**Supplementary Table 4. Mutations of ARID1A in TCGA dataset**

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| --- | --- | --- | --- | --- | --- | --- |
| **Sample ID** | **Protein change** | **Functional impact** | **Mutation type** | **Variant type** | **HGVSg** | **HGVSc** |
| TCGA-ZS-A9CD-01 | G2087E | MutationAssessor: impact: medium, score: 2.65; SIFT: impact: deleterious, score: 0; Polyphen-2: impact: probably\_damaging, score: 1 | Missense\_Mutation | SNP | 1:g.27106649G>A | ENST00000324856.7:c.6260G>A |
| TCGA-DD-A1EH-01 | R1721\* | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Nonsense\_Mutation | SNP | 1:g.27105550C>T | ENST00000324856.7:c.5161C>T |
| TCGA-FV-A23B-01 | E1542\* | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Nonsense\_Mutation | SNP | 1:g.27101342G>T | ENST00000324856.7:c.4624G>T |
| TCGA-CC-5262-01 | Q1142\* | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Nonsense\_Mutation | SNP | 1:g.27099008C>T | ENST00000324856.7:c.3424C>T |
| TCGA-DD-A39W-01 | Q1142\* | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Nonsense\_Mutation | SNP | 1:g.27099008C>T | ENST00000324856.7:c.3424C>T |
| TCGA-CC-5258-01 | P728Qfs\*87 | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Frame\_Shift\_Del | DEL | 1:g.27087894\_27087898del | ENST00000324856.7:c.2181\_2185del |
| TCGA-DD-A1EE-01 | P728Qfs\*87 | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Frame\_Shift\_Del | DEL | 1:g.27087894\_27087898del | ENST00000324856.7:c.2181\_2185del |
| TCGA-G3-A3CJ-01 | N917Ifs\*2 | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Frame\_Shift\_Del | DEL | 1:g.27092724del | ENST00000324856.7:c.2748del |
| TCGA-LG-A6GG-01 | X1665\_splice | MutationAssessor: impact: , score: undefined;SIFT: NA;Polyphen-2: NA | Splice\_Site | SNP | 1:g.27102066A>T | ENST00000324856.7:c.4994-2A>T |
| TCGA-DD-AADR-01 | A165Gfs\*67 | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Frame\_Shift\_Del | DEL | 1:g.27023388del | ENST00000324856.7:c.494del |
| TCGA-CC-A9FS-01 | K1129\* | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Nonsense\_Mutation | SNP | 1:g.27097796A>T | ENST00000324856.7:c.3385A>T |
| TCGA-2V-A95S-01 | A1687Dfs\*2 | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Frame\_Shift\_Del | DEL | 1:g.27102134del | ENST00000324856.7:c.5060del |
| TCGA-DD-A1EH-01 | V2169Cfs\*56 | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Frame\_Shift\_Ins | INS | 1:g.27106893\_27106894insT | ENST00000324856.7:c.6504\_6505insT |
| TCGA-DD-AADP-01 | I1130Tfs\*28 | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Frame\_Shift\_Del | DEL | 1:g.27097800\_27097809del | ENST00000324856.7:c.3389\_3398del |
| TCGA-DD-AACG-01 | P109Afs\*6 | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Frame\_Shift\_Del | DEL | 1:g.27023218\_27023222del | ENST00000324856.7:c.324\_328del |
| TCGA-DD-AAE7-01 | Q1499\* | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Nonsense\_Mutation | SNP | 1:g.27101213C>T | ENST00000324856.7:c.4495C>T |
| TCGA-DD-A39V-01 | E1733Gfs\*3 | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Frame\_Shift\_Ins | INS | 1:g.27105581\_27105582insA | ENST00000324856.7:c.5195dup |
| TCGA-KR-A7K8-01 | S1930Qfs\*26 | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Frame\_Shift\_Del | DEL | 1:g.27106176del | ENST00000324856.7:c.5788del |
| TCGA-BW-A5NQ-01 | Q1974Tfs\*43 | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Frame\_Shift\_Ins | INS | 1:g.27106299\_27106300insCTGGA | ENST00000324856.7:c.5915\_5919dup |
| TCGA-EP-A2KB-01 | Q2039Hfs\*60 | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Frame\_Shift\_Ins | INS | 1:g.27106505\_27106506insT | ENST00000324856.7:c.6116\_6117insT |
| TCGA-DD-AAVX-01 | K2033Rfs\*9 | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Frame\_Shift\_Del | DEL | 1:g.27106484del | ENST00000324856.7:c.6098del |
| TCGA-CC-A123-01 | A2234Gfs\*34 | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Frame\_Shift\_Ins | INS | 1:g.27107084\_27107085insGC | ENST00000324856.7:c.6697\_6698dup |
| TCGA-BC-A10W-01 | Q450= | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Splice\_Region | SNP | 1:g.27056354G>A | ENST00000324856.7:c.1350G>A |
| TCGA-XR-A8TF-01 | V2228Afs\*2 | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Frame\_Shift\_Del | DEL | 1:g.27107072\_27107075del | ENST00000324856.7:c.6683\_6686del |
| TCGA-G3-A3CG-01 | L1681Yfs\*8 | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Frame\_Shift\_Del | DEL | 1:g.27102114\_27102139del | ENST00000324856.7:c.5040\_5065del |
| TCGA-DD-A39Y-01 | S735Afs\*7 | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | Frame\_Shift\_Del | DEL | 1:g.27087916del | ENST00000324856.7:c.2203del |
| TCGA-ES-A2HT-01 | Y1027C | MutationAssessor: impact: medium, score: 2.175;SIFT: impact: deleterious, score: 0;Polyphen-2: impact: probably\_damaging, score: 0.997 | Missense\_Mutation | SNP | 1:g.27094372A>G | ENST00000324856.7:c.3080A>G |
| TCGA-UB-A7ME-01 | S1001C | MutationAssessor: impact: medium, score: 2.05;SIFT: impact: deleterious, score: 0;Polyphen-2: impact: probably\_damaging, score: 0.983 | Missense\_Mutation | SNP | 1:g.27094294C>G | ENST00000324856.7:c.3002C>G |
| TCGA-CC-A5UD-01 | S2214C | MutationAssessor: impact: medium, score: 2.14;SIFT: impact: deleterious, score: 0;Polyphen-2: impact: probably\_damaging, score: 0.956 | Missense\_Mutation | SNP | 1:g.27107029A>T | ENST00000324856.7:c.6640A>T |
| TCGA-DD-A4NR-01 | N1475T | MutationAssessor: impact: low, score: 1.32;SIFT: impact: tolerated, score: 0.42;Polyphen-2: impact: benign, score: 0 | Missense\_Mutation | SNP | 1:g.27101142A>C | ENST00000324856.7:c.4424A>C |
| TCGA-UB-A7MD-01 | S2068W | MutationAssessor: impact: medium, score: 2.43;SIFT: impact: deleterious, score: 0;Polyphen-2: impact: probably\_damaging, score: 0.998 | Missense\_Mutation | SNP | 1:g.27106592C>G | ENST00000324856.7:c.6203C>G |
| TCGA-DD-AAEG-01 | P136T | MutationAssessor: impact: neutral, score: 0;SIFT: impact: tolerated\_low\_confidence, score: 0.46;Polyphen-2: impact: benign, score: 0.161 | Missense\_Mutation | SNP | 1:g.27023300C>A | ENST00000324856.7:c.406C>A |
| TCGA-XR-A8TF-01 | M2230\_R2236delinsS | MutationAssessor: NA;SIFT: NA;Polyphen-2: NA | In\_Frame\_Del | DEL | 1:g.27107078\_27107095del | ENST00000324856.7:c.6689\_6706del |
| TCGA-DD-A39X-01 | S514P | MutationAssessor: impact: neutral, score: 0.695;SIFT: impact: tolerated\_low\_confidence, score: 0.06;Polyphen-2: impact: benign, score: 0.203 | Missense\_Mutation | SNP | 1:g.27057832T>C | ENST00000324856.7:c.1540T>C |

DEL, deletion; HGVSc, Human Genome Variation Society coding nomenclature; HGVSg, Human Genome Variation Society genomic nomenclature; SNP, single nucleotide polymorphism.