		Ramaswami, 2013	Ramaswami, 2012	Peng, 2012	Park, 2013	Zhu, 2013	Bahn, 2012	Gu, 2012	Dillman, 2013	Lagarrigue, 2013	Rodriguez, 2012	Graveley, 2011
<u>Data</u>	DNA-seq											
	RNA-seq		PolyA+	PolyA+/-	PolyA+	PolyA+				PolyA+		PolyA+
	Adar null strain											
	Replicates		2								2	
<u>Aligner</u>		BWA	BWA	SOAP2/ SOAPSplice	Bowtie	Bowtie	Bowtie/BLAT/ Tophat	Bowtie		mrsFAST/Tophat	TopHat	
Reference	Genome	hg19	hg19	hg18	hg19	hg19	hg18	mm9	mm9	mm9	dm3	dm3
	Transcripts		Gencode, RefSeq, Ensembl and UCSC		GENCODE							
<u>pre-filter</u>	Remove duplicate reads	Picard	Samtools rmdup		Samtools rmdup							
	Realign to indel											
	Recalibrate baq											
	Uniquely mapped reads											
	Caller	GATK	In house	SOAPsnp	In house	In house	In house	In house	samtools		In house	In house
post-filter	Base call quality	> 25	>= 25	>= 20				>= 20				
	Mapping quality	> 21	>21									
	Coverage		>10	5					>= 5	>= 10	>= 10	
	Alternative N bases		>2	>2	>2	>= 2						
	Base modification									(DNA+RNA)/depth >= 90%		
	1 variant within N bp span			5						5		
	Discard mismatch in the Nbp	6	6				5					
	Highly similar region	BLAT	BLAT	BLAT					BLAT			
	Supporting mismatch			> 2 reads	>10%	> 5%		>= 5%		>= 10%		>= 5 reads
	Expression level					5(FPKM)						
	Effective signal					> 95%						
	Strand bias											
	Extreme edited sites			100%								
	Ubiquitous events					> 3 tissues/cell lines			Shared by all samples	Shared by 5/6 samples	Shared by 5/6 samples	least 2 adult samples
	N bp of splice junction	5	4		5							6
	N bp repeat	>6		>1						>= 3		
	Homo-polymer		>6bp									
Knowledge filter	SNP sites	dbSNP	dbSNP, 1000 genomes, EVS	dbSNP, 1000 genomes								
	ChIP-seq data				call CNV							
	CNV sites			CNVnator								
	Mask repeat seq.		RepeatMasker annotation							SciRoKo		
	hypervariable sites	abParts in UCSC										
	Bidirectional transcripts											