**Supplementary Table 1**　The Correlation between clinicopathologic features and TGFβR2 protein expression in NPC

| Characteristics | n | TGFBR2 (%) | | P |
| --- | --- | --- | --- | --- |
| | | High expression | Low expression | |
| Gender | | | | |
| Male | 103 | 50(48.5) | 53 (51.5) | |
| Female | 53 | 28(52.8) | 25 (47.2) | 0.735 |
| Age(y) | | | | |
| ≥50 | 71 | 31 (43.7) | 40 (56.3) | |
| <50 | 85 | 47 (55.3) | 38(44.7) | 0.198 |
| Smoking | | | | |
| Yes | 31 | 18 (58.1) | 13 (41.9) | |
| No | 125 | 60 (48.0) | 65 (52.0) | 0.423 |
| Family tumor history | | | | |
| Yes | 5 | 4(80.0) | 1(20.0) | |
| No | 151 | 74(49.0) | 77(51.0) | 0.367 |
| Recurrence | | | | |
| Yes | 39 | 17(43.6) | 22(56.4) | |
| No | 117 | 61(52.1) | 56(47.9) | 0.460 |
| T classification | | | | |
| $T_1$-$T_2$ | 109 | 62(56.9) | 40 (43.1) | |
| $T_3$-$T_4$ | 47 | 16 (51.7) | 38(48.3) | <0.001 |
| N classification | | | | |
| $N_0$-$N_1$ | 87 | 45 (51.7) | 28(48.3) | |
| $N_2$-$N_3$ | 69 | 33(47.8) | 50 (52.2) | 0.010 |
| Distant metastasis [#] | | | | |
| Yes | 9 | 3 (33.3) | 6 (66.7) | |
| No | 147 | 75 (51.0) | 72 (49.0) | 0.495 |
| TNM Clinical stage | | | | |
| I-II | 47 | 31 (66.0) | 16 (34.0) | |
| III-IV | 109 | 47(43.1) | 62(56.9) | 0.014 |

[#] The difference that was not statistically significant, possibly due to few patients with distant metastasis

**Supplementary Table 2** Summary of univariate and multivariate Cox regression analysis of overall survival duration

| Parameter | Univariate analysis | | | Multivariate analysis | | |
|---|---|---|---|---|---|---|
| | *P* | HR | 95%CI | *P* | HR | 95%CI |
| Gender | | | | | | |
| Male vs. female | 0.880 | 1.041 | 0.617-1.755 | | | |
| Age | | | | | | |
| ≥50 vs. <50 years | 0.073 | 1.576 | 0.959-2.592 | | | |
| Family tumor history | | | | | | |
| Yes vs. No | 0.369 | 0.404 | 0.056-2.917 | | | |
| Smoking | | | | | | |
| Yes vs. No | 0.536 | 0.814 | 0.425-1.560 | | | |
| Biotherapy | | | | | | |
| Yes vs. No | 0.554 | 0.653 | 0.159-2.677 | | | |
| T classification | | | | | | |
| $T_1$-$T_2$ vs. $T_3$-$T_4$ | <0.001 | 2.574 | 1.573-4.215 | 0.040 | 1.867 | 1.030-3.383 |
| N classification | | | | | | |
| $N_0$-N1 vs. $N_2$-$N_3$ | <0.001 | 3.553 | 2.011-6.277 | 0.002 | 3.562 | 1.583-8.014 |
| M classification | | | | | | |
| $M_0$ vs. $M_1$ | <0.001 | 6.367 | 3.002-13.507 | 0.000 | 7.689 | 3.388-17.448 |
| Clinical stage | | | | | | |
| I-II vs. III-IV | <0.001 | 3.563 | 1.755-7.234 | 0.628 | 0.759 | 0.249-2.314 |
| TGFBR2 expression | | | | | | |
| High vs. low | <0.001 | 0.181 | 0.098-0.333 | 0.000 | 0.239 | 0.125-0.458 |

**Supplementary Table 3.** Differentially expressed miRNAs in three subgroups of tissue samples

| Description | Parametric p-value | FDR | Permutation p-value | Geom mean of ratios | | | Unique id |
|---|---|---|---|---|---|---|---|
| | | | | group 1 | group 2 | Group 2 | |
| hsa-miR-20a | 0.00339 | 0.1932708 | 0.0012 | 0.489626 | 0.4907058 | 0.9801892 | 6519885 |
| hsa-miR-93 | 0.00621 | 0.1932708 | 0.0025 | 0.5247165 | 0.5789282 | 1.0329631 | 6520210 |
| hsa-miR-20b | 0.00793 | 0.1932708 | 0.0095 | 0.5672913 | 0.4738735 | 1.3353771 | 6520264 |
| hsa-miR-18a | 0.04642 | 0.3629741 | 0.0727 | 0.2738743 | 0.3217721 | 0.6608565 | 6520174 |

**Supplementary Table 4**  The information of TGFBR2 interference fragments

| The interference fragment | Base sequence |
|---|---|
| SiRNA-TGFBR2-homo-462 | Sense ; 5'-GUUCAGAAGUCGGUUAAUATT-3'<br>Antisense ; 5'-UAUUAACCGACUUCUGAACTT-3' |
| SiRNA-TGFBR2-homo-663 | Sense ; 5'-GUGGCUGUAUGGAGAAAGATT-3'<br>Antisense ; 5'-UCUUUCUCCAUACAGCCACTT-3' |
| SiRNA-TGFBR2-homo-796 | Sense ; 5'-GCUCUGAUGAGUGCAAUGATT-3'<br>Antisense ; 5'-UCAUUGCACUCAUCAGAGCTT-3' |
| SiRNA-TGFBR2-homo-1141 | Sense ; 5'-GCUUUGCUGAGGUCUAUAATT-3'<br>Antisense ; 5'-UUAUAGACCUCAGCAAAGCTT-3' |
| SiRNA-TGFBR2-homo-1515 | Sense ; 5'-GACCUCAAGAGCUCCAAUATT-3'<br>Antisense ; 5'-UAUUGGAGCUCUUGAGGUCTT-3' |
| SiRNA-negative control | Sense ; 5'-UUCUCCGAACGUGUCACGUTT-3'<br>Antisense ; 5'-ACGUGACACGUUCGGAGAATT-3' |