

Supplementary table S1

Genetic background of used primary cultures

| Culture | Gender | Recurrent | MGMT | PTEN | IDH | EGFR/chr 7 | 1p19q | TP53 |
|---------|--------|-----------|--------------|-----------|-----|---------------|-----------------|----------|
| GS755 | M | N | Unmethylated | Mutation | WT | Amplification | WT | Mutation |
| GS838 | M | Y | Unmethylated | Mutation | WT | Amplification | WT | WT |
| GS786 | M | N | Methylated | Loss | WT | Amplification | 1p imbalance | WT |
| GS607 | M | N | Unmethylated | Loss | WT | Amplification | 19q imbalance | Mutation |
| GS799 | M | N | Methylated | Loss | WT | Amplification | 1p19q loss | Mutation |
| GS502 | F | N | Methylated | Loss | WT | Amplification | 19q imbalance | Mutation |
| GS916 | M | Y | Unmethylated | Loss | WT | Amplification | 1p loss | WT |
| GS824 | M | N | Methylated | Loss | WT | Amplification | WT | WT |
| GS627 | F | N | Unmethylated | WT | WT | Amplification | 19q imbalance | WT |
| GS832 | M | N | Unmethylated | Loss | WT | Amplification | 19q imbalance | WT |
| GS851 | M | N | Methylated | WT | WT | Amplification | 19q imbalance | WT |
| GS741 | M | N | Unmethylated | Loss | WT | Amplification | WT | Mutation |
| GS636 | M | N | Unmethylated | Loss | WT | Amplification | WT | WT |
| GS622 | F | N | Methylated | Loss | WT | Amplification | 1p loss | Mutation |
| GS630 | M | N | Unmethylated | Imbalance | WT | WT | WT | WT |
| GS784 | F | Y | Unmethylated | Mutation | WT | Amplification | 1p imbalance | WT |
| GS820 | F | N | Methylated | Loss | WT | Amplification | 1p19q imbalance | WT |
| GS968 | M | N | Methylated | Loss | WT | Amplification | 1p loss | WT |
| GS802 | M | N | Unmethylated | Loss | WT | Amplification | WT | Mutation |
| GS612 | M | N | Unmethylated | Mutation | WT | Amplification | WT | WT |