

CALEYDO StratomeX ANALYSIS

Workgroup leader: Nils Gehlenborg (nils@hms.harvard.edu)

Analyses were conducted in Caleydo StratomeX 3.1.2 (Lex et al., 2012; Streit et al., 2014) with Firehose THCA AWG freeze run data from 14 July 2013 and standard data from 23 June 2013 (for mRNA and microRNA expression matrices). mRNA, microRNA, methylation and RPPA cluster assignments, *RAS* and *BRAF*^{V600E} mutation status, driver fusion events, histology classes, and risk information were imported from the master data table of 14 March 2014 (see Table S2). Results are shown in Figure 1, Figure 2 and Figure 3 below.

References

A Lex, M Streit, H-J Schulz, C Partl, D Schmalstieg, PJ Park, N Gehlenborg, "StratomeX: Visual Analysis of Large-Scale Heterogeneous Genomics Data for Cancer Subtype Characterization". *Computer Graphics Forum* **31**:1175-1184 (2012).

M Streit, A Lex, S Gratzl, C Partl, D Schmalstieg, H Pfister, PJ Park, N Gehlenborg, "Guided visual exploration of genomic stratifications in cancer". *Nature Methods* **11**:884-885 (2014).

Software

<http://stratomex.caleydo.org>

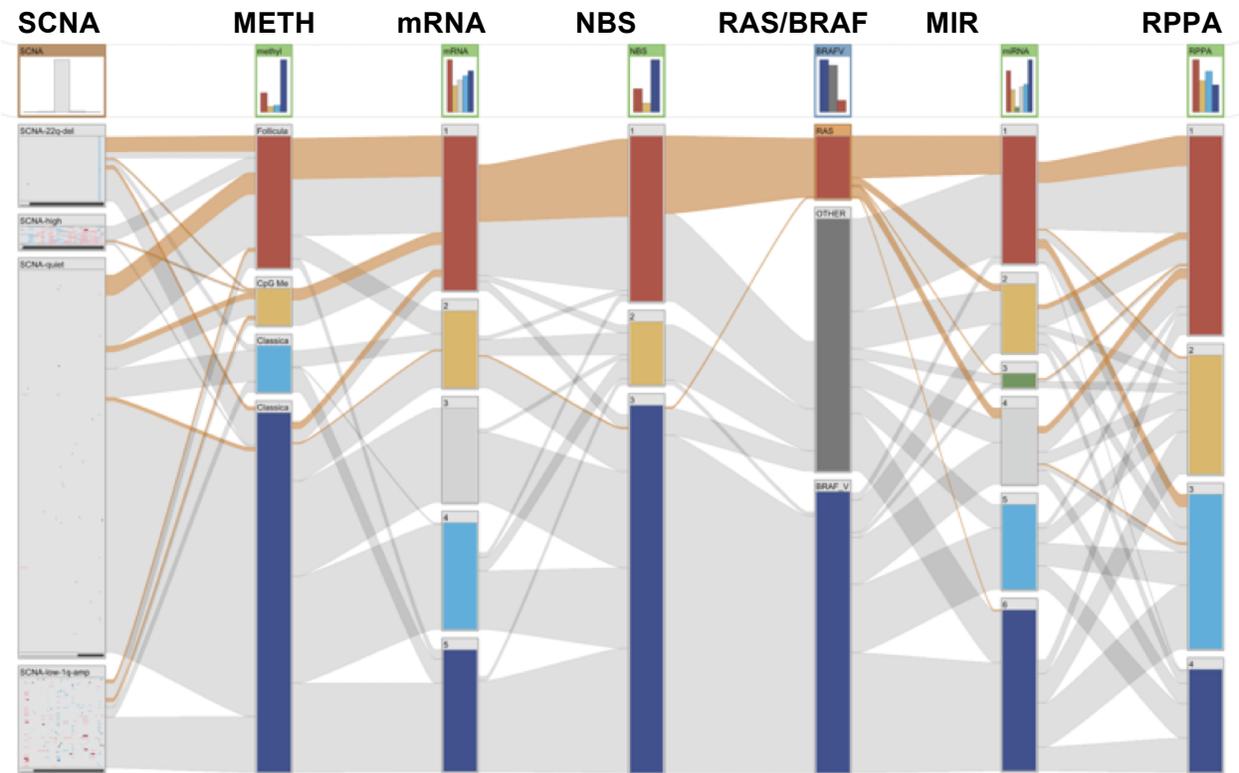


Figure 1. mRNA subclass exploration with Caleydo StratomeX. Columns represent patient assignments for SCNA clusters, methylation clusters, mRNA clusters, NBS clusters, *RAS* and *BRAF*^{V600E} mutation status, microRNA clusters and RPPA clusters (from left to right). The orange bands indicate the patients with *RAS* mutations and their distributions across SCNA, NBS, mRNA, microRNA, methylation and RPPA clusters, emphasizing that they largely form a distinct group of patients that tend to co-occur in clusters across multiple data types.

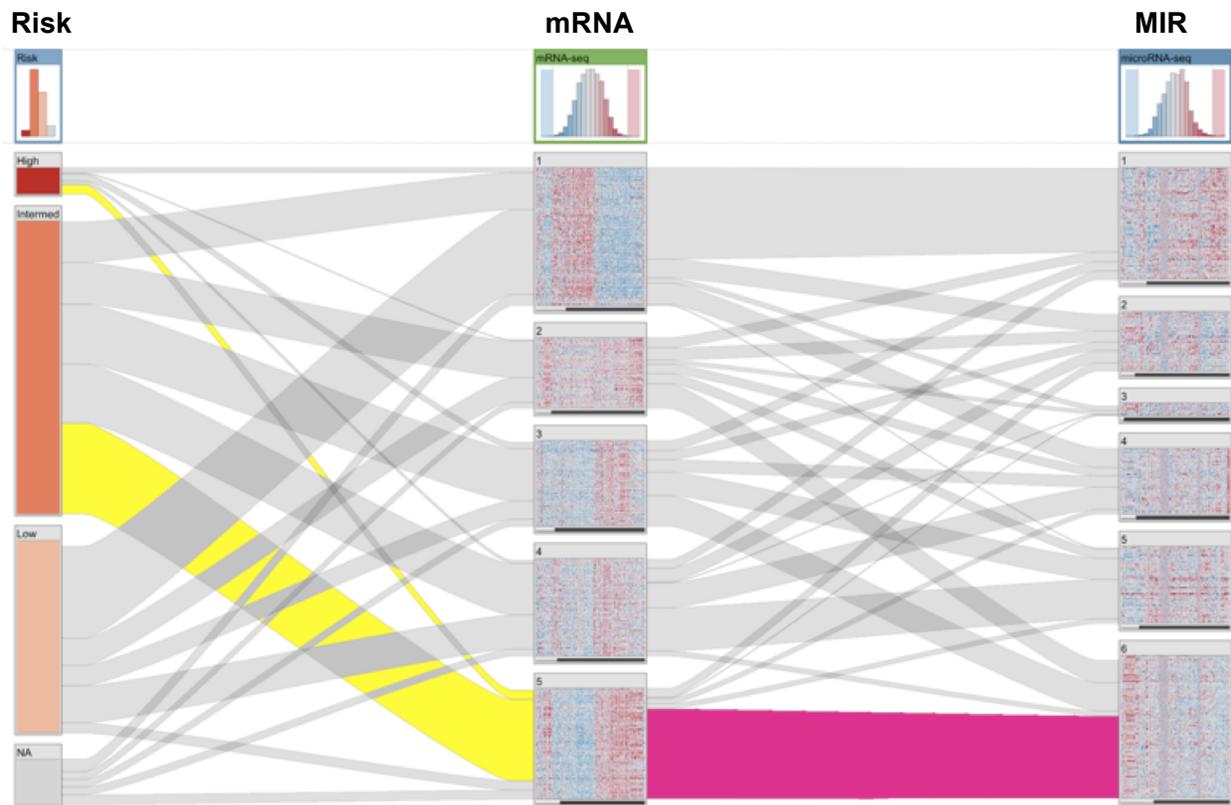


Figure 2. mRNA subclass exploration with Caleydo StratomeX. Columns represent patient assignments for risk (left), mRNA clusters (center; cluster 1 = *RAS*-like, clusters 2-5 = *BRAF*-like), and microRNA clusters (right). Heat maps for 1,500 and 514 most variable mRNAs and microRNAs, respectively, are shown (rows = patients, columns = genes; blue = lower than cohort mean, red = higher than cohort mean). Bands show intersection between patient sets: the wider the band, the larger the overlap. Yellow bands between risk and mRNA columns indicate very large number of intermediate and high risk patients in *mRNA cluster 4*. The pink band between mRNA and microRNA columns highlights strong overlap between *mRNA cluster 5* and *microRNA cluster 6*.

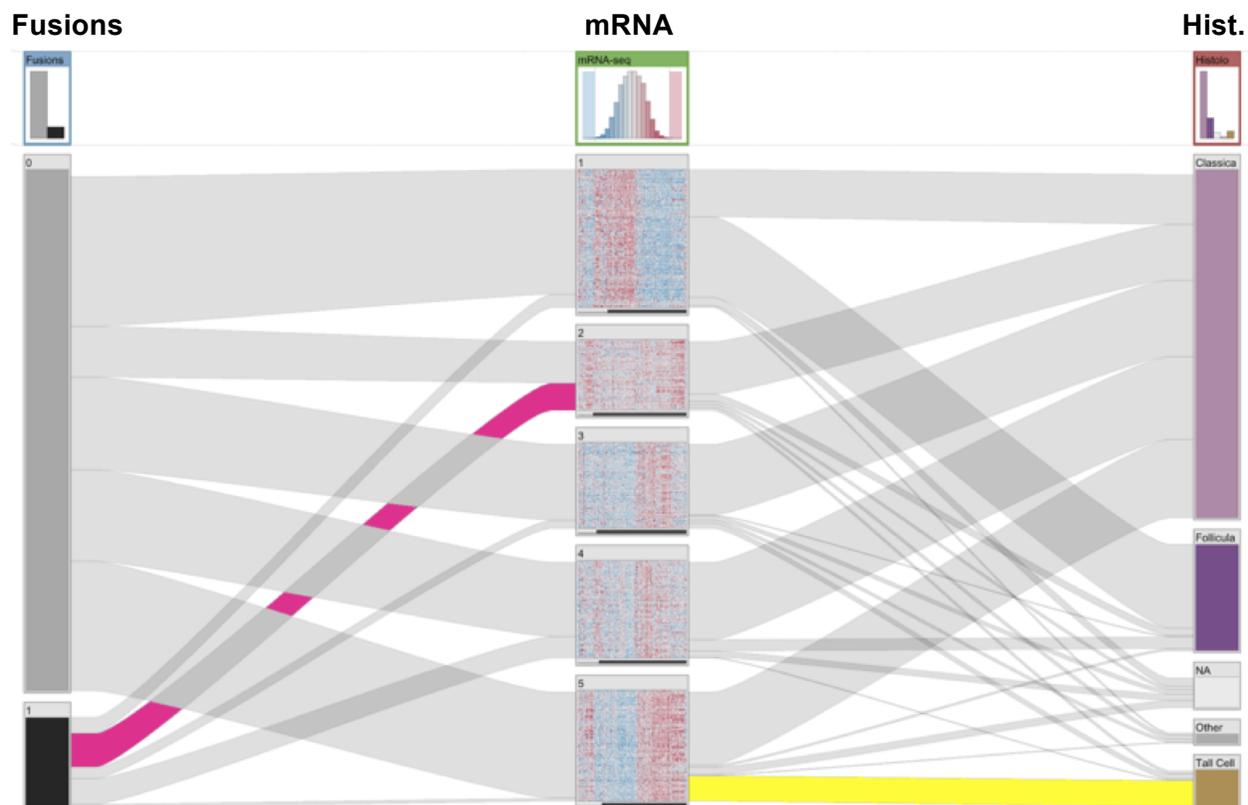


Figure 3. mRNA subclass exploration with Caleydo StratomeX as in Figure S73. Columns represent patient assignments for driver fusion events (left; gray = no driver fusion event reported, black = at least one fusion driver event reported), mRNA clusters (center; cluster 1 = RAS-like, clusters 2-5 = BRAF-like), and histology classes (right). Heat maps for 1,500 most variable mRNAs are shown (rows = patients, columns = genes). The pink band between fusion driver and mRNA columns indicate large number of driver fusion events in cluster 2 (in 37% percent of cases in cluster 2). The yellow band between mRNA and histology columns illustrates that almost all tall cell cases (71%) are contained in mRNA cluster 5.