**S. Table 1: Comparison of the *nNMF* clusters with IntNMF, SNF and iCluster methods on Glioblastoma study.** All four methods result in three subtypes of the disease. The clustering assignment from the proposed nNMF method matches closely with the clustering assignment given by IntNMF as measured by Adjusted Rand Index. Also, the clustering assignment by nNMF has good match with the clustering assignment given by iCluster and SNF methods.

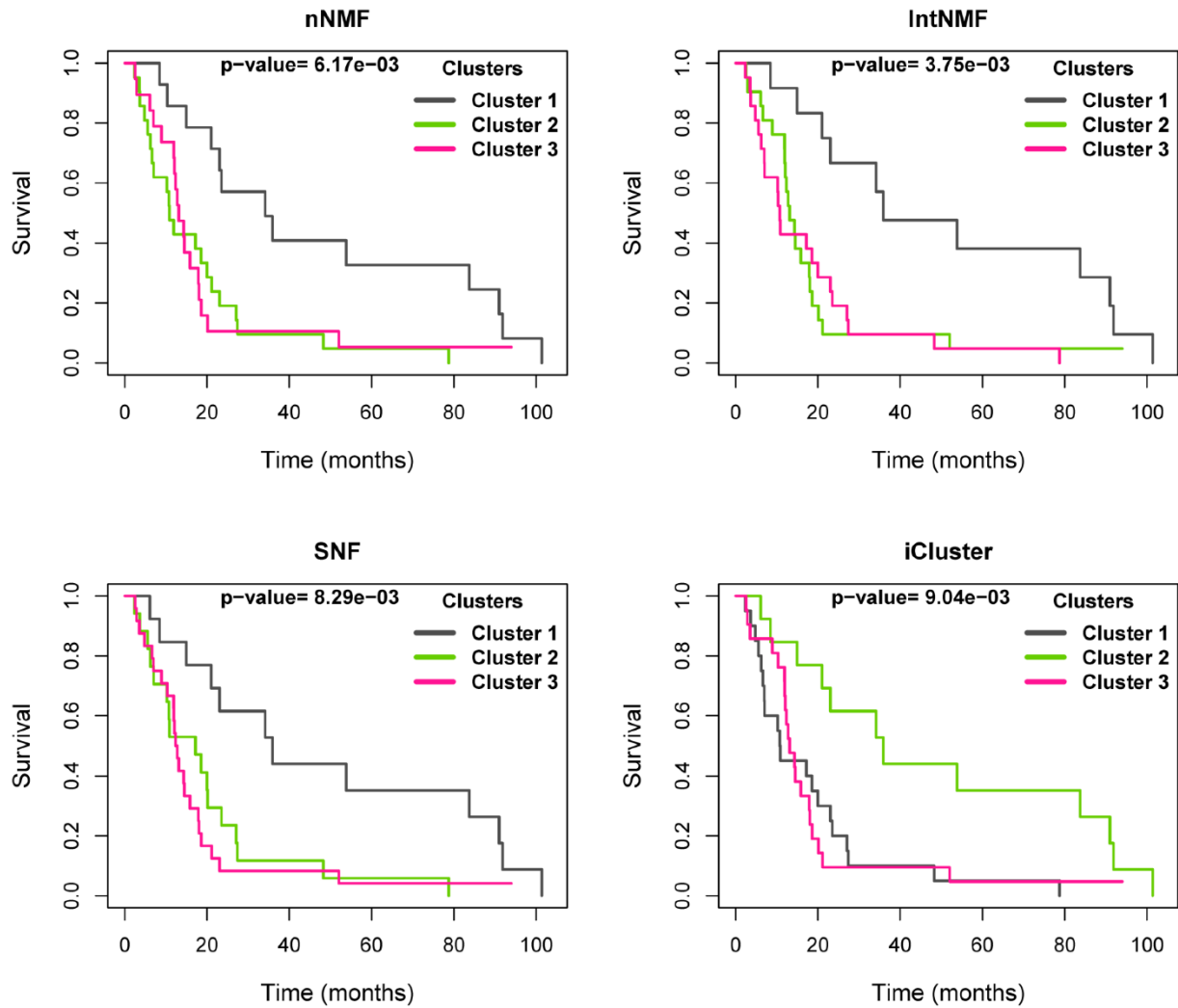| | | nNMF subtypes | | | | Adjusted Rand Index |
|---|---|---|---|---|---|---|
| | | C1 | C2 | C3 | Total | |
| IntNMF | C1 | 12 | 0 | 0 | 12 | |
| Subtypes | C2 | 0 | 3 | 19 | 22 | 0.6831 |
| | C3 | 2 | 18 | 1 | 21 | |
| | Total | 14 | 21 | 20 | 55 | |
| SNF | C1 | 12 | 0 | 1 | 13 | |
| Subtypes | C2 | 1 | 15 | 1 | 17 | 0.5083 |
| | C3 | 1 | 6 | 18 | 25 | |
| | Total | 14 | 21 | 20 | 55 | |
| iCluster | C1 | 1 | 18 | 1 | 20 | |
| Subtypes | C2 | 12 | 0 | 1 | 13 | 0.6363 |
| | C3 | 1 | 3 | 18 | 22 | |
| | Total | 14 | 21 | 20 | 55 | |

# Glioblastoma



**Fig S42: Comparison of the survival probabilities of the subtypes identified by *nNMF* with IntNMF, SNF and iCluster methods on Glioblastoma study.** The survival probabilities of the subjects in the identified subtypes are significantly different with all methods. In each case, the survival probability of one group is clearly better than that of the remaining two subtypes.

**S. Table 2: Comparison of the *nNMF* clusters with IntNMF, SNF and iCluster methods on Lower Grade Glioma study.** All four methods result in three subtypes of the disease. The clustering assignment from the proposed nNMF method matches closely with the clustering assignment given by IntNMF as measured by Adjusted Rand Index. Also, the clustering assignment by nNMF has good match with the clustering assignment given by SNF method. However, the clustering assignment from nNMF matches least with iCluster method.

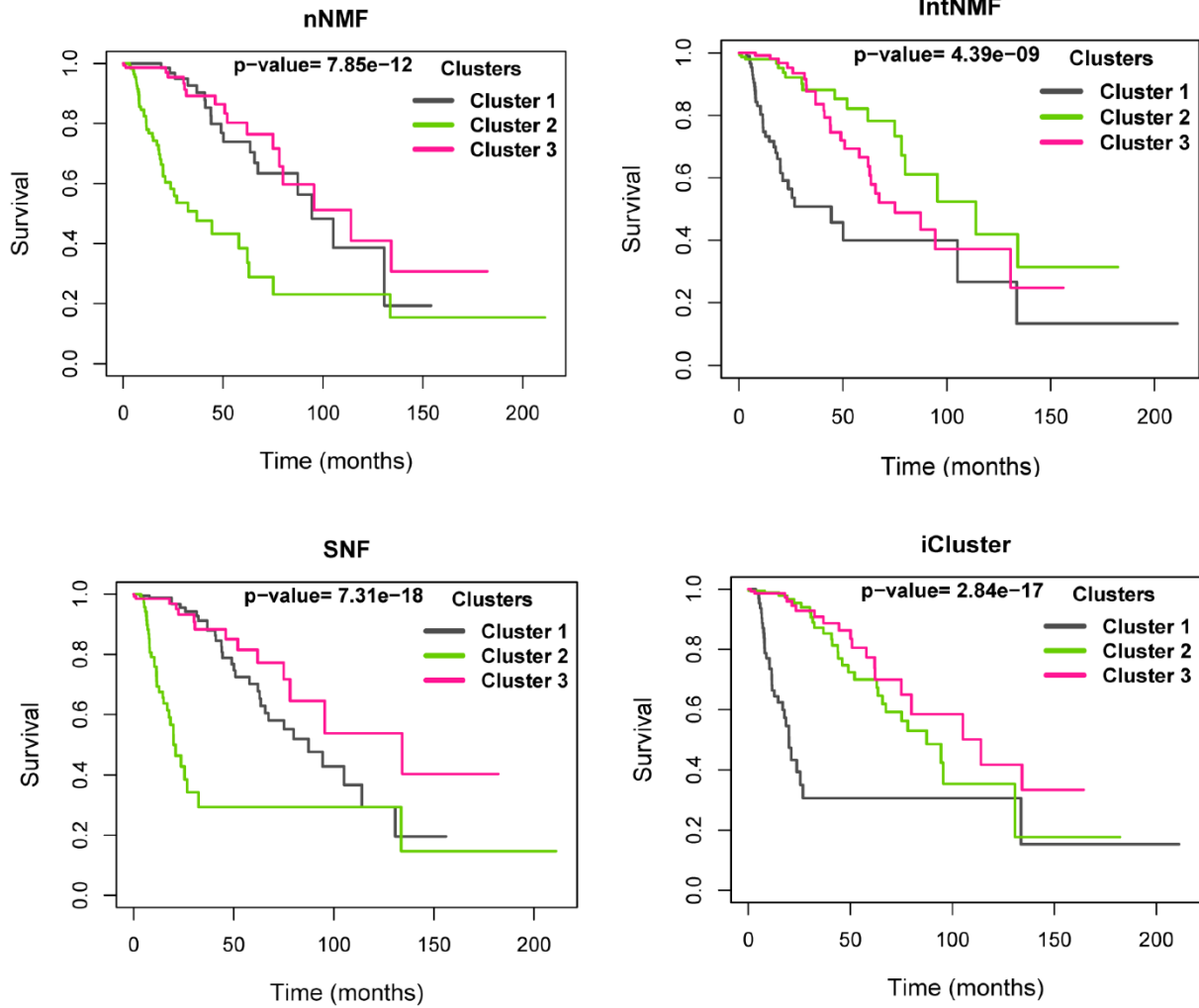| | | nNMF subtypes | | | | Adjusted Rand Index |
|---|---|---|---|---|---|---|
| | | C1 | C2 | C3 | Total | |
| **IntNMF** | **C1** | 12 | 109 | 1 | **122** | |
| **Subtypes** | **C2** | 2 | 17 | 166 | **185** | **0.6201** |
| | **C3** | 157 | 36 | 8 | **201** | |
| | **Total** | **171** | **162** | **175** | **508** | |
| **SNF** | **C1** | 171 | 58 | 22 | **251** | |
| **Subtypes** | **C2** | 0 | 99 | 0 | **99** | **0.5667** |
| | **C3** | 0 | 5 | 153 | **158** | |
| | **Total** | **171** | **162** | **175** | **508** | |
| **iCluster** | **C1** | 0 | 92 | 0 | **92** | |
| **Subtypes** | **C2** | 130 | 30 | 82 | **242** | **0.2073** |
| | **C3** | 41 | 40 | 93 | **174** | |
| | **Total** | **171** | **162** | **175** | **508** | |

**Fig S43: Comparison of the survival probabilities of the subtypes identified by *nNMF* with IntNMF, SNF and iCluster methods on Lower Grade Glioma study.** The survival probabilities of the subjects in the identified subtypes are significantly different with all methods. In each case, the survival probability of one group is clearly worse than that of the remaining two subtypes.

**S. Table 3: Comparison of the *nNMF* clusters with IntNMF, SNF and iCluster methods on Head and Neck Squamous Cell Carcinoma (HNSCC) study.** nNMF and IntNMF result in four subtypes of the disease, SNF results in three subtypes and iCluster results in two clusters. The clustering assignment from the proposed nNMF method matches closely with the clustering assignment given by IntNMF as measured by Adjusted Rand Index. The clustering assignment by nNMF has least match with the clustering assignment given by SNF and iCluster methods.

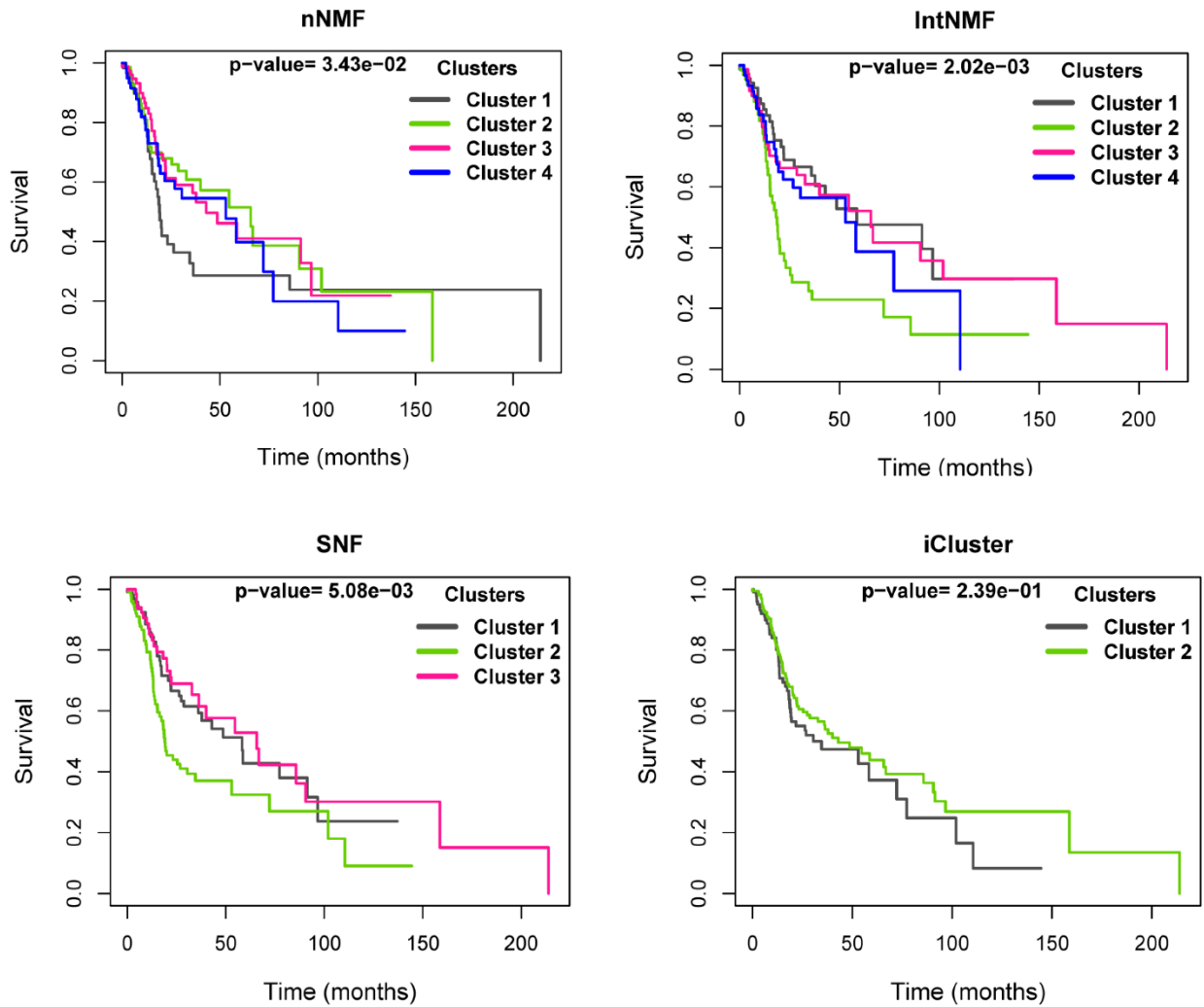| | | nNMF subtypes | | | | | Adjusted Rand Index |
|---|---|---|---|---|---|---|---|
| | | C1 | C2 | C3 | C4 | Total | |
| **IntNMF** | **C1** | 2 | 2 | 69 | 1 | **74** | |
| **Subtypes** | **C2** | 46 | 7 | 6 | 6 | **65** | **0.602** |
| | **C3** | 8 | 61 | 7 | 0 | **76** | |
| | **C4** | 4 | 4 | 1 | 55 | **64** | |
| | **Total** | **60** | **74** | **83** | **62** | **279** | |
| **SNF** | **C1** | 12 | 10 | 75 | 5 | **102** | |
| **Subtypes** | **C2** | 35 | 19 | 2 | 49 | **105** | **0.3232** |
| | **C3** | 13 | 45 | 6 | 8 | **72** | |
| | **Total** | **60** | **74** | **83** | **62** | **279** | |
| **iCluster** | **C1** | 20 | 17 | 5 | 62 | **104** | |
| **Subtypes** | **C2** | 40 | 57 | 78 | 0 | **175** | **0.2426** |
| | **Total** | **60** | **74** | **83** | **62** | **279** | |

# Head and Neck Squamous Cell Carcinoma



**Fig S44: Comparison of the survival probabilities of the subtypes identified by *nNMF* with IntNMF, SNF and iCluster methods on Head and Neck Squamous Cell Carcinoma study.** The survival probabilities of the subjects in the identified subtypes are significantly different with all methods except iCluster method.