**The genefile file**

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| **Name** | **Length of CDS** | **Hallmark type** | **Oncogene or suppressor** | **weights** |
| GA1 | 1 | apoptosis | o | 0.1 |
| GA2 | 1 | apoptosis | o | 0.2 |
| GA3 | 1 | apoptosis | o | 0.3 |
| GA4 | 1 | apoptosis | o | 0.4 |
| GB1 | 1 | angiogenesis | o | 0.1 |
| GB2 | 1 | angiogenesis | o | 0.2 |
| GB3 | 1 | angiogenesis | o | 0.3 |
| GB4 | 1 | angiogenesis | o | 0.4 |
| GIM1 | 1 | invasion | o | 0.1 |
| GIM2 | 1 | invasion | o | 0.2 |
| GIM3 | 1 | invasion | o | 0.3 |
| GIM4 | 1 | invasion | o | 0.4 |
| GI1 | 1 | immortalization | o | 0.1 |
| GI2 | 1 | immortalization | o | 0.2 |
| GI3 | 1 | immortalization | o | 0.3 |
| GI4 | 1 | immortalization | o | 0.4 |
| GD1 | 1 | growth | o | 0.1 |
| GD2 | 1 | anti-growth | o | 0.2 |
| GD3 | 1 | growth | o | 0.3 |
| GD4 | 1 | anti-growth | o | 0.4 |

The sum of weights is equal 1. The oncogene or suppressor parameter and length of CDS do not matter, they are important only for mutation processes. The weights are different in order to make different combinations in cells. Please, check the **FIRST and SECOND** steps, because the invasion/metastasis transformation occurs only after trial !!!!!

**The cloneinit file**

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| **N** | **Destroyed Genes** | **Calculation example** | **Notes** |
| 1 | GB1,GB2,GB3,GB4,GI1,GI2,GI3,GI4,GD1,GD2,GD3,GD4 | a=0.73… , Ha=0 | For normal clones  a=sigma\_function – Ha,  the mutation rates are same for different cells and rate = 12/20, s0=10 and sigma=function = 0.73… |
| 2 | GA1,GB1,GB2,GB3,GB4,GI1,GI2,GI3,GI4,GD1,GD2,GD3 | a=0.63…, Ha=0.1 |
| 3 | GA1,GA2,GB1,GB2,GB3,GB4,GI1,GI2,GI3,GI4,GD1,GD2 | a=0.43…, Ha=0.3 |
| 4 | GA1,GA2,GA3,GB1,GB2,GB3,GB4,GI1,GI2,GI3,GI4,GD1 | a=0.13…, Ha=0.6 |
| 5 | GA1,GA2,GA3,GA4,GB1,GB2,GB3,GB4,GI1,GI2,GI3,GI4 | a=0, Ha=1 |
| 6 | GIM1,GIM2,GIM3,GIM4,GA1,GB2,GB3,GB4,GI1,GI2,GI3 | a=0, Ha=1 | For metastasis clones  a=sigma\_function – Ha,  Values are same as for normal cells |
| 7 | GIM1,GIM2,GIM3,GIM4,GA1,GA2,GB4,GI1,GI2,GI3,GI4 | a=0.13…, Ha=0.6 |
| 8 | GIM1,GIM2,GIM3,GIM4,GA1,GA2,GA3,GI2,GI3,GI4,GD1 | a=0.43…, Ha=0.3 |
| 9 | GIM1,GIM2,GIM3,GIM4,GA1,GA2,GA3,GA4,GI4,GD1,GD2 | a=0.63…, Ha=0.1 |
| 10 |  |  | Normal clone |
| 11 | GB1,GD1,GD2,GD3,GD4 | *Hb*=0.1, *Nmax*=24, *d*=0.083… | where , what is why we have Hd=1  with 4 genes (GD1-GD4) |
| 12 | GB1,GB2,GD1,GD2,GD3,GD4 | *Hb*=0.3, *Nmax*=32, *d*=0.3125 |
| 13 | GB1,GB2,GB3,GD1,GD2,GD3,GD4 | *Hb*=0.6, *Nmax*=44, *d*=0.5 |
| 14 | GB1,GB2,GB3,GB4,GD1,GD2,GD3,GD4 | *Hb*=1.0, *Nmax*=60, *d*=0.633… |
| 15 | GIM1,GIM2,GIM3,GIM4,GB1,GB2,GB3,GB4,GD1,GD2,GD3,GD4 | *Hb*=1.0, *Nmax*=60, *d*=1 | *F0=2, E0=0.05, so Nmax=(20-60) to check formula,* ***N=22*** |
| 16 | GIM1,GIM2,GIM3,GIM4,GB1,GB2,GB3,GD1,GD2,GD3,GD4 | *Hb*=0.6, *Nmax*=32, *d*=1 |
| 17 | GIM1,GIM2,GIM3,GIM4,GB1,GB2,GD1,GD2,GD3,GD4 | *Hb*=0.3, *Nmax*=44, *d*=1 |
| 18 | GIM1,GIM2,GIM3,GIM4,GB1,GD1,GD2,GD3,GD4 | *Hb*=0.1, *Nmax*=24, *d*=1 |
| 19 |  |  | Normal clone |
| 20 | GIM1 | *Him*=0.1, *im`*=0.1 | This is a invasion/metastasis transformation, the probability **im` = Him** *before* transformation and if **im` = 1** then *becomes*  metastasis transformation |
| 21 | GIM1,GIM2 | *Him*=0.3, *im`*=0.3 |
| 22 | GIM1,GIM2,GIM3 | *Him*=0.6, *im`*=0.6 |
| 23 | GIM1,GIM2,GIM3,GIM4 | *Him*=1.0, *im`*=1.0 and 1 |
| 24 |  |  | Normal clone |
| 25 | GI1 | *Hi* = 0.1, *i`* = 0.9 | *i`* = 1 - *Hi* |
| 26 | GI1,GI2 | *Hi* = 0.3, *i`* = 0.7 |
| 27 | GI1,GI2,GI3 | *Hi* = 0.6, *i`* = 0.4 |
| 28 | GI1,GI2,GI3,GI4 | *Hi* = 1.0, *i`* = 0 |
| 29 | GIM3,GI1,GI2,GI3,GI4 | *Hi* = 1.0, *i`* = 0 | Same formula |
| 30 | GIM3,GI1,GI2,GI3 | *Hi* = 0.6, *i`* = 0.4 |
| 31 | GIM3,GI1,GI2 | *Hi* = 0.3, *i`* = 0.7 |
| 32 | GIM3,GI1 | *Hi* = 0.1, *i`* = 0.9 |
| 33 |  |  | Normal clone |
| 34 | GD1 | *Hd* = 0.1, *d`* = 0 | where , *d0* = 0, *N*/*Nmax* = 22/20 > 1,  so *d* = 0. |
| 35 | GD1,GD2 | *Hd* = 0.3, *d`* = 0 |
| 36 | GD1,GD2,GD3 | *Hd* = 0.6, *d`* = 0 |
| 37 | GD1,GD2,GD3,GD4 | *Hd* = 1.0, *d`* = 0 |
| 38 | GIM1,GIM2,GIM3,GIM4, GD1,GD2,GD3,GD4 | *Hd* = 1.0, *d`* = 1.0 | , *d0* = 0 |
| 39 | GIM1,GIM2,GIM3,GIM4,GD1,GD2,GD3 | *Hd* = 0.6, *d`* = 0.6 |
| 40 | GIM1,GIM2,GIM3,GIM4,GD1,GD2 | *Hd* = 0.3, *d`* = 0.3 |
| 41 | GIM1,GIM2,GIM3,GIM4,GD1 | *Hd* = 0.1, *d`* = 0.1 |
| 42 |  |  | Normal clone |