

R workspace - additional information

The following variable names are used in the R workspace - important ones in **bold**.

Used acronyms:

BC' : alias: uni / unique, a set not having an overlap to other sets, e.g. BCuni, BCunique

NSP', SP', MSC' : alias: NSPunique, SPunique, MSCunique.

'i', 'I' denote intersection between, e.g. BC i H1 i H2 or BCuni I H1 i H2

'sv' : variables including sample associated splice variants subdivided by splice events

'joined', 'join' : variables where the splice events are joined to one set per sample

JC+JCEC based list variables contain 10 (sv) or two (joined) sub-variables.

Description	R variables: prefix	Examples
Significant rMATS results	s.	s.B, s.BC, s.x.sp
strip position from gene symbol	s. -> s1.	s1.BC
join splice events	s1. -> u.	u.BC
downstream intersections	u. -> u.2.	u.2.BCiH1iH2
downstream intersections	s1. -> s1.2.	s1.2.BCiH1iH2
gene symbols plus position	s. -> s2.	s2.G1
join splice events	s2. -> u2.	u2.E1
downstream intersections	u2. -> u.3.	u.3.NSPiG1iG2
strip position again	u.3. -> u.3.1.	u.3.1.BCuniIH1iH2
gene symbols plus PSI + counts	s. -> c.s. + counts.	c.s.B, counts.B.A3.JC
plot genomic distribution	c.s. -> g.s. (sv)	g.s.B
GO analysis	s1. -> ba. (sv)	ba.BC
	u. -> bb. (joined)	bb.BC.joined
CORUM analysis	s. -> cx. (sv)	cx.BC
	s. -> cx. (joined)	cx.BC.joined
Search		
compare overlap between splice variants	a3.	a3.bb.sp.nsp.msc.ic
compare expression results	nde.	nde.312onco43
search for gene names	search.	search.s1.set01