

# pmartR coverage - 60.12%

Files	Source					
File	Lines	Relevant	Covered	Missed	Hits / Line	Coverage
R/as.trelliData.R	587	179	179	0	39	100.00%
src/calculate_cv.cpp	244	65	65	0	3290	100.00%
R/summary_trelliData.R	147	57	57	0	4	100.00%
R/edata_transform.R	171	43	43	0	18	100.00%
R/normRes_tests.R	116	43	43	0	4	100.00%
R/edata_replace.R	130	41	41	0	18	100.00%
src/nonmissing_per_grp.cpp	86	38	38	0	22403	100.00%
R/normalize_quantile.R	140	33	33	0	9	100.00%
R/nonmissing_per_group.R	87	17	17	0	91	100.00%
src/count_missing_cpp.cpp	35	11	11	0	31527	100.00%
R/trelliPlots.R	2000	715	710	5	5	99.30%
R/as.omicsData.R	2019	544	538	6	75	98.90%
R/combine_omicsdata.R	313	152	148	4	8	97.37%
R/combine_techreps.R	222	101	98	3	24	97.03%
R/subset_funcs.R	279	61	59	2	23	96.72%
R/seqData_wrappers.R	1301	588	530	58	3	90.14%
R/bpquant.R	368	142	125	17	83	88.03%
R/cor_result.R	88	25	22	3	2	88.00%
src/kw_rcpp.cpp	250	102	89	13	45777	87.25%
R/protein_quant.R	1065	334	290	44	40	86.83%
R/imd_anova.R	2091	733	632	101	216	86.22%
R/filter_objects.R	1922	554	477	77	8	86.10%

File	Lines	Relevant	Covered	Missed	Hits / Line	Coverage
src/imd_anova.cpp	694	321	270	51	4436	84.11%
R/applyFilt.R	2654	907	760	147	9	83.79%
R/MSnSet2pepData.R	81	30	25	5	1	83.33%
R/normalize_nmr.R	761	233	187	46	5	80.26%
R/normalize_isobaric.R	444	131	103	28	2	78.63%
R/norm_funcs.R	692	171	132	39	24	77.19%
R/dim_reduction.R	131	38	29	9	1	76.32%
R/normalize_loess.R	59	12	9	3	1	75.00%
R/group_designation.R	829	259	194	65	43	74.90%
R/edata_summary.R	466	303	223	80	17	73.60%
R/helper_fn.R	1074	209	152	57	156	72.73%
R/custom_sampnames.R	149	60	43	17	16	71.67%
R/as.multiData.R	381	154	110	44	6	71.43%
R/spans.R	730	248	174	74	62	70.16%
R/normalize_global.R	584	156	102	54	38	65.38%
R/rmd_conversion.R	75	15	9	6	1	60.00%
R/missingval_result.R	118	41	24	17	1	58.54%
R/summary_pmartR.R	259	77	42	35	4	54.55%
R/filter_summary.R	1182	368	193	175	1	52.45%
R/statRes_class.R	163	68	32	36	29	47.06%
R/plot_fns.R	6539	2511	18	2493	0	0.72%
R/print_data_objects.R	719	418	0	418	0	0.00%
R/print_filter_objects.R	312	167	0	167	0	0.00%
R/report_dataRes.R	225	136	0	136	0	0.00%

File	Lines	Relevant	Covered	Missed	Hits / Line	Coverage
R/write_stat_results.R	120	49	0	49	0	0.00%
R/write_stat_results_omics.R	97	45	0	45	0	0.00%
R/results_summary.R	110	34	0	34	0	0.00%
R/survival.R	157	28	0	28	0	0.00%
R/get_comparisons.R	78	27	0	27	0	0.00%
R/summary_isobaricnormRes.R	83	23	0	23	0	0.00%
R/summary_nmrnormRes.R	67	16	0	16	0	0.00%
R/pre_imdanova_melt.R	42	11	0	11	0	0.00%
R/analysis_log.R	33	10	0	10	0	0.00%
R/surv_designation.R	24	2	0	2	0	0.00%