

Supplementary Table 1. Nanopore sequencing, alignment, and read statistics for P2-seq samples.

Sample	Total reads	Total aligned reads	Mean coverage	Mean read length, bp	Remaining Reads after Filtering Plus Strand	Remaining Reads after Filtering Minus Strand	Mean read quality
PromethION (R10 flowcell)							
Low_Salt_Control	692542	643259	540708	2109	n/a	n/a	38.9
Low_Salt_S1	696358	639631	527592	2074	249562	270642	37.9
Low_Salt_S2	512722	467842	386589	2072	183295	198126	38.1
Low_Salt_S3	640317	574964	468736	2046	220615	240752	37.7
Low_Salt_S4	674463	615857	495296	2020	230475	250230	37.3
Low_Salt_S5	635299	567213	444531	1968	204531	220858	37.1
Low_Salt_S6	604283	544577	417469	1922	190863	203258	36.9
Low_Salt_S7	543551	476431	356411	1866	161395	173893	36.8
Low_Salt_S8	473721	415242	296658	1788	131538	145493	36.4
High_Salt_Control	1263392	421468	376096	2539	n/a	n/a	34.3
High_Salt_S1	364646	344075	283288	2065	100749	100876	35.4
High_Salt_S2	447705	416093	341632	2030	125900	124843	35.4
High_Salt_S3	342144	323046	265384	2069	97042	96205	35.4
High_Salt_S4	358996	338835	274026	2030	96730	95859	35
High_Salt_S5	370523	348380	278126	2009	97369	96886	34.7
High_Salt_S6	388297	364576	284890	1967	96614	97028	34.2
High_Salt_S7	2708054	306384	226547	10232*	70674	71827	39.7
High_Salt_S8	1963761	384866	283883	2205*	89997	91110	31.5
Low_Salt_Topoisoimer Lk22	500476	451262	312297	1760	92766	92345	36.5
Low_Salt_Topoisoimer Lk23	587546	539550	390752	1857	123359	124539	35.9
MiniON (R9 flowcell)							
Low_High_Salt_Control	153262	147147	134500	2287	n/a	n/a	21.8
Low_Salt_S1	146147	141373	127447	2268	76601	76307	21.6
Low_Salt_S2	141229	136486	122210	2252	73862	72977	21.6
Low_Salt_S3	140943	135163	117299	2175	73176	73108	21.4
Low_Salt_S4	156854	149039	125529	2104	80915	79404	21.3
Low_Salt_S5	159909	151350	125084	2061	81731	80330	21.2
Low_Salt_S6	165057	155546	126146	2014	83741	83177	21.1
High_Salt_S1	109136	106305	93640	2234	52516	50983	22.2
High_Salt_S2	113382	109898	96167	2210	53944	52822	22.2
High_Salt_S3	102435	98761	83630	2138	48141	47710	22
High_Salt_S4	108710	104432	84693	2051	51099	50174	21.9
High_Salt_S5	104907	100083	76715	1935	48901	47834	21.7
High_Salt_S6	108687	102413	75173	1841	50165	48816	21.7

n/a = used only as a control for p-value calculation

* These samples were sequenced together with S2 gDNA libraries using shared barcodes; after demultiplexing, reads were assigned to each sample by alignment to the appropriate reference sequence.