## Deletions (CNV) detected by GqCNV and PennCNV in at least 3 tumors

| | Locus (Mb) | | | | | | Detected in database |
|---|---|---|---|---|---|---|---|
| **Chr** | **Start** | **End** | **Size** | **Nb SNP** | **Nb tumors** | **Genes** | **of Genomic Variants** |
| 1p36.13 | 17086767 | 17155012 | 68246 | 11 | 6 | 3 genes LOC100129182, TRNAN2, CROCC | no |
| 2p22.3 | 34544587 | 34592120 | 35482 | 32 | 5 | no gene | no |
| 2q33.3 | 208057503 | 208071307 | 13805 | 17 | 4 | no gene | no |
| 3q26.1 | 163746526 | 164238477 | 491952 | 105 | 5 | no gene | no |
| 3q28 | 192547222 | 192555922 | 8701 | 18 | 5 | 1 gene CCD50 | no |
| 4q13.1 | 64350537 | 64392223 | 41687 | 18 | 4 | no gene | no |
| 5q23.1 | 117414333 | 117421055 | 6723 | 13 | 4 | no gene | no |
| 6p21.33-6p21.32 | 29965944 | 32763196 | 37147 | 123 | 10 | 168 genes | no |
| 6q14.1 | 79036117 | 79086086 | 49970 | 46 | 6 | no gene | no |
| 7q34 | 141419097 | 141439888 | 20792 | 21 | 5 | 1 MGAM | no |
| 8p11.23-8p11.22 | 39350791 | 39509376 | 158586 | 38 | 12 | 2 genes ADAM5P, ADAM3A | no |
| 9p11.2 | 44683090 | 44797463 | 114374 | 20 | 4 | 1 gene LOC100131427 | no |
| 12p13 | 9526879 | 9607393 | 80515 | 15 | 5 | 1 OVOS | no |
| 12p11.22 | 30125165 | 30134898 | 9734 | 10 | 4 | no gene | no |

## Amplifications (CNV) detected by GqCVN and PennCNV in at least 3 tumors

| | Locus (Mb) | | | | | | Detected in database |
|---|---|---|---|---|---|---|---|
| **Chr** | **Start** | **End** | **Size** | **Nb SNP** | **Nb tumors** | **Genes** | **of Genomic Variants** |
| 6q27 | 168091860 | 168319676 | 227817 | 209 | 3 | 4 genes MLLT4, LOC100128124, KIF25, FRMD1 | yes |
| **7q34** | **139501685** | **140079362** | **577678** | **124** | **20** | **region of interest** | **NO** |
| 10q11.22 | 47007374 | 47167032 | 74264 | 82 | 3 | 3 genes LOC340844, LOC728684, ANTXRL | yes |
| 12p11.21 | 31157554 | 31300846 | 143293 | 55 | 9 | 3 genes LOC100132881, OVOS2, LOC441632 | no |
| 19q13.42 | 59971240 | 60054671 | 83432 | 14 | 6 | 6 genes KIR2DL1-4, KIR3DP1, KIR3DL1, KIR2DS1-4 | no |

**Supplementary Table 2**: Genomic alterations in the data set generated on the Hap300-Duo and 610-Qad human arrays detected by both GqCNV and PennCNV algo

rithms.