

MAQCsubsetILM: MAQC reference subset for the Illumina platform

Laurent Gatto

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1 The MAQC reference datasets

The MAQC (MicroArray Quality Control) project¹ provides a set of reference datasets for a set of 10 platforms (see *Summary of the MAQC Data Sets*² for more details). This package provides a subset of the Illumina MAQC dataset³.

Regarding the Illumina platform (ILM prefix), a total of 59 Human-6 BeadChip 48K v1.0 have been generated. Four different reference RNAs have been used: (A) 100% of Stratagene's *Universal Human Reference RNA*, (B) 100% of Ambion's Human Brain Reference RNA, (C) 75% of A and 25% of B and (D) 25% of A and 75% of B. Each reference has been repeated 5⁴ times (noted _A1_ to _A5_) on three different test sites (noted _1_ to _3_). As an example, the .CEL result file for the first replicate of test site 2, for the reference ARN C is named ILM_2_C1.CEL.

¹<http://www.fda.gov/nctr/science/centers/toxicoinformatics/maqc>

²http://edkb.fda.gov/MAQC/MainStudy/upload/Summary_MAQC_DataSets.pdf

³Packages for the datasets of other platforms will follow and will all be named MAQCsubsetXXX where XXX is the three-letter code used by the MAQC consortium.

⁴except for site 1, reference C, where 4 replicates are available

⁵the replicates for site 2, reference D are labelled _D1_, _D2_, _D4_, _D6_ and _D7_

These datasets are freely available and allow, for example, researchers to compare the reproducibility of their own Human-6 BeadChip 48K v1.0 data with the MAQC data. *MAQCsubsetILM* offers 3 randomly chosen BeadChips for each reference RNA, one for each test site. Each reference RNA subset is accessible as an R data object, respectively called `refA`, `refB`, `refC` and `refD`.

More information concerning the MAQC initiative can be found in the September 2006 special issue of *Nature Biotechnology*.

2 Loading the reference data

Once the library has been installed and loaded, the reference datasets can be loaded using the `(data())` function as shown below.

```
> library("MAQCsubsetILM")
> data(refA)
> refA
```

Summary of data information:

Major Operation History:

	submitted		finished	
1	2008-02-29	12:24:41	2008-02-29	12:24:43
2	2008-02-29	12:24:43	2008-02-29	12:24:43
3	2008-02-29	12:24:46	2008-02-29	12:24:46
4	2008-02-29	12:24:43	2008-02-29	12:24:45
5	2008-02-29	12:24:45	2008-02-29	12:24:45
6	2008-02-29	12:24:46	2008-02-29	12:24:46
7	2008-02-29	12:24:46	2008-02-29	12:24:46
8	2008-02-29	12:24:48	2008-02-29	12:24:48
9	2008-02-29	12:24:46	2008-02-29	12:24:48
10	2008-02-29	12:24:48	2008-02-29	12:24:48
11	2008-02-29	12:24:48	2008-02-29	12:24:49
12	2008-02-29	12:24:49	2008-02-29	12:24:49
13	2008-02-29	12:24:51	2008-02-29	12:24:51
14	2008-02-29	12:24:49	2008-02-29	12:24:51
15	2008-02-29	12:24:51	2008-02-29	12:24:51
16	2008-02-29	12:24:51	2008-02-29	12:24:51
17	2008-02-29	12:24:51	2008-02-29	12:24:51

18	2008-02-29	12:24:54	2008-02-29	12:24:54
19	2008-02-29	12:24:51	2008-02-29	12:24:54
20	2008-02-29	12:24:54	2008-02-29	12:24:54
21	2008-02-29	12:24:54	2008-02-29	12:24:54
22	2008-02-29	12:24:54	2008-02-29	12:24:54
23	2008-02-29	12:24:57	2008-02-29	12:24:57
24	2008-02-29	12:24:54	2008-02-29	12:24:56
25	2008-02-29	12:24:56	2008-02-29	12:24:56
26	2008-02-29	12:24:57	2008-02-29	12:24:57
27	2008-02-29	12:24:57	2008-02-29	12:24:57
28	2008-02-29	12:24:59	2008-02-29	12:25:00
29	2008-02-29	12:24:57	2008-02-29	12:24:59
30	2008-02-29	12:24:59	2008-02-29	12:24:59
31	2008-02-29	12:25:00	2008-02-29	12:25:00
32	2008-02-29	12:25:00	2008-02-29	12:25:00
33	2008-02-29	12:25:02	2008-02-29	12:25:02
34	2008-02-29	12:25:00	2008-02-29	12:25:02
35	2008-02-29	12:25:02	2008-02-29	12:25:02
36	2008-02-29	12:25:02	2008-02-29	12:25:03
37	2008-02-29	12:25:03	2008-02-29	12:25:03
38	2008-02-29	12:25:05	2008-02-29	12:25:05
39	2008-02-29	12:25:03	2008-02-29	12:25:04
40	2008-02-29	12:25:04	2008-02-29	12:25:05
41	2008-02-29	12:25:05	2008-02-29	12:25:05
42	2008-02-29	12:25:05	2008-02-29	12:25:05
43	2008-02-29	12:25:08	2008-02-29	12:25:08
44	2008-02-29	12:25:05	2008-02-29	12:25:07
45	2008-02-29	12:25:07	2008-02-29	12:25:07
46	2008-02-29	12:25:08	2008-02-29	12:25:08
47	2008-02-29	12:25:08	2008-02-29	12:25:08
48	2008-02-29	12:25:10	2008-02-29	12:25:10
49	2008-02-29	12:25:08	2008-02-29	12:25:10
50	2008-02-29	12:25:10	2008-02-29	12:25:10
51	2008-02-29	12:25:10	2008-02-29	12:25:11
52	2008-02-29	12:25:11	2008-02-29	12:25:11
53	2008-02-29	12:25:13	2008-02-29	12:25:13
54	2008-02-29	12:25:11	2008-02-29	12:25:13
55	2008-02-29	12:25:13	2008-02-29	12:25:13
56	2008-02-29	12:25:13	2008-02-29	12:25:13
57	2008-02-29	12:25:13	2008-02-29	12:25:13
58	2008-02-29	12:25:16	2008-02-29	12:25:16
59	2008-02-29	12:25:13	2008-02-29	12:25:15

```

60 2008-02-29 12:25:15 2008-02-29 12:25:16
61 2008-02-29 12:25:16 2008-02-29 12:25:16
62 2008-02-29 12:25:16 2008-02-29 12:25:16
63 2008-02-29 12:25:19 2008-02-29 12:25:19
64 2008-02-29 12:25:16 2008-02-29 12:25:18
65 2008-02-29 12:25:18 2008-02-29 12:25:18
66 2008-02-29 12:25:19 2008-02-29 12:25:19
67 2008-02-29 12:25:19 2008-02-29 12:25:19
68 2008-02-29 12:25:22 2008-02-29 12:25:22
69 2008-02-29 12:25:19 2008-02-29 12:25:21
70 2008-02-29 12:25:21 2008-02-29 12:25:21
71 2008-02-29 12:25:22 2008-02-29 12:25:22
72 2008-02-29 12:25:22 2008-02-29 12:25:22
73 2008-02-29 12:27:25 2008-02-29 12:27:25

```

```

                                command lumiVersion
1      lumiR("ILM_1_A1.txt", parseColumnName = FALSE)      1.5.17
2  lumiQ(x.lumi = x.lumi, detectionTh = detectionTh)      1.5.17
3                                Subsetting 47293 features.  1.5.17
4      lumiR("ILM_1_A2.txt", parseColumnName = FALSE)      1.5.17
5  lumiQ(x.lumi = x.lumi, detectionTh = detectionTh)      1.5.17
6                                Subsetting 47293 features.  1.5.17
7                                combine(x = x.lumi, y = x.lumi.i) 1.5.17
8                                Subsetting 47293 features.  1.5.17
9      lumiR("ILM_1_A3.txt", parseColumnName = FALSE)      1.5.17
10 lumiQ(x.lumi = x.lumi, detectionTh = detectionTh)      1.5.17
11                                Subsetting 47293 features.  1.5.17
12                                combine(x = x.lumi, y = x.lumi.i) 1.5.17
13                                Subsetting 47293 features.  1.5.17
14      lumiR("ILM_1_A4.txt", parseColumnName = FALSE)      1.5.17
15 lumiQ(x.lumi = x.lumi, detectionTh = detectionTh)      1.5.17
16                                Subsetting 47293 features.  1.5.17
17                                combine(x = x.lumi, y = x.lumi.i) 1.5.17
18                                Subsetting 47293 features.  1.5.17
19      lumiR("ILM_1_A5.txt", parseColumnName = FALSE)      1.5.17
20 lumiQ(x.lumi = x.lumi, detectionTh = detectionTh)      1.5.17
21                                Subsetting 47293 features.  1.5.17
22                                combine(x = x.lumi, y = x.lumi.i) 1.5.17
23                                Subsetting 47293 features.  1.5.17
24      lumiR("ILM_2_A1.txt", parseColumnName = FALSE)      1.5.17
25 lumiQ(x.lumi = x.lumi, detectionTh = detectionTh)      1.5.17
26                                Subsetting 47293 features.  1.5.17
27                                combine(x = x.lumi, y = x.lumi.i) 1.5.17

```

28	Subsetting 47293 features.	1.5.17
29	lumiR("ILM_2_A2.txt", parseColumnName = FALSE)	1.5.17
30	lumiQ(x.lumi = x.lumi, detectionTh = detectionTh)	1.5.17
31	Subsetting 47293 features.	1.5.17
32	combine(x = x.lumi, y = x.lumi.i)	1.5.17
33	Subsetting 47293 features.	1.5.17
34	lumiR("ILM_2_A3.txt", parseColumnName = FALSE)	1.5.17
35	lumiQ(x.lumi = x.lumi, detectionTh = detectionTh)	1.5.17
36	Subsetting 47293 features.	1.5.17
37	combine(x = x.lumi, y = x.lumi.i)	1.5.17
38	Subsetting 47293 features.	1.5.17
39	lumiR("ILM_2_A4.txt", parseColumnName = FALSE)	1.5.17
40	lumiQ(x.lumi = x.lumi, detectionTh = detectionTh)	1.5.17
41	Subsetting 47293 features.	1.5.17
42	combine(x = x.lumi, y = x.lumi.i)	1.5.17
43	Subsetting 47293 features.	1.5.17
44	lumiR("ILM_2_A5.txt", parseColumnName = FALSE)	1.5.17
45	lumiQ(x.lumi = x.lumi, detectionTh = detectionTh)	1.5.17
46	Subsetting 47293 features.	1.5.17
47	combine(x = x.lumi, y = x.lumi.i)	1.5.17
48	Subsetting 47293 features.	1.5.17
49	lumiR("ILM_3_A1.txt", parseColumnName = FALSE)	1.5.17
50	lumiQ(x.lumi = x.lumi, detectionTh = detectionTh)	1.5.17
51	Subsetting 47293 features.	1.5.17
52	combine(x = x.lumi, y = x.lumi.i)	1.5.17
53	Subsetting 47293 features.	1.5.17
54	lumiR("ILM_3_A2.txt", parseColumnName = FALSE)	1.5.17
55	lumiQ(x.lumi = x.lumi, detectionTh = detectionTh)	1.5.17
56	Subsetting 47293 features.	1.5.17
57	combine(x = x.lumi, y = x.lumi.i)	1.5.17
58	Subsetting 47293 features.	1.5.17
59	lumiR("ILM_3_A3.txt", parseColumnName = FALSE)	1.5.17
60	lumiQ(x.lumi = x.lumi, detectionTh = detectionTh)	1.5.17
61	Subsetting 47293 features.	1.5.17
62	combine(x = x.lumi, y = x.lumi.i)	1.5.17
63	Subsetting 47293 features.	1.5.17
64	lumiR("ILM_3_A4.txt", parseColumnName = FALSE)	1.5.17
65	lumiQ(x.lumi = x.lumi, detectionTh = detectionTh)	1.5.17
66	Subsetting 47293 features.	1.5.17
67	combine(x = x.lumi, y = x.lumi.i)	1.5.17
68	Subsetting 47293 features.	1.5.17
69	lumiR("ILM_3_A5.txt", parseColumnName = FALSE)	1.5.17

70	<code>lumiQ(x.lumi = x.lumi, detectionTh = detectionTh)</code>	1.5.17
71	Subsetting 47293 features.	1.5.17
72	<code>combine(x = x.lumi, y = x.lumi.i)</code>	1.5.17
73	Subsetting 3 samples.	1.5.17

Object Information:

LumiBatch (storageMode: lockedEnvironment)

assayData: 47293 features, 3 samples

 element names: beadNum, detection, exprs, se.exprs

protocolData: none

phenoData

 sampleNames: ILM_1_A5, ILM_2_A1, ILM_3_A2

 varLabels and varMetadata description:

 sampleID: The unique Illumina microarray Id

 site: NA

 ref: NA

 replicate: NA

featureData

 featureNames: GI_10047089-S, GI_10047091-S, ..., trpF (47293 total)

 fvarLabels and fvarMetadata description:

 TargetID: The Illumina microarray identifier

experimentData: use 'experimentData(object)'

Annotation:

Control Data: Available

QC information: Please run `summary(x, 'QC')` for details!