i>	76	480	6.30	4.83E-02
<i>EML4</i>	1021	173	-5.91	4.84E-02
<i>HHLA2</i>	1021	173	-5.91	4.84E-02
PAPD4	1280	230	-5.56	4.84E-02
<i>CTD-2587H24.5</i>	107	634	5.94	4.84E-02
<i>CDH12</i>	1235	230	-5.36	4.87E-02
C22orf26	122	691	5.67	4.87E-02
<i>RP1-225E12.2</i>	823	134	-6.12	4.88E-02
<i>TIA1</i>	823	134	-6.12	4.88E-02
DSCAML1	183	941	5.14	4.89E-02
<i>RP4-791M13.4</i>	579	96	-6.03	4.89E-02
<i>FCN1</i>	76	250	3.28	4.90E-02
<i>NCR2</i>	107	595	5.58	4.91E-02
<i>GBA</i>	107	634	5.94	4.92E-02
<i>SUCLG2</i>	594	96	-6.19	4.92E-02
<i>PPP6R1</i>	137	807	5.88	4.92E-02
<i>SIGLEC8</i>	198	1095	5.52	4.92E-02
<i>VIPR1-AS1</i>	76	480	6.30	4.93E-02
<i>AKAP9</i>	3033	711	-4.27	4.96E-02
NAALAD2	899	154	-5.85	4.96E-02
<i>FLOT1</i>	122	711	5.83	4.97E-02
<i>VPS9D1</i>	122	711	5.83	4.97E-02
<i>PIAS1</i>	549	96	-5.71	4.97E-02
PKD1	351	1517	4.33	4.97E-02
<i>CENPV</i>	76	346	4.54	4.98E-02
<i>NOX3</i>	76	346	4.54	4.98E-02
<i>ADAM33</i>	76	499	6.55	4.99E-02
<i>C19orf44</i>	76	461	6.05	5.00E-02

Table S9. Statistically significant pathways for differentially expressed transcripts in BPH and LS samples ($n=327$).

	-log(p-value)
Aldosterone signaling in epithelial cells	9.94×10^{-4}
Protein Ubiquitination Pathway	3.35×10^{-3}
Glioma signaling	2.8×10^{-3}
iCOS signaling in T helper cells	8.52×10^{-3}
Antiproliferative role of TOB in T cell signaling	4.7×10^{-3}
PI3K signaling in B lymphocytes	2.27×10^{-2}
Neuregulin signaling	3.14×10^{-2}
Ceramide biosynthesis	4.12×10^{-2}

Serotonin and melatonin biosynthesis	4.2×10^{-2}
Glycogen biosynthesis	4.2×10^{-2}
Role of OCT4 in mammalian embryonic stem cell pluripotency	4.26×10^{-2}
Tryptophan degradation	4.89×10^{-2}

Table S10. Statistically significant pathways for differentially expressed transcripts in BPH and HS samples ($n = 63$).

	$-\log(p\text{-value})$
NER pathway	2.71×10^{-2}
Assembly of RNA I polymerase complex	2.94×10^{-2}
NAD phosphorylation and dephosphorylation	3.14×10^{-2}
RAN signaling	4.15×10^{-2}

Table S11. Statistically significant pathways for differentially expressed transcripts in LS and HS samples ($n = 341$).

	$-\log(p\text{-value})$
RAN Signaling	1.42×10^{-3}
Clathrin-mediated Endocytosis Signaling	4.87×10^{-3}
Sumoylation Pathway	1.28×10^{-2}
Axonal Guidance Signaling	1.52×10^{-2}
Paxillin Signaling	1.66×10^{-2}
Caveolar-mediated Endocytosis Signaling	1.69×10^{-2}
D-myo-inositol (1,4,5)-trisphosphate Degradation	2.15×10^{-2}
D-myo-inositol Hexakisphosphate Biosynthesis II	2.39×10^{-2}
D-myo-inositol (1,3,4)-trisphosphate Biosynthesis	2.39×10^{-2}
Palmitate Biosynthesis I (Animals)	2.67×10^{-2}
Fatty Acid Biosynthesis Initiation II	2.67×10^{-2}
Protein Ubiquitination Pathway	3.2×10^{-2}
Tryptophan Degradation III (Eukaryotic)	3.29×10^{-2}
D-myo-inositol (1,4,5)-trisphosphate Metabolism	3.79×10^{-2}
S-adenosyl-L-methionine Biosynthesis	3.98×10^{-2}
4-aminobutyrate Degradation I	3.98×10^{-2}
Hepatic Fibrosis / Hepatic Stellate Cell Activation	4.03×10^{-2}
Apelin Cardiomyocyte Signaling Pathway	4.61×10^{-2}
Apelin Liver Signaling Pathway	4.74×10^{-2}
RAR Activation	4.77×10^{-2}
Regulation of the Epithelial-Mesenchymal Transition Pathway	4.77×10^{-2}

Table S12. Sequences used for Taqman probe design.

OSBP (Chr 11:59,337,733-59,387,385 (NM_02556.3)), exon sequence 2171 to 2391:

CATCCTCTGTGGCTTTCATAGCTTCCGCTTCTCTCTTTCTGGAAGTCTTTGTTTTCCTCCAGGCGC
TGCTTCTCCGCATTTGCTTCATCCCAGCGTCCATTTCCATAGTCTCTGGTCAGGTCGTAACCGGCTGTC
TGTGGGGGCGAGTGCCACTTCCCAACATTGAGAGTCAGAGCAAGCTCTGAGAAGTAGTACATGTTTTC
TGCATTCTTC

PHC3 (Chr 3:169,795,957 - 169,908,936 (NM_024947.4)), exon sequence 938 to 1182:

CTGAATCGGTGAACAATGCTGTGACTGGGCATTACTGGGAGCTGGAGGAAGGCCATGGTTCTGGAGTG
GTATACAGTGCTGGGATGGGGGTGGGTCTTGAGTTGAATTCTGAAGTGTGATTGGCTGAATTTGCTGTT
GCTGCTGTTGTAATATCAGCTGATGATGGGAACTTTGGAAGGTGGTGAATGAAGAGGAATCTGCTGA
TGTTTTATTAGAGAATGAGGCTGAATTGGAGAATATGAAG

UACA (Chr 15:70,935,992 - 71,066,798 (NM_018003.4), exon sequence 1642 to 2090:

CTTCTCATTCACTTCATTTGATAATGAGCTCTTCATGTTTTCAAATTTTTCAGCTGGAATGGAAAGGGC
 CAACTTCGCTGACAATTCTTTTGCCTGGCCTTCCATCTCTGTGACCTTTCTTCCTTTCTTCTCTCGCTCCA
 TTTCACACATACTAAGTTCCTTCTGTAATCGCTTATTTTCTTCTATCAGCTTGCCTTCATCCCTCTTAAAC
 TCTTCTACTATCATCTCATTTTGTGTTGATTTGGTTTCTTAATTTCCCCACTTCTGCTGAAGCACCTTCATAT
 TTTACTTTCAAGTCTTTCAACTGATCCTTCAGTTCCTCGGTTAGTCTGTGATTCCCTGAGGCTGCTTCACT
 TGTTAAGTGTTCTTTAAGGGCAAGAAAATGGGTCTGCATTTGTTTAACTTTACCTTCTGACTCATACATC
 CTCTTCTGCACATCTTTAATGCACATCCTCTGTGGCTTTCATAGCTTCCGCTTCTCTCTTCTTTCTGGAA
 AGTCTTTGTTTTTCTCCAGGCGCTGCTTCTCCGCATTTGCTTCATCCCAGCGTCCATTTTCCATCAGTCT
 CTGGTCAGGTCGTAACCGGCTGTCTGTGGGGCAGTGCCACTTTCCCAAGCATTGAGAGTCAGAGCAA
 GCTCTGAGAAGTAGTACATGTTTTCTGCATTCTTC

***BRPF1* (Chr 3:9,771,791 - 9,791,327 (NM_001003694.2)), exon sequence 1014 to 1973:**

GTACATCGAGAAGTCTGCAGAGGAGCTGGACGAGGAAGTAGAGTATGACATGGACGAGGAGGACTA
 CATCTGGCTGGATATCATGAATGAGCGTCGGAAGACAGAGGGTGTAAGTCCCATCCCGCAGGAGATC
 TTTGAGTACCTAATGGACCGACTGGAGAAGGAGTCGTACTTTGAGAGTCATAATAAAGGCGACCCTA
 ATGCGCTAGTGGACGAGGATGCTGTTTGTGTATCTGCAATGATGGTGAGTGCCAGAACAGCAATGTC
 ACCTCTTCTGTGACATGTGCAACCTGGCCGTGCACCAGGAGTGCTACGGTGTCCCCTATATCCCTGAGG
 GCCAGTGGCTGTGCCGCCGTGCTGTCAGTCACCTCTCGTGCTGTGGATTGTGCCCTGTGCCCAACA
 AGGGCGGTGCCTTCAAGCAGACAGATGACGGGCGCTGGGCCCATGTGGTGTGTGCCTTGTGGATCCCT
 GAGGTCTGCTTCGCCAACACGGTCTTCTAGAGCCTATTGACAGCATTGAGCACATCCCACCAGCTCG
 CTGGAAGCTCACCTGCTACATTTGCAAACAACGGGGCTCAGGGGCCTGCATCCAGGCCACAAGGCCA
 ACTGTTACACAGCTTTCCATGTGACATGCGCCCAGCAGGCTGGCCTTTACATGAAGATGGAGCCTGTG
 CGGGAGACAGGCGCCAACGGCACCTCTTTCAGTGTCCGCAAGACAGCCTACTGCGACATCCACACGC
 CTCCAGGTTACGACGCGGACTGCCTGCCCTGTCCCACAGCGAGGGTGAGGAGGATGAAGATGAGGA
 GGAGGATGAGGGTAAGGGCTGGAGCTCAGAGAAAGTCAAGAAGGCCAAGGCCAAGTCCCGGATCAA
 AATGAAGAAGGCACGGAAGATCCTGGCAGAGAAGCGGGCAGCAGCACCTGTGGTGTCAGTGCCCTG
 CATCCCACCACACAG

***FTH1* (Chr 11:61,731,419 - 61,735,470 (AC004228.2)), exon sequence 188806 to 189645:**

TCAATCTTTGAGGCTGCAGGCAGGCACCCATCTCCCCATTTACAGGCAGGGAAACTGAGGTCCAGAG
 AGAGGGAGAGATTCTCCAAGTCATCAGGCACATAAAGGTCTGCTGGGATGATCTTTCTGTGGGA
 CTTCTTCTGTCCCTGGTGACCAGGTGTCCCTGTTGGCTGTGGATGAGATGCACCAGGACCTGCCTCGGA
 TGGAGCCGGACATGTACTGGAATAAGCCCGAGCCACAGCCCCCTACACAGCTGCTTCGCCCAGTTC
 CGTCGAGCCTCCTTTATGGGCTCCACCTTCAACATCAGGTGTGGCCAGAGCCAGGGGGCTGGGTGGGA
 AGCCCCCTCCTAGTGAGGGGTCTGCCTAGGAACCTAGAATAGCACTAGTTAATGCATACAGGTTGCTT
 CAGTAAGTGTGAGGCACTGTACTATGCTCTTTATAAACATTAACCTATTTTTTCTCCCAATAATTCTGG
 TTTGTTATCCCAAGTTTTTTCAGATAATTAAAGTACAGGTTTCAGAGAGAGTAAGTTGTCCAAGGCCACAT
 AGCTACCAAATGGTGCATTTGCTACTCGAAGGACAGCCTGTGATCAGTGATGCAGTGGAACGTTAGGA
 CCTGGCTCTTGTATCCAGAACTATGTTTTCTTTCTTTTGTGAGACAGTATCTCGCTCTGTGCCCCAGGTT
 GGAGCGCAGTGGCGTGATCTTGGCTCACTGCAACCTCCGCCTCTGGGTTCAAGTGATTCTCTGCTTC

AGCCTCCCCAGTAGCTGGGATTACAGGTGCCACACAACCACAACCTGGCTAATTTTTGTACTTTTAGTAGA
GATGAGGTTTCACCAT

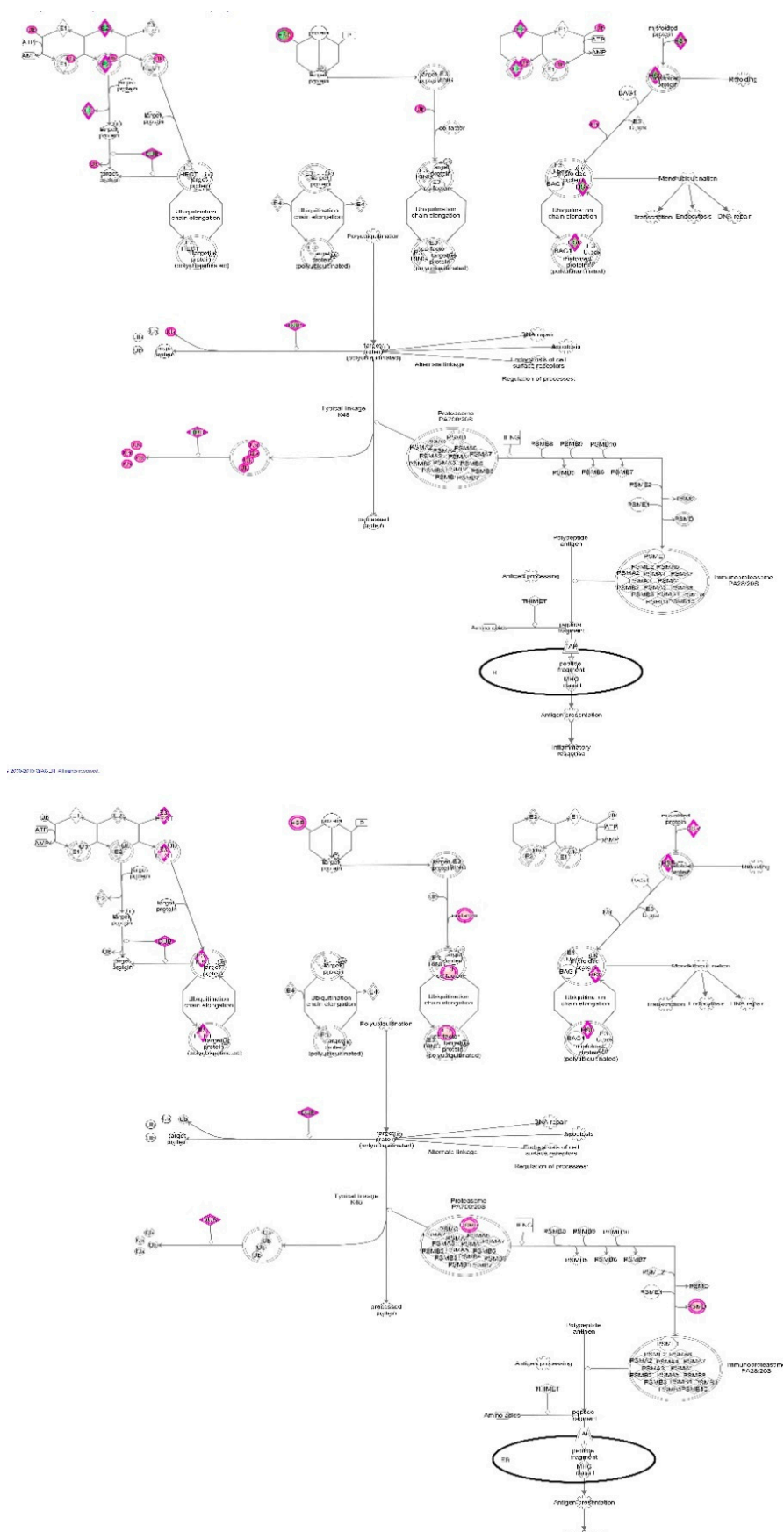


Figure S1. Differentially expressed genes in LS vs. HS (top) and BPH vs. LS (bottom) in the context of the protein ubiquitination pathway. Differentially expressed genes are depicted in pink. .

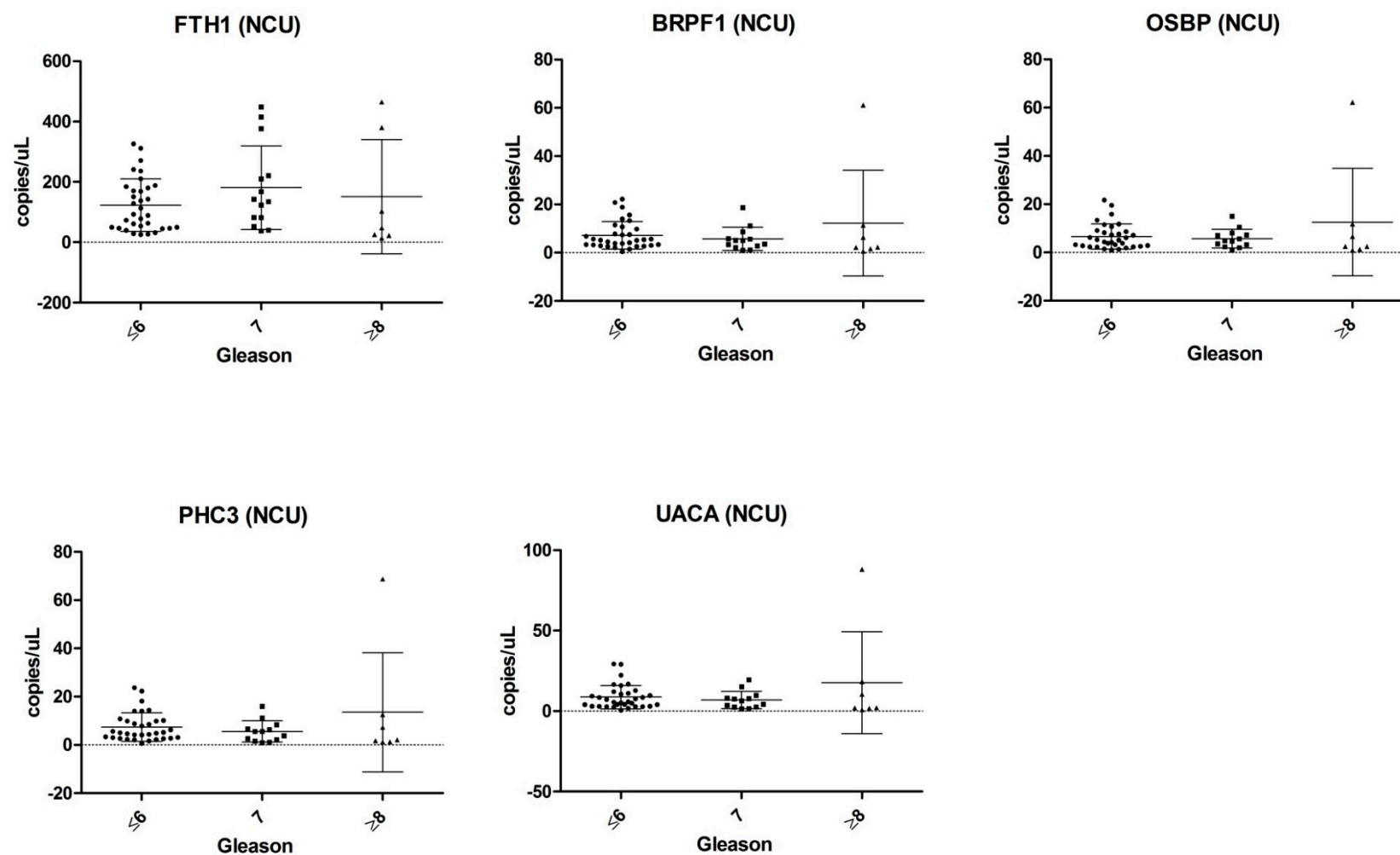


Figure S2. Expression levels of selected genes in non-centrifuged urine samples (NCU), classified according to the Gleason score. Expression levels were compared using the Mann–Whitney independent t -test (* $p \leq 0.05$).

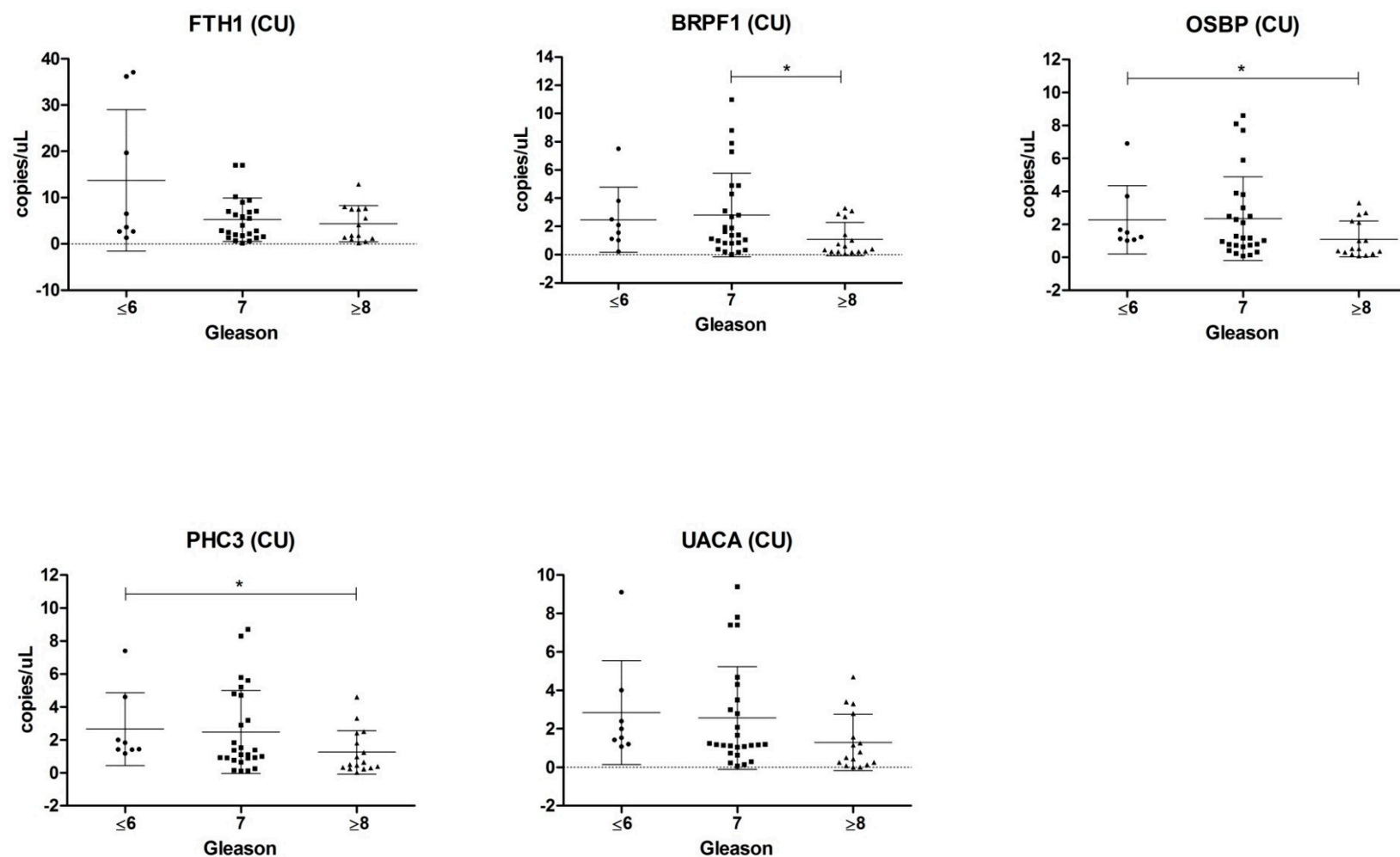


Figure S3. Expression levels of selected genes in centrifuged urine samples (CU), classified according to the Gleason score. Expression levels were compared using the Mann–Whitney independent t-test (* $p \leq 0.05$).