Supplementary Table 4: High confidence somatic nonsynonymous mutations identified by target gene sequence

Sample	*Location*	*Gene*	*Variant classification*	*Reference allele*	*Variant allele*	*AA change*	*Filtered coverage*	*Variant allele frequency*	*RefSeq*	*dbSNP ID*	*COSMIC ID*
PR101	chrX:70360666	MED12	Stop_Gained	C	T	p.Q2076*	52	0.077	NM_005120.2		
PR101	chr5:112162851	APC	Non_Synonymous_Coding	G	A	p.M485I	5924	0.469	NM_001127510.2		
PR102	chr3:178922301	PIK3CA	Non_Synonymous_Coding	G	A	p.R357Q	3977	0.137	NM_006218.2		COSM276752
PR103	chr12:49446101	KMT2D	Codon_Change_Plus_Coding	TTCCTCAGGTGGTGGGGACAGGGGTGAC	T	p.ESPLSPPPEE446E	2846	0.223	NM_003482.3		
PR103	chr12:49432245	KMT2D	Non_Synonymous_Coding	T	C	p.N2965S	6929	0.489	NM_003482.3		
PR103	chr14:95916416	SYNE3	Non_Synonymous_Coding	C	T	p.R434H	2238	0.492	NM_152592.3	rs183604014	
PR104	chr7:91731945	AKAP9	Non_Synonymous_Coding	G	A	p.R3712Q	4052	0.456	NM_005751.4	rs186148498	
PR104	chr17:37673806	CDK12	Non_Synonymous_Coding	C	T	p.S987F	8795	0.479	NM_016507.2	rs201661022	
PR105	chr12:49446101	KMT2D	Codon_Change_Plus_Coding	TTCCTCAGGTGGTGGGGACAGGGGTGAC	T	p.ESPLSPPPEE446E	5408	0.224	NM_003482.3		
PR105	chr16:72828867	ZFHX3	Non_Synonymous_Coding	T	C	p.M2572V	4624	0.51	NM_006885.3	rs147672861	
PR105	chrX:70360579	MED12	Non_Synonymous_Coding	A	G	p.I2047V	548	0.969	NM_005120.2		
PR106	chr12:57865558	GLI1	Non_Synonymous_Coding	G	T	p.G1012V	312	0.417	NM_005269.2	rs2229300	
PR106	chr16:72984669	ZFHX3	Non_Synonymous_Coding	G	A	p.S972L	942	0.499	NM_006885.3	rs77124117	
PR106	chr19:5131419	KDM4B	Non_Synonymous_Coding	G	A	p.A550T	1370	0.503	NM_015015.2		
PR107	chr12:49421002	KMT2D	Non_Synonymous_Coding	G	A	p.P4916L	110	0.073	NM_003482.3		
PR107	chr15:23019819	NIPA2	Non_Synonymous_Coding	C	G	p.W59C	34	0.118	NM_030922.6		
PR107	chr12:49446101	KMT2D	Codon_Change_Plus_Coding	TTCCTCAGGTGGTGGGGACAGGGGTGAC	T	p.ESPLSPPPEE446E	4141	0.205	NM_003482.3		
PR107	chr3:38888862	SCN11A	Non_Synonymous_Coding	A	G	p.C1567R	4641	0.467	NM_014139.2	rs201595463	
PR108	chr7:91715706	AKAP9	Stop_Gained	T	A	p.C3063*	420	0.043	NM_005751.4		
PR108	chr10:89653841	PTEN	Non_Synonymous_Coding	A	G	p.R47G	91	0.077	NM_000314.4		COSM28887
PR108	chr12:49446101	KMT2D	Codon_Change_Plus_Coding	TTCCTCAGGTGGTGGGGACAGGGGTGAC	T	p.ESPLSPPPEE446E	4216	0.228	NM_003482.3		
PR108	chr7:91731945	AKAP9	Non_Synonymous_Coding	G	A	p.R3712Q	2572	0.478	NM_005751.4	rs186148498	
PR108	chr12:57865558	GLI1	Non_Synonymous_Coding	G	T	p.G1012V	365	0.499	NM_005269.2	rs2229300	
PR108	chr7:91646406	AKAP9	Non_Synonymous_Coding	G	A	p.R1276Q	2288	0.505	NM_005751.4	rs146797353	
PR108	chr8:71037059	NCOA2	Non_Synonymous_Coding	T	A	p.T1320S	1423	0.515	NM_006540.2		
PR108	chr16:72831357	ZFHX3	Coding_Deletion	CTTGTTG	C	p.QQ1740-	2233	0.563	NM_006885.3		COSM1731926
PR109	chr12:49446101	KMT2D	Codon_Change_Plus_Coding	TTCCTCAGGTGGTGGGGACAGGGGTGAC	T	p.ESPLSPPPEE446E	5095	0.242	NM_003482.3		
PR109	chr16:72829385	ZFHX3	Non_Synonymous_Coding	T	C	p.N2399S	5581	0.467	NM_006885.3		
PR110	chr12:49421003	KMT2D	Non_Synonymous_Coding	G	A	p.P4916S	148	0.061	NM_003482.3		
PR110	chr7:91682269	AKAP9	Non_Synonymous_Coding	T	A	p.S1866R	113	0.071	NM_005751.4		
PR110	chr16:72828408	ZFHX3	Non_Synonymous_Coding	C	A	p.A2725S	5104	0.073	NM_006885.3		
PR110	chr17:37619359	CDK12	Non_Synonymous_Coding	T	A	p.S345R	32	0.094	NM_016507.2		
PR110	chr17:47696426	SPOP	Non_Synonymous_Coding	A	C	p.F133V	3470	0.223	NM_001007230.1		COSM219965
PR110	chr12:49446101	KMT2D	Codon_Change_Plus_Coding	TTCCTCAGGTGGTGGGGACAGGGGTGAC	T	p.ESPLSPPPEE446E	3688	0.368	NM_003482.3		
PR110	chr7:91712512	AKAP9	Non_Synonymous_Coding	A	G	p.Q2730R	4012	0.44	NM_005751.4	rs80191629	
PR110	chr5:112174665	APC	Non_Synonymous_Coding	T	C	p.V1125A	2958	0.494	NM_001127510.2	rs377278397	
PR110	chr10:89711909	PTEN	Non_Synonymous_Coding	A	G	p.Y176C	1004	0.536	NM_000314.4		
PR110	chr2:138000044	THSD7B	Non_Synonymous_Coding	G	A	p.R692Q	3741	0.985	NM_001080427.1	rs76693568	COSM148945
PR111	chr17:7578427	TP53	Non_Synonymous_Coding	T	G	p.H168P	4091	0.058	NM_000546.5		COSM44808
PR111	chr12:49446101	KMT2D	Codon_Change_Plus_Coding	TTCCTCAGGTGGTGGGGACAGGGGTGAC	T	p.ESPLSPPPEE446E	3900	0.255	NM_003482.3		
PR111	chr14:95916404	SYNE3	Non_Synonymous_Coding	G	A	p.A438V	3236	0.5	NM_152592.3	rs376830751	COSM198717
PR111	chr12:49444996	KMT2D	Frame_shift	A	AG	p.-823?	93	0.677	NM_003482.3		

Contd...

Supplementary Table 4: Contd...

Sample	*Location*	*Gene*	*Variant classification*	*Reference allele*	*Variant allele*	*AA change*	*Filtered coverage*	*Variant allele frequency*	*RefSeq*	*dbSNP ID*	*COSMIC ID*
PR111	chrX:66937337	AR	Non_Synonymous_Coding	G	A	p.V731M	2059	0.997	NM_000044.3	rs137852571	COSM1468985
PR112	chr17:47696425	SPOP	Non_Synonymous_Coding	A	C	p.F133C	2480	0.189	NM_001007230.1		COSM242645
PR112	chr12:57865558	GLI1	Non_Synonymous_Coding	G	T	p.G1012V	137	0.263	NM_005269.2	rs2229300	
PR112	chr12:49446101	KMT2D	Codon_Change_Plus_Coding	TTCCTCAGGTGGTGGGGACAGGGGTGAC	T	p.ESPLSPPPEE446E	3359	0.286	NM_003482.3		
PR112	chr16:72832153	ZFHX3	Non_Synonymous_Coding	C	T	p.M1476I	1266	0.509	NM_006885.3	rs200133878	
PR113	chr17:37687207	CDK12	Non_Synonymous_Coding	G	C	p.V1371L	272	0.04	NM_016507.2		
PR113	chr12:57864588	GLI1	Non_Synonymous_Coding	C	T	p.P689S	178	0.067	NM_005269.2		
PR113	chr16:72828408	ZFHX3	Non_Synonymous_Coding	C	A	p.A2725S	5110	0.068	NM_006885.3		
PR113	chr12:49446101	KMT2D	Codon_Change_Plus_Coding	TTCCTCAGGTGGTGGGGACAGGGGTGAC	T	p.ESPLSPPPEE446E	10 048	0.241	NM_003482.3		
PR113	chr12:49445021	KMT2D	Frame_shift	C	CG, CGG	p.-815?	173	0.422	NM_003482.3		
PR114	chr2:137988662	THSD7B	Non_Synonymous_Coding	G	T	p.R560M	124	0.04	NM_001080427.1		
PR114	chr3:73433708	PDZRN3	Non_Synonymous_Coding	G	A	p.P670L	261	0.05	NM_015009.1		
PR114	chr7:91739463	AKAP9	Non_Synonymous_Coding	T	C	p.M3905T	4221	0.589	NM_005751.4	rs77447750	
PR115	chr14:95932477	SYNE3	Non_Synonymous_Coding	T	C	p.I140V	7018	0.496	NM_152592.3		
PR115	chr12:49424475	KMT2D	Non_Synonymous_Coding	C	T	p.C4583Y	3132	0.522	NM_003482.3		
PR201	chr19:5144388	KDM4B	Non_Synonymous_Coding	T	C	p.S956P	9471	0.031	NM_015015.2		
PR201	chr17:37619118	CDK12	Non_Synonymous_Coding	G	T	p.S265I	75	0.04	NM_016507.2		
PR201	chr3:100467047	TFG	Non_Synonymous_Coding	G	T	p.G292V	197	0.041	NM_006070.5		
PR201	chr2:138400097	THSD7B	Non_Synonymous_Coding	A	C	p.K1251Q	95	0.042	NM_001080427.1		
PR201	chr12:56428856	IKZF4	Non_Synonymous_Coding	A	G	p.K500R	88	0.045	NM_022465.3		
PR201	chr7:91714912	AKAP9	Non_Synonymous_Coding	C	T	p.P2979L	2084	0.047	NM_005751.4		
PR201	chr16:72821079	ZFHX3	Non_Synonymous_Coding	T	G	p.D3699A	1342	0.047	NM_006885.3		
PR201	chr5:112173687	APC	Non_Synonymous_Coding	A	C	p.Y799S	105	0.048	NM_001127510.2		
PR201	chr2:138163363	THSD7B	Non_Synonymous_Coding	G	T	p.R863L	348	0.052	NM_001080427.1		
PR201	chr17:37687207	CDK12	Non_Synonymous_Coding	G	T	p.V1371L	111	0.054	NM_016507.2		
PR201	chr19:50549280	ZNF473	Non_Synonymous_Coding	G	A	p.G527D	3327	0.057	NM_001006656.1		
PR201	chr3:100467073	TFG	Non_Synonymous_Coding	G	C	p.A301P	198	0.061	NM_006070.5		
PR201	chr5:112111327	APC	Non_Synonymous_Coding	T	A	p.S142T	63	0.063	NM_001127510.2		
PR201	chr12:49421002	KMT2D	Non_Synonymous_Coding	G	A	p.P4916L	126	0.063	NM_003482.3		
PR201	chr12:49425616	KMT2D	Non_Synonymous_Coding	G	C	p.A4291G	157	0.064	NM_003482.3		
PR201	chr19:5071040	KDM4B	Non_Synonymous_Coding	C	T	p.H216Y	240	0.071	NM_015015.2		
PR201	chrX:66766249	AR	Non_Synonymous_Coding	G	A	p.G421R	84	0.071	NM_000044.3		
PR201	chr4:87217	ZNF595	Non_Synonymous_Coding	C	A	p.T607N	626	0.073	NM_182524.2		
PR201	chr12:56428449	IKZF4	Non_Synonymous_Coding	C	G	p.S364R	112	0.08	NM_022465.3		
PR201	chr3:73437120	PDZRN3	Non_Synonymous_Coding	T	C	p.Q506R	285	0.084	NM_015009.1		
PR201	chr16:72828408	ZFHX3	Non_Synonymous_Coding	C	A	p.A2725S	2338	0.147	NM_006885.3		
PR201	chr4:86822	ZNF595	Coding_Deletion	CGAGAAACCCTACAAATGTGAAGAATGT GGCAAAGCTTTCATATGGTCCGCAAGC CTGAATGAACATAAGAATATTCATACTGGA	C	p.EKPYKCEECGKAF IWSASLNEHKNIH TG476-	212	0.302	NM_182524.2		
PR201	chr17:37673806	CDK12	Non_Synonymous_Coding	C	T	p.S987F	10 151	0.506	NM_016507.2	rs201661022	
PR201	chr4:87313	ZNF595	Frame_shift	G	GA	p.-639?	184	0.783	NM_182524.2	rs60154095	
PR201	chr7:91714911	AKAP9	Non_Synonymous_Coding	C	T	p.P2979S	2076	0.947	NM_005751.4	rs1063242	
PR201	chrX:66765516	AR	Non_Synonymous_Coding	C	A	p.S176R	1550	0.995	NM_000044.3		

Contd...

Supplementary Table 4: Contd...

Sample	*Location*	*Gene*	*Variant classification*	*Reference allele*	*Variant allele*	*AA change*	*Filtered coverage*	*Variant allele frequency*	*RefSeq*	*dbSNP ID*	*COSMIC ID*
PR202	chr19:5150397	KDM4B	Non_Synonymous_Coding	C	T	p.T1017M	161	0.043	NM_015015.2		
PR202	chr12:49444986	KMT2D	Non_Synonymous_Coding	T	C	p.Q827R	27	0.074	NM_003482.3		
PR202	chr5:112175043	APC	Non_Synonymous_Coding	T	C	p.V1251A	107	0.075	NM_001127510.2		
PR202	chrX:70339696	MED12	Non_Synonymous_Coding	G	T	p.G122V	53	0.075	NM_005120.2		
PR202	chr16:72821887	ZFHX3	Frame_shift	C	CG	p.-3429?	1432	0.214	NM_006885.3		
PR202	chr7:91646406	AKAP9	Non_Synonymous_Coding	G	A	p.R1276Q	1608	0.631	NM_005751.4	rs146797353	
PR202	chr4:87313	ZNF595	Frame_shift	G	GA	p.-639?	142	0.965	NM_182524.2	rs60154095	
PR203	chr16:72991626	ZFHX3	Non_Synonymous_Coding	C	T	p.E807K	216	0.042	NM_006885.3		
PR203	chr15:23006222	NIPA2	Stop_Lost	T	A	p.*361L	836	0.045	NM_030922.6		
PR203	chr12:49445310	KMT2D	Non_Synonymous_Coding	G	A	p.P719L	59	0.085	NM_003482.3	rs185660524	
PR203	chr5:112173644	APC	Non_Synonymous_Coding	C	G	p.H785D	1781	0.127	NM_001127510.2		
PR203	chr17:47696425	SPOP	Non_Synonymous_Coding	A	G	p.F133S	1070	0.133	NM_001007230.1		COSM247573
PR203	chr9:21974694	CDKN2A	Non_Synonymous_Coding	C	G	p.G45R	2296	0.501	NM_001195132.1		
PR203	chr16:72831357	ZFHX3	Coding_Deletion	CTTGTTG	C	p.QQ1740-	1886	0.512	NM_006885.3		COSM1731926
PR203	chr7:91690697	AKAP9	Non_Synonymous_Coding	G	A	p.A1909T	2874	0.558	NM_005751.4	rs200844952	
PR203	chr4:87313	ZNF595	Frame_shift	G	GA	p.-639?	110	0.936	NM_182524.2	rs60154095	
PR203	chr7:91714911	AKAP9	Non_Synonymous_Coding	C	T	p.P2979S	1553	0.958	NM_005751.4	rs1063242	
PR205	chr19:50549280	ZNF473	Non_Synonymous_Coding	G	A	p.G527D	14 424	0.041	NM_001006656.1		
PR205	chr12:49427950	KMT2D	Non_Synonymous_Coding	C	T	p.R3547H	6749	0.045	NM_003482.3		COSM240685
PR205	chr17:37687204	CDK12	Non_Synonymous_Coding	C	A	p.L1370M	437	0.046	NM_016507.2		
PR205	chr2:138400100	THSD7B	Non_Synonymous_Coding	G	C	p.E1252Q	312	0.048	NM_001080427.1		
PR205	chr5:112176407	APC	Non_Synonymous_Coding	T	A	p.S1706T	548	0.049	NM_001127510.2		
PR205	chr12:49424422	KMT2D	Non_Synonymous_Coding	G	T	p.P4601T	201	0.05	NM_003482.3		
PR205	chr3:178942538	PIK3CA	Non_Synonymous_Coding	A	G	p.N782S	791	0.053	NM_006218.2		
PR205	chr12:56428447	IKZF4	Non_Synonymous_Coding	A	T	p.S364C	431	0.053	NM_022465.3		
PR205	chr12:56428445	IKZF4	Non_Synonymous_Coding	A	T	p.H363L	404	0.054	NM_022465.3		
PR205	chr19:5119672	KDM4B	Non_Synonymous_Coding	G	A	p.R375Q	403	0.062	NM_015015.2		
PR205	chr16:72991377	ZFHX3	Non_Synonymous_Coding	C	T	p.G890R	496	0.067	NM_006885.3		
PR205	chr12:49444990	KMT2D	Non_Synonymous_Coding	G	T	p.P826T	292	0.068	NM_003482.3		
PR205	chr2:138400097	THSD7B	Non_Synonymous_Coding	A	C	p.K1251Q	318	0.097	NM_001080427.1		
PR205	chr16:72828408	ZFHX3	Non_Synonymous_Coding	C	A	p.A2725S	8996	0.105	NM_006885.3		
PR205	chr16:72828405	ZFHX3	Frame_shift	GA	G	p.-2725	8808	0.107	NM_006885.3		
PR205	chr12:49445334	KMT2D	Non_Synonymous_Coding	G	A	p.P711L	44	0.136	NM_003482.3		
PR205	chr17:7577147	TP53	Non_Synonymous_Coding	A	T	p.L264Q	98	0.184	NM_000546.5		
PR205	chr7:91682269	AKAP9	Non_Synonymous_Coding	T	A	p.S1866R	83	0.193	NM_005751.4		
PR205	chr17:37627784	CDK12	Non_Synonymous_Coding	C	G	p.P567A	92	0.196	NM_016507.2		
PR205	chr12:49446101	KMT2D	Codon_Change_Plus_Coding	TTCCTCAGGTGGTGGGGACAGGGGTGAC	T	p.ESPLSPPPEE446E	7007	0.463	NM_003482.3		
PR206	chr8:71078935	NCOA2	Non_Synonymous_Coding	T	C	p.N199S	4974	0.035	NM_006540.2		
PR206	chr3:178928073	PIK3CA	Non_Synonymous_Coding	G	A	p.G451R	4034	0.037	NM_006218.2		
PR206	chr14:95932477	SYNE3	Non_Synonymous_Coding	T	C	p.I140V	8892	0.041	NM_152592.3		
PR206	chr3:178916833	PIK3CA	Non_Synonymous_Coding	A	G	p.T74A	7255	0.106	NM_006218.2		
PR206	chr17:37649079	CDK12	Coding_Deletion	CATT	C	p.I729-	13 486	0.22	NM_016507.2		

Contd...

Supplementary Table 4: Contd...

Sample	*Location*	*Gene*	*Variant classification*	*Reference allele*	*Variant allele*	*AA change*	*Filtered coverage*	*Variant allele frequency*	*RefSeq*	*dbSNP ID*	*COSMIC ID*
PR206	chr12:49446101	KMT2D	Codon_Change_Plus_Coding	TTCCTCAGGTGGTGGGGACAGGGGTGAC	T	p.ESPLSPPPEE446E	5541	0.243	NM_003482.3		
PR206	chr7:107823354	NRCAM	Non_Synonymous_Coding	C	T	p.G772D	5502	0.486	NM_001037132.2		
PR207	chr3:38888625	SCN11A	Non_Synonymous_Coding	G	T	p.L1646I	6475	0.127	NM_014139.2		
PR208	chr12:49445341	KMT2D	Non_Synonymous_Coding	G	A	p.P709S	100	0.04	NM_003482.3		
PR208	chr12:57865549	GLI1	Non_Synonymous_Coding	C	T	p.P1009L	81	0.074	NM_005269.2		
PR208	chr16:72828408	ZFHX3	Non_Synonymous_Coding	C	A	p.A2725S	8350	0.082	NM_006885.3		
PR208	chr12:49446101	KMT2D	Codon_Change_Plus_Coding	TTCCTCAGGTGGTGGGGACAGGGGTGAC	T	p.ESPLSPPPEE446E	7658	0.303	NM_003482.3		
PR208	chr3:73433697	PDZRN3	Non_Synonymous_Coding	C	G	p.G674R	390	0.454	NM_015009.1		
PR210	chr16:72828408	ZFHX3	Non_Synonymous_Coding	C	A	p.A2725S	9425	0.06	NM_006885.3		
PR210	chr19:5144410	KDM4B	Non_Synonymous_Coding	C	G	p.P963R	105	0.105	NM_015015.2		
PR210	chr16:72821887	ZFHX3	Frame_shift	C	CG	p.-3429?	3674	0.201	NM_006885.3		
PR210	chr12:49446101	KMT2D	Codon_Change_Plus_Coding	TTCCTCAGGTGGTGGGGACAGGGGTGAC	T	p.ESPLSPPPEE446E	7636	0.323	NM_003482.3		
PR210	chr14:95942049	SYNE3	Non_Synonymous_Coding	C	T	p.R37H	7754	0.401	NM_152592.3		
PR210	chr14:95932477	SYNE3	Non_Synonymous_Coding	T	C	p.I140V	10 415	0.499	NM_152592.3		
PR210	chr7:91646406	AKAP9	Non_Synonymous_Coding	G	A	p.R1276Q	2452	0.529	NM_005751.4	rs146797353	
PR210	chr8:71078935	NCOA2	Non_Synonymous_Coding	T	C	p.N199S	4847	0.56	NM_006540.2		
PR210	chr16:72991697	ZFHX3	Codon_Change_Plus_Coding	GCCGCCGCCGCCGCAGCCA	G	p.VAAAAAA777A	390	0.985	NM_006885.3		
PR212	chr3:178917586	PIK3CA	Non_Synonymous_Coding	G	C	p.R154T	30	0.1	NM_006218.2		
PR212	chrX:70348499	MED12	Non_Synonymous_Coding	A	T	p.I1136F	799	0.149	NM_005120.2		
PR212	chr19:5144410	KDM4B	Non_Synonymous_Coding	C	A	p.P963H	83	0.205	NM_015015.2		
PR212	chr12:49446101	KMT2D	Codon_Change_Plus_Coding	TTCCTCAGGTGGTGGGGACAGGGGTGAC	T	p.ESPLSPPPEE446E	6707	0.211	NM_003482.3		
PR212	chr12:57865558	GLI1	Non_Synonymous_Coding	G	T	p.G1012V	168	0.357	NM_005269.2	rs2229300	
PR212	chr12:49420078	KMT2D	Non_Synonymous_Coding	C	T	p.R5224H	3045	0.5	NM_003482.3	rs3782356	
PR213	chr12:49446101	KMT2D	Codon_Change_Plus_Coding	TTCCTCAGGTGGTGGGGACAGGGGTGAC	T	p.ESPLSPPPEE446E	5577	0.203	NM_003482.3		
PR213	chrX:70349256	MED12	Non_Synonymous_Coding	T	G	p.V1223G	3524	0.442	NM_005120.2		
PR213	chr12:49420078	KMT2D	Non_Synonymous_Coding	C	T	p.R5224H	4335	0.493	NM_003482.3	rs3782356	
PR214	chr3:178917586	PIK3CA	Non_Synonymous_Coding	G	T	p.R154M	86	0.058	NM_006218.2		
PR214	chr2:138000044	THSD7B	Non_Synonymous_Coding	G	A	p.R692Q	6899	0.492	NM_001080427.1	rs76693568	COSM148945
PR215	chr16:72828408	ZFHX3	Non_Synonymous_Coding	C	A	p.A2725S	12 278	0.059	NM_006885.3		
PR215	chr7:91699374	AKAP9	Non_Synonymous_Coding	A	C	p.K2121Q	55	0.091	NM_005751.4		
PR215	chr12:57865558	GLI1	Non_Synonymous_Coding	G	T	p.G1012V	45	0.178	NM_005269.2	rs2229300	
PR215	chr12:49446101	KMT2D	Codon_Change_Plus_Coding	TTCCTCAGGTGGTGGGGACAGGGGTGAC	T	p.ESPLSPPPEE446E	8010	0.342	NM_003482.3		
PR215	chr3:38962696	SCN11A	Non_Synonymous_Coding	T	G	p.N255H	1634	0.523	NM_014139.2	rs371647806	
PR302	chr8:23540243	NKX3-1	Non_Synonymous_Coding	G	A	p.P54S	96	0.052	NM_006167.3		
PR302	chr16:72828408	ZFHX3	Non_Synonymous_Coding	C	A	p.A2725S	7963	0.061	NM_006885.3		
PR302	chr7:91682269	AKAP9	Non_Synonymous_Coding	T	A	p.S1866R	60	0.117	NM_005751.4		
PR302	chr8:71036150	NCOA2	Non_Synonymous_Coding	G	A	p.T1421M	5550	0.451	NM_006540.2		
PR302	chr3:38941459	SCN11A	Non_Synonymous_Coding	G	A	p.L650F	7862	0.483	NM_014139.2		COSM136332
PR304	chr12:57865558	GLI1	Non_Synonymous_Coding	G	T	p.G1012V	115	0.461	NM_005269.2	rs2229300	
PR305	chrX:70360666	MED12	Stop_Gained	C	T	p.Q2076*	50	0.06	NM_005120.2		
PR305	chr12:57865558	GLI1	Non_Synonymous_Coding	G	T	p.G1012V	309	0.469	NM_005269.2	rs2229300	
PR306	chr12:49444990	KMT2D	Non_Synonymous_Coding	G	C	p.P826A	106	0.057	NM_003482.3		

Contd...

Supplementary Table 4: Contd...

Sample	*Location*	*Gene*	*Variant classification*	*Reference allele*	*Variant allele*	*AA change*	*Filtered coverage*	*Variant allele frequency*	*RefSeq*	*dbSNP ID*	*COSMIC ID*
PR306	chr2:137988661	THSD7B	Non_Synonymous_Coding	A	C, G	p.R560G	32	0.094	NM_001080427.1		
PR306	chr12:57865558	GLI1	Non_Synonymous_Coding	G	T	p.G1012V	117	0.496	NM_005269.2	rs2229300	
PR307	chr12:57865558	GLI1	Non_Synonymous_Coding	G	T	p.G1012V	377	0.44	NM_005269.2	rs2229300	
PR307	chr7:91668025	AKAP9	Non_Synonymous_Coding	G	C	p.C1544S	2296	0.472	NM_005751.4		
PR307	chr7:91709065	AKAP9	Non_Synonymous_Coding	A	G	p.I2540V	1978	0.502	NM_005751.4		
PR307	chr16:72832320	ZFHX3	Non_Synonymous_Coding	G	C	p.Q1421E	7856	0.516	NM_006885.3		
PR307	chr16:72829373	ZFHX3	Non_Synonymous_Coding	G	A	p.S2403F	4584	0.517	NM_006885.3		
PR308	chr12:49425853	KMT2D	Non_Synonymous_Coding	C	T	p.R4212Q	3047	0.493	NM_003482.3		
PR309	chr2:138417295	THSD7B	Non_Synonymous_Coding	A	C	p.N1450T	2559	0.032	NM_001080427.1		
PR309	chr16:72821079	ZFHX3	Non_Synonymous_Coding	T	G	p.D3699A	3002	0.033	NM_006885.3		
PR309	chr19:50549280	ZNF473	Non_Synonymous_Coding	G	A	p.G527D	10 005	0.034	NM_001006656.1		
PR309	chr12:49431013	KMT2D	Non_Synonymous_Coding	C	G	p.V3376L	594	0.042	NM_003482.3		
PR309	chr3:178916786	PIK3CA	Non_Synonymous_Coding	T	C	p.L58P	1431	0.043	NM_006218.2		
PR309	chr3:38904766	SCN11A	Non_Synonymous_Coding	T	C	p.T1326A	2150	0.045	NM_014139.2		
PR309	chr5:112173291	APC	Non_Synonymous_Coding	A	G	p.Q667R	736	0.045	NM_001127510.2		
PR309	chr3:73450149	PDZRN3	Non_Synonymous_Coding	G	A	p.A393V	1574	0.047	NM_015009.1		COSM1425294
PR309	chr12:49436006	KMT2D	Non_Synonymous_Coding	T	C	p.E1992G	64	0.047	NM_003482.3		
PR309	chr2:138163363	THSD7B	Non_Synonymous_Coding	G	A	p.R863Q	915	0.048	NM_001080427.1		
PR309	chr16:72991476	ZFHX3	Non_Synonymous_Coding	C	T	p.A857T	1570	0.049	NM_006885.3	rs146607776	COSM1379726
PR309	chr5:112176066	APC	Non_Synonymous_Coding	A	G	p.K1592R	1204	0.052	NM_001127510.2		
PR309	chr13:48934201	RB1	Non_Synonymous_Coding	T	C	p.M219T	538	0.052	NM_000321.2		
PR309	chr13:48934204	RB1	Non_Synonymous_Coding	T	C	p.L220P	534	0.052	NM_000321.2		
PR309	chr17:37687207	CDK12	Non_Synonymous_Coding	G	C	p.V1371L	323	0.053	NM_016507.2		
PR309	chrX:70346837	MED12	Non_Synonymous_Coding	G	A	p.V902I	668	0.054	NM_005120.2		COSM1124669
PR309	chr2:138425344	THSD7B	Non_Synonymous_Coding	A	G	p.M1522V	1208	0.058	NM_001080427.1		
PR309	chr16:72828408	ZFHX3	Non_Synonymous_Coding	C	A	p.A2725S	9128	0.058	NM_006885.3		
PR309	chr5:112174845	APC	Non_Synonymous_Coding	C	T	p.T1185I	461	0.059	NM_001127510.2		
PR309	chr5:112179113	APC	Non_Synonymous_Coding	G	A	p.A2608T	494	0.059	NM_001127510.2		
PR309	chr5:112177895	APC	Non_Synonymous_Coding	A	G	p.K2202E	275	0.062	NM_001127510.2		
PR309	chr7:91631131	AKAP9	Non_Synonymous_Coding	G	A	p.E634K	699	0.062	NM_005751.4	rs368006874	
PR309	chr3:178943760	PIK3CA	Non_Synonymous_Coding	A	T	p.Q809H	302	0.063	NM_006218.2		
PR309	chr12:56428449	IKZF4	Non_Synonymous_Coding	C	G	p.S364R	560	0.066	NM_022465.3		
PR309	chrX:70347260	MED12	Non_Synonymous_Coding	T	C	p.L975P	2086	0.07	NM_005120.2		
PR309	chr7:91609645	AKAP9	Non_Synonymous_Coding	G	C	p.E117Q	113	0.08	NM_005751.4		
PR309	chr8:23540200	NKX3-1	Non_Synonymous_Coding	C	T	p.R68H	191	0.089	NM_006167.3		
PR309	chr16:72828173	ZFHX3	Non_Synonymous_Coding	G	A	p.S2803F	357	0.098	NM_006885.3		
PR309	chr17:7577147	TP53	Non_Synonymous_Coding	A	T	p.L264Q	61	0.098	NM_000546.5		
PR309	chr12:57865549	GLI1	Non_Synonymous_Coding	C	T	p.P1009L	29	0.172	NM_005269.2		
PR309	chr7:91682269	AKAP9	Non_Synonymous_Coding	T	G	p.S1866R	47	0.255	NM_005751.4		
PR309	chr12:49446101	KMT2D	Codon_Change_Plus_Coding	TTCCTCAGGTGGTGGGGACAGGGGTGAC	T	p.ESPLSPPPEE446E	8861	0.35	NM_003482.3		
PR309	chr16:72831357	ZFHX3	Coding_Deletion	CTTGTTG	C	p.QQ1740-	2881	0.431	NM_006885.3		COSM1731926
PR309	chr16:72832153	ZFHX3	Non_Synonymous_Coding	C	T	p.M1476I	1414	0.592	NM_006885.3	rs200133878	

Contd...

Supplementary Table 4: Contd...

Sample	*Location*	*Gene*	*Variant classification*	*Reference allele*	*Variant allele*	*AA change*	*Filtered coverage*	*Variant allele frequency*	*RefSeq*	*dbSNP ID*	*COSMIC ID*
PR310	chr2:137988662	THSD7B	Non_Synonymous_Coding	G	C	p.R560T	49	0.102	NM_001080427.1		
PR311	chr16:72993731	ZFHX3	Non_Synonymous_Coding	G	A	p.P105L	1658	0.154	NM_006885.3	rs199521581	COSM130307
PR312	chr16:72821887	ZFHX3	Frame_shift	C	CG	p.-3429?	3536	0.154	NM_006885.3		
PR313	chr2:137988662	THSD7B	Non_Synonymous_Coding	G	A	p.R560K	39	0.077	NM_001080427.1		
PR313	chr7:91712775	AKAP9	Non_Synonymous_Coding	A	C	p.T2818P	62	0.113	NM_005751.4		
PR313	chr12:49432474	KMT2D	Non_Synonymous_Coding	C	T	p.G2889R	31	0.129	NM_003482.3		
PR313	chr3:73657760	PDZRN3	Non_Synonymous_Coding	G	A	p.R267W	1517	0.477	NM_015009.1	rs373980887	
PR315	chr19:5144410	KDM4B	Non_Synonymous_Coding	C	T	p.P963L	21	0.238	NM_015015.2		
PR315	chr7:91739463	AKAP9	Non_Synonymous_Coding	T	C	p.M3905T	2857	0.476	NM_005751.4	rs77447750	
PR315	chr19:5134026	KDM4B	Non_Synonymous_Coding	C	T	p.T680M	3383	0.514	NM_015015.2	rs149752315	
PR315	chr12:57865558	GLI1	Non_Synonymous_Coding	G	T	p.G1012V	498	0.552	NM_005269.2	rs2229300	
PR401	chr12:49444992	KMT2D	Non_Synonymous_Coding	G	C	p.S825C	155	0.052	NM_003482.3		
PR401	chr12:57865558	GLI1	Non_Synonymous_Coding	G	T	p.G1012V	63	0.349	NM_005269.2	rs2229300	
PR401	chr8:71071746	NCOA2	Non_Synonymous_Coding	A	G	p.L373P	24	0.375	NM_006540.2		
PR401	chr12:49444996	KMT2D	Frame_shift	A	AG	p.-823?	127	0.701	NM_003482.3		
PR403	chr16:72821887	ZFHX3	Frame_shift	C	CG	p.-3429?	3159	0.172	NM_006885.3		
PR403	chr12:49445021	KMT2D	Frame_shift	C	CG, CGG	p.-815?	85	0.376	NM_003482.3		
PR403	chr12:57865558	GLI1	Non_Synonymous_Coding	G	T	p.G1012V	517	0.472	NM_005269.2	rs2229300	
PR404	chr16:72991476	ZFHX3	Non_Synonymous_Coding	C	T	p.A857T	2706	0.04	NM_006885.3	rs146607776	COSM1379726
PR404	chr16:72991494	ZFHX3	Non_Synonymous_Coding	C	T	p.G851S	2731	0.044	NM_006885.3		
PR404	chr16:72991473	ZFHX3	Non_Synonymous_Coding	C	T	p.E858K	2757	0.051	NM_006885.3		
PR404	chr12:49436073	KMT2D	Non_Synonymous_Coding	C	T	p.D1970N	138	0.094	NM_003482.3		
PR404	chr16:72991700	ZFHX3	Non_Synonymous_Coding	G	A	p.A782V	54	0.148	NM_006885.3	rs62639304	
PR404	chr16:72991706	ZFHX3	Non_Synonymous_Coding	G	A	p.A780V	53	0.151	NM_006885.3		
PR404	chr12:49446101	KMT2D	Codon_Change_Plus_Coding	TTCCTCAGGTGGTGGGGACAGGGGTGAC	T	p.ESPLSPPPEE446E	6052	0.282	NM_003482.3		
PR414	chr12:49416542	KMT2D	Non_Synonymous_Coding	C	T	p.R5390Q	5172	0.485	NM_003482.3		
PR414	chr19:50549441	ZNF473	Non_Synonymous_Coding	G	A	p.E581K	10 668	0.487	NM_001006656.1	rs150885598	
PRY01	chr12:49445021	KMT2D	Frame_shift	C	CG, CGG	p.-815?	191	0.424	NM_003482.3		
PRY02	chr19:50549280	ZNF473	Non_Synonymous_Coding	G	A	p.G527D	2445	0.034	NM_001006656.1		
PRY02	chr16:72821887	ZFHX3	Frame_shift	C	CG	p.-3429?	1603	0.224	NM_006885.3		
PRY02	chr4:87313	ZNF595	Frame_shift	G	GA	p.-639?	62	0.968	NM_182524.2	rs60154095	
PRY04	chr16:72827613	ZFHX3	Non_Synonymous_Coding	C	T	p.V2990I	509	0.063	NM_006885.3		
PRY04	chr16:72821887	ZFHX3	Frame_shift	C	CG	p.-3429?	1684	0.249	NM_006885.3		
PRY04	chr16:72821887	ZFHX3	Frame_shift	C	CG	p.-3429?	1684	0.249	NM_006885.3		
PRY04	chr4:87313	ZNF595	Frame_shift	G	GA	p.-639?	66	0.879	NM_182524.2	rs60154095	

PTEN: phosphatase and tensin homolog; AR: androgen receptor