Table S1. Primers used for preparing non-coding mutation sequencing libraries by multiplex-PCR. Coordinates are Hg19. The sequences of the adapters for subsequent barcoding are, CS1: ACACTGACGACATGGTTCTACA and CS2: TACGGTAGCAGAGACTTGGTCT.



Table S2. Non-recurrent variants and polymorphisms. Variants that occurred once in 302 UBCs or were recurrent but confirmed as polymorphisms by germline DNA sequencing (indicated with an asterisk are listed). These variants were excluded from all data analyses.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| GENE | COORDINATE | BASE CHANGE | MAF(%) | dbSBNP | SAMPLE |
| PLEKHS1 | chr10:115511555 | C/G | 33.9 | NA | 1 |
| PLEKHS1 | chr10:115511559 | G/A | 46.3 | rs150946996 | 1 |
| PLEKHS1 | chr10:115511578 | T/C | ave=54 | rs79409239 | 8\* |
| PLEKHS1 | chr10:115511588 | T/A | 45.8 | NA | 1 |
| PLEKHS1 | chr10:115511590 | G/T | 17.8 | NA | 1 |
| PLEKHS1 | chr10:115511607 | G/C | 42.0 | NA | 1 |
| TBC1D12 | chr10:96162342 | C/T | 50.4 | rs199804945 | 1 |
| TBC1D12 | chr10:96162370 | G/C | 16.8 | NA | 1 |
| WDR74 | chr11:62609175 | T/C | 36.0 | rs548405016 | 1 |
| WDR74 | chr11:62609176 | C/T | 10.4 | NA | 1 |
| WDR74 | chr11:62609176 | C/A | 38.9 | NA | 1 |
| WDR74 | chr11:62609182 | A/G | 25.1 | NA | 1 |
| WDR74 | chr11:62609200 | C/T | 46.7 | rs534780060 | 1 |
| WDR74 | chr11:62609204 | G/C | 2.9 | NA | 1 |
| WDR74 | chr11:62609207 | T/G | 63.1 | NA | 1 |
| WDR74 | chr11:62609212 | G/A | ave=48 | rs370494108 | 13\* |
| WDR74 | chr11:62609232 | G/A | 29.9 | NA | 1 |
| WDR74 | chr11:62609237 | G/C | 34.5 | NA | 1 |
| WDR74 | chr11:62609254 | G/T | 22.7 | NA | 1 |
| WDR74 | chr11:62609261 | G/T | 37.2 | NA | 1 |
| WDR74 | chr11:62609272 | G/A | 46.4 | NA | 1 |
| WDR74 | chr11:62609279 | G/C | 34.4 | NA | 1 |
| WDR74 | chr11:62609283 | C/T | 47.4 | rs547036809 | 1 |
| WDR74 | chr11:62609284 | C/T | 21.2 | rs114330587 | 1 |
| GPR126 | chr6:142706198 | C/T | 42.4 | NA | 1 |
| GPR126 | chr6:142706206 | G/T | 29.0 | NA | 1 |
| GPR126 | chr6:142706217 | G/T | 28.6 | NA | 1 |
| GPR126 | chr6:142706217 | G/A | 47.9 | NA | 1 |
| LEPROTL1 | chr8:29952874 | C/T | 42.6 | NA | 1 |
| LEPROTL1 | chr8:29952897 | G/A | 41.4 | NA | 1 |
| LEPROTL1 | chr8:29952915 | C/A | 4.9 | NA | 1 |
| LEPROTL1 | chr8:29952919 | G/T | 35.5 | NA | 1 |
| LEPROTL1 | chr8:29952922 | G/A | 55.7 | NA | 1 |
| LEPROTL1 | chr8:29952946 | C/T | ave=50 | rs143899166 | 22\* |

Table S3. Frequencies of recurrent non-coding mutations across patient groups.



Table S4. Effects of mutation status on gene expression. Data shown are median normalised read counts for each gene product. For grade 1 UBC n=15, grade 3 UBC n=45. \* = p<0.05. For comparison, median GAPDH expression = 17756.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | All UBCs | wt | mut | Grade 1 | Grade 3 |
| GPR126 | 2241 | 3247 | 1861\* | 3290 | 1805\* |
| PLEKHS1 | 36 | 46 | 33 | 11 | 47\* |
| LEPROTL1 | 473 | 468 | 493 | 536 | 447 |
| TBC1D12 | 317 | 309 | 335 | 333 | 317 |
| WDR74 | 330 | 327 | 398 | 329 | 340 |