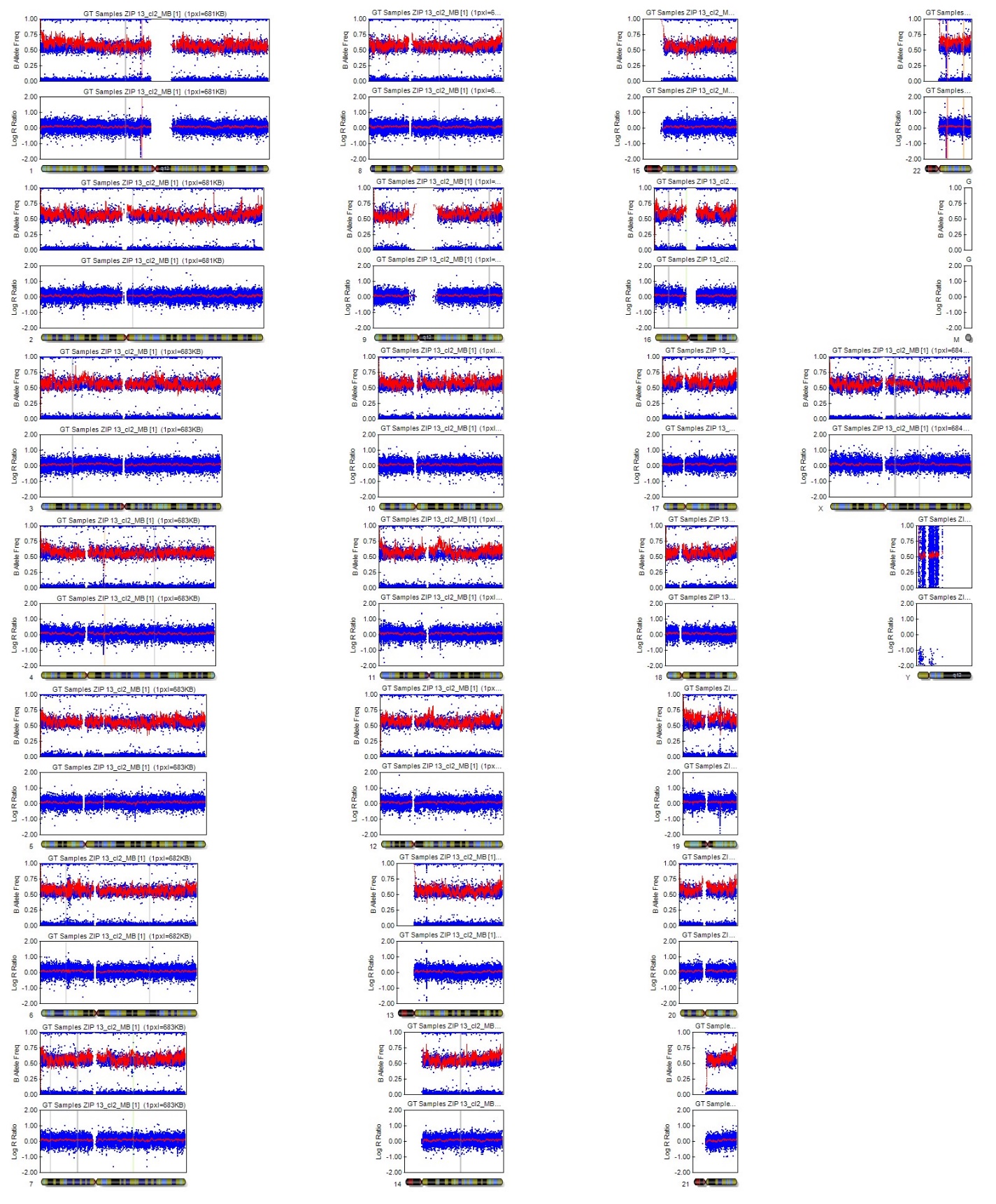
**Supplementary Fig. 2**

|  |
| --- |
| **Virtual karyotype** |

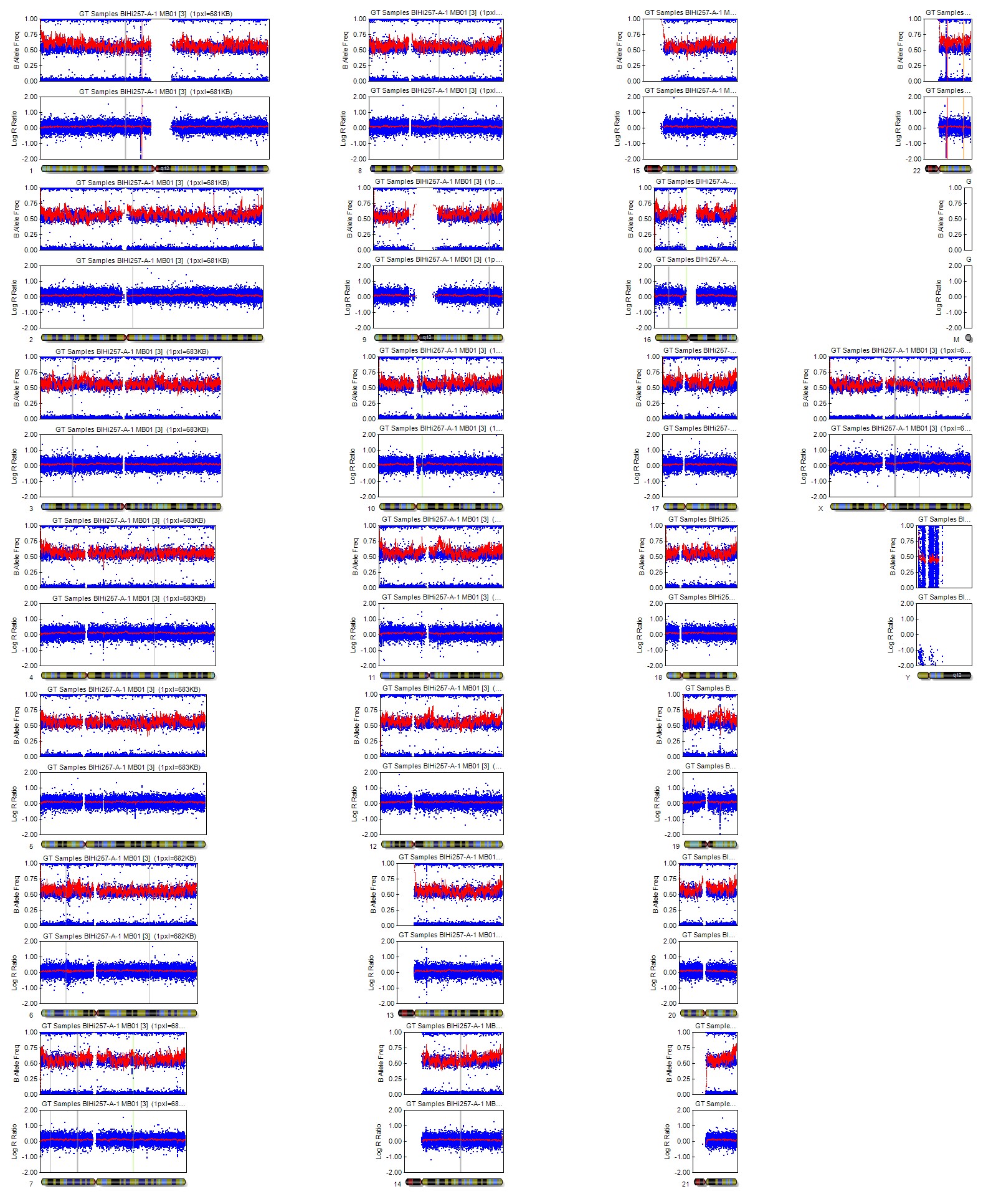
Parameters are set to detect copy number variations (CNVs) ≥ 45 kb and loss of heterozygosity (LOH) regions > 1 Mb with a confidence value > 35. Balanced translocations and inversions cannot be detected with this method. Aberrant copy number regions are identified by log R ratio and B allele frequency. Copy number changes (gains and losses) greater than **0.4 Mb** and regions of LOH above **5 Mb** are considered reportable and taken into account for interpretation. Genomic positions are based on genome build GRCh37/hg19.

|  |  |  |  |
| --- | --- | --- | --- |
| **Color** | **CNV Value** | **Aberration** | **Genotype** |
| Red | 0 | Loss | 00 |
| Organge | 1 | Loss | X0 |
| Grey | 2 | LOH | XX |
| Light green | 3 | Gain | XXX |
| Dark green | 4 | Gain | XXXX |

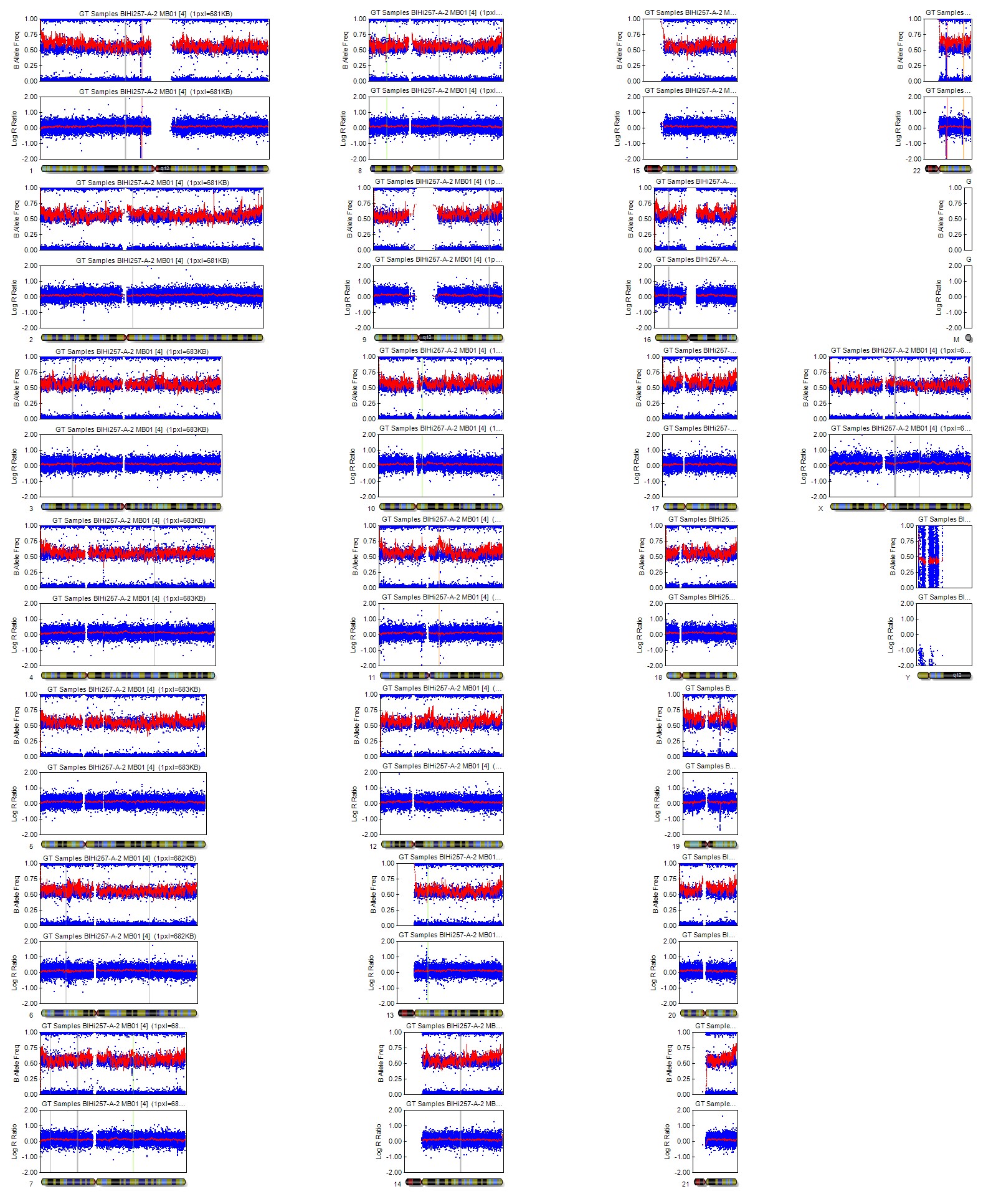
**ZIPi013-B**



**ZIPi013-B-1**



**ZIPi013-B-2**



|  |
| --- |
| **Western blot: TRPM4** |

