Shared Columns Between All Splicing Events:

- **ID:** rMATS event ID
- **GeneID:** Gene ID
- **geneSymbol:** Gene name
- **chr:** Chromosome
- **strand:** Gene strand
- **IJC_SAMPLE_1:** Inclusion counts for sample 1 (comma-separated replicates)
  - This column contains the raw read counts for sample 1 that support inclusion of an exon or splicing event.
- **SJC_SAMPLE_1:** Skipping counts for sample 1 (comma-separated replicates)
  - This column contains the raw read counts for sample 1 that support skipping of an exon or splicing event.
- **IJC_SAMPLE_2:** Inclusion counts for sample 2 (comma-separated replicates)
  - This column contains the raw read counts for sample 2 that support inclusion of an exon or splicing event.
- **SJC_SAMPLE_2:** Skipping counts for sample 2 (comma-separated replicates)
  - This column contains the raw read counts for sample 2 that support skipping of an exon or splicing event.
- **IncFormLen:** Length of the inclusion form (used for normalization)
- **SkipFormLen:** Length of the skipping form (used for normalization)
- **PValue:** Significance of the splicing difference between two groups
- **FDR:** False Discovery Rate based on the p-value
- **IncLevel1:** Inclusion level for sample 1 (comma-separated replicates, based on normalized counts)
  - This column represents the proportion or percentage of transcripts in sample 1 where a particular exon (or splicing event) is included, across multiple replicates.
- **IncLevel2:** Inclusion level for sample 2 (comma-separated replicates, based on normalized counts)
  - This column represents the proportion or percentage of transcripts in sample 2 where a particular exon (or splicing event) is included, across multiple replicates.
- **IncLevelDifference:** This column represents the difference in transcript inclusion levels between two conditions or time points. A larger positive value indicates that the inclusion level is higher in IncLevel1 compared to IncLevel2, while a larger negative value suggests it is lower in IncLevel1.

Event-Specific Columns:

Key Terms:

- **EE =** Exon End
- **ES =** Exon Start
- **UpstreamES/EE:** Start/end position of the exon upstream of the event.
- **DownstreamES/EE:** Start/end position of the exon downstream of the event.
- **exonStart_0base:** Start position of splicing event
- **exonEnd:** End position of splicing event

1. **SE (Skipped Exon):**
    - **Coordinates:** exonStart_0base, exonEnd, upstreamES, upstreamEE, downstreamES, downstreamEE
    - **Inclusion form:** Includes the target exon (exonStart_0base, exonEnd).
2. **MXE (Mutually Exclusive Exon):**
    - **Coordinates:** 1stExonStart_0base, 1stExonEnd, 2ndExonStart_0base, 2ndExonEnd, upstreamES, upstreamEE, downstreamES, downstreamEE
    - **If the strand is +:** The inclusion form includes the 1st exon (1stExonStart_0base, 1stExonEnd).
    - **If the strand is -:** The inclusion form includes the 2nd exon (2ndExonStart_0base, 2ndExonEnd).
3. **A3SS/A5SS (Alternative 3' or 5' Splice Site):**
    - **Coordinates:** longExonStart_0base, longExonEnd, shortES, shortEE, flankingES, flankingEE
    - **Inclusion form:** Includes the long exon instead of the short exon (longExonStart_0base, longExonEnd).
4. **RI (Retained Intron):**
    - **Coordinates:** riExonStart_0base, riExonEnd, upstreamES, upstreamEE, downstreamES, downstreamEE
    - **Inclusion form:** Retains the intron between upstreamEE and downstreamES (riExonStart_0base, riExonEnd).