**Table 2a.** *Yersinia pestis* specific probes **(supplementary)**.

|  |  |  |
| --- | --- | --- |
| **Probe ID** | **Sequence** | **Description** |
| Yp1 | TTCATTGTCTCATGGCATCTATGGGAAACAGAC | ***pst*: pesticin**Context: pPCP1-[4815-5888] |
| Yp2 | TTAAATACCTTTGGCAATTCATTGTCTCATGGCAT |
| Yp3 | ACCGTGTCATGGTTCTTGAGGGAACGA |
| Yp4 | TCCGATTGATACGGAGATGGAGAAAGACAGTG |
| Yp5 | TTGACCACGATATTTTCTCCAGTAATGGTTTTGAA |
| Yp6 | TCAATGACGCTAATATCGGTCTTCGGTTCAGC |
| Yp7 | TGCAGATAGACTTGATGGGTATTATATGCTTCGAG |
| Yp8 | TCGTTCGGTAAATATTGTTGACCACGATATTTTCT |
| Yp9 | CTGAAGGAATTTTTACGTCGTTCGGTAAATATTGT |
| Yp10 | GGTATTATATGCTTCGAGGGAAGGAGGCTTATGA |
| Yp11 | TCTTGAGGGAACGATTGCCGAATCTATTGAAC |
| Yp12 | GGTGTCCCTCAGTATATTGCAGATAGACTTGATGG |
| Yp13 | AATAACCGAAATCGCATCGTCCTAGCGGA |
| Yp14 | GTCATTTTCCGTCTAATCCTAGTAGCGATTATTTT |
| Yp15 | TCAAAAACTGAAGGGACCGTGTCTTACGAAC |
| Yp16 | ATGTCAGATACAATGGTAGTGAATGGTTCAGGTGG |
| Yp17 | TCTGTCTCTATTGGCGGAGATGCTGCC | ***pla***: **plasminogen activator protease** **precursor**Context: pPCP1+[6665-7603] |
| Yp18 | TTAACGCTGGATATTATGTCACACCTAATGCCAAA |
| Yp19 | AGGTACTCAGACCATTGATAAGAATAGTGGAGATT |
| Yp20 | AAACACGTTTCAGTTGGACAGCTACAGGTG |
| Yp21 | GGACTTGCAGGCCAGTATCGCATTAATGA |
| Yp22 | GAGTGCTAATGCAGCATCATCTCAGTTAATACCA |
| Yp23 | ATTATAAAGCAGGTATAACAGCAGGATATCAGGAA |
| Yp24 | AAACTTCCCGAAAGGAGTGCGGGTAATAGG |
| Yp25 | AATATATCCCCTGACAGCTTTACAGTTGCAGC |
| Yp26 | TTACATACAGTAAATATGATGAGGGCAAAGGAGGT |
| Yp27 | ACTATTCTGTCCGGGAGTGCTAATGCAGC |
| Yp28 | GGTATTTCCAATAAAAATTATACTGTGACGGCGGG |
| Yp29 | ATTCTTGAGGTCGGCTTGCAGATGATGC | **putative transcriptional regulator**Context: pPCP1-[7790-8089]similar to predicted transcriptional regulator TR:P95258 (EMBL:Z84498) |
| Yp30 | TCACAAAAACAAGTTGCTGAGGCGATGGG |
| Yp31 | ATGGCAGATGAGATGATTCTTGAGGTCGGC |
| Yp32 | AAATGATTTAAAGCTGGCGACGTTAAAGCGTTAC |
| Yp33 | CGACGTTAAAGCGTTACGTTGAAGCAATGG |
| Yp34 | ATGAGAACATTAGATGAGGTGATTGCCAGTCGT |
| Yp35 | CCGATTCGTCGGGCTATCGTTCTTTGTG | **hypothetical protein**Context: pPCP1-[8089-8436] |
| Yp36 | TCCGATAAGAGCCTTTTATGCGTTCGATCCG |
| Yp37 | GGCTGATTTGAAAAAGCTACAGGTTTACGGACC |

**Table 2b.** *B. anthracis* specific probes **(supplementary)**.

| **Probe ID** | **Sequence** | **Description** |
| --- | --- | --- |
| Ba1 | AATTTGTATCCTGTTTTCACATTTGGGCATTACGA | **acetyltransferase**; gnat family; (pxo1-37) |
| Ba2 | AGAGGAAATTCCGTTCTTCTTCTGTAAACCCAGC | **bacterial type ii/iv secretion system protein** (pxo1-59) |
| Ba3 | CTCCTGTGGCACTTATTTCAATTGTTCTTCTTGC | **caax amino terminal protease family protein** (pxo1-85) |
| Ba4 | GGCTAAAAATGTAGAAGGGGTCTTGAAGCCG | **calmodulin-sensitive adenylate cyclase** Context:pXO1+[122608-125010] |
| Ba5 | TACAAGCACATAAGATCCCAGCAAGCTCGG | **conjugation protein; trag/trad family** (pxo1-42) |
| Ba6 | GCAGAGCAACTACAAATACTTGTTAAACTGTTACA | **DNA topoisomerase I**Context:pXO1-[176759-179371] |
| Ba7 | TAACAGATTCCCTAAGTCAACAACTGGAGGTAAAA | **group ii intron reverse transcriptase/maturase**(pxo1-23) |
| Ba8 | GCCTACCGCAATATTAAGGGGAACAAAGGAA |
| Ba9 | TAAAGAAATTTCGAAGCCCAACGGACAAACCA |
| Ba10 | CCTGTCATTATTGTAAAAAGGCTGCACCAGATATC | **hypothetical protein**Context:pXO1 |
| Ba11 | CCAAAACGCTATATTGAAATTGAGTTACCACATGG |
| Ba12 | AAGGATTCAAACGTAGGACGTATCCCTTTAAGTAA |
| Ba13 | GCCTCTATTGACAAGTTAAAGTTACGAGGACAACG |
| Ba14 | GAGAGCTTTCTAGGGAGAACCCAGCTAAAATGG |
| Ba15 | ACCCTAATGCATATGAATTTGATTATAATGGCGCT |
| Ba16 | CAATCCGTTACTCGCGCTAGAAAACAAATTATGTT |
| Ba17 | GGCCAAAACTTTAATGGTGAAGCAATAAGGAGAAT |
| Ba18 | TGCAACTGAATAGAGGATTAAATGCACATGGAGT |
| Ba19 | TGAAGCAATAAGGAGAATGCAACTGAATAGAGGAT |
| Ba20 | TTAAATGCACATGGAGTTCTAGGGCAAGAATTTGA |
| Ba21 | AATGATTACCCACAAGGTATATCGCCAGGTGA |
| Ba22 | TAACCGTAGATTGAAACCGAGAGAACATGAGGA |
| Ba23 | CGGATTACGAACTCGAAAAGTATTACAAAGGAAAA |
| Ba24 | AACCATATCAAATTGGCTGAGAGAGGCTTATATAG |
| Ba25 | AGCAAAAACAGCGTGAAACCATATCAAATTGGC |
| Ba26 | AGTGGGGAATTGAATCATCGACATTACGTAAAAGG |
| Ba27 | ATTGGCACGACATATGCTGTGACTCGATTT |
| Ba28 | TGGTCCGCTAGAAAAAGCATTAGAAGCCATG |
| Ba29 | ATTCTGTCTATTGAGACGGGGTATTCAAAACACG |
| Ba30 | CATATTGTATATAGATTTGGTCCGCTAGAAAAAGC |
| Ba31 | TCATTAGCATTAGGATTCGTAGAGATGGTGATAAA |
| Ba32 | CCAACTTTGGCGTCATTGAAAAACCAGTCAA |
| Ba33 | CGTAATAGGTCTATCTATCTATTTTTCCTCTGTTG |
| Ba34 | ACTTTTAGATAGAGGATTATTGCCTTTTGGCGTAG |
| Ba35 | ACTCACATGAACCCTTTCCCTACTGCAATTATTT |
| Ba36 | CACTTACCTATCGACAATAAATACTGAGGATCTTA |
| Ba37 | CATCGTTTTTAGGACATGTTATGCACCCATCTATT |
| Ba38 | GGAAAGATTTCGTAGAGTCAGGAAGAGATGTTATT |
| Ba39 | CATCTGCGTTATGCACCATCGTTTTTAGGACA |
| Ba40 | GTGCGCTATGAAAAGAAACAAGTCCAGGTATTACG |
| Ba41 | GGCGTAATGATTTAAAACATGCAAGTGATGTGATG |
| Ba42 | CTGTTCAACAAAGAGTAGCTGATGTTAAAGATATG |
| Ba43 | ATGTACCAAATTCGTGGGTCAGTTCACTTAGTATG |
| Ba44 | CCAATTAAGAGGATTCGTGCAATTAAAGGTGAAAT |
| Ba45 | CAGAACATTACATCAACAGAGAATCAGAAATGCAT |
| Ba46 | ATATTTTTCGTCATCCCAACTCAGCTAGATACAAT |
| Ba47 | TGGATTTGAGAAAGTTTTTAAAGAGGTTCAAGAGG |
| Ba48 | CCGCGAAGTATTGTTAAAACGAAAAGATTGGCT |
| Ba49 | AAGAGAACCTTCTACTAAGTAATTGCTGGAATAAC |
| Ba50 | TTCCAAAAGGATGATTGAAGAGAACCTTCTACTAA |
| Ba51 | GGCTACAAGAAGTTTGCTGAAGACATTTTATCTGC |
| Ba52 | ATCAGATGTTTAATGAAGCGAAGCCAATGATGTTT |
| Ba53 | AGATCCATTGAATTCACACATACACCAGCAACT |
| Ba54 | ATAAAGACGCAATATGGTATGGGTCAGTAAACTAT |
| Ba55 | AGTATTGGCCCCTTTAATCATGAAAACCCCAT |
| Ba56 | TTAATTTCGCACCTTATAATGGATGATACTGAAGC |
| Ba57 | TATTGATACCGTTAGTAGGTGAAAAAGTGGTGCG |
| Ba58 | TGCAGAAGAATATCGATATATGGAGTTTAAGGAGG |
| Ba59 | TCGTCTTTTTGCTATTACGCCTTCAATTAATGGAG |
| Ba60 | TTGACGACCCTTTTATTGAGGTTGCTGAGG |
| Ba61 | AAAAATATATGGAAGTCTCAATGGCTCTGAATGTG |
| Ba62 | CGTTATGACGGAAAAGTATGGACTTGTAGGACAAA |
| Ba63 | AAACATCAGTGATTCCAAGCTCTTCAATCGCT | **is231-related; transposase**(pxo1-35) |
| Ba64 | TAGCTATTATCTGTTTCTGGATTAGTCAACATGTC |
| Ba65 | CAACATCTTACTCCCTCATTTTTAGAGAATCTGGC |
| Ba66 | TGAAAATTGGCGATCATTAGTAGATCCTGGTGATG | **protective antigen-related protein**(pxo1-111) |
| Ba67 | ACGCCATAACTTAGGTTTAATGTATTCAGGTCAAA | **response regulator; putative**Context:pXO1+[172308-173402] |
| Ba68 | CGGATCAGTTTTTACAATACTACTACCACTTCTTT |
| Ba69 | AATGATGCAATTAGTGCTTTACAGTCGAATCAACT | **s-layer protein**; (pxo1-90) |
| Ba70 | AAAGGACGCAAACGAAGGTGGGACTTTT | **spore germination protein xa**Context:pXO1 |
| Ba71 | CGCATTCCTGCTGCATTTGGACAAACTTT |
| Ba72 | CCCAGTAATAAAAGGGATGATTTATCCAGCCGC | **spore germination protein xb**Context:pXO1 |
| Ba73 | ACTCGTTATTTTTCTCATTCCAGATGTGCTACAAG |
| Ba74 | GATTTGTAGATGAAAAGAACCGTCATTATAACCGT | **thermonuclease family protein**; (pxo1-141) |
| Ba75 | ATGACAACTATTCAAGCAGGTAATGAAATGCACAA | **transcriptional regulator; arsr family**(pxo1-138) |
| Ba76 | TTAGATATTCCTCAATCTACCGTATCTCAGCATTT |
| Ba77 | AGGTAATGAAATGCACAAAATCCCAGAGGCG |
| Ba78 | CTCGCTCTTGCTTAGATGATGTTCAGGAGTACA | **tyrosinerecombinase**Context:pXO1 |
| Ba79 | TCTTCCGTATTAGCTACTCGCTCTTGCTTAGAT |
| Ba80 | TTCCTATTTCTATGCTAGTTGAAAAACCACCTCTG | **utp-glucose-1-phosphate uridylyltransferase** (pxo1-94) |
| Ba81 | GATTTTGCACTTCAGAGAGAAAGTCTAAAAGAAGA |
| Ba82 | TCGCCTTTGAATTTGATGGGAAAAGATATGATGTA |
| Ba83 | ATGTCTCAAGCAATTGATAGATGTTTATGAGGAAC |