**Supplementary Table S1. Expression of CD133, KLF8 and miR-429 in osteosarcoma samples**

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| --- | --- | --- | --- | --- | --- | --- | --- |
| **Case** | **Age** | **TNM** | **Clinical****stage** | **Percentage of CD133+cells** | **aNormalized KLF8 amount 2-ΔΔ Ct**  | **aNormalized miR-429 amount 2-ΔΔ Ct**  | **Sphere****formation** |
| 1 | 56 | T1N0M0 | IA | 0.07% | 4.3600 | 0.3027 | Yes |
| 2 | 61 | T2N0M0 | IB | 0.03% | 4.6023 | 0.2964 | Yes |
| 3 | 44 | T1N1M0 | IIA | 1.06% | 2.1854 | 0.1392 | No |
| 4 | 57 | T2N1M0 | IIA | 1.83% | 3.0938 | 0.4336 | Yes |
| 5 | 49 | T2N2M0 | IIB | 1.20% | 2.6927 | 0.2578 | Yes |
| 6 | 67 | T3N0M0 | IIIA | 1.38% | 3.2247 | 0.1937 | Yes |
| 7 | 58 | T3N3M1 | IV | 0.95% | 5.3219 | 0.2026 | Yes |
| 8 | 59 | T2N2M0 | IIIA | 0.84% | 4.3963 | 0.1962 | Yes |
| 9 | 51 | T2N0M0 | IB | 0.69% | 5.2014 | 0.3525 | No |
| 10 |  72 | T2N3M0 | IIIB | 1.81% | 4.0390 | 0.4669 | Yes |

a Relative quantification was performed by the 2-ΔΔCt method with the adjacent osteosarcoma tissue sample as a calibrator. Data show the means from three independent analyses. Every independent analysis was carried out after the RNA extraction step. Total RNA was poly-A tailed, reverse transcript, and then real-time PCR tested. ΔCT obtained from real-time PCR was subject to paired t-test (ΔCT = CTKLF8 -CT GAPDH). ΔCT obtained from real-time PCR was subject to paired t-test (ΔCT = CTmiR-429-CT U6). The expression levels of KLF8 in tumor tissues were significantly higher than normal tissues (P < 0.01). The expression levels of miR-429 in tumor tissues were significantly lower than normal tissues (P < 0.01).