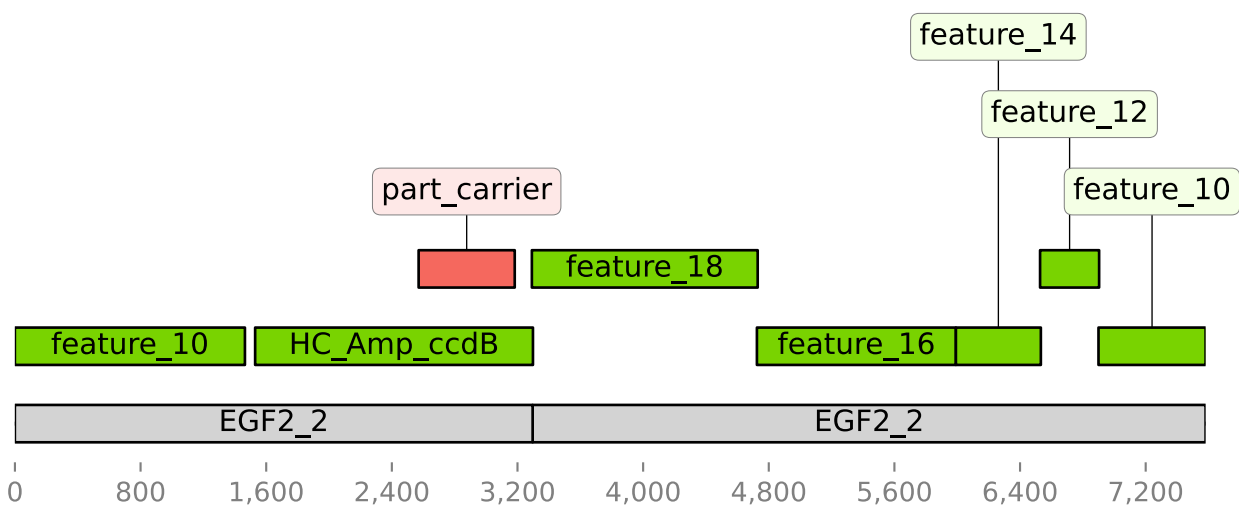Edinburgh Genome Foundry

Assembly analysis report

This document reports the sequencing results of the **EGF demo review** project. Each chapter details the results of a plasmid (assembly). Please see the Appendix on the last page for an explanation of the report.

EGF2_2

Note: the assembly is in reverse complement, compared to the reference.

Plot of the aligning parts:

Alignment table:

Name	Length	Start	End	Strand	T Start	T End	Matches	Size	Quality
EGF2_2	7604	3307	7604	-	3297	7582	4285	4297	60
EGF2_2	7604	0	3307	-	0	3297	3297	3307	60
HC_Amp_ccdB	2721	947	2721	-	1530	3299	1769	1774	60
feature_10	2166	6	1475	-	0	1465	1465	1469	60
feature_10	2166	1475	2159	-	6900	7582	682	684	60
feature_12	390	7	383	-	6528	6904	376	376	60
feature_14	554	6	547	-	5992	6533	541	541	60
feature_16	1294	15	1287	-	4725	5992	1267	1272	60
feature_18	1451	6	1445	-	3292	4730	1438	1439	60
part_carrier	2329	235	852	+	2571	3183	611	617	60

EGF2_13

Note: the assembly is in reverse complement, compared to the reference.

Plot of the aligning parts:
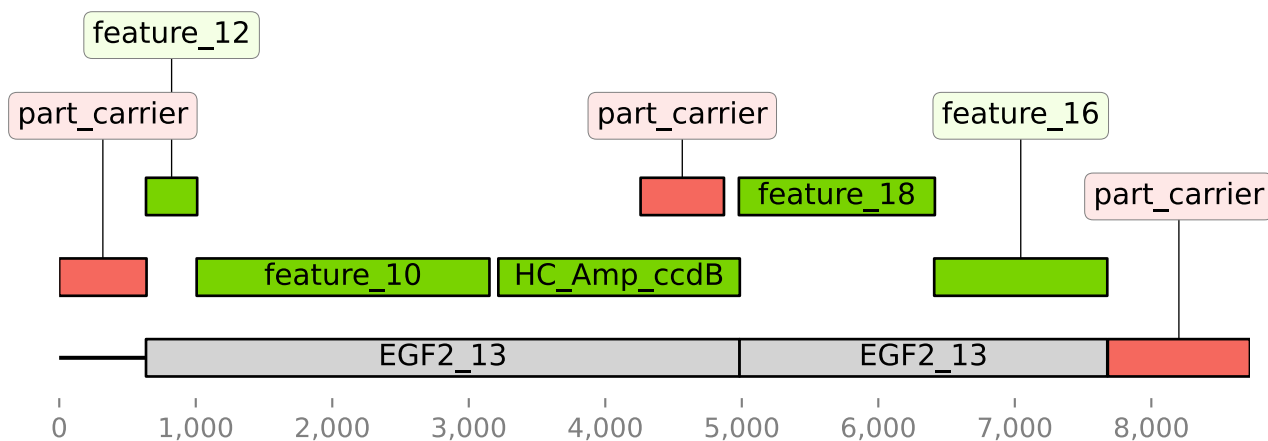
Alignment table:

Name	Length	Start	End	Strand	T Start	T End	Matches	Size	Quality
EGF2_13	8939	0	4362	-	636	4984	4348	4362	60
EGF2_13	8939	6238	8939	-	4984	7678	2694	2701	60
HC_Amp_ccdB	2721	947	2721	-	3217	4986	1769	1774	60
feature_10	2166	6	2159	-	1007	3152	2145	2153	60
feature_12	390	7	382	-	636	1011	375	375	60
feature_16	1294	15	1287	-	6410	7678	1268	1272	60
feature_18	1451	6	1445	-	4979	6415	1436	1439	60
part_carrier	2329	1287	2329	-	7682	8723	1041	1042	60
part_carrier	2329	646	1287	-	0	640	640	641	60
part_carrier	2329	235	852	+	4259	4870	610	617	60

Appendix

Each chapter describes results on a plasmid sequence (*de novo* assembly). The provided (part) sequences were aligned against the sequence assembled from the reads. The plot shows alignment regions as annotations. If there are unannotated segments, then none of the parts aligned there. If an assembly plan is provided, then annotations are coloured based on whether they are expected in the plasmid: green: part is expected in the construct; red: part shouldn't be in the construct. Grey is the reference expected sequence for the plasmid. The alignments are provided in a PAF (pairwise mapping format) table. The columns of the table are:

- Name: Query sequence name
- Length: Query sequence length
- Start: Query start coordinate
- End: Query end coordinate
- Strand: `+` if query and target on the same strand; `-` if opposite
- T Start: Target start coordinate on the original strand
- T End: Target end coordinate on the original strand
- Matches: Number of matching bases in the mapping (includes mismatches but not indels)
- Size: Number bases, including gaps (indels), in the mapping
- Quality: Mapping quality (0–255 with 255 for missing)