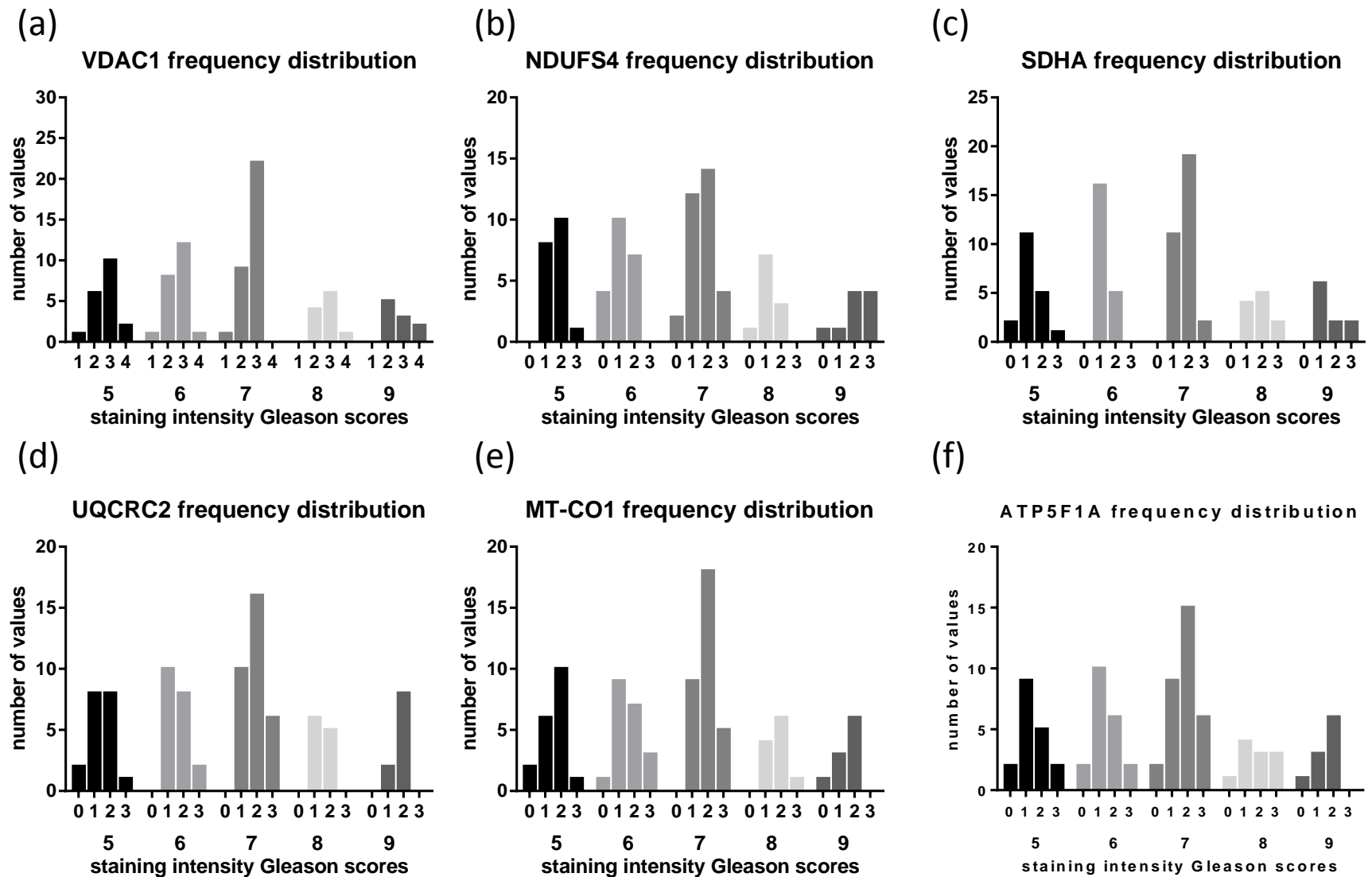
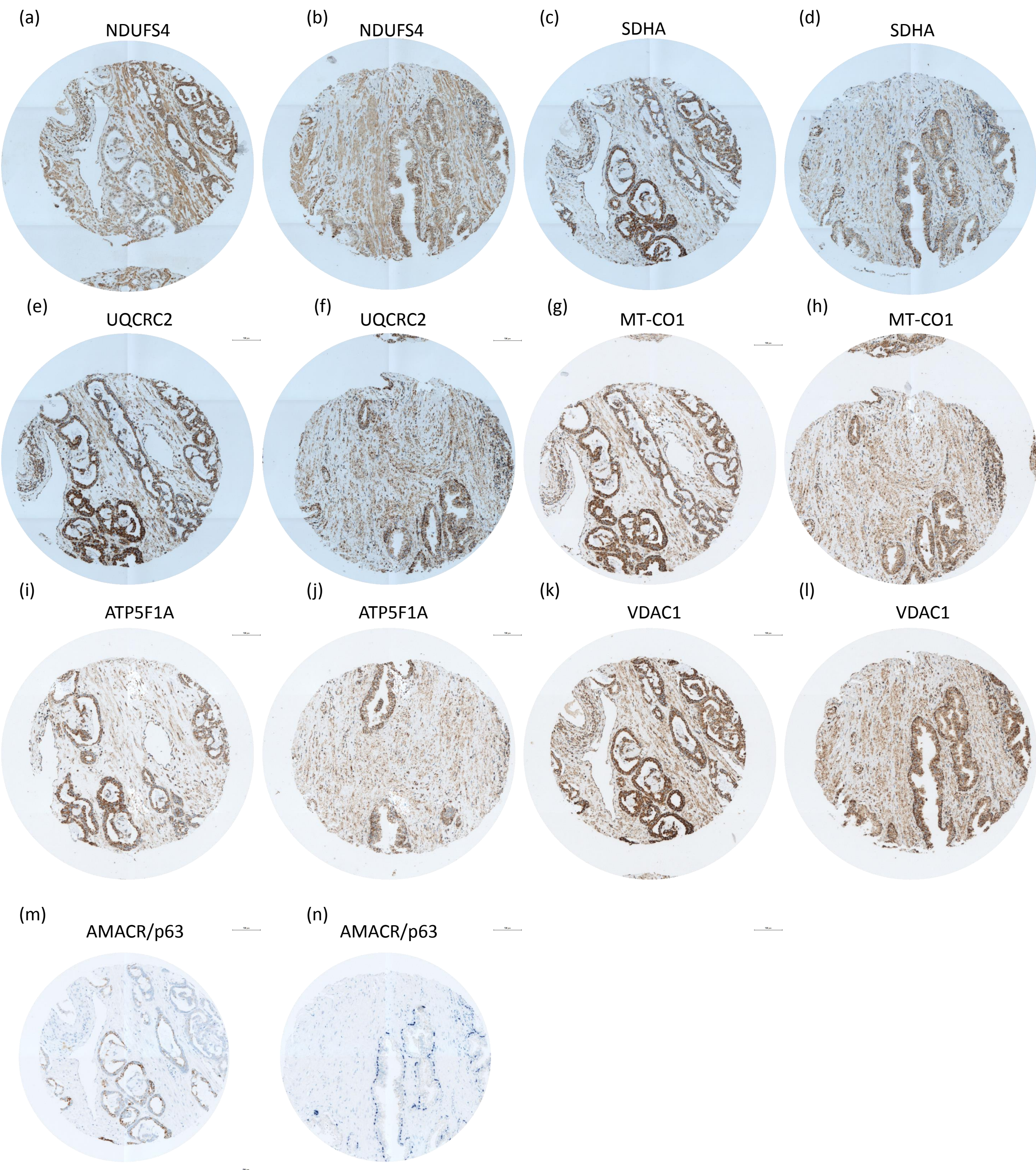


Supplementary figure 1: OXPHOS complex expression in prostate carcinomas of different Gleason scores. (a) VDAC1, (b) NDUF54, (c) SDHA, (d) UQCRC2, (e) MT-CO1, (f) ATP5F1A. The intensities of the stainings are given as median \pm SD. *** $p < 0.001$, ** $p > 0.01$, * $p > 0.05$.



Supplementary figure 2: Frequency distribution of the lowest staining intensities found in prostate carcinoma tissue punches of different Gleason scores. (a) VDAC1, (b) NDUFS4, (c) SDHA, (d) UQCRC2, (e) MT-CO1, (f) ATP5F1A. The frequencies are given in percent. The staining intensities are: 0 = no staining, 1 = weak staining, 2 = moderate staining, 3 = strong staining, 4 = very strong staining.



Supplementary figure 3: Staining of the OXPHOS complexes, VDAC1 and AMACR/p63 in a prostate carcinoma Gleason score 7 and the adjacent benign prostate tissue. (a, b) NDUFS4, (c, d) SDHA, (e, f) UQCRC2, (g, h) MT-CO1, (i, j) ATP5F1A, (k, l) VDAC1, (m, n) AMACR/p63. (a, c, e, g, i, k) carcinoma; (b, d, f, h, j, l, n) benign prostate tissue. The punches are 0.6 mm in diameter. The AMACR/p63 staining was used to visualize the carcinoma cells in brown and the benign prostate tissue in blue.

Supplementary table 1A: Staining intensities

Tumor	Punch	VDAC1				NDUFS4				SDHA				UQCRC2				MT-CO1				ATP5F1A			
		CA		BE		CA		BE		CA		BE		CA		BE		CA		BE		CA		BE	
		Low/High	Low/High	Low/High	Low/High	Low/High	Low/High	Low/High	Low/High	Low/High	Low/High	Low/High	Low/High	Low/High	Low/High	Low/High	Low/High	Low/High	Low/High	Low/High	Low/High	Low/High	Low/High	Low/High	Low/High
9932197	B1	3				2	3	2	2	1	2	0	1	2	3	2	3	2	3						
9932197	B2			3	4			3	3			1	3			3			2	3			2	3	
9935954	B3	3				2	3			1	2			1	2			2	3			2	3		
9935954	B4	3	4			2	3			1	2			1	3			2	3			2	3		
9935954	B5	2	3					1	2			1	2					1	3					2	3
9935954	B6			3				1	2			1	3			1	2	2	3			2	3		
10338726	B7	3	4			0	2			1	4			1	3			1	3						
10338726	B8			3	4			1	3			1	3			2	3			2	3			2	3
10343434	B9	3	4			2	3			2	3			1	3			2	3			2	3		
10343434	B10	3	4			2	3			2	3			3	3			2	3			2	3		
10343434	B11	3	4			2	3	2	3	3	3	2	3	3	3	2	3	2	3	2	3	2	3		
10343434	B12			3	4			1	3			1	3			2	3			1	3			1	2
10631521	B13	3	4					2	3			2	3			2	3			2	3				
10631521	B14			3	4			1	3			2	3			3	3			2	3			2	3
10637255	B15	3	4			2	3			2	2			2	3			2	3			2	3		
10637255	B16	3	4			3	3			2	2			2	3			2	3			2	3		
10637255	B17	3	4			2	3			1	2			2	3			2	3			2	3		
10637255	B18			2	3			2	3			1	2	3	3	2	3	2	3					2	3
9916972	C1	3	4			3	3			1	3			2	3			2	3						
9916972	C2	3	4			3	4			1	3			2	3			2	3			3	3		
9916972	C3	3	4			2	3			1	3			1	3			2	3			1	3		
9916972	C4			3	4			2	3			2	2			2	3							2	3
9932197	C5	3	4					1	3			2	2			2	3							2	3
9932197	C6	3	4			2	3			2	3			2	3	2	3	2	3			2	3	2	3
10325091	C7	3	4			2	3	2	3	3	3	1	3	2	3	2	3	2	3						
10325091	C8	3	4			1	3			3	3			2	3			2	3			3	3		
10325091	C9	3	4			1	3			2	3			1	3			2	3			3	3		
10325091	C10			3				2	3			2	2			3	3			2	3			2	3
10338726	C11	3																3	3	1	2			1	3
10338726	C12	3	4			1	3	2	3	2	3	1	2	2	3	2	3	0	1	2	3	1	3		
10630526	C13	3	4			2	3			3	4			2	3			2	3			2	3		
10630526	C14	3	4			3	3			3	3			2	3			2	3			2	3		
10630526	C15	3	4			2	4	3	3	3	4	3	3	2	3			1	3			2	3		
10630526	C16			3	4			2	3			2	3	2	3	2	3	2	3					2	3
10631521	C17	3	4			2	3			2	3			2	3			2	3			2	3		
10631521	C18	2	4			3	3	3	3	2	3	1	3			3		2	3			2	3		
10904082	C19	3	4	2		2	3	2	3	3	4	1	2	2	3			2	3			1	3		
10904082	C20	2	4			2	3			3	4			2	3			2	3			2	3		
10904082	C21	2	4			1	3	3	3	3	4	1	3	2	3	2	3	2	3			2	3		
10904082	C22			2	3			2	3			2	3			2	3			2	3			2	3
9908111	D1	3	4					1	2			0	1			2	3			2	3			2	3

9908111	D2			2	3			1	2			0	1			2	2			2	2			0	1
9909768	D3	3	4			1	3			1	3			3	3			3	3			2	3		
9909768	D4	4				3	4	2	2	3	4	2	3	3			3	3			2	3			
9909768	D5	4				1	2	3	3	3	4	1	2				2	3			2	3	2	2	
9909768	D6			3	4			1	2			1	2	2	3			2	3			1	2		
10310392	D7	4				1	3			2	3			3	3			3	3						
10310392	D8			3				2	3			1	2			3	3			3	3			2	2
10311955	D9	3	4			2	3			3	3			3	3			3	3			2	3		
10311955	D10	3	4			2	3			3	3			3	3			3	3			2	3		
10311955	D11	3	4			2	3			3	3					2	3			2	3	2	3		
10311955	D12			2	3	2	2	2	3	2	3	2	3			2	3			2	3			1	3
10625132	D13	3	4			3	3	3	3	3	3	2	3	2	3			2	3			2	3	2	3
10625132	D14			3	4			2	3			1	3			2	3			2	3			2	3
10627970	D15	3				3	4			3	3			2	3			2	3			2	3		
10627970	D16	3				3	3			2	3			2	3			2	3			2	3		
10627970	D17	2	3					2	3			1	2			2	3			2	3			1	2
10627970	D18			2	4			2	3			1	3			2	3			2	3			2	2
10817500	D19	4				4	4			4	4			2	3			2	3			3	3		
10817500	D20			3	4			3	3			1	3			2	3			2	3			2	3
10821594	D21	4				2	3			1	4			1	3			1	3			3	3		
10821594	D22	3	4			2	3	2	3	2	4	0	1	1	3			1	3			1	3		
10821594	D23	2	4			2	4	2	3	2	4	0	1	1	3			1	3			2	3		
10821594	D24			3				2	3			1	2			1	3			1	3			1	3
9902802	E1	4				1	3			1	3			2	3			2	3			2	3		
9902802	E2	4				2	3	3	3	1	4	2	3	1	3			1	3					1	3
9902802	E3	2	4			2	3	2	2	1	3	1	1	2	3			2	3			2	3		
9902802	E4			2				1	2			0	1			1	2			1	2			0	1
9908111	E5	3	4			2	3			1	3							2	3			2	3		
9908111	E6	3	4			3	3	1	2	2	3	1	2	1	3	1	2	2	3			1	2		
10239624	E7	2	4			2	3			1	2			2	3			2	3						
10239624	E8	3	4			3	3			2	2			2	3			2	3			1	3		
10239624	E9	3	4			2	3			1	3			1	3			1	3			1	3		
10239624	E10			4				2	3			2	2			2	3			2	3			1	2
10310392	E11	4				2	3	1	2	3	4	1	2	2	3			2	3			2	3		
10310392	E12	3	4			3	3			3	4			2	3			2	3			2	3		
10624826	E13	4				3	3			1	2			2	3			2	3			2	3		
10624826	E14	4				4	4			1	2			2	3			2	3			2	3		
10624826	E15	2	4			3	3			1	2			2	3			2	3			2	3		
10624826	E16			3	4			1	3			1	2			2	3			2	3			1	2
10625132	E17	4				2	3			1	3			2	3			2	3			2	3		
10625132	E18	4				3	3	2	3	2	3	2	3	2	3			2	3			2	3		
10812983	E19	4				3	3			2	3			2	3			2	3			2	3		
10812983	E20	3	4			3	4			2	3			2	3			2	3			2	3		
10812983	E21	4				3	3			2	3			2	3			2	3			2	3		
10812983	E22			3				3	3			3	3			2	3			2	3			1	3
10817500	E23	3	4			2	4			3	3			2	3			2	3			2	3		

10817500	E24	3	4			3	3	3	4	3	3	3	3	3	3	3	0	1	2	2	3	3				
9901335	F1	2	4					1	3			0	2			1	2			1	2			1	1	
9901335	F2			3	4										2	2			2	2			1	2		
9901797	F3	2	4			2	3			1	3			2	3			2	3			1	3			
9901797	F4	2	4			2	3			1	3			2	3			2	3			1	3			
9901797	F5	3	4			2	3			1	3			2	3			2	3			1	3			
9901797	F6			4				2	3			2	3			2	3			2	3			3	3	
10238998	F7	2	4			1	2	3	3	1	2	2	3			2	3			2	3	1	2	2	3	
10238998	F8			4				2	2			2	2			2	3			2	3			2	3	
10239551	F9	3	4			1	2	1	2	3	3	2	2	2	3			2	3			2	3			
10239551	F10	3	4			2	2	2	3	1	2	2	2	2	3			2	3			1	3	1	3	
10239551	F11	4						1	3			2	2					2	3			2	3			
10239551	F12			4																						
10613128	F13	4				3	4			3	4			2	3			2	3			2	3			
10613128	F14			4				2	3			2	2			2	3			2	3			2	3	
10622130	F15	3	4			2	3	2	3	2	3	2	3	2	3	2	3	2	3	2	3	1	3	1	3	
10622130	F16	4												3	3			3	3							
10622130	F17	3	4			2	3	2	3	2	3	2	3	3	3			3	3			2	3			
10622130	F18			2	4	3	3	1	2	1	1	2	3	2	3			2	3			2	3			
10736608	F19	3	4			2	3	2	2	2	3	2	2	2	3			2	3			2	3			
10736608	F20			2	4			1	2			1	2				2	3			2	3			1	3
10811752	F21	3	4			3	4			3	4			2	3			2	3			3	3			
10811752	F22	3	4			3	4			3	3			2	3			2	3			1	3			
10811752	F23	3	4			2	3			2	3			2	3			2	3			2	3			
10811752	F24			2	4			2	3			1	2			1	3			1	3			1	3	
9901036	G1	4				3	3			3	4			3	3			3	3			2	3			
9901036	G2	4				1	3			1	3			1	3			1	3			0	3			
9901036	G3	4				3	4			3	4			3	3			3	3			3	3			
9901036	G4			4				2	3			2	4			2	3			2	3			2	3	
9901335	G5	3	4			2	3			2	3						2	3			2	3				
9901335	G6	4										2	3	1	2	1	2	1	3			0	3	1	3	
10217305	G7	1	4			1	2			1	2			1	3			1	3			0	3			
10217305	G8	2	4			2	3			2	3			1	3			1	3			0	3			
10217305	G9	2	4			1	3			1	3			1	3			1	3			0	3			
10217305	G10			3	4			2	3			2	2	2	3			2	3					2	3	
10238998	G11																					2	3			
10238998	G12							1	1			1	2			1	2			1	2			2	3	
10607452	G13	2	4			2	3			1	2			1	3			1	3			1	3			
10607452	G14	3	4			2	3			1	2			1	3			1	3			1	3			
10607452	G15	3	4			2	3			1	3			1	3			1	3			1	3			
10607452	G16			3	4			2	3			1	2			1	3			1	3			1	3	
10613128	G17	4				4	4			3	4			2	3			2	3			3	3			
10613128	G18	4				3	4			3	4			2	3			2	3			3	3			
10734364	G19	3	4			2	3	1	2	3	4	2	3	3	3	1	2	3	3	1	2	3	3			
10734364	G20	3	4			2	3	1	1	3	4	3	3	2	3			2	3			3	3	2	3	
10734364	G21	3	4			1	3	2	2	3	4	3	3	2	3			2	3			3	3			

10734364	G22			3	4			2	3			2	3	2	3			2	3					1	2
10736608	G23	3	4			2	3	2	2	3	4	2	3	2	3			2	3			2	3		
10736608	G24	3	4			1	3			2	3			1	3			1	3			1	3		
9841708	H1	3	4			2	3			2	3			1	3			1	3			3	3		
9841708	H2			3	4			1	2			1	2			1	2			1	2			1	3
9842434	H3	4				1	3			1	3			2	3			2	3			1	3		
9842434	H4	4				2	3			2	3			3	3			3	3			3	3		
9842434	H5	4				1	3			2	3			3	3			3	3			3	3		
9842434	H6			3	4			2	3			2	2			2	3			2	3			2	3
10213893	H7	3	4					2	2			2	2			2	3			2	3			2	3
10213893	H8			4		3	3	2	3	2	3	2	3			3	3			3	3			2	3
10217220	H9	3	4			1	3			1	3			1	3			1	3			0	3		
10217220	H10	3	4			1	3			1	2			1	3			1	3			1	3		
10217220	H11	3	4			3	4			3	3			3	3			3	3			2	3		
10217220	H12			3	4			2	3			1	3			1	3			1	3				
10604940	H13	4				3	4			3	4			3	3			3	3			2	3		
10604940	H14			3	4	2	3			2	2					2	3			2	3			1	3
10606082	H15	4				1	3	3	3	1	3	3	4	1	3			1	3			2	3	2	3
10606082	H16	3	4			3	3			1	2			2	3			2	3			2	3		
10606082	H17	3	4			3	3			1	2			2	3			2	3			2	3	0	1
10606082	H18			4				2	3			1	2			2	3			2	3			2	3
10729892	H19	4				2	4	3	3	2	3	1	3	2	3			2	3			1	3		
10729892	H20			3	4	2	3	3	4	2	3	1	3	2	3	2	3	2	3	2	3	2	3	0	2
10732505	H21	3	4			2	3			2	3			2	2			2	2			2	3		
10732505	H22	3	4			3	4			2	3			2	3			2	3			2	3		
10732505	H23	3	4			3	4			2	3			2	3			2	3			2	3		
10732505	H24			3	4			2	4			1	3			2	3			2	3			0	1
9839857	I1	3	4			2	3			1	3			2	3			2	3			2	3		
9839857	I2	4				1	1	2	3	2	3	2	3	3	3			3	3					2	3
9839857	I3	4						2	2			1	2			2	3			2	3			0	3
9839857	I4			4				2	3			1	2			2	3			2	3			2	3
9841708	I5					2	3			1	3			2	3			2	3			3	3		
9841708	I6	2	4			1	2	1	2	1	3	2	2	2	3			2	3			3	3		
10212172	I7																								
10212172	I8	3	4			1	2			2	3			1	3			1	3			2	3		
10212172	I9	3	4			0	2			1	2			1	3			1	3			1	3		
10212172	I10			3	4			2	3			2	3			2	3			2	3			1	3
10213893	I11	4				2	2	2	3	3	3	2	3	2	3			2	3			2	3		
10213893	I12	3	4			1	3			2	3			1	3			1	3			2	3		
10601619	I13	3	4			2	3	2	3	2	3	2	3	2	3	2	3	2	3	2	3	2	3		
10601619	I14	3	4			3	3	1	3	1	3	2	3	2	3	2	3	2	3	2	3	2	3	2	3
10601619	I15	4				3	3	2	3	2	3	2	3	2	3	2	3	2	3	2	3	2	3	1	3
10601619	I16			4				1	3			2	3			2	3			2	3			2	3
10604940	I17	4				2	4			2	4			3	3			3	3			3	3		
10604940	I18	3	4			3	3			2	4			3	3			3	3			3	3		
10729632	I19	4				3	4			2	4			3	3			3	3			3	3		

10729632	I20	4				3	4			2	4			3	3			3	3			3	3		
10729632	I21	3	4			3	4			2	3			2	3			2	3			3	3		
10729632	I22			3	4			1	1			1	2			1	3			1	3			0	1
10729892	I23	3	4			2	3			2	3			2	3			2	3			2	3	2	2
10729892	I24	3	4			2	4			2	3			2	3			2	3			2	3	2	3
9832740S	J01	3	4			1	2	1	2	3	3	1	1	3	3	1	1	3	3	1	1	3	3	1	2
9832740S	J02			3	4			1	2			1	2			1	2			1	2			1	3
9838248	J03	3	4			2	3	2	3	1	3	1	2	1	3			1	3			1	2	3	3
9838248	J04	3	4			2	3			1	2			1	3			1	3			1	2		
9838248	J05	4				2	3	1	3	1	3	1	3	2	3			2	3			1	2	2	3
9838248	J06			4				2	3			2	3			2	3			2	3			0	2
10203428	J07	4				2	3			1	4			2	3			2	3			1	3		
10203428	J08			4				2	3			1	3			2	3			2	3			1	3
10204696	J09	4						1	2			1	3			2	3			2	3			1	2
10204696	J10	3	4			2	3			2	3			2	3			2	3			2	3		
10204696	J11	4				2	3			2	4			2	3			2	3			2	3		
10204696	J12			2	4			1	2			0	1			2	3			2	3			1	2
10514489	J13	2	4			2	3			2	3	1	1	1	3			1	3			2	3	2	3
10514489	J14			2	4			1	2			1	2			1	3			1	3			1	3
10529151	J15	2	4			1	3			1	3	1	2	1	3			2	3			0	2		
10529151	J16	2	4			1	3			1	3			1	3			2	3			1	2		
10529151	J17	2	4			1	3			1	3			2	3			2	3			1	2		
10529151	J18			3	4	2	3			2	4			3	3			3	3			2	3		
10727106	J19	4				2	4			2	4			2	3			2	3			3	3		
10727106	J20			4		3	4					3	3			2	3			2	3			2	3
10728457	J21																								
10728457	J22	3	4			3	4			2	4			2	3			2	3			2	3		
10728457	J23	3	4			3	4			3	3			2	3			2	3			1	3		
10728457	J24			3	4			2	3			2	3			2	3			2	3			2	3
9832588	K1	2	4			2	3			1	3			2	3			2	3			2	3		
9832588	K2	3	4			2	3			1	3	2	3	2	3			2	3			2	3		
9832588	K3	3	4			2	3			1	2			2	3			2	3			3	3		
9832588	K4			4		2	3			2	3					1	2			1	2			0	3
9832740S	K5	4						2	3			1	3	3	3			3	3			3	3		
9832740S	K6	4				2	3			2	3			3	3			3	3			3	3		
10136806	K7	4				1	2			1	3			2	2			3	3			2	3		
10136806	K8	3	4			2	3	1	2	1	2	1	2	2	3	2	2	3	3	2	3	2	3	1	2
10136806	K9	4				2	3			1	2	1	2	2	3	3		3	3			2	3		
10136806	K10			4				1	2			1	2			2	3			2	3			1	2
10203428	K11	2	4			2	3			1	3			2	3			2	3			3	3		
10203428	K12	4				2	3			1	3			2	3			2	3			2	3		
10513260	K13																								
10513260	K14																								
10513260	K15	3	4			1	2			2	3			2	3			2	3			2	3	1	2
10513260	K16			2	4	2	3	0	1	3	3	1	2	2	3	1	2	2	3	1	2	2	3	1	2
10514489	K17	4				2	3			3	3			2	3			2	3			2	3	3	3

10443208	M16			3	4			1	2			1	3			2	3			2	3			1	3
10511812	M17	2	4			0	2			1	3			1	3			1	3			0	3		
10511812	M18	3	4			1	2			1	2			1	3			1	3			1	3		
10725463	M19																								
10725463	M20	4				2	3	1	1	3	4	1	2	2	3			2	3			3	3		
10725463	M21	4				3	3			3	4			2	3			2	3			3	3		
10725463	M22			3				1	2			1	2			1	3			1	3			1	3
10726179	M23	3	4			1	3			1	3			2	3			2	3			1	3		
10726179	M24	3	4			2	4			1	2			2	3			2	3			2	3		
9823371	N1	3	4											2	3			2	3			3	3	2	3
9823371	N2			3	4			2	3			2	3			2	3			2	3			2	2
9826099S	N3																								
9826099S	N4	3	4					1	2			1	1			3	3			3	3			2	2
9826099S	N5	2	4			1	2	1	2	1	2	1	2	2	2	2	3	2	2	2	3			2	2
9826099S	N6			3	4	2	3	1	2	2	3	1	2			2	3			2	3			2	3
10022186	N7	3	4			2	3			3	3			3	3			3	3			3	3		
10022186	N8															2	3							2	3
10027530	N9	3	4			1	3			2	3			2	3			2	3			1	3		
10027530	N10	1		3	4	0	3	2	3	1	2	2	2	1	3	2	3	1	3	2	3	1	3		
10027530	N11	2	4			0	3	2	3	1	2	2	2	2	3	2	3	2	3	2	3	2	3		
10027530	N12			2	3			1	2			1	2			2	2			2	2			2	3
10431981	N13	3	4			0	3			2	4	2	4	3	3			3	3			1	3		
10431981	N14			4				2	3			2	3			3	3			3	3			2	3
10433224	N15	4						1	2			2	3			2	3			2	3			1	2
10433224	N16	3	4			1	3	1	2	3	3	2	2	1	3	2	3	1	3	2	3	2	3	1	1
10433224	N17	3	4			3	4	1	1	2	3	2	2	3	3			3	3			2	3		
10433224	N18			3	4			1	1			2	3	2	3	2	3			2	3			0	3
10718773	N19	3	4			0	1			3	4			3	3			3	3						
10718773	N20			3	4			1	2			2	3			2	3			2	3			1	2
10720178	N21	3	4					2	3			3	3			2	3			2	3			2	3
10720178	N22	3	4			2	3			2	3			2	3			2	3			1	3		
10720178	N23	3	4			1	3			2	3	3	3	2	3			2	3			2	3		
10720178	N24			3	4			1	1			1	2	2	3			2	3					1	2
9823060	O1	2	4					1	3			1	2			2	3			2	3			1	3
9823060	O2	3	4			2	3	1	3	1	2	1	3	2	3	1	3	2	3	1	3	2	3	1	2
9823060	O3	4				2	3	2	3	2	3	1	2			2	3			2	3			1	2
9823060	O4			4				3	3			2	2			2	3			2	3			2	3
9823371	O5	4																							
9823371	O6	3	4			2	3	3	3	2	3	3	3	2	3	3	3	2	3	3	3			3	3
10015784	O7	4				3	3	3	3	3	3	3	3	2	3	2	3	2	3	2	3			3	3
10015784	O8	3	4			3	3			2	3			3	3			3	3			3	3		
10015784	O9	3	4			3	4			3	4			3	3			3	3			3	3		
10015784	O10			3	4			3	3			2	3			2	3			2	3			2	3
10022186	O11	3	4			3	3	3	3	2	3	2	3	3	3			3	3			3	3		
10022186	O12	3	4			3	3			3	3			3	3			3	3			3	3		
10426270	O13	3	4			2	3			1	3			1	3			1	3			1	3		

10426270	O14	2	4			1	3	1	2	1	3	1	3	1	3			1	3			1	3		
10426270	O15	2	4			1	3			1	3			1	3			1	3			1	3		
10426270	O16			3	4			3	3			2	3			3	3			3	3			1	3
10431981	O17	2	4			0	2			1	2	3	3	1	1	3	3	1	1	3	3	0	1		
10431981	O18	2	4			0	2			1	3	2	3	1	1	3	3	1	1	3	3	0	1		
10709663	O19	3	4			2	2	2	2	1	2	2	3	2	3	2	2	2	3	2	2	3	3		
10709663	O20	2	4					2	3			1	3			2	3			2	3			2	2
10709663	O21	3	4			2	3	1	2	1	3	1	3	2	3	2	3	2	3	2	3	2	3	1	2
10709663	O22			3	4			1	3			1	3			2	3			2	3			1	2
10718773	O23	3	4			1	2			2	3			3	3			3	3			2	3		
10718773	O24	3	4			1	3	1	2	2	3	1	2	3	3	2	3	3	3	2	3	2	3	1	2
9815043	P1	3	4			2	3	2	3	1	3	1	3	1	3			1	3			2	3		
9815043	P2			3	4			1	2			1	2			2	3			2	3			1	2
9818278	P3	2	3	3	4	2	3	2	3	1	3	2	2	2	3	2	3	2	3	2	3	1	3	1	2
9818278	P4	2	3	3	4	1	3	1	2	1	3	1	2	2	3	2	3	2	3	2	3	2	3	2	3
9818278	P5	3	4			2	3			1	3			3	3			3	3			2	3	1	1
9818278	P6			3	4			2	3			1	3			2	3			2	3			2	2
10003847	P7	3	4			3	4			3	3			3	3			3	3			3	3		
10003847	P8																							2	3
10006811	P9	2	4			2	3			2	3			2	3			2	3			2	2		
10006811	P10																					2	3		
10006811	P11	2	4			3	4	2	2	2	3	1	1	2	3			2	3			1	3		
10006811	P12			3	4			3	3			1	3			3	3			3	3			1	2
10400680	P13	2	4	2	4	2	3	1	2	2	3	2	2	2	3	2	3	2	3	2	3	1	3	1	3
10400680	P14			3	4			1	3			1	2			0	2			2	3	2	2		
10402495	P15	3	4			1	2			2	3			3	3			3	3			2	3		
10402495	P16	3	4			1	2	1	2	1	2	2	2	3	3			3	3			2	2		
10402495	P17	3	4			2	3			1	2			3	3			3	3			2	3		
10402495	P18			3	4			2	3			2	2			3	3			3	3				
10700693	P19	3	4			3	3			2	3			3	3			3	3			2	2		
10700693	P20			2	4	3	3	3	3	2	3	2	3	1	3	2	3	1	3	2	3	1	3	1	3
10701686	P21	2	4			3	3	3	3	2	3			2	3			2	3			2	2		
10701686	P22	3	4			3	4	3	3	3	4	3	3	2	3			2	3			2	2		
10701686	P23	3	4			3	3	3	4	2	4	3	4	2	3			2	3			2	3		
10701686	P24			3	4			2	3			1	3			2	3			2	3			2	2
9740516	Q1	1	4			1	3			0	2			0	3			0	3			0	2		
9740516	Q2	3	4			1	3			1	3			2	3			2	3			1	3		
9740516	Q3	3	4			2	3			1	3			1	3			1	3			1	3		
9740516	Q4			2	4	1	3			1	2			1	3			1	3			1	2		
9815043	Q5	2	4			2	2	2	3	2	3	2	3	3	3	3	3	3	3	3	3	1	3		
9815043	Q6	2	4			2	3			1	3			3	3			3	3			1	3		
9940301	Q7	4				1	2			3	4			1	2			3	3			3	3		
9940301	Q8	4				1	2			3	4			3	3			3	3			3	3		
9940301	Q9	4				1	2			3	4			1	2			3	3			3	3		
9940301	Q10			4				1	3			2	3			3	3			3	3			2	3
10003847	Q11	4				2	3	1	2	3	3	1	2	3	3	3	3	3	3	3	3	2	3	1	3

10003847	Q12																				3	3	1	1		
10345627	Q13	4				2	2			2	3			3	3			3	3			2	2			
10345627	Q14	3	4			2	3			3	3				2	3			2	3		2	3			
10345627	Q15	3	4			2	3			3	3			3	3			3	3			2	3			
10345627	Q16			3	4			2	3			1	3			2	3			2	3			2	2	
10400680	Q17	3	4					2	3			1	3			2	3			2	3			1	3	
10400680	Q18	2	4			1	2	2	3	0	3	1	3	0	1	2	3	0	1	2	3			2	3	
10639881	Q19	2	3			1	3			1	3	2	2	1	3	2	3	1	3	2	3	1	3	1	3	
10639881	Q20	3	4			1	3	1	3	3	4	2	3	2	3	2	3	2	3	2	3	1	3	1	3	
10639881	Q21	3	4			1	3			1	3				3	3			3	3			3	3	1	2
10639881	Q22			2	3	1	1	2				2	2			1	3			1	3			1	2	
10700693	Q23	3	4			3				3	3			3	3			3	3			1	2			
10700693	Q24	3	4			3				2	3			3	3			3	3			1	3			

CA: Prostate carcinoma; BE: benign tissue. The intensities are given as 0=no staining, 1=weak, 2=moderate, 3=strong, 4=very strong. Low=lowest staining intensity of a tissue punch. High= highest staining intensity of a tissue punch.

Supplementary table 1B: Mean staining intensities and clinical data

Tumor	VDAC1		NDUF54		SDHA		UQCRC2		MT-CO1		ATP5F1A		Age at diagnosis [years]	Age at radical prostatectomy [years]	Gleason score	Gleason pattern 1 at RPE	Gleason pattern 2 at RPE	Resection border; 0=without tumor, 1=tumor positive	Tumor stage at RPE	Prostate volume at RPE	PSA levels at diagnosis	fPSA% at diagnosis	PSA progression	Time to PSA progression
	CA	BE	CA	BE	CA	BE	CA	BE	CA	BE	CA	BE												
9740516	3.2	3.0	2.1	1.6	2.0	2.0	2.0	2.0	2.0	2.0	1.8		67	67	5	2	3	0	2b	47	8.5	14.6	unknown	0
9815043	3.2	3.5	2.3	2.2	2.2	2.0	2.7	2.8	2.7	2.8	2.2	1.5	68	69	6	3	3	0	2b	26	7.3	12.6	unknown	0
9818278	2.8	3.5	2.3	2.2	2.0	1.8	2.7	2.5	2.7	2.5	2.3	1.8	53	53	7	3	4	0	2a	24.5	2.2	10.5	no	0
9823060	3.5		2.5	2.4	2.0	1.8	2.5	2.4	2.5	2.4	2.5	1.9	57	57	5	2	3	0	2c	20	2.6	12.3	no	0
9823371	3.7	3.5	2.5	2.8	2.5	2.8	2.5	2.8	2.5	2.8	3.0	2.5	55	55	8	4	4	0	2b	25	7.4	7.6	unknown	0
9826099S	3.3	3.5	2.0	1.5	2.0	1.3	2.0	2.7	2.0	2.7		2.2	57	58	5	3	2	0	2c	25	7.9	8.7	unknown	0
9827917	3.7		2.7	1.8	2.5	1.0	2.5	2.0	2.5	1.5	3.0	2.2	69	69	6	3	3	0	3a	26	6.8	16.3	unknown	0
9828722	3.5	3.0	0.5	1.0	2.5	2.0	2.0	2.0	2.0	2.0		2.0	56	56	6	3	3	0	3a	17	3.1	4.5	noRad	0
9832436	3.7		1.3	1.5	2.2	1.5	3.0	2.0	3.0	2.0	3.0	2.0	52	52	6	3	3	0	2b	20	2.9	15.2	unknown	0
9832588	3.3		2.5		2.0	2.5	2.5	1.5	2.5	1.5	2.7	1.5	57	58	7	4	3	0	2c	50	12.4	14.9	no	0
9832740S	3.8	3.5	2.0	1.8	2.8	1.5	3.0	1.3	3.0	1.3	3.0	1.8	59	59	7	3	4	0	3a	20	2.1	16	noRad	0
9838248	3.7		2.5	2.3	1.8	2.0	2.2	2.5	2.2	2.5	1.5	2.2	54	54	6	3	3	0	2c	17	7.8	10	no	0
9839857	3.8		1.8	2.3	2.3	1.8	2.8	2.5	2.8	2.5	2.5	2.2	67	68	6	3	3	0	2c	17	4.1	13.7	no	0
9841708	3.3	3.5	2.2	1.5	2.2	1.8	2.3	1.5	2.3	1.5	3.0	2.5	72	73	7	3	4	0	3a	22	4.6	16.5	unknown	0
9842434		3.5	2.2	2.5	2.3	2.0	3.0	2.5	3.0	2.5	3.0	2.5	57	57	5	2	3	0	2b	40	6.2	13.2	no	0
9901036			2.8	2.5	3.0	3.0	3.0	2.5	3.0	2.5	2.8	2.5	52	52	6	3	3	0	2c	28	3.6	13.9	yes	3676
9901335	3.5	3.5	2.5	2.0	2.5	1.8	1.5	1.7	2.3	1.8	2.0	1.5	57	57	5	2	3	0	2b	31	8.2	11.2	no	0
9901797	3.2		2.5	2.5	2.0	2.5	2.5	2.5	2.5	2.5	2.0	3.0	55	55	6	3	3	1	2c	28.5	8.3	6.3	no	0
9902802	3.7		2.3	2.2	2.2	1.3	2.3	1.5	2.3	1.5	2.5	1.3	50	50	7	3	4	0	2c	18	8.5	3.4	unknown	0
9908111	3.5	2.5	2.8	1.5	2.3	0.8	2.0	2.0	2.5	2.3	2.0	1.5	54	54	5	3	2	0	2c	30	4.2	21.7	unknown	0
9909768	3.8	3.5	2.3	2.2	3.0	1.8	2.8		2.8		2.3	2.0	48	48	6	3	3	0	2a	22	2	9.5	no	0
9916972	3.5	3.5	3.0	2.5	2.0	2.0	2.3	2.5	2.5		2.5	2.5	49	50	5	2	3	0	2b	40	4.5	13.1	no	0
9932197	3.5	3.5	2.5	2.3	2.0	1.5	2.5	2.4	2.5	2.5	2.5	2.5	60	61	5	3	2	0	2c	n.a.	5.8	15	no	0
9935954	3.1		2.5	1.5	1.5	1.8	1.8	1.5	2.4		2.5	2.5	64	65	6	3	3	0	2a	42	2.1	17.6	unknown	0
9940301			1.5	2.0	3.5	2.5	2.0	3.0	3.0	3.0	3.0	2.5	68	68	8	3	5	0	2b	20	44.55	n.a.	yes	351
10003847	3.8		3.0	1.5	3.0	1.5	3.0	3.0	3.0	3.0	2.8	1.8	57	57	7	3	4	0	2c	24.8	8.2	12	no	0
10006811	3.0	3.5	3.0	2.5	2.5	1.5	2.5	3.0	2.5	3.0	2.2	1.5	49	49	6	3	3	0	2c	16.9	4.3	7	no	0
10015784	3.7	3.5	3.2	3.0	3.0	2.8	2.8	2.5	2.8	2.5	3.0	2.8	68	68	7	3	4	1	3a	30	5.8	11.9	no	0
10022186	3.5		2.8	3.0	2.8	2.5	3.0	2.5	3.0		3.0	2.5	52	52	7	3	4	0	2a	18	6	9	no	0
10027530	3.0	3.0	1.7	2.2	1.8	1.8	2.5	2.3	2.5	2.3	2.3	2.5	59	59	7	3	4	x	2c	27	9	9.7	no	0
10038130	3.5	3.5	2.0	1.5	1.8	2.0	2.2		2.2		1.8	2.0	62	62	5	2	3	0	2c	n.a.	5.4	12	no	0
10115487	3.5		1.7	1.3	1.5	1.3	2.5	2.5	2.5	2.5	2.3	2.3	56	56	5	2	3	0	3a	30	5.03	11.4	unknown	0
10134427	3.5		2.2	1.7	2.3	2.0	2.5	2.5	2.5	2.5	2.8	1.8	62	62	7	3	4	0	2c	n.a.	5.4	0	no	0
10136806	3.8		2.2	1.5	1.7	1.5	2.5	2.3	3.0	2.5	2.5	1.5	55	56	6	3	3	0	2a	25	2.8	15	no	0
10203428	3.7		2.5	2.5	2.2	2.0	2.5	2.5	2.5	2.5	2.5	2.0	58	58	7	4	3	0	2c	21	14.6	6.8	no	0
10204696	3.8	3.0	2.5	1.5	2.8	1.3	2.5	2.5	2.5	2.5	2.5	1.5	60	60	7	4	3	0	2c	29	2.5	14	no	0
10212172	3.5	3.5	1.3	2.5	2.0	2.5	2.0	2.5	2.0	2.5	2.0	2.0	65	65	6	3	3	0	2b	36.6	5.5	23.8	unknown	0
10213893	3.7		2.3	2.3	2.7	2.3	2.5	2.8	2.5	2.8	2.5	2.5	55	55	5	3	2	0	2c	46	3.3	12	no	0
10217220	3.5	3.5	2.5	2.5	2.2	2.0	3.0	2.0	3.0	2.0	2.5		72	72	7	3	4	1	2b	21	7.79	16.8	yes	2093
10217305	2.8	3.5	2.0	2.5	2.0	2.0	2.5		2.5			2.5	63	63	6	3	3	0	2b	28	6.28	6.1	no	0
10238998	3.0		1.5	2.0	1.5	2.0		2.2		2.2	2.0	2.5	51	52	6	3	3	0	2c	36	2.04	13.2	no	0
10239551	3.7		1.8	2.0	2.3	2.0	2.5	2.5	2.5	2.5	2.3	2.3	57	57	8	3	5	0	2a	35	3.68	12	no	0
10239624	3.3		2.7	2.5	1.8	2.0	2.3	2.5	2.3	2.5	2.0	1.5	67	68	5	2	3	0	2c	75	16.45	23.7	no	0
10310392	3.8		2.5	2.0	3.2	1.5	2.7	3.0	2.7	3.0	2.5	2.0	56	57	7	3	4	1	2c	30	1.85	15.1	no	0
10311955	3.5	2.5	2.4	2.5	2.9	2.5	3.0	2.5	3.0	2.5	2.5	2.0	61	61	7	3	4	1	2b	26	5.16	8.7	no	0
10325091	3.5		2.2	2.5	2.8	2.0	2.3	2.8	2.5	2.5	3.0	2.5	58	59	8	3	5	0	3a	24	2.31	15.6	no	0
10338726	3.5	3.5	1.5	2.3	2.5	1.8	2.3	2.5	1.9	2.2	2.0	2.3	56	56	6	3	3	0	2c	23	3.19	12.5	no	0
10343434	3.5	3.5	2.5	2.3	2.7	2.3	2.7	2.5	2.5	2.3	2.5	1.5	55	55	7	3	4	0	2c	35	3.15	12.1	unknown	0
10345627	3.7	3.5	2.3	2.5	2.8	2.0	3.0	2.5	3.0	2.5	2.3	2.0	52	52	5	3	2	0	2a	33	4.9	13	no	0
10400680	3.2	3.3	2.0	2.1	2.0	1.9	1.5	2.0	1.5	2.5	2.0	2.2	61	61	5	3	2	0	2c	80	9.24	17.2	no	0
10402495	3.5	3.5	1.8	2.0	1.8	2.0	3.0	3.0	3.0	3.0	2.3		60	61	6	3	3	1	2c	50	10.78	7.1	no	0
10426270	3.2	3.5	2.2	2.3	2.0	2.3		3.0		3.0		2.0	64	65	8	3	5	0	2c	30	7.61	11	no	0
10431981	3.2		1.2	2.5	2.2	2.8	1.7	3.0	1.7	3.0	1.0	2.5	58	58	8	3	5	0	2c	24	4.63	6.5	no	0
10433224	3.7	3.5	2.8	1.3	2.8	2.3	2.8	2.5	2.8	2.5	2.5	1.3	59	59	6	3	3	0	2a	28	4.21	12.1	no	0
10443208	3.5	3.5		1.3		1.8		2.8		2.8		2.3	58	59	6	3	3	0	2c	60	6.44	11.3	unknown	0

10511812	3,5		1,8	2,0	1,8	2,5	3,0	2,0	3,0	2,0	3,0	2,0	70	71	9	5	4	0	3a	30	8,23	17,7	yes	435
10512852	3,1	3,5	2,5	2,0	2,7	2,2	2,3	2,0	2,3	2,0	2,3	2,0	56	56	7	4	3	1	2c	30	6,66	15,5	yes	1319
10513260	3,5	3,0	2,0	0,5	2,8	1,5	2,5	1,5	2,5	1,5	2,5	1,5	65	66	8	5	3	0	2c	20	4,63	8,2	no	0
10514489	3,7	3,0	2,5	2,0	2,7	1,7	2,3	2,0	2,3	2,0	2,5	2,6	61	61	8	3	5	0	2c	34	2,52	10,6	no	0
10529151	3,0	3,5	2,1		2,3	1,5	2,4		2,6		1,6		56	56	7	3	4	0	2b	33	29,2	8	unknown	0
10601619	3,7		2,8	2,3	2,3	2,5	2,5	2,5	2,5	2,5	2,5	2,3	67	67	7	3	4	1	2c	30	7,11	10,1	no	0
10604940	3,8	3,5	3,0		2,9		3,0	2,5	3,0	2,5	2,8	2,0	71	71	7	3	4	0	2c	62	6,19	15,5	no	0
10606082	3,7		2,7	2,8	1,7	2,5	2,5	2,5	2,5	2,5	2,5	1,8	57	57	8	3	5	1	2c	30	6,28	12	no	0
10607452	3,3	3,5	2,5	2,5	1,7	1,5		2,0		2,0		2,0	64	64	6	3	3	0	2c	35	4,27	15	no	0
10613128			3,7	2,5	3,5	2,0	2,5	2,5	2,5	2,5	2,8	2,5	62	62	9	4	5	1	2c	42	3,46	28,3	yes	1087
10622130	3,7	3,0	2,7	2,2	2,0	2,5	2,8	2,5	2,8	2,5	2,3	2,0	59	60	5	3	2	0	2c	28,5	4,84	13	no	0
10624826	3,7	3,5	3,3	2,0	1,5	1,5	2,5	2,5	2,5	2,5	2,5	1,5	67	67	9	4	5	0	2c	30	9,1	8	yes	894
10625132	3,8	3,5	2,8	2,7	2,5	2,3	2,5	2,5	2,5	2,5	2,5	2,5	67	67	5	3	2	0	2c	40	9,03	14,5	no	0
10627970	2,8	3,0	3,3	2,5	2,8	1,8	2,5	2,5	2,5	2,5	2,5	1,8	70	70	7	3	4	0	2c	30	5,8	5,8	unknown	0
10630526	3,5	3,5	2,8	2,8	3,3	2,8	2,5		2,5		2,5	2,5	66	66	7	3	4	0	3b	40	16,9	0	unknown	0
10631521	3,3	3,5	2,8	2,5	2,5	2,3	2,5	2,8	2,5	2,5	2,5	2,5	60	61	6	3	3	0	2c	30	3,5	15,3	no	0
10637255	3,5	2,5	2,7	2,5	1,8	1,5	2,6	2,5	2,5	2,5	2,5	2,5	63	63	7	3	4	1	2c	42	3,77	17	yes	970
10639881	3,2	2,5	1,8	2,3	2,5	2,2	2,5	2,3	2,5	2,3	2,3	1,8	64	64	6	3	3	0	2c	41	3,64	14	unknown	0
10700693	3,5	3,0	3,0	3,0	2,6	2,5	2,8	2,5	2,8	2,5	1,9	2,0	57	57	5	3	2	0	2c	30	4,88	11,6	no	0
10701686	3,3	3,5	3,2	3,0	3,0	2,8	2,5	2,5	2,5	2,5	2,2	2,0	67	67	9	4	5	0	3a	20	6,91	6,1	no	0
10709663	3,3	3,5	2,3	2,0	1,8	2,1	2,5	2,4	2,5	2,4	2,8	1,7	65	65	9	4	5	0	3a	38,9	2,65	17,1	no	0
10718773	3,5	3,5	1,3	1,5	2,8	2,0	3,0	2,5	3,0	2,5	2,5	1,5	66	67	7	4	3	0	3a	25	6,1	20,1	yes	1261
10720178	3,5	3,5	2,3	1,8	2,5	2,5	2,5	2,5	2,5	2,5	2,3	2,0	59	60	7	3	4	0	2c	28	3,21	8,1	no	0
10725463			2,8	1,3	3,5	1,5	2,5	2,0	2,5	2,0	3,0	2,0	70	70	5	3	2	0	2a	30	3,18	11,2	no	0
10726179	3,5	3,5	2,8		2,2		2,5	2,5	2,6	2,5	2,3		51	52	9	5	4	1	3b	30	15,2	12	yes	153
10726359	3,5	3,5	2,8	3,2	2,5	2,5	2,2	2,5	2,2	2,5	2,2	2,3	57	57	7	3	4	1	2c	47	9,85	7,6	yes	513
10726906	3,8	3,5	2,0	1,8	2,8	1,8	2,0	2,4	1,0	2,5	3,0	1,9	67	68	5	3	2	0	2c	63	7,27	39,9	no	0
10727106	3,7		2,9		2,3	3,0	2,8	2,5	2,2	2,5	2,2	2,5	65	66	9	5	4	1	3b	80	8,6	0	yes	63
10728457	3,5	3,5	3,5	2,5	3,0	2,5	2,5	2,5	2,5	2,5	2,3	2,5	67	68	7	3	4	0	3a	30	5,52	13	no	0
10729632	3,8	3,5	3,5	1,0	2,8	1,5	2,8	2,0	2,8	2,0	3,0	0,5	64	65	7	3	4	1	2c	30	5,63	15,1	no	0
10729892	3,7	3,5	2,8	3,3	2,5	2,0	2,5	2,5	2,5	2,5	2,4	1,8	69	69	7	4	3	1	3a	30	3,39	12	yes	414
10732505	3,5	3,5	3,2	3,0	2,5	2,0	2,3	2,5	2,3	2,5	2,5	0,5	62	63	7	3	4	1	2c	n.a.	7,24	0	unknown	0
10734364	3,5	3,5	2,3	1,8	3,5	2,8	2,6	1,5	2,6	1,5	3,0	2,0	60	60	7	3	4	1	3a	25	6,45	9,9	unknown	0
10736608	3,5	3,0	2,3	1,8	2,8	2,0	2,3	2,5	2,3	2,5	2,3	2,0	65	65	7	3	4	0	3a	35	7,9	0	unknown	0
10811752	3,5	3,0	3,2	2,5	3,0	1,5	2,5	2,0	2,5	2,0	2,5	2,0	67	68	8	4	4	1	3b	50	20,75	10,46	noMed	0
10812983	3,8		3,2	3,0	2,5	3,0	2,5	2,5	2,5	2,5	2,5	2,0	67	67	9	5	4	0	3b	28	5,9	15	no	0
10817500	3,7	3,5	3,3	3,3	3,3	2,5	2,5	2,8	2,2	2,3	2,8	2,5	72	72	9	4	5	1	3b	40	18,09	8,96	unknown	0
10821594	3,5		2,7	2,5	2,8	0,8	2,0	2,0	2,0	2,0	2,5	2,0	50	51	9	5	4	0	2c	25	6,9	5,22	unknown	0
10904082	3,2	2,5	2,3	2,7	3,5	2,0	2,5	2,5	2,5	2,5	2,5	2,5	59	59	8	3	5	0	2c	50	4,4	10	unknown	0

Mean staining intensities of tumors (CA) and benign tissue (BE). n.a. = not available; noRAD = no PSA progression, patient received immediately after the radical prostatectomy a radiation therapy. It was indicated when the tumor had a high Gleason score and high risk of progression. noMED = no PSA Progression, same as noRAD with drug therapy (often short androgen withdrawal); RPE = radical prostatectomy; PSA = prostate specific antigen; fPSA% = percent free PSA compared to total PSA.

Supplementary table 2: Comparison of the expression of the OXPPOS subunits and VDAC1 in benign prostate hyperplasia and carcinomas in different Gleason scores

VDAC1							
	Hyperplasia			Carcinoma			
	mean	SEM	n	mean	SEM	p value	n
Gleason score 5	3.307	0.084	14	3.512	0.045	0.0316	17
Gleason score 6	3.385	0.083	13	3.419	0.065	0.7467	21
Gleason score 7	3.333	0.065	24	3.488	0.050	0.0605	32
Gleason score 8	3.083	0.154	6	3.490	0.069	0.0153	10
Gleason score 9	3.500	0.000	5	3.556	0.060	0.5132	9
NDUFS4							
Gleason score 5	2.106	0.121	18	2.416	0.089	0.044	19
Gleason score 6	2.045	0.103	22	2.114	0.140	0.6921	21
Gleason score 7	2.221	0.108	29	2.572	0.086	0.0126	32
Gleason score 8	2.236	0.197	11	2.191	0.169	0.8624	11
Gleason score 9	2.538	0.183	8	2.920	0.175	0.1535	10
SDHA							
Gleason score 5	1.850	0.104	18	2.247	0.113	0.0145	19
Gleason score 6	1.945	0.091	22	2.214	0.099	0.0522	21
Gleason score 7	2.039	0.083	31	2.597	0.075	<0.0001	32
Gleason score 8	2.145	0.142	11	2.636	0.173	0.0403	11
Gleason score 9	2.244	0.244	9	2.470	0.213	0.4940	10
UQCRC2							
Gleason score 5	2.376	0.069	17	2.337	0.099	0.7498	19
Gleason score 6	2.410	0.086	20	2.521	0.080	0.3494	19
Gleason score 7	2.303	0.080	30	2.609	0.045	0.0012	32
Gleason score 8	2.509	0.149	11	2.330	0.087	0.3237	10
Gleason score 9	2.420	0.077	10	2.530	0.080	0.3365	10
MT-CO1							
Gleason score 5	2.438	0.060	16	2.363	0.111	0.5811	19
Gleason score 6	2.411	0.085	19	2.558	0.080	0.2170	19
Gleason score 7	2.282	0.085	28	2.606	0.044	0.0009	32
Gleason score 8	2.482	0.146	11	2.450	0.100	0.8619	10
Gleason score 9	2.370	0.065	10	2.450	0.086	0.4676	10
ATP5F1A							
Gleason score 5	2.083	0.082	18	2.328	0.094	0.0578	18
Gleason score 6	2.110	0.092	21	2.339	0.089	0.0844	18
Gleason score 7	1.900	0.096	30	2.550	0.054	<0.0001	32
Gleason score 8	2.245	0.110	11	2.480	0.184	0.2766	10
Gleason score 9	2.078	0.120	9	2.560	0.088	0.0044	10

The mean \pm SEM of the staining intensities, the p values and the number of the analyzed samples (n) is given.