

1.2 Release Notes

| T | Key | Summary | Status |
|---|-----------|--|----------|
| | BARNA-257 | Error in read ID: could not parse read identifier in indexed bam generated by GEMtools | RESOLVED |
| | BARNA-256 | When an error occurs solving the linear system, the matrix is written on stderr and an exception is thrown even if the deconvolution continues | RESOLVED |
| | BARNA-248 | Capacitor complains about READ_DESCRIPTOR when given a unindexed BAM file | RESOLVED |
| | BARNA-247 | Capacitor still wants the -p <parameterfile> option even if I specify all mandatory paramters on the command line | RESOLVED |
| | BARNA-246 | UnixSorter line interceptor called for each merge step instead of just the final one | RESOLVED |
| | BARNA-242 | When counting Splice Junctions and Introns, output the correct GeneID of a locus if multiple Genes are contained | RESOLVED |
| | BARNA-240 | Capacitor runs out of Heap Space with some BAM files | RESOLVED |
| | BARNA-239 | Parameter Schema relative path parser extends Windows paths | RESOLVED |
| | BARNA-238 | Wrong number of reads detected in some BAM input files | RESOLVED |

9 issues