Contaminating DNA in Human Saliva Alters the Detection of Variants from Whole Genome Sequencing.

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Supplementary Table 1- Examples of anomalous variant calls which lead to the identification of atypically aligning reads. Variants displayed are derived from the alignment of internal sample A

Chromosome	Position	Reference allele	Alternate Allele	Genotype	Allelic Depth Ratio (Ref,Alt)	GQ Score
1	1443328	C	CCGCGTGCGCCGTGAGCGCATGGGTCACATCGACCTGGCCG	0/1	30,3	78
1	3019209	T	TCGTTTCGCCATGCACTCTGCCTATTTGCGCCATCTTATCAAAGGCGAGAGCGTCTTCTTGGTGAAAGACGGCGTTATCAAATTTAAGAACTTCAAGCGTA	0/1	24,3	53
1	3431499	G	GTACGCGCCTTCCTTAGCGAAAACCGCACGGACAGTACGCAGAAGAATAATGAAGTCACCGGTAAGCGACCAGTTCTCAACATAGTAGAGATCCAGACGAACCGACTCTTCCCAAGAGAGATCA	0/1	25,3	49
1	4213486	T	TCCGCACTGGCTCAATTTTTGGGCACAACGTTTGAATATCGCGATTAAAAAATCAGTGTTTGAACCGGATATAAAAAGGCCGTCTGAAATCAAGGTTTCAGACGGCCTGCTATTTTCAAATCAAGAAGGA	0/1	29,11	99

1	4282539	G	GCGCTACTGAGGGCAGCGTTTTTGCCGCCGTCACGGATAATGCCGAGCACGTAGGCTCGCA	0/1	31,6	99
1	4282543	C	CGTTGA	0/1	31,6	99
1	4282545	C	CTCAATCATGTTCCGCCCGGGCTCAGTACTGACCCCTAGCTCTTTCGCG	0/1	29,6	99
1	5509136	A	ATCGCAGCCGCACCGGCTACGATTTCATTT	0/1	24,3	53
1	5509138	A	ATTCATTTGTGATACTTGCTTGACGAGCTTTGTTATACACCAACCGCAGATCATTAATTAAATTACCTGCAT	0/1	23,3	53
1	6392150	C	CATCGCCTCCCTCTTCGTTGAG	0/1	18,3	67
1	6392152	A	AGG	0/1	19,3	69
1	6392155	G	GCATTCCTGGTGGATGCGGACGCTATCTCCCGCTCCCTCATGGAGCCCGGCGAGGCGGTGCTCGCCCGCACGGTCGCGGAGTTCGGTGAGCA	0/1	19,3	69
1	7830320	T	TCGCGCTGGCTG	0/1	28,12	99
1	7830322	C	CCGTTCGTTGACCTTGCCCGGCGCAATGGAGGG	0/1	29,12	99
1	7830325	T	TGGCATTTTTGTTGAAACCGGATTGGTCGTATTTGAAACCGGGTACGATGCTGACTG	0/1	31,12	99
1	8579657	A	C	0/1	24,3	54
1	8579660	C	CAGCCTGGTTCAACAACACGAAGTCCGCTGGACTTGGGTAAAAGGCCATGCCGGACACCCTGAAAACGAAAAAGCCGACGAGCTCGCCAACCGAGGCGCAGCAAAATTTTT	0/1	24,3	54
1	8658064	G	GTTTTTA	0/1	36,11	99
1	8658066	C	CGTGTTATTGCCCTA	0/1	37,11	99
1	8658069	T	TGAAAATCTTTTTACCATATTGGATATAATCCAA	0/1	37,10	99
1	8658073	C	A	0/1	39,9	99
1	8658076	C	CTTAA	0/1	38,9	99
1	8658078	C	CGCACTGCAAAATTACGAAATATATATGGCAACAACCAACAATTTCAAAATATT	0/1	38,9	99

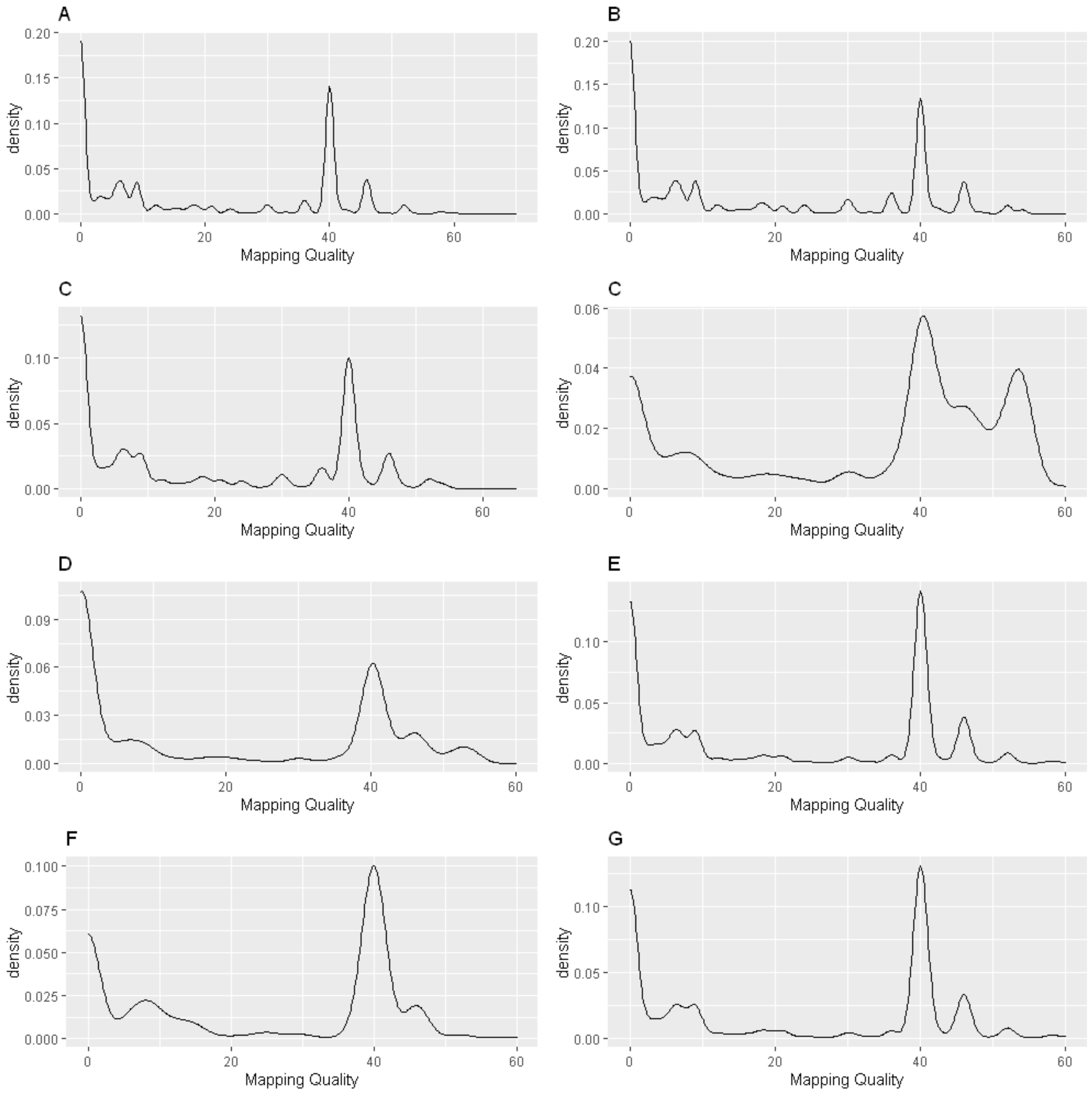
Supplementary Table 2- Top 77 genera used for decoy development

Species	Number of Sequences Returning with Match	% of Submitted Sequences	Accession of Sequence(s) Used
Prevotella	56417122	22.78228	NZ_CP013195.1
Neisseria	24623277	9.943334	NC_003112.2
Streptococcus	17799602	7.187808	NC_015678.1
Haemophilus	11684583	4.718451	NC_000907.1
Veillonella	8964212	3.619915	ACIK02000001.2-ACIK02000025.2
Rothia	5967605	2.409829	NC_013715.1
Actinomyces	5504468	2.222806	NZ_CP012590.1
Porphyromonas	5503687	2.222491	NC_010729.1
Eubacterium	3554132	1.435224	NZ_CP012068.1
Fusobacterium	3470611	1.401497	NC_003454.1
Campylobacter	3267852	1.319619	NZ_CP012541.1
Granulicatella	2538844	1.025232	NZ_KI391971
Atopobium	2138896	0.863726	NC_013203.1
Gemella	2052068	0.828663	NZ_CP014233.1
Leptotrichia	1945440	0.785605	CP014231.1
Oribacterium	1515533	0.612	ACKX01000001.1-ACKX01000254.1
Capnocytophaga	1515252	0.611887	NZ_CP012589.1
Solobacterium	1506910	0.608518	AECQ01000001.1-AECQ01000066.1
Selenomonas	1380182	0.557343	NZ_CP012071.1
Lautropia	1010801	0.40818	AEQP01000001.1-AEQP01000030.1
Megasphaera	875359	0.353486	AECS01000001.1-AECS01000049.1
Peptoniphilus	812443	0.32808	PNGX01000001.1-PNGX01000004.1
Achromobacter	481071	0.194265	NZ_LN831029.1
Aggregatibacter	462896	0.186926	NZ_CP012067.1
Corynebacterium	454905	0.183699	NZ_LN831026.1
Candidatus	363746	0.146887	NZ_CP007496.1
Lachnospiraceae	264750	0.106911	NBBL01000001.1-NBBL01000017.1
Catonella	236983	0.095698	ACIL03000001.3-ACIL03000026.3
Eikenella	152940	0.06176	NHRS01000001.1-NHRS01000006.1
Treponema	139123	0.05618	NZ_CP009228.1
Cardiobacterium	139052	0.056152	FKLO01000001.1-FKLO01000088.1
Kingella	125553	0.050701	AEWV01000001.1-AEWV01000057.1
Tannerella	108155	0.043675	CP017038.1
Lactobacillus	55357	0.022354	NC_013198.1
Abiotrophia	51159	0.020659	ACIN03000001.3-ACIN03000020.3
Peptostreptococcus	46552	0.018799	FOVA01000001.1-FOVA01000060.1
Dialister	45854	0.018517	GG698602.1

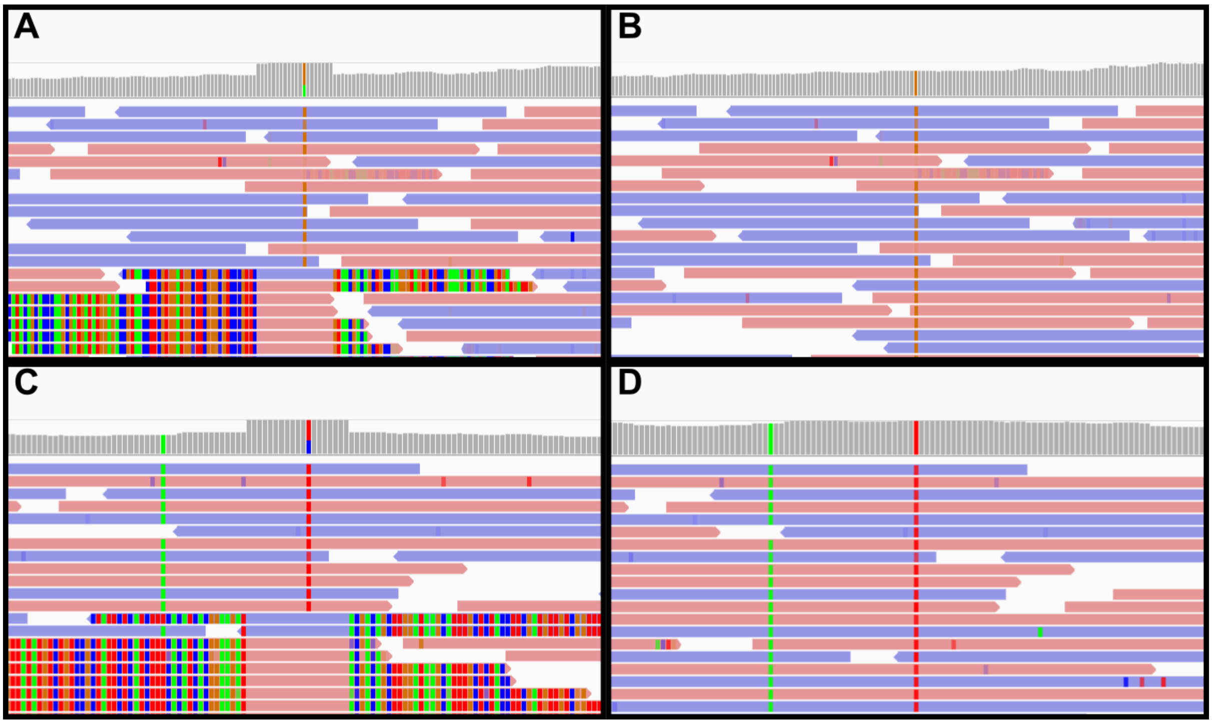
Lachnoanaerobaculum	35132	0.014187	AEPW01000001.1-AEPW01000150.1
Propionibacterium	33231	0.013419	NC_006085.1
Parvimonas	19673	0.007944	NZ_CP009761.1
Bacteroides	17869	0.007216	BAIU01000001.1-BAIU01000095.1
Mogibacterium	17277	0.006977	JALU01000001.1-JALU01000030.1
Centipeda	16449	0.006642	AFHQ01000001.1-AFHQ01000072.1
Pseudomonas	16277	0.006573	NC_002516.2
Bacteroidetes	15771	0.006369	NVWV01000001.1-NVWV01000022.1
Mycoplasma	15486	0.006254	NC_000912.1
Simonsiella	14083	0.005687	ADCY02000001.2-ADCY02000082.2
Klebsiella	12982	0.005242	NC_016845.1
Enterococcus	11871	0.004794	NC_004668.1
Actinobaculum	10155	0.004101	AWSB01000001.1-AWSB01000117.1
Staphylococcus	8968	0.003621	NC_004461.1
Finegoldia	8754	0.003535	NC_010376.1
Mitsuokella	7349	0.002968	ABWK02000001.2-ABWK02000031.2
Johnsonella	7300	0.002948	ACZL01000001.1-ACZL01000080.1
Eggerthia	7203	0.002909	ACZL01000001.1-ACZL01000080.1
Bifidobacterium	7003	0.002828	NZ_AP012324.1
Bulleidia	6923	0.002796	ADFR01000001.1-ADFR01000016.1
Olsenella	6791	0.002742	CP012069.2
Peptostreptococcaceae	6427	0.002595	AWVB01000001.1-AWVB01000160.1
Filifactor	6208	0.002507	NC_016630.1
Escherichia	5763	0.002327	NC_002695.1
Bacillus	4668	0.001885	NC_003997.3
Shuttleworthia	4517	0.001824	ACIP02000001.2-ACIP02000010.2
Gardnerella	4261	0.001721	NC_014644.1
Lactococcus	4257	0.001719	NC_002662.1
Eggerthella	4138	0.001671	AGEJ01000001.1
Stenotrophomonas	3691	0.00149	NC_010943.1
Listeria	3284	0.001326	NC_003210.1
Scardovia	3261	0.001317	AKCI00000000.1
Anaerococcus	3033	0.001225	NC_013171.1
Lysinibacillus	2993	0.001209	NZ_CP010820.1
Anaeroglobus	2816	0.001137	AGCJ01000001.1-AGCJ01000103.1
Gracilibacteria	2812	0.001136	PDRB01000001.1-PDRB01000010.1
Moraxella	2745	0.001108	NZ_CP014234.1
Enterobacter	2597	0.001049	NZ_CP025225.1
Desulfobulbus	2594	0.001048	NZ_CP021255.1
Bordetella	2586	0.001044	NC_002929.2

Supplementary Table 3- Species representing at least 2% of BLAST results for atypically aligning reads

Species	**Number of Sequences Returning with Match**	**% of Submitted Sequences**	**Accession of Sequence(s) Used**
Prevotella jejuni	69100	25.22634	NZ_CP023863.1-NZ_CP023864.1
Prevotella intermedia	35311	12.89099	NZ_CP019300.1-NZ_CP019301.1
Haemophilus influenzae	15001	5.476416	NC_000907.1
Capnocytophaga sputigena	9521	3.475832	NZ_CP022385.1
Prevotella scopos	8342	3.045415	NZ_CP016204.1-NZ_CP016206.1
Rothia aeria	6759	2.467509	AP017895.1
Neisseria elongata	5914	2.159025	NZ_CP007726



Supplementary Figure 1 – The distribution of mapping qualities of atypically aligning reads. For all samples density peaks are seen in the distributions as 0 and 40. The distributions of internal sample A (A), internal sample B (B), internal sample C (C) ERX1462737 (D), ERX1462740 (E), SRX2830689 (F), SRX2830684 (G), and SRX2830689 (H) are shown.



Supplementary Figure 2 – Examples of SNVs altered by the presence of atypical read pairs. A heterozygous, non-coding, SNV (A>G) in internal sample B (A) is called as homozygous when the atypical pairs are removed (B). The same effect is observed in SRX2830689 for a coding SNV (C-D).