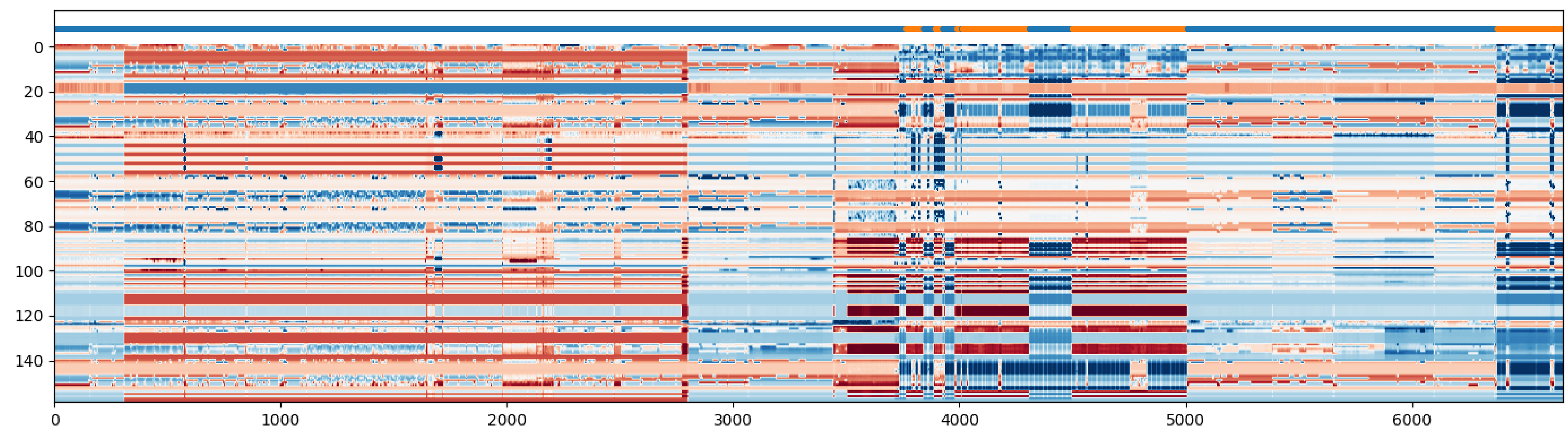
GMMs for Anomaly Detection

Back to our HPC Problem

Let's go back to our anomaly detection problem

In [2]:
```
hpcsv = hpc.copy()
hpcsv[inputs] = (hpcsv[inputs] - hpcsv[inputs].mean()) / hpcsv[inputs].std()
labels = pd.Series(index=hpcsv.index, data=(hpcsv['anomaly'] != 0), dtype=int)
util.plot_dataframe(hpcsv[inputs], labels, figsize=figsize)
```



The colored line on the top identifies anomalies (in orange)

Preprocessing

We proceed to standardize the data again

- This is not strictly needed for GMMs
- ...but many optimization algorithms are designed for standardized data

```
In [4]: tr_end, val_end = 3000, 4500

        hpcs = hpc.copy()
        tmp = hpcs.iloc[:tr_end]
        hpcs[inputs] = (hpcs[inputs] - tmp[inputs].mean()) / tmp[inputs].std()
```

We separate the training, validation, and test set

```
In [5]: trdata = hpcs.iloc[:tr_end]
        valdata = hpcs.iloc[tr_end:val_end]
        tsdata = hpcs.iloc[val_end:]
```

- This time, we keep the validation set distinct from the training set

Training and Number of Components

We now need to pick a number of components

We'll do this by using grid search and cross validation

- We would have used other method (e.g. elbow method or BIC)
- There are also variants of GMMs that can infer the number of components

In [6]:
```
%%time
opt = GridSearchCV(GaussianMixture(), {'n_components': [2, 4, 8]}, cv=5)
opt.fit(trdata[inputs])
print(f'Best parameters: {opt.best_params_}')
```

```
Best parameters: {'n_components': 8}
CPU times: user 1min, sys: 2min 16s, total: 3min 16s
Wall time: 16.9 s
```

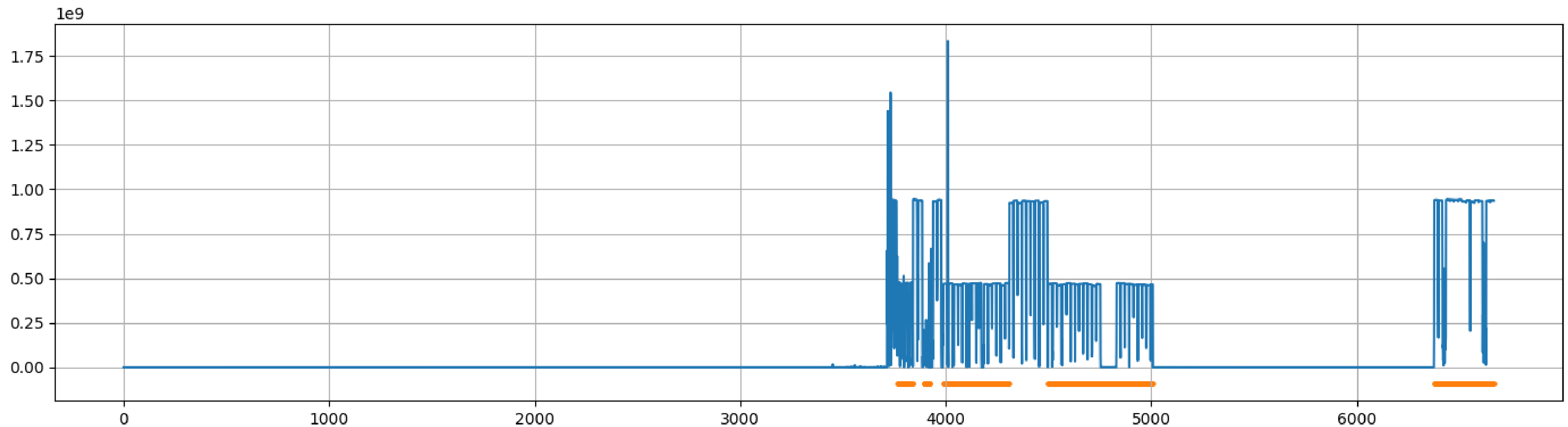
- While training is slow
- ...Generating the alarm signal is now much faster

In [7]:
```
ldens = opt.score_samples(hpcs[inputs])
signal = pd.Series(index=hpcs.index, data=-ldens)
```

Inspecting the Alarm Signal

Let's have a look at the alarm signal

In [8]:
```
util.plot_signal(signal, labels, figsize=figsize)
```



It's very similar to the one provided by KDE

Threshold Optimization

We can optimize the threshold in the usual fashion

The cost model is the same as before

In [9]:
```
c_alarm, c_missed, tolerance = 1, 5, 12
cmodel =  util.HPCMetrics(c_alarm, c_missed, tolerance)

th_range = np.linspace(1e4, 1e9, 1000)
th, val_cost = util.opt_threshold(signal[tr_end:val_end],
                                        valdata['anomaly'],
                                        th_range, cmodel)
print(f'Best threshold: {th:.3f}')
tr_cost = cmodel.cost(signal[:tr_end], hpcs['anomaly'][:tr_end], th)
print(f'Cost on the training set: {tr_cost}')
print(f'Cost on the validation set: {val_cost}')
ts_cost = cmodel.cost(signal[val_end:], hpcs['anomaly'][val_end:], th)
print(f'Cost on the test set: {ts_cost}')
```

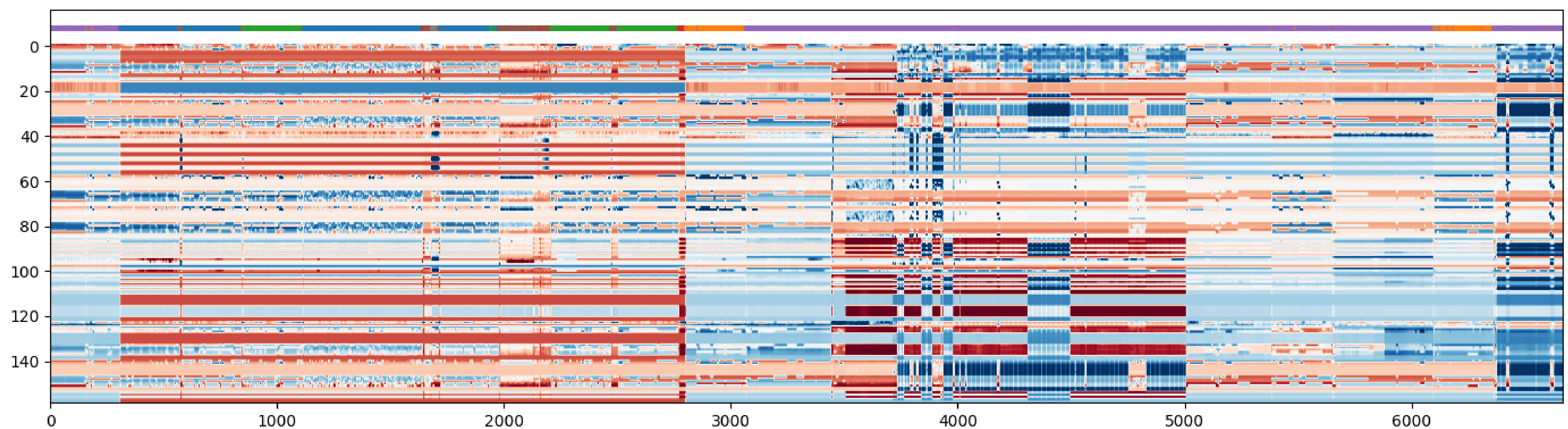
```
Best threshold: 258265675.676
Cost on the training set: 0
Cost on the validation set: 245
Cost on the test set: 275
```

The results are also similar to those from KDE

Behavior Clusters

Finally, we can have a look at how the model is using its components

In [10]:
```
zvals = opt.predict(hpcs[inputs])
zsignal = pd.Series(index=hpcs.index, data=zvals)
util.plot_dataframe(hpcsv[inputs], zsignal, figsize=figsize)
```



- The results may vary, since some steps of the process are stochastic
- ...But typically one or more component will be use for a single, long job