

# Gene Set Enrichment (GSEA)

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## Running GSEA for RNAseq

- .rnk file      Cut/paste to new excel file:  
                  *filter on minimum expression (e.g. baseMean > 5)*  
                  col1 = gene names/IDs  
                  col2 = log2FC  
                  Save as txt file, change file extension to .rnk
- .gmt file      workshop: use built-in MSigDB gene sets  
                  also option to create your own custom gene set
- .rnk file gene identifiers must match gene set!***

Use GSEA parameters recommended for RNAseq  
[http://software.broadinstitute.org/cancer/software/gsea/wiki/index.php/Using\\_RNA-seq\\_Datasets\\_with\\_GSEA](http://software.broadinstitute.org/cancer/software/gsea/wiki/index.php/Using_RNA-seq_Datasets_with_GSEA)