**Supplementary Table S3. Summary for structural alterations detected by paired-end WGS for 25 TCGA ovarian tumors**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **SampleID** | **Deletions** | **Seq** | **Duplications** | **Seq** | **Translocations** | **Seq** | **Inversions** | **Dup<30kb^** |
| TCGA-04-1371 | 29 (14) | 9 | 25 (11) | 0 | 57 (34) | 11 | 21 (12) | 14 |
| TCGA-04-1542 | 34 (15) | 13 | 4 (1) | 0 | 20 (9) | 0 | 11 (6) | 7 |
| TCGA-09-20503 | 25 (13) | 10 | 7 (4) | 0 | 42 (27) | 7 | 9 (4) | 9 |
| TCGA-10-0934 | 18 (12) | 55 | 54 (46) | 34 | 56 (50) | 15 | 9 (9) | 20 |
| TCGA-10-0938 | 38 (18) | 12 | 17 (11) | 0 | 21 (11) | 4 | 42 (33) | 9 |
| TCGA-13-07252 | 11 (11) | 7 | 6 (3) | 0 | 19 (6) | 0 | 4 (2) | 38 |
| TCGA-13-0727 | 13 (5) | 3 | 34 (23) | 15 | 18 (3) | 1 | 11 (4) | 11 |
| TCGA-13-0751 | 13 (7) | 1 | 62 (54) | 27 | 30 (26) | 7 | 20 (14) | 8 |
| TCGA-13-0906 | 13 (7) | 3 | 12 (3) | 0 | 49 (13) | 6 | 13 (3) | 13 |
| TCGA-13-0912 | 16 (11) | 11 | 23 (18) | 0 | 24 (10) | 4 | 11 (7) | 11 |
| TCGA-13-1477 | 2 (1) | 0 | 3 (0) | 0 | 17 (1) | 2 | 3 (3) | 7 |
| TCGA-13-1487\* | 38 (29) | 26 | 116 (84) | 52 | 71 (41) | 13 | 16 (12) | 38 |
| TCGA-13-1491 | 18 (7) | 5 | 35 (22) | 0 | 23 (13) | 4 | 8 (4) | 11 |
| TCGA-23-11181 | 26 (16) | 12 | 74 (35) | 24 | 49 (20) | 6 | 21 (9) | 105 |
| TCGA-23-11242 | 30 (14) | 8 | 42 (18) | 9 | 96 (65) | 28 | 30 (17) | 155 |
| TCGA-24-0982 | 8 (5) | 3 | 18 (16) | 0 | 7 (3) | 1 | 6 (4) | 5 |
| TCGA-24-1466\*\* | 31 (20) | 26 | 347 (304) | 216 | 51 (45) | 16 | 36 (33) | 19 |
| TCGA-24-1544 | 36 (23) | 13 | 31 (17) | 0 | 44 (18) | 8 | 25 (15) | 18 |
| TCGA-24-15572 | 14 (11) | 10 | 69 (31) | 25 | 82 (38) | 13 | 17 (8) | 106 |
| TCGA-24-1562 | 16 (10) | 8 | 22 (13) | 0 | 8 (2) | 0 | 15 (8) | 11 |
| TCGA-24-16142 | 11 (9) | 6 | 16 (10) | 0 | 49 (28) | 13 | 16 (2) | 118 |
| TCGA-25-1319 | 20 (16) | 9 | 16 (13) | 0 | 44 (26) | 10 | 30 (20) | 5 |
| TCGA-25-16321 | 25 (14) | 8 | 30 (16) | 0 | 29 (7) | 5 | 23 (20) | 50 |
| TCGA-25-1634 | 25 (7) | 6 | 12 (3) | 0 | 20 (7) | 2 | 19 (10) | 11 |
| TCGA-25-2400 | 33 (26) | 18 | 23 (16) | 0 | 45 (23) | 13 | 32 (21) | 4 |

The numbers in parenthesis correspond to SNP-array validated alterations. Column “Seq” shows the number of junction sequences found for the corresponding alterations.

\*Tumor with a high rate of TDs not *CDK12* mutated; \*\**CDK12*-mutated tumor; 1*BRCA1* mutated tumor; 2*BRCA1* promoter methylated tumor; 3*BRCA2*-mutated tumor; ^ number of tandem duplications of the size less than 30kb.