drugMatrix changes in tSet construction

**From s\_hepatocyte**

* All NA columns removed
* Following cols removed: Accession.Number, Term.Accession.Number, Term.Source.REF.4, Term.Accession.Number.4, Characteristics.StdInChIKey., Term.Accession.Number.6, .Source.REF.6, Protocol.REF, Sample.Name, Term.Accession.Number, Term.Accession.Number.5

Col Name Changes:

* old = c('Source.Name', 'Characteristics.Subject.ID.', "Characteristics.Strain.", "Characteristics.Organism.","Characteristics.Sex.", "Characteristics.Cell.", "Characteristics.Assay.Type.", "Characteristics.Biological.Replicate.", "Characteristics.Technical.Replicate. "Factor.Value.Compound.","Characteristics.Control.", "Characteristics.Sample.Match.", "Factor.Value.Dose.", "Characteristics.DoseUnit.", "Factor.Value.Dose.Duration.", "Characteristics.Treatment.Group.","Term.Source.REF", "Characteristics.Vehicle.")
* new = c("source\_name", "samplename", "STRAIN\_TYPE", "species", "sex\_type", "cellid", "test\_type", "biological\_replicate", "individual\_id", "drugid", "Control", "sample\_match.", "concentration", "dose\_unit" ,"dose\_duration\_inDays", "treatment\_group", "org\_id\_abbr", "Vehicle")

Adding Cols

* Chiptype, xptype, batchid, organ\_id, drugmatrix.drugid, individual\_id, celfilename, duration, dose\_level

Changing Cols

* All Control rows drug changed to DMSO
  + phenodata$drugmatrix.drugid[827:939] <- "DMSO"
  + to improve compatibility with plotting functions
* phenodata$drugmatrix.drugid[19:24] <- "4,4'-diaminodiphenylmethane"
* phenodata$drugmatrix.drugid[531:537] <- "N,N-dimethylformamide"
* phenodata$drugmatrix.drugid[773:778] <- "tgf beta-1, human recombinant"
  + Above names changed to be compatible with given lab list of drugs

Note: modularized pipeline for drugmatrix