

## Supplementary Data file

### Supplementary Data S1



**Identification of *IGH::EPOR* gene fusions.** *IGH::EPOR* fusions were confirmed through inspection of the sequencing reads in the BAM using IGV (Integrative Genomics Viewer). Above you can see the mismatches at the end of the sequencing reads that are mapped to *EPOR*.

## Supplementary Data S2

The default commands used to run the standard pipeline.

Gene Fusion Detection Algorithm	Version	Alignment algorithm (version)	Default parameters
Arriba	2.1.0	STAR (v2.7.9a)	<pre> arriba \ -x /dev/stdin \ -o \${filename}.fusions.tsv \ -O \${filename}.fusions.discarded. tsv \ -a \${assembly} \ -g \${gtf} \ -b \${blacklist} \ -k \${knownfus} \ -p \${proteindom} </pre>
FusionCatcher	1.33	Bowtie (v1.2.3) Bowtie2 (v2.3.5.1) STAR (v2.7.2b)	<pre> fusioncatcher \ -p \${task.cpus} \ -d \${fusioncatcher_db} \ -i \${reads[0]},\${reads[1]} \ -o \\${PWD} \ --skip-blat </pre>
Star-Fusion	1.10.0	STAR (v2.7.8)	<pre> STAR-Fusion \ --genome_lib_dir \${ctat_dir} \ --left_fq \${reads[0]} \ --right_fq \${reads[1]} \ --CPU \${task.cpus} \ --output_dir \\${PWD} </pre>

### Supplementary Data S3

The default and altered values for the parameters used for each test of STAR-Fusion. Results from Read Support (3) and Read Support + FFPM (3) were used for the manuscript as they were the best performing for the given parameter combination.

Test Name	Parameter	Default Value	Altered Value
Read Support (1)	--min_novel_junction_support	1	0
Read Support (2)	--min_junction_reads	2	1
Read Support (3)	--min_junction_reads --min_novel_junction_support	1 2	0 1
Read Support + FFPM (1)	--min_novel_junction_support --min_FFPM	1 0.1	0 0.001
Read Support + FFPM (2)	--min_junction_reads --min_FFPM	2 0.1	1 0.001
Read Support + FFPM (3)	--min_junction_reads --min_novel_junction_support --min_FFPM	1 2 0.1	0 1 0.001
Max Sensitivity	--max_sensitivity Includes: --min_junction_reads --min_sum_frags --require_LDAS --min_spanning_frags_only --min_novel_junction_support --skip_FFPM -- no_single_fusion_per_breakpoint --skip_EM	 1 2 1 5 3 0.1 n/a n/a	 0 1 0 1 1 1 n/a TRUE TRUE
Full Monty	--full_Monty Includes --max_sensitivity, and: --max_promiscuity --min_pct_dom_promiscuity --min_alt_pct_junction --no_annotation_filter --no_RT_artifact_filter	 10 20 10.0 n/a n/a	 1000000 1 1e-3 TRUE TRUE