Table.1 The characteristics and clinical features of KEAP1 and NRF2 gene mutations identified in the study group.

No	Gene	Nt change	Rs number	Mutation type	Localization	Mutation position	Previously identified patient/project type	Patient/control carrier status.	Clinical importance	
									Poly-Phen2	SIFT
C-1	*KEAP1*	c.1708+22A>T	rs777552118	SNP	Intron	-	Current study	Control/ Male- Low Grade- 62 years	NA	NA
C-2	*KEAP1*	c.767A>G	COSV50634305	Missense variant	IVR Domain	p.D256G	Current study / Breast carcinoma	Male-High Grade-63 years	Possibly Damaging 0.81	NA
C-3	*KEAP1*	c.1708+11G>A	rs977175626	SNP	Intron	-	Current study	Control/ Male- Low Grade- 67 years	NA	NA
C-4	*KEAP1*	c.1708+40T>C	rs188184784	SNP	Intron	-	Current study	Control / Male- Low Grade- 65 years	NA	NA
C-5	*KEAP1*	c.344T>A	COSV99407626	Missense variant	BTB Domain	p.L115Q	Current study /Hepatocellular carcinoma	Male-High Grade- 76 years	Probably Damaging 0.98	Deleterious 0.00
C-6	*KEAP1*	c.830C>T	COSV50262958	Missense variant	IVR Domain	p.T277M	Current study / Squamous cell carcinoma	Male-Low Grade- 78 years	Probably Damaging 0.99	NA
C-7	*KEAP1*	c.533C>A	COSV99408354	Missense variant	BTB Domain	p.Q178L	Current study / Head and Neck carcinoma	Male-High Grade- 66 years	Possibly Damaging 0.90	Deleterious 0.00
C-8	*KEAP1*	c.411_423delinsGG	COSV50262244	Frame shift variant	BTB Domain	p.I137Mfs*33	Current study /Squamous cell carcinoma	Male- High Grade - 70 years	NA	NA
C-9	*NRF2*	c.472G>T	rs754950910	Missense variant	Transaktivasyon domain	p.A158P	Current study	Male-High Grade - 84 years	Probably Damaging 1.00	Deleterious 0.00
C-10	*NRF2*	c.246A>T	COSV67960221	Missense variant	Neh2 Domain	p.E82D	cbioportal	BLCA cohort	Probably Damaging 1.00	Deleterious 0.00
C-11	*NRF2*	c.92G>C	COSV67959995	Missense variant	Neh2 Domain	p.G31A	cbioportal	BLCA cohort	Probably Damaging 1.00	Deleterious 0.00
C-12	*NRF2*	c.235G>C	COSV67960008	Missense variant	Neh2 Domain	p.E79Q	cbioportal	BLCA cohort	Probably Damaging 1.00	Deleterious 0.00
C-13	*NRF2*	c.235G>A	COSV67959999	Missense	Neh2 Domain	p.E79K	cbioportal	BLCA cohort	Probably Damaging	Deleterious

				variant					1.00	0.00
C-14	*NRF2*	c.245A>T	COSV67961061	Missense variant	Neh2 Domain	p.E82V	cbioportal	BLCA cohort	Probably Damaging 1.00	Deleterious 0.00
C-15	*NRF2*	c.239C>T	COSV67960012	Missense variant	Neh2 Domain	p.T80I	cbioportal	BLCA cohort	Probably Damaging 1.00	Deleterious 0.00
C-16	*NRF2*	c.242G>C	COSV67960680	Missense variant	Neh2 Domain	p.G81A	cbioportal	BLCA cohort	Probably Damaging 1.00	Deleterious 0.00
C-17	*NRF2*	c.91G>A	COSV67959995	Missense variant	Neh2 Domain	p.G31R	cbioportal	BLCA cohort	Probably Damaging 1.00	Deleterious 0.00
C-18	*NRF2*	c.70T>C	COSV67960091	Missense variant	Neh2 Domain	p.W24R	cbioportal	BLCA cohort	Probably Damaging 1.00	Deleterious 0.00
C-19	*NRF2*	c.100C>G	COSV67960061	Missense variant	Neh2 Domain	p.R34G	cbioportal	BLCA cohort	Probably Damaging 1.00	Deleterious 0.00
C-20	*NRF2*	c.85G>T	COSV67960852	Missense variant	Neh2 Domain	p.D29Y	cbioportal	BLCA cohort	Probably Damaging 1.00	Deleterious 0.00
C-21	*NRF2*	c.101G>C	COSV67960096	Missense variant	Neh2 Domain	p.R34P	cbioportal	BLCA cohort	Probably Damaging 1.00	Deleterious 0.00
C-22	*NRF2*	c.85G>C	COSV67960002	Missense variant	Neh2 Domain	p.D29H	cbioportal	BLCA cohort	Probably Damaging 1.00	Deleterious 0.00
C-23	*NRF2*	:c.89_100del	UNK	Frame shift variant	-	p.L30_S33del	cbioportal	BLCA cohort	NA	NA
C-24	*NRF2*	c.481C>G	COSV67960927	Missense variant	Neh5 Domain	p.Q161E	cbioportal	BLCA cohort	Benign 0.14	Tolerated 0.51
C-25	*NRF2*	c.1597A>C	COSV67961715	Missense variant	Neh1 Domain	p.K533Q	cbioportal	BLCA cohort	Probably Damaging 1.00	Tolerated 0.09
C-26	*NRF2*	c.1799C>G	UNK	Missense variant	Neh3 Domain	p.P600R	cbioportal	BLCA cohort	Benign 0.22	Deleterious 0.04
C-27	*NRF2*	c.1570G>C	UNK	Missense variant	Neh1Domain	p.E524Q	cbioportal	BLCA cohort	Probably Damaging 0.98	Tolerated 0.20
C-28	*NRF2*	c.1249G>A	COSV67960306	Missense variant	-	p.V417M	cbioportal	BLCA cohort	Benign 0.01	Tolerated 0.04
C-29	*NRF2*	c.105A>C	UNK	Missense variant	Neh2 Domain	p.E35D	cbioportal	BLCA cohort	Benign 0.04	Deleterious 0.03
C-30	*NRF2*	c.1267G>T	UNK	Nonsense variant	-	p.E423*	cbioportal	BLCA cohort	NA	NA
C-31	*NRF2*	c.157A>C	COSV67961715	Missense variant	Neh2 Domain	p.K53Q	cbioportal	BLCA cohort	Benign 0.01	Tolerated 0.10
C-32	*KEAP1*	c.1607_1608insTG	UNK	Frame shift variant	-	p.Y537Afs*12	cbioportal	BLCA cohort	NA	NA
C-33	*KEAP1*	c.1709-2A>G	UNK	Splice site	-	p.X570_splice	cbioportal	BLCA cohort	NA	NA

				variant						
C-34	*KEAP1*	c.652G>C	COSV50261023	Missense variant	IVR Domain	p.E218Q	cbioportal	BLCA cohort	Possibly Damaging 0.90	Deleterious 0.00
C-35	*KEAP1*	c.73G>A		Missense variant	NTR Domain	p.E25K	cbioportal	BLCA cohort	Benign 0.00	Tolerated 0.06
C-36	*KEAP1*	c.347G>C		Missense variant	BTB Domain	p.R116P	cbioportal	BLCA cohort	Possibly Damaging 0.86	Deleterious 0.00
C-37	*KEAP1*	c.730G>A	COSV50280201	Missense variant	IVR Domain	p.E244K	cbioportal	BLCA cohort	Possibly Damaging 0.77	Deleterious 0.00
C-38	*KEAP1*	c.134C>T	COSV50263607	Missense variant	NTR Domain	p.S45F	cbioportal	BLCA cohort	Probably Damaging 1.00	Deleterious 0.00
C-39	*KEAP1*	c.1411C>T	UNK	Missense variant	KELC/DGR Domain	p.L471F	cbioportal	BLCA cohort	Benign 0.17	Tolerated 0.09
C-40	*KEAP1*	c.706G>A	COSV50260398	Missense variant	IVR Domain	D236N	cbioportal	BLCA cohort	Benign 0.05	Tolerated 0.06
UNK: Unknown, NA: Not available, SNP: Single nucleotide polymorphism, C: Change, UTR: Untranslated Region; P: Patient: BLCA: Bladder Cancer										