Supplementary Table S1. Output and transitional tables columns description. All columns are listed in an alphabetical order. Related to Steps 1-5 and Expected outcomes.

Column name	Column description	Possible values
alg	algorithm used for detection of mutations	e.g.: mutect2, somatic sniper
alt	alternative allele	e.g.: G, A, GAA
arm	in which part of miRNA precursor mutation is located	5p, loop, 3p
balance	arm from which the main miRNA is generated; defined based on deep sequencing reeds (miRBase), [for details see (Urbanek-Trzeciak et al., 2020)]	5p, 3p, both, undefined
based_on_coordinates	indicates whether used coordinates were defined based on miRBase annotations or were predicted based on miRNA structure	yes, no
BQ_alt_norm	BQ metric from VCF file for alternative allele in normal sample	e.g.: 0
BQ_alt_tum	BQ metric from VCF file for alternative allele in tumor sample	e.g.: 32
BQ_ref_norm	BQ metric from VCF file for reference allele in normal sample	e.g.: 30
BQ_ref_tum	BQ metric from VCF file for reference allele in tumor sample	e.g.: 31
chrom	chromosome	e.g.: chr1, chrX
complex	if mutations are complex (multiple mutations in single miRNA gene in single sample)	0 (no), 1 (yes)
confidence	as high-confidence miRNA genes, we considered genes coding for miRNA precursors annotated as “high confidence” in miRBase and/or deposited in MiRGeneDB v2.0	High, Low
cut_region	whether the mutation is within Drosha or Dicer cut region	0 (no), 1 (yes)
duplex	whether the mutation is within duplex	0 (no), 1 (yes)
eval	if filtering is performed it indicates if a mutation passed the filtering	True, False
filename	path to analysed VCF file	e.g.: /home/Documents/0001.vcf.gz
filter	filter column from VCF file	e.g.: PASS
format	format column from VCF file	e.g.: GT:AD:BQ:DP:SS
from_start	nucleotide position from start of miRNA region in which mutation is located (e.g., within seed, 5’ flanking sequence)	e.g.: 1, 3

from_end	nucleotide position from end of miRNA region in which mutation is located (e.g., within seed, 5' flanking sequence)	e.g.: -1, -25
hgvs	noncoding HGVS nomenclature of the mutation in the reference to the miRBase coordinates *Note that annotation of some indels may not match the latest HGVS recommendations; for multimutations (multiple changes in a single position in one sample) HGVS nomenclature is not available	e.g.: n.90G>A, n.67+21G>A, n.1-15delA
hgvs_g	genomic HGVS nomenclature of the mutation; for multimutations HGVS is not available	e.g.: NC_000010.11:g.17845137C>A, NC_000001.11:g.1167872_1167873insT
if_complex	if there was any complex mutations in the gene	0 (no), 1 (yes)
ID	miRBase ID	e.g.: MI0000737
indiv_ID	identifier of the sample	e.g.: 001
indiv_name	sample identifier	e.g.: sample01
indiv_name_count	how many mutations were found in a position (or in a indicated gene)	e.g.: 1
indiv_name_nunique	how many samples had specific mutation (or mutation in a indicated gene)	e.g.: 1
info	info column from VCF file	e.g.: ACGTNacgtnMINUS=0,0,23,1,0,0,0,11,4,0...
mirgenedb_ID	miRgeneDB ID	e.g.: Hsa-Mir-8-P1a_pre
motifs	whether any motif was disturbed as a result of the mutation	0 (no), 1 (yes)
motifs_{}	information for each checked motif if there was loss of a motif as a result of the mutation	-, loss
mutation_type	mutation type: substitution, insertion, deletion, insertion-deletion, multimutation	subst, ins, del, indel, multimutation
name	miRNA region name built by pre-miRNA name and precursor region connected by an underscore	e.g.: hsa-mir-200a_flanking-5, hsa-mir-511_post-seed
no_of_loc	internal check column	1
norm_alt_count	count of reads supporting alternative allele in normal sample	e.g.: 0
norm_ref_count	count of reads supporting reference allele in normal sample	e.g.: 20
normal	normal column from VCF file in a structure as format column dictates	e.g.: 0/0:53,0:34,0:53

orientation	miRNA gene orientation	"+, -"
pos	genomic position of the mutation	e.g.: 1167859, 20633667
pos_count	number of mutations in a miRNA gene	e.g.: 3
pos_nunique	number of unique mutated positions in a miRNA gene	e.g.: 1
pre_name	precursor name	e.g.: hsa-mir-200a, hsa-mir-6084
QSS_alt_nor	quality score for alternative allele for normal sample	e.g.: 0
QSS_alt_tum	quality score for alternative allele for tumor sample	e.g.: 99
QSS_ref_nor	quality score for reference allele for normal sample	e.g.: 3001
QSS_ref_tum	quality score for reference allele for tumor sample	e.g.: 1650
qual	qual column from VCF file	e.g.: .
ref	reference allele	e.g.: C, GCA
sample_ID_normal_aliQ	ID of aliquote of normal sample from VCF file	e.g.: 534gjhg345-sdfv689
sample_ID_normal_name	name of normal sample from VCF file	e.g.: TCGA-66678-asasd
sample_ID_tumor_aliQ	ID of aliquote of tumor sample from VCF file	e.g.: skdjf879xc-xcv6s8df
sample_ID_tumor_name	name of tumor sample from VCF file	e.g.: TCGA-2934592-msandf8
seed	whether mutation is located within seed	0 (no), 1 (yes)
SPV	somatic P-value for somatic/LOH events (Varscan)	e.g.: 0.0187
SSC	somatic score from Somatic Sniper	e.g.: 123
start	miRNA region start coordinate	e.g.: 1167853, 20633667
start_pre_build	miRBase start coordinate	e.g.: 1167863, 20633679
stop	miRNA region stop coordinate	e.g.: 1167877, 20633691
stop_pre_build	miRBase stop coordinate	e.g.: 1167952, 20633788
tumor	tumor column from VCF file in a structure as format column dictates	e.g.: 0/1:26,38:35,34:64:2
tumor_alt_count	count of reads supporting alternative allele in tumor sample	e.g.: 25
tumor_ref_count	count of reads supporting reference allele in tumor sample	e.g.: 21
type	region of miRNA precursor	flanking-5, pre-seed, seed, post-seed, loop, flanking-3
type_of_file	algorithm used to create VCF file	e.g.: somaticsniper, varscan2
type_of_subst	substitution type, n.a. for non-substitution mutations	transition, transversion, n.a.
weight	weight score	1, 1.5, 2